



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 09:40 AM UTC

PDB ID : 5TRS / pdb\_00005trs  
Title : Structure of Mycobacterium tuberculosis proteasome in complex with N,C-capped dipeptide PKS2144  
Authors : Hsu, H.-C.; Fan, H.; Singh, P.K.; Wang, R.; Sukenick, G.; Nathan, C.; Lin, G.; Li, H.  
Deposited on : 2016-10-27  
Resolution : 3.08 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

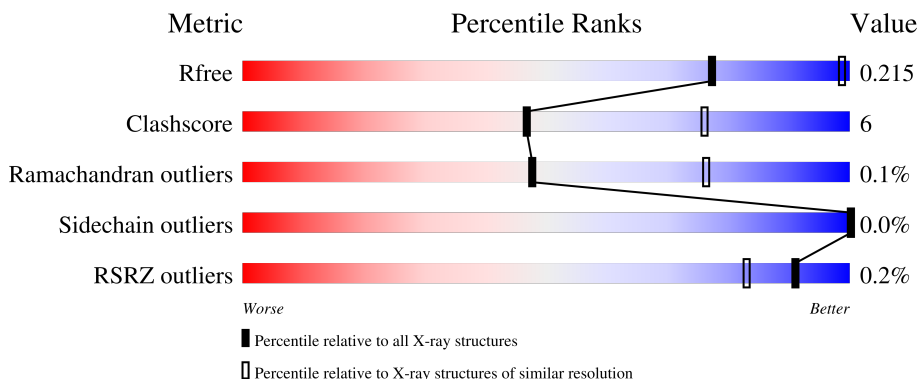
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


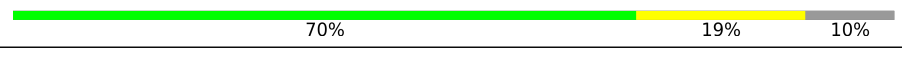
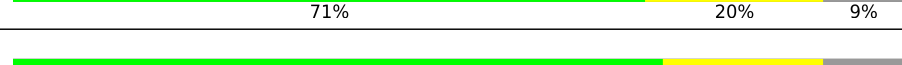

The reported resolution of this entry is 3.08 Å.

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.






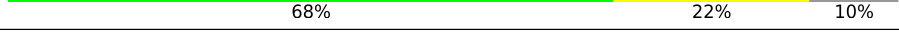


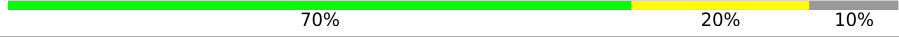


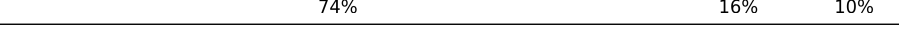
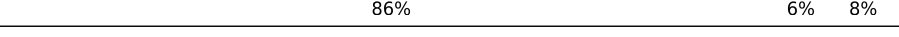
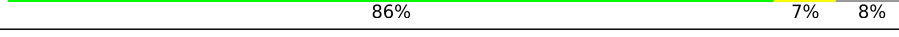

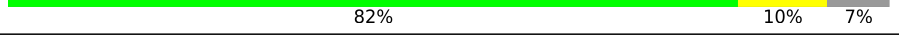
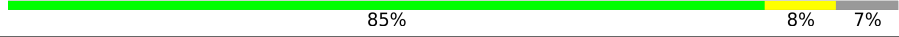









Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	240	 78% 13% 9%
1	B	240	 70% 19% 10%
1	C	240	 71% 20% 9%
1	D	240	 73% 18% 9%

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Mol	Chain	Length	Quality of chain
1	E	240	
1	F	240	
1	G	240	
1	O	240	
1	P	240	
1	Q	240	
1	R	240	
1	S	240	
1	T	240	
1	U	240	
2	H	240	
2	I	240	
2	J	240	
2	K	240	
2	L	240	
2	M	240	
2	N	240	
2	V	240	
2	W	240	
2	X	240	
2	Y	240	
2	Z	240	
2	a	240	
2	b	240	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 47019 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 Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	Total 1684	C 1055	N 307	O 318	S 4	0	0	0
1	B	216	Total 1668	C 1045	N 304	O 315	S 4	0	0	0
1	C	218	Total 1678	C 1050	N 306	O 318	S 4	0	0	0
1	D	218	Total 1677	C 1050	N 306	O 317	S 4	0	0	0
1	E	217	Total 1671	C 1047	N 305	O 315	S 4	0	0	0
1	F	216	Total 1663	C 1041	N 304	O 314	S 4	0	0	0
1	G	216	Total 1662	C 1040	N 304	O 314	S 4	0	0	0
1	O	217	Total 1671	C 1047	N 305	O 315	S 4	0	0	0
1	P	219	Total 1685	C 1054	N 307	O 320	S 4	0	0	0
1	Q	216	Total 1668	C 1045	N 304	O 315	S 4	0	0	0
1	R	216	Total 1663	C 1041	N 304	O 314	S 4	0	0	0
1	S	218	Total 1678	C 1050	N 306	O 318	S 4	0	0	0
1	T	217	Total 1671	C 1047	N 305	O 315	S 4	0	0	0
1	U	216	Total 1664	C 1043	N 304	O 313	S 4	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	initiating methionine	UNP A5U4D5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	9	MET	-	initiating methionine	UNP A5U4D5
C	9	MET	-	initiating methionine	UNP A5U4D5
D	9	MET	-	initiating methionine	UNP A5U4D5
E	9	MET	-	initiating methionine	UNP A5U4D5
F	9	MET	-	initiating methionine	UNP A5U4D5
G	9	MET	-	initiating methionine	UNP A5U4D5
O	9	MET	-	initiating methionine	UNP A5U4D5
P	9	MET	-	initiating methionine	UNP A5U4D5
Q	9	MET	-	initiating methionine	UNP A5U4D5
R	9	MET	-	initiating methionine	UNP A5U4D5
S	9	MET	-	initiating methionine	UNP A5U4D5
T	9	MET	-	initiating methionine	UNP A5U4D5
U	9	MET	-	initiating methionine	UNP A5U4D5

- Molecule 2 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	222	1638	1027	282	324	5	0	0	0
2	I	222	1638	1027	282	324	5	0	0	0
2	J	222	1638	1027	282	324	5	0	0	0
2	K	223	1642	1029	283	325	5	0	0	0
2	L	223	1642	1029	283	325	5	0	0	0
2	M	222	1638	1027	282	324	5	0	0	0
2	N	223	1642	1029	283	325	5	0	0	0
2	V	223	1642	1029	283	325	5	0	0	0
2	W	223	1642	1029	283	325	5	0	0	0
2	X	222	1638	1027	282	324	5	0	0	0
2	Y	223	1642	1029	283	325	5	0	0	0
2	Z	222	1638	1027	282	324	5	0	0	0
2	a	223	1642	1029	283	325	5	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	b	223	1642	1029	283	325	5	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	235	HIS	-	expression tag	UNP A5U4D6
H	236	HIS	-	expression tag	UNP A5U4D6
H	237	HIS	-	expression tag	UNP A5U4D6
H	238	HIS	-	expression tag	UNP A5U4D6
H	239	HIS	-	expression tag	UNP A5U4D6
H	240	HIS	-	expression tag	UNP A5U4D6
I	235	HIS	-	expression tag	UNP A5U4D6
I	236	HIS	-	expression tag	UNP A5U4D6
I	237	HIS	-	expression tag	UNP A5U4D6
I	238	HIS	-	expression tag	UNP A5U4D6
I	239	HIS	-	expression tag	UNP A5U4D6
I	240	HIS	-	expression tag	UNP A5U4D6
J	235	HIS	-	expression tag	UNP A5U4D6
J	236	HIS	-	expression tag	UNP A5U4D6
J	237	HIS	-	expression tag	UNP A5U4D6
J	238	HIS	-	expression tag	UNP A5U4D6
J	239	HIS	-	expression tag	UNP A5U4D6
J	240	HIS	-	expression tag	UNP A5U4D6
K	235	HIS	-	expression tag	UNP A5U4D6
K	236	HIS	-	expression tag	UNP A5U4D6
K	237	HIS	-	expression tag	UNP A5U4D6
K	238	HIS	-	expression tag	UNP A5U4D6
K	239	HIS	-	expression tag	UNP A5U4D6
K	240	HIS	-	expression tag	UNP A5U4D6
L	235	HIS	-	expression tag	UNP A5U4D6
L	236	HIS	-	expression tag	UNP A5U4D6
L	237	HIS	-	expression tag	UNP A5U4D6
L	238	HIS	-	expression tag	UNP A5U4D6
L	239	HIS	-	expression tag	UNP A5U4D6
L	240	HIS	-	expression tag	UNP A5U4D6
M	235	HIS	-	expression tag	UNP A5U4D6
M	236	HIS	-	expression tag	UNP A5U4D6
M	237	HIS	-	expression tag	UNP A5U4D6
M	238	HIS	-	expression tag	UNP A5U4D6
M	239	HIS	-	expression tag	UNP A5U4D6
M	240	HIS	-	expression tag	UNP A5U4D6

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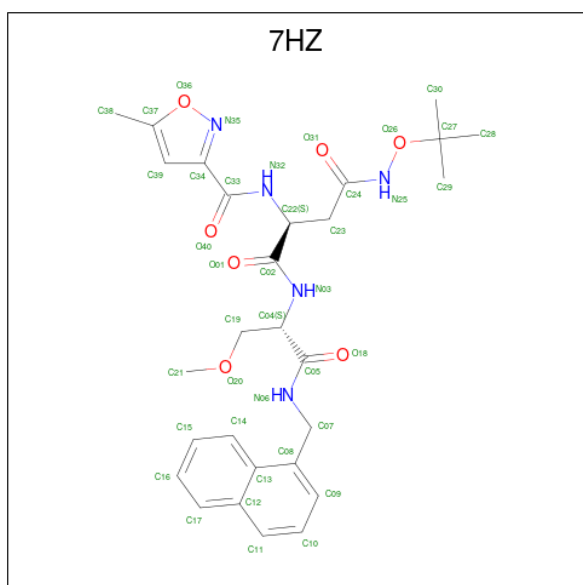
Chain	Residue	Modelled	Actual	Comment	Reference
N	235	HIS	-	expression tag	UNP A5U4D6
N	236	HIS	-	expression tag	UNP A5U4D6
N	237	HIS	-	expression tag	UNP A5U4D6
N	238	HIS	-	expression tag	UNP A5U4D6
N	239	HIS	-	expression tag	UNP A5U4D6
N	240	HIS	-	expression tag	UNP A5U4D6
V	235	HIS	-	expression tag	UNP A5U4D6
V	236	HIS	-	expression tag	UNP A5U4D6
V	237	HIS	-	expression tag	UNP A5U4D6
V	238	HIS	-	expression tag	UNP A5U4D6
V	239	HIS	-	expression tag	UNP A5U4D6
V	240	HIS	-	expression tag	UNP A5U4D6
W	235	HIS	-	expression tag	UNP A5U4D6
W	236	HIS	-	expression tag	UNP A5U4D6
W	237	HIS	-	expression tag	UNP A5U4D6
W	238	HIS	-	expression tag	UNP A5U4D6
W	239	HIS	-	expression tag	UNP A5U4D6
W	240	HIS	-	expression tag	UNP A5U4D6
X	235	HIS	-	expression tag	UNP A5U4D6
X	236	HIS	-	expression tag	UNP A5U4D6
X	237	HIS	-	expression tag	UNP A5U4D6
X	238	HIS	-	expression tag	UNP A5U4D6
X	239	HIS	-	expression tag	UNP A5U4D6
X	240	HIS	-	expression tag	UNP A5U4D6
Y	235	HIS	-	expression tag	UNP A5U4D6
Y	236	HIS	-	expression tag	UNP A5U4D6
Y	237	HIS	-	expression tag	UNP A5U4D6
Y	238	HIS	-	expression tag	UNP A5U4D6
Y	239	HIS	-	expression tag	UNP A5U4D6
Y	240	HIS	-	expression tag	UNP A5U4D6
Z	235	HIS	-	expression tag	UNP A5U4D6
Z	236	HIS	-	expression tag	UNP A5U4D6
Z	237	HIS	-	expression tag	UNP A5U4D6
Z	238	HIS	-	expression tag	UNP A5U4D6
Z	239	HIS	-	expression tag	UNP A5U4D6
Z	240	HIS	-	expression tag	UNP A5U4D6
a	235	HIS	-	expression tag	UNP A5U4D6
a	236	HIS	-	expression tag	UNP A5U4D6
a	237	HIS	-	expression tag	UNP A5U4D6
a	238	HIS	-	expression tag	UNP A5U4D6
a	239	HIS	-	expression tag	UNP A5U4D6
a	240	HIS	-	expression tag	UNP A5U4D6

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Chain	Residue	Modelled	Actual	Comment	Reference
b	235	HIS	-	expression tag	UNP A5U4D6
b	236	HIS	-	expression tag	UNP A5U4D6
b	237	HIS	-	expression tag	UNP A5U4D6
b	238	HIS	-	expression tag	UNP A5U4D6
b	239	HIS	-	expression tag	UNP A5U4D6
b	240	HIS	-	expression tag	UNP A5U4D6

