



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 01:10 am BST

PDB ID : 3IBG
Title : Crystal structure of Aspergillus fumigatus Get3 with bound ADP
Authors : Suloway, C.J.M.; Chartron, J.W.; Zaslaver, M.; Clemons Jr., W.M.
Deposited on : 2009-07-15
Resolution : 3.20 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 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 : 2.11
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) : 2.11

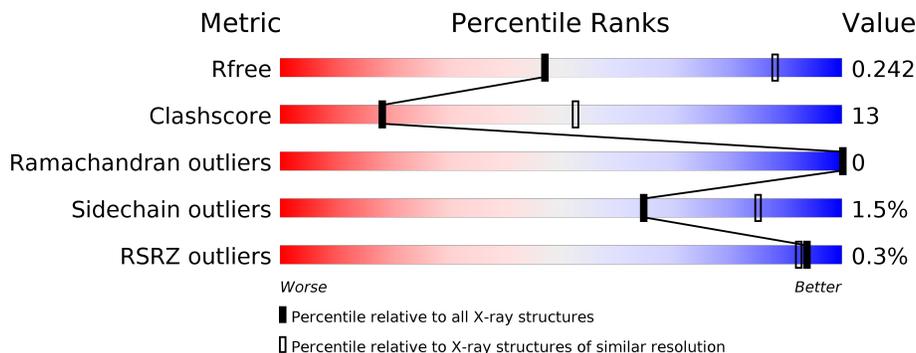
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	348	
1	B	348	
1	C	348	
1	D	348	
1	E	348	
1	F	348	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 14238 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 ATPase, subunit of the Get complex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	300	2346	1495	388	449	14	0	0	0
1	B	300	2346	1495	388	449	14	0	0	0
1	C	300	2346	1495	388	449	14	0	0	0
1	D	300	2346	1495	388	449	14	0	0	0
1	E	300	2346	1495	388	449	14	0	0	0
1	F	300	2346	1495	388	449	14	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q4WY07
A	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
A	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
A	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
A	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
A	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
A	345	HIS	-	EXPRESSION TAG	UNP Q4WY07
A	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
A	347	HIS	-	EXPRESSION TAG	UNP Q4WY07
A	348	HIS	-	EXPRESSION TAG	UNP Q4WY07
B	1	MET	-	EXPRESSION TAG	UNP Q4WY07
B	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
B	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
B	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
B	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
B	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
B	345	HIS	-	EXPRESSION TAG	UNP Q4WY07

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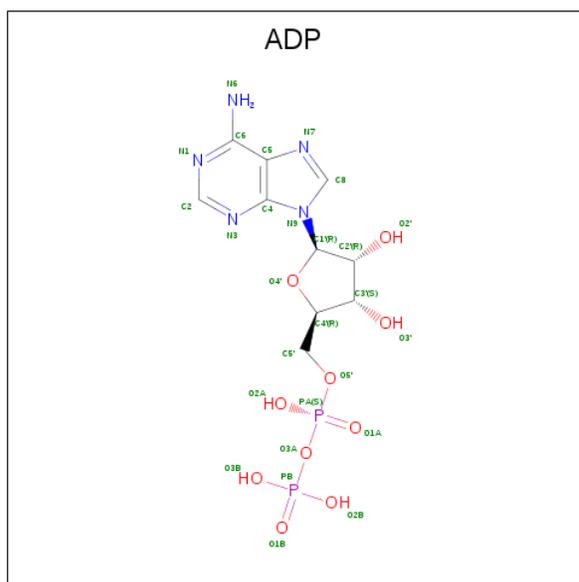
Chain	Residue	Modelled	Actual	Comment	Reference
B	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
B	347	HIS	-	EXPRESSION TAG	UNP Q4WY07
B	348	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	1	MET	-	EXPRESSION TAG	UNP Q4WY07
C	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
C	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
C	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
C	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	345	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	347	HIS	-	EXPRESSION TAG	UNP Q4WY07
C	348	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	1	MET	-	EXPRESSION TAG	UNP Q4WY07
D	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
D	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
D	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
D	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	345	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	347	HIS	-	EXPRESSION TAG	UNP Q4WY07
D	348	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	1	MET	-	EXPRESSION TAG	UNP Q4WY07
E	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
E	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
E	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
E	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	345	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	347	HIS	-	EXPRESSION TAG	UNP Q4WY07
E	348	HIS	-	EXPRESSION TAG	UNP Q4WY07
F	1	MET	-	EXPRESSION TAG	UNP Q4WY07
F	2	GLY	-	EXPRESSION TAG	UNP Q4WY07
F	341	LEU	-	EXPRESSION TAG	UNP Q4WY07
F	342	GLU	-	EXPRESSION TAG	UNP Q4WY07
F	343	HIS	-	EXPRESSION TAG	UNP Q4WY07
F	344	HIS	-	EXPRESSION TAG	UNP Q4WY07
F	345	HIS	-	EXPRESSION TAG	UNP Q4WY07
F	346	HIS	-	EXPRESSION TAG	UNP Q4WY07
F	347	HIS	-	EXPRESSION TAG	UNP Q4WY07

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Chain	Residue	Modelled	Actual	Comment	Reference
F	348	HIS	-	EXPRESSION TAG	UNP Q4WY07

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

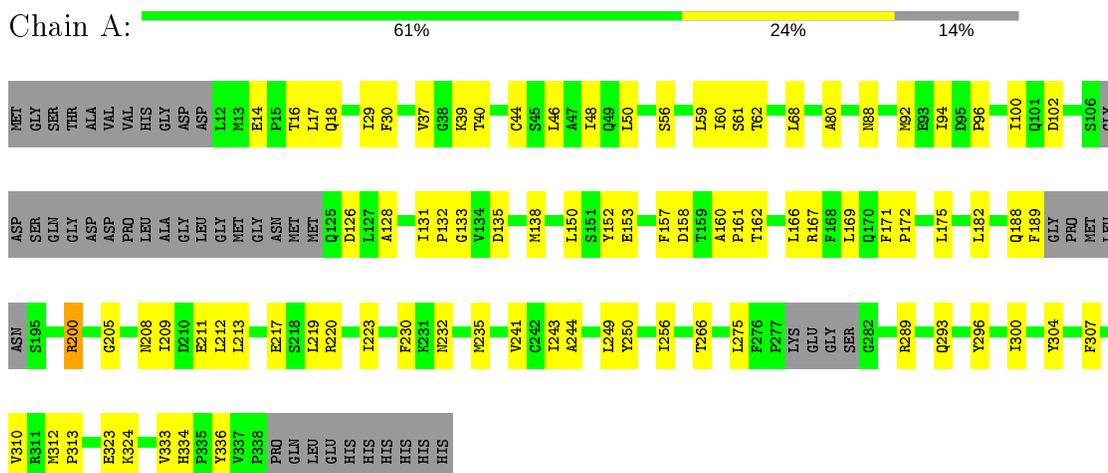


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
		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

