



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:18 PM UTC

PDB ID : 2IXE / pdb_00002ixe
Title : Crystal structure of the ATPase domain of TAP1 with ATP (D645N mutant)
Authors : Procko, E.; Ferrin-O'Connell, I.; Ng, S.-L.; Gaudet, R.
Deposited on : 2006-07-07
Resolution : 2.00 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

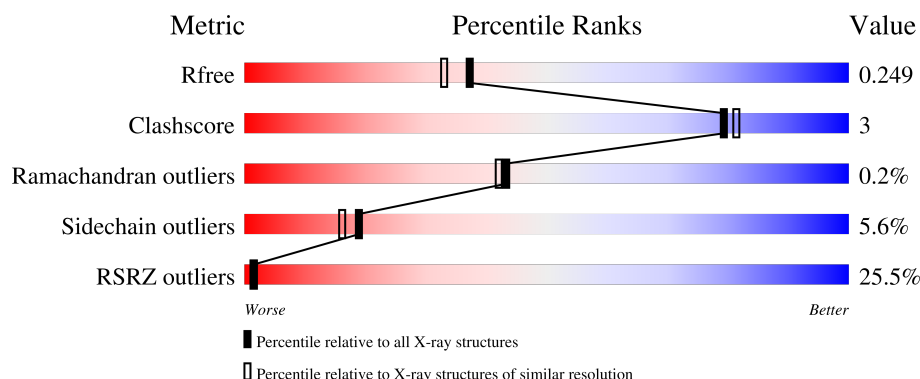
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	271	23% 83% 7% 7%
1	D	271	24% 83% 8% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4203 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 ANTIGEN PEPTIDE TRANSPORTER 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	2	0
			1902	1203	336	356	7			
1	D	248	Total	C	N	O	S	0	5	0
			1900	1205	337	351	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	464	MET	-	expression tag	UNP P36370
A	726	ALA	-	expression tag	UNP P36370
A	727	ALA	-	expression tag	UNP P36370
A	728	ALA	-	expression tag	UNP P36370
A	729	HIS	-	expression tag	UNP P36370
A	730	HIS	-	expression tag	UNP P36370
A	731	HIS	-	expression tag	UNP P36370
A	732	HIS	-	expression tag	UNP P36370
A	733	HIS	-	expression tag	UNP P36370
A	734	HIS	-	expression tag	UNP P36370
A	645	ASN	ASP	engineered mutation	UNP P36370
D	464	MET	-	expression tag	UNP P36370
D	726	ALA	-	expression tag	UNP P36370
D	727	ALA	-	expression tag	UNP P36370
D	728	ALA	-	expression tag	UNP P36370
D	729	HIS	-	expression tag	UNP P36370
D	730	HIS	-	expression tag	UNP P36370
D	731	HIS	-	expression tag	UNP P36370
D	732	HIS	-	expression tag	UNP P36370
D	733	HIS	-	expression tag	UNP P36370
D	734	HIS	-	expression tag	UNP P36370
D	645	ASN	ASP	engineered mutation	UNP P36370

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

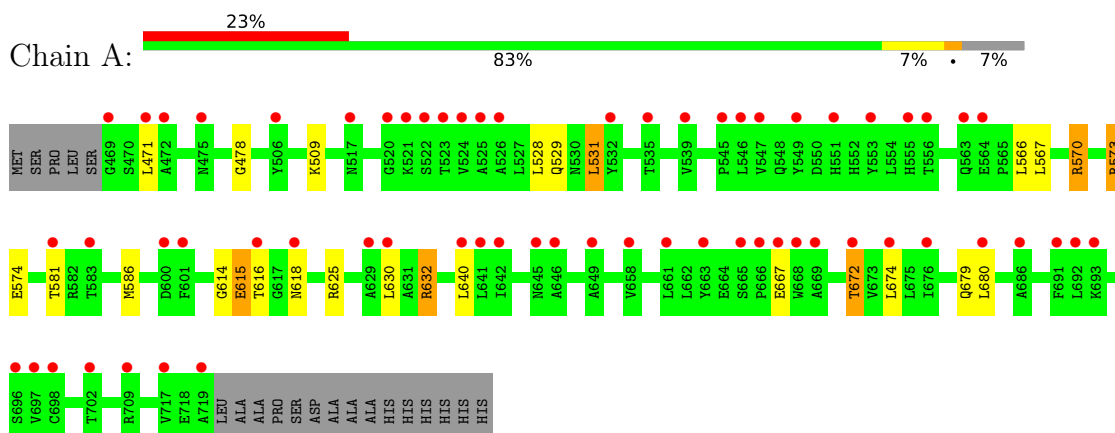
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	159	Total	O	0	0
			159	159		
5	D	173	Total	O	0	0
			173	173		

