WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2025 – 12:24 PM JST

PDB ID	:	9ISB / pdb_00009isb
Title	:	Ligand bound AGD of enzyme
Authors	:	Park, J.B.; Roh, S.H.
Deposited on	:	2024-07-17
Resolution	:	2.24 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

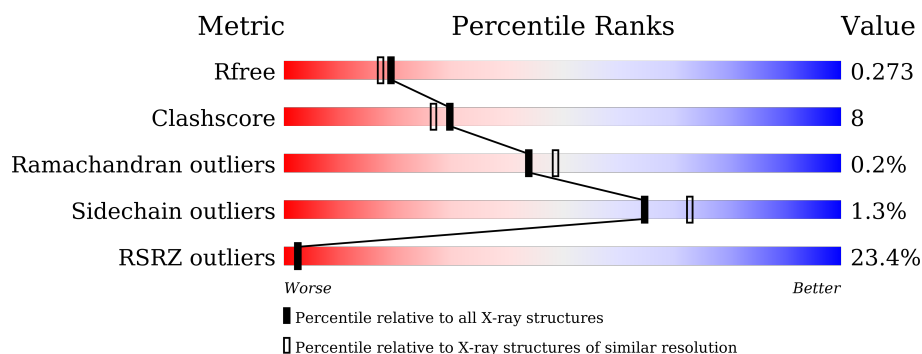|		
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 2.24 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	Percentile Ranks	Value
Rfree		0.273
Clashscore		8
Ramachandran outliers		0.2%
Sidechain outliers		1.3%
RSRZ outliers		23.4%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3139 (2.26-2.22)
Clashscore	180529	3381 (2.26-2.22)
Ramachandran outliers	177936	3334 (2.26-2.22)
Sidechain outliers	177891	3335 (2.26-2.22)
RSRZ outliers	164620	3138 (2.26-2.22)

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 <=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	234	24% / 77% / 18% · ·
1	B	234	22% / 83% / 15% ·

WORLDWIDE PDB
PROTEIN DATA BANK

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 3629 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 Protein acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1717	1087	300	323	7			
1	B	232	Total	C	N	O	S	0	0	0
			1770	1118	312	332	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	462	MET	-	initiating methionine	UNP W8T0A9
A	563	ALA	TRP	variant	UNP W8T0A9
A	605	ALA	GLY	variant	UNP W8T0A9
B	462	MET	-	initiating methionine	UNP W8T0A9
B	563	ALA	TRP	variant	UNP W8T0A9
B	605	ALA	GLY	variant	UNP W8T0A9

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).
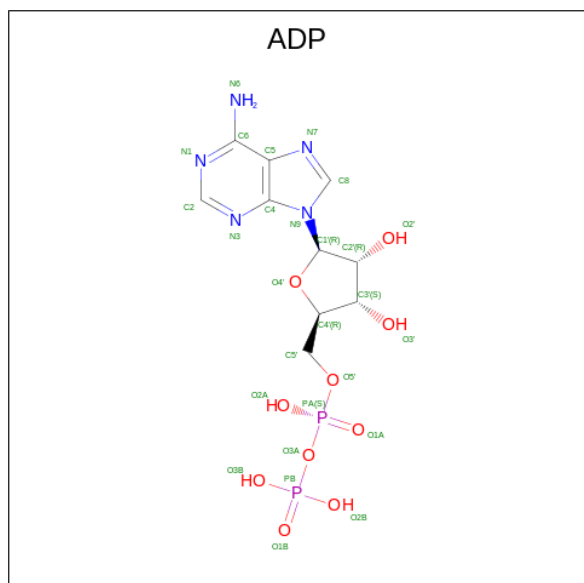
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	27	10	5	10	2	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).
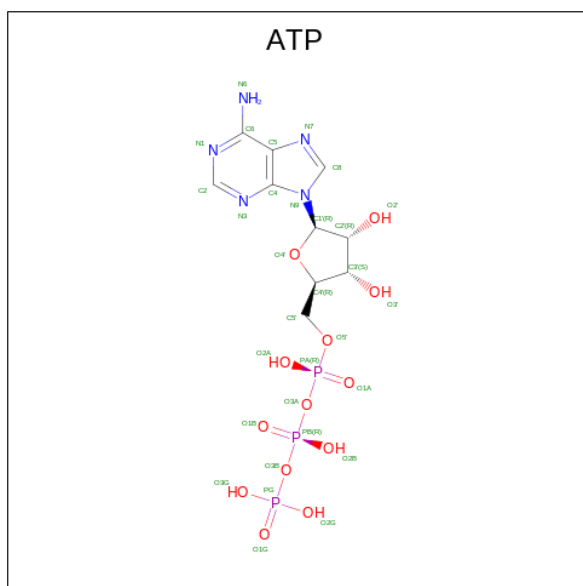
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	B	1	31	10	5	13	3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	27	27	27	0	0
4	B	57	57	57	0	0

