



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 12:16 PM UTC

PDB ID : 1KYI / pdb_00001kyi
Title : HslUV (H. influenzae)-NLVS Vinyl Sulfone Inhibitor Complex
Authors : Sousa, M.C.; Kessler, B.M.; Overkleeft, H.S.; McKay, D.B.
Deposited on : 2002-02-04
Resolution : 3.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

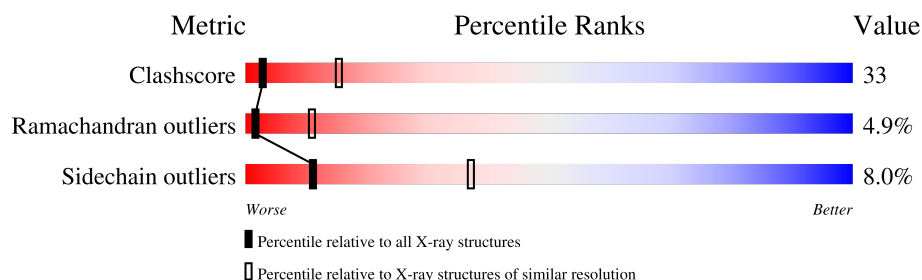
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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))
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)

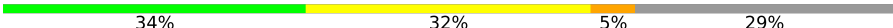
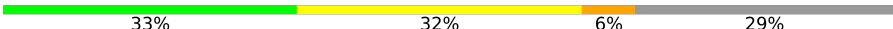
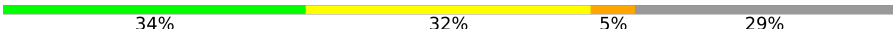
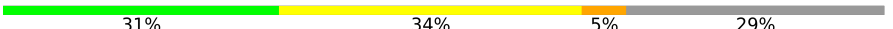
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	444	36% 29% 7% 28%
1	B	444	36% 30% 6% 28%
1	C	444	37% 30% 5% 28%
1	D	444	37% 29% 6% 28%
1	E	444	37% 29% 6% 28%
1	F	444	38% 29% 6% 28%
1	S	444	31% 35% 5% 29%
1	T	444	32% 33% 6% 29%

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Mol	Chain	Length	Quality of chain
1	U	444	
1	V	444	
1	W	444	
1	X	444	
2	G	174	
2	H	174	
2	I	174	
2	J	174	
2	K	174	
2	L	174	
2	M	174	
2	N	174	
2	O	174	
2	P	174	
2	Q	174	
2	R	174	

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	LVS	J	175	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 45756 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 ATP-dependent hsl protease ATP-binding subunit hslU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	B	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	C	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	D	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	E	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	F	321	Total	C	N	O	S	0	0	0
			2488	1557	444	477	10			
1	S	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			
1	T	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			
1	U	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			
1	V	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			
1	W	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			
1	X	317	Total	C	N	O	S	0	0	0
			2469	1543	444	472	10			

- Molecule 2 is a protein called ATP-dependent protease hslV.

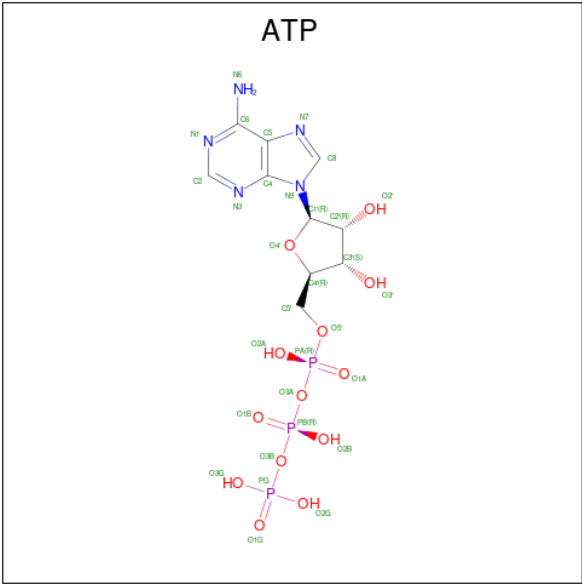
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			
2	H	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			
2	J	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			
2	K	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			
2	L	173	Total	C	N	O	S	0	0	0
			1290	809	228	249	4			
2	M	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			
2	N	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			
2	O	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			
2	P	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			
2	Q	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			
2	R	173	Total	C	N	O	S	0	0	0
			1261	791	226	241	3			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



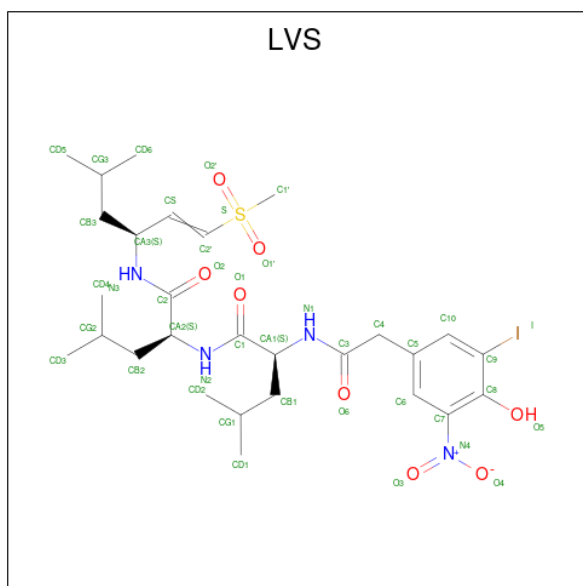
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	S	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	T	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	U	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	V	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	W	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	X	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 4 is 4-iodo-3-nitrophenyl acetyl-leucinyll-leucinyll-leucinyll-vinylsulfone (CCD ID: LVS) (formula: $C_{28}H_{43}IN_4O_8S$).



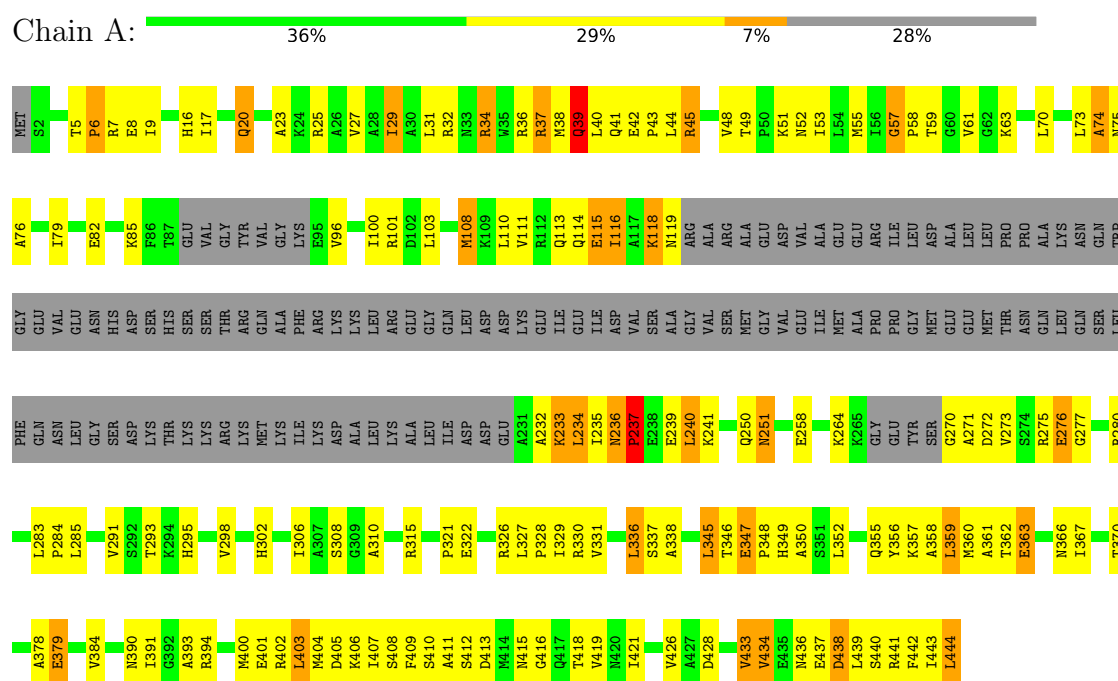
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	H	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	I	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	J	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	K	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	L	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	M	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	N	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	O	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	P	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	Q	1	Total 28	C 20	N 3	O 4	S 1	0	0
4	R	1	Total 28	C 20	N 3	O 4	S 1	0	0

3 Residue-property plots

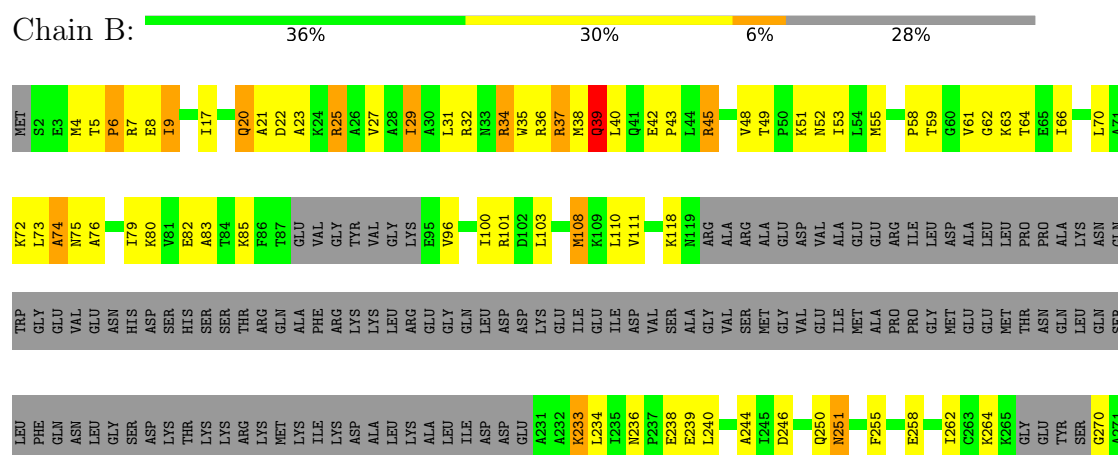
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

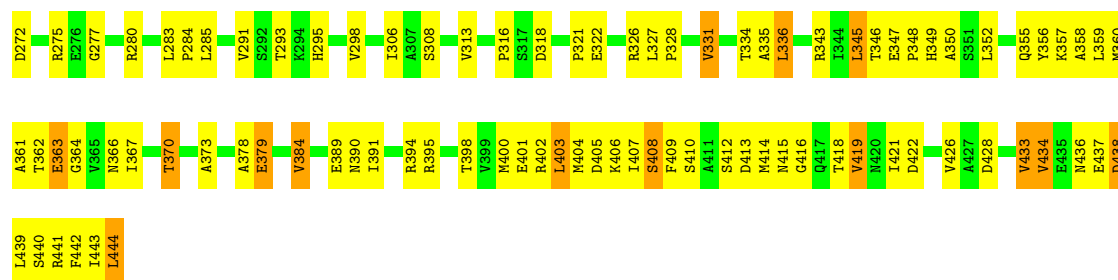
Note EDS was not executed.

- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU



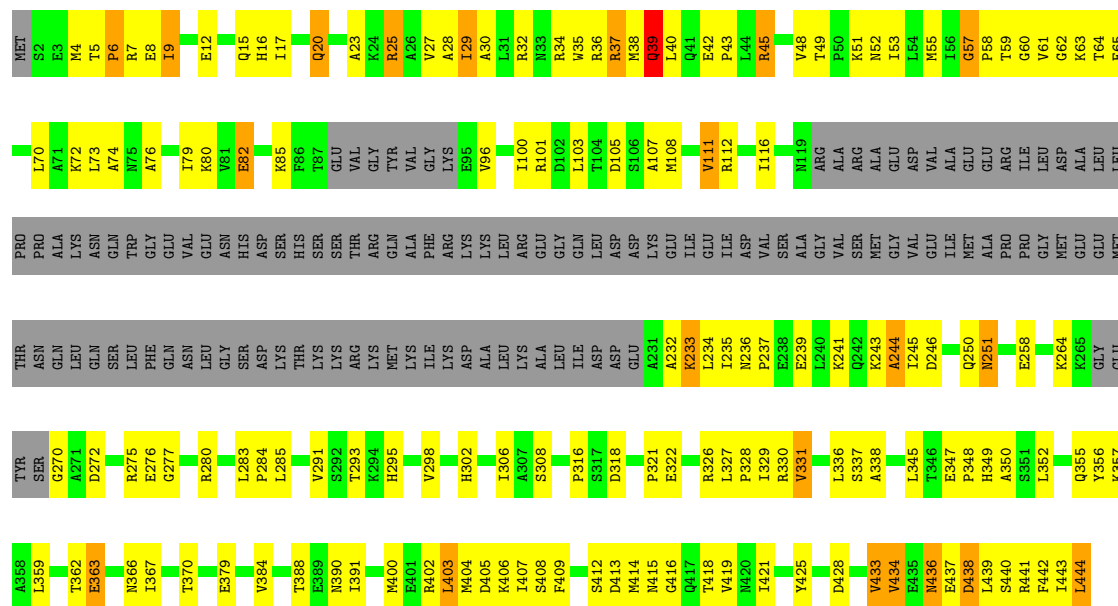
- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU





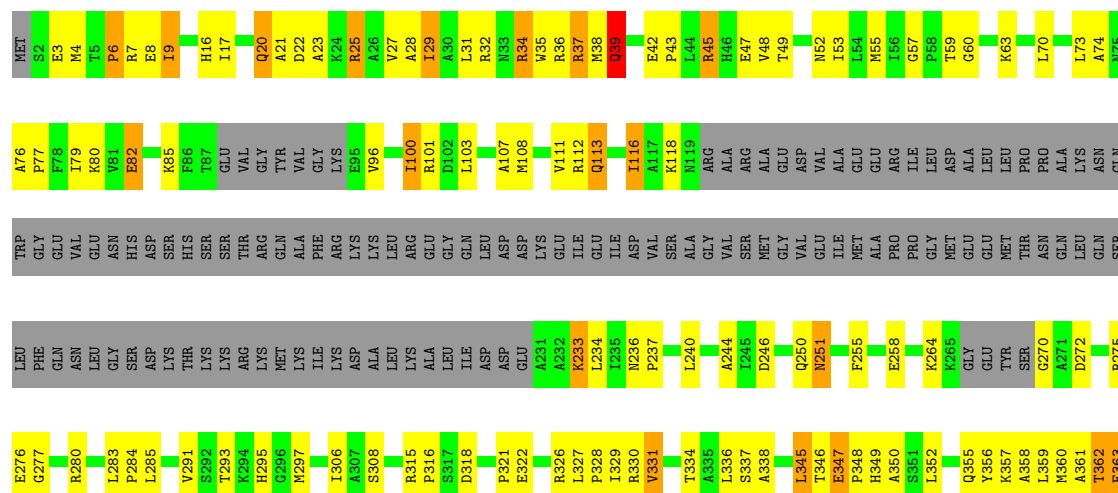
- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

Chain C: 37% 30% 5% 28%



- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

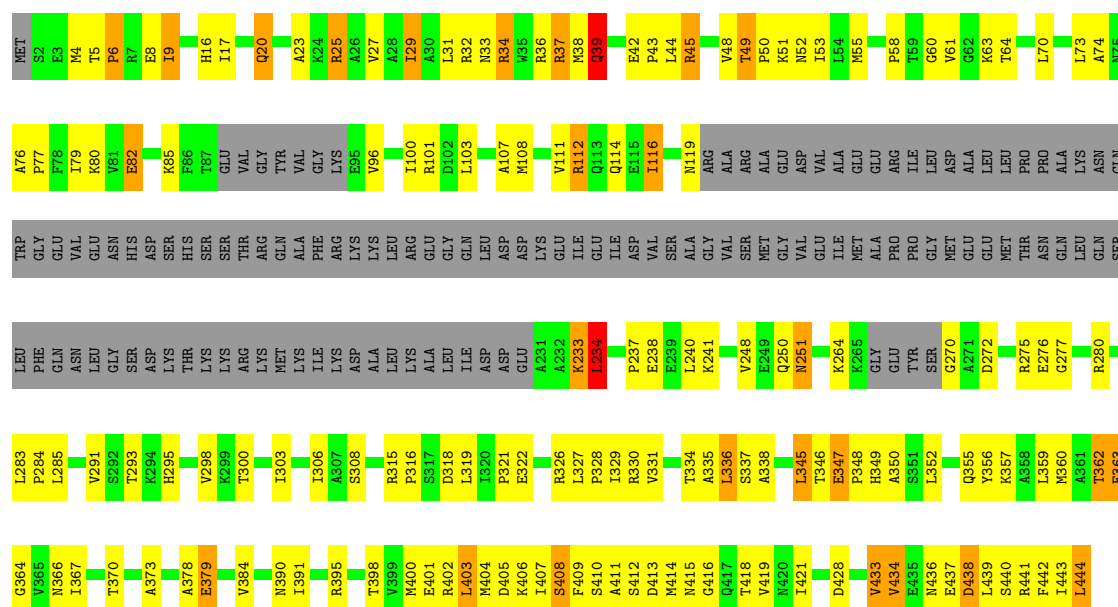
Chain D: 37% 29% 6% 28%





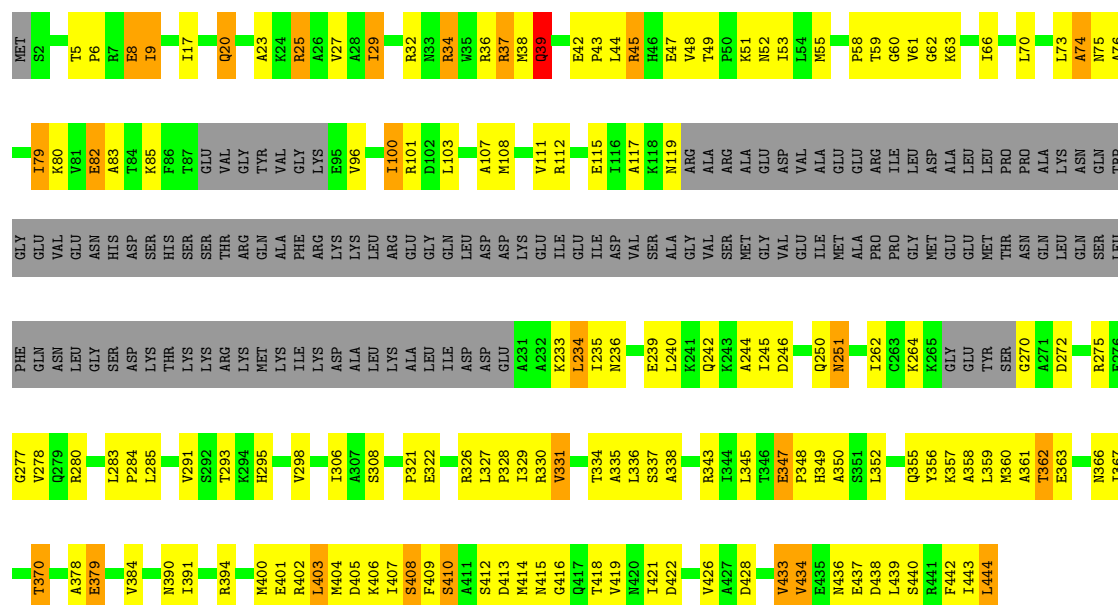
• Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