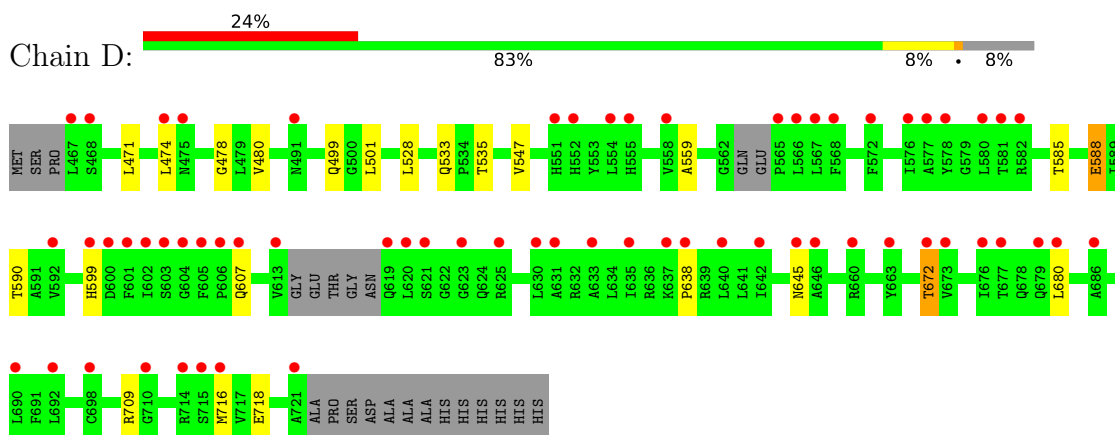
3 Residue-property plots [i](#)

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: ANTIGEN PEPTIDE TRANSPORTER 1



• Molecule 1: ANTIGEN PEPTIDE TRANSPORTER 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.43Å 80.43Å 168.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.55 – 2.00 72.55 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (72.55-2.00) 99.7 (72.55-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.199 , 0.241 0.204 , 0.249	Depositor DCC
R_{free} test set	2705 reflections (7.12%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4203	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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: PO4, MG, 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	0.47	0/1946	0.70	0/2648
1	D	0.47	0/1951	0.69	0/2648
All	All	0.47	0/3897	0.69	0/5296

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

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	1902	0	1875	13	0
1	D	1900	0	1906	8	0
2	A	31	0	12	0	0
2	D	31	0	12	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
4	A	5	0	0	0	0
5	A	159	0	0	2	0
5	D	173	0	0	1	0
All	All	4203	0	3805	21	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 3.

All (21) 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:D:478:GLY:O	1:D:672:THR:HG21	1.86	0.76
1:A:570:ARG:HD3	1:A:574:GLU:OE1	1.91	0.71
1:A:618[A]:ASN:HA	1:A:625[A]:ARG:HH21	1.56	0.69
1:A:529:GLN:HB2	1:A:531:LEU:HD13	1.84	0.60
1:D:680:LEU:HD21	1:D:716:MET:HG2	1.86	0.57
1:A:573:ARG:CZ	1:A:586:MET:HE3	2.35	0.55
1:A:478:GLY:O	1:A:672:THR:HG21	2.07	0.54
1:A:679:GLN:OE1	5:A:2141:HOH:O	2.20	0.48
1:A:567:LEU:O	1:A:616:THR:HA	2.13	0.48
1:A:632:ARG:HD2	5:A:2109:HOH:O	2.14	0.47
1:D:559:ALA:HB3	1:D:638:PRO:HG3	1.98	0.46
1:A:529:GLN:CB	1:A:531:LEU:HD13	2.47	0.45
1:D:480:VAL:HG11	1:D:528:LEU:HD21	1.98	0.44
1:A:615:GLU:CD	1:A:618[A]:ASN:HD21	2.25	0.44
1:D:645:ASN:ND2	5:D:2112:HOH:O	2.50	0.44
1:D:533:GLN:NE2	1:D:547:VAL:CG1	2.81	0.43
1:D:585:THR:OG1	1:D:588:GLU:OE1	2.38	0.41
1:A:614:GLY:O	1:A:615:GLU:C	2.63	0.41
1:D:590:THR:HG23	1:D:599:HIS:CD2	2.56	0.41
1:A:528:LEU:CD1	1:A:674:LEU:HD22	2.52	0.40
1:A:566:LEU:O	1:A:632:ARG:NH2	2.48	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	251/271 (93%)	248 (99%)	2 (1%)	1 (0%)	30 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	247/271 (91%)	246 (100%)	1 (0%)	0	100	100
All	All	498/542 (92%)	494 (99%)	3 (1%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	615	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	198/219 (90%)	186 (94%)	12 (6%)	17	14
1	D	201/219 (92%)	190 (94%)	11 (6%)	19	17
All	All	399/438 (91%)	376 (94%)	23 (6%)	19	15

