



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 05:43 AM UTC

PDB ID : 4U01 / pdb_00004u01
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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtrriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

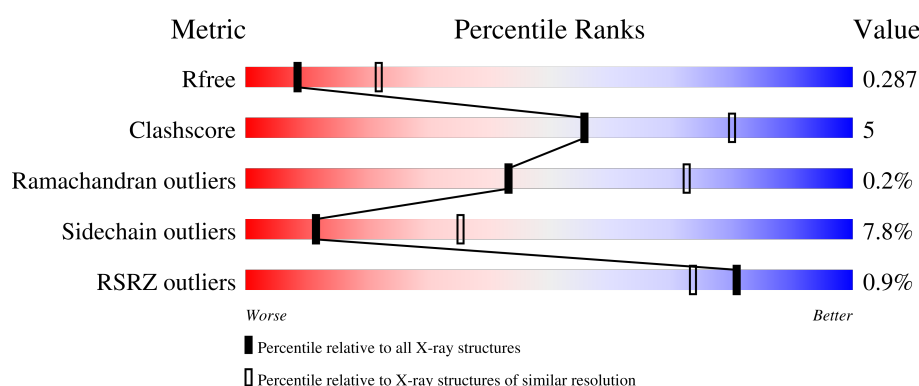
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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.



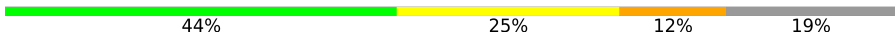
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	74% 15% • 10%
1	B	203	% 74% 14% • 10%
1	C	203	78% 11% • 10%
1	D	203	78% 9% • 10%
1	E	203	80% 8% • 10%

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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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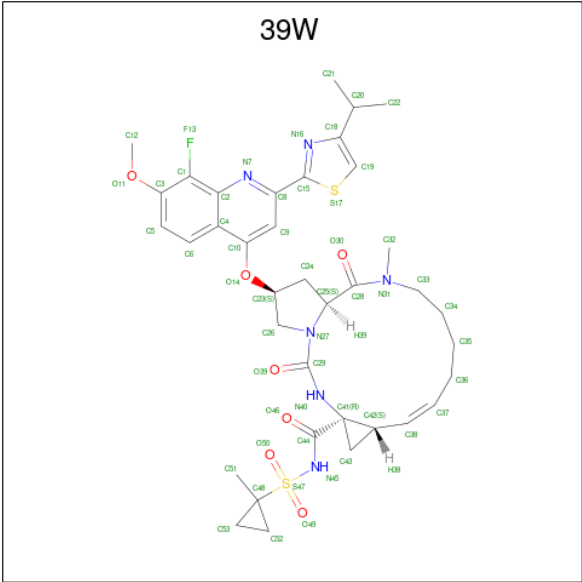
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	L	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	M	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	N	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	O	13	Total	C	N	O	0	0	0
			93	61	17	15			
2	P	13	Total	C	N	O	0	0	0
			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 (CCD ID: 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 (CCD ID: 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 (CCD ID: CL) (formula: Cl).

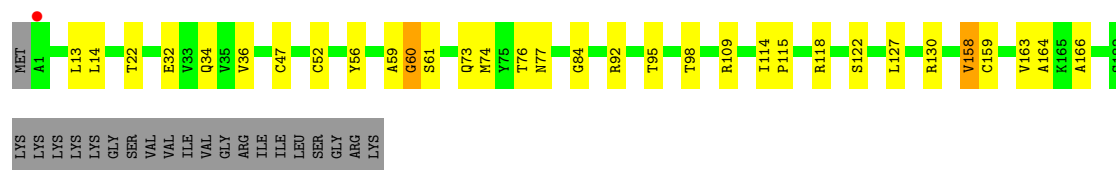
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Cl 1	0	0
5	D	1	Total 1	Cl 1	0	0
5	E	1	Total 1	Cl 1	0	0
5	G	1	Total 1	Cl 1	0	0

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.

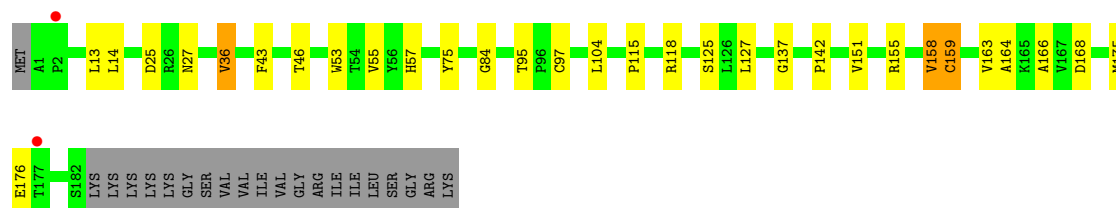
- Molecule 1: Non-structural 3 protease

Chain A: 



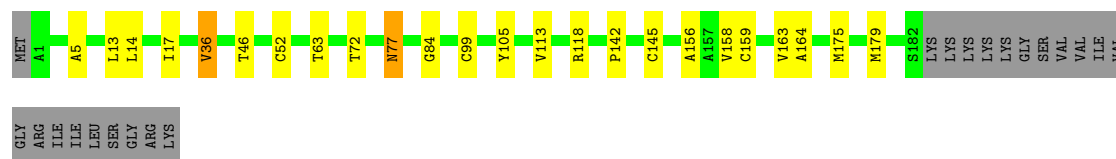
- Molecule 1: Non-structural 3 protease

Chain B: 



- Molecule 1: Non-structural 3 protease

Chain C: 



- Molecule 1: Non-structural 3 protease

Chain D: 



ILE
LEU
SER
GLY
ARG
LYS

- Molecule 1: Non-structural 3 protease

Chain E:  80% 8% 10%

MET A1 P2 L13 L14 N27 V36 T40 H57 T63 T72 Q73 T76 N77 R118 K136 V151 R155 V168 V163 D168 M175 S182 LYS LYS LYS LYS LYS GLY SER VAL ILE VAL ARG ILE ILE LEU SER GLY ARG LYS

- Molecule 1: Non-structural 3 protease

Chain F:  74% 13% 10%

MET A1 P2 L13 L14 E52 V36 S37 T38 A39 T40 F43 C47 V48 C52 T63 T72 Y75 T76 N77 R82 T95 T98 S102 R118 R119 G120 L126 L127 S128 G137 V151 V158 V163 A166 M175 E176 M179 R180 A181 S182 LYS LYS LYS SER VAL ILE VAL GLY ARG ILE ILE LEU SER GLY ARG LYS

- Molecule 1: Non-structural 3 protease

Chain G:  76% 11% 10%

MET A1 L13 I17 R26 N27 V36 V48 W53 H57 Y75 T76 N77 D81 C97 T98 P115 R118 R119 G120 L127 R130 Y134 V158 C159 V163 A164 K165 A166 M175 E176 M179 R180 A181 S182 LYS LYS LYS LYS LYS GLY SER VAL ILE ILE ARG ILE LEU SER GLY ARG LYS

- Molecule 1: Non-structural 3 protease

Chain H:  77% 11% 10%

MET A1 P2 G12 L13 L14 L21 V36 V48 C52 W53 H57 M74 Y75 G84 W85 Q86 T98 R118 R119 G120 C145 H149 V158 C159 V163 A164 K165 A166 V172 M175 M179 S182 LYS LYS LYS LYS LYS GLY VAL VAL ILE ILE ARG ILE LEU SER GLY ARG LYS

- Molecule 1: Non-structural 3 protease

Chain J:  82% 5% 10%

MET A1 L13 L14 N27 V36 T40 C47 C52 N77 L106 F129 A156 A157 V158 C159 T160 R161 V163 G162 A164 K165 A166 V167 E176 S182 LYS LYS LYS LYS LYS GLY SER VAL ILE ILE VAL VAL GLY ARG ILE ILE LEU SER GLY ARG LYS

- Molecule 2: NS4A protein

Chain K:  56% 25% 19%



- Molecule 2: NS4A protein



- Molecule 2: NS4A protein



- Molecule 2: NS4A protein



- Molecule 2: NS4A protein



- Molecule 2: NS4A protein



- Molecule 2: NS4A protein

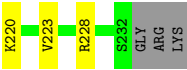


- Molecule 2: NS4A protein





● 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 43.23 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.23-2.80) 96.9 (43.23-2.80)	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 , 73.9	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	0.94	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: CL, ZN, 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	0.64	0/1363	0.83	0/1857
1	B	0.55	0/1363	0.80	1/1857 (0.1%)
1	C	0.56	0/1363	0.81	0/1857
1	D	0.58	0/1363	0.84	1/1857 (0.1%)
1	E	0.57	0/1363	0.79	0/1857
1	F	0.57	0/1363	0.76	0/1857
1	G	0.57	0/1363	0.77	0/1857
1	H	0.53	0/1363	0.75	0/1857
1	J	0.53	0/1363	0.71	0/1857
2	K	0.65	0/92	0.77	0/122
2	L	0.70	0/92	0.75	0/122
2	M	0.62	0/92	0.67	0/122
2	N	0.64	0/92	0.76	0/122
2	O	0.73	0/92	0.75	0/122
2	P	0.53	0/92	0.62	0/122
2	Q	0.66	0/92	0.72	0/122
2	T	0.56	0/92	0.73	0/122
2	U	0.54	0/92	0.68	0/122
All	All	0.57	0/13095	0.78	2/17811 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	37	SER	N-CA-C	5.58	117.58	108.76
1	B	159	CYS	N-CA-C	5.20	115.40	108.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1337	0	1344	15	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	16	0
1	G	1337	0	1346	17	0
1	H	1337	0	1344	14	0
1	J	1337	0	1344	8	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	3	0
2	U	93	0	112	3	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	127	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 5.

