



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:19 PM UTC

PDB ID : 5B0O / pdb_00005b0o
Title : Structure of the FliH-FliI complex
Authors : Imada, K.; Uchida, Y.; Kinoshita, M.; Namba, K.; Minamino, T.
Deposited on : 2015-11-02
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

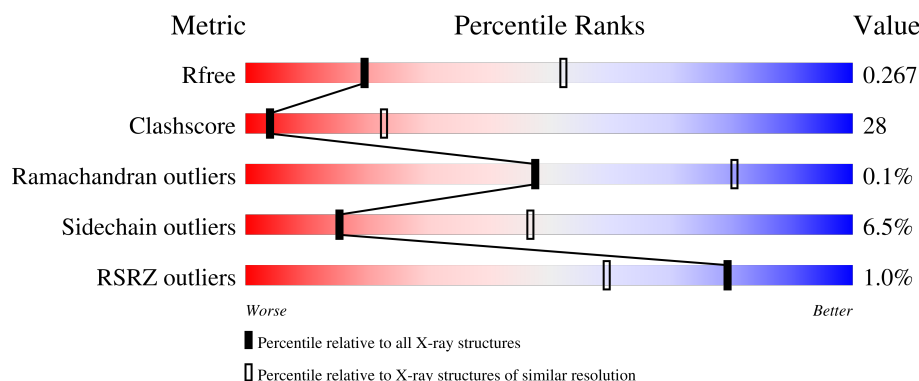
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	456	% 55% 39% • •
1	B	456	61% 34% 5%
1	C	456	% 47% 45% 5% •
1	D	456	57% 38% 5%
2	E	140	61% 34% • •

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Mol	Chain	Length	Quality of chain
2	F	140	4% 40% 47% • 10%
2	G	140	% 46% 46% 5% •
2	H	140	2% 41% 52% • •
2	I	140	% 60% 34% • 5%
2	J	140	% 41% 49% 5% • 5%
2	K	140	% 51% 41% • 5%
2	L	140	% 42% 43% 6% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21982 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 Flagellum-specific ATP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	0	0
			3391	2148	607	625	11			
1	B	455	Total	C	N	O	S	0	0	0
			3460	2187	621	641	11			
1	C	445	Total	C	N	O	S	0	0	0
			3395	2151	607	626	11			
1	D	454	Total	C	N	O	S	0	0	0
			3452	2182	620	639	11			

- Molecule 2 is a protein called Flagellar assembly protein FliH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	135	Total	C	N	O	S	0	0	0
			1040	645	193	196	6			
2	F	126	Total	C	N	O	S	0	0	0
			966	599	177	185	5			
2	G	136	Total	C	N	O	S	0	0	0
			1048	651	194	197	6			
2	H	136	Total	C	N	O	S	0	0	0
			1049	651	194	198	6			
2	I	133	Total	C	N	O	S	0	0	0
			1029	638	191	194	6			
2	J	133	Total	C	N	O	S	0	0	0
			1029	638	191	194	6			
2	K	133	Total	C	N	O	S	0	0	0
			1029	638	191	194	6			
2	L	127	Total	C	N	O	S	0	0	0
			986	612	185	183	6			

There are 24 discrepancies between the modelled and reference sequences:

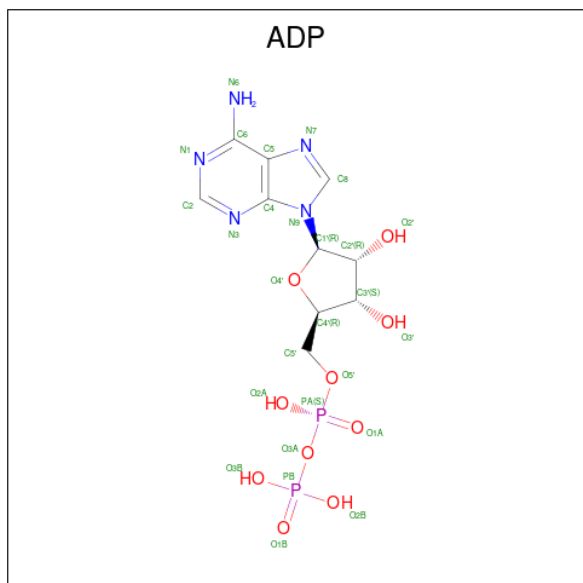
Chain	Residue	Modelled	Actual	Comment	Reference
E	96	GLY	-	expression tag	UNP P15934

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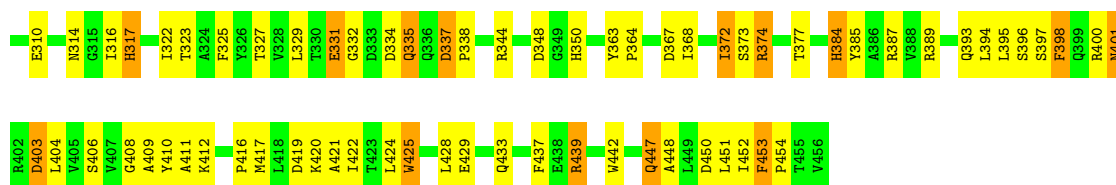
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Chain	Residue	Modelled	Actual	Comment	Reference
E	97	SER	-	expression tag	UNP P15934
E	98	HIS	-	expression tag	UNP P15934
F	96	GLY	-	expression tag	UNP P15934
F	97	SER	-	expression tag	UNP P15934
F	98	HIS	-	expression tag	UNP P15934
G	96	GLY	-	expression tag	UNP P15934
G	97	SER	-	expression tag	UNP P15934
G	98	HIS	-	expression tag	UNP P15934
H	96	GLY	-	expression tag	UNP P15934
H	97	SER	-	expression tag	UNP P15934
H	98	HIS	-	expression tag	UNP P15934
I	96	GLY	-	expression tag	UNP P15934
I	97	SER	-	expression tag	UNP P15934
I	98	HIS	-	expression tag	UNP P15934
J	96	GLY	-	expression tag	UNP P15934
J	97	SER	-	expression tag	UNP P15934
J	98	HIS	-	expression tag	UNP P15934
K	96	GLY	-	expression tag	UNP P15934
K	97	SER	-	expression tag	UNP P15934
K	98	HIS	-	expression tag	UNP P15934
L	96	GLY	-	expression tag	UNP P15934
L	97	SER	-	expression tag	UNP P15934
L	98	HIS	-	expression tag	UNP P15934

