



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 06:54 PM UTC

PDB ID : 6TP6 / pdb\_00006tp6  
Title : Crystal structure of the Orexin-1 receptor in complex with filorexant  
Authors : Rappas, M.; Ali, A.; Bennett, K.A.; Brown, J.D.; Bucknell, S.J.; Congreve, M.; Cooke, R.M.; Cseke, G.; de Graaf, C.; Dore, A.S.; Errey, J.C.; Jazayeri, A.; Marshall, F.H.; Mason, J.S.; Mould, R.; Patel, J.C.; Tehan, B.G.; Weir, M.; Christopher, J.A.  
Deposited on : 2019-12-12  
Resolution : 2.34 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](mailto: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>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

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

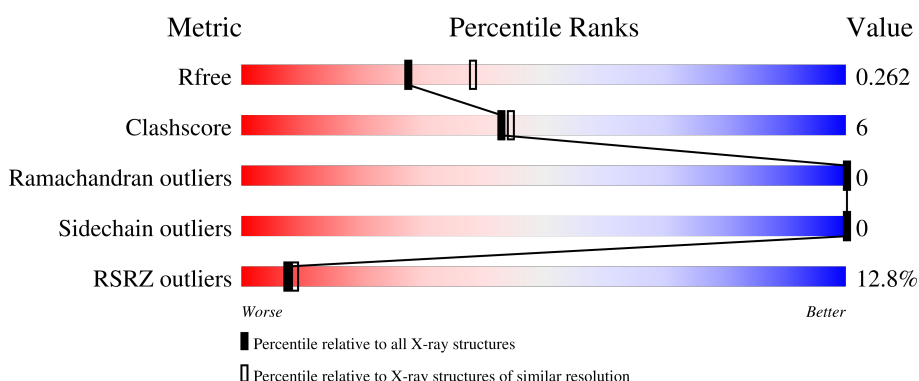
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.34 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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  $\geq 3$ , 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	368	
1	B	368	

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
7	PGW	A	411	X	-	-	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5301 atoms, of which 50 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 Orexin receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	305	2447	1627	402	401	17	0	0	0
1	B	303	2404	1592	403	392	17	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

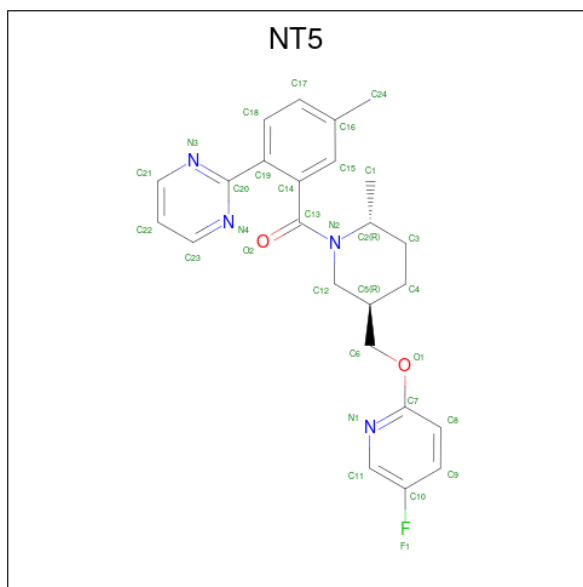
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	ALA	-	expression tag	UNP O43613
A	26	ALA	-	expression tag	UNP O43613
A	27	SER	-	expression tag	UNP O43613
A	46	ALA	GLU	engineered mutation	UNP O43613
A	85	LEU	ILE	engineered mutation	UNP O43613
A	95	ALA	VAL	engineered mutation	UNP O43613
A	162	LEU	ARG	engineered mutation	UNP O43613
A	194	ALA	ASN	engineered mutation	UNP O43613
A	198	ALA	LEU	engineered mutation	UNP O43613
A	211	ALA	TYR	engineered mutation	UNP O43613
A	304	VAL	LEU	engineered mutation	UNP O43613
A	339	ALA	CYS	engineered mutation	UNP O43613
A	375	TRP	CYS	engineered mutation	UNP O43613
A	376	TRP	CYS	engineered mutation	UNP O43613
A	381	ALA	-	expression tag	UNP O43613
A	382	ALA	-	expression tag	UNP O43613
A	383	ALA	-	expression tag	UNP O43613
A	384	HIS	-	expression tag	UNP O43613
A	385	HIS	-	expression tag	UNP O43613
A	386	HIS	-	expression tag	UNP O43613
A	387	HIS	-	expression tag	UNP O43613
A	388	HIS	-	expression tag	UNP O43613
A	389	HIS	-	expression tag	UNP O43613
A	390	HIS	-	expression tag	UNP O43613
A	391	HIS	-	expression tag	UNP O43613

