



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 01:24 AM UTC

PDB ID : 9O0V / pdb_00009o0v
Title : Crystal structure of CRAF/MEK1 complex with PLX4720, CH5126766, and AMPPNP
Authors : Jang, D.M.; Eck, M.J.
Deposited on : 2025-04-03
Resolution : 3.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

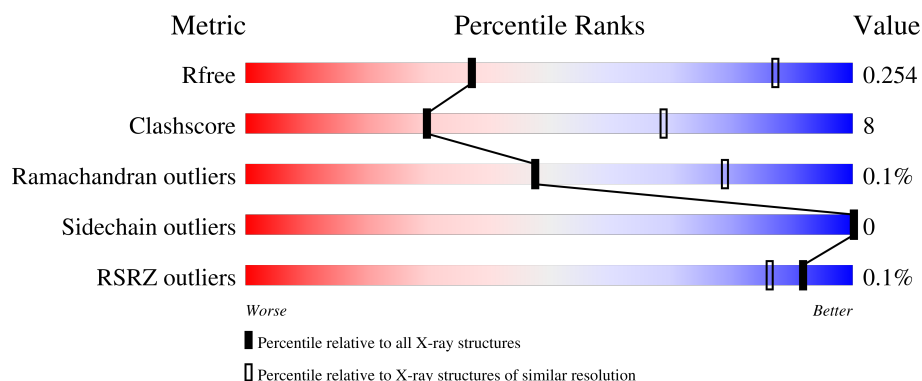
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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

Mol	Chain	Length	Quality of chain
1	A	280	 83% 12% 5%
1	C	280	 80% 14% 6%
1	E	280	 78% 16% 7%
1	G	280	 82% 13% 5%
2	B	395	 66% 16% 18%

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Mol	Chain	Length	Quality of chain
2	D	395	% 54% 25% 20%
2	F	395	59% 22% • 18%
2	H	395	64% 17% 19%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18879 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 RAF proto-oncogene serine/threonine-protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	1	0
			2137	1369	368	386	14			
1	C	264	Total	C	N	O	S	0	0	0
			2115	1355	362	384	14			
1	E	261	Total	C	N	O	S	0	0	0
			2098	1346	359	379	14			
1	G	265	Total	C	N	O	S	0	1	0
			2135	1368	366	387	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	336	SER	-	expression tag	UNP P04049
A	340	ASP	TYR	engineered mutation	UNP P04049
A	341	ASP	TYR	engineered mutation	UNP P04049
C	336	SER	-	expression tag	UNP P04049
C	340	ASP	TYR	engineered mutation	UNP P04049
C	341	ASP	TYR	engineered mutation	UNP P04049
E	336	SER	-	expression tag	UNP P04049
E	340	ASP	TYR	engineered mutation	UNP P04049
E	341	ASP	TYR	engineered mutation	UNP P04049
G	336	SER	-	expression tag	UNP P04049
G	340	ASP	TYR	engineered mutation	UNP P04049
G	341	ASP	TYR	engineered mutation	UNP P04049

- Molecule 2 is a protein called Dual specificity mitogen-activated protein kinase kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	322	Total	C	N	O	S	0	0	0
			2532	1618	430	467	17			
2	D	315	Total	C	N	O	S	0	0	0
			2465	1578	413	459	15			

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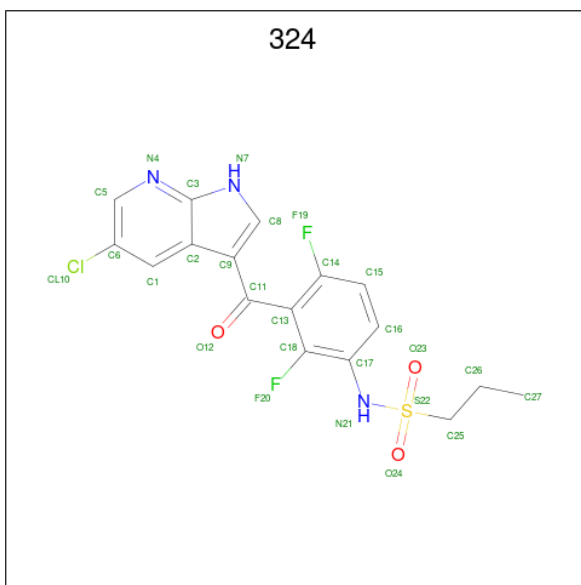
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	322	Total	C	N	O	S	0	0	0
			2522	1613	427	465	17			
2	H	318	Total	C	N	O	S	0	0	0
			2503	1599	426	463	15			

There are 16 discrepancies between the modelled and reference sequences:

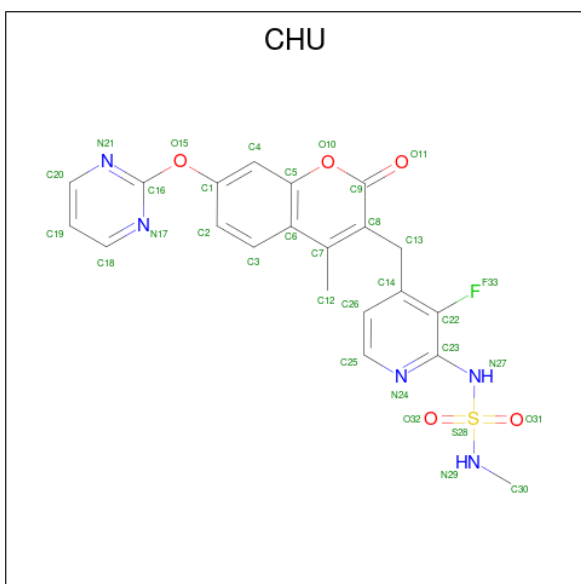
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP Q02750
B	0	GLY	-	expression tag	UNP Q02750
B	218	ALA	SER	engineered mutation	UNP Q02750
B	222	ALA	SER	engineered mutation	UNP Q02750
D	-1	GLY	-	expression tag	UNP Q02750
D	0	GLY	-	expression tag	UNP Q02750
D	218	ALA	SER	engineered mutation	UNP Q02750
D	222	ALA	SER	engineered mutation	UNP Q02750
F	-1	GLY	-	expression tag	UNP Q02750
F	0	GLY	-	expression tag	UNP Q02750
F	218	ALA	SER	engineered mutation	UNP Q02750
F	222	ALA	SER	engineered mutation	UNP Q02750
H	-1	GLY	-	expression tag	UNP Q02750
H	0	GLY	-	expression tag	UNP Q02750
H	218	ALA	SER	engineered mutation	UNP Q02750
H	222	ALA	SER	engineered mutation	UNP Q02750

- Molecule 3 is N-{3-[(5-chloro-1H-pyrrolo[2,3-b]pyridin-3-yl)carbonyl]-2,4-difluorophenyl}propane-1-sulfonamide (CCD ID: 324) (formula: C₁₇H₁₄ClF₂N₃O₃S) (labeled as "Ligand of Interest" by depositor).



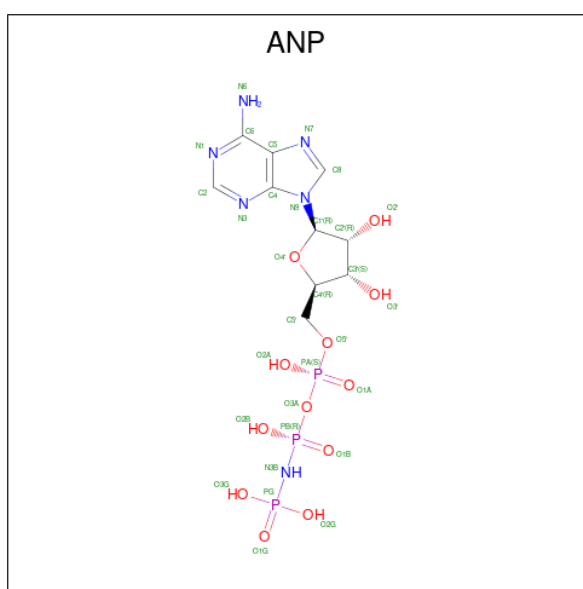
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	F	N	O	S	0	0
			27	17	1	2	3	3	1		
3	C	1	Total	C	Cl	F	N	O	S	0	0
			27	17	1	2	3	3	1		
3	E	1	Total	C	Cl	F	N	O	S	0	0
			27	17	1	2	3	3	1		
3	G	1	Total	C	Cl	F	N	O	S	0	0
			27	17	1	2	3	3	1		

- Molecule 4 is N-(3-fluoro-4-{[4-methyl-2-oxo-7-(pyrimidin-2-yloxy)-2H-chromen-3-yl]methyl}pyridin-2-yl)-N'-methylsulfuric diamide (CCD ID: CHU) (formula: $C_{21}H_{18}FN_5O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	F	N	O	S	
			33	21	1	5	5	1	0
4	D	1	Total	C	F	N	O	S	
			33	21	1	5	5	1	0
4	F	1	Total	C	F	N	O	S	
			33	21	1	5	5	1	0
4	H	1	Total	C	F	N	O	S	
			33	21	1	5	5	1	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P		
			31	10	6	12	3	0	0
5	D	1	Total	C	N	O	P		
			31	10	6	12	3	0	0
5	F	1	Total	C	N	O	P		
			31	10	6	12	3	0	0
5	H	1	Total	C	N	O	P		
			31	10	6	12	3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	3	Total O 3	0	0

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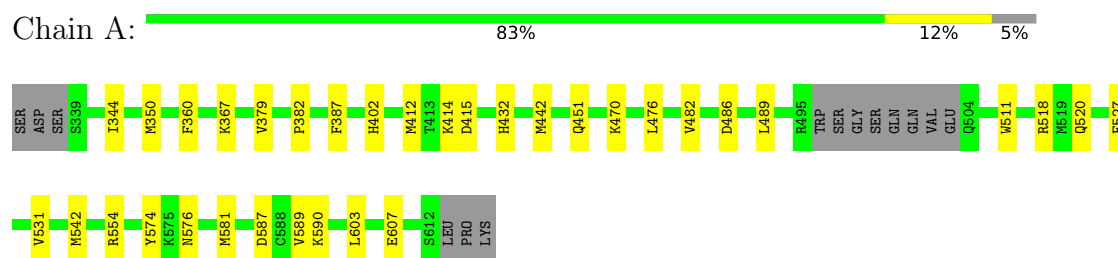
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	2	Total	O	0	0
			2	2		
6	G	3	Total	O	0	0
			3	3		

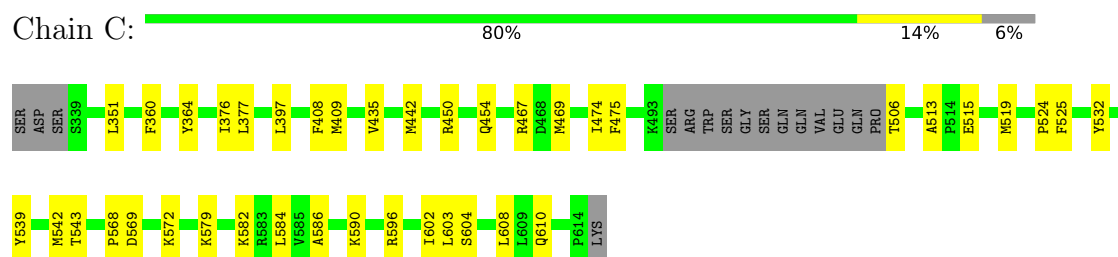
3 Residue-property plots

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.