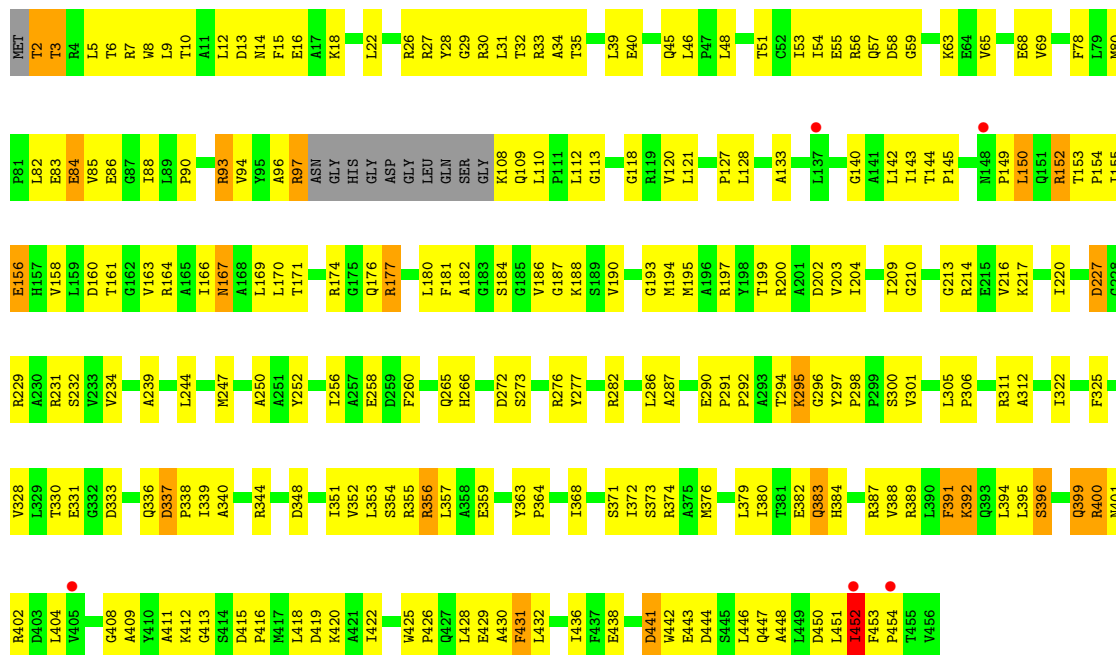
- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



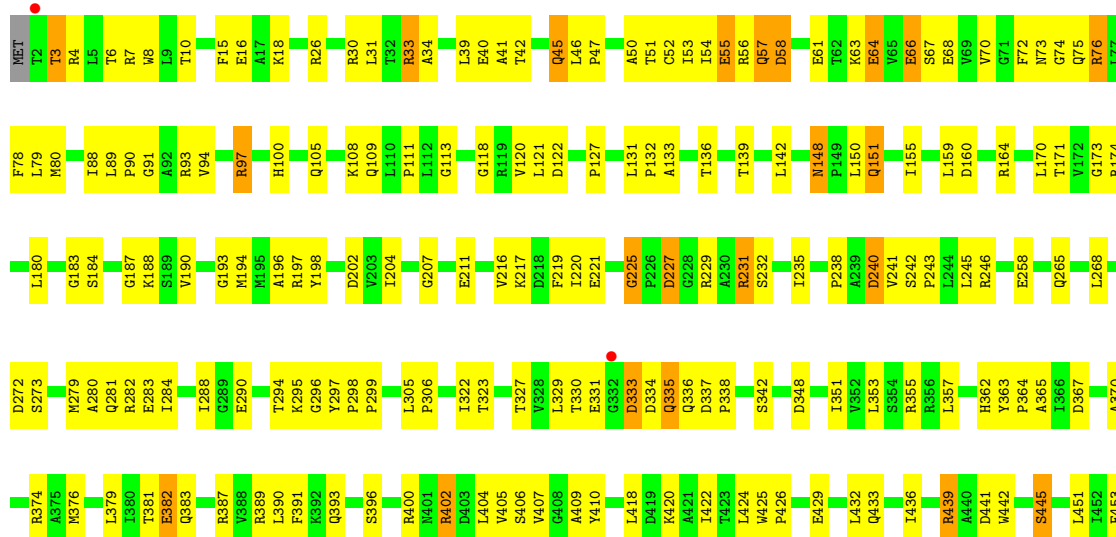
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		



• Molecule 1: Flagellum-specific ATP synthase



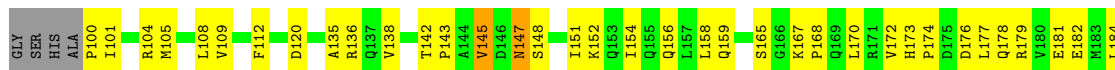
• Molecule 1: Flagellum-specific ATP synthase





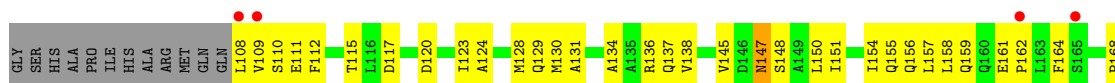
• Molecule 2: Flagellar assembly protein FliH

Chain E: 61% 34% . .