Chain E: 37% 29% 6% 28%



• Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

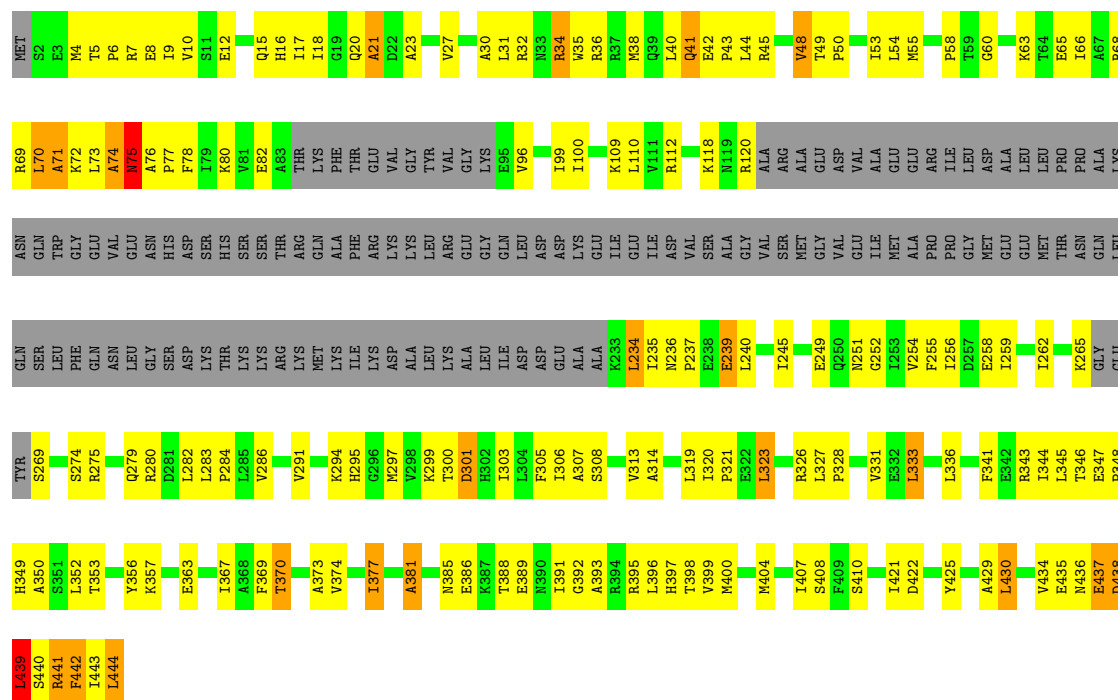
Chain F: 38% 29% 6% 28%



• Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

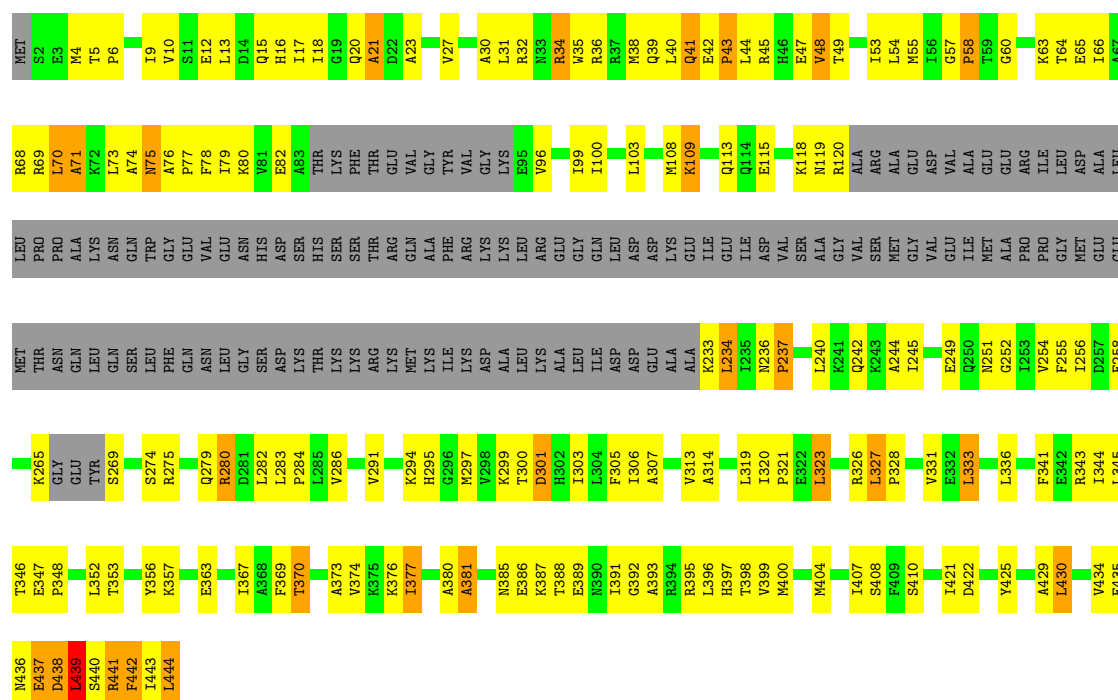
Chain S: 31% 35% 5% 29%





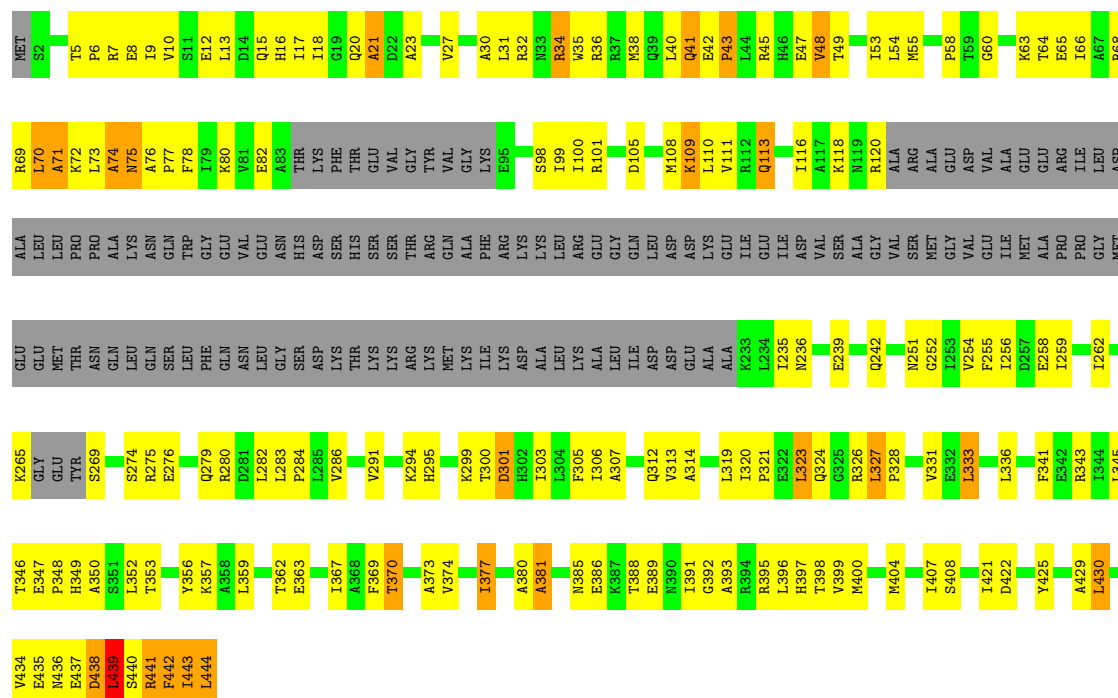
- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

Chain V: 33% 32% 6% 29%



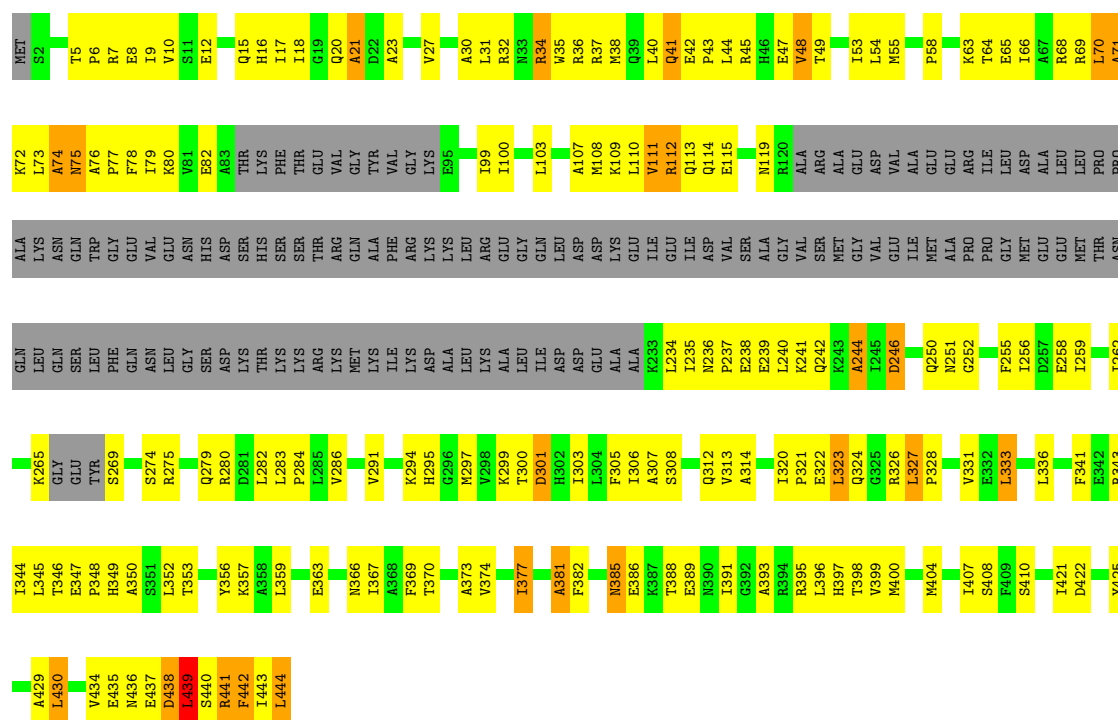
- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

Chain W: 34% 32% 5% 29%



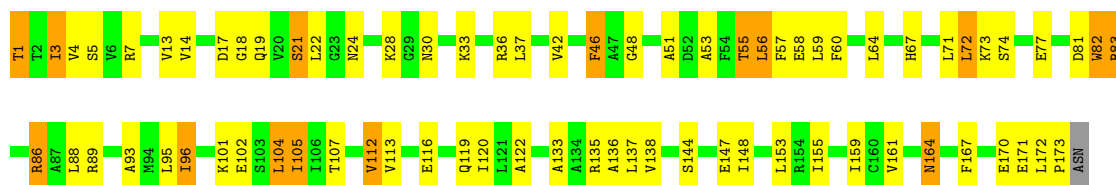
- Molecule 1: ATP-dependent hsl protease ATP-binding subunit hslU

Chain X: 31% 34% 5% 29%



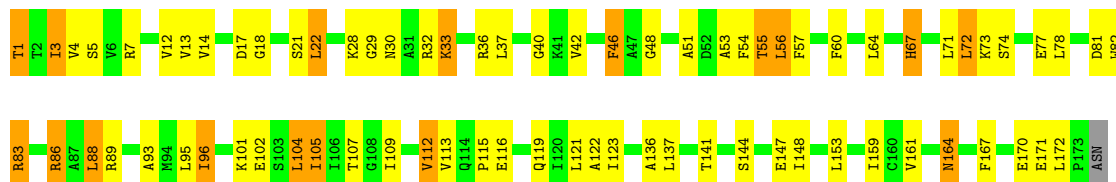
- Molecule 2: ATP-dependent protease hslV

Chain G: 57% 34% 9%



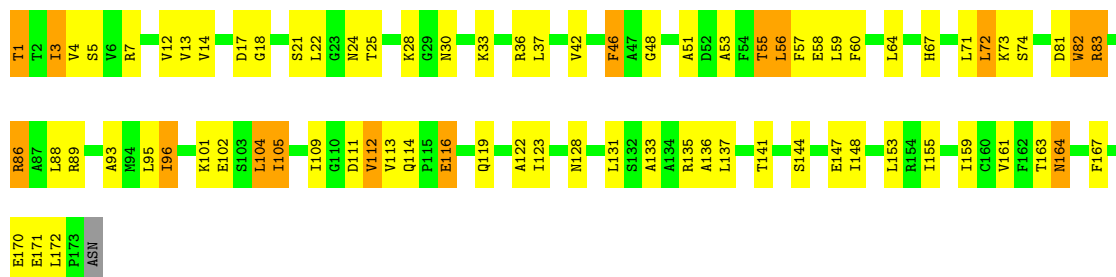
- Molecule 2: ATP-dependent protease hslV

Chain H: 56% 33% 10% .



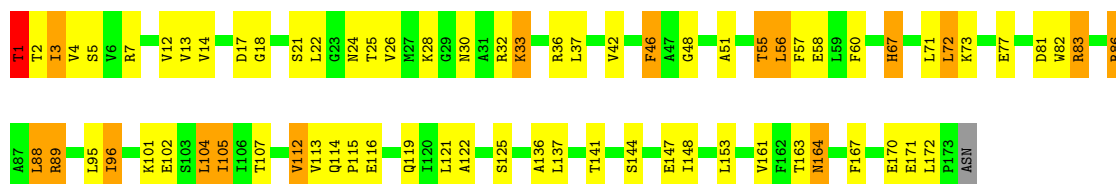
- Molecule 2: ATP-dependent protease hslV

Chain I: 55% 36% 9% .



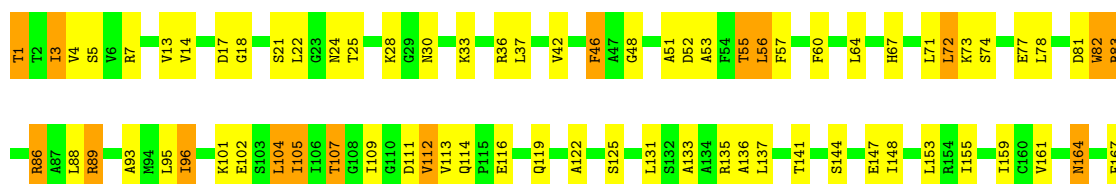
- Molecule 2: ATP-dependent protease hslV

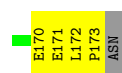
Chain J: 58% 32% 9% ..



- Molecule 2: ATP-dependent protease hslV

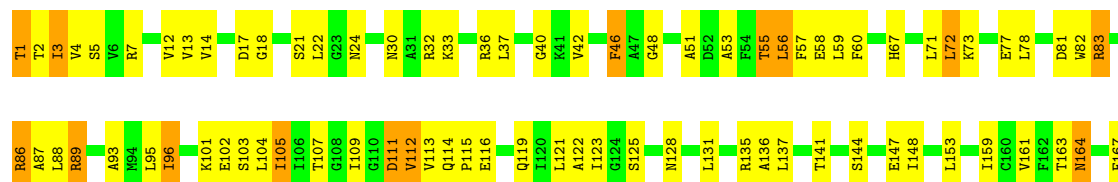
Chain K: 55% 36% 9% .