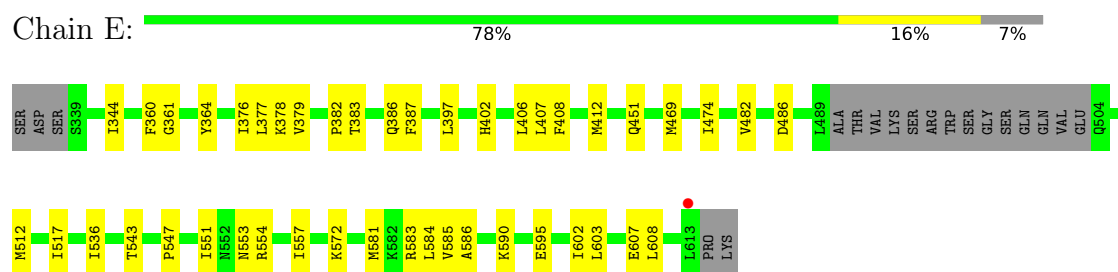
- Molecule 1: RAF proto-oncogene serine/threonine-protein kinase



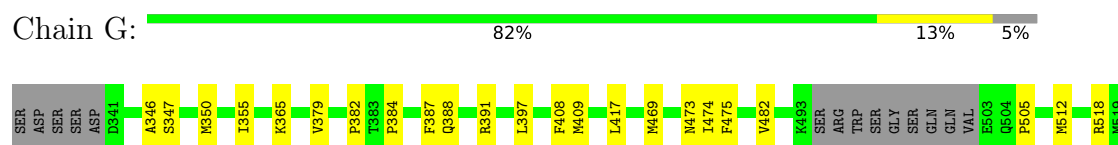
- Molecule 1: RAF proto-oncogene serine/threonine-protein kinase



- Molecule 1: RAF proto-oncogene serine/threonine-protein kinase



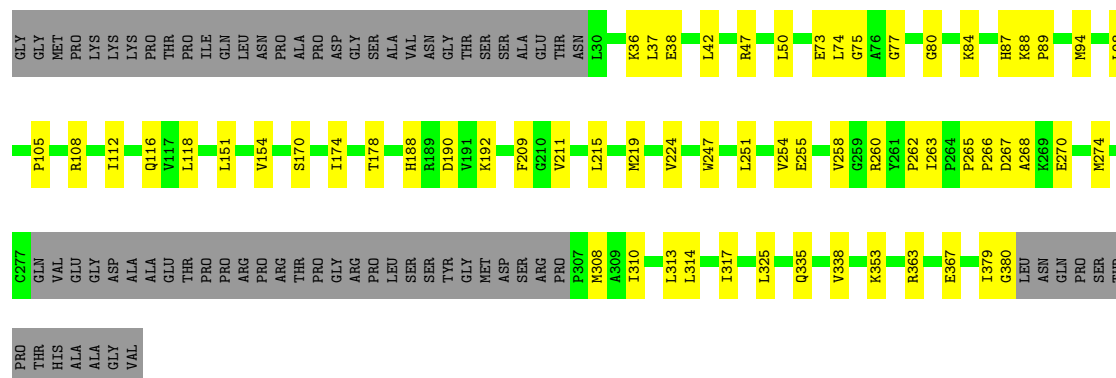
- Molecule 1: RAF proto-oncogene serine/threonine-protein kinase





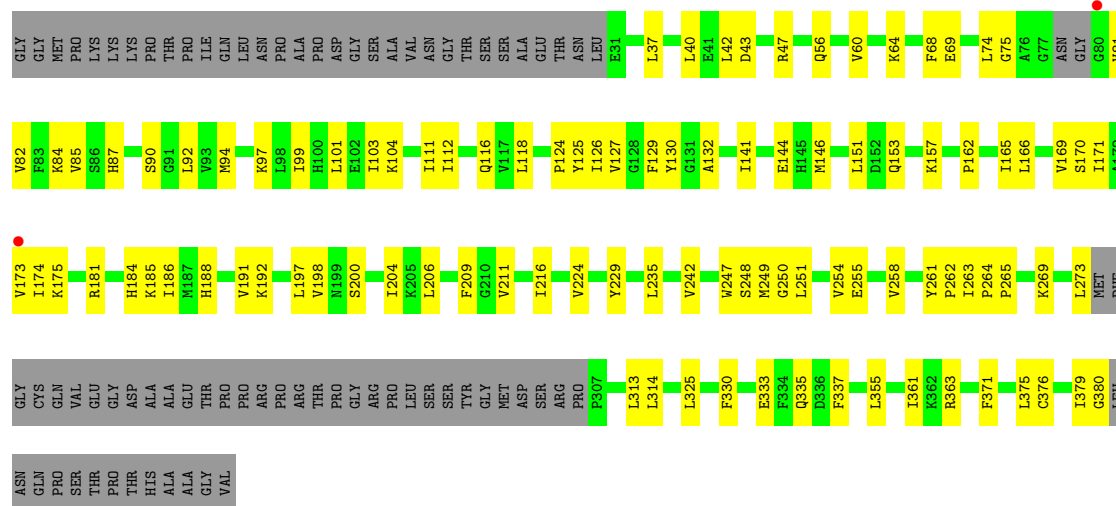
- Molecule 2: Dual specificity mitogen-activated protein kinase kinase 1

Chain B: 66% 16% 18%



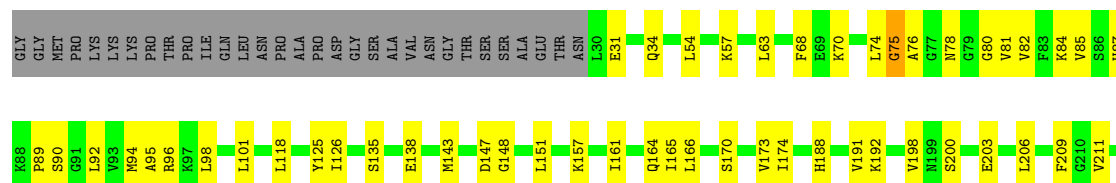
- Molecule 2: Dual specificity mitogen-activated protein kinase kinase 1

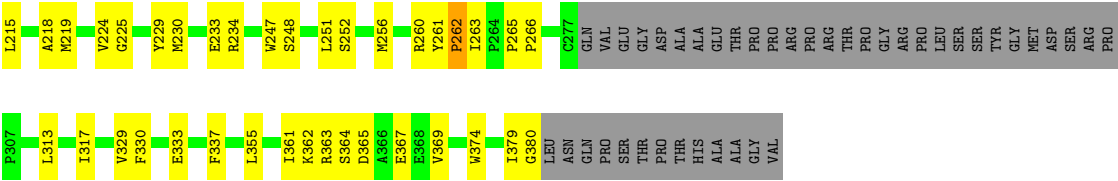
Chain D: 54% 25% 20%



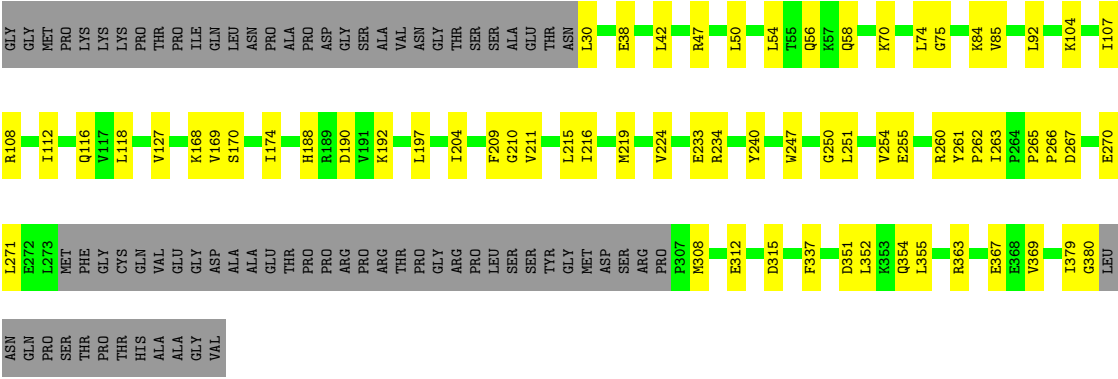
- Molecule 2: Dual specificity mitogen-activated protein kinase kinase 1

Chain F: 59% 22% 18%





- Molecule 2: Dual specificity mitogen-activated protein kinase kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	180.94Å 180.94Å 366.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.03 – 3.50 48.03 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.03-3.50) 99.6 (48.03-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.205 , 0.254 0.205 , 0.254	Depositor DCC
R_{free} test set	2269 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	96.9	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 91.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18879	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, CHU, 324

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	0.15	0/2187	0.41	0/2952
1	C	0.15	0/2161	0.45	0/2918
1	E	0.15	0/2145	0.42	0/2896
1	G	0.16	0/2182	0.40	0/2947
2	B	0.13	0/2580	0.42	0/3471
2	D	0.20	0/2511	0.52	0/3381
2	F	0.17	0/2570	0.46	0/3459
2	H	0.16	0/2550	0.47	0/3432
All	All	0.16	0/18886	0.45	0/25456

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2137	0	2145	28	0
1	C	2115	0	2125	28	0
1	E	2098	0	2102	35	0
1	G	2135	0	2144	25	0
2	B	2532	0	2574	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2465	0	2494	75	0
2	F	2522	0	2559	67	0
2	H	2503	0	2548	40	0
3	A	27	0	14	1	0
3	C	27	0	14	1	0
3	E	27	0	14	3	0
3	G	27	0	14	2	0
4	B	33	0	18	1	0
4	D	33	0	18	2	0
4	F	33	0	18	0	0
4	H	33	0	18	1	0
5	B	31	0	13	1	0
5	D	31	0	13	1	0
5	F	31	0	13	1	0
5	H	31	0	13	1	0
6	A	3	0	0	0	0
6	E	2	0	0	0	0
6	G	3	0	0	0	0
All	All	18879	0	18871	321	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 8.

