



# wwPDB X-ray Structure Validation Summary Report i

Jan 4, 2024 – 06:13 am GMT

PDB ID : 5DOU  
Title : Crystal Structure of Human Carbamoyl phosphate synthetase I (CPS1), ligand-bound form  
Authors : de Cima, S.; Polo, L.M.; Fita, I.; Rubio, V.  
Deposited on : 2015-09-11  
Resolution : 2.60 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 i 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](#) i) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, 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

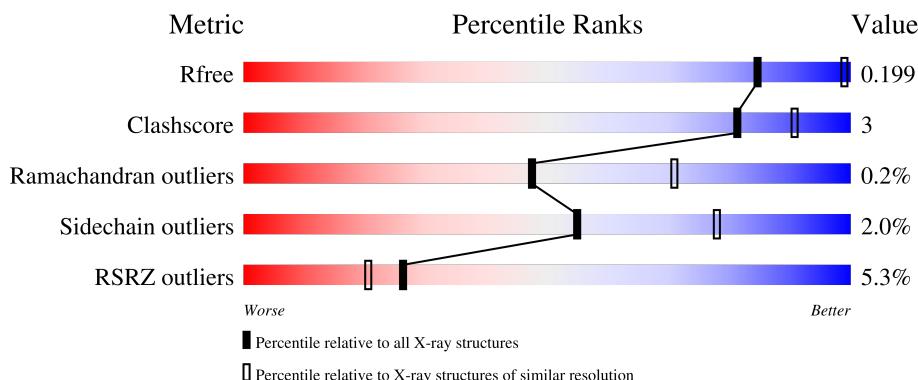
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

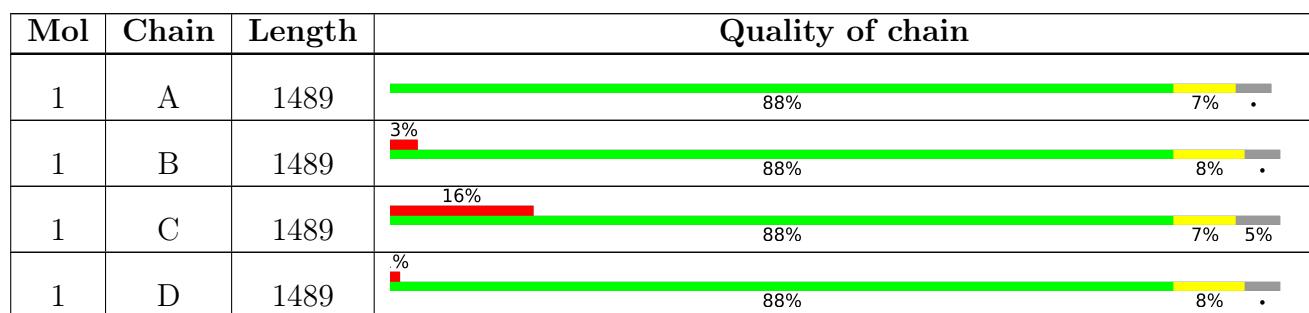
The reported resolution of this entry is 2.60 Å.

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 <sub>free</sub>	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.



## 2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 45021 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 Carbamoyl-phosphate synthase [ammonia], mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	1422	Total	C 10991	N 6980	O 1863	S 2090	58	0	2	0
1	B	1426	Total	C 11018	N 6997	O 1864	S 2098	59	0	0	0
1	C	1421	Total	C 10975	N 6969	O 1859	S 2089	58	0	1	0
1	D	1430	Total	C 11056	N 7023	O 1872	S 2102	59	0	1	0

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MET	-	initiating methionine	UNP P31327
A	13	SER	-	expression tag	UNP P31327
A	14	TYR	-	expression tag	UNP P31327
A	15	TYR	-	expression tag	UNP P31327
A	16	HIS	-	expression tag	UNP P31327
A	17	HIS	-	expression tag	UNP P31327
A	18	HIS	-	expression tag	UNP P31327
A	19	HIS	-	expression tag	UNP P31327
A	20	HIS	-	expression tag	UNP P31327
A	21	HIS	-	expression tag	UNP P31327
A	22	ASP	-	expression tag	UNP P31327
A	23	TYR	-	expression tag	UNP P31327
A	24	ASP	-	expression tag	UNP P31327
A	25	ILE	-	expression tag	UNP P31327
A	26	PRO	-	expression tag	UNP P31327
A	27	THR	-	expression tag	UNP P31327
A	28	THR	-	expression tag	UNP P31327
A	29	GLU	-	expression tag	UNP P31327
A	30	ASN	-	expression tag	UNP P31327
A	31	LEU	-	expression tag	UNP P31327
A	32	TYR	-	expression tag	UNP P31327

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Chain	Residue	Modelled	Actual	Comment	Reference
A	33	PHE	-	expression tag	UNP P31327
A	34	GLN	-	expression tag	UNP P31327
A	35	GLY	-	expression tag	UNP P31327
A	36	ALA	-	expression tag	UNP P31327
A	37	MET	-	expression tag	UNP P31327
A	38	ASP	-	expression tag	UNP P31327
A	39	PRO	-	expression tag	UNP P31327
B	12	MET	-	initiating methionine	UNP P31327
B	13	SER	-	expression tag	UNP P31327
B	14	TYR	-	expression tag	UNP P31327
B	15	TYR	-	expression tag	UNP P31327
B	16	HIS	-	expression tag	UNP P31327
B	17	HIS	-	expression tag	UNP P31327
B	18	HIS	-	expression tag	UNP P31327
B	19	HIS	-	expression tag	UNP P31327
B	20	HIS	-	expression tag	UNP P31327
B	21	HIS	-	expression tag	UNP P31327
B	22	ASP	-	expression tag	UNP P31327
B	23	TYR	-	expression tag	UNP P31327
B	24	ASP	-	expression tag	UNP P31327
B	25	ILE	-	expression tag	UNP P31327
B	26	PRO	-	expression tag	UNP P31327
B	27	THR	-	expression tag	UNP P31327
B	28	THR	-	expression tag	UNP P31327
B	29	GLU	-	expression tag	UNP P31327
B	30	ASN	-	expression tag	UNP P31327
B	31	LEU	-	expression tag	UNP P31327
B	32	TYR	-	expression tag	UNP P31327
B	33	PHE	-	expression tag	UNP P31327
B	34	GLN	-	expression tag	UNP P31327
B	35	GLY	-	expression tag	UNP P31327
B	36	ALA	-	expression tag	UNP P31327
B	37	MET	-	expression tag	UNP P31327
B	38	ASP	-	expression tag	UNP P31327
B	39	PRO	-	expression tag	UNP P31327
C	12	MET	-	initiating methionine	UNP P31327
C	13	SER	-	expression tag	UNP P31327
C	14	TYR	-	expression tag	UNP P31327
C	15	TYR	-	expression tag	UNP P31327
C	16	HIS	-	expression tag	UNP P31327
C	17	HIS	-	expression tag	UNP P31327
C	18	HIS	-	expression tag	UNP P31327

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Chain	Residue	Modelled	Actual	Comment	Reference
C	19	HIS	-	expression tag	UNP P31327
C	20	HIS	-	expression tag	UNP P31327
C	21	HIS	-	expression tag	UNP P31327
C	22	ASP	-	expression tag	UNP P31327
C	23	TYR	-	expression tag	UNP P31327
C	24	ASP	-	expression tag	UNP P31327
C	25	ILE	-	expression tag	UNP P31327
C	26	PRO	-	expression tag	UNP P31327
C	27	THR	-	expression tag	UNP P31327
C	28	THR	-	expression tag	UNP P31327
C	29	GLU	-	expression tag	UNP P31327
C	30	ASN	-	expression tag	UNP P31327
C	31	LEU	-	expression tag	UNP P31327
C	32	TYR	-	expression tag	UNP P31327
C	33	PHE	-	expression tag	UNP P31327
C	34	GLN	-	expression tag	UNP P31327
C	35	GLY	-	expression tag	UNP P31327
C	36	ALA	-	expression tag	UNP P31327
C	37	MET	-	expression tag	UNP P31327
C	38	ASP	-	expression tag	UNP P31327
C	39	PRO	-	expression tag	UNP P31327
D	12	MET	-	initiating methionine	UNP P31327
D	13	SER	-	expression tag	UNP P31327
D	14	TYR	-	expression tag	UNP P31327
D	15	TYR	-	expression tag	UNP P31327
D	16	HIS	-	expression tag	UNP P31327
D	17	HIS	-	expression tag	UNP P31327
D	18	HIS	-	expression tag	UNP P31327
D	19	HIS	-	expression tag	UNP P31327
D	20	HIS	-	expression tag	UNP P31327
D	21	HIS	-	expression tag	UNP P31327
D	22	ASP	-	expression tag	UNP P31327
D	23	TYR	-	expression tag	UNP P31327
D	24	ASP	-	expression tag	UNP P31327
D	25	ILE	-	expression tag	UNP P31327
D	26	PRO	-	expression tag	UNP P31327
D	27	THR	-	expression tag	UNP P31327
D	28	THR	-	expression tag	UNP P31327
D	29	GLU	-	expression tag	UNP P31327
D	30	ASN	-	expression tag	UNP P31327
D	31	LEU	-	expression tag	UNP P31327
D	32	TYR	-	expression tag	UNP P31327

