



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 02:07 AM EDT

PDB ID : 2AOB
Title : Crystal structures of a high-affinity macrocyclic peptide mimetic in complex with the Grb2 SH2 domain
Authors : Phan, J.; Shi, Z.D.; Burke, T.R.; Waugh, D.S.
Deposited on : 2005-08-12
Resolution : 1.80 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

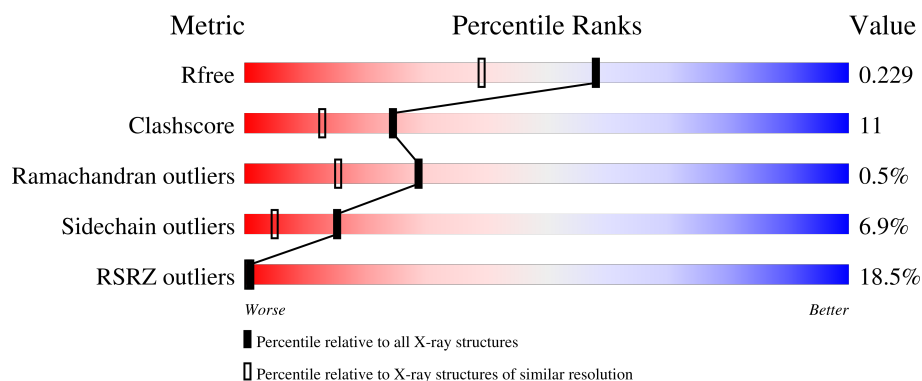
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	99	<div> <div>16%</div> <div>76%</div> <div>18%</div> <div>• • •</div> </div>
1	B	99	<div> <div>18%</div> <div>68%</div> <div>23%</div> <div>• 6%</div> </div>
1	C	99	<div> <div>14%</div> <div>75%</div> <div>16%</div> <div>5% • •</div> </div>
1	D	99	<div> <div>22%</div> <div>70%</div> <div>20%</div> <div>• • 6%</div> </div>

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
2	S1S	A	1201	X	-	-	-
2	S1S	A	1401	X	-	-	-
2	S1S	A	1501	X	-	-	-
2	S1S	A	1601	X	-	-	-
2	S1S	A	1701	X	-	-	-
2	S1S	B	1301	X	-	-	-
2	S1S	C	2201	X	-	-	-
2	S1S	C	2501	X	-	-	-
2	S1S	C	2601	X	-	-	-
2	S1S	D	2301	X	-	-	-
2	S1S	D	2701	X	-	-	-

2 Entry composition [i](#)

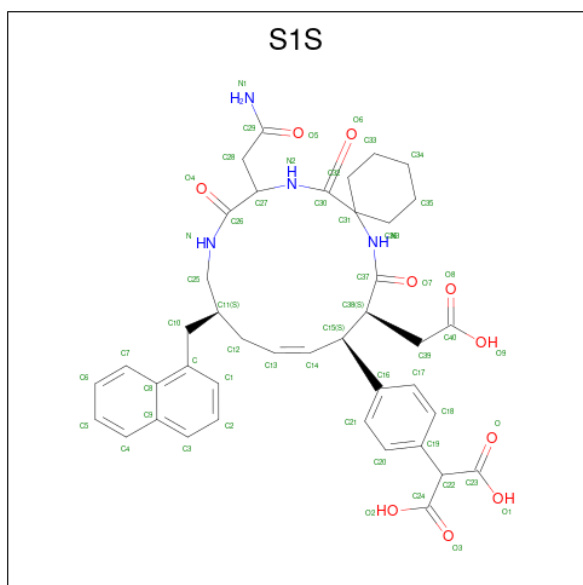
There are 3 unique types of molecules in this entry. The entry contains 4036 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Growth factor receptor-bound protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	0	0	0
			765	495	134	135	1			
1	B	93	Total	C	N	O		0	0	0
			741	477	134	130				
1	C	96	Total	C	N	O	S	0	0	0
			775	501	138	135	1			
1	D	93	Total	C	N	O		0	0	0
			722	464	129	129				

- Molecule 2 is 2-(4-((9S,10S,14S,Z)-18-(2-AMINO-2-OXOETHYL)-9-(CARBOXYMETHYL)-14-(NAPHTHALEN-1-YLMETHYL)-8,17,20-TRIOXO-7,16,19-TRIAZASPIRO [5.14]ICOS-11-EN-10-YL)PHENYL)MALONIC ACID (three-letter code: S1S) (formula: $C_{41}H_{46}N_4O_{10}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			55	41	4	10		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			55	41	4	10		
2	A	1	Total	C	N	O	0	0
			55	41	4	10		
2	A	1	Total	C	N	O	0	0
			55	41	4	10		
2	A	1	Total	C	N	O	0	0
			55	41	4	10		
2	B	1	Total	C	N	O	0	0
			55	41	4	10		
2	C	1	Total	C	N	O	0	0
			55	41	4	10		
2	C	1	Total	C	N	O	0	0
			55	41	4	10		
2	C	1	Total	C	N	O	0	0
			55	41	4	10		
2	C	1	Total	C	N	O	0	0
			55	41	4	10		
2	D	1	Total	C	N	O	0	0
			55	41	4	10		
2	D	1	Total	C	N	O	0	0
			55	41	4	10		

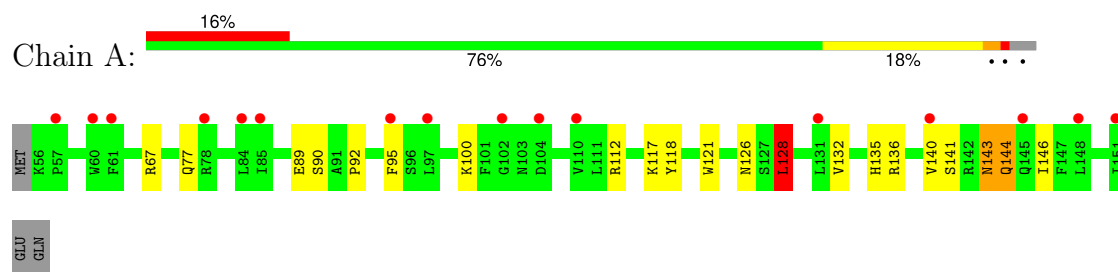
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	115	Total	O	0	0
			115	115		
3	B	84	Total	O	0	0
			84	84		
3	C	106	Total	O	0	0
			106	106		
3	D	68	Total	O	0	0
			68	68		

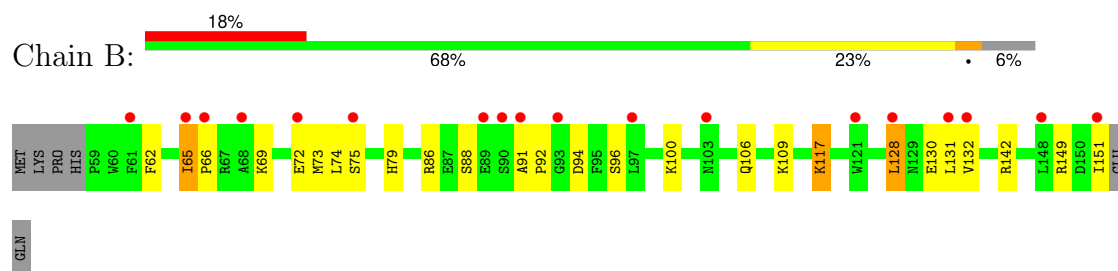
3 Residue-property plots [i](#)

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.

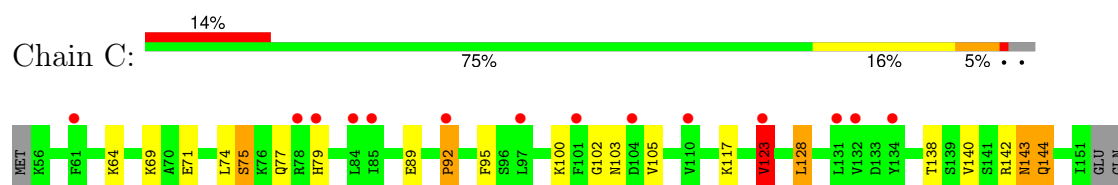
- Molecule 1: Growth factor receptor-bound protein 2



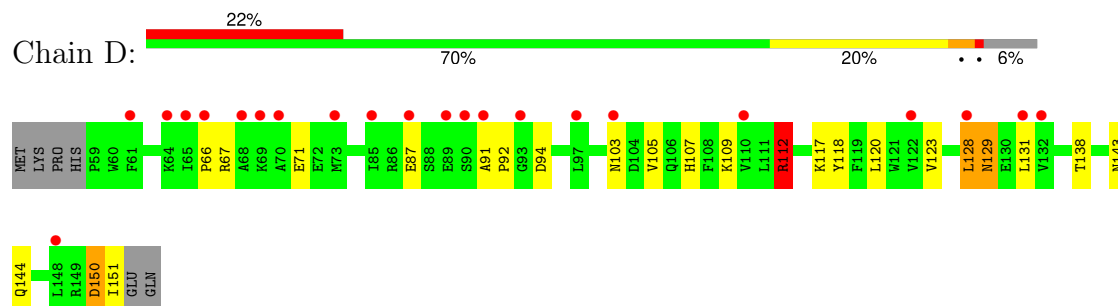
- Molecule 1: Growth factor receptor-bound protein 2



- Molecule 1: Growth factor receptor-bound protein 2



- Molecule 1: Growth factor receptor-bound protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.82Å 106.19Å 102.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.80 24.70 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (25.00-1.80) 99.7 (24.70-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.232 , 0.293 0.234 , 0.229	Depositor DCC
R_{free} test set	2212 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4036	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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 80.90 % 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 4.0181e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: S1S

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	1.09	1/787 (0.1%)	1.04	4/1063 (0.4%)
1	B	1.02	1/760 (0.1%)	1.01	3/1025 (0.3%)
1	C	1.07	1/797 (0.1%)	1.03	3/1074 (0.3%)
1	D	0.99	0/740	1.09	4/1000 (0.4%)
All	All	1.04	3/3084 (0.1%)	1.04	14/4162 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	121	TRP	CB-CG	6.69	1.62	1.50
1	B	132	VAL	CB-CG2	5.27	1.64	1.52
1	C	140	VAL	CB-CG2	5.12	1.63	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	ARG	NE-CZ-NH2	-7.24	116.68	120.30
1	A	112	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	B	66	PRO	N-CA-CB	6.67	111.31	103.30
1	C	123	VAL	CG1-CB-CG2	6.09	120.64	110.90
1	C	142	ARG	NE-CZ-NH1	-5.89	117.36	120.30

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	765	0	726	15	0
1	B	741	0	697	20	0
1	C	775	0	748	14	0
1	D	722	0	654	17	0
2	A	275	0	208	16	0
2	B	55	0	42	3	0
2	C	220	0	166	12	0
2	D	110	0	82	2	0
3	A	115	0	0	1	0
3	B	84	0	0	4	0
3	C	106	0	0	4	0
3	D	68	0	0	1	0
All	All	4036	0	3323	76	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 11.