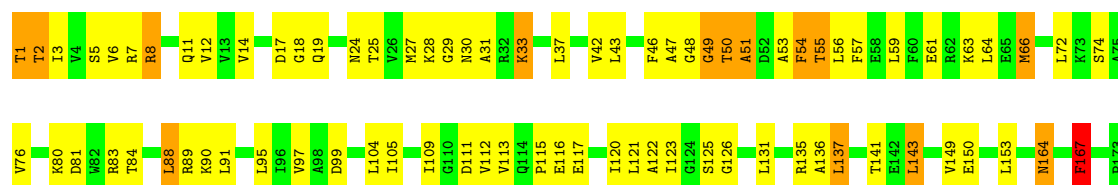
• Molecule 2: ATP-dependent protease hslV

Chain L: 52% 40% 8%



• Molecule 2: ATP-dependent protease hslV

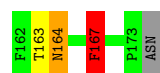
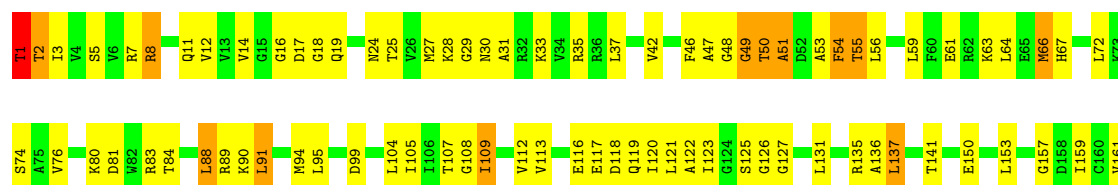
Chain M: 53% 37% 8%



ASN

• Molecule 2: ATP-dependent protease hslV

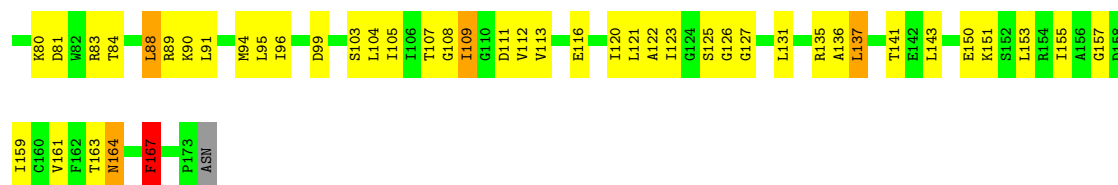
Chain N: 51% 40% 7%



• Molecule 2: ATP-dependent protease hslV

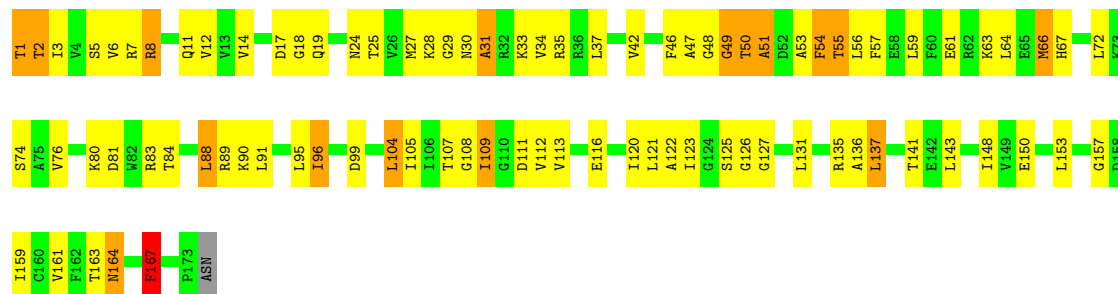
Chain O: 50% 41% 7%





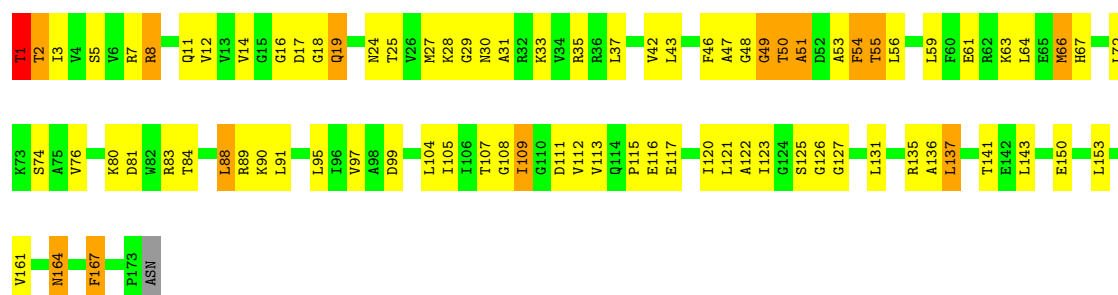
• Molecule 2: ATP-dependent protease hslV

Chain P: 49% 40% 9% ..



• Molecule 2: ATP-dependent protease hslV

Chain Q: 51% 40% 8% ..



• Molecule 2: ATP-dependent protease hslV

Chain R: 52% 40% 6% ..



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	208.51Å 219.97Å 242.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10	Depositor
% Data completeness (in resolution range)	92.9 (30.00-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.266 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	45756	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, LVS

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	0.72	1/2515 (0.0%)	1.26	32/3391 (0.9%)
1	B	0.73	0/2515	1.19	21/3391 (0.6%)
1	C	0.73	0/2515	1.20	24/3391 (0.7%)
1	D	0.76	0/2515	1.18	24/3391 (0.7%)
1	E	0.78	0/2515	1.19	27/3391 (0.8%)
1	F	0.74	0/2515	1.19	21/3391 (0.6%)
1	S	0.36	0/2495	0.99	13/3360 (0.4%)
1	T	0.36	0/2495	0.96	15/3360 (0.4%)
1	U	0.37	0/2495	0.97	8/3360 (0.2%)
1	V	0.37	0/2495	0.99	13/3360 (0.4%)
1	W	0.37	0/2495	0.96	15/3360 (0.4%)
1	X	0.37	0/2495	0.98	18/3360 (0.5%)
2	G	0.72	0/1304	1.08	6/1765 (0.3%)
2	H	0.73	0/1304	1.10	7/1765 (0.4%)
2	I	0.73	0/1304	1.11	7/1765 (0.4%)
2	J	0.78	3/1304 (0.2%)	1.10	8/1765 (0.5%)
2	K	0.71	0/1304	1.10	6/1765 (0.3%)
2	L	0.78	1/1304 (0.1%)	1.13	7/1765 (0.4%)
2	M	0.58	1/1275 (0.1%)	1.02	3/1732 (0.2%)
2	N	0.62	2/1275 (0.2%)	1.04	4/1732 (0.2%)
2	O	0.58	1/1275 (0.1%)	1.01	4/1732 (0.2%)
2	P	0.58	1/1275 (0.1%)	1.01	5/1732 (0.3%)
2	Q	0.59	2/1275 (0.2%)	1.04	3/1732 (0.2%)
2	R	0.69	1/1275 (0.1%)	1.01	3/1732 (0.2%)
All	All	0.62	13/45534 (0.0%)	1.08	294/61488 (0.5%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	1	THR	C-N	14.62	1.52	1.33
2	N	2	THR	N-CA	8.16	1.56	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	1	THR	C-N	7.55	1.43	1.33
2	J	2	THR	CA-C	6.30	1.59	1.52
2	M	2	THR	N-CA	6.16	1.53	1.46

The worst 5 of 294 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	438	ASP	N-CA-C	-12.55	97.07	112.38
1	A	39	GLN	N-CA-C	-11.80	99.58	114.56
1	E	438	ASP	N-CA-C	-11.76	98.03	112.38
1	D	438	ASP	N-CA-C	-11.37	97.56	112.34
1	A	438	ASP	N-CA-C	-11.33	98.56	112.38

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	2488	0	2546	164	0
1	B	2488	0	2546	168	0
1	C	2488	0	2546	161	0
1	D	2488	0	2546	155	0
1	E	2488	0	2546	153	0
1	F	2488	0	2546	160	0
1	S	2469	0	2540	175	0
1	T	2469	0	2540	161	0
1	U	2469	0	2540	160	0
1	V	2469	0	2540	160	0
1	W	2469	0	2540	155	0
1	X	2469	0	2540	163	1
2	G	1290	0	1288	98	0
2	H	1290	0	1288	108	0
2	I	1290	0	1288	110	0
2	J	1290	0	1288	110	0
2	K	1290	0	1288	101	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	1290	0	1288	102	0
2	M	1261	0	1239	113	0
2	N	1261	0	1239	117	0
2	O	1261	0	1239	111	0
2	P	1261	0	1239	127	0
2	Q	1261	0	1239	116	0
2	R	1261	0	1239	115	0
3	A	31	0	12	3	0
3	B	31	0	12	5	0
3	C	31	0	12	8	0
3	D	31	0	12	5	0
3	E	31	0	12	6	0
3	F	31	0	12	4	0
3	S	31	0	12	4	0
3	T	31	0	12	4	0
3	U	31	0	12	5	0
3	V	31	0	12	2	0
3	W	31	0	12	4	0
3	X	31	0	12	3	0
4	G	28	0	36	12	0
4	H	28	0	36	14	0
4	I	28	0	36	16	0
4	J	28	0	36	23	0
4	K	28	0	36	16	0
4	L	28	0	36	14	0
4	M	28	0	36	12	0
4	N	28	0	36	19	0
4	O	28	0	36	13	0
4	P	28	0	36	13	0
4	Q	28	0	36	14	0
4	R	28	0	36	13	0
All	All	45756	0	46254	3015	1

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 33.

The worst 5 of 3015 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:1:THR:HG21	2:P:33:LYS:CD	1.47	1.44
2:G:1:THR:CG2	2:G:33:LYS:CE	1.98	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:1:THR:HG21	2:O:33:LYS:CD	1.50	1.40
2:H:1:THR:HG21	2:H:33:LYS:CE	1.53	1.38
2:G:1:THR:HG21	2:G:33:LYS:CD	1.53	1.38

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:7:ARG:NH2	1:X:7:ARG:NH2[2_765]	2.04	0.16

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	49/444 (11%)	47 (96%)	2 (4%)	0	100	100
1	S	309/444 (70%)	235 (76%)	57 (18%)	17 (6%)	1	9
1	T	294/444 (66%)	224 (76%)	50 (17%)	20 (7%)	1	5
1	U	309/444 (70%)	235 (76%)	55 (18%)	19 (6%)	1	7
1	V	309/444 (70%)	237 (77%)	54 (18%)	18 (6%)	1	8
1	W	309/444 (70%)	233 (75%)	57 (18%)	19 (6%)	1	7
1	X	309/444 (70%)	237 (77%)	55 (18%)	17 (6%)	1	9
2	G	57/174 (33%)	54 (95%)	3 (5%)	0	100	100
2	H	62/174 (36%)	56 (90%)	5 (8%)	1 (2%)	7	30
2	I	18/174 (10%)	18 (100%)	0	0	100	100
2	L	141/174 (81%)	128 (91%)	9 (6%)	4 (3%)	4	20
2	M	171/174 (98%)	145 (85%)	19 (11%)	7 (4%)	2	13
2	N	171/174 (98%)	143 (84%)	21 (12%)	7 (4%)	2	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	O	171/174 (98%)	141 (82%)	24 (14%)	6 (4%)	3	16
2	P	171/174 (98%)	143 (84%)	22 (13%)	6 (4%)	3	16
2	Q	171/174 (98%)	142 (83%)	21 (12%)	8 (5%)	2	11
2	R	171/174 (98%)	144 (84%)	20 (12%)	7 (4%)	2	13
All	All	3192/4848 (66%)	2562 (80%)	474 (15%)	156 (5%)	1	11

5 of 156 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	89	ARG
2	M	50	THR
2	M	51	ALA
2	N	50	THR
2	O	50	THR

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	267/373 (72%)	240 (90%)	27 (10%)	7	28
1	B	267/373 (72%)	239 (90%)	28 (10%)	6	26
1	C	267/373 (72%)	243 (91%)	24 (9%)	9	33
1	D	267/373 (72%)	241 (90%)	26 (10%)	8	30
1	E	267/373 (72%)	243 (91%)	24 (9%)	9	33
1	F	267/373 (72%)	240 (90%)	27 (10%)	7	28
1	S	267/373 (72%)	257 (96%)	10 (4%)	30	61
1	T	267/373 (72%)	256 (96%)	11 (4%)	27	59
1	U	267/373 (72%)	257 (96%)	10 (4%)	30	61
1	V	267/373 (72%)	257 (96%)	10 (4%)	30	61
1	W	267/373 (72%)	256 (96%)	11 (4%)	27	59
1	X	267/373 (72%)	257 (96%)	10 (4%)	30	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	132/140 (94%)	115 (87%)	17 (13%)	4	18
2	H	132/140 (94%)	114 (86%)	18 (14%)	3	16
2	I	132/140 (94%)	116 (88%)	16 (12%)	5	20
2	J	132/140 (94%)	114 (86%)	18 (14%)	3	16
2	K	132/140 (94%)	115 (87%)	17 (13%)	4	18
2	L	132/140 (94%)	116 (88%)	16 (12%)	5	20
2	M	125/140 (89%)	114 (91%)	11 (9%)	9	33
2	N	125/140 (89%)	116 (93%)	9 (7%)	13	40
2	O	125/140 (89%)	115 (92%)	10 (8%)	11	37
2	P	125/140 (89%)	115 (92%)	10 (8%)	11	37
2	Q	125/140 (89%)	115 (92%)	10 (8%)	11	37
2	R	125/140 (89%)	115 (92%)	10 (8%)	11	37
All	All	4746/6156 (77%)	4366 (92%)	380 (8%)	11	37

5 of 380 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	72	LEU
2	O	164	ASN
2	K	107	THR
2	M	33	LYS
2	Q	54	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 172 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	436	ASN
1	V	397	HIS
1	U	113	GLN
1	U	397	HIS
1	W	242	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](#)

24 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$
4	LVS	I	175	2	25,27,42	2.79	4 (16%)	30,37,59	1.55	3 (10%)
4	LVS	M	175	2	25,27,42	2.90	4 (16%)	30,37,59	1.65	6 (20%)
3	ATP	W	460	-	32,33,33	0.62	1 (3%)	48,52,52	0.75	1 (2%)
4	LVS	H	175	2	25,27,42	2.88	4 (16%)	30,37,59	1.44	3 (10%)
3	ATP	B	451	-	32,33,33	0.93	1 (3%)	48,52,52	0.80	1 (2%)
4	LVS	L	175	2	25,27,42	2.91	4 (16%)	30,37,59	1.48	3 (10%)
3	ATP	T	457	-	32,33,33	0.68	1 (3%)	48,52,52	0.70	1 (2%)
4	LVS	R	175	2	25,27,42	2.96	4 (16%)	30,37,59	1.69	7 (23%)
3	ATP	U	458	-	32,33,33	0.72	1 (3%)	48,52,52	0.70	1 (2%)
4	LVS	Q	175	2	25,27,42	2.87	4 (16%)	30,37,59	1.62	6 (20%)
4	LVS	P	175	2	25,27,42	3.06	4 (16%)	30,37,59	1.65	6 (20%)
4	LVS	O	175	2	25,27,42	3.05	4 (16%)	30,37,59	1.71	8 (26%)
3	ATP	V	459	-	32,33,33	0.67	1 (3%)	48,52,52	0.75	1 (2%)
3	ATP	D	453	-	32,33,33	0.84	1 (3%)	48,52,52	0.95	4 (8%)
3	ATP	A	450	-	32,33,33	0.79	1 (3%)	48,52,52	0.92	2 (4%)
3	ATP	C	452	-	32,33,33	1.05	1 (3%)	48,52,52	0.89	3 (6%)
3	ATP	E	454	-	32,33,33	1.02	1 (3%)	48,52,52	0.95	2 (4%)
4	LVS	N	175	2	25,27,42	3.20	4 (16%)	30,37,59	1.67	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ATP	S	456	-	32,33,33	0.73	1 (3%)	48,52,52	0.71	1 (2%)
4	LVS	J	175	2	25,27,42	2.85	4 (16%)	30,37,59	1.53	5 (16%)
4	LVS	K	175	2	25,27,42	3.05	4 (16%)	30,37,59	1.63	4 (13%)
3	ATP	F	455	-	32,33,33	1.03	1 (3%)	48,52,52	0.87	2 (4%)
4	LVS	G	175	2	25,27,42	3.02	4 (16%)	30,37,59	1.53	3 (10%)
3	ATP	X	461	-	32,33,33	0.69	0	48,52,52	0.72	1 (2%)

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
4	LVS	I	175	2	-	10/33/34/46	-
4	LVS	M	175	2	-	4/33/34/46	-
3	ATP	W	460	-	-	3/22/38/38	0/3/3/3
4	LVS	H	175	2	-	12/33/34/46	-
3	ATP	B	451	-	-	9/22/38/38	0/3/3/3
4	LVS	L	175	2	-	11/33/34/46	-
3	ATP	T	457	-	-	0/22/38/38	0/3/3/3
4	LVS	R	175	2	-	4/33/34/46	-
3	ATP	U	458	-	-	4/22/38/38	0/3/3/3
4	LVS	Q	175	2	-	5/33/34/46	-
4	LVS	P	175	2	-	4/33/34/46	-
4	LVS	O	175	2	-	4/33/34/46	-
3	ATP	V	459	-	-	0/22/38/38	0/3/3/3
3	ATP	D	453	-	-	6/22/38/38	0/3/3/3
3	ATP	A	450	-	-	2/22/38/38	0/3/3/3
3	ATP	C	452	-	-	5/22/38/38	0/3/3/3
3	ATP	E	454	-	-	6/22/38/38	0/3/3/3
4	LVS	N	175	2	-	4/33/34/46	-
3	ATP	S	456	-	-	2/22/38/38	0/3/3/3
4	LVS	J	175	2	-	10/33/34/46	-
4	LVS	K	175	2	-	11/33/34/46	-
3	ATP	F	455	-	-	4/22/38/38	0/3/3/3
4	LVS	G	175	2	-	13/33/34/46	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	X	461	-	-	0/22/38/38	0/3/3/3

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	175	LVS	C2'-CS	14.47	1.54	1.31
4	P	175	LVS	C2'-CS	14.06	1.54	1.31
4	R	175	LVS	C2'-CS	14.02	1.53	1.31
4	O	175	LVS	C2'-CS	13.98	1.53	1.31
4	K	175	LVS	C2'-CS	13.19	1.52	1.31

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	175	LVS	CS-CA3-N3	5.70	121.04	110.36
4	L	175	LVS	CS-CA3-N3	5.59	120.84	110.36
4	G	175	LVS	CS-CA3-N3	5.29	120.27	110.36
4	I	175	LVS	CS-CA3-N3	5.24	120.19	110.36
4	H	175	LVS	CS-CA3-N3	5.21	120.12	110.36

There are no chirality outliers.

5 of 133 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	450	ATP	PB-O3B-PG-O2G
3	B	451	ATP	PB-O3B-PG-O2G
3	B	451	ATP	C5'-O5'-PA-O1A
3	B	451	ATP	C5'-O5'-PA-O2A
3	B	451	ATP	C5'-O5'-PA-O3A

There are no ring outliers.