The worst 5 of 321 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:234:ARG:HG2	2:H:240:TYR:CD1	2.13	0.83
1:C:469:MET:HE1	1:C:474:ILE:HD11	1.65	0.78
1:A:476:LEU:HD23	1:A:482:VAL:HG12	1.67	0.76
2:H:174:ILE:HG23	2:H:352:LEU:HD22	1.69	0.74
2:D:325:LEU:HD13	2:D:335:GLN:HA	1.71	0.73

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	263/280 (94%)	251 (95%)	12 (5%)	0	100	100
1	C	260/280 (93%)	247 (95%)	13 (5%)	0	100	100
1	E	257/280 (92%)	247 (96%)	10 (4%)	0	100	100
1	G	262/280 (94%)	248 (95%)	14 (5%)	0	100	100
2	B	318/395 (80%)	301 (95%)	17 (5%)	0	100	100
2	D	309/395 (78%)	289 (94%)	19 (6%)	1 (0%)	36	67
2	F	318/395 (80%)	302 (95%)	14 (4%)	2 (1%)	21	54
2	H	314/395 (80%)	303 (96%)	11 (4%)	0	100	100
All	All	2301/2700 (85%)	2188 (95%)	110 (5%)	3 (0%)	48	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	262	PRO
2	D	81	VAL
2	F	75	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	236/250 (94%)	236 (100%)	0	100	100
1	C	234/250 (94%)	234 (100%)	0	100	100
1	E	232/250 (93%)	232 (100%)	0	100	100
1	G	236/250 (94%)	236 (100%)	0	100	100
2	B	278/336 (83%)	278 (100%)	0	100	100
2	D	270/336 (80%)	270 (100%)	0	100	100
2	F	276/336 (82%)	276 (100%)	0	100	100
2	H	275/336 (82%)	275 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2037/2344 (87%)	2037 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	386	GLN
2	H	354	GLN
2	D	110	GLN
2	D	188	HIS
2	D	354	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	324	E	701	-	29,29,29	0.94	1 (3%)	38,43,43	1.00	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CHU	B	401	-	35,36,36	0.78	1 (2%)	45,52,52	1.17	4 (8%)
4	CHU	F	401	-	35,36,36	0.81	0	45,52,52	1.08	3 (6%)
3	324	A	701	-	29,29,29	0.87	1 (3%)	38,43,43	1.03	2 (5%)
3	324	G	701	-	29,29,29	0.87	1 (3%)	38,43,43	0.90	1 (2%)
5	ANP	D	402	-	33,33,33	2.32	6 (18%)	45,52,52	1.70	10 (22%)
5	ANP	B	402	-	33,33,33	2.37	5 (15%)	45,52,52	1.27	4 (8%)
5	ANP	F	402	-	33,33,33	2.42	6 (18%)	45,52,52	1.28	5 (11%)
5	ANP	H	402	-	33,33,33	2.45	5 (15%)	45,52,52	1.34	3 (6%)
3	324	C	701	-	29,29,29	0.89	1 (3%)	38,43,43	0.91	0
4	CHU	H	401	-	35,36,36	0.77	0	45,52,52	1.16	5 (11%)
4	CHU	D	401	-	35,36,36	0.79	0	45,52,52	1.13	5 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	324	E	701	-	-	0/17/17/17	0/3/3/3
4	CHU	B	401	-	-	0/15/16/16	0/4/4/4
4	CHU	F	401	-	-	0/15/16/16	0/4/4/4
3	324	A	701	-	-	3/17/17/17	0/3/3/3
3	324	G	701	-	-	7/17/17/17	0/3/3/3
5	ANP	D	402	-	-	8/18/38/38	0/3/3/3
5	ANP	B	402	-	-	2/18/38/38	0/3/3/3
5	ANP	F	402	-	-	7/18/38/38	0/3/3/3
5	ANP	H	402	-	-	10/18/38/38	0/3/3/3
3	324	C	701	-	-	4/17/17/17	0/3/3/3
4	CHU	H	401	-	-	0/15/16/16	0/4/4/4
4	CHU	D	401	-	-	0/15/16/16	0/4/4/4

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	402	ANP	PB-O3A	9.62	1.71	1.59
5	F	402	ANP	PB-O3A	9.31	1.70	1.59
5	B	402	ANP	PB-O3A	9.14	1.70	1.59
5	D	402	ANP	PB-O3A	8.82	1.70	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	402	ANP	PG-N3B	6.42	1.80	1.63

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	402	ANP	O2B-PB-O1B	5.43	121.51	109.87
5	H	402	ANP	O1G-PG-N3B	-5.13	104.21	111.77
5	F	402	ANP	O2B-PB-O1B	5.01	120.62	109.87
5	H	402	ANP	O2B-PB-O1B	4.72	120.00	109.87
5	B	402	ANP	O1B-PB-N3B	4.10	117.80	111.77

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	701	324	C13-C11-C9-C8
3	C	701	324	C13-C11-C9-C2
3	C	701	324	O12-C11-C9-C8
3	C	701	324	O12-C11-C9-C2
5	B	402	ANP	PA-O3A-PB-O2B

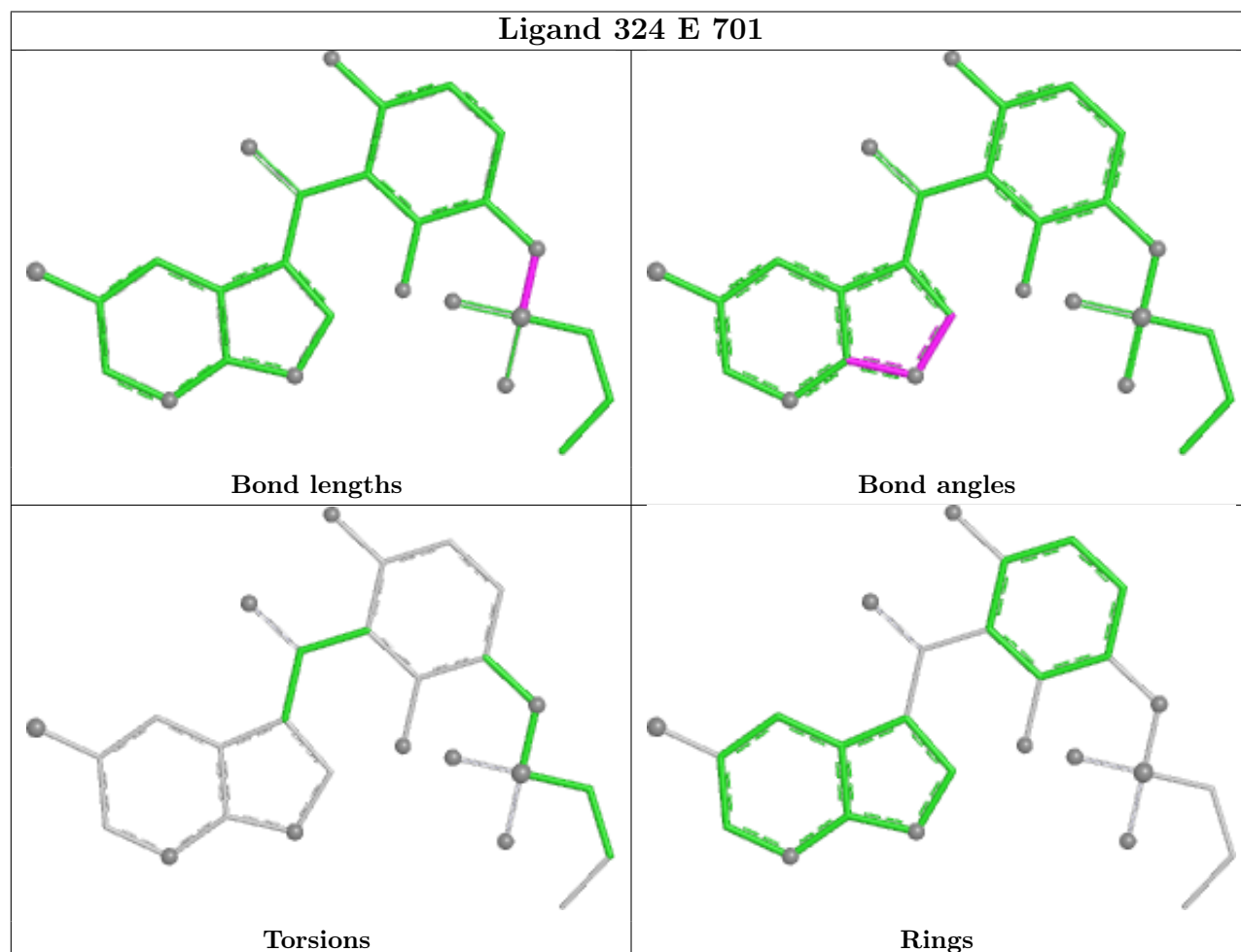
There are no ring outliers.

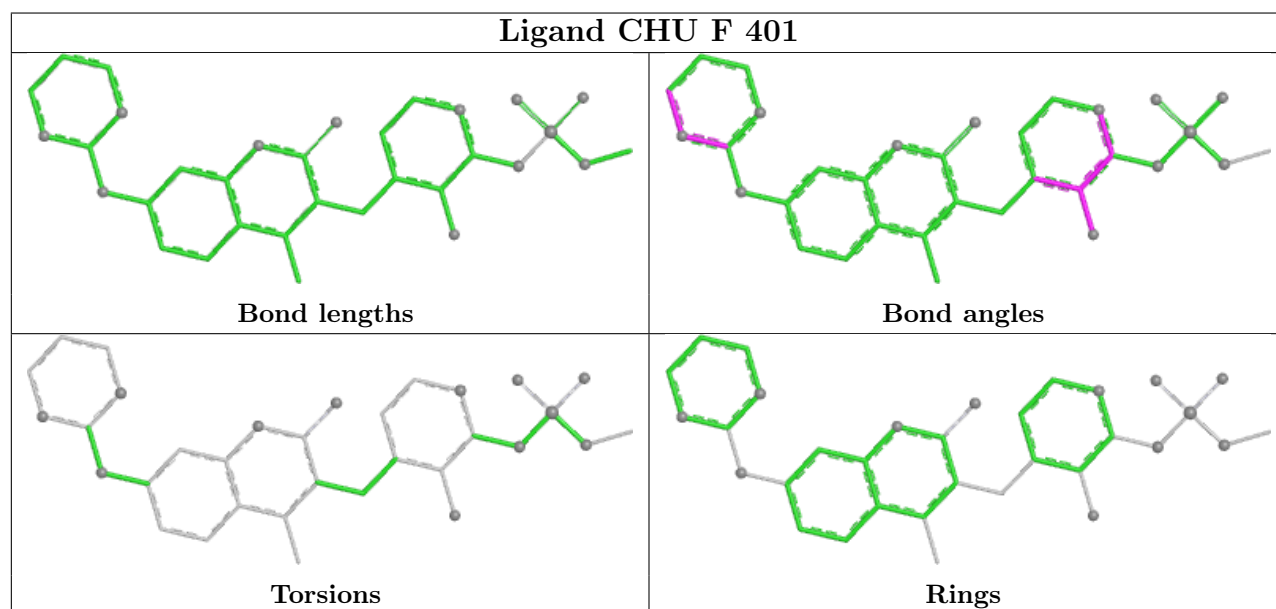
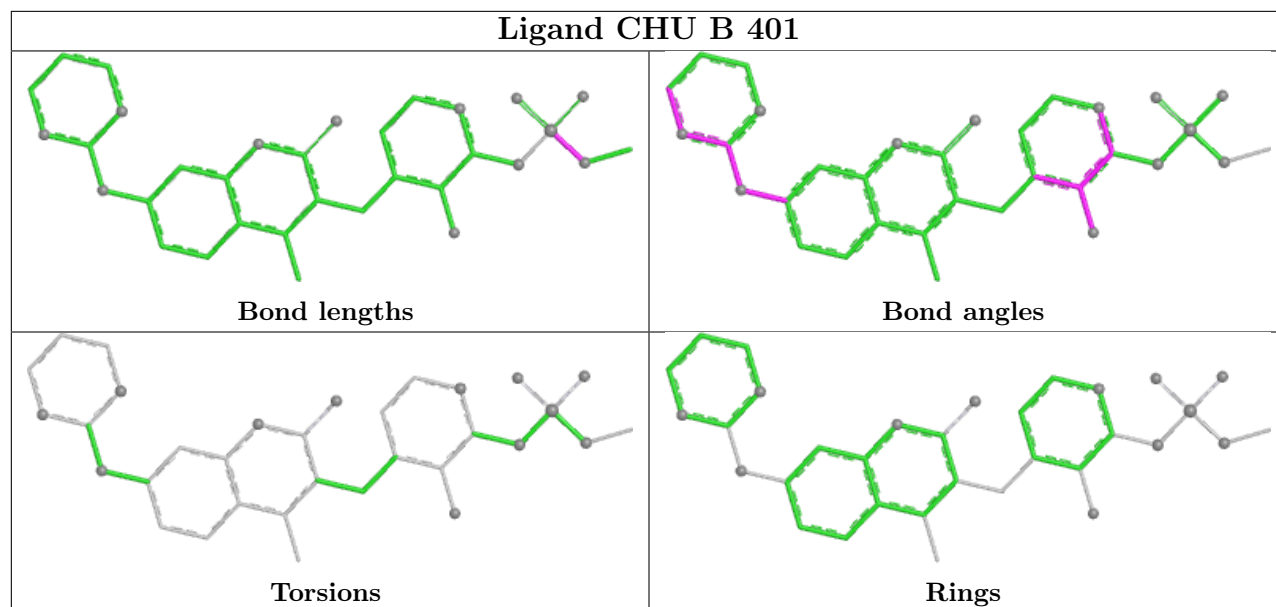
11 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	701	324	3	0
4	B	401	CHU	1	0
3	A	701	324	1	0
3	G	701	324	2	0
5	D	402	ANP	1	0
5	B	402	ANP	1	0
5	F	402	ANP	1	0
5	H	402	ANP	1	0
3	C	701	324	1	0
4	H	401	CHU	1	0
4	D	401	CHU	2	0