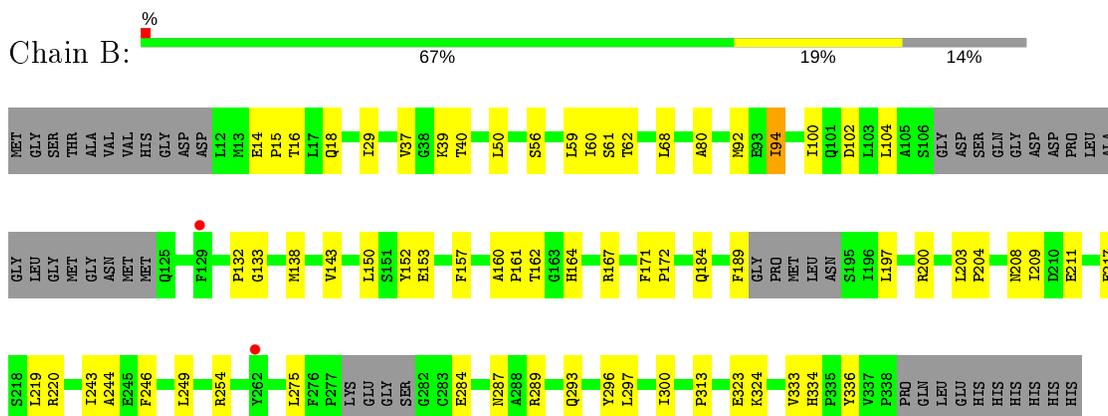
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

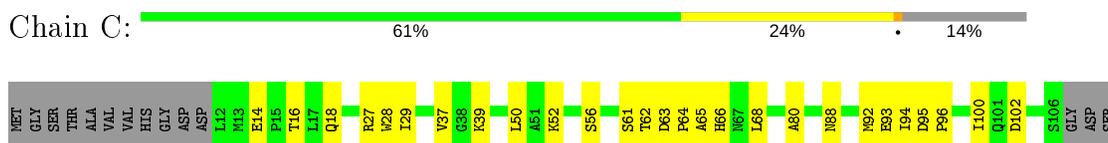
- Molecule 1: ATPase, subunit of the Get complex

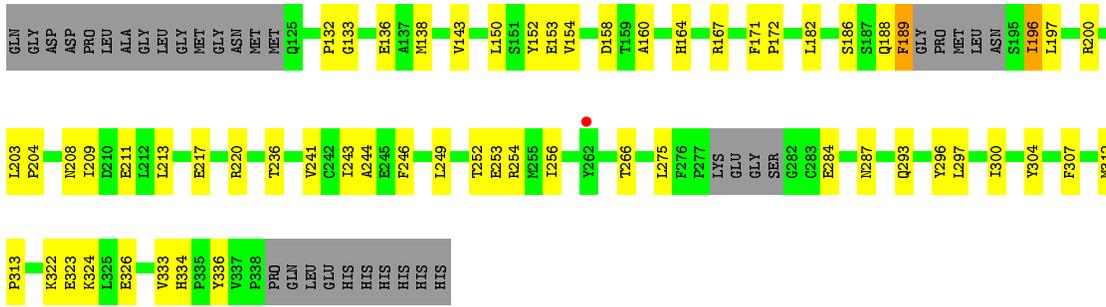


- Molecule 1: ATPase, subunit of the Get complex



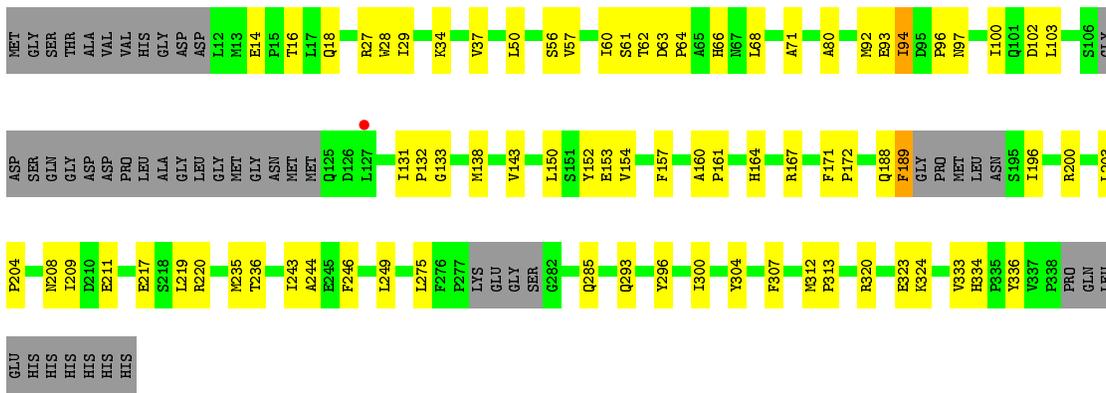
- Molecule 1: ATPase, subunit of the Get complex





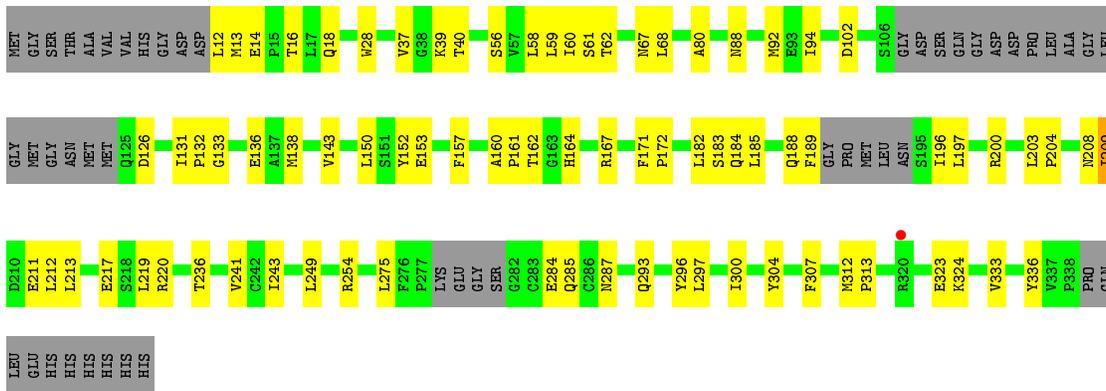
- Molecule 1: ATPase, subunit of the Get complex