The worst 5 of 76 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:A:95:PHE:CE2	2:A:1601:S1S:O	2.36	0.78
1:B:62:PHE:HB3	1:B:65:ILE:HD11	1.65	0.78
1:C:95:PHE:CE2	2:C:2601:S1S:O1	2.38	0.76
1:C:103:ASN:O	3:C:2657:HOH:O	2.05	0.72
1:D:94:ASP:OD2	1:D:109:LYS:NZ	2.24	0.71

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	94/99 (95%)	93 (99%)	1 (1%)	0	100	100
1	B	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
1	C	94/99 (95%)	91 (97%)	2 (2%)	1 (1%)	14	4
1	D	91/99 (92%)	86 (94%)	4 (4%)	1 (1%)	14	4
All	All	370/396 (93%)	355 (96%)	13 (4%)	2 (0%)	29	15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	91	ALA
1	C	92	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	79/88 (90%)	75 (95%)	4 (5%)	24	10
1	B	74/88 (84%)	71 (96%)	3 (4%)	30	16
1	C	81/88 (92%)	74 (91%)	7 (9%)	10	3
1	D	69/88 (78%)	62 (90%)	7 (10%)	7	2
All	All	303/352 (86%)	282 (93%)	21 (7%)	15	5

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	87	GLU
1	D	117	LYS
1	D	150	ASP
1	D	128	LEU
1	D	112	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	144	GLN
1	C	143	ASN
1	B	144	GLN
1	B	79	HIS
1	C	106	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](#)

12 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	$\# Z > 2$
2	S1S	A	1201	-	59,59,59	1.32	6 (10%)	77,83,83	2.62	21 (27%)
2	S1S	D	2701	-	59,59,59	1.67	13 (22%)	77,83,83	4.36	27 (35%)
2	S1S	A	1701	-	59,59,59	1.65	12 (20%)	77,83,83	4.51	32 (41%)
2	S1S	B	1301	-	59,59,59	1.77	16 (27%)	77,83,83	3.85	27 (35%)
2	S1S	C	2201	-	59,59,59	1.33	7 (11%)	77,83,83	2.99	29 (37%)
2	S1S	D	2301	-	59,59,59	1.65	9 (15%)	77,83,83	3.84	32 (41%)
2	S1S	C	2401	-	59,59,59	1.34	8 (13%)	77,83,83	3.78	27 (35%)
2	S1S	A	1401	-	59,59,59	1.46	9 (15%)	77,83,83	3.62	30 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	S1S	A	1601	-	59,59,59	1.30	5 (8%)	77,83,83	3.23	22 (28%)
2	S1S	A	1501	-	59,59,59	1.35	6 (10%)	77,83,83	2.05	20 (25%)
2	S1S	C	2501	-	59,59,59	1.49	7 (11%)	77,83,83	2.46	29 (37%)
2	S1S	C	2601	-	59,59,59	1.38	8 (13%)	77,83,83	2.41	23 (29%)

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	S1S	A	1201	-	2/2/13/18	17/66/76/76	0/4/5/5
2	S1S	D	2701	-	1/1/13/18	24/66/76/76	0/4/5/5
2	S1S	A	1701	-	1/1/13/18	17/66/76/76	0/4/5/5
2	S1S	B	1301	-	2/2/13/18	10/66/76/76	0/4/5/5
2	S1S	C	2201	-	2/2/13/18	20/66/76/76	0/4/5/5
2	S1S	D	2301	-	2/2/13/18	15/66/76/76	0/4/5/5
2	S1S	C	2501	-	1/1/13/18	13/66/76/76	0/4/5/5
2	S1S	A	1401	-	2/2/13/18	15/66/76/76	0/4/5/5
2	S1S	A	1601	-	1/1/13/18	16/66/76/76	0/4/5/5
2	S1S	A	1501	-	1/1/13/18	19/66/76/76	0/4/5/5
2	S1S	C	2401	-	-	18/66/76/76	0/4/5/5
2	S1S	C	2601	-	1/1/13/18	15/66/76/76	0/4/5/5

The worst 5 of 106 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2301	S1S	C16-C15	-4.50	1.47	1.52
2	A	1701	S1S	C16-C15	-4.38	1.47	1.52
2	B	1301	S1S	C36-C31	4.36	1.59	1.54
2	D	2701	S1S	C36-C31	4.25	1.59	1.54
2	D	2301	S1S	C19-C22	-4.17	1.48	1.53

The worst 5 of 319 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2701	S1S	C39-C38-C37	16.23	129.13	109.49
2	D	2301	S1S	C38-C37-N3	15.51	136.44	116.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1301	S1S	O7-C37-C38	-14.75	104.02	121.67
2	B	1301	S1S	C38-C37-N3	14.58	135.23	116.18
2	D	2701	S1S	C36-C31-N3	-14.38	82.20	109.57

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1201	S1S	C38
2	A	1201	S1S	C27
2	A	1401	S1S	C27
2	A	1401	S1S	C38
2	A	1501	S1S	C38

5 of 199 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	S1S	C15-C38-C39-C40
2	A	1201	S1S	C37-C38-C39-C40
2	A	1201	S1S	C16-C15-C38-C39
2	A	1201	S1S	C14-C15-C38-C39
2	A	1201	S1S	C14-C15-C38-C37

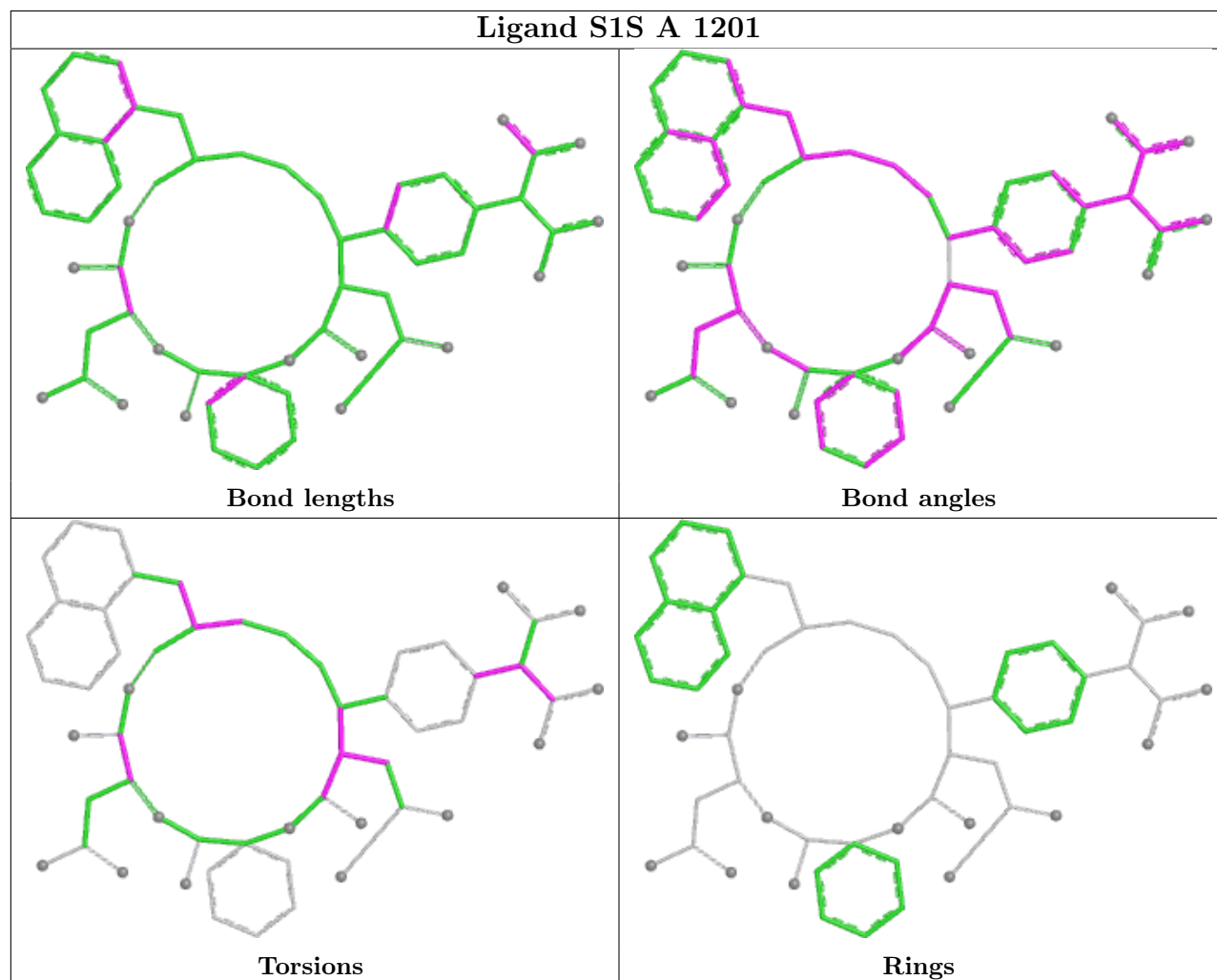
There are no ring outliers.

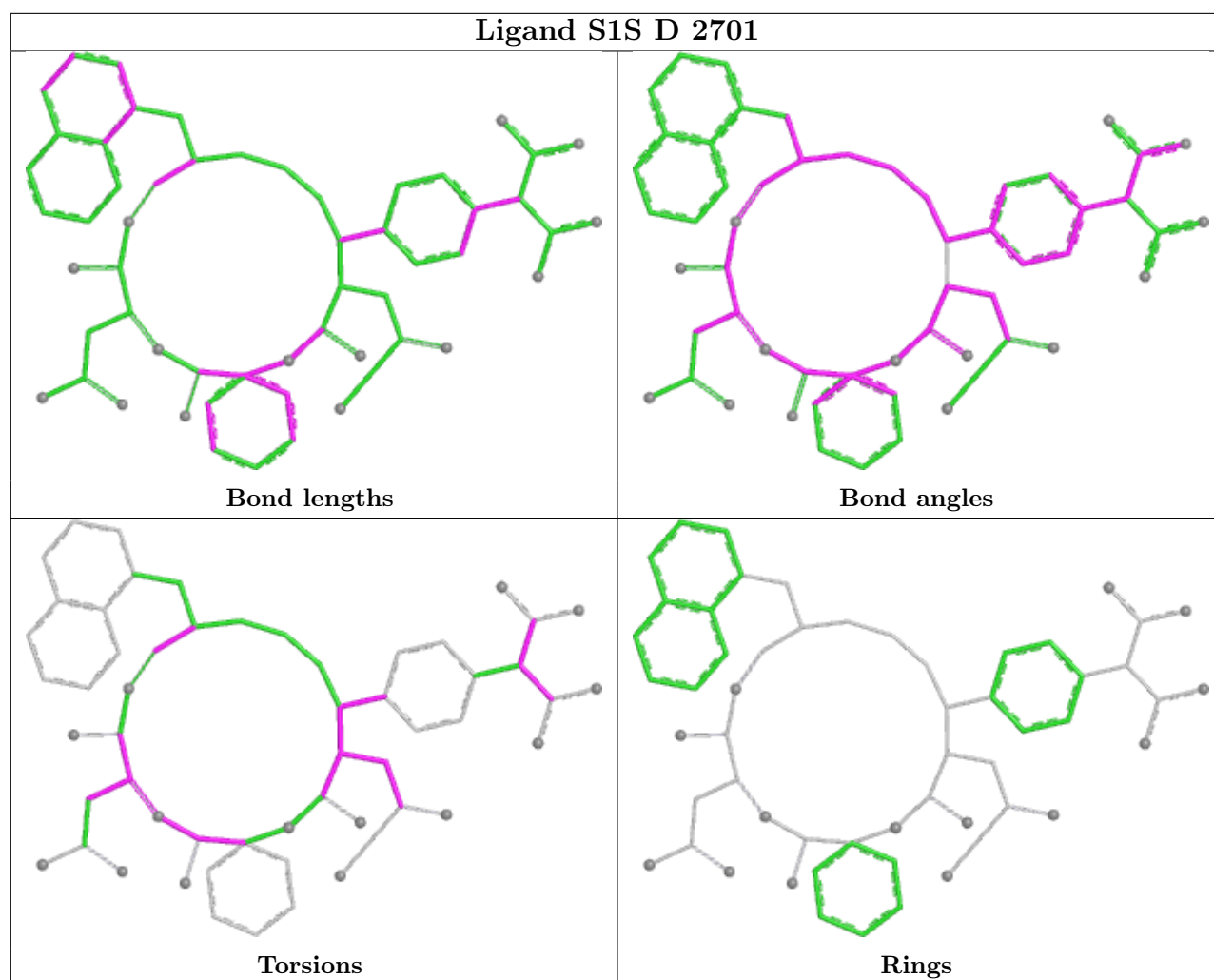
10 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	S1S	2	0
2	B	1301	S1S	3	0
2	C	2201	S1S	2	0
2	D	2301	S1S	2	0
2	C	2401	S1S	1	0
2	A	1401	S1S	5	0
2	A	1601	S1S	6	0
2	A	1501	S1S	5	0
2	C	2501	S1S	5	0
2	C	2601	S1S	5	0

