



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2020 – 12:00 PM BST

PDB ID : 6UXN
Title : Crystal structure of BAK core domain BH3-groove-dimer in complex with phosphatidylserine
Authors : Cowan, A.D.; Colman, P.M.; Czabotar, P.E.
Deposited on : 2019-11-07
Resolution : 2.49 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 following versions of software and data (see [references ⓘ](#)) 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	:	2.13
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)	:	2.13

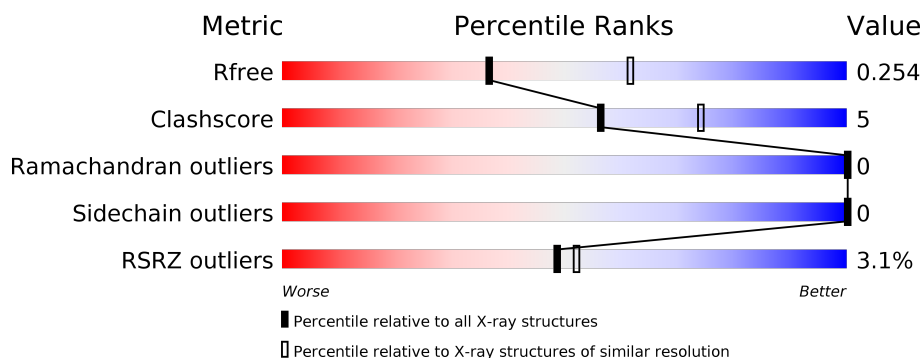
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	85	<div> <div>2%</div> <div>94%</div> <div>••</div> </div>
1	B	85	<div> <div>4%</div> <div>78%</div> <div>14%</div> <div>8%</div> </div>
1	C	85	<div> <div>7%</div> <div>82%</div> <div>13%</div> <div>5%</div> </div>
1	D	85	<div> <div>2%</div> <div>80%</div> <div>11%</div> <div>9%</div> </div>
1	E	85	<div> <div>2%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	F	85	<div> <div>2%</div> <div>71%</div> <div>22%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	85	<div><div></div><div>2%</div><div>86%</div><div>8%</div><div>6%</div></div>
1	H	85	<div><div></div><div>%</div><div>81%</div><div>9%</div><div>9%</div></div>
1	I	85	<div><div></div><div>%</div><div>86%</div><div>11%</div><div>•</div></div>
1	J	85	<div><div></div><div>5%</div><div>80%</div><div>13%</div><div>7%</div></div>
1	K	85	<div><div></div><div>5%</div><div>87%</div><div>8%</div><div>5%</div></div>
1	L	85	<div><div></div><div>%</div><div>82%</div><div>9%</div><div>8%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8306 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 Bcl-2 homologous antagonist/killer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	82	Total	C	N	O	S	0	0	0
			651	414	114	121	2			
1	B	78	Total	C	N	O	S	0	2	0
			638	406	112	118	2			
1	C	81	Total	C	N	O	S	0	0	0
			644	410	113	119	2			
1	D	77	Total	C	N	O	S	0	0	0
			622	397	109	114	2			
1	E	79	Total	C	N	O	S	0	0	0
			634	405	111	116	2			
1	F	79	Total	C	N	O	S	0	0	0
			634	405	111	116	2			
1	G	80	Total	C	N	O	S	0	0	0
			640	408	112	118	2			
1	H	77	Total	C	N	O	S	0	0	0
			622	397	109	114	2			
1	I	82	Total	C	N	O	S	0	0	0
			651	414	114	121	2			
1	J	79	Total	C	N	O	S	0	0	0
			632	402	111	117	2			
1	K	81	Total	C	N	O	S	0	0	0
			644	410	113	119	2			
1	L	78	Total	C	N	O	S	0	1	0
			636	405	113	116	2			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	64	GLY	-	expression tag	UNP Q16611
A	65	PRO	-	expression tag	UNP Q16611
A	66	LEU	-	expression tag	UNP Q16611
A	67	GLY	-	expression tag	UNP Q16611
B	64	GLY	-	expression tag	UNP Q16611

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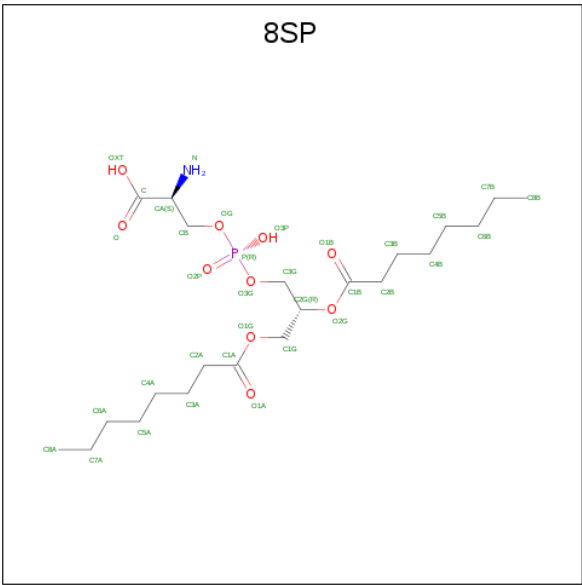
Chain	Residue	Modelled	Actual	Comment	Reference
B	65	PRO	-	expression tag	UNP Q16611
B	66	LEU	-	expression tag	UNP Q16611
B	67	GLY	-	expression tag	UNP Q16611
C	64	GLY	-	expression tag	UNP Q16611
C	65	PRO	-	expression tag	UNP Q16611
C	66	LEU	-	expression tag	UNP Q16611
C	67	GLY	-	expression tag	UNP Q16611
D	64	GLY	-	expression tag	UNP Q16611
D	65	PRO	-	expression tag	UNP Q16611
D	66	LEU	-	expression tag	UNP Q16611
D	67	GLY	-	expression tag	UNP Q16611
E	64	GLY	-	expression tag	UNP Q16611
E	65	PRO	-	expression tag	UNP Q16611
E	66	LEU	-	expression tag	UNP Q16611
E	67	GLY	-	expression tag	UNP Q16611
F	64	GLY	-	expression tag	UNP Q16611
F	65	PRO	-	expression tag	UNP Q16611
F	66	LEU	-	expression tag	UNP Q16611
F	67	GLY	-	expression tag	UNP Q16611
G	64	GLY	-	expression tag	UNP Q16611
G	65	PRO	-	expression tag	UNP Q16611
G	66	LEU	-	expression tag	UNP Q16611
G	67	GLY	-	expression tag	UNP Q16611
H	64	GLY	-	expression tag	UNP Q16611
H	65	PRO	-	expression tag	UNP Q16611
H	66	LEU	-	expression tag	UNP Q16611
H	67	GLY	-	expression tag	UNP Q16611
I	64	GLY	-	expression tag	UNP Q16611
I	65	PRO	-	expression tag	UNP Q16611
I	66	LEU	-	expression tag	UNP Q16611
I	67	GLY	-	expression tag	UNP Q16611
J	64	GLY	-	expression tag	UNP Q16611
J	65	PRO	-	expression tag	UNP Q16611
J	66	LEU	-	expression tag	UNP Q16611
J	67	GLY	-	expression tag	UNP Q16611
K	64	GLY	-	expression tag	UNP Q16611
K	65	PRO	-	expression tag	UNP Q16611
K	66	LEU	-	expression tag	UNP Q16611
K	67	GLY	-	expression tag	UNP Q16611
L	64	GLY	-	expression tag	UNP Q16611
L	65	PRO	-	expression tag	UNP Q16611
L	66	LEU	-	expression tag	UNP Q16611

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Chain	Residue	Modelled	Actual	Comment	Reference
L	67	GLY	-	expression tag	UNP Q16611

- Molecule 2 is O-[(R)-{[(2R)-2,3-bis(octanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (three-letter code: 8SP) (formula: C₂₂H₄₂NO₁₀P) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			26	17	8	1		
2	A	1	Total	C	N	O	P	0
			28	16	1	10	1	
2	B	1	Total	C	N	O	P	0
			25	15	1	8	1	
2	B	1	Total	C	N	O	P	0
			30	18	1	10	1	
2	D	1	Total	C	O	P	0	0
			27	18	8	1		
2	D	1	Total	C	O	P	0	0
			18	11	6	1		
2	E	1	Total	C	O	P	0	0
			27	18	8	1		
2	F	1	Total	C	O	P	0	0
			29	20	8	1		
2	F	1	Total	C	N	O	P	0
			31	19	1	10	1	
2	G	1	Total	C	O	P	0	0
			25	16	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	P	0	0
			28	16	1	10	1		
2	H	1	Total	C	N	O	P	0	0
			33	21	1	10	1		
2	I	1	Total	C	O	P		0	0
			20	13	6	1			
2	J	1	Total	C	N	O	P	0	0
			29	17	1	10	1		
2	J	1	Total	C	N	O	P	0	0
			24	14	1	8	1		
2	K	1	Total	C	O	P		0	0
			25	16	8	1			
2	L	1	Total	C	N	O	P	0	0
			25	15	1	8	1		
2	L	1	Total	C	N	O	P	0	0
			34	22	1	10	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	B	9	Total	O	0	0
			9	9		
5	C	4	Total	O	0	0
			4	4		
5	D	9	Total	O	0	0
			9	9		
5	E	7	Total	O	0	0
			7	7		
5	F	8	Total	O	0	0
			8	8		
5	G	5	Total	O	0	0
			5	5		
5	H	5	Total	O	0	0
			5	5		
5	I	2	Total	O	0	0
			2	2		
5	J	10	Total	O	0	0
			10	10		
5	K	3	Total	O	0	0
			3	3		

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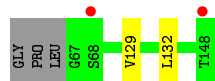
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	7	Total	O	0	0
			7	7		

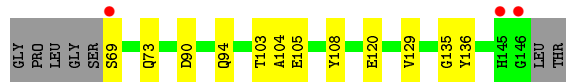
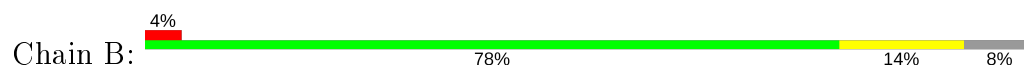
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

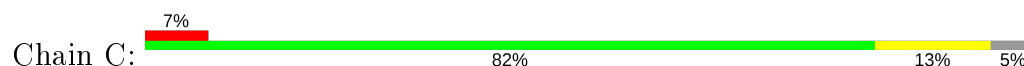
- Molecule 1: Bcl-2 homologous antagonist/killer



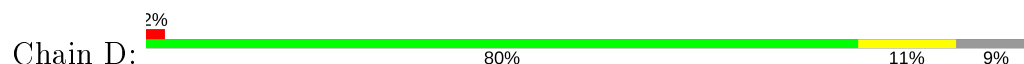
- Molecule 1: Bcl-2 homologous antagonist/killer



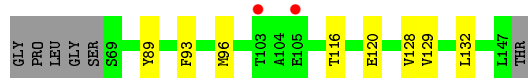
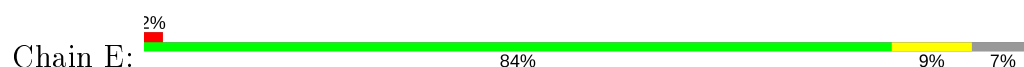
- Molecule 1: Bcl-2 homologous antagonist/killer



- Molecule 1: Bcl-2 homologous antagonist/killer



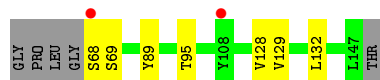
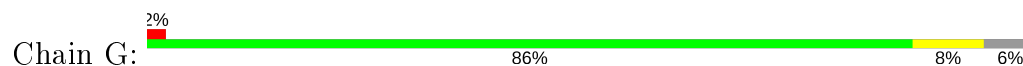
- Molecule 1: Bcl-2 homologous antagonist/killer



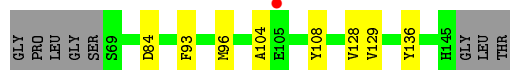
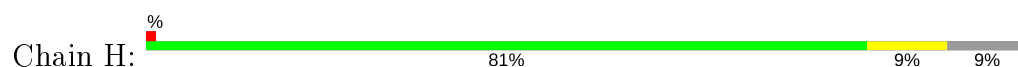
- Molecule 1: Bcl-2 homologous antagonist/killer



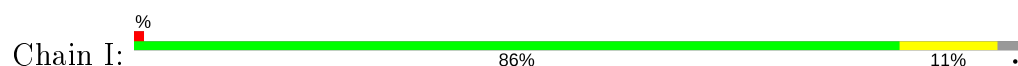
- Molecule 1: Bcl-2 homologous antagonist/killer



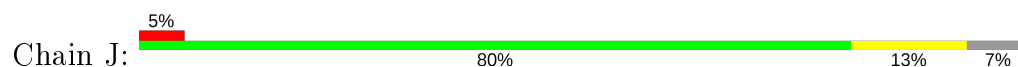
- Molecule 1: Bcl-2 homologous antagonist/killer



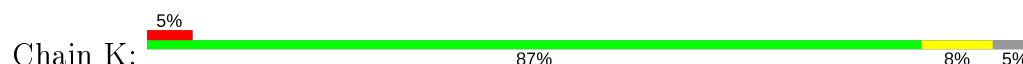
- Molecule 1: Bcl-2 homologous antagonist/killer



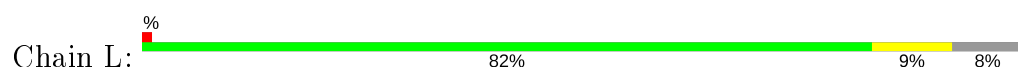
- Molecule 1: Bcl-2 homologous antagonist/killer



- Molecule 1: Bcl-2 homologous antagonist/killer



- Molecule 1: Bcl-2 homologous antagonist/killer



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.76 Å 91.09 Å 96.39 Å 90.00° 107.07° 90.00°	Depositor
Resolution (Å)	45.74 – 2.49 45.74 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.6 (45.74-2.49) 88.8 (45.74-2.49)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.16 (at 2.48 Å)	Xtriage
Refinement program	PHENIX 1.14	Depositor
R, R_{free}	0.205 , 0.253 0.204 , 0.254	Depositor DCC
R_{free} test set	2000 reflections (4.40%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8306	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0918e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 8SP, SO4

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	0.25	0/665	0.40	0/899
1	B	0.24	0/655	0.38	0/885
1	C	0.25	0/658	0.39	0/889
1	D	0.24	0/636	0.39	0/860
1	E	0.25	0/648	0.39	0/876
1	F	0.25	0/648	0.43	0/876
1	G	0.25	0/654	0.38	0/884
1	H	0.24	0/636	0.39	0/860
1	I	0.25	0/665	0.40	0/899
1	J	0.25	0/646	0.40	0/873
1	K	0.24	0/658	0.40	0/889
1	L	0.24	0/651	0.40	0/880
All	All	0.25	0/7820	0.40	0/10570

