



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 15, 2024 – 04:36 PM EDT

PDB ID : 4U01
Title : HCV NS3/4A serine protease in complex with 6570
Authors : Parsy, C.C.; Alexandre, F.-R.; Brandt, G.; Caillet, C.; Chaves, D.; Derock, M.; Gloux, D.; Griffon, Y.; Lallo, L.B.; Leroy, F.; Liuzzi, M.; Loi, A.-G.; Mayes, B.; Moulat, L.; Moussa, A.; Chiara, M.; Roques, V.; Rosinovsky, E.; Seifer, M.; Stewart, A.; Wang, J.; Standring, D.; Surleraux, D.
Deposited on : 2014-07-11
Resolution : 2.80 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](#) ①) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

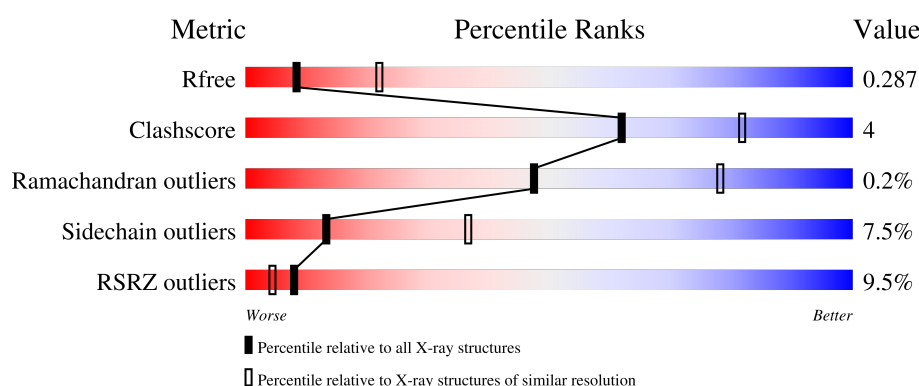
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	203	
1	B	203	
1	C	203	
1	D	203	
1	E	203	

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Mol	Chain	Length	Quality of chain
1	F	203	
1	G	203	
1	H	203	
1	J	203	
2	K	16	
2	L	16	
2	M	16	
2	N	16	
2	O	16	
2	P	16	
2	Q	16	
2	T	16	
2	U	16	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ZN	G	302	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13360 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 Non-structural 3 protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	B	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	C	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	D	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	E	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	F	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	G	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	H	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			
1	J	182	Total	C	N	O	S	0	0	0
			1337	829	244	254	10			

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A6N4J4
A	26	ARG	LYS	conflict	UNP A6N4J4
A	181	ALA	-	expression tag	UNP A6N4J4
A	182	SER	-	expression tag	UNP A6N4J4
A	183	LYS	-	expression tag	UNP A6N4J4
A	184	LYS	-	expression tag	UNP A6N4J4
A	185	LYS	-	expression tag	UNP A6N4J4
A	186	LYS	-	expression tag	UNP A6N4J4
A	187	LYS	-	expression tag	UNP A6N4J4
A	188	GLY	-	expression tag	UNP A6N4J4
A	189	SER	-	expression tag	UNP A6N4J4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	190	VAL	-	expression tag	UNP A6N4J4
A	191	VAL	-	expression tag	UNP A6N4J4
A	192	ILE	-	expression tag	UNP A6N4J4
A	193	VAL	-	expression tag	UNP A6N4J4
A	194	GLY	-	expression tag	UNP A6N4J4
A	195	ARG	-	expression tag	UNP A6N4J4
A	196	ILE	-	expression tag	UNP A6N4J4
A	197	ILE	-	expression tag	UNP A6N4J4
A	198	LEU	-	expression tag	UNP A6N4J4
A	199	SER	-	expression tag	UNP A6N4J4
A	200	GLY	-	expression tag	UNP A6N4J4
A	201	ARG	-	expression tag	UNP A6N4J4
A	202	LYS	-	expression tag	UNP A6N4J4
B	0	MET	-	initiating methionine	UNP A6N4J4
B	26	ARG	LYS	conflict	UNP A6N4J4
B	181	ALA	-	expression tag	UNP A6N4J4
B	182	SER	-	expression tag	UNP A6N4J4
B	183	LYS	-	expression tag	UNP A6N4J4
B	184	LYS	-	expression tag	UNP A6N4J4
B	185	LYS	-	expression tag	UNP A6N4J4
B	186	LYS	-	expression tag	UNP A6N4J4
B	187	LYS	-	expression tag	UNP A6N4J4
B	188	GLY	-	expression tag	UNP A6N4J4
B	189	SER	-	expression tag	UNP A6N4J4
B	190	VAL	-	expression tag	UNP A6N4J4
B	191	VAL	-	expression tag	UNP A6N4J4
B	192	ILE	-	expression tag	UNP A6N4J4
B	193	VAL	-	expression tag	UNP A6N4J4
B	194	GLY	-	expression tag	UNP A6N4J4
B	195	ARG	-	expression tag	UNP A6N4J4
B	196	ILE	-	expression tag	UNP A6N4J4
B	197	ILE	-	expression tag	UNP A6N4J4
B	198	LEU	-	expression tag	UNP A6N4J4
B	199	SER	-	expression tag	UNP A6N4J4
B	200	GLY	-	expression tag	UNP A6N4J4
B	201	ARG	-	expression tag	UNP A6N4J4
B	202	LYS	-	expression tag	UNP A6N4J4
C	0	MET	-	initiating methionine	UNP A6N4J4
C	26	ARG	LYS	conflict	UNP A6N4J4
C	181	ALA	-	expression tag	UNP A6N4J4
C	182	SER	-	expression tag	UNP A6N4J4
C	183	LYS	-	expression tag	UNP A6N4J4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	184	LYS	-	expression tag	UNP A6N4J4
C	185	LYS	-	expression tag	UNP A6N4J4
C	186	LYS	-	expression tag	UNP A6N4J4
C	187	LYS	-	expression tag	UNP A6N4J4
C	188	GLY	-	expression tag	UNP A6N4J4
C	189	SER	-	expression tag	UNP A6N4J4
C	190	VAL	-	expression tag	UNP A6N4J4
C	191	VAL	-	expression tag	UNP A6N4J4
C	192	ILE	-	expression tag	UNP A6N4J4
C	193	VAL	-	expression tag	UNP A6N4J4
C	194	GLY	-	expression tag	UNP A6N4J4
C	195	ARG	-	expression tag	UNP A6N4J4
C	196	ILE	-	expression tag	UNP A6N4J4
C	197	ILE	-	expression tag	UNP A6N4J4
C	198	LEU	-	expression tag	UNP A6N4J4
C	199	SER	-	expression tag	UNP A6N4J4
C	200	GLY	-	expression tag	UNP A6N4J4
C	201	ARG	-	expression tag	UNP A6N4J4
C	202	LYS	-	expression tag	UNP A6N4J4
D	0	MET	-	initiating methionine	UNP A6N4J4
D	26	ARG	LYS	conflict	UNP A6N4J4
D	181	ALA	-	expression tag	UNP A6N4J4
D	182	SER	-	expression tag	UNP A6N4J4
D	183	LYS	-	expression tag	UNP A6N4J4
D	184	LYS	-	expression tag	UNP A6N4J4
D	185	LYS	-	expression tag	UNP A6N4J4
D	186	LYS	-	expression tag	UNP A6N4J4
D	187	LYS	-	expression tag	UNP A6N4J4
D	188	GLY	-	expression tag	UNP A6N4J4
D	189	SER	-	expression tag	UNP A6N4J4
D	190	VAL	-	expression tag	UNP A6N4J4
D	191	VAL	-	expression tag	UNP A6N4J4
D	192	ILE	-	expression tag	UNP A6N4J4
D	193	VAL	-	expression tag	UNP A6N4J4
D	194	GLY	-	expression tag	UNP A6N4J4
D	195	ARG	-	expression tag	UNP A6N4J4
D	196	ILE	-	expression tag	UNP A6N4J4
D	197	ILE	-	expression tag	UNP A6N4J4
D	198	LEU	-	expression tag	UNP A6N4J4
D	199	SER	-	expression tag	UNP A6N4J4
D	200	GLY	-	expression tag	UNP A6N4J4
D	201	ARG	-	expression tag	UNP A6N4J4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	202	LYS	-	expression tag	UNP A6N4J4
E	0	MET	-	initiating methionine	UNP A6N4J4
E	26	ARG	LYS	conflict	UNP A6N4J4
E	181	ALA	-	expression tag	UNP A6N4J4
E	182	SER	-	expression tag	UNP A6N4J4
E	183	LYS	-	expression tag	UNP A6N4J4
E	184	LYS	-	expression tag	UNP A6N4J4
E	185	LYS	-	expression tag	UNP A6N4J4
E	186	LYS	-	expression tag	UNP A6N4J4
E	187	LYS	-	expression tag	UNP A6N4J4
E	188	GLY	-	expression tag	UNP A6N4J4
E	189	SER	-	expression tag	UNP A6N4J4
E	190	VAL	-	expression tag	UNP A6N4J4
E	191	VAL	-	expression tag	UNP A6N4J4
E	192	ILE	-	expression tag	UNP A6N4J4
E	193	VAL	-	expression tag	UNP A6N4J4
E	194	GLY	-	expression tag	UNP A6N4J4
E	195	ARG	-	expression tag	UNP A6N4J4
E	196	ILE	-	expression tag	UNP A6N4J4
E	197	ILE	-	expression tag	UNP A6N4J4
E	198	LEU	-	expression tag	UNP A6N4J4
E	199	SER	-	expression tag	UNP A6N4J4
E	200	GLY	-	expression tag	UNP A6N4J4
E	201	ARG	-	expression tag	UNP A6N4J4
E	202	LYS	-	expression tag	UNP A6N4J4
F	0	MET	-	initiating methionine	UNP A6N4J4
F	26	ARG	LYS	conflict	UNP A6N4J4
F	181	ALA	-	expression tag	UNP A6N4J4
F	182	SER	-	expression tag	UNP A6N4J4
F	183	LYS	-	expression tag	UNP A6N4J4
F	184	LYS	-	expression tag	UNP A6N4J4
F	185	LYS	-	expression tag	UNP A6N4J4
F	186	LYS	-	expression tag	UNP A6N4J4
F	187	LYS	-	expression tag	UNP A6N4J4
F	188	GLY	-	expression tag	UNP A6N4J4
F	189	SER	-	expression tag	UNP A6N4J4
F	190	VAL	-	expression tag	UNP A6N4J4
F	191	VAL	-	expression tag	UNP A6N4J4
F	192	ILE	-	expression tag	UNP A6N4J4
F	193	VAL	-	expression tag	UNP A6N4J4
F	194	GLY	-	expression tag	UNP A6N4J4
F	195	ARG	-	expression tag	UNP A6N4J4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	196	ILE	-	expression tag	UNP A6N4J4
F	197	ILE	-	expression tag	UNP A6N4J4
F	198	LEU	-	expression tag	UNP A6N4J4
F	199	SER	-	expression tag	UNP A6N4J4
F	200	GLY	-	expression tag	UNP A6N4J4
F	201	ARG	-	expression tag	UNP A6N4J4
F	202	LYS	-	expression tag	UNP A6N4J4
G	0	MET	-	initiating methionine	UNP A6N4J4
G	26	ARG	LYS	conflict	UNP A6N4J4
G	181	ALA	-	expression tag	UNP A6N4J4
G	182	SER	-	expression tag	UNP A6N4J4
G	183	LYS	-	expression tag	UNP A6N4J4
G	184	LYS	-	expression tag	UNP A6N4J4
G	185	LYS	-	expression tag	UNP A6N4J4
G	186	LYS	-	expression tag	UNP A6N4J4
G	187	LYS	-	expression tag	UNP A6N4J4
G	188	GLY	-	expression tag	UNP A6N4J4
G	189	SER	-	expression tag	UNP A6N4J4
G	190	VAL	-	expression tag	UNP A6N4J4
G	191	VAL	-	expression tag	UNP A6N4J4
G	192	ILE	-	expression tag	UNP A6N4J4
G	193	VAL	-	expression tag	UNP A6N4J4
G	194	GLY	-	expression tag	UNP A6N4J4
G	195	ARG	-	expression tag	UNP A6N4J4
G	196	ILE	-	expression tag	UNP A6N4J4
G	197	ILE	-	expression tag	UNP A6N4J4
G	198	LEU	-	expression tag	UNP A6N4J4
G	199	SER	-	expression tag	UNP A6N4J4
G	200	GLY	-	expression tag	UNP A6N4J4
G	201	ARG	-	expression tag	UNP A6N4J4
G	202	LYS	-	expression tag	UNP A6N4J4
H	0	MET	-	initiating methionine	UNP A6N4J4
H	26	ARG	LYS	conflict	UNP A6N4J4
H	181	ALA	-	expression tag	UNP A6N4J4
H	182	SER	-	expression tag	UNP A6N4J4
H	183	LYS	-	expression tag	UNP A6N4J4
H	184	LYS	-	expression tag	UNP A6N4J4
H	185	LYS	-	expression tag	UNP A6N4J4
H	186	LYS	-	expression tag	UNP A6N4J4
H	187	LYS	-	expression tag	UNP A6N4J4
H	188	GLY	-	expression tag	UNP A6N4J4
H	189	SER	-	expression tag	UNP A6N4J4