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	LEU
1	A	509	LYS
1	A	531	LEU
1	A	570	ARG
1	A	573	ARG
1	A	581	THR
1	A	630	LEU
1	A	632	ARG
1	A	640	LEU
1	A	667	GLU
1	A	672	THR
1	A	680	LEU
1	D	471	LEU
1	D	474	LEU
1	D	499	GLN

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Mol	Chain	Res	Type
1	D	501	LEU
1	D	535[A]	THR
1	D	535[B]	THR
1	D	588	GLU
1	D	607	GLN
1	D	672	THR
1	D	709	ARG
1	D	718	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	483	GLN
1	A	557	GLN
1	A	659	GLN
1	A	700	GLN
1	D	483	GLN
1	D	494	ASN
1	D	530	ASN
1	D	533	GLN
1	D	555	HIS
1	D	599	HIS
1	D	607	GLN
1	D	619	GLN
1	D	659	GLN
1	D	700	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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
2	ATP	D	1	3	32,33,33	1.45	6 (18%)	48,52,52	1.82	10 (20%)
4	PO4	A	3	-	4,4,4	0.94	0	6,6,6	0.41	0
2	ATP	A	1	3	32,33,33	1.62	7 (21%)	48,52,52	1.85	11 (22%)

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	D	1	3	-	2/22/38/38	0/3/3/3
2	ATP	A	1	3	-	1/22/38/38	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	ATP	C5-C4	4.54	1.47	1.39
2	D	1	ATP	C5-C4	4.43	1.47	1.39
2	A	1	ATP	PB-O3A	3.79	1.63	1.59
2	A	1	ATP	PA-O3A	3.52	1.63	1.59
2	A	1	ATP	C5-C6	2.75	1.48	1.41
2	D	1	ATP	PA-O3A	2.72	1.62	1.59
2	D	1	ATP	PB-O3B	2.67	1.62	1.59
2	D	1	ATP	C5-C6	2.57	1.48	1.41
2	A	1	ATP	PB-O3B	2.39	1.62	1.59
2	D	1	ATP	C5-N7	-2.36	1.34	1.39
2	A	1	ATP	C5-N7	-2.33	1.34	1.39
2	A	1	ATP	C8-N7	2.23	1.36	1.31
2	D	1	ATP	C8-N7	2.17	1.35	1.31