• Molecule 2: Flagellar assembly protein FliH

Chain F: 4% 40% 47% . 10%



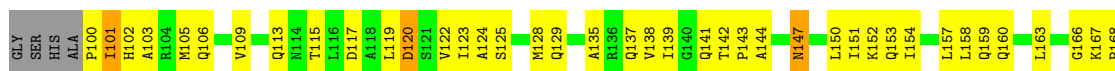
• Molecule 2: Flagellar assembly protein FliH

Chain G: % 46% 46% 5% .



• Molecule 2: Flagellar assembly protein FliH

Chain H: 2% 41% 52% . .

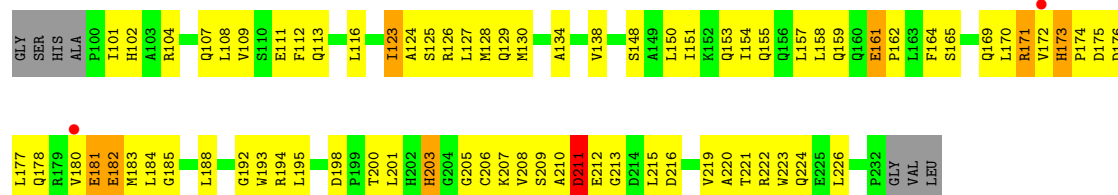
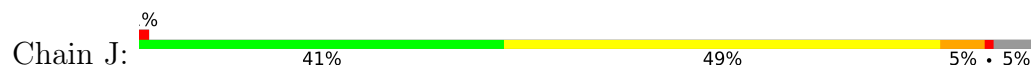


• Molecule 2: Flagellar assembly protein FliH

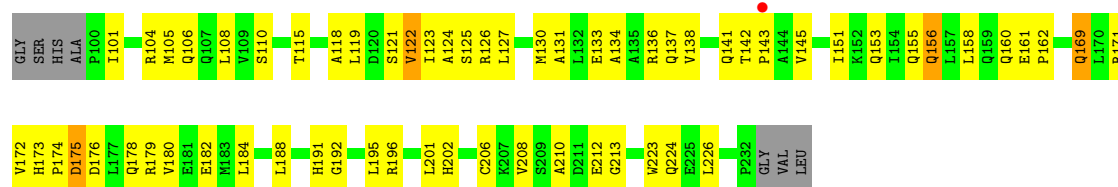
Chain I: % 60% 34% . 5%



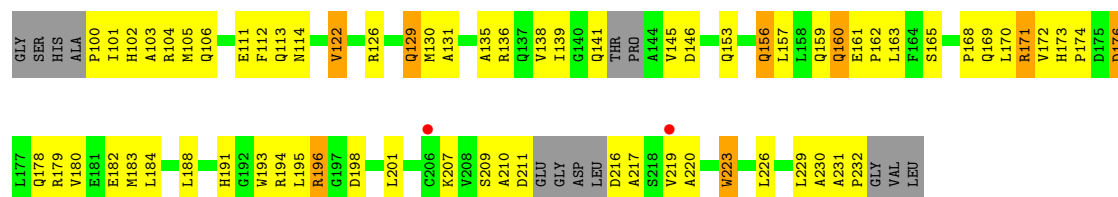
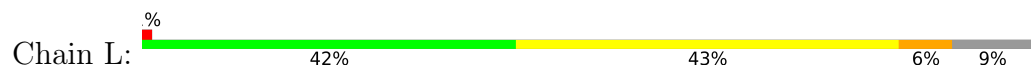
- Molecule 2: Flagellar assembly protein FliH



- Molecule 2: Flagellar assembly protein FliH



- Molecule 2: Flagellar assembly protein FliH



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	133.66Å 147.31Å 164.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.31 – 3.00 51.31 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (51.31-3.00) 99.2 (51.31-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.7.1 _743	Depositor
R, R_{free}	0.218 , 0.270 0.214 , 0.267	Depositor DCC
R_{free} test set	3293 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	21982	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.42	0/3452	0.92	9/4683 (0.2%)
1	B	0.39	0/3523	0.89	11/4779 (0.2%)
1	C	0.39	0/3456	0.89	15/4688 (0.3%)
1	D	0.42	0/3515	0.91	9/4769 (0.2%)
2	E	0.40	0/1057	0.77	0/1432
2	F	0.34	0/981	0.82	1/1330 (0.1%)
2	G	0.36	0/1065	0.85	1/1443 (0.1%)
2	H	0.37	0/1066	0.91	2/1443 (0.1%)
2	I	0.37	0/1046	0.75	0/1417
2	J	0.35	0/1046	0.88	4/1417 (0.3%)
2	K	0.35	0/1046	0.80	1/1417 (0.1%)
2	L	0.36	0/1000	0.84	1/1350 (0.1%)
All	All	0.39	0/22253	0.88	54/30168 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	337	ASP	CA-C-N	9.45	129.54	119.05
1	B	337	ASP	C-N-CA	9.45	129.54	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	GLY	N-CA-C	-7.99	104.01	115.27
1	C	144	THR	CA-C-N	7.86	125.40	119.66
1	C	144	THR	C-N-CA	7.86	125.40	119.66

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	333	ASP	Peptide
1	C	452	ILE	Peptide

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	3391	0	3464	174	1
1	B	3460	0	3524	174	3
1	C	3395	0	3470	216	0
1	D	3452	0	3515	174	0
2	E	1040	0	1043	40	0
2	F	966	0	965	69	0
2	G	1048	0	1054	91	0
2	H	1049	0	1054	115	0
2	I	1029	0	1031	58	0
2	J	1029	0	1031	96	1
2	K	1029	0	1031	61	2
2	L	986	0	991	84	3
3	A	27	0	12	5	0
3	B	27	0	12	7	0
3	C	27	0	12	3	0
3	D	27	0	12	5	0
All	All	21982	0	22221	1229	5

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 28.