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	651	0	630	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	638	0	616	9	0
1	C	644	0	623	8	0
1	D	622	0	601	8	0
1	E	634	0	615	6	0
1	F	634	0	615	17	0
1	G	640	0	620	6	0
1	H	622	0	601	8	0
1	I	651	0	630	7	0
1	J	632	0	609	10	0
1	K	644	0	623	5	0
1	L	636	0	610	9	0
2	A	54	0	52	2	0
2	B	55	0	54	4	0
2	D	45	0	49	5	0
2	E	27	0	28	3	0
2	F	60	0	67	3	0
2	G	25	0	24	2	0
2	H	61	0	62	5	0
2	I	20	0	20	2	0
2	J	53	0	53	4	0
2	K	25	0	24	1	0
2	L	59	0	65	5	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	15	0	0	0	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
3	H	15	0	0	0	0
3	I	5	0	0	1	0
3	K	10	0	0	0	0
3	L	15	0	0	0	0
4	C	6	0	8	1	0
5	A	4	0	0	0	0
5	B	9	0	0	0	0
5	C	4	0	0	0	0
5	D	9	0	0	0	0
5	E	7	0	0	0	0
5	F	8	0	0	0	0
5	G	5	0	0	0	0
5	H	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	2	0	0	0	0
5	J	10	0	0	0	0
5	K	3	0	0	0	0
5	L	7	0	0	0	0
All	All	8306	0	7899	80	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 80 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:J:73:GLN:HE21	1:L:122:GLY:HA2	1.41	0.83
1:F:105:GLU:OE2	1:J:99:HIS:NE2	2.15	0.79
1:B:104:ALA:O	2:B:202:8SP:N	2.18	0.76
1:F:104:ALA:O	2:F:202:8SP:N	2.21	0.74
1:J:108:TYR:HB3	2:J:201:8SP:HA	1.70	0.72

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	80/85 (94%)	79 (99%)	1 (1%)	0	100	100
1	B	78/85 (92%)	77 (99%)	1 (1%)	0	100	100
1	C	79/85 (93%)	79 (100%)	0	0	100	100
1	D	75/85 (88%)	75 (100%)	0	0	100	100
1	E	77/85 (91%)	77 (100%)	0	0	100	100
1	F	77/85 (91%)	77 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	78/85 (92%)	76 (97%)	2 (3%)	0	100	100
1	H	75/85 (88%)	75 (100%)	0	0	100	100
1	I	80/85 (94%)	80 (100%)	0	0	100	100
1	J	77/85 (91%)	76 (99%)	1 (1%)	0	100	100
1	K	79/85 (93%)	78 (99%)	1 (1%)	0	100	100
1	L	77/85 (91%)	77 (100%)	0	0	100	100
All	All	932/1020 (91%)	926 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	67/69 (97%)	67 (100%)	0	100	100
1	B	66/69 (96%)	66 (100%)	0	100	100
1	C	66/69 (96%)	66 (100%)	0	100	100
1	D	64/69 (93%)	64 (100%)	0	100	100
1	E	65/69 (94%)	65 (100%)	0	100	100
1	F	65/69 (94%)	65 (100%)	0	100	100
1	G	66/69 (96%)	66 (100%)	0	100	100
1	H	64/69 (93%)	64 (100%)	0	100	100
1	I	67/69 (97%)	67 (100%)	0	100	100
1	J	65/69 (94%)	65 (100%)	0	100	100
1	K	66/69 (96%)	66 (100%)	0	100	100
1	L	65/69 (94%)	65 (100%)	0	100	100
All	All	786/828 (95%)	786 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	94	GLN
1	G	94	GLN
1	I	141	HIS
1	I	145	HIS
1	J	73	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

38 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	H	203	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	E	204	-	4,4,4	0.14	0	6,6,6	0.06	0
3	SO4	H	204	-	4,4,4	0.14	0	6,6,6	0.07	0
2	8SP	B	202	-	26,29,33	1.14	1 (3%)	28,36,40	1.59	4 (14%)
3	SO4	L	203	-	4,4,4	0.15	0	6,6,6	0.05	0
2	8SP	J	201	-	20,23,33	1.13	1 (5%)	21,28,40	1.17	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	8SP	F	202	-	27,30,33	1.13	1 (3%)	29,37,40	1.62	4 (13%)
3	SO4	H	205	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	G	202	-	4,4,4	0.14	0	6,6,6	0.06	0
2	8SP	I	201	-	19,19,33	1.29	2 (10%)	21,23,40	1.96	3 (14%)
3	SO4	E	202	-	4,4,4	0.15	0	6,6,6	0.04	0
3	SO4	I	202	-	4,4,4	0.15	0	6,6,6	0.05	0
4	GOL	C	201	-	5,5,5	0.89	0	5,5,5	1.03	0
3	SO4	A	203	-	4,4,4	0.14	0	6,6,6	0.04	0
2	8SP	B	201	-	24,24,33	1.14	1 (4%)	27,29,40	1.53	3 (11%)
3	SO4	L	205	-	4,4,4	0.14	0	6,6,6	0.05	0
2	8SP	H	202	-	29,32,33	1.10	1 (3%)	31,39,40	1.46	4 (12%)
2	8SP	A	201	-	25,25,33	1.15	1 (4%)	28,30,40	1.27	3 (10%)
3	SO4	K	203	-	4,4,4	0.14	0	6,6,6	0.05	0
2	8SP	L	202	-	30,33,33	1.10	1 (3%)	32,40,40	1.35	4 (12%)
2	8SP	H	201	-	24,27,33	1.13	1 (4%)	26,34,40	1.67	4 (15%)
3	SO4	E	203	-	4,4,4	0.15	0	6,6,6	0.04	0
2	8SP	L	201	-	24,24,33	1.14	1 (4%)	27,29,40	1.42	3 (11%)
2	8SP	D	202	-	17,17,33	1.60	3 (17%)	20,20,40	0.98	1 (5%)
2	8SP	A	202	-	24,27,33	1.12	1 (4%)	26,34,40	1.63	4 (15%)
3	SO4	K	202	-	4,4,4	0.14	0	6,6,6	0.08	0
3	SO4	B	204	-	4,4,4	0.13	0	6,6,6	0.06	0
2	8SP	D	201	-	26,26,33	1.30	1 (3%)	30,31,40	1.25	3 (10%)
3	SO4	D	203	-	4,4,4	0.14	0	6,6,6	0.07	0
2	8SP	K	201	-	24,24,33	1.17	1 (4%)	27,29,40	1.29	3 (11%)
2	8SP	F	201	-	28,28,33	1.10	1 (3%)	31,33,40	1.23	3 (9%)
3	SO4	F	203	-	4,4,4	0.14	0	6,6,6	0.07	0
2	8SP	G	201	-	24,24,33	1.16	1 (4%)	27,29,40	1.37	3 (11%)
2	8SP	E	201	-	26,26,33	1.14	1 (3%)	29,31,40	1.27	3 (10%)
2	8SP	J	200	-	25,28,33	1.14	1 (4%)	27,35,40	1.77	5 (18%)
3	SO4	L	204	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	C	202	-	4,4,4	0.14	0	6,6,6	0.06	0
3	SO4	B	203	-	4,4,4	0.14	0	6,6,6	0.05	0

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
2	8SP	F	201	-	-	13/32/32/39	-
2	8SP	I	201	-	-	11/21/21/39	-
2	8SP	G	201	-	-	15/28/28/39	-
2	8SP	H	202	-	-	24/34/38/39	-
2	8SP	A	201	-	-	12/29/29/39	-
2	8SP	L	202	-	-	20/35/39/39	-
2	8SP	E	201	-	-	13/30/30/39	-
2	8SP	H	201	-	-	13/28/32/39	-
4	GOL	C	201	-	-	2/4/4/4	-
2	8SP	B	202	-	-	12/31/35/39	-
2	8SP	L	201	-	-	12/27/27/39	-
2	8SP	D	202	-	-	6/16/16/39	-
2	8SP	J	201	-	-	14/22/26/39	-
2	8SP	F	202	-	-	20/32/36/39	-
2	8SP	J	200	-	-	11/30/34/39	-
2	8SP	A	202	-	-	11/28/32/39	-
2	8SP	D	201	-	-	16/28/28/39	-
2	8SP	B	201	-	-	11/27/27/39	-
2	8SP	K	201	-	-	9/28/28/39	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	8SP	P-O3P	4.62	1.72	1.54
2	D	202	8SP	P-O3P	4.60	1.72	1.54
2	A	201	8SP	P-O3P	3.69	1.72	1.55
2	K	201	8SP	P-O3P	3.69	1.72	1.55
2	F	202	8SP	P-O3P	3.68	1.72	1.55

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	201	8SP	C2G-O2G-C1B	7.66	127.73	117.88
2	J	200	8SP	OG-CB-CA	5.94	113.24	108.06
2	F	202	8SP	OG-CB-CA	5.56	112.91	108.06
2	B	201	8SP	C1G-O1G-C1A	4.98	129.63	117.10
2	H	202	8SP	C2G-O2G-C1B	4.80	129.61	117.79

There are no chirality outliers.

5 of 245 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	202	8SP	N-CA-CB-OG
2	B	202	8SP	C-CA-CB-OG
2	B	202	8SP	O1G-C1G-C2G-O2G
2	B	202	8SP	C2G-C3G-O3G-P
2	J	201	8SP	CB-OG-P-O2P

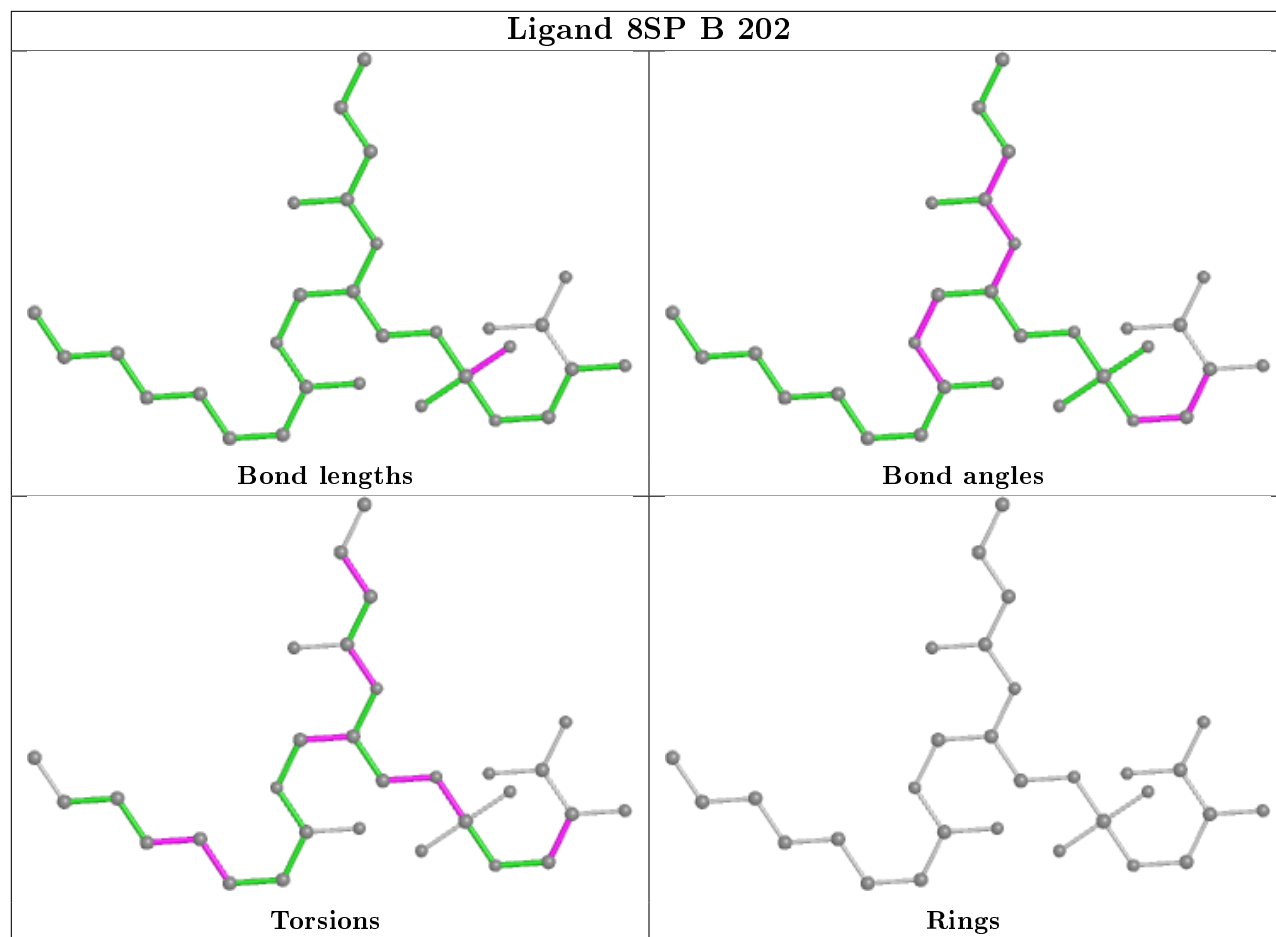
There are no ring outliers.

19 monomers are involved in 38 short contacts:

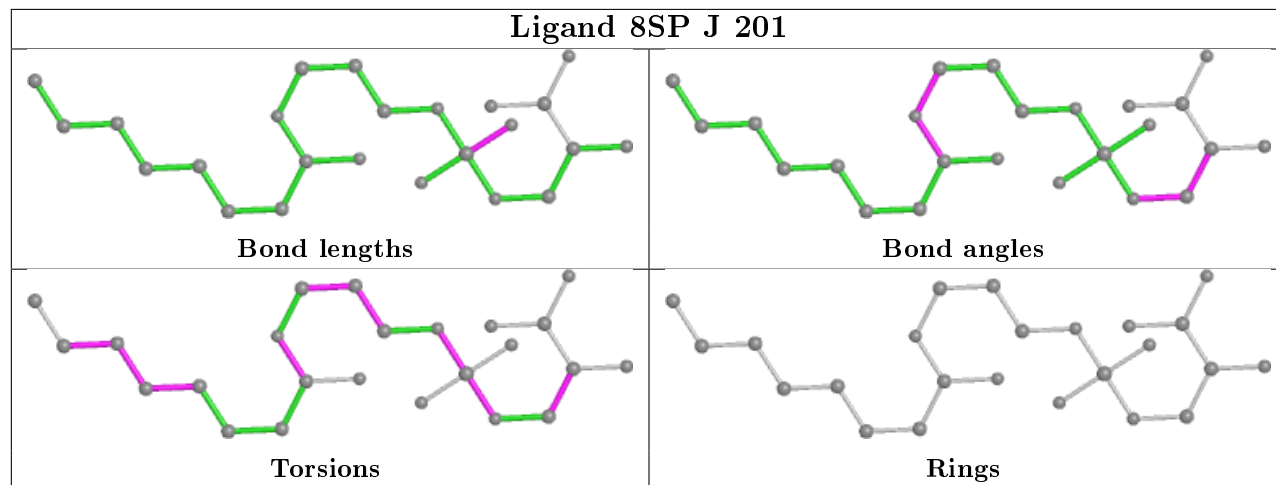
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	202	8SP	3	0
2	J	201	8SP	2	0
2	F	202	8SP	2	0
2	I	201	8SP	2	0
3	I	202	SO4	1	0
4	C	201	GOL	1	0
2	B	201	8SP	1	0
2	H	202	8SP	3	0
2	A	201	8SP	1	0
2	L	202	8SP	3	0
2	H	201	8SP	2	0
2	L	201	8SP	2	0
2	A	202	8SP	1	0
2	D	201	8SP	5	0
2	K	201	8SP	1	0
2	F	201	8SP	1	0
2	G	201	8SP	2	0
2	E	201	8SP	3	0
2	J	200	8SP	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.

