



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2023 – 03:25 AM EDT

PDB ID : 7LZ4  
Title : Crystal structure of A211D mutant of Protein Kinase A RIa subunit, a Carney Complex mutation  
Authors : Del Rio, J.; Wu, J.; Taylor, S.S.  
Deposited on : 2021-03-08  
Resolution : 4.16 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 : 2.35.1  
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) : 2.35.1

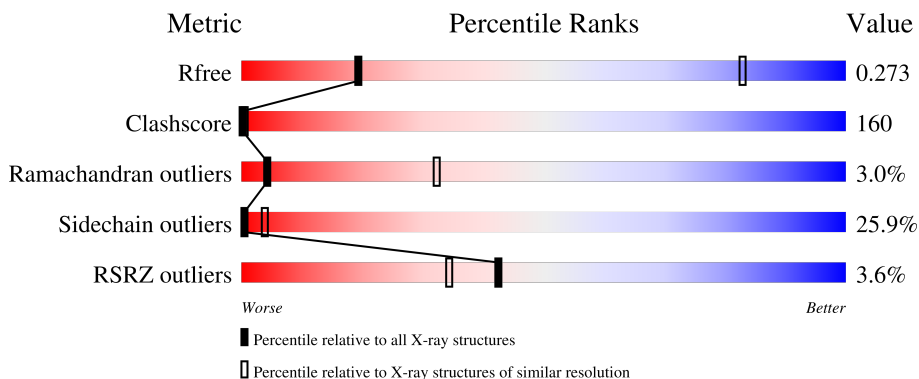
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.16 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	1020 (4.54-3.76)
Clashscore	141614	1028 (4.52-3.80)
Ramachandran outliers	138981	1005 (4.54-3.78)
Sidechain outliers	138945	1024 (4.54-3.76)
RSRZ outliers	127900	1055 (4.62-3.70)

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	269	
1	B	269	
1	C	269	
1	D	269	
1	E	269	

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Mol	Chain	Length	Quality of chain
1	F	269	
1	G	269	
1	H	269	

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
2	CMP	A	401	-	-	X	-
2	CMP	A	402	-	-	X	-
2	CMP	B	401	-	-	X	-
2	CMP	B	402	-	-	X	-
2	CMP	C	401	-	-	X	-
2	CMP	C	402	-	-	X	-
2	CMP	D	401	-	-	X	-
2	CMP	D	402	-	-	X	-
2	CMP	E	401	-	-	X	-
2	CMP	E	402	-	-	X	-
2	CMP	F	401	-	-	X	-
2	CMP	F	402	-	-	X	-
2	CMP	G	401	-	-	X	-
2	CMP	G	402	-	-	X	-
2	CMP	H	401	-	-	X	-
2	CMP	H	402	-	-	X	-

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 17138 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.

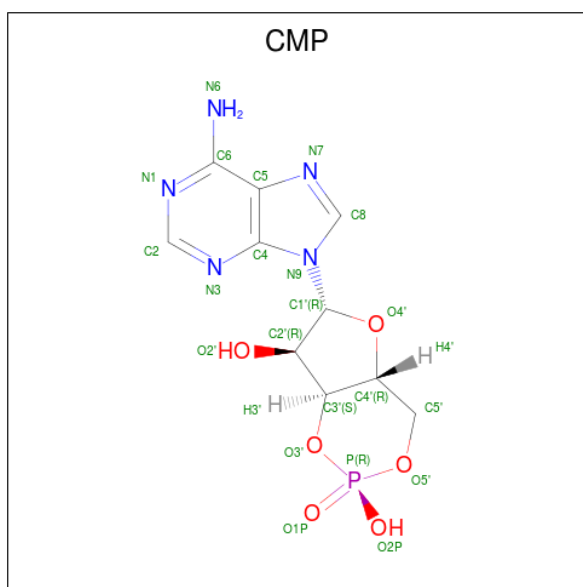
- Molecule 1 is a protein called cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	268	2100	1333	358	401	8	0	0	0
1	B	268	2100	1333	358	401	8	0	0	0
1	C	268	2100	1333	358	401	8	0	0	0
1	D	266	2086	1325	356	397	8	0	0	0
1	E	268	2100	1333	358	401	8	0	0	0
1	F	268	2100	1333	358	401	8	0	0	0
1	G	268	2100	1333	358	401	8	0	0	0
1	H	268	2100	1333	358	401	8	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	ASP	ALA	engineered mutation	UNP P00514
B	211	ASP	ALA	engineered mutation	UNP P00514
C	211	ASP	ALA	engineered mutation	UNP P00514
D	211	ASP	ALA	engineered mutation	UNP P00514
E	211	ASP	ALA	engineered mutation	UNP P00514
F	211	ASP	ALA	engineered mutation	UNP P00514
G	211	ASP	ALA	engineered mutation	UNP P00514
H	211	ASP	ALA	engineered mutation	UNP P00514

- Molecule 2 is ADENOSINE-3',5'-CYCLIC-MONOPHOSPHATE (three-letter code: CMP) (formula: C<sub>10</sub>H<sub>12</sub>N<sub>5</sub>O<sub>6</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

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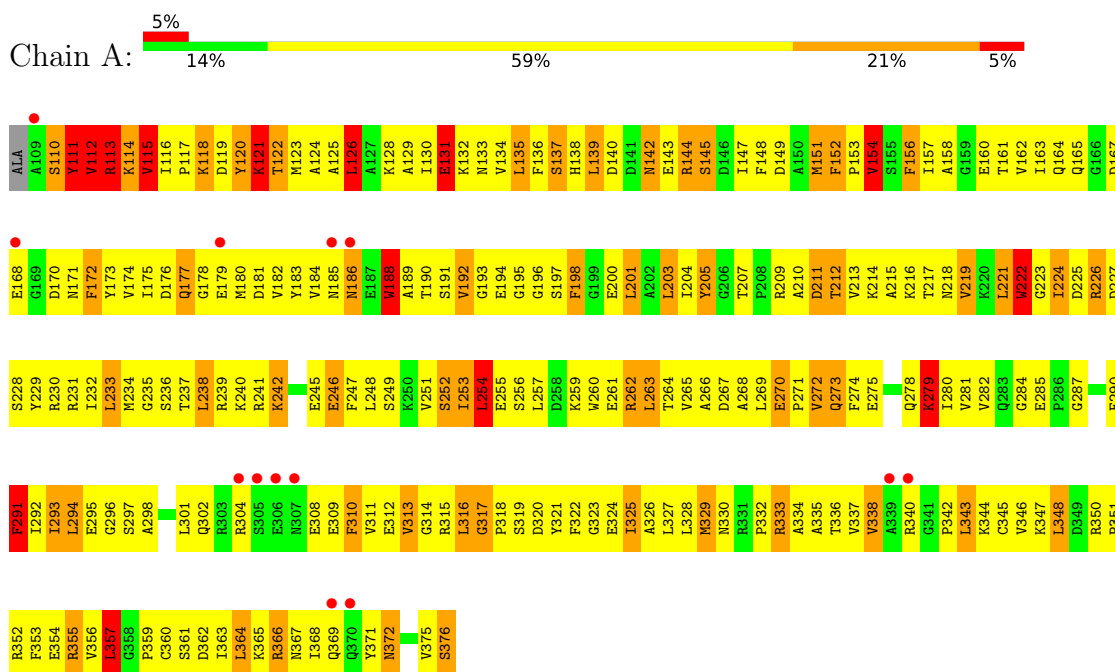
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>					<b>ZeroOcc</b>	<b>AltConf</b>
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

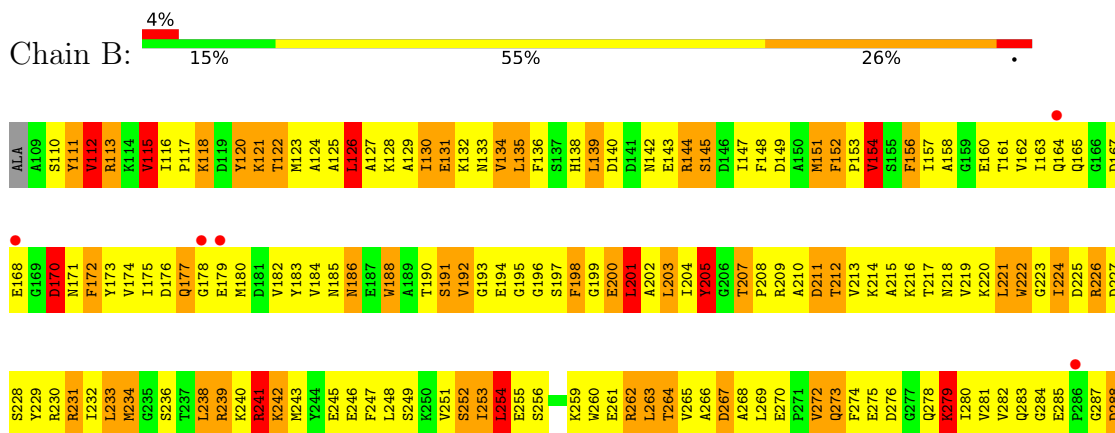
### 3 Residue-property plots

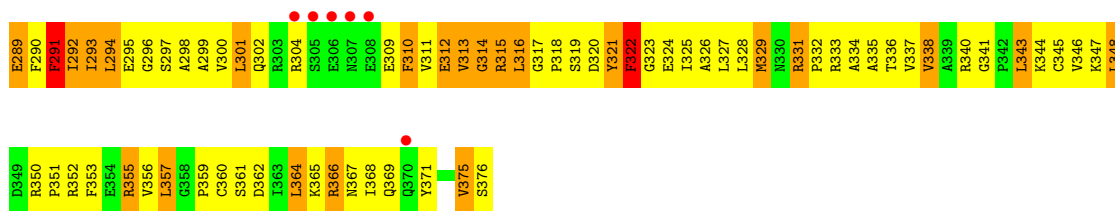
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

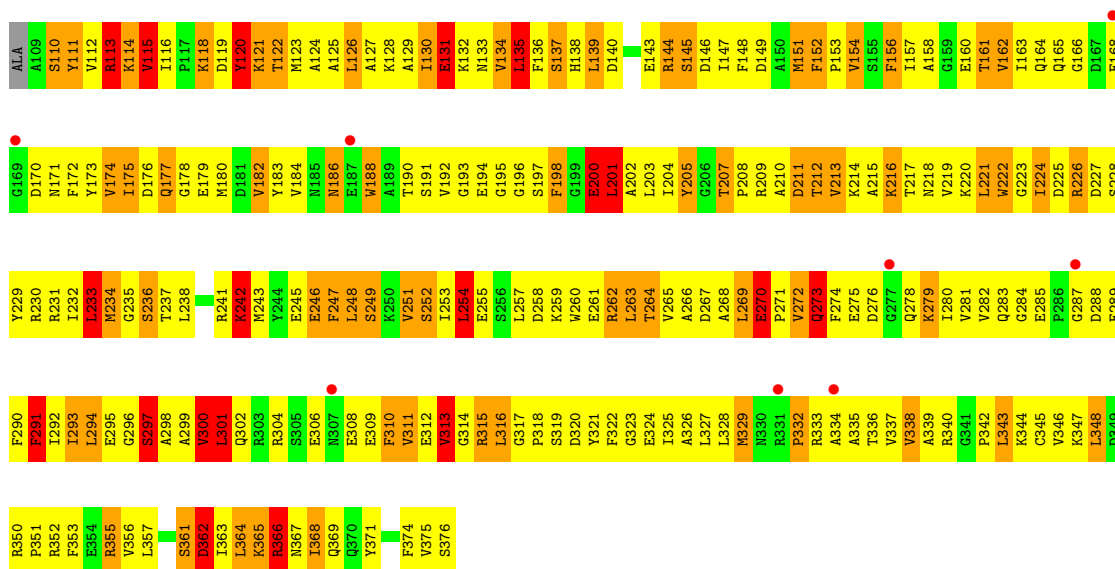
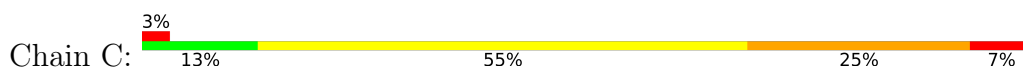


- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

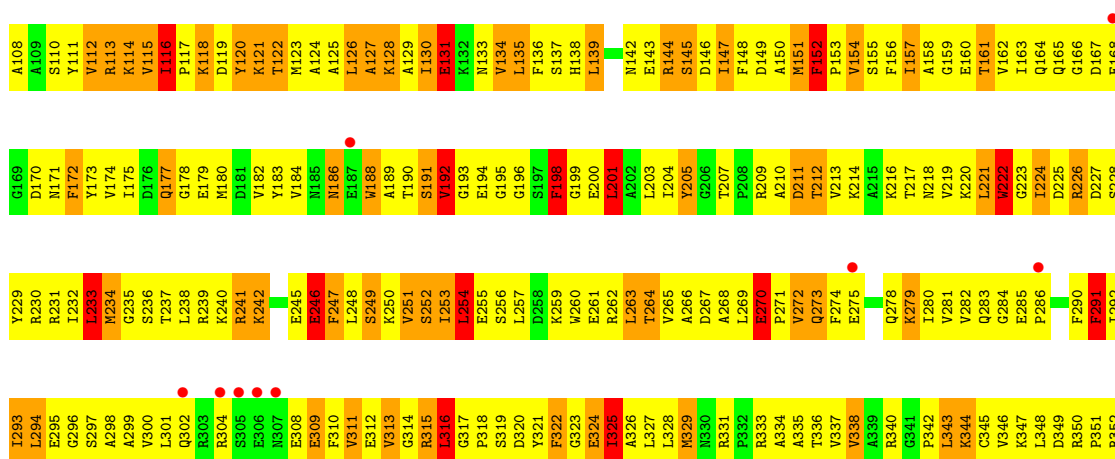
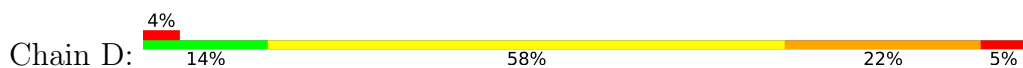




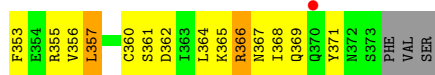
- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



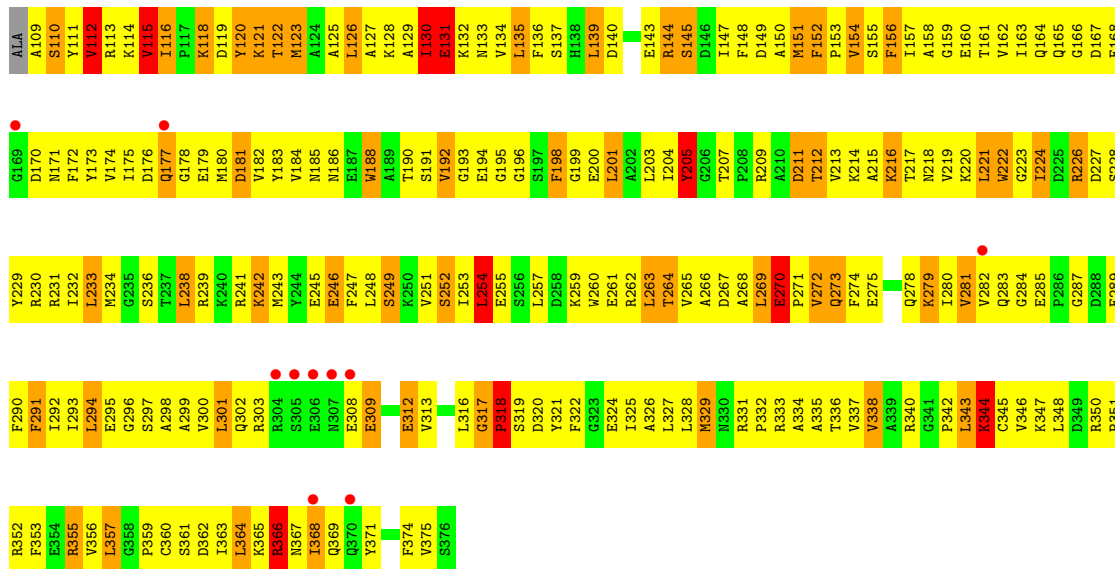
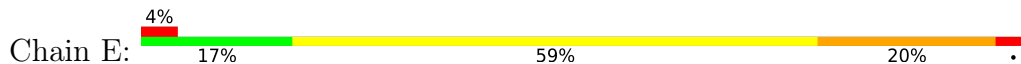
- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



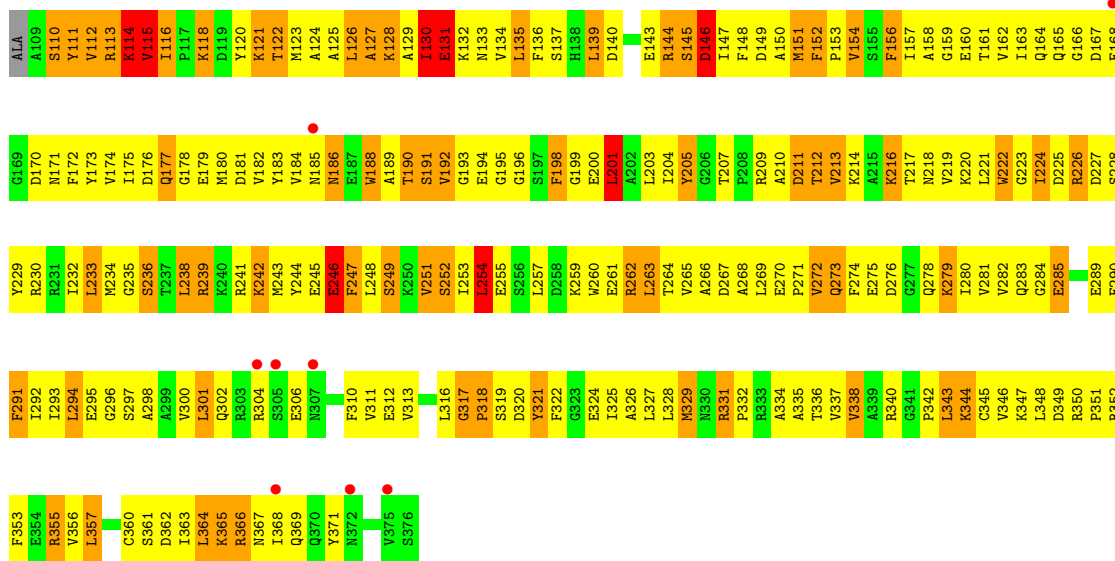
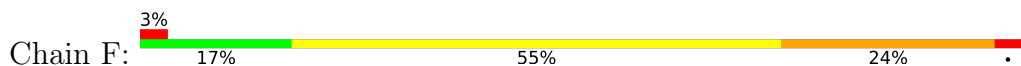




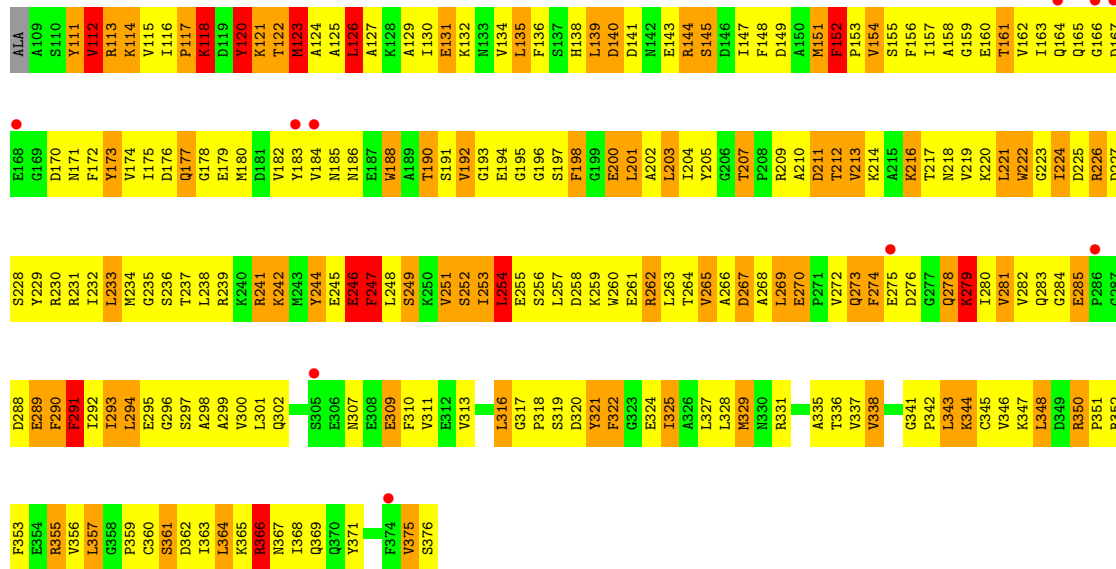
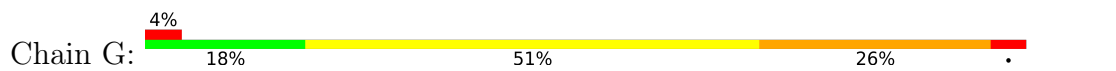
• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



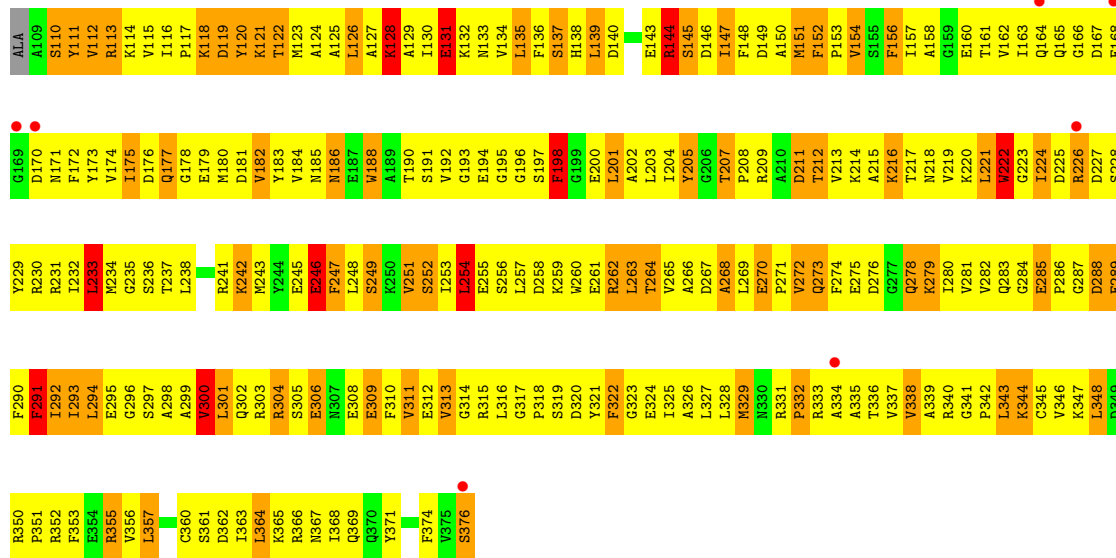
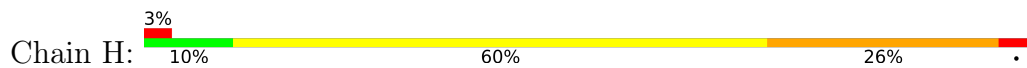
• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



• Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	176.79Å 176.79Å 345.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.25 – 4.16 48.25 – 4.15	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.25-4.16) 99.4 (48.25-4.15)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.69 (at 4.14Å)	Xtrriage
Refinement program	PHENIX 1.7_650	Depositor
R, $R_{free}$	0.221 , 0.270 0.225 , 0.273	Depositor DCC
$R_{free}$ test set	1526 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	125.7	Xtrriage
Anisotropy	0.440	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 97.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.418 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	17138	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	135.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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 i