The worst 5 of 1229 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)
2:L:231:ALA:HB1	2:L:232:PRO:HD2	1.23	1.18
1:A:450:ASP:HA	1:A:454:PRO:HD2	1.40	1.04
1:C:387:ARG:NH1	1:C:450:ASP:OD1	1.93	1.01
1:B:450:ASP:HA	1:B:454:PRO:HG2	1.42	1.00
2:I:194:ARG:NH1	2:I:211:ASP:OD2	1.94	1.00

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:GLU:OE2	2:L:196:ARG:NH2[3_445]	2.08	0.12
1:B:13:ASP:OD2	2:K:121:SER:OG[1_655]	2.10	0.10
2:J:125:SER:O	2:K:125:SER:OG[1_655]	2.15	0.05
1:A:6:THR:OG1	2:L:114:ASN:OD1[1_655]	2.16	0.04
1:B:332:GLY:N	2:L:211:ASP:OD1[3_445]	2.18	0.02

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	441/456 (97%)	429 (97%)	12 (3%)	0	100	100
1	B	453/456 (99%)	438 (97%)	13 (3%)	2 (0%)	30	65
1	C	441/456 (97%)	426 (97%)	13 (3%)	2 (0%)	24	60
1	D	452/456 (99%)	440 (97%)	12 (3%)	0	100	100
2	E	133/140 (95%)	131 (98%)	2 (2%)	0	100	100
2	F	124/140 (89%)	121 (98%)	3 (2%)	0	100	100
2	G	134/140 (96%)	124 (92%)	10 (8%)	0	100	100
2	H	134/140 (96%)	127 (95%)	7 (5%)	0	100	100
2	I	131/140 (94%)	127 (97%)	4 (3%)	0	100	100
2	J	131/140 (94%)	126 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	131/140 (94%)	129 (98%)	2 (2%)	0	100	100
2	L	121/140 (86%)	115 (95%)	6 (5%)	0	100	100
All	All	2826/2944 (96%)	2733 (97%)	89 (3%)	4 (0%)	48	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	294	THR
1	C	295	LYS
1	C	452	ILE
1	B	317	HIS

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	350/358 (98%)	327 (93%)	23 (7%)	15	46
1	B	357/358 (100%)	335 (94%)	22 (6%)	16	49
1	C	351/358 (98%)	324 (92%)	27 (8%)	12	40
1	D	356/358 (99%)	333 (94%)	23 (6%)	15	47
2	E	112/115 (97%)	105 (94%)	7 (6%)	16	48
2	F	104/115 (90%)	95 (91%)	9 (9%)	9	35
2	G	113/115 (98%)	105 (93%)	8 (7%)	13	43
2	H	113/115 (98%)	108 (96%)	5 (4%)	25	60
2	I	111/115 (96%)	106 (96%)	5 (4%)	24	59
2	J	111/115 (96%)	105 (95%)	6 (5%)	20	53
2	K	111/115 (96%)	103 (93%)	8 (7%)	13	43
2	L	106/115 (92%)	99 (93%)	7 (7%)	15	46
All	All	2295/2352 (98%)	2145 (94%)	150 (6%)	15	47

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	172	VAL
2	L	129	GLN
2	H	101	ILE
2	J	173	HIS
1	C	14	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	159	GLN
2	I	202	HIS
2	H	173	HIS
2	I	147	ASN
2	J	153	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	ADP	C	601	-	28,29,29	1.43	4 (14%)	43,45,45	1.86	9 (20%)
3	ADP	B	601	-	28,29,29	1.44	4 (14%)	43,45,45	1.92	9 (20%)
3	ADP	D	601	-	28,29,29	1.40	4 (14%)	43,45,45	1.85	8 (18%)
3	ADP	A	601	-	28,29,29	1.47	5 (17%)	43,45,45	1.82	9 (20%)

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	ADP	C	601	-	-	2/16/32/32	0/3/3/3
3	ADP	B	601	-	-	2/16/32/32	0/3/3/3
3	ADP	D	601	-	-	1/16/32/32	0/3/3/3
3	ADP	A	601	-	-	5/16/32/32	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	ADP	C5-C4	5.04	1.48	1.39
3	A	601	ADP	C5-C4	4.95	1.47	1.39
3	C	601	ADP	C5-C4	4.84	1.47	1.39
3	D	601	ADP	C5-C4	4.82	1.47	1.39
3	A	601	ADP	C5-C6	2.83	1.48	1.41

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	601	ADP	C5-C4-N3	-6.14	118.26	126.72
3	C	601	ADP	C5-C4-N3	-6.10	118.32	126.72
3	B	601	ADP	C5-C4-N3	-6.07	118.36	126.72
3	A	601	ADP	C5-C4-N3	-5.74	118.81	126.72
3	B	601	ADP	N3-C4-N9	4.98	135.65	127.17