- Molecule 3 is N-tert-butoxy-N 2 -(5-methyl-1,2-oxazole-3-carbonyl)-L-asparaginyl-O-methyl-N-[(naphthalen-1-yl)methyl]-L-serinamide (CCD ID: 7HZ) (formula: C<sub>28</sub>H<sub>35</sub>N<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
3	H	1	Total	C	N	O	0	0
			40	28	5	7		
3	I	1	Total	C	N	O	0	0
			40	28	5	7		
3	J	1	Total	C	N	O	0	0
			40	28	5	7		
3	K	1	Total	C	N	O	0	0
			40	28	5	7		
3	L	1	Total	C	N	O	0	0
			40	28	5	7		
3	M	1	Total	C	N	O	0	0
			40	28	5	7		
3	N	1	Total	C	N	O	0	0
			40	28	5	7		
3	V	1	Total	C	N	O	0	0
			40	28	5	7		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	W	1	Total	C	N	O	0	0
			40	28	5	7		
3	X	1	Total	C	N	O	0	0
			40	28	5	7		
3	Y	1	Total	C	N	O	0	0
			40	28	5	7		
3	Z	1	Total	C	N	O	0	0
			40	28	5	7		
3	a	1	Total	C	N	O	0	0
			40	28	5	7		
3	b	1	Total	C	N	O	0	0
			40	28	5	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		
4	B	1	Total	O	0	0
			1	1		
4	D	2	Total	O	0	0
			2	2		
4	F	2	Total	O	0	0
			2	2		
4	G	1	Total	O	0	0
			1	1		
4	H	7	Total	O	0	0
			7	7		
4	I	5	Total	O	0	0
			5	5		
4	J	5	Total	O	0	0
			5	5		
4	K	6	Total	O	0	0
			6	6		
4	L	5	Total	O	0	0
			5	5		
4	M	7	Total	O	0	0
			7	7		
4	N	5	Total	O	0	0
			5	5		
4	O	1	Total	O	0	0
			1	1		

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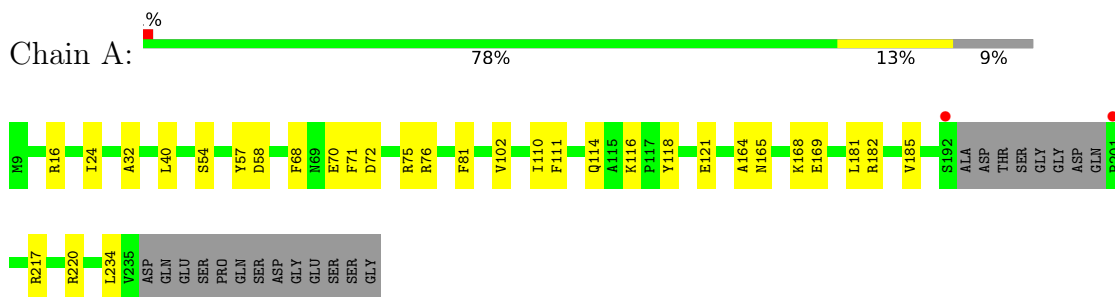
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	P	1	Total O 1 1	0	0
4	Q	1	Total O 1 1	0	0
4	R	1	Total O 1 1	0	0
4	S	2	Total O 2 2	0	0
4	T	1	Total O 1 1	0	0
4	U	1	Total O 1 1	0	0
4	V	4	Total O 4 4	0	0
4	W	3	Total O 3 3	0	0
4	X	5	Total O 5 5	0	0
4	Y	7	Total O 7 7	0	0
4	Z	5	Total O 5 5	0	0
4	a	6	Total O 6 6	0	0
4	b	6	Total O 6 6	0	0

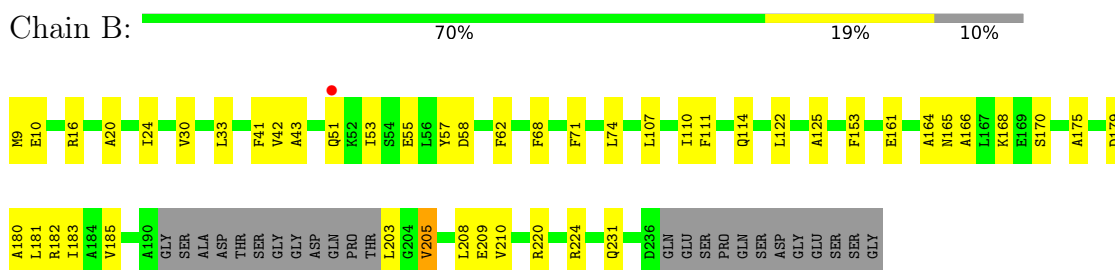
### 3 Residue-property plots [i](#)

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.

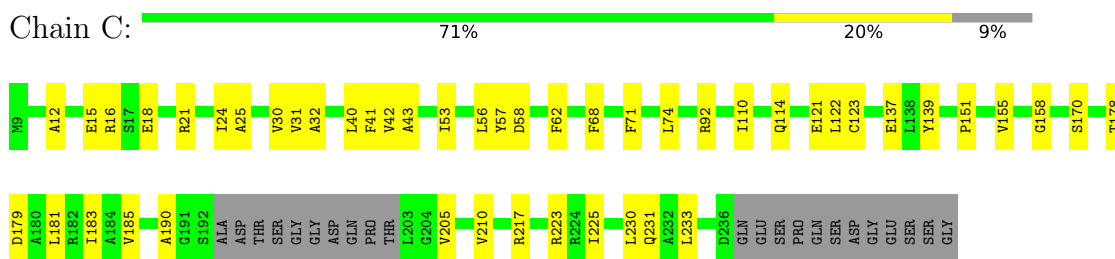
- Molecule 1: Proteasome subunit alpha



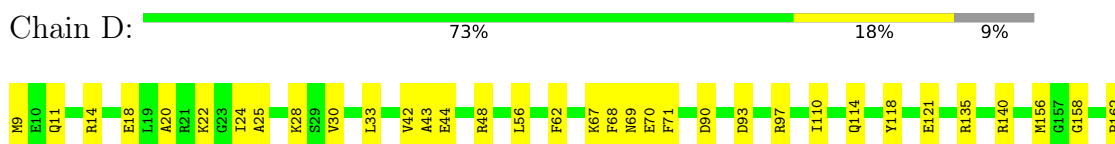
- Molecule 1: Proteasome subunit alpha



- Molecule 1: Proteasome subunit alpha

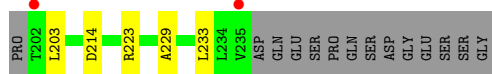
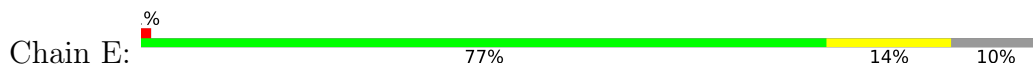


- Molecule 1: Proteasome subunit alpha

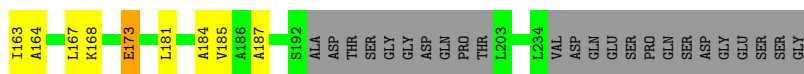




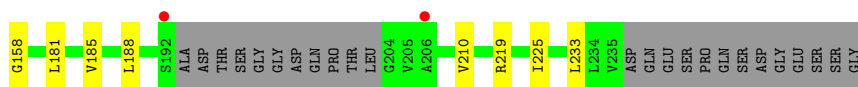
• Molecule 1: Proteasome subunit alpha



• Molecule 1: Proteasome subunit alpha



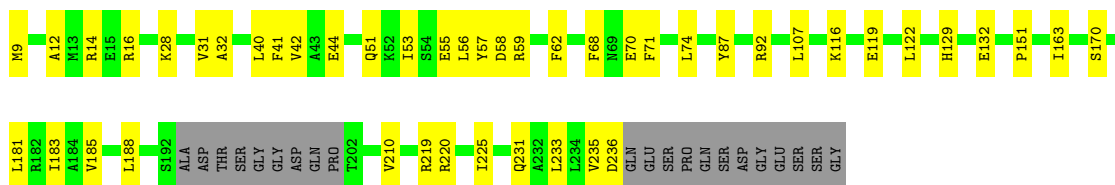
• Molecule 1: Proteasome subunit alpha



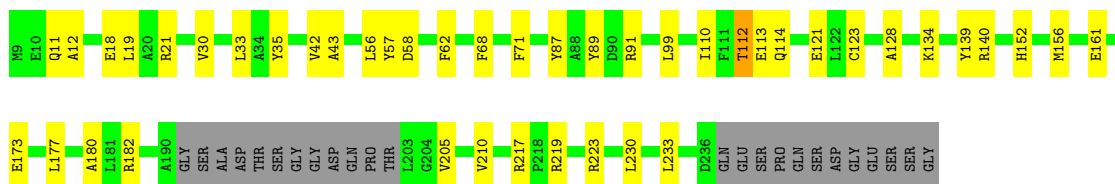
• Molecule 1: Proteasome subunit alpha



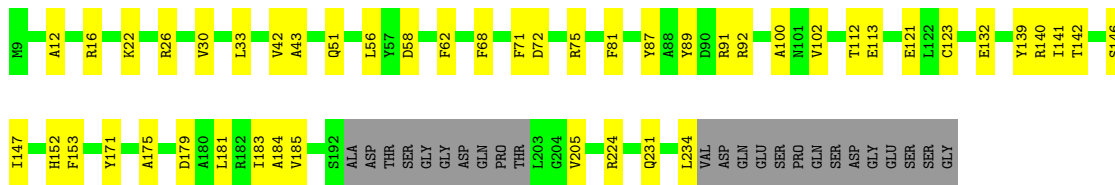
• Molecule 1: Proteasome subunit alpha



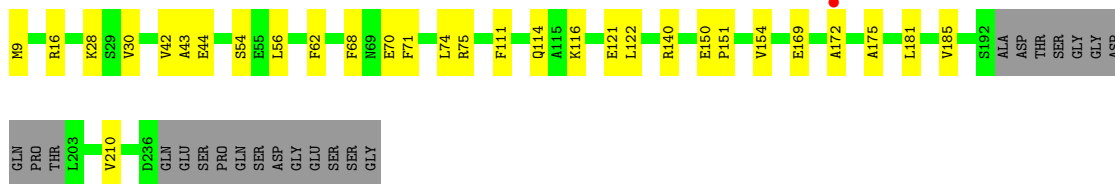
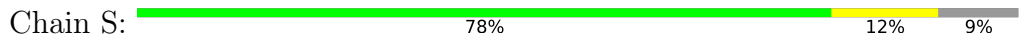
● Molecule 1: Proteasome subunit alpha



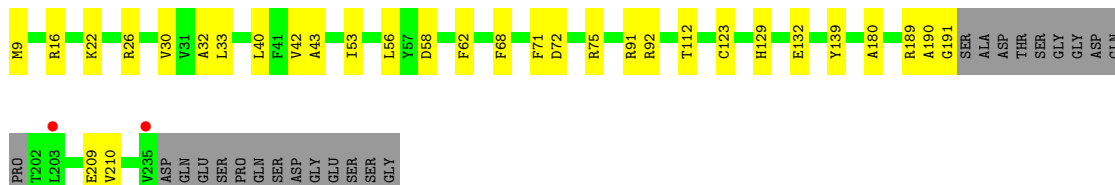
● Molecule 1: Proteasome subunit alpha



● Molecule 1: Proteasome subunit alpha

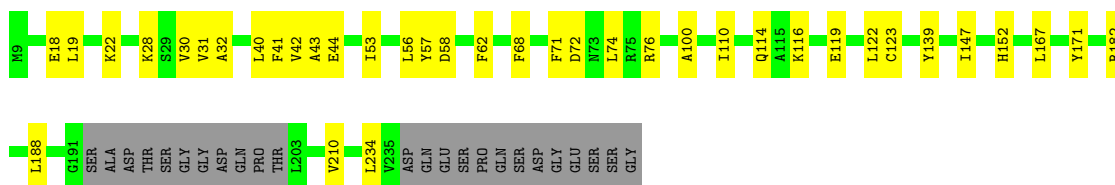


● Molecule 1: Proteasome subunit alpha




- Molecule 1: Proteasome subunit alpha

Chain U:  74% 16% 10%




- Molecule 2: Proteasome subunit beta

Chain H:  86% 6% 8%




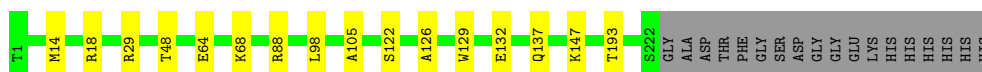
- Molecule 2: Proteasome subunit beta

Chain I:  86% 7% 8%




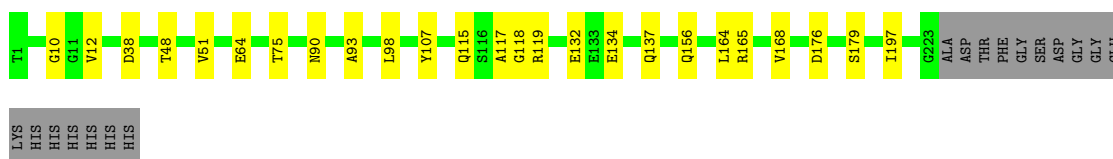
- Molecule 2: Proteasome subunit beta

Chain J:  86% 7% 8%




- Molecule 2: Proteasome subunit beta

Chain K:  82% 10% 7%




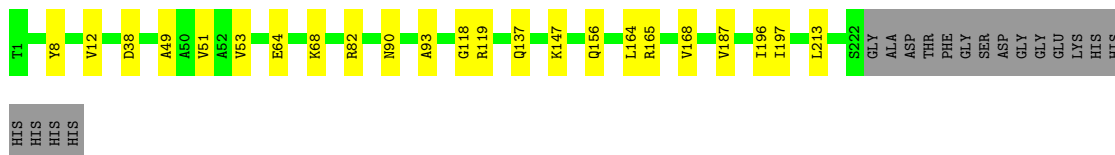
- Molecule 2: Proteasome subunit beta

Chain L:  85% 8% 7%

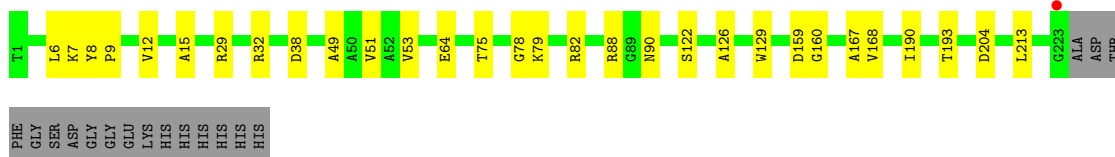
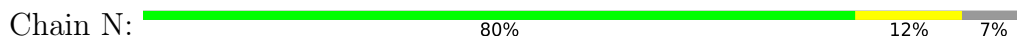