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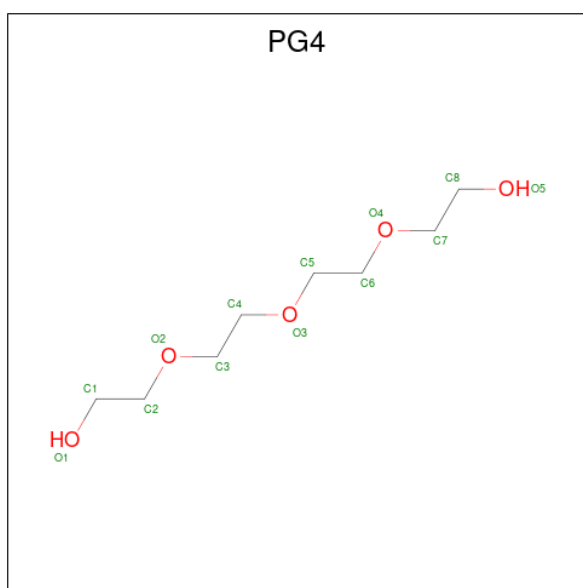
Chain	Residue	Modelled	Actual	Comment	Reference
A	392	HIS	-	expression tag	UNP O43613
B	25	ALA	-	expression tag	UNP O43613
B	26	ALA	-	expression tag	UNP O43613
B	27	SER	-	expression tag	UNP O43613
B	46	ALA	GLU	engineered mutation	UNP O43613
B	85	LEU	ILE	engineered mutation	UNP O43613
B	95	ALA	VAL	engineered mutation	UNP O43613
B	162	LEU	ARG	engineered mutation	UNP O43613
B	194	ALA	ASN	engineered mutation	UNP O43613
B	198	ALA	LEU	engineered mutation	UNP O43613
B	211	ALA	TYR	engineered mutation	UNP O43613
B	304	VAL	LEU	engineered mutation	UNP O43613
B	339	ALA	CYS	engineered mutation	UNP O43613
B	375	TRP	CYS	engineered mutation	UNP O43613
B	376	TRP	CYS	engineered mutation	UNP O43613
B	381	ALA	-	expression tag	UNP O43613
B	382	ALA	-	expression tag	UNP O43613
B	383	ALA	-	expression tag	UNP O43613
B	384	HIS	-	expression tag	UNP O43613
B	385	HIS	-	expression tag	UNP O43613
B	386	HIS	-	expression tag	UNP O43613
B	387	HIS	-	expression tag	UNP O43613
B	388	HIS	-	expression tag	UNP O43613
B	389	HIS	-	expression tag	UNP O43613
B	390	HIS	-	expression tag	UNP O43613
B	391	HIS	-	expression tag	UNP O43613
B	392	HIS	-	expression tag	UNP O43613

- Molecule 2 is [(2 {R},5 {R})-5-[(5-fluoranylpyridin-2-yl)oxymethyl]-2-methyl-piperidin-1-yl)-(5-methyl-2-pyrimidin-2-yl-phenyl)methanone (CCD ID: NT5) (formula: C<sub>24</sub>H<sub>25</sub>FN<sub>4</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



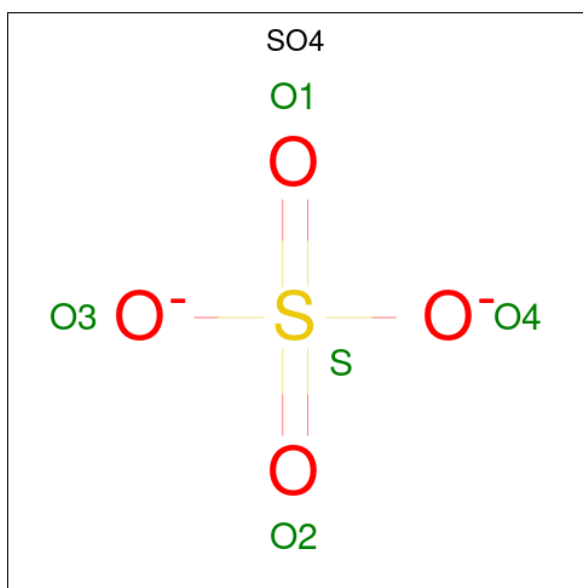
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	H	N			O
2	A	1	Total	C	F	H	N	O	0	0
			56	24	1	25	4	2		
2	B	1	Total	C	F	H	N	O	0	0
			56	24	1	25	4	2		

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula:  $C_8H_{18}O_5$ ).



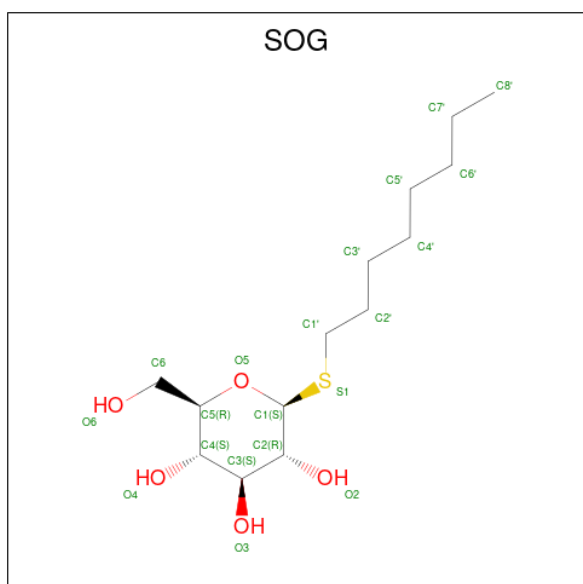
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	Total	C	O	0	0
			13	8	5		
3	B	1	Total	C	O	0	0
			9	6	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 5 is octyl 1-thio-beta-D-glucopyranoside (CCD ID: SOG) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>5</sub>S).