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	ATP	C5-C4-N3	-5.70	118.88	126.72
2	D	1	ATP	C5-C4-N3	-5.41	119.27	126.72
2	A	1	ATP	N3-C4-N9	4.65	135.08	127.17
2	D	1	ATP	N3-C4-N9	4.59	134.97	127.17
2	A	1	ATP	C2-N3-C4	3.84	121.22	111.83
2	D	1	ATP	N3-C2-N1	-3.77	122.88	128.58
2	D	1	ATP	C2-N3-C4	3.73	120.93	111.83
2	A	1	ATP	N3-C2-N1	-3.67	123.03	128.58
2	A	1	ATP	C4-C5-N7	-3.60	106.47	110.58
2	D	1	ATP	C4-N9-C8	3.26	109.16	105.74
2	A	1	ATP	C4-N9-C8	3.15	109.04	105.74
2	D	1	ATP	C4-C5-N7	-3.13	107.00	110.58
2	A	1	ATP	C5-N7-C8	2.98	108.14	103.45
2	D	1	ATP	C5-N7-C8	2.62	107.57	103.45
2	A	1	ATP	O2B-PB-O3B	2.57	114.23	107.27
2	A	1	ATP	N9-C8-N7	-2.56	110.30	113.94
2	D	1	ATP	O3A-PB-O1B	-2.42	103.42	110.70
2	D	1	ATP	N9-C8-N7	-2.41	110.51	113.94
2	A	1	ATP	C6-C5-N7	2.25	136.43	132.09
2	D	1	ATP	C6-C5-N7	2.12	136.17	132.09
2	A	1	ATP	O3G-PG-O2G	2.08	115.61	107.80

There are no chirality outliers.

All (3) torsion outliers are listed below:

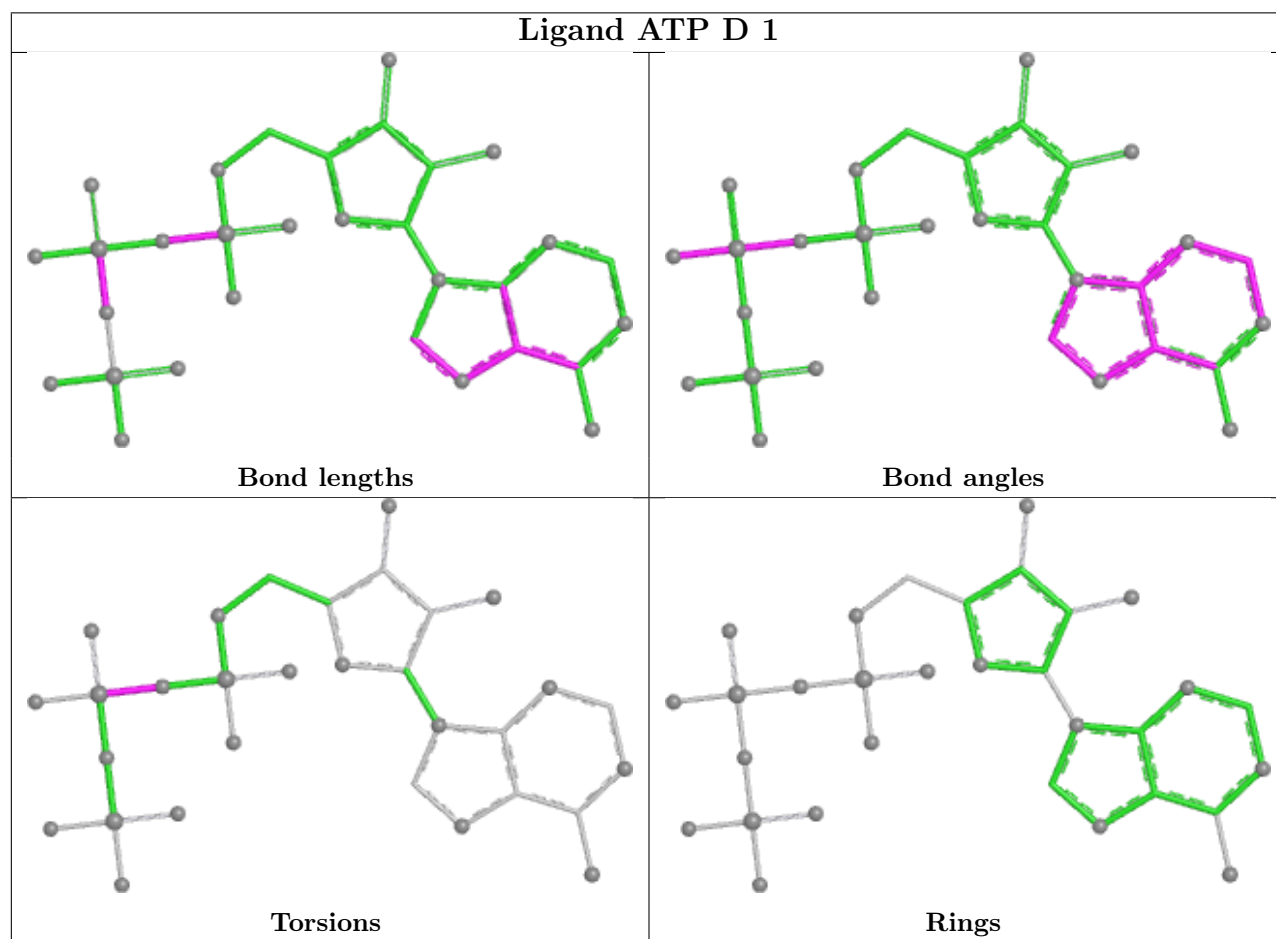
Mol	Chain	Res	Type	Atoms
2	D	1	ATP	PA-O3A-PB-O2B
2	A	1	ATP	PA-O3A-PB-O2B
2	D	1	ATP	PA-O3A-PB-O1B