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	ADP	PA-O3A-PB-O2B
3	A	601	ADP	PA-O3A-PB-O3B

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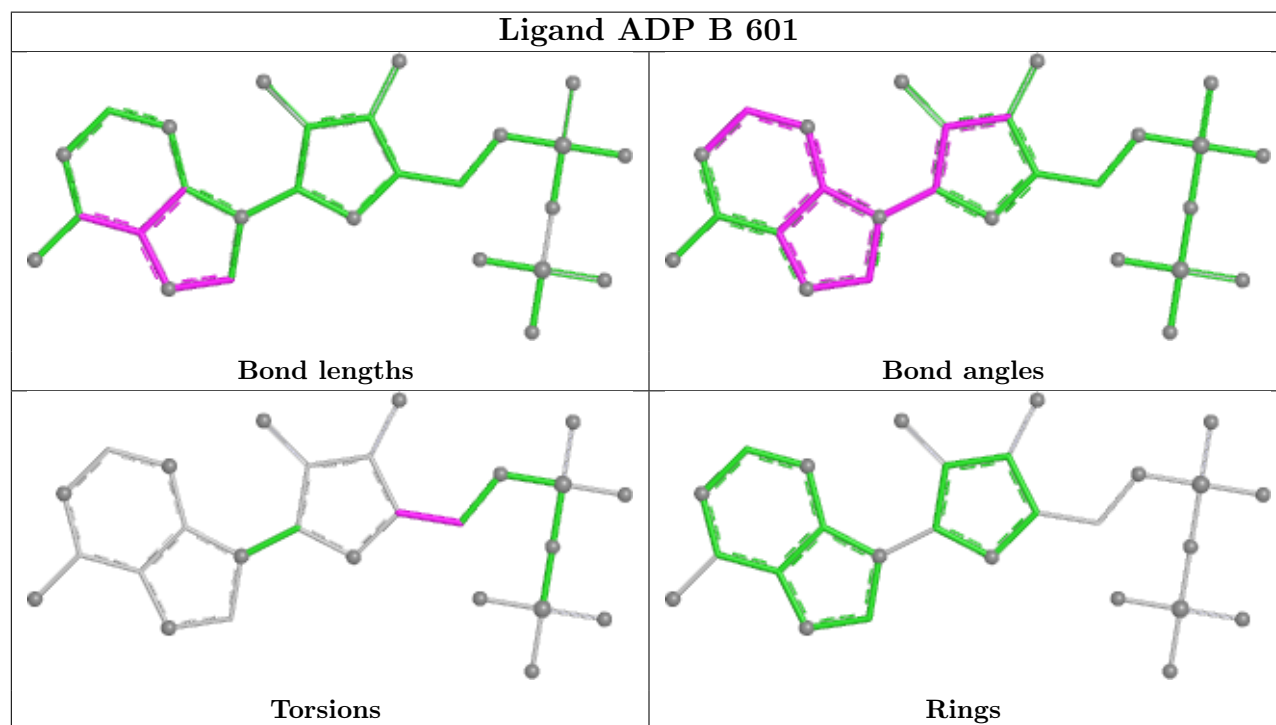
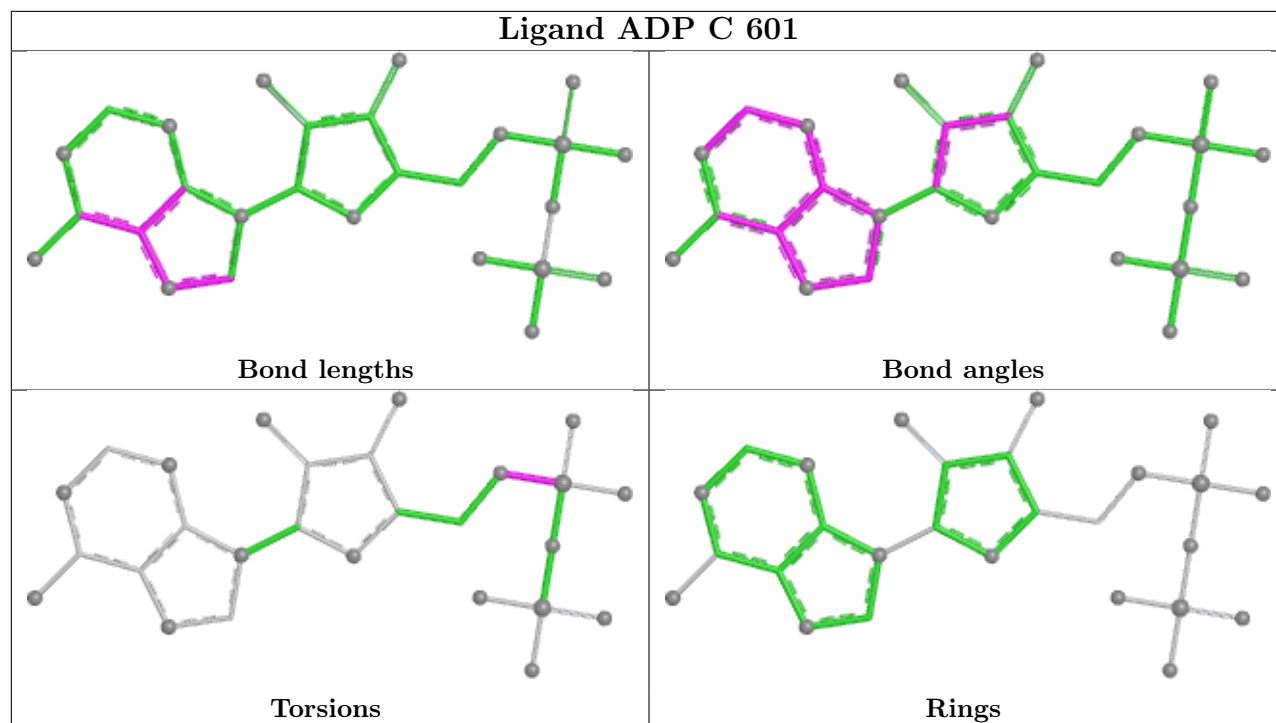
Mol	Chain	Res	Type	Atoms
3	A	601	ADP	C5'-O5'-PA-O1A
3	A	601	ADP	C5'-O5'-PA-O3A
3	C	601	ADP	C5'-O5'-PA-O1A

