



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2024 – 12:34 AM EST

PDB ID : 4GI7  
Title : Crystal structure of *Klebsiella pneumoniae* pantothenate kinase in complex with a pantothenate analogue  
Authors : Li, B.; Tempel, W.; Smil, D.; Bolshan, Y.; Hong, B.S.; Park, H.W.; Structural Genomics Consortium (SGC)  
Deposited on : 2012-08-08  
Resolution : 1.95 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

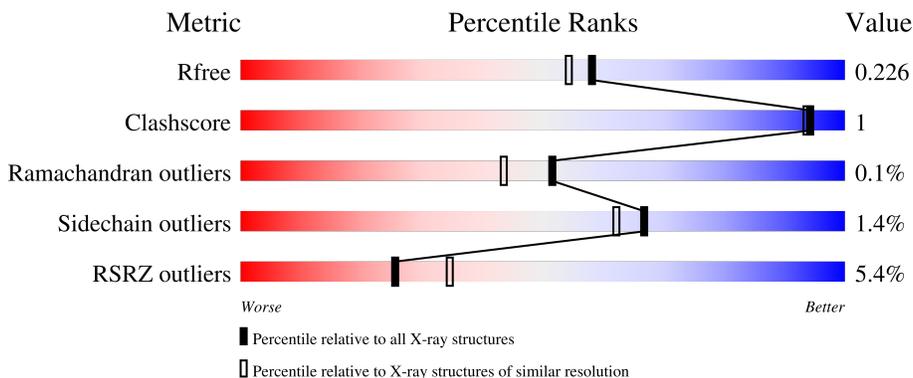
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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  $\geq 3$ , 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	334	 7% 89% 7%
1	B	334	 7% 88% 7%
1	C	334	 4% 87% 5% 7%
1	D	334	 2% 88% 8%

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Mol	Chain	Length	Quality of chain
1	E	334	
1	F	334	
1	G	334	
1	H	334	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	UNX	G	1408	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21291 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 Pantothenate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	309	2499	1600	431	461	7	0	0	0
1	C	309	2499	1600	431	461	7	0	0	0
1	B	309	2502	1602	431	462	7	0	1	0
1	D	308	2491	1594	430	460	7	0	0	0
1	E	304	2463	1578	426	453	6	0	0	0
1	F	309	2499	1600	431	461	7	0	0	0
1	G	308	2491	1594	430	460	7	0	0	0
1	H	303	2452	1572	422	452	6	0	0	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	983	MET	-	expression tag	UNP B5XYG3
A	984	HIS	-	expression tag	UNP B5XYG3
A	985	HIS	-	expression tag	UNP B5XYG3
A	986	HIS	-	expression tag	UNP B5XYG3
A	987	HIS	-	expression tag	UNP B5XYG3
A	988	HIS	-	expression tag	UNP B5XYG3
A	989	HIS	-	expression tag	UNP B5XYG3
A	990	SER	-	expression tag	UNP B5XYG3
A	991	SER	-	expression tag	UNP B5XYG3
A	992	GLY	-	expression tag	UNP B5XYG3
A	993	ARG	-	expression tag	UNP B5XYG3
A	994	GLU	-	expression tag	UNP B5XYG3
A	995	ASN	-	expression tag	UNP B5XYG3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	996	LEU	-	expression tag	UNP B5XYG3
A	997	TYR	-	expression tag	UNP B5XYG3
A	998	PHE	-	expression tag	UNP B5XYG3
A	999	GLN	-	expression tag	UNP B5XYG3
A	1000	GLY	-	expression tag	UNP B5XYG3
C	983	MET	-	expression tag	UNP B5XYG3
C	984	HIS	-	expression tag	UNP B5XYG3
C	985	HIS	-	expression tag	UNP B5XYG3
C	986	HIS	-	expression tag	UNP B5XYG3
C	987	HIS	-	expression tag	UNP B5XYG3
C	988	HIS	-	expression tag	UNP B5XYG3
C	989	HIS	-	expression tag	UNP B5XYG3
C	990	SER	-	expression tag	UNP B5XYG3
C	991	SER	-	expression tag	UNP B5XYG3
C	992	GLY	-	expression tag	UNP B5XYG3
C	993	ARG	-	expression tag	UNP B5XYG3
C	994	GLU	-	expression tag	UNP B5XYG3
C	995	ASN	-	expression tag	UNP B5XYG3
C	996	LEU	-	expression tag	UNP B5XYG3
C	997	TYR	-	expression tag	UNP B5XYG3
C	998	PHE	-	expression tag	UNP B5XYG3
C	999	GLN	-	expression tag	UNP B5XYG3
C	1000	GLY	-	expression tag	UNP B5XYG3
B	983	MET	-	expression tag	UNP B5XYG3
B	984	HIS	-	expression tag	UNP B5XYG3
B	985	HIS	-	expression tag	UNP B5XYG3
B	986	HIS	-	expression tag	UNP B5XYG3
B	987	HIS	-	expression tag	UNP B5XYG3
B	988	HIS	-	expression tag	UNP B5XYG3
B	989	HIS	-	expression tag	UNP B5XYG3
B	990	SER	-	expression tag	UNP B5XYG3
B	991	SER	-	expression tag	UNP B5XYG3
B	992	GLY	-	expression tag	UNP B5XYG3
B	993	ARG	-	expression tag	UNP B5XYG3
B	994	GLU	-	expression tag	UNP B5XYG3
B	995	ASN	-	expression tag	UNP B5XYG3
B	996	LEU	-	expression tag	UNP B5XYG3
B	997	TYR	-	expression tag	UNP B5XYG3
B	998	PHE	-	expression tag	UNP B5XYG3
B	999	GLN	-	expression tag	UNP B5XYG3
B	1000	GLY	-	expression tag	UNP B5XYG3
D	983	MET	-	expression tag	UNP B5XYG3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	984	HIS	-	expression tag	UNP B5XYG3
D	985	HIS	-	expression tag	UNP B5XYG3
D	986	HIS	-	expression tag	UNP B5XYG3
D	987	HIS	-	expression tag	UNP B5XYG3
D	988	HIS	-	expression tag	UNP B5XYG3
D	989	HIS	-	expression tag	UNP B5XYG3
D	990	SER	-	expression tag	UNP B5XYG3
D	991	SER	-	expression tag	UNP B5XYG3
D	992	GLY	-	expression tag	UNP B5XYG3
D	993	ARG	-	expression tag	UNP B5XYG3
D	994	GLU	-	expression tag	UNP B5XYG3
D	995	ASN	-	expression tag	UNP B5XYG3
D	996	LEU	-	expression tag	UNP B5XYG3
D	997	TYR	-	expression tag	UNP B5XYG3
D	998	PHE	-	expression tag	UNP B5XYG3
D	999	GLN	-	expression tag	UNP B5XYG3
D	1000	GLY	-	expression tag	UNP B5XYG3
E	983	MET	-	expression tag	UNP B5XYG3
E	984	HIS	-	expression tag	UNP B5XYG3
E	985	HIS	-	expression tag	UNP B5XYG3
E	986	HIS	-	expression tag	UNP B5XYG3
E	987	HIS	-	expression tag	UNP B5XYG3
E	988	HIS	-	expression tag	UNP B5XYG3
E	989	HIS	-	expression tag	UNP B5XYG3
E	990	SER	-	expression tag	UNP B5XYG3
E	991	SER	-	expression tag	UNP B5XYG3
E	992	GLY	-	expression tag	UNP B5XYG3
E	993	ARG	-	expression tag	UNP B5XYG3
E	994	GLU	-	expression tag	UNP B5XYG3
E	995	ASN	-	expression tag	UNP B5XYG3
E	996	LEU	-	expression tag	UNP B5XYG3
E	997	TYR	-	expression tag	UNP B5XYG3
E	998	PHE	-	expression tag	UNP B5XYG3
E	999	GLN	-	expression tag	UNP B5XYG3
E	1000	GLY	-	expression tag	UNP B5XYG3
F	983	MET	-	expression tag	UNP B5XYG3
F	984	HIS	-	expression tag	UNP B5XYG3
F	985	HIS	-	expression tag	UNP B5XYG3
F	986	HIS	-	expression tag	UNP B5XYG3
F	987	HIS	-	expression tag	UNP B5XYG3
F	988	HIS	-	expression tag	UNP B5XYG3
F	989	HIS	-	expression tag	UNP B5XYG3

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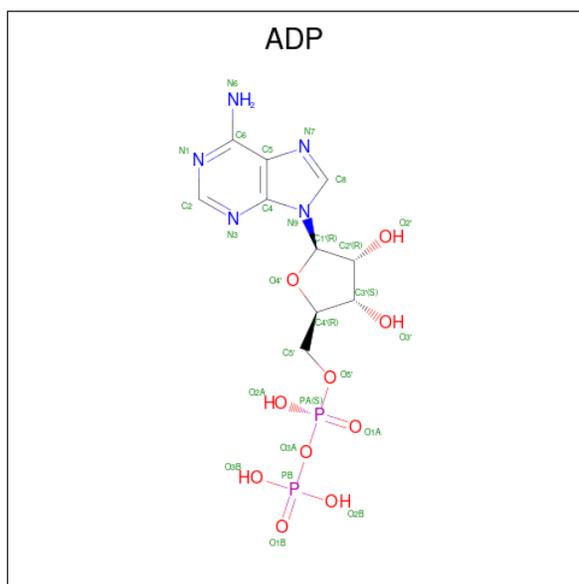
Chain	Residue	Modelled	Actual	Comment	Reference
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F	991	SER	-	expression tag	UNP B5XYG3
F	992	GLY	-	expression tag	UNP B5XYG3
F	993	ARG	-	expression tag	UNP B5XYG3
F	994	GLU	-	expression tag	UNP B5XYG3
F	995	ASN	-	expression tag	UNP B5XYG3
F	996	LEU	-	expression tag	UNP B5XYG3
F	997	TYR	-	expression tag	UNP B5XYG3
F	998	PHE	-	expression tag	UNP B5XYG3
F	999	GLN	-	expression tag	UNP B5XYG3
F	1000	GLY	-	expression tag	UNP B5XYG3
G	983	MET	-	expression tag	UNP B5XYG3
G	984	HIS	-	expression tag	UNP B5XYG3
G	985	HIS	-	expression tag	UNP B5XYG3
G	986	HIS	-	expression tag	UNP B5XYG3
G	987	HIS	-	expression tag	UNP B5XYG3
G	988	HIS	-	expression tag	UNP B5XYG3
G	989	HIS	-	expression tag	UNP B5XYG3
G	990	SER	-	expression tag	UNP B5XYG3
G	991	SER	-	expression tag	UNP B5XYG3
G	992	GLY	-	expression tag	UNP B5XYG3
G	993	ARG	-	expression tag	UNP B5XYG3
G	994	GLU	-	expression tag	UNP B5XYG3
G	995	ASN	-	expression tag	UNP B5XYG3
G	996	LEU	-	expression tag	UNP B5XYG3
G	997	TYR	-	expression tag	UNP B5XYG3
G	998	PHE	-	expression tag	UNP B5XYG3
G	999	GLN	-	expression tag	UNP B5XYG3
G	1000	GLY	-	expression tag	UNP B5XYG3
H	983	MET	-	expression tag	UNP B5XYG3
H	984	HIS	-	expression tag	UNP B5XYG3
H	985	HIS	-	expression tag	UNP B5XYG3
H	986	HIS	-	expression tag	UNP B5XYG3
H	987	HIS	-	expression tag	UNP B5XYG3
H	988	HIS	-	expression tag	UNP B5XYG3
H	989	HIS	-	expression tag	UNP B5XYG3
H	990	SER	-	expression tag	UNP B5XYG3
H	991	SER	-	expression tag	UNP B5XYG3
H	992	GLY	-	expression tag	UNP B5XYG3
H	993	ARG	-	expression tag	UNP B5XYG3
H	994	GLU	-	expression tag	UNP B5XYG3
H	995	ASN	-	expression tag	UNP B5XYG3