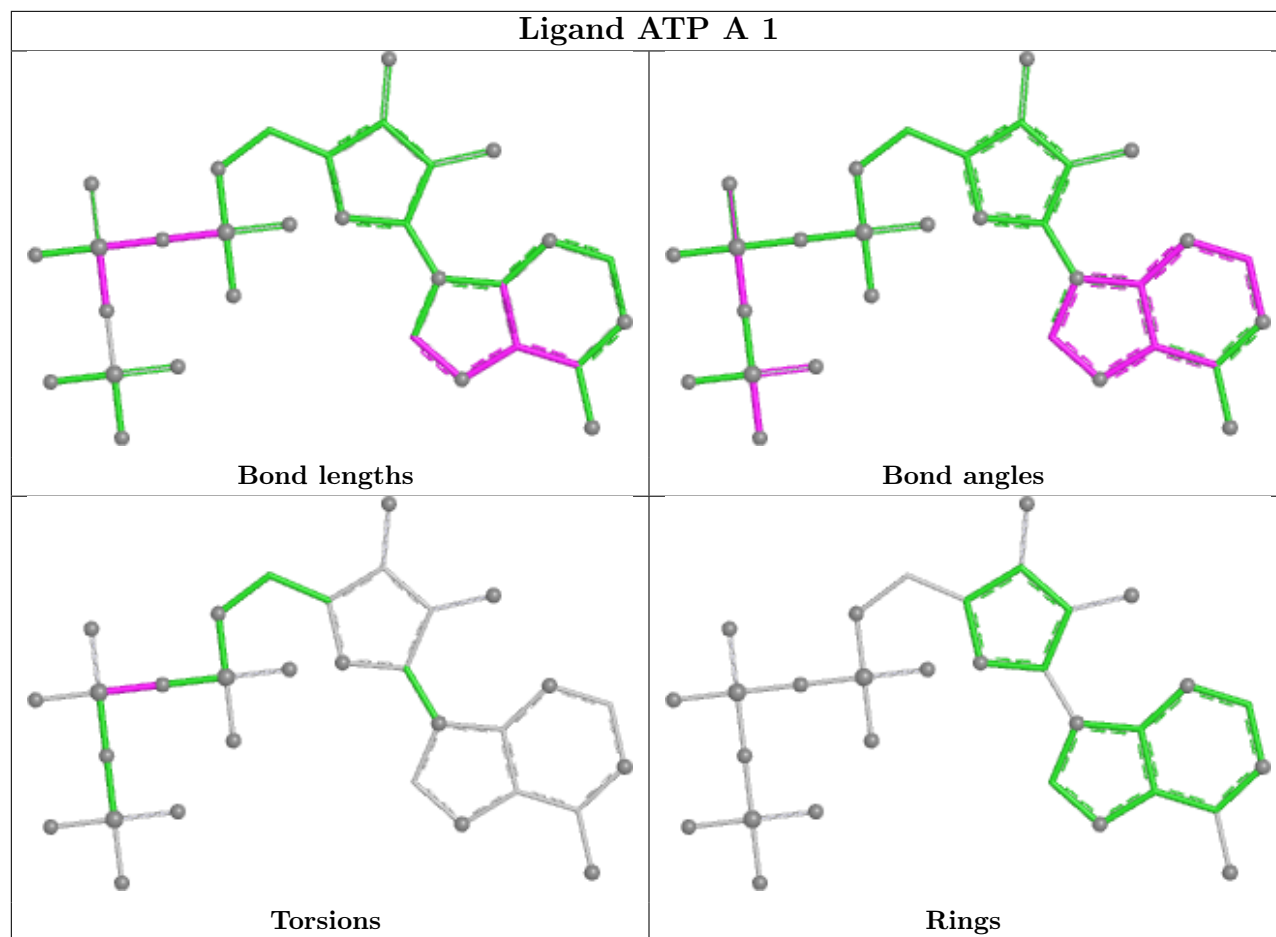
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	251/271 (92%)	1.57	63 (25%)	1 1	23, 45, 52, 58	2 (0%)
1	D	248/271 (91%)	1.52	64 (25%)	1 1	26, 44, 52, 55	5 (2%)
All	All	499/542 (92%)	1.54	127 (25%)	1 1	23, 44, 52, 58	7 (1%)