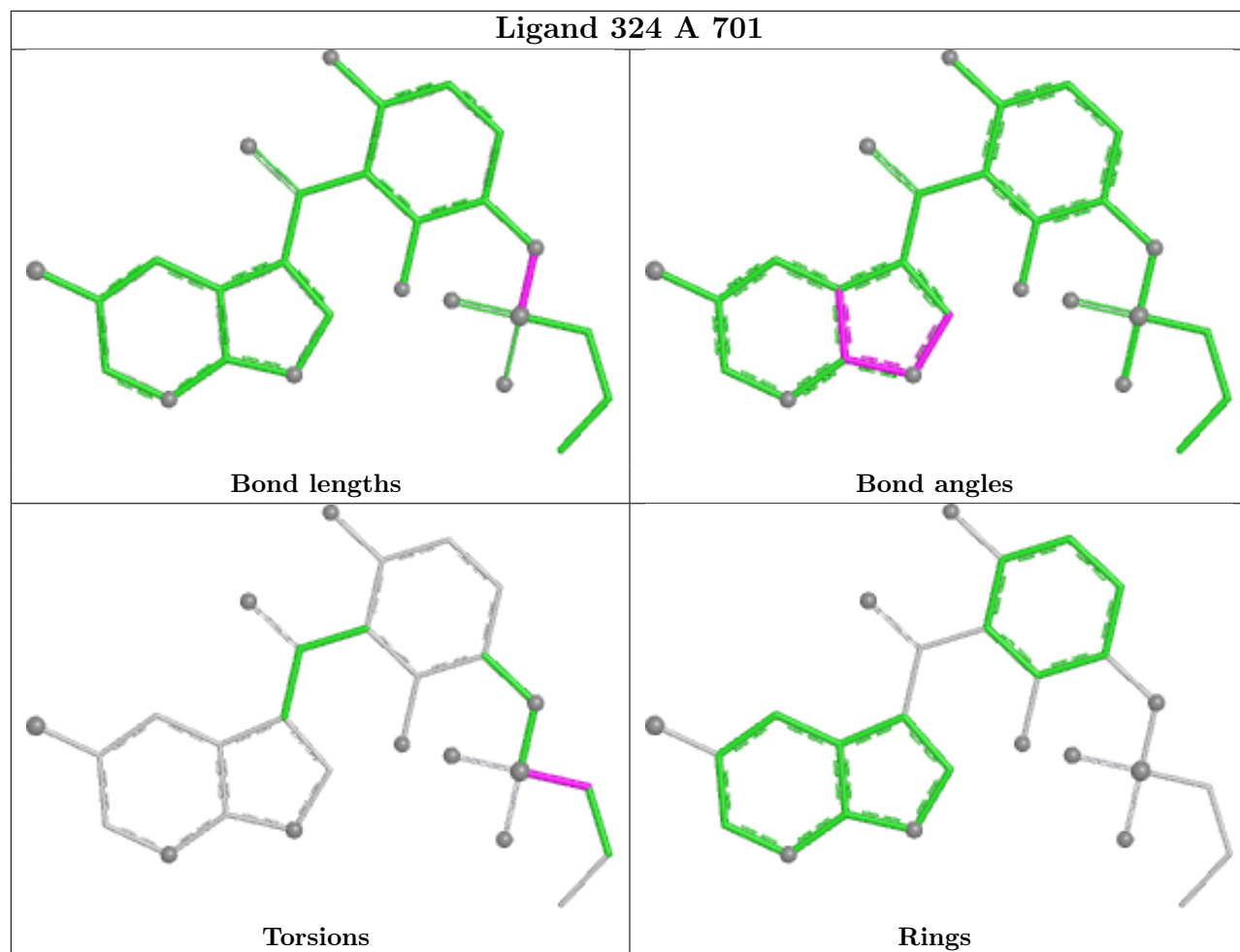
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