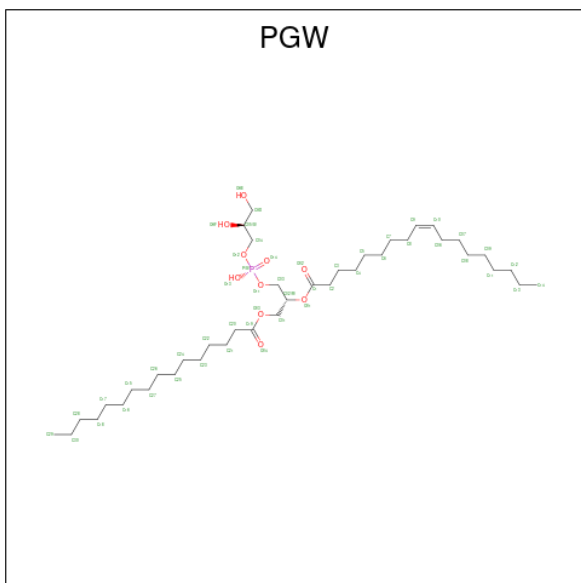


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O S 20 14 5 1	0	0
5	A	1	Total C O S 20 14 5 1	0	0
5	A	1	Total C O S 13 7 5 1	0	0
5	A	1	Total C O S 20 14 5 1	0	0
5	A	1	Total C 4 4	0	0
5	B	1	Total C O S 20 14 5 1	0	0
5	B	1	Total C O S 20 14 5 1	0	0
5	B	1	Total C O S 20 14 5 1	0	0
5	B	1	Total C S 6 5 1	0	0

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0

- Molecule 7 is (1R)-2-[[[(S)-{[(2S)-2,3-dihydroxypropyl]oxy}(hydroxy)phosphoryl]oxy}-1-[(hexadecanoyloxy)methyl]ethyl (9Z)-octadec-9-enoate (CCD ID: PGW) (formula: C<sub>40</sub>H<sub>77</sub>O<sub>10</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			51	40	10	1		
7	B	1	Total	C	O	P	0	0
			51	40	10	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	20	Total	O	0	0
			20	20		
8	B	30	Total	O	0	0
			30	30		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.89Å 146.20Å 72.33Å 90.00° 111.12° 90.00°	Depositor
Resolution (Å)	34.99 – 2.34 34.99 – 2.34	Depositor EDS
% Data completeness (in resolution range)	60.0 (34.99-2.34) 81.6 (34.99-2.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.27 (at 2.34Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.211 , 0.244 0.233 , 0.262	Depositor DCC
$R_{free}$ test set	2472 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.0	Xtrriage
Anisotropy	0.150	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 50.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5301	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: PGW, NT5, CL, SO4, SOG, PG4

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	0.12	0/2516	0.33	0/3429
1	B	0.13	0/2470	0.35	0/3368
All	All	0.13	0/4986	0.34	0/6797

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	2447	0	2489	26	0
1	B	2404	0	2474	39	0
2	A	31	25	0	0	0
2	B	31	25	0	1	0
3	A	13	0	18	2	0
3	B	9	0	11	1	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
5	A	77	0	102	1	0
5	B	66	0	92	1	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	51	0	76	5	0
7	B	51	0	76	8	0
8	A	20	0	0	0	0
8	B	30	0	0	0	0
All	All	5251	50	5338	65	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 6.

The worst 5 of 65 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:B:234:ALA:HB2	7:B:409:PGW:H7	1.46	0.96
1:A:234:ALA:HB2	7:A:411:PGW:H7	1.52	0.90
1:B:184:GLU:HG2	1:B:205:ARG:HG2	1.55	0.86
1:B:237:GLN:HG2	7:B:409:PGW:H05	1.71	0.71
1:B:105:LEU:HD12	1:B:114:PHE:HZ	1.55	0.70

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	299/368 (81%)	295 (99%)	4 (1%)	0	100	100
1	B	301/368 (82%)	297 (99%)	4 (1%)	0	100	100
All	All	600/736 (82%)	592 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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	256/305 (84%)	256 (100%)	0	100	100
1	B	252/305 (83%)	252 (100%)	0	100	100
All	All	508/610 (83%)	508 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	A	126	GLN
1	A	368	GLN
1	B	150	HIS