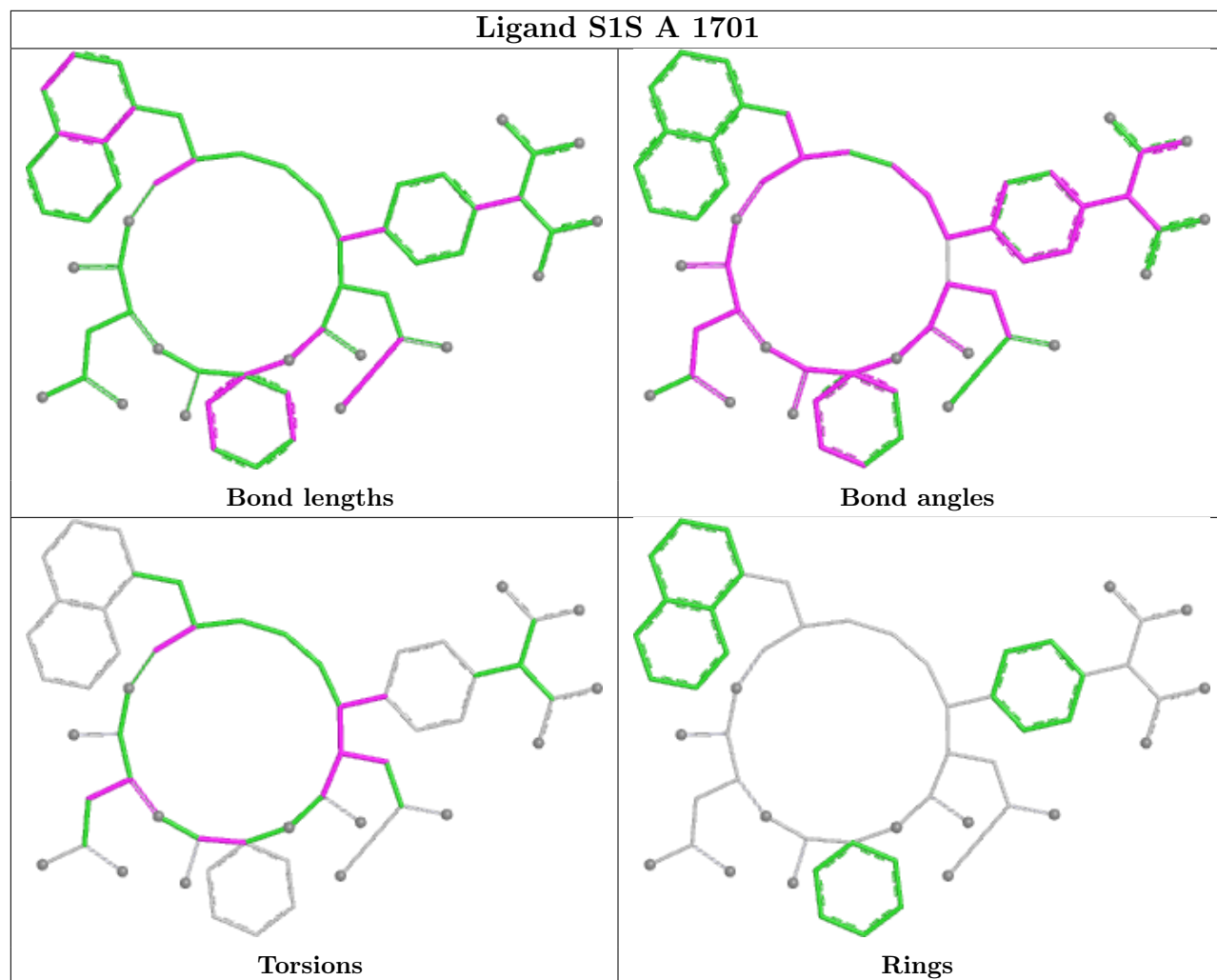
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