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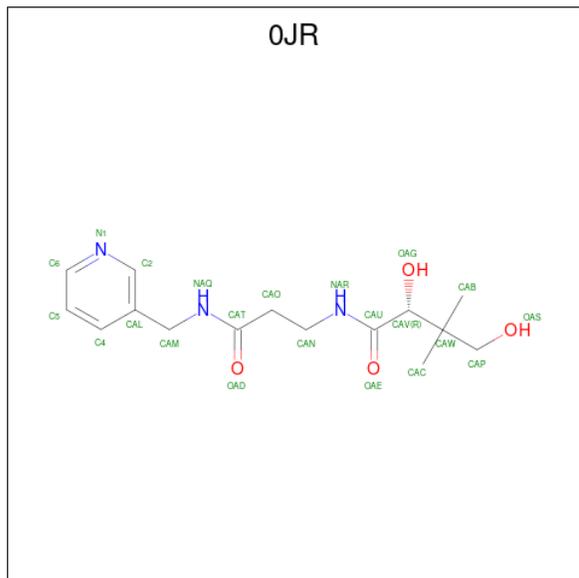
Chain	Residue	Modelled	Actual	Comment	Reference
H	996	LEU	-	expression tag	UNP B5XYG3
H	997	TYR	-	expression tag	UNP B5XYG3
H	998	PHE	-	expression tag	UNP B5XYG3
H	999	GLN	-	expression tag	UNP B5XYG3
H	1000	GLY	-	expression tag	UNP B5XYG3

- 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	C	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	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		
2	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is (2R)-2,4-dihydroxy-3,3-dimethyl-N-{3-oxo-3-[(pyridin-3-ylmethyl)amino]propyl}butanamide (three-letter code: OJR) (formula: C<sub>15</sub>H<sub>23</sub>N<sub>3</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	22	15	3	4	0	0
3	C	1	22	15	3	4	0	0
3	B	1	22	15	3	4	0	0
3	D	1	22	15	3	4	0	1
3	F	1	22	15	3	4	0	1

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	X	0	0
			4	4		
4	C	7	Total	X	0	0
			7	7		
4	B	5	Total	X	0	0
			5	5		
4	D	8	Total	X	0	0
			8	8		
4	E	3	Total	X	0	0
			3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	7	Total X 7 7	0	0
4	G	7	Total X 7 7	0	0
4	H	4	Total X 4 4	0	0

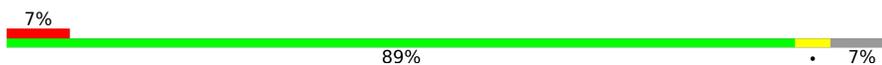
- Molecule 5 is water.

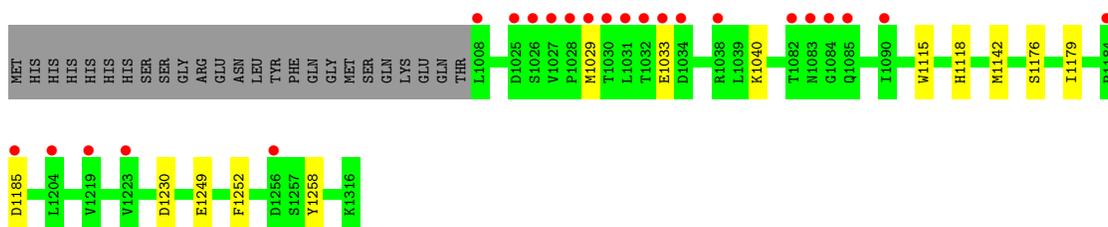
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	125	Total O 125 125	0	0
5	C	158	Total O 158 158	0	0
5	B	126	Total O 126 126	0	0
5	D	136	Total O 136 136	0	0
5	E	67	Total O 67 67	0	0
5	F	113	Total O 113 113	0	0
5	G	153	Total O 153 153	0	0
5	H	145	Total O 146 146	0	1

### 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.

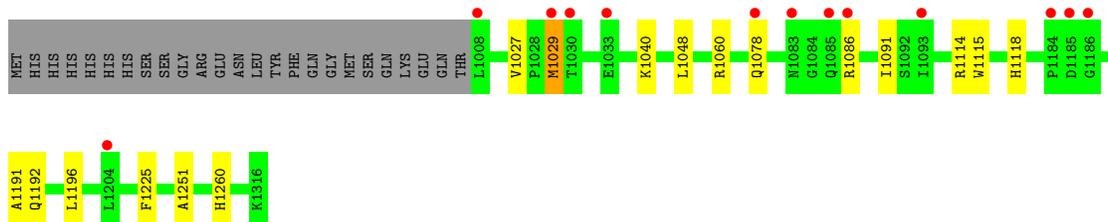
- Molecule 1: Pantothenate kinase

Chain A: 

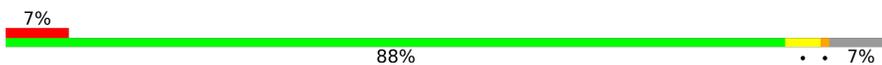


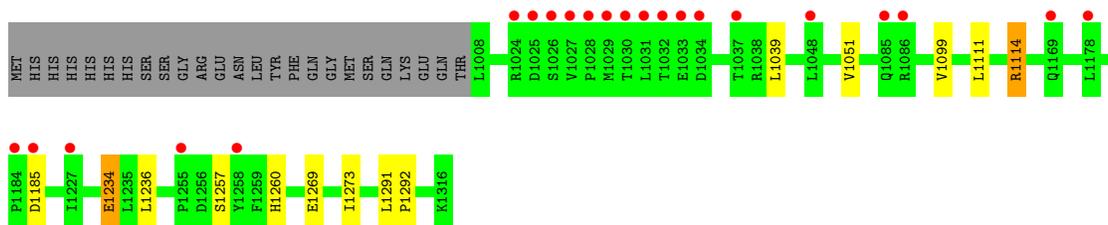
- Molecule 1: Pantothenate kinase

Chain C: 



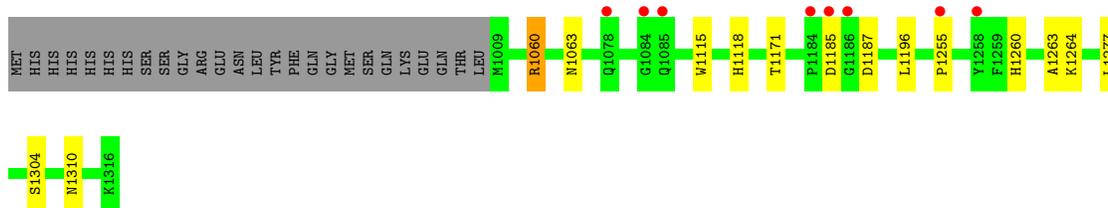
- Molecule 1: Pantothenate kinase

Chain B: 

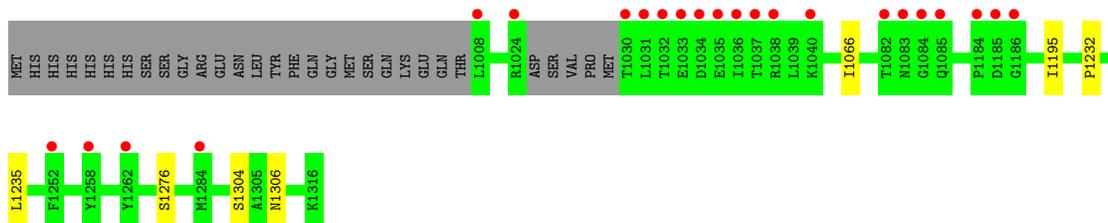
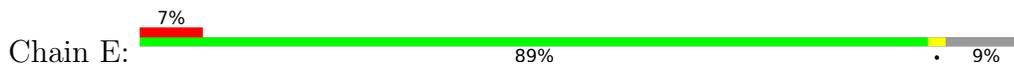


- Molecule 1: Pantothenate kinase

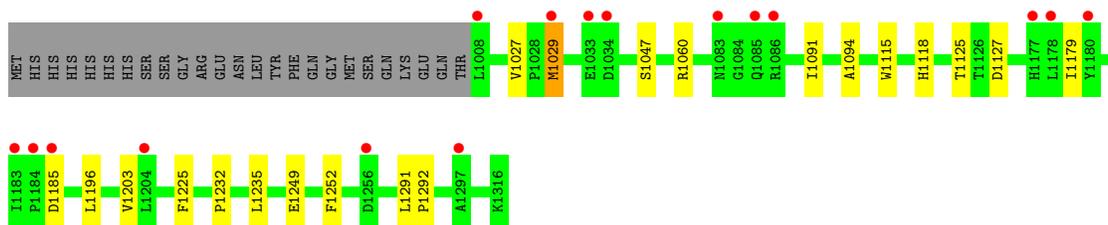
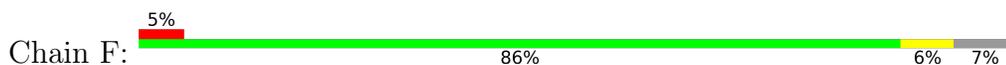
Chain D: 