24 monomers are involved in 232 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	175	LVS	16	0
4	M	175	LVS	12	0
3	W	460	ATP	4	0
4	H	175	LVS	14	0
3	B	451	ATP	5	0
4	L	175	LVS	14	0
3	T	457	ATP	4	0

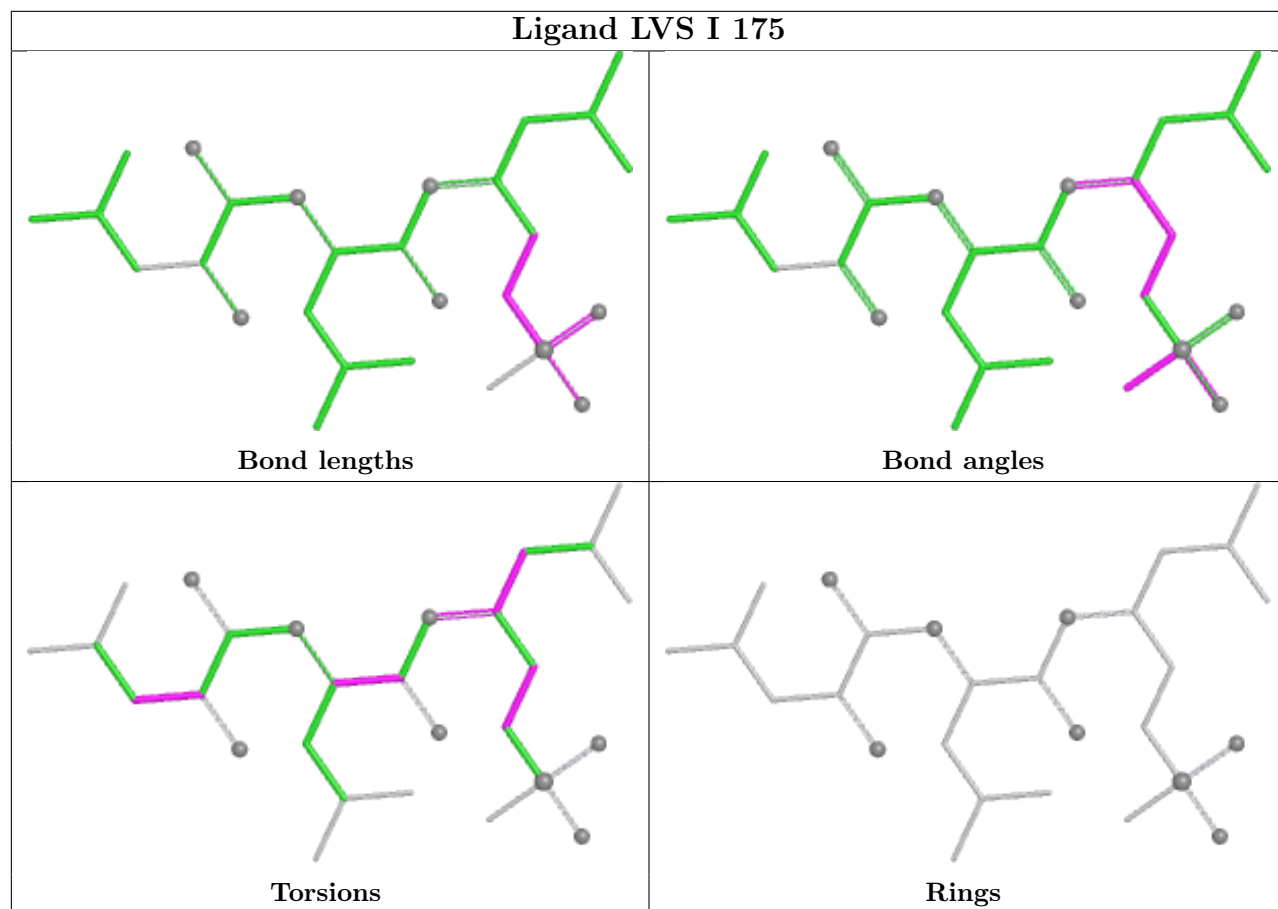
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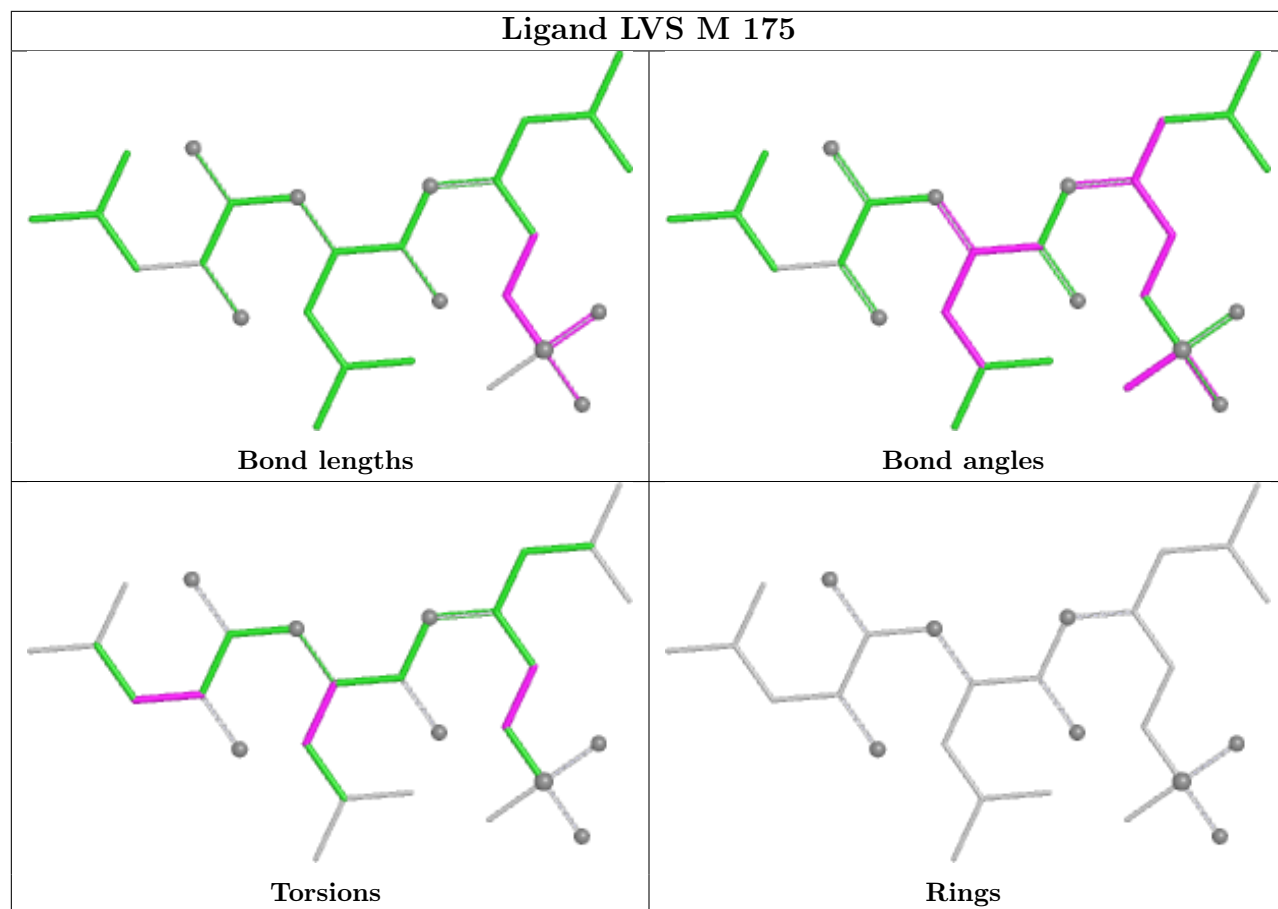
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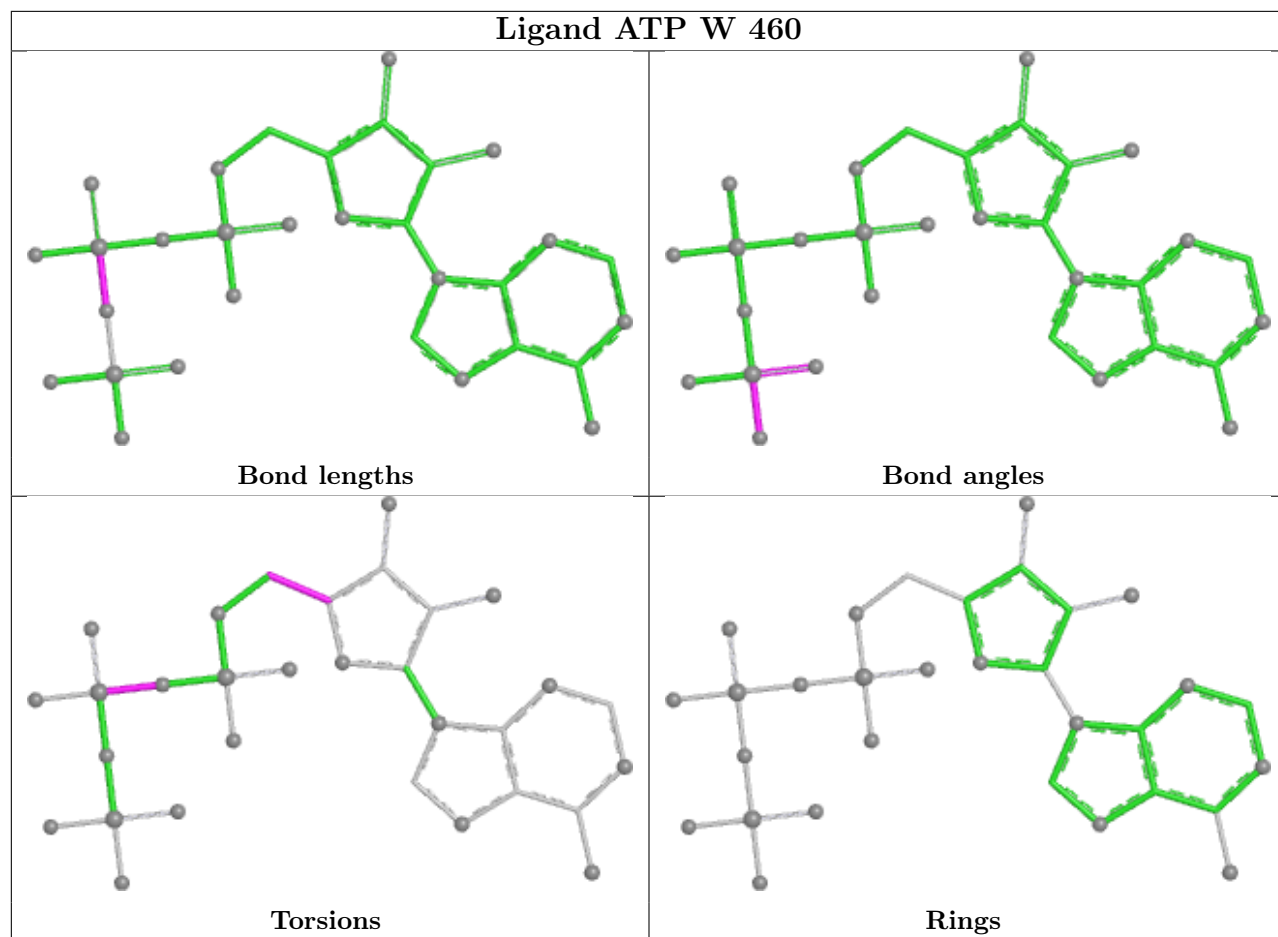
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	175	LVS	13	0
3	U	458	ATP	5	0
4	Q	175	LVS	14	0
4	P	175	LVS	13	0
4	O	175	LVS	13	0
3	V	459	ATP	2	0
3	D	453	ATP	5	0
3	A	450	ATP	3	0
3	C	452	ATP	8	0
3	E	454	ATP	6	0
4	N	175	LVS	19	0
3	S	456	ATP	4	0
4	J	175	LVS	23	0
4	K	175	LVS	16	0
3	F	455	ATP	4	0
4	G	175	LVS	12	0
3	X	461	ATP	3	0

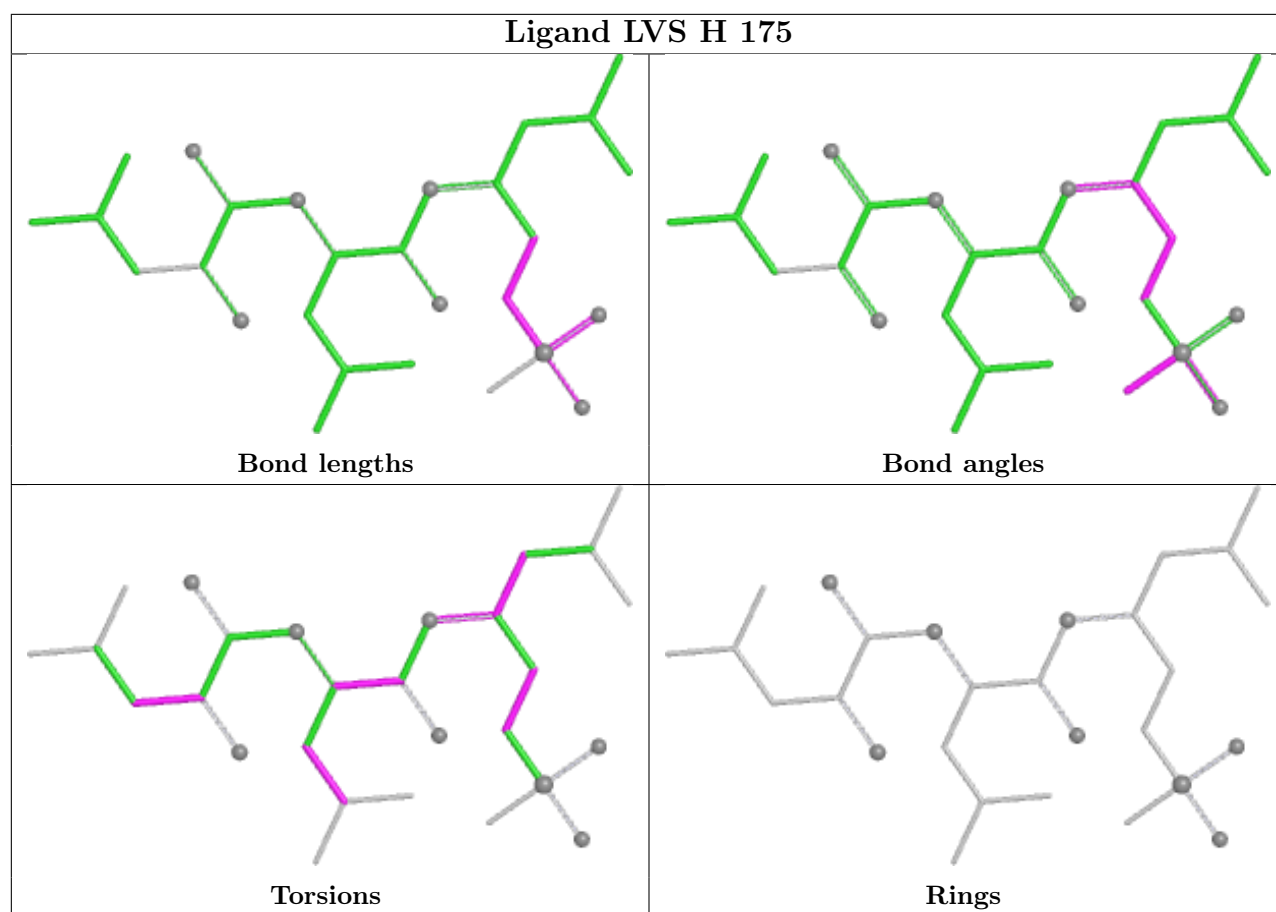
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