- Molecule 2: Proteasome subunit beta

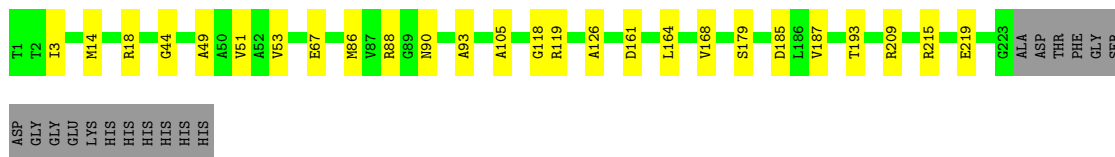
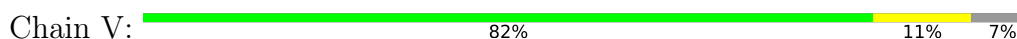
Chain M:  83% 10% 8%



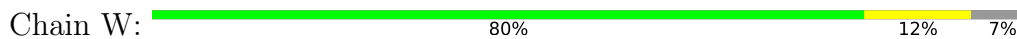
• Molecule 2: Proteasome subunit beta



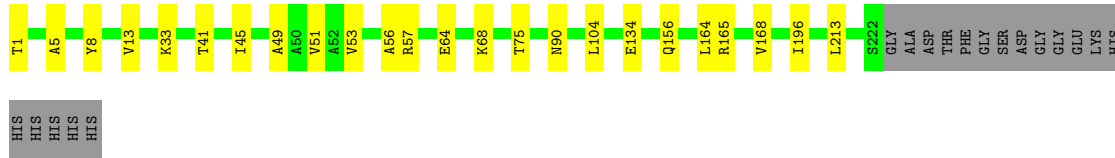
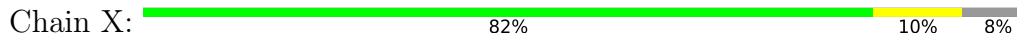
• Molecule 2: Proteasome subunit beta



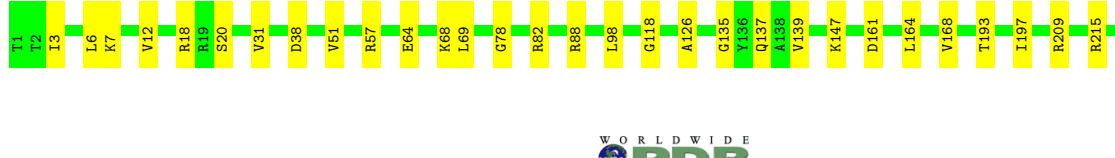
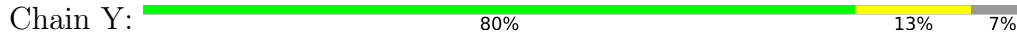
• Molecule 2: Proteasome subunit beta

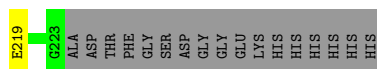


• Molecule 2: Proteasome subunit beta

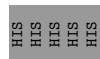
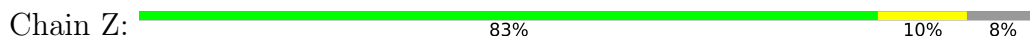


• Molecule 2: Proteasome subunit beta

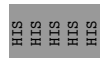
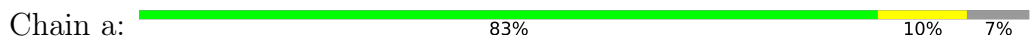




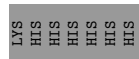
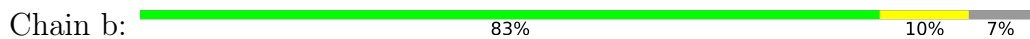
• Molecule 2: Proteasome subunit beta



• Molecule 2: Proteasome subunit beta



• Molecule 2: Proteasome subunit beta



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	120.51Å 198.30Å 165.94Å 90.00° 103.13° 90.00°	Depositor
Resolution (Å)	49.87 – 3.08 49.87 – 3.08	Depositor EDS
% Data completeness (in resolution range)	98.1 (49.87-3.08) 93.0 (49.87-3.08)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 3.07Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.181 , 0.211 0.189 , 0.215	Depositor DCC
$R_{free}$ test set	6701 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.1	Xtrriage
Anisotropy	0.030	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 20.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	47019	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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: 7HZ

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	0.29	0/1709	0.50	0/2308
1	B	0.25	0/1692	0.49	0/2285
1	C	0.26	0/1702	0.48	0/2298
1	D	0.25	0/1701	0.48	0/2297
1	E	0.26	0/1695	0.45	0/2289
1	F	0.27	0/1687	0.48	0/2277
1	G	0.29	0/1686	0.48	0/2276
1	O	0.27	0/1695	0.47	0/2289
1	P	0.26	0/1709	0.50	0/2308
1	Q	0.28	0/1692	0.49	0/2285
1	R	0.28	0/1687	0.49	0/2277
1	S	0.29	0/1702	0.48	0/2298
1	T	0.27	0/1695	0.49	0/2289
1	U	0.27	0/1688	0.48	0/2279
2	H	0.30	0/1662	0.45	0/2254
2	I	0.31	0/1662	0.45	0/2254
2	J	0.29	0/1662	0.43	0/2254
2	K	0.31	0/1666	0.47	0/2259
2	L	0.31	0/1666	0.45	0/2259
2	M	0.28	0/1662	0.44	0/2254
2	N	0.29	0/1666	0.45	0/2259
2	V	0.30	0/1666	0.46	0/2259
2	W	0.32	0/1666	0.45	0/2259
2	X	0.29	0/1662	0.45	0/2254
2	Y	0.30	0/1666	0.48	0/2259
2	Z	0.30	0/1662	0.45	0/2254
2	a	0.29	0/1666	0.42	0/2259
2	b	0.30	0/1666	0.45	0/2259
All	All	0.29	0/47040	0.47	0/63651

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	1684	0	1688	18	0
1	B	1668	0	1669	33	0
1	C	1678	0	1677	29	0
1	D	1677	0	1680	25	0
1	E	1671	0	1675	22	0
1	F	1663	0	1664	29	0
1	G	1662	0	1662	25	0
1	O	1671	0	1675	35	0
1	P	1685	0	1684	30	0
1	Q	1668	0	1669	30	0
1	R	1663	0	1664	30	0
1	S	1678	0	1677	15	0
1	T	1671	0	1675	18	0
1	U	1664	0	1668	23	0
2	H	1638	0	1633	10	0
2	I	1638	0	1633	9	0
2	J	1638	0	1633	10	0
2	K	1642	0	1636	16	0
2	L	1642	0	1636	12	0
2	M	1638	0	1633	15	0
2	N	1642	0	1636	21	0
2	V	1642	0	1636	15	0
2	W	1642	0	1636	21	0
2	X	1638	0	1633	16	0
2	Y	1642	0	1636	19	0
2	Z	1638	0	1633	14	0
2	a	1642	0	1636	15	0
2	b	1642	0	1636	16	0
3	H	40	0	0	0	0
3	I	40	0	0	0	0
3	J	40	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	40	0	0	0	0
3	L	40	0	0	0	0
3	M	40	0	0	0	0
3	N	40	0	0	0	0
3	V	40	0	0	0	0
3	W	40	0	0	0	0
3	X	40	0	0	0	0
3	Y	40	0	0	0	0
3	Z	40	0	0	0	0
3	a	40	0	0	0	0
3	b	40	0	0	0	0
4	A	2	0	0	2	0
4	B	1	0	0	0	0
4	D	2	0	0	1	0
4	F	2	0	0	0	0
4	G	1	0	0	0	0
4	H	7	0	0	0	0
4	I	5	0	0	0	0
4	J	5	0	0	0	0
4	K	6	0	0	0	0
4	L	5	0	0	0	0
4	M	7	0	0	0	0
4	N	5	0	0	0	0
4	O	1	0	0	0	0
4	P	1	0	0	0	0
4	Q	1	0	0	0	0
4	R	1	0	0	0	0
4	S	2	0	0	0	0
4	T	1	0	0	0	0
4	U	1	0	0	0	0
4	V	4	0	0	0	0
4	W	3	0	0	0	0
4	X	5	0	0	0	0
4	Y	7	0	0	0	0
4	Z	5	0	0	0	0
4	a	6	0	0	0	0
4	b	6	0	0	0	0
All	All	47019	0	46313	527	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 6.

The worst 5 of 527 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:GLN:HG3	1:D:14:ARG:HH12	1.37	0.90
1:F:123:CYS:HB2	1:F:156:MET:HE1	1.57	0.87
1:E:140:ARG:NH1	1:E:155:VAL:O	2.10	0.83
2:N:159:ASP:OD1	2:N:160:GLY:N	2.15	0.80
1:S:16:ARG:NH2	1:S:114:GLN:O	2.16	0.78

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	215/240 (90%)	206 (96%)	9 (4%)	0	100	100
1	B	212/240 (88%)	203 (96%)	8 (4%)	1 (0%)	24	54
1	C	214/240 (89%)	205 (96%)	7 (3%)	2 (1%)	14	41
1	D	214/240 (89%)	203 (95%)	11 (5%)	0	100	100
1	E	213/240 (89%)	204 (96%)	9 (4%)	0	100	100
1	F	212/240 (88%)	204 (96%)	6 (3%)	2 (1%)	14	41
1	G	212/240 (88%)	201 (95%)	11 (5%)	0	100	100
1	O	213/240 (89%)	201 (94%)	12 (6%)	0	100	100
1	P	215/240 (90%)	205 (95%)	9 (4%)	1 (0%)	24	54
1	Q	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
1	R	212/240 (88%)	203 (96%)	9 (4%)	0	100	100
1	S	214/240 (89%)	203 (95%)	9 (4%)	2 (1%)	14	41
1	T	213/240 (89%)	204 (96%)	8 (4%)	1 (0%)	24	54
1	U	212/240 (88%)	205 (97%)	7 (3%)	0	100	100
2	H	220/240 (92%)	217 (99%)	3 (1%)	0	100	100
2	I	220/240 (92%)	215 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	220/240 (92%)	217 (99%)	3 (1%)	0	100	100
2	K	221/240 (92%)	216 (98%)	5 (2%)	0	100	100
2	L	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
2	M	220/240 (92%)	216 (98%)	4 (2%)	0	100	100
2	N	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
2	V	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
2	W	221/240 (92%)	216 (98%)	5 (2%)	0	100	100
2	X	220/240 (92%)	216 (98%)	4 (2%)	0	100	100
2	Y	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
2	Z	220/240 (92%)	217 (99%)	3 (1%)	0	100	100
2	a	221/240 (92%)	216 (98%)	5 (2%)	0	100	100
2	b	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
All	All	6071/6720 (90%)	5883 (97%)	179 (3%)	9 (0%)	48	76

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	169	GLU
1	F	173	GLU
1	T	190	ALA
1	C	151	PRO
1	C	190	ALA

### 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	168/184 (91%)	168 (100%)	0	100	100
1	B	166/184 (90%)	166 (100%)	0	100	100
1	C	167/184 (91%)	167 (100%)	0	100	100
1	D	167/184 (91%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	166/184 (90%)	166 (100%)	0	100	100
1	F	165/184 (90%)	164 (99%)	1 (1%)	78	81
1	G	165/184 (90%)	165 (100%)	0	100	100
1	O	166/184 (90%)	166 (100%)	0	100	100
1	P	168/184 (91%)	168 (100%)	0	100	100
1	Q	166/184 (90%)	165 (99%)	1 (1%)	78	81
1	R	165/184 (90%)	165 (100%)	0	100	100
1	S	167/184 (91%)	167 (100%)	0	100	100
1	T	166/184 (90%)	166 (100%)	0	100	100
1	U	165/184 (90%)	165 (100%)	0	100	100
2	H	165/178 (93%)	165 (100%)	0	100	100
2	I	165/178 (93%)	165 (100%)	0	100	100
2	J	165/178 (93%)	165 (100%)	0	100	100
2	K	165/178 (93%)	165 (100%)	0	100	100
2	L	165/178 (93%)	165 (100%)	0	100	100
2	M	165/178 (93%)	165 (100%)	0	100	100
2	N	165/178 (93%)	165 (100%)	0	100	100
2	V	165/178 (93%)	165 (100%)	0	100	100
2	W	165/178 (93%)	165 (100%)	0	100	100
2	X	165/178 (93%)	165 (100%)	0	100	100
2	Y	165/178 (93%)	165 (100%)	0	100	100
2	Z	165/178 (93%)	165 (100%)	0	100	100
2	a	165/178 (93%)	165 (100%)	0	100	100
2	b	165/178 (93%)	165 (100%)	0	100	100
All	All	4637/5068 (92%)	4635 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	112	THR
1	Q	112	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	W	130	ASN
2	a	130	ASN
2	X	130	ASN
2	N	130	ASN
1	U	129	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