### 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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NT5	B	401	-	34,34,34	1.10	2 (5%)	47,47,47	1.55	7 (14%)
5	SOG	A	406	-	20,20,20	0.27	0	24,25,25	0.27	0
7	PGW	B	409	-	50,50,50	0.27	0	53,56,56	0.44	0
5	SOG	B	407	-	20,20,20	0.27	0	24,25,25	0.35	0
4	SO4	B	404	-	4,4,4	0.23	0	6,6,6	0.13	0
7	PGW	A	411	-	50,50,50	0.28	0	53,56,56	0.36	0
3	PG4	A	402	-	12,12,12	0.15	0	11,11,11	0.10	0
5	SOG	A	405	-	20,20,20	0.34	0	24,25,25	0.58	0
5	SOG	B	406	-	20,20,20	0.24	0	24,25,25	0.25	0
3	PG4	B	402	-	8,8,12	0.20	0	7,7,11	0.17	0
2	NT5	A	401	-	34,34,34	1.09	1 (2%)	47,47,47	1.61	5 (10%)
4	SO4	A	403	-	4,4,4	0.23	0	6,6,6	0.13	0
5	SOG	A	408	-	20,20,20	0.23	0	24,25,25	0.38	0
4	SO4	B	403	-	4,4,4	0.24	0	6,6,6	0.15	0
5	SOG	B	408	-	5,5,20	0.28	0	4,4,25	0.21	0
5	SOG	A	407	-	12,13,20	0.45	0	17,18,25	0.34	0
5	SOG	B	405	-	20,20,20	0.27	0	24,25,25	0.24	0
5	SOG	A	409	-	3,3,20	0.19	0	2,2,25	0.48	0
4	SO4	A	404	-	4,4,4	0.24	0	6,6,6	0.12	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
5	SOG	B	405	-	-	5/11/31/31	0/1/1/1
3	PG4	A	402	-	-	5/10/10/10	-
2	NT5	B	401	-	-	0/17/30/30	0/4/4/4