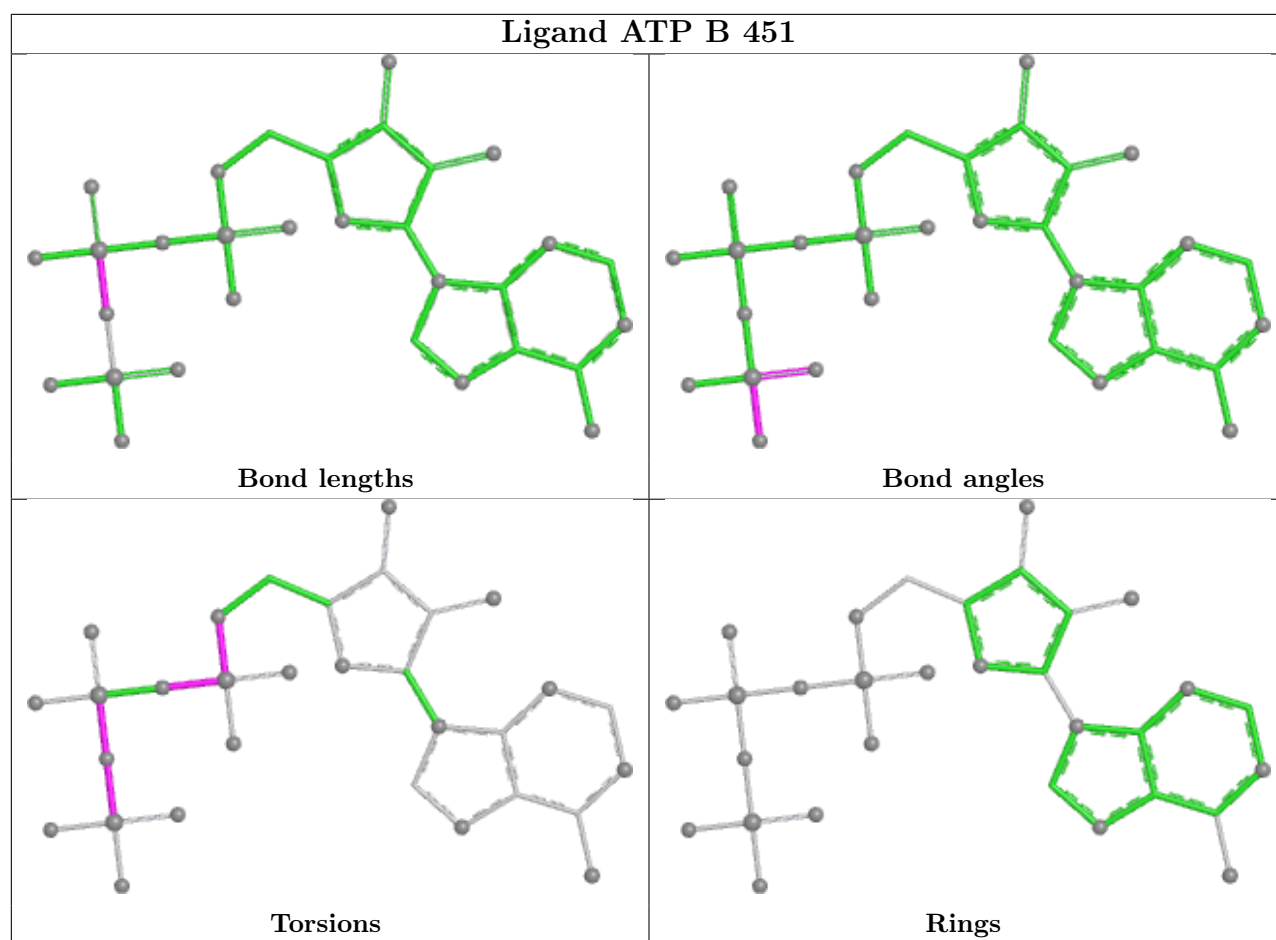
Ligand LVS I 175

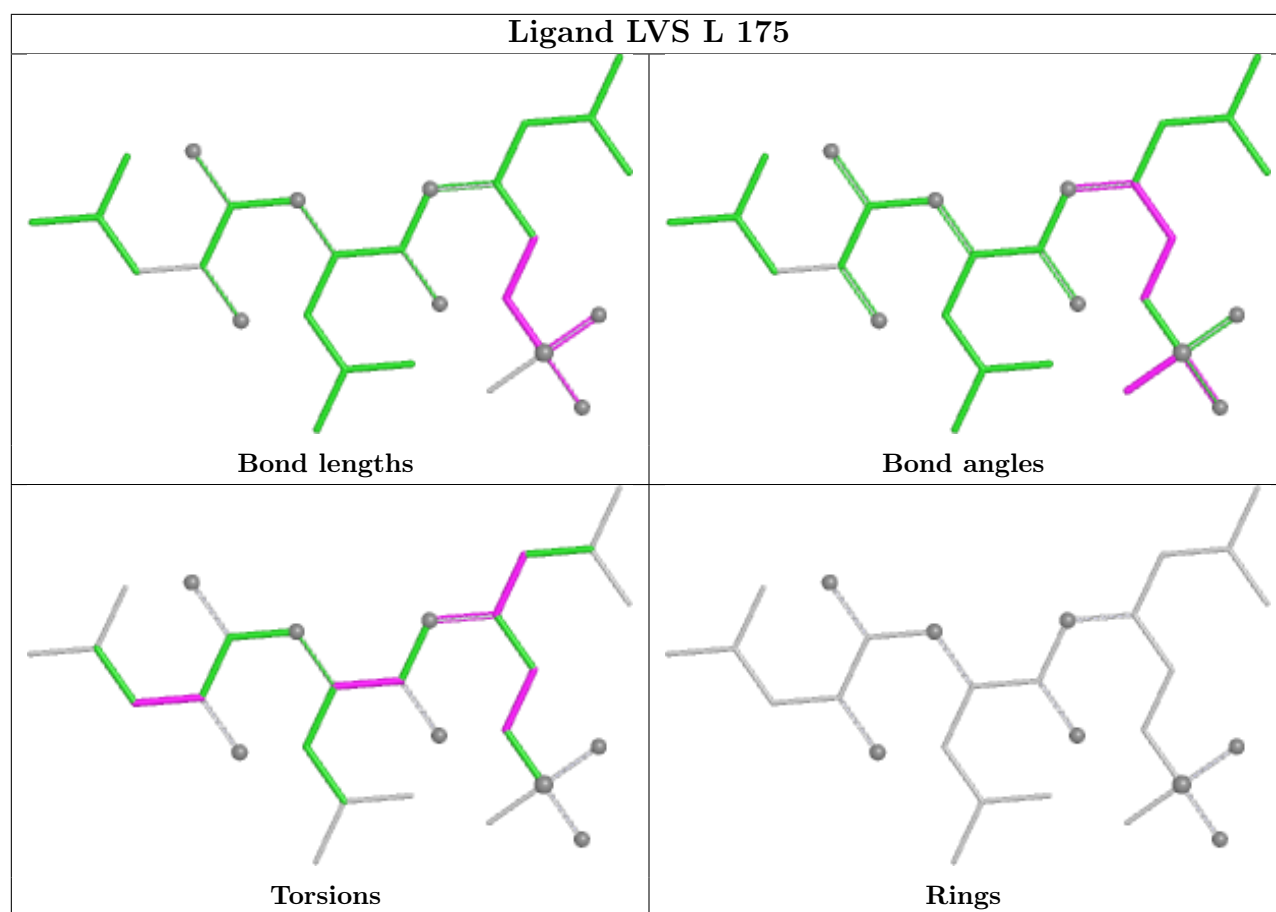


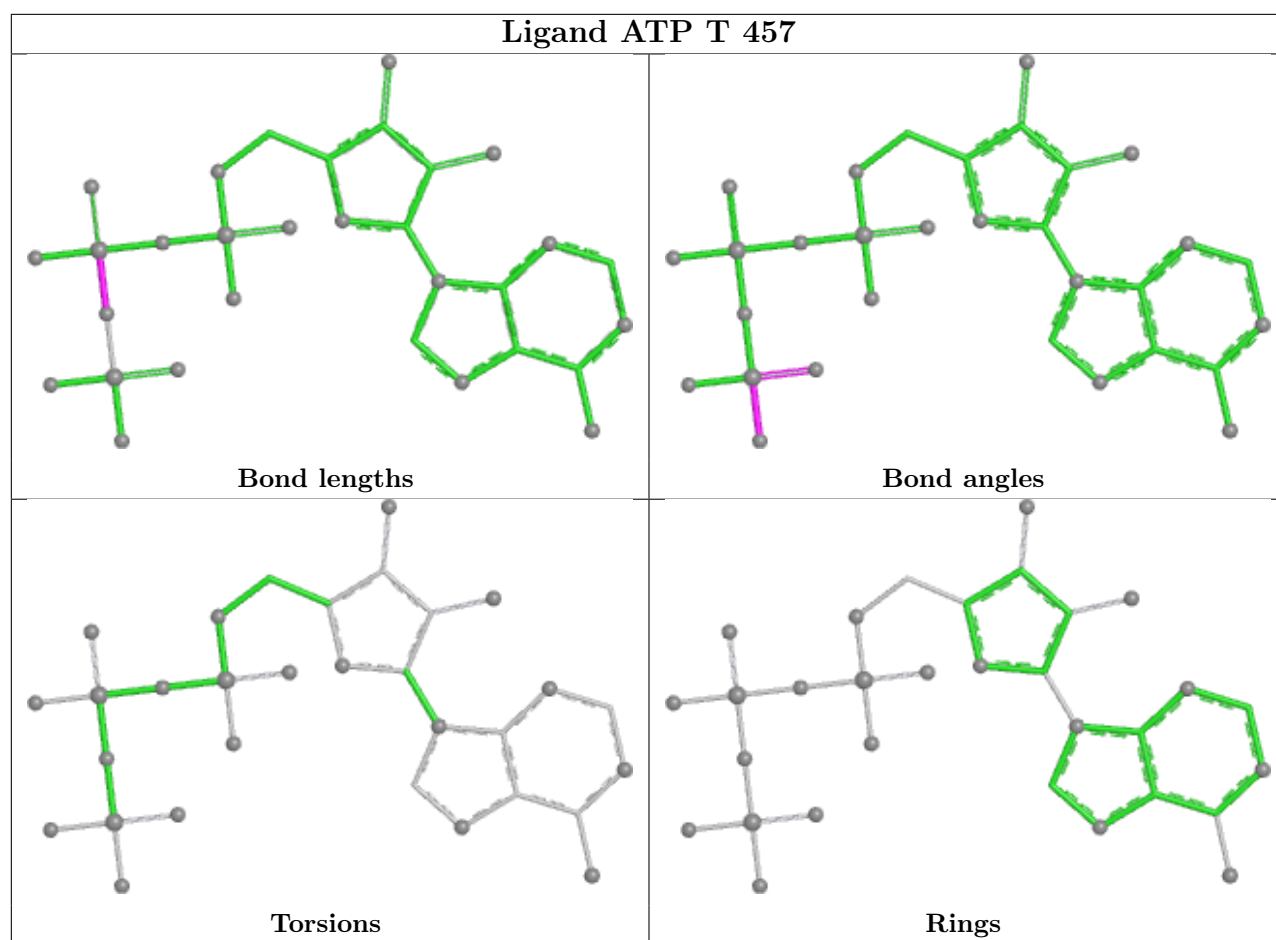


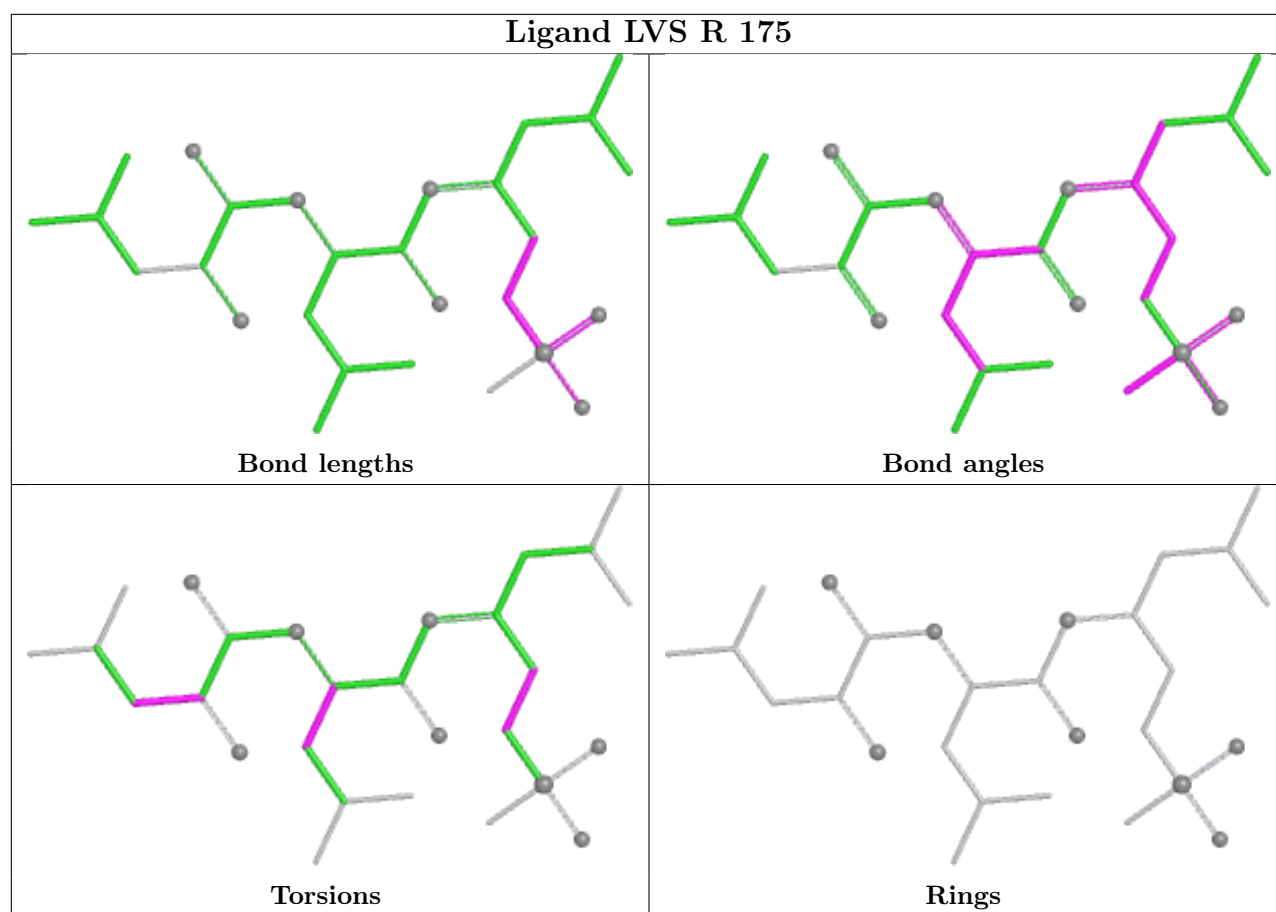


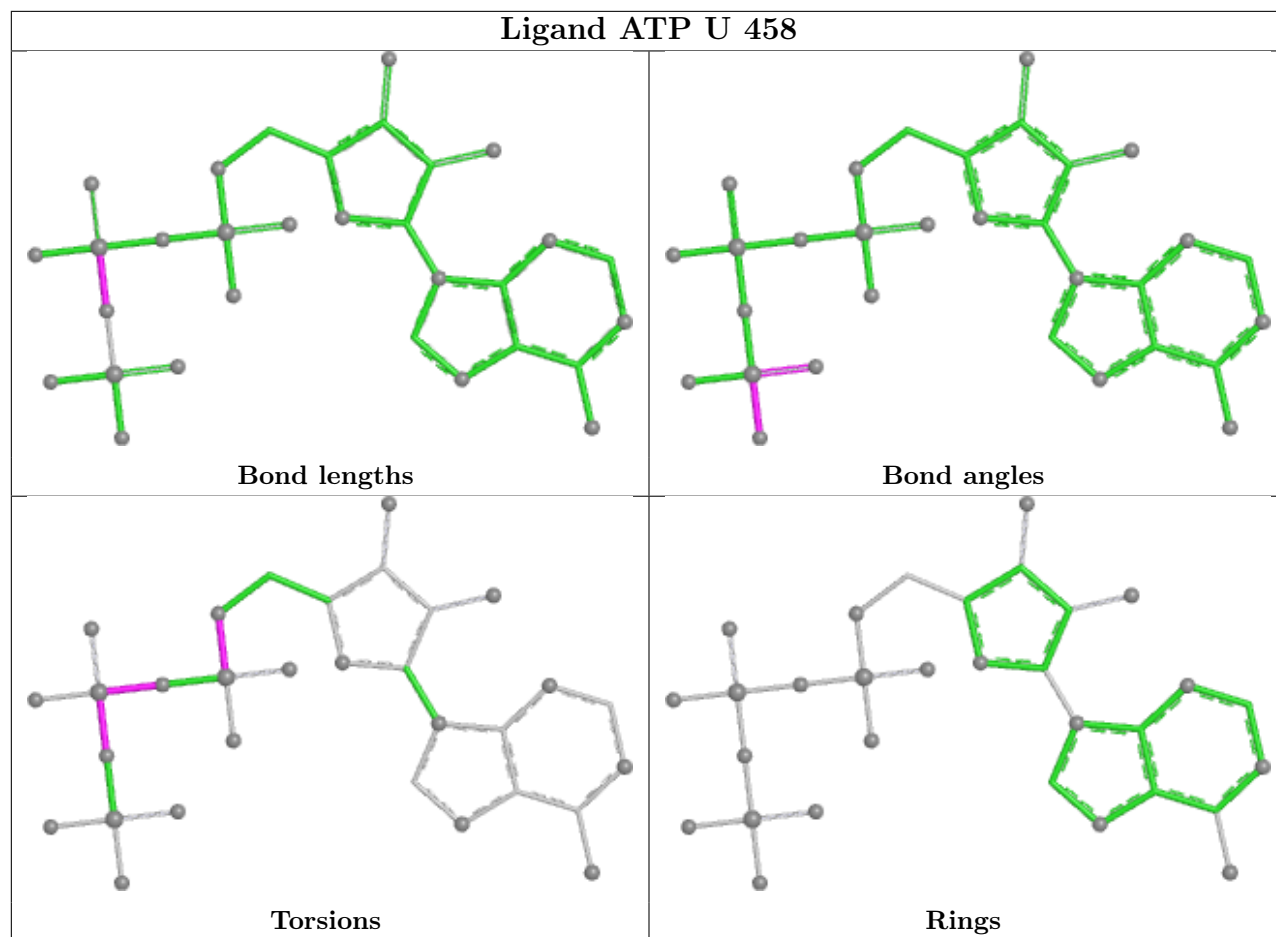


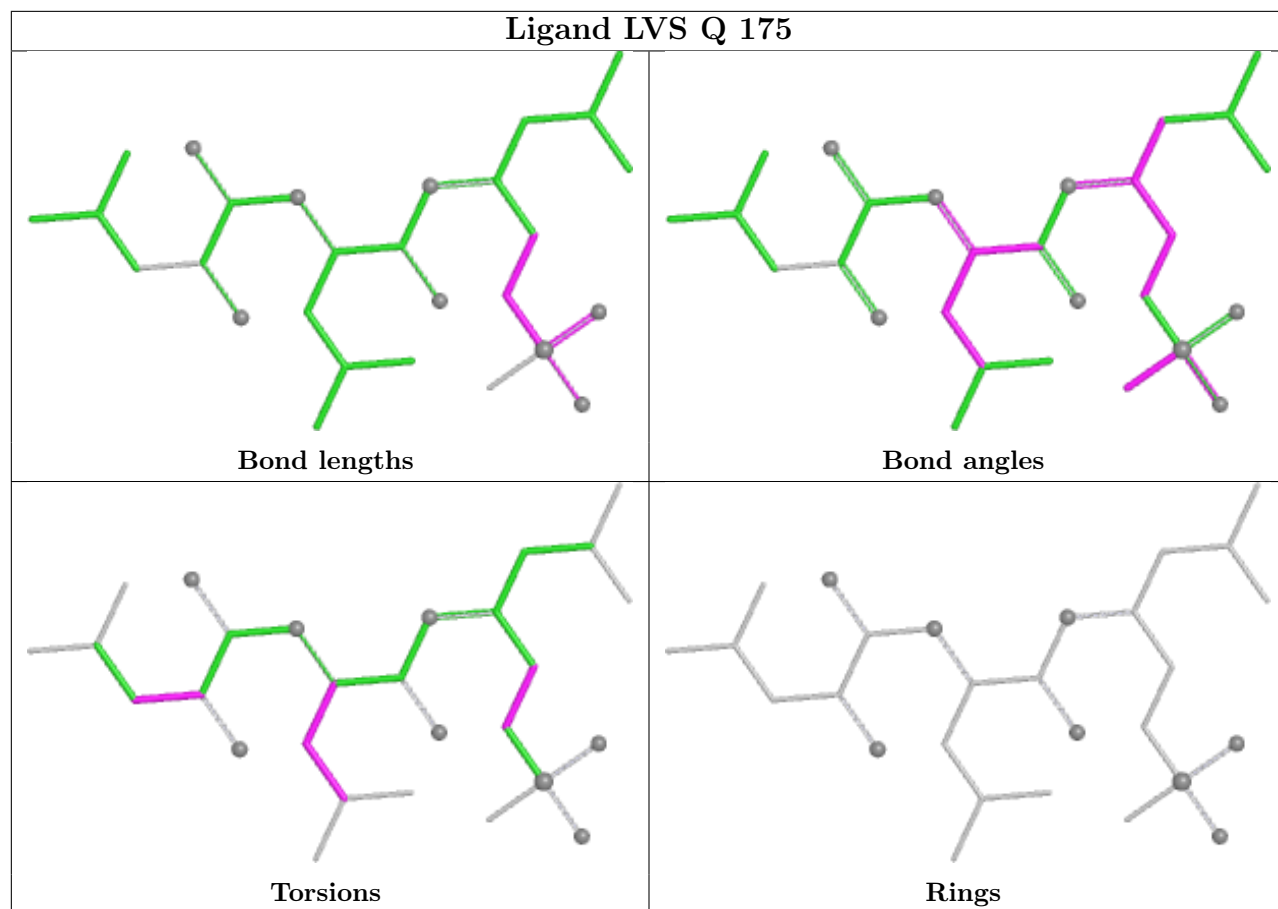