3 Residue-property plots ⓘ

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: Protein acetyltransferase

Chain A:

• Molecule 1: Protein acetyltransferase

Chain B:
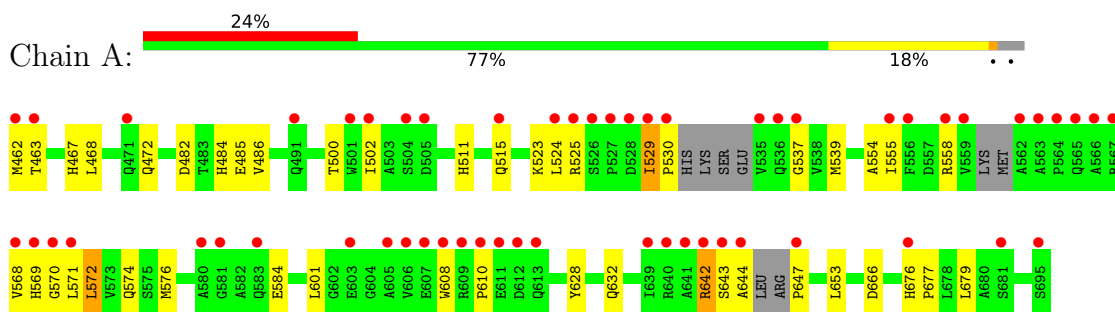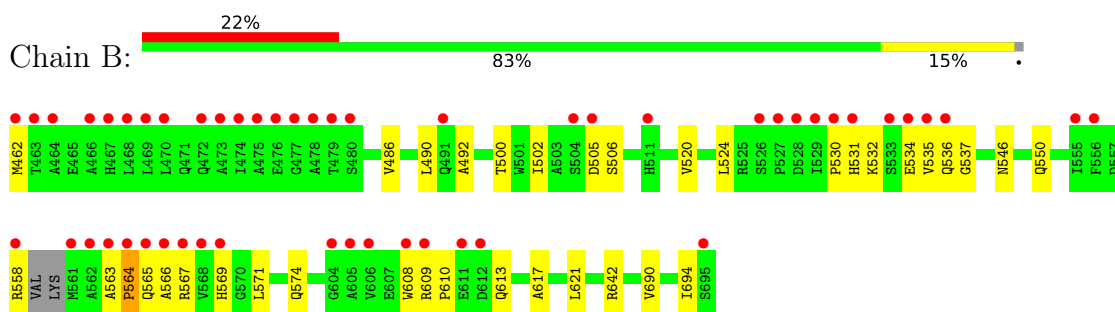
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	76.05Å 76.05Å 199.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.05 – 2.24 71.05 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.7 (71.05-2.24) 99.7 (71.05-2.24)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.01 (at 2.25Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.236 , 0.270 0.237 , 0.273	Depositor DCC
R_{free} test set	1408 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	36.3	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 30.5	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3629	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9790e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

---

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, ADP

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	0.45	0/1744	0.63	0/2374
1	B	0.45	0/1800	0.68	1/2451 (0.0%)
All	All	0.45	0/3544	0.65	1/4825 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	564	PRO	N-CA-C	-12.28	101.91	114.68