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Chain	Residue	Modelled	Actual	Comment	Reference
H	190	VAL	-	expression tag	UNP A6N4J4
H	191	VAL	-	expression tag	UNP A6N4J4
H	192	ILE	-	expression tag	UNP A6N4J4
H	193	VAL	-	expression tag	UNP A6N4J4
H	194	GLY	-	expression tag	UNP A6N4J4
H	195	ARG	-	expression tag	UNP A6N4J4
H	196	ILE	-	expression tag	UNP A6N4J4
H	197	ILE	-	expression tag	UNP A6N4J4
H	198	LEU	-	expression tag	UNP A6N4J4
H	199	SER	-	expression tag	UNP A6N4J4
H	200	GLY	-	expression tag	UNP A6N4J4
H	201	ARG	-	expression tag	UNP A6N4J4
H	202	LYS	-	expression tag	UNP A6N4J4
J	0	MET	-	initiating methionine	UNP A6N4J4
J	26	ARG	LYS	conflict	UNP A6N4J4
J	181	ALA	-	expression tag	UNP A6N4J4
J	182	SER	-	expression tag	UNP A6N4J4
J	183	LYS	-	expression tag	UNP A6N4J4
J	184	LYS	-	expression tag	UNP A6N4J4
J	185	LYS	-	expression tag	UNP A6N4J4
J	186	LYS	-	expression tag	UNP A6N4J4
J	187	LYS	-	expression tag	UNP A6N4J4
J	188	GLY	-	expression tag	UNP A6N4J4
J	189	SER	-	expression tag	UNP A6N4J4
J	190	VAL	-	expression tag	UNP A6N4J4
J	191	VAL	-	expression tag	UNP A6N4J4
J	192	ILE	-	expression tag	UNP A6N4J4
J	193	VAL	-	expression tag	UNP A6N4J4
J	194	GLY	-	expression tag	UNP A6N4J4
J	195	ARG	-	expression tag	UNP A6N4J4
J	196	ILE	-	expression tag	UNP A6N4J4
J	197	ILE	-	expression tag	UNP A6N4J4
J	198	LEU	-	expression tag	UNP A6N4J4
J	199	SER	-	expression tag	UNP A6N4J4
J	200	GLY	-	expression tag	UNP A6N4J4
J	201	ARG	-	expression tag	UNP A6N4J4
J	202	LYS	-	expression tag	UNP A6N4J4

- Molecule 2 is a protein called NS4A protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	K	13	Total	C	N	O	0	0	0
			93	61	17	15			

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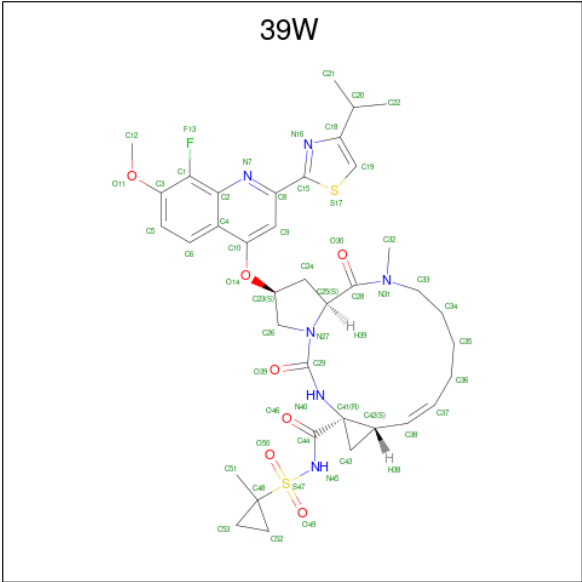
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	L	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	M	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	N	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	O	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	P	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	Q	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	T	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	U	13	Total	C	N	O	0	0	0
			93	61	17	15			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	220	LYS	-	expression tag	UNP F0UY39
K	235	LYS	-	expression tag	UNP F0UY39
L	220	LYS	-	expression tag	UNP F0UY39
L	235	LYS	-	expression tag	UNP F0UY39
M	220	LYS	-	expression tag	UNP F0UY39
M	235	LYS	-	expression tag	UNP F0UY39
N	220	LYS	-	expression tag	UNP F0UY39
N	235	LYS	-	expression tag	UNP F0UY39
O	220	LYS	-	expression tag	UNP F0UY39
O	235	LYS	-	expression tag	UNP F0UY39
P	220	LYS	-	expression tag	UNP F0UY39
P	235	LYS	-	expression tag	UNP F0UY39
Q	220	LYS	-	expression tag	UNP F0UY39
Q	235	LYS	-	expression tag	UNP F0UY39
T	220	LYS	-	expression tag	UNP F0UY39
T	235	LYS	-	expression tag	UNP F0UY39
U	220	LYS	-	expression tag	UNP F0UY39
U	235	LYS	-	expression tag	UNP F0UY39

- Molecule 3 is (2S,3aS,10Z,11aS,12aR)-2-({8-fluoro-7-methoxy-2-[4-(propan-2-yl)-1,3-thiazol-2-yl]quinolin-4-yl}oxy)-5-methyl-N-[(1-methylcyclopropyl)sulfonyl]-4,14-dioxo-1,2,3,3a,4,5,6,7,8,9,11a,12,13,14-tetradecahydro-12aH-cyclopropa[m]pyrrolo[1,2-c][1,3,6]triazacyclotetradecine-12a-carboxamide (three-letter code: 39W) (formula: C₃₇H₄₅FN₆O₇S₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	B	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	C	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	D	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	E	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	F	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	G	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	H	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		
3	J	1	Total	C	F	N	O	S	0	0
			53	37	1	6	7	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		

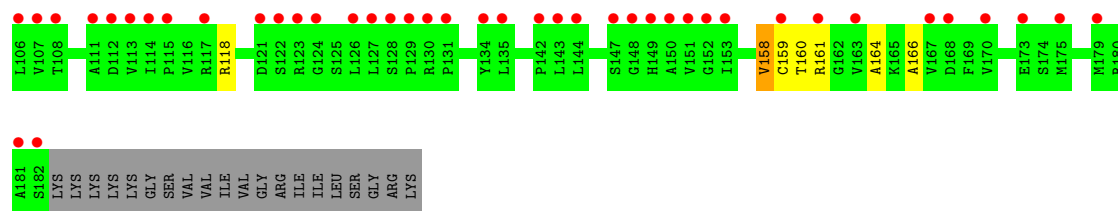
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total 1	Zn 1	0	0
4	E	1	Total 1	Zn 1	0	0
4	F	1	Total 1	Zn 1	0	0
4	G	1	Total 1	Zn 1	0	0
4	H	1	Total 1	Zn 1	0	0
4	J	1	Total 1	Zn 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Cl 1	0	0
5	D	1	Total 1	Cl 1	0	0
5	E	1	Total 1	Cl 1	0	0
5	G	1	Total 1	Cl 1	0	0



● Molecule 2: NS4A protein



● Molecule 2: NS4A protein



● Molecule 2: NS4A protein



● Molecule 2: NS4A protein



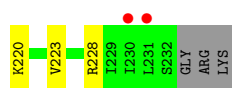
● Molecule 2: NS4A protein



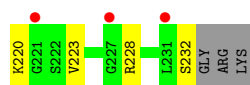
● Molecule 2: NS4A protein



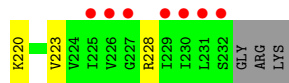
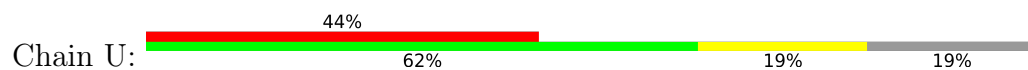
● Molecule 2: NS4A protein



● Molecule 2: NS4A protein



● Molecule 2: NS4A protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	150.03Å 174.36Å 133.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.23 – 2.80 43.22 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.23-2.80) 97.0 (43.22-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.233 , 0.290 0.234 , 0.287	Depositor DCC
R_{free} test set	2088 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	72.3	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13360	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.27% 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: ZN, CL, 39W

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	0.47	0/1363	0.63	0/1857
1	B	0.38	0/1363	0.58	0/1857
1	C	0.42	0/1363	0.59	0/1857
1	D	0.42	0/1363	0.61	0/1857
1	E	0.40	0/1363	0.57	0/1857
1	F	0.41	0/1363	0.56	0/1857
1	G	0.40	0/1363	0.58	0/1857
1	H	0.37	0/1363	0.54	0/1857
1	J	0.35	0/1363	0.50	0/1857
2	K	0.40	0/92	0.72	0/122
2	L	0.52	0/92	0.66	0/122
2	M	0.45	0/92	0.71	0/122
2	N	0.57	0/92	0.71	0/122
2	O	0.46	0/92	0.67	0/122
2	P	0.41	0/92	0.64	0/122
2	Q	0.45	0/92	0.57	0/122
2	T	0.43	0/92	0.75	0/122
2	U	0.39	0/92	0.65	0/122
All	All	0.41	0/13095	0.58	0/17811

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	1337	0	1344	14	0
1	B	1337	0	1345	13	0
1	C	1337	0	1344	13	0
1	D	1337	0	1344	12	0
1	E	1337	0	1344	11	0
1	F	1337	0	1345	14	0
1	G	1337	0	1346	15	0
1	H	1337	0	1344	12	0
1	J	1337	0	1344	6	0
2	K	93	0	112	3	0
2	L	93	0	112	1	0
2	M	93	0	112	5	0
2	N	93	0	112	2	0
2	O	93	0	112	2	0
2	P	93	0	112	2	0
2	Q	93	0	112	4	0
2	T	93	0	112	4	0
2	U	93	0	112	4	0
3	A	53	0	44	4	0
3	B	53	0	44	0	0
3	C	53	0	44	2	0
3	D	53	0	44	6	0
3	E	53	0	44	3	0
3	F	53	0	44	1	0
3	G	53	0	44	0	0
3	H	53	0	44	3	0
3	J	53	0	44	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	1	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	2	0
4	H	1	0	0	0	0
4	J	1	0	0	0	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
All	All	13360	0	13504	119	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 4.