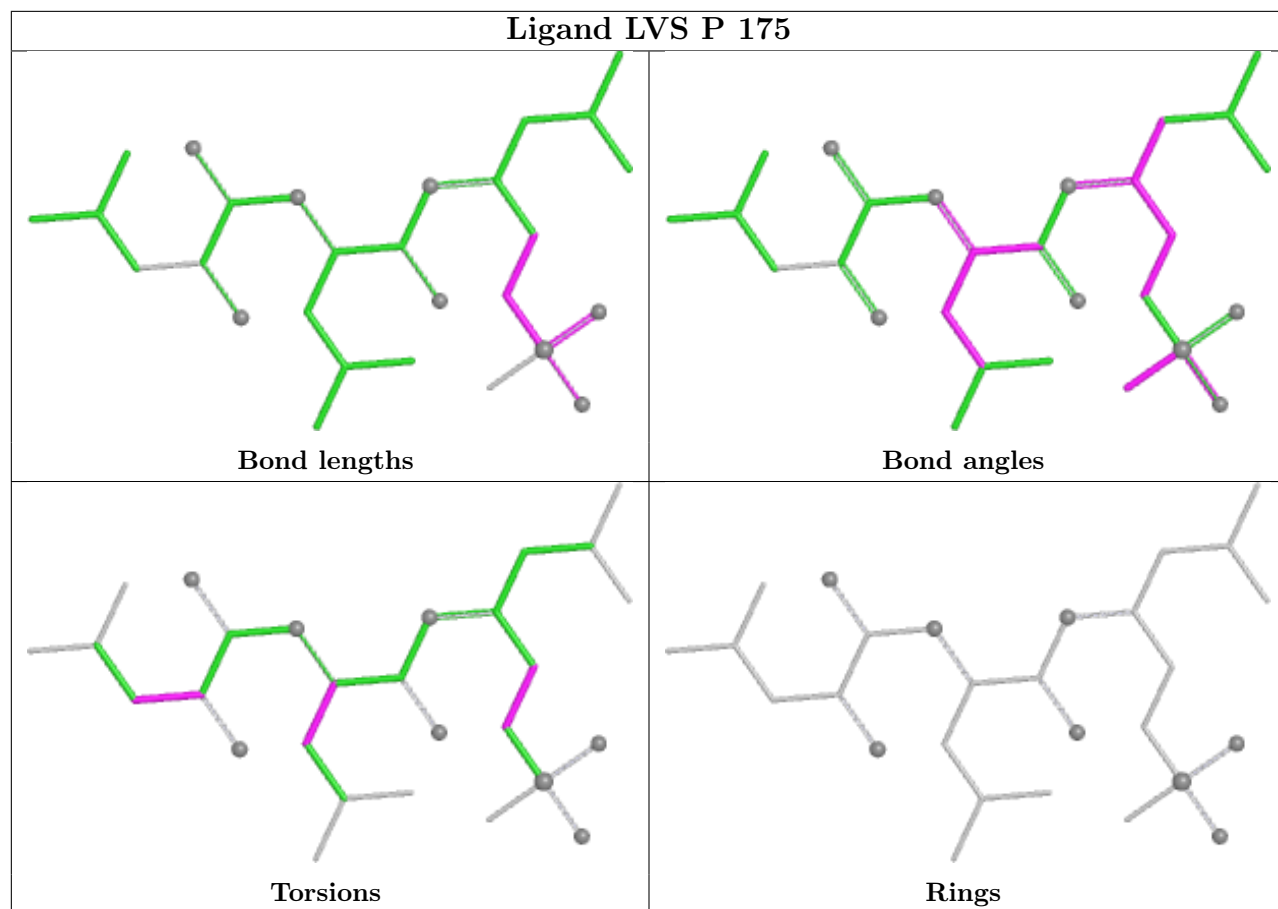


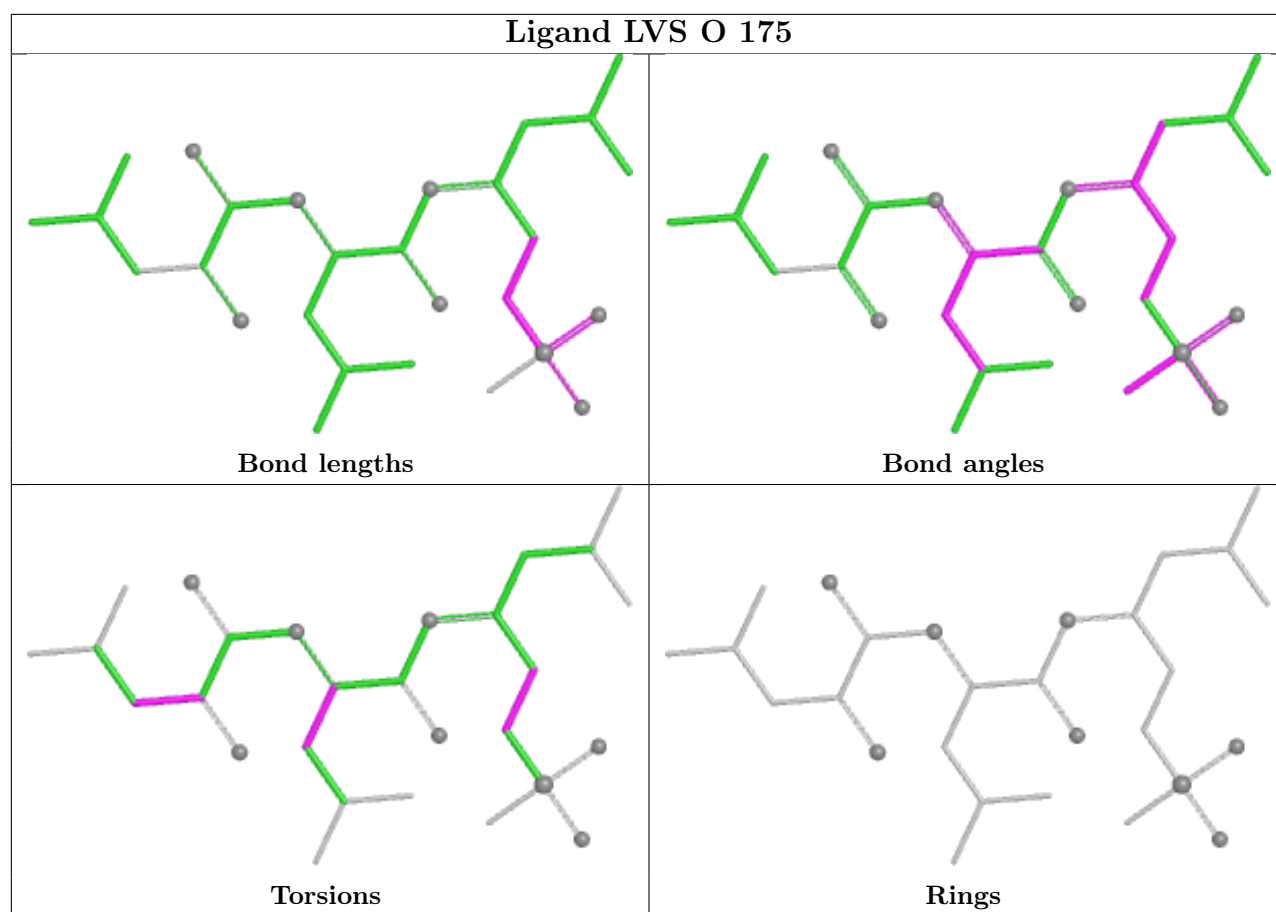


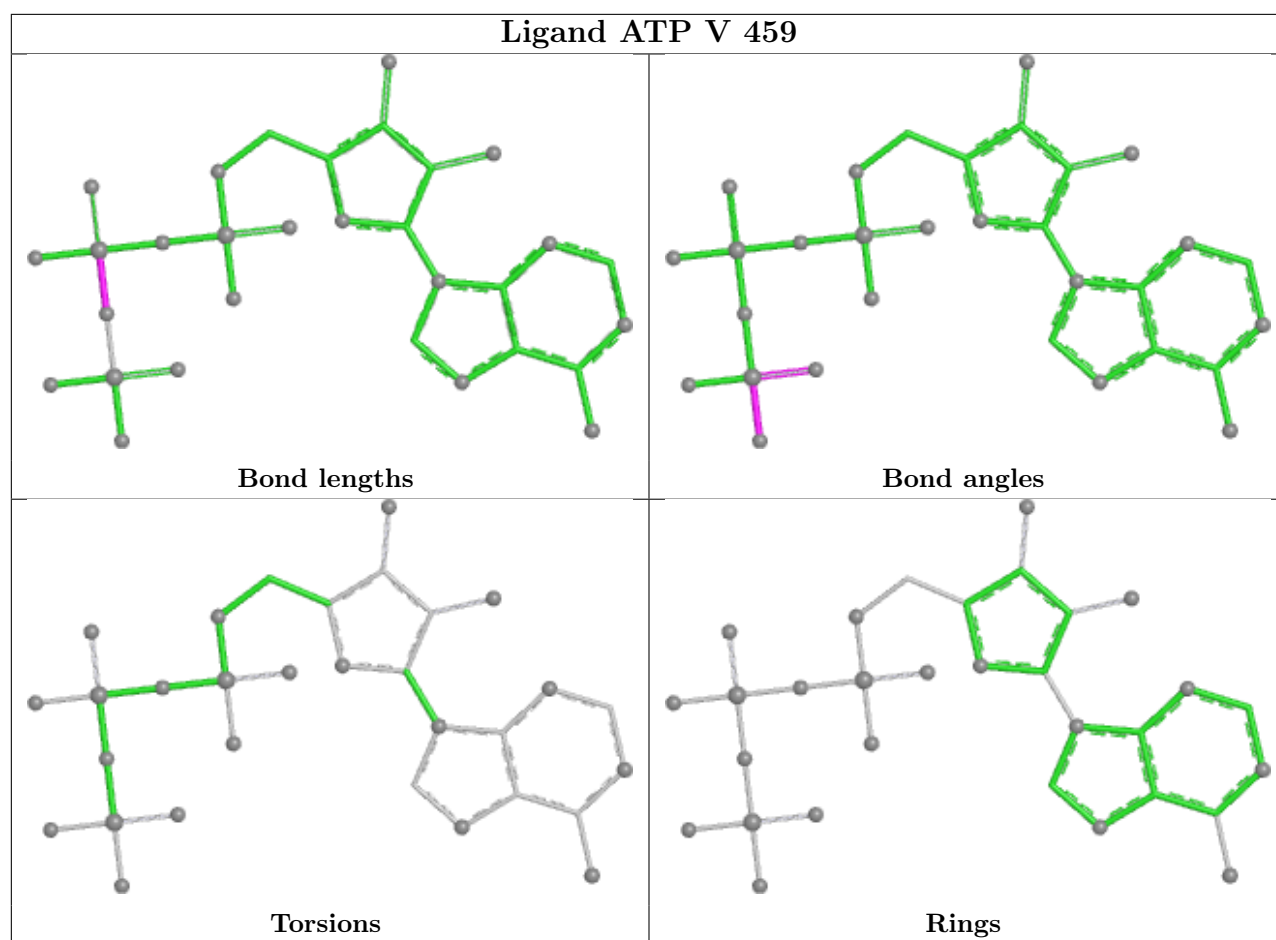


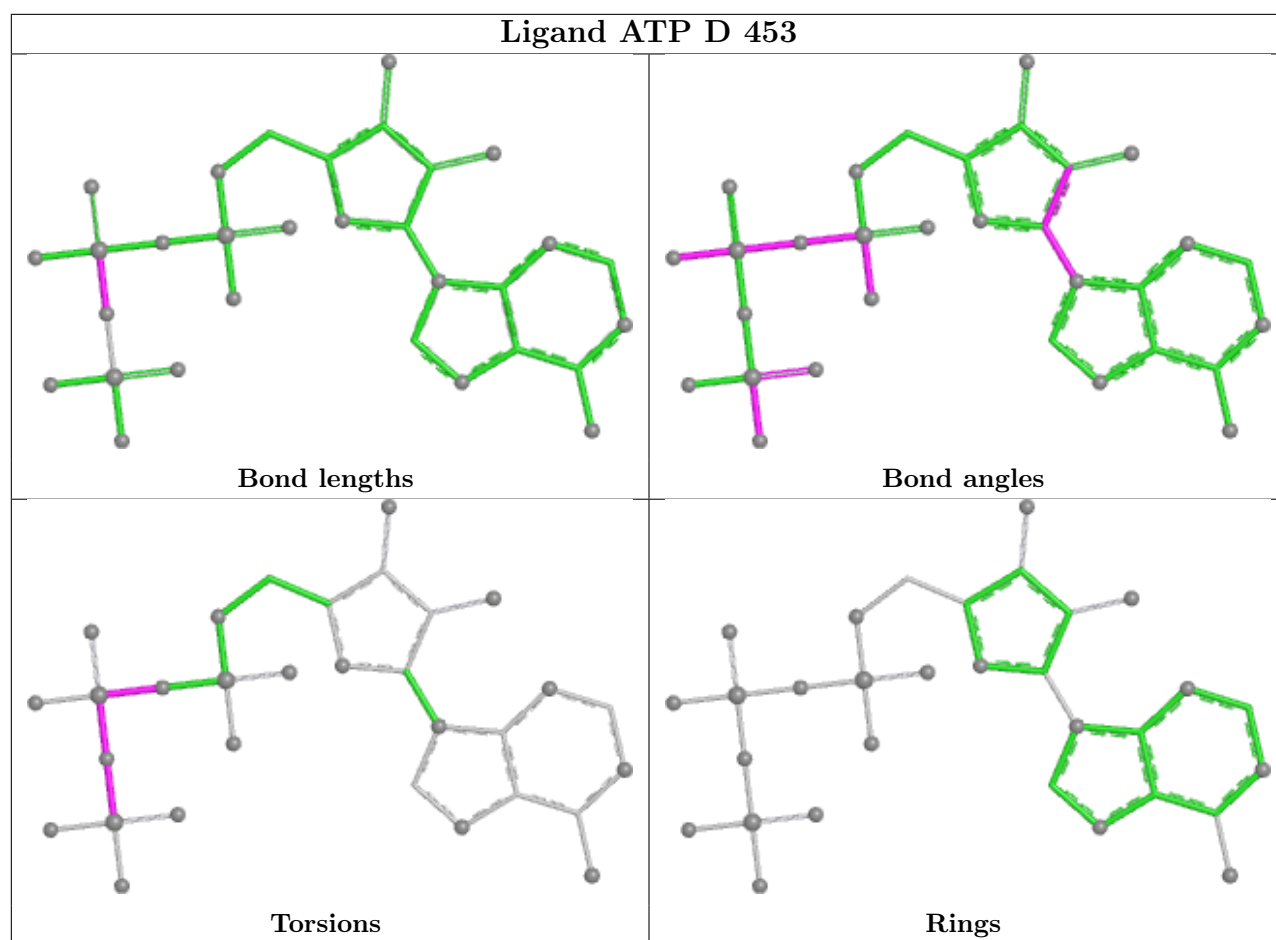


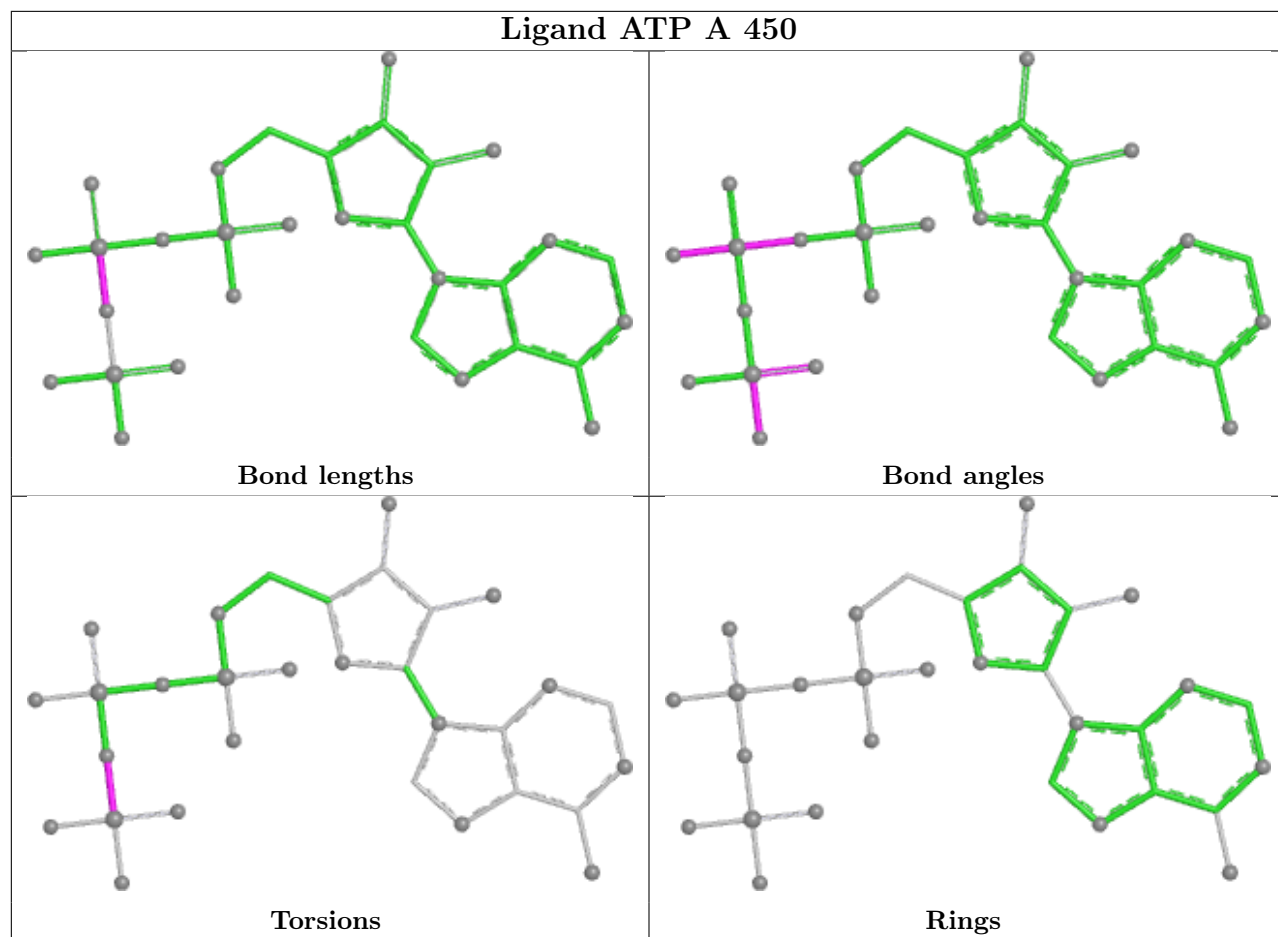
Ligand LVS P 175