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	642	ARG	Sidechain

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	1717	0	1748	38	0
1	B	1770	0	1801	22	0
2	A	27	0	12	0	0
3	B	31	0	12	0	0
4	A	27	0	0	0	0
4	B	57	0	0	1	0
All	All	3629	0	3573	60	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 (60) 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:609:ARG:HB2	1:B:613:GLN:HG3	1.41	0.98
1:B:532:LYS:HG3	1:B:537:GLY:HA3	1.55	0.86
1:A:525:ARG:HB2	1:A:572:LEU:HD22	1.64	0.80
1:A:524:LEU:HA	1:A:571:LEU:HD23	1.65	0.78
1:A:500:THR:HG22	1:A:572:LEU:HD12	1.64	0.78
1:A:529:ILE:HG13	1:A:530:PRO:HD2	1.71	0.73
1:A:482:ASP:OD1	1:A:484:HIS:ND1	2.23	0.72
1:A:484:HIS:CG	1:A:502:ILE:HD11	2.26	0.70
1:A:642:ARG:HG2	1:A:647:PRO:HA	1.79	0.64
1:A:484:HIS:CE1	1:A:525:ARG:HD2	2.32	0.63
1:B:536:GLN:HG2	1:B:558:ARG:HE	1.63	0.62
1:A:643:SER:O	1:A:644:ALA:C	2.43	0.61
1:A:554:ALA:O	1:A:558:ARG:HB2	2.01	0.60
1:A:500:THR:CG2	1:A:572:LEU:HD12	2.32	0.59
1:B:546:ASN:O	1:B:550:GLN:HG2	2.03	0.58
1:A:468:LEU:HD22	1:A:472:GLN:HE21	1.68	0.58
1:B:563:ALA:C	1:B:565:GLN:H	2.12	0.58
1:B:564:PRO:C	1:B:566:ALA:H	2.12	0.57
1:B:505:ASP:OD1	1:B:506:SER:N	2.36	0.57
1:B:536:GLN:HE21	1:B:558:ARG:HB2	1.69	0.57
1:A:568:VAL:C	1:A:570:GLY:H	2.12	0.56
1:A:484:HIS:CD2	1:A:502:ILE:HD11	2.42	0.54
1:A:525:ARG:NH2	1:A:569:HIS:C	2.65	0.54
1:A:568:VAL:O	1:A:570:GLY:N	2.34	0.54
1:B:617:ALA:HB1	1:B:621:LEU:HD21	1.90	0.53
1:A:502:ILE:HG23	1:A:525:ARG:CZ	2.39	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:531:HIS:O	1:B:534:GLU:HG2	2.09	0.52
1:A:568:VAL:C	1:A:570:GLY:N	2.67	0.52
1:B:535:VAL:HG22	1:B:536:GLN:H	1.75	0.52
1:A:529:ILE:CG1	1:A:530:PRO:HD2	2.41	0.48
1:B:567:ARG:HG2	1:B:569:HIS:NE2	2.28	0.48
1:A:523:LYS:HE2	1:A:574:GLN:OE1	2.13	0.48
1:A:462:MET:HG3	1:A:463:THR:H	1.77	0.47
1:B:462:MET:HG3	1:B:492:ALA:HB2	1.96	0.47
1:B:642:ARG:HD2	4:B:810:HOH:O	2.13	0.47
1:A:628:TYR:O	1:A:632:GLN:HG2	2.16	0.46
1:A:642:ARG:CG	1:A:647:PRO:HA	2.45	0.46
1:B:490:LEU:HD11	1:B:690:VAL:HG21	1.97	0.46
1:B:608:TRP:NE1	1:B:610:PRO:HG3	2.31	0.46
1:A:525:ARG:NH2	1:A:570:GLY:N	2.63	0.45
1:A:568:VAL:O	1:A:569:HIS:HB2	2.17	0.45
1:A:608:TRP:CD1	1:A:610:PRO:HG3	2.52	0.44
1:A:482:ASP:O	1:A:486:VAL:HG13	2.18	0.43
1:A:484:HIS:CE1	1:A:485:GLU:HG3	2.54	0.43
1:A:511:HIS:O	1:A:515:GLN:HG3	2.19	0.43
1:B:486:VAL:HG21	1:B:690:VAL:CG1	2.49	0.43
1:B:535:VAL:HG22	1:B:536:GLN:N	2.34	0.43
1:A:676:HIS:HA	1:A:677:PRO:HA	1.86	0.43
1:B:563:ALA:C	1:B:565:GLN:N	2.75	0.43
1:A:584:GLU:HG2	1:A:679:LEU:HD12	2.00	0.42
1:A:576:MET:HE3	1:A:576:MET:HB3	1.72	0.42
1:B:500:THR:HG22	1:B:574:GLN:HB3	2.01	0.42
1:B:564:PRO:C	1:B:566:ALA:N	2.76	0.42
1:A:539:MET:HG3	1:A:555:ILE:HD11	2.02	0.42
1:A:601:LEU:HD21	1:A:653:LEU:HD21	2.03	0.41
1:A:523:LYS:HA	1:A:537:GLY:O	2.21	0.41
1:A:467:HIS:HE1	1:A:666:ASP:O	2.03	0.41
1:A:484:HIS:CD2	1:A:502:ILE:CD1	3.04	0.41
1:A:502:ILE:HG23	1:A:502:ILE:HD12	1.65	0.40
1:B:524:LEU:HA	1:B:571:LEU:HD23	2.04	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	218/234 (93%)	210 (96%)	8 (4%)	0	100	100
1	B	228/234 (97%)	220 (96%)	7 (3%)	1 (0%)	30	31
All	All	446/468 (95%)	430 (96%)	15 (3%)	1 (0%)	44	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	530	PRO