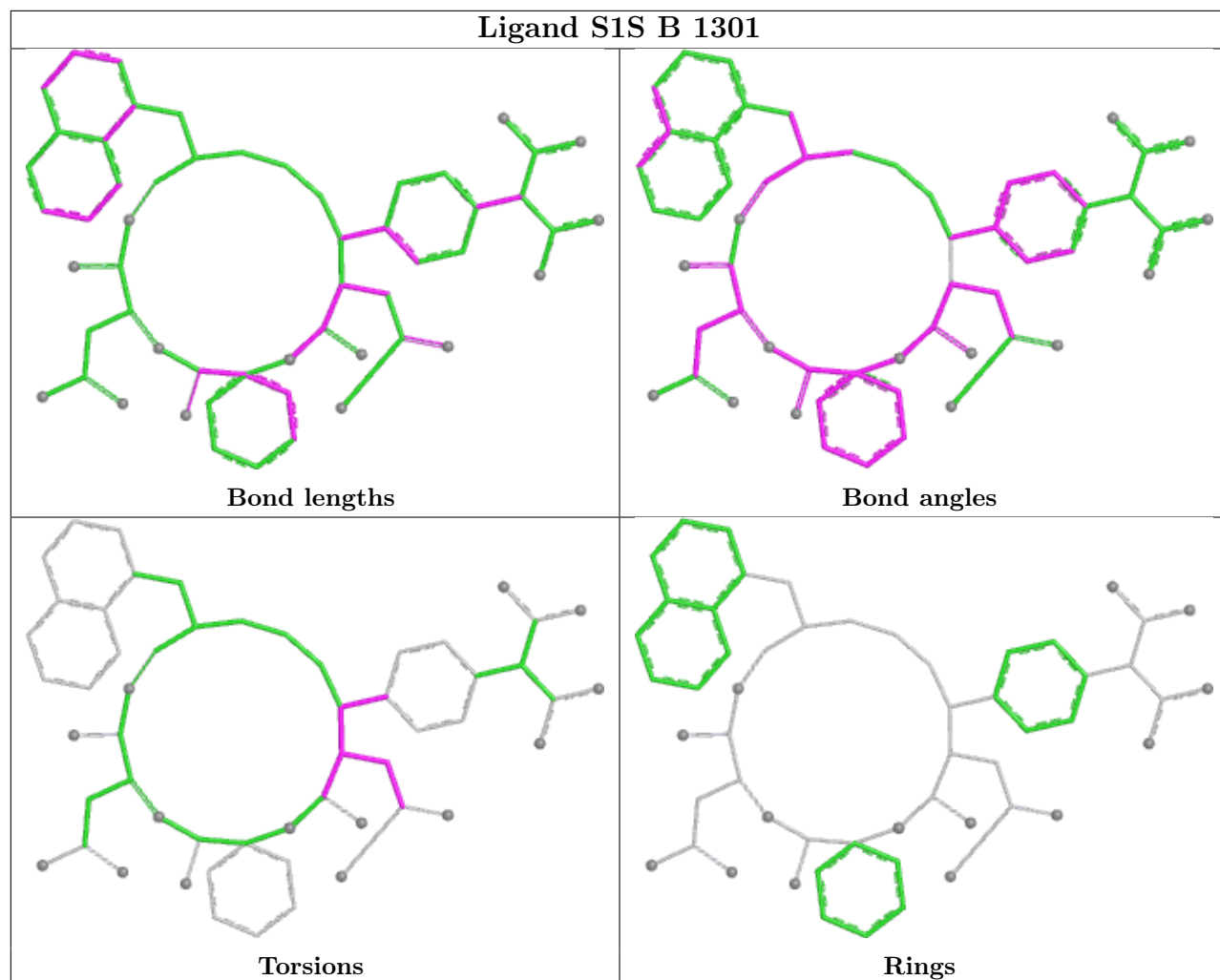


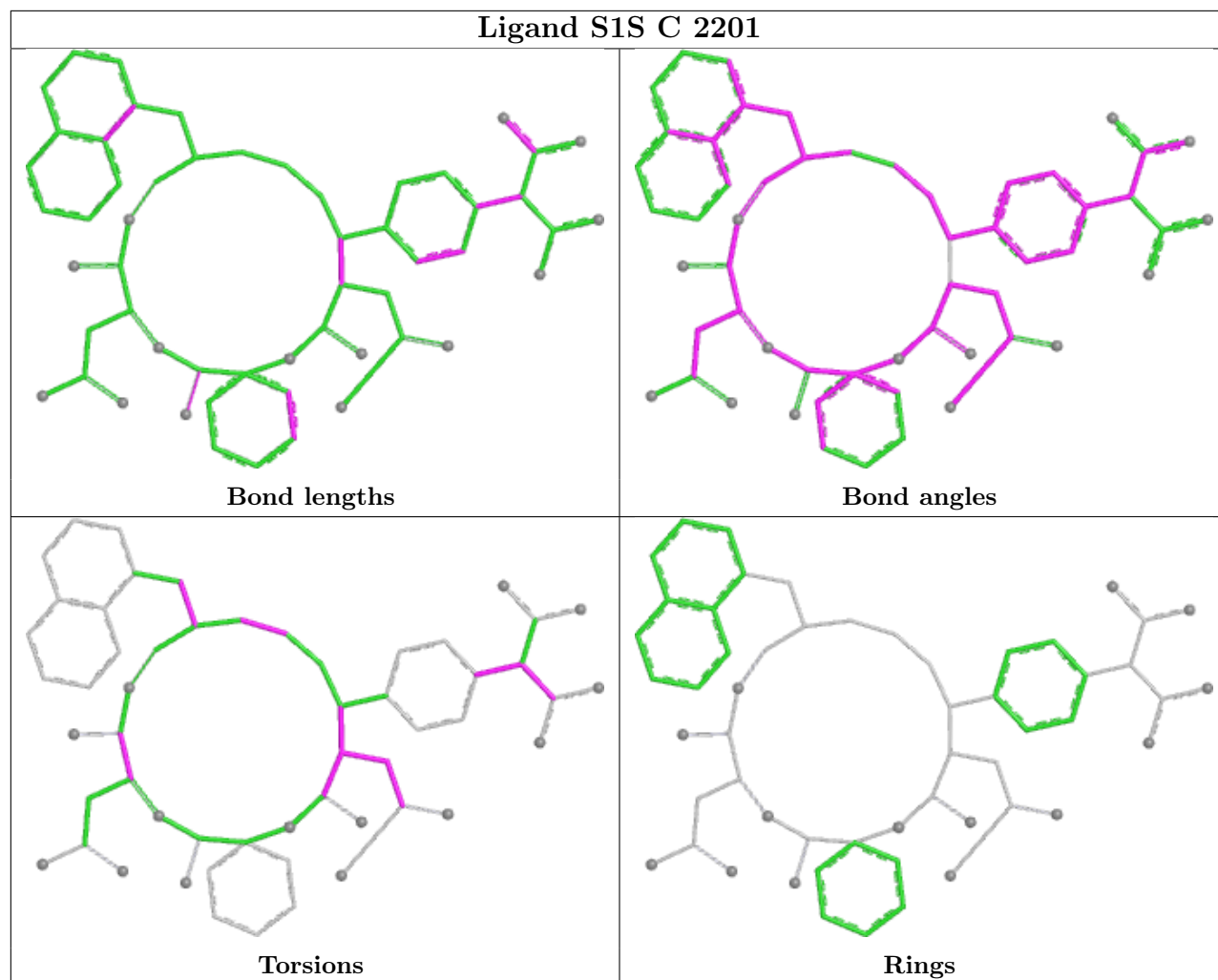


Ligand S1S A 1701

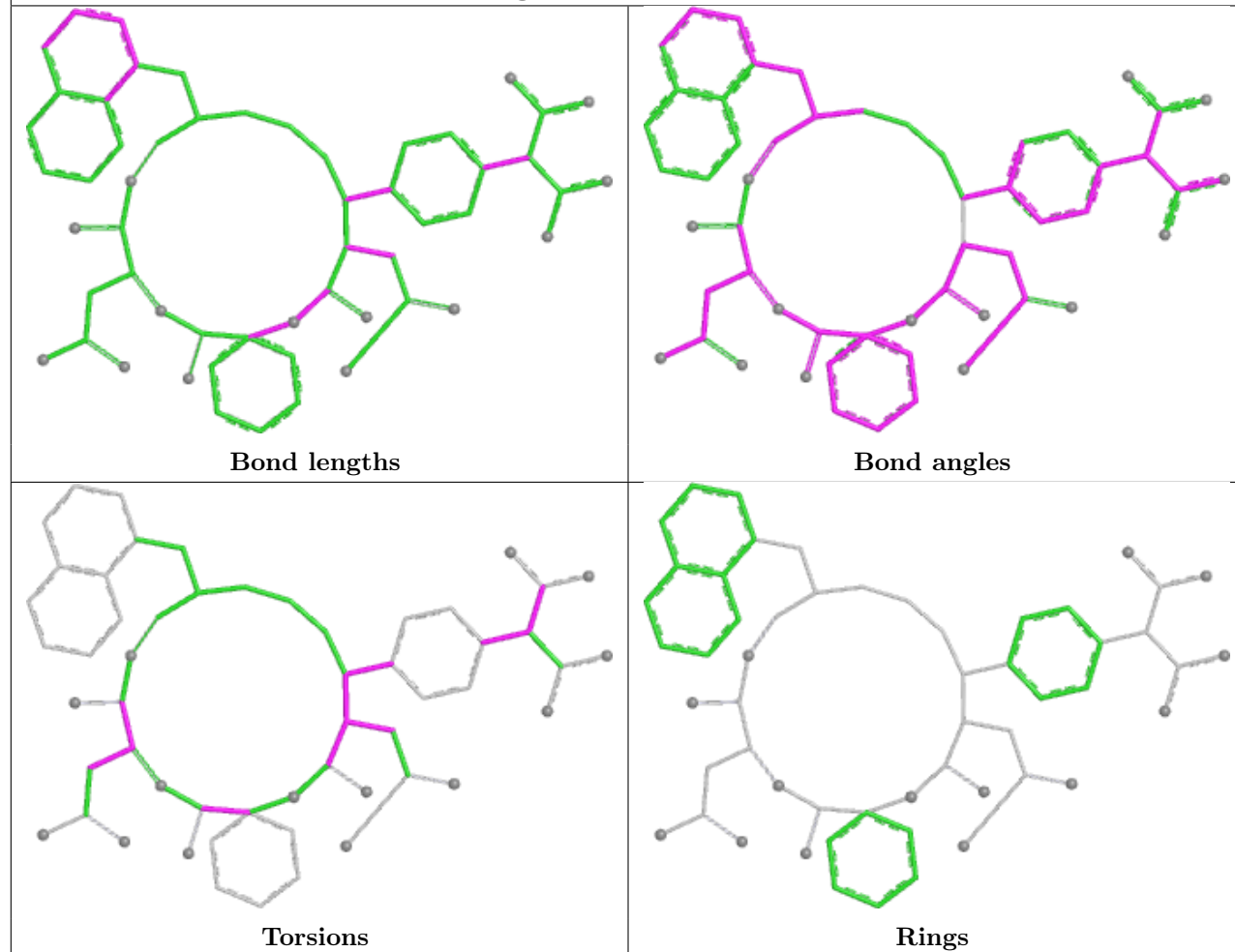


Ligand S1S B 1301

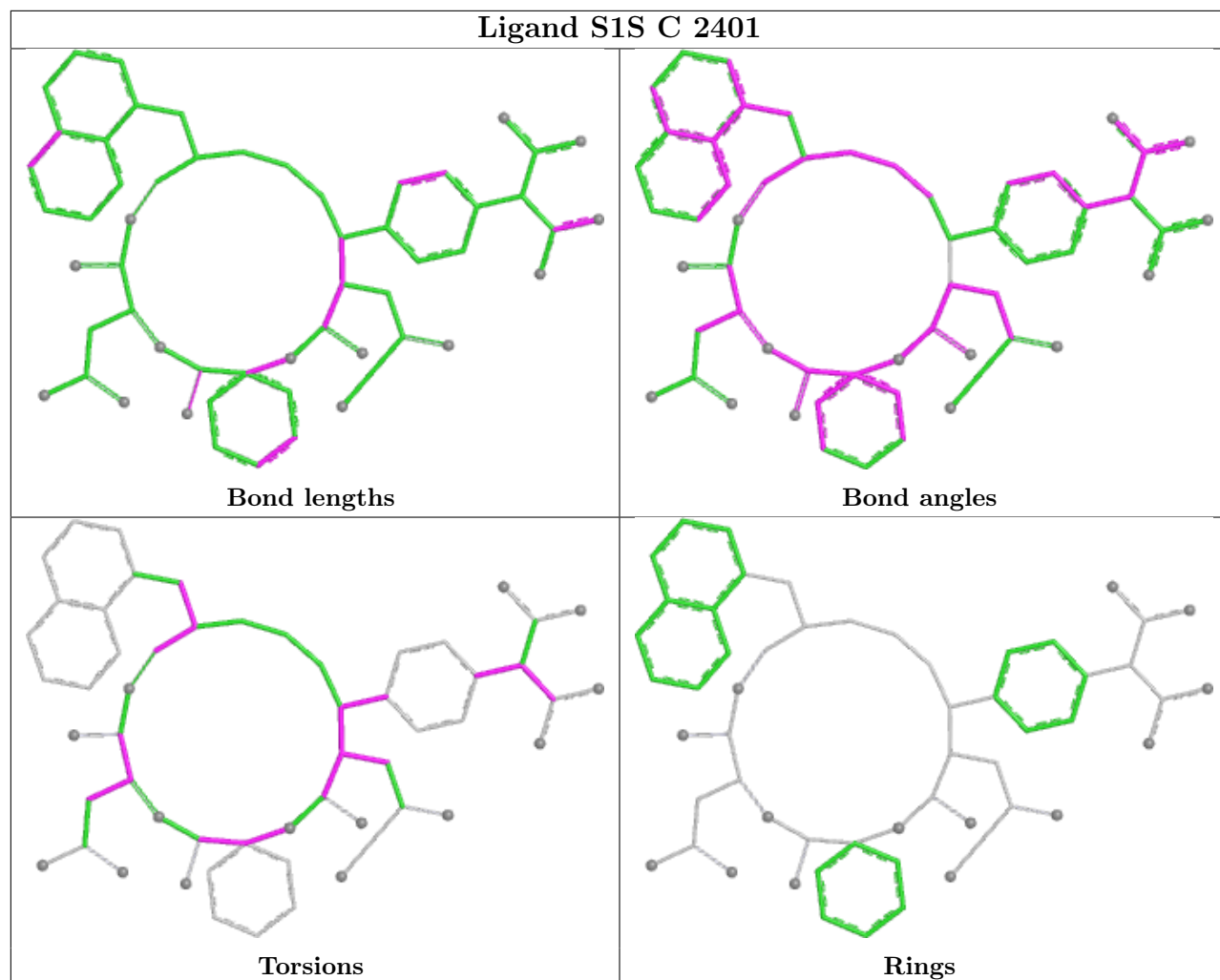




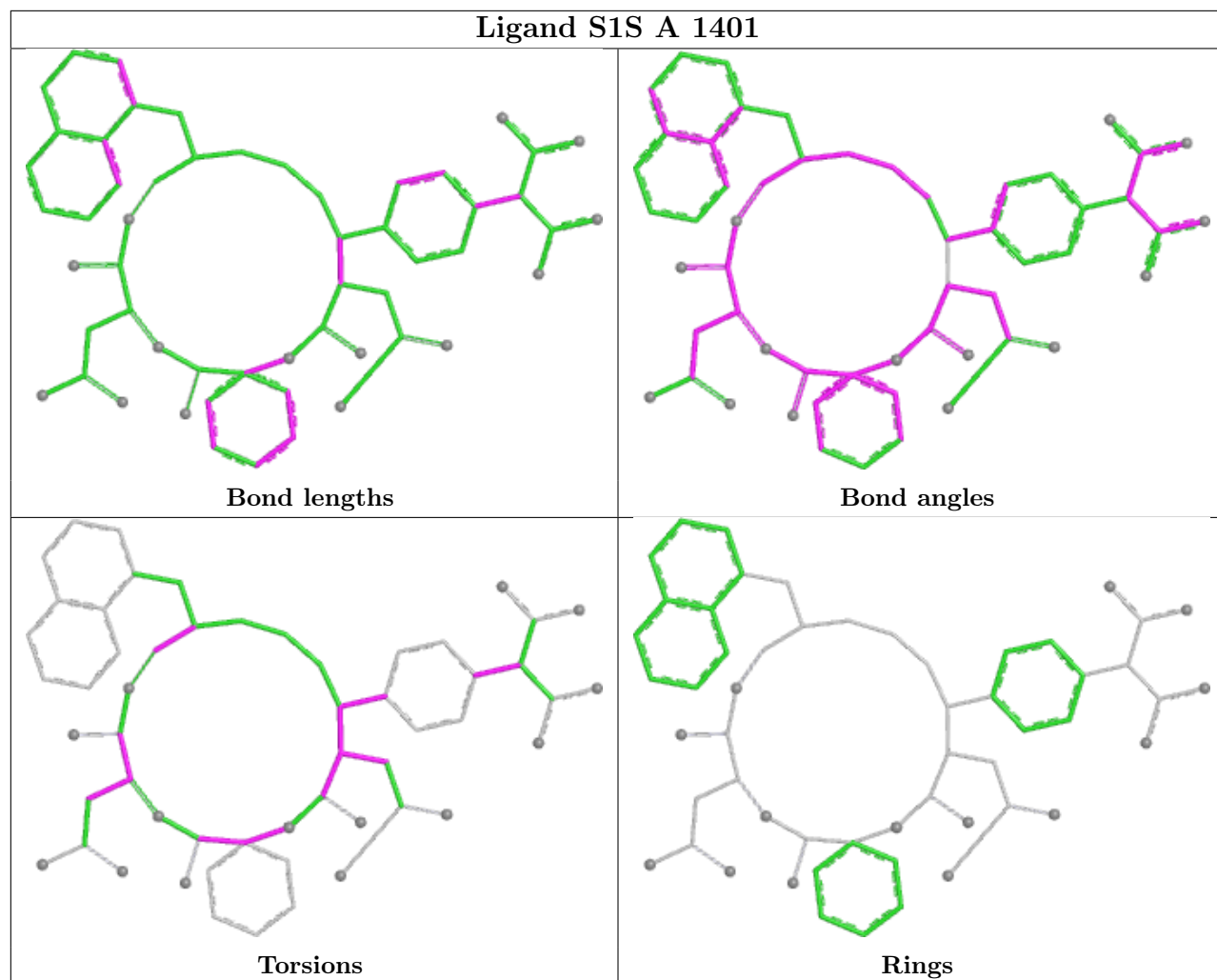
Ligand S1S D 2301



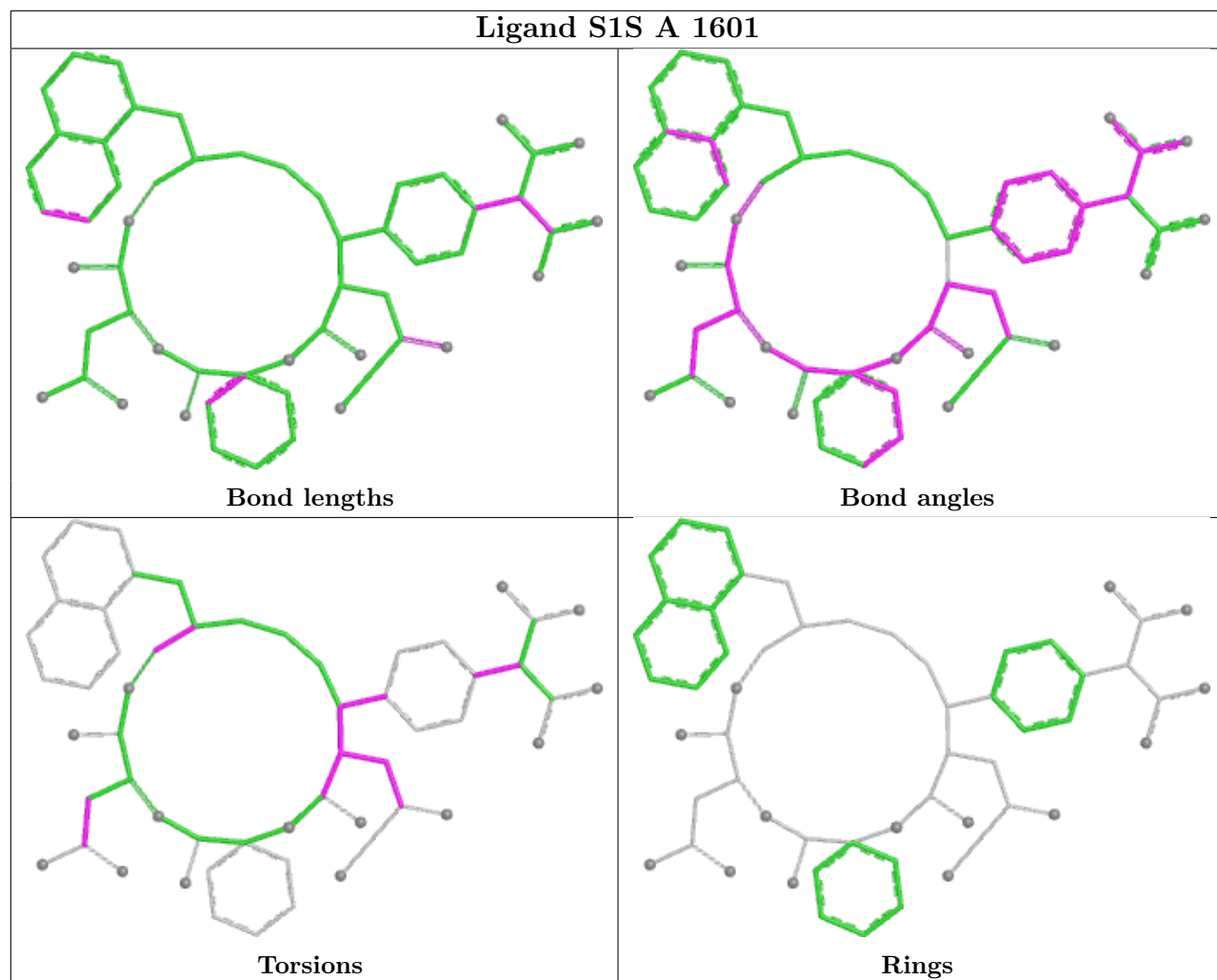
Ligand S1S C 2401

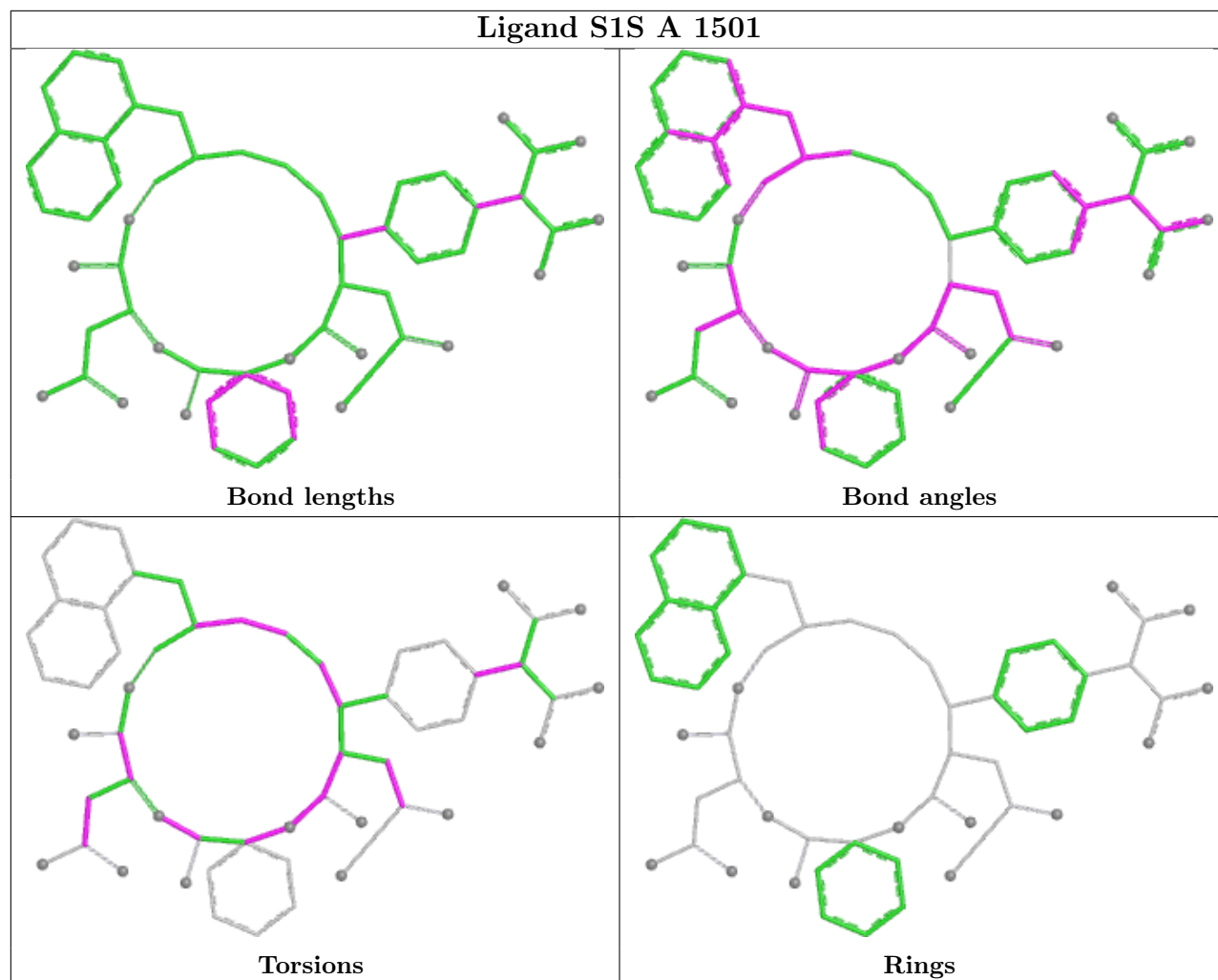


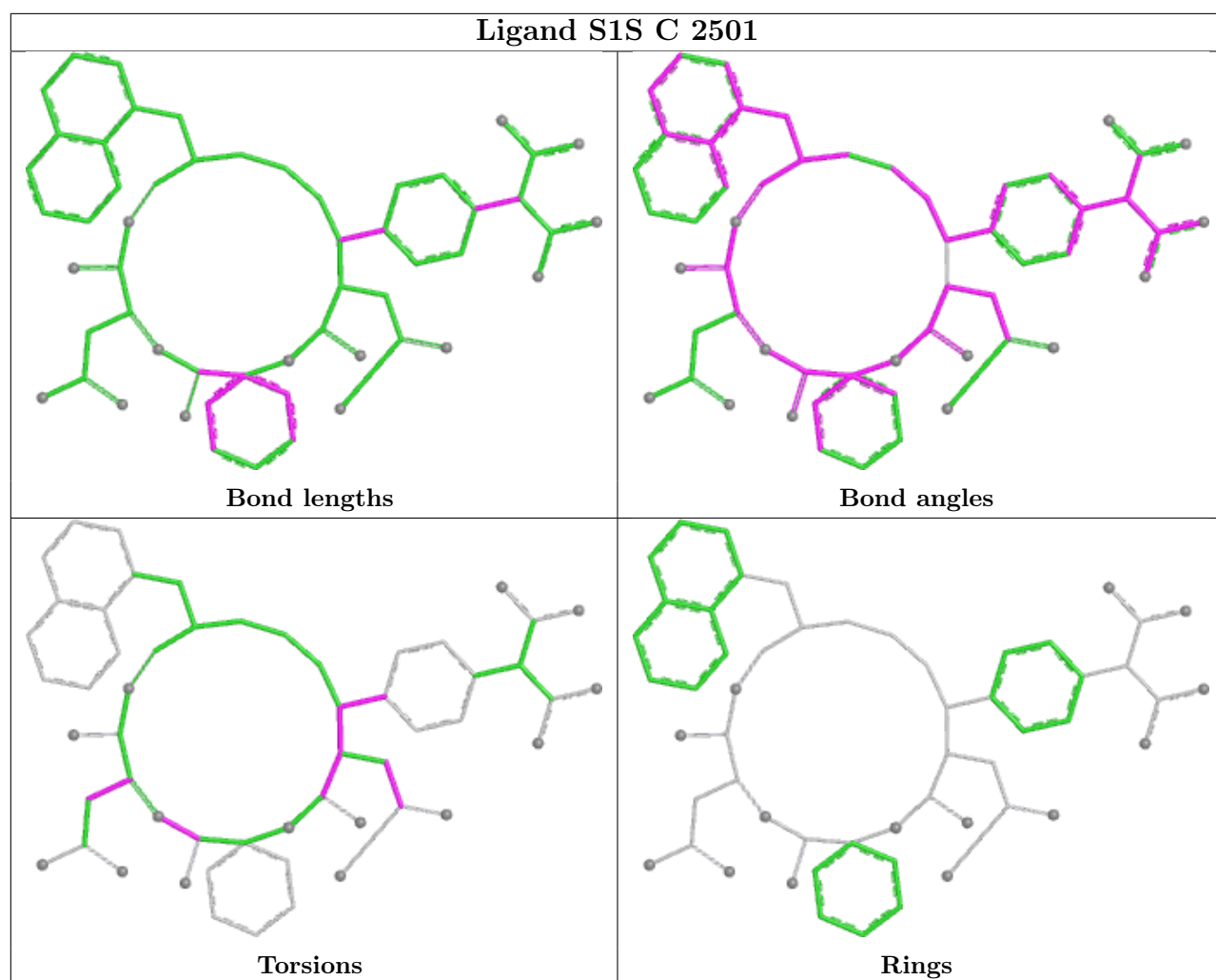
Ligand S1S A 1401

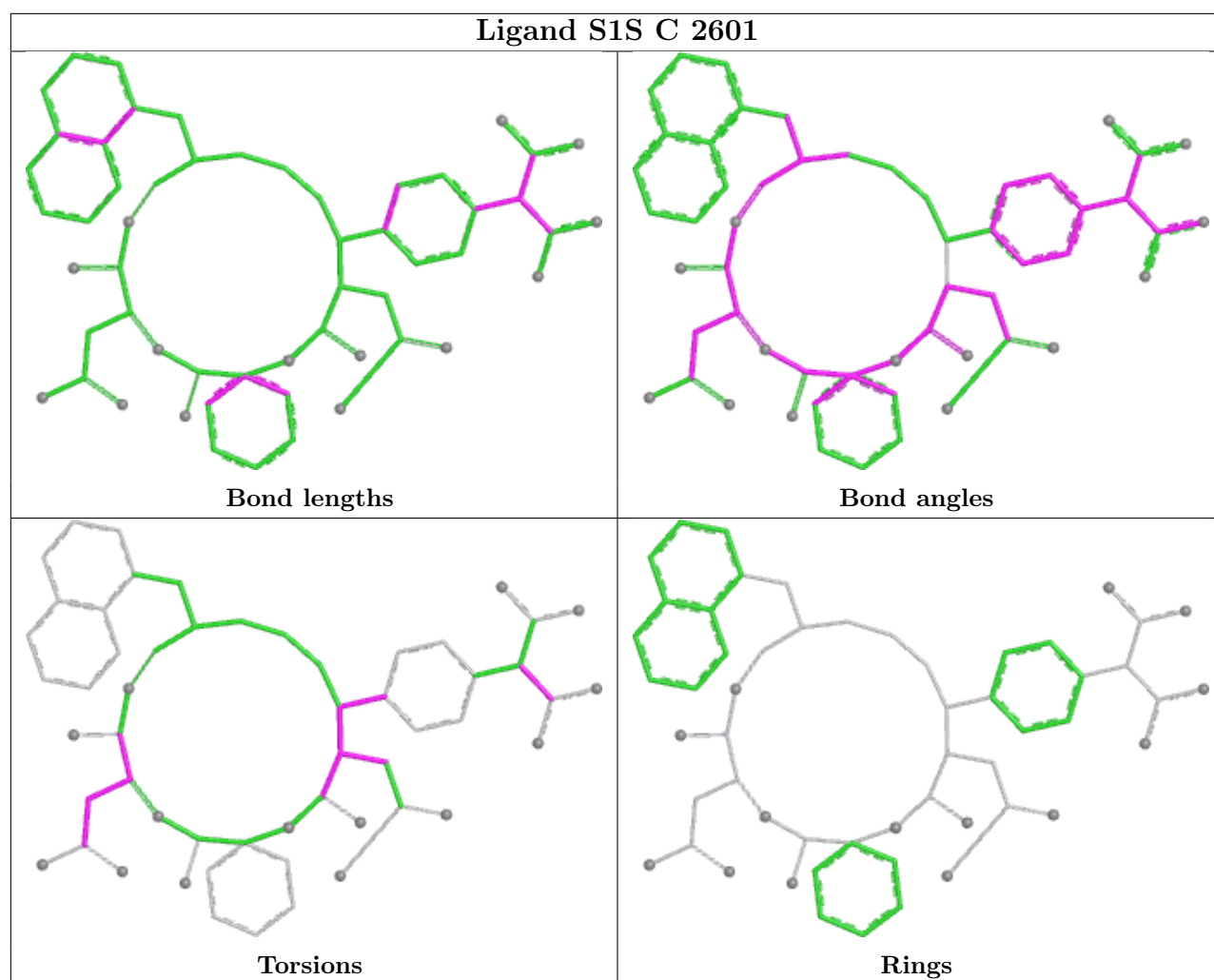


Ligand S1S A 1601









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	96/99 (96%)	1.00	16 (16%) 1 1	25, 33, 44, 53	0
1	B	93/99 (93%)	1.31	18 (19%) 1 0	23, 34, 45, 52	0
1	C	96/99 (96%)	0.98	14 (14%) 2 1	26, 33, 48, 52	0