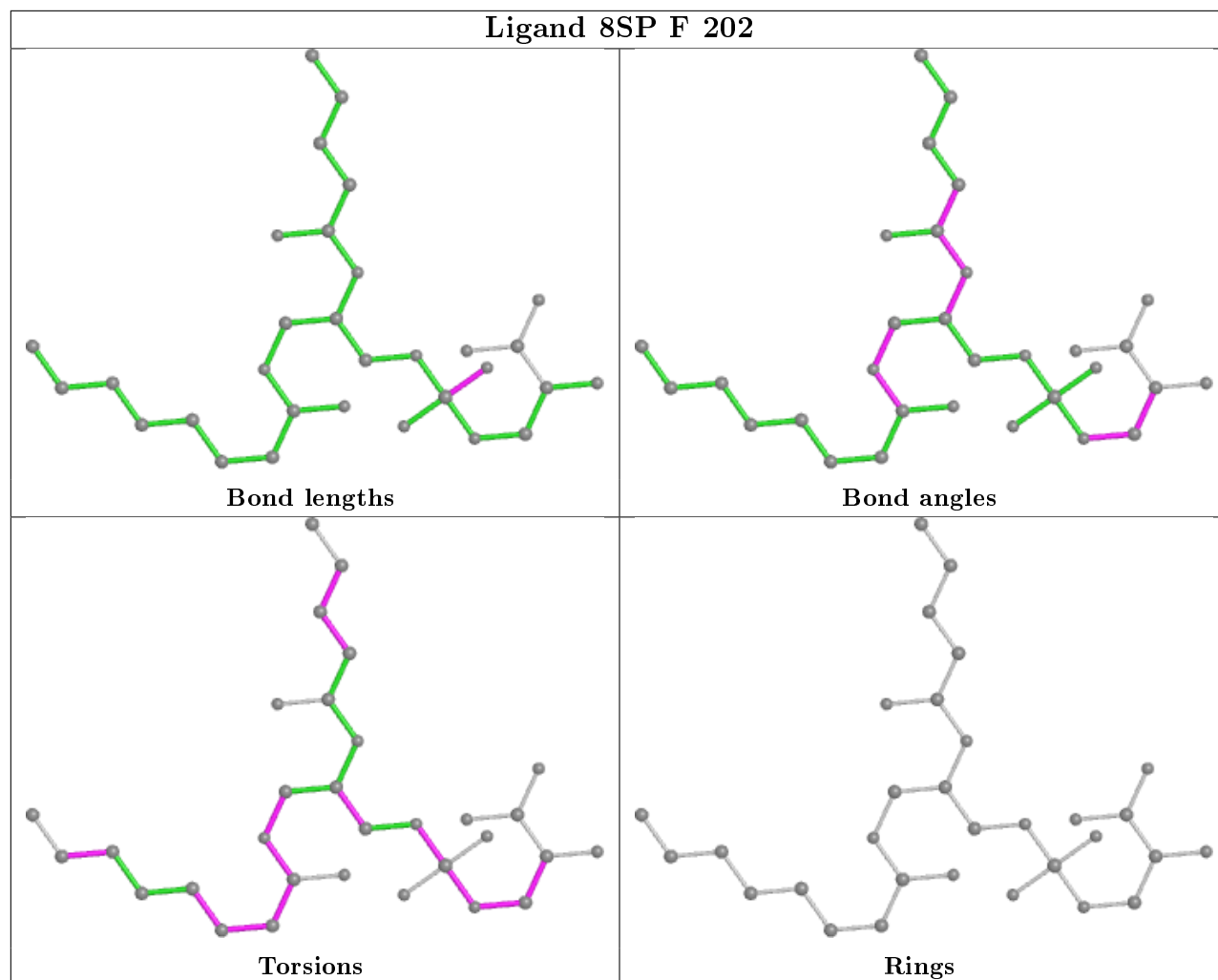
Ligand 8SP B 202



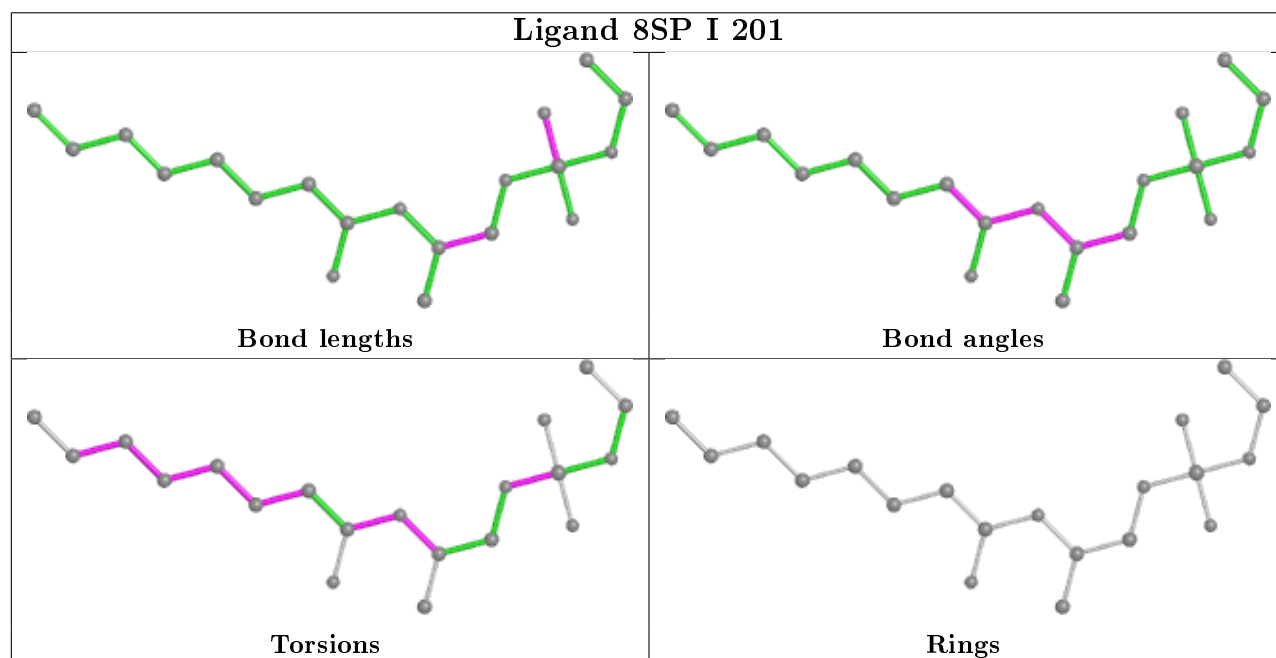
Ligand 8SP J 201

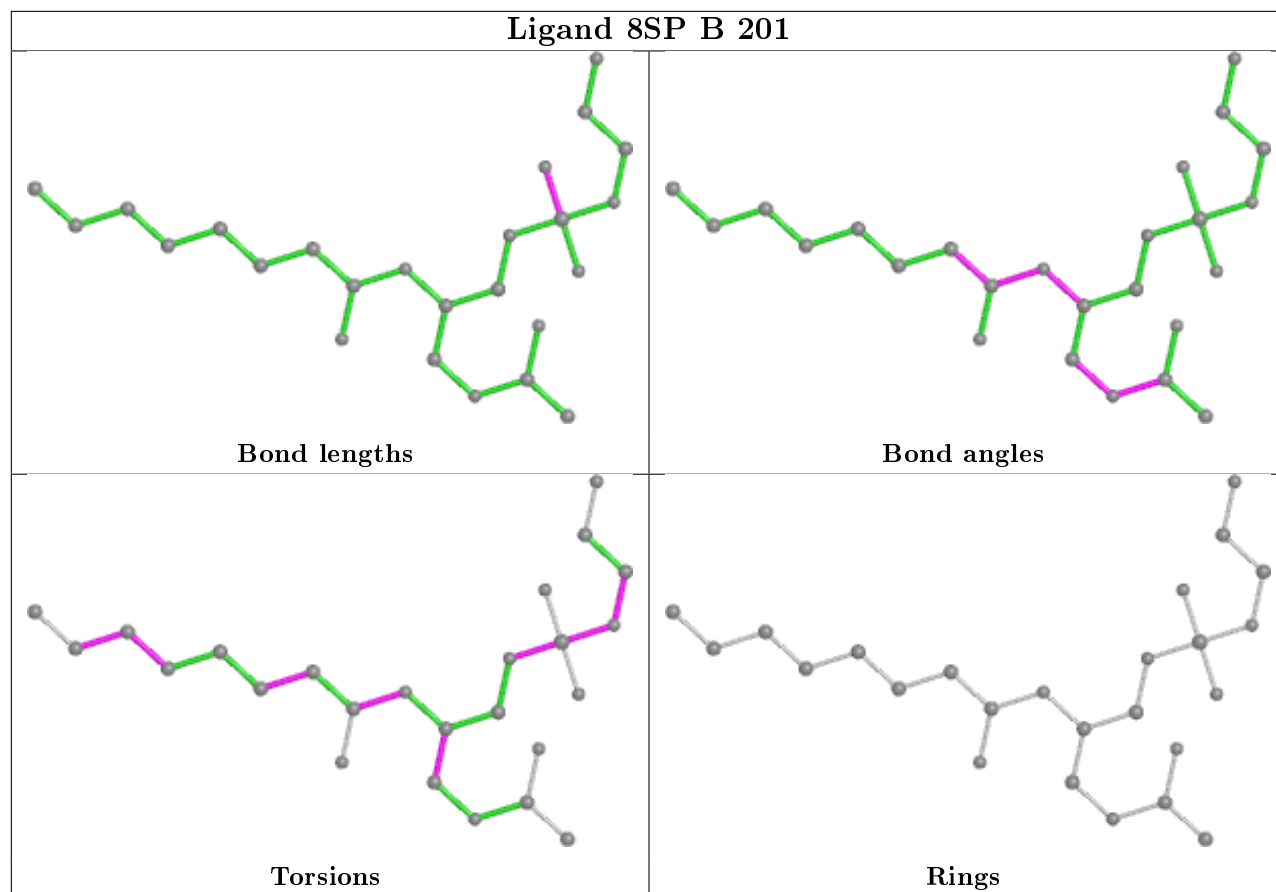


Ligand 8SP F 202

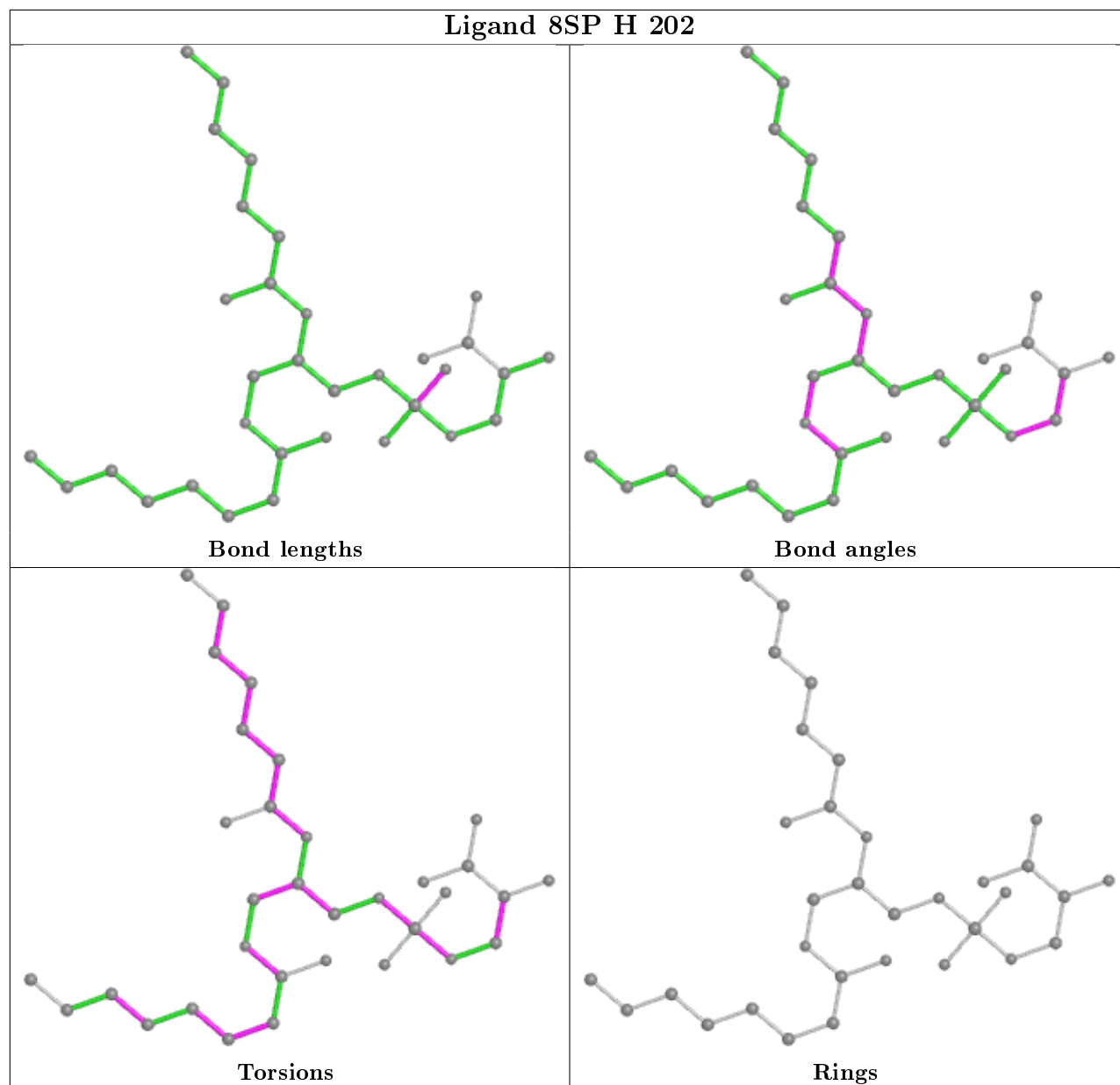


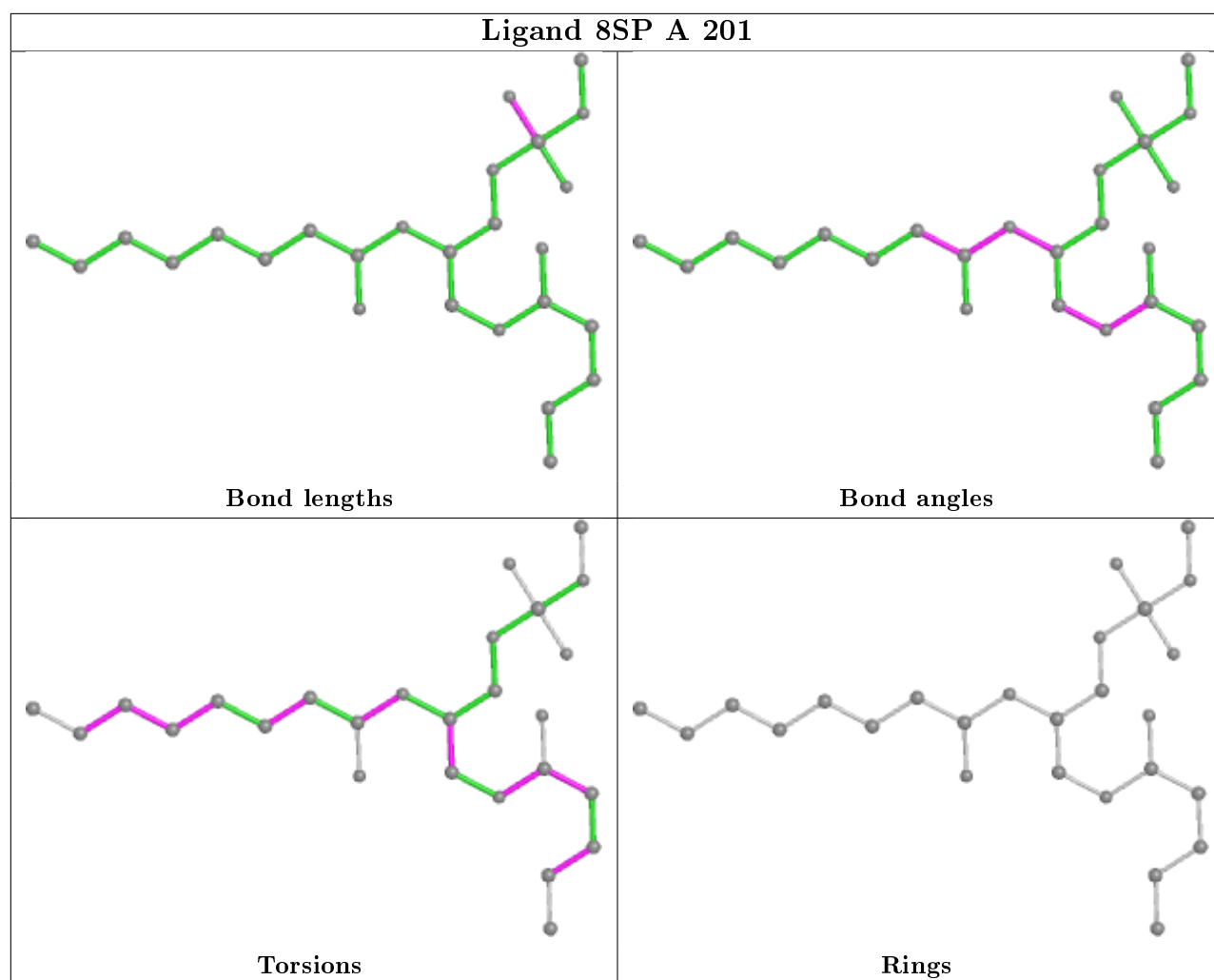
Ligand 8SP I 201

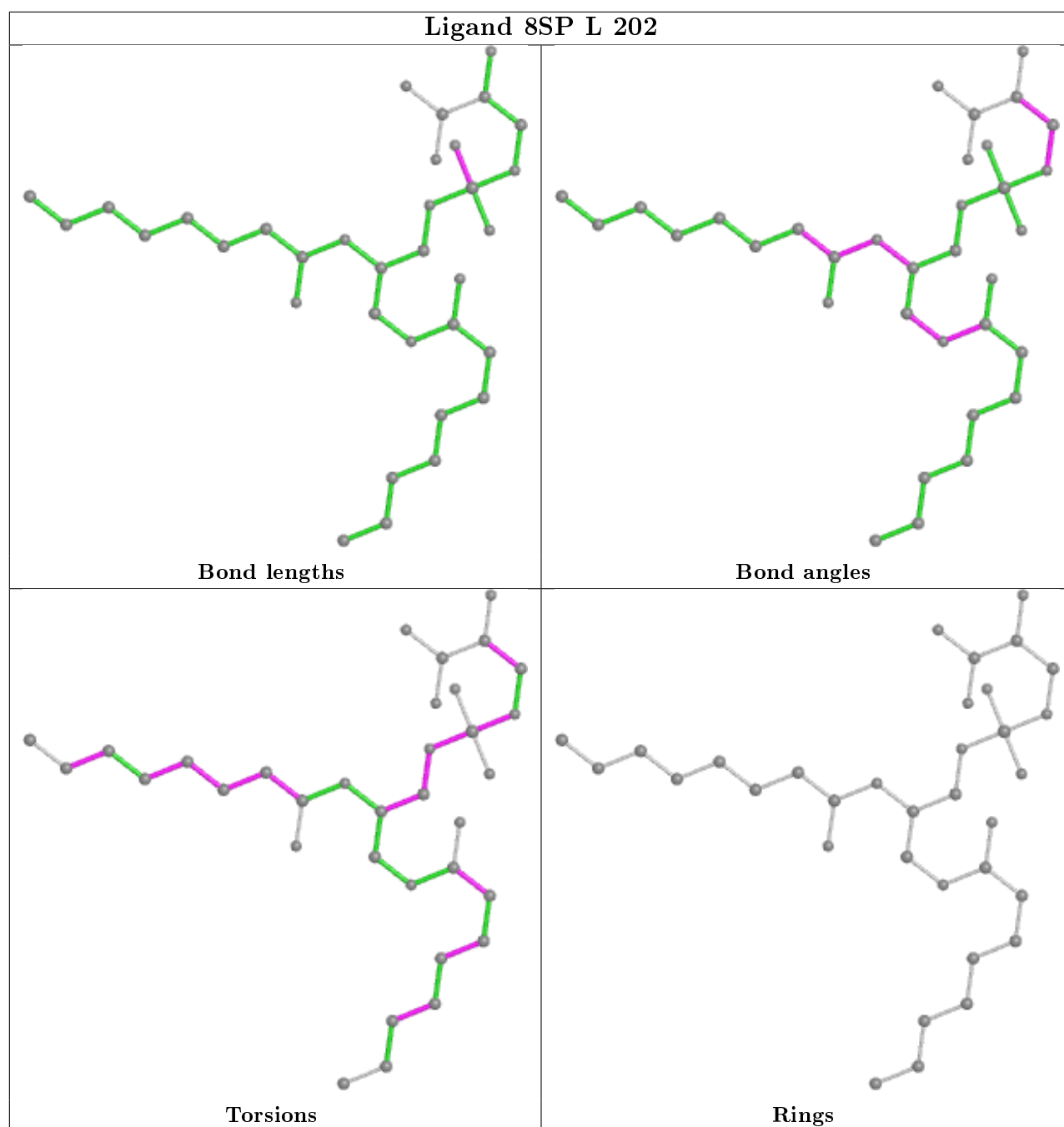


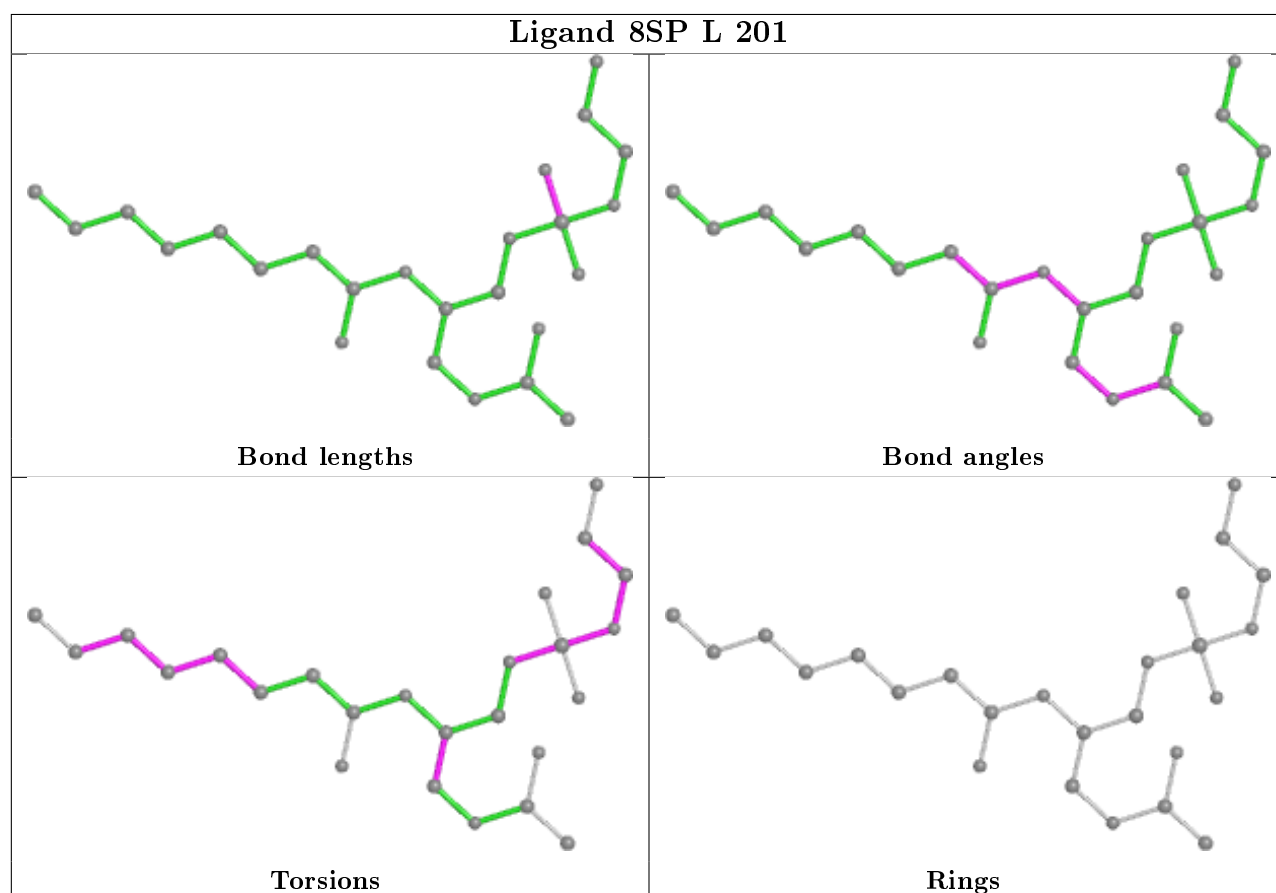
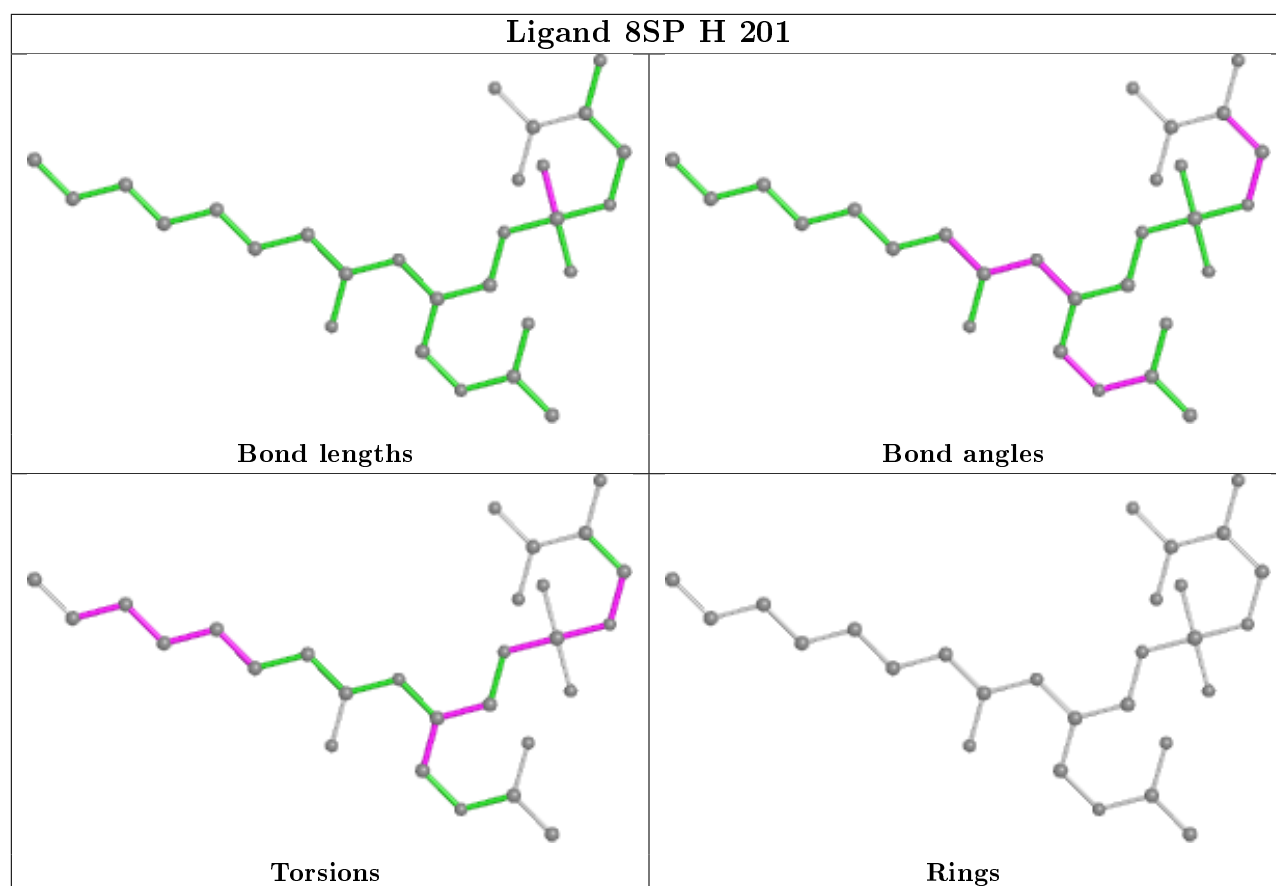


