



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:17 AM UTC

PDB ID : 5TS0 / pdb_00005ts0
Title : Structure of Mycobacterium tuberculosis proteasome in complex with N,C-capped dipeptide PKS2208
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 : 2.85 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

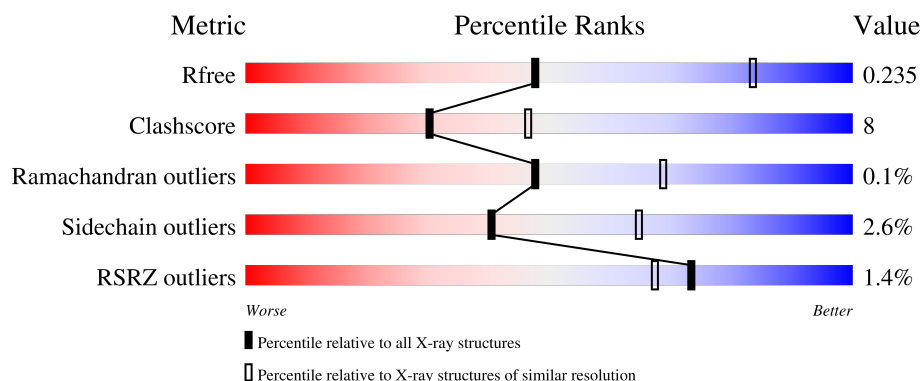
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	240	2% 72% 19% 9%
1	B	240	0% 68% 21% 10%
1	C	240	2% 64% 25% 10%
1	D	240	3% 67% 23% 10%

Continued on next page...

Continued from previous page...

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

There are 4 unique types of molecules in this entry. The entry contains 47311 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
1	A	218	Total	C	N	O	S	0	0	0
			1677	1050	306	317	4			
1	B	216	Total	C	N	O	S	0	0	0
			1668	1045	304	315	4			
1	C	217	Total	C	N	O	S	0	0	0
			1672	1047	305	316	4			
1	D	217	Total	C	N	O	S	0	0	0
			1670	1046	305	315	4			
1	E	218	Total	C	N	O	S	0	0	0
			1677	1050	306	317	4			
1	F	215	Total	C	N	O	S	0	0	0
			1655	1035	303	313	4			
1	G	220	Total	C	N	O	S	0	0	0
			1690	1057	308	321	4			
1	O	216	Total	C	N	O	S	0	0	0
			1664	1043	304	313	4			
1	P	218	Total	C	N	O	S	0	0	0
			1677	1050	306	317	4			
1	Q	218	Total	C	N	O	S	0	0	0
			1678	1050	306	318	4			
1	R	217	Total	C	N	O	S	0	0	0
			1670	1046	305	315	4			
1	S	218	Total	C	N	O	S	0	0	0
			1678	1050	306	318	4			
1	T	218	Total	C	N	O	S	0	0	0
			1679	1051	306	318	4			
1	U	217	Total	C	N	O	S	0	0	0
			1670	1046	305	315	4			

There are 14 discrepancies between the modelled and reference sequences:

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

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

Continued on next page...

Continued from previous page...

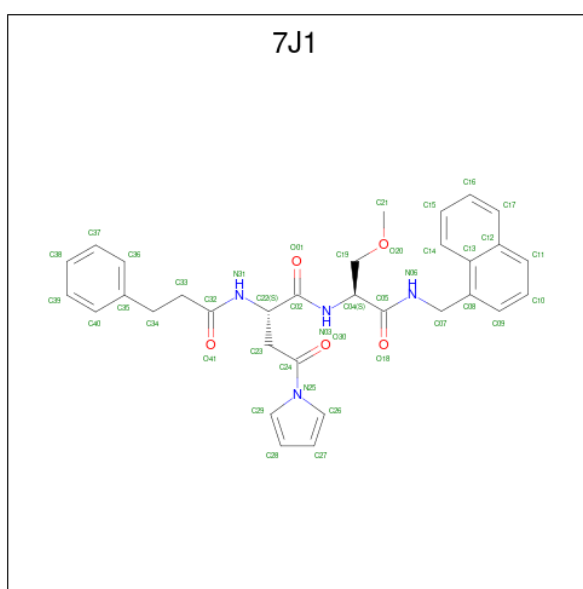
Chain	Residue	Modelled	Actual	Comment	Reference
N	235	HIS	-	expression tag	UNP A5U4D6
N	236	HIS	-	expression tag	UNP A5U4D6
N	237	HIS	-	expression tag	UNP A5U4D6
N	238	HIS	-	expression tag	UNP A5U4D6
N	239	HIS	-	expression tag	UNP A5U4D6
N	240	HIS	-	expression tag	UNP A5U4D6
V	235	HIS	-	expression tag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

Continued on next page...

Continued from previous page...

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 (2S)-N-{(2S)-3-methoxy-1-[(naphthalen-1-ylmethyl)amino]-1-oxopropan-2-yl}-4-oxo-2-[(3-phenylpropanoyl)amino]-4-(1H-pyrrol-1-yl)butanamide (non-preferred name) (CCD ID: 7J1) (formula: C₃₂H₃₄N₄O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			41	32	4	5		
3	I	1	Total	C	N	O	0	0
			41	32	4	5		
3	J	1	Total	C	N	O	0	0
			41	32	4	5		
3	K	1	Total	C	N	O	0	0
			41	32	4	5		
3	L	1	Total	C	N	O	0	0
			41	32	4	5		
3	M	1	Total	C	N	O	0	0
			41	32	4	5		
3	N	1	Total	C	N	O	0	0
			41	32	4	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	V	1	Total	C	N	O	0	0
			41	32	4	5		
3	W	1	Total	C	N	O	0	0
			41	32	4	5		
3	X	1	Total	C	N	O	0	0
			41	32	4	5		
3	Y	1	Total	C	N	O	0	0
			41	32	4	5		
3	Z	1	Total	C	N	O	0	0
			41	32	4	5		
3	a	1	Total	C	N	O	0	0
			41	32	4	5		
3	b	1	Total	C	N	O	0	0
			41	32	4	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	O	0	0
			12	12		
4	B	7	Total	O	0	0
			7	7		
4	C	9	Total	O	0	0
			9	9		
4	D	5	Total	O	0	0
			5	5		
4	E	7	Total	O	0	0
			7	7		
4	F	8	Total	O	0	0
			8	8		
4	G	4	Total	O	0	0
			4	4		
4	H	14	Total	O	0	0
			14	14		
4	I	25	Total	O	0	0
			25	25		
4	J	13	Total	O	0	0
			13	13		
4	K	19	Total	O	0	0
			19	19		
4	L	14	Total	O	0	0
			14	14		

Continued on next page...

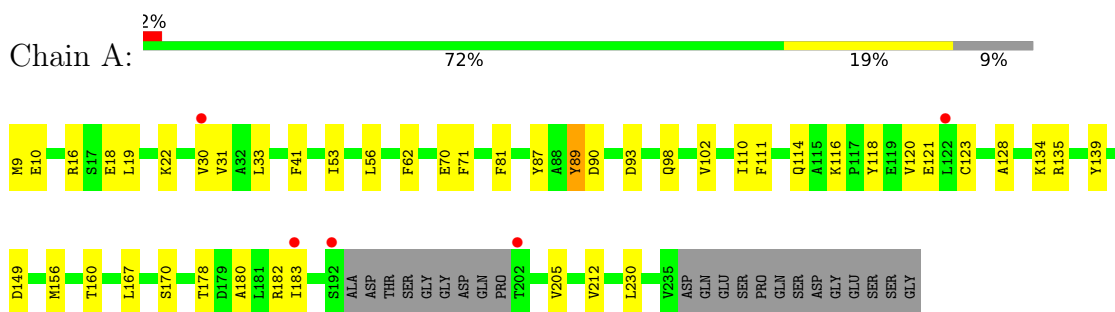
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	M	20	Total 20	O 20	0	0
4	N	11	Total 11	O 11	0	0
4	O	10	Total 10	O 10	0	0
4	P	4	Total 4	O 4	0	0
4	Q	5	Total 5	O 5	0	0
4	R	9	Total 9	O 9	0	0
4	S	15	Total 15	O 15	0	0
4	T	6	Total 6	O 6	0	0
4	U	10	Total 10	O 10	0	0
4	V	19	Total 19	O 19	0	0
4	W	12	Total 12	O 12	0	0
4	X	13	Total 13	O 13	0	0
4	Y	26	Total 26	O 26	0	0
4	Z	19	Total 19	O 19	0	0
4	a	16	Total 16	O 16	0	0
4	b	16	Total 16	O 16	0	0

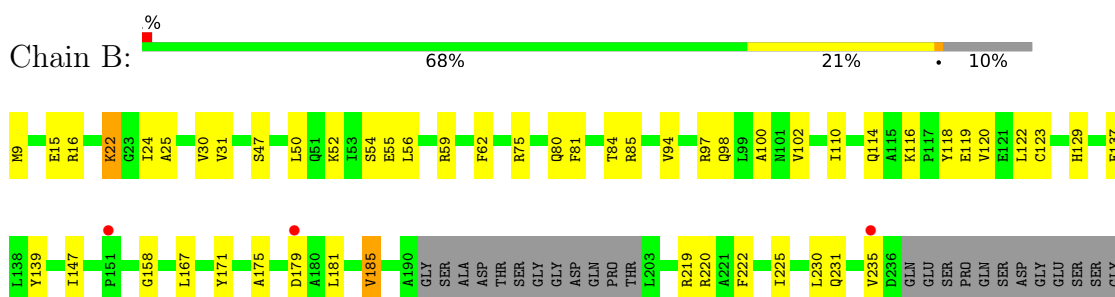
3 Residue-property plots

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.