14 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	7HZ	b	301	-	42,42,42	2.16	7 (16%)	55,58,58	2.50	18 (32%)
3	7HZ	N	301	-	42,42,42	2.17	8 (19%)	55,58,58	2.58	16 (29%)
3	7HZ	a	301	-	42,42,42	2.15	10 (23%)	55,58,58	2.46	18 (32%)
3	7HZ	W	301	-	42,42,42	2.05	9 (21%)	55,58,58	2.50	17 (30%)
3	7HZ	Z	301	-	42,42,42	2.07	7 (16%)	55,58,58	2.59	17 (30%)
3	7HZ	I	301	-	42,42,42	2.08	8 (19%)	55,58,58	2.53	17 (30%)
3	7HZ	K	301	-	42,42,42	2.47	9 (21%)	55,58,58	2.59	18 (32%)
3	7HZ	H	301	-	42,42,42	1.98	8 (19%)	55,58,58	2.59	19 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	7HZ	Y	301	-	42,42,42	2.22	10 (23%)	55,58,58	2.42	17 (30%)
3	7HZ	V	301	-	42,42,42	1.99	7 (16%)	55,58,58	2.63	17 (30%)
3	7HZ	J	301	-	42,42,42	1.97	8 (19%)	55,58,58	2.53	17 (30%)
3	7HZ	X	301	-	42,42,42	2.02	7 (16%)	55,58,58	2.53	17 (30%)
3	7HZ	M	301	-	42,42,42	2.08	7 (16%)	55,58,58	2.61	17 (30%)
3	7HZ	L	301	-	42,42,42	2.26	9 (21%)	55,58,58	2.48	18 (32%)

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	7HZ	b	301	-	-	11/38/38/38	0/3/3/3
3	7HZ	N	301	-	-	12/38/38/38	0/3/3/3
3	7HZ	a	301	-	-	10/38/38/38	0/3/3/3
3	7HZ	W	301	-	-	11/38/38/38	0/3/3/3
3	7HZ	Z	301	-	-	12/38/38/38	0/3/3/3
3	7HZ	I	301	-	-	8/38/38/38	0/3/3/3
3	7HZ	K	301	-	-	8/38/38/38	0/3/3/3
3	7HZ	H	301	-	-	8/38/38/38	0/3/3/3
3	7HZ	Y	301	-	-	6/38/38/38	0/3/3/3
3	7HZ	V	301	-	-	7/38/38/38	0/3/3/3
3	7HZ	J	301	-	-	6/38/38/38	0/3/3/3
3	7HZ	X	301	-	-	7/38/38/38	0/3/3/3
3	7HZ	M	301	-	-	7/38/38/38	0/3/3/3
3	7HZ	L	301	-	-	7/38/38/38	0/3/3/3

The worst 5 of 114 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	301	7HZ	O26-N25	-11.20	1.34	1.41
3	L	301	7HZ	O26-N25	-10.13	1.35	1.41
3	b	301	7HZ	O26-N25	-9.24	1.35	1.41
3	Y	301	7HZ	O26-N25	-8.78	1.36	1.41
3	M	301	7HZ	O26-N25	-8.23	1.36	1.41

The worst 5 of 243 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Z	301	7HZ	C34-C33-N32	8.70	127.59	115.22
3	I	301	7HZ	C34-C33-N32	8.65	127.51	115.22
3	N	301	7HZ	C34-C33-N32	8.54	127.36	115.22
3	M	301	7HZ	C34-C33-N32	8.40	127.16	115.22
3	H	301	7HZ	C34-C33-N32	8.35	127.09	115.22

There are no chirality outliers.

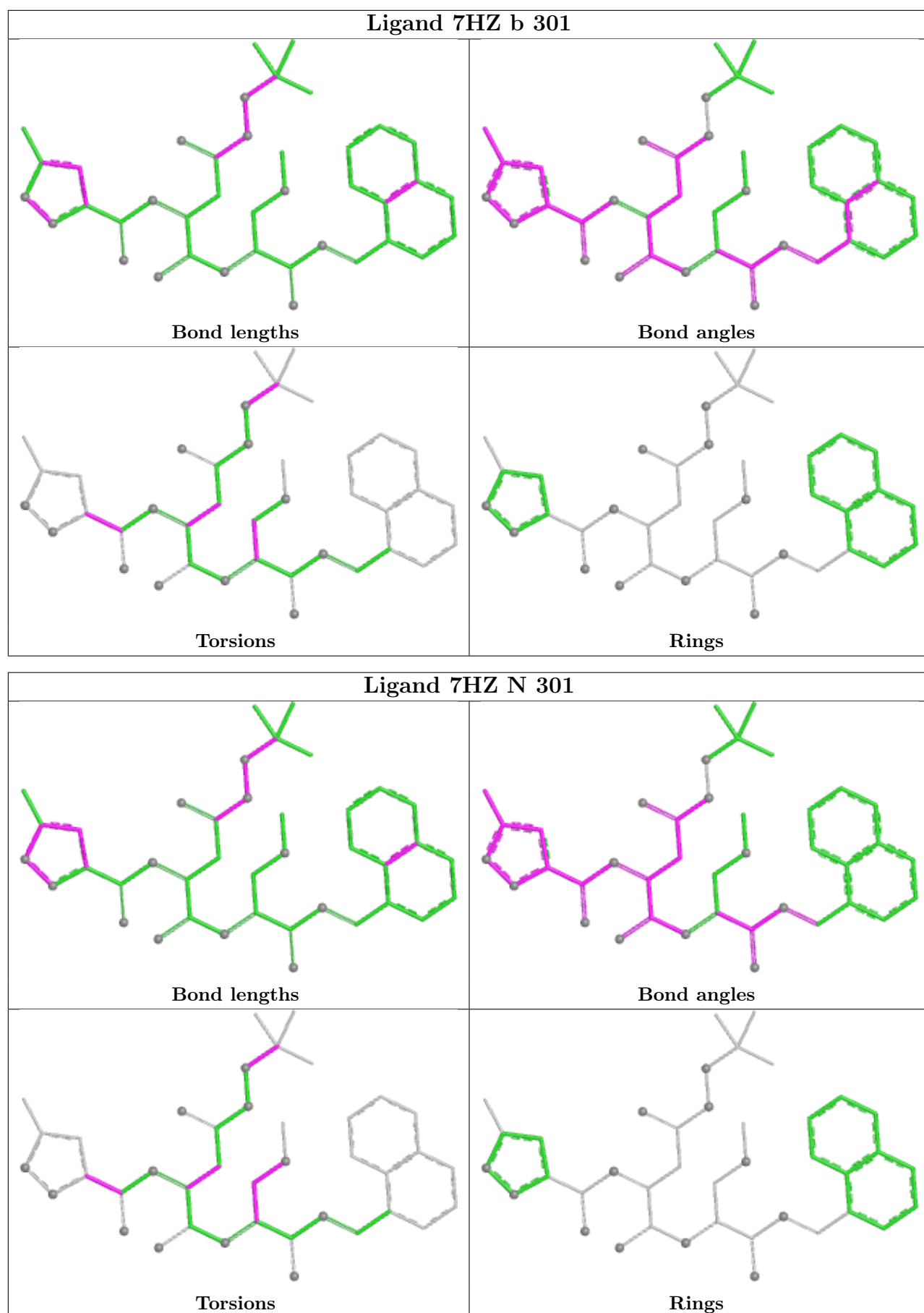
5 of 120 torsion outliers are listed below:

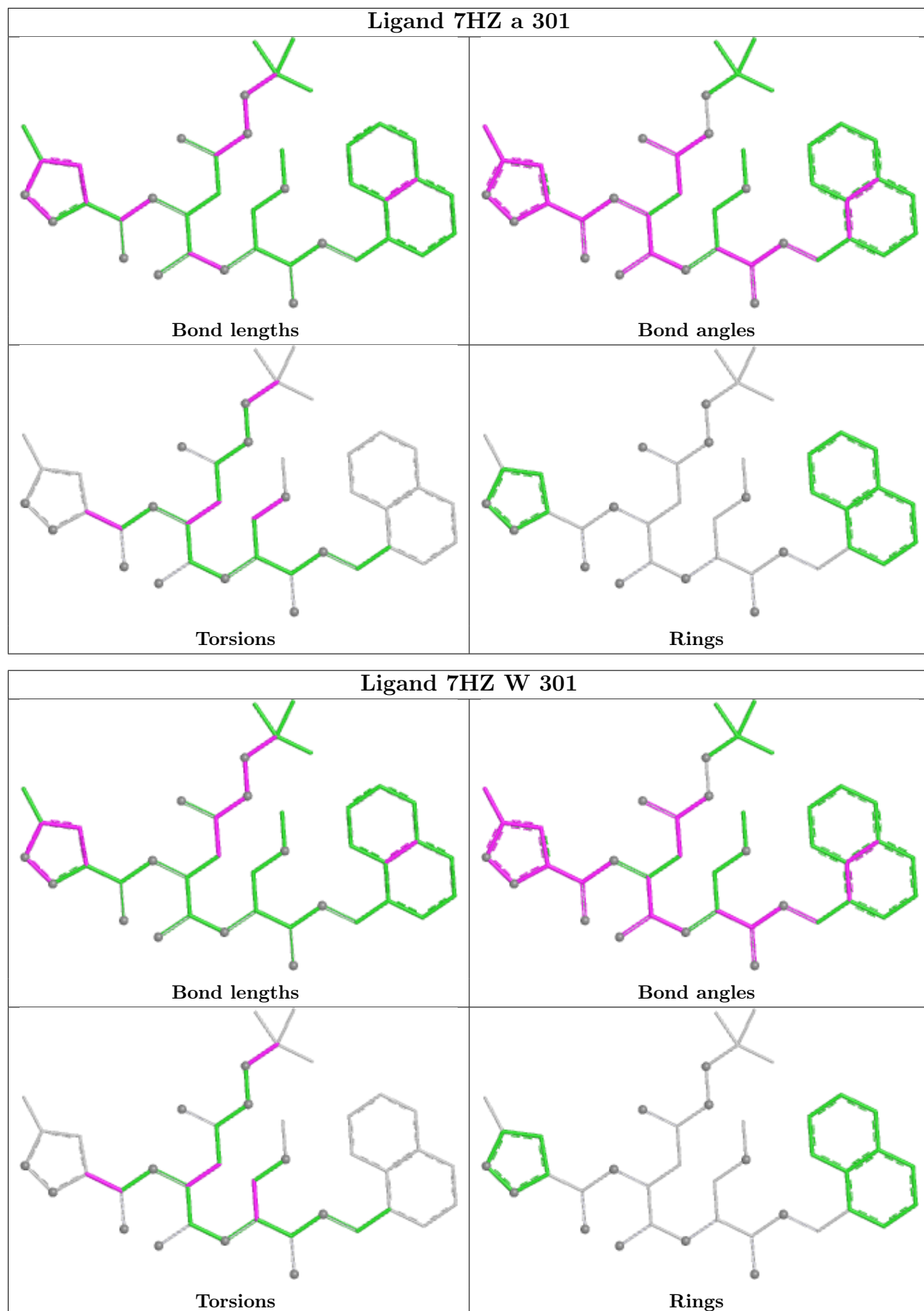
Mol	Chain	Res	Type	Atoms
3	I	301	7HZ	O40-C33-C34-C39
3	I	301	7HZ	N32-C33-C34-C39
3	I	301	7HZ	O40-C33-C34-N35
3	I	301	7HZ	N32-C33-C34-N35
3	J	301	7HZ	O40-C33-C34-C39