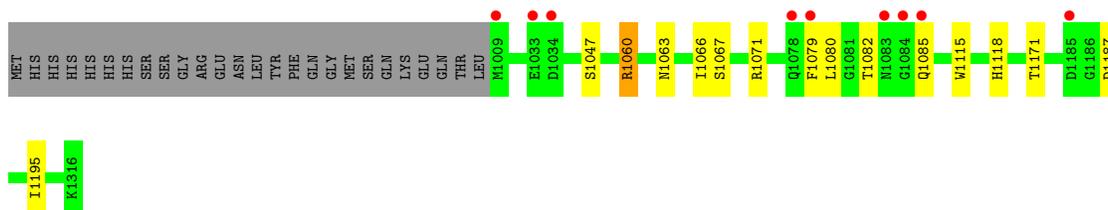
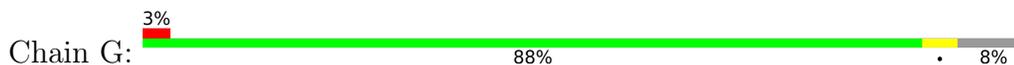
- Molecule 1: Pantothenate kinase



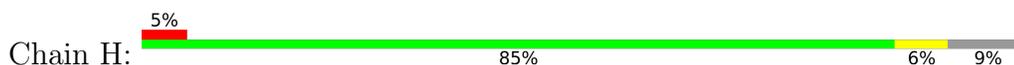
- Molecule 1: Pantothenate kinase



- Molecule 1: Pantothenate kinase



- Molecule 1: Pantothenate kinase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	127.93Å 130.94Å 193.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.68 – 1.95 39.68 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.68-1.95) 99.8 (39.68-1.95)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 1.95Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.186 , 0.220 0.194 , 0.226	Depositor DCC
$R_{free}$ test set	11741 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtrriage
Anisotropy	0.045	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.049 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21291	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 0JR, UNX, 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	0.51	0/2558	0.66	1/3471 (0.0%)
1	B	0.48	0/2564	0.64	0/3479
1	C	0.54	0/2558	0.71	3/3471 (0.1%)
1	D	0.53	0/2550	0.66	0/3460
1	E	0.46	0/2520	0.61	0/3417
1	F	0.52	0/2558	0.68	2/3471 (0.1%)
1	G	0.54	0/2550	0.69	0/3460
1	H	0.52	0/2509	0.66	1/3403 (0.0%)
All	All	0.51	0/20367	0.67	7/27632 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	1029	MET	CB-CG-SD	6.19	130.98	112.40
1	A	1230	ASP	CB-CG-OD1	6.11	123.80	118.30
1	F	1029	MET	CB-CA-C	5.70	121.79	110.40
1	C	1029	MET	CB-CG-SD	5.69	129.47	112.40
1	C	1029	MET	CG-SD-CE	5.44	108.90	100.20

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	2499	0	2500	5	0
1	B	2502	0	2506	6	0
1	C	2499	0	2500	9	0
1	D	2491	0	2489	7	0
1	E	2463	0	2465	2	0
1	F	2499	0	2501	10	0
1	G	2491	0	2489	9	0
1	H	2452	0	2452	10	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
2	C	27	0	12	0	0
2	D	27	0	12	0	0
2	E	27	0	12	0	0
2	F	27	0	12	0	0
2	G	27	0	12	0	0
2	H	27	0	12	0	0
3	A	22	0	23	1	0
3	B	22	0	23	0	0
3	C	22	0	23	0	0
3	D	22	0	7	1	0
3	F	22	0	7	0	0
4	A	4	0	0	0	0
4	B	5	0	0	0	0
4	C	7	0	0	0	0
4	D	8	0	0	0	0
4	E	3	0	0	0	0
4	F	7	0	0	0	0
4	G	7	0	0	0	0
4	H	4	0	0	0	0
5	A	125	0	0	1	0
5	B	126	0	0	1	0
5	C	158	0	0	1	0
5	D	136	0	0	0	0
5	E	67	0	0	0	0
5	F	113	0	0	0	0
5	G	153	0	0	0	0
5	H	146	0	0	0	0
All	All	21291	0	20081	54	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 1.

The worst 5 of 54 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:1060:ARG:HH12	1:D:1063:ASN:HD22	1.35	0.75
1:C:1078:GLN:HG3	5:C:1585:HOH:O	1.96	0.65
1:F:1125:THR:HG22	1:F:1127:ASP:H	1.65	0.61
1:G:1060:ARG:HH12	1:G:1063:ASN:HD22	1.48	0.61
1:G:1079:PHE:CZ	1:H:1023:LEU:HB3	2.37	0.59

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	307/334 (92%)	302 (98%)	5 (2%)	0	100	100
1	B	308/334 (92%)	300 (97%)	8 (3%)	0	100	100
1	C	307/334 (92%)	301 (98%)	6 (2%)	0	100	100
1	D	306/334 (92%)	300 (98%)	5 (2%)	1 (0%)	41	30
1	E	300/334 (90%)	295 (98%)	5 (2%)	0	100	100
1	F	307/334 (92%)	302 (98%)	5 (2%)	0	100	100
1	G	306/334 (92%)	297 (97%)	8 (3%)	1 (0%)	41	30
1	H	299/334 (90%)	292 (98%)	7 (2%)	0	100	100
All	All	2440/2672 (91%)	2389 (98%)	49 (2%)	2 (0%)	51	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1263	ALA
1	G	1085	GLN

### 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	278/301 (92%)	274 (99%)	4 (1%)	67	62
1	B	279/301 (93%)	274 (98%)	5 (2%)	59	53
1	C	278/301 (92%)	276 (99%)	2 (1%)	84	82
1	D	277/301 (92%)	273 (99%)	4 (1%)	67	62
1	E	273/301 (91%)	270 (99%)	3 (1%)	73	71
1	F	278/301 (92%)	274 (99%)	4 (1%)	67	62
1	G	277/301 (92%)	274 (99%)	3 (1%)	73	71
1	H	272/301 (90%)	266 (98%)	6 (2%)	52	44
All	All	2212/2408 (92%)	2181 (99%)	31 (1%)	67	62

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1264	LYS
1	H	1032	THR
1	E	1306	ASN
1	H	1192	GLN
1	G	1082	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	1073	GLN
1	H	1311	GLN
1	F	1205	GLN
1	H	1063	ASN
1	F	1014	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 58 ligands modelled in this entry, 45 are unknown - leaving 13 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	ADP	F	1401	-	24,29,29	1.01	1 (4%)	29,45,45	1.06	2 (6%)
2	ADP	E	1401	-	24,29,29	0.93	0	29,45,45	1.34	3 (10%)
2	ADP	C	1401	-	24,29,29	1.02	1 (4%)	29,45,45	1.43	3 (10%)
3	0JR	C	1402	-	20,22,22	1.73	4 (20%)	27,29,29	1.31	3 (11%)
2	ADP	H	1401	-	24,29,29	1.05	2 (8%)	29,45,45	1.44	3 (10%)
2	ADP	G	1401	-	24,29,29	1.04	3 (12%)	29,45,45	1.51	6 (20%)
3	0JR	B	1402	-	20,22,22	1.59	3 (15%)	27,29,29	1.05	1 (3%)
2	ADP	D	1401	-	24,29,29	1.06	2 (8%)	29,45,45	1.34	4 (13%)
2	ADP	A	1401	-	24,29,29	1.18	1 (4%)	29,45,45	1.28	1 (3%)
2	ADP	B	1401	-	24,29,29	1.06	1 (4%)	29,45,45	1.31	5 (17%)
3	0JR	A	1402	-	20,22,22	1.59	3 (15%)	27,29,29	1.13	2 (7%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	F	1401	-	-	1/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	E	1401	-	-	1/12/32/32	0/3/3/3
2	ADP	C	1401	-	-	1/12/32/32	0/3/3/3
3	0JR	C	1402	-	-	6/24/24/24	0/1/1/1
2	ADP	H	1401	-	-	1/12/32/32	0/3/3/3
2	ADP	G	1401	-	-	1/12/32/32	0/3/3/3
3	0JR	B	1402	-	-	2/24/24/24	0/1/1/1
2	ADP	D	1401	-	-	2/12/32/32	0/3/3/3
2	ADP	A	1401	-	-	2/12/32/32	0/3/3/3
2	ADP	B	1401	-	-	0/12/32/32	0/3/3/3
3	0JR	A	1402	-	-	2/24/24/24	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1402	0JR	CAM-CAL	-4.89	1.40	1.51
3	A	1402	0JR	CAM-CAL	-4.87	1.40	1.51
3	C	1402	0JR	C2-N1	4.18	1.43	1.34
3	C	1402	0JR	CAM-CAL	-3.93	1.42	1.51
2	A	1401	ADP	C2-N3	3.25	1.37	1.32

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1401	ADP	N3-C2-N1	-4.61	121.47	128.68
2	E	1401	ADP	N3-C2-N1	-4.34	121.90	128.68
2	C	1401	ADP	N3-C2-N1	-4.19	122.13	128.68
2	A	1401	ADP	N3-C2-N1	-4.01	122.42	128.68
2	G	1401	ADP	N3-C2-N1	-3.55	123.13	128.68