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	638	PRO	5.5
1	A	669	ALA	4.9
1	A	469	GLY	4.6
1	A	520	GLY	4.6
1	A	719	ALA	4.4
1	D	602	ILE	4.4
1	D	568	PHE	4.3
1	A	668	TRP	4.0
1	D	581	THR	3.8
1	D	613	VAL	3.7
1	A	698	CYS	3.6
1	D	605	PHE	3.6
1	D	491	ASN	3.5
1	D	604	GLY	3.5
1	D	600	ASP	3.4
1	A	692	LEU	3.3
1	A	709	ARG	3.3
1	A	583	THR	3.3
1	A	680	LEU	3.1
1	D	620	LEU	3.1
1	D	565	PRO	3.1
1	D	601	PHE	3.1
1	D	592	VAL	3.1
1	D	578	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	567	LEU	3.0
1	D	606	PRO	3.0
1	D	680	LEU	3.0
1	A	618[A]	ASN	3.0
1	A	553	TYR	3.0
1	D	603	SER	2.9
1	A	601	PHE	2.9
1	A	666	PRO	2.9
1	A	667	GLU	2.9
1	A	686	ALA	2.8
1	D	721	ALA	2.8
1	D	599	HIS	2.8
1	A	535	THR	2.8
1	A	658	VAL	2.8
1	A	551	HIS	2.7
1	D	635	ILE	2.7
1	D	580	LEU	2.7
1	A	676	ILE	2.7
1	D	582	ARG	2.7
1	A	525	ALA	2.7
1	D	633	ALA	2.7
1	D	566	LEU	2.7
1	A	523	THR	2.6
1	A	556	THR	2.6
1	A	672	THR	2.6
1	A	642	ILE	2.6
1	A	661	LEU	2.6
1	A	522	SER	2.6
1	D	468[A]	SER	2.6
1	D	637	LYS	2.6
1	A	471	LEU	2.6
1	D	692	LEU	2.6
1	D	621	SER	2.5
1	D	572	PHE	2.5
1	D	642	ILE	2.5
1	D	467	LEU	2.5
1	A	581	THR	2.5
1	A	702	THR	2.5
1	D	686	ALA	2.5
1	D	475	ASN	2.5
1	A	547	VAL	2.4
1	D	676	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	698	CYS	2.4
1	A	546	LEU	2.4
1	D	640	LEU	2.4
1	D	710	GLY	2.4
1	A	506	TYR	2.4
1	A	532	TYR	2.4
1	D	677	THR	2.4
1	A	472	ALA	2.4
1	A	640	LEU	2.4
1	A	697	VAL	2.4
1	D	552	HIS	2.4
1	A	674	LEU	2.3
1	D	623	GLY	2.3
1	A	691	PHE	2.3
1	D	673	VAL	2.3
1	A	521	LYS	2.3
1	A	555	HIS	2.3
1	A	524	VAL	2.3
1	A	564	GLU	2.3
1	A	630	LEU	2.3
1	D	474	LEU	2.3
1	D	554	LEU	2.3
1	A	526	ALA	2.3
1	D	551[A]	HIS	2.2
1	A	616	THR	2.2
1	A	693	LYS	2.2
1	D	576	ILE	2.2
1	D	716	MET	2.2
1	A	649	ALA	2.2
1	D	577	ALA	2.2
1	D	630	LEU	2.2
1	A	665	SER	2.2
1	D	715	SER	2.2
1	A	717	VAL	2.2
1	D	607	GLN	2.2
1	A	696	SER	2.2
1	D	672	THR	2.2
1	A	539	VAL	2.1
1	D	660	ARG	2.1
1	A	563	GLN	2.1
1	D	631	ALA	2.1
1	D	646	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	517	ASN	2.1
1	D	645	ASN	2.1
1	A	549	TYR	2.1
1	A	641	LEU	2.1
1	A	645	ASN	2.1
1	A	629	ALA	2.1
1	D	619	GLN	2.0
1	D	714	ARG	2.0
1	D	558	VAL	2.0
1	A	646	ALA	2.0
1	A	475	ASN	2.0
1	D	679	GLN	2.0
1	D	690	LEU	2.0
1	A	600	ASP	2.0
1	D	625	ARG	2.0
1	D	555	HIS	2.0
1	A	545	PRO	2.0
1	A	663	TYR	2.0
1	D	663	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