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Chain	Residue	Modelled	Actual	Comment	Reference
D	33	PHE	-	expression tag	UNP P31327
D	34	GLN	-	expression tag	UNP P31327
D	35	GLY	-	expression tag	UNP P31327
D	36	ALA	-	expression tag	UNP P31327
D	37	MET	-	expression tag	UNP P31327
D	38	ASP	-	expression tag	UNP P31327
D	39	PRO	-	expression tag	UNP P31327

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ni 1 1	0	0
2	B	1	Total Ni 1 1	0	0
2	C	1	Total Ni 1 1	0	0
2	D	1	Total Ni 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

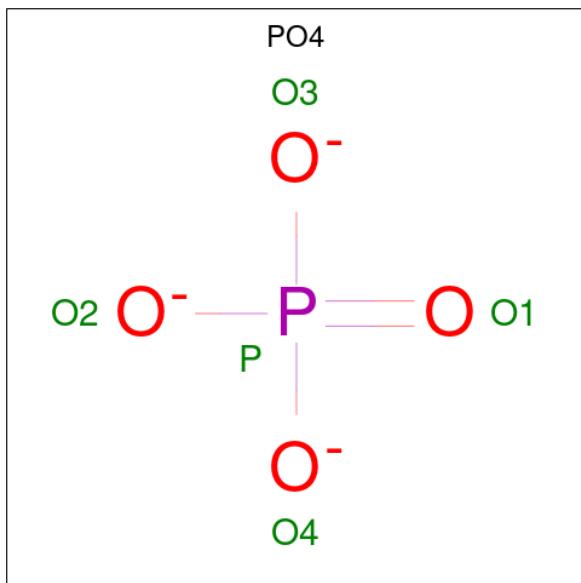
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total K 5 5	0	0
4	B	4	Total K 4 4	0	0
4	C	4	Total K 4 4	0	0

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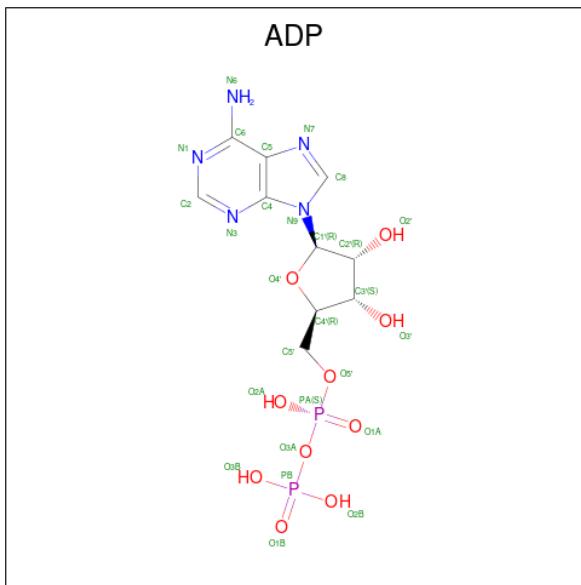
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	5	Total K 5 5	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



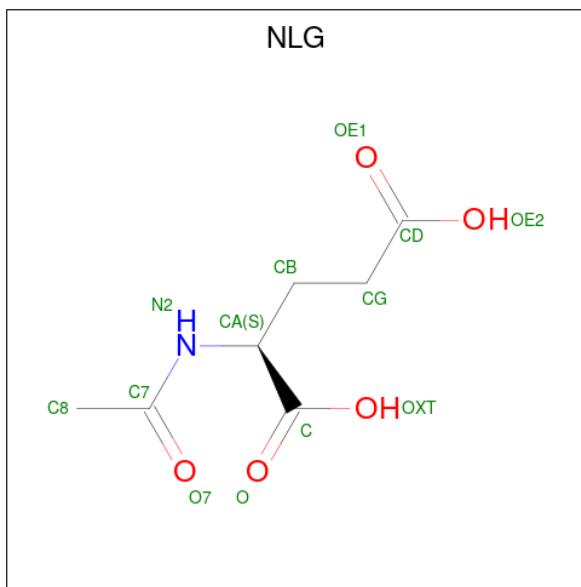
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	B	1	Total O P 5 4 1	0	0
5	C	1	Total O P 5 4 1	0	0
5	D	1	Total O P 5 4 1	0	0

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



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

- Molecule 7 is N-ACETYL-L-GLUTAMATE (three-letter code: NLG) (formula: C<sub>7</sub>H<sub>11</sub>NO<sub>5</sub>).

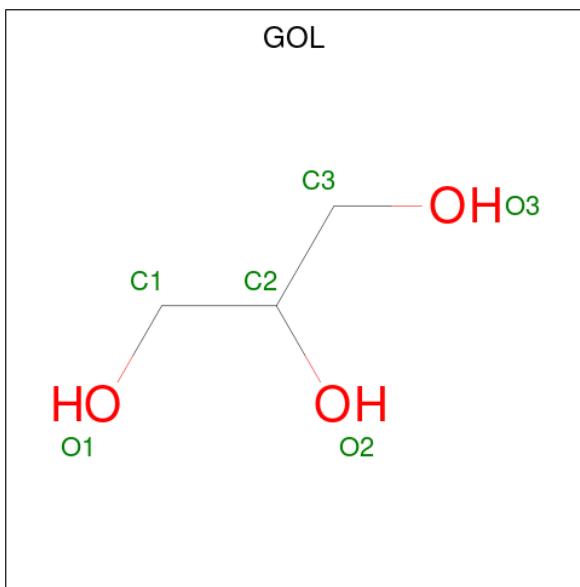


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 13 7 1 5	0	0
7	B	1	Total C N O 13 7 1 5	0	0
7	C	1	Total C N O 13 7 1 5	0	0
7	D	1	Total C N O 13 7 1 5	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

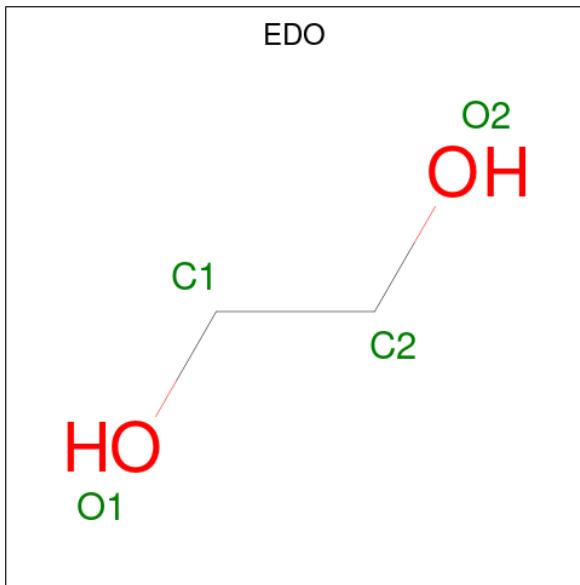
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0
8	B	1	Total Cl 1 1	0	0
8	D	1	Total Cl 1 1	0	0

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 6 3 3	0	0
9	D	1	Total C O 6 3 3	0	0

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C O 4 2 2	0	0

- Molecule 11 is water.

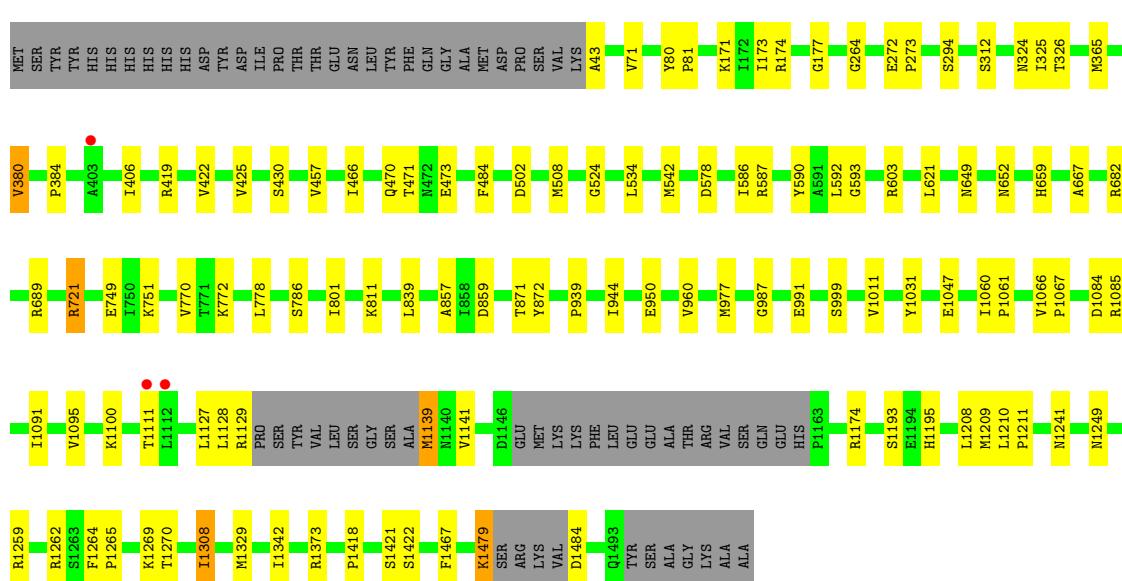
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	264	Total O 264 264	0	0
11	B	79	Total O 79 79	0	0
11	C	65	Total O 65 65	0	0
11	D	232	Total O 232 232	0	0