1	D	93/99 (93%)	1.29	22 (23%) 0 0	25, 35, 54, 58	0
All	All	378/396 (95%)	1.14	70 (18%) 1 0	23, 33, 50, 58	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	90	SER	7.6
1	D	90	SER	5.6
1	B	68	ALA	4.8
1	D	68	ALA	4.6
1	B	89	GLU	4.5

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 monosaccharides in this entry.

6.4 Ligands [i](#)

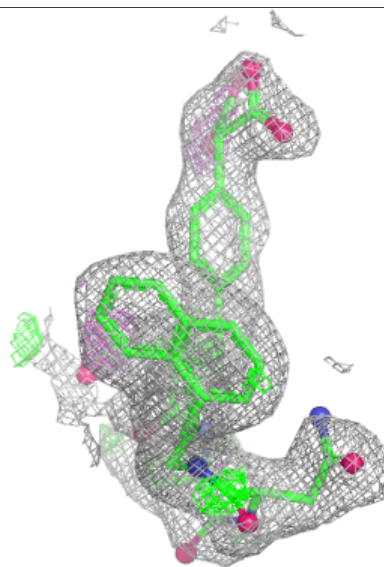
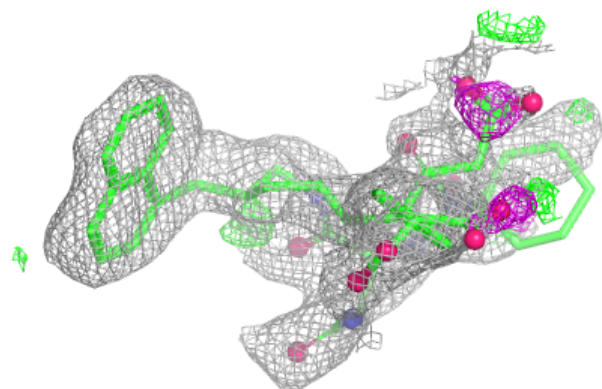
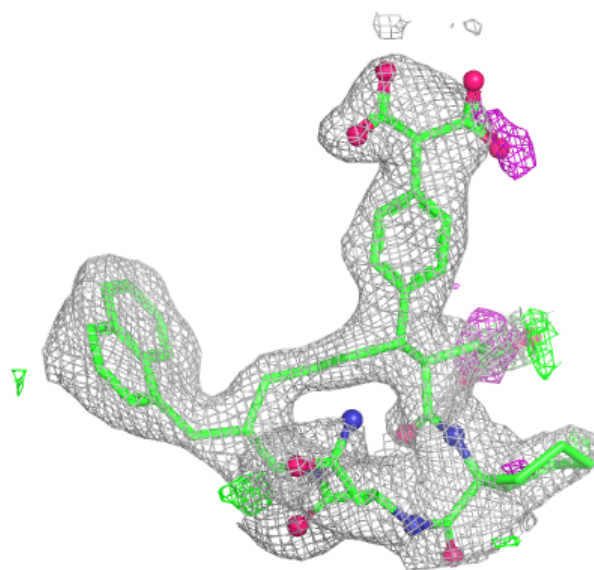
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	S1S	A	1501	55/55	0.79	0.21	35,53,61,61	0
2	S1S	C	2501	55/55	0.79	0.23	31,46,54,62	0
2	S1S	A	1701	55/55	0.80	0.20	21,33,54,56	0
2	S1S	D	2701	55/55	0.82	0.19	20,33,50,53	0
2	S1S	A	1601	55/55	0.86	0.17	19,29,47,55	0