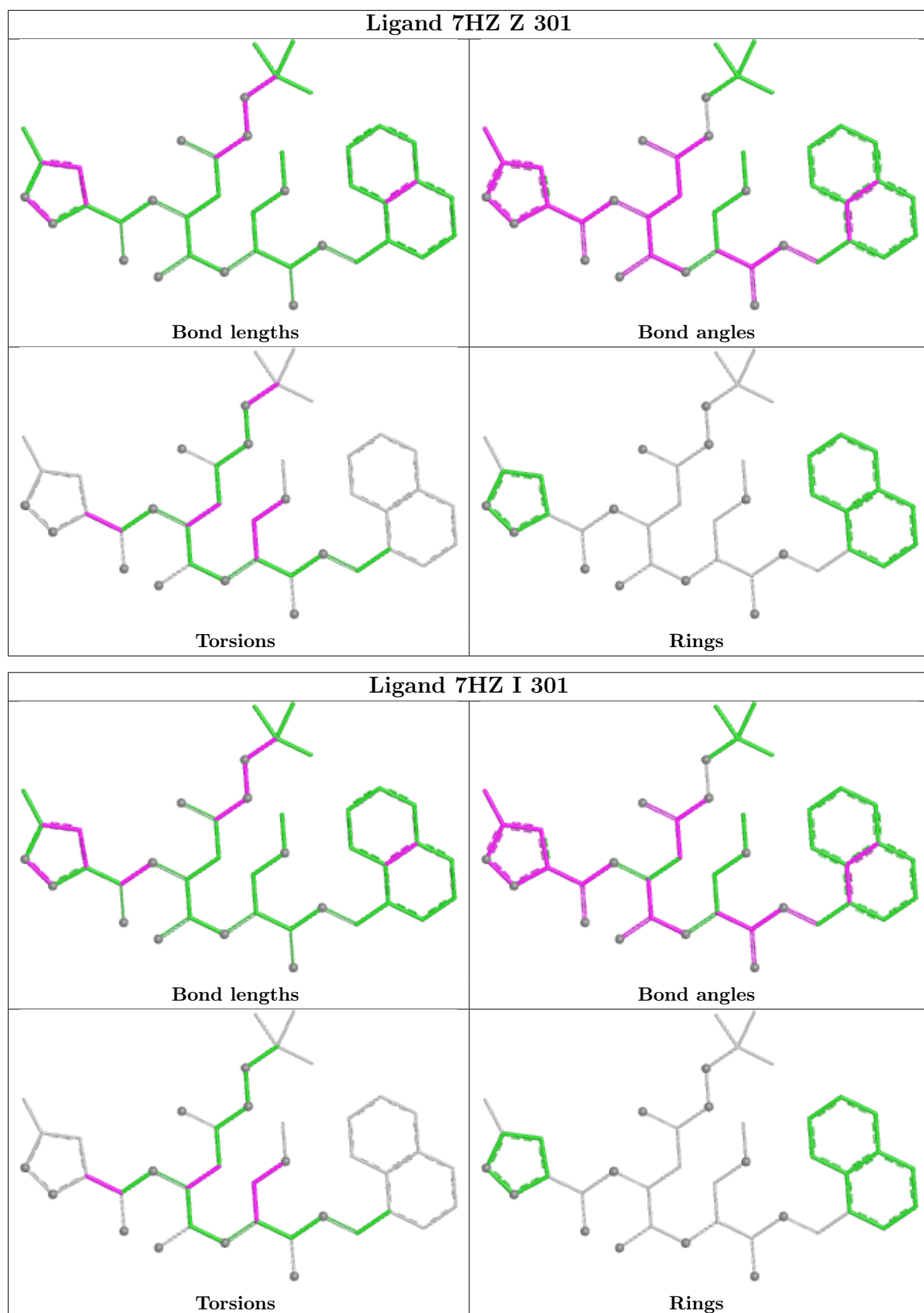
There are no ring outliers.

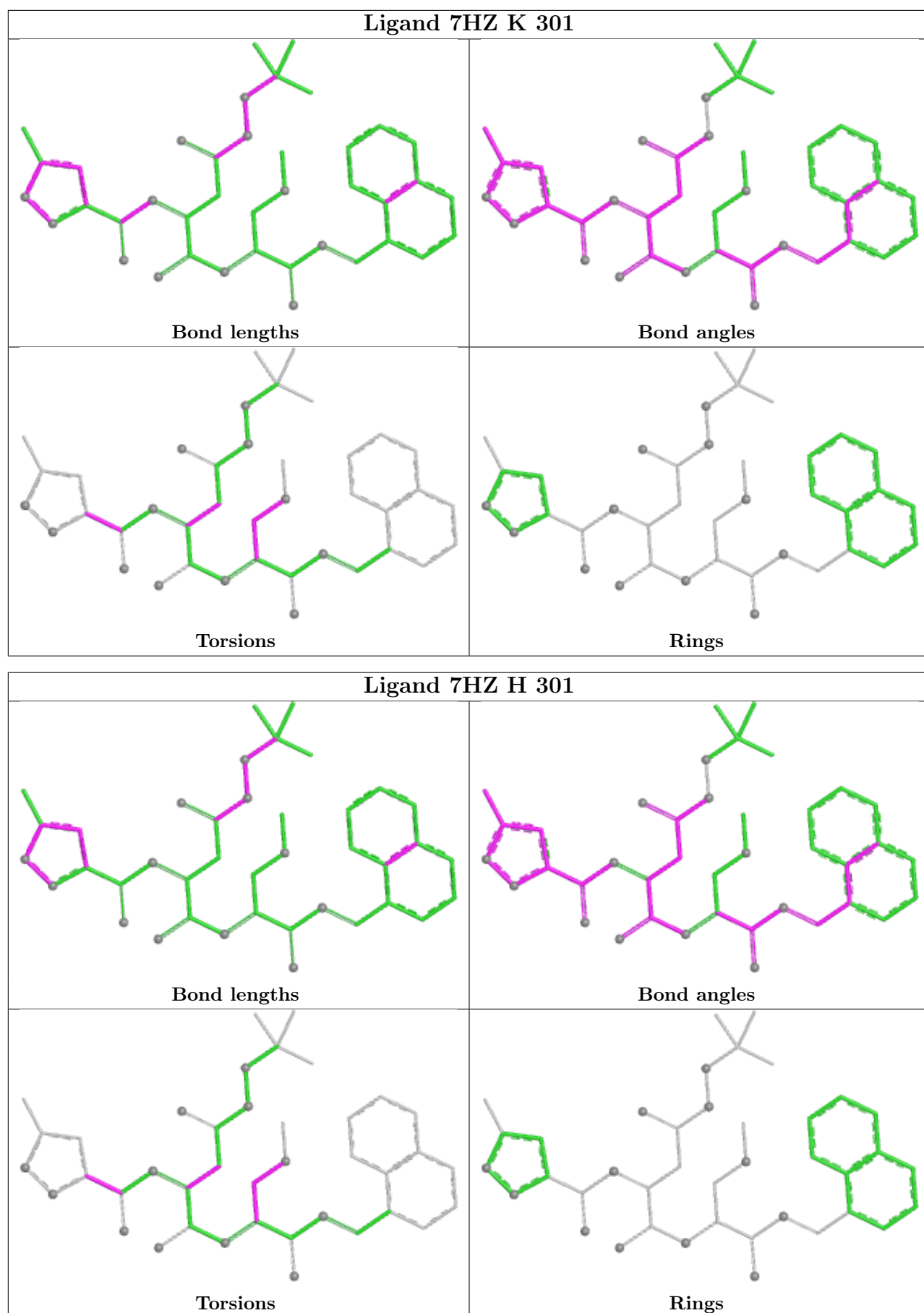
No monomer is involved in short contacts.

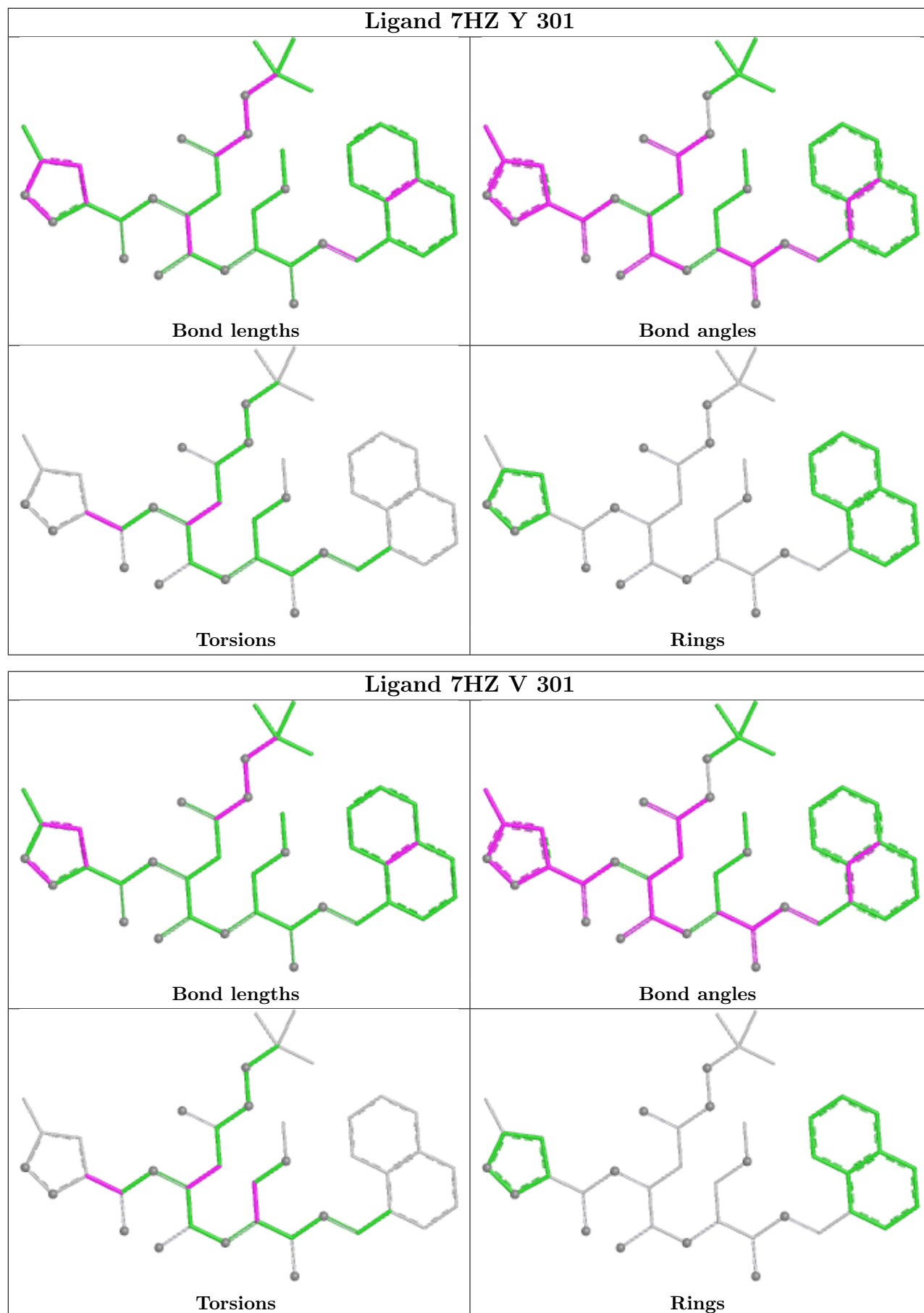
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