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

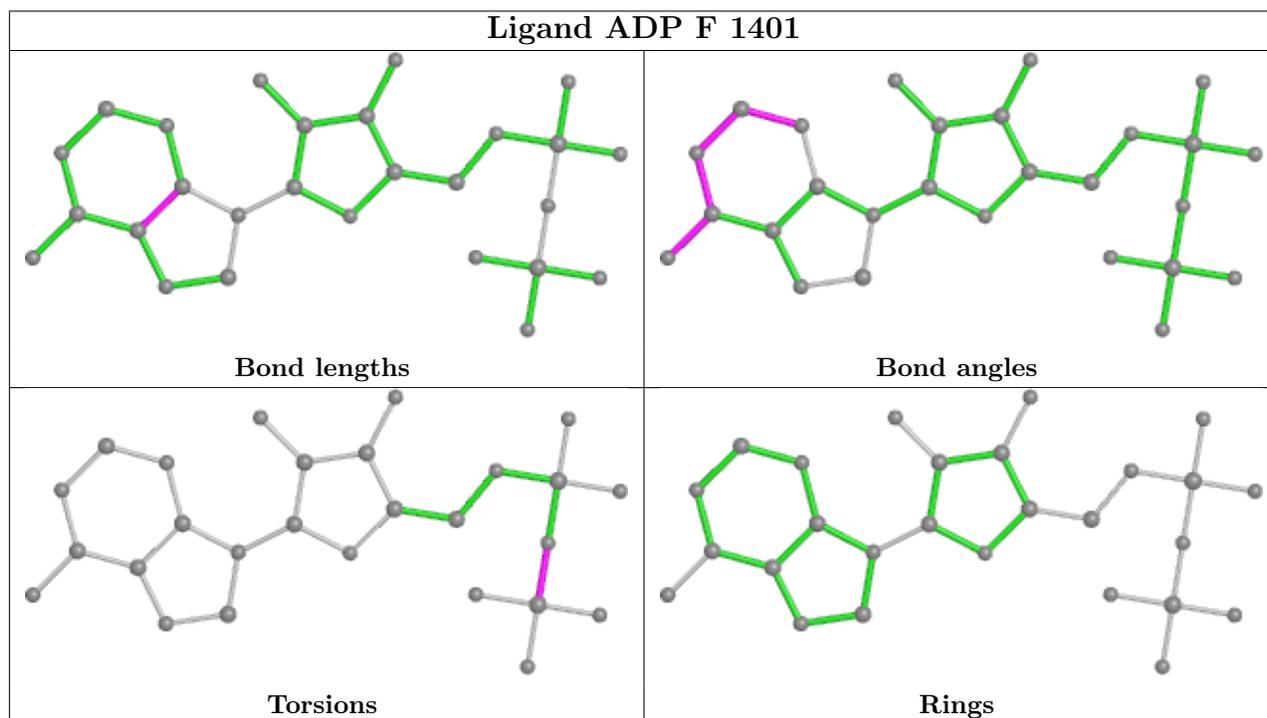
Mol	Chain	Res	Type	Atoms
2	A	1401	ADP	PA-O3A-PB-O2B
2	D	1401	ADP	PA-O3A-PB-O2B
2	E	1401	ADP	PA-O3A-PB-O2B
2	G	1401	ADP	PA-O3A-PB-O2B
3	C	1402	0JR	OAS-CAP-CAW-CAV

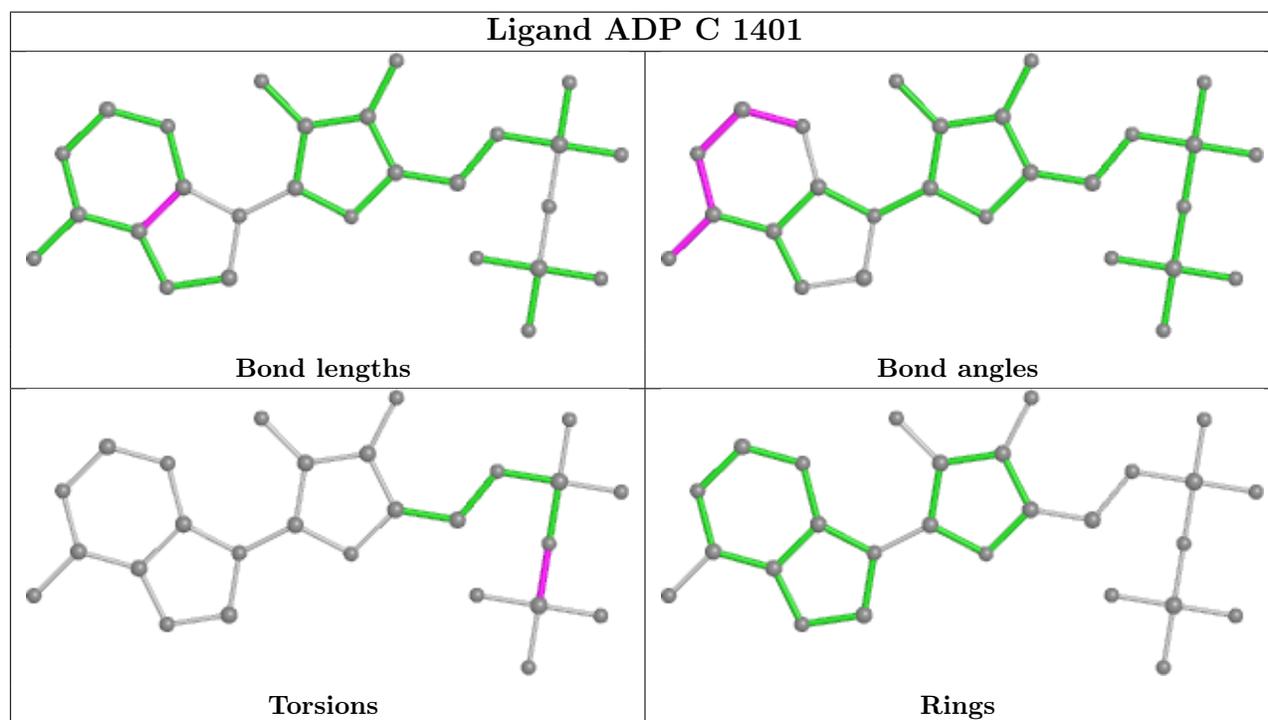
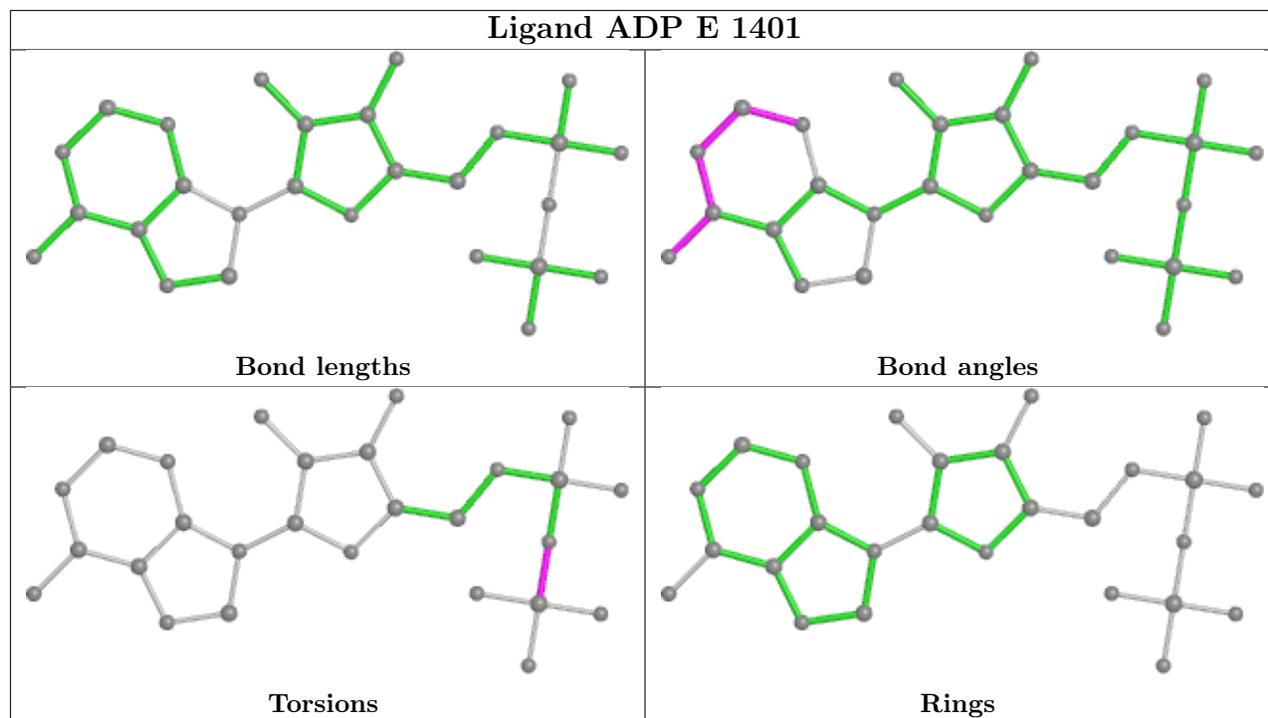
There are no ring outliers.