### 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.

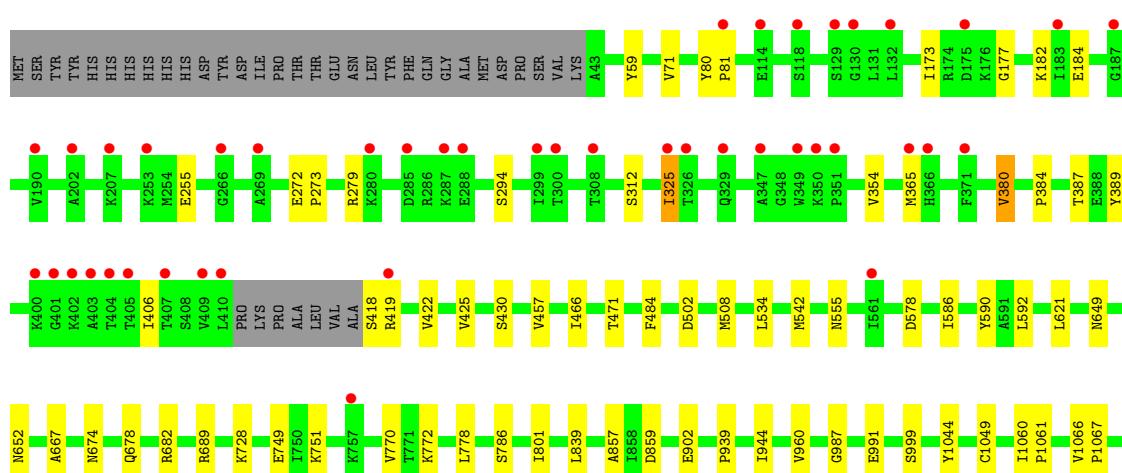
- Molecule 1: Carbamoyl-phosphate synthase [ammonia], mitochondrial

Chain A:



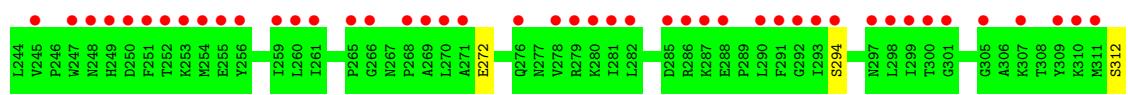
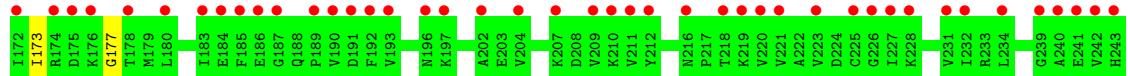
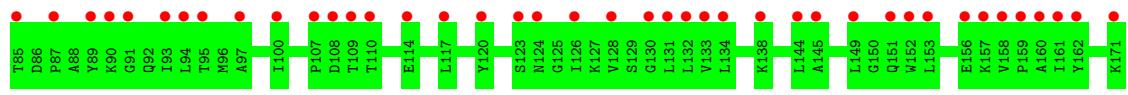
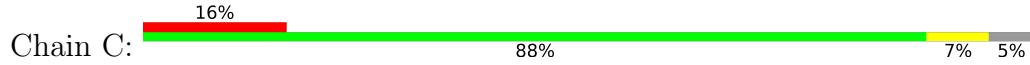
- Molecule 1: Carbamoyl-phosphate synthase [ammonia], mitochondrial

Chain B:

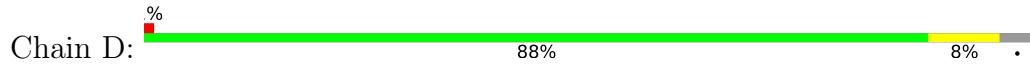


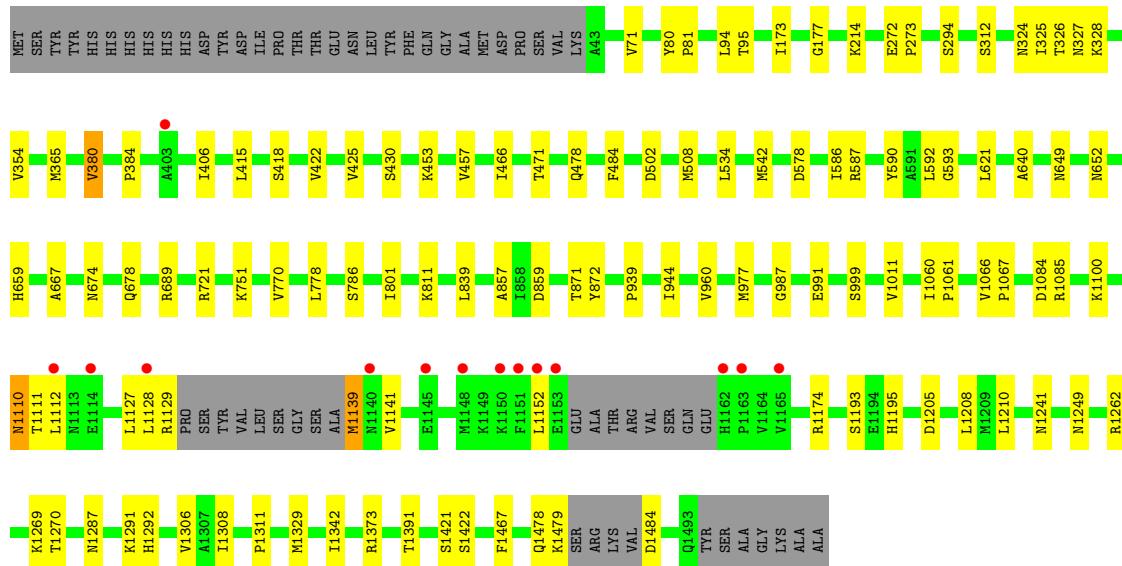


- Molecule 1: Carbamoyl-phosphate synthase [ammonia], mitochondrial



- Molecule 1: Carbamoyl-phosphate synthase [ammonia], mitochondrial





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.92 Å   98.56 Å   214.89 Å 90.66°   98.65°   90.08°	Depositor
Resolution (Å)	40.00 – 2.60 39.98 – 2.60	Depositor EDS
% Data completeness (in resolution range)	90.7 (40.00-2.60) 87.6 (39.98-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	2.83 (at 2.61 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
$R$ , $R_{free}$	0.195 , 0.229 0.202 , 0.199	Depositor DCC
$R_{free}$ test set	8964 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.4	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 14.2	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.45$ , $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-1 0.247 for -h,k,-l 0.030 for -h,-k,h+1	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	45021	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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  $< |L| >$ ,  $< L^2 >$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [\(i\)](#)

### 5.1 Standard geometry [\(i\)](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, PO4, CL, EDO, K, NI, NLG, GOL

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	0.65	0/11210	0.71	6/15188 (0.0%)
1	B	0.51	0/11231	0.67	4/15213 (0.0%)
1	C	0.48	0/11191	0.66	4/15162 (0.0%)
1	D	0.64	0/11274	0.71	5/15273 (0.0%)
All	All	0.58	0/44906	0.69	19/60836 (0.0%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	C	1174	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	D	689	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	A	689	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	B	1428	ARG	NE-CZ-NH2	6.08	123.34	120.30
1	A	1174	ARG	NE-CZ-NH2	-6.02	117.29	120.30

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	10991	0	11065	63	0
1	B	11018	0	11072	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	10975	0	11038	51	1
1	D	11056	0	11125	57	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
4	A	5	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	5	0	0	0	0
5	A	5	0	0	1	0
5	B	5	0	0	0	0
5	C	5	0	0	1	0
5	D	5	0	0	0	0
6	A	54	0	24	2	0
6	B	54	0	24	0	0
6	C	54	0	24	0	0
6	D	54	0	24	2	0
7	A	13	0	9	0	0
7	B	13	0	9	0	0
7	C	13	0	9	0	0
7	D	13	0	9	1	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	D	1	0	0	0	0
9	A	6	0	8	0	0
9	D	6	0	8	1	0
10	A	4	0	6	2	0
11	A	264	0	0	5	0
11	B	79	0	0	4	1
11	C	65	0	0	8	0
11	D	232	0	0	3	0
All	All	45021	0	44454	227	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 227 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:A:419[B]:ARG:HH11	1:A:419[B]:ARG:CG	1.72	1.03
1:A:419[B]:ARG:HH11	1:A:419[B]:ARG:HG3	0.86	1.03
1:A:419[B]:ARG:HG3	1:A:419[B]:ARG:NH1	1.67	0.98
1:C:419:ARG:NH1	1:C:749:GLU:OE1	1.97	0.98
1:C:894:LEU:O	11:C:2101:HOH:O	2.01	0.79