Chain D: 64% 22% 14%



- Molecule 1: ATPase, subunit of the Get complex

Chain E: 63% 23% 14%



- Molecule 1: ATPase, subunit of the Get complex

Chain F: 60% 26% 14%



D102	S106	R200	F307
GLY	GLY	P313	P313
ASP	ASP	V319	V319
SER	SER	E323	E323
GLN	GLN	K324	K324
GLY	GLY	L325	L325
ASP	ASP	V333	V333
PRO	PRO	H334	H334
LEU	LEU	F335	F335
ALA	ALA	Y336	Y336
GLY	GLY	V337	V337
LEU	LEU	F338	F338
GLY	GLY	PRO	PRO
GLY	GLY	GLN	GLN
GLY	GLY	LEU	LEU
ASN	ASN	GLU	GLU
MET	MET	HIS	HIS
MET	MET	HIS	HIS
Q125	D126	HIS	HIS
P132	G133	HIS	HIS
G133	G133	HIS	HIS
M138	M138	L249	L249
V143	V143	Y250	Y250
L150	S151	T252	T252
S151	Y152	E253	E253
Y152	E153	R254	R254
E153	E153	M255	M255
F157	D158	I256	I256
D158	I159	T266	T266
I159	A160	L275	L275
P161	P161	F276	F276
L166	R167	P277	P277
R167	F168	LYS	LYS
F168	L169	GLU	GLU
Q170	Q170	GLY	GLY
F171	F171	SER	SER
P172	P172	G282	G282
Q188	F189	C283	C283
F189	GLY	E284	E284
GLY	PRO	M287	M287
PRO	MET	Q293	Q293
LEU	LEU	Y296	Y296
ASN	ASN	L297	L297
S195	I196	I300	I300
I196	L197	Y304	Y304
L197	L197	Y304	Y304

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.76Å 154.78Å 242.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.26 – 3.20 65.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (65.26-3.20) 100.0 (65.27-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.4 _62	Depositor
R, R_{free}	0.212 , 0.251 0.206 , 0.242	Depositor DCC
R_{free} test set	2660 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	77.3	Xtrriage
Anisotropy	0.278	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14238	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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: 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	0.28	0/2382	0.45	0/3211
1	B	0.26	0/2382	0.43	0/3211
1	C	0.26	0/2382	0.43	0/3211
1	D	0.26	0/2382	0.44	0/3211
1	E	0.28	0/2382	0.45	0/3211
1	F	0.31	0/2382	0.48	0/3211
All	All	0.28	0/14292	0.45	0/19266

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	2346	0	2379	68	0
1	B	2346	0	2379	61	0
1	C	2346	0	2379	70	0
1	D	2346	0	2379	64	0
1	E	2346	0	2379	77	0
1	F	2346	0	2379	76	0
2	A	27	0	12	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	27	0	12	4	0
2	C	27	0	12	2	0
2	D	27	0	12	1	0
2	E	27	0	12	5	0
2	F	27	0	12	6	0
All	All	14238	0	14346	383	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 13.

The worst 5 of 383 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:E:16:THR:HG23	1:E:333:VAL:HA	1.57	0.85
1:A:275:LEU:H	1:A:293:GLN:HE22	1.33	0.77
1:B:16:THR:HG22	1:B:18:GLN:H	1.51	0.76
1:E:94:ILE:HD12	1:E:143:VAL:HG11	1.68	0.76
1:B:16:THR:HG23	1:B:333:VAL:HA	1.67	0.76

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	292/348 (84%)	278 (95%)	14 (5%)	0	100	100
1	B	292/348 (84%)	279 (96%)	13 (4%)	0	100	100
1	C	292/348 (84%)	278 (95%)	14 (5%)	0	100	100
1	D	292/348 (84%)	279 (96%)	13 (4%)	0	100	100
1	E	292/348 (84%)	279 (96%)	13 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	292/348 (84%)	277 (95%)	15 (5%)	0	100	100
All	All	1752/2088 (84%)	1670 (95%)	82 (5%)	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	264/301 (88%)	259 (98%)	5 (2%)	57	81
1	B	264/301 (88%)	260 (98%)	4 (2%)	65	85
1	C	264/301 (88%)	260 (98%)	4 (2%)	65	85
1	D	264/301 (88%)	260 (98%)	4 (2%)	65	85
1	E	264/301 (88%)	260 (98%)	4 (2%)	65	85
1	F	264/301 (88%)	261 (99%)	3 (1%)	73	88
All	All	1584/1806 (88%)	1560 (98%)	24 (2%)	65	85

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	196	ILE
1	D	94	ILE
1	F	217	GLU
1	C	217	GLU
1	C	220	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	293	GLN
1	C	334	HIS
1	F	97	ASN

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Mol	Chain	Res	Type
1	C	66	HIS
1	C	164	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	ADP	F	349	-	24,29,29	1.36	3 (12%)	29,45,45	1.63	6 (20%)
2	ADP	D	349	-	24,29,29	1.35	3 (12%)	29,45,45	1.60	7 (24%)
2	ADP	A	349	-	24,29,29	1.27	2 (8%)	29,45,45	1.61	6 (20%)
2	ADP	E	349	-	24,29,29	1.27	2 (8%)	29,45,45	1.61	6 (20%)
2	ADP	C	349	-	24,29,29	1.69	4 (16%)	29,45,45	1.50	5 (17%)
2	ADP	B	349	-	24,29,29	1.27	2 (8%)	29,45,45	1.61	6 (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
2	ADP	F	349	-	-	5/12/32/32	0/3/3/3
2	ADP	D	349	-	-	3/12/32/32	0/3/3/3
2	ADP	A	349	-	-	2/12/32/32	0/3/3/3
2	ADP	E	349	-	-	2/12/32/32	0/3/3/3
2	ADP	C	349	-	-	5/12/32/32	0/3/3/3
2	ADP	B	349	-	-	2/12/32/32	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	349	ADP	C8-N7	5.08	1.43	1.34
2	C	349	ADP	PB-O3B	-3.38	1.41	1.54
2	D	349	ADP	C5-C4	2.96	1.48	1.40
2	D	349	ADP	PB-O3B	-2.83	1.43	1.54
2	C	349	ADP	C5-C4	2.72	1.48	1.40

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	349	ADP	PA-O3A-PB	-4.17	118.52	132.83
2	B	349	ADP	PA-O3A-PB	-4.16	118.54	132.83
2	E	349	ADP	PA-O3A-PB	-4.16	118.54	132.83
2	F	349	ADP	PA-O3A-PB	-4.01	119.06	132.83
2	D	349	ADP	C4-C5-N7	-3.45	105.80	109.40