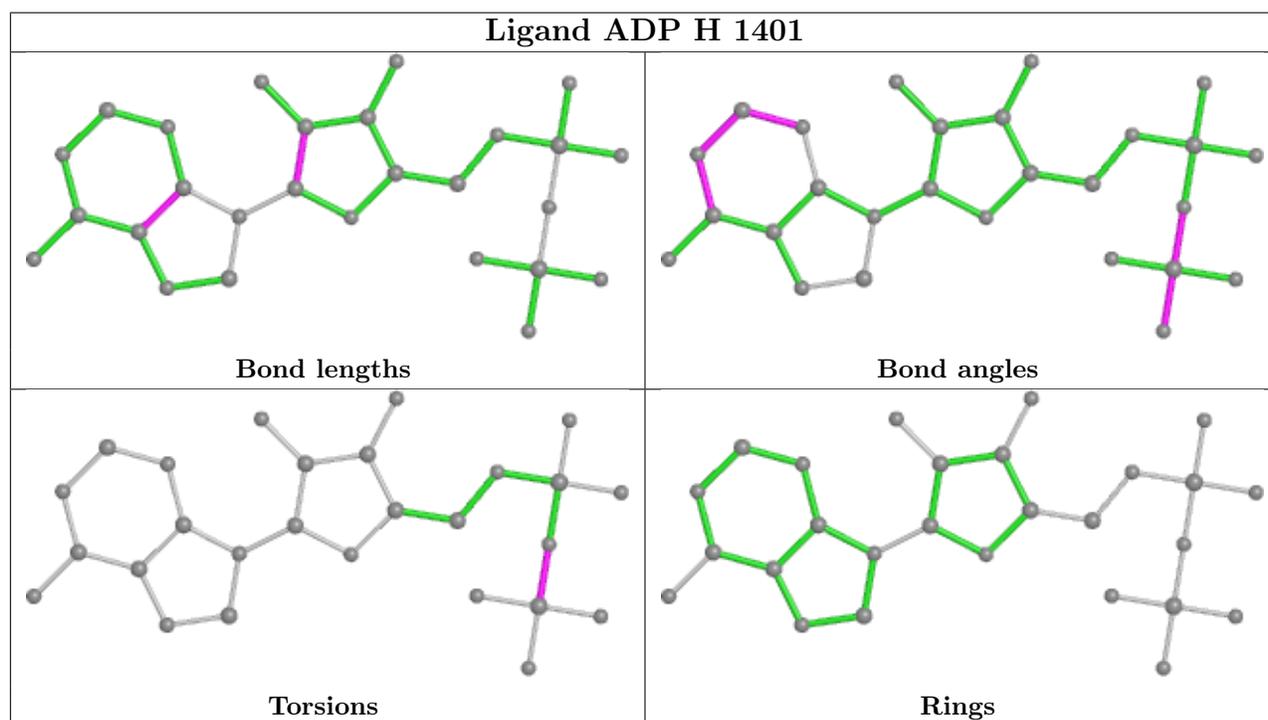
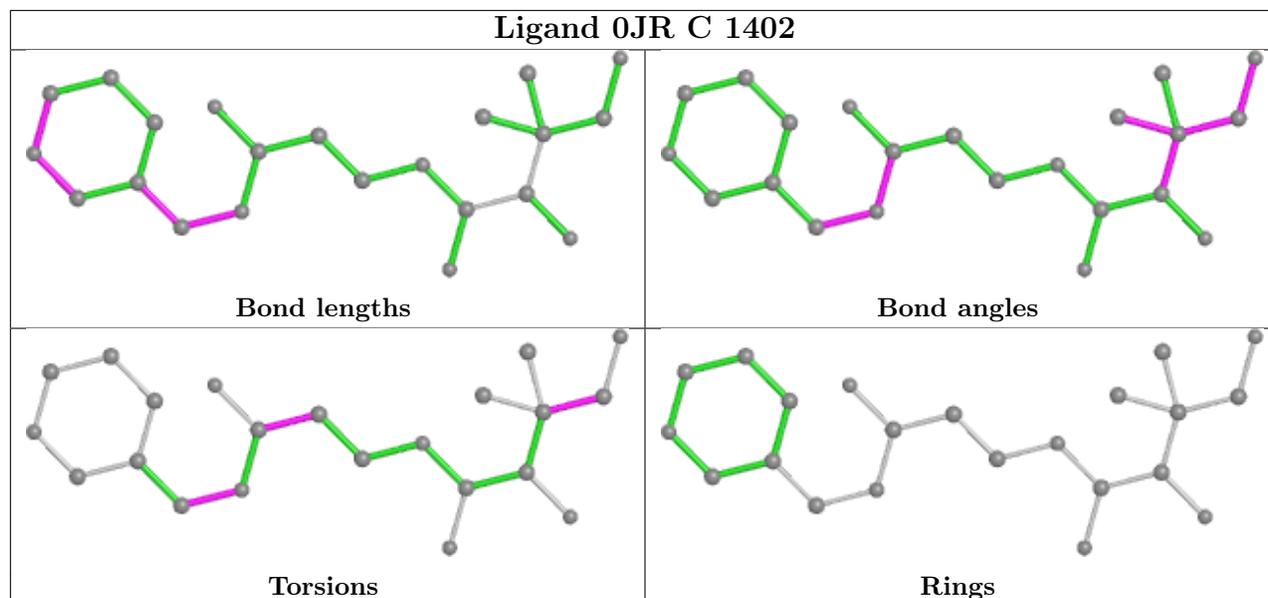
1 monomer is involved in 1 short contact:

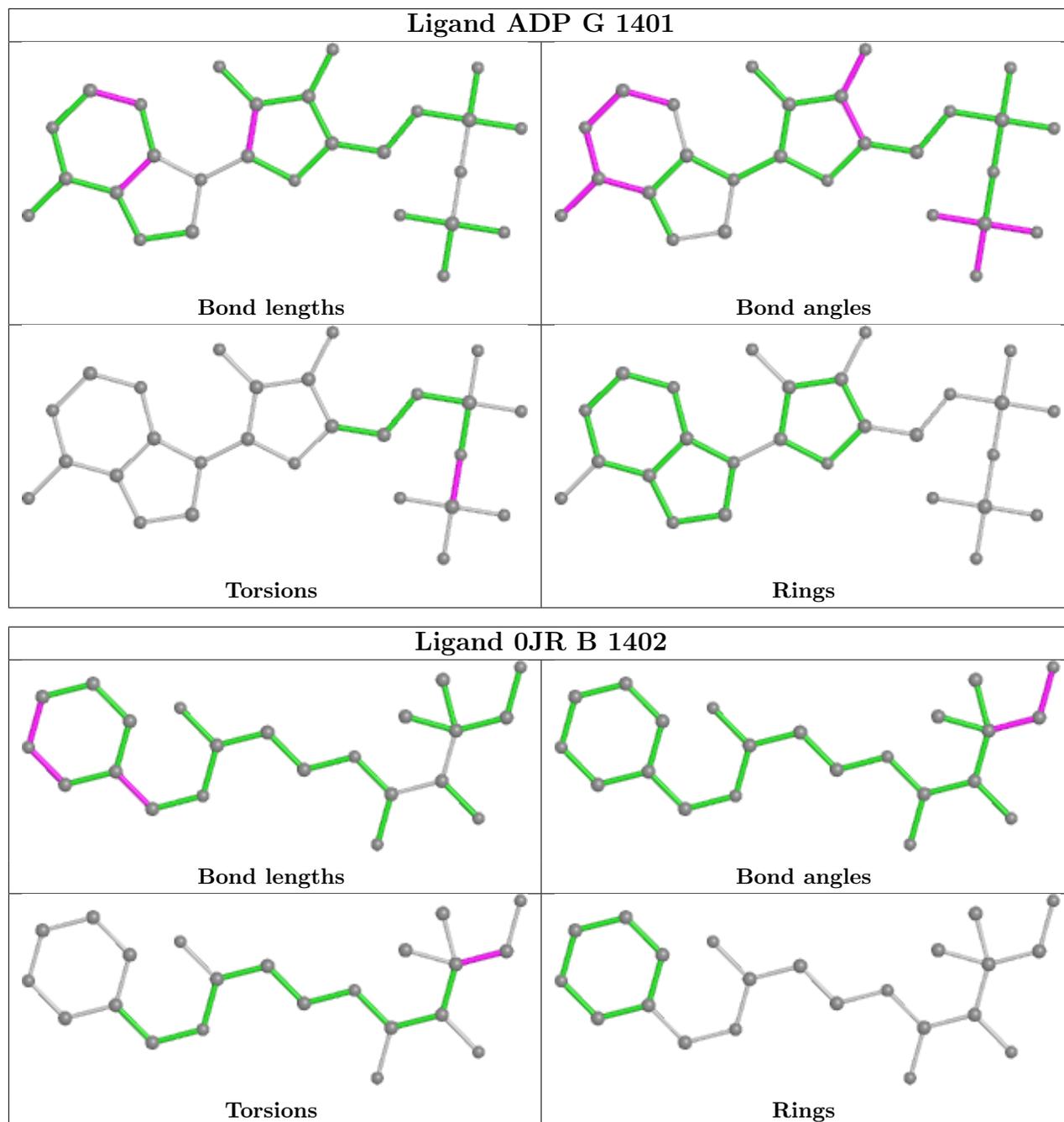
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1402	OJR	1	0

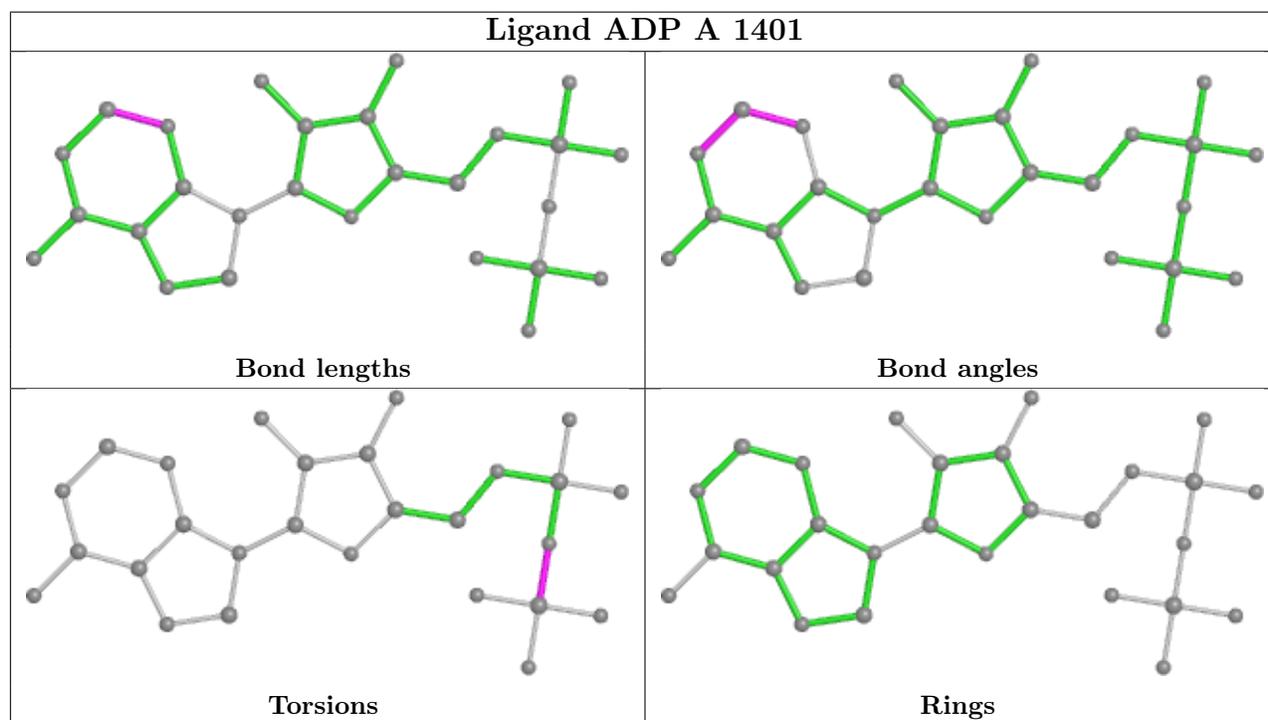
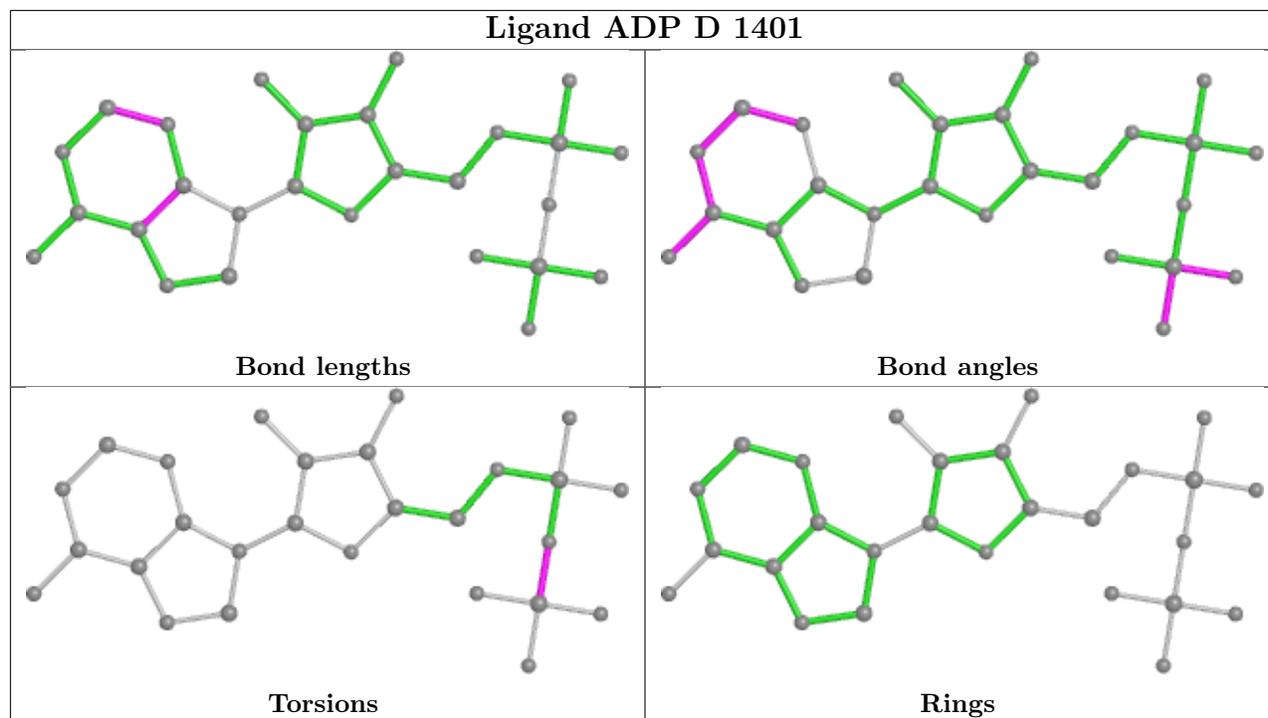
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