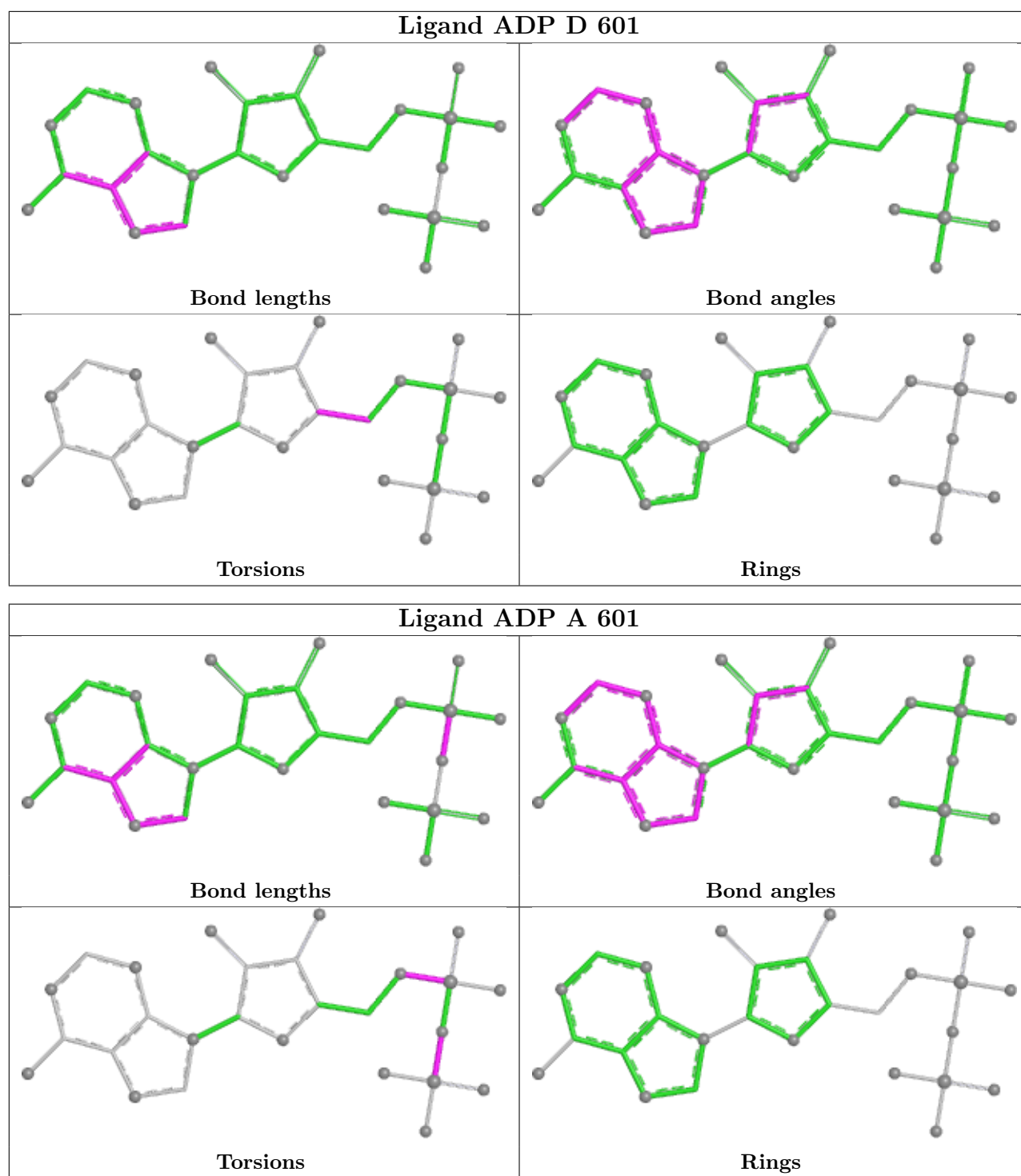
There are no ring outliers.

4 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	601	ADP	3	0
3	B	601	ADP	7	0
3	D	601	ADP	5	0
3	A	601	ADP	5	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	445/456 (97%)	-0.40	3 (0%) 84 66	28, 50, 94, 139	0
1	B	455/456 (99%)	-0.32	1 (0%) 91 83	33, 58, 118, 147	0
1	C	445/456 (97%)	-0.08	5 (1%) 78 57	40, 71, 132, 157	0
1	D	454/456 (99%)	-0.40	2 (0%) 88 76	28, 49, 90, 134	0
2	E	135/140 (96%)	-0.41	0 100 100	28, 45, 108, 138	0
2	F	126/140 (90%)	0.27	6 (4%) 35 19	63, 109, 132, 139	0
2	G	136/140 (97%)	0.19	2 (1%) 72 49	54, 101, 136, 160	0
2	H	136/140 (97%)	0.42	3 (2%) 62 39	62, 107, 145, 148	0
2	I	133/140 (95%)	-0.21	1 (0%) 82 64	32, 61, 105, 116	0
2	J	133/140 (95%)	0.22	2 (1%) 72 49	70, 108, 147, 158	0
2	K	133/140 (95%)	0.04	1 (0%) 82 64	39, 85, 116, 131	0
2	L	127/140 (90%)	0.19	2 (1%) 70 47	41, 89, 139, 147	1 (0%)
All	All	2858/2944 (97%)	-0.16	28 (0%) 79 59	28, 67, 130, 160	1 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	206	CYS	3.6
2	J	172	VAL	3.5
2	H	191	HIS	3.1
2	F	109	VAL	3.0
2	H	187	THR	3.0