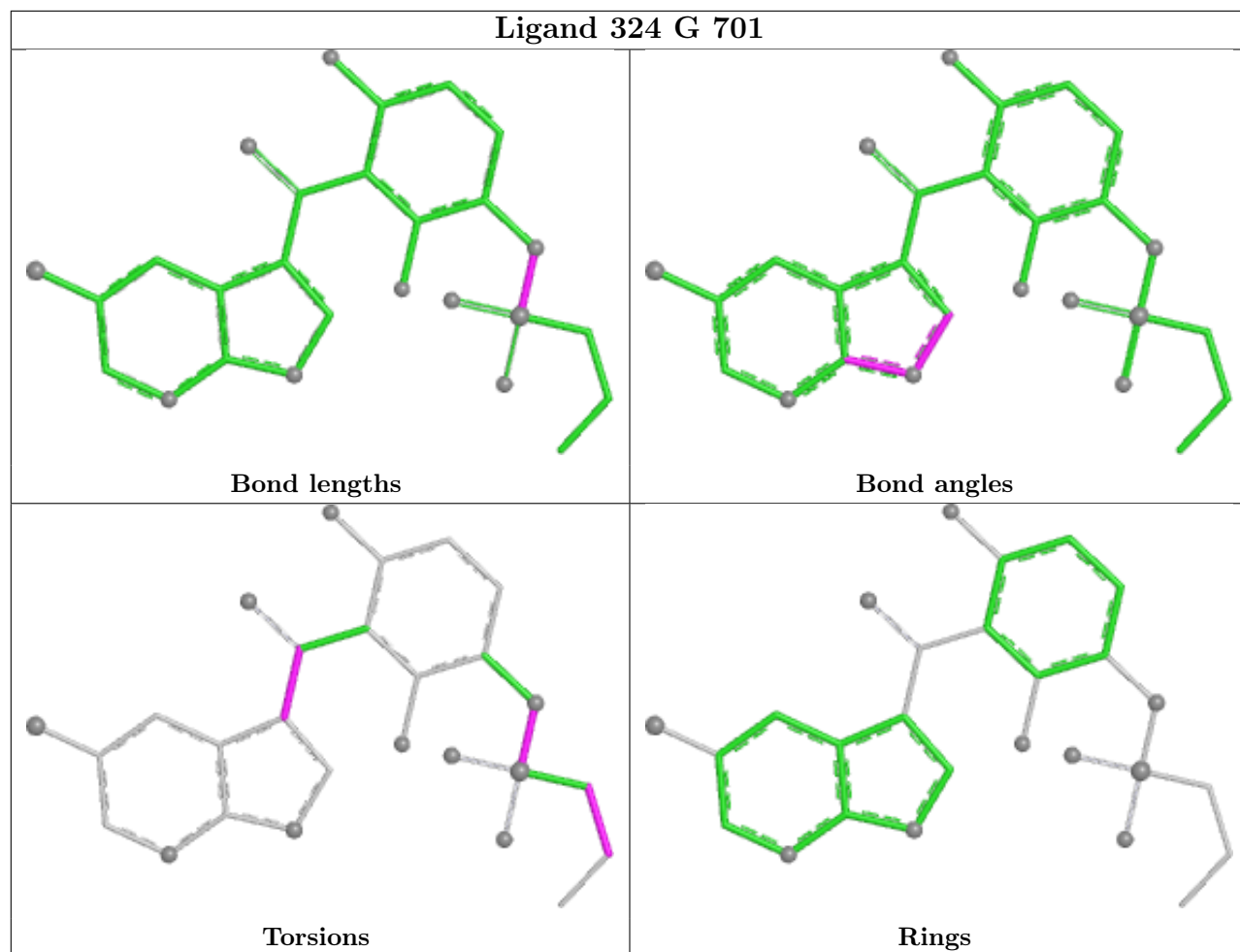


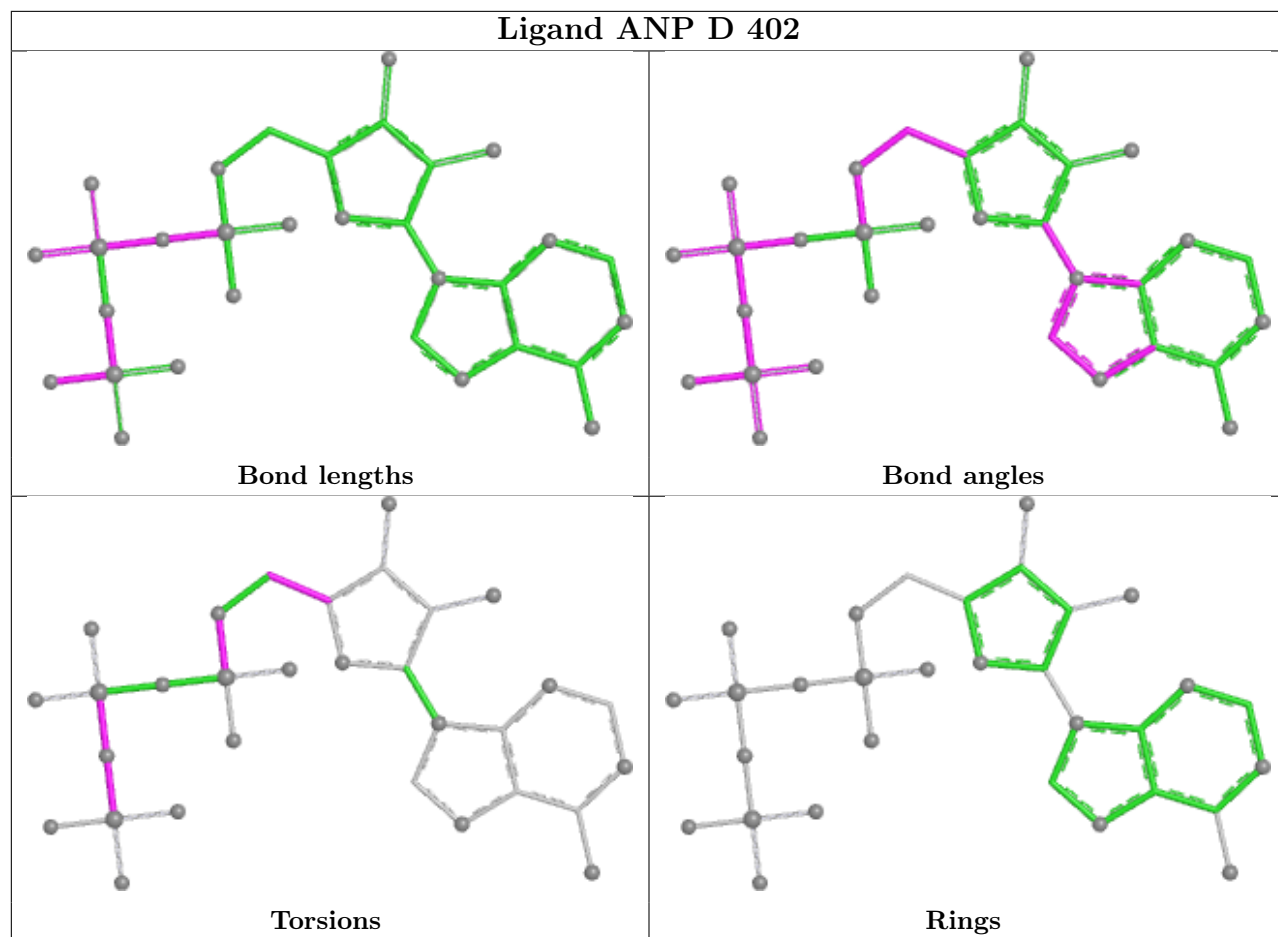


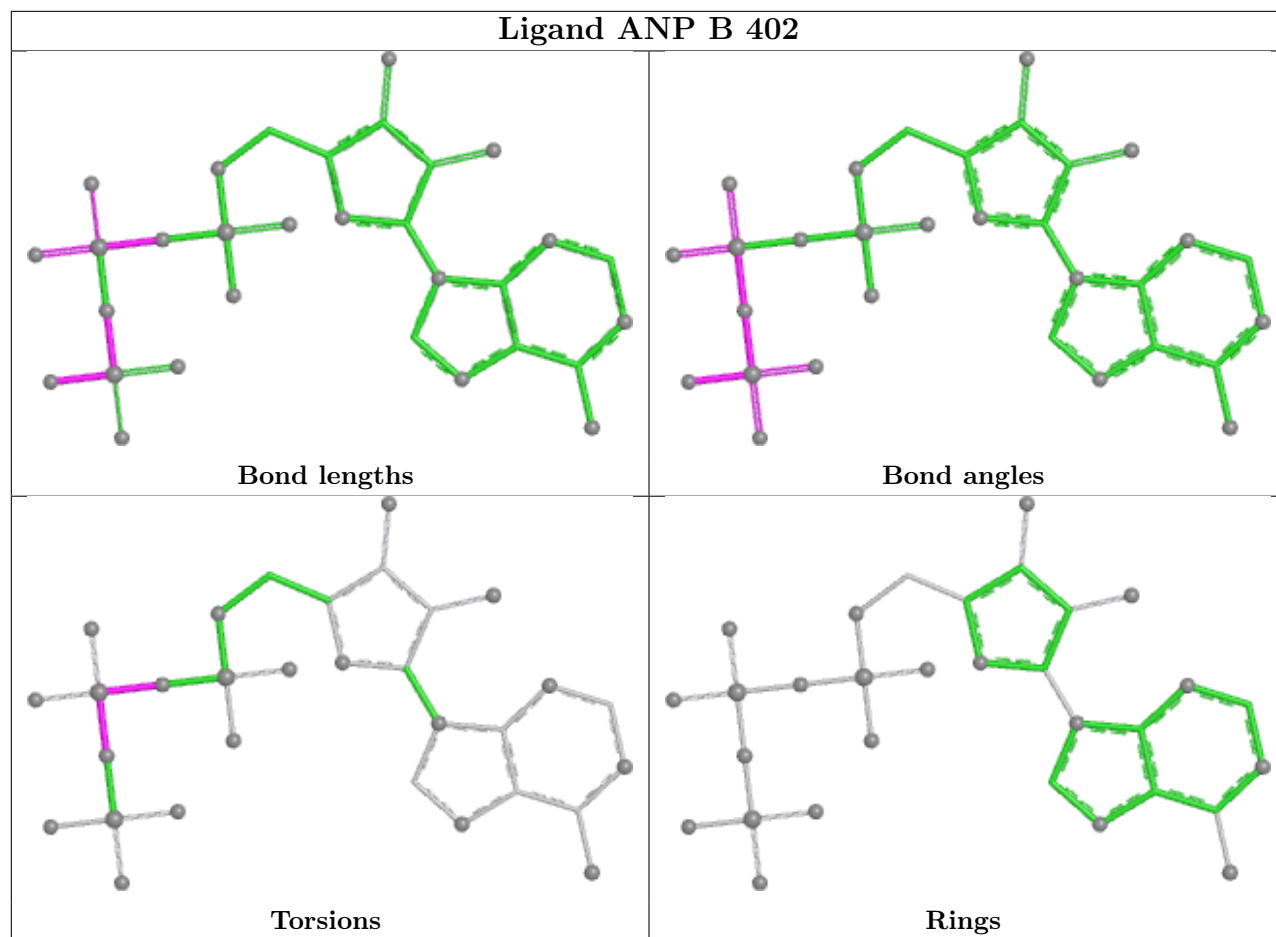
Ligand 324 A 701

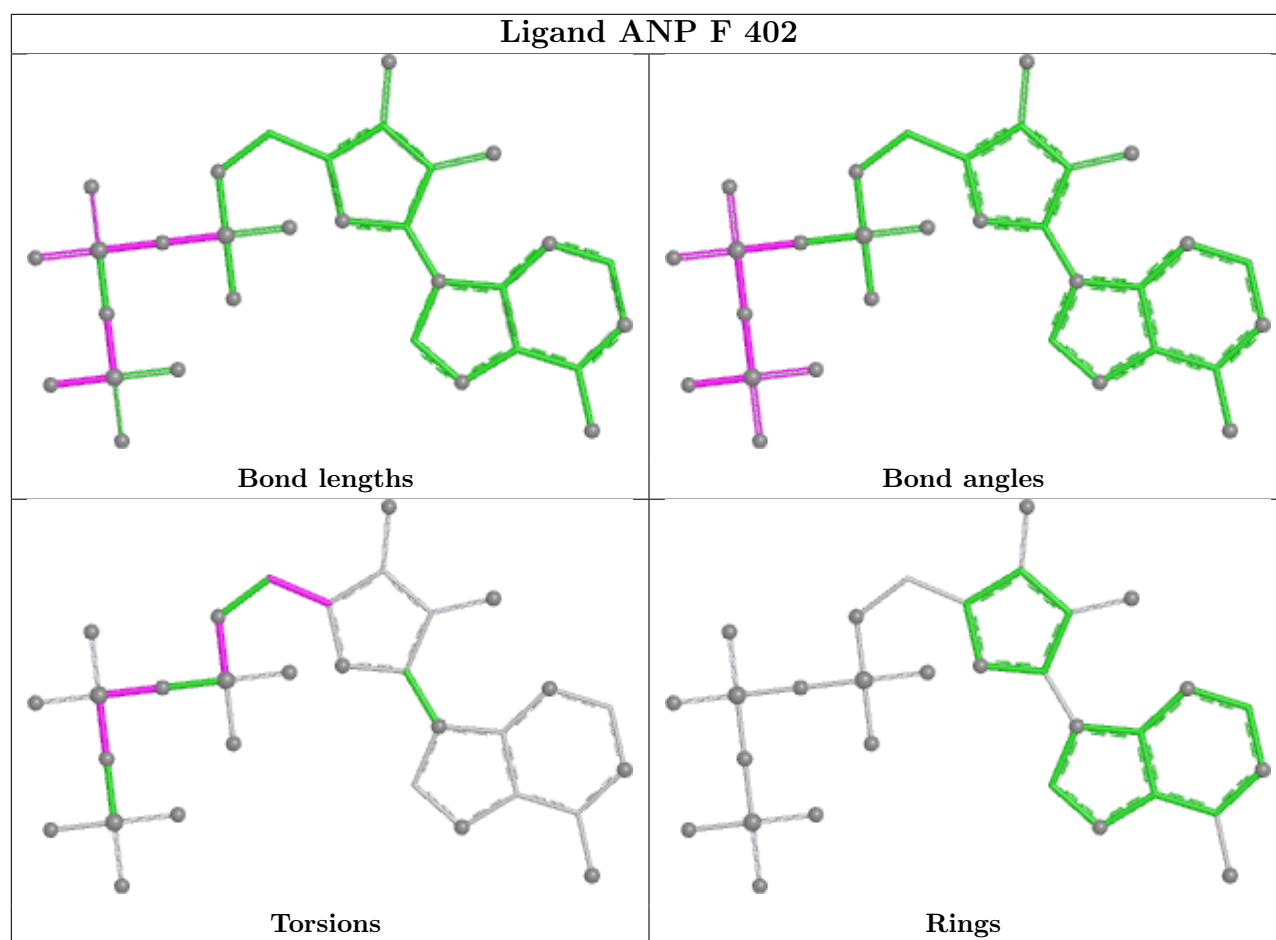


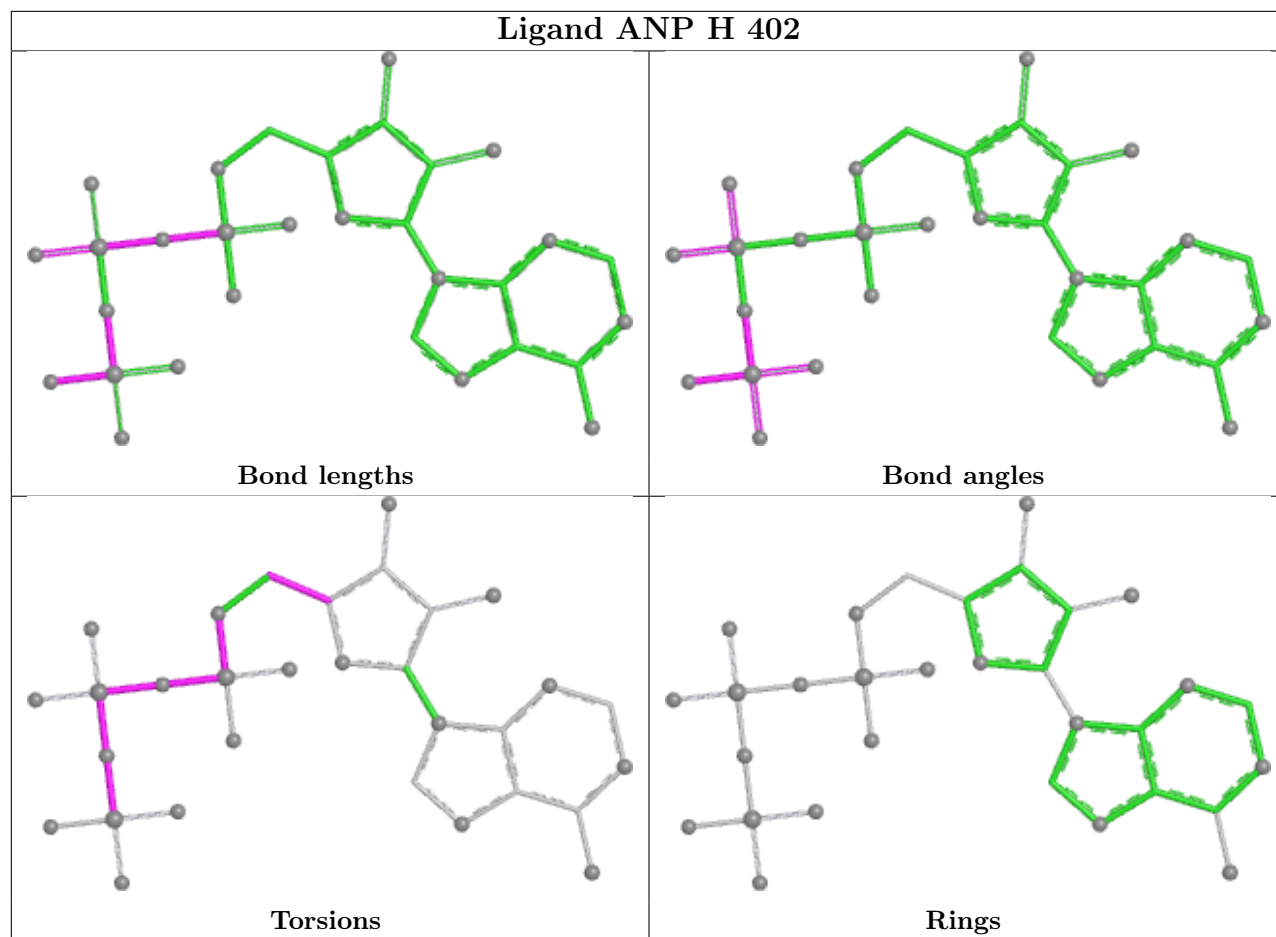
Ligand 324 G 701



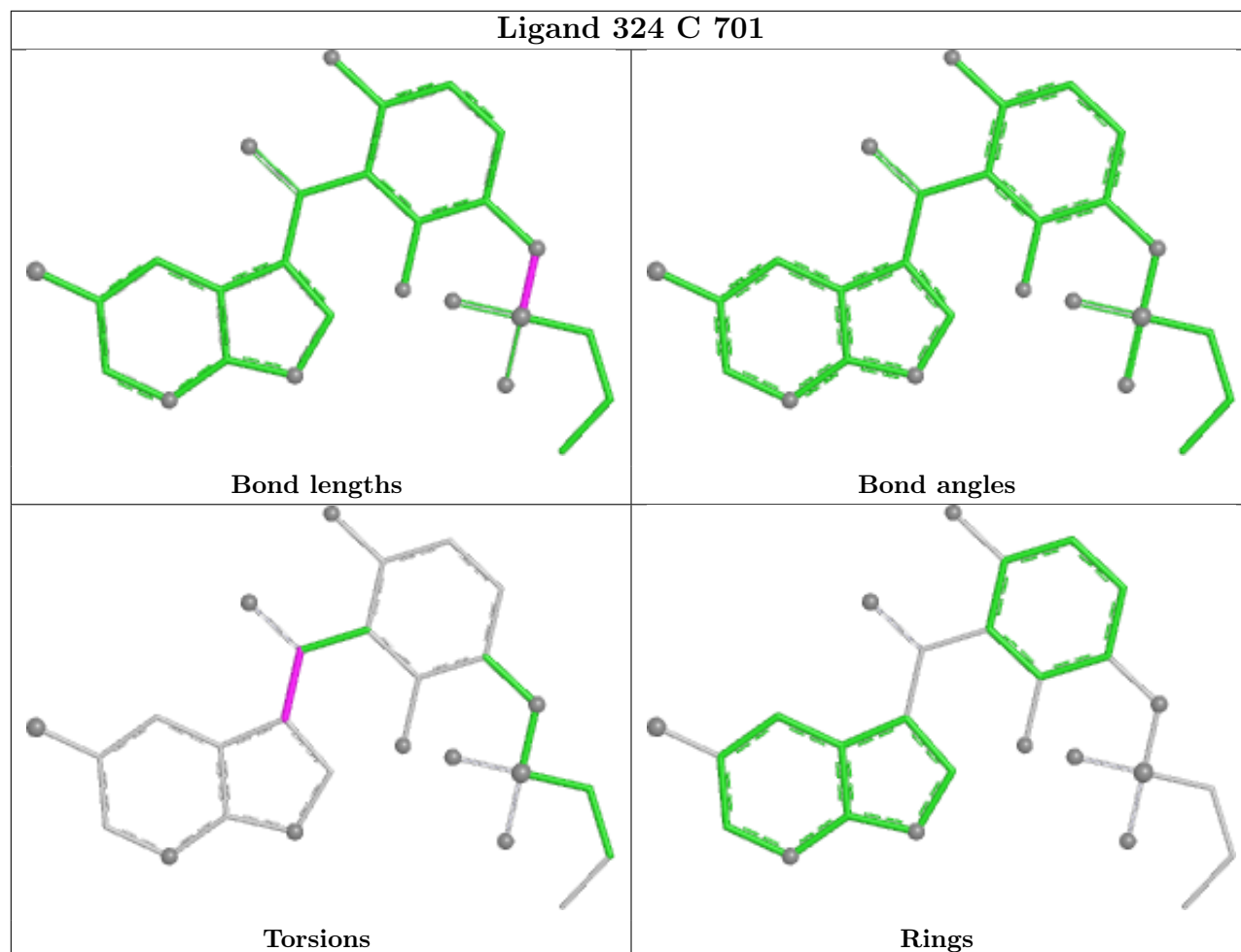




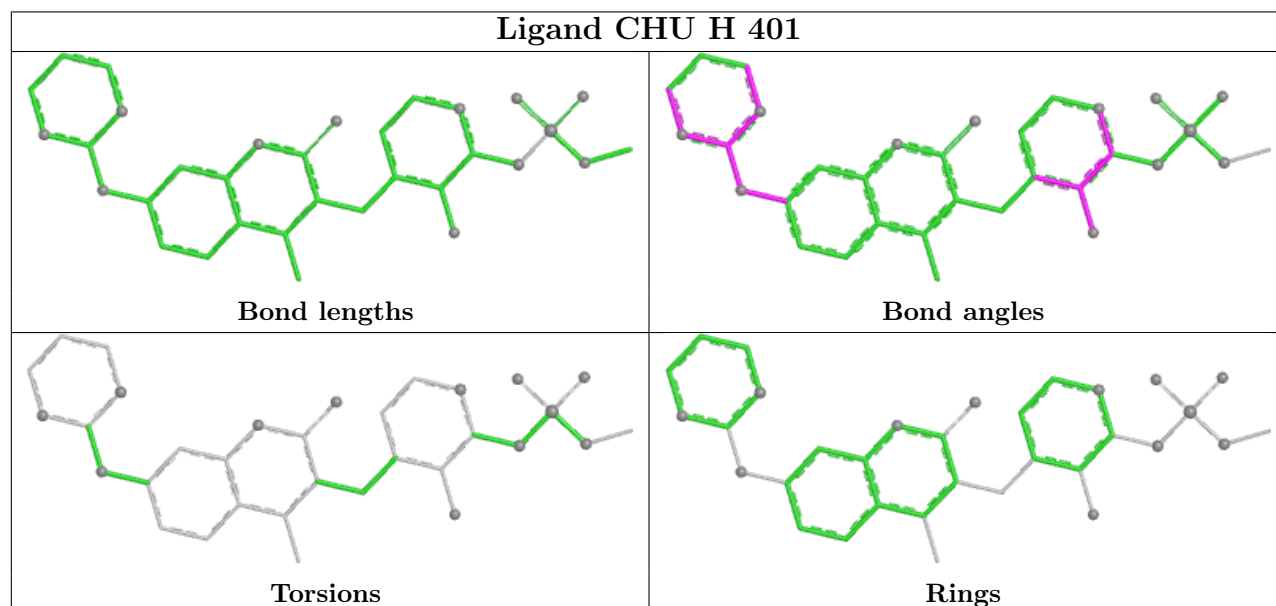


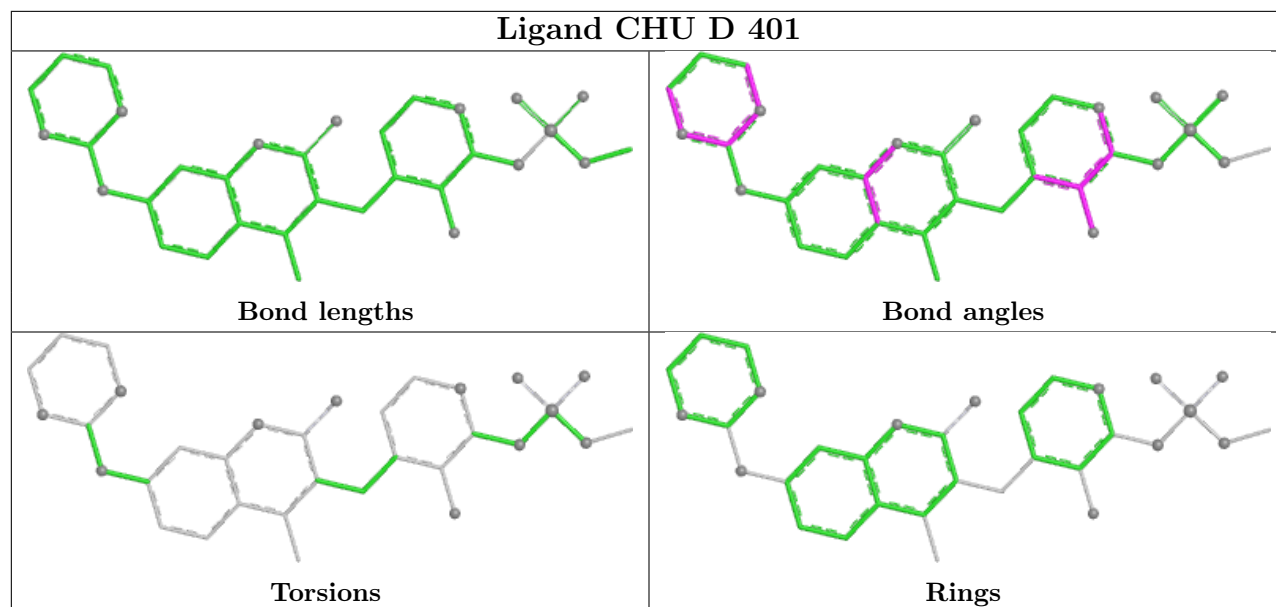


Ligand 324 C 701



Ligand CHU H 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	266/280 (95%)	-0.56	0	100	100	44, 72, 134, 168	1 (0%)
1	C	264/280 (94%)	-0.28	0	100	100	51, 100, 150, 188	0
1	E	261/280 (93%)	-0.41	1 (0%)	88	72	47, 78, 128, 168	0
1	G	265/280 (94%)	-0.45	0	100	100	37, 71, 140, 171	1 (0%)
2	B	322/395 (81%)	-0.30	0	100	100	52, 95, 146, 186	0
2	D	315/395 (79%)	0.13	2 (0%)	85	65	124, 174, 202, 216	0
2	F	322/395 (81%)	-0.19	0	100	100	74, 120, 168, 194	0
2	H	318/395 (80%)	-0.21	0	100	100	54, 101, 163, 194	0
All	All	2333/2700 (86%)	-0.27	3 (0%)	92	86	37, 100, 183, 216	2 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	613	LEU	2.6
2	D	80	GLY	2.3
2	D	173	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