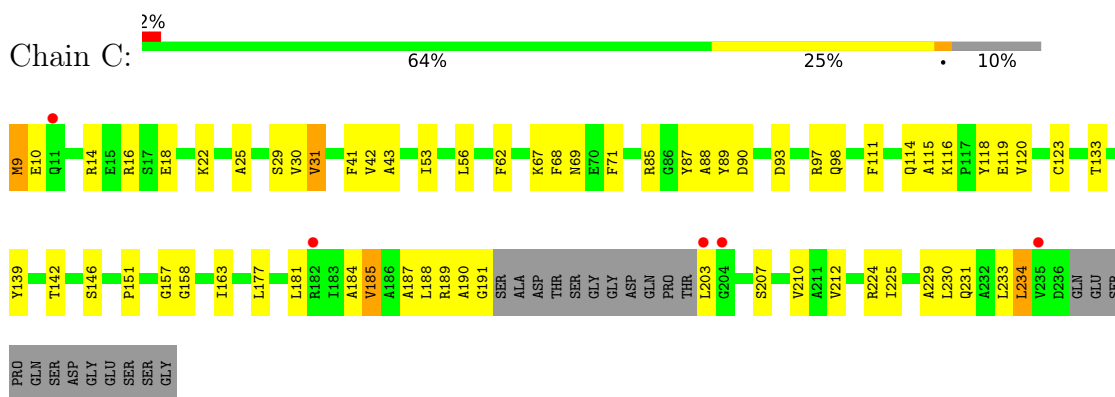
- Molecule 1: Proteasome subunit alpha



- Molecule 1: Proteasome subunit alpha

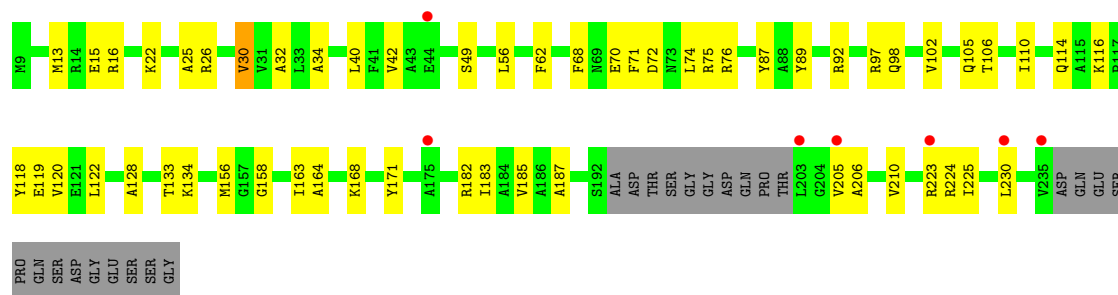


- Molecule 1: Proteasome subunit alpha

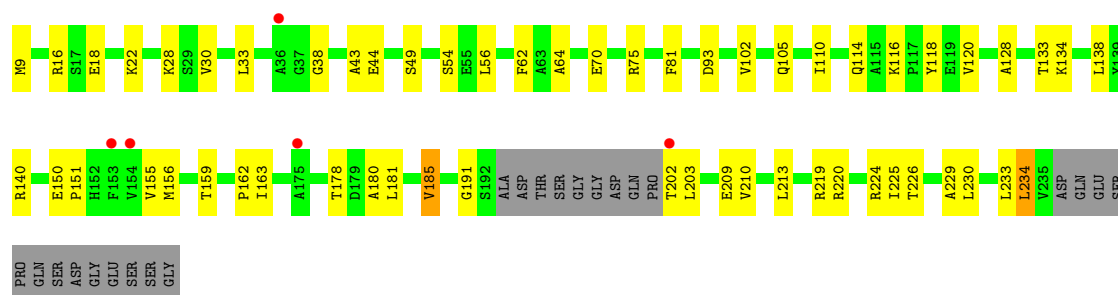


- Molecule 1: Proteasome subunit alpha

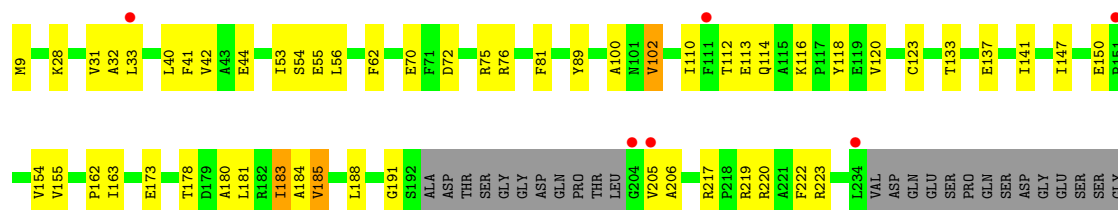




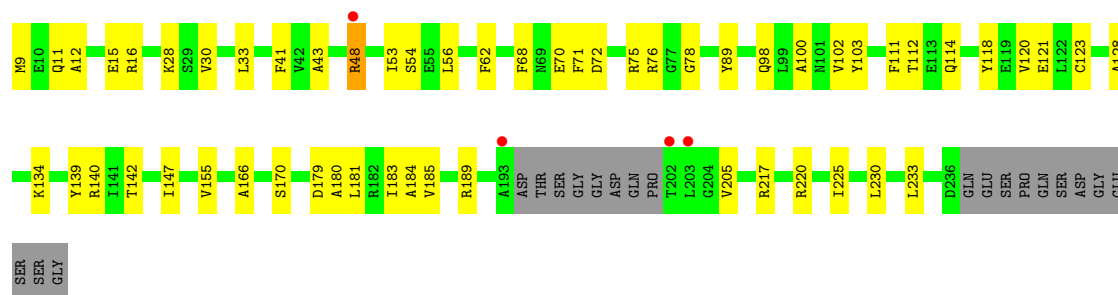
- Molecule 1: Proteasome subunit alpha



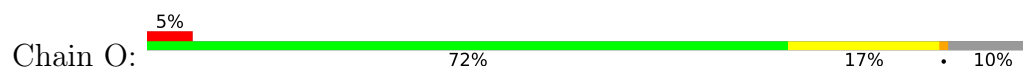
- Molecule 1: Proteasome subunit alpha

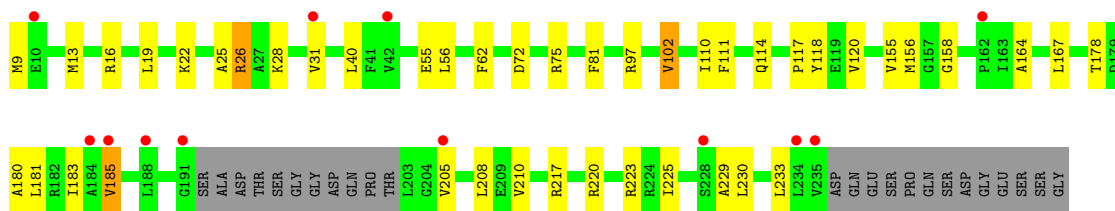


- Molecule 1: Proteasome subunit alpha

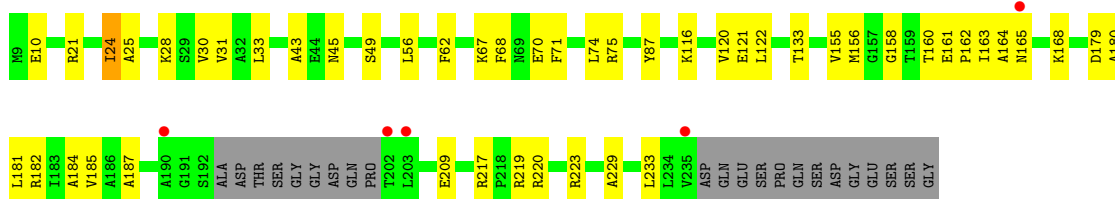


- Molecule 1: Proteasome subunit alpha

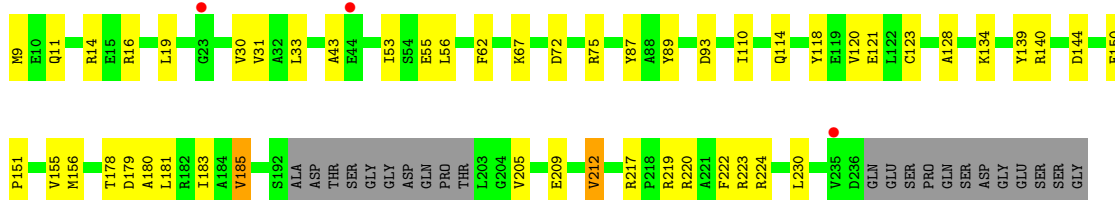




• Molecule 1: Proteasome subunit alpha



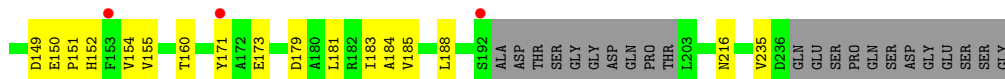
• Molecule 1: Proteasome subunit alpha



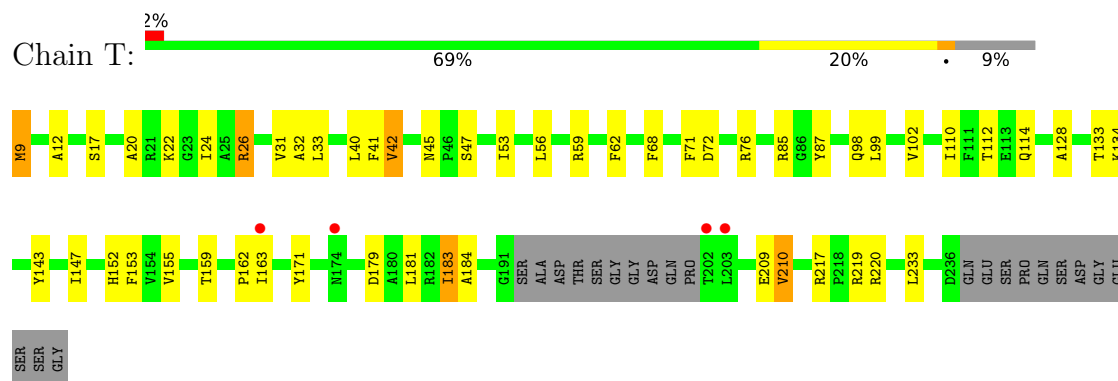
• Molecule 1: Proteasome subunit alpha



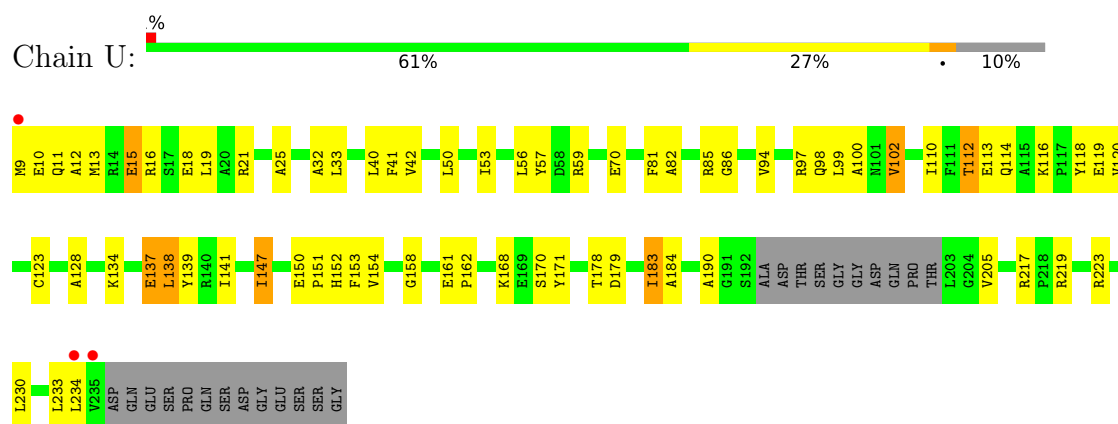
• Molecule 1: Proteasome subunit alpha



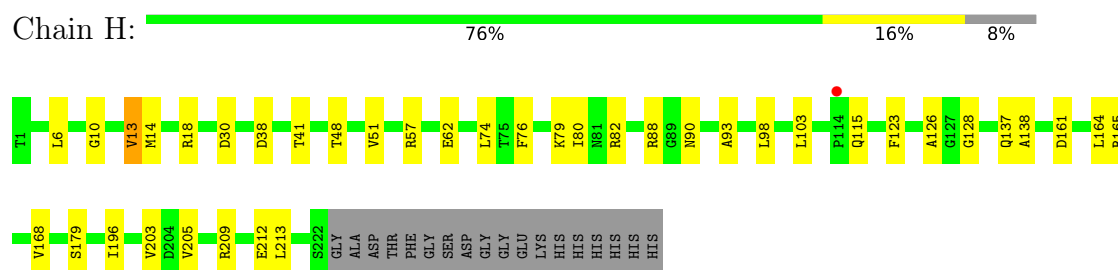
- Molecule 1: Proteasome subunit alpha



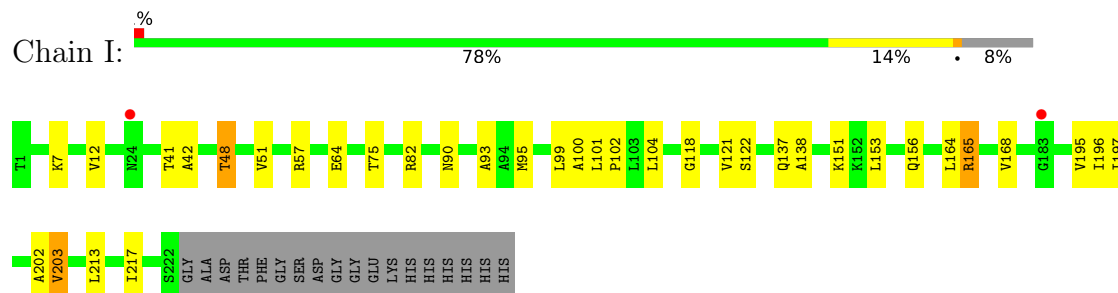
- Molecule 1: Proteasome subunit alpha



- Molecule 2: Proteasome subunit beta



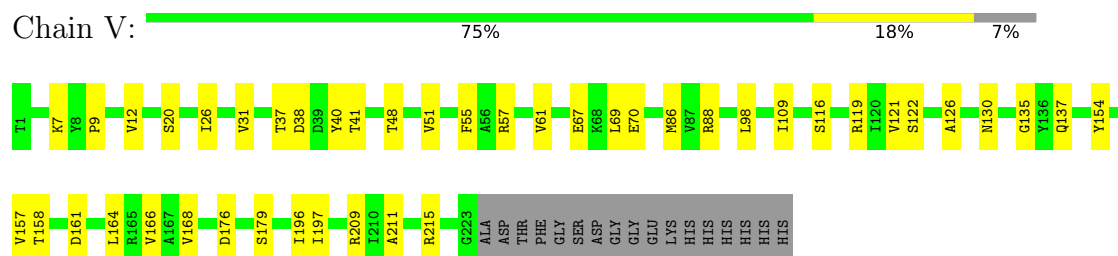
- Molecule 2: Proteasome subunit beta



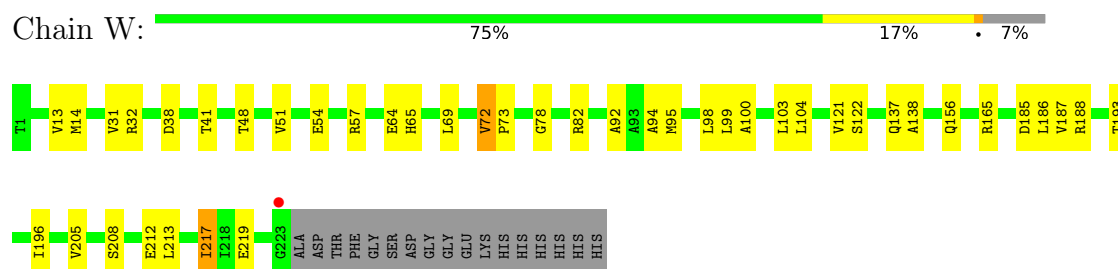
- Molecule 2: Proteasome subunit beta



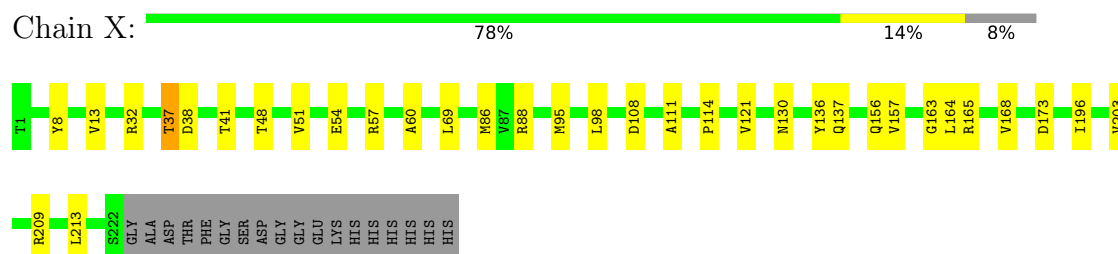
- Molecule 2: Proteasome subunit beta



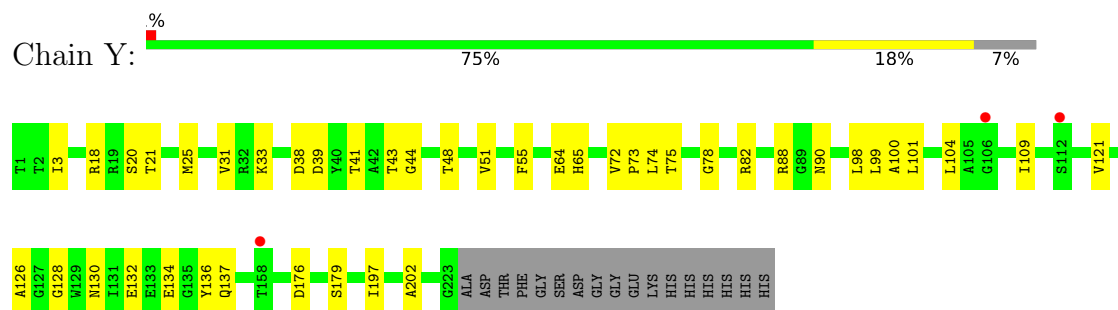
- Molecule 2: Proteasome subunit beta



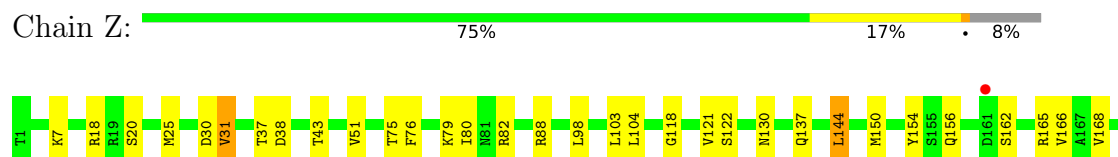
- Molecule 2: Proteasome subunit beta



- Molecule 2: Proteasome subunit beta

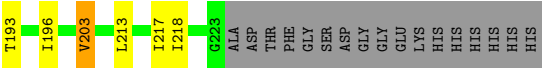


- Molecule 2: Proteasome subunit beta

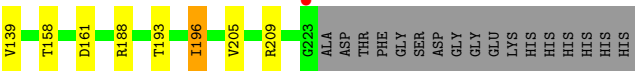
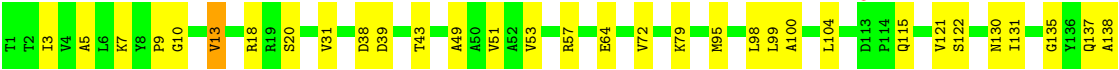
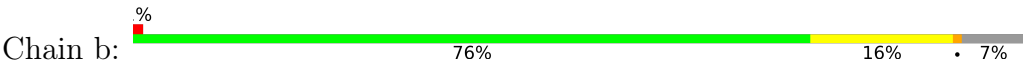




• Molecule 2: Proteasome subunit beta



• 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, α , β , γ	120.55Å 198.54Å 165.72Å 90.00° 103.24° 90.00°	Depositor
Resolution (Å)	49.61 – 2.85 49.61 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.9 (49.61-2.85) 94.2 (49.61-2.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.177 , 0.235 0.179 , 0.235	Depositor DCC
R_{free} test set	8304 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	48.8	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	47311	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: 7J1

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	0.50	1/1701 (0.1%)	0.72	0/2297
1	B	0.46	0/1692	0.71	0/2285
1	C	0.42	0/1696	0.68	0/2290
1	D	0.46	0/1694	0.71	0/2287
1	E	0.44	0/1701	0.72	0/2297
1	F	0.45	0/1679	0.72	0/2266
1	G	0.43	0/1714	0.71	0/2315
1	O	0.45	0/1688	0.71	0/2279
1	P	0.45	0/1701	0.73	0/2297
1	Q	0.46	0/1702	0.71	0/2298
1	R	0.46	0/1694	0.73	0/2287
1	S	0.47	0/1702	0.72	0/2298
1	T	0.49	0/1703	0.77	4/2300 (0.2%)
1	U	0.52	0/1694	0.81	3/2287 (0.1%)
2	H	0.45	0/1662	0.69	0/2254
2	I	0.49	0/1662	0.71	0/2254
2	J	0.45	0/1662	0.70	0/2254
2	K	0.46	0/1666	0.74	0/2259
2	L	0.46	0/1666	0.68	0/2259
2	M	0.43	0/1662	0.67	0/2254
2	N	0.45	0/1666	0.73	0/2259
2	V	0.44	0/1666	0.69	0/2259
2	W	0.48	0/1666	0.69	0/2259
2	X	0.49	0/1662	0.72	0/2254
2	Y	0.48	0/1666	0.73	0/2259
2	Z	0.48	0/1662	0.72	0/2254
2	a	0.44	0/1666	0.67	0/2259
2	b	0.49	0/1666	0.72	0/2259
All	All	0.46	1/47061 (0.0%)	0.72	7/63679 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	Y	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	TYR	CA-C	-6.43	1.49	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	15	GLU	CA-CB-CG	-10.73	92.64	114.10
1	T	9	MET	CB-CG-SD	6.60	132.49	112.70
1	T	9	MET	N-CA-C	6.43	129.00	111.00
1	T	9	MET	CA-C-N	-5.70	112.07	120.28
1	T	9	MET	C-N-CA	-5.70	112.07	120.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Y	128	GLY	Peptide