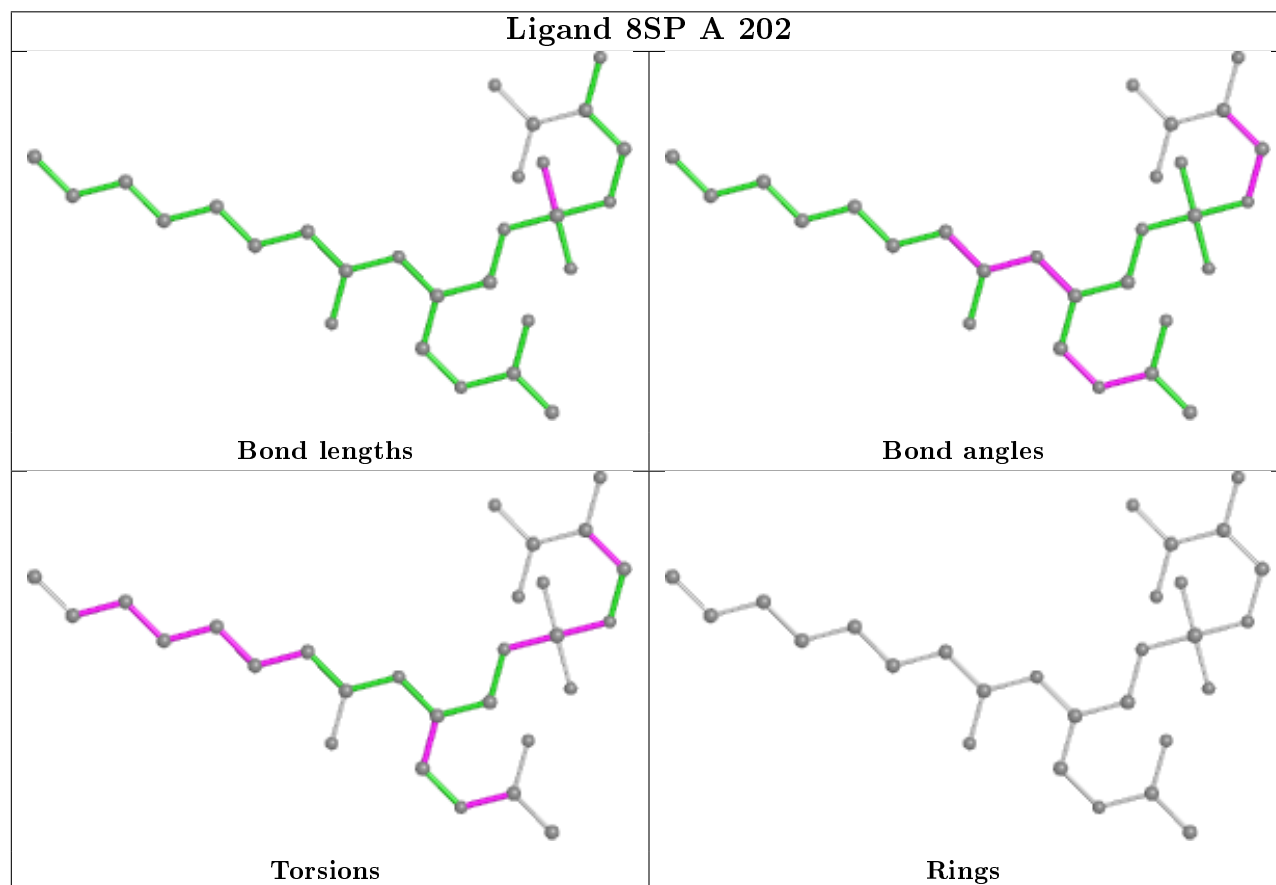
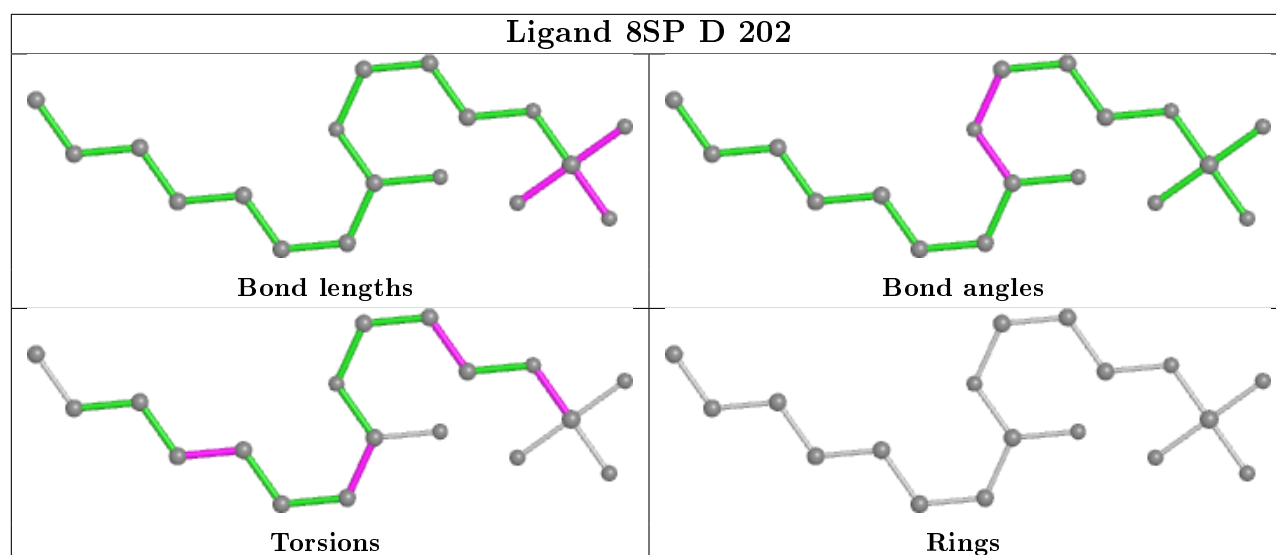
Ligand 8SP H 202