The worst 5 of 119 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:G:97:CYS:SG	4:G:302:ZN:ZN	1.57	0.92
1:A:159:CYS:HB3	1:A:164:ALA:HA	1.57	0.86
1:D:36:VAL:HG13	2:N:223:VAL:CG1	2.20	0.71
1:H:159:CYS:HB3	1:H:164:ALA:HA	1.76	0.68
1:D:159:CYS:HB3	1:D:164:ALA:HA	1.76	0.68

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	180/203 (89%)	174 (97%)	5 (3%)	1 (1%)	25	56
1	B	180/203 (89%)	172 (96%)	8 (4%)	0	100	100
1	C	180/203 (89%)	170 (94%)	10 (6%)	0	100	100
1	D	180/203 (89%)	171 (95%)	8 (4%)	1 (1%)	25	56
1	E	180/203 (89%)	173 (96%)	7 (4%)	0	100	100
1	F	180/203 (89%)	170 (94%)	10 (6%)	0	100	100
1	G	180/203 (89%)	174 (97%)	6 (3%)	0	100	100
1	H	180/203 (89%)	170 (94%)	10 (6%)	0	100	100
1	J	180/203 (89%)	173 (96%)	6 (3%)	1 (1%)	25	56
2	K	11/16 (69%)	11 (100%)	0	0	100	100
2	L	11/16 (69%)	11 (100%)	0	0	100	100
2	M	11/16 (69%)	11 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N	11/16 (69%)	11 (100%)	0	0	100	100
2	O	11/16 (69%)	11 (100%)	0	0	100	100
2	P	11/16 (69%)	11 (100%)	0	0	100	100
2	Q	11/16 (69%)	11 (100%)	0	0	100	100
2	T	11/16 (69%)	11 (100%)	0	0	100	100
2	U	11/16 (69%)	11 (100%)	0	0	100	100
All	All	1719/1971 (87%)	1646 (96%)	70 (4%)	3 (0%)	47	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	GLY
1	D	109	ARG
1	J	161	ARG

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	147/165 (89%)	135 (92%)	12 (8%)	11	33
1	B	147/165 (89%)	140 (95%)	7 (5%)	25	58
1	C	147/165 (89%)	141 (96%)	6 (4%)	30	64
1	D	147/165 (89%)	134 (91%)	13 (9%)	10	29
1	E	147/165 (89%)	134 (91%)	13 (9%)	10	29
1	F	147/165 (89%)	134 (91%)	13 (9%)	10	29
1	G	147/165 (89%)	138 (94%)	9 (6%)	18	48
1	H	147/165 (89%)	140 (95%)	7 (5%)	25	58
1	J	147/165 (89%)	138 (94%)	9 (6%)	18	48
2	K	11/13 (85%)	9 (82%)	2 (18%)	1	5
2	L	11/13 (85%)	10 (91%)	1 (9%)	9	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	11/13 (85%)	7 (64%)	4 (36%)	0	0
2	N	11/13 (85%)	10 (91%)	1 (9%)	9	27
2	O	11/13 (85%)	9 (82%)	2 (18%)	1	5
2	P	11/13 (85%)	8 (73%)	3 (27%)	0	1
2	Q	11/13 (85%)	10 (91%)	1 (9%)	9	27
2	T	11/13 (85%)	9 (82%)	2 (18%)	1	5
2	U	11/13 (85%)	10 (91%)	1 (9%)	9	27
All	All	1422/1602 (89%)	1316 (92%)	106 (8%)	13	37

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	98	THR
1	G	158	VAL
2	P	220	LYS
1	F	118	ARG
1	G	26	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	8	GLN
1	G	9	GLN
1	F	9	GLN
1	F	73	GLN
1	G	34	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 13 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	39W	G	301	-	54,59,59	2.03	9 (16%)	70,91,91	2.56	21 (30%)
3	39W	J	301	-	54,59,59	2.12	9 (16%)	70,91,91	2.23	19 (27%)
3	39W	A	301	-	54,59,59	2.17	8 (14%)	70,91,91	2.52	16 (22%)
3	39W	D	301	-	54,59,59	2.21	7 (12%)	70,91,91	2.81	23 (32%)
3	39W	F	301	-	54,59,59	2.11	8 (14%)	70,91,91	2.35	19 (27%)
3	39W	H	301	-	54,59,59	2.14	8 (14%)	70,91,91	2.53	19 (27%)
3	39W	C	301	-	54,59,59	2.01	9 (16%)	70,91,91	2.57	18 (25%)
3	39W	B	301	-	54,59,59	2.18	8 (14%)	70,91,91	2.54	20 (28%)
3	39W	E	301	-	54,59,59	2.05	9 (16%)	70,91,91	2.32	20 (28%)

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	39W	G	301	-	-	12/48/84/84	0/6/7/7
3	39W	J	301	-	-	12/48/84/84	0/6/7/7
3	39W	A	301	-	-	12/48/84/84	0/6/7/7
3	39W	D	301	-	-	13/48/84/84	0/6/7/7
3	39W	F	301	-	-	10/48/84/84	0/6/7/7
3	39W	H	301	-	-	11/48/84/84	0/6/7/7
3	39W	C	301	-	-	13/48/84/84	0/6/7/7

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	39W	B	301	-	-	11/48/84/84	0/6/7/7
3	39W	E	301	-	-	11/48/84/84	0/6/7/7

The worst 5 of 75 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	39W	C15-S17	-10.88	1.58	1.73
3	D	301	39W	C15-S17	-10.67	1.58	1.73
3	A	301	39W	C15-S17	-10.50	1.59	1.73
3	F	301	39W	C15-S17	-10.17	1.59	1.73
3	H	301	39W	C15-S17	-10.08	1.59	1.73

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	301	39W	O11-C3-C1	13.45	125.83	116.27
3	B	301	39W	O11-C3-C1	11.69	124.58	116.27
3	G	301	39W	O11-C3-C1	10.95	124.05	116.27
3	C	301	39W	O11-C3-C1	10.63	123.82	116.27
3	A	301	39W	O11-C3-C1	10.04	123.41	116.27

There are no chirality outliers.

5 of 105 torsion outliers are listed below:

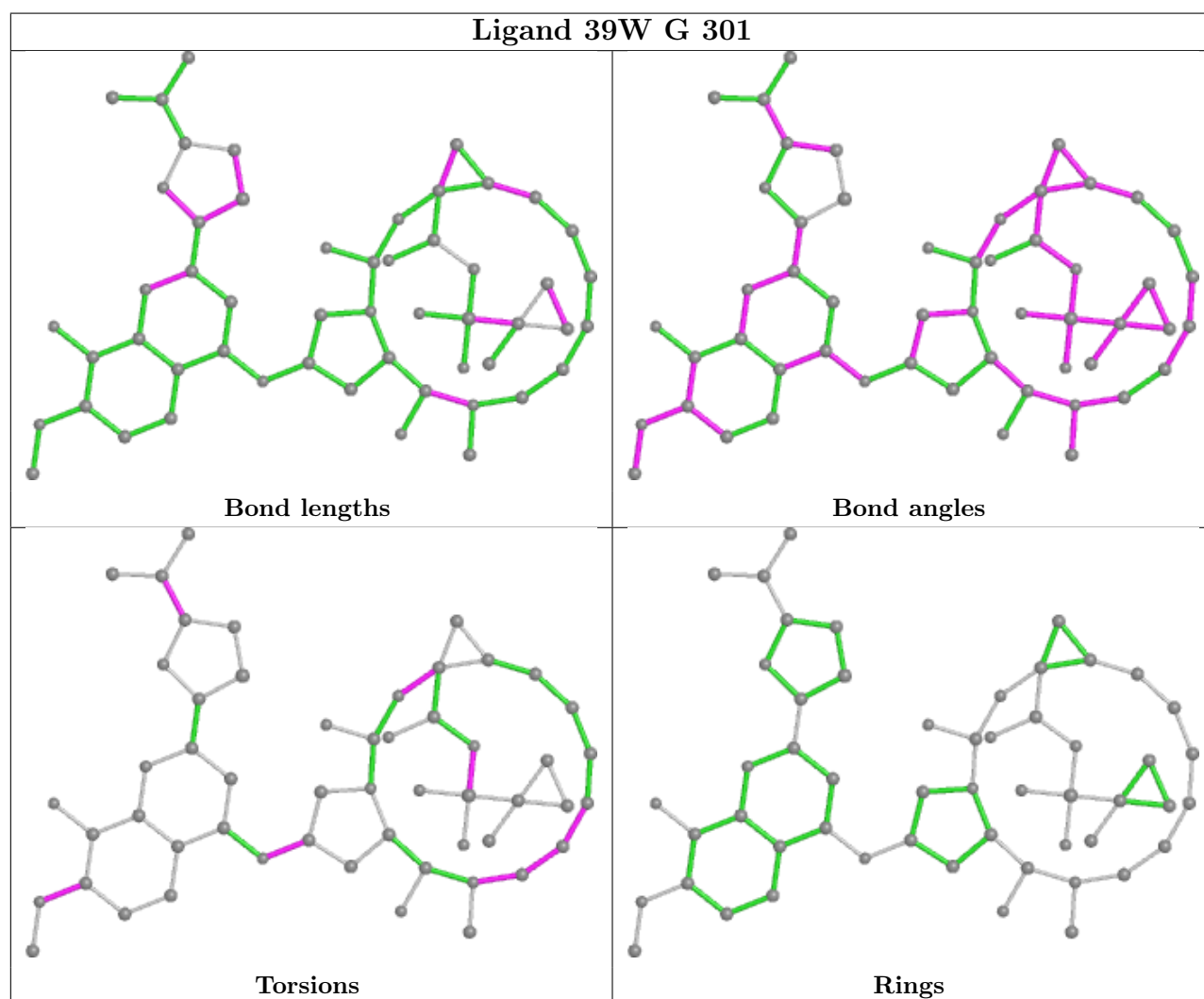
Mol	Chain	Res	Type	Atoms
3	A	301	39W	C1-C3-O11-C12
3	A	301	39W	C24-C23-O14-C10
3	A	301	39W	C44-N45-S47-C48
3	B	301	39W	C1-C3-O11-C12
3	B	301	39W	C24-C23-O14-C10

There are no ring outliers.