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	1677	0	1680	32	0
1	B	1668	0	1669	33	0
1	C	1672	0	1672	42	0
1	D	1670	0	1673	39	0
1	E	1677	0	1680	32	0
1	F	1655	0	1653	37	0
1	G	1690	0	1689	37	0
1	O	1664	0	1668	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1677	0	1680	28	0
1	Q	1678	0	1677	35	0
1	R	1670	0	1673	38	0
1	S	1678	0	1677	29	0
1	T	1679	0	1679	33	0
1	U	1670	0	1673	53	0
2	H	1638	0	1633	23	0
2	I	1638	0	1633	23	0
2	J	1638	0	1633	24	0
2	K	1642	0	1636	34	0
2	L	1642	0	1636	23	0
2	M	1638	0	1633	27	0
2	N	1642	0	1636	27	0
2	V	1642	0	1636	26	0
2	W	1642	0	1636	27	0
2	X	1638	0	1633	24	0
2	Y	1642	0	1636	32	0
2	Z	1638	0	1633	30	0
2	a	1642	0	1636	21	0
2	b	1642	0	1636	23	0
3	H	41	0	0	0	0
3	I	41	0	0	0	0
3	J	41	0	0	0	0
3	K	41	0	0	0	0
3	L	41	0	0	0	0
3	M	41	0	0	0	0
3	N	41	0	0	0	0
3	V	41	0	0	0	0
3	W	41	0	0	0	0
3	X	41	0	0	1	0
3	Y	41	0	0	1	0
3	Z	41	0	0	0	0
3	a	41	0	0	0	0
3	b	41	0	0	0	0
4	A	12	0	0	1	0
4	B	7	0	0	0	0
4	C	9	0	0	0	0
4	D	5	0	0	0	0
4	E	7	0	0	1	0
4	F	8	0	0	0	0
4	G	4	0	0	0	0
4	H	14	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	25	0	0	0	0
4	J	13	0	0	2	0
4	K	19	0	0	2	0
4	L	14	0	0	0	0
4	M	20	0	0	0	0
4	N	11	0	0	1	0
4	O	10	0	0	0	0
4	P	4	0	0	0	0
4	Q	5	0	0	0	0
4	R	9	0	0	1	0
4	S	15	0	0	1	0
4	T	6	0	0	0	0
4	U	10	0	0	2	0
4	V	19	0	0	0	0
4	W	12	0	0	0	0
4	X	13	0	0	1	0
4	Y	26	0	0	1	0
4	Z	19	0	0	1	0
4	a	16	0	0	0	0
4	b	16	0	0	1	0
All	All	47311	0	46329	783	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 783 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:P:24:ILE:HD11	1:P:121:GLU:HB2	1.50	0.94
1:R:112:THR:HG22	1:R:113:GLU:HG3	1.55	0.89
1:T:9:MET:HA	1:T:12:ALA:HB3	1.52	0.88
1:D:16:ARG:NH2	1:D:114:GLN:O	2.06	0.88
1:G:16:ARG:NH1	1:G:111:PHE:O	2.08	0.86

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	214/240 (89%)	208 (97%)	6 (3%)	0	100	100
1	B	212/240 (88%)	208 (98%)	4 (2%)	0	100	100
1	C	213/240 (89%)	205 (96%)	5 (2%)	3 (1%)	9	18
1	D	213/240 (89%)	204 (96%)	9 (4%)	0	100	100
1	E	214/240 (89%)	207 (97%)	7 (3%)	0	100	100
1	F	211/240 (88%)	204 (97%)	7 (3%)	0	100	100
1	G	216/240 (90%)	211 (98%)	5 (2%)	0	100	100
1	O	212/240 (88%)	204 (96%)	8 (4%)	0	100	100
1	P	214/240 (89%)	208 (97%)	6 (3%)	0	100	100
1	Q	214/240 (89%)	207 (97%)	7 (3%)	0	100	100
1	R	213/240 (89%)	209 (98%)	4 (2%)	0	100	100
1	S	214/240 (89%)	205 (96%)	9 (4%)	0	100	100
1	T	214/240 (89%)	207 (97%)	7 (3%)	0	100	100
1	U	213/240 (89%)	205 (96%)	8 (4%)	0	100	100
2	H	220/240 (92%)	216 (98%)	4 (2%)	0	100	100
2	I	220/240 (92%)	216 (98%)	4 (2%)	0	100	100
2	J	220/240 (92%)	215 (98%)	5 (2%)	0	100	100
2	K	221/240 (92%)	217 (98%)	3 (1%)	1 (0%)	24	43
2	L	221/240 (92%)	218 (99%)	3 (1%)	0	100	100
2	M	220/240 (92%)	215 (98%)	5 (2%)	0	100	100
2	N	221/240 (92%)	215 (97%)	6 (3%)	0	100	100
2	V	221/240 (92%)	218 (99%)	3 (1%)	0	100	100
2	W	221/240 (92%)	217 (98%)	4 (2%)	0	100	100
2	X	220/240 (92%)	213 (97%)	6 (3%)	1 (0%)	24	43
2	Y	221/240 (92%)	217 (98%)	4 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Z	220/240 (92%)	218 (99%)	2 (1%)	0	100	100
2	a	221/240 (92%)	216 (98%)	5 (2%)	0	100	100
2	b	221/240 (92%)	218 (99%)	3 (1%)	0	100	100
All	All	6075/6720 (90%)	5921 (98%)	149 (2%)	5 (0%)	48	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	190	ALA
1	C	234	LEU
1	C	151	PRO
2	X	114	PRO
2	K	114	PRO

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	167/184 (91%)	162 (97%)	5 (3%)	36	60
1	B	166/184 (90%)	162 (98%)	4 (2%)	43	67
1	C	166/184 (90%)	161 (97%)	5 (3%)	36	60
1	D	166/184 (90%)	163 (98%)	3 (2%)	51	74
1	E	167/184 (91%)	159 (95%)	8 (5%)	23	46
1	F	164/184 (89%)	158 (96%)	6 (4%)	30	55
1	G	168/184 (91%)	165 (98%)	3 (2%)	51	74
1	O	165/184 (90%)	161 (98%)	4 (2%)	43	67
1	P	167/184 (91%)	161 (96%)	6 (4%)	31	56
1	Q	167/184 (91%)	162 (97%)	5 (3%)	36	60
1	R	166/184 (90%)	162 (98%)	4 (2%)	43	67
1	S	167/184 (91%)	163 (98%)	4 (2%)	43	67

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T	167/184 (91%)	162 (97%)	5 (3%)	36	60
1	U	166/184 (90%)	160 (96%)	6 (4%)	31	56
2	H	165/178 (93%)	160 (97%)	5 (3%)	36	60
2	I	165/178 (93%)	160 (97%)	5 (3%)	36	60
2	J	165/178 (93%)	162 (98%)	3 (2%)	51	74
2	K	165/178 (93%)	160 (97%)	5 (3%)	36	60
2	L	165/178 (93%)	165 (100%)	0	100	100
2	M	165/178 (93%)	163 (99%)	2 (1%)	63	80
2	N	165/178 (93%)	157 (95%)	8 (5%)	23	46
2	V	165/178 (93%)	163 (99%)	2 (1%)	63	80
2	W	165/178 (93%)	160 (97%)	5 (3%)	36	60
2	X	165/178 (93%)	163 (99%)	2 (1%)	63	80
2	Y	165/178 (93%)	164 (99%)	1 (1%)	78	89
2	Z	165/178 (93%)	158 (96%)	7 (4%)	26	51
2	a	165/178 (93%)	159 (96%)	6 (4%)	31	56
2	b	165/178 (93%)	162 (98%)	3 (2%)	51	74
All	All	4639/5068 (92%)	4517 (97%)	122 (3%)	40	65

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	N	166	VAL
2	Z	208	SER
1	P	160	THR
2	Z	196	ILE
2	a	203	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
2	X	65	HIS
2	Z	130	ASN
2	a	130	ASN
2	I	81	ASN
2	I	65	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	7J1	M	301	-	44,44,44	2.05	9 (20%)	54,58,58	1.86	12 (22%)
3	7J1	V	301	-	44,44,44	2.41	8 (18%)	54,58,58	1.31	8 (14%)
3	7J1	Y	301	-	44,44,44	2.05	9 (20%)	54,58,58	1.51	10 (18%)
3	7J1	H	301	-	44,44,44	2.43	8 (18%)	54,58,58	1.37	9 (16%)
3	7J1	W	301	-	44,44,44	2.20	11 (25%)	54,58,58	1.41	7 (12%)
3	7J1	N	301	-	44,44,44	2.22	8 (18%)	54,58,58	1.39	8 (14%)
3	7J1	J	301	-	44,44,44	2.16	9 (20%)	54,58,58	1.66	10 (18%)
3	7J1	X	301	-	44,44,44	2.15	9 (20%)	54,58,58	1.31	8 (14%)
3	7J1	b	301	-	44,44,44	2.41	10 (22%)	54,58,58	1.45	9 (16%)
3	7J1	K	301	-	44,44,44	2.56	9 (20%)	54,58,58	1.36	7 (12%)
3	7J1	L	301	-	44,44,44	2.39	9 (20%)	54,58,58	1.24	7 (12%)
3	7J1	Z	301	-	44,44,44	2.32	7 (15%)	54,58,58	1.26	6 (11%)
3	7J1	a	301	-	44,44,44	2.34	9 (20%)	54,58,58	1.22	5 (9%)
3	7J1	I	301	-	44,44,44	2.45	10 (22%)	54,58,58	1.24	4 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	7J1	M	301	-	-	2/37/37/37	0/4/4/4
3	7J1	V	301	-	-	2/37/37/37	0/4/4/4
3	7J1	Y	301	-	-	2/37/37/37	0/4/4/4
3	7J1	H	301	-	-	5/37/37/37	0/4/4/4
3	7J1	W	301	-	-	5/37/37/37	0/4/4/4
3	7J1	N	301	-	-	4/37/37/37	0/4/4/4
3	7J1	J	301	-	-	3/37/37/37	0/4/4/4
3	7J1	X	301	-	-	3/37/37/37	0/4/4/4
3	7J1	b	301	-	-	2/37/37/37	0/4/4/4
3	7J1	K	301	-	-	5/37/37/37	0/4/4/4
3	7J1	L	301	-	-	2/37/37/37	0/4/4/4
3	7J1	Z	301	-	-	4/37/37/37	0/4/4/4
3	7J1	a	301	-	-	3/37/37/37	0/4/4/4
3	7J1	I	301	-	-	3/37/37/37	0/4/4/4

The worst 5 of 125 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	301	7J1	C26-C27	9.52	1.57	1.37
3	K	301	7J1	C29-C28	9.31	1.57	1.37
3	K	301	7J1	C26-C27	9.09	1.56	1.37
3	Z	301	7J1	C29-C28	8.70	1.55	1.37
3	L	301	7J1	C29-C28	8.54	1.55	1.37

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	301	7J1	C26-C27-C28	-5.92	102.47	107.74
3	J	301	7J1	C26-C27-C28	-5.92	102.47	107.74
3	Y	301	7J1	C26-C27-C28	-5.30	103.02	107.74
3	M	301	7J1	C29-C28-C27	-4.94	103.34	107.74
3	b	301	7J1	C26-C27-C28	-4.92	103.36	107.74

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	301	7J1	N03-C04-C19-O20
3	H	301	7J1	C05-C04-C19-O20
3	I	301	7J1	N03-C04-C19-O20
3	I	301	7J1	C05-C04-C19-O20
3	J	301	7J1	C05-C04-C19-O20

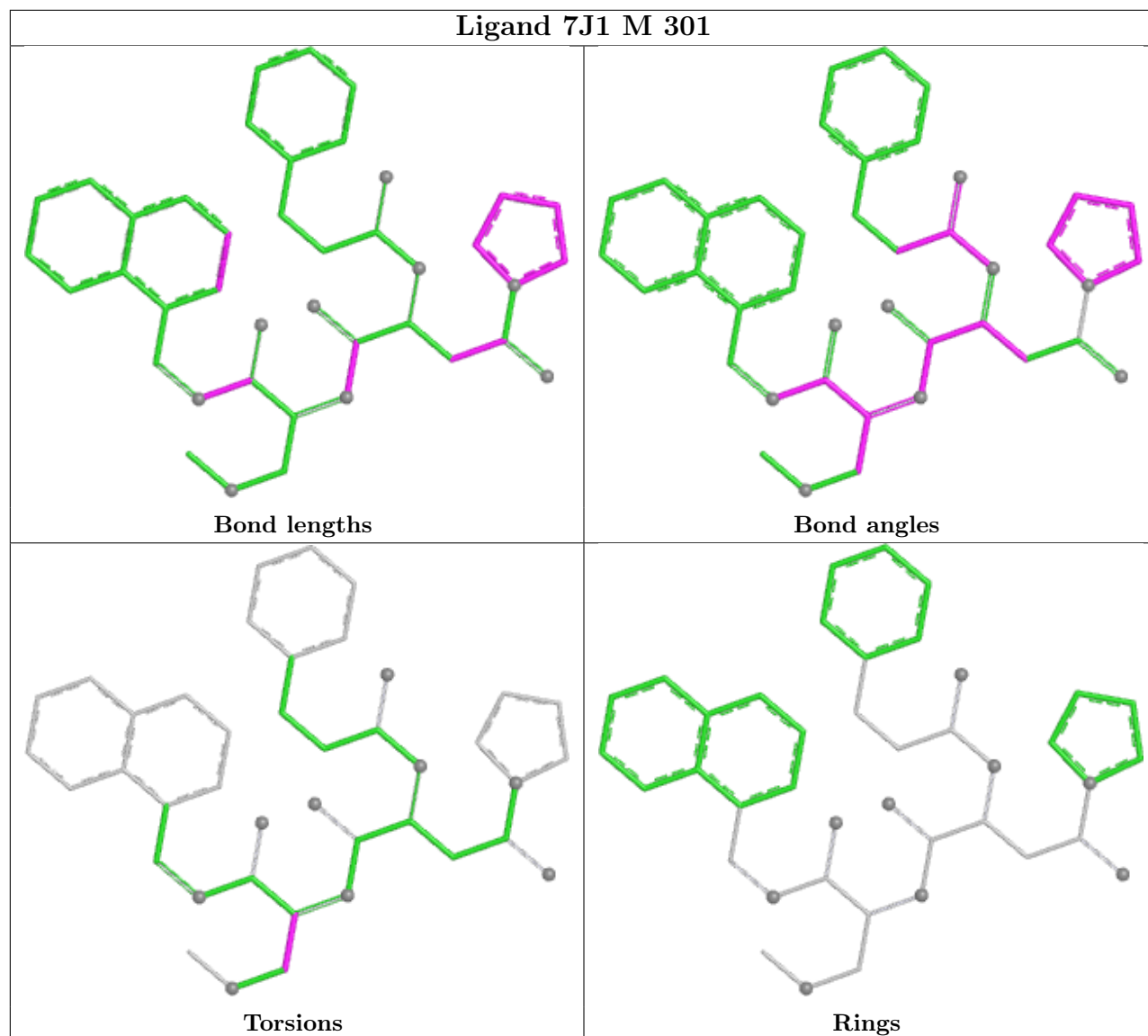
There are no ring outliers.

2 monomers are involved in 2 short contacts:

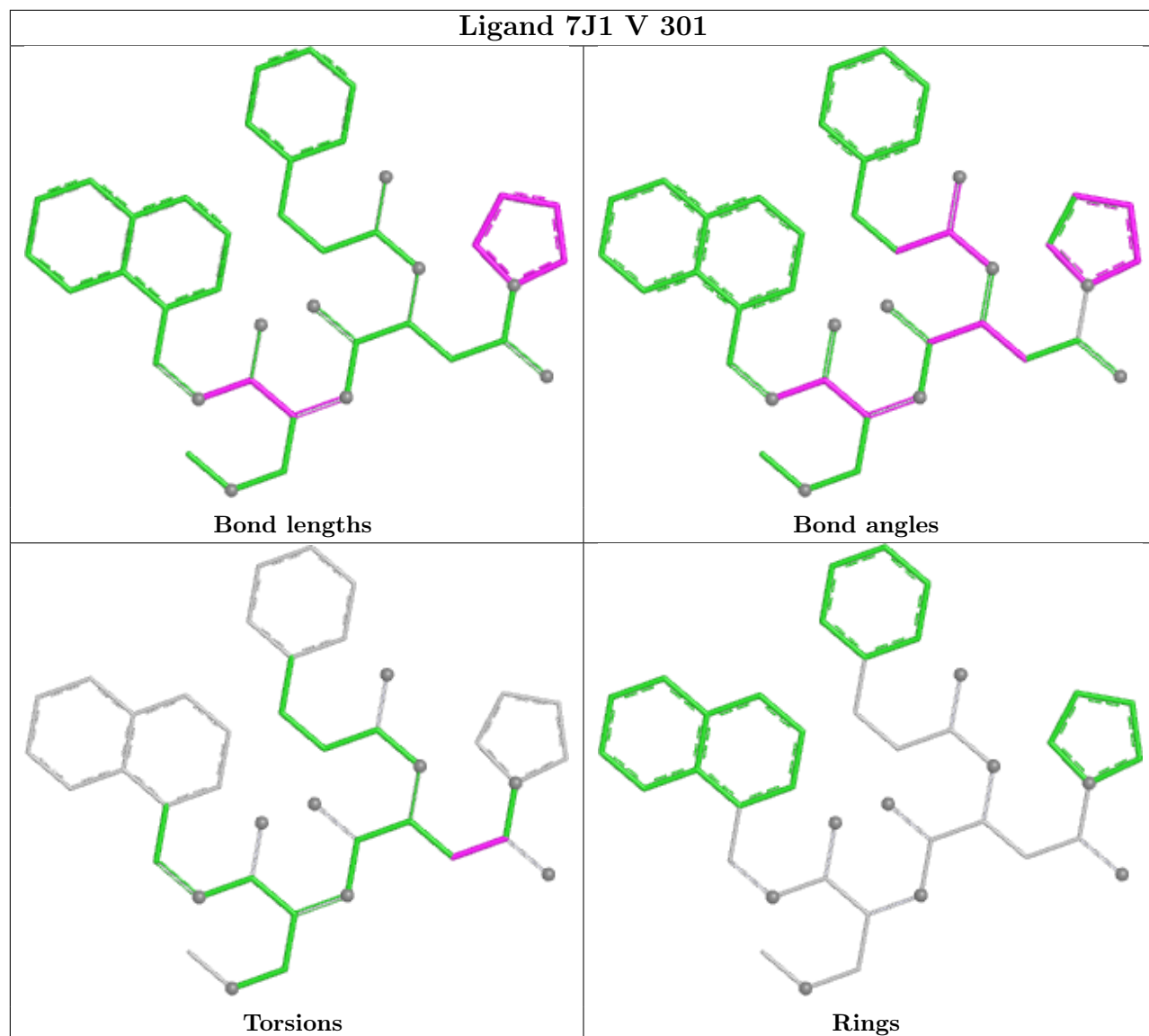
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Y	301	7J1	1	0
3	X	301	7J1	1	0