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](#)

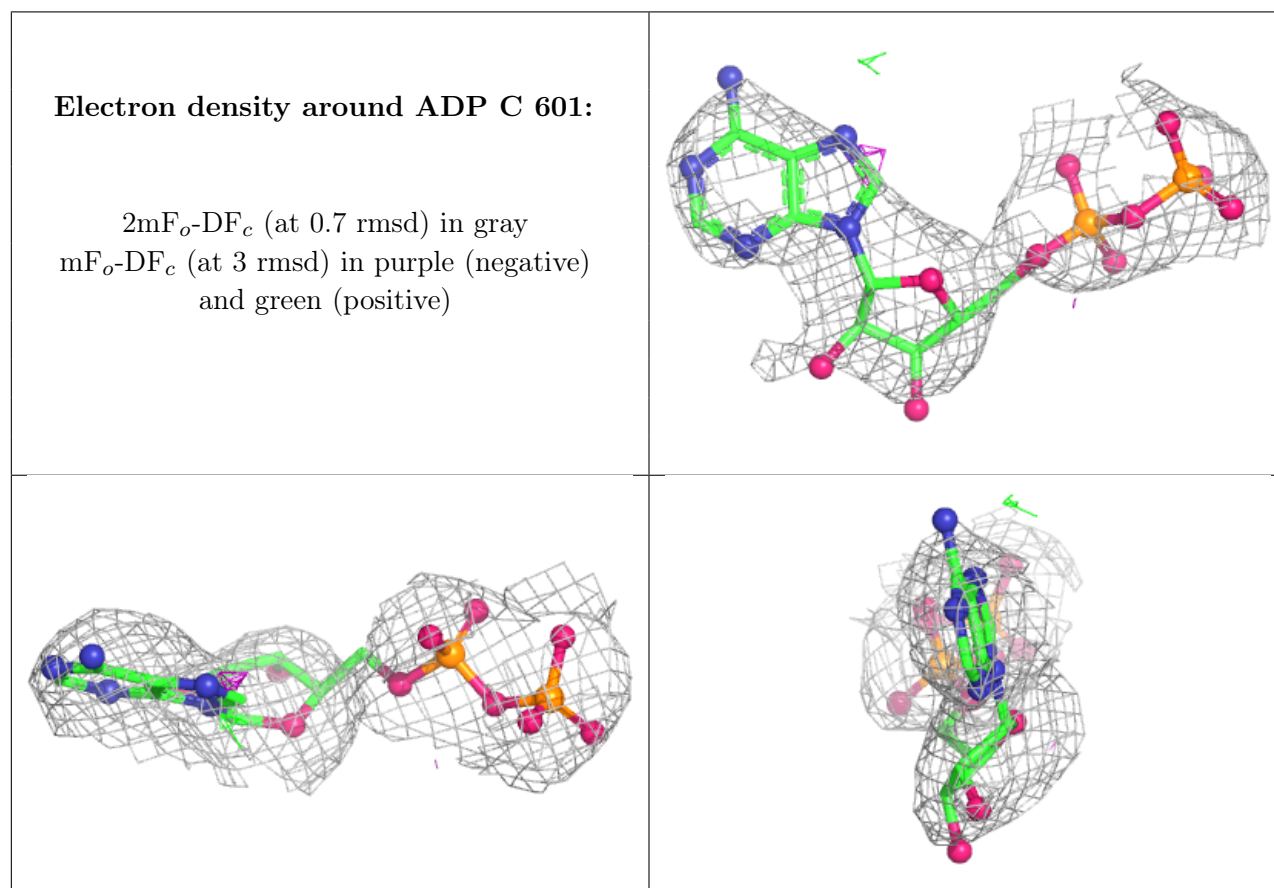
There are no oligosaccharides in this entry.

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.

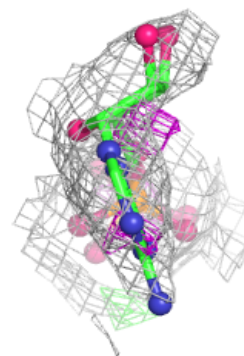
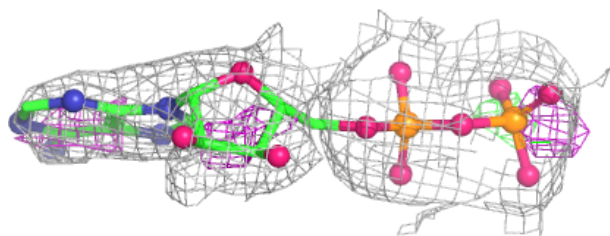
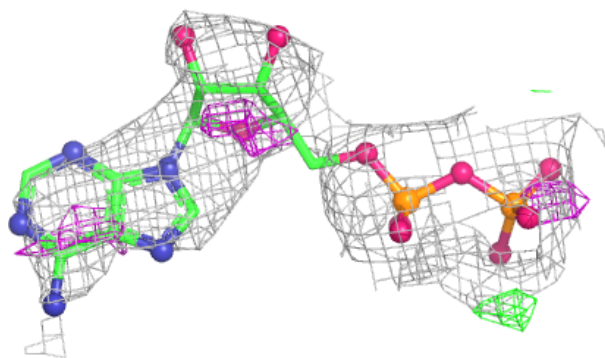
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ADP	C	601	27/27	0.84	0.10	72,89,104,111	0
3	ADP	B	601	27/27	0.87	0.10	59,79,92,92	0
3	ADP	A	601	27/27	0.92	0.09	47,57,74,77	0
3	ADP	D	601	27/27	0.94	0.08	51,63,73,81	0

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.