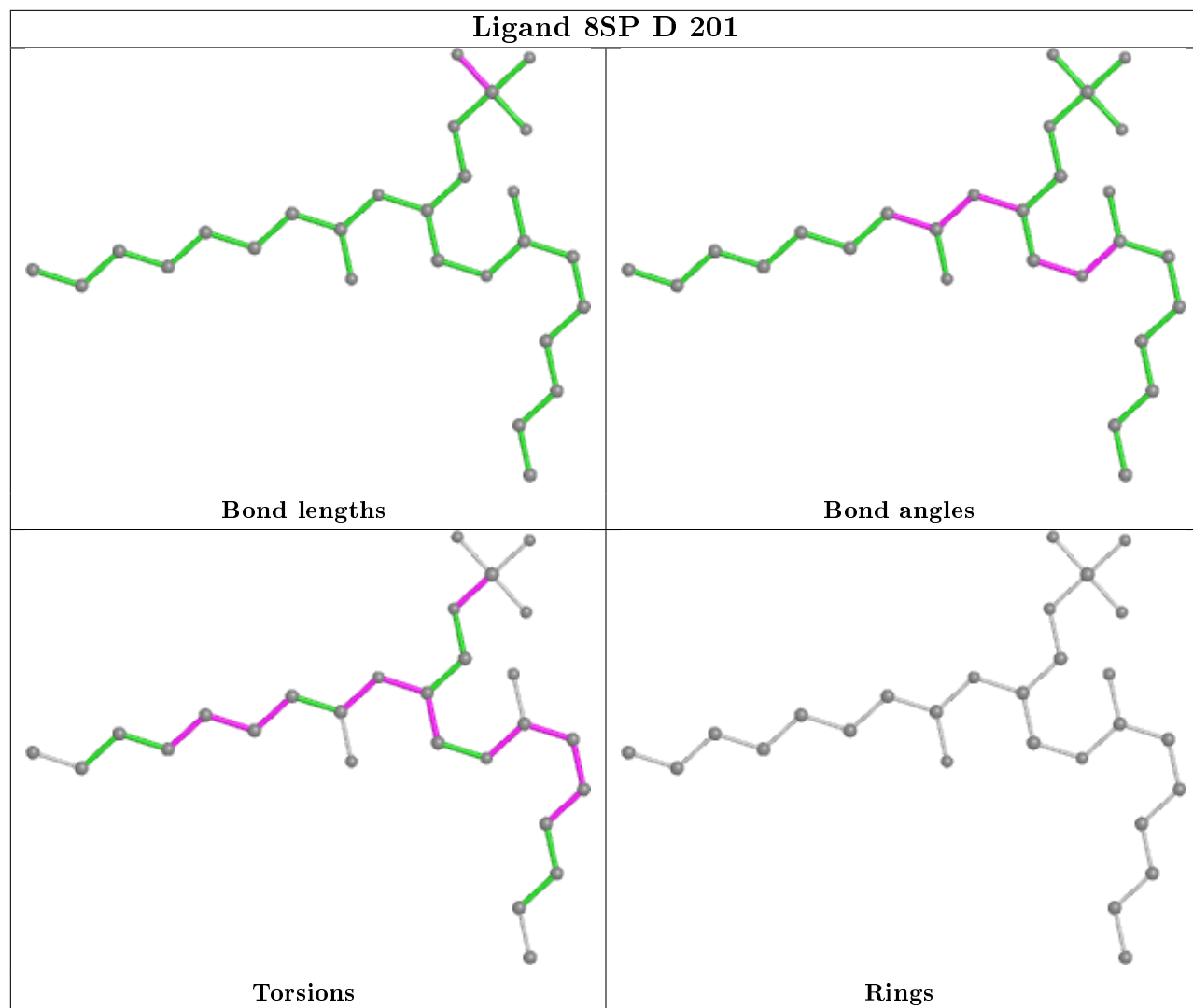


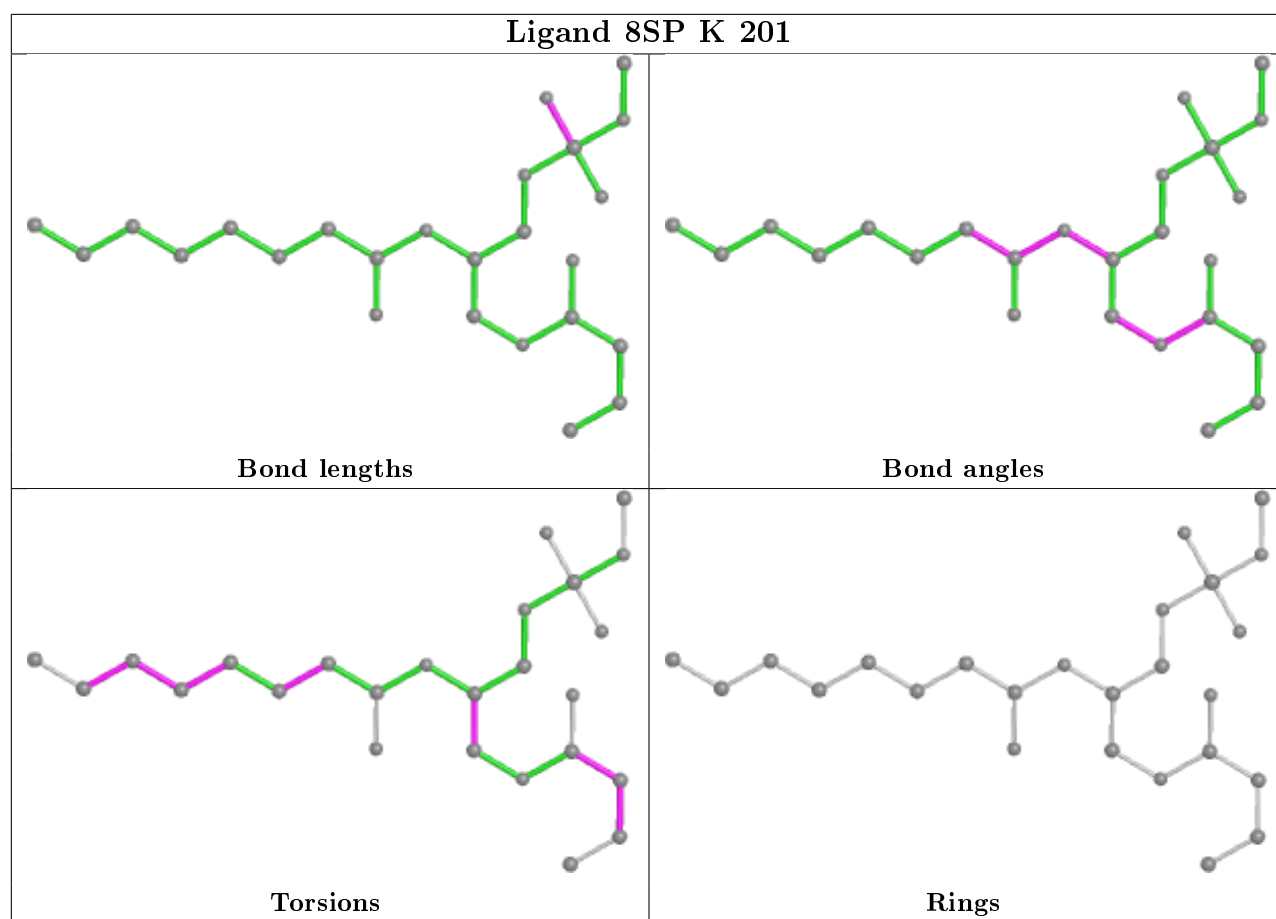


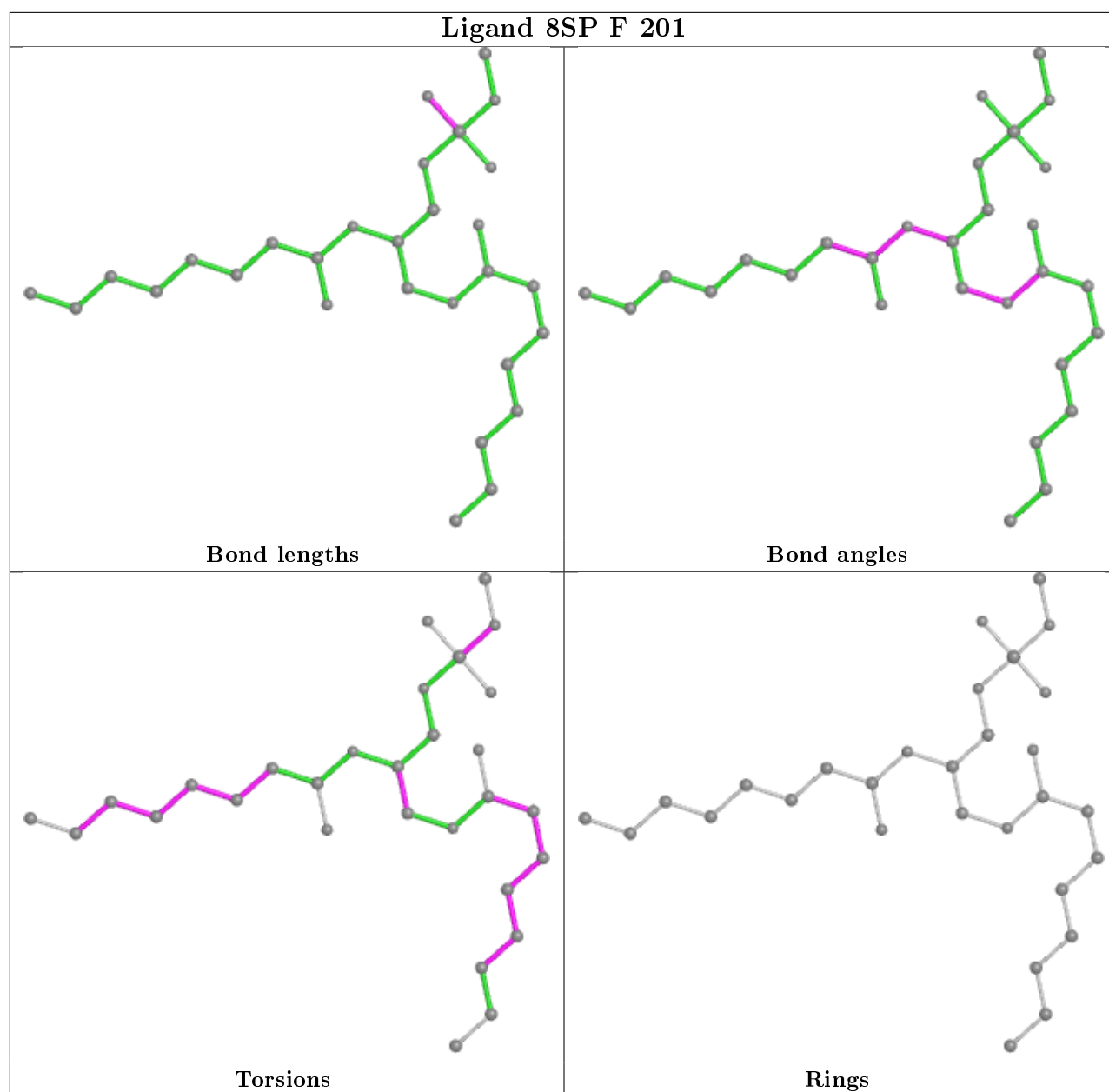


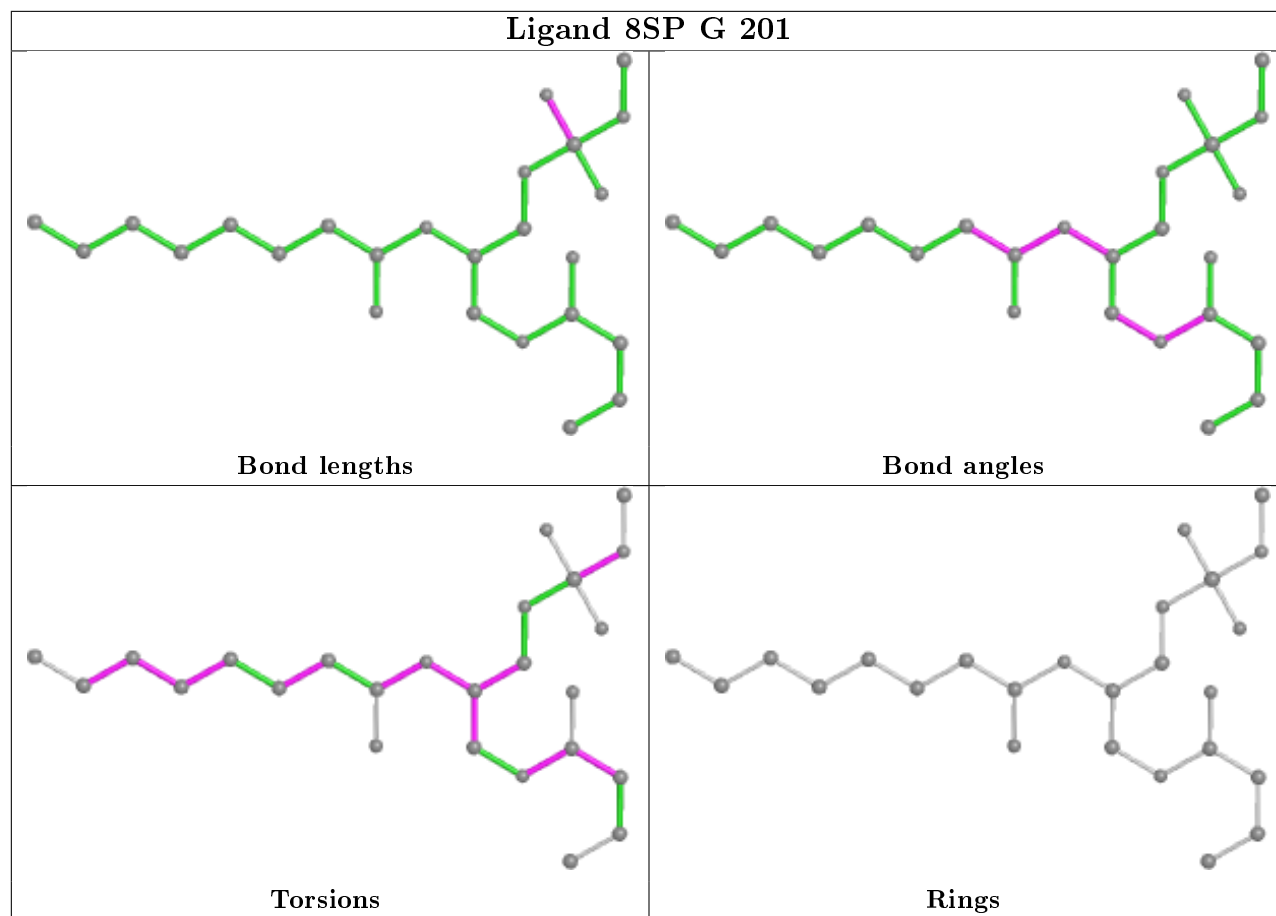


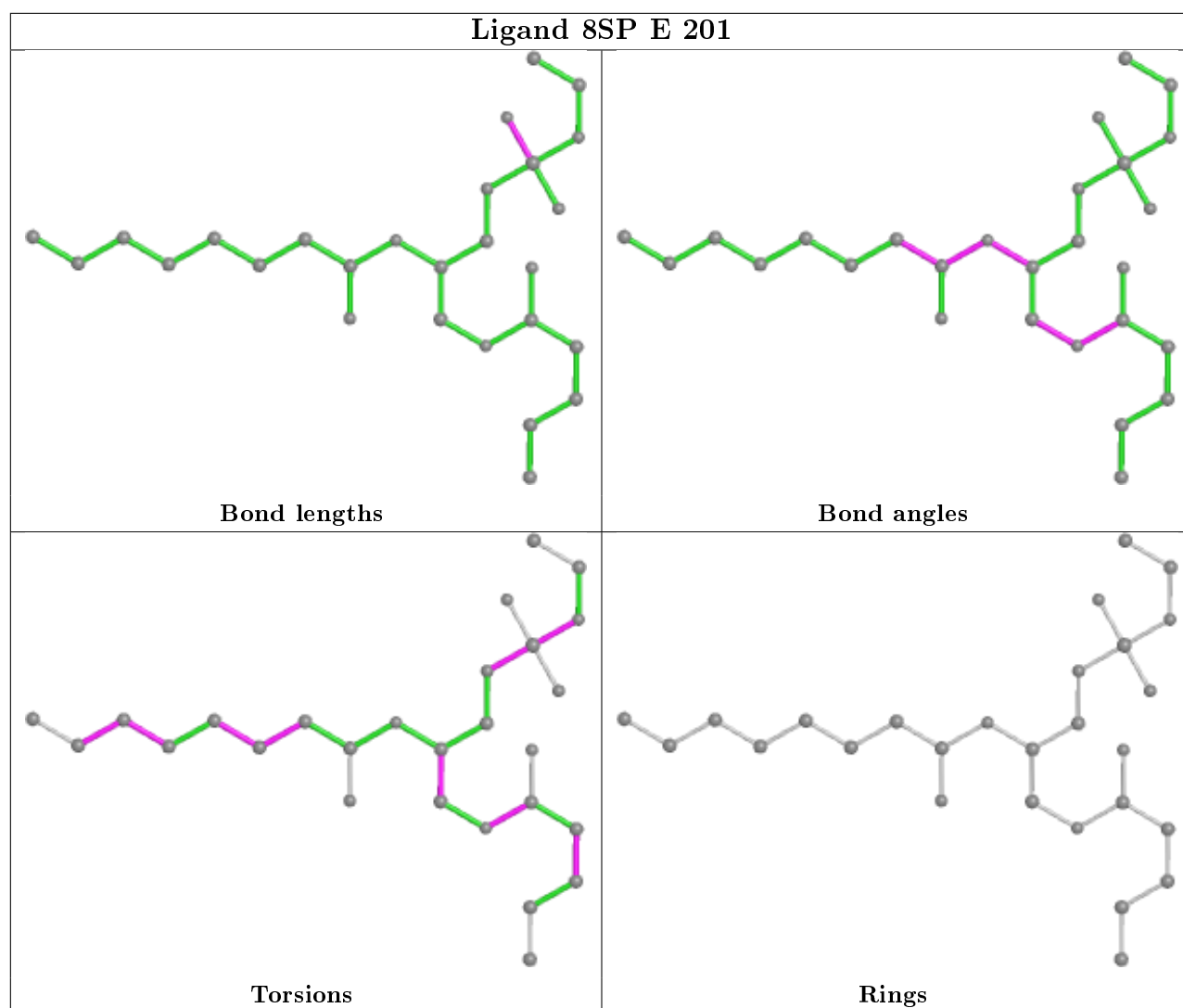


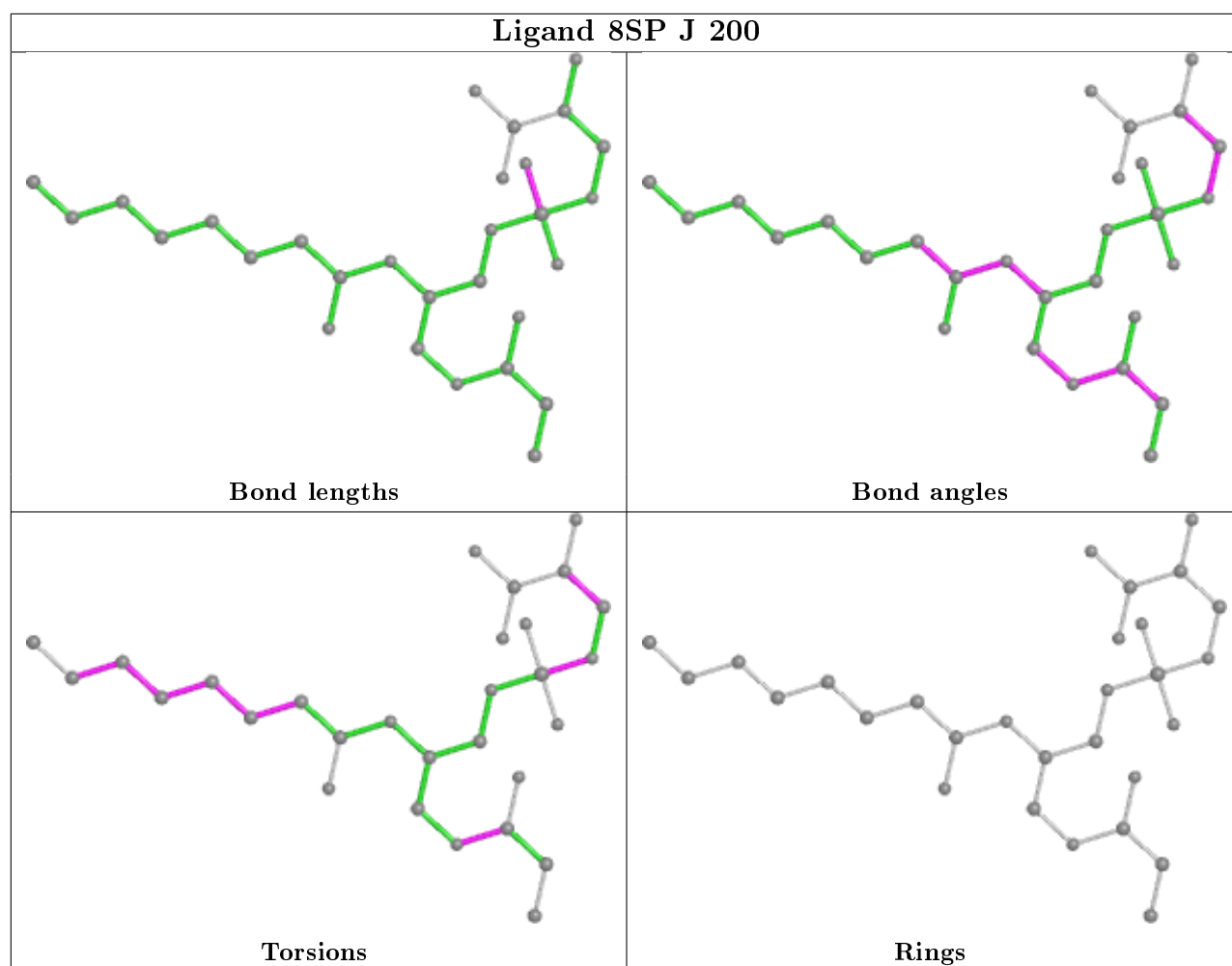












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	82/85 (96%)	0.25	2 (2%) 59 62	40, 65, 91, 122	0
1	B	78/85 (91%)	0.30	3 (3%) 40 43	41, 60, 91, 118	0
1	C	81/85 (95%)	0.29	6 (7%) 14 15	40, 61, 96, 115	0
1	D	77/85 (90%)	0.22	2 (2%) 56 59	38, 57, 81, 117	0
1	E	79/85 (92%)	0.31	2 (2%) 57 61	39, 59, 92, 117	0
1	F	79/85 (92%)	0.17	2 (2%) 57 61	42, 58, 86, 99	0
1	G	80/85 (94%)	0.42	2 (2%) 57 61	39, 64, 100, 118	0
1	H	77/85 (90%)	0.26	1 (1%) 77 79	45, 58, 86, 107	0
1	I	82/85 (96%)	0.12	1 (1%) 79 80	41, 61, 95, 129	0
1	J	79/85 (92%)	0.22	4 (5%) 28 29	38, 56, 87, 106	0
1	K	81/85 (95%)	0.25	4 (4%) 29 31	39, 62, 94, 103	0
1	L	78/85 (91%)	0.04	1 (1%) 77 79	37, 56, 86, 117	0
All	All	953/1020 (93%)	0.24	30 (3%) 49 52	37, 60, 93, 129	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	146	GLY	5.5
1	A	148	THR	5.5
1	K	147	LEU	3.7
1	L	146	GLY	3.6
1	J	102	PRO	3.5

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	K	203	5/5	0.50	0.39	175,180,183,186	0
3	SO4	E	203	5/5	0.62	0.27	147,155,158,159	0
4	GOL	C	201	6/6	0.67	0.38	82,96,109,109	0
3	SO4	C	202	5/5	0.70	0.34	137,142,143,146	0
2	8SP	H	202	33/34	0.72	0.36	59,103,153,161	0
2	8SP	B	202	30/34	0.77	0.35	41,110,141,145	0
2	8SP	L	202	34/34	0.77	0.30	57,86,137,143	0
3	SO4	A	203	5/5	0.78	0.27	138,142,144,147	0
2	8SP	D	202	18/34	0.79	0.35	57,97,134,148	0