The worst 5 of 127 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
2:T:220:LYS:HZ1	2:U:220:LYS:HG2	1.56	0.70
1:H:159:CYS:HB3	1:H: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%)	21	51
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%)	21	51
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	180/203 (89%)	170 (94%)	10 (6%)	0	100	100
1	J	180/203 (89%)	173 (96%)	6 (3%)	1 (1%)	21	51
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
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%)	43	72

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%)	10	33
1	B	147/165 (89%)	138 (94%)	9 (6%)	17	46
1	C	147/165 (89%)	139 (95%)	8 (5%)	20	51
1	D	147/165 (89%)	133 (90%)	14 (10%)	8	26
1	E	147/165 (89%)	138 (94%)	9 (6%)	17	46
1	F	147/165 (89%)	133 (90%)	14 (10%)	8	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	147/165 (89%)	138 (94%)	9 (6%)	17	46
1	H	147/165 (89%)	141 (96%)	6 (4%)	27	62
1	J	147/165 (89%)	137 (93%)	10 (7%)	14	42
2	K	11/13 (85%)	9 (82%)	2 (18%)	2	6
2	L	11/13 (85%)	9 (82%)	2 (18%)	2	6
2	M	11/13 (85%)	6 (54%)	5 (46%)	0	0
2	N	11/13 (85%)	10 (91%)	1 (9%)	9	28
2	O	11/13 (85%)	9 (82%)	2 (18%)	2	6
2	P	11/13 (85%)	8 (73%)	3 (27%)	0	1
2	Q	11/13 (85%)	9 (82%)	2 (18%)	2	6
2	T	11/13 (85%)	9 (82%)	2 (18%)	2	6
2	U	11/13 (85%)	10 (91%)	1 (9%)	9	28
All	All	1422/1602 (89%)	1311 (92%)	111 (8%)	11	35

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	98	THR
2	U	228	ARG
1	G	118	ARG
2	T	232	SER
2	M	232	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	8	GLN
1	G	77	ASN
1	F	9	GLN
1	G	8	GLN
1	H	28	GLN

5.3.3 RNA ⓘ

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](#)

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	A	301	-	56,59,59	1.69	7 (12%)	74,91,91	3.02	19 (25%)
3	39W	E	301	-	56,59,59	1.60	6 (10%)	74,91,91	2.74	25 (33%)
3	39W	G	301	-	56,59,59	1.61	8 (14%)	74,91,91	2.95	22 (29%)
3	39W	F	301	-	56,59,59	1.64	7 (12%)	74,91,91	2.84	21 (28%)
3	39W	D	301	-	56,59,59	1.74	7 (12%)	74,91,91	3.36	26 (35%)
3	39W	H	301	-	56,59,59	1.67	8 (14%)	74,91,91	2.97	22 (29%)
3	39W	J	301	-	56,59,59	1.65	8 (14%)	74,91,91	2.71	21 (28%)
3	39W	B	301	-	56,59,59	1.70	7 (12%)	74,91,91	3.00	25 (33%)
3	39W	C	301	-	56,59,59	1.57	7 (12%)	74,91,91	3.04	20 (27%)

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	A	301	-	-	15/51/84/84	0/6/7/7
3	39W	E	301	-	-	15/51/84/84	0/6/7/7
3	39W	G	301	-	-	14/51/84/84	0/6/7/7

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	39W	F	301	-	-	13/51/84/84	0/6/7/7
3	39W	D	301	-	-	16/51/84/84	0/6/7/7
3	39W	H	301	-	-	14/51/84/84	0/6/7/7
3	39W	J	301	-	-	16/51/84/84	0/6/7/7
3	39W	B	301	-	-	15/51/84/84	0/6/7/7
3	39W	C	301	-	-	15/51/84/84	0/6/7/7

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	39W	C15-S17	-7.62	1.58	1.73
3	D	301	39W	C15-S17	-7.47	1.58	1.73
3	A	301	39W	C15-S17	-7.34	1.59	1.73
3	F	301	39W	C15-S17	-7.10	1.59	1.73
3	H	301	39W	C15-S17	-7.04	1.59	1.73

The worst 5 of 201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	301	39W	C19-S17-C15	14.10	98.55	89.51
3	A	301	39W	C19-S17-C15	13.60	98.23	89.51
3	C	301	39W	C19-S17-C15	13.13	97.93	89.51
3	F	301	39W	C19-S17-C15	13.13	97.93	89.51
3	H	301	39W	C19-S17-C15	13.13	97.93	89.51

There are no chirality outliers.

5 of 133 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	C19-C18-C20-C21
3	A	301	39W	N16-C18-C20-C21
3	A	301	39W	N16-C18-C20-C22