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

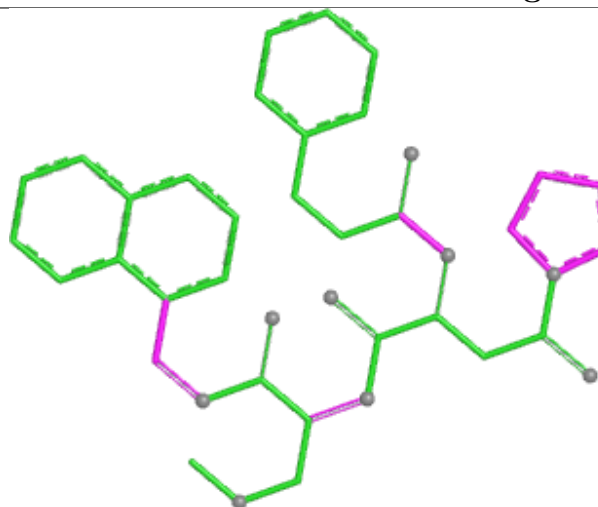
Ligand 7J1 M 301



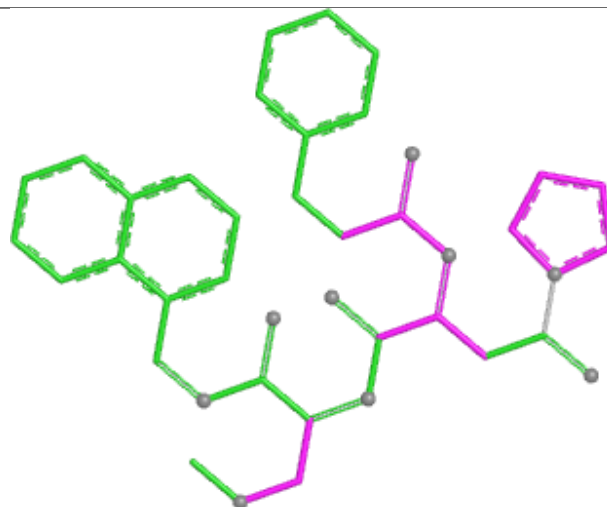
Ligand 7J1 V 301



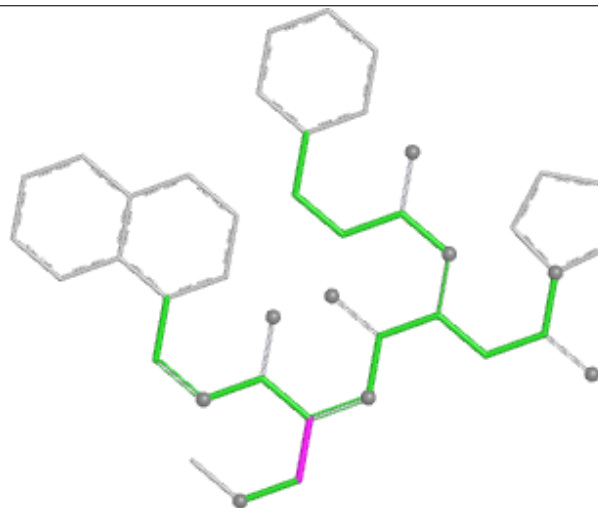
Ligand 7J1 Y 301



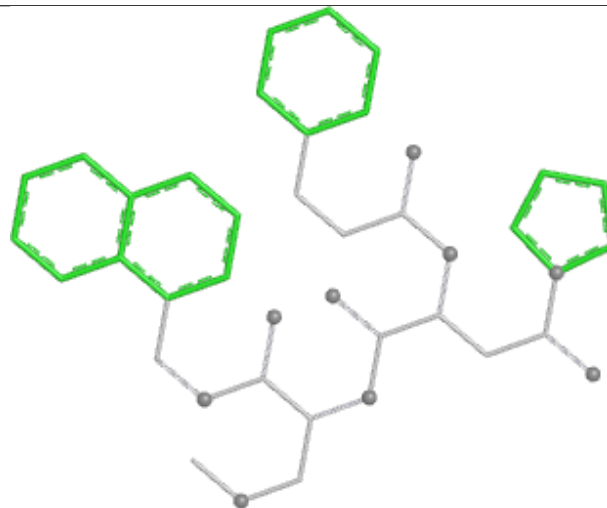
Bond lengths



Bond angles

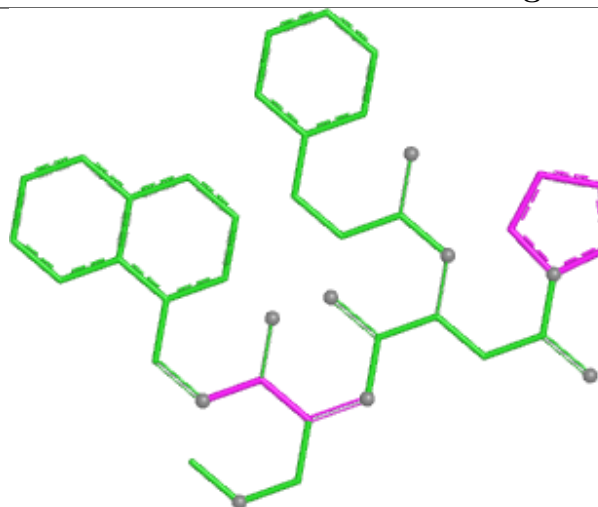


Torsions

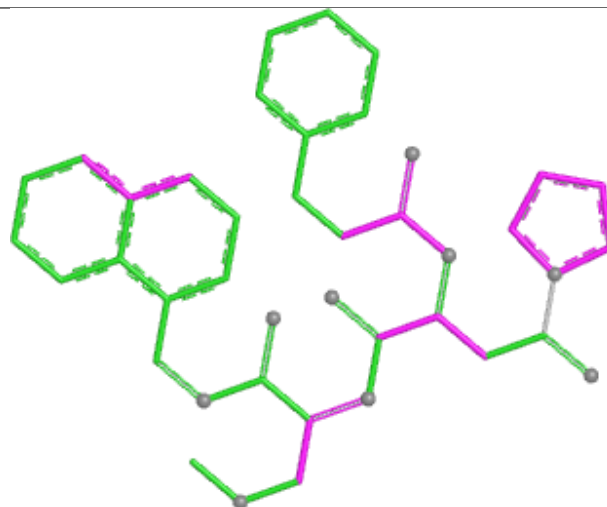


Rings

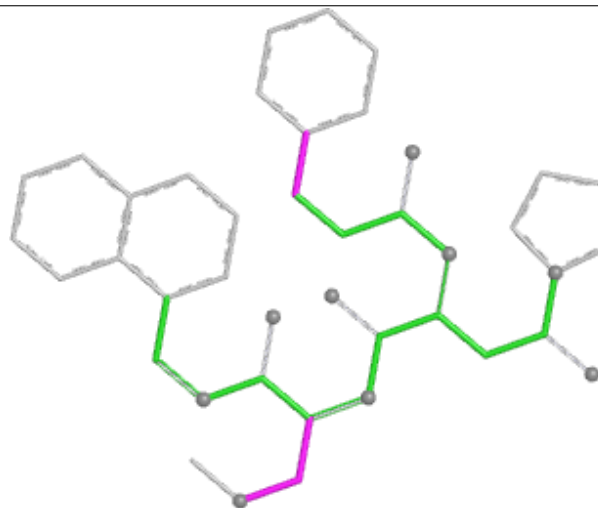
Ligand 7J1 H 301



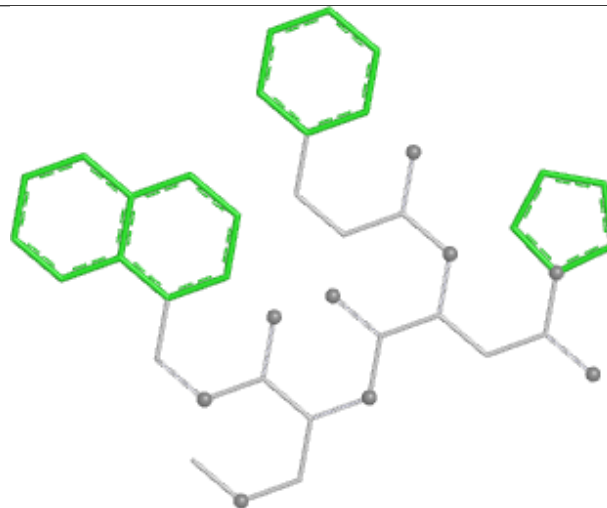
Bond lengths



Bond angles

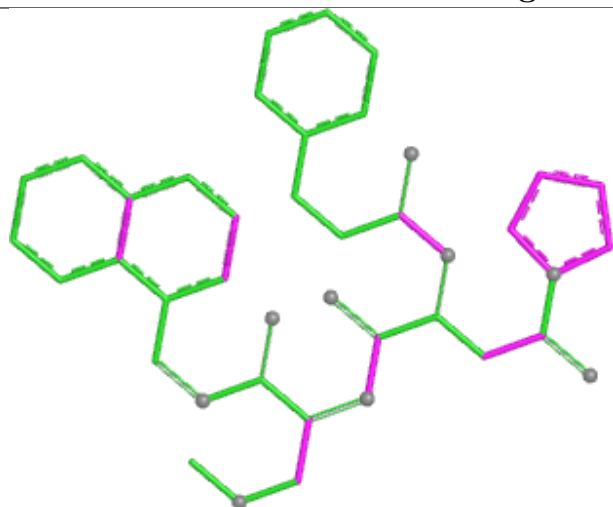


Torsions

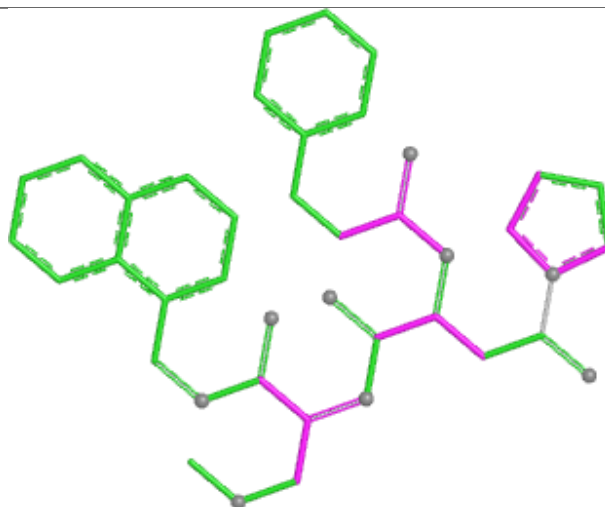


Rings

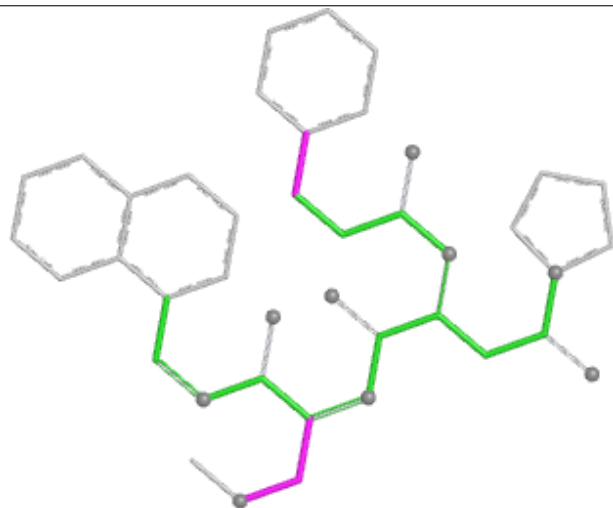
Ligand 7J1 W 301



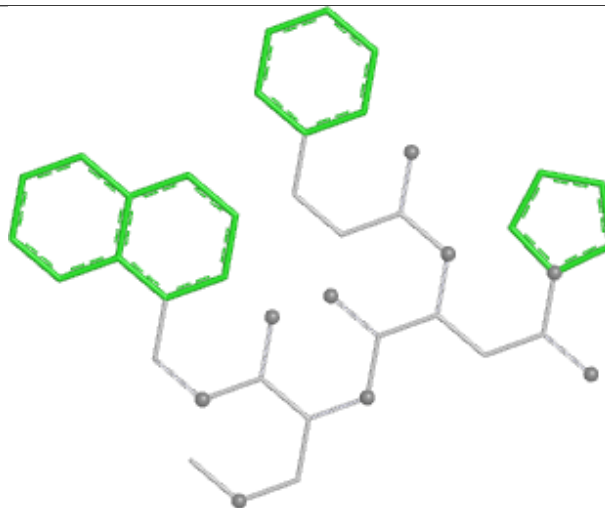
Bond lengths



Bond angles

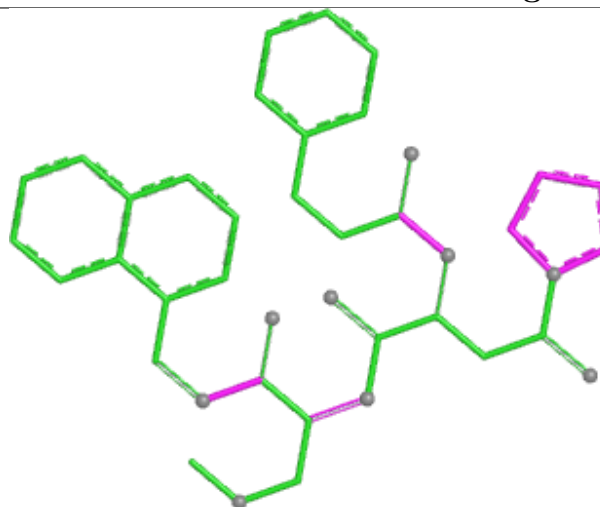


Torsions

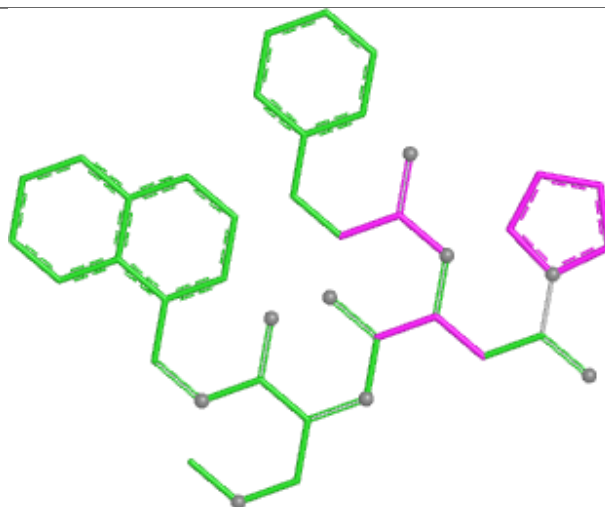


Rings

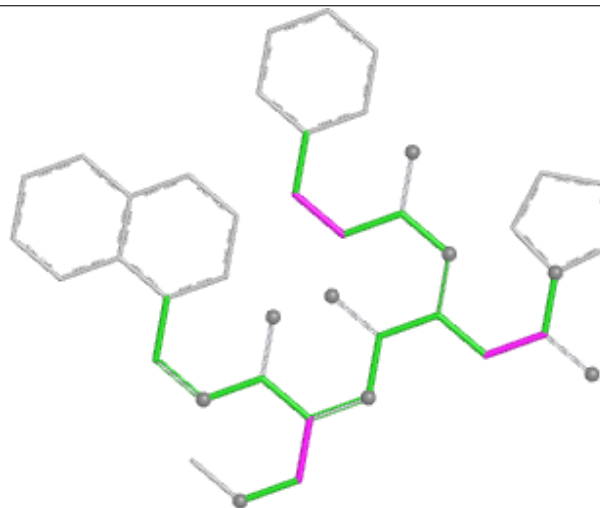
Ligand 7J1 N 301



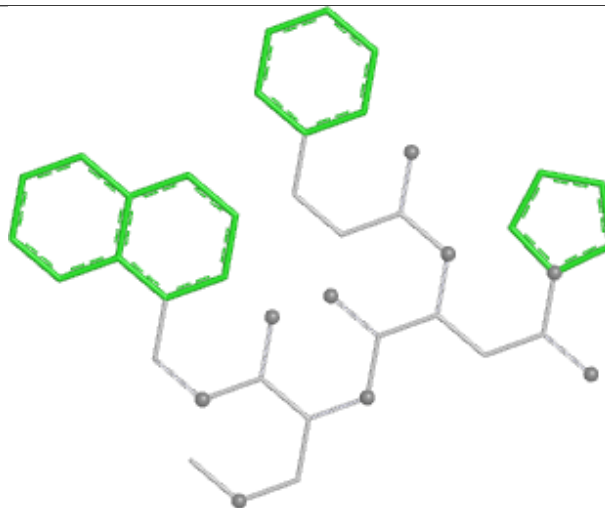
Bond lengths



Bond angles

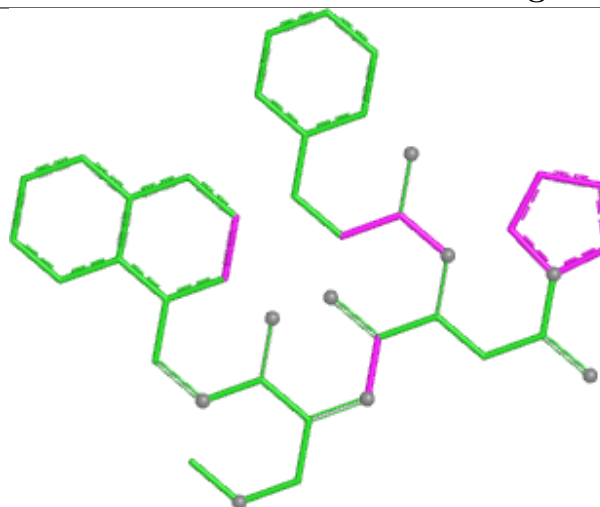


Torsions

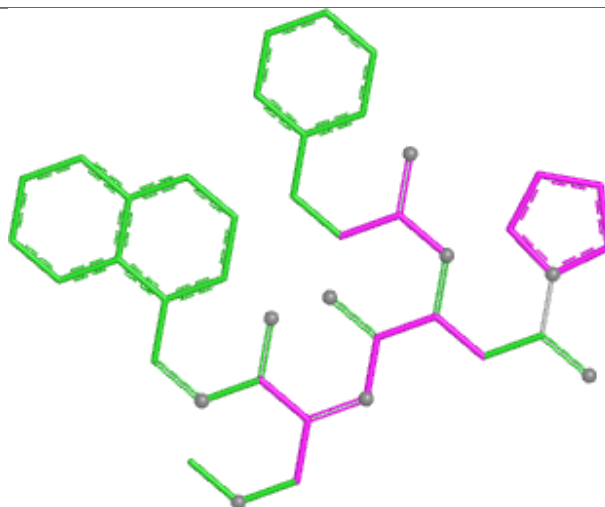


Rings

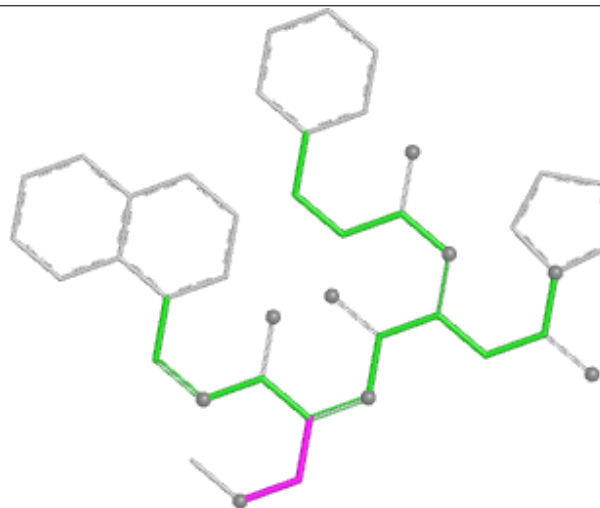
Ligand 7J1 J 301



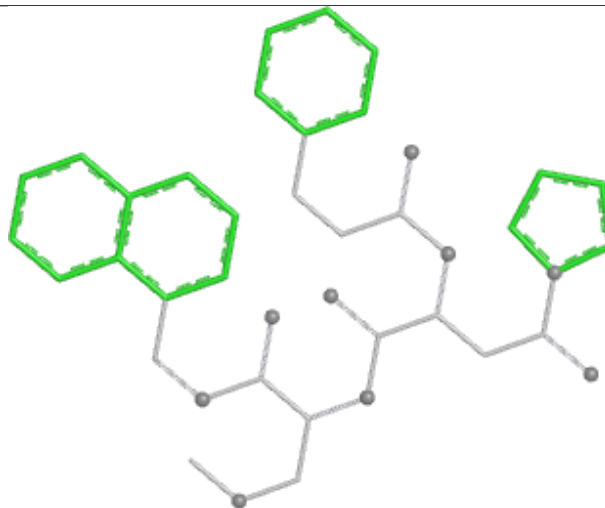
Bond lengths



Bond angles

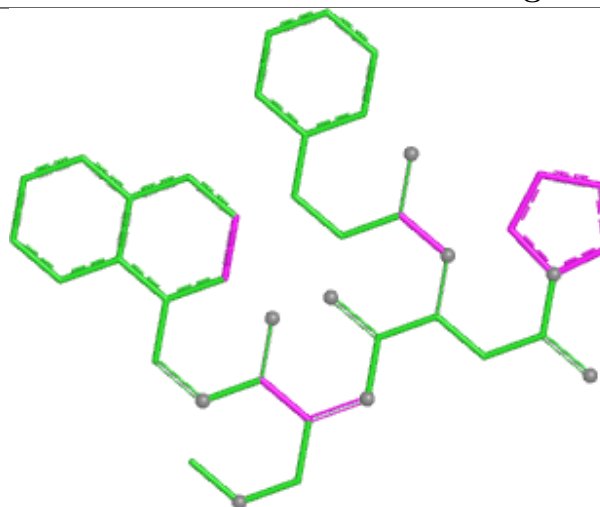


Torsions

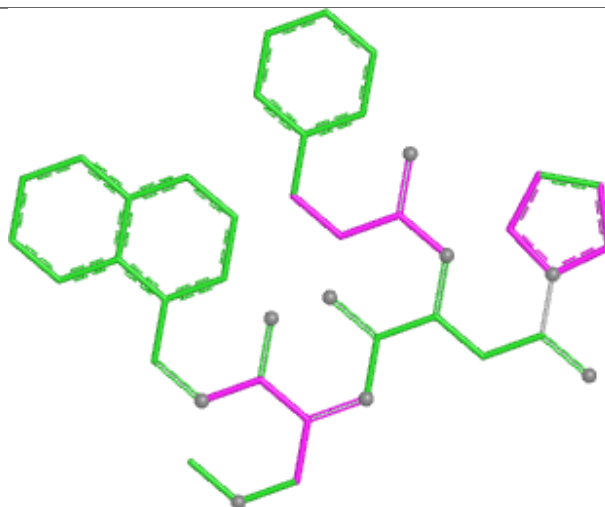


Rings

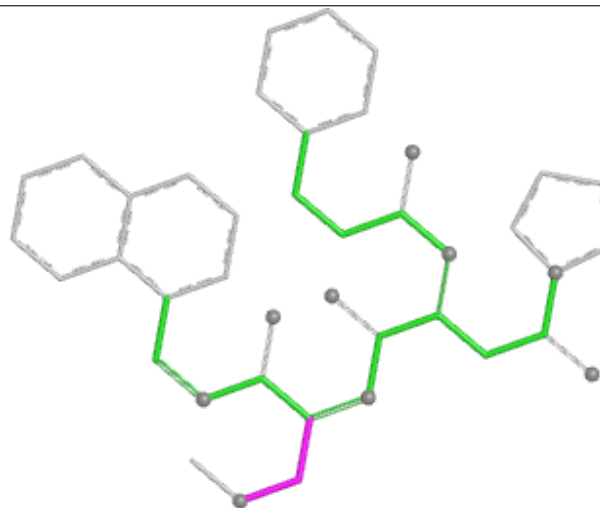
Ligand 7J1 X 301



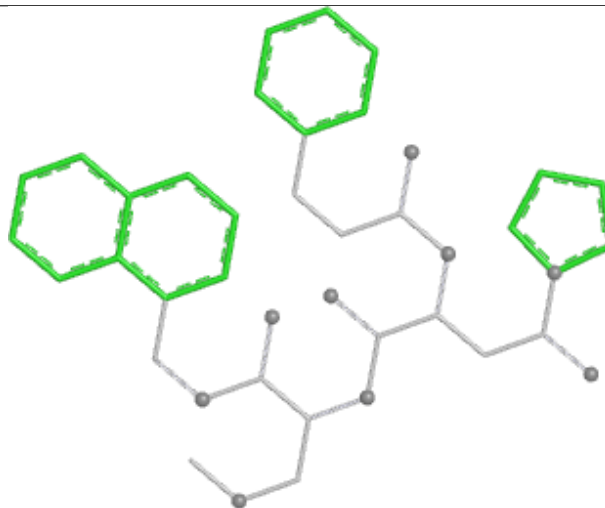
Bond lengths



Bond angles

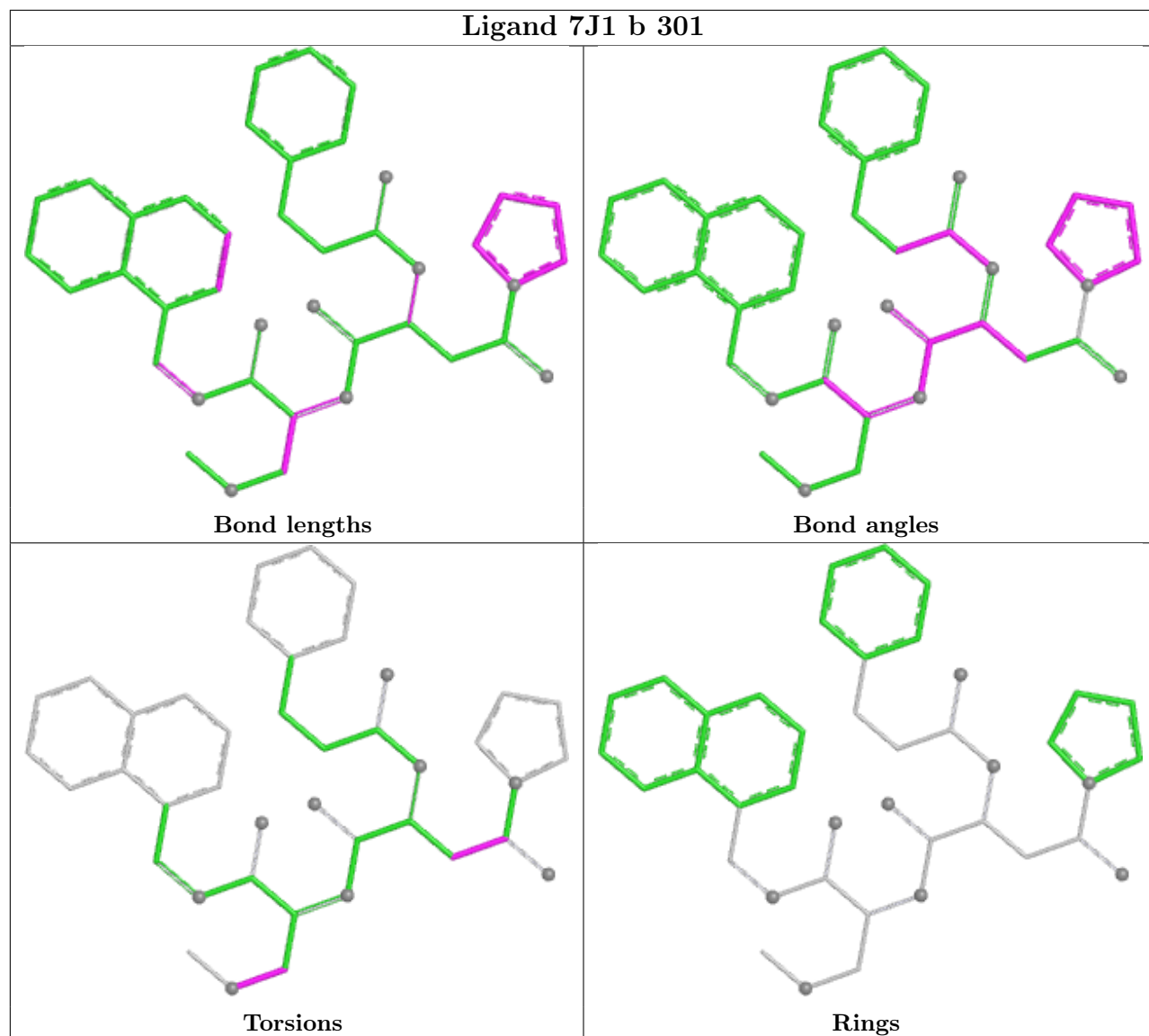


Torsions