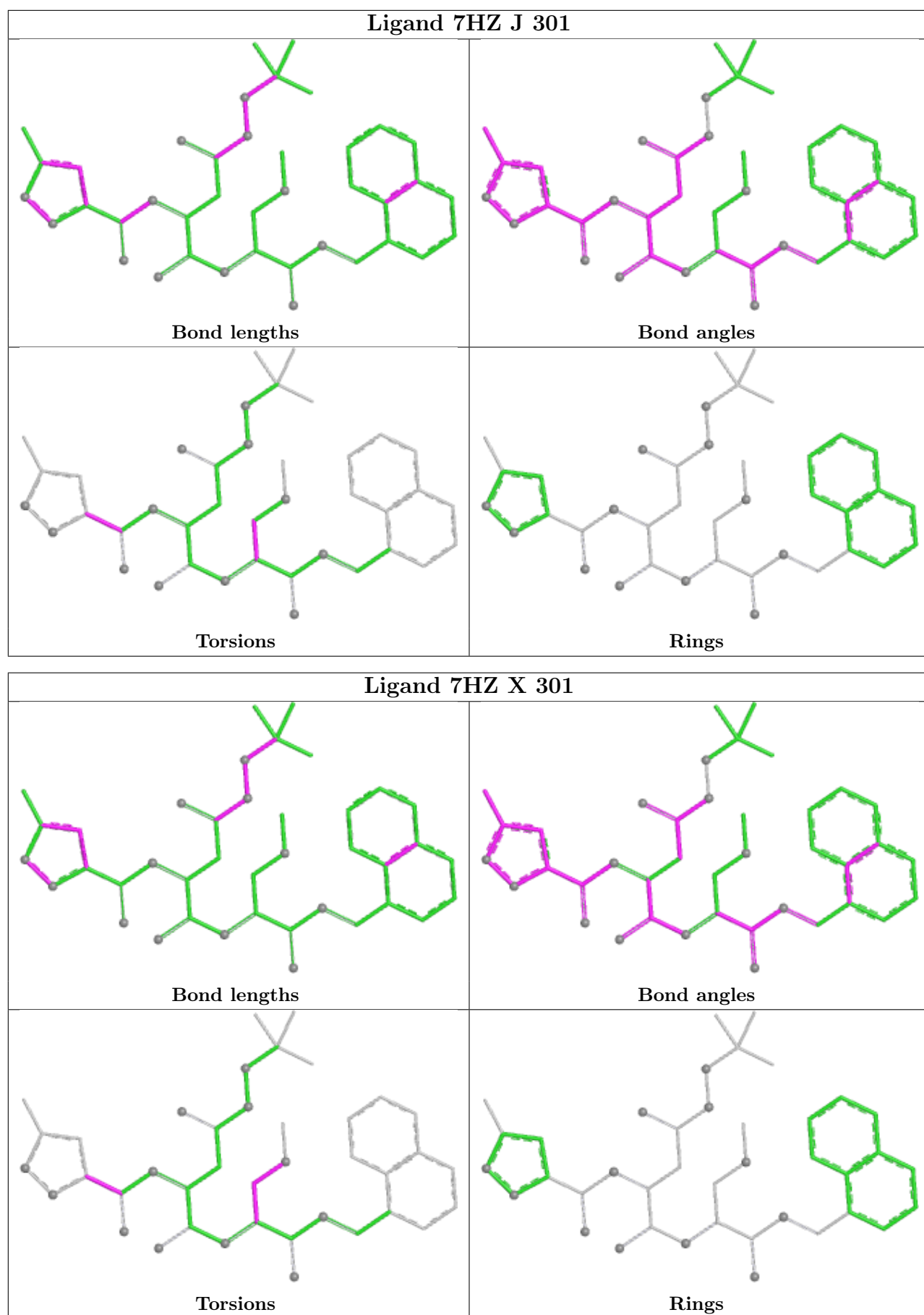


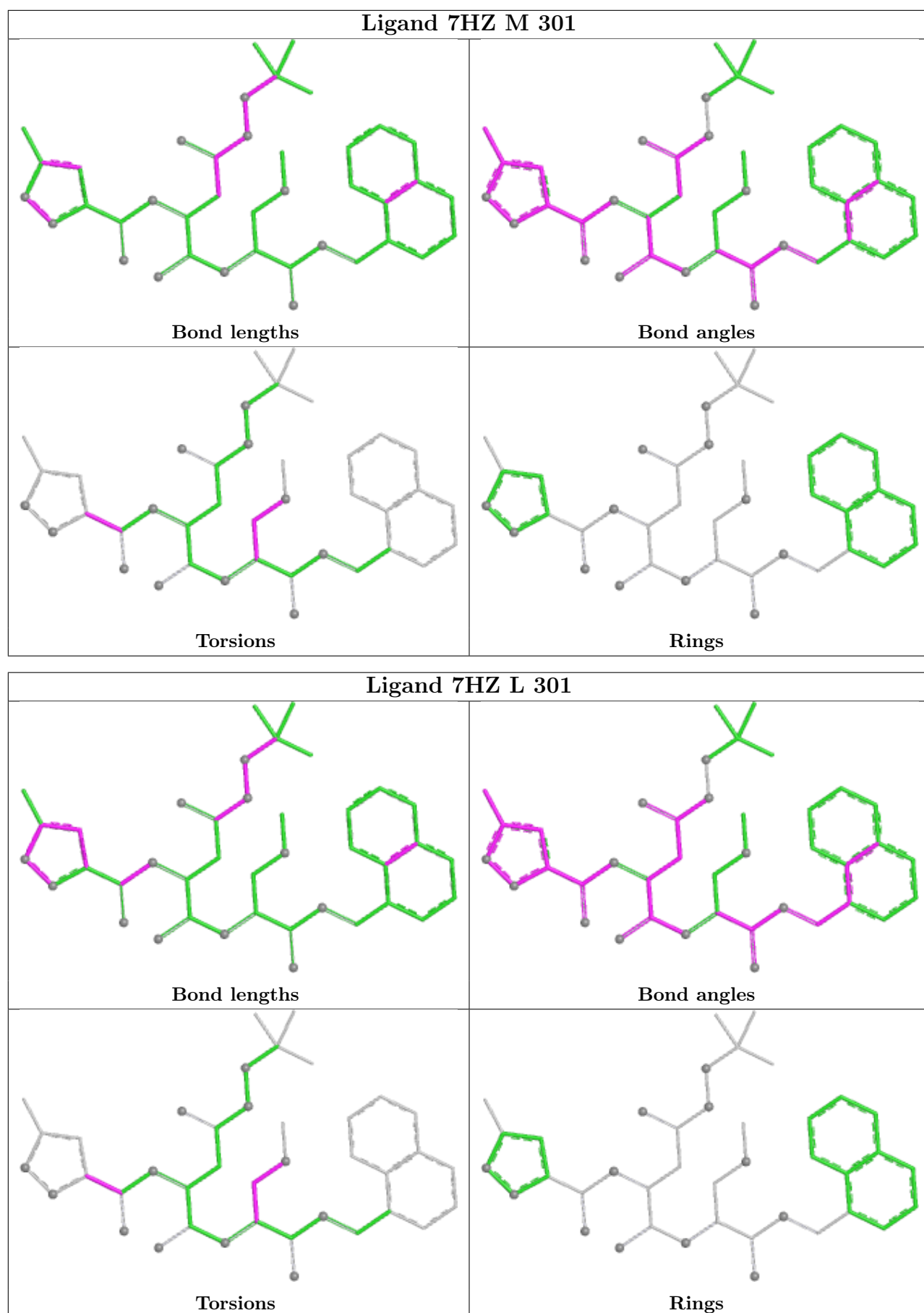












## 5.7 Other polymers [i](#)

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	219/240 (91%)	-0.42	2 (0%) 81 61	41, 56, 84, 118	0
1	B	216/240 (90%)	-0.23	1 (0%) 87 72	42, 66, 105, 162	0
1	C	218/240 (90%)	-0.19	0 100 100	42, 66, 103, 151	0
1	D	218/240 (90%)	-0.24	1 (0%) 87 72	44, 71, 105, 121	0
1	E	217/240 (90%)	-0.26	3 (1%) 73 51	40, 62, 90, 121	0
1	F	216/240 (90%)	-0.22	0 100 100	41, 67, 101, 127	0
1	G	216/240 (90%)	-0.40	2 (0%) 81 61	39, 57, 87, 135	0
1	O	217/240 (90%)	-0.12	1 (0%) 87 72	44, 70, 110, 159	0
1	P	219/240 (91%)	-0.21	0 100 100	43, 65, 97, 129	0
1	Q	216/240 (90%)	-0.36	0 100 100	42, 61, 89, 130	0
1	R	216/240 (90%)	-0.33	0 100 100	40, 61, 91, 108	0
1	S	218/240 (90%)	-0.35	1 (0%) 87 72	40, 56, 90, 119	0
1	T	217/240 (90%)	-0.26	2 (0%) 81 61	43, 64, 95, 117	0
1	U	216/240 (90%)	-0.38	0 100 100	40, 59, 89, 118	0
2	H	222/240 (92%)	-0.53	0 100 100	40, 49, 74, 97	0
2	I	222/240 (92%)	-0.54	0 100 100	40, 47, 66, 83	0
2	J	222/240 (92%)	-0.53	0 100 100	41, 50, 74, 93	0
2	K	223/240 (92%)	-0.51	0 100 100	40, 49, 71, 88	0
2	L	223/240 (92%)	-0.56	0 100 100	39, 48, 69, 92	0
2	M	222/240 (92%)	-0.52	0 100 100	39, 50, 72, 109	0
2	N	223/240 (92%)	-0.35	1 (0%) 88 75	41, 54, 80, 130	0
2	V	223/240 (92%)	-0.59	0 100 100	39, 48, 67, 84	0
2	W	223/240 (92%)	-0.57	0 100 100	39, 49, 72, 98	0
2	X	222/240 (92%)	-0.54	0 100 100	40, 49, 72, 93	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
2	Y	223/240 (92%)	-0.49	0 100 100	41, 48, 72, 93	0
2	Z	222/240 (92%)	-0.56	0 100 100	39, 49, 73, 92	0
2	a	223/240 (92%)	-0.50	0 100 100	41, 52, 77, 106	0
2	b	223/240 (92%)	-0.53	0 100 100	40, 49, 76, 88	0
All	All	6155/6720 (91%)	-0.40	14 (0%) 91 83	39, 54, 91, 162	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	PRO	3.8
1	O	235	VAL	3.2
1	G	206	ALA	2.7
1	B	51	GLN	2.6
1	D	235	VAL	2.6

## 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 oligosaccharides 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.

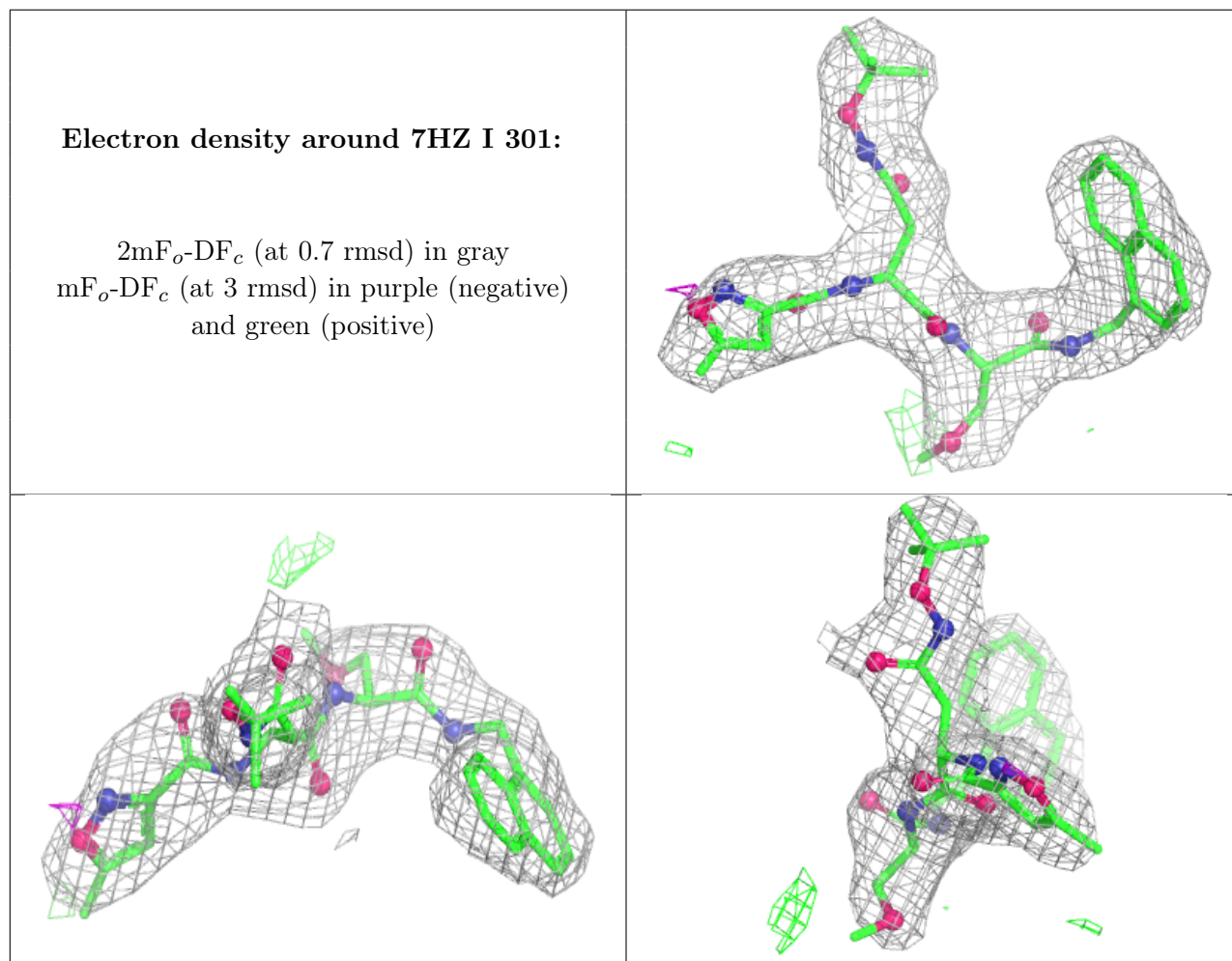
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	7HZ	I	301	40/40	0.93	0.10	41,52,66,91	0
3	7HZ	K	301	40/40	0.93	0.10	49,54,75,87	0
3	7HZ	L	301	40/40	0.93	0.10	40,48,62,75	0
3	7HZ	N	301	40/40	0.93	0.11	48,51,70,82	0
3	7HZ	M	301	40/40	0.94	0.10	44,51,69,76	0
3	7HZ	V	301	40/40	0.94	0.09	45,52,65,72	0
3	7HZ	W	301	40/40	0.94	0.09	44,49,70,73	0

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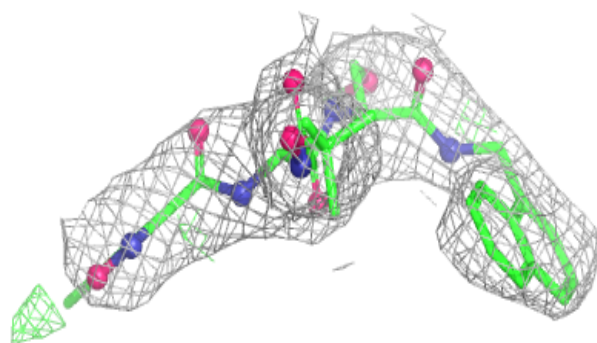
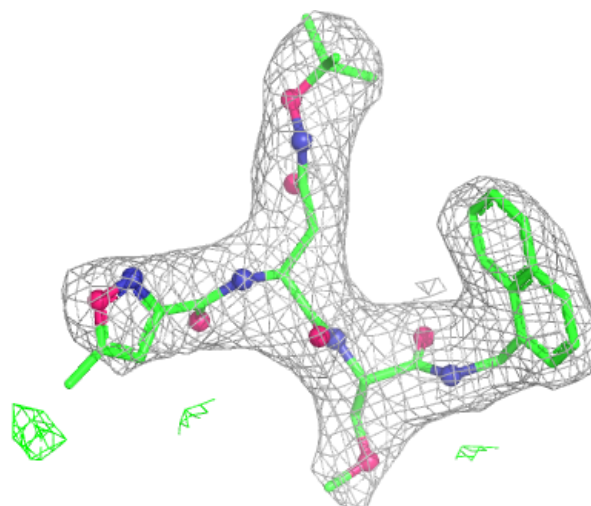
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	7HZ	Y	301	40/40	0.94	0.10	41,52,71,75	0
3	7HZ	a	301	40/40	0.94	0.09	45,51,61,62	0
3	7HZ	b	301	40/40	0.94	0.10	43,47,56,62	0
3	7HZ	H	301	40/40	0.95	0.10	43,49,74,76	0
3	7HZ	Z	301	40/40	0.95	0.09	41,47,58,67	0
3	7HZ	J	301	40/40	0.95	0.09	44,47,59,63	0
3	7HZ	X	301	40/40	0.95	0.09	42,50,60,71	0