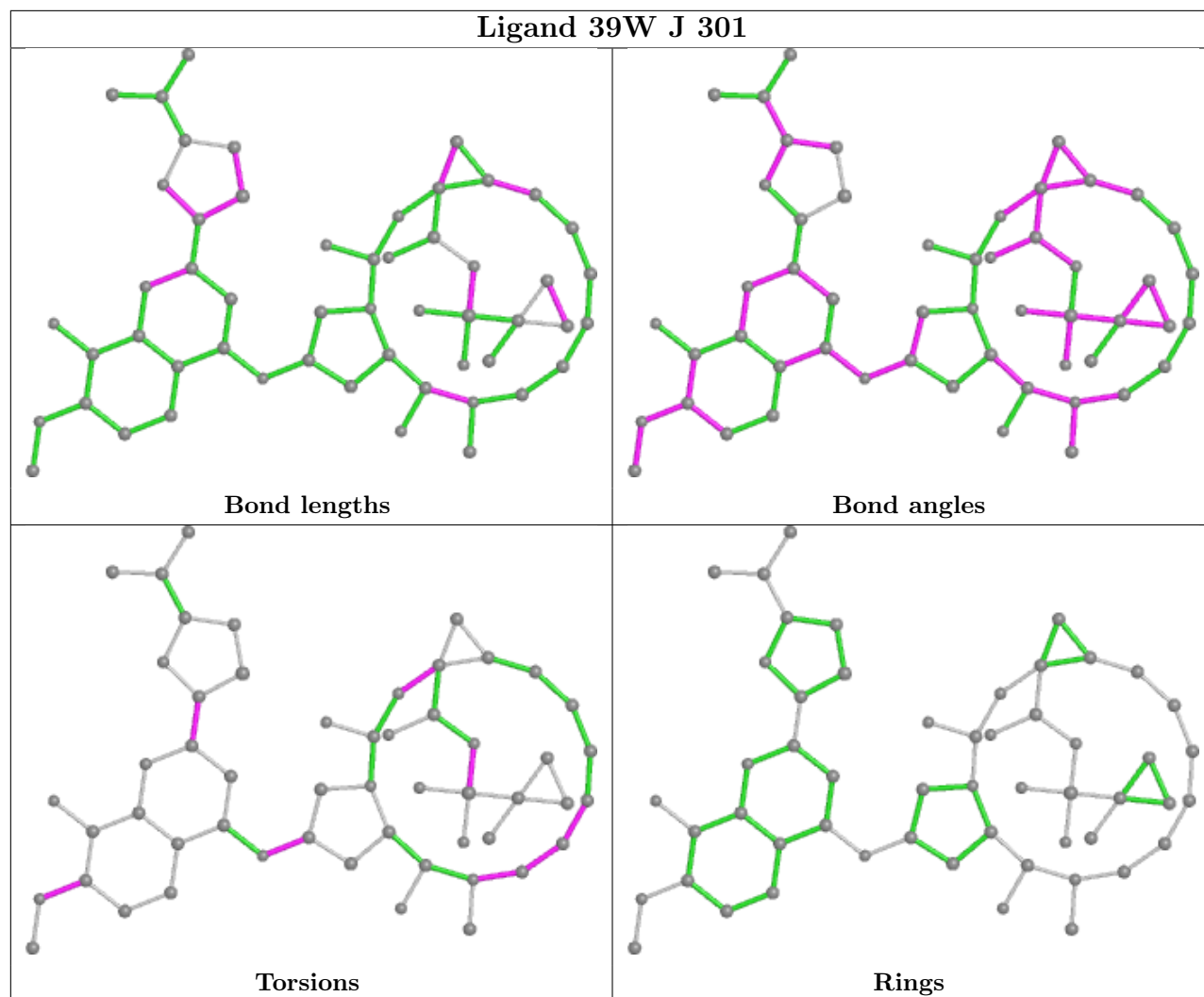
6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	39W	4	0
3	D	301	39W	6	0
3	F	301	39W	1	0
3	H	301	39W	3	0
3	C	301	39W	2	0
3	E	301	39W	3	0

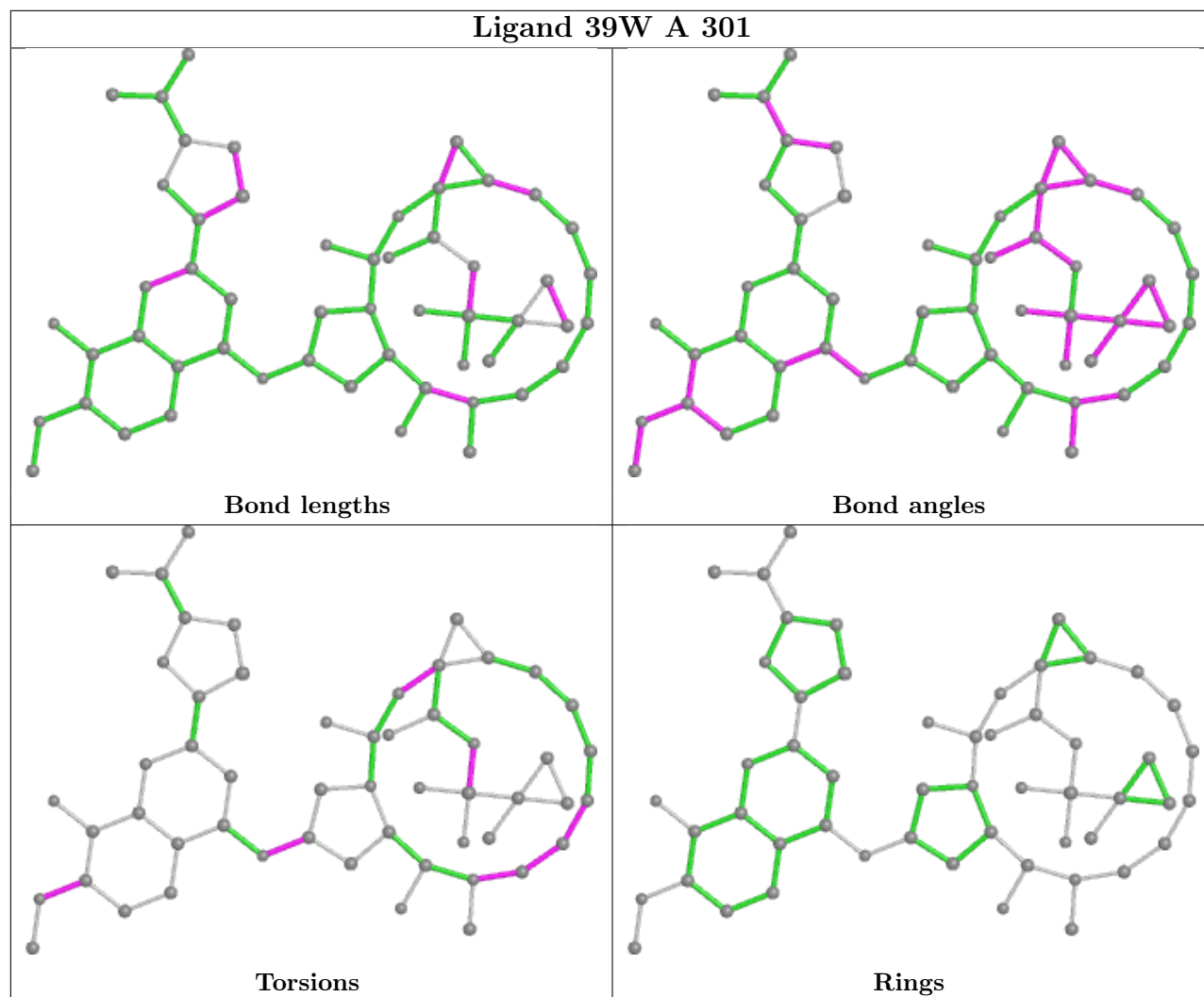
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