All (1) 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:C:1289:ASP:OD2	11:B:2101:HOH:O[1_656]	2.10	0.10

## 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	1416/1489 (95%)	1367 (96%)	46 (3%)	3 (0%)	47 71
1	B	1416/1489 (95%)	1375 (97%)	38 (3%)	3 (0%)	47 71
1	C	1412/1489 (95%)	1369 (97%)	41 (3%)	2 (0%)	51 75
1	D	1423/1489 (96%)	1379 (97%)	42 (3%)	2 (0%)	51 75
All	All	5667/5956 (95%)	5490 (97%)	167 (3%)	10 (0%)	47 71

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1153	GLU
1	A	294	SER
1	A	380	VAL
1	B	294	SER
1	B	380	VAL

### 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	1210/1266 (96%)	1187 (98%)	23 (2%)	57 <b>79</b>
1	B	1212/1266 (96%)	1185 (98%)	27 (2%)	52 <b>76</b>
1	C	1208/1266 (95%)	1184 (98%)	24 (2%)	55 <b>78</b>
1	D	1217/1266 (96%)	1192 (98%)	25 (2%)	53 <b>77</b>
All	All	4847/5064 (96%)	4748 (98%)	99 (2%)	55 <b>78</b>

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	859	ASP
1	C	1428	ARG
1	C	1084	ASP
1	C	1193	SER
1	D	430	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1249	ASN
1	C	1359	GLN
1	D	1359	GLN
1	D	1110	ASN
1	D	1243	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 56 ligands modelled in this entry, 37 are monoatomic - leaving 19 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
9	GOL	D	2015	-	5,5,5	0.70	0	5,5,5	0.91	0
6	ADP	C	2009	3	24,29,29	1.17	2 (8%)	29,45,45	1.30	4 (13%)
10	EDO	A	2016	-	3,3,3	0.48	0	2,2,2	0.32	0
6	ADP	C	2008	3	24,29,29	1.01	2 (8%)	29,45,45	1.44	4 (13%)
5	PO4	D	2007	3,4	4,4,4	1.13	0	6,6,6	1.08	0
6	ADP	A	2009	3	24,29,29	1.01	2 (8%)	29,45,45	1.13	1 (3%)
7	NLG	A	2010	-	12,12,12	0.89	0	15,15,15	1.73	3 (20%)
6	ADP	D	2009	3	24,29,29	1.02	1 (4%)	29,45,45	1.42	4 (13%)
7	NLG	D	2010	-	12,12,12	0.96	0	15,15,15	1.66	4 (26%)
9	GOL	A	2015	-	5,5,5	0.88	0	5,5,5	0.83	0
5	PO4	C	2007	3,4	4,4,4	0.91	0	6,6,6	0.85	0
6	ADP	D	2008	3	24,29,29	1.38	3 (12%)	29,45,45	1.50	6 (20%)
7	NLG	C	2010	-	12,12,12	0.86	0	15,15,15	1.06	1 (6%)
7	NLG	B	2010	-	12,12,12	0.86	0	15,15,15	0.90	0
5	PO4	A	2007	3,4	4,4,4	1.12	0	6,6,6	0.98	0
6	ADP	B	2008	3	24,29,29	1.16	2 (8%)	29,45,45	1.37	5 (17%)
6	ADP	B	2009	3	24,29,29	1.06	3 (12%)	29,45,45	1.27	3 (10%)
5	PO4	B	2007	3,4	4,4,4	0.97	0	6,6,6	0.78	0
6	ADP	A	2008	3	24,29,29	1.36	5 (20%)	29,45,45	1.45	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
9	GOL	D	2015	-	-	4/4/4/4	-
6	ADP	A	2008	3	-	2/12/32/32	0/3/3/3
6	ADP	D	2008	3	-	3/12/32/32	0/3/3/3
7	NLG	C	2010	-	-	0/13/13/13	-
6	ADP	C	2009	3	-	3/12/32/32	0/3/3/3
10	EDO	A	2016	-	-	1/1/1/1	-
7	NLG	B	2010	-	-	0/13/13/13	-
6	ADP	A	2009	3	-	3/12/32/32	0/3/3/3
7	NLG	A	2010	-	-	4/13/13/13	-
6	ADP	D	2009	3	-	5/12/32/32	0/3/3/3
6	ADP	B	2009	3	-	4/12/32/32	0/3/3/3
7	NLG	D	2010	-	-	2/13/13/13	-
6	ADP	C	2008	3	-	1/12/32/32	0/3/3/3
9	GOL	A	2015	-	-	4/4/4/4	-
6	ADP	B	2008	3	-	1/12/32/32	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	2008	ADP	C2-N3	2.97	1.36	1.32
6	A	2008	ADP	C2-N1	2.90	1.39	1.33
6	C	2009	ADP	C2-N3	2.88	1.36	1.32
6	D	2009	ADP	C5-C4	2.80	1.48	1.40
6	A	2008	ADP	O4'-C1'	2.72	1.44	1.41

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	2008	ADP	N3-C2-N1	-4.23	122.06	128.68
6	D	2008	ADP	C5-C6-N6	-4.02	114.25	120.35
6	B	2008	ADP	N3-C2-N1	-3.70	122.89	128.68
7	A	2010	NLG	C-CA-N2	3.49	118.81	110.55
7	A	2010	NLG	CB-CA-C	-3.40	102.14	110.35

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2009	ADP	PA-O3A-PB-O3B
6	B	2009	ADP	PA-O3A-PB-O3B

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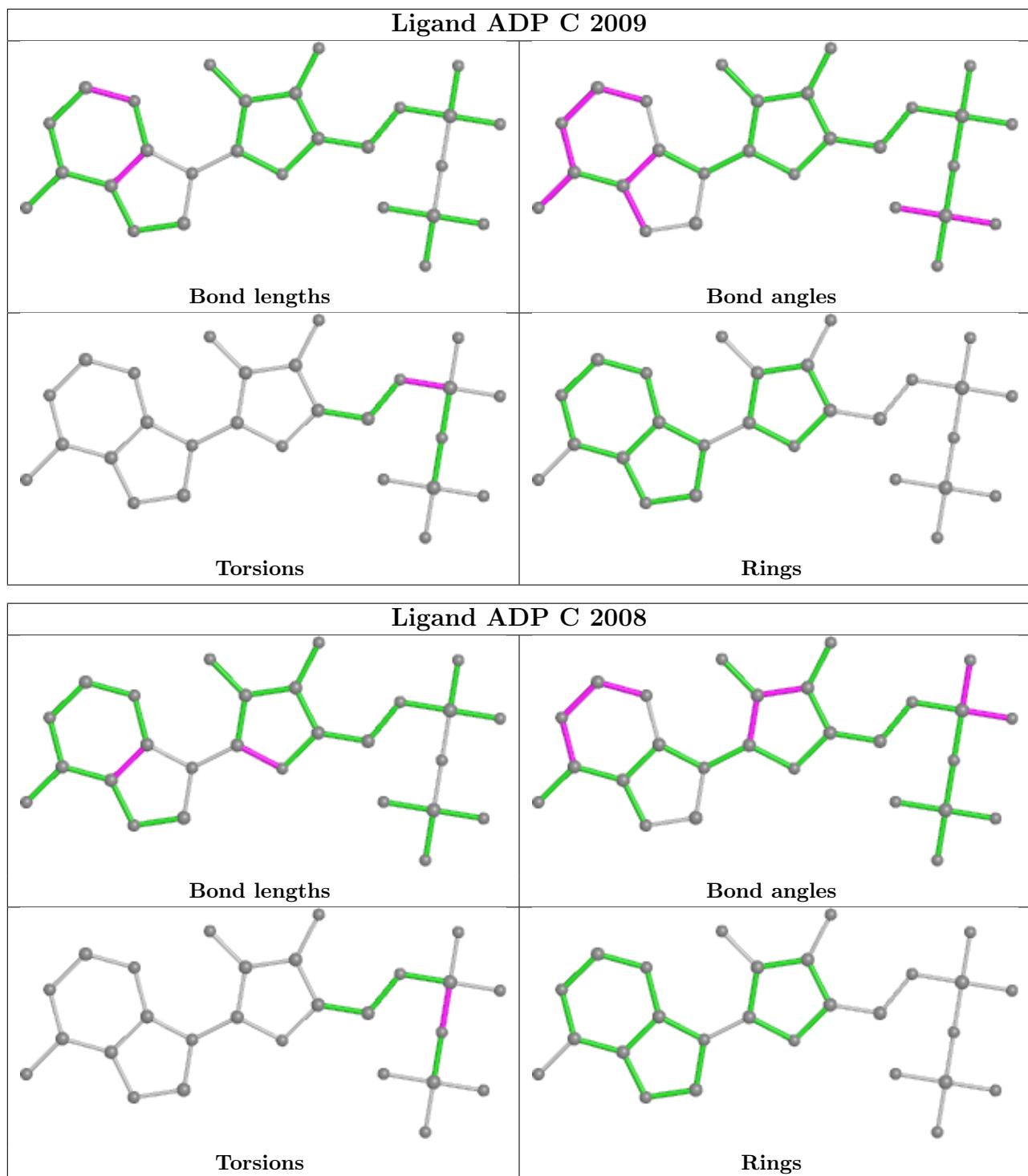
Mol	Chain	Res	Type	Atoms
6	C	2009	ADP	C5'-O5'-PA-O1A
6	C	2009	ADP	C5'-O5'-PA-O2A
6	C	2009	ADP	C5'-O5'-PA-O3A