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	185/193 (96%)	183 (99%)	2 (1%)	70	77
1	B	190/193 (98%)	187 (98%)	3 (2%)	58	66
All	All	375/386 (97%)	370 (99%)	5 (1%)	65	73

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	529	ILE
1	A	572	LEU
1	B	502	ILE
1	B	520	VAL
1	B	694	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	467	HIS
1	A	487	GLN
1	A	511	HIS
1	A	546	ASN
1	A	569	HIS
1	B	536	GLN
1	B	546	ASN
1	B	550	GLN
1	B	655	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 ⓘ

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	$\#|Z| > 2$
3	ATP	B	701	-	26,33,33	0.56	0	31,52,52	0.77	2 (6%)
2	ADP	A	701	-	24,29,29	1.00	2 (8%)	29,45,45	1.34	3 (10%)

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
3	ATP	B	701	-	-	5/18/38/38	0/3/3/3
2	ADP	A	701	-	-	0/12/32/32	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	ADP	C5-C4	2.62	1.47	1.40
2	A	701	ADP	O4'-C1'	2.10	1.44	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	ADP	N3-C2-N1	-3.56	123.11	128.68
2	A	701	ADP	PA-O3A-PB	-2.67	123.66	132.83
2	A	701	ADP	C4-C5-N7	-2.36	106.94	109.40
3	B	701	ATP	C5-C6-N6	2.30	123.85	120.35
3	B	701	ATP	PB-O3B-PG	2.03	139.78	132.83

There are no chirality outliers.

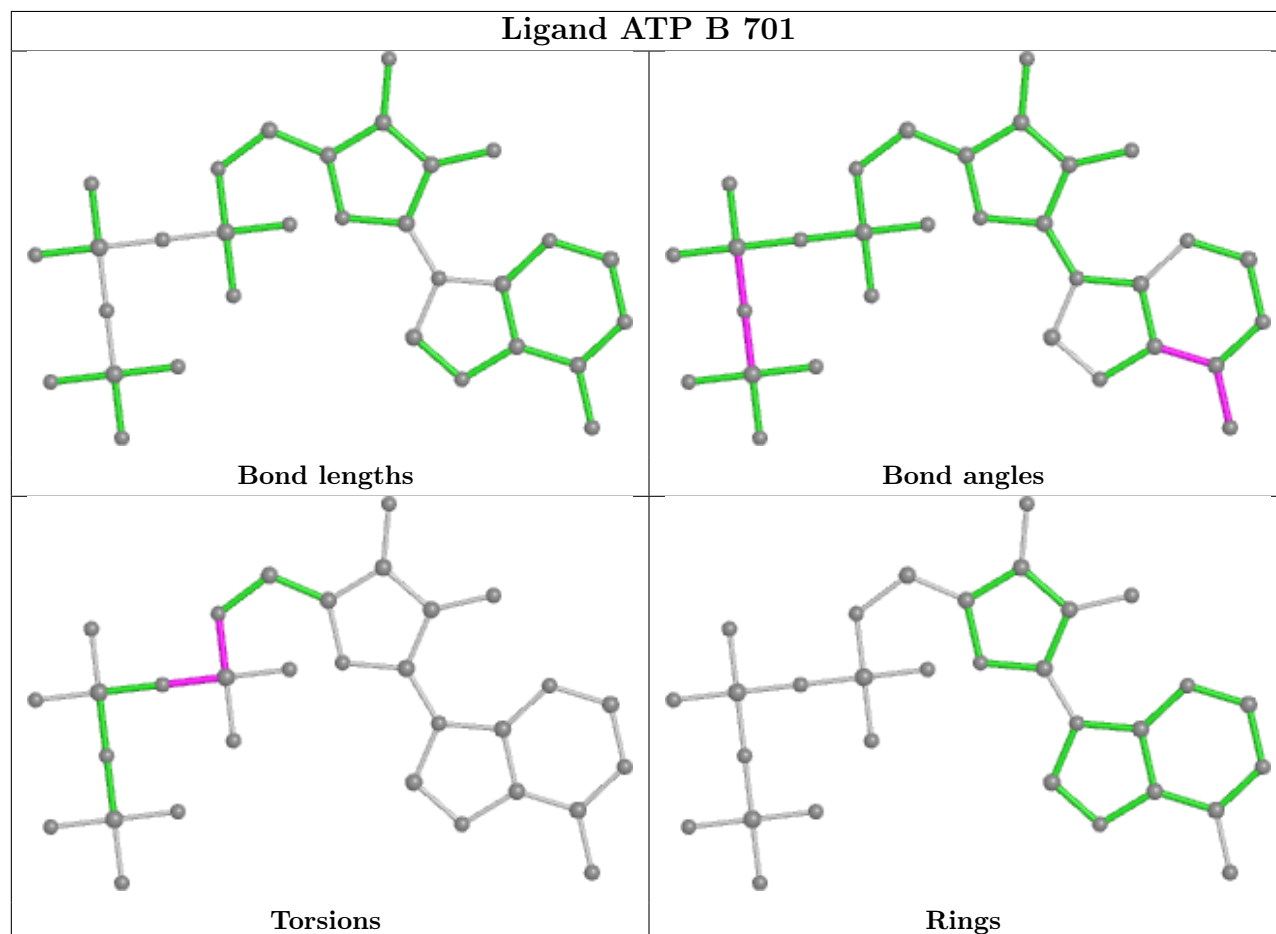All (5) torsion outliers are listed below:

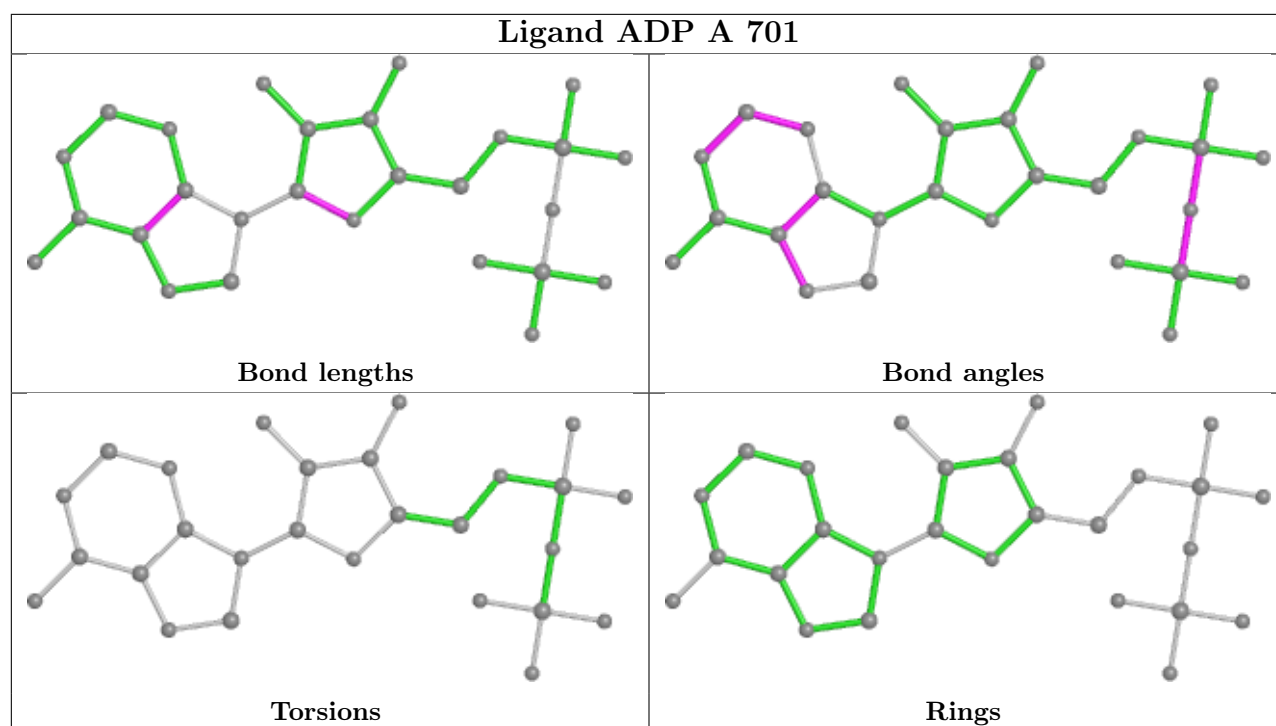| Mol	Chain	Res	Type	Atoms
3	B	701	ATP	C5'-O5'-PA-O1A
3	B	701	ATP	C5'-O5'-PA-O3A
3	B	701	ATP	PB-O3A-PA-O1A
3	B	701	ATP	PB-O3A-PA-O2A
3	B	701	ATP	C5'-O5'-PA-O2A