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

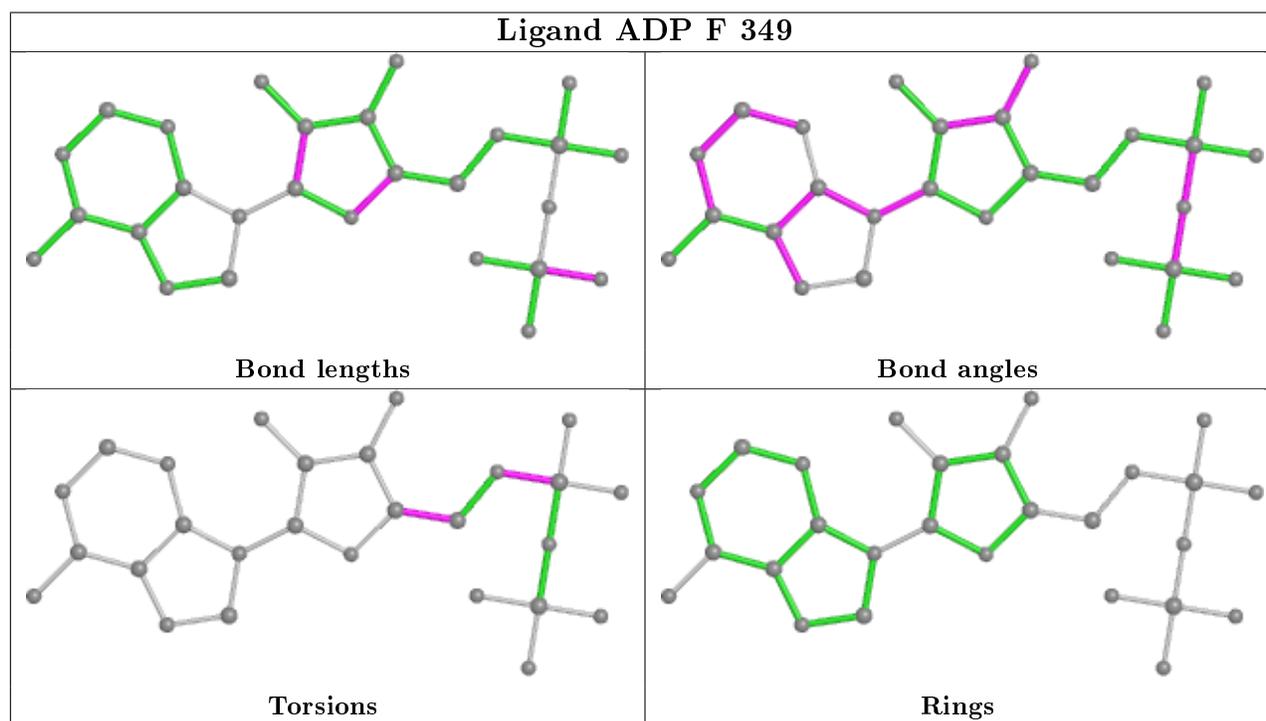
Mol	Chain	Res	Type	Atoms
2	F	349	ADP	C5'-O5'-PA-O1A
2	F	349	ADP	C5'-O5'-PA-O2A
2	C	349	ADP	C5'-O5'-PA-O2A
2	F	349	ADP	O4'-C4'-C5'-O5'
2	F	349	ADP	C3'-C4'-C5'-O5'

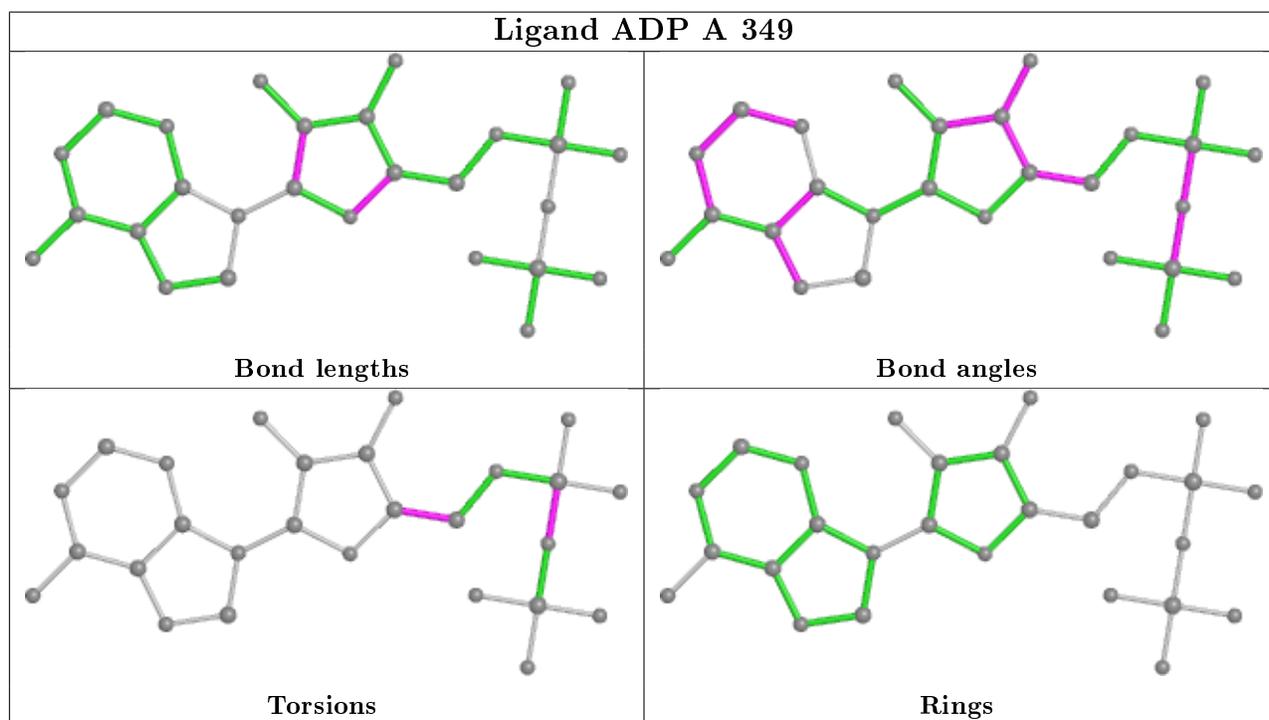
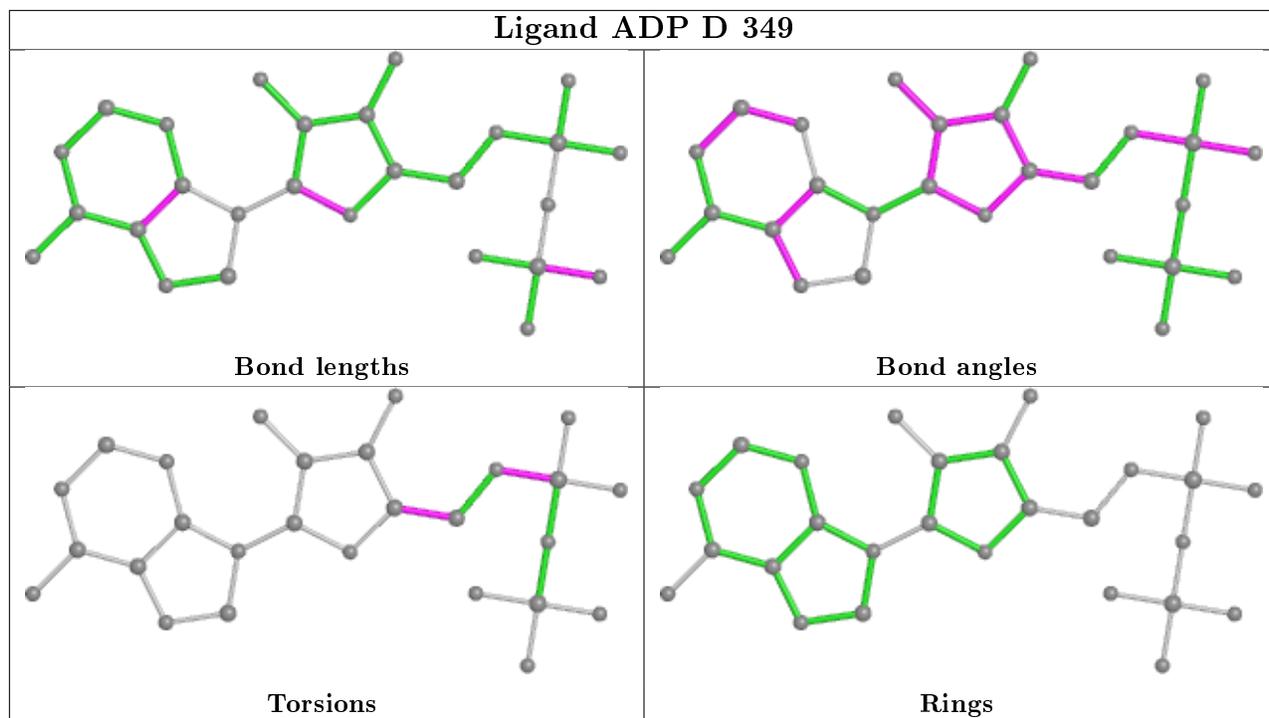
There are no ring outliers.