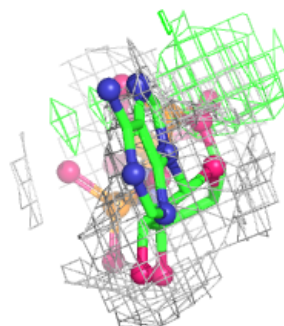
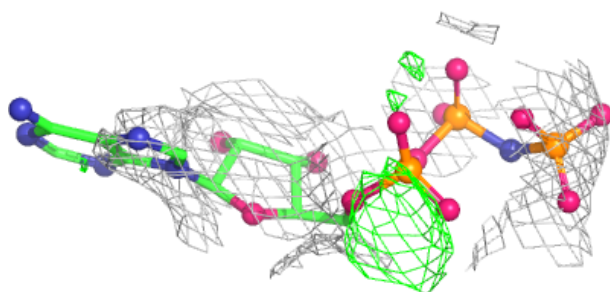
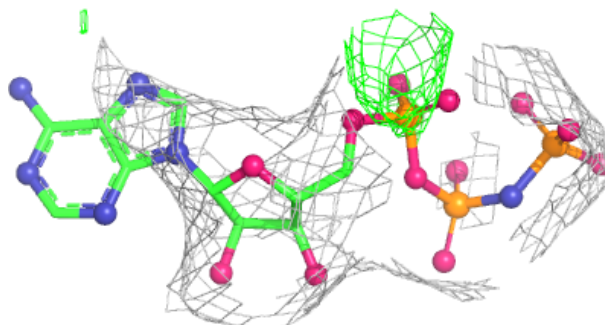
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	ANP	D	402	31/31	0.77	0.12	174,204,228,235	0
4	CHU	D	401	33/33	0.85	0.11	135,155,174,176	0
5	ANP	B	402	31/31	0.86	0.12	93,118,167,190	0
5	ANP	F	402	31/31	0.87	0.08	112,130,171,206	0
3	324	C	701	27/27	0.89	0.10	52,97,127,140	0
5	ANP	H	402	31/31	0.90	0.09	85,100,138,167	0
3	324	G	701	27/27	0.94	0.08	35,75,111,144	0
4	CHU	F	401	33/33	0.96	0.08	56,88,116,119	0
4	CHU	H	401	33/33	0.96	0.07	52,70,90,101	0
3	324	A	701	27/27	0.97	0.07	47,62,84,104	0
3	324	E	701	27/27	0.97	0.06	50,64,94,104	0
4	CHU	B	401	33/33	0.98	0.06	47,66,90,102	0

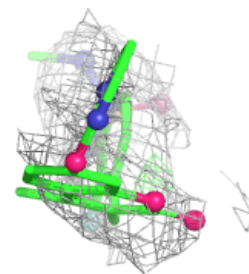
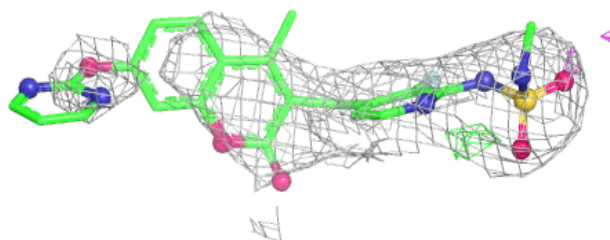
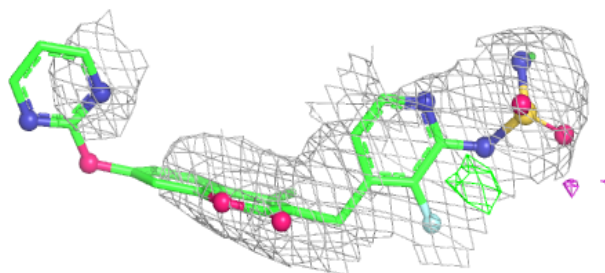
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP 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)

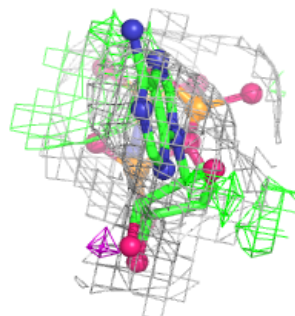
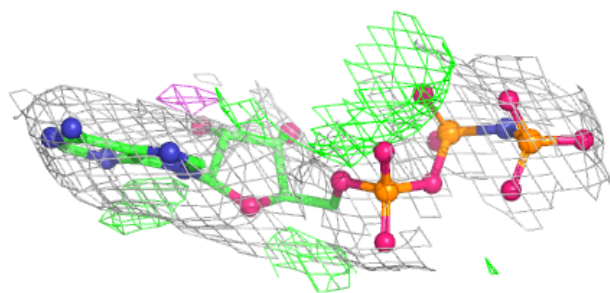
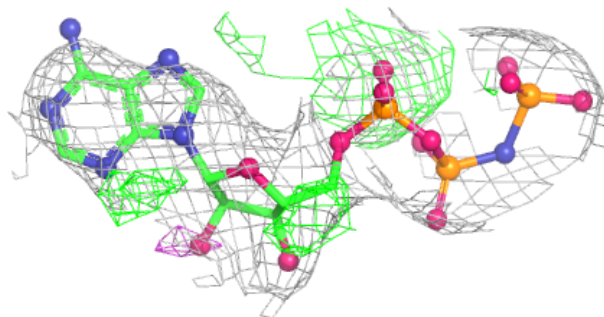
**Electron density around CHU D 401:**

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

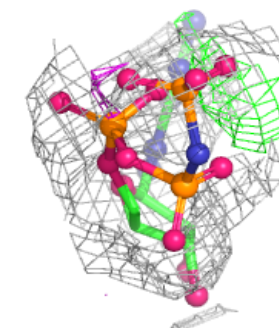
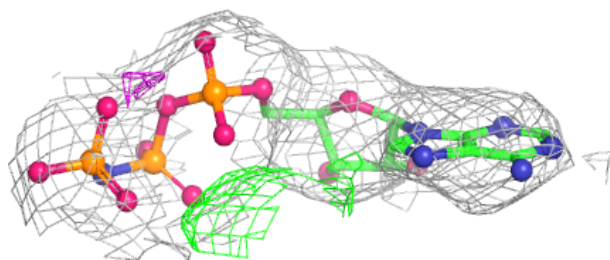
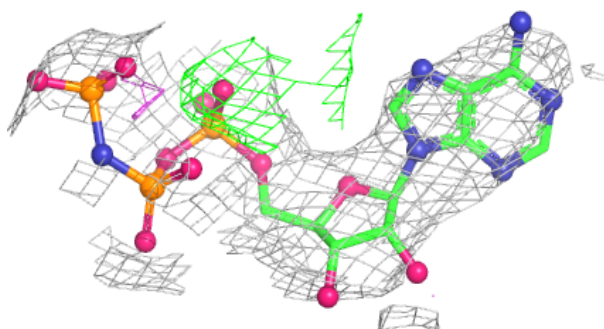


Electron density around ANP B 402:

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

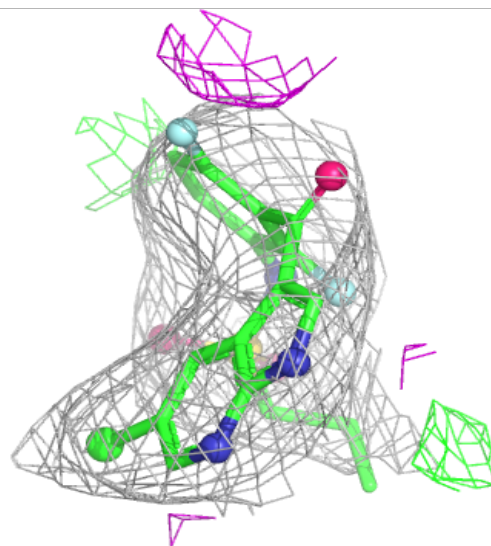
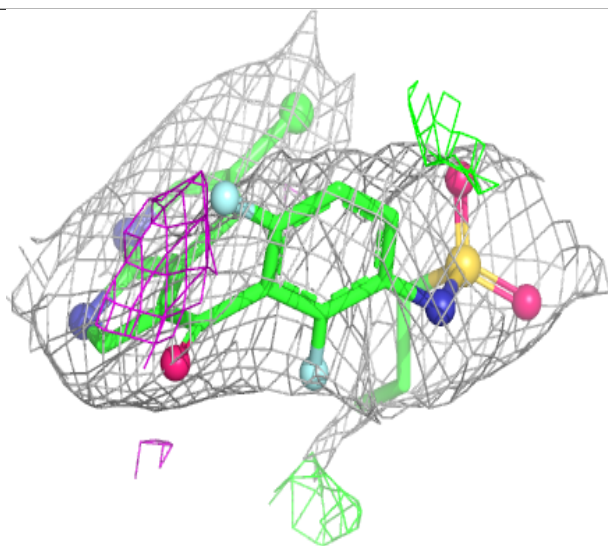
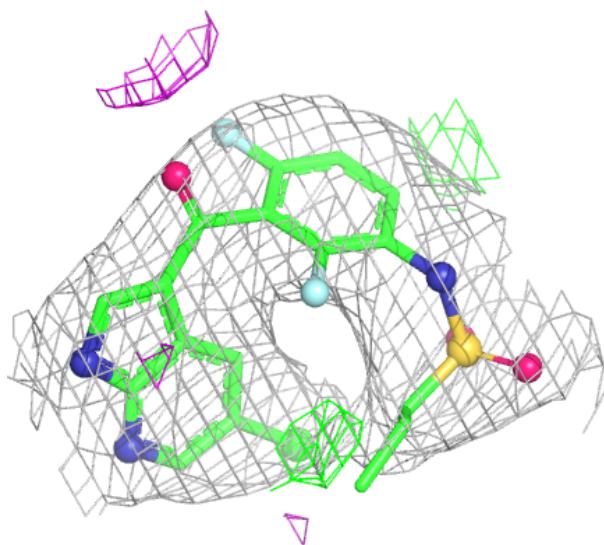
**Electron density around ANP F 402:**

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



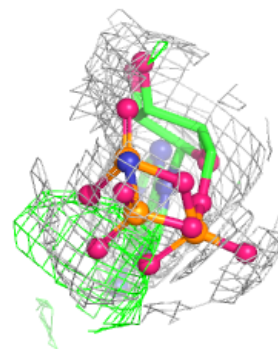
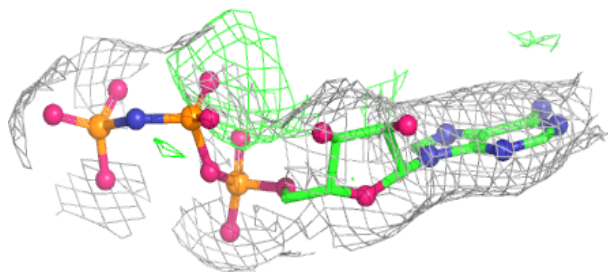
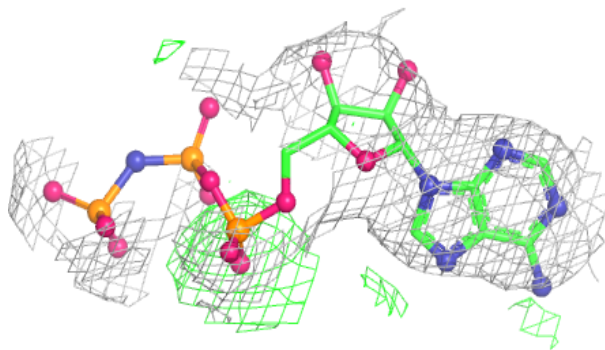
Electron density around 324 C 701:

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



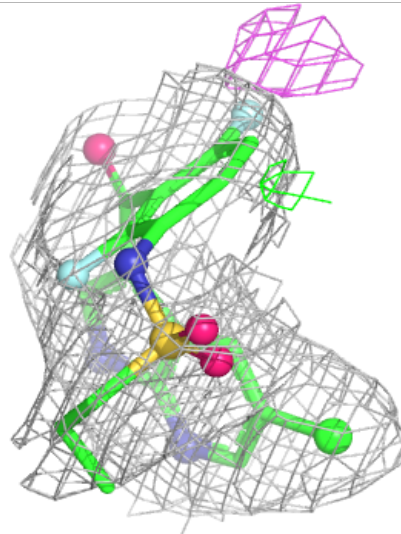
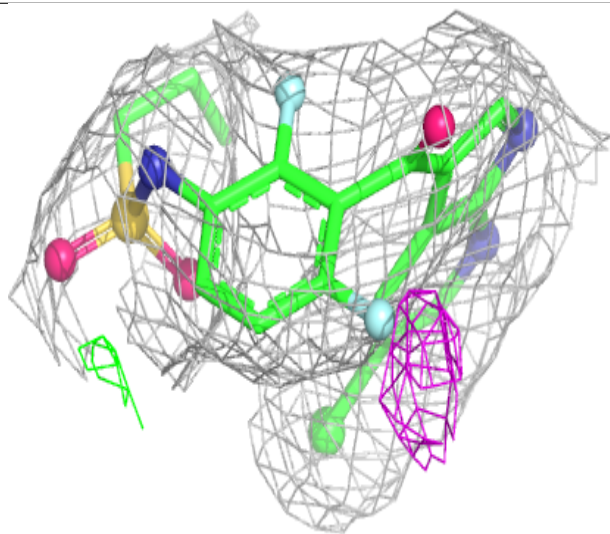
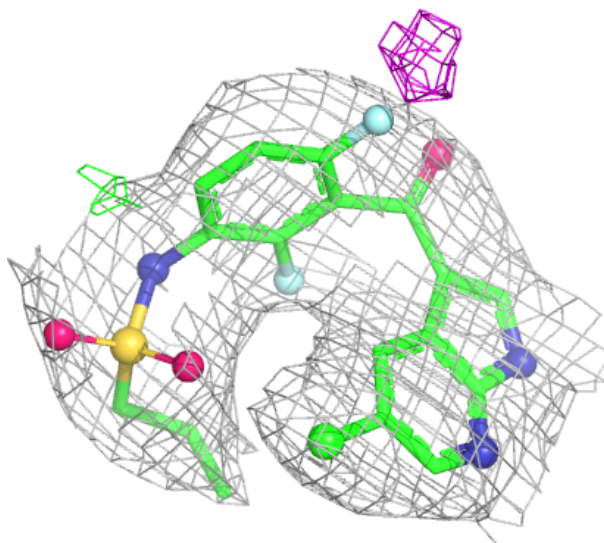
Electron density around ANP H 402:

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



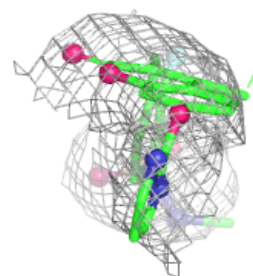
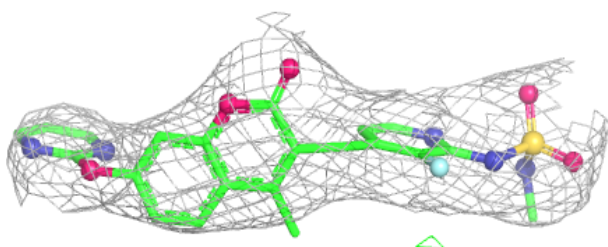
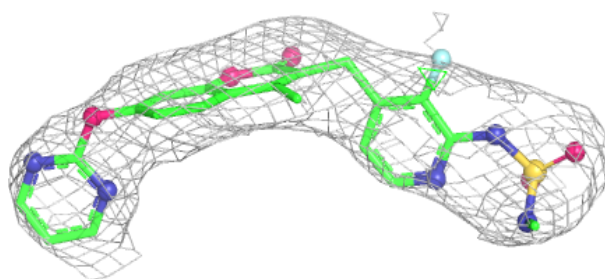
Electron density around 324 G 701:

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

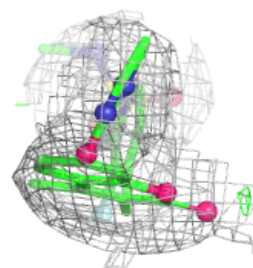
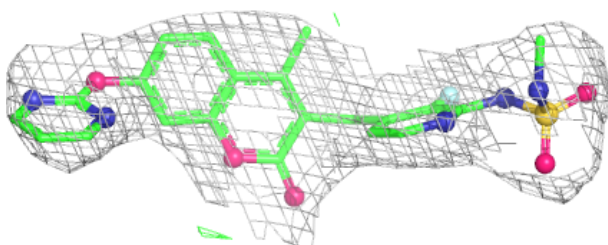
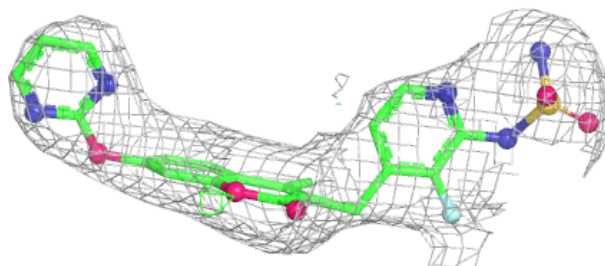


Electron density around CHU F 401:

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

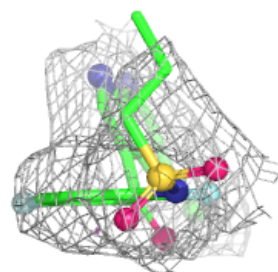
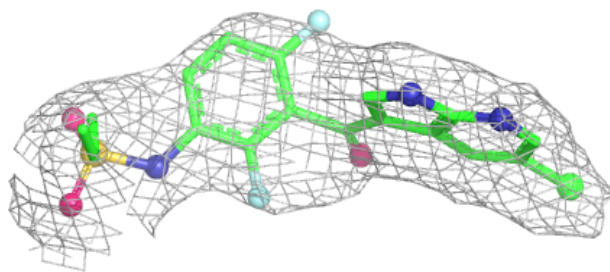
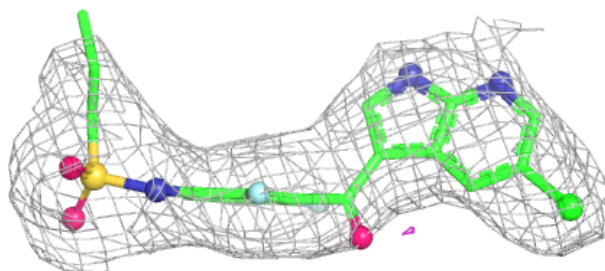
**Electron density around CHU H 401:**

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and green (positive)

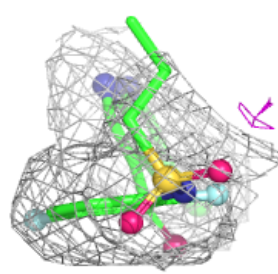
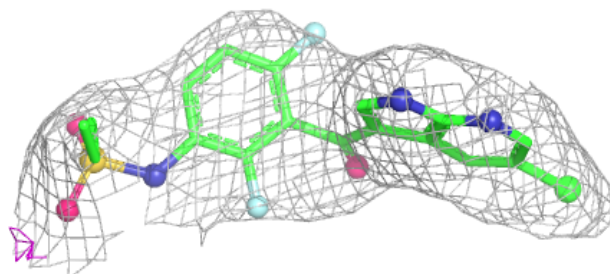
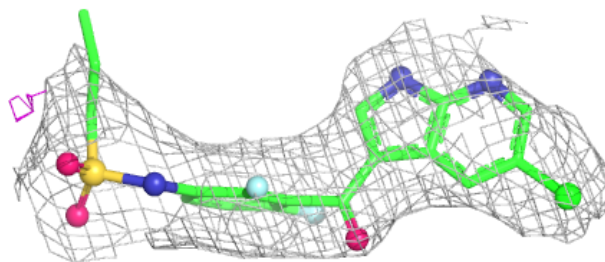


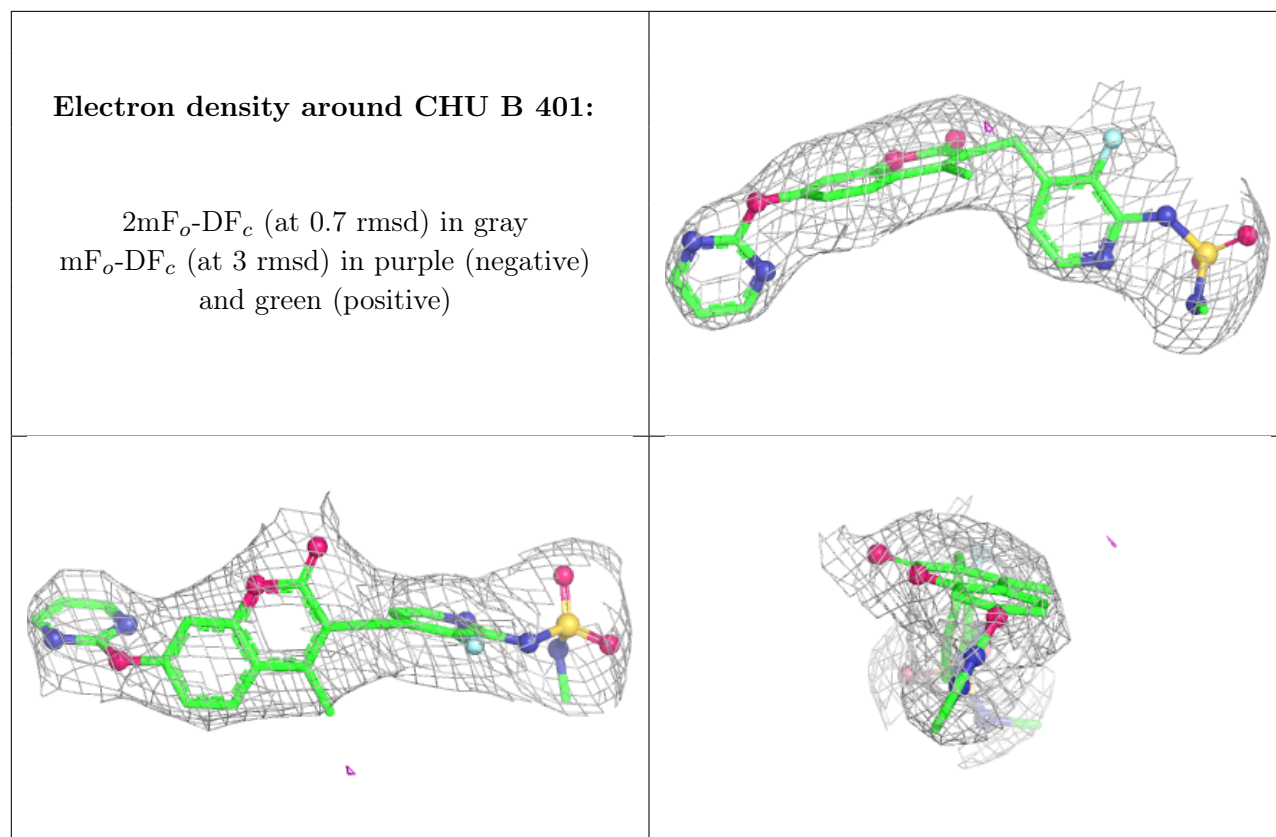
Electron density around 324 A 701:

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

**Electron density around 324 E 701:**

$2mF_o-DF_c$ (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.