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 then 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.

Ligand ATP B 701

Bond lengths

Bond angles

Torsions

Rings

Ligand ADP A 701

Bond lengths

Bond angles

Torsions

Rings

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(Å²)	Q<0.9
1	A	226/234 (96%)	1.20	56 (24%)	2	2	22, 41, 110, 123	0
1	B	232/234 (99%)	0.84	51 (21%)	3	3	19, 38, 106, 137	0
All	All	458/468 (97%)	1.02	107 (23%)	2	2	19, 40, 109, 137	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	535	VAL	7.3
1	A	568	VAL	7.2
1	A	606	VAL	7.1
1	B	562	ALA	6.7
1	A	559	VAL	6.6
1	A	529	ILE	6.3
1	A	530	PRO	5.6
1	A	647	PRO	5.5
1	B	563	ALA	5.4
1	A	527	PRO	5.4
1	A	608	TRP	5.2
1	A	525	ARG	5.2
1	A	562	ALA	5.0
1	B	564	PRO	5.0
1	B	605	ALA	4.9
1	B	468	LEU	4.9
1	B	695	SER	4.8
1	A	502	ILE	4.6
1	B	464	ALA	4.6
1	A	564	PRO	4.6
1	A	644	ALA	4.4
1	A	610	PRO	4.4
1	B	561	MET	4.4
1	B	566	ALA	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	605	ALA	4.2
1	A	524	LEU	4.2
1	B	475	ALA	4.1
1	A	556	PHE	4.1
1	B	606	VAL	4.0
1	A	462	MET	4.0
1	B	535	VAL	4.0
1	A	563	ALA	3.9
1	A	643	SER	3.9
1	A	580	ALA	3.9
1	B	530	PRO	3.8
1	B	473	ALA	3.8
1	A	569	HIS	3.7
1	B	463	THR	3.7
1	A	641	ALA	3.7
1	B	558	ARG	3.7
1	B	565	GLN	3.6
1	B	612	ASP	3.6
1	A	565	GLN	3.6
1	B	477	GLY	3.5
1	B	608	TRP	3.5
1	B	569	HIS	3.4
1	B	567	ARG	3.4
1	A	639	ILE	3.4
1	A	537	GLY	3.4
1	B	505	ASP	3.4
1	A	555	ILE	3.3
1	B	462	MET	3.2
1	B	568	VAL	3.1
1	A	571	LEU	3.1
1	B	531	HIS	3.0
1	B	476	GLU	3.0
1	A	642	ARG	3.0
1	B	529	ILE	3.0
1	A	558	ARG	3.0
1	A	567	ARG	3.0
1	A	570	GLY	3.0
1	B	527	PRO	2.9
1	B	478	ALA	2.9
1	A	695	SER	2.9
1	A	526	SER	2.8
1	B	526	SER	2.8