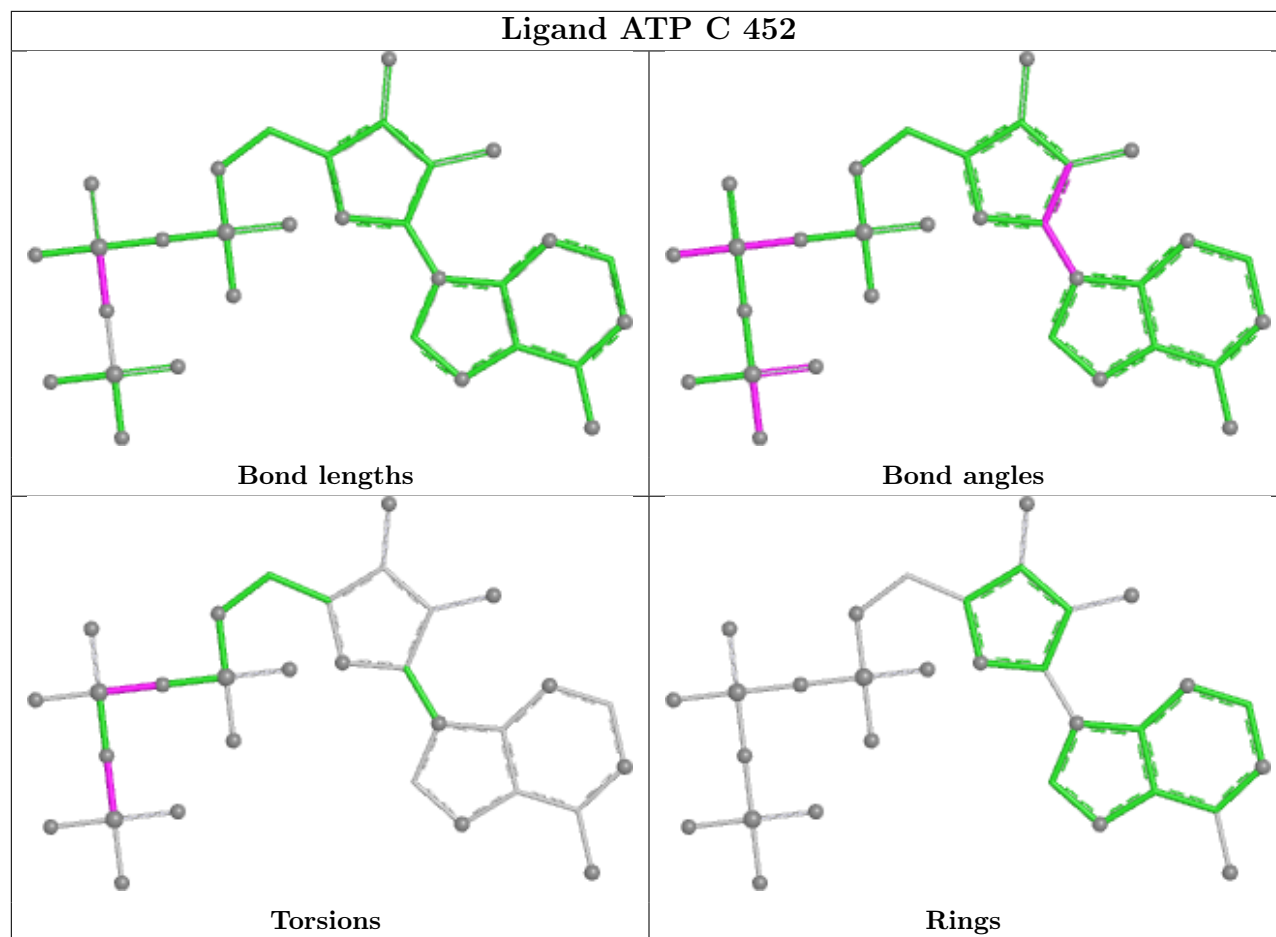


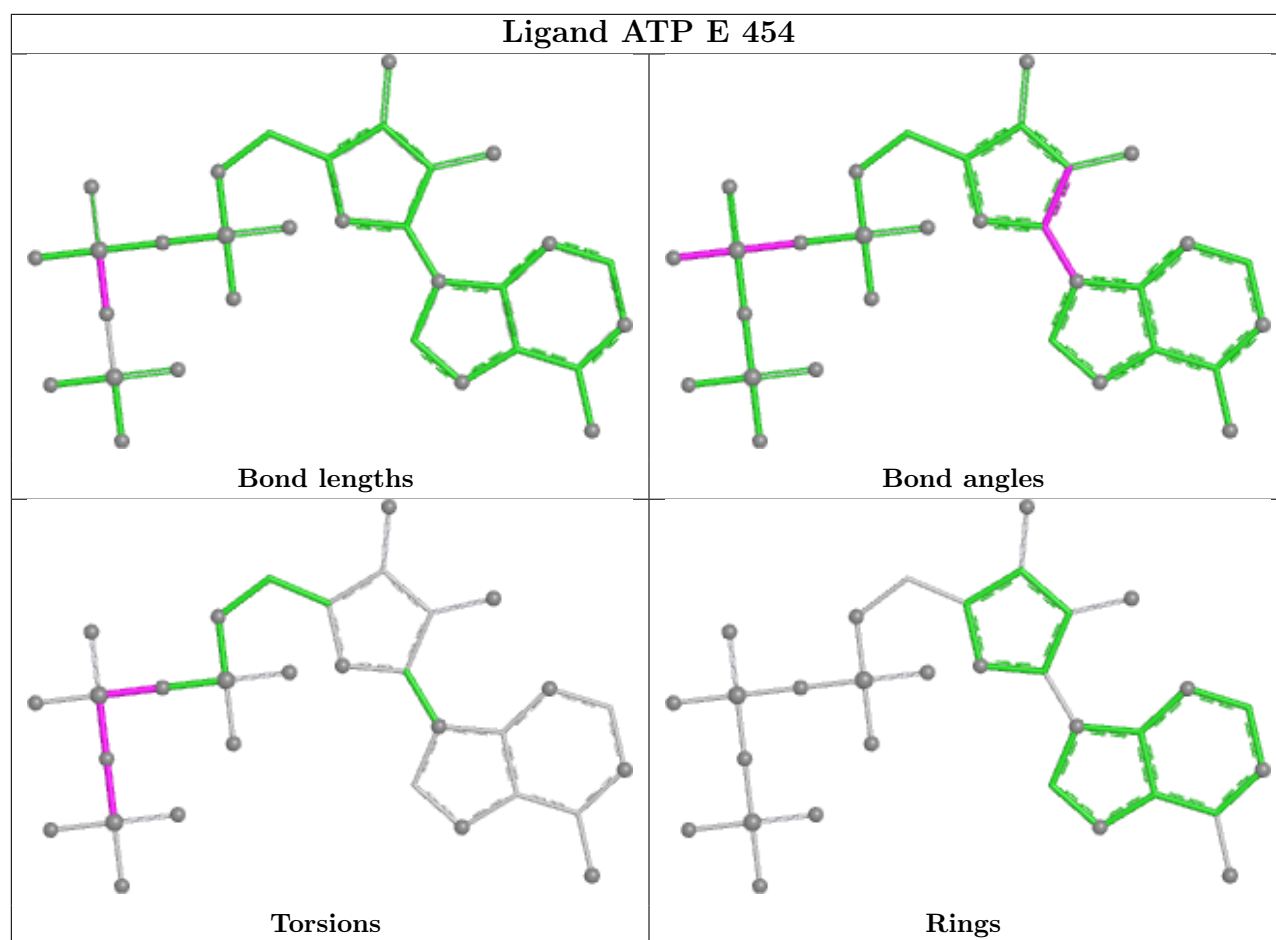


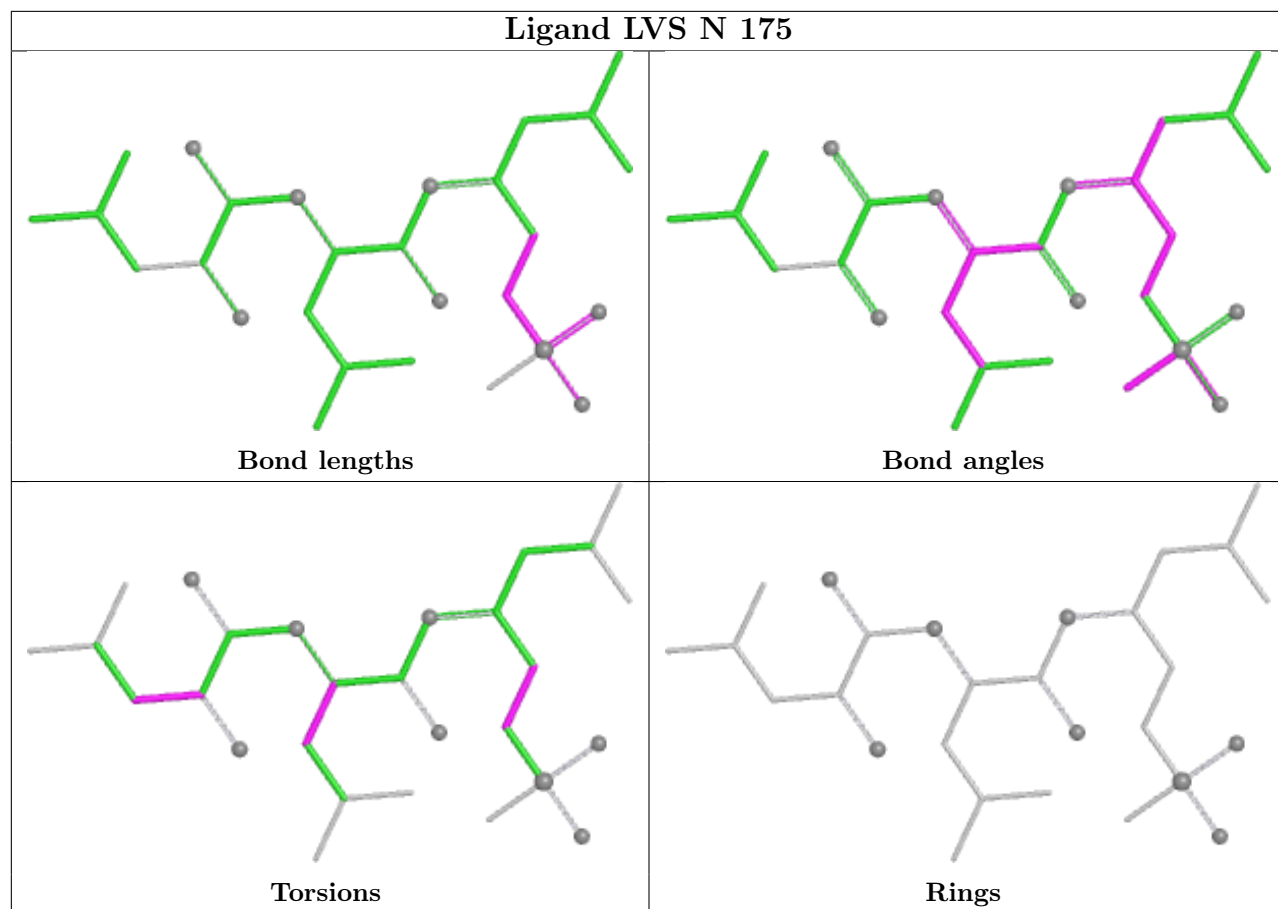


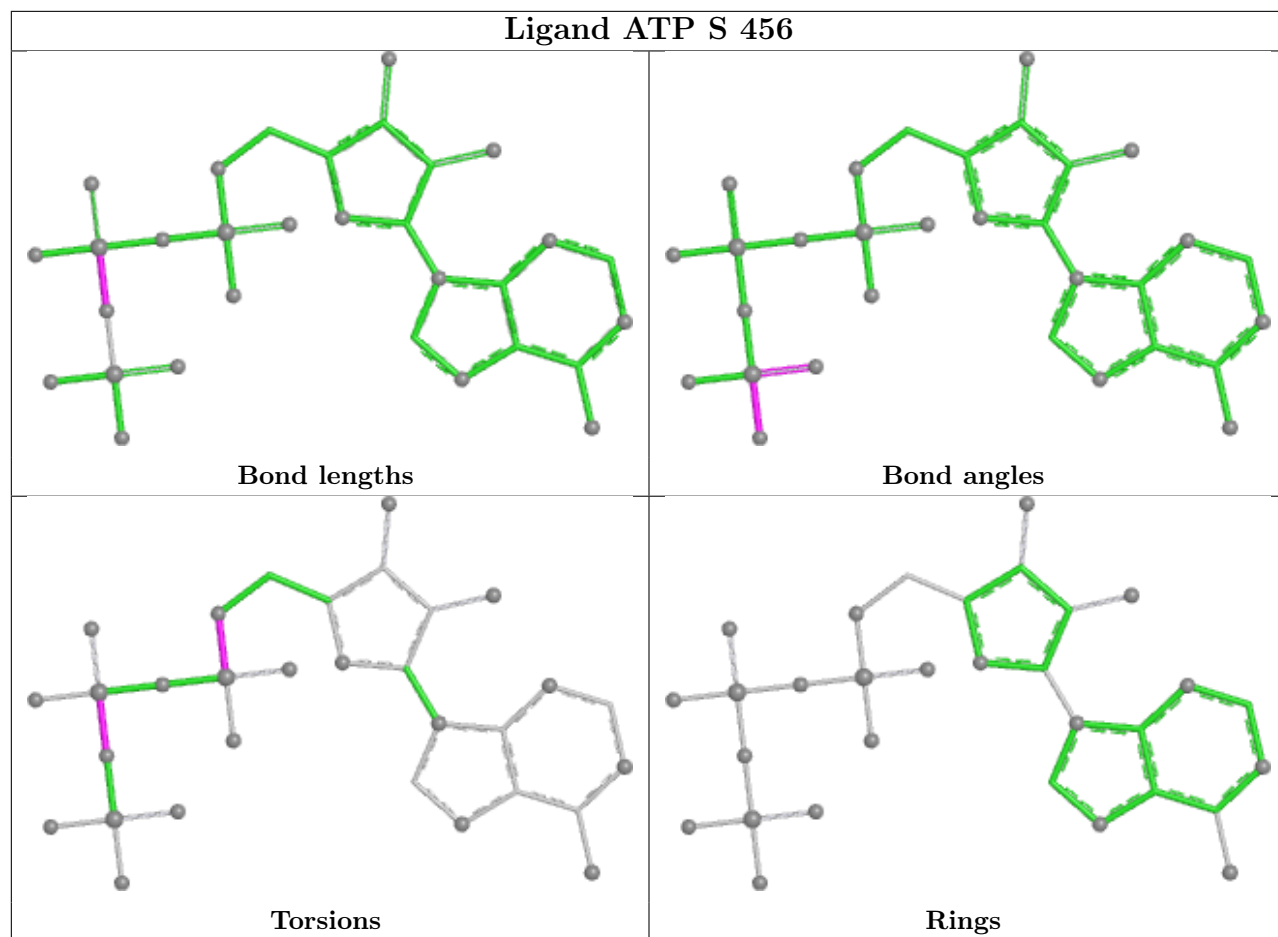




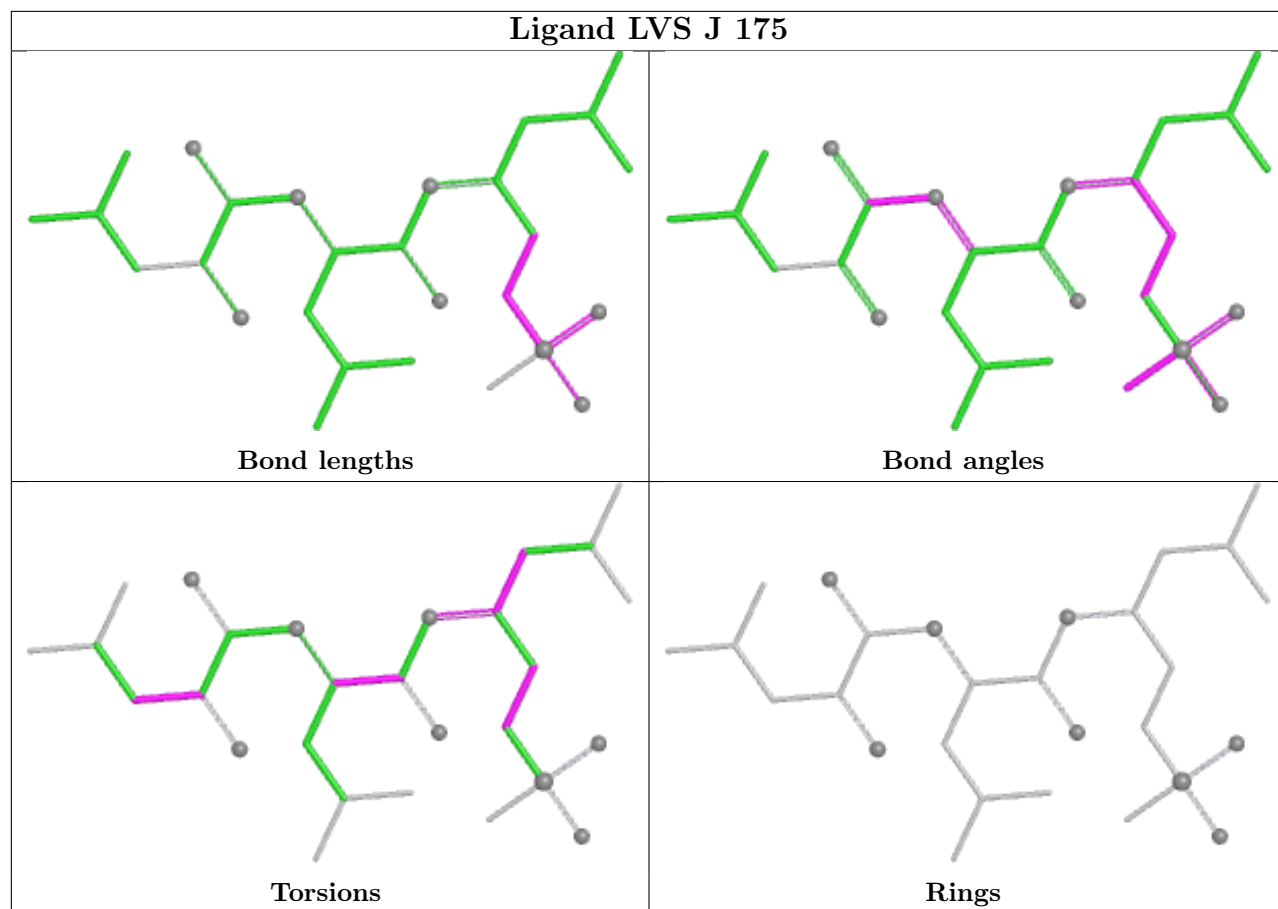


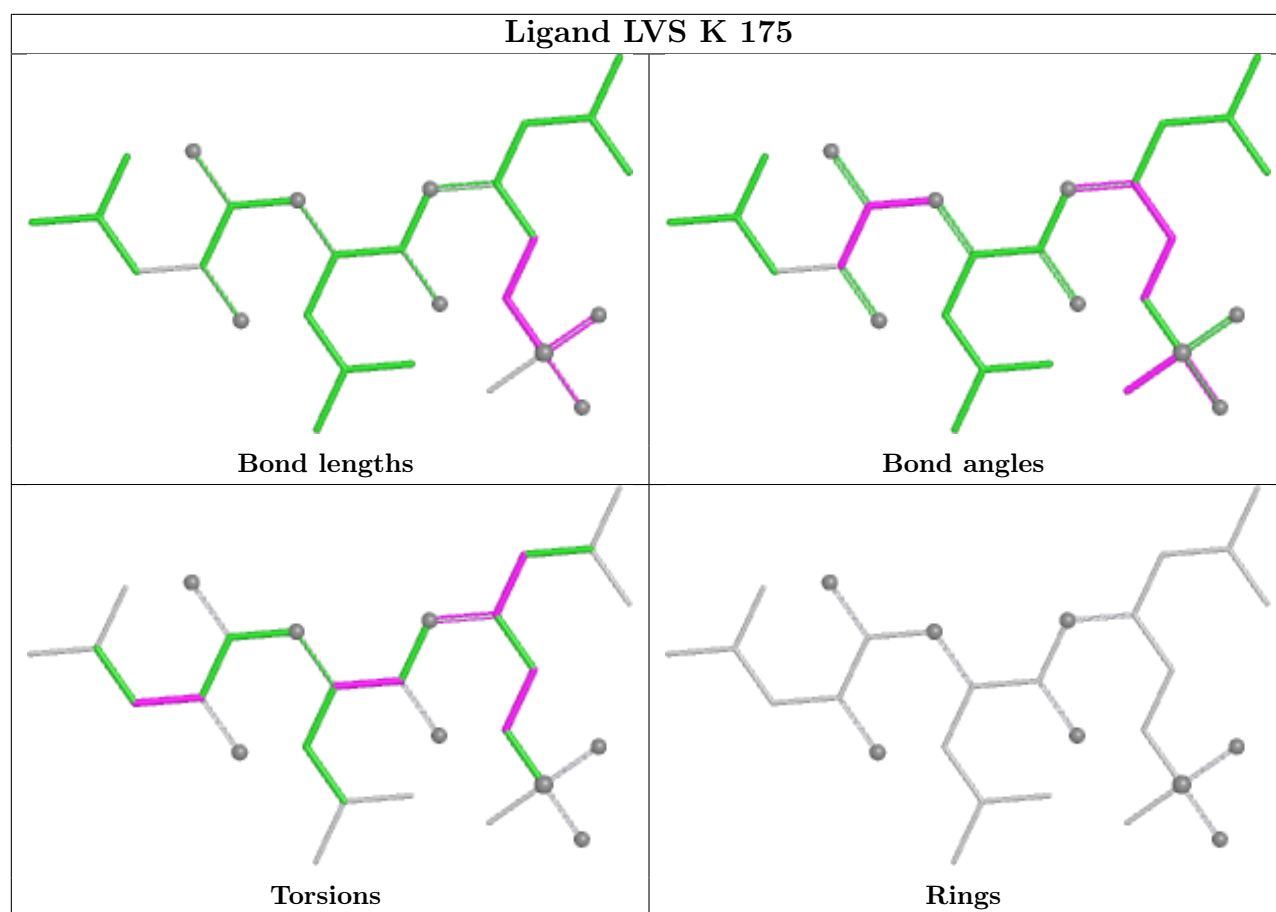