### 5.1 Standard geometry i

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

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	1.35	15/2138 (0.7%)	1.60	33/2887 (1.1%)
1	B	1.31	13/2138 (0.6%)	1.55	31/2887 (1.1%)
1	C	1.27	5/2138 (0.2%)	1.61	34/2887 (1.2%)
1	D	1.33	20/2124 (0.9%)	1.44	27/2869 (0.9%)
1	E	1.12	8/2138 (0.4%)	1.39	19/2887 (0.7%)
1	F	1.26	14/2138 (0.7%)	1.48	27/2887 (0.9%)
1	G	1.60	32/2138 (1.5%)	1.82	58/2887 (2.0%)
1	H	1.27	12/2138 (0.6%)	1.56	33/2887 (1.1%)
All	All	1.32	119/17090 (0.7%)	1.56	262/23078 (1.1%)

The worst 5 of 119 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	131	GLU	CB-CG	-16.50	1.20	1.52
1	D	152	PHE	CE1-CZ	-12.97	1.12	1.37
1	A	112	VAL	CA-CB	12.67	1.81	1.54
1	G	289	GLU	CB-CG	-12.20	1.28	1.52
1	B	241	ARG	CZ-NH1	11.78	1.48	1.33

The worst 5 of 262 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	288	ASP	CB-CG-OD1	-22.79	97.79	118.30
1	A	357	LEU	CB-CG-CD1	-21.79	73.97	111.00
1	H	288	ASP	CB-CG-OD2	21.11	137.30	118.30
1	C	279	LYS	CD-CE-NZ	-19.95	65.81	111.70
1	G	121	LYS	CA-CB-CG	17.60	152.12	113.40

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	2100	0	2069	737	0
1	B	2100	0	2071	708	0
1	C	2100	0	2069	789	0
1	D	2086	0	2060	702	0
1	E	2100	0	2071	683	0
1	F	2100	0	2071	684	0
1	G	2100	0	2071	605	0
1	H	2100	0	2071	748	0
2	A	44	0	22	40	0
2	B	44	0	22	55	0
2	C	44	0	22	36	0
2	D	44	0	22	37	0
2	E	44	0	22	35	0
2	F	44	0	22	29	0
2	G	44	0	22	30	0
2	H	44	0	22	38	0
All	All	17138	0	16729	5432	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 160.

The worst 5 of 5432 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:112:VAL:CA	1:A:112:VAL:CB	1.81	1.53
1:A:112:VAL:CA	1:A:112:VAL:C	1.74	1.50
2:C:402:CMP:H2	2:C:402:CMP:C2	0.97	1.50
2:A:401:CMP:H2	2:A:401:CMP:C2	0.97	1.49
2:A:402:CMP:H2	2:A:402:CMP:C2	0.97	1.49

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	266/269 (99%)	225 (85%)	32 (12%)	9 (3%)	3	30
1	B	266/269 (99%)	218 (82%)	40 (15%)	8 (3%)	4	32
1	C	266/269 (99%)	221 (83%)	34 (13%)	11 (4%)	3	26
1	D	264/269 (98%)	226 (86%)	31 (12%)	7 (3%)	5	34
1	E	266/269 (99%)	219 (82%)	41 (15%)	6 (2%)	6	37
1	F	266/269 (99%)	224 (84%)	37 (14%)	5 (2%)	8	41
1	G	266/269 (99%)	224 (84%)	31 (12%)	11 (4%)	3	26
1	H	266/269 (99%)	225 (85%)	35 (13%)	6 (2%)	6	37
All	All	2126/2152 (99%)	1782 (84%)	281 (13%)	63 (3%)	4	32

5 of 63 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	VAL
1	A	252	SER
1	A	253	ILE
1	B	112	VAL
1	B	252	SER

### 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	222/229 (97%)	165 (74%)	57 (26%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	222/229 (97%)	158 (71%)	64 (29%)	0	3
1	C	222/229 (97%)	155 (70%)	67 (30%)	0	2
1	D	220/229 (96%)	156 (71%)	64 (29%)	0	2
1	E	222/229 (97%)	169 (76%)	53 (24%)	0	5
1	F	222/229 (97%)	168 (76%)	54 (24%)	0	4
1	G	222/229 (97%)	179 (81%)	43 (19%)	1	9
1	H	222/229 (97%)	164 (74%)	58 (26%)	0	4
All	All	1774/1832 (97%)	1314 (74%)	460 (26%)	0	4

5 of 460 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	254	LEU
1	H	273	GLN
1	E	254	LEU
1	H	254	LEU
1	G	338	VAL

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	E	273	GLN
1	F	142	ASN
1	H	302	GLN
1	G	273	GLN
1	H	273	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

16 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	CMP	F	401	-	22,25,25	1.76	3 (13%)	24,39,39	1.71	5 (20%)
2	CMP	D	402	-	22,25,25	1.80	6 (27%)	24,39,39	1.60	4 (16%)
2	CMP	C	402	-	22,25,25	1.89	6 (27%)	24,39,39	2.15	5 (20%)
2	CMP	H	401	-	22,25,25	2.15	5 (22%)	24,39,39	2.52	6 (25%)
2	CMP	C	401	-	22,25,25	1.72	4 (18%)	24,39,39	2.14	6 (25%)
2	CMP	G	401	-	22,25,25	1.93	6 (27%)	24,39,39	1.65	5 (20%)
2	CMP	H	402	-	22,25,25	1.81	5 (22%)	24,39,39	1.90	6 (25%)
2	CMP	E	402	-	22,25,25	1.92	5 (22%)	24,39,39	1.65	5 (20%)
2	CMP	A	401	-	22,25,25	1.68	3 (13%)	24,39,39	2.27	9 (37%)
2	CMP	B	402	-	22,25,25	2.22	6 (27%)	24,39,39	2.03	8 (33%)
2	CMP	D	401	-	22,25,25	1.89	4 (18%)	24,39,39	1.70	7 (29%)
2	CMP	F	402	-	22,25,25	1.91	5 (22%)	24,39,39	1.82	5 (20%)
2	CMP	E	401	-	22,25,25	1.76	7 (31%)	24,39,39	1.96	7 (29%)
2	CMP	G	402	-	22,25,25	1.63	6 (27%)	24,39,39	2.46	7 (29%)
2	CMP	B	401	-	22,25,25	1.77	4 (18%)	24,39,39	2.57	8 (33%)
2	CMP	A	402	-	22,25,25	2.07	7 (31%)	24,39,39	2.44	7 (29%)

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	CMP	F	401	-	-	0/0/31/31	0/4/4/4
2	CMP	D	402	-	-	0/0/31/31	0/4/4/4
2	CMP	C	402	-	-	0/0/31/31	0/4/4/4
2	CMP	H	401	-	-	0/0/31/31	0/4/4/4
2	CMP	C	401	-	-	0/0/31/31	0/4/4/4
2	CMP	G	401	-	-	0/0/31/31	0/4/4/4
2	CMP	H	402	-	-	0/0/31/31	0/4/4/4
2	CMP	E	402	-	-	0/0/31/31	0/4/4/4
2	CMP	A	401	-	-	0/0/31/31	0/4/4/4
2	CMP	B	402	-	-	0/0/31/31	0/4/4/4
2	CMP	D	401	-	-	0/0/31/31	0/4/4/4
2	CMP	F	402	-	-	0/0/31/31	0/4/4/4
2	CMP	E	401	-	-	0/0/31/31	0/4/4/4
2	CMP	G	402	-	-	0/0/31/31	0/4/4/4
2	CMP	B	401	-	-	0/0/31/31	0/4/4/4
2	CMP	A	402	-	-	0/0/31/31	0/4/4/4

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	CMP	P-O3'	6.88	1.69	1.57
2	H	401	CMP	P-O3'	6.86	1.69	1.57
2	D	401	CMP	P-O3'	5.93	1.67	1.57
2	A	402	CMP	P-O5'	5.43	1.63	1.57
2	A	401	CMP	P-O3'	5.41	1.66	1.57

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	402	CMP	C1'-N9-C4	8.60	141.76	126.64
2	H	401	CMP	C4-C5-N7	-7.18	101.92	109.40
2	A	402	CMP	O3'-P-O1P	-6.46	96.56	110.39
2	B	401	CMP	N3-C2-N1	-6.19	119.01	128.68
2	A	401	CMP	N3-C2-N1	-6.05	119.22	128.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 300 short contacts:

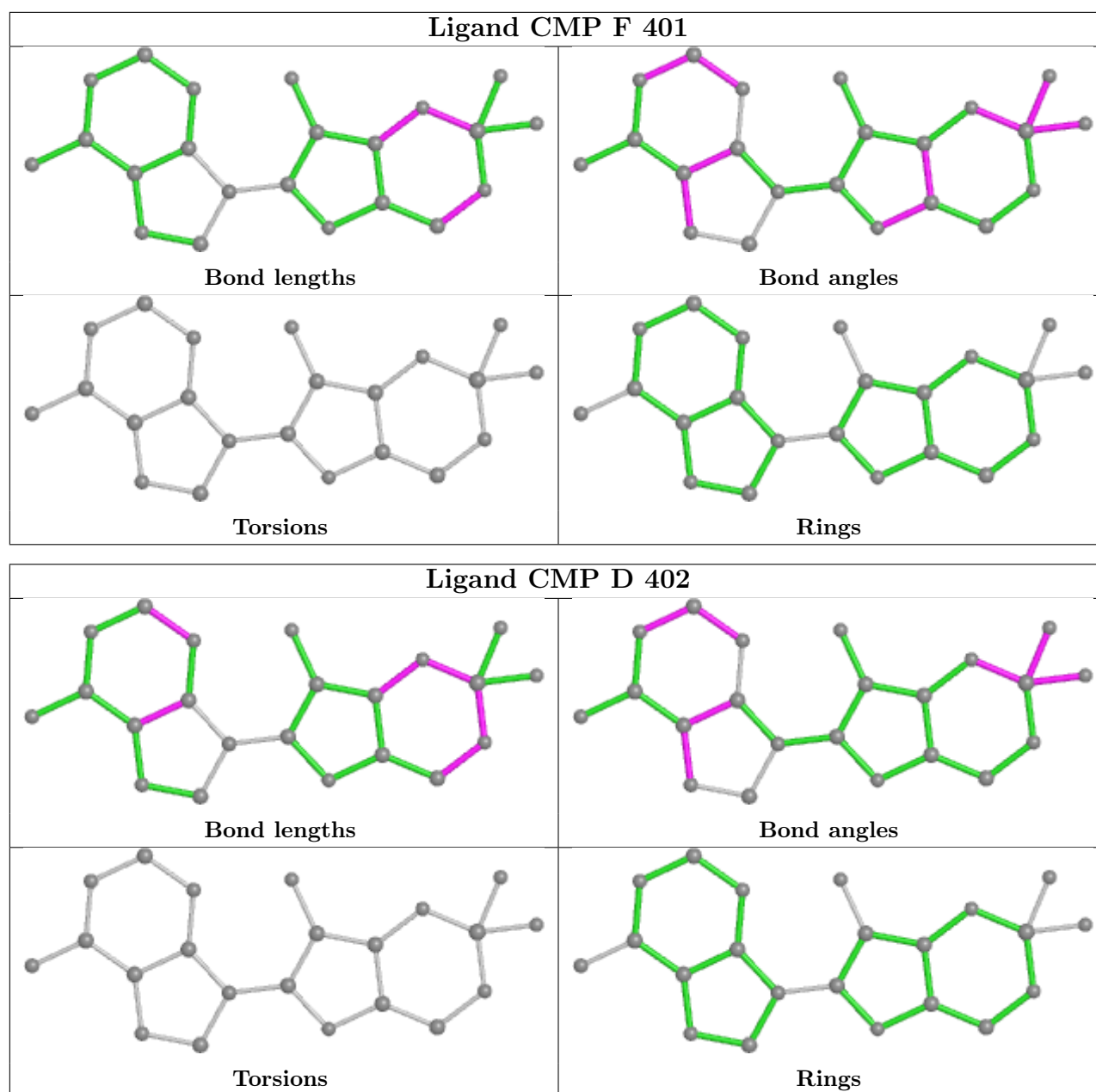
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	CMP	22	0