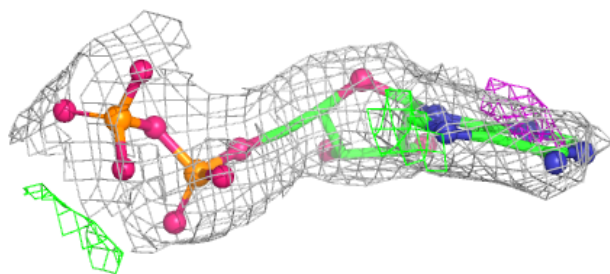
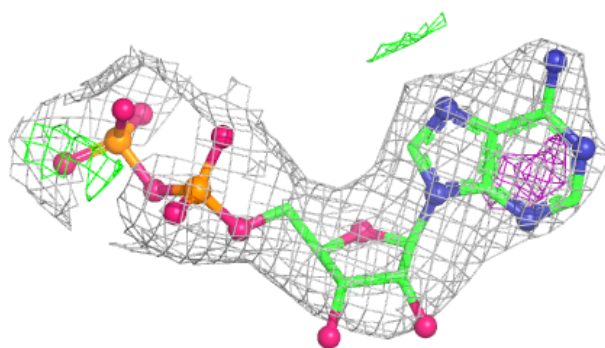


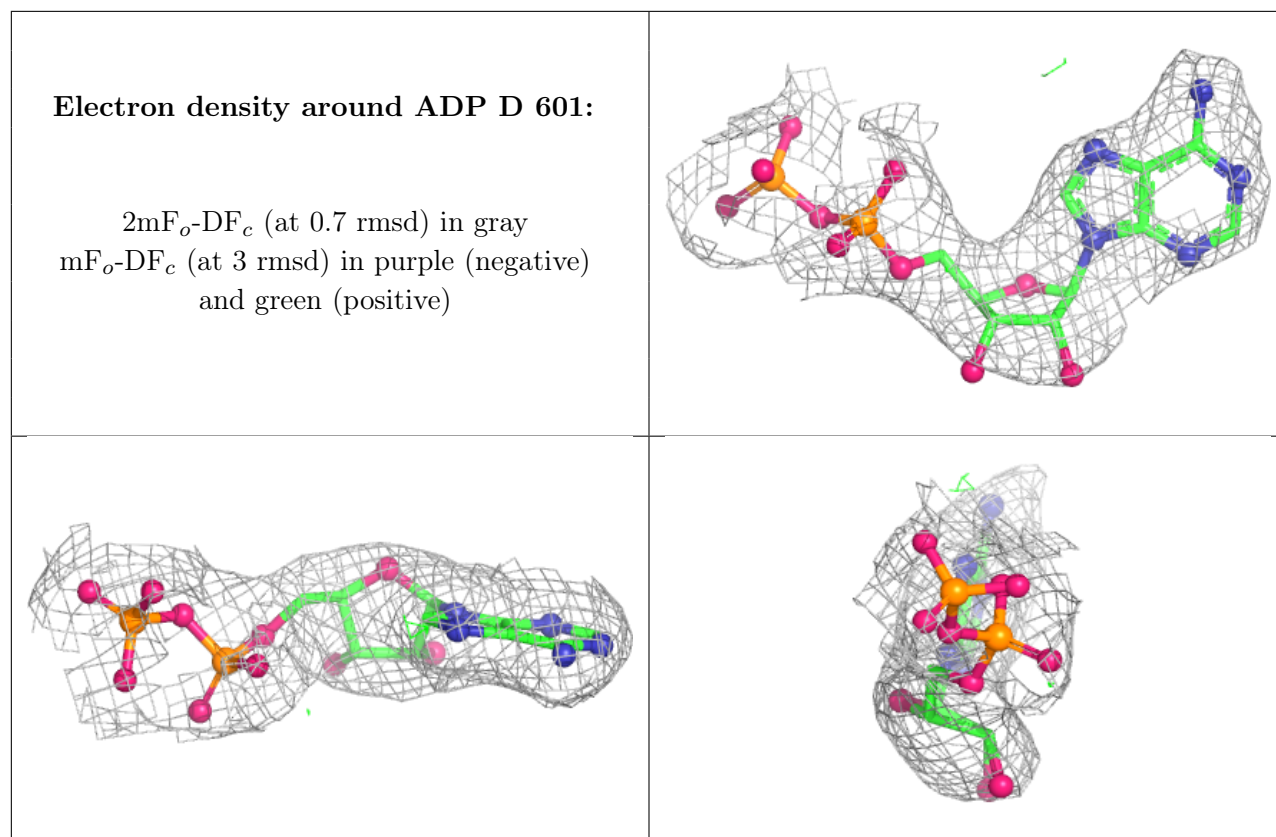
Electron density around ADP B 601:

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

**Electron density around ADP A 601:**

$2mF_o-DF_c$ (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.