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

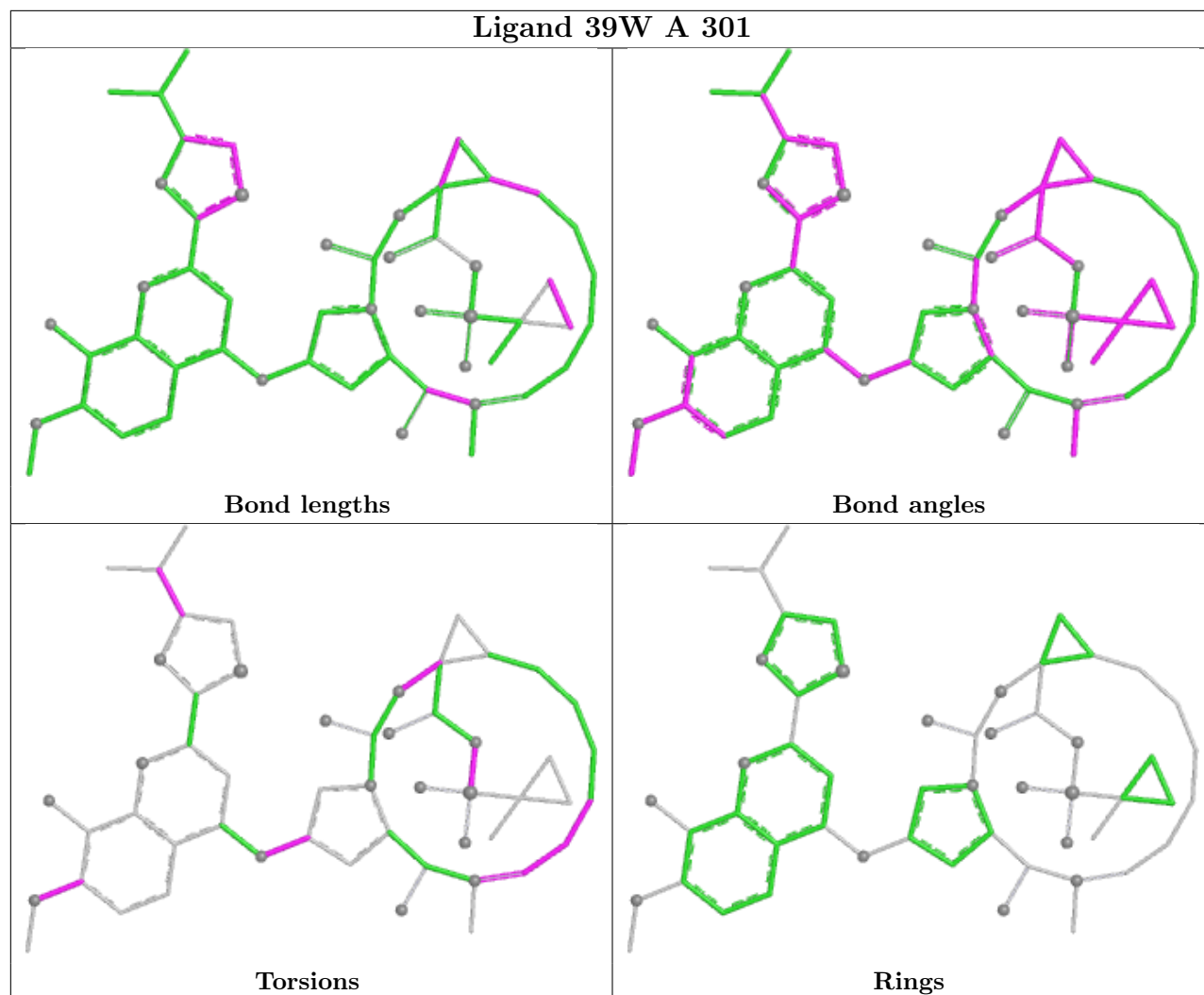
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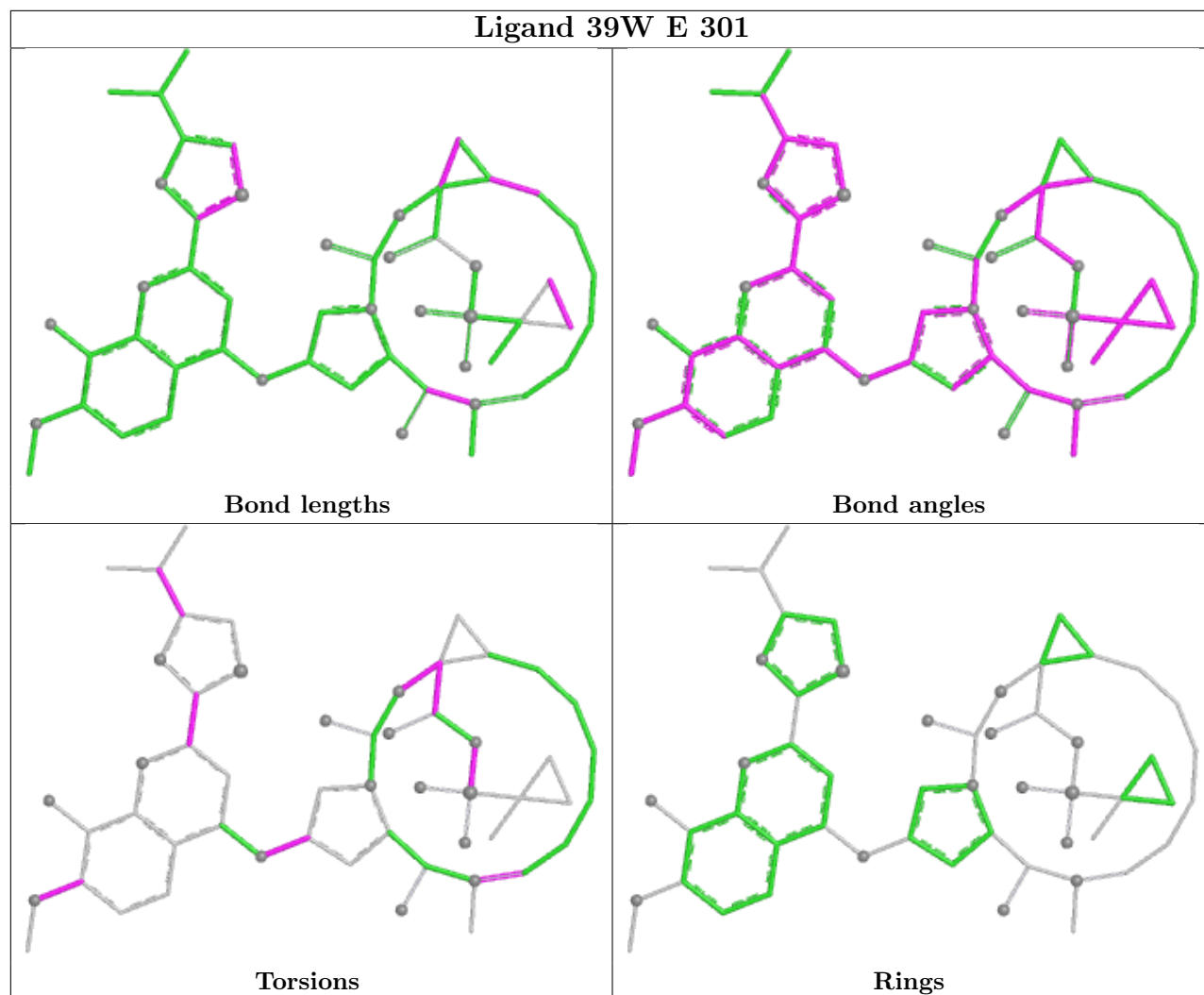
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	301	39W	3	0
3	F	301	39W	1	0
3	D	301	39W	6	0
3	H	301	39W	3	0
3	C	301	39W	2	0