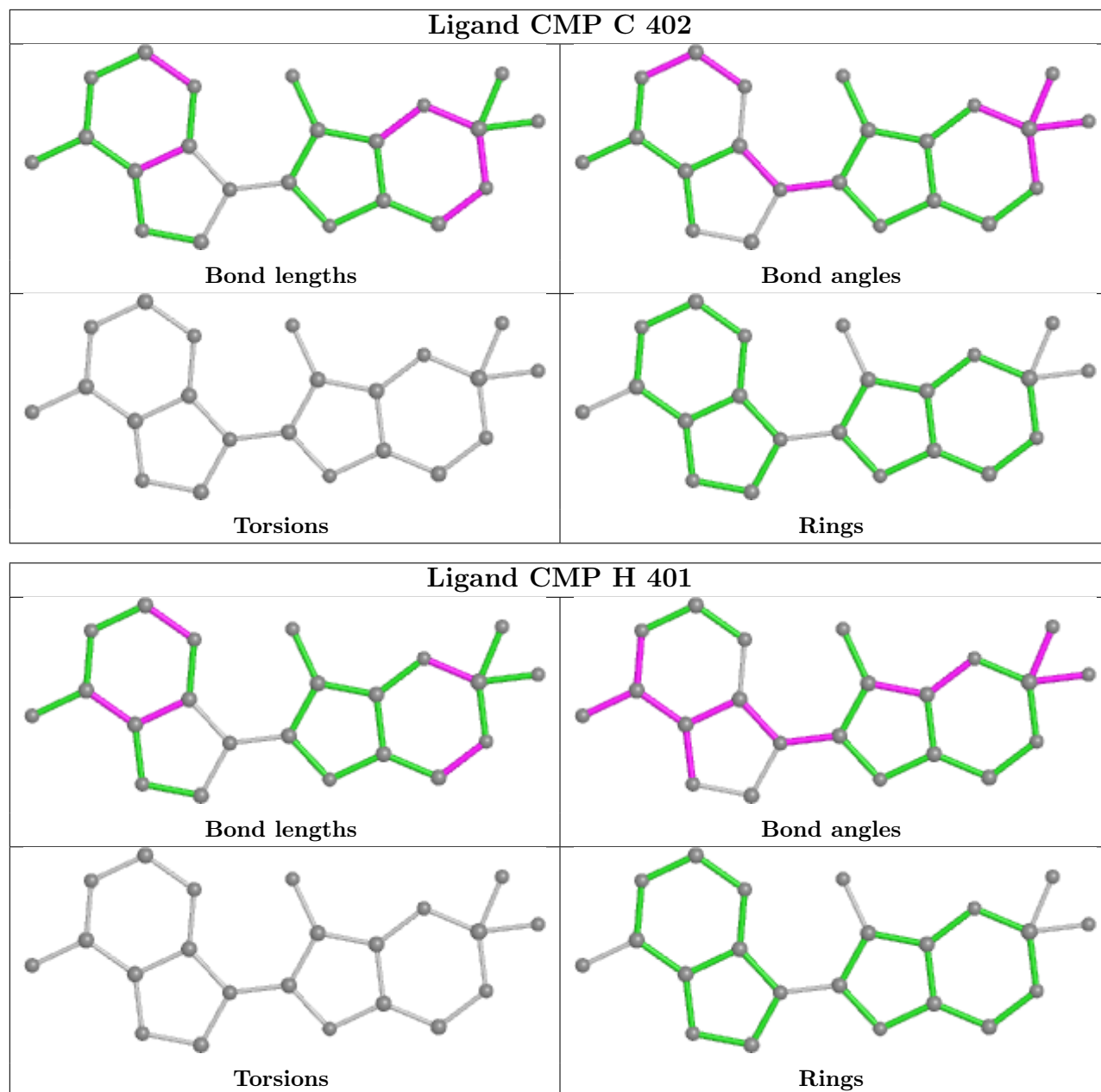
*Continued on next page...*

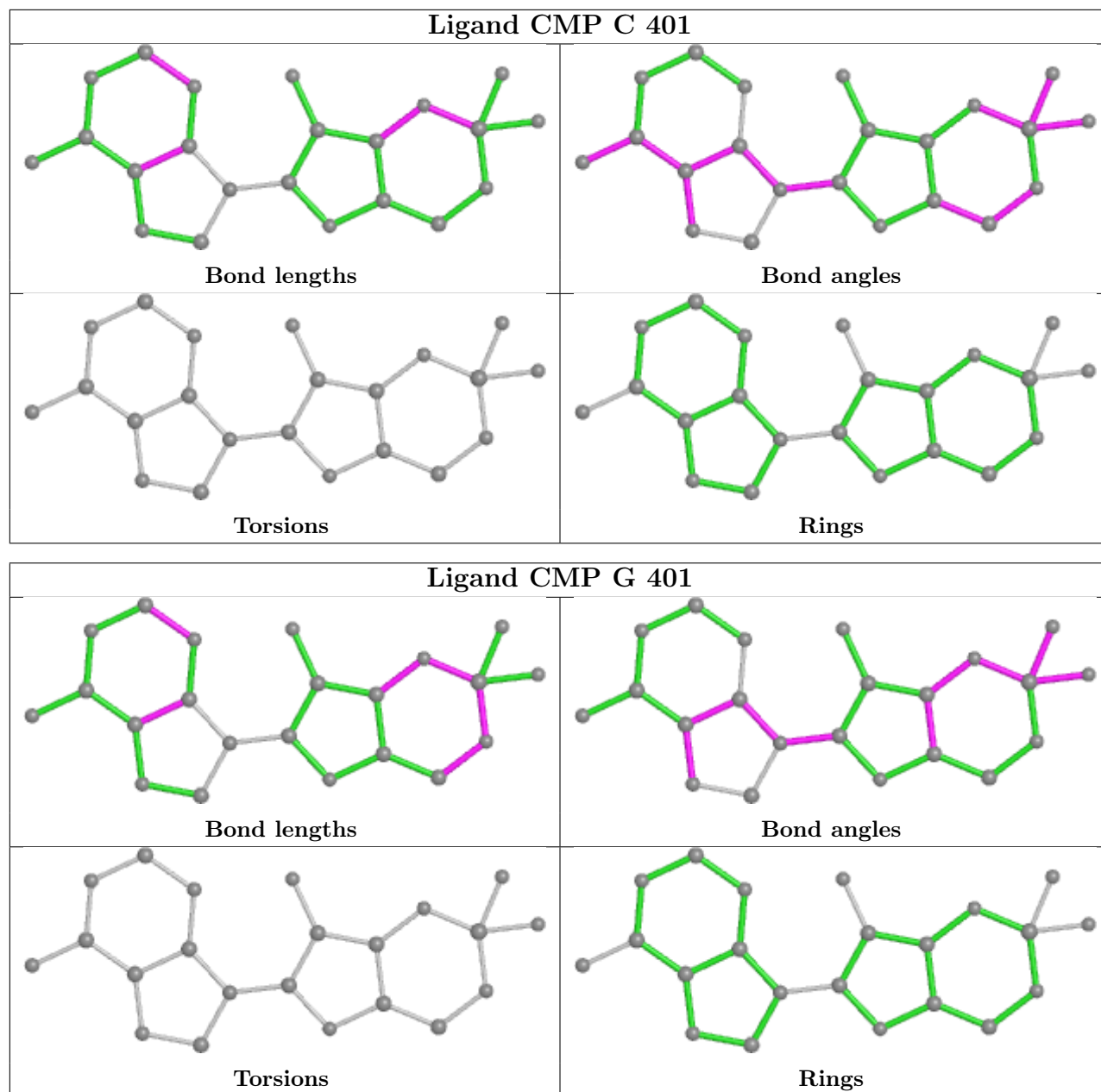
*Continued from previous page...*

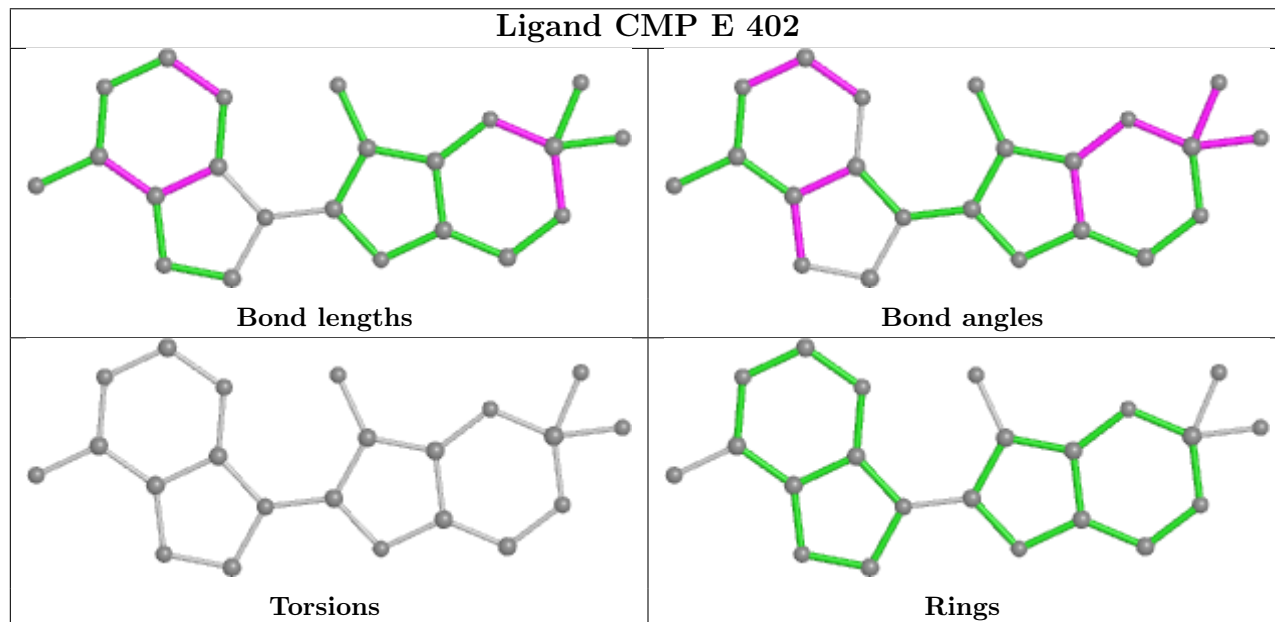
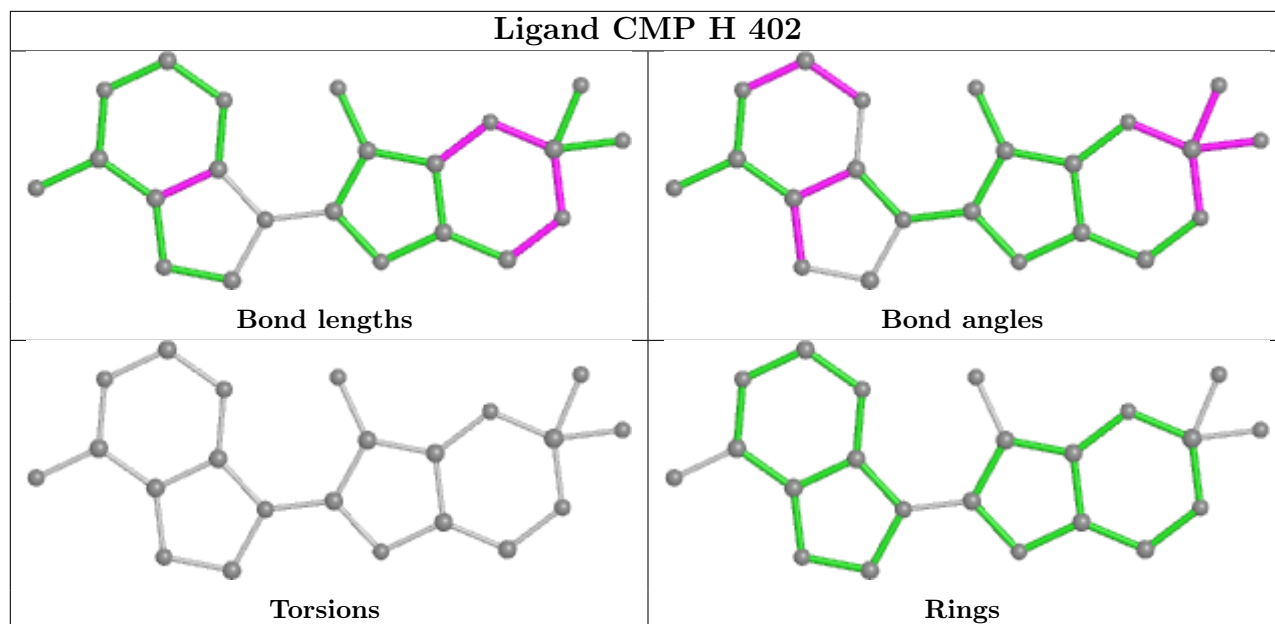
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	402	CMP	21	0
2	C	402	CMP	19	0
2	H	401	CMP	22	0
2	C	401	CMP	17	0
2	G	401	CMP	19	0
2	H	402	CMP	16	0
2	E	402	CMP	11	0
2	A	401	CMP	25	0
2	B	402	CMP	21	0
2	D	401	CMP	16	0
2	F	402	CMP	7	0
2	E	401	CMP	24	0
2	G	402	CMP	11	0
2	B	401	CMP	34	0
2	A	402	CMP	15	0