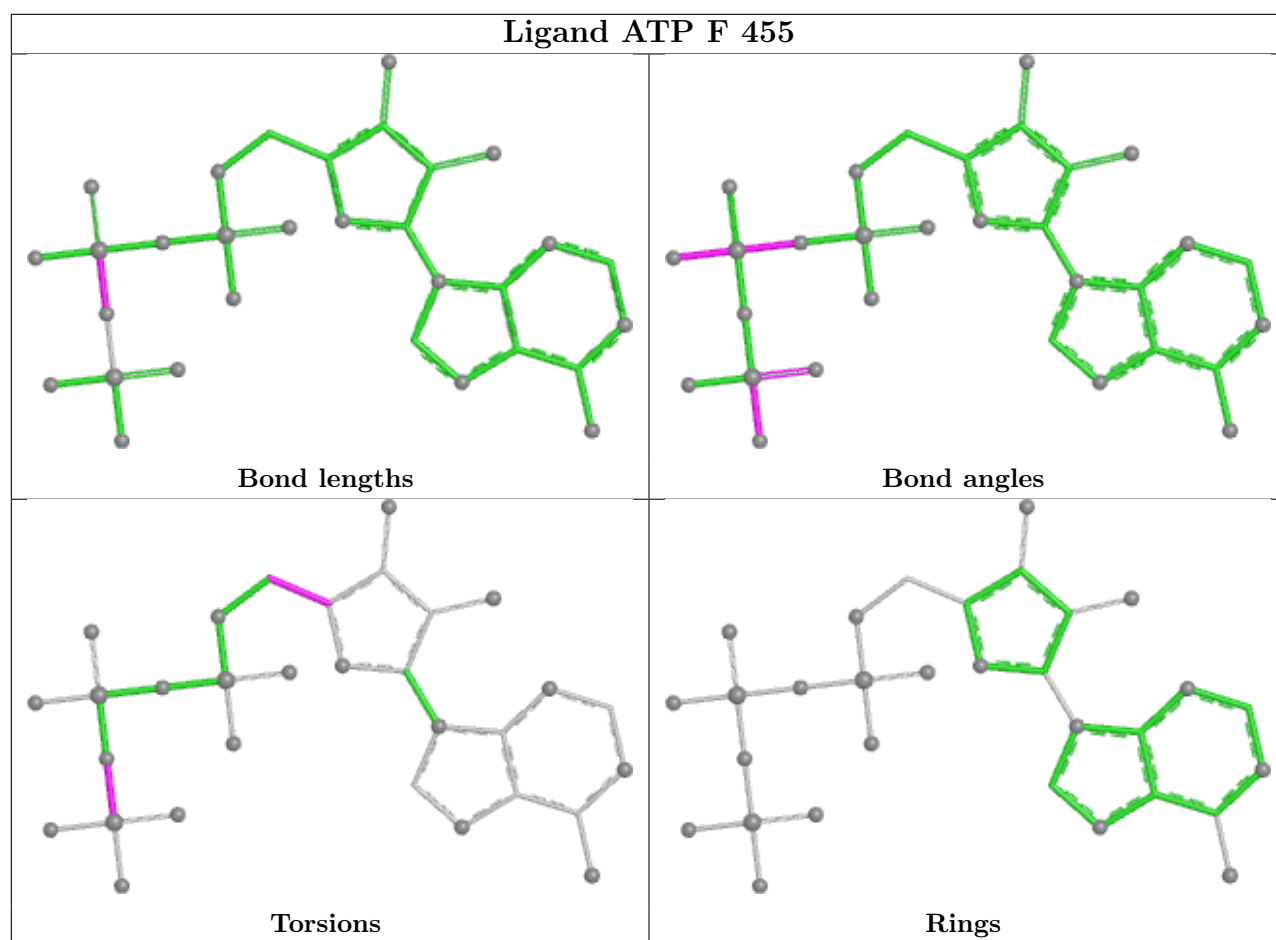


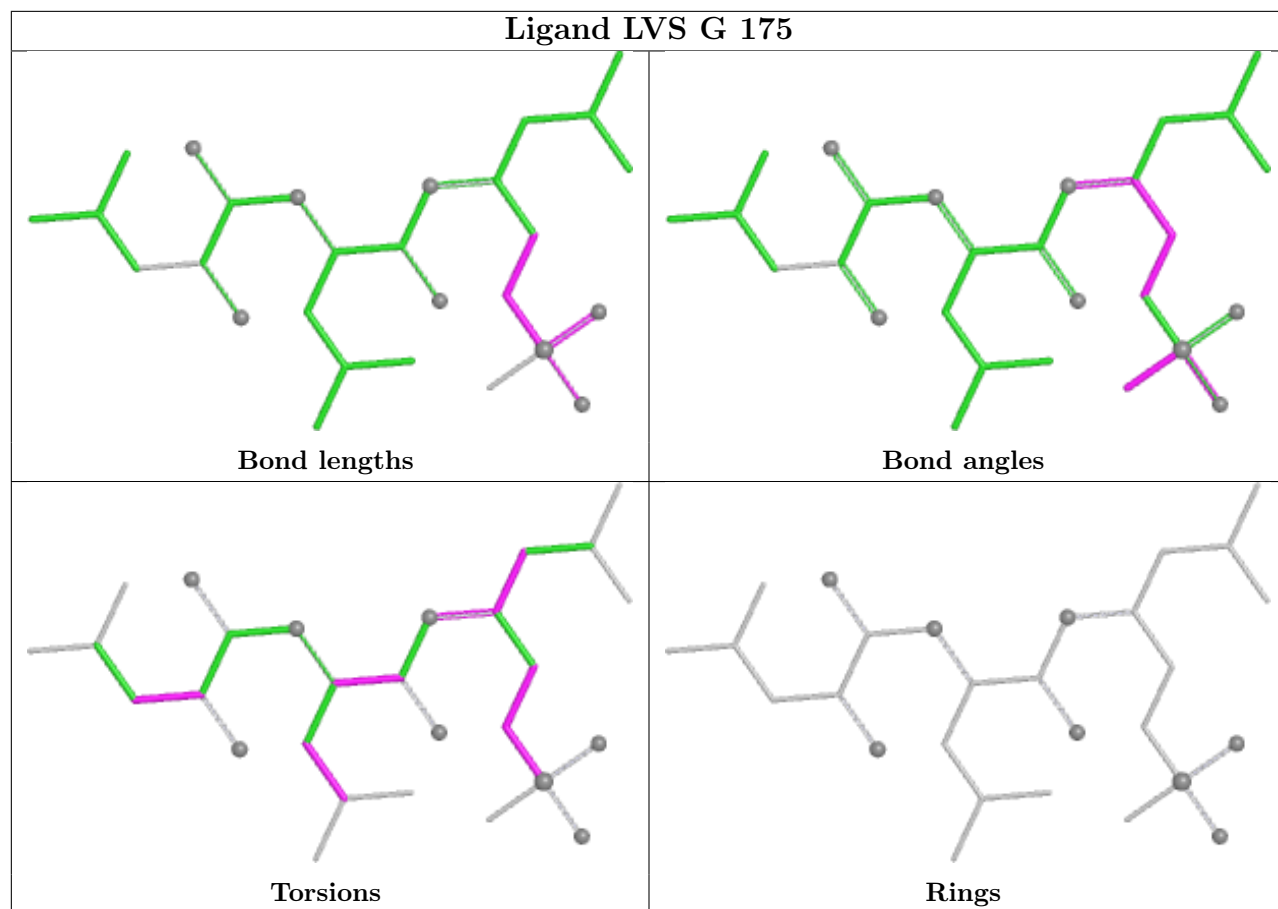


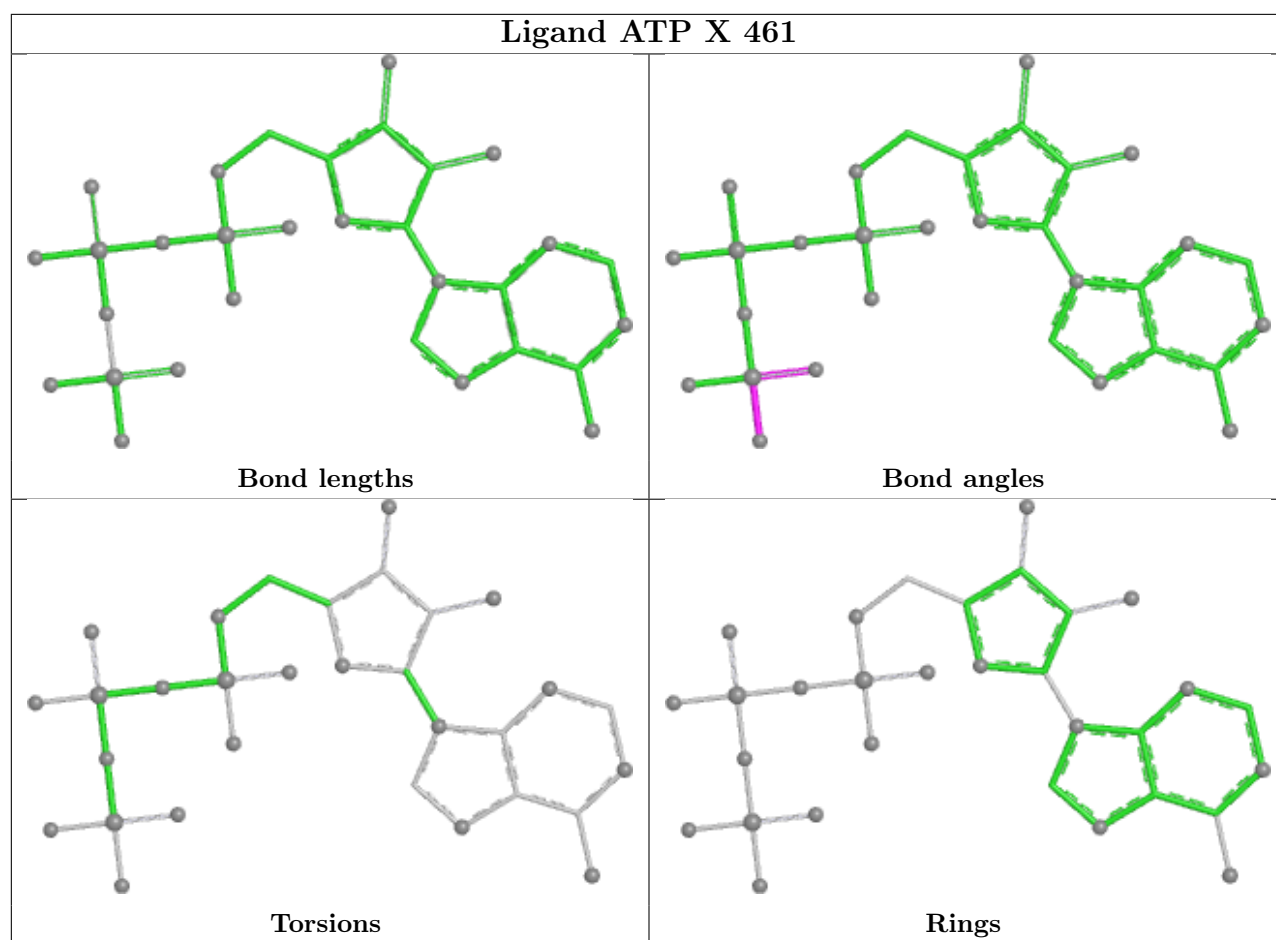
Ligand LVS J 175











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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.