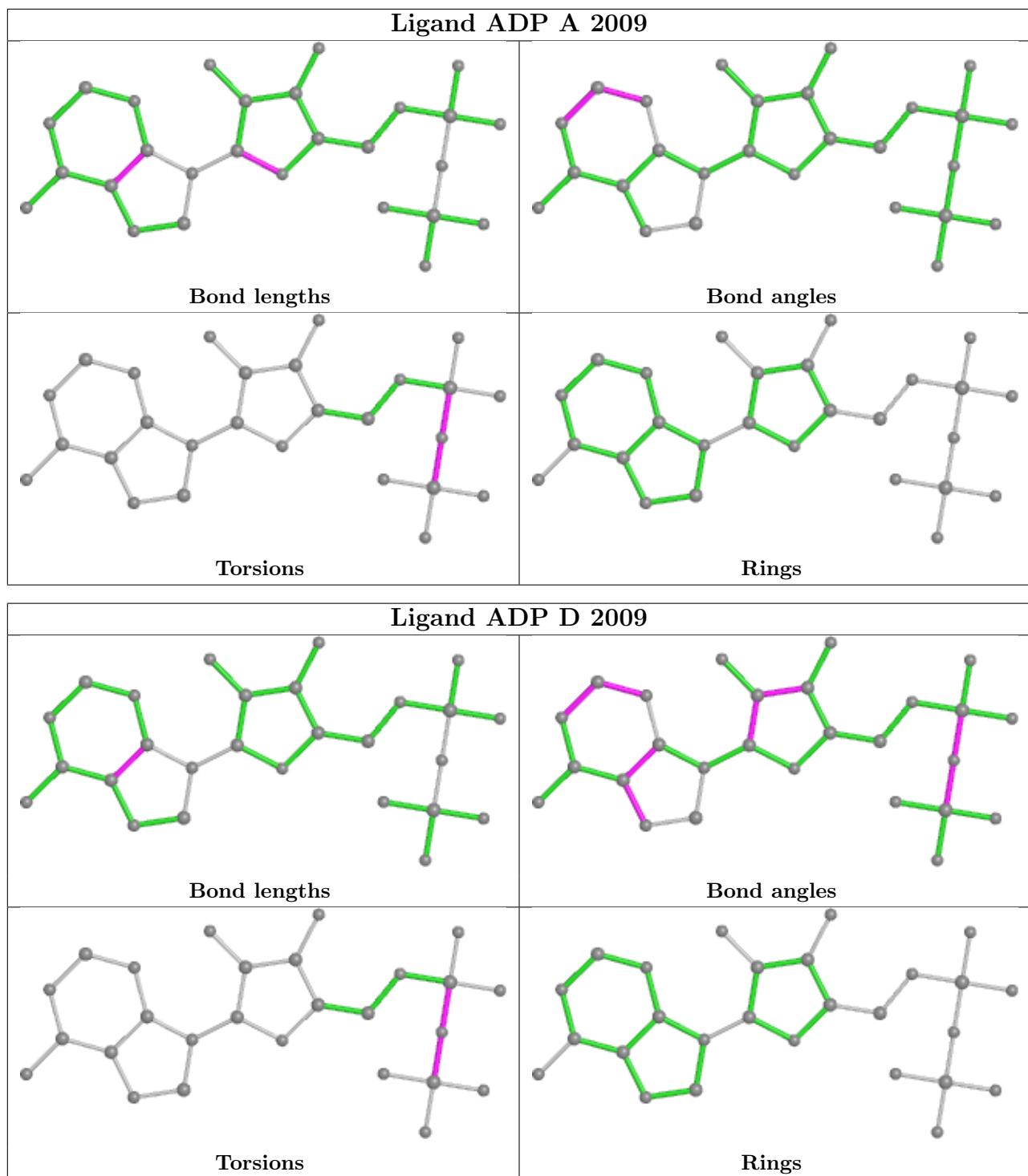
There are no ring outliers.

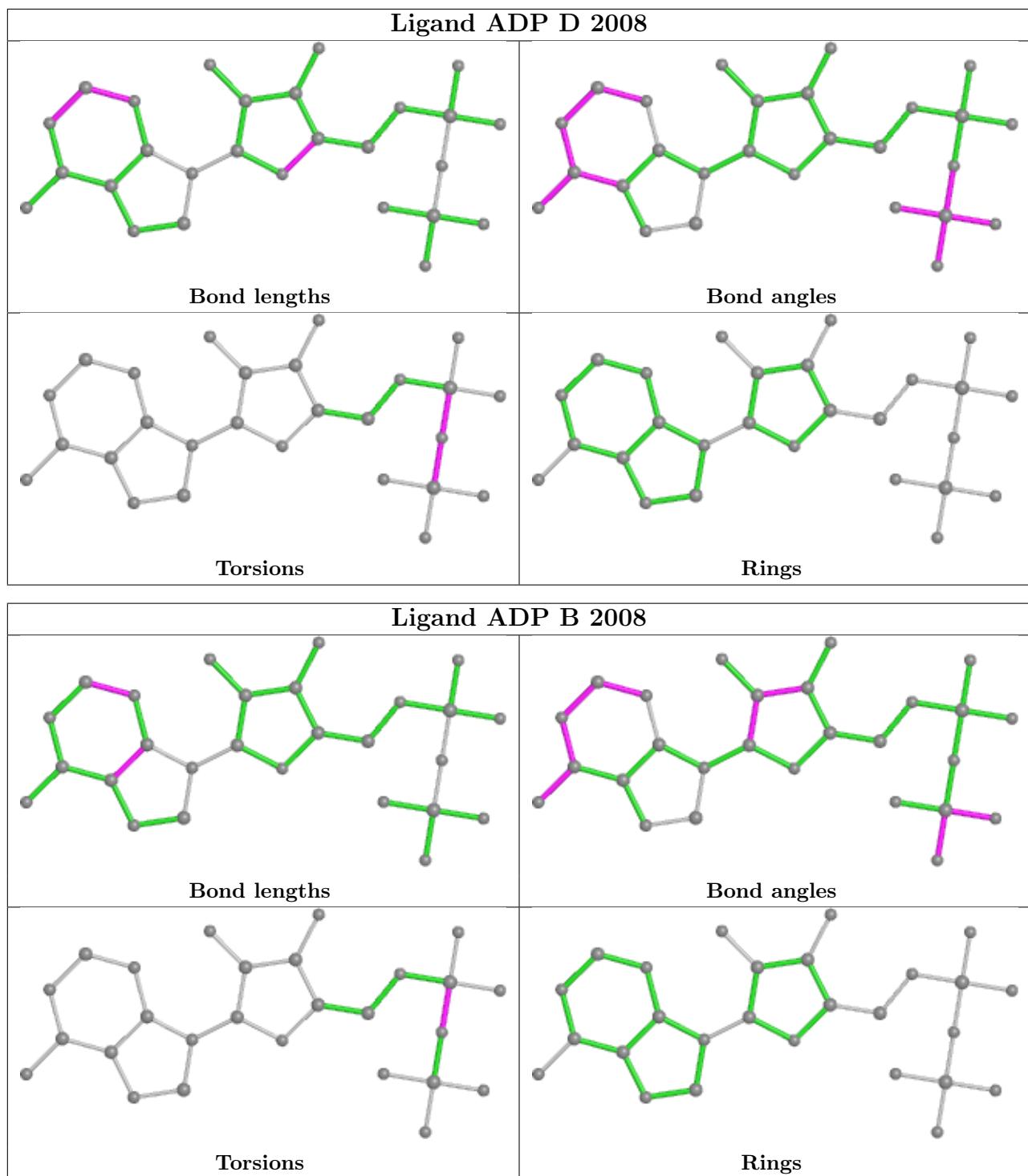
8 monomers are involved in 10 short contacts:

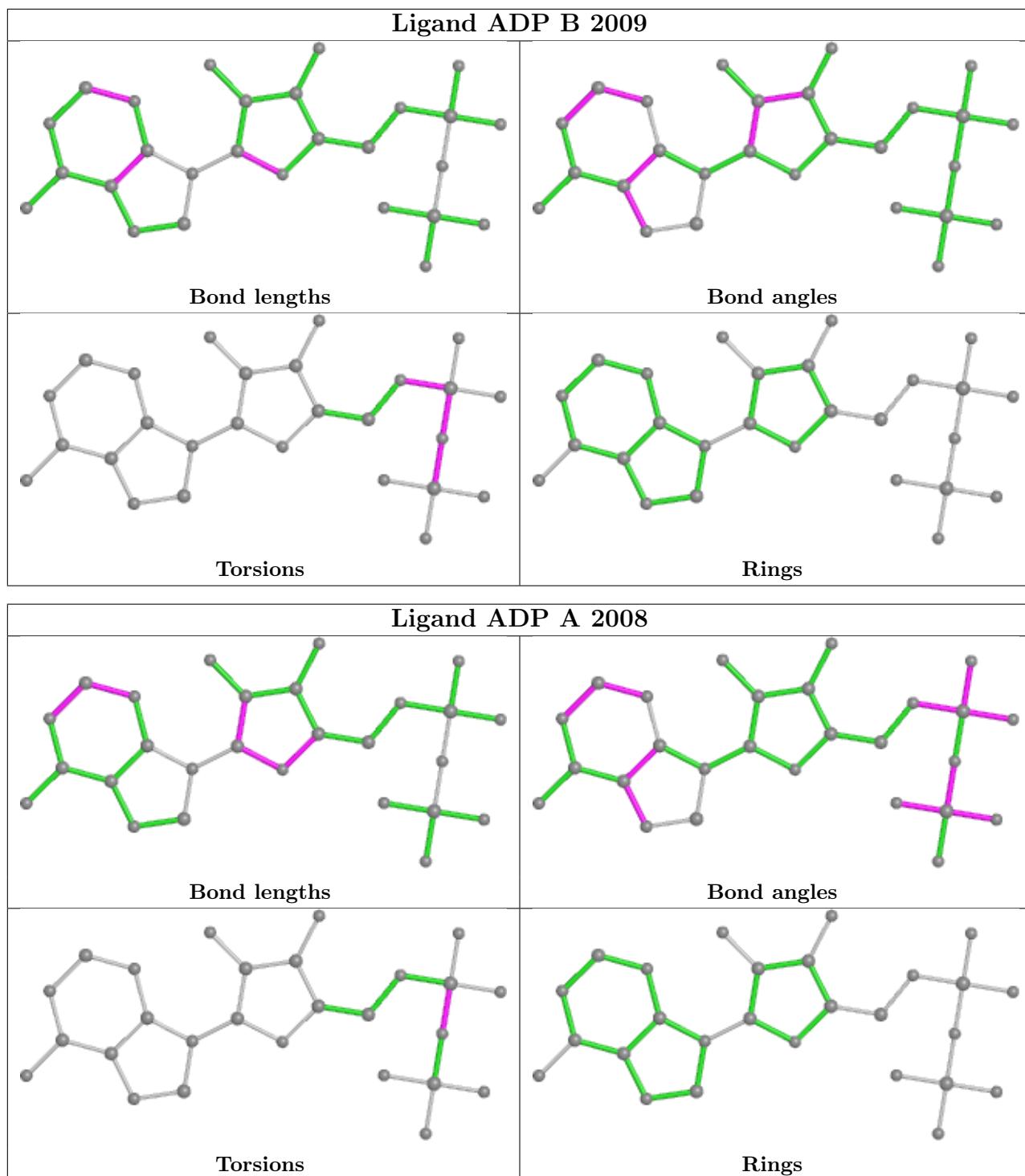
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	2015	GOL	1	0
10	A	2016	EDO	2	0
6	D	2009	ADP	1	0
7	D	2010	NLG	1	0
5	C	2007	PO4	1	0
6	D	2008	ADP	1	0
5	A	2007	PO4	1	0
6	A	2008	ADP	2	0

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	1422/1489 (95%)	-0.51	3 (0%) 95 95	12, 24, 47, 94	3 (0%)
1	B	1426/1489 (95%)	0.08	45 (3%) 47 40	19, 55, 87, 116	3 (0%)
1	C	1421/1489 (95%)	0.72	239 (16%) 1 1	20, 64, 144, 172	3 (0%)
1	D	1430/1489 (96%)	-0.51	14 (0%) 82 80	12, 24, 48, 113	3 (0%)
All	All	5699/5956 (95%)	-0.05	301 (5%) 26 20	12, 34, 111, 172	12 (0%)

The worst 5 of 301 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	404	THR	13.0
1	C	343	ASN	9.5
1	C	403	ALA	9.5
1	C	368	SER	9.0
1	C	130	GLY	8.6

### 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 [\(i\)](#)

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, 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.

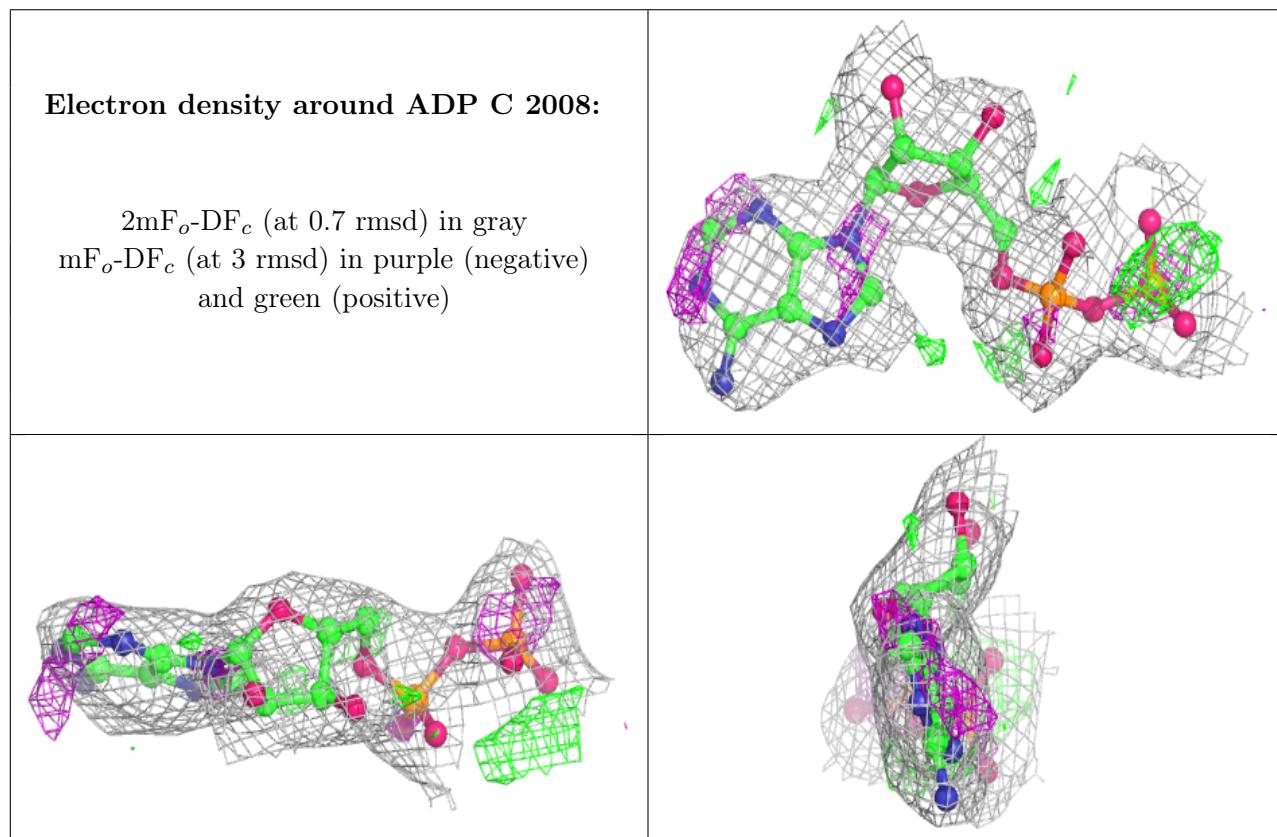
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å²)	Q<0.9
3	MG	C	2003	1/1	0.82	0.07	20,20,20,20	0
3	MG	B	2003	1/1	0.89	0.07	35,35,35,35	0
2	NI	C	2001	1/1	0.89	0.17	56,56,56,56	0
4	K	C	2006	1/1	0.91	0.09	78,78,78,78	0
4	K	C	2004	1/1	0.92	0.09	44,44,44,44	0
4	K	C	2012	1/1	0.92	0.23	75,75,75,75	0
10	EDO	A	2016	4/4	0.92	0.17	39,40,40,41	0
3	MG	A	2011	1/1	0.93	0.05	41,41,41,41	0
6	ADP	C	2008	27/27	0.94	0.13	26,29,36,38	0
3	MG	B	2011	1/1	0.94	0.05	15,15,15,15	0
3	MG	D	2002	1/1	0.95	0.14	13,13,13,13	0
4	K	C	2005	1/1	0.95	0.18	45,45,45,45	0
7	NLG	A	2010	13/13	0.95	0.15	17,18,19,21	0
9	GOL	A	2015	6/6	0.95	0.11	26,29,29,29	0
3	MG	D	2011	1/1	0.95	0.08	34,34,34,34	0
6	ADP	A	2009	27/27	0.96	0.11	28,31,46,47	0
6	ADP	B	2009	27/27	0.96	0.12	24,28,35,37	0
3	MG	C	2002	1/1	0.96	0.06	20,20,20,20	0
6	ADP	C	2009	27/27	0.96	0.14	28,31,37,38	0
3	MG	B	2002	1/1	0.96	0.08	21,21,21,21	0
7	NLG	B	2010	13/13	0.96	0.13	16,23,25,26	0
7	NLG	C	2010	13/13	0.96	0.13	18,22,25,26	0
5	PO4	B	2007	5/5	0.96	0.11	26,26,29,29	0
5	PO4	C	2007	5/5	0.96	0.08	32,34,34,35	0
3	MG	A	2002	1/1	0.97	0.11	13,13,13,13	0
6	ADP	B	2008	27/27	0.97	0.10	25,29,32,32	0
7	NLG	D	2010	13/13	0.97	0.15	20,21,24,25	0
8	CL	B	2012	1/1	0.97	0.10	43,43,43,43	0
6	ADP	D	2009	27/27	0.97	0.09	27,31,44,45	0
9	GOL	D	2015	6/6	0.97	0.15	30,34,37,38	0
4	K	A	2013	1/1	0.97	0.04	32,32,32,32	0
6	ADP	D	2008	27/27	0.98	0.11	7,7,10,10	0
4	K	D	2005	1/1	0.98	0.06	30,30,30,30	0
4	K	B	2005	1/1	0.98	0.04	42,42,42,42	0
4	K	B	2006	1/1	0.98	0.22	65,65,65,65	0
6	ADP	A	2008	27/27	0.98	0.11	7,8,11,12	0
4	K	B	2013	1/1	0.98	0.23	61,61,61,61	0
2	NI	B	2001	1/1	0.98	0.06	75,75,75,75	0
3	MG	D	2003	1/1	0.98	0.11	13,13,13,13	0
3	MG	A	2003	1/1	0.98	0.09	9,9,9,9	0
3	MG	C	2011	1/1	0.98	0.04	41,41,41,41	0
4	K	D	2006	1/1	0.99	0.10	53,53,53,53	0
4	K	D	2013	1/1	0.99	0.04	18,18,18,18	0