2	S1S	C	2601	55/55	0.88	0.17	20,30,43,47	0
2	S1S	C	2201	55/55	0.89	0.12	22,29,34,35	0
2	S1S	A	1201	55/55	0.91	0.12	21,28,36,38	0
2	S1S	B	1301	55/55	0.91	0.11	16,23,41,47	0
2	S1S	D	2301	55/55	0.92	0.12	15,24,46,50	0
2	S1S	A	1401	55/55	0.92	0.12	16,23,38,40	0
2	S1S	C	2401	55/55	0.93	0.12	16,22,36,38	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.

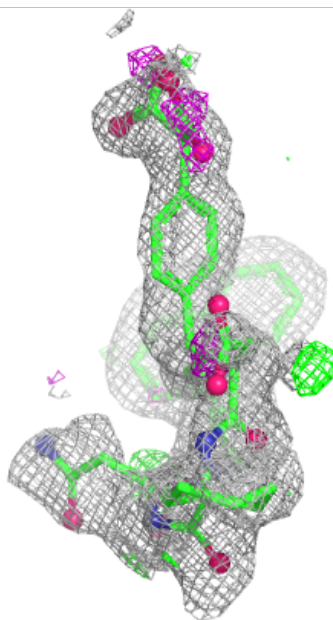
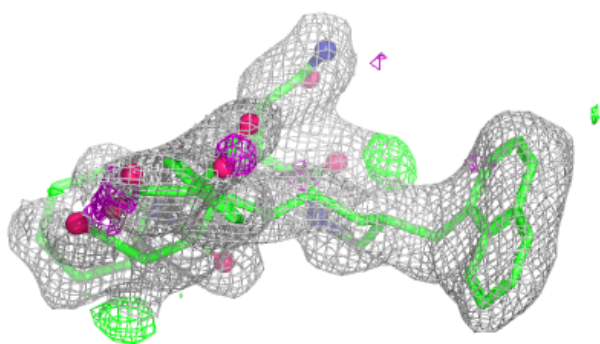
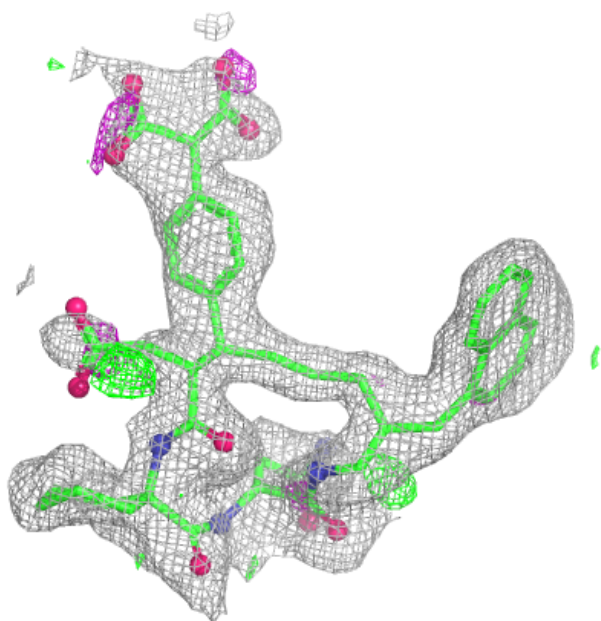
Electron density around S1S A 1501:

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



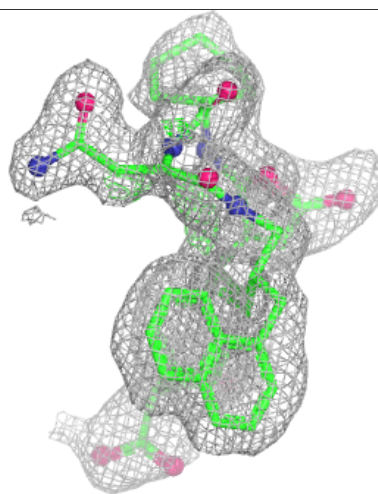
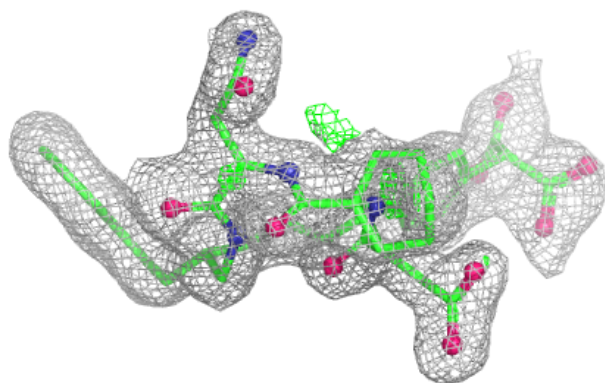
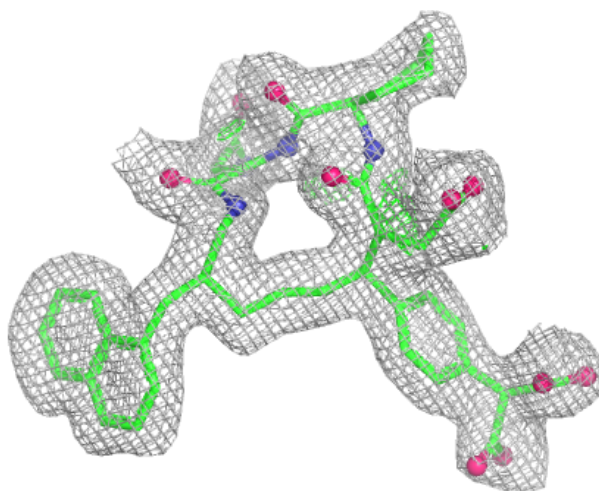
Electron density around S1S C 2501:

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



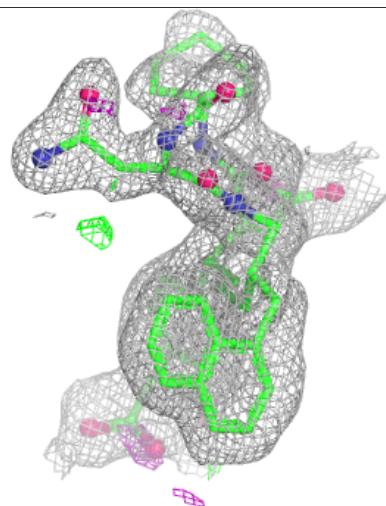
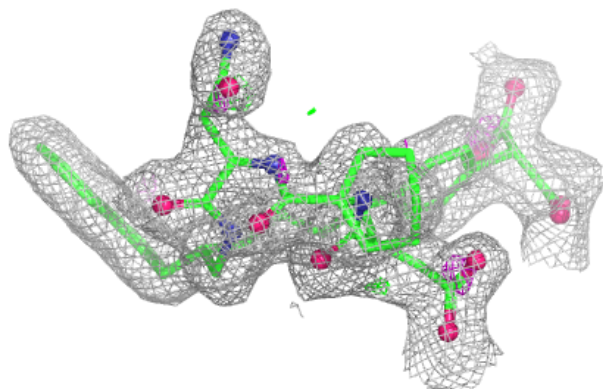
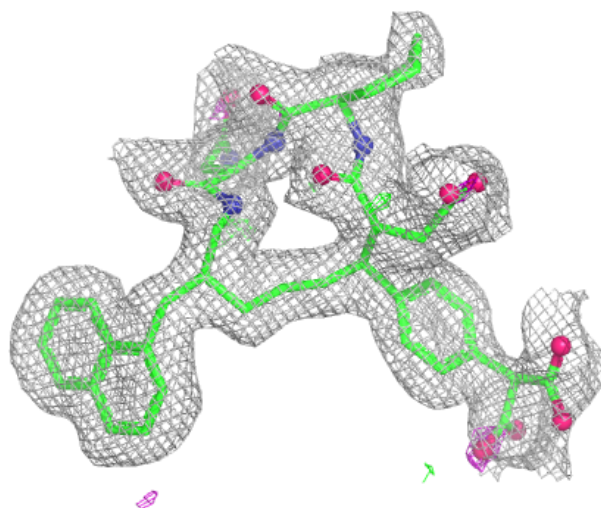
Electron density around S1S A 1701:

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



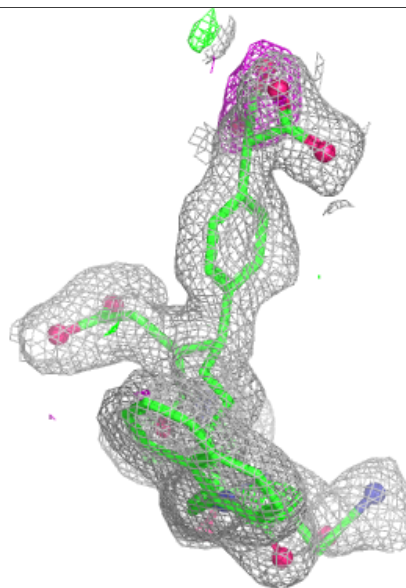
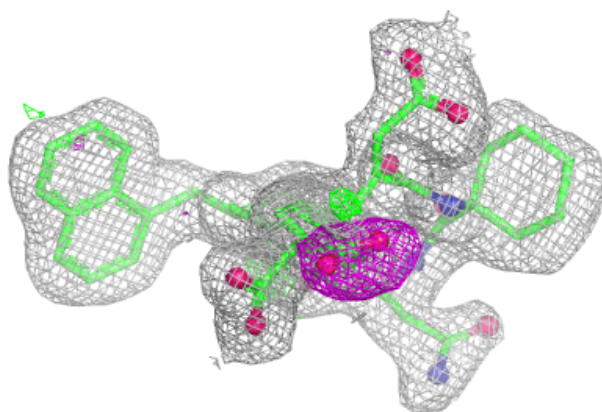
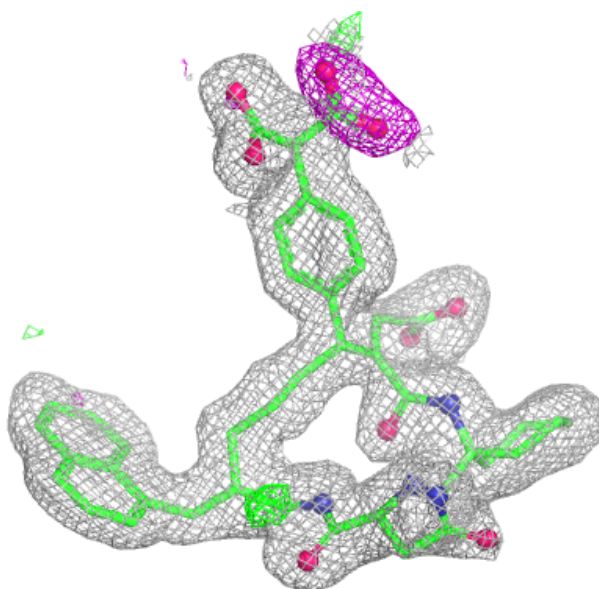
Electron density around S1S D 2701:

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



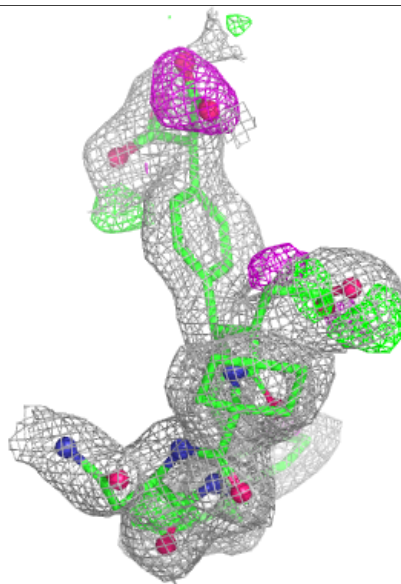
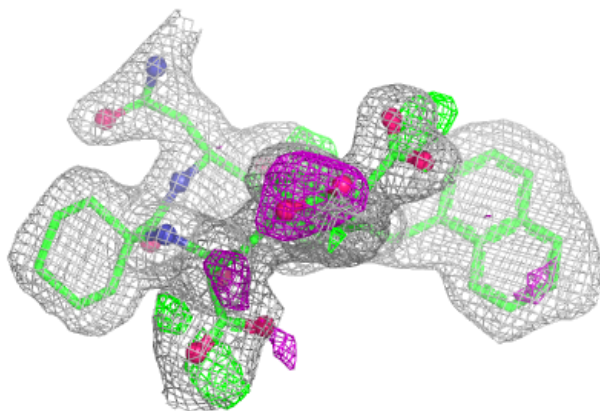
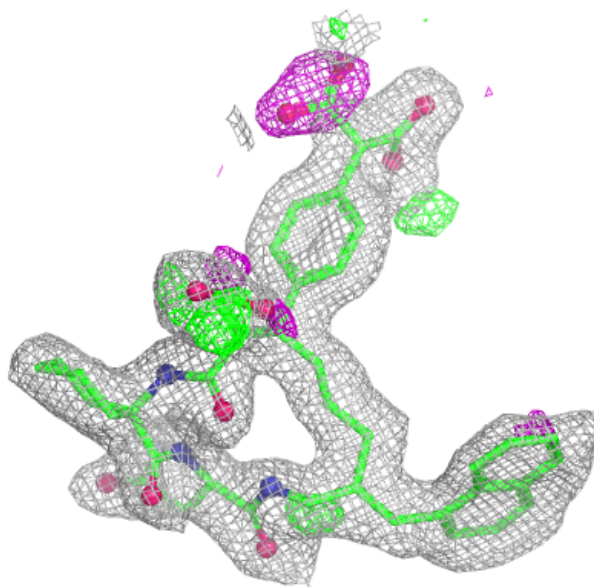
Electron density around S1S A 1601:

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



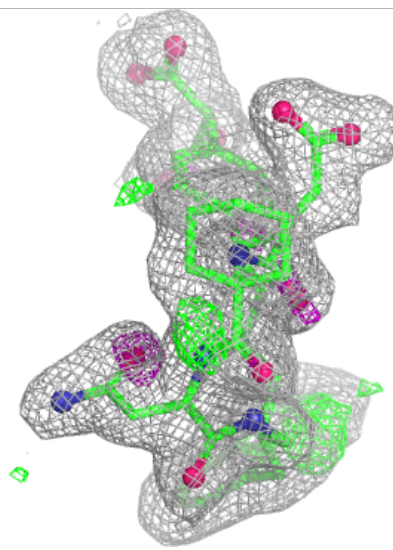
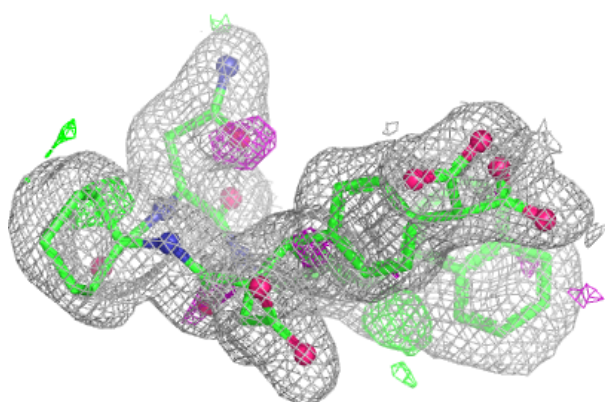
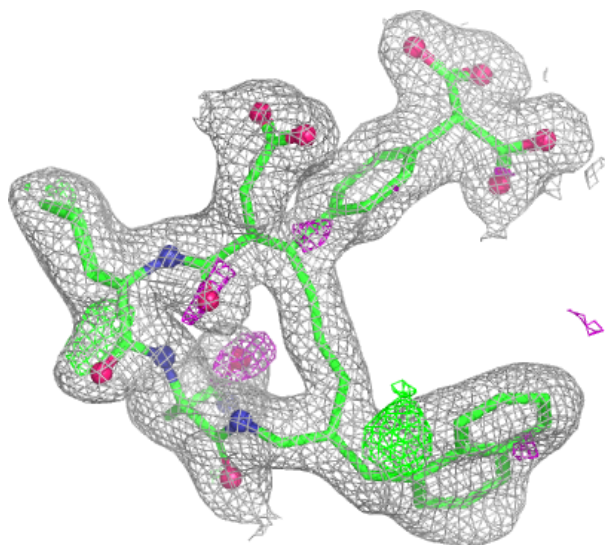
Electron density around S1S C 2601:

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



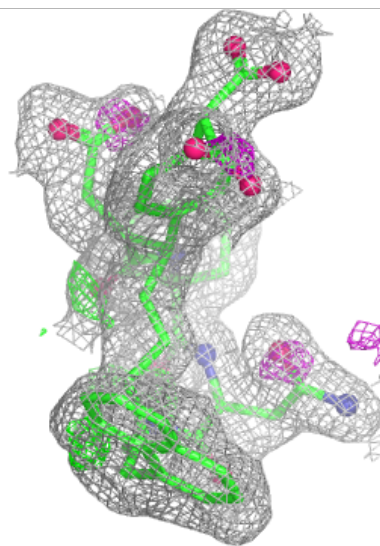
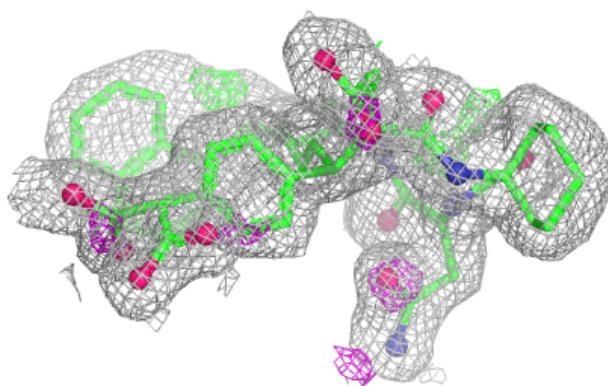
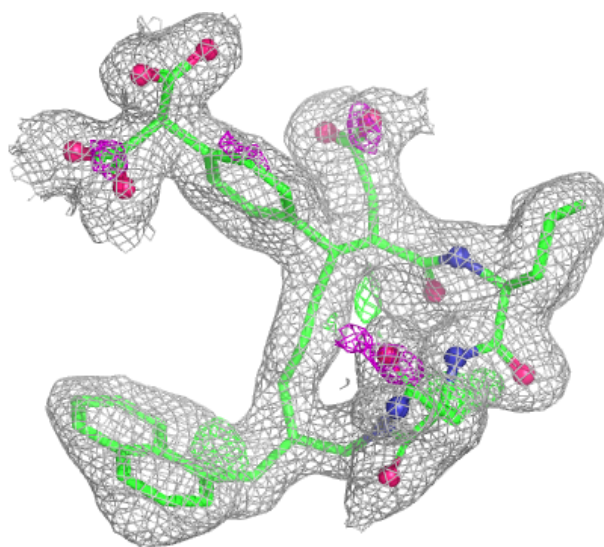
Electron density around S1S C 2201:

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



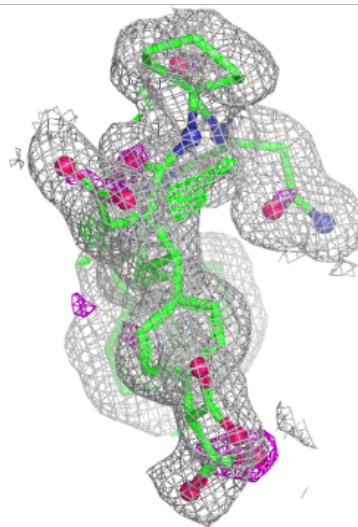
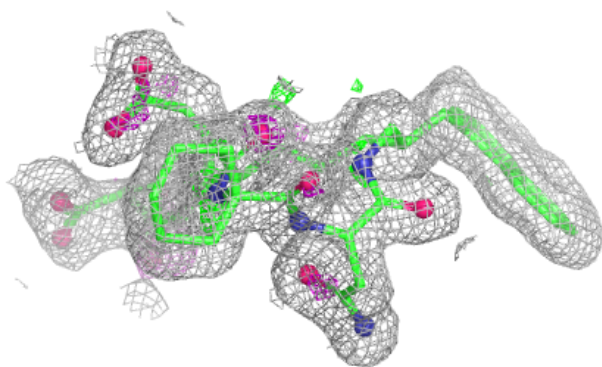
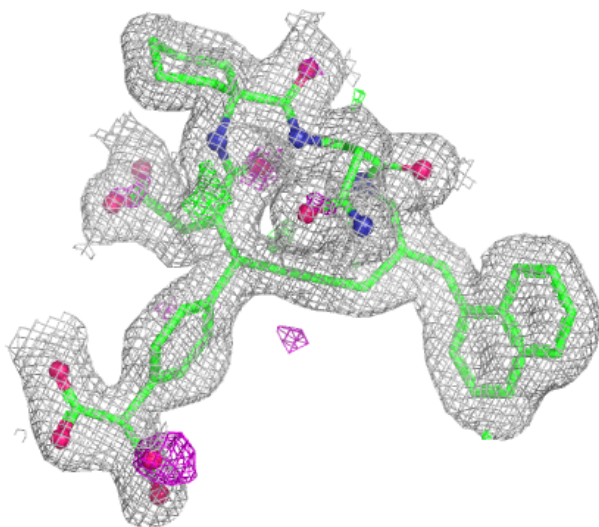
Electron density around S1S A 1201:

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



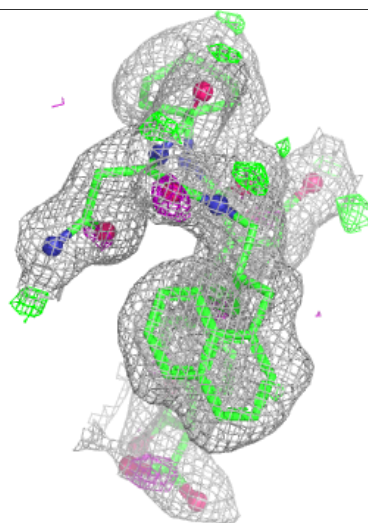
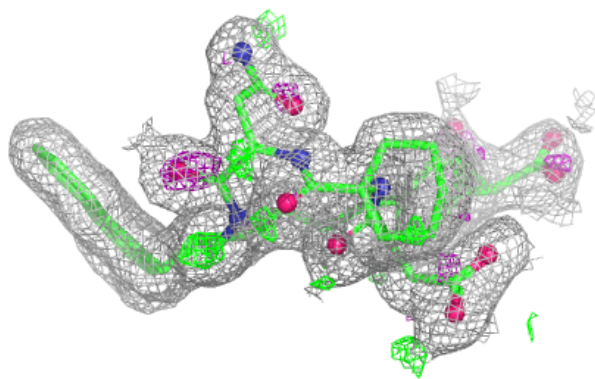
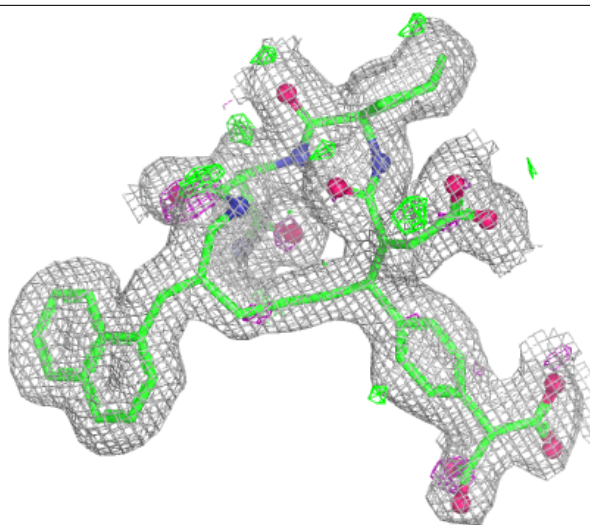
Electron density around S1S B 1301:

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



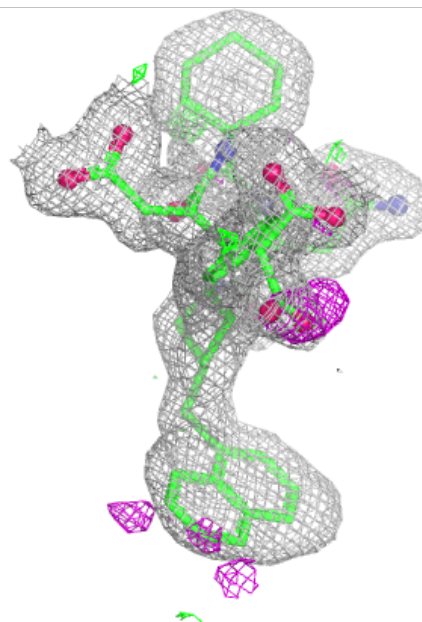
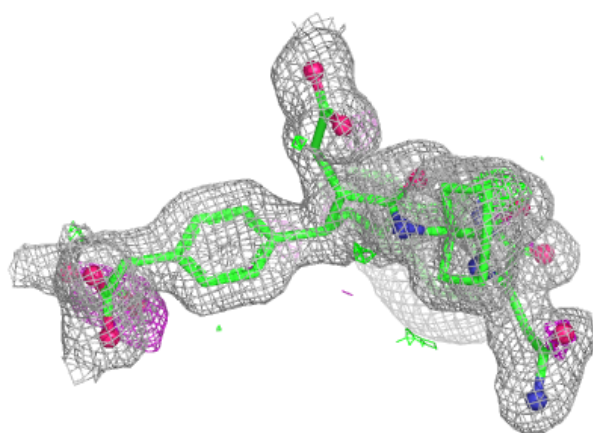
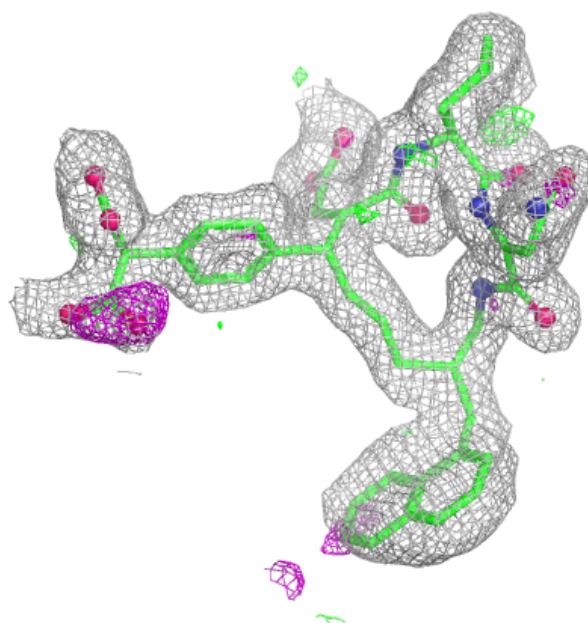
Electron density around S1S D 2301:

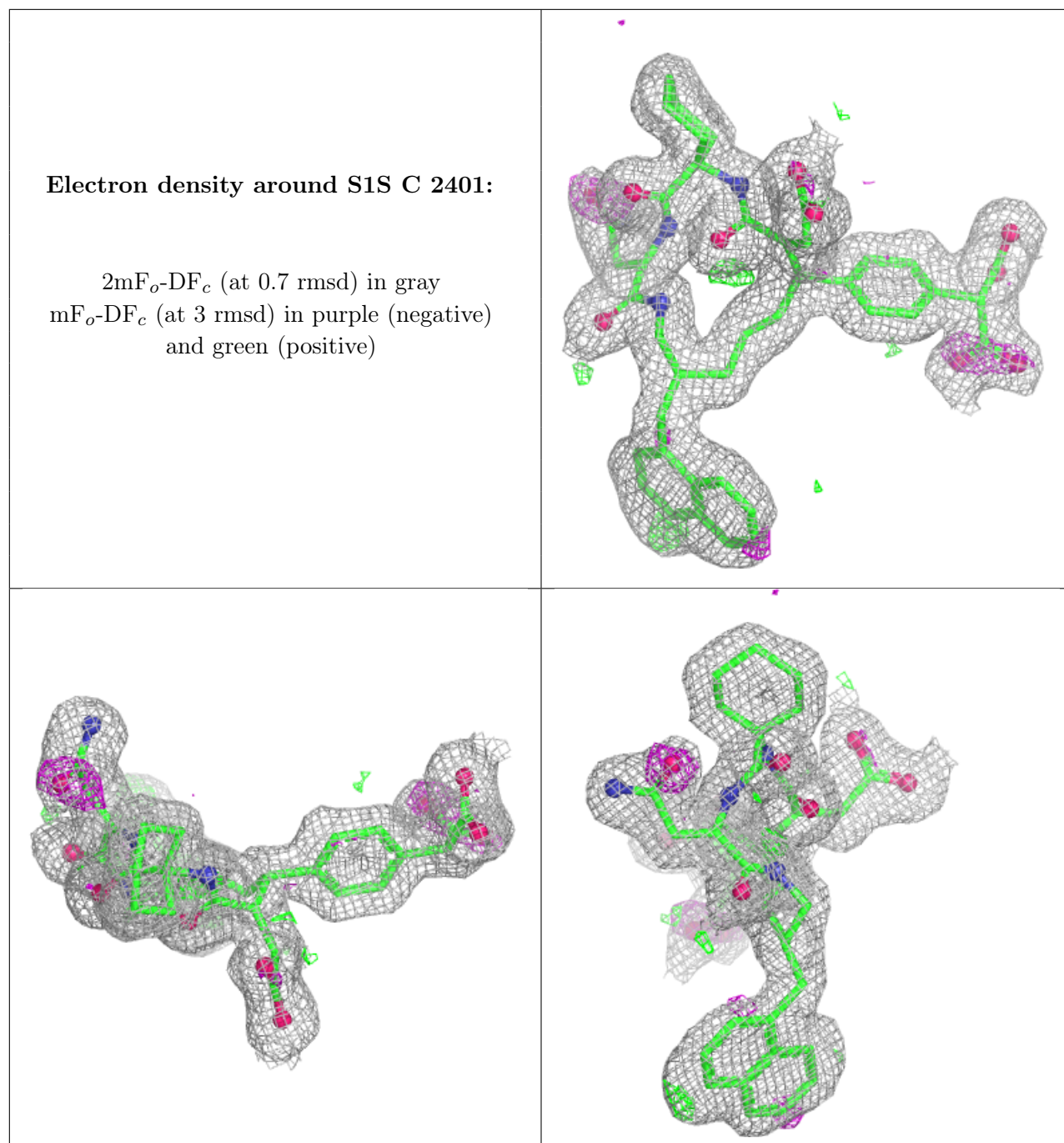
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around S1S A 1401:

$2mF_o-DF_c$ (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.