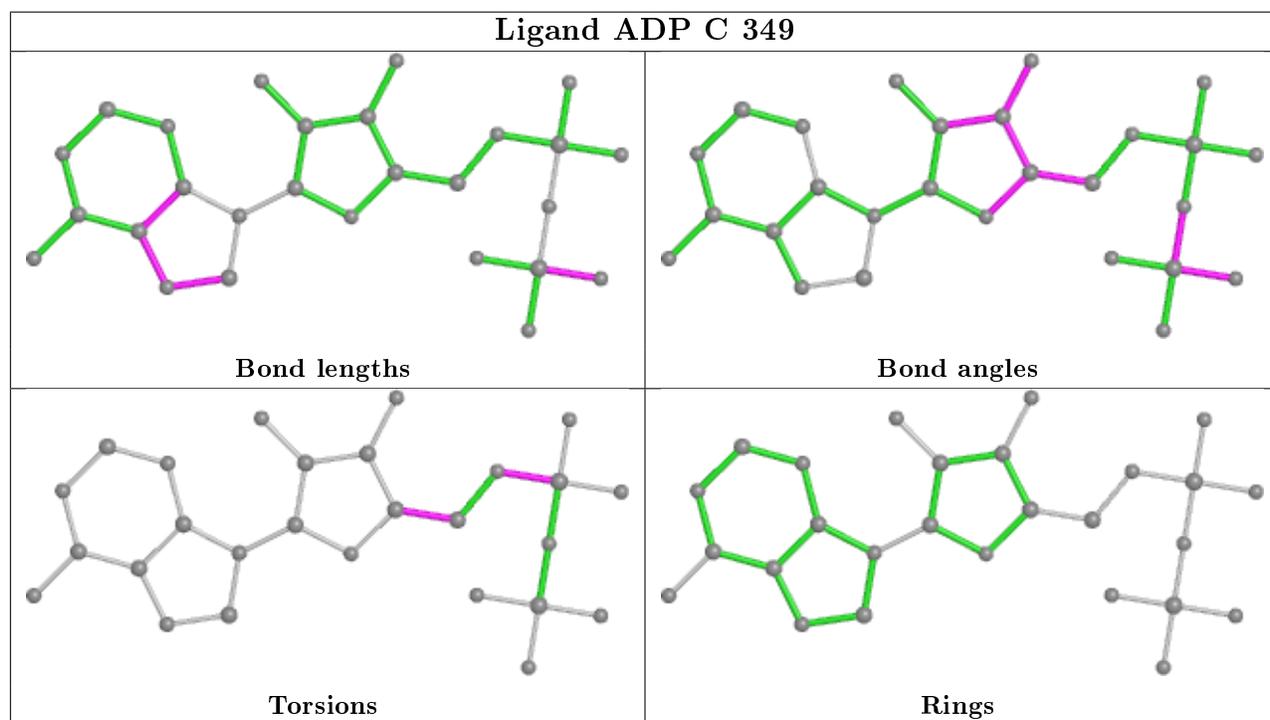
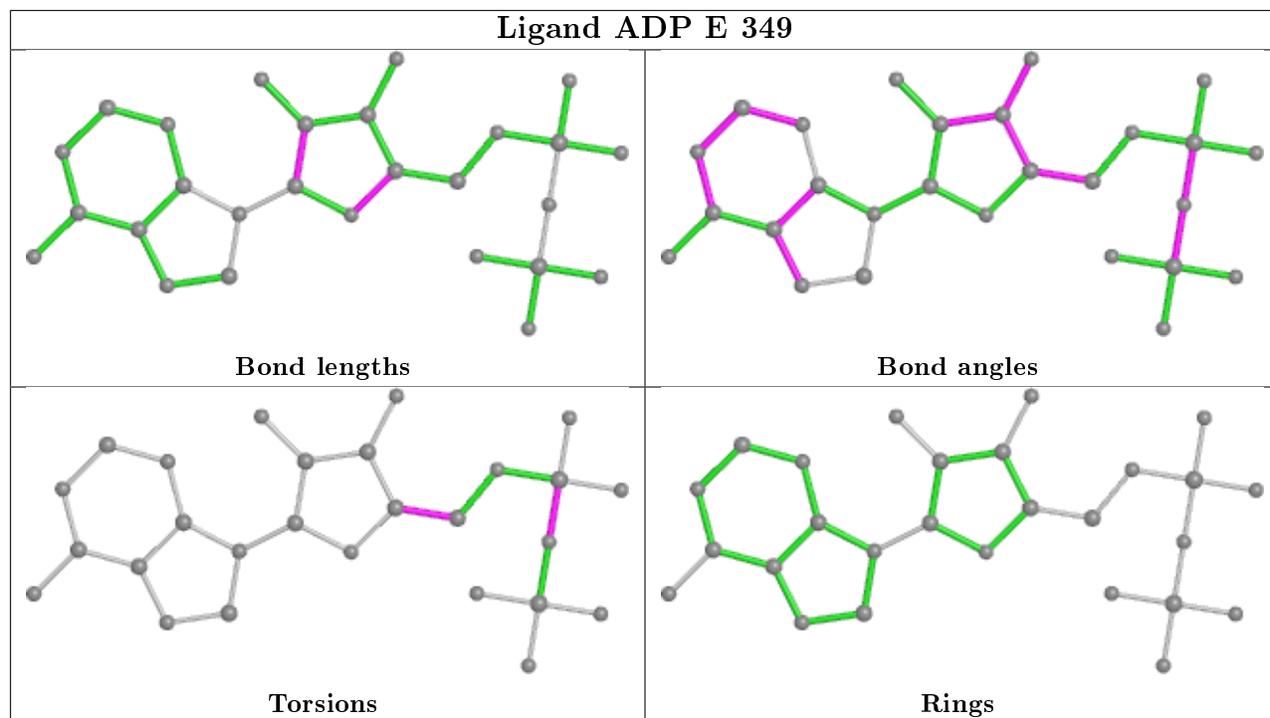
6 monomers are involved in 22 short contacts:

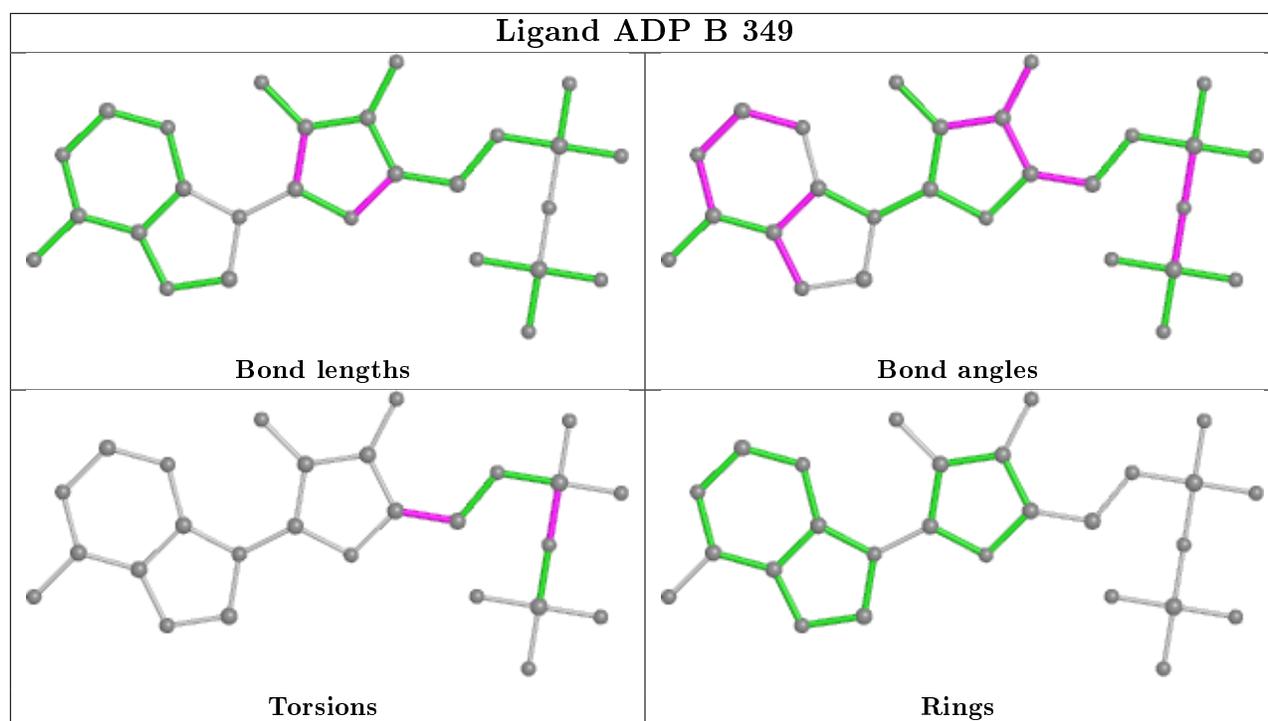
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	349	ADP	6	0
2	D	349	ADP	1	0
2	A	349	ADP	4	0
2	E	349	ADP	5	0
2	C	349	ADP	2	0
2	B	349	ADP	4	0

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	300/348 (86%)	-0.13	0 100 100	33, 71, 121, 156	0
1	B	300/348 (86%)	-0.04	2 (0%) 87 81	51, 94, 138, 177	0
1	C	300/348 (86%)	-0.03	1 (0%) 94 92	51, 88, 134, 175	0
1	D	300/348 (86%)	-0.08	1 (0%) 94 92	52, 91, 141, 176	0
1	E	300/348 (86%)	-0.07	1 (0%) 94 92	38, 74, 124, 165	0
1	F	300/348 (86%)	-0.08	1 (0%) 94 92	34, 64, 114, 155	0
All	All	1800/2088 (86%)	-0.07	6 (0%) 94 92	33, 82, 131, 177	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	129	PHE	3.3
1	B	262	TYR	2.9
1	D	127	LEU	2.9
1	F	67	ASN	2.6
1	E	320	ARG	2.2

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](#)