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



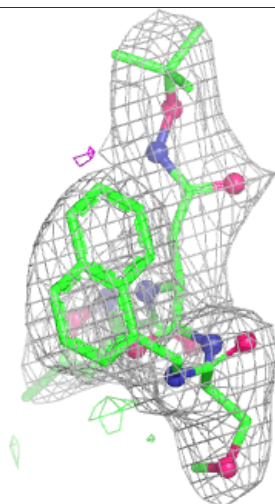
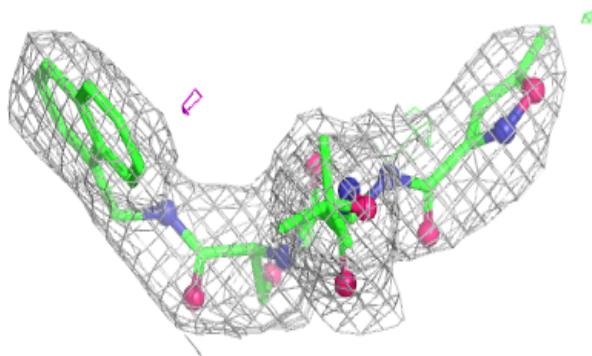
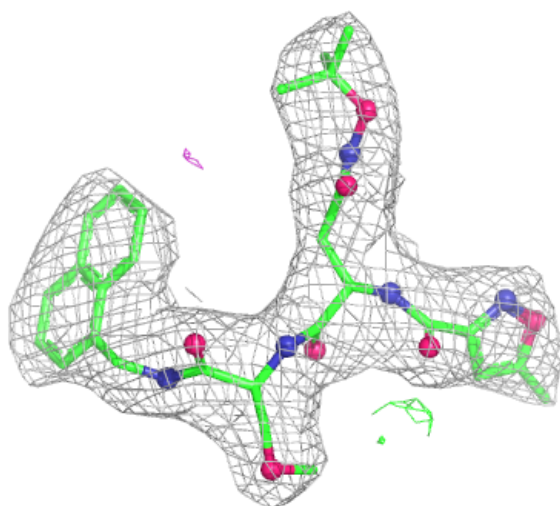
**Electron density around 7HZ K 301:**

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



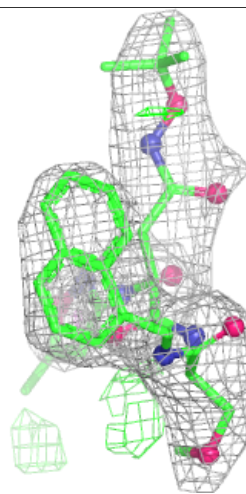
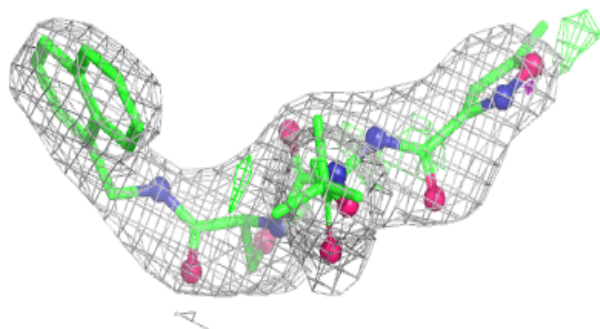
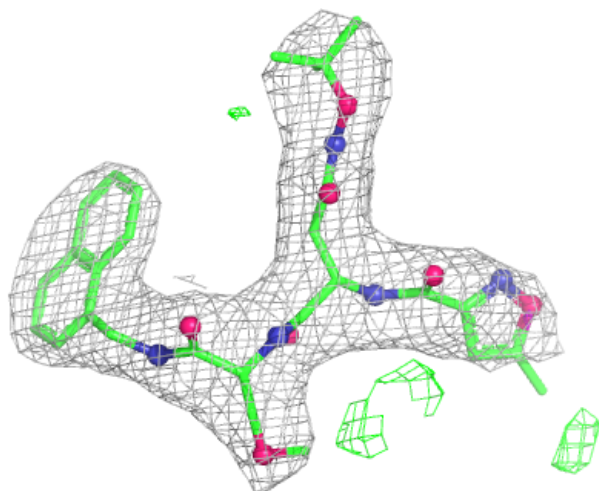
**Electron density around 7HZ L 301:**

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



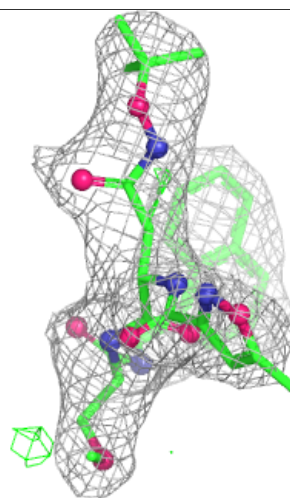
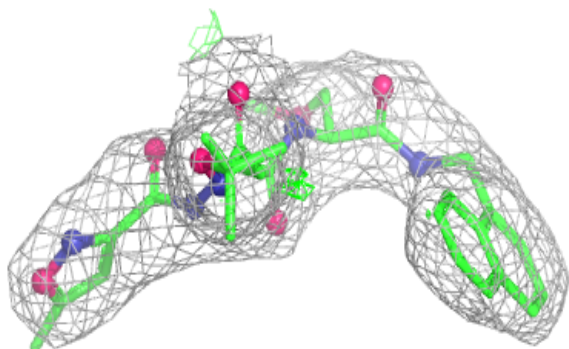
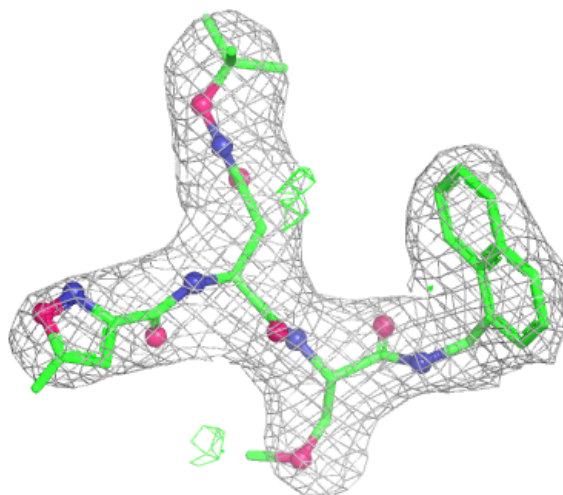
**Electron density around 7HZ N 301:**

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



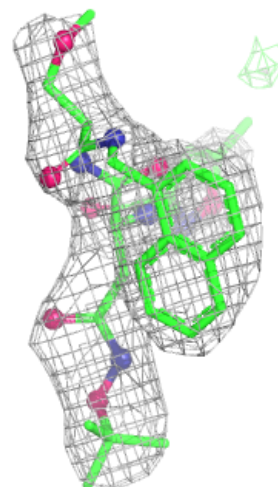
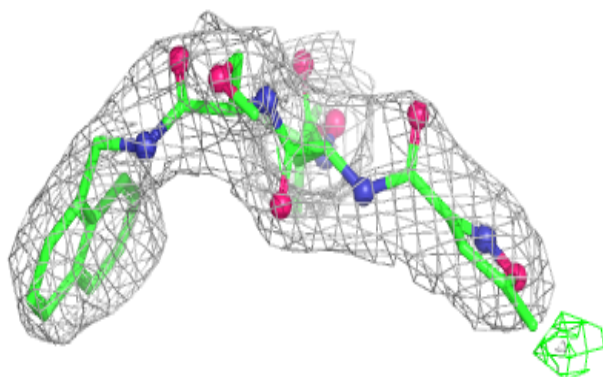
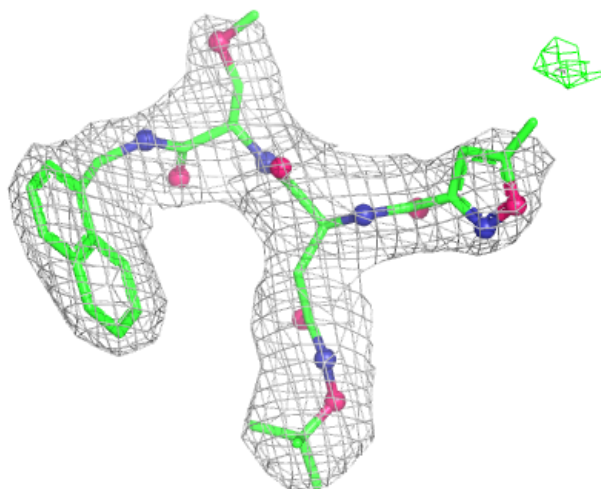
**Electron density around 7HZ M 301:**

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



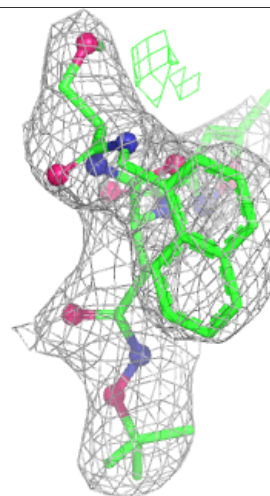
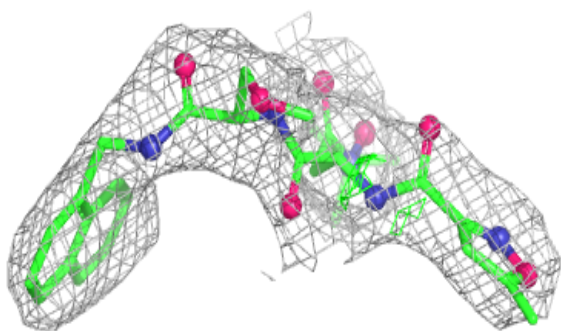
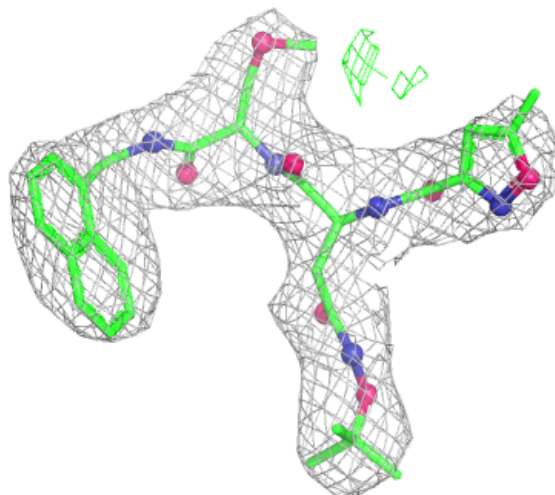
**Electron density around 7HZ V 301:**

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



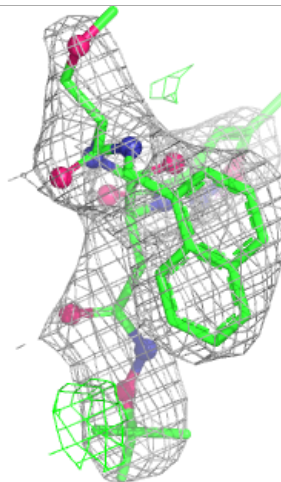
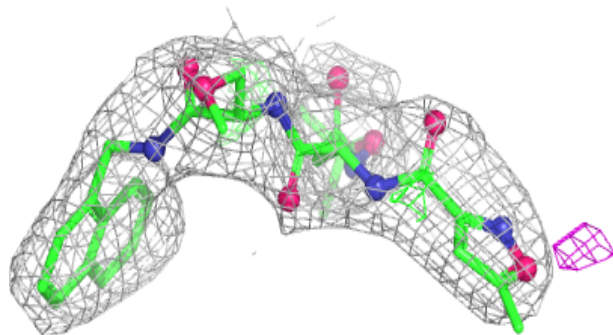
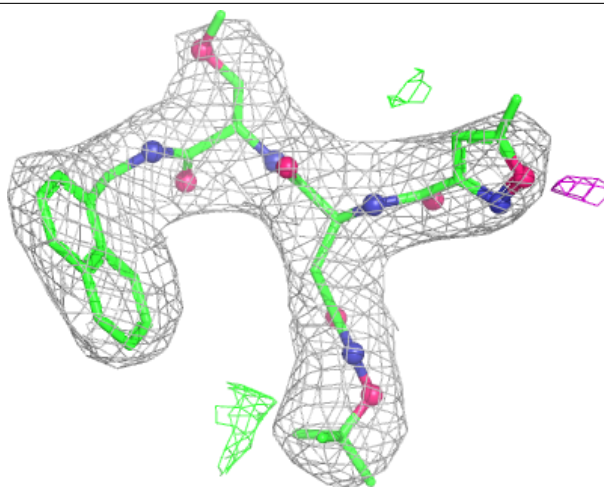
**Electron density around 7HZ W 301:**