3	SO4	H	204	5/5	0.79	0.20	96,111,120,128	0
2	8SP	J	201	24/34	0.81	0.40	51,96,156,169	0
2	8SP	D	201	27/34	0.81	0.34	54,91,132,142	0
3	SO4	L	204	5/5	0.81	0.21	147,149,154,157	0
2	8SP	F	202	31/34	0.81	0.35	53,102,121,128	0
3	SO4	L	203	5/5	0.82	0.14	128,134,138,140	0
2	8SP	G	201	25/34	0.84	0.31	57,85,140,146	0
3	SO4	B	204	5/5	0.84	0.17	121,126,130,130	0
2	8SP	A	201	26/34	0.84	0.29	58,94,157,165	0
3	SO4	G	202	5/5	0.85	0.23	129,132,133,137	0
2	8SP	I	201	20/34	0.85	0.33	54,102,145,146	0
3	SO4	H	205	5/5	0.85	0.21	152,154,158,161	0
2	8SP	K	201	25/34	0.86	0.25	51,91,137,142	0
2	8SP	E	201	27/34	0.86	0.27	48,86,123,126	0
3	SO4	F	203	5/5	0.89	0.17	105,106,113,114	0
3	SO4	I	202	5/5	0.91	0.21	111,119,122,124	0
2	8SP	B	201	25/34	0.91	0.23	48,70,87,103	0
2	8SP	F	201	29/34	0.91	0.25	44,74,105,106	0
2	8SP	H	201	28/34	0.91	0.22	53,80,122,131	0
2	8SP	A	202	28/34	0.92	0.21	50,81,116,123	0
2	8SP	J	200	29/34	0.92	0.19	54,73,108,116	0
3	SO4	D	203	5/5	0.92	0.12	110,117,120,132	0
3	SO4	L	205	5/5	0.92	0.15	138,143,146,148	0

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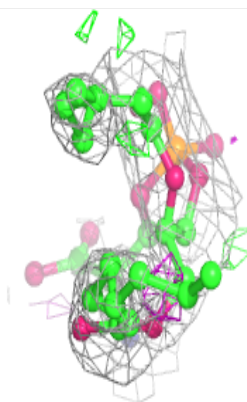
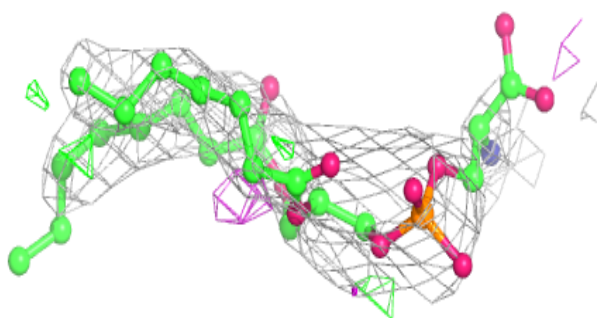
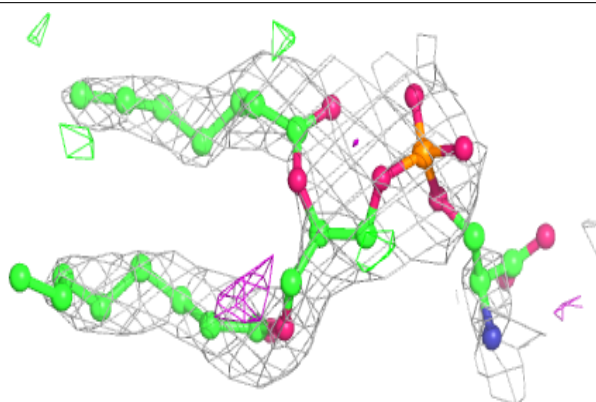
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	K	202	5/5	0.93	0.19	110,110,114,115	0
3	SO4	E	204	5/5	0.93	0.11	79,99,102,112	0
2	8SP	L	201	25/34	0.93	0.20	44,76,91,102	0
3	SO4	E	202	5/5	0.96	0.16	90,98,108,113	0
3	SO4	B	203	5/5	0.98	0.28	75,78,84,86	0
3	SO4	H	203	5/5	0.99	0.22	73,77,92,100	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.