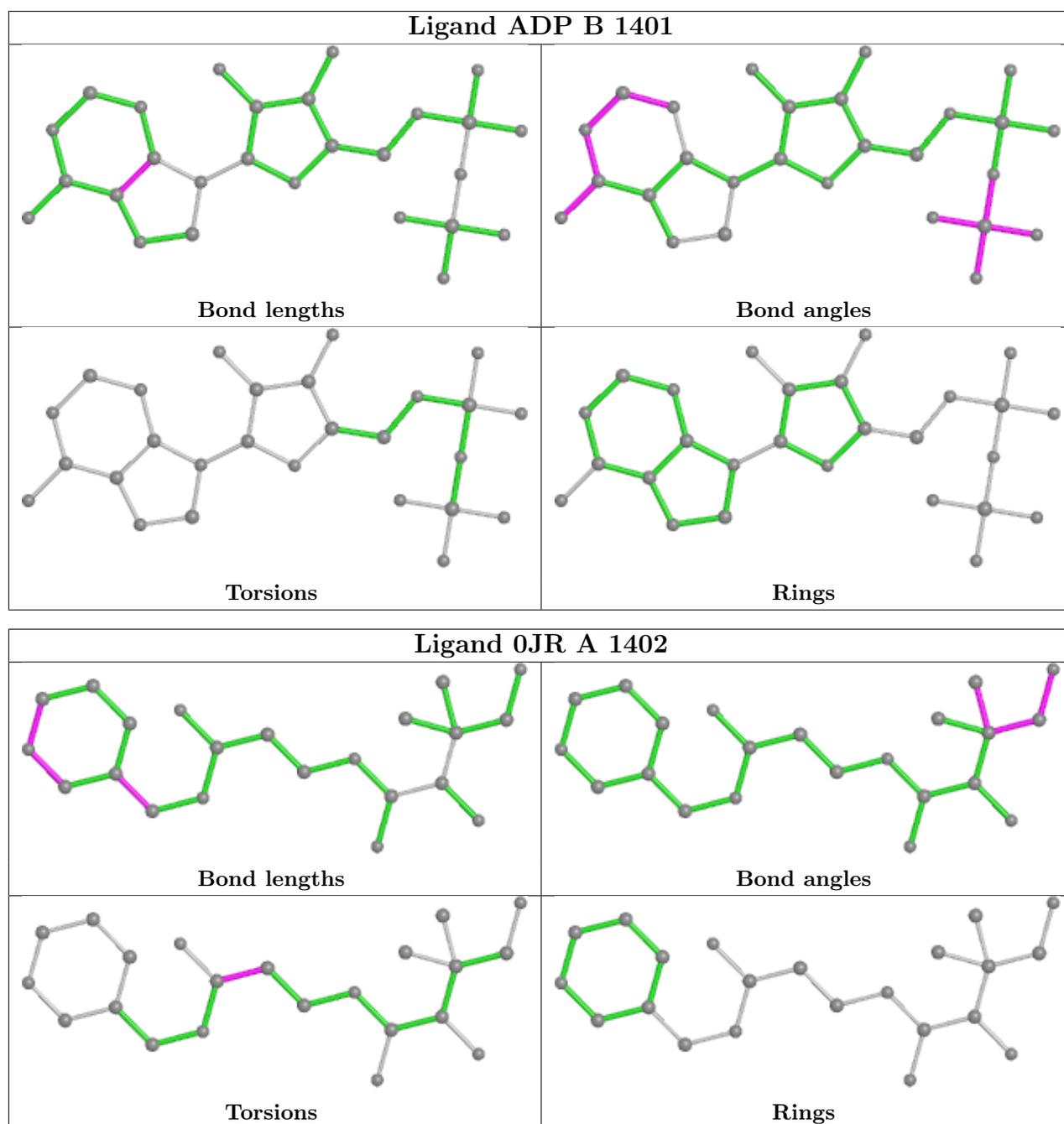












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	309/334 (92%)	0.24	23 (7%) 14 22	17, 28, 63, 110	0
1	B	309/334 (92%)	0.29	22 (7%) 16 24	19, 33, 71, 95	0
1	C	309/334 (92%)	0.12	13 (4%) 36 45	16, 27, 49, 66	0
1	D	308/334 (92%)	0.13	8 (2%) 56 65	16, 28, 54, 71	0
1	E	304/334 (91%)	0.45	23 (7%) 13 21	21, 38, 64, 94	0
1	F	309/334 (92%)	0.16	16 (5%) 27 37	17, 29, 57, 77	0
1	G	308/334 (92%)	0.07	9 (2%) 51 60	17, 27, 48, 86	0
1	H	303/334 (90%)	0.17	18 (5%) 22 30	17, 28, 58, 77	0
All	All	2459/2672 (92%)	0.20	132 (5%) 25 34	16, 29, 60, 110	0

The worst 5 of 132 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1026	SER	8.9
1	A	1027	VAL	8.7
1	B	1026	SER	8.0
1	G	1084	GLY	5.7
1	A	1028	PRO	5.6

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	UNX	G	1408	1/1	0.78	0.54	49,49,49,49	0
4	UNX	H	1405	1/1	0.78	0.24	36,36,36,36	0
4	UNX	C	1409	1/1	0.81	0.77	29,29,29,29	0
3	0JR	D	1402[A]	22/22	0.82	0.20	35,44,71,74	0
3	0JR	F	1402[A]	22/22	0.83	0.24	46,52,60,61	0
4	UNX	G	1403	1/1	0.83	0.51	34,34,34,34	0
4	UNX	C	1405	1/1	0.83	0.40	41,41,41,41	0
4	UNX	C	1408	1/1	0.83	0.35	31,31,31,31	0
4	UNX	G	1407	1/1	0.84	0.73	38,38,38,38	0
4	UNX	E	1403	1/1	0.84	0.54	40,40,40,40	0
4	UNX	B	1406	1/1	0.84	0.30	39,39,39,39	0
4	UNX	E	1404	1/1	0.85	0.29	34,34,34,34	0
4	UNX	B	1404	1/1	0.86	0.27	37,37,37,37	0
3	0JR	C	1402	22/22	0.86	0.15	35,39,42,45	0
4	UNX	G	1406	1/1	0.88	0.17	36,36,36,36	0
4	UNX	H	1403	1/1	0.88	0.25	36,36,36,36	0
4	UNX	F	1407	1/1	0.88	0.19	28,28,28,28	0
3	0JR	A	1402	22/22	0.90	0.15	29,34,49,51	0
4	UNX	C	1404	1/1	0.90	0.48	31,31,31,31	0
4	UNX	D	1405	1/1	0.91	0.21	31,31,31,31	0
4	UNX	D	1404	1/1	0.91	0.29	35,35,35,35	0
4	UNX	C	1403	1/1	0.92	0.18	29,29,29,29	0
3	0JR	B	1402	22/22	0.92	0.14	38,42,64,65	0
4	UNX	H	1404	1/1	0.92	0.57	32,32,32,32	0
4	UNX	A	1405	1/1	0.92	0.27	40,40,40,40	0
4	UNX	A	1404	1/1	0.93	0.29	22,22,22,22	0
4	UNX	F	1404	1/1	0.93	0.43	33,33,33,33	0
4	UNX	G	1404	1/1	0.93	0.14	23,23,23,23	0
4	UNX	E	1402	1/1	0.94	0.16	29,29,29,29	0
4	UNX	F	1409	1/1	0.94	0.14	16,16,16,16	0
4	UNX	G	1405	1/1	0.94	0.21	33,33,33,33	0
4	UNX	D	1408	1/1	0.95	0.34	35,35,35,35	0
4	UNX	F	1405	1/1	0.95	0.11	22,22,22,22	0
4	UNX	F	1406	1/1	0.95	0.14	32,32,32,32	0
4	UNX	C	1406	1/1	0.95	0.19	25,25,25,25	0
4	UNX	D	1403	1/1	0.95	0.20	32,32,32,32	0
4	UNX	D	1406	1/1	0.95	0.62	42,42,42,42	0