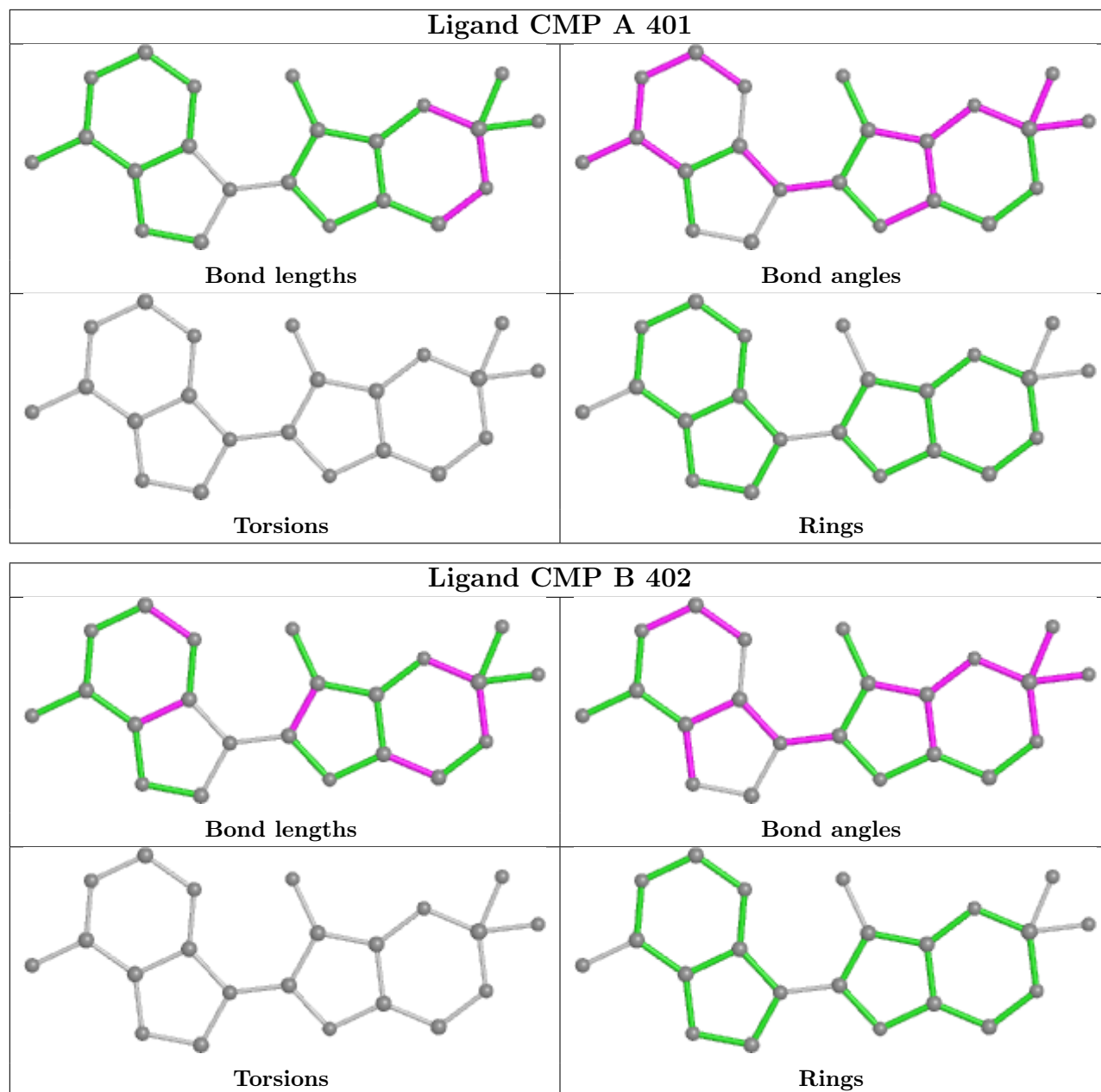
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