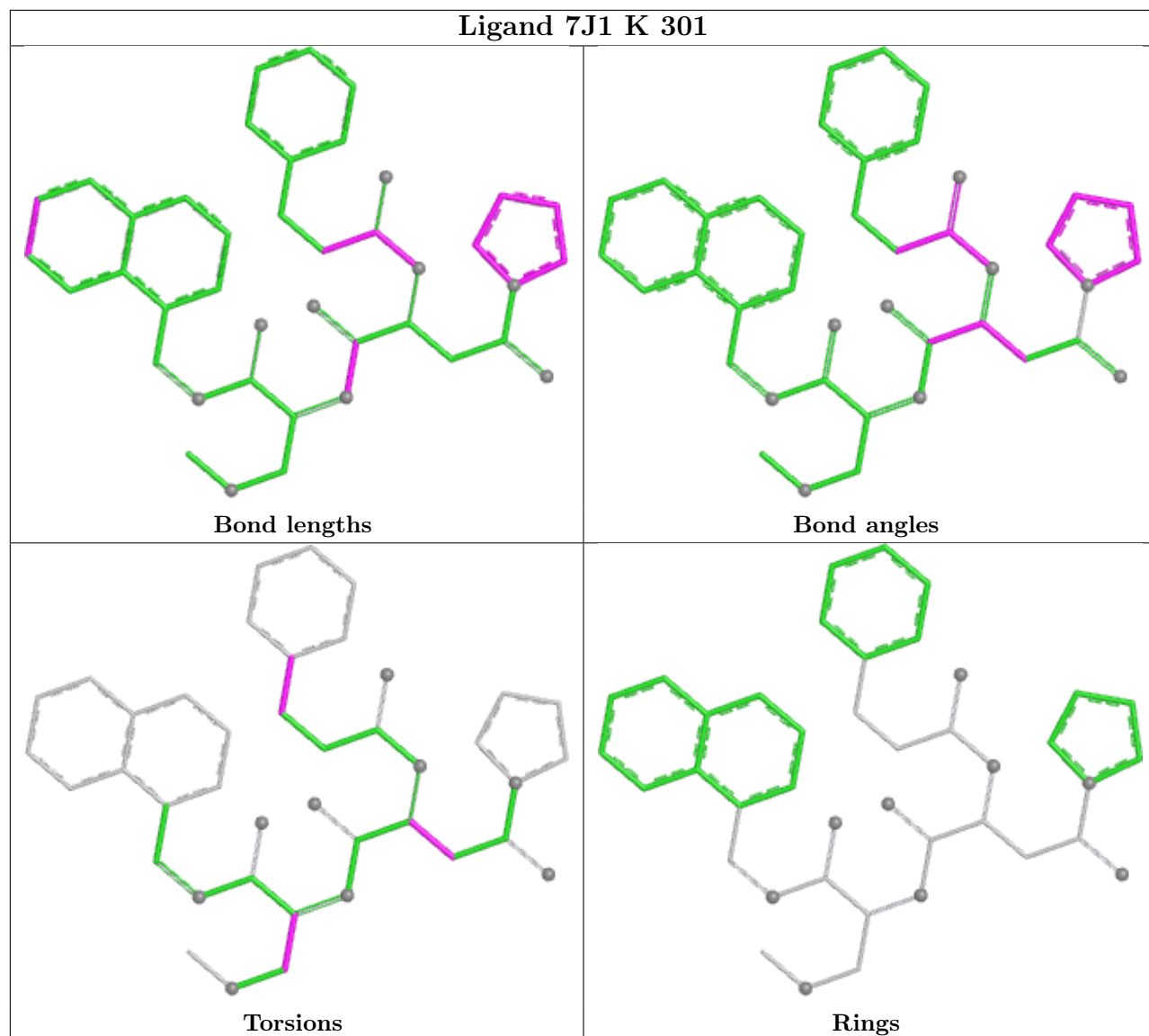


Rings

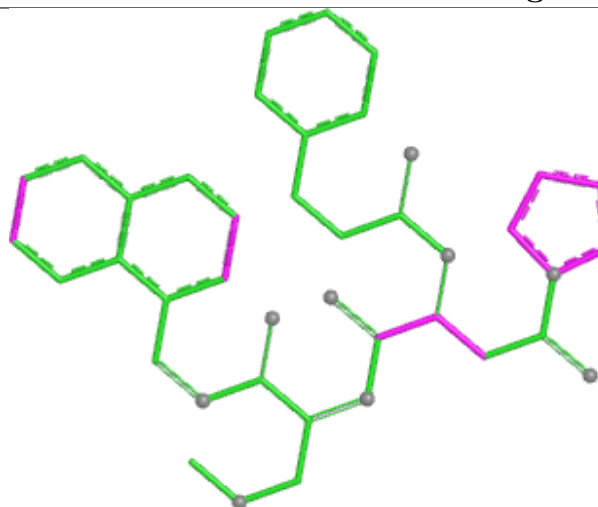
Ligand 7J1 b 301



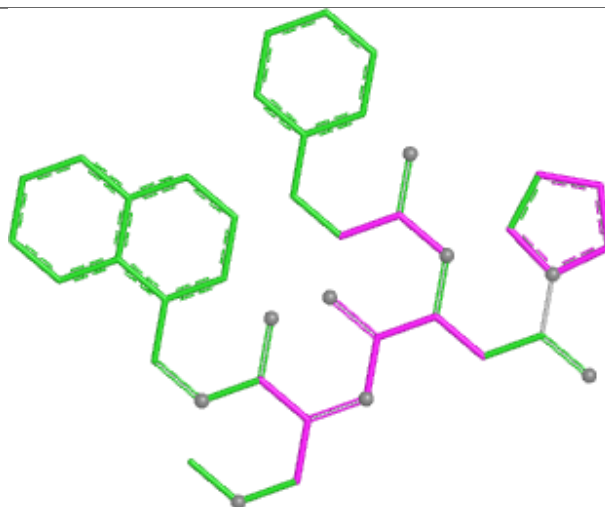
Ligand 7J1 K 301



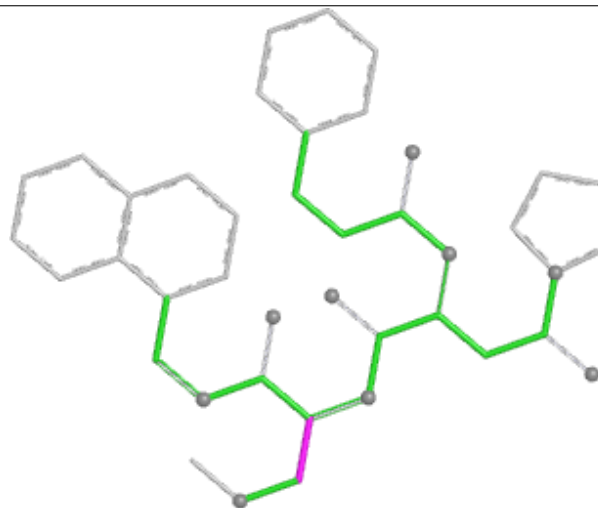
Ligand 7J1 L 301



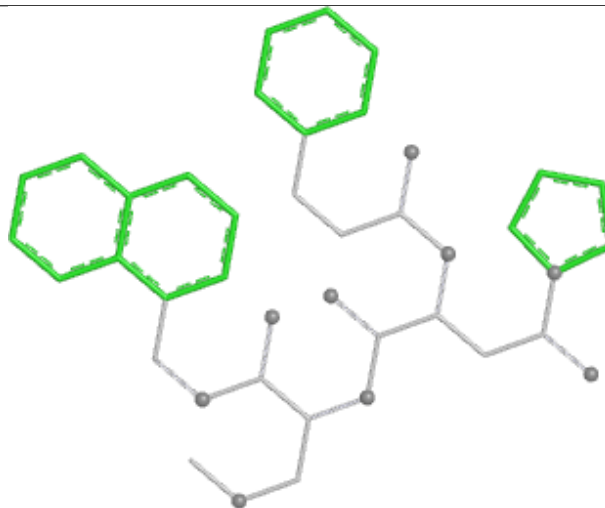
Bond lengths



Bond angles

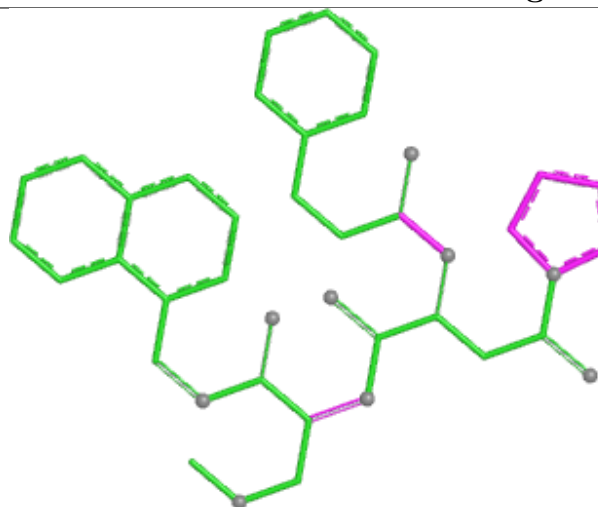


Torsions

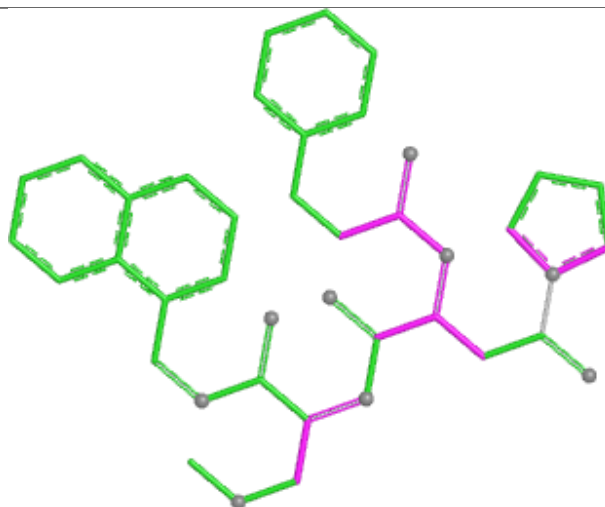


Rings

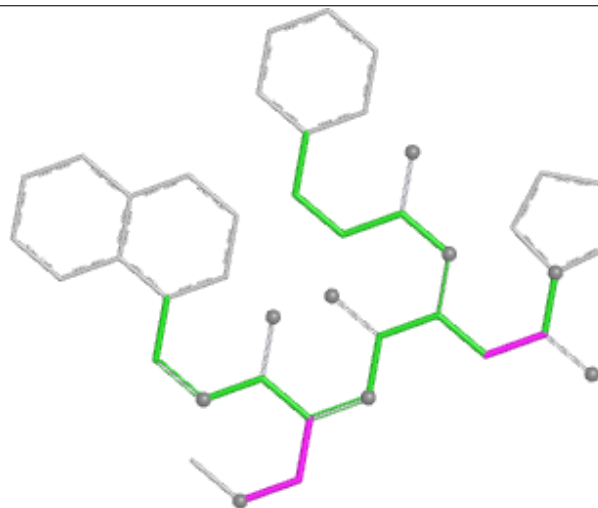
Ligand 7J1 Z 301



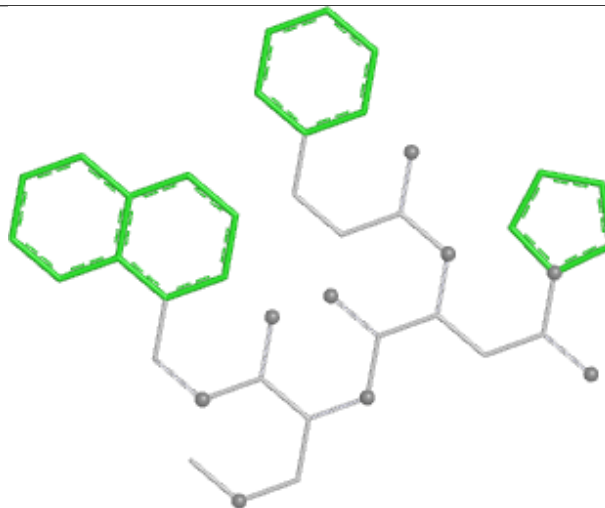
Bond lengths



Bond angles

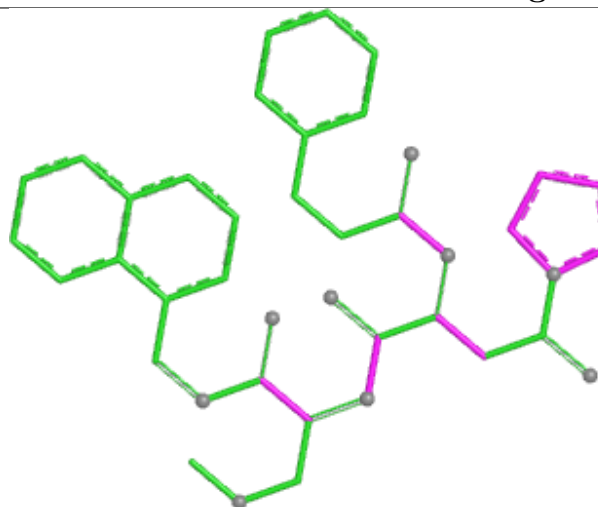


Torsions

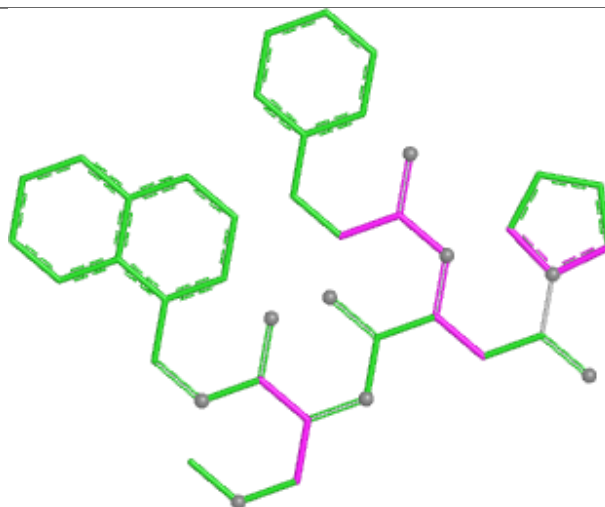


Rings

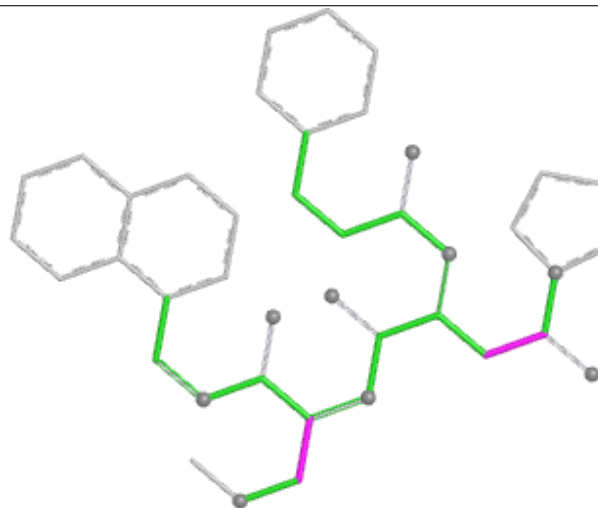
Ligand 7J1 a 301



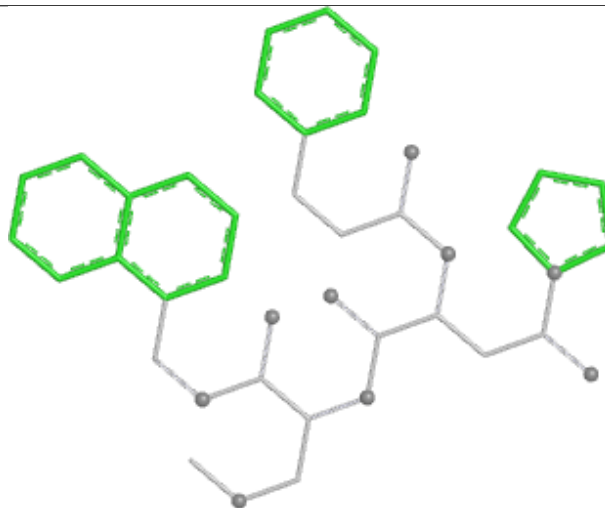
Bond lengths



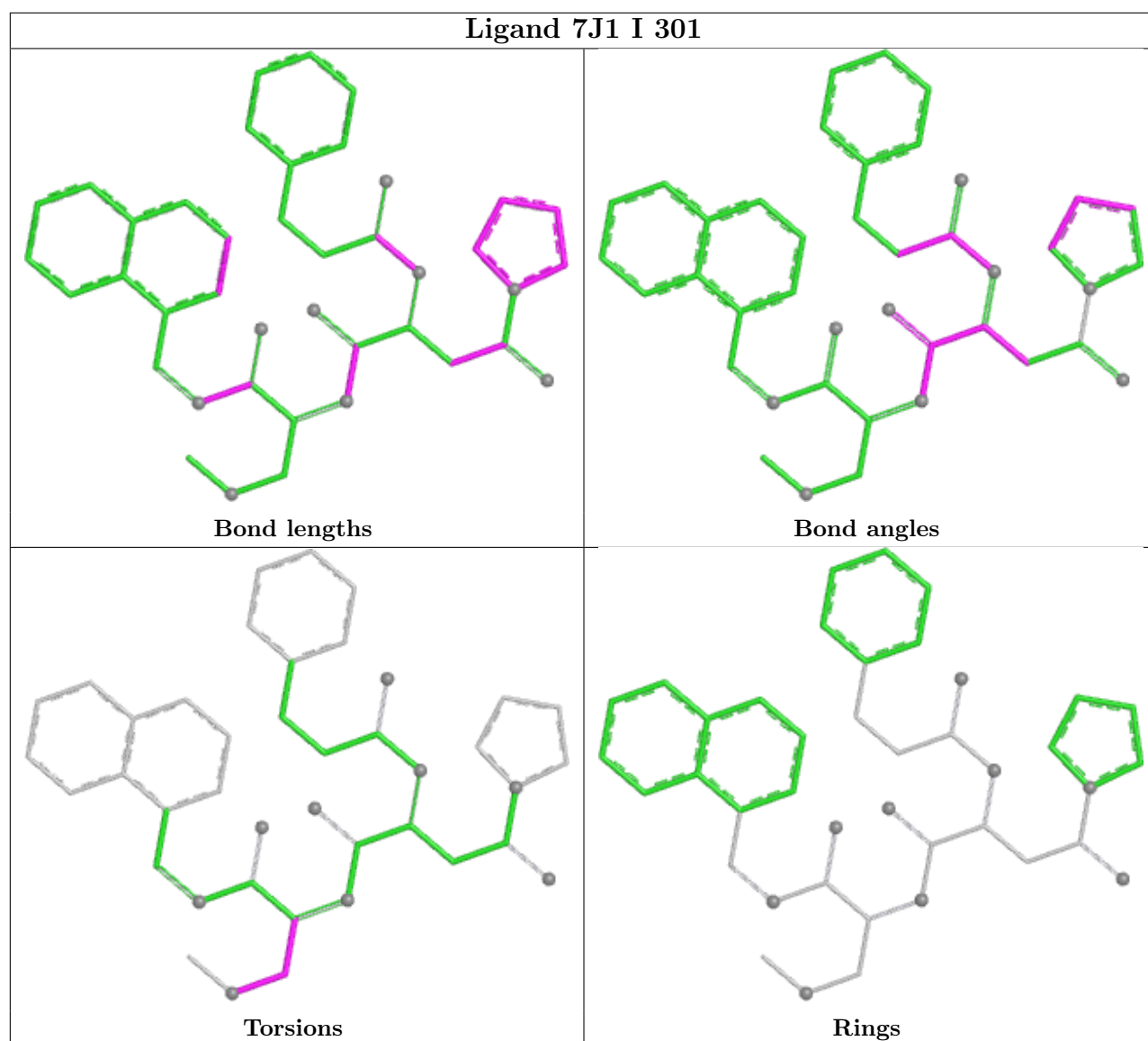
Bond angles



Torsions



Rings



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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	218/240 (90%)	0.19	5 (2%) 61 52	30, 50, 78, 104	0
1	B	216/240 (90%)	0.28	3 (1%) 73 67	34, 59, 93, 129	0
1	C	217/240 (90%)	0.42	5 (2%) 61 52	34, 63, 97, 118	0
1	D	217/240 (90%)	0.38	7 (3%) 50 40	34, 61, 91, 112	0
1	E	218/240 (90%)	0.26	5 (2%) 61 52	28, 59, 87, 129	0
1	F	215/240 (89%)	0.49	6 (2%) 55 45	34, 63, 93, 108	0
1	G	220/240 (91%)	0.13	4 (1%) 67 60	33, 53, 83, 103	0
1	O	216/240 (90%)	0.50	12 (5%) 30 23	30, 65, 99, 127	0
1	P	218/240 (90%)	0.30	5 (2%) 61 52	34, 58, 90, 117	0
1	Q	218/240 (90%)	0.09	3 (1%) 73 67	30, 53, 81, 124	0
1	R	217/240 (90%)	0.16	3 (1%) 73 67	30, 53, 81, 99	0