5	SOG	A	405	-	-	3/11/31/31	0/1/1/1
5	SOG	A	406	-	-	3/11/31/31	0/1/1/1
5	SOG	A	409	-	-	0/1/1/31	-
5	SOG	B	406	-	-	3/11/31/31	0/1/1/1
5	SOG	A	408	-	-	3/11/31/31	0/1/1/1
5	SOG	A	407	-	-	2/4/24/31	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PG4	B	402	-	-	2/6/6/10	-
7	PGW	B	409	-	-	13/55/55/55	-
5	SOG	B	407	-	-	0/11/31/31	0/1/1/1
5	SOG	B	408	-	-	0/3/3/31	-
2	NT5	A	401	-	-	0/17/30/30	0/4/4/4
7	PGW	A	411	-	1/1/5/7	13/55/55/55	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NT5	C7-N1	3.12	1.37	1.32
2	A	401	NT5	C7-N1	3.12	1.37	1.32
2	B	401	NT5	C19-C20	2.03	1.53	1.48

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NT5	C9-C10-C11	-5.77	118.52	121.55
2	B	401	NT5	C9-C10-C11	-5.37	118.73	121.55
2	A	401	NT5	C4-C5-C12	4.00	113.33	108.59
2	B	401	NT5	C4-C5-C12	3.46	112.69	108.59
2	A	401	NT5	C21-N3-C20	3.44	119.47	116.07

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	411	PGW	C05

5 of 52 torsion outliers are listed below:

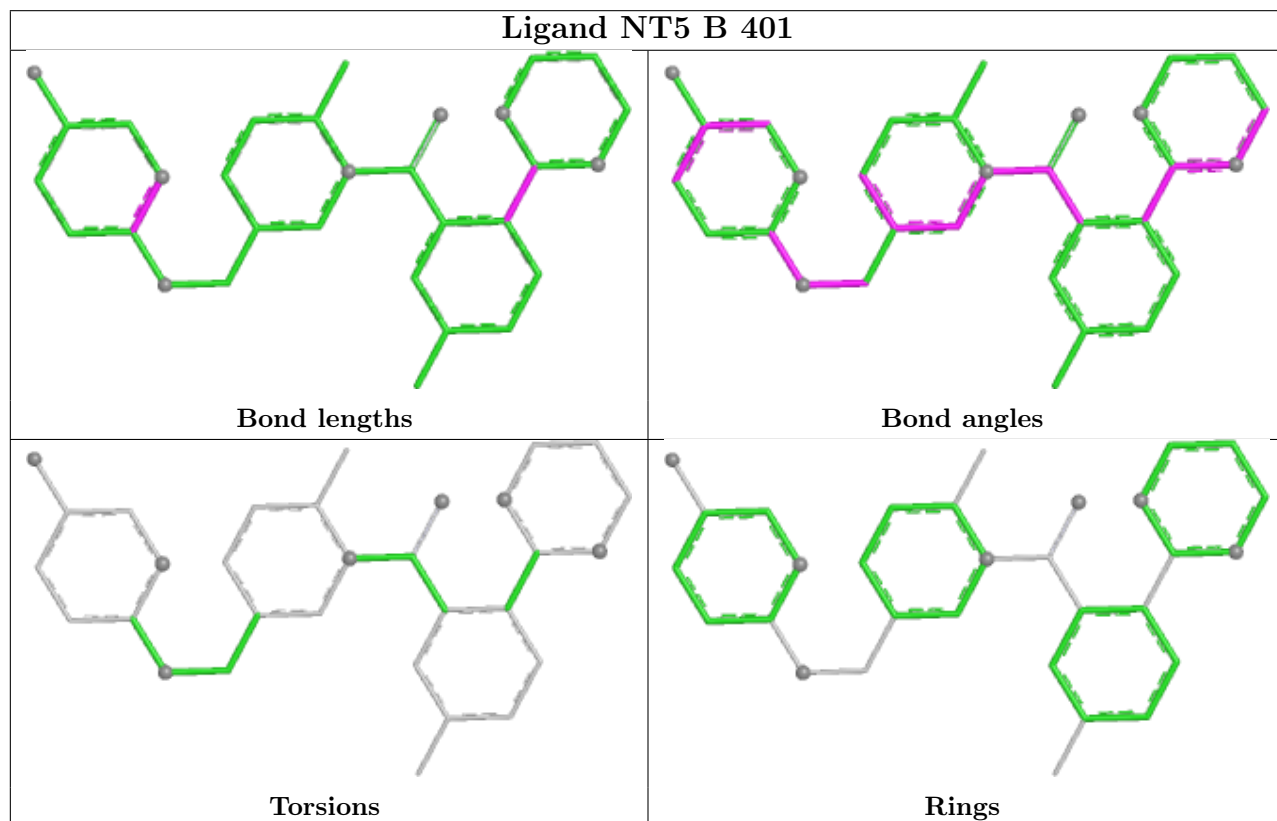
Mol	Chain	Res	Type	Atoms
5	A	408	SOG	O5-C1-S1-C1'
7	A	411	PGW	C03-O11-P-O14
5	A	407	SOG	O5-C5-C6-O6
5	A	405	SOG	O5-C5-C6-O6
5	A	407	SOG	C4-C5-C6-O6