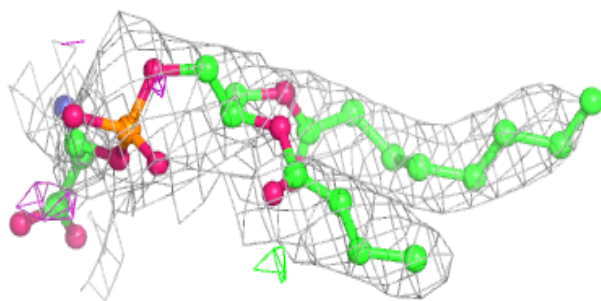
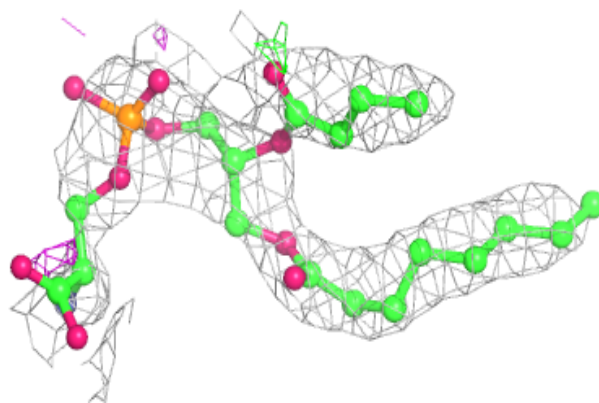
Electron density around 8SP H 202:

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

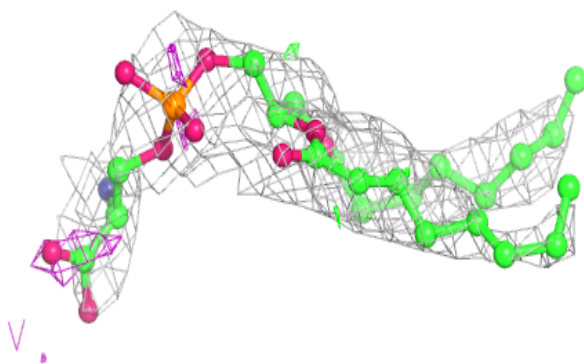
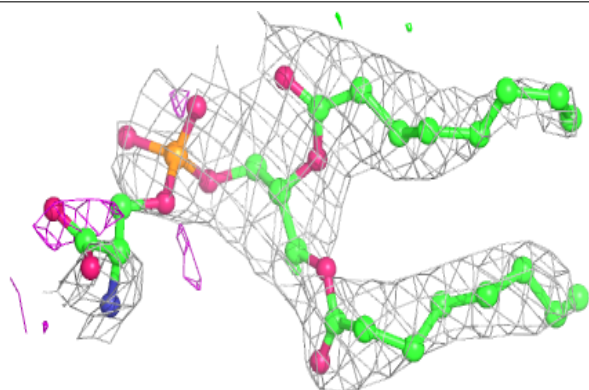


Electron density around 8SP B 202:

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

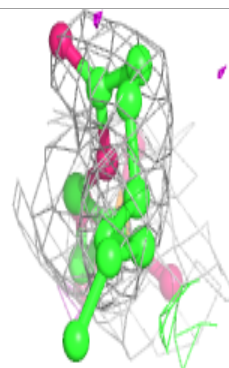
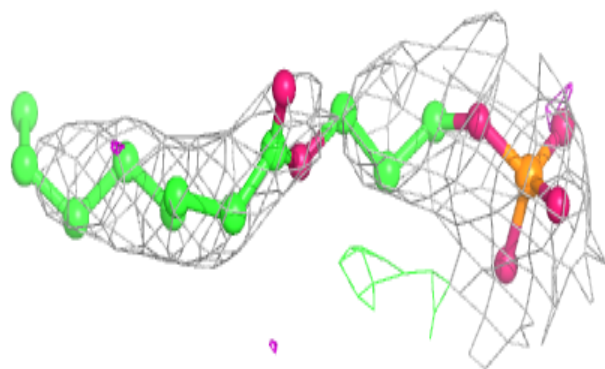
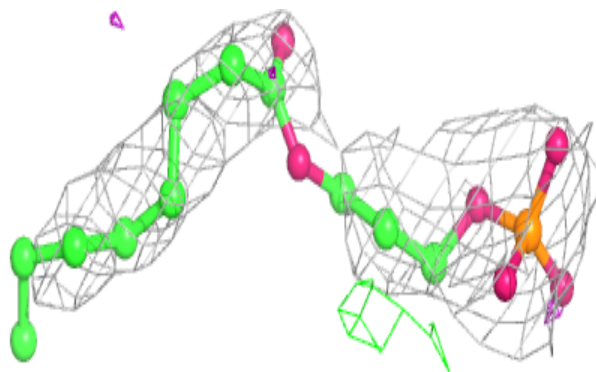
**Electron density around 8SP L 202:**

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

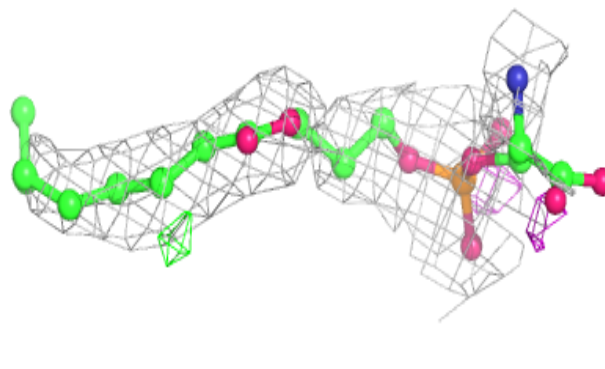
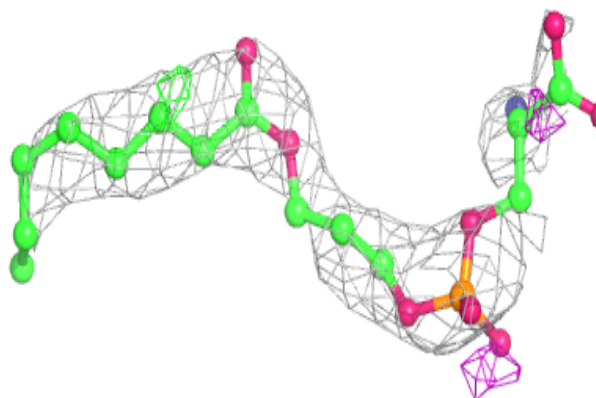


Electron density around 8SP D 202:

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

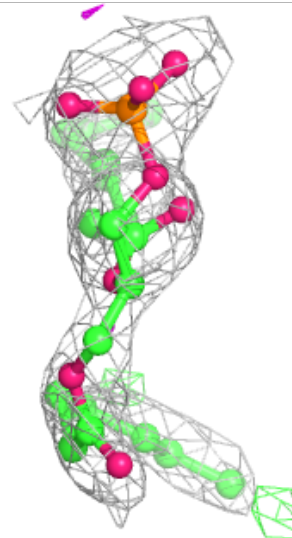
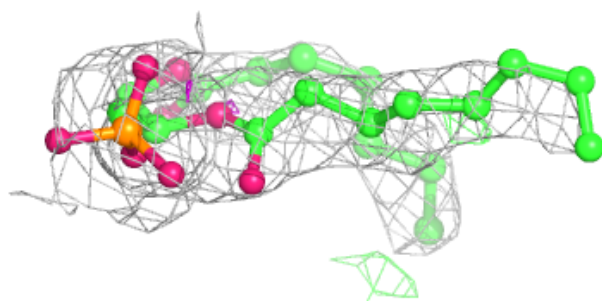
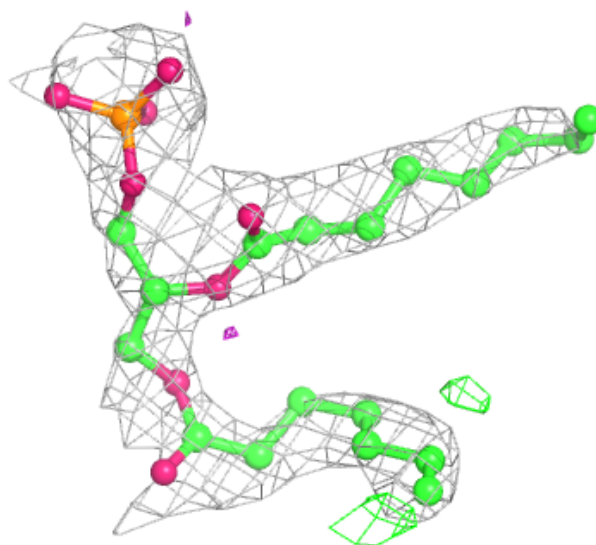
**Electron density around 8SP J 201:**

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



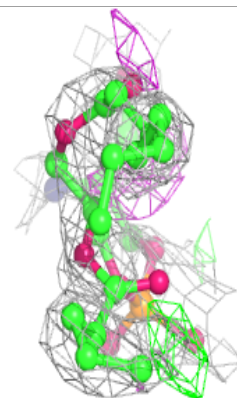
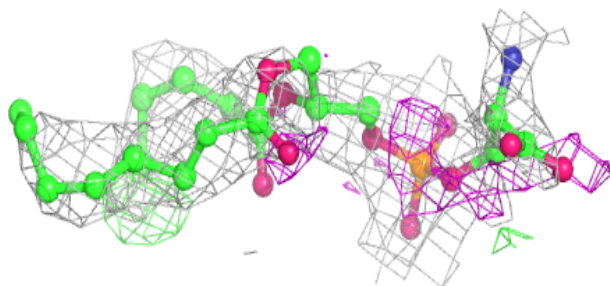
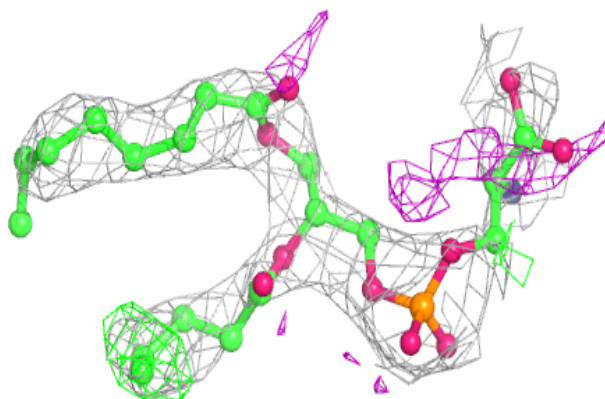
Electron density around 8SP D 201:

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



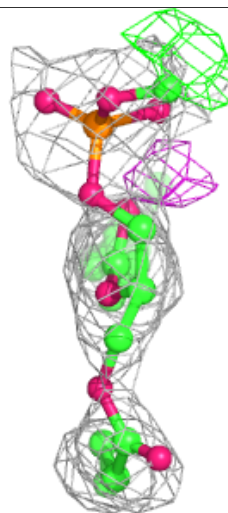
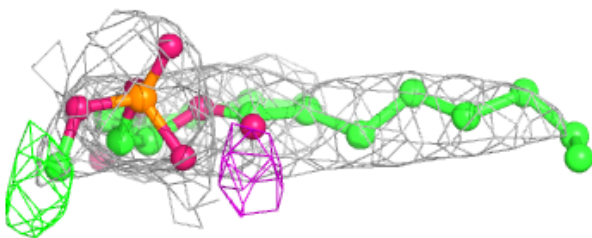
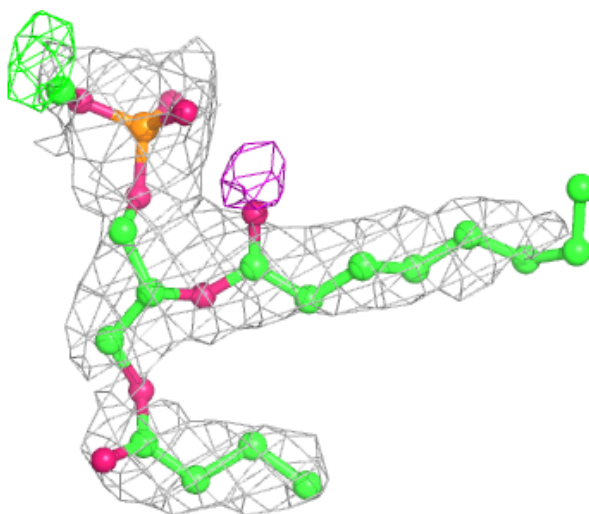
Electron density around 8SP F 202:

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



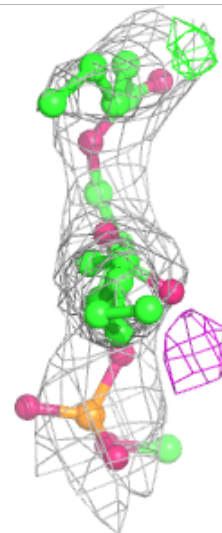
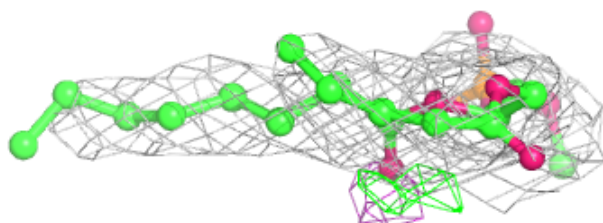
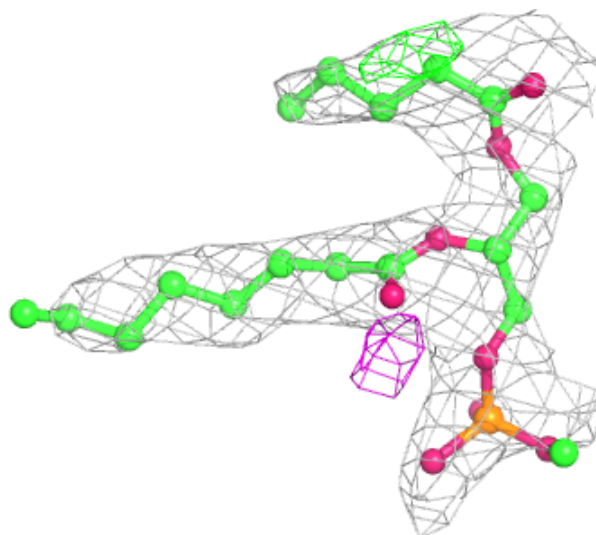
Electron density around 8SP G 201:

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



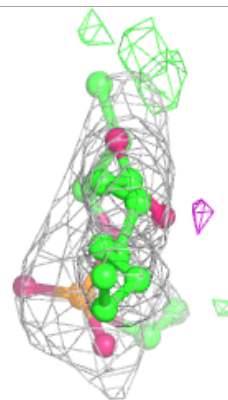
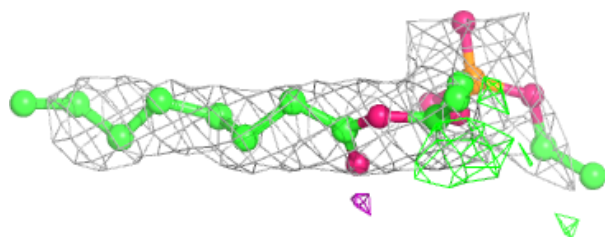
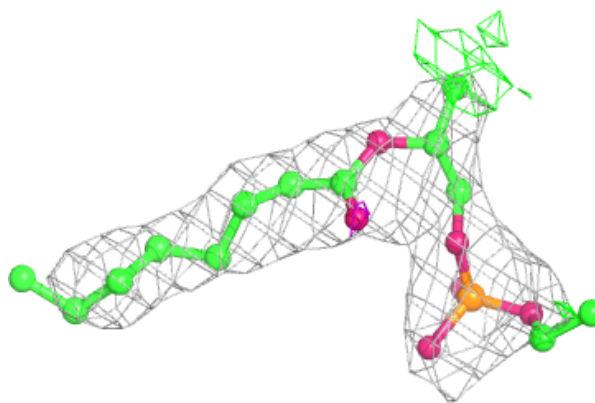
Electron density around 8SP A 201:

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



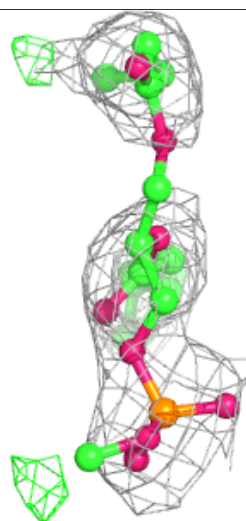
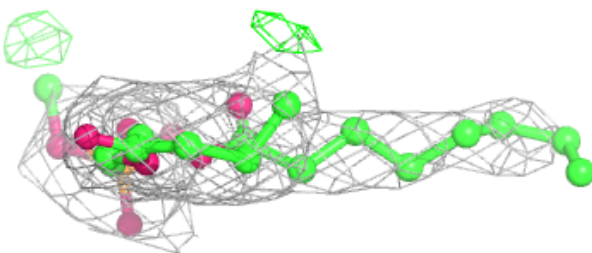
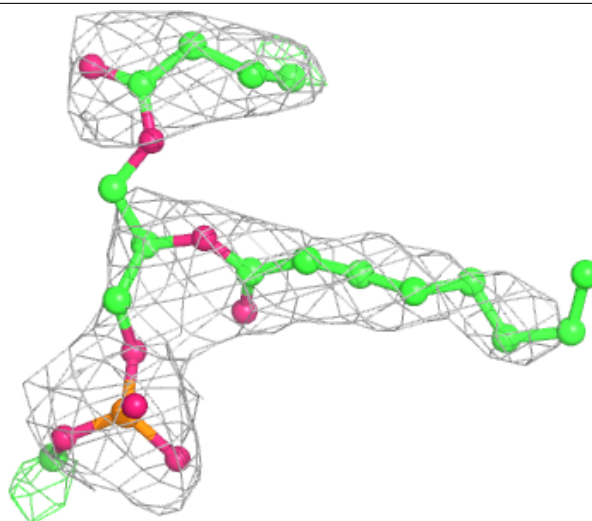
Electron density around 8SP I 201:

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and green (positive)



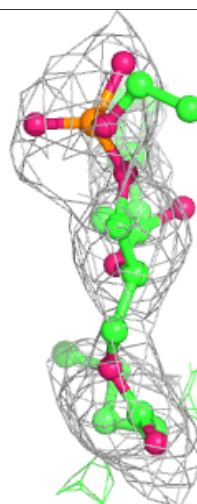
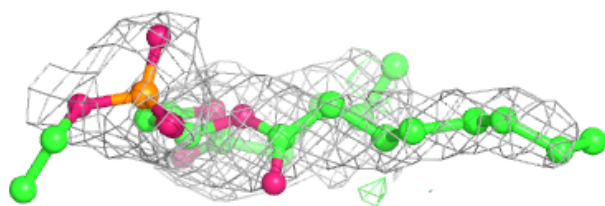
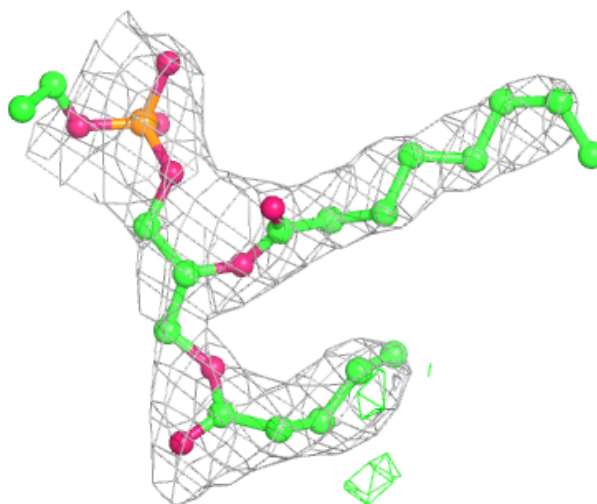
Electron density around 8SP K 201:

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and green (positive)



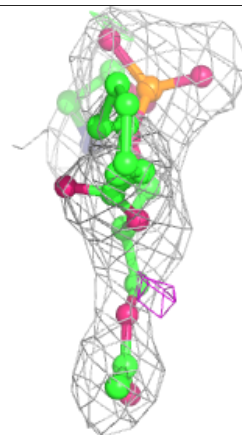
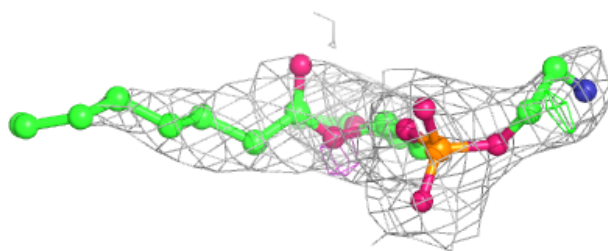
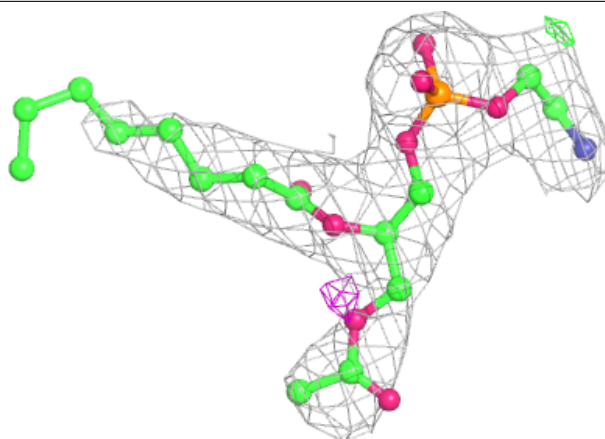
Electron density around 8SP E 201:

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and green (positive)



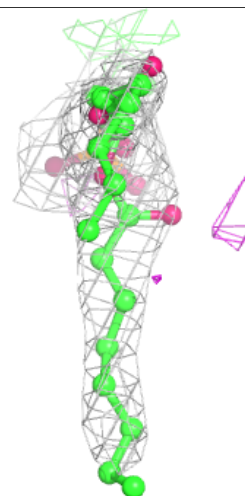
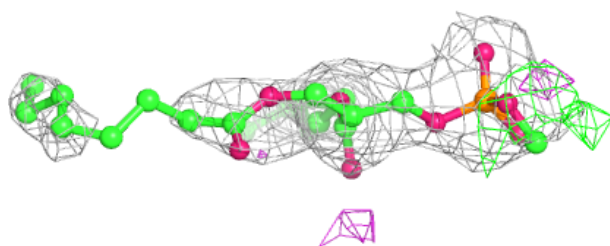
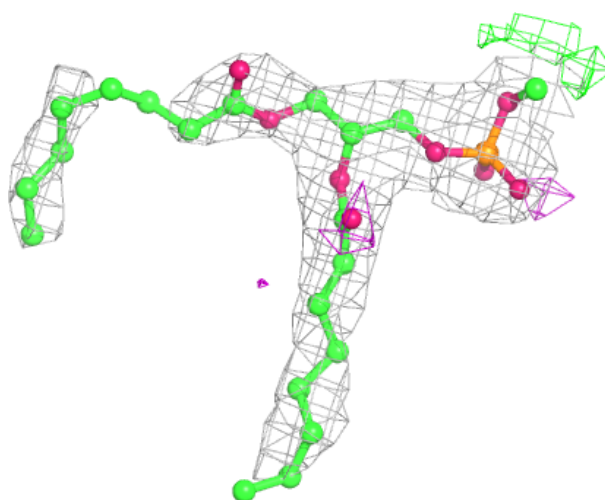
Electron density around 8SP B 201:

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



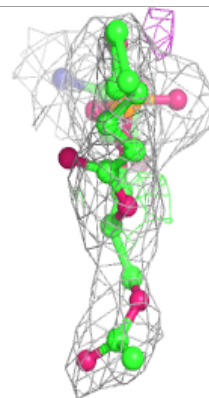
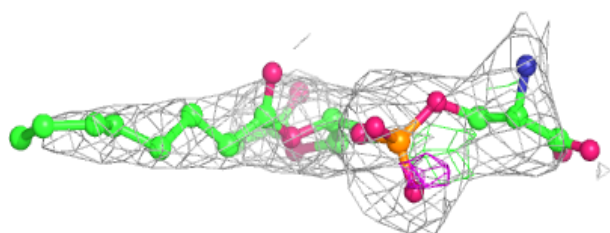
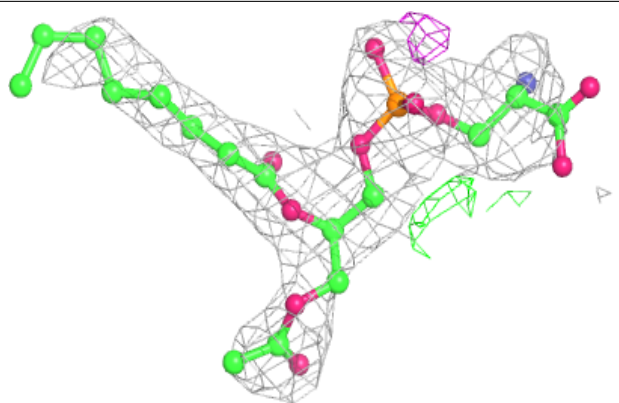
Electron density around 8SP F 201:

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

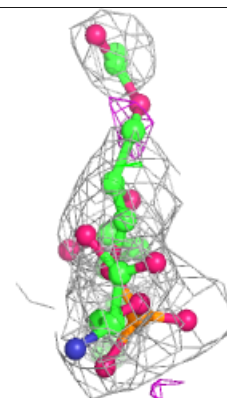
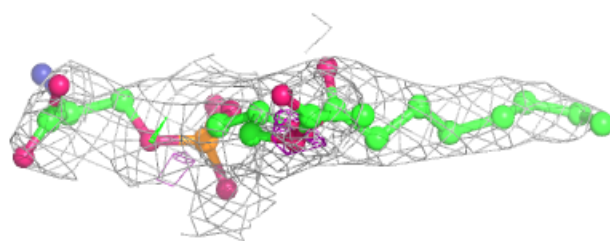
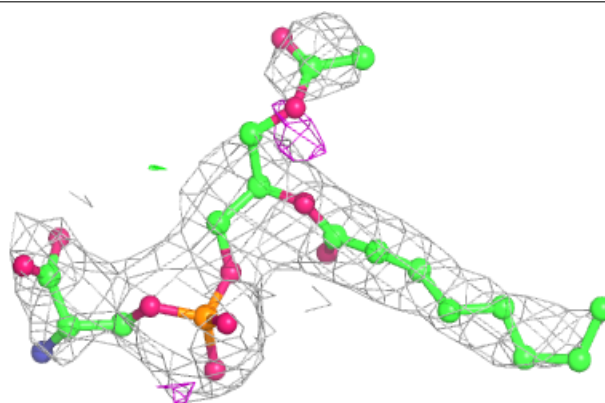


Electron density around 8SP H 201:

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

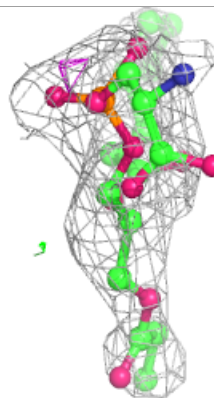
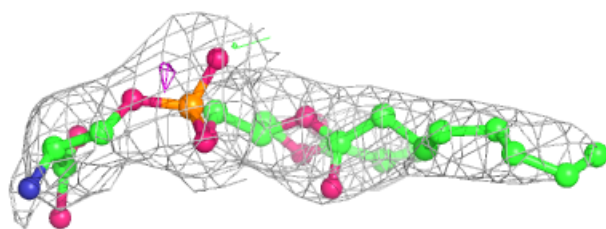
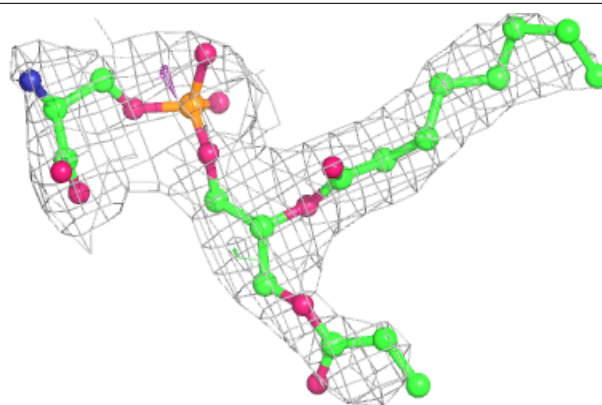
**Electron density around 8SP A 202:**

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

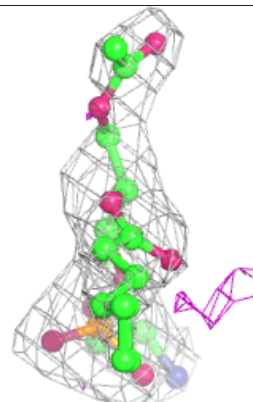
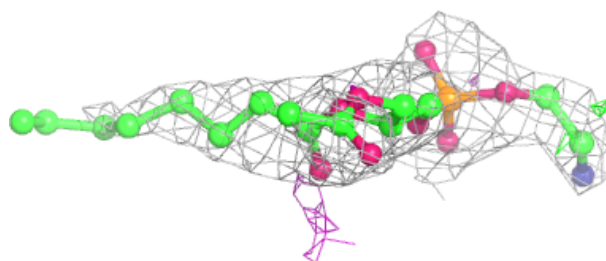
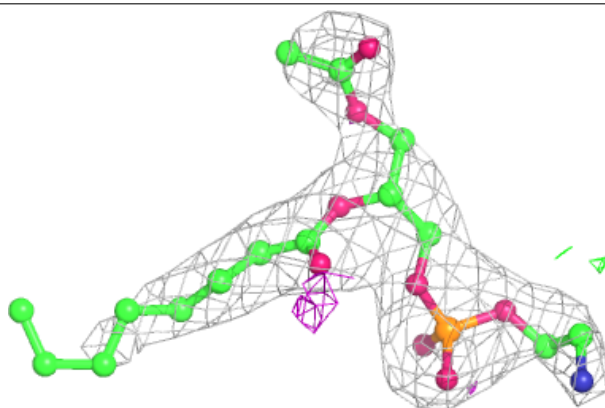


Electron density around 8SP J 200:

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

**Electron density around 8SP L 201:**

$2mF_o-DF_c$ (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.