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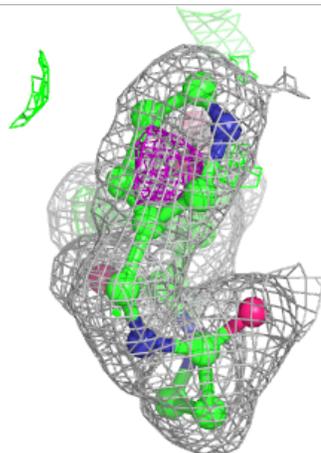
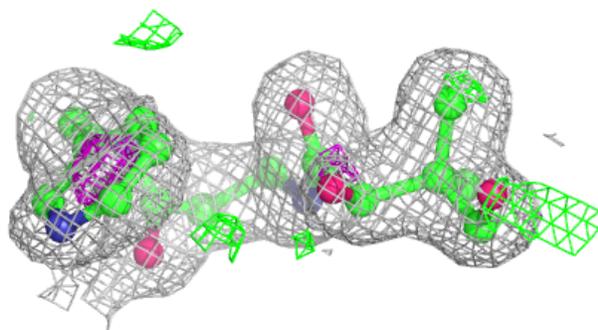
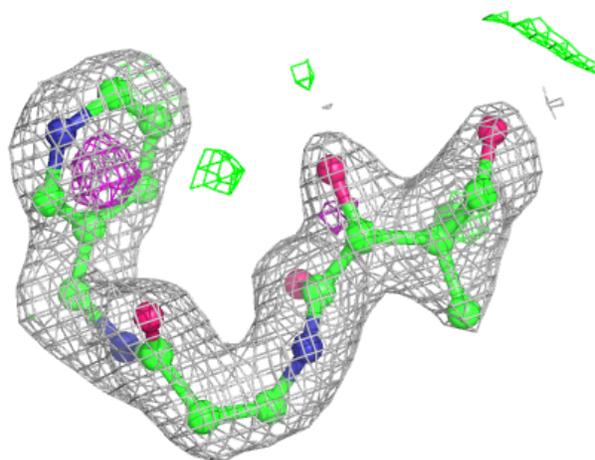
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	UNX	F	1403	1/1	0.95	0.20	33,33,33,33	0
4	UNX	B	1405	1/1	0.96	0.30	30,30,30,30	0
4	UNX	D	1410	1/1	0.96	0.30	23,23,23,23	0
4	UNX	G	1402	1/1	0.96	0.25	23,23,23,23	0
4	UNX	D	1407	1/1	0.96	0.11	21,21,21,21	0
4	UNX	A	1406	1/1	0.97	0.24	32,32,32,32	0
2	ADP	E	1401	27/27	0.97	0.07	30,36,43,44	0
4	UNX	C	1407	1/1	0.97	0.14	25,25,25,25	0
4	UNX	F	1408	1/1	0.97	0.13	25,25,25,25	0
4	UNX	A	1403	1/1	0.97	0.15	22,22,22,22	0
2	ADP	D	1401	27/27	0.98	0.09	21,24,28,29	0
4	UNX	B	1403	1/1	0.98	0.17	28,28,28,28	0
4	UNX	H	1402	1/1	0.98	0.13	23,23,23,23	0
2	ADP	B	1401	27/27	0.98	0.08	24,29,35,36	0
4	UNX	D	1409	1/1	0.98	0.19	25,25,25,25	0
2	ADP	H	1401	27/27	0.98	0.09	22,23,27,27	0
4	UNX	B	1407	1/1	0.99	0.18	28,28,28,28	0
2	ADP	A	1401	27/27	0.99	0.08	17,21,25,28	0
2	ADP	F	1401	27/27	0.99	0.08	20,23,24,25	0
2	ADP	G	1401	27/27	0.99	0.07	20,23,27,29	0
2	ADP	C	1401	27/27	0.99	0.09	19,22,25,25	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.

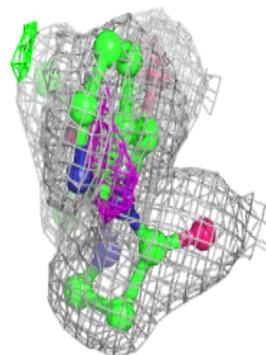
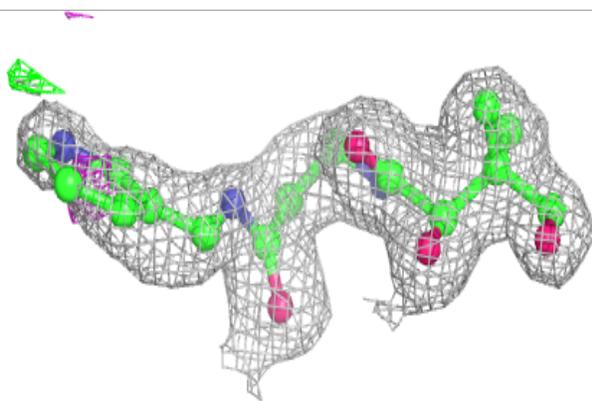
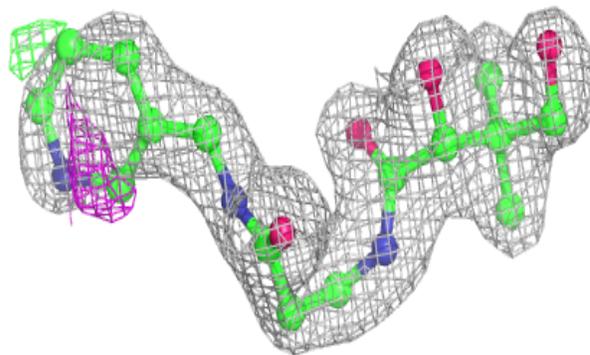
**Electron density around 0JR C 1402:**

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

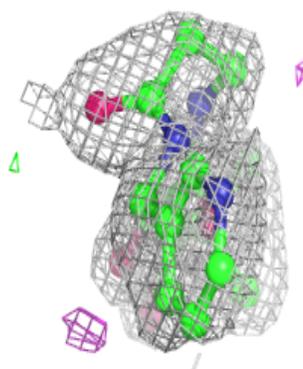
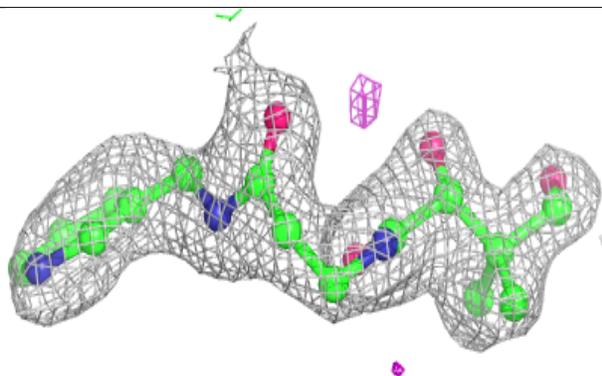
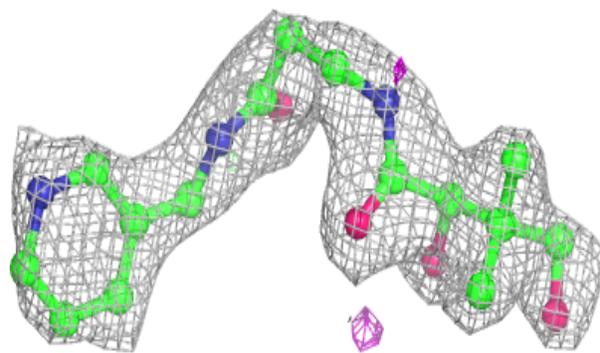


**Electron density around 0JR A 1402:**

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

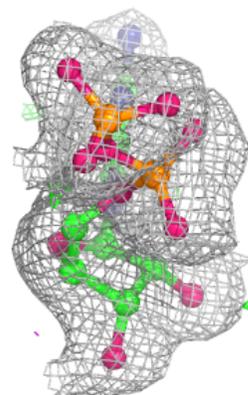
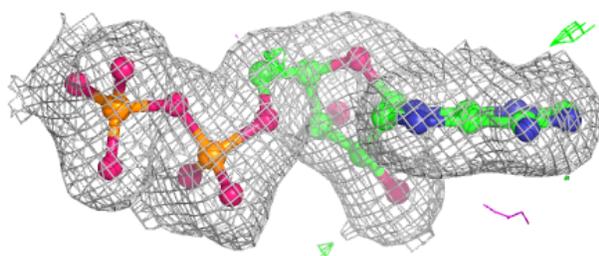
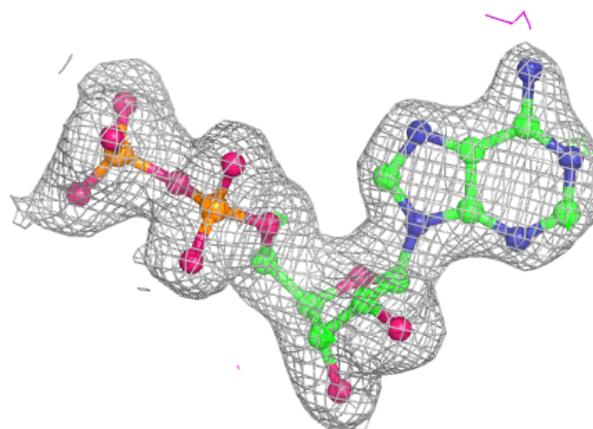
**Electron density around 0JR B 1402:**

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

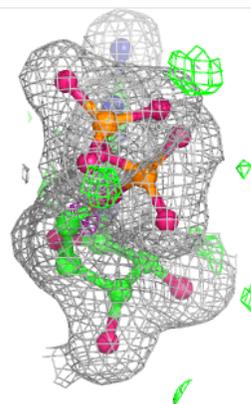
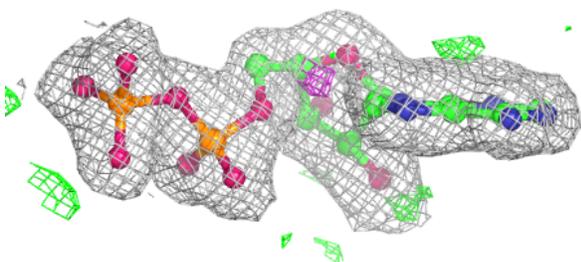
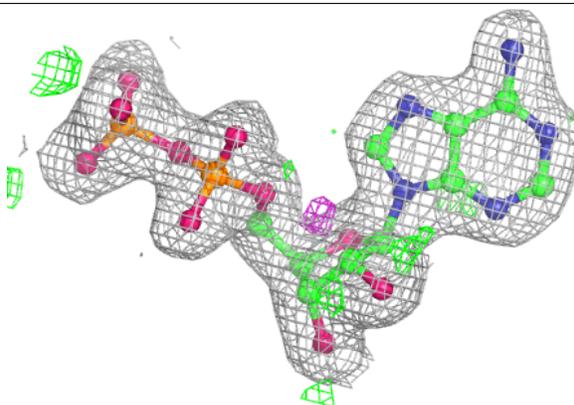