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

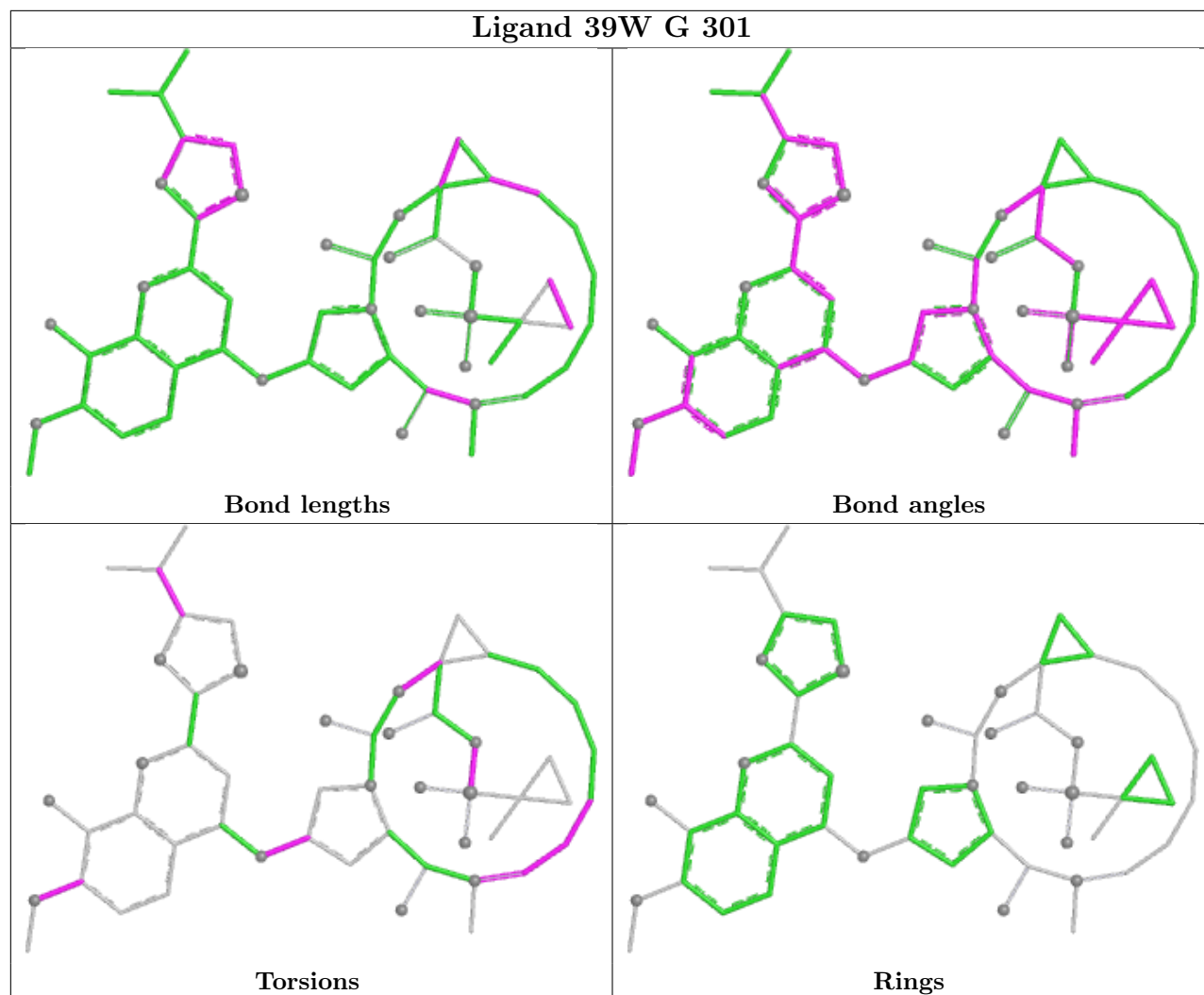
Ligand 39W A 301



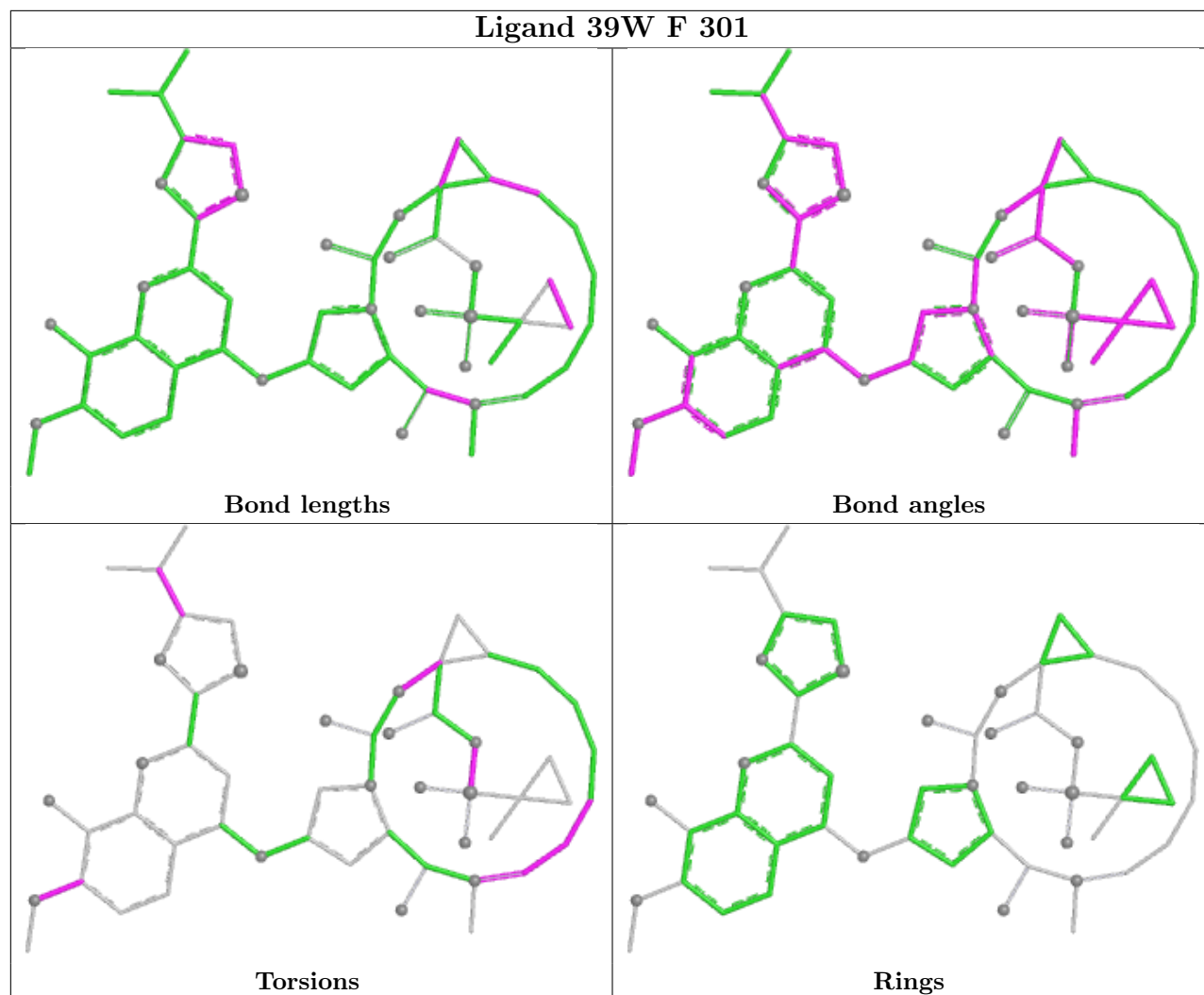
Ligand 39W E 301



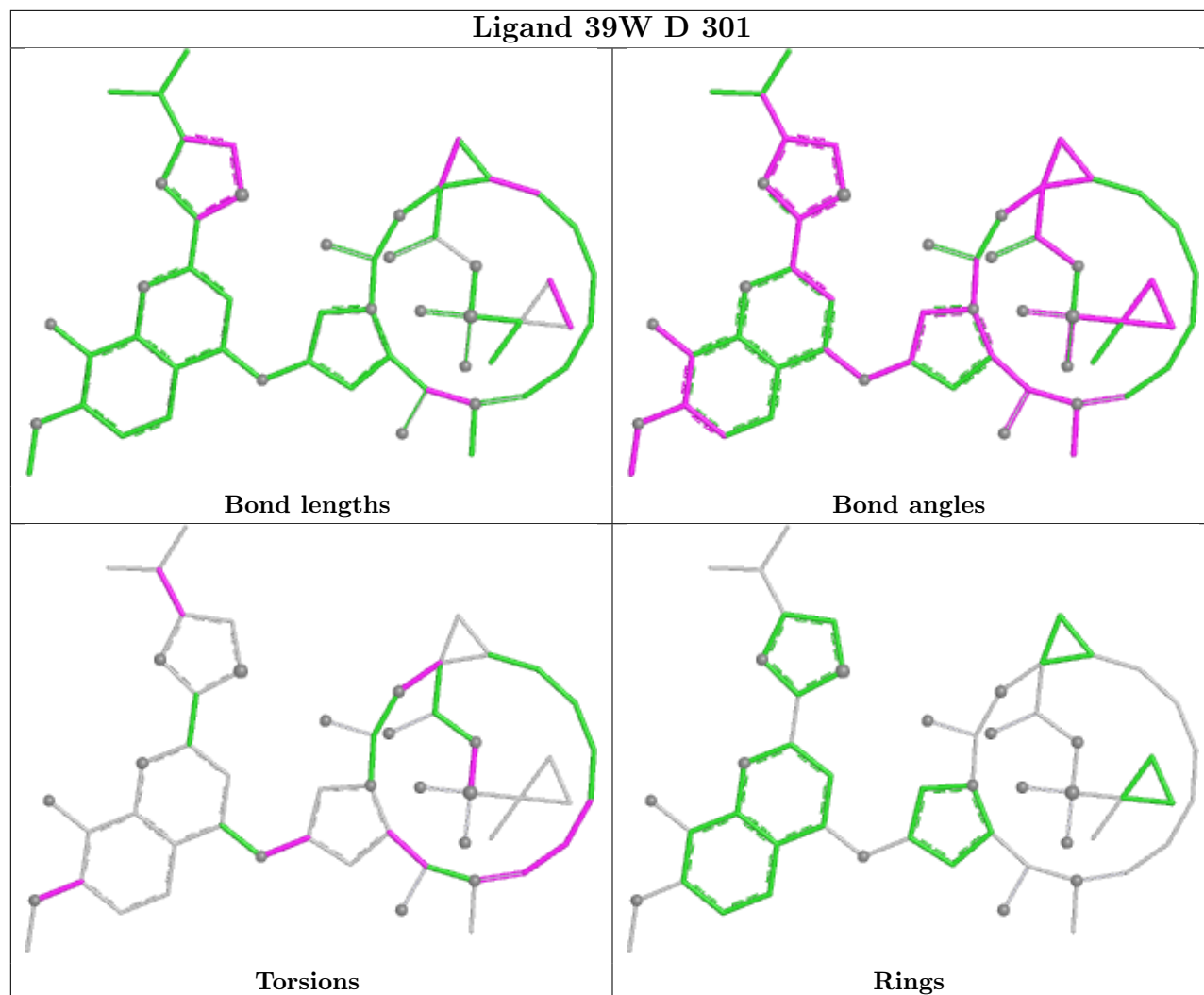
Ligand 39W G 301



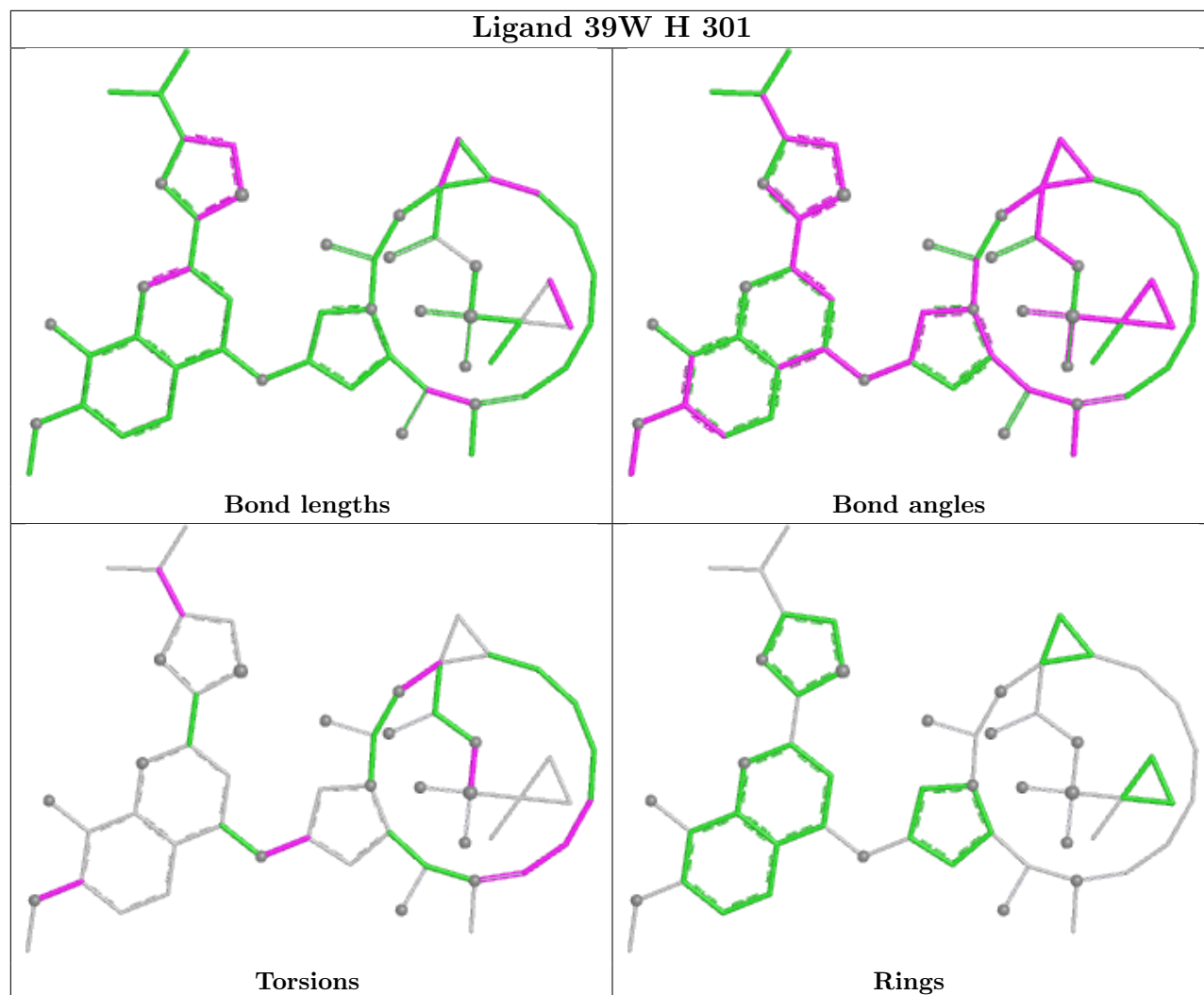
Ligand 39W F 301



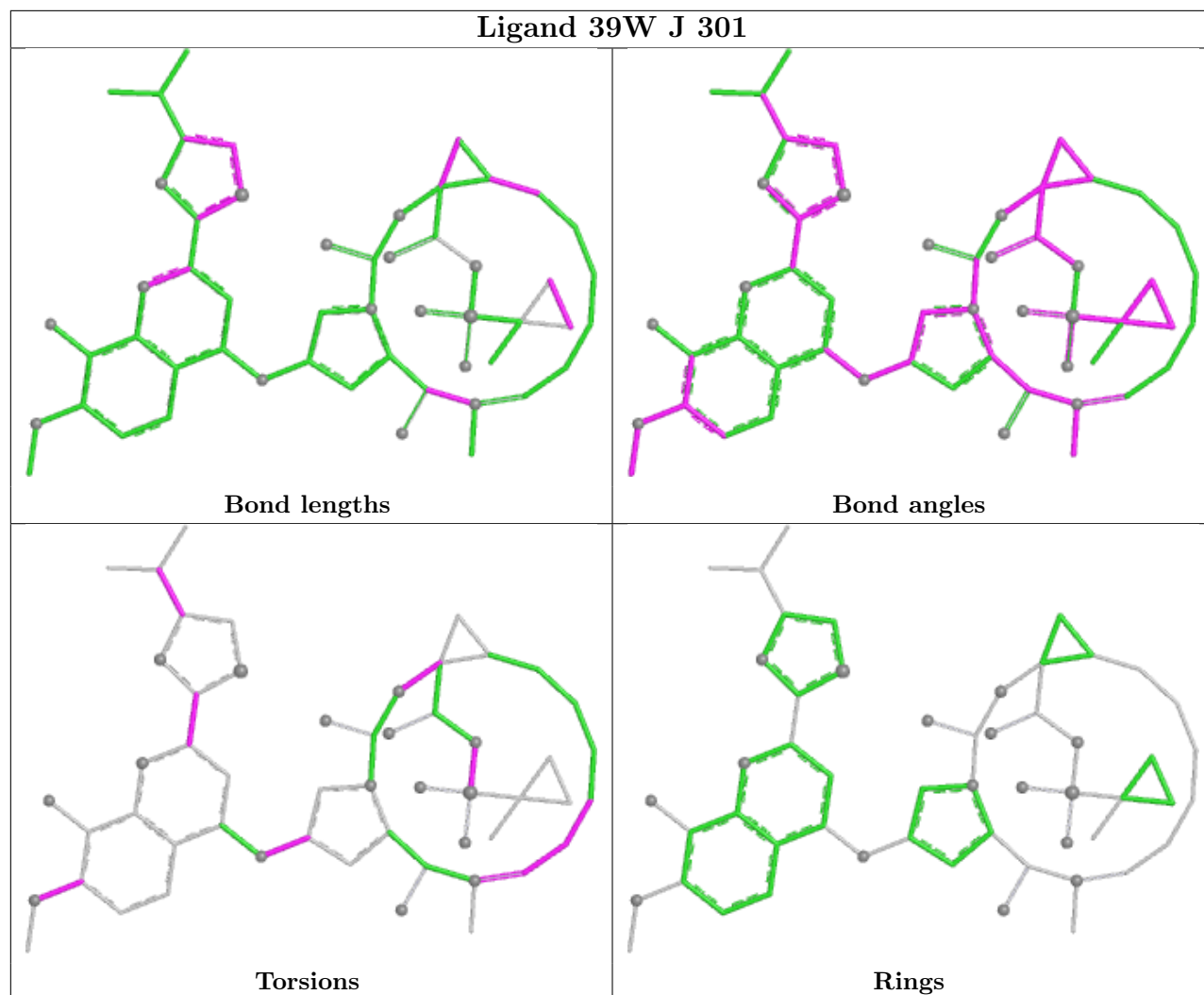
Ligand 39W D 301



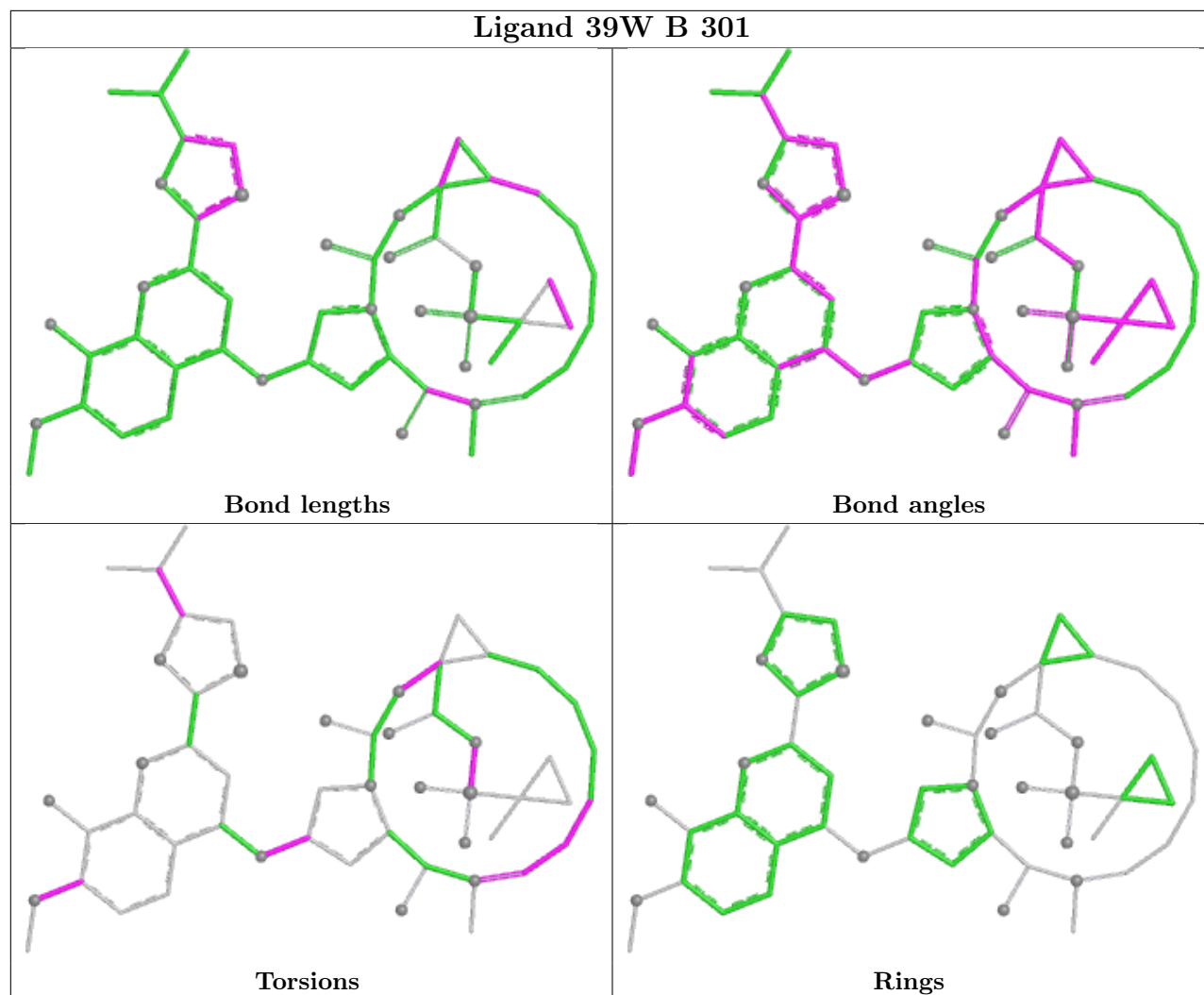
Ligand 39W H 301

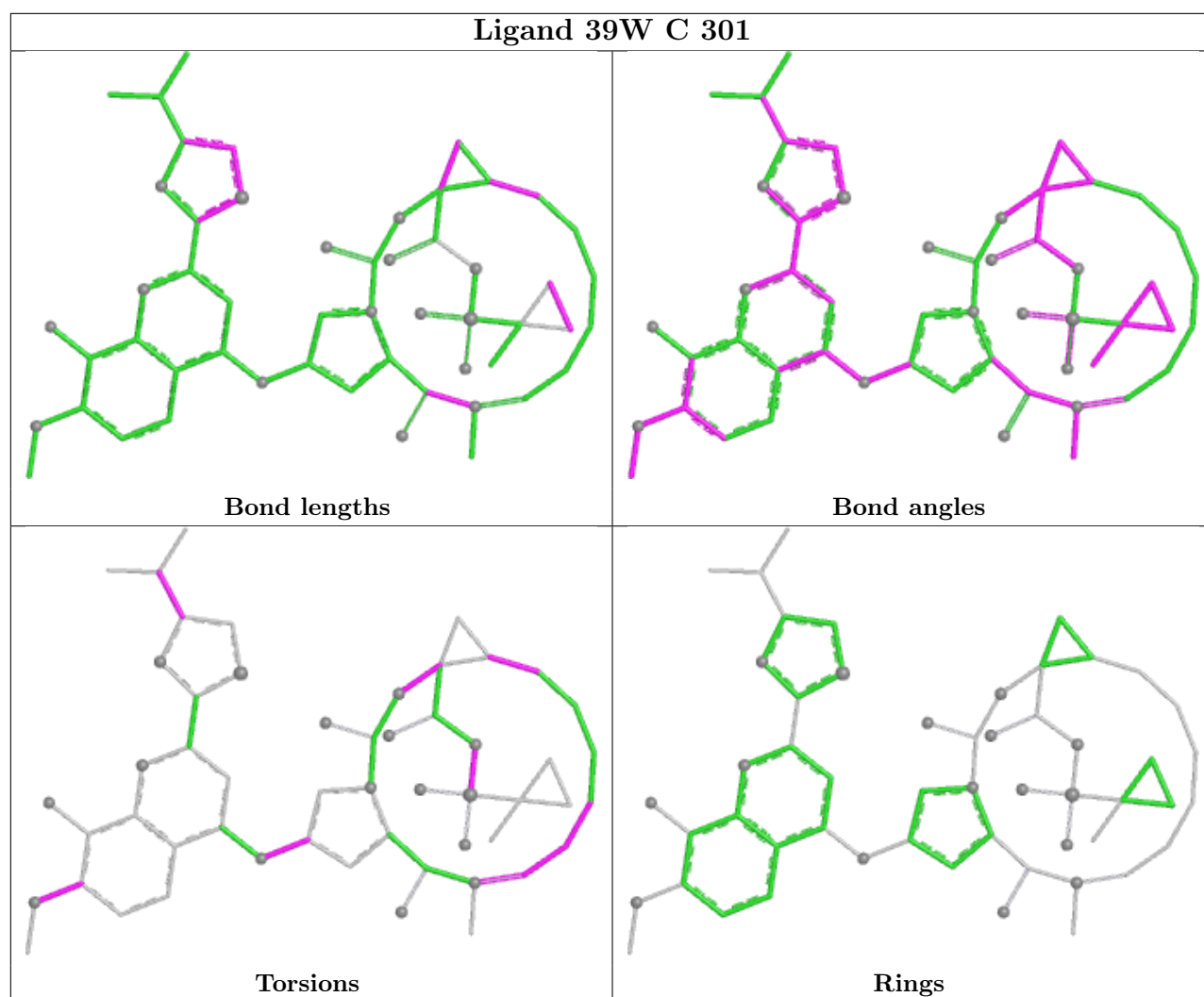


Ligand 39W J 301



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%)	-0.18	1 (0%) 87 82	40, 63, 100, 127	1 (0%)
1	B	182/203 (89%)	0.13	2 (1%) 78 70	52, 89, 137, 173	0
1	C	182/203 (89%)	0.06	0 100 100	51, 88, 123, 176	0
1	D	182/203 (89%)	-0.13	1 (0%) 87 82	42, 76, 110, 155	1 (0%)
1	E	182/203 (89%)	-0.11	1 (0%) 87 82	52, 81, 125, 147	0
1	F	182/203 (89%)	0.10	1 (0%) 87 82	47, 85, 125, 167	0