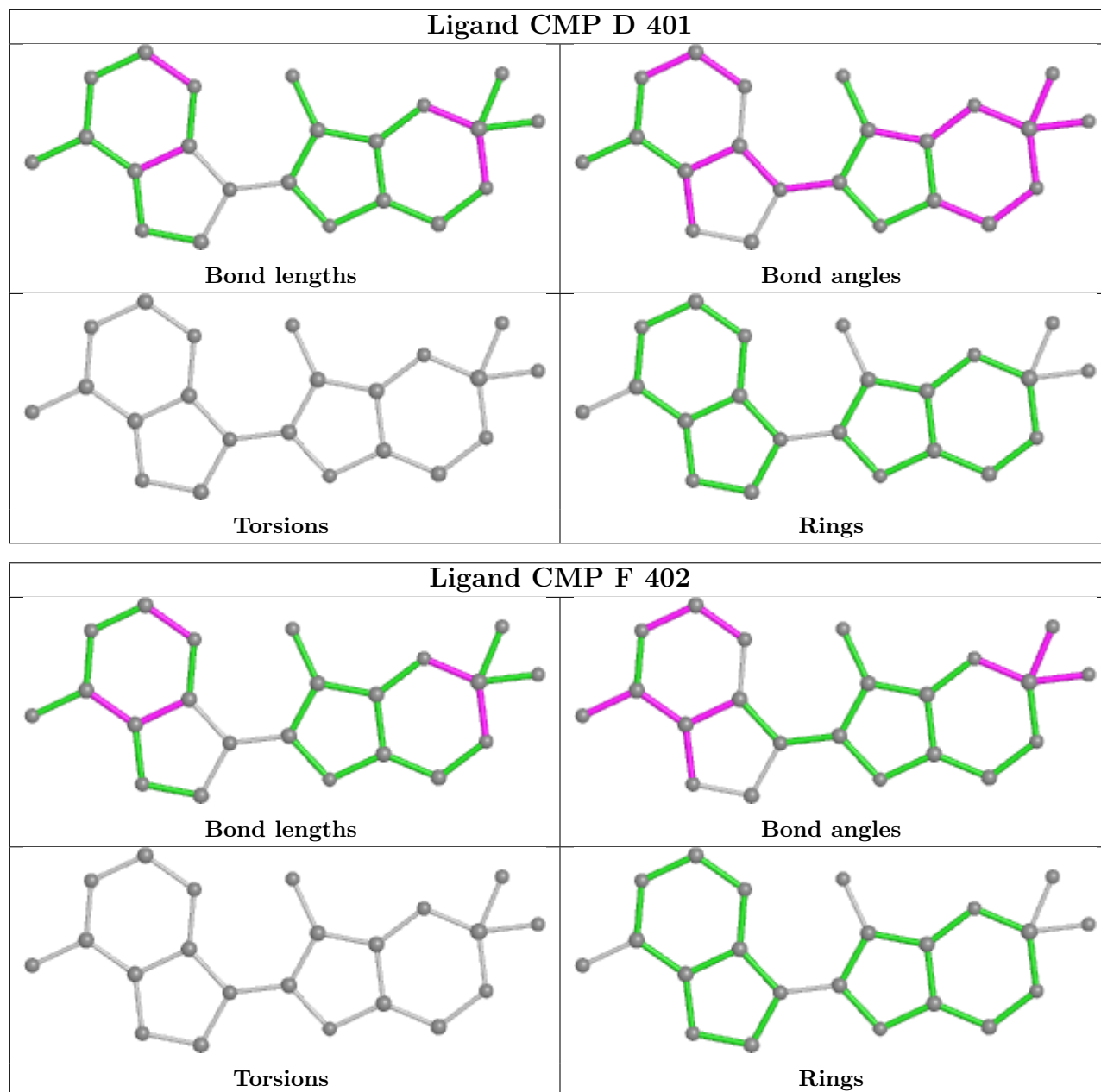




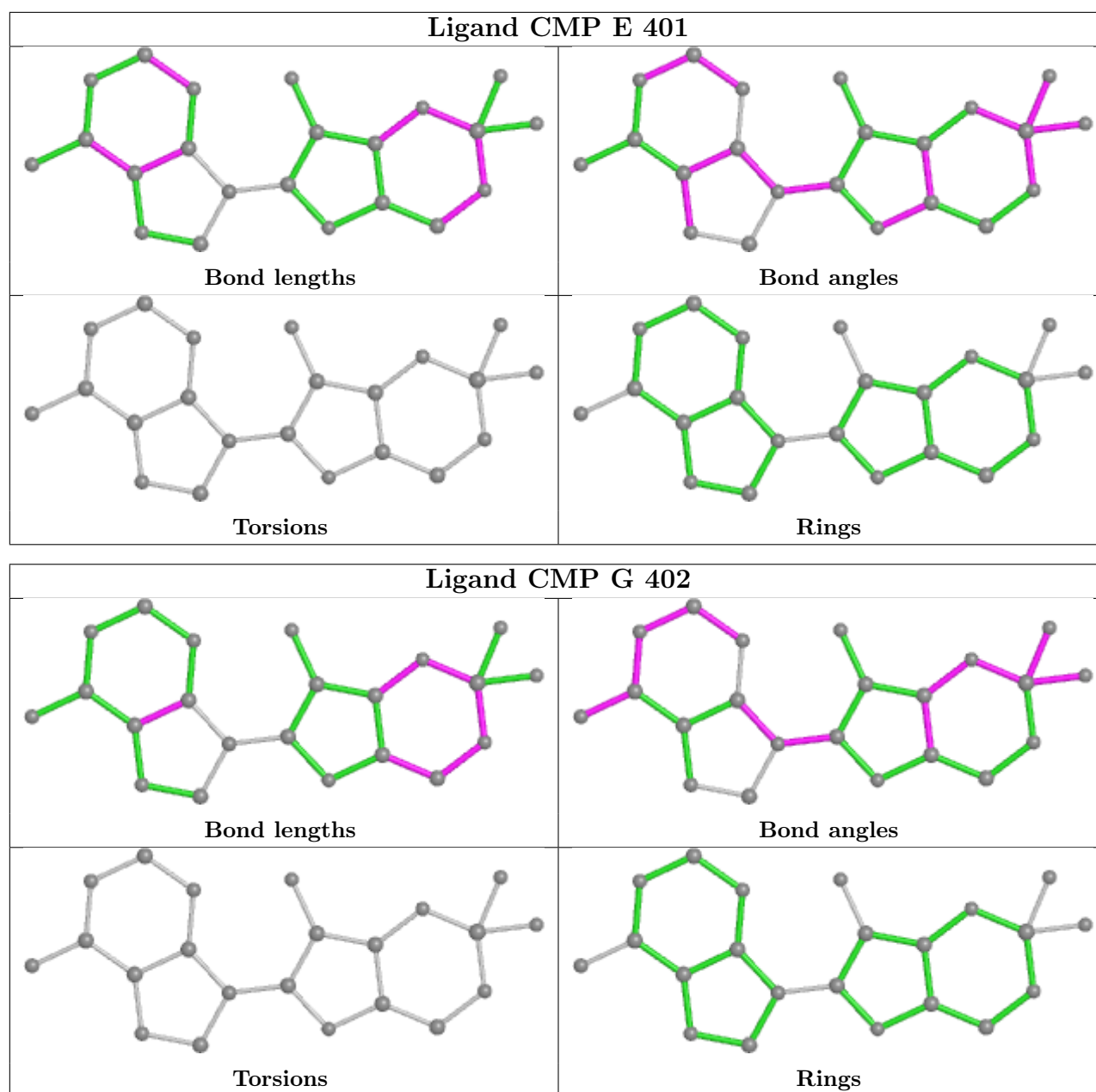


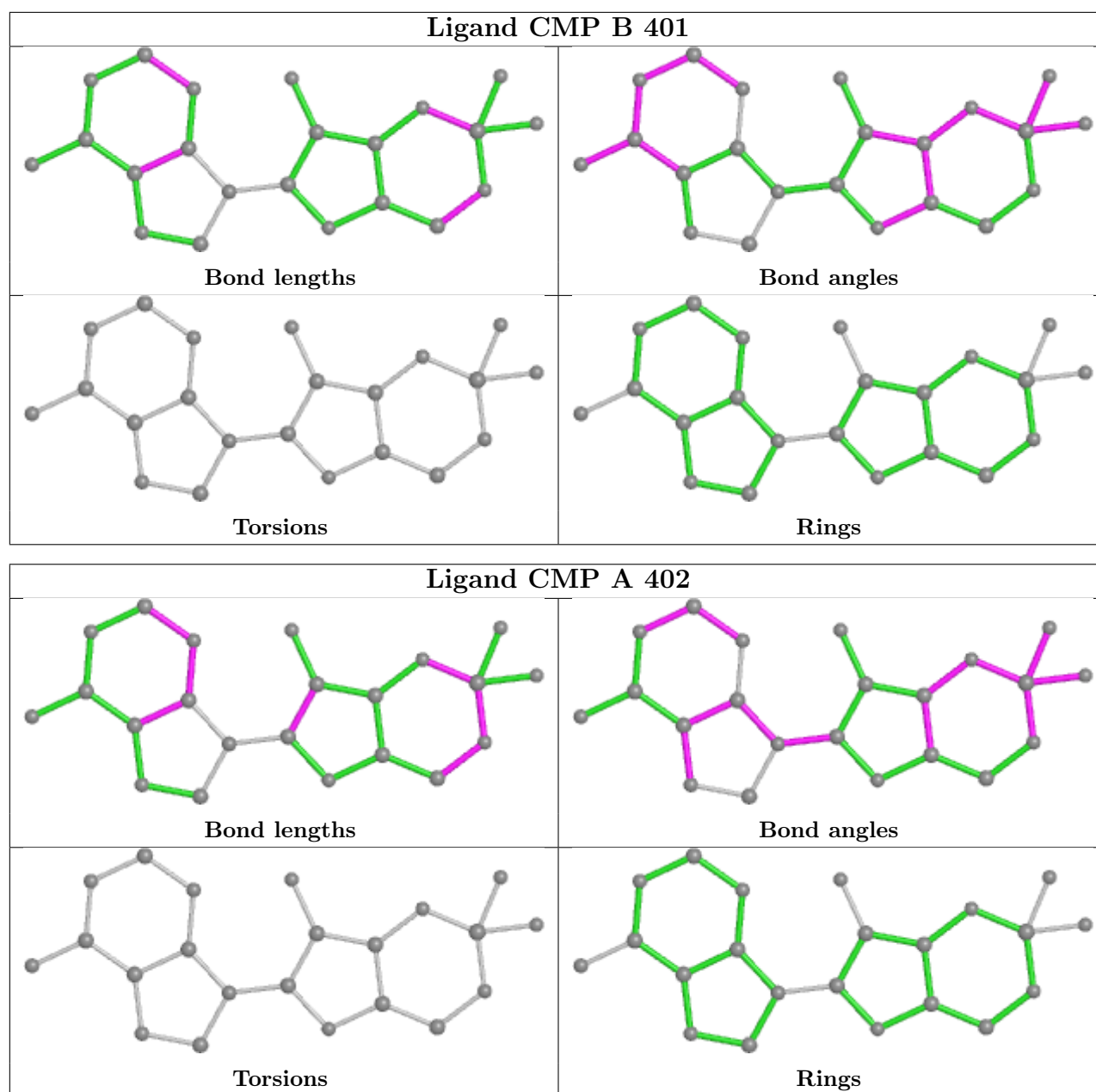












## 5.7 Other polymers [i](#)

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	268/269 (99%)	0.03	13 (4%) 29 25	70, 133, 202, 260	0
1	B	268/269 (99%)	-0.04	11 (4%) 37 30	70, 133, 202, 266	0
1	C	268/269 (99%)	-0.09	8 (2%) 50 39	71, 131, 201, 286	0
1	D	266/269 (98%)	-0.05	10 (3%) 40 32	75, 133, 194, 246	0
1	E	268/269 (99%)	0.02	10 (3%) 41 33	75, 139, 215, 259	0
1	F	268/269 (99%)	0.04	8 (2%) 50 39	75, 138, 212, 261	0
1	G	268/269 (99%)	-0.06	10 (3%) 41 33	77, 135, 201, 268	0
1	H	268/269 (99%)	-0.05	7 (2%) 56 45	71, 132, 199, 274	0
All	All	2142/2152 (99%)	-0.03	77 (3%) 42 34	70, 134, 205, 286	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	306	GLU	7.7
1	B	304	ARG	6.4
1	B	305	SER	6.4
1	A	306	GLU	5.1
1	H	169	GLY	5.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

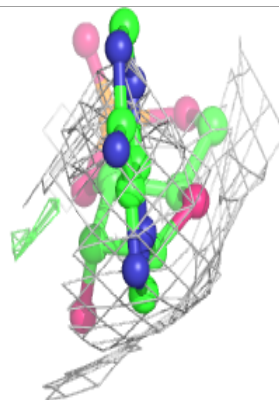
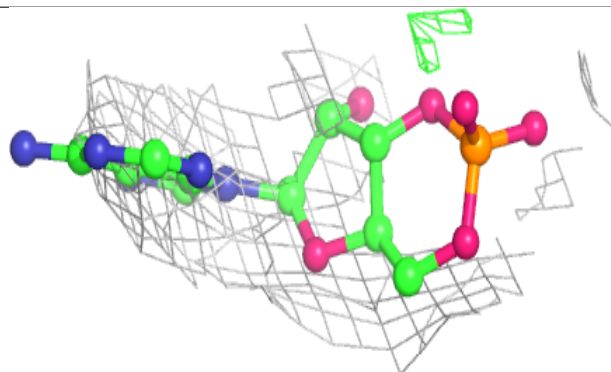
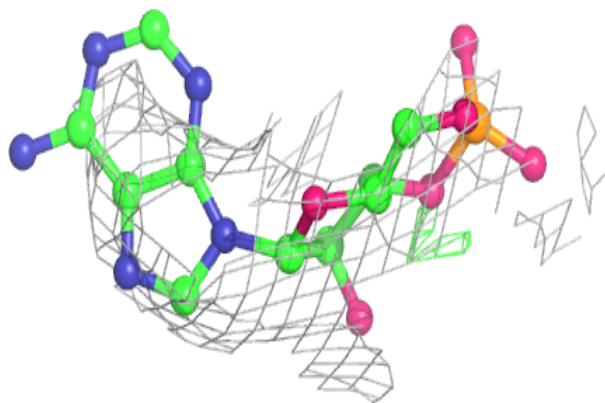
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CMP	A	402	22/22	0.92	0.33	79,151,186,198	0
2	CMP	B	402	22/22	0.92	0.26	86,150,175,194	0
2	CMP	C	401	22/22	0.94	0.29	77,107,140,155	0
2	CMP	E	402	22/22	0.94	0.15	118,201,228,242	0
2	CMP	G	402	22/22	0.94	0.32	101,148,200,208	0
2	CMP	H	401	22/22	0.94	0.30	74,105,125,133	0
2	CMP	F	402	22/22	0.95	0.18	137,185,218,227	0
2	CMP	G	401	22/22	0.95	0.23	79,112,144,145	0
2	CMP	D	402	22/22	0.95	0.28	112,143,193,210	0
2	CMP	D	401	22/22	0.95	0.21	84,111,128,131	0
2	CMP	B	401	22/22	0.96	0.22	70,102,127,132	0
2	CMP	C	402	22/22	0.96	0.28	79,130,177,213	0
2	CMP	A	401	22/22	0.96	0.28	77,102,123,128	0
2	CMP	E	401	22/22	0.97	0.28	73,108,130,140	0
2	CMP	F	401	22/22	0.97	0.28	69,96,132,143	0
2	CMP	H	402	22/22	0.97	0.27	81,139,165,200	0

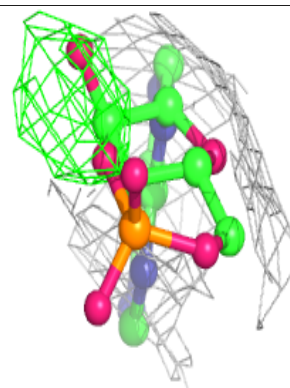
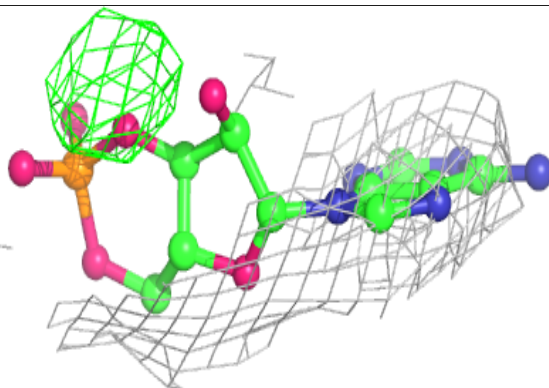
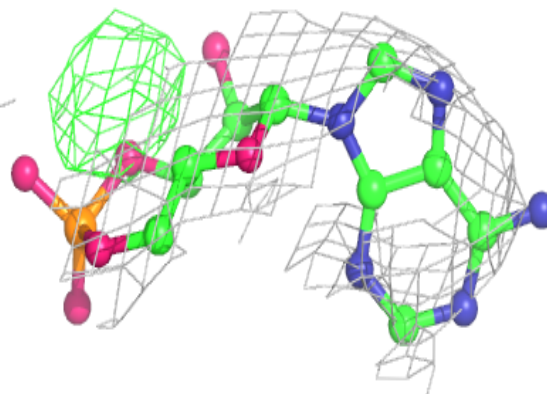
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around CMP A 402:**

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

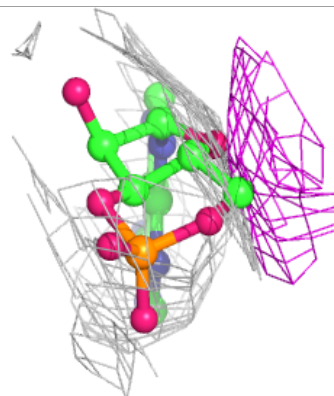
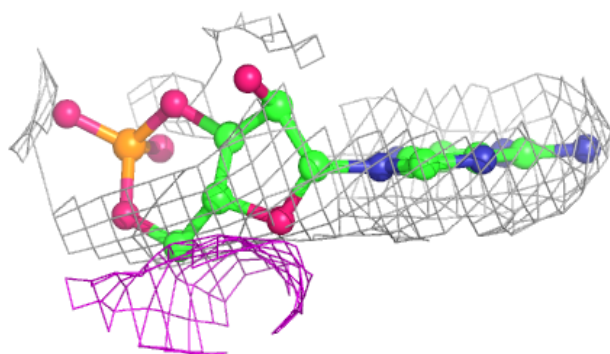
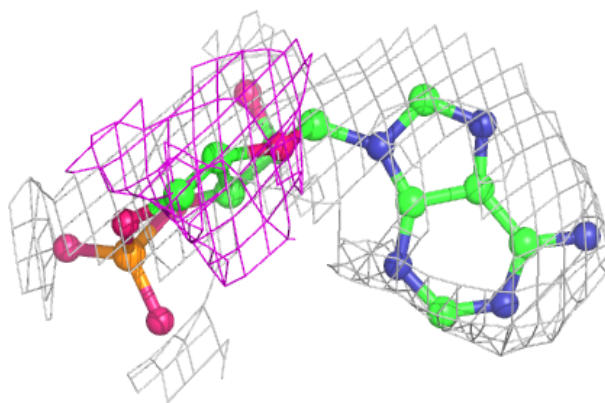
**Electron density around CMP B 402:**