1	S	218/240 (90%)	0.07	3 (1%) 73 67	28, 50, 89, 104	0
1	T	218/240 (90%)	0.36	4 (1%) 67 60	33, 59, 91, 118	0
1	U	217/240 (90%)	0.10	3 (1%) 73 67	32, 52, 87, 105	0
2	H	222/240 (92%)	-0.12	1 (0%) 87 85	30, 44, 67, 111	0
2	I	222/240 (92%)	-0.19	2 (0%) 81 76	29, 40, 60, 77	0
2	J	222/240 (92%)	-0.21	0 100 100	30, 42, 65, 103	0
2	K	223/240 (92%)	0.03	1 (0%) 88 87	28, 45, 66, 84	0
2	L	223/240 (92%)	-0.01	2 (0%) 81 76	31, 43, 70, 95	0
2	M	222/240 (92%)	-0.04	3 (1%) 73 67	30, 44, 68, 111	0
2	N	223/240 (92%)	0.13	3 (1%) 75 69	34, 49, 76, 115	0
2	V	223/240 (92%)	-0.19	0 100 100	31, 41, 63, 79	0
2	W	223/240 (92%)	-0.05	1 (0%) 88 87	30, 42, 67, 92	0
2	X	222/240 (92%)	-0.22	0 100 100	29, 40, 64, 108	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	Y	223/240 (92%)	0.02	3 (1%) 75 69	28, 41, 63, 99	0
2	Z	222/240 (92%)	-0.09	1 (0%) 87 85	29, 42, 68, 95	0
2	a	223/240 (92%)	-0.06	1 (0%) 88 87	32, 46, 75, 99	0
2	b	223/240 (92%)	-0.16	2 (0%) 81 76	28, 42, 64, 97	0
All	All	6159/6720 (91%)	0.09	88 (1%) 73 67	28, 48, 86, 129	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	U	9	MET	4.9
1	A	183	ILE	4.8
1	O	235	VAL	4.7
1	P	235	VAL	4.0
1	F	204	GLY	3.9

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, 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
3	7J1	N	301	41/41	0.93	0.11	35,46,62,67	0
3	7J1	b	301	41/41	0.93	0.11	27,36,53,66	0
3	7J1	J	301	41/41	0.94	0.09	20,33,54,57	0
3	7J1	X	301	41/41	0.94	0.10	29,36,57,63	0
3	7J1	a	301	41/41	0.94	0.10	29,38,49,59	0
3	7J1	K	301	41/41	0.94	0.10	39,50,63,72	0
3	7J1	W	301	41/41	0.95	0.09	24,36,55,63	0