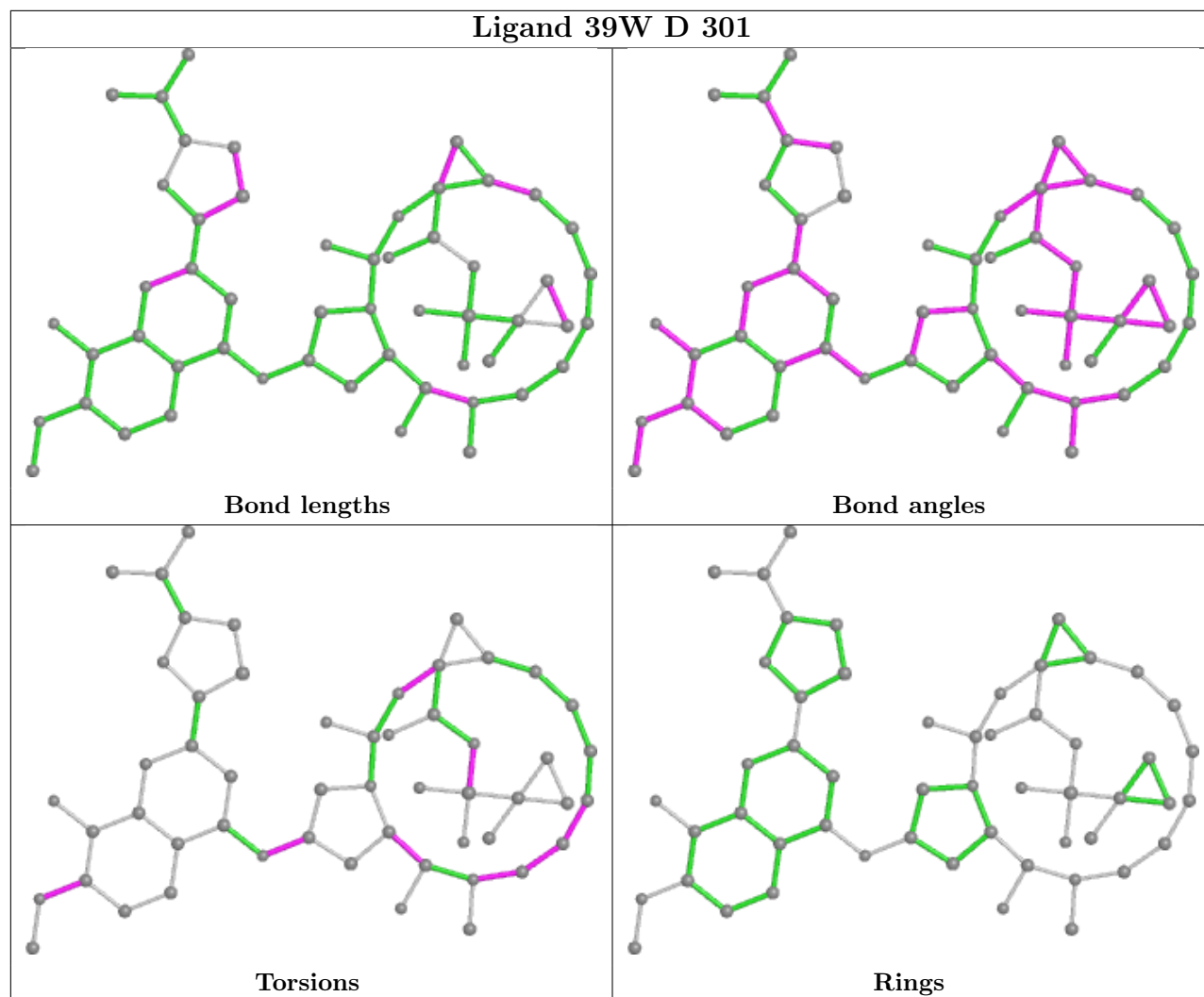
Ligand 39W J 301



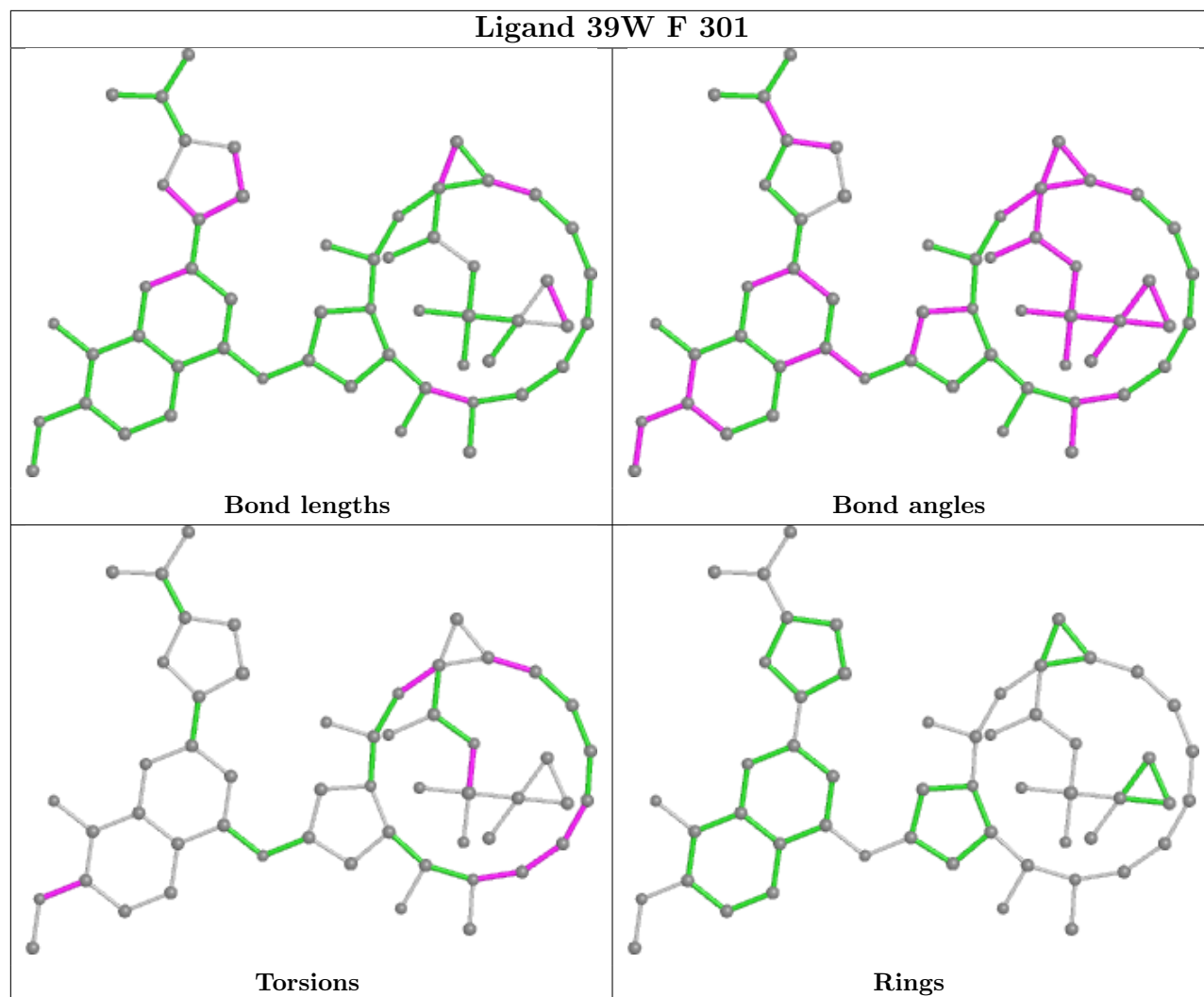
Ligand 39W A 301



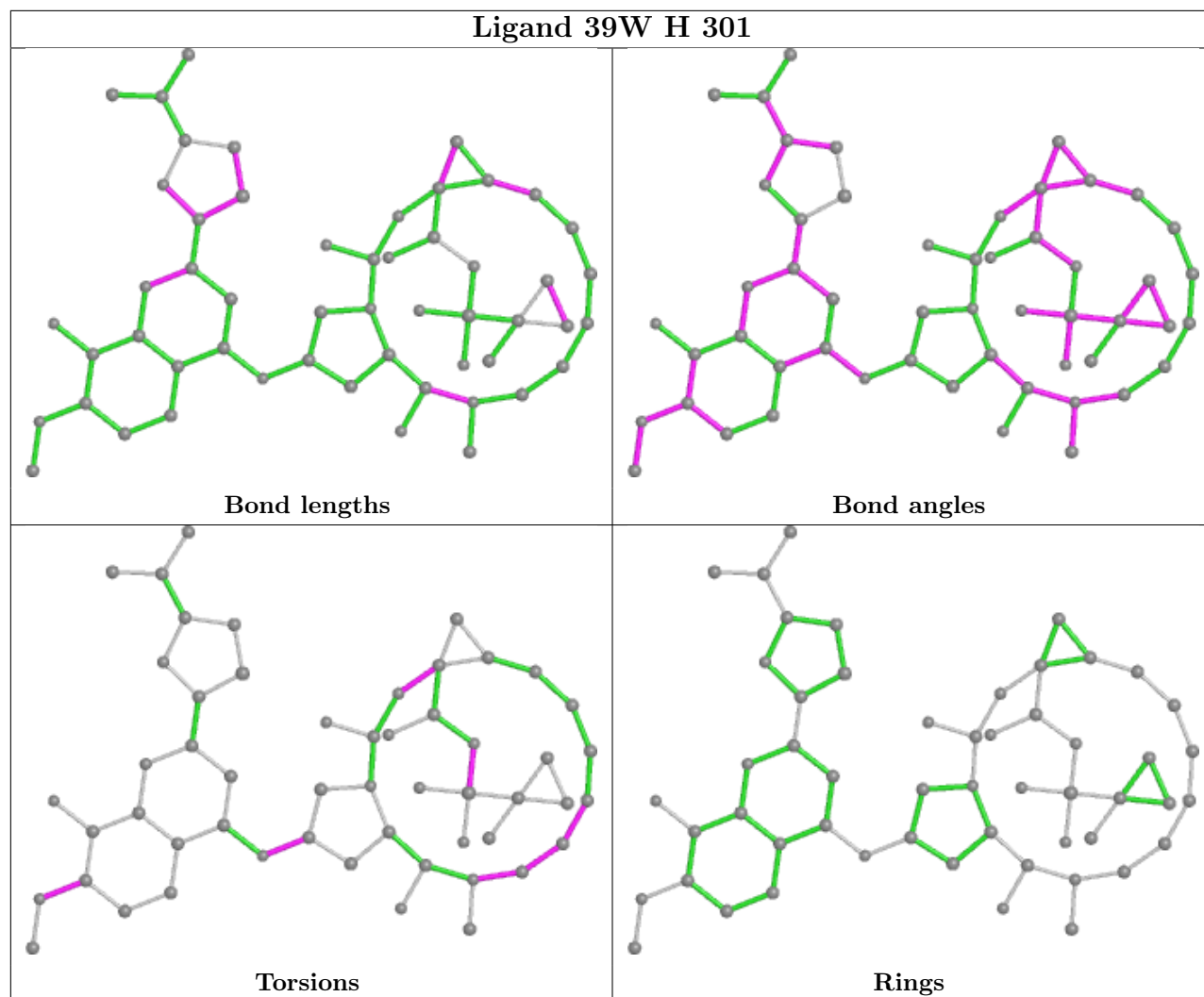
Ligand 39W D 301



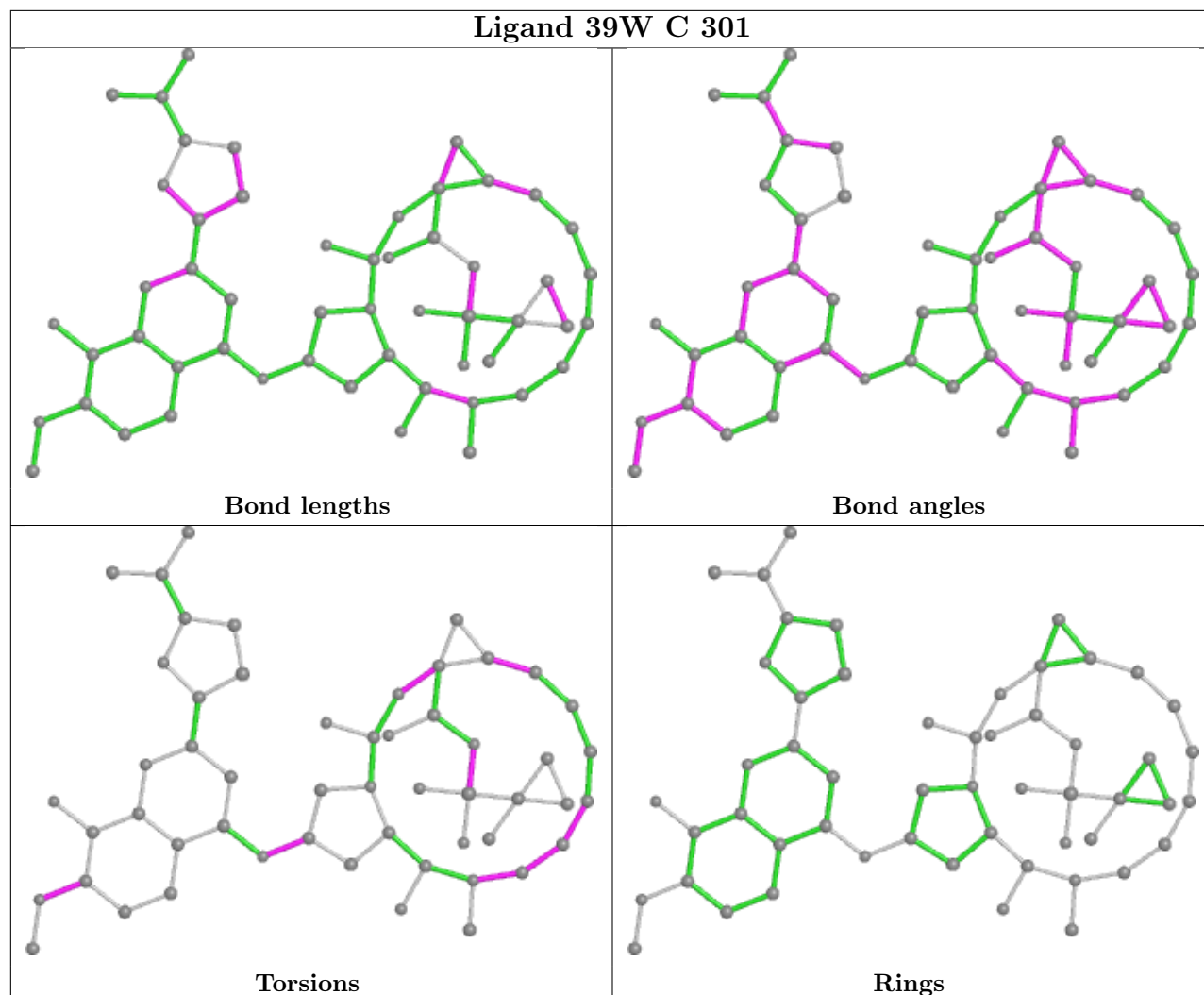
Ligand 39W F 301



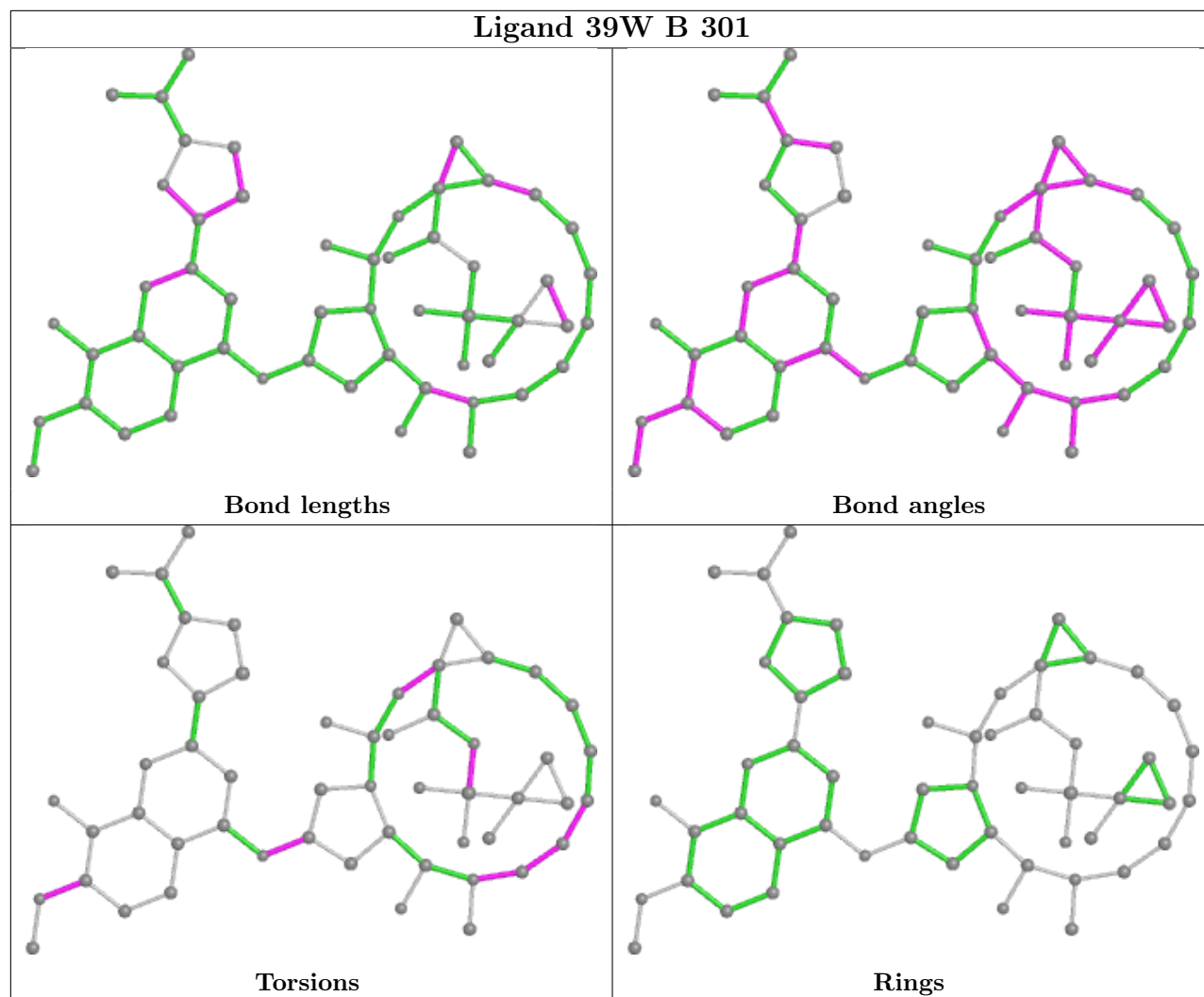
Ligand 39W H 301

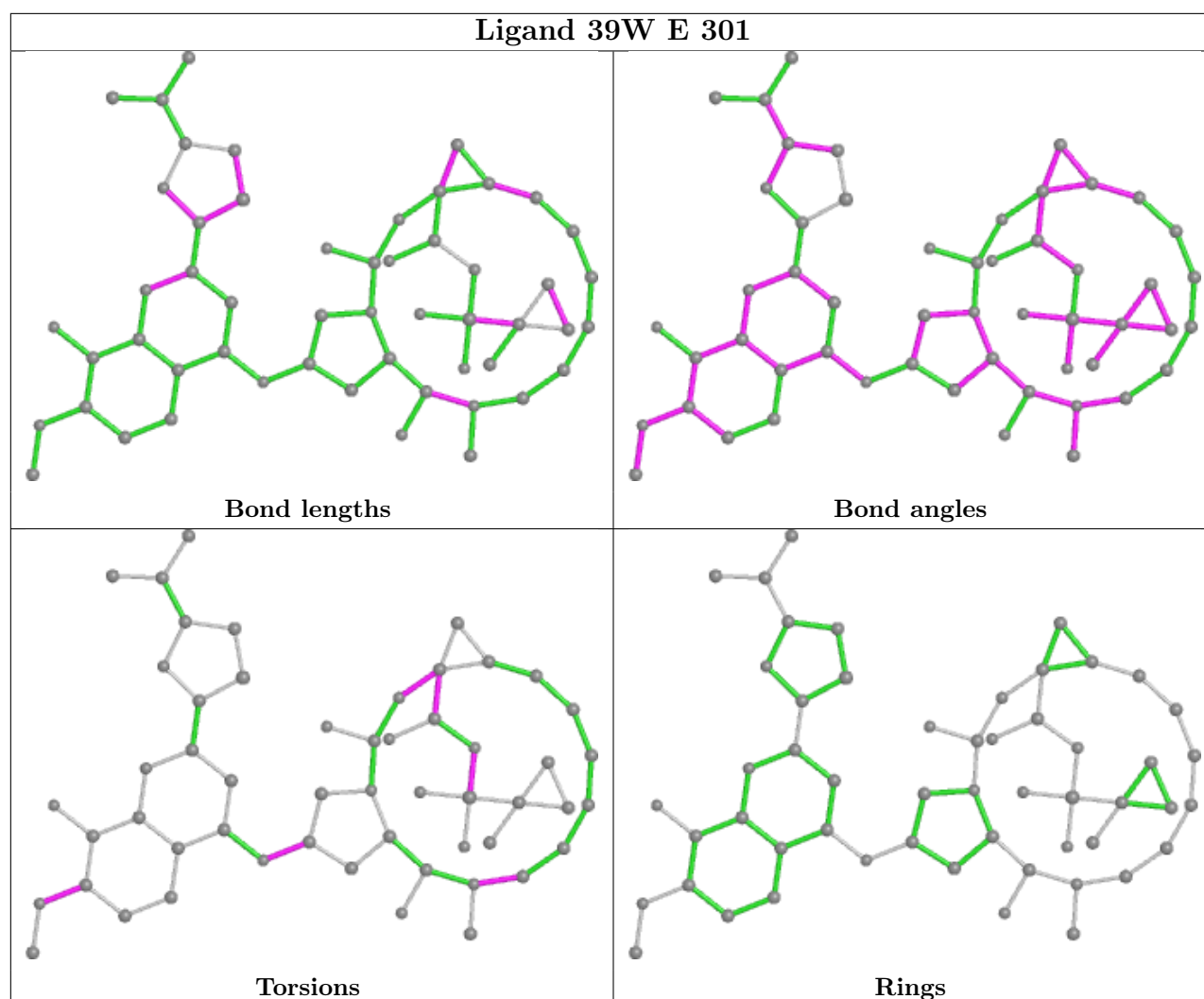


Ligand 39W C 301



Ligand 39W B 301





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	182/203 (89%)	0.13	3 (1%) 72 66	40, 63, 100, 127	1 (0%)
1	B	182/203 (89%)	0.42	17 (9%) 8 4	52, 89, 137, 173	0
1	C	182/203 (89%)	0.33	6 (3%) 46 36	51, 88, 123, 176	0
1	D	182/203 (89%)	0.16	6 (3%) 46 36	42, 76, 110, 155	1 (0%)
1	E	182/203 (89%)	0.21	8 (4%) 34 24	52, 81, 125, 147	0
1	F	182/203 (89%)	0.32	6 (3%) 46 36	47, 85, 125, 167	0
1	G	182/203 (89%)	0.16	6 (3%) 46 36	51, 84, 131, 173	0