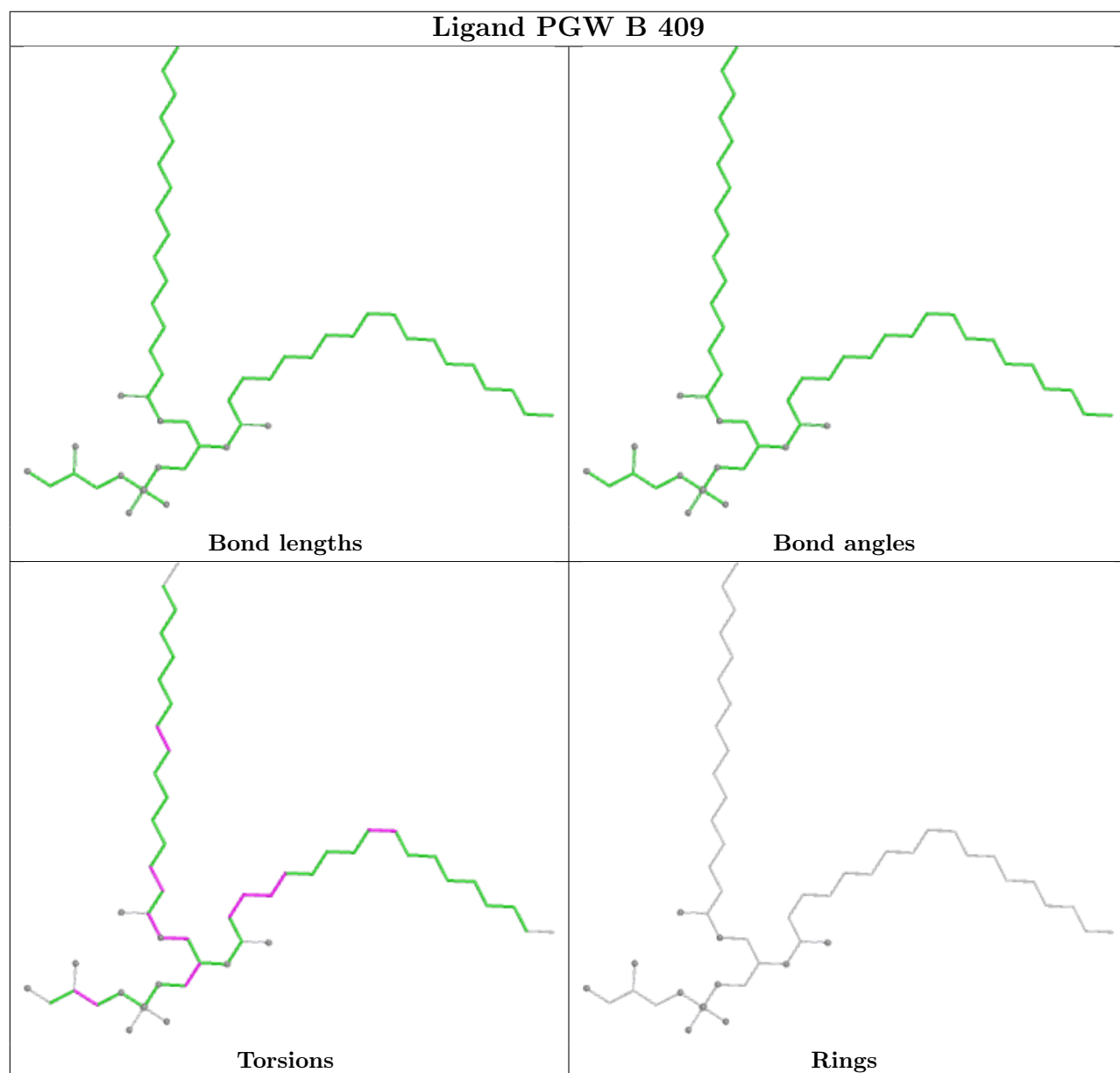
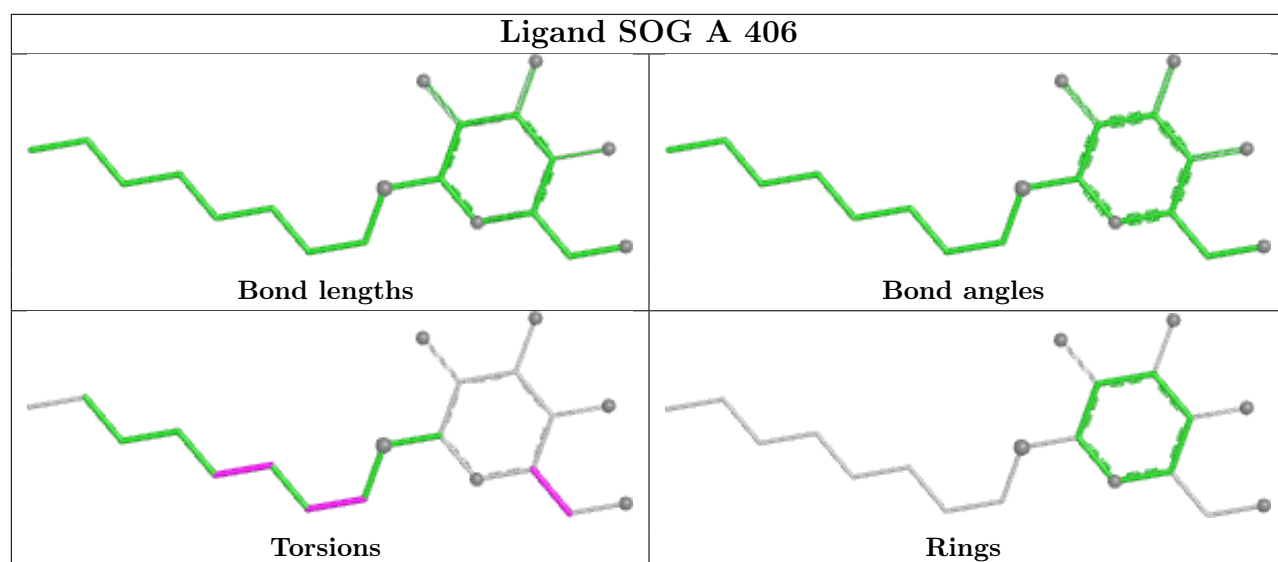
There are no ring outliers.