Continued on next page...

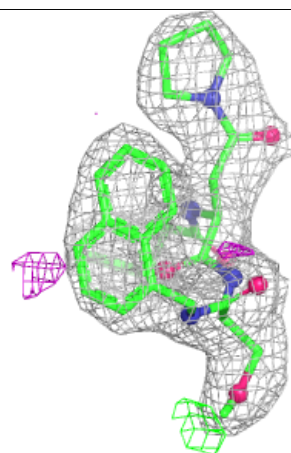
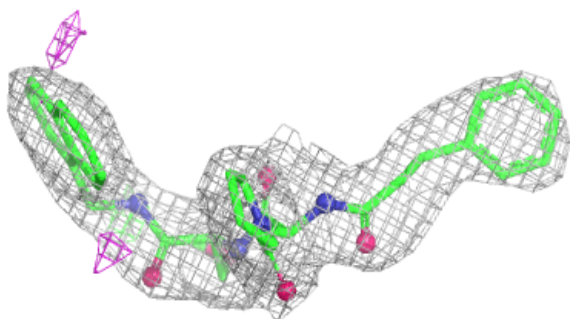
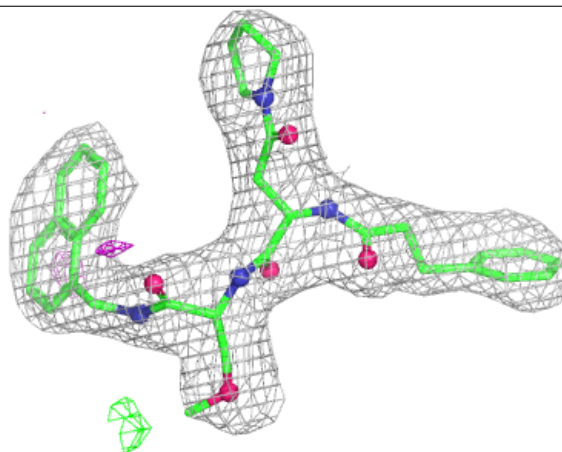
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	7J1	M	301	41/41	0.95	0.10	30,37,53,58	0
3	7J1	Y	301	41/41	0.95	0.09	21,38,57,63	0
3	7J1	L	301	41/41	0.95	0.09	23,38,55,59	0
3	7J1	V	301	41/41	0.95	0.09	31,43,50,55	0
3	7J1	Z	301	41/41	0.96	0.09	29,38,53,60	0
3	7J1	I	301	41/41	0.96	0.09	25,38,47,54	0
3	7J1	H	301	41/41	0.96	0.08	24,36,51,63	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.

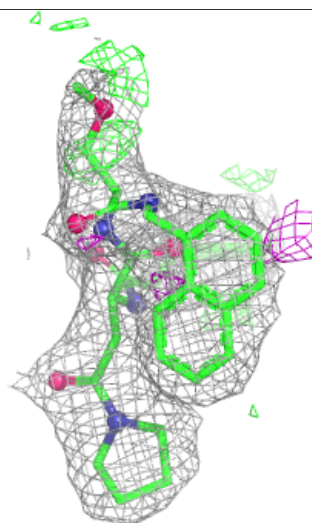
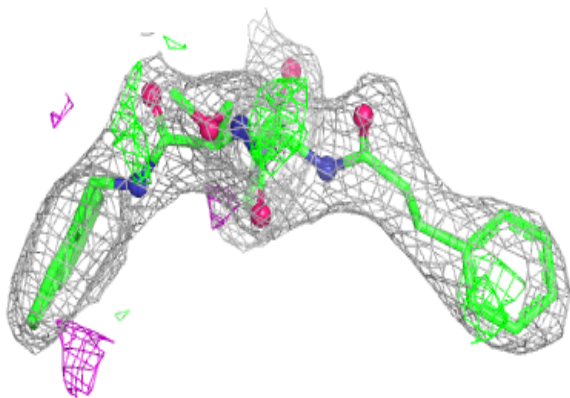
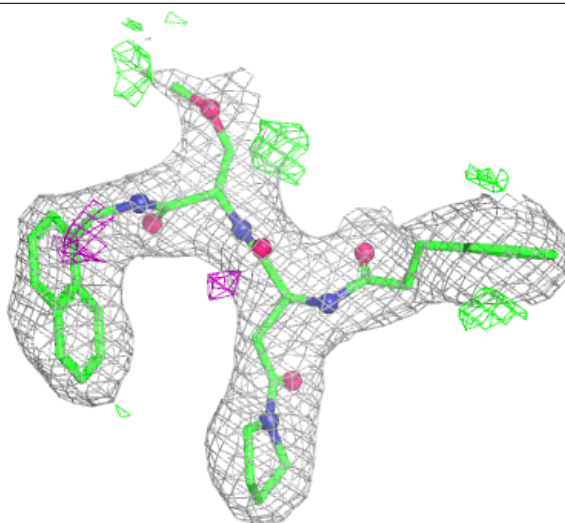
Electron density around 7J1 N 301:

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



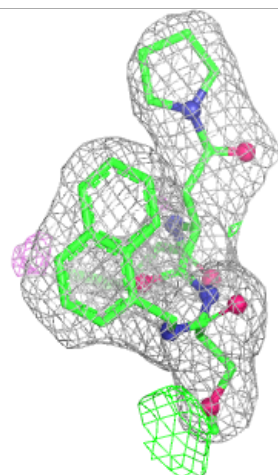
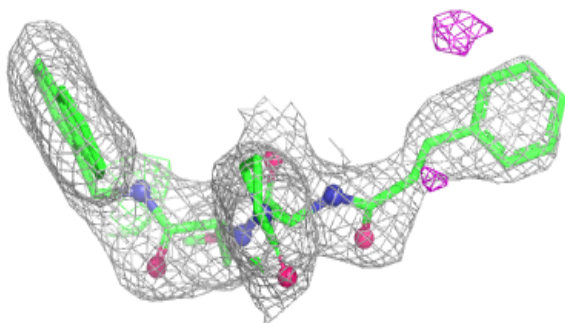
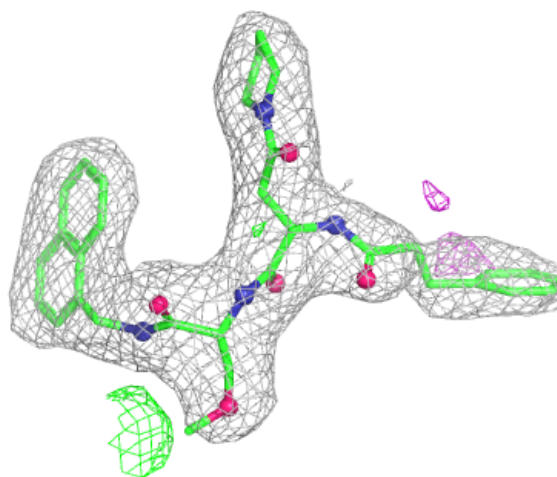
Electron density around 7J1 b 301:

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



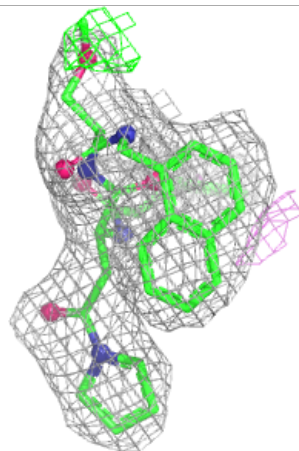
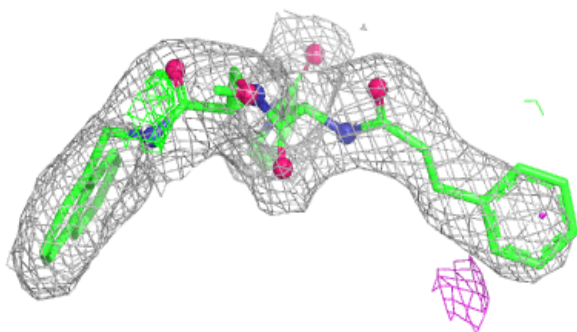
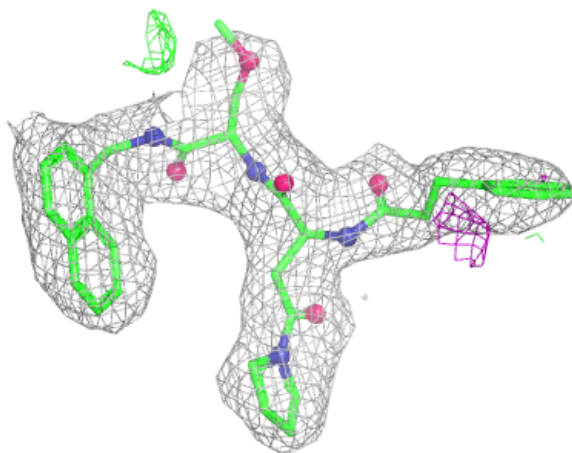
Electron density around 7J1 J 301:

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



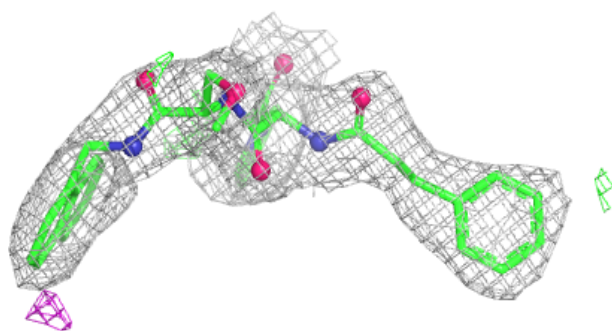
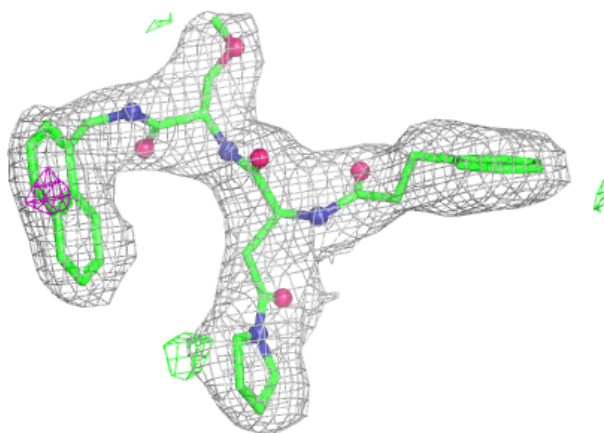
Electron density around 7J1 X 301:

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



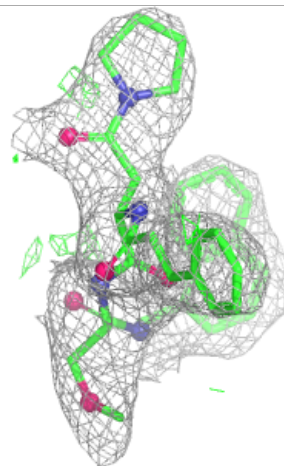
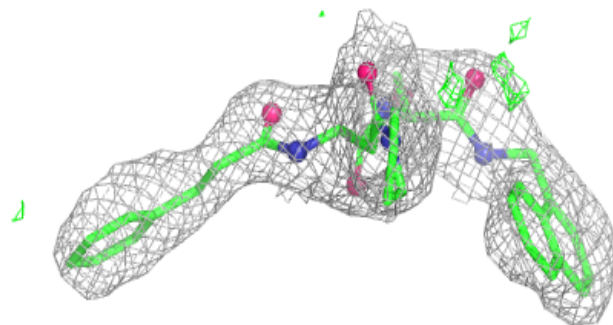
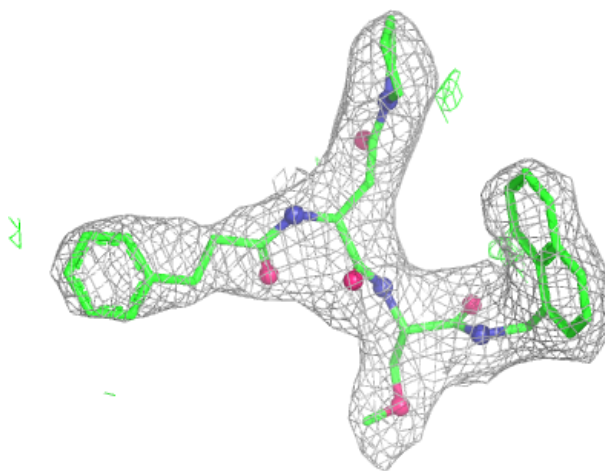
Electron density around 7J1 a 301:

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



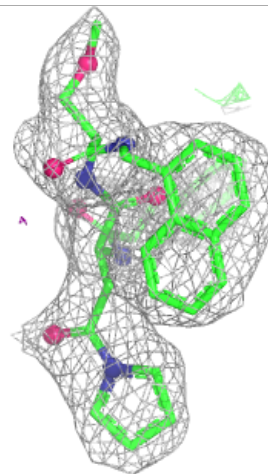
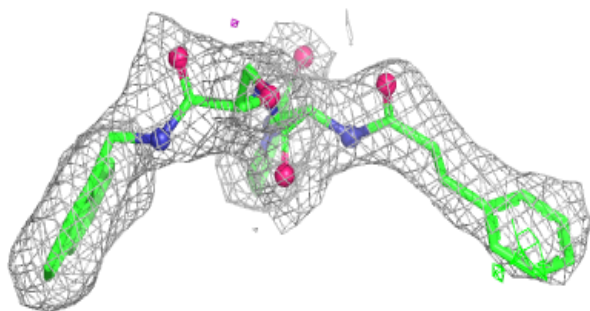
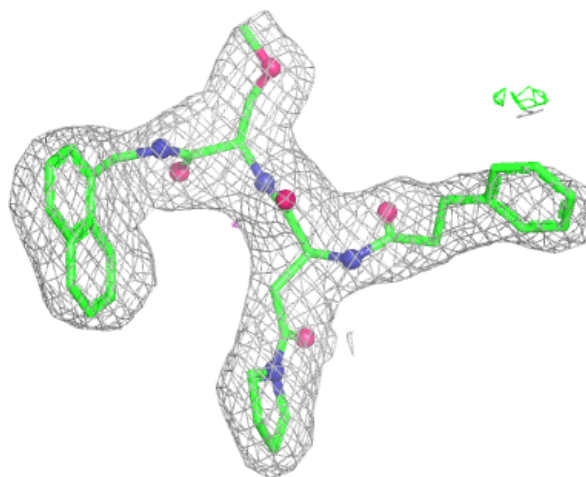
Electron density around 7J1 K 301:

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



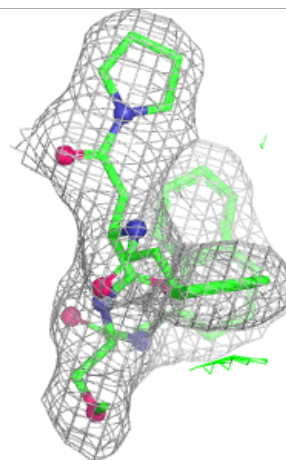
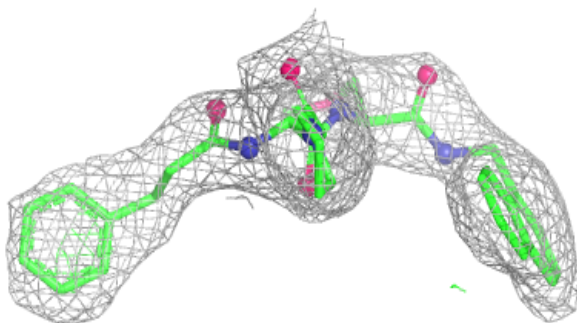
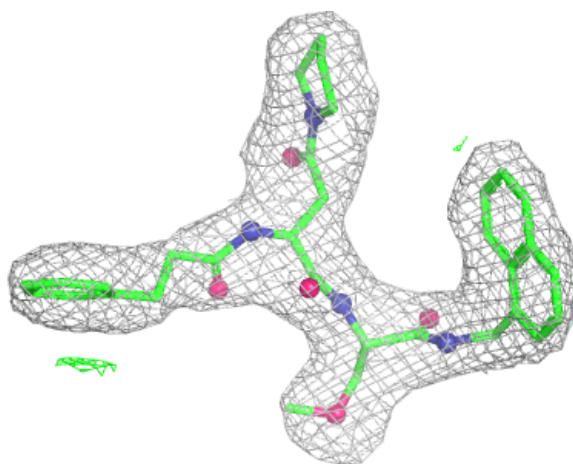
Electron density around 7J1 W 301:

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



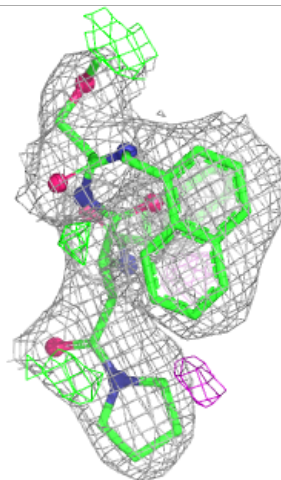
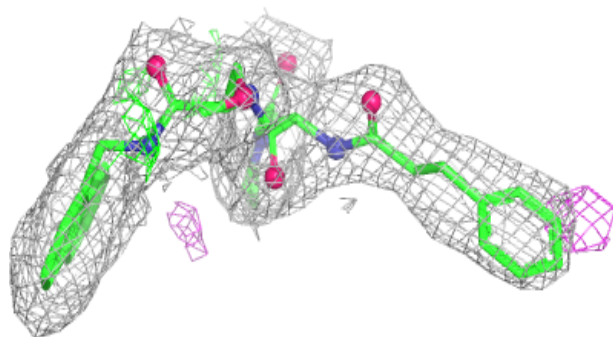
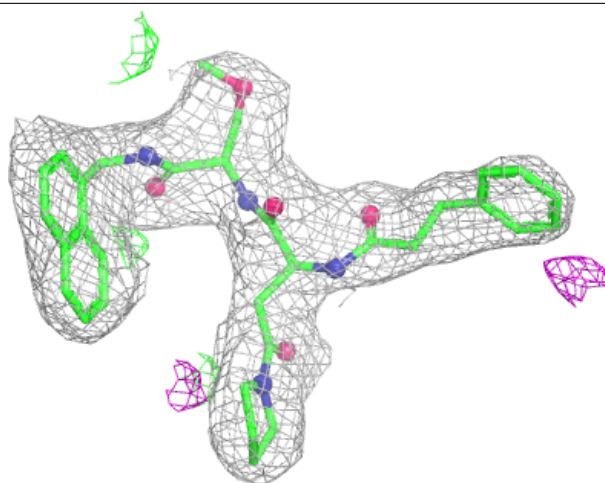
Electron density around 7J1 M 301:

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



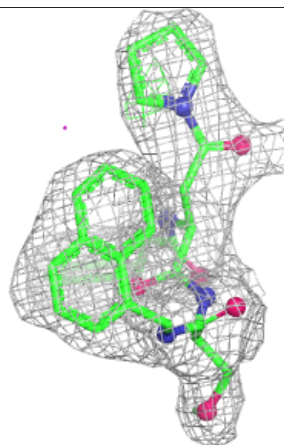
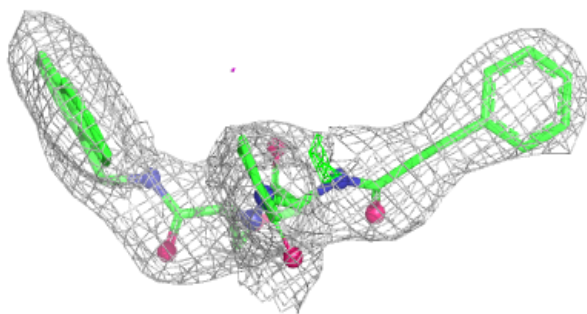
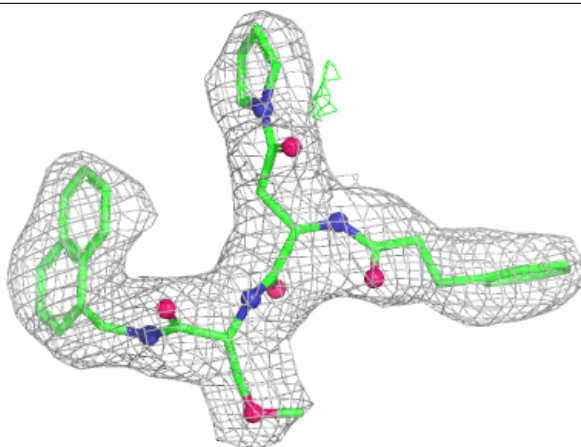
Electron density around 7J1 Y 301:

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



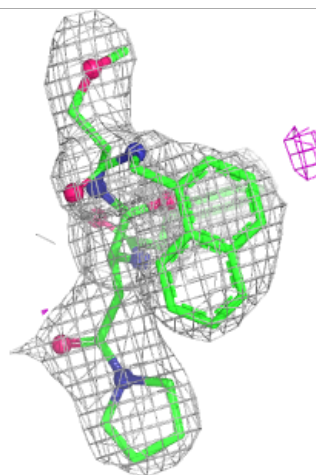
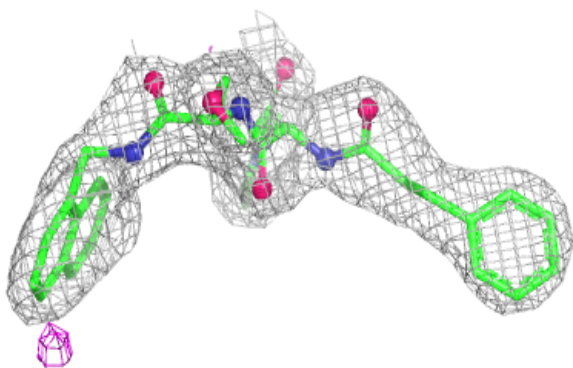
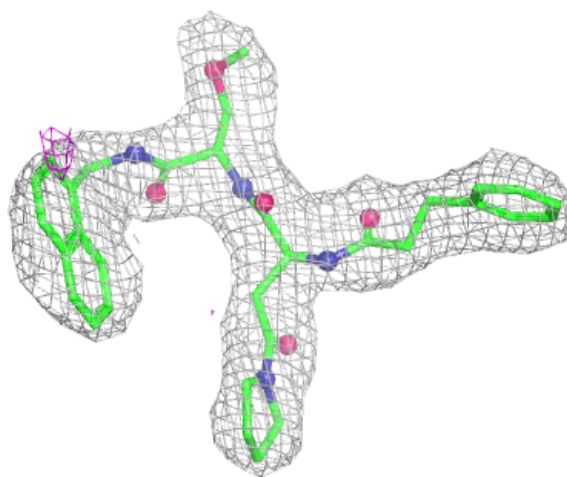
Electron density around 7J1 L 301:

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



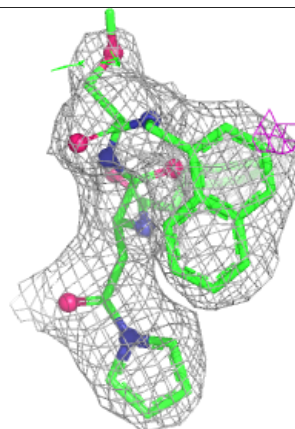
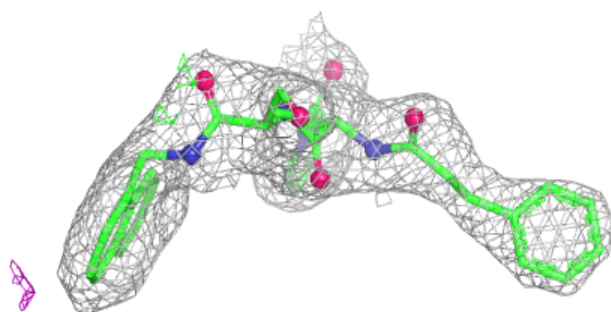
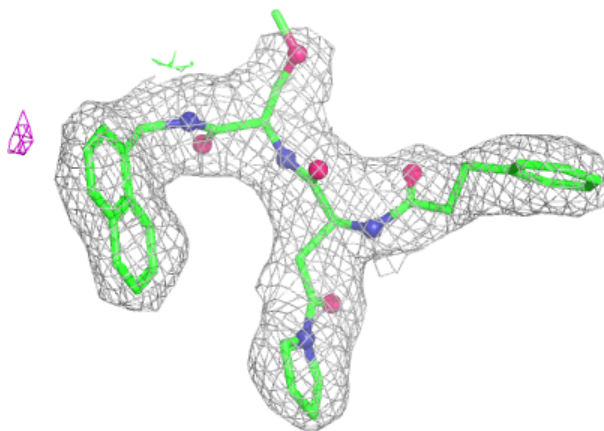
Electron density around 7J1 V 301:

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



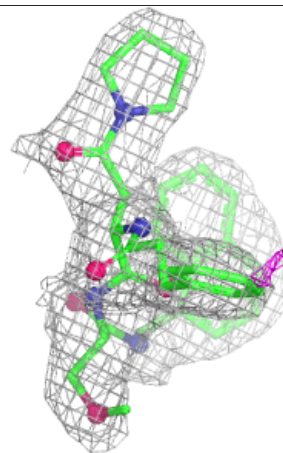
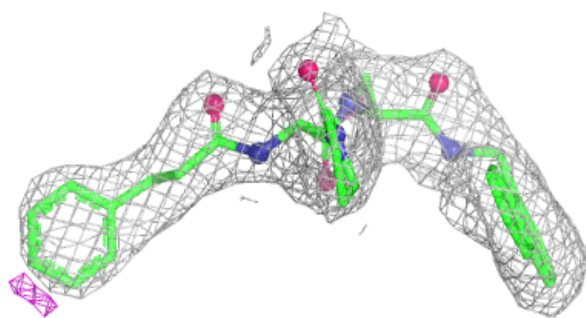
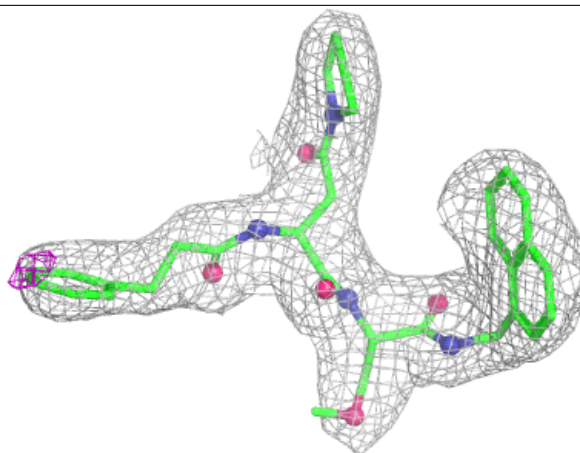
Electron density around 7J1 Z 301:

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



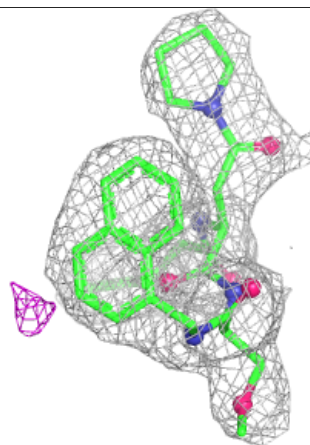
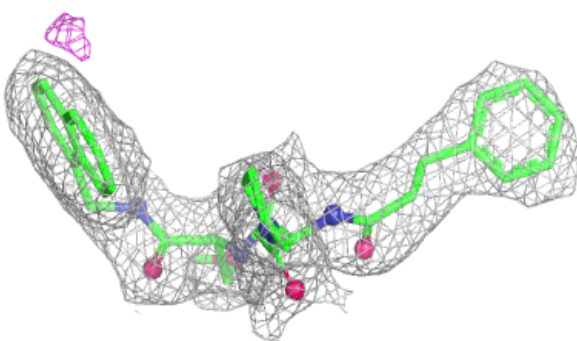
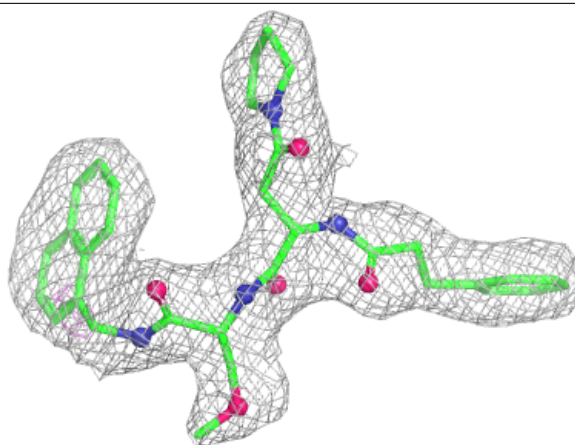
Electron density around 7J1 I 301:

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



Electron density around 7J1 H 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.