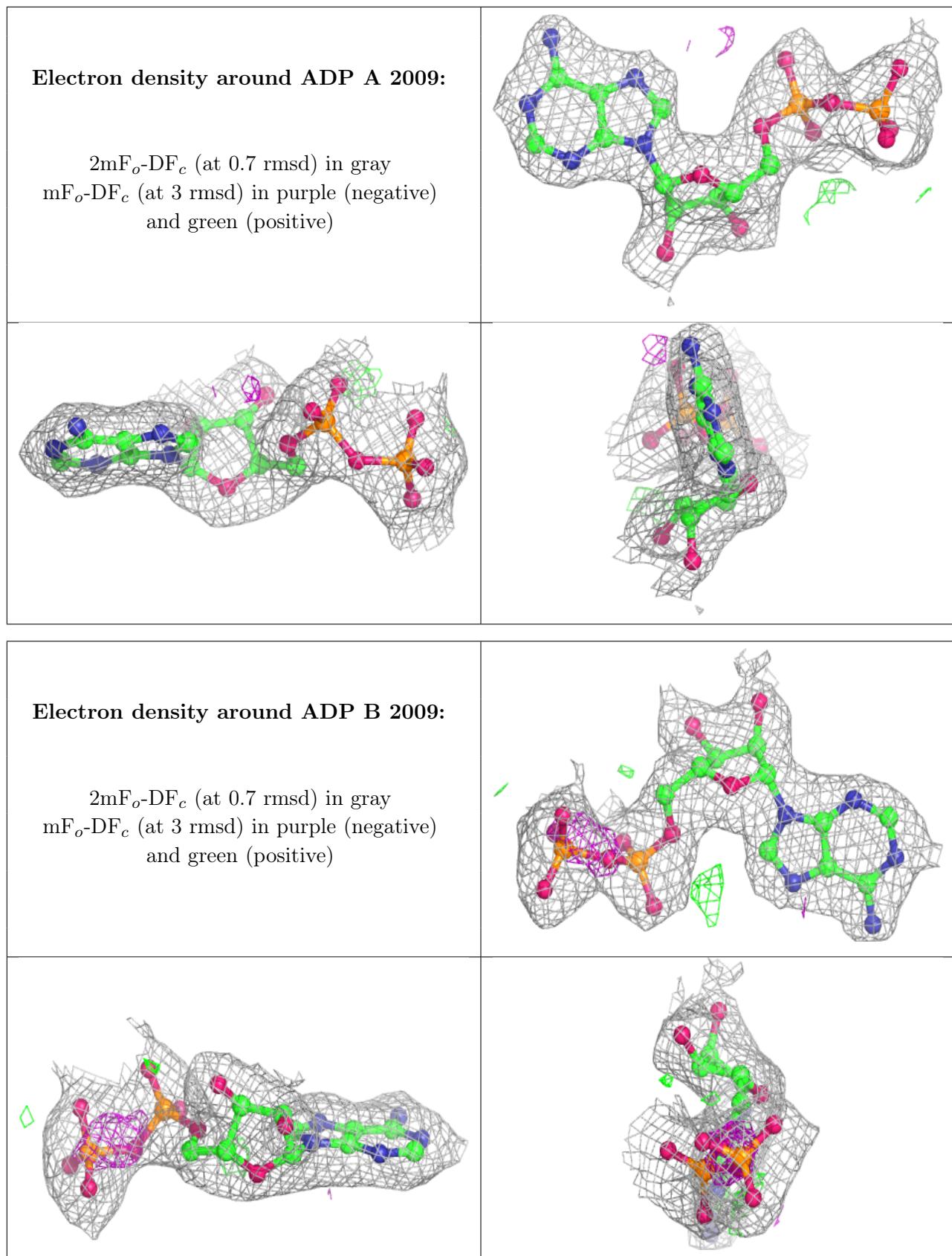
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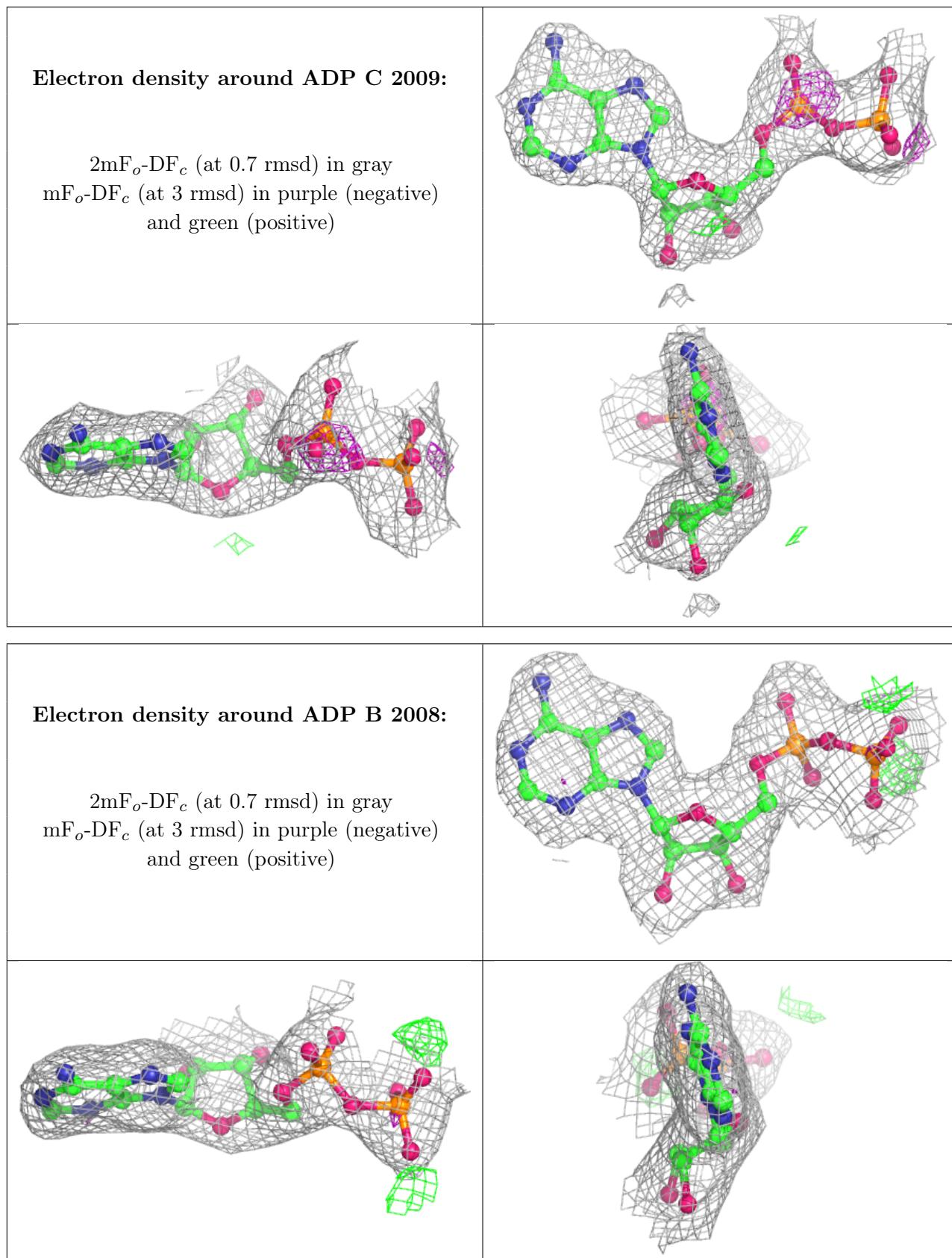
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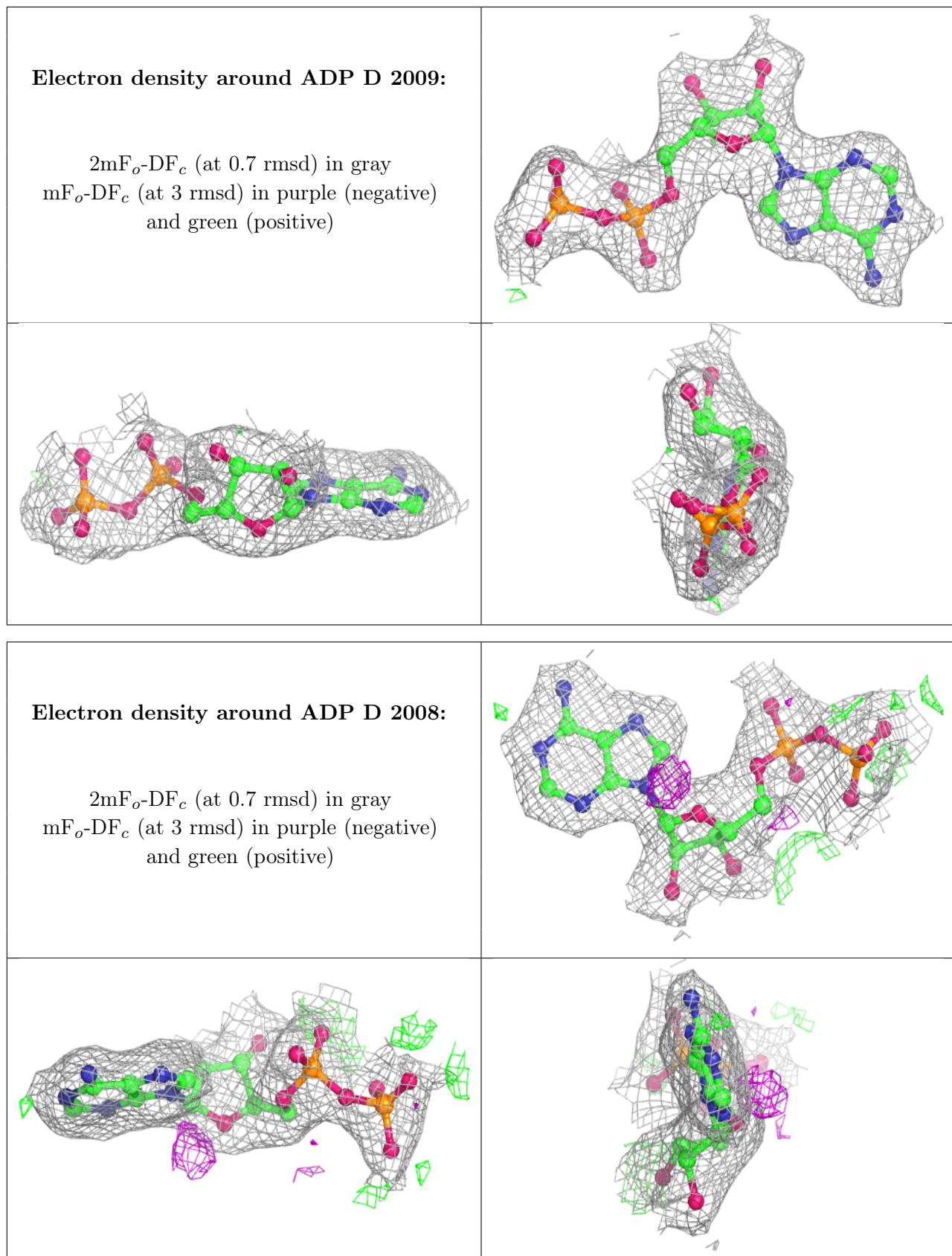
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	K	D	2014	1/1	0.99	0.05	37,37,37,37	0
5	PO4	A	2007	5/5	0.99	0.12	11,12,12,13	0
4	K	A	2006	1/1	0.99	0.09	46,46,46,46	0
2	NI	D	2001	1/1	0.99	0.07	34,34,34,34	0
4	K	A	2014	1/1	0.99	0.04	24,24,24,24	0
8	CL	A	2012	1/1	0.99	0.06	31,31,31,31	0
4	K	B	2004	1/1	0.99	0.05	39,39,39,39	0
8	CL	D	2012	1/1	0.99	0.12	26,26,26,26	0
4	K	A	2004	1/1	0.99	0.08	9,9,9,9	0
4	K	D	2004	1/1	0.99	0.09	8,8,8,8	0
4	K	A	2005	1/1	0.99	0.10	31,31,31,31	0
2	NI	A	2001	1/1	1.00	0.04	34,34,34,34	0
5	PO4	D	2007	5/5	1.00	0.11	11,11,13,14	0