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	463	THR	2.7
1	A	613	GLN	2.7
1	B	479	THR	2.7
1	B	467	HIS	2.6
1	A	581	GLY	2.6
1	B	534	GLU	2.6
1	A	501	TRP	2.6
1	A	612	ASP	2.6
1	A	566	ALA	2.5
1	B	469	LEU	2.5
1	B	470	LEU	2.5
1	B	609	ARG	2.5
1	B	466	ALA	2.5
1	A	609	ARG	2.5
1	A	681	SER	2.4
1	A	607	GLU	2.3
1	A	640	ARG	2.3
1	A	491	GLN	2.3
1	A	536	GLN	2.3
1	B	604	GLY	2.3
1	B	528	ASP	2.3
1	B	555	ILE	2.3
1	A	583	GLN	2.2
1	B	480	SER	2.2
1	B	504	SER	2.2
1	A	505	ASP	2.2
1	A	528	ASP	2.2
1	B	556	PHE	2.2
1	A	471	GLN	2.1
1	A	611	GLU	2.1
1	A	515	GLN	2.1
1	B	472	GLN	2.1
1	B	474	ILE	2.1
1	B	511	HIS	2.1
1	B	536	GLN	2.1
1	A	504	SER	2.0
1	B	491	GLN	2.0
1	A	603	GLU	2.0
1	B	611	GLU	2.0
1	A	676	HIS	2.0
1	B	533	SER	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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.

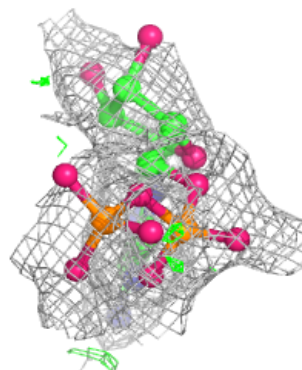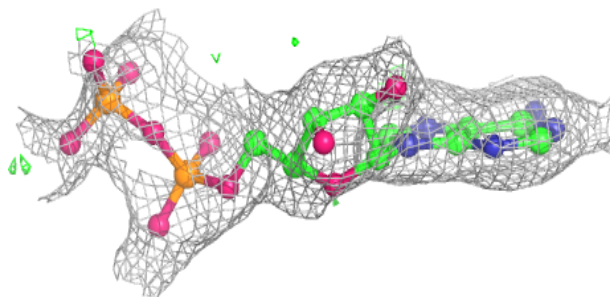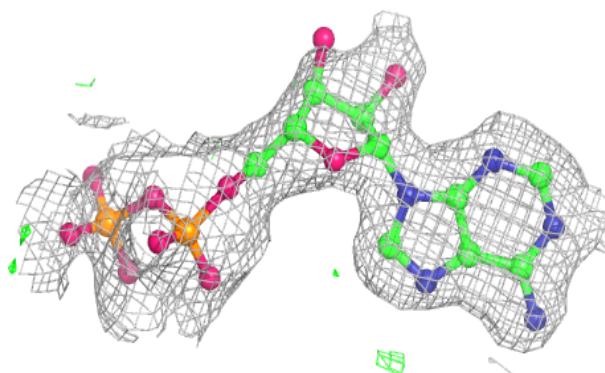| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\mathring{A}^2$)	Q<0.9
3	ATP	B	701	31/31	0.66	0.15	40,70,124,124	0
2	ADP	A	701	27/27	0.71	0.13	44,69,121,129	0

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)
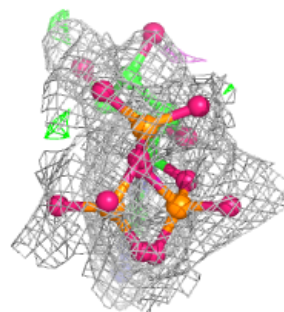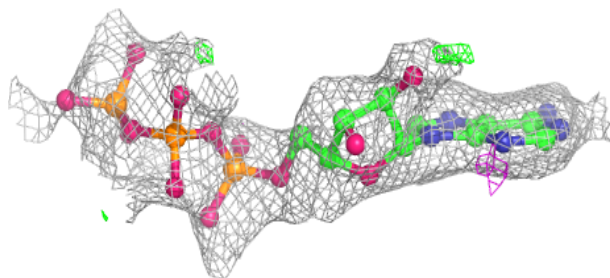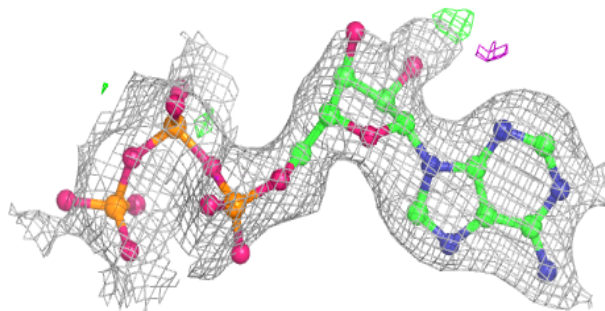
Electron density around ADP A 701:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.