1	G	182/203 (89%)	-0.08	0 100 100	51, 84, 131, 173	0
1	H	182/203 (89%)	0.22	3 (1%) 70 61	70, 106, 146, 187	0
1	J	182/203 (89%)	0.58	6 (3%) 49 39	69, 143, 185, 215	0
2	K	13/16 (81%)	-0.22	0 100 100	45, 59, 79, 95	0
2	L	13/16 (81%)	0.04	0 100 100	50, 68, 99, 118	0
2	M	13/16 (81%)	-0.05	0 100 100	57, 64, 104, 126	0
2	N	13/16 (81%)	-0.02	0 100 100	51, 61, 93, 103	0
2	O	13/16 (81%)	-0.18	0 100 100	57, 69, 98, 112	0
2	P	13/16 (81%)	0.57	0 100 100	78, 95, 115, 118	0
2	Q	13/16 (81%)	-0.16	0 100 100	57, 67, 98, 121	0
2	T	13/16 (81%)	0.46	0 100 100	98, 112, 139, 158	0
2	U	13/16 (81%)	0.73	0 100 100	104, 110, 173, 195	0
All	All	1755/1971 (89%)	0.07	15 (0%) 81 74	40, 87, 153, 215	2 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	PRO	2.9
1	A	1	ALA	2.9
1	H	2	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	H	12	GLY	2.5
1	J	106	LEU	2.5

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