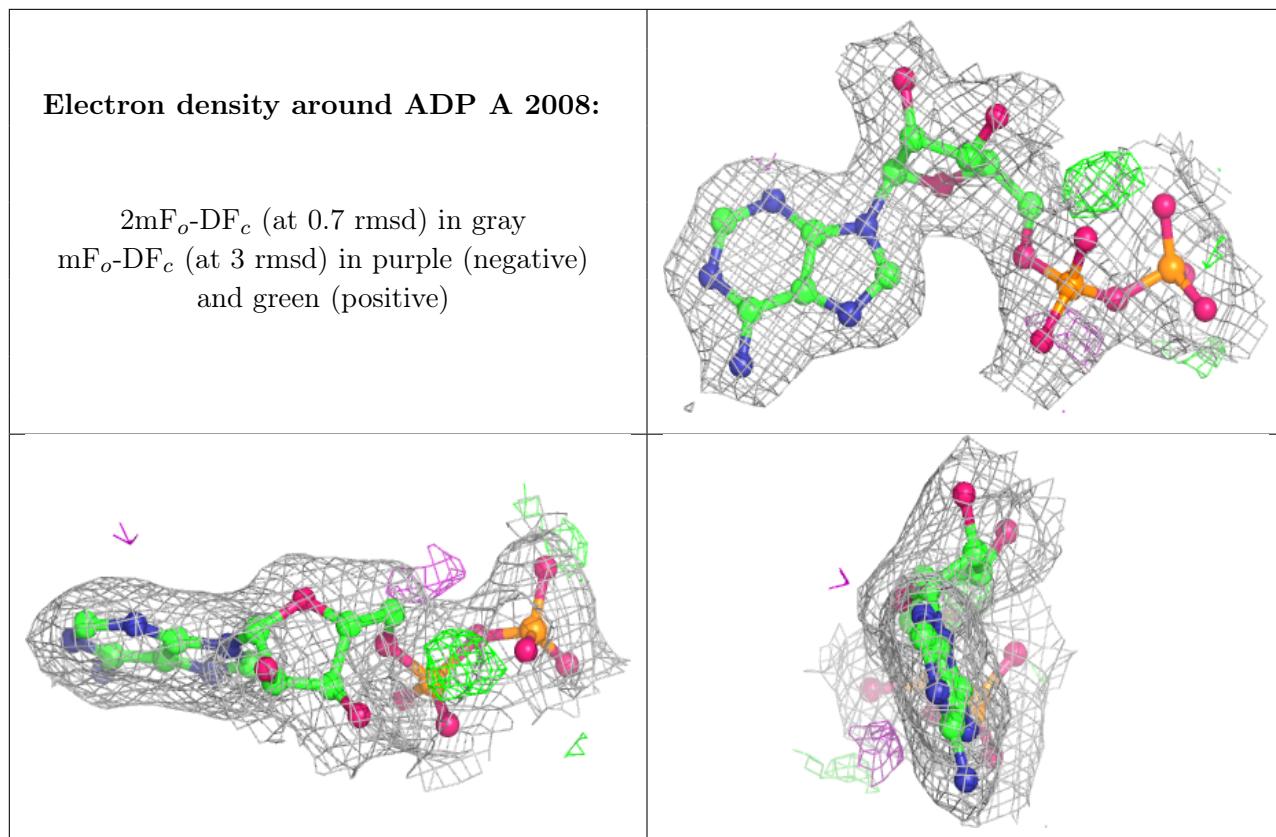
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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











## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.