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



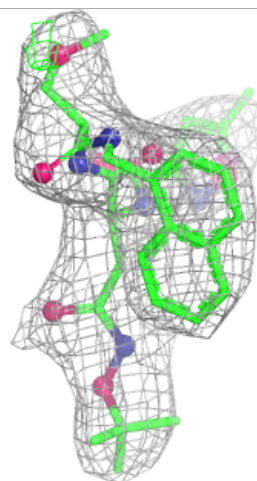
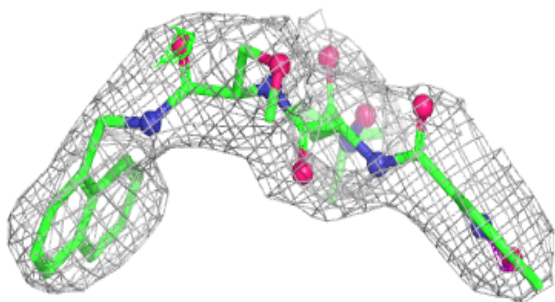
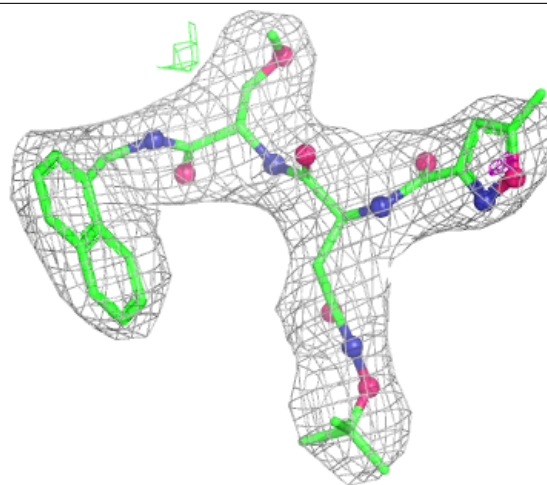
**Electron density around 7HZ Y 301:**

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



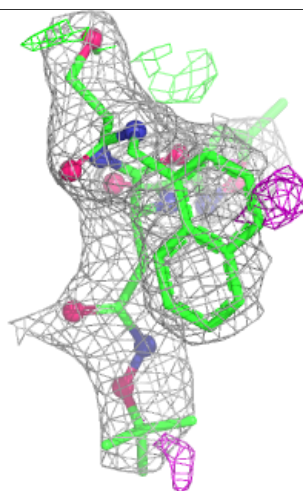
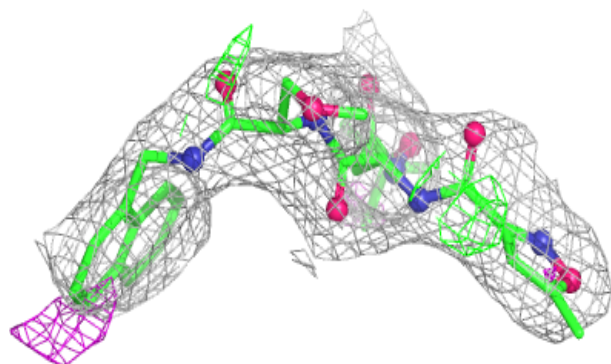
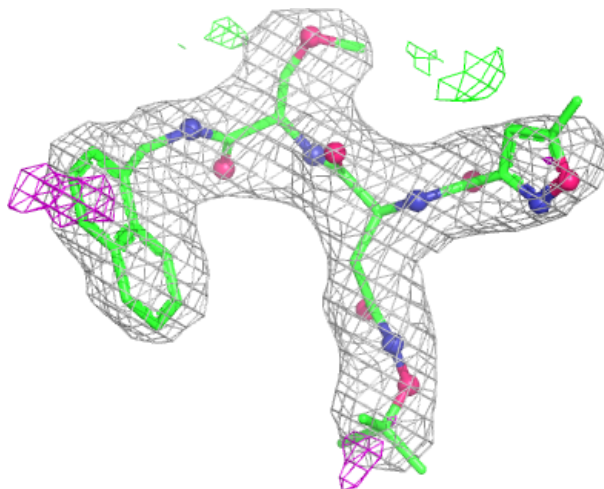
**Electron density around 7HZ a 301:**

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and green (positive)



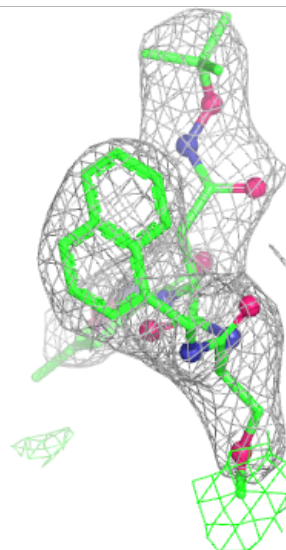
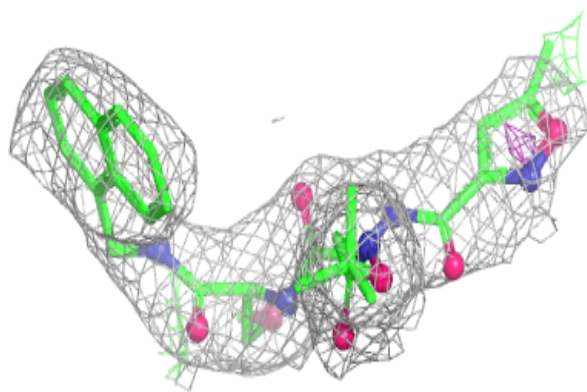
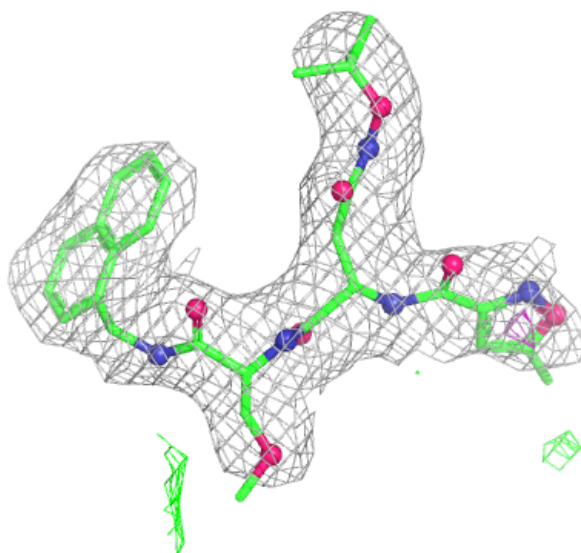
**Electron density around 7HZ b 301:**

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and green (positive)



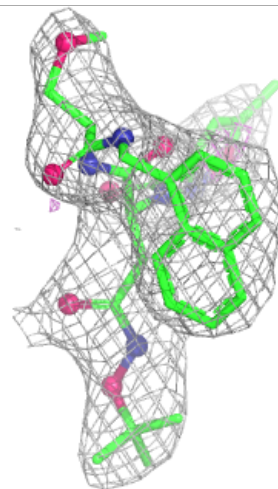
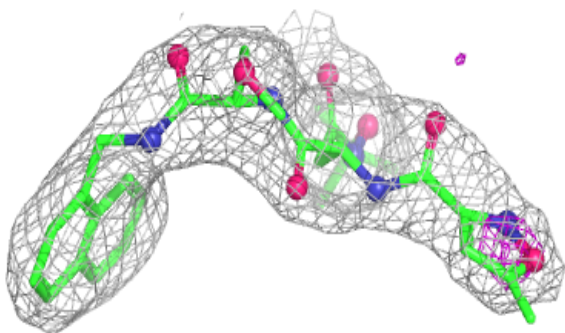
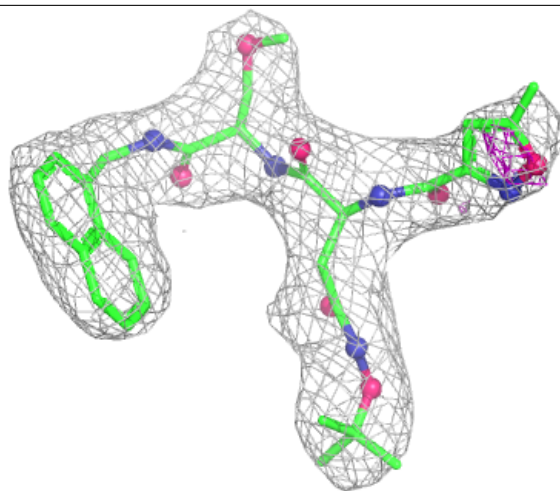
**Electron density around 7HZ H 301:**

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



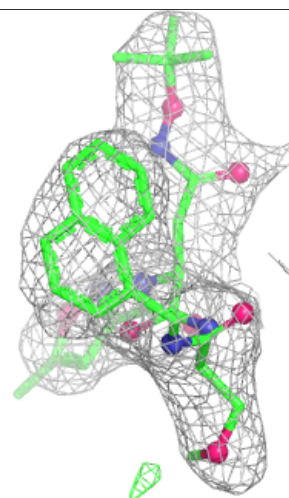
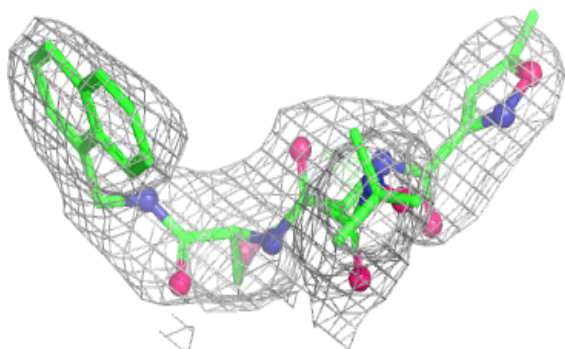
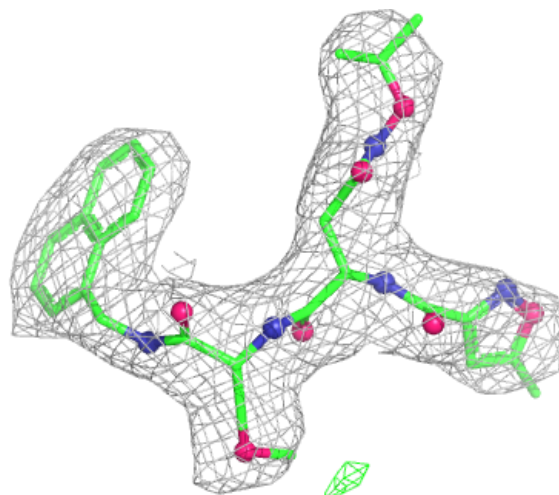
**Electron density around 7HZ Z 301:**

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and green (positive)



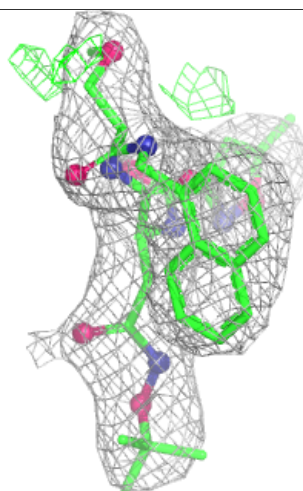
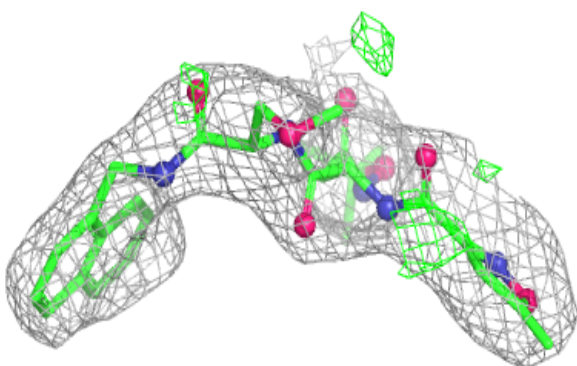
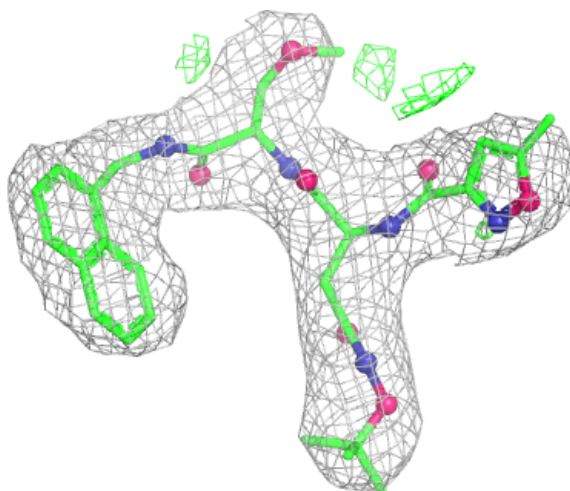
**Electron density around 7HZ J 301:**

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



**Electron density around 7HZ X 301:**

$2mF_o-DF_c$  (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.