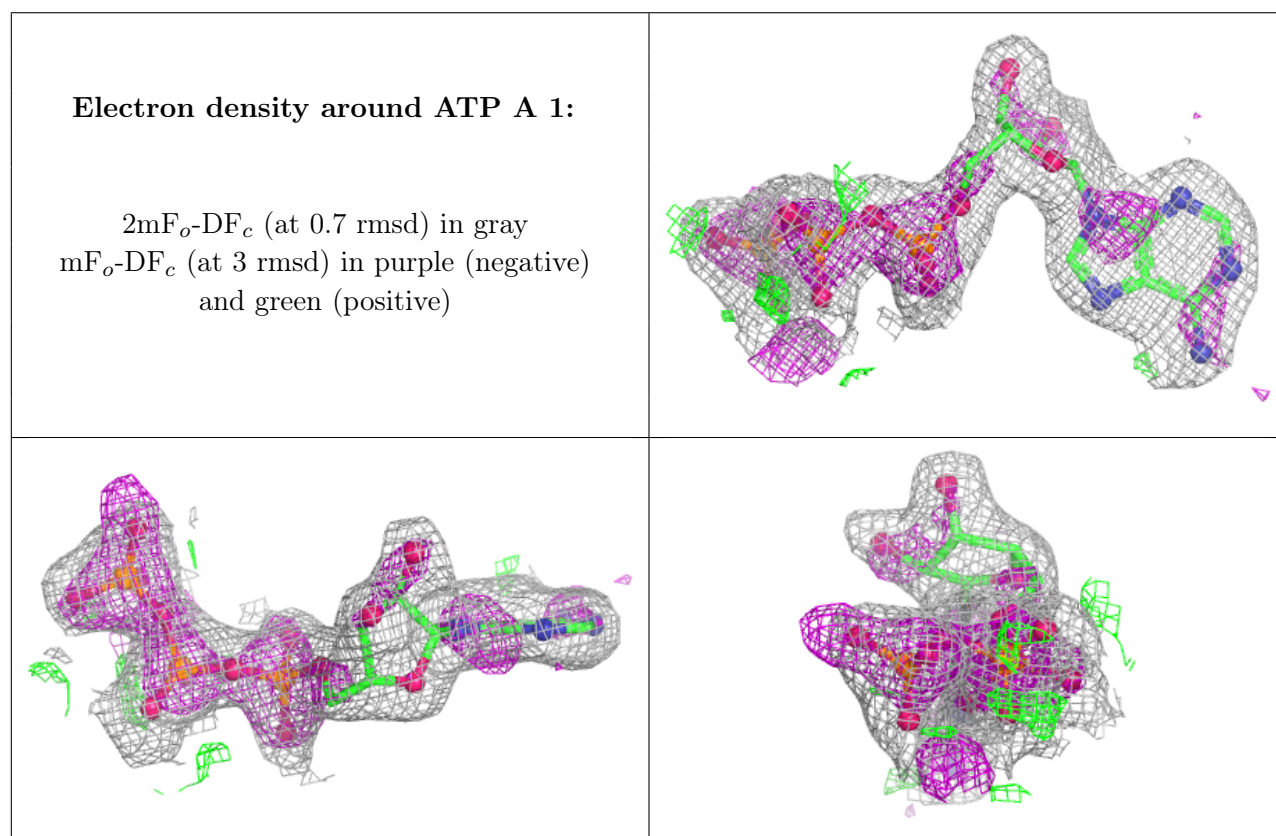
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PO4	A	3	5/5	0.61	0.13	96,96,97,97	0
2	ATP	A	1	31/31	0.92	0.13	30,43,46,47	0
3	MG	D	2	1/1	0.96	0.24	32,32,32,32	0
2	ATP	D	1	31/31	0.96	0.11	24,36,39,39	0