1	H	182/203 (89%)	0.80	26 (14%) 2 1	70, 106, 146, 187	0
1	J	182/203 (89%)	1.91	74 (40%) 0 0	69, 143, 185, 215	0
2	K	13/16 (81%)	-0.01	0 100 100	45, 59, 79, 95	0
2	L	13/16 (81%)	0.34	0 100 100	50, 68, 99, 118	0
2	M	13/16 (81%)	0.17	0 100 100	57, 64, 104, 126	0
2	N	13/16 (81%)	0.30	1 (7%) 13 7	51, 61, 93, 103	0
2	O	13/16 (81%)	0.27	1 (7%) 13 7	57, 69, 98, 112	0
2	P	13/16 (81%)	0.81	1 (7%) 13 7	78, 95, 115, 118	0
2	Q	13/16 (81%)	0.54	2 (15%) 2 1	57, 67, 98, 121	0
2	T	13/16 (81%)	1.44	3 (23%) 0 0	98, 112, 139, 158	0
2	U	13/16 (81%)	2.41	7 (53%) 0 0	104, 110, 173, 195	0
All	All	1755/1971 (89%)	0.51	167 (9%) 8 4	40, 87, 153, 215	2 (0%)

The worst 5 of 167 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	152	GLY	13.6
1	J	124	GLY	10.9
1	J	113	VAL	10.4

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Mol	Chain	Res	Type	RSRZ
1	A	1	ALA	9.5
2	U	231	LEU	8.2