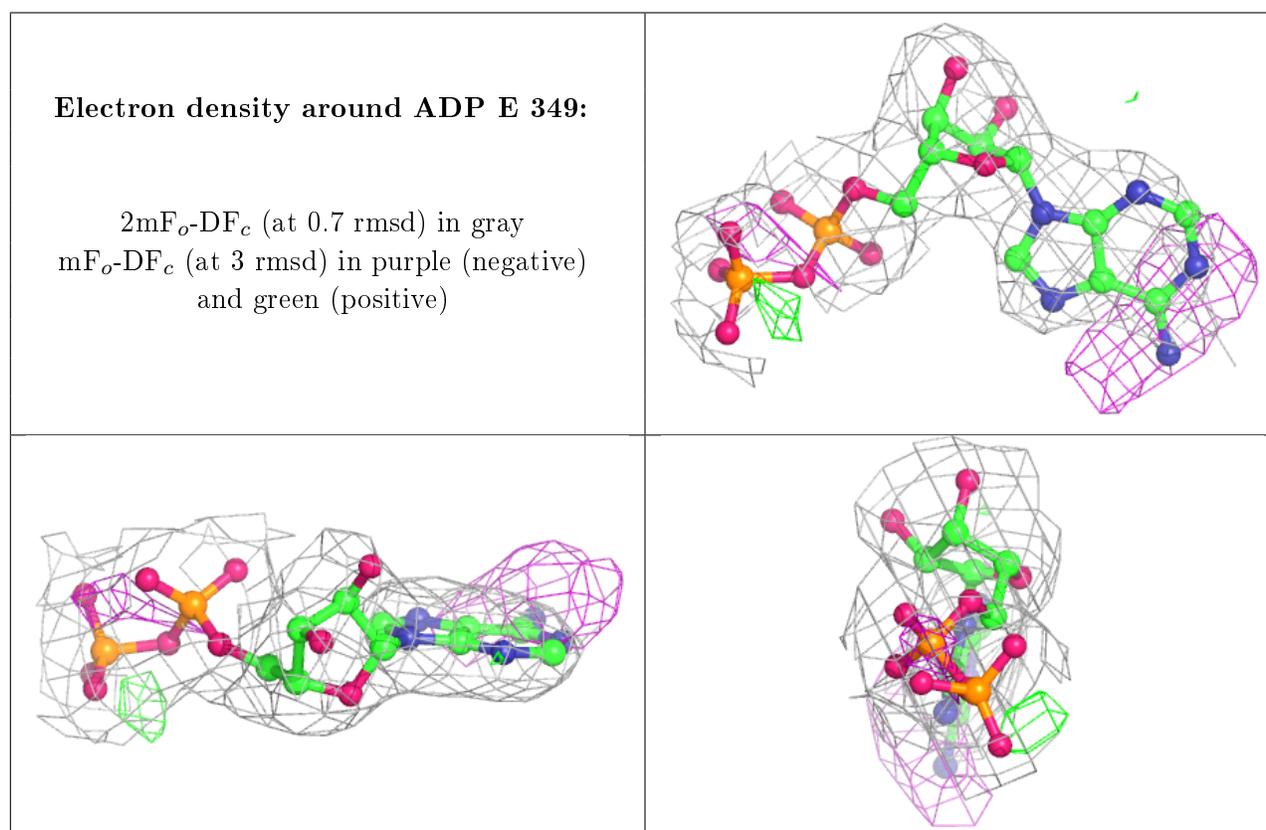
There are no carbohydrates in this entry.

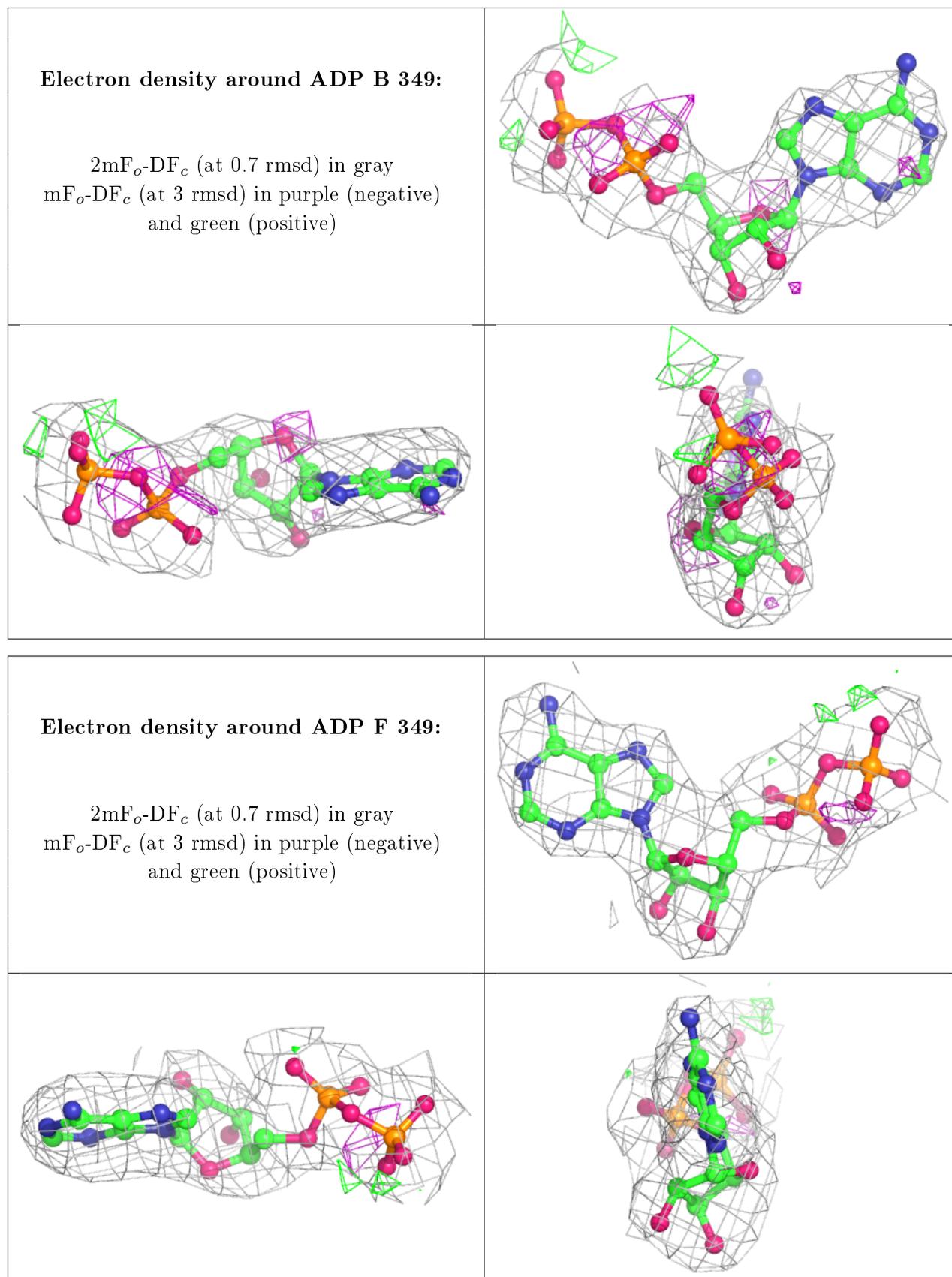
6.4 Ligands [i](#)

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	ADP	E	349	27/27	0.92	0.23	58,58,58,58	0
2	ADP	B	349	27/27	0.93	0.22	75,75,75,75	0
2	ADP	F	349	27/27	0.95	0.21	64,64,64,64	0
2	ADP	D	349	27/27	0.96	0.20	74,74,74,74	0
2	ADP	C	349	27/27	0.96	0.19	75,75,75,75	0
2	ADP	A	349	27/27	0.96	0.19	71,71,71,71	0