4	ZN	J	302	1/1	0.73	0.09	314,314,314,314	0
3	39W	J	301	53/53	0.85	0.11	67,74,77,79	0
5	CL	D	303	1/1	0.85	0.12	97,97,97,97	0
4	ZN	E	302	1/1	0.86	0.11	141,141,141,141	0
4	ZN	C	302	1/1	0.88	0.09	127,127,127,127	0
5	CL	G	303	1/1	0.90	0.09	81,81,81,81	0
4	ZN	B	302	1/1	0.91	0.10	117,117,117,117	0
5	CL	B	303	1/1	0.93	0.09	76,76,76,76	0
3	39W	G	301	53/53	0.93	0.10	57,62,66,70	0
4	ZN	A	302	1/1	0.93	0.09	89,89,89,89	0
3	39W	H	301	53/53	0.94	0.08	55,62,67,70	0
3	39W	E	301	53/53	0.94	0.08	48,63,65,67	0
4	ZN	F	302	1/1	0.94	0.08	93,93,93,93	0
4	ZN	H	302	1/1	0.94	0.09	114,114,114,114	0
3	39W	C	301	53/53	0.95	0.07	53,60,63,66	0
3	39W	A	301	53/53	0.95	0.10	47,54,63,64	0
3	39W	F	301	53/53	0.95	0.08	54,59,64,66	0
3	39W	B	301	53/53	0.95	0.08	56,62,65,68	0
4	ZN	G	302	1/1	0.96	0.05	115,115,115,115	0
3	39W	D	301	53/53	0.96	0.08	47,55,62,65	0
4	ZN	D	302	1/1	0.96	0.06	87,87,87,87	0