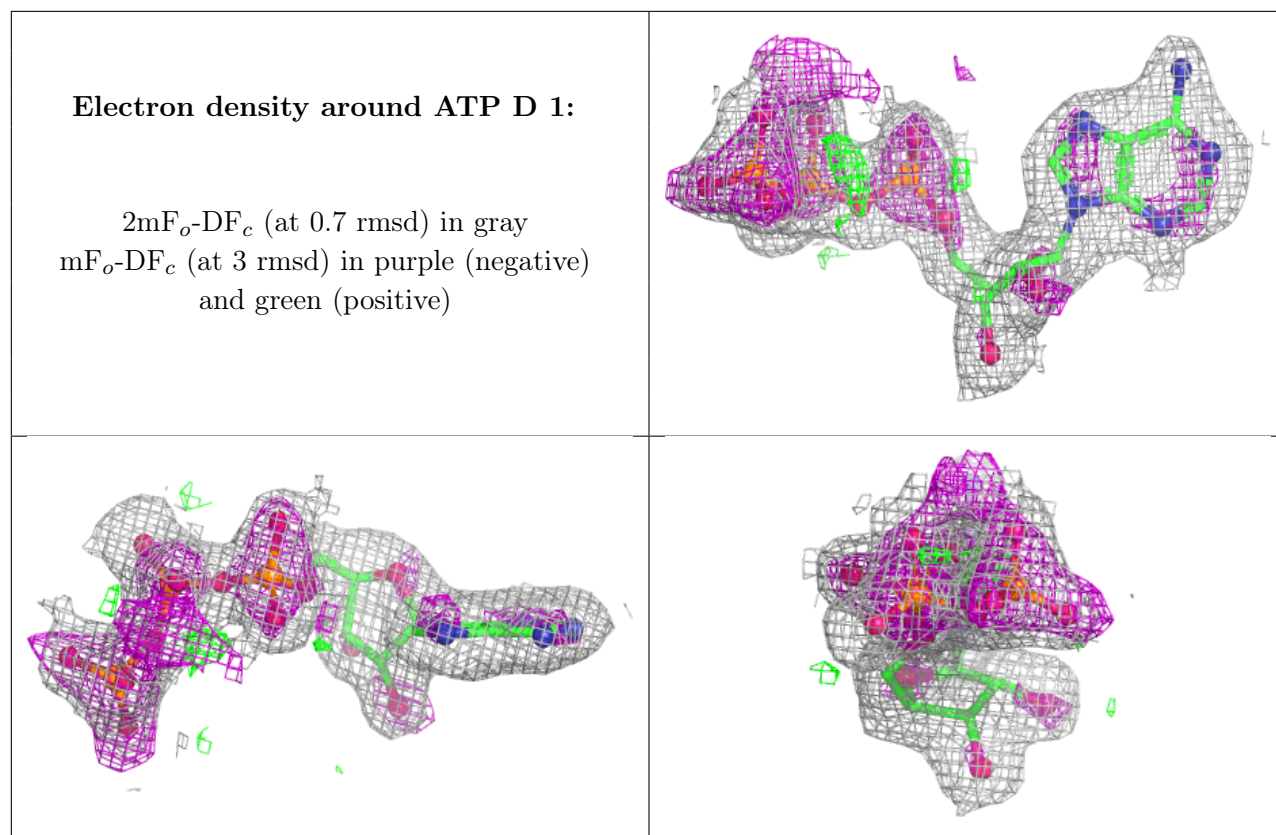
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	2	1/1	0.99	0.16	32,32,32,32	0

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.





6.5 Other polymers ⓘ

There are no such residues in this entry.