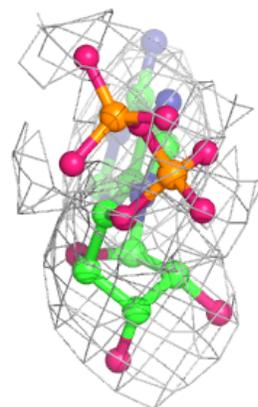
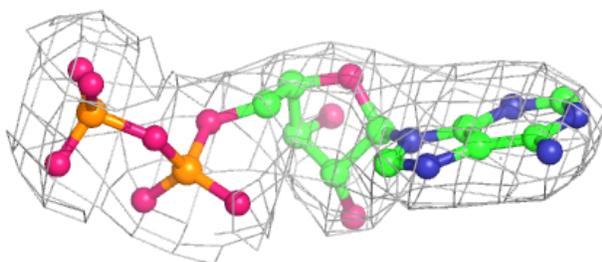
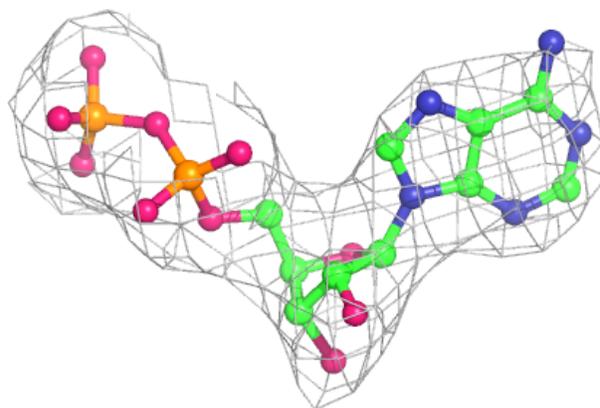
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



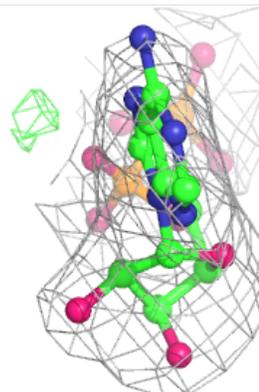
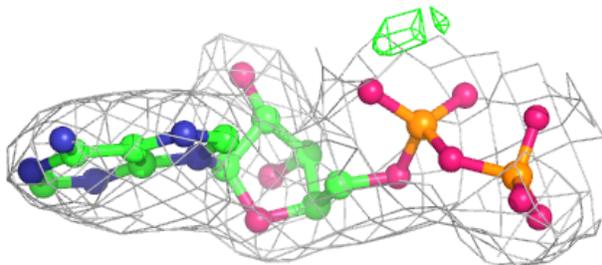
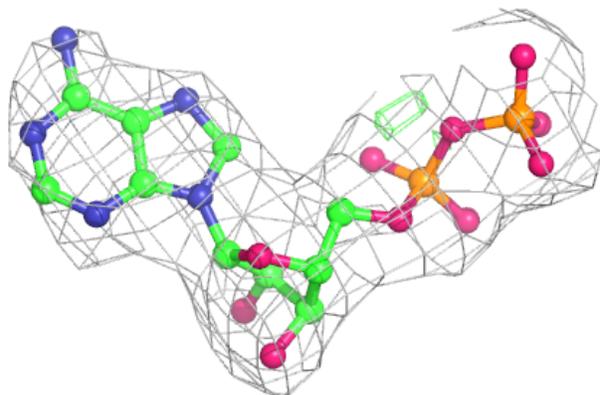


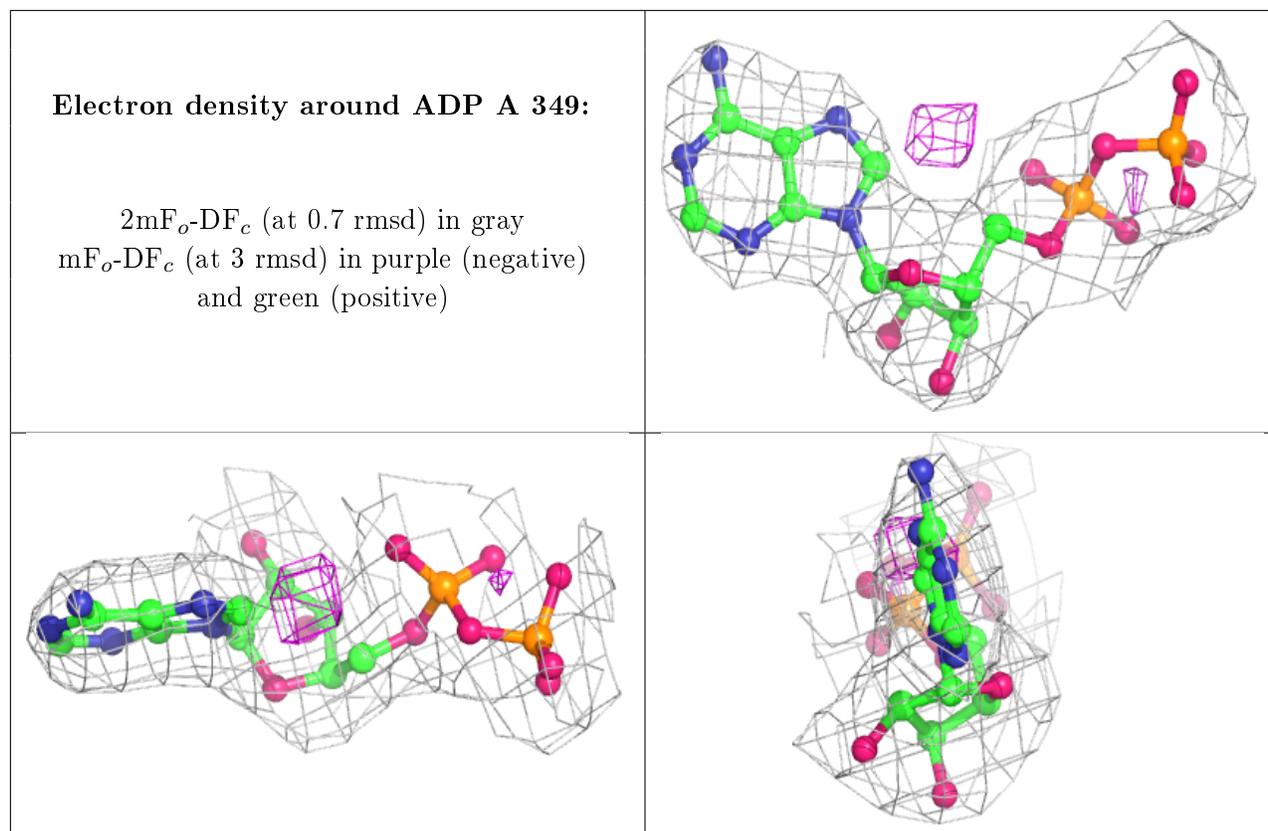
Electron density around ADP D 349:

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

**Electron density around ADP C 349:**

$2mF_o-DF_c$ (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.