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

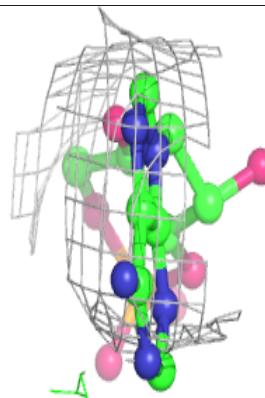
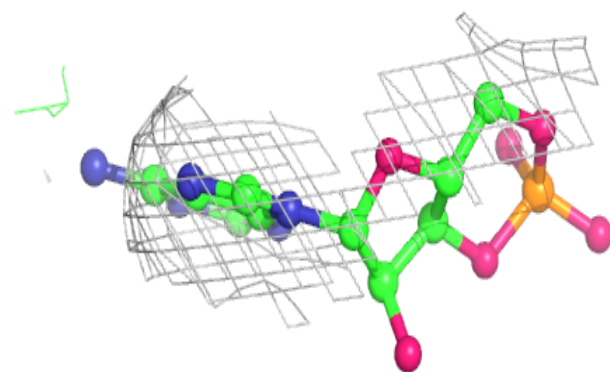
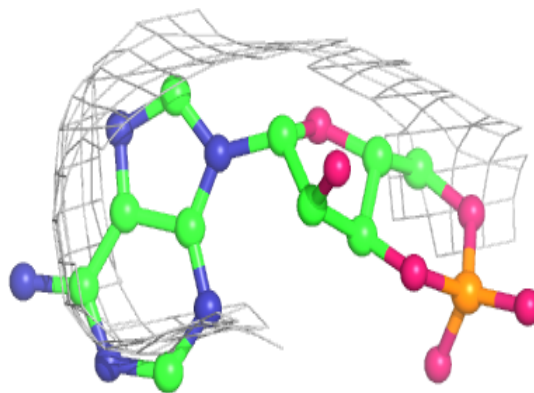


**Electron density around CMP C 401:**

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

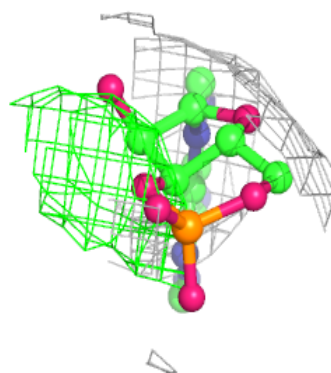
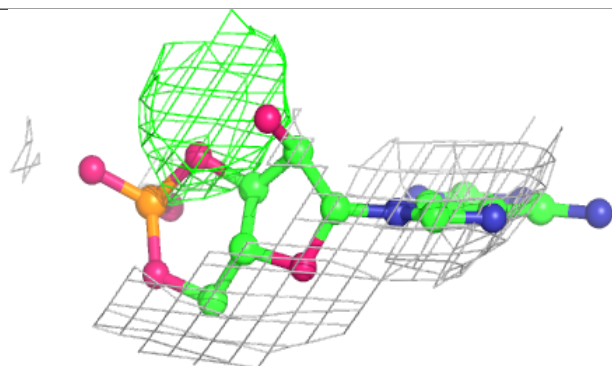
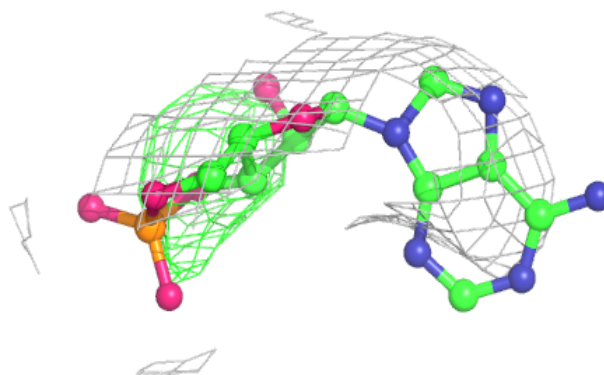
**Electron density around CMP E 402:**

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

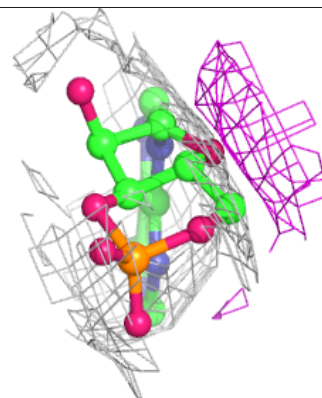
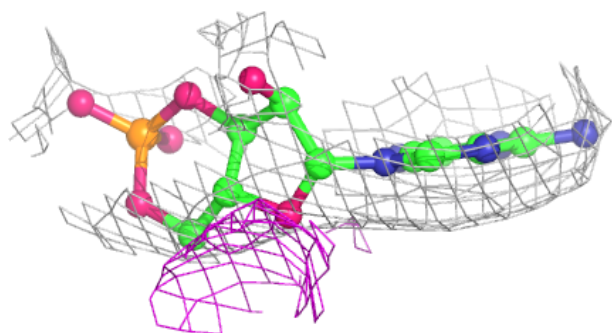
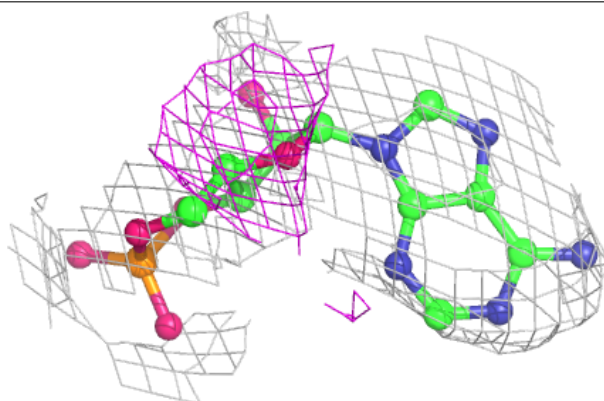


**Electron density around CMP G 402:**

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

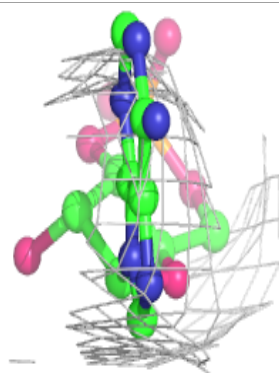
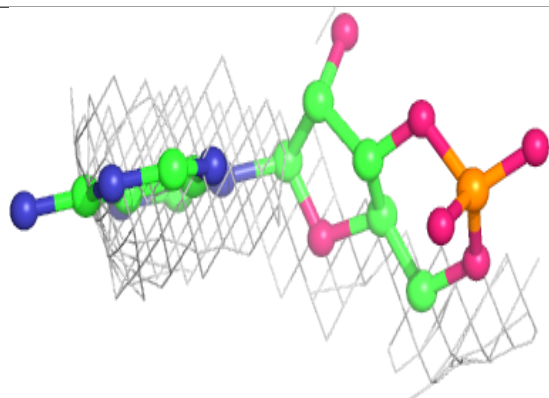
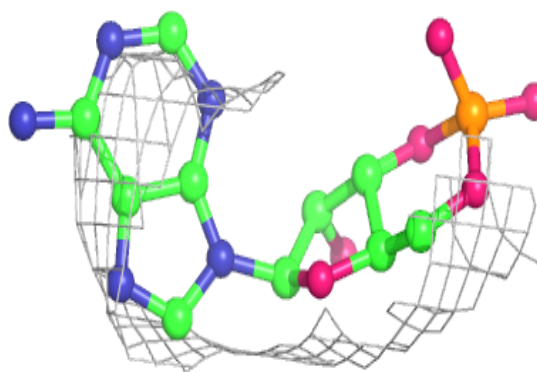
**Electron density around CMP H 401:**

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and green (positive)

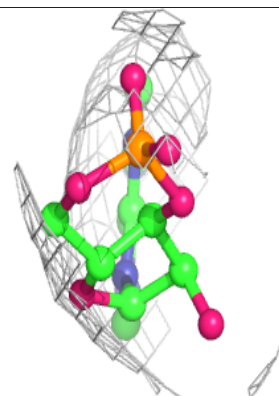
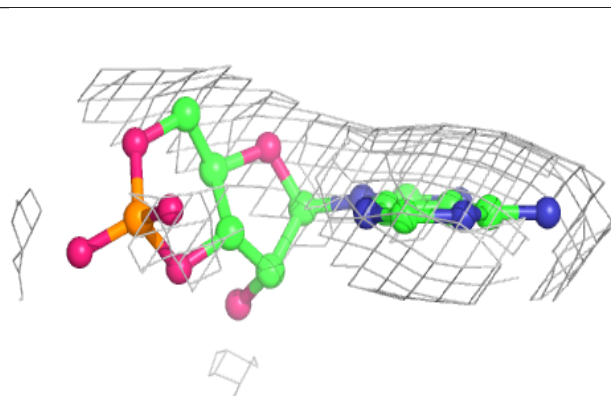
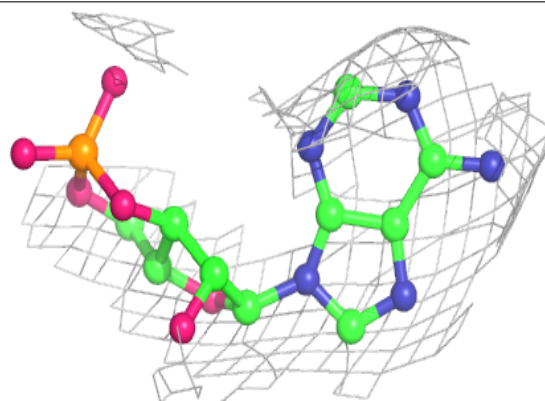


**Electron density around CMP F 402:**

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

**Electron density around CMP G 401:**

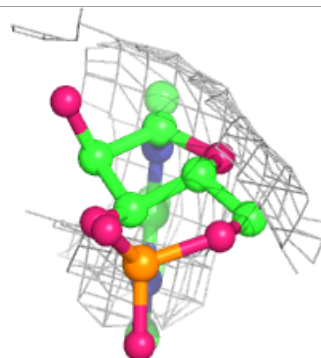
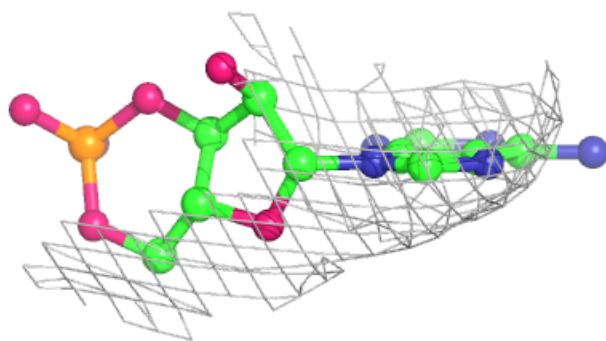
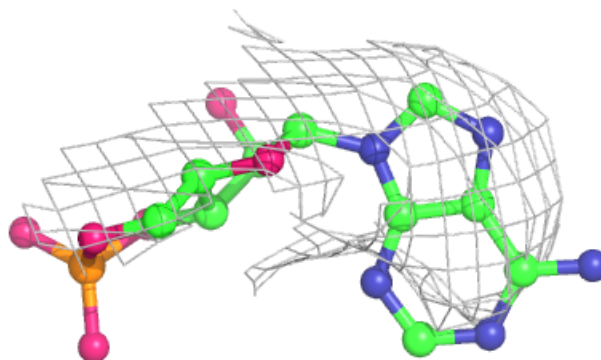
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



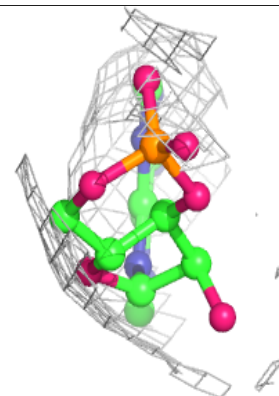
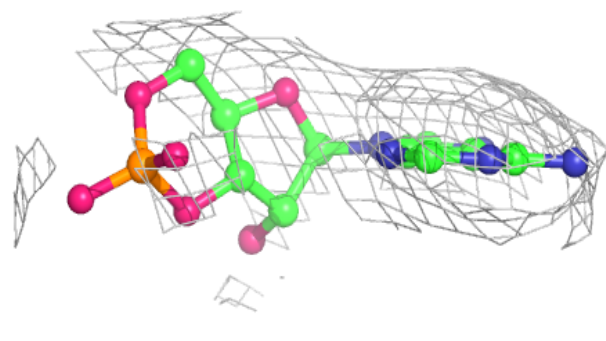
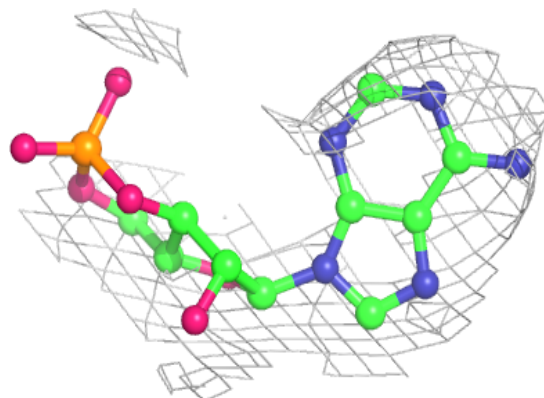