**Electron density around ADP E 1401:**

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

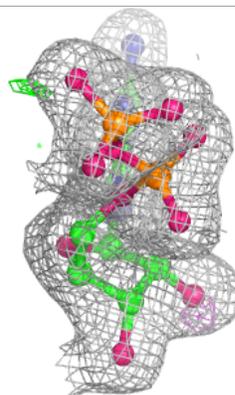
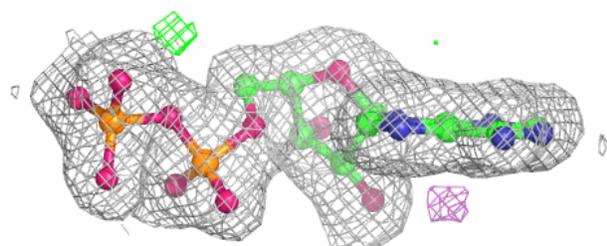
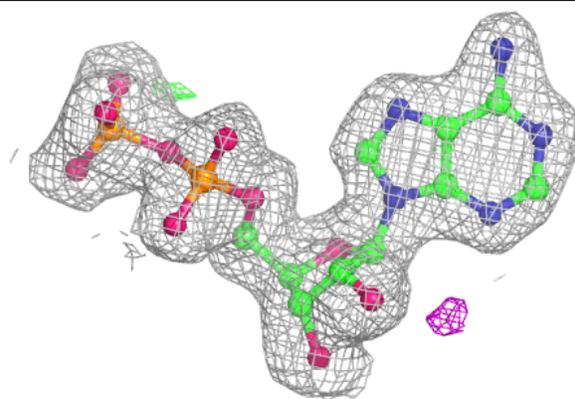
**Electron density around ADP D 1401:**

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

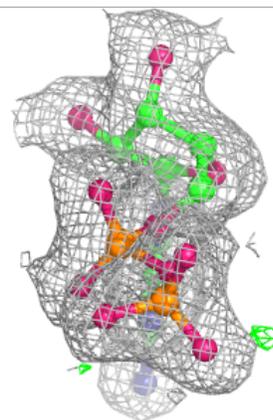
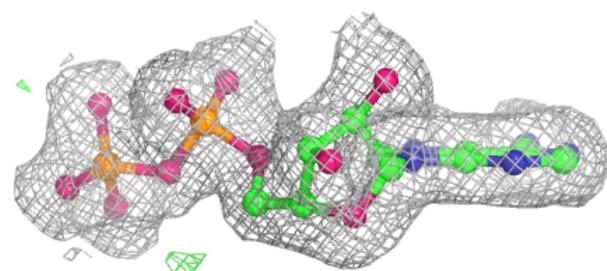
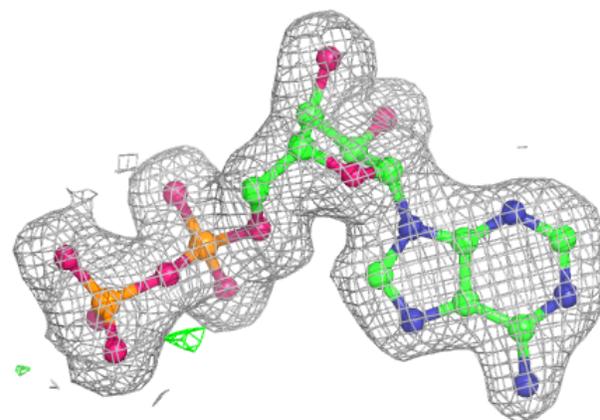


**Electron density around ADP B 1401:**

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

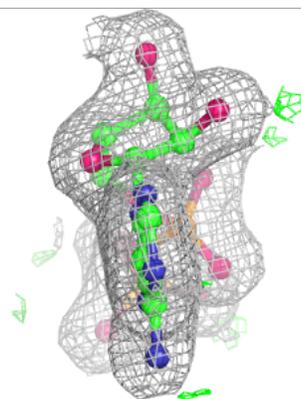
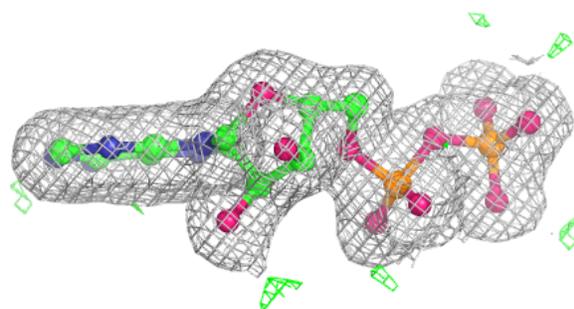
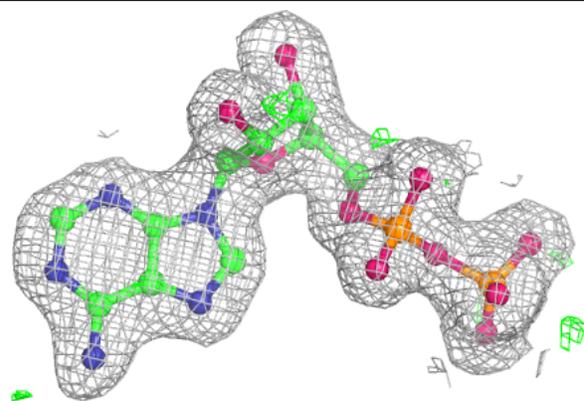
**Electron density around ADP H 1401:**

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

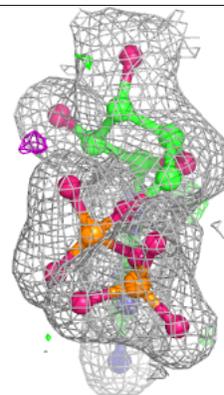
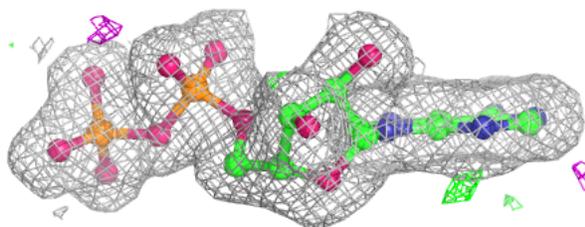
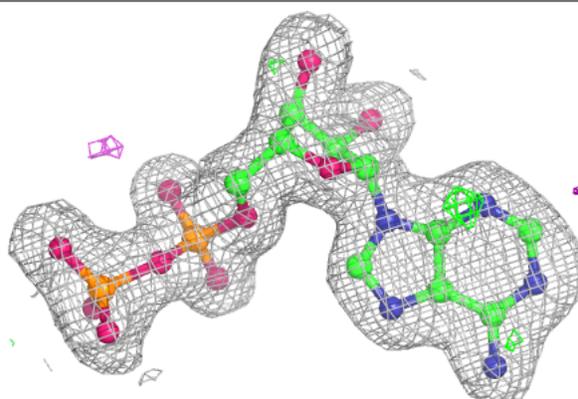


**Electron density around ADP A 1401:**

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

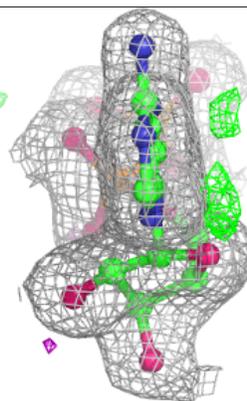
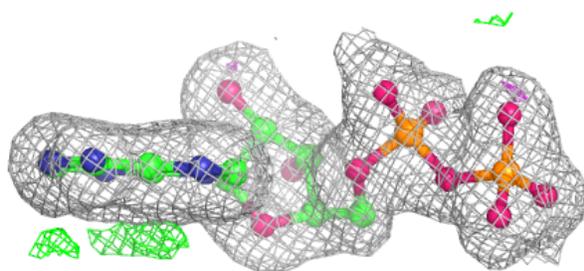
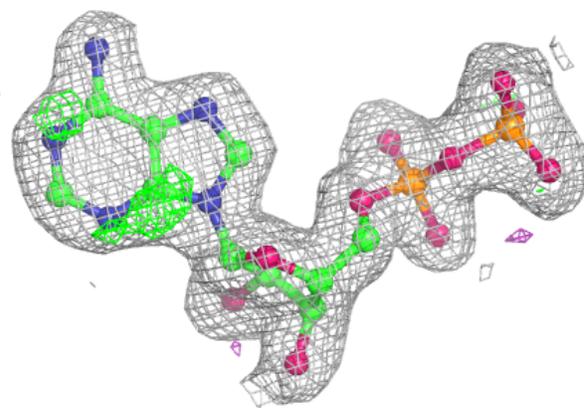
**Electron density around ADP F 1401:**

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

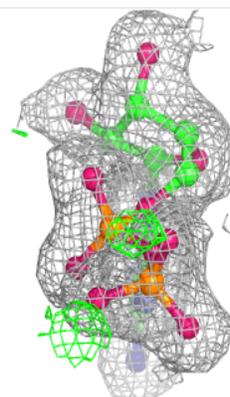
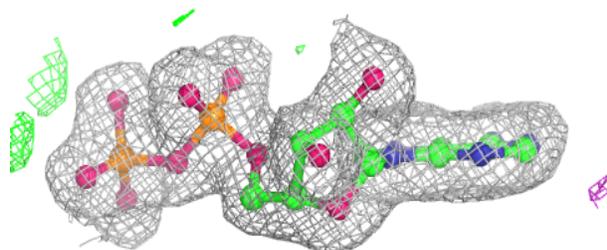
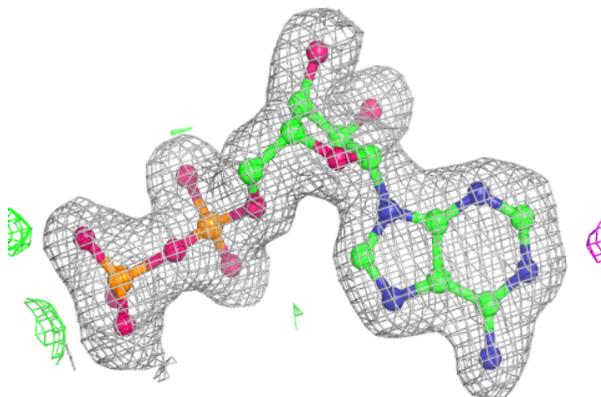


**Electron density around ADP G 1401:**

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

**Electron density around ADP C 1401:**

$2mF_o-DF_c$  (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.