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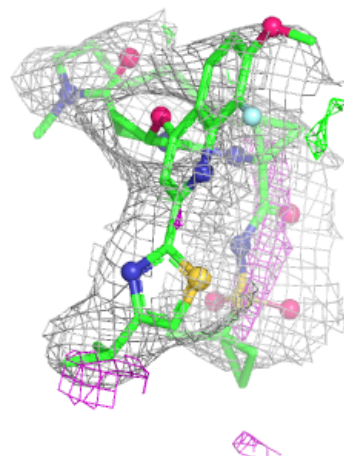
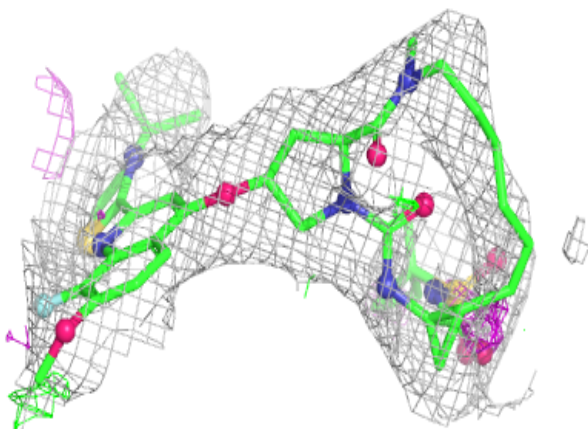
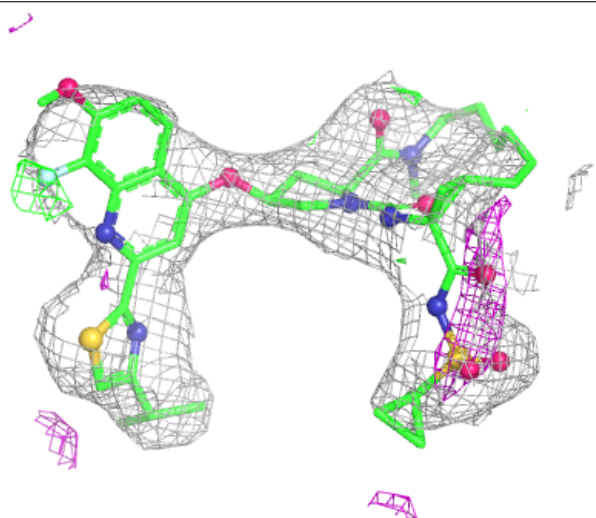
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CL	E	303	1/1	0.97	0.15	91,91,91,91	0

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.

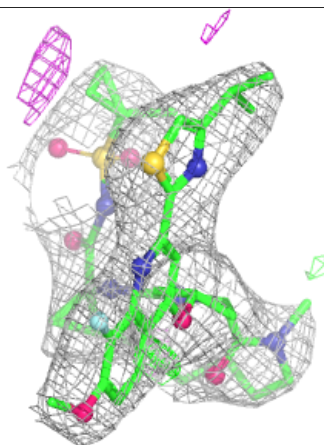
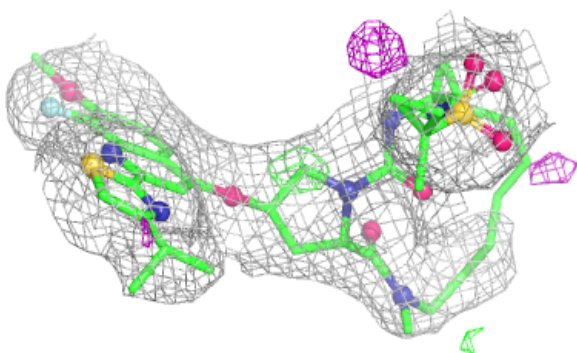
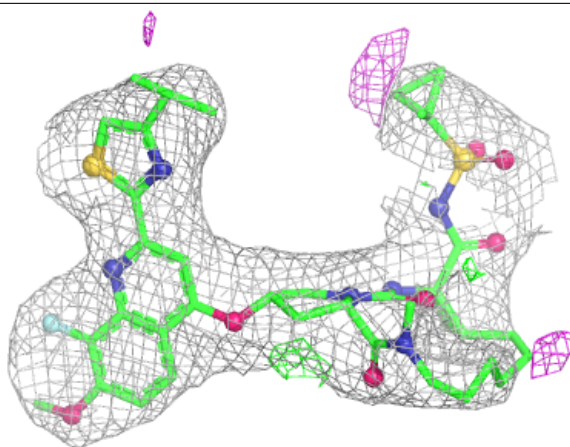
Electron density around 39W J 301:

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



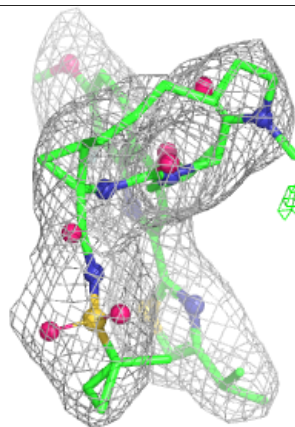
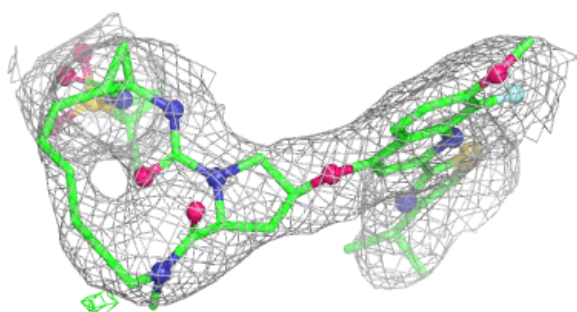
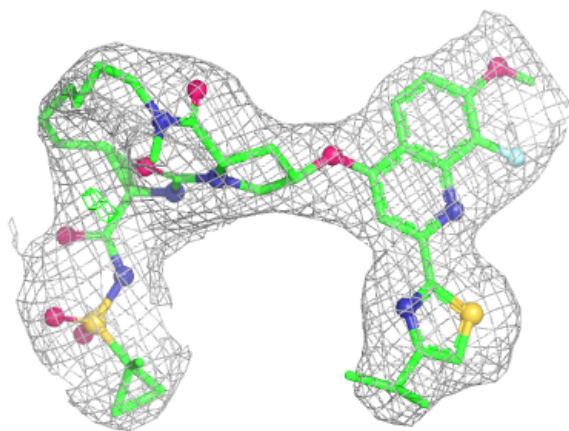
Electron density around 39W G 301:

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



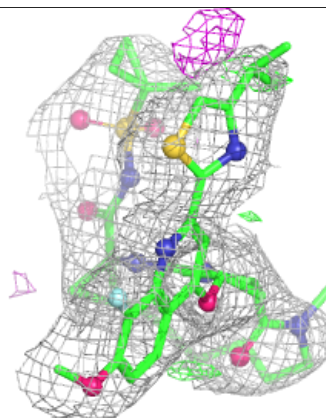
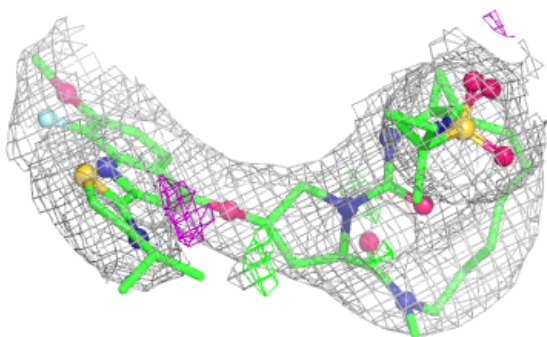
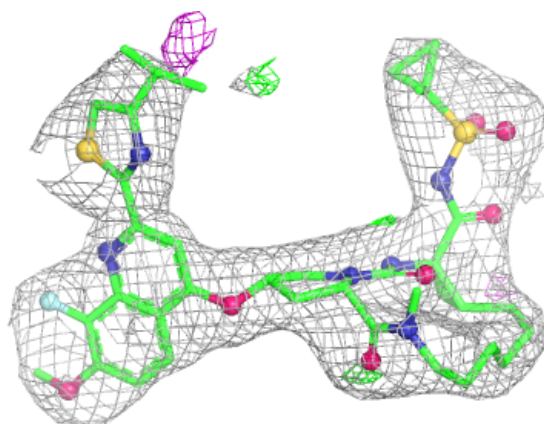
Electron density around 39W H 301:

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and green (positive)



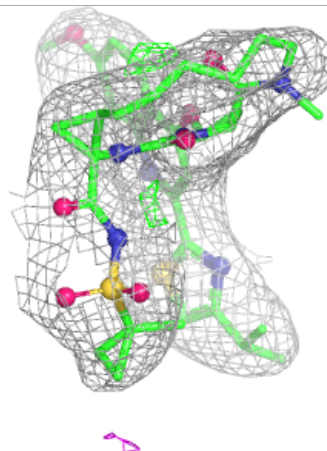
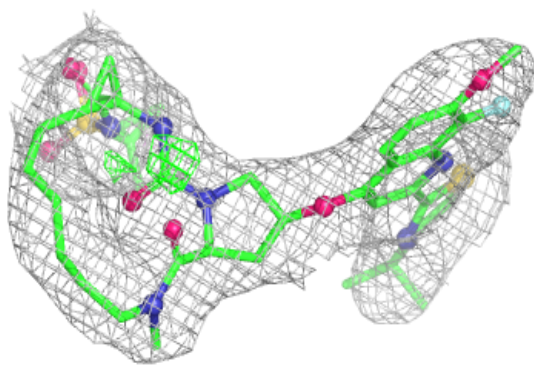
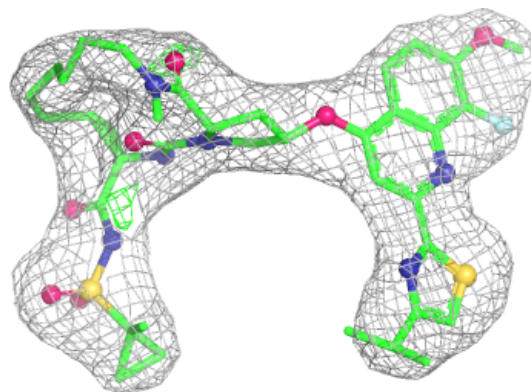
Electron density around 39W E 301:

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



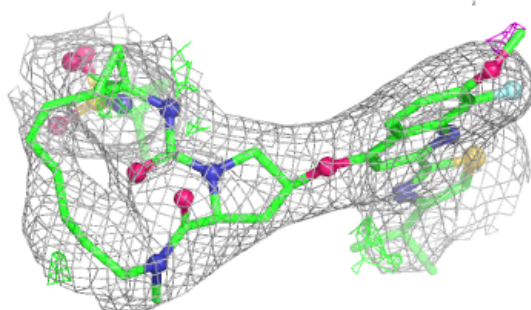
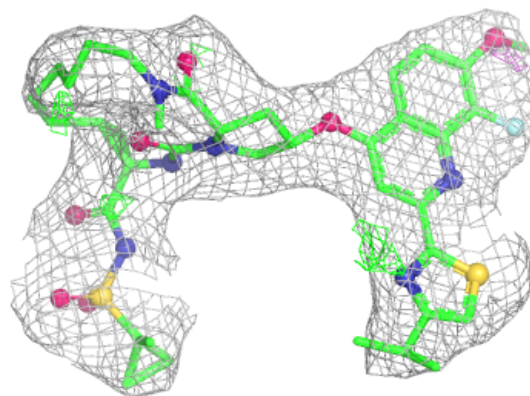
Electron density around 39W C 301:

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

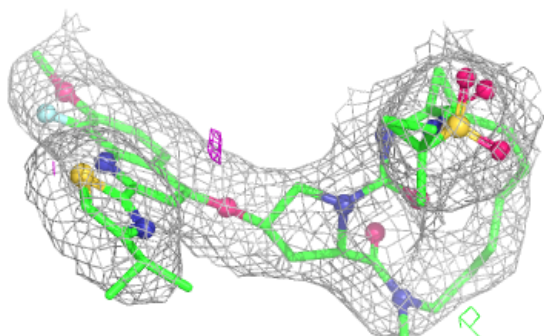
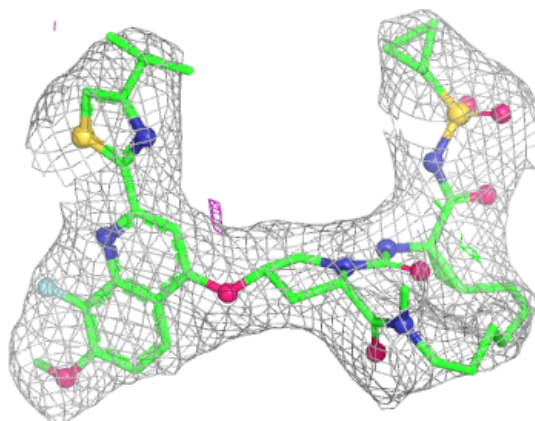


Electron density around 39W A 301:

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and green (positive)

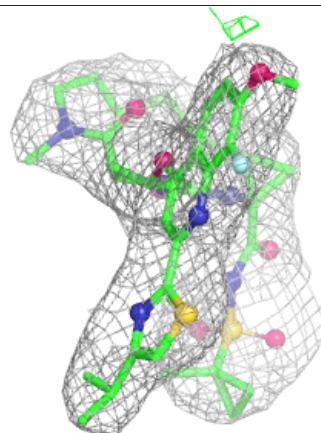
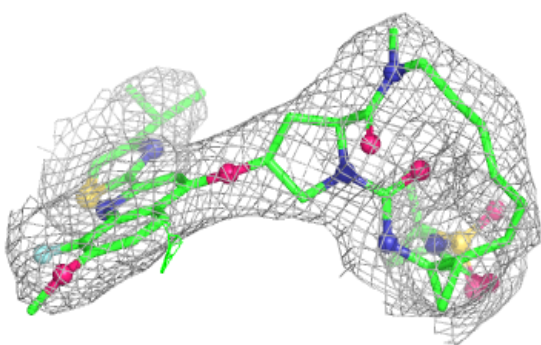
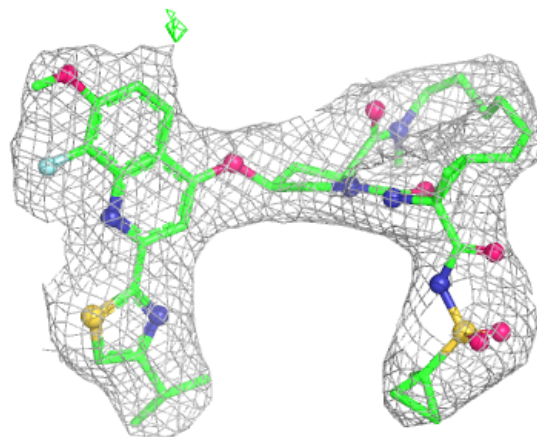
**Electron density around 39W F 301:**

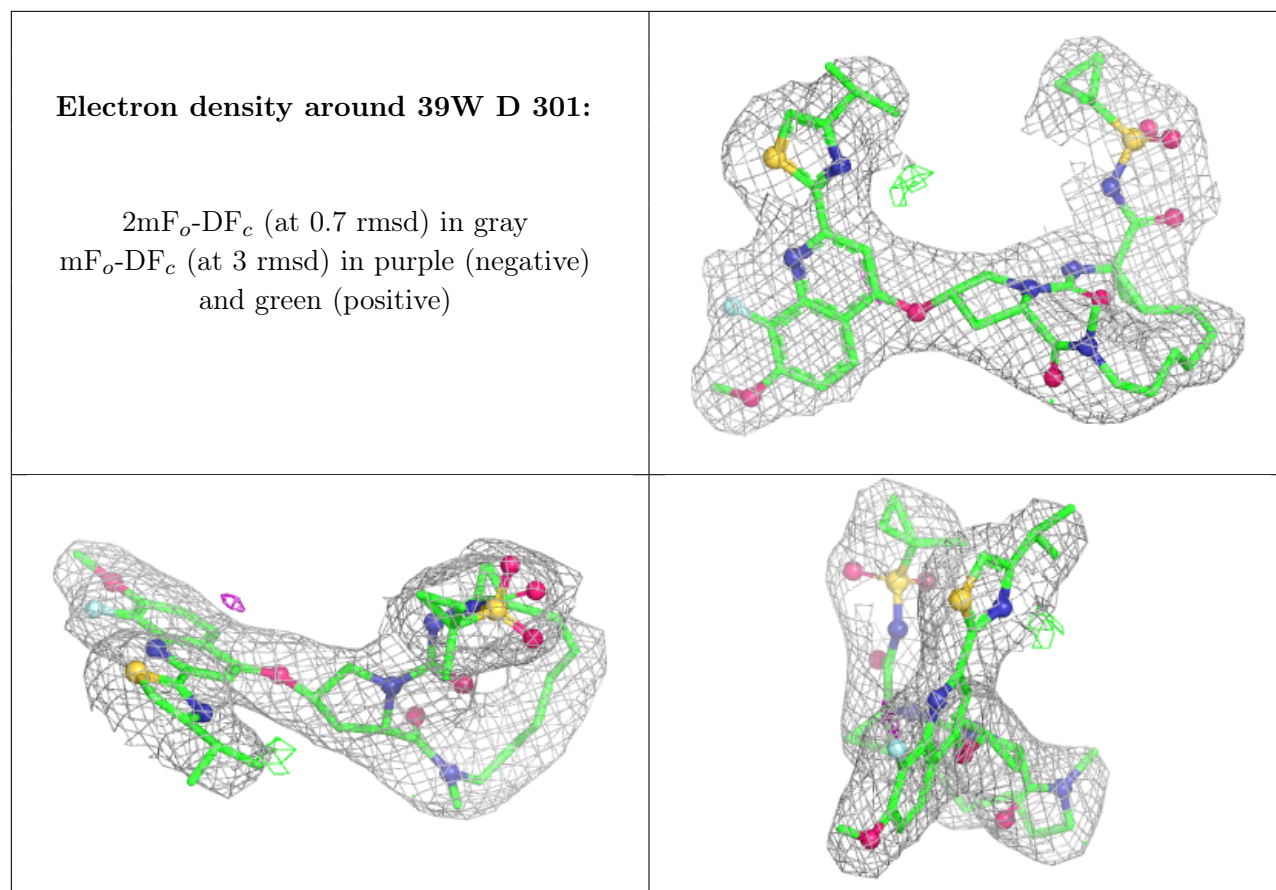
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 39W 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)





6.5 Other polymers ⓘ

There are no such residues in this entry.