**Electron density around CMP D 402:**

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

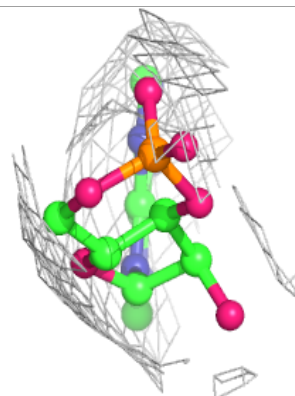
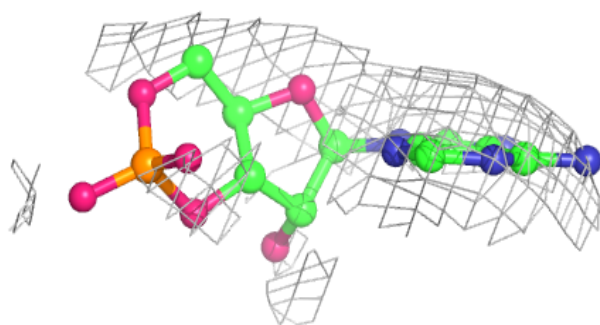
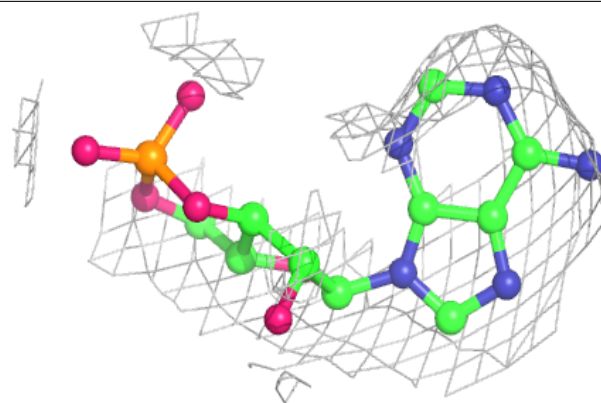
**Electron density around CMP D 401:**

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

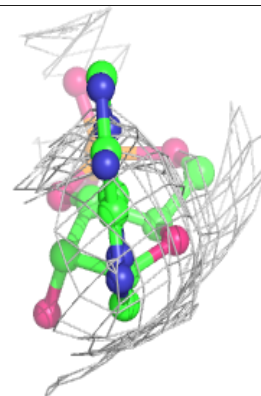
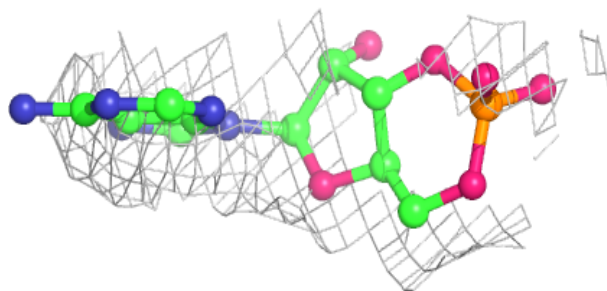
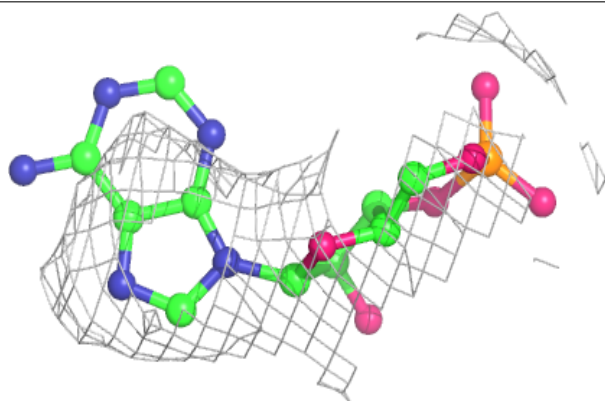


**Electron density around CMP B 401:**

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

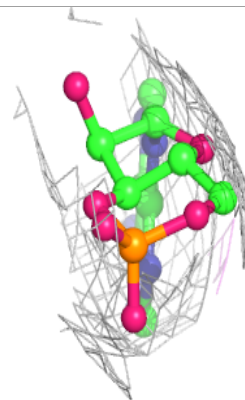
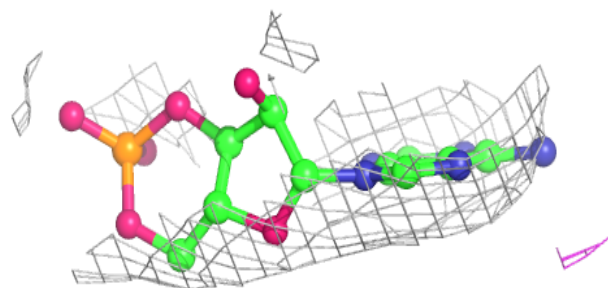
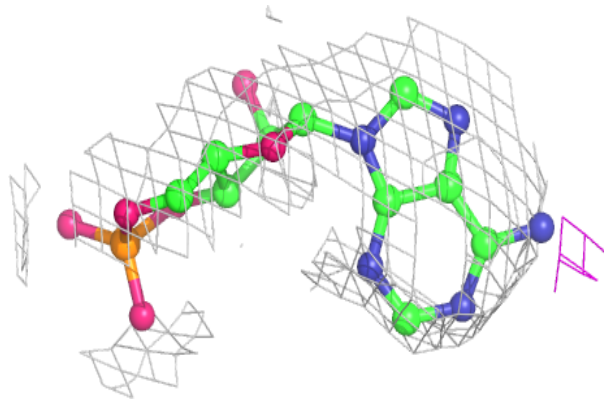
**Electron density around CMP C 402:**

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

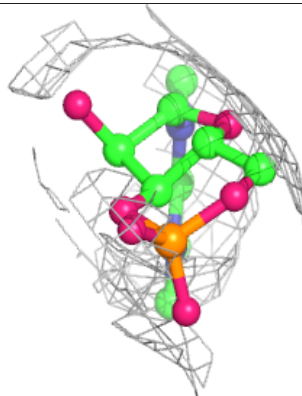
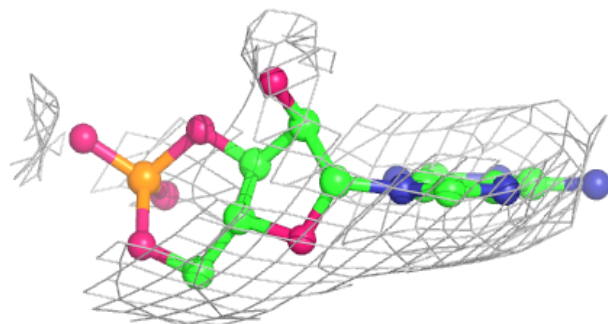
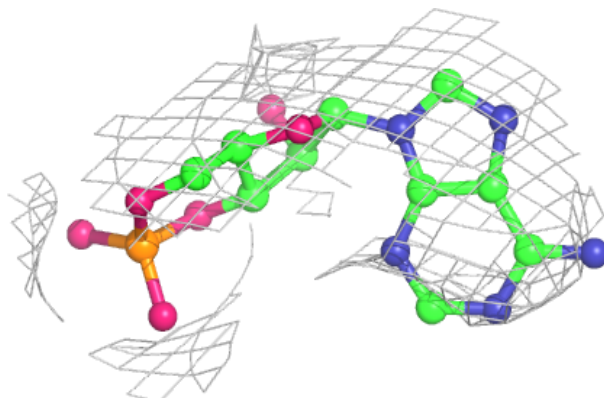


**Electron density around CMP A 401:**

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

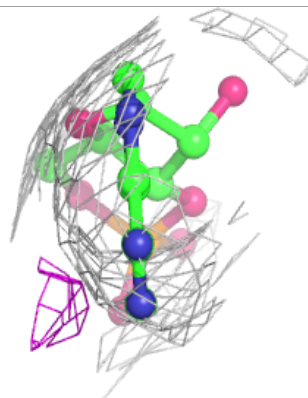
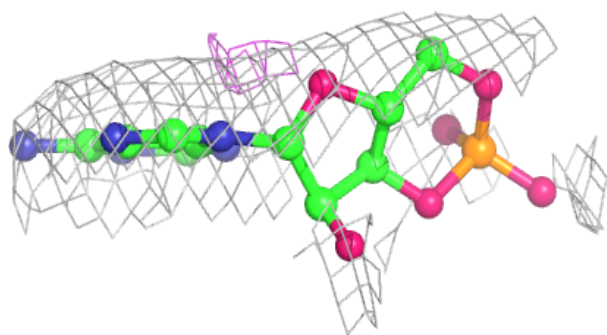
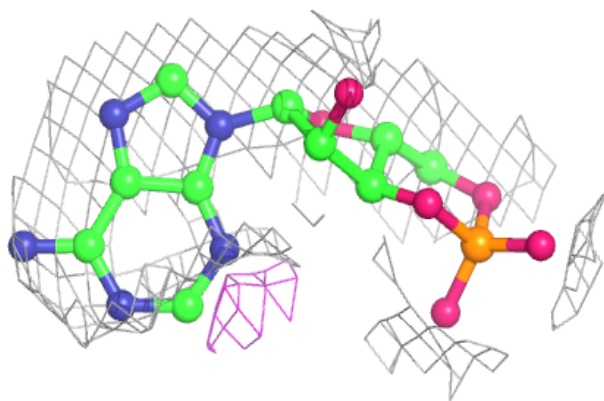
**Electron density around CMP E 401:**

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

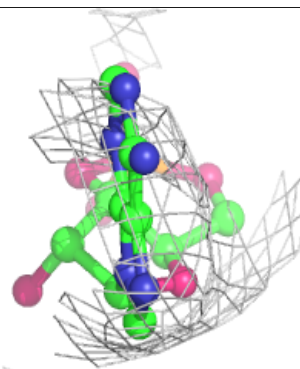
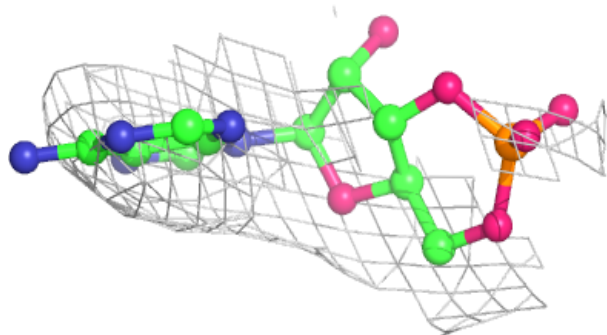
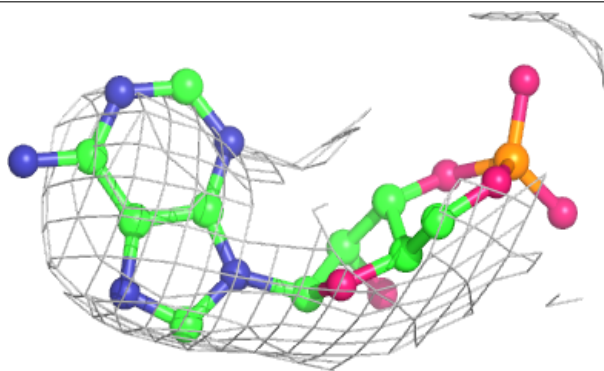


**Electron density around CMP F 401:**

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

**Electron density around CMP H 402:**

$2mF_o-DF_c$  (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.