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CL	D	303	1/1	0.42	0.27	97,97,97,97	0
4	ZN	J	302	1/1	0.67	0.07	314,314,314,314	0
4	ZN	C	302	1/1	0.82	0.16	127,127,127,127	0
5	CL	G	303	1/1	0.82	0.27	81,81,81,81	0
5	CL	B	303	1/1	0.85	0.17	76,76,76,76	0
4	ZN	D	302	1/1	0.86	0.14	87,87,87,87	0
4	ZN	H	302	1/1	0.87	0.14	114,114,114,114	0
4	ZN	B	302	1/1	0.89	0.13	117,117,117,117	0
3	39W	J	301	53/53	0.91	0.20	67,74,77,79	0
5	CL	E	303	1/1	0.92	0.25	91,91,91,91	0
4	ZN	E	302	1/1	0.93	0.10	141,141,141,141	0
3	39W	G	301	53/53	0.95	0.20	57,62,66,70	0
3	39W	B	301	53/53	0.96	0.17	56,62,65,68	0
4	ZN	A	302	1/1	0.96	0.18	89,89,89,89	0
3	39W	E	301	53/53	0.96	0.20	48,63,65,67	0
3	39W	F	301	53/53	0.96	0.20	54,59,64,66	0
3	39W	A	301	53/53	0.96	0.21	47,54,63,64	0
3	39W	H	301	53/53	0.96	0.20	55,62,67,70	0
3	39W	C	301	53/53	0.97	0.18	53,60,63,66	0
4	ZN	F	302	1/1	0.97	0.18	93,93,93,93	0
4	ZN	G	302	1/1	0.97	0.16	115,115,115,115	0

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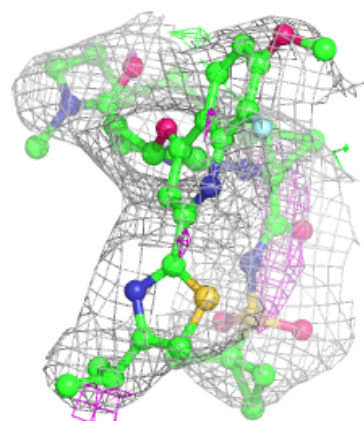
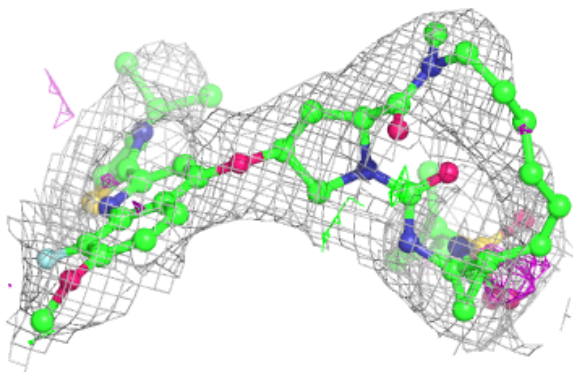
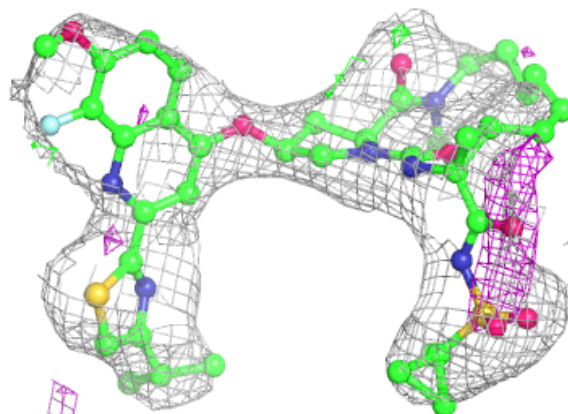
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	39W	D	301	53/53	0.98	0.20	47,55,62,65	0

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.

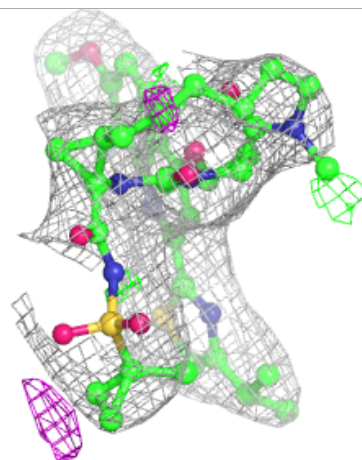
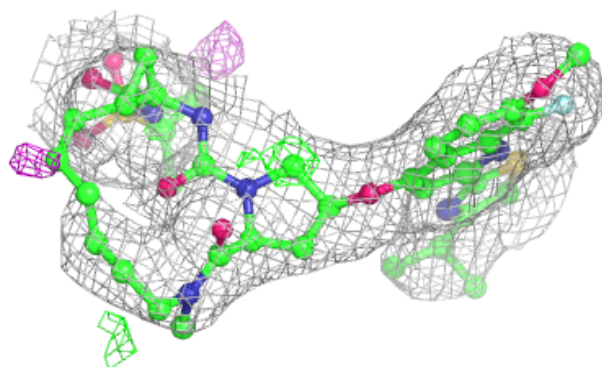
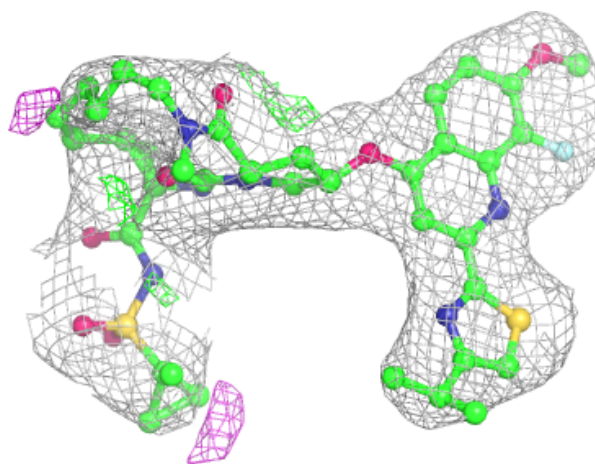
Electron density around 39W J 301:

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



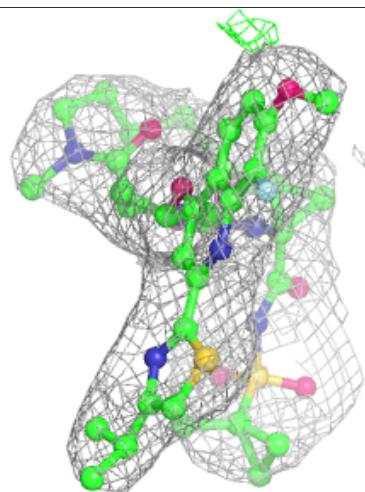
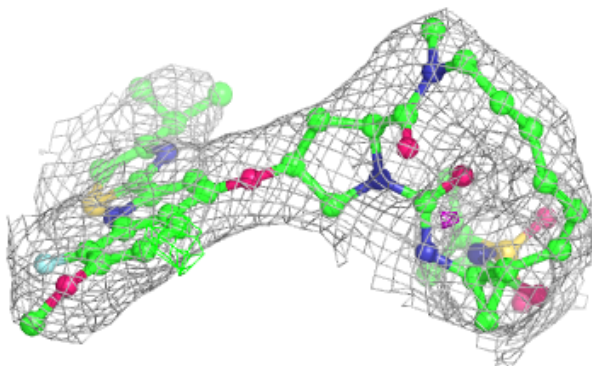
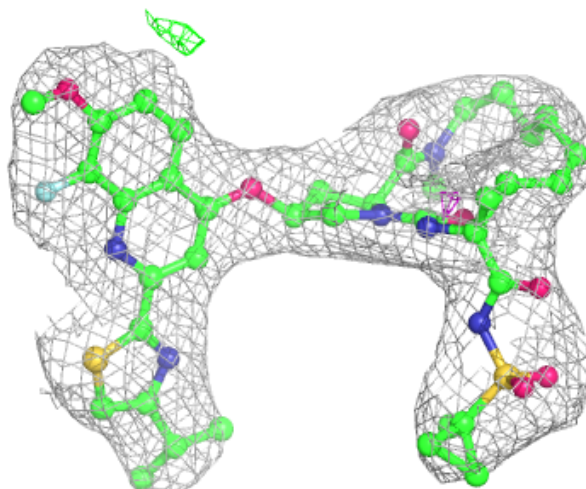
Electron density around 39W G 301:

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



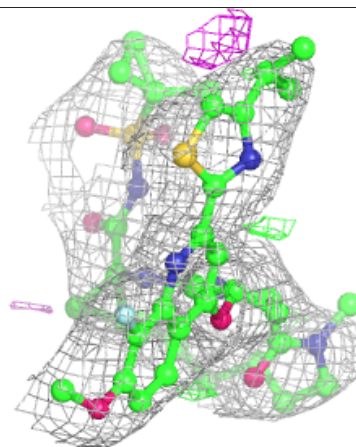
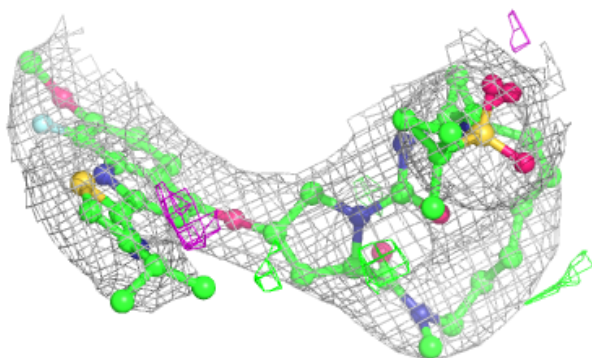
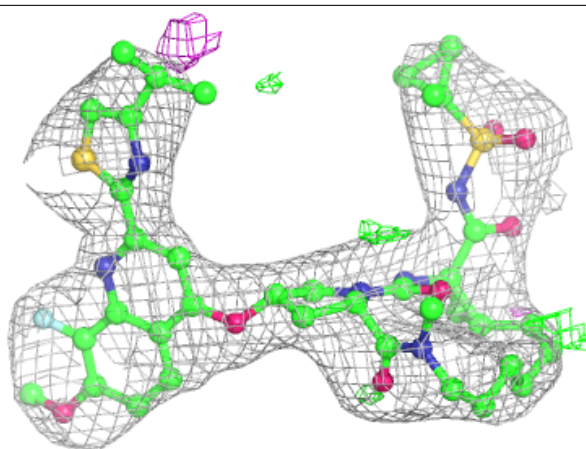
Electron density around 39W B 301:

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



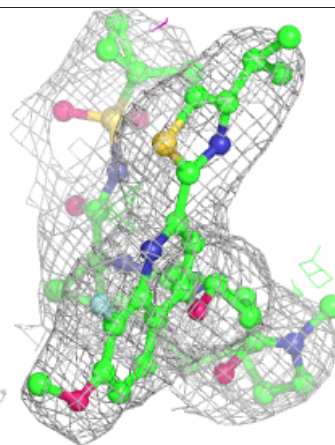
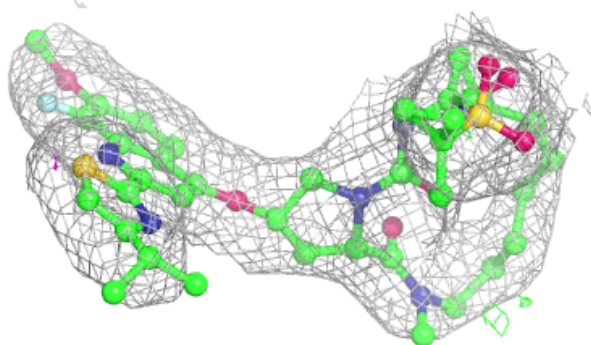
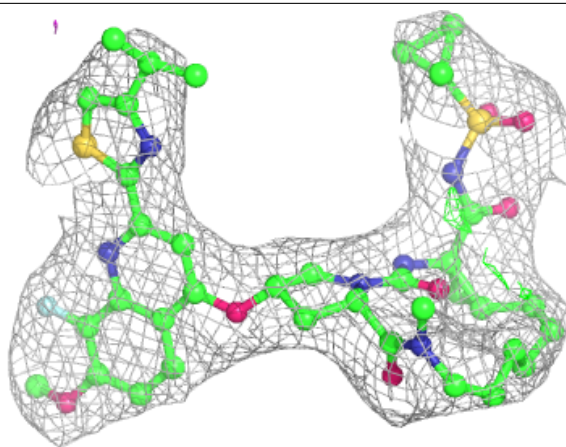
Electron density around 39W E 301:

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

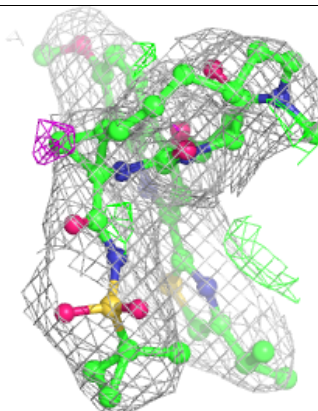
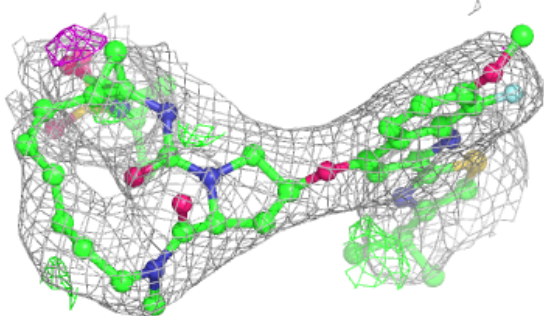
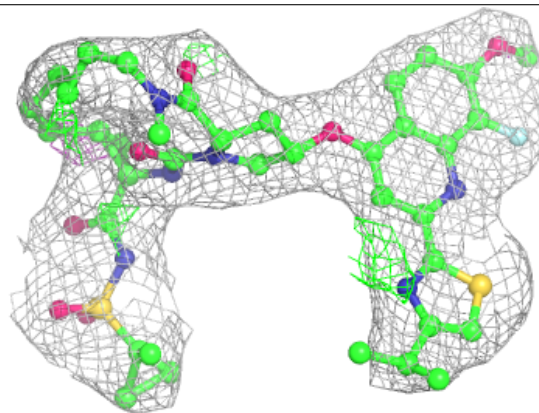


Electron density around 39W F 301:

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

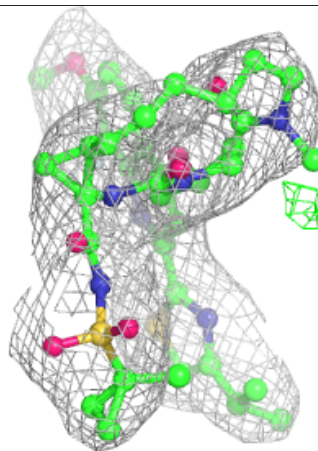
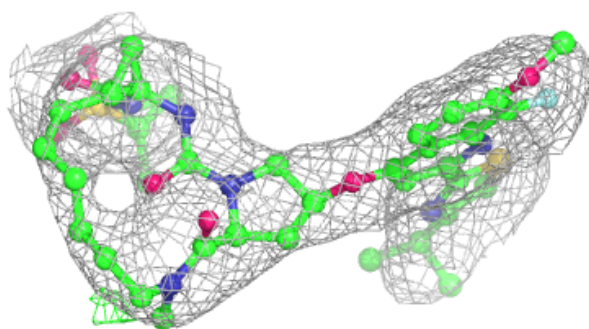
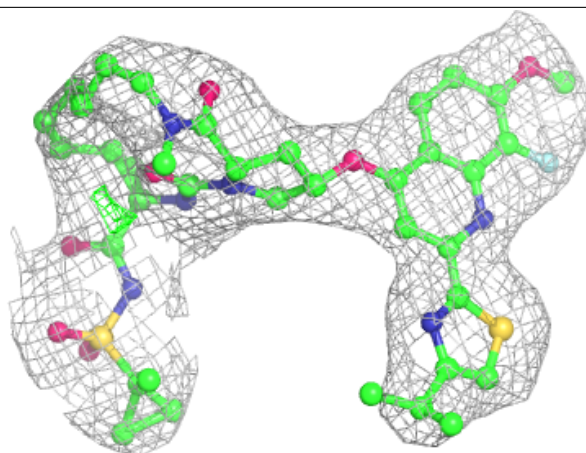
**Electron density around 39W A 301:**

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



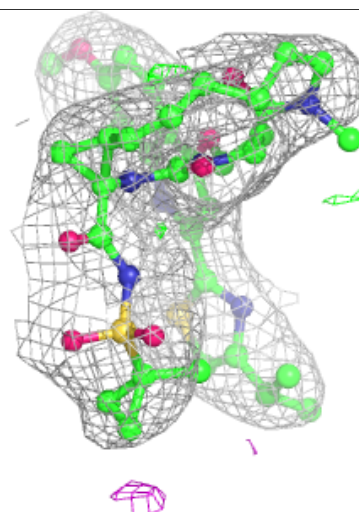
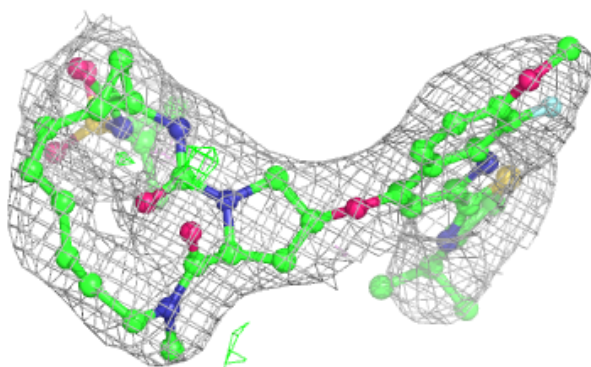
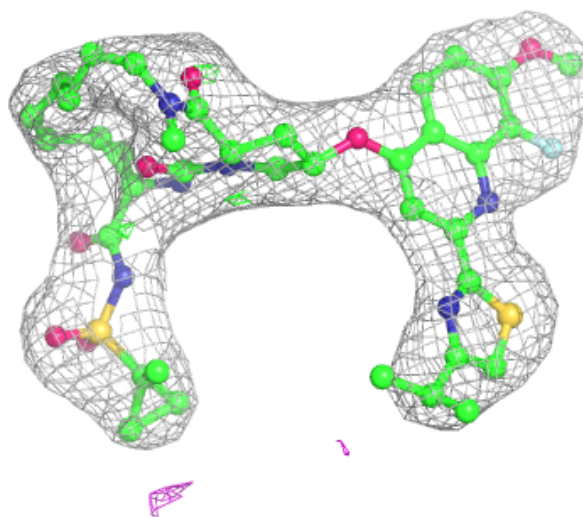
Electron density around 39W H 301:

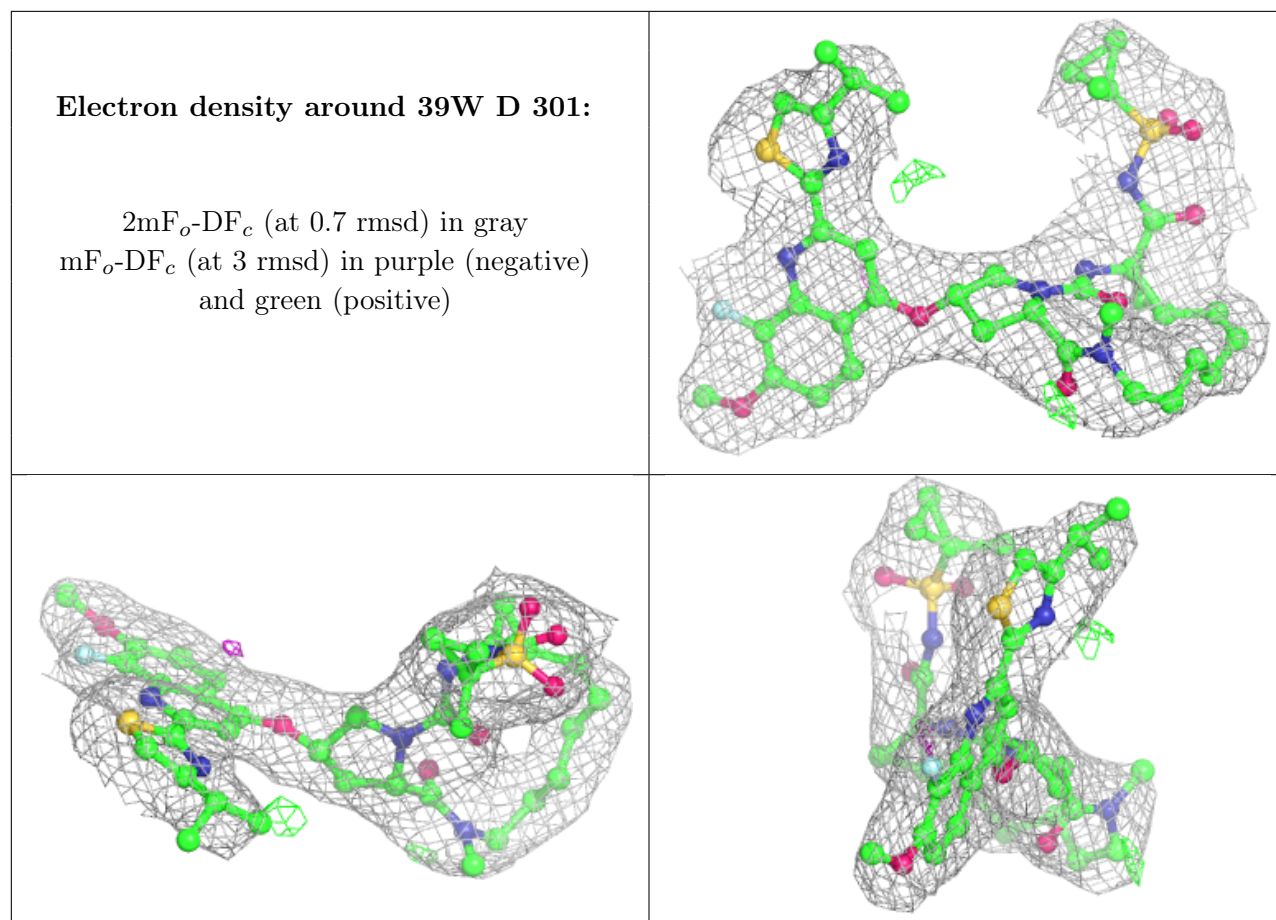
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 39W C 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.