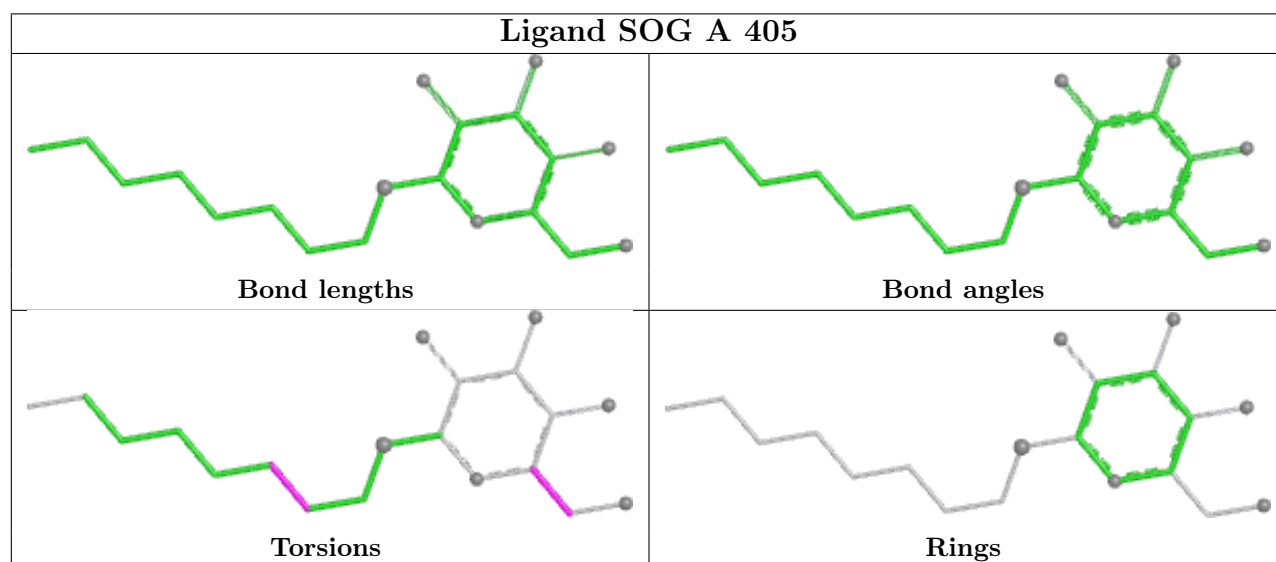
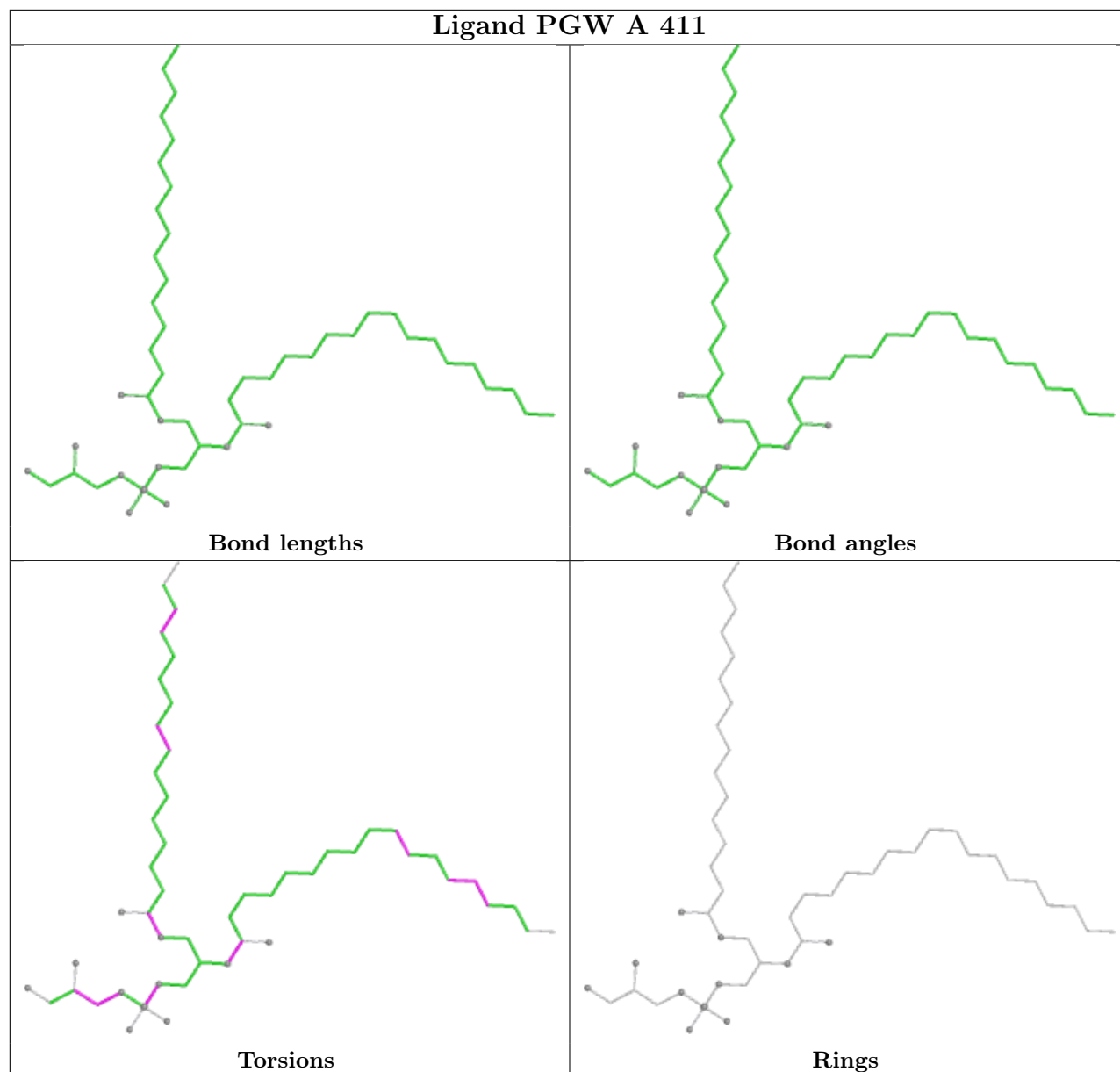
7 monomers are involved in 19 short contacts:

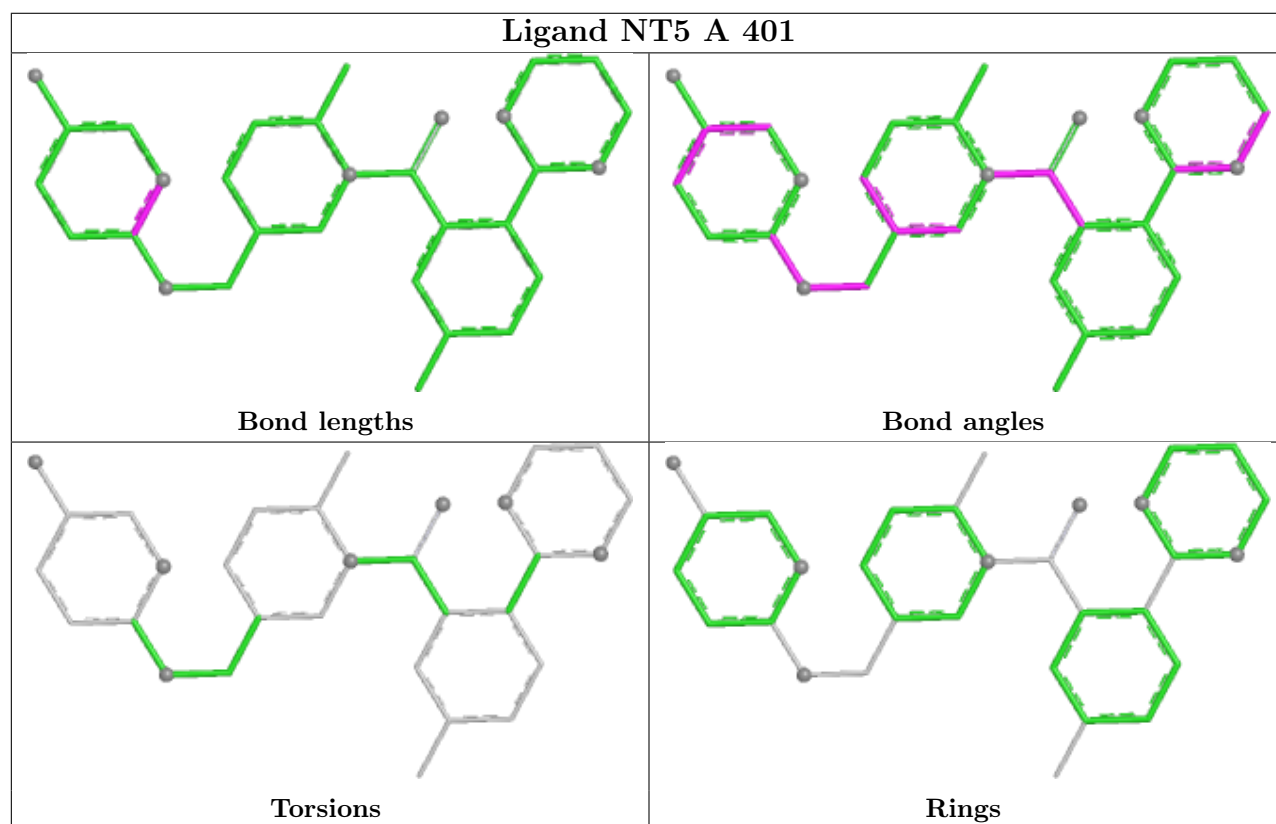
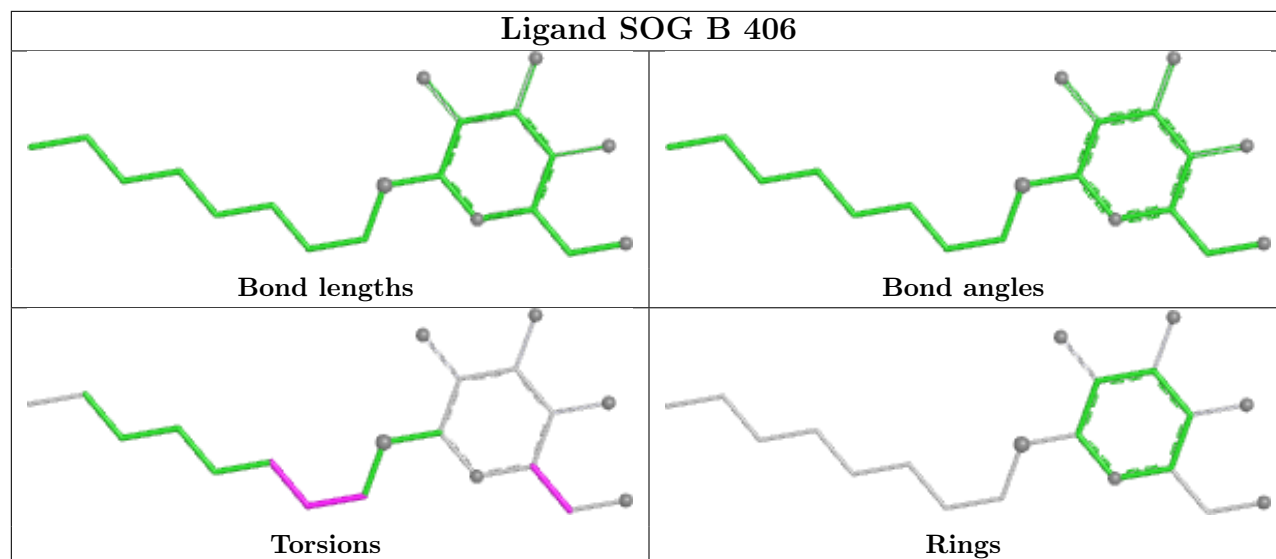
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	NT5	1	0
7	B	409	PGW	8	0
5	B	407	SOG	1	0
7	A	411	PGW	5	0
3	A	402	PG4	2	0
3	B	402	PG4	1	0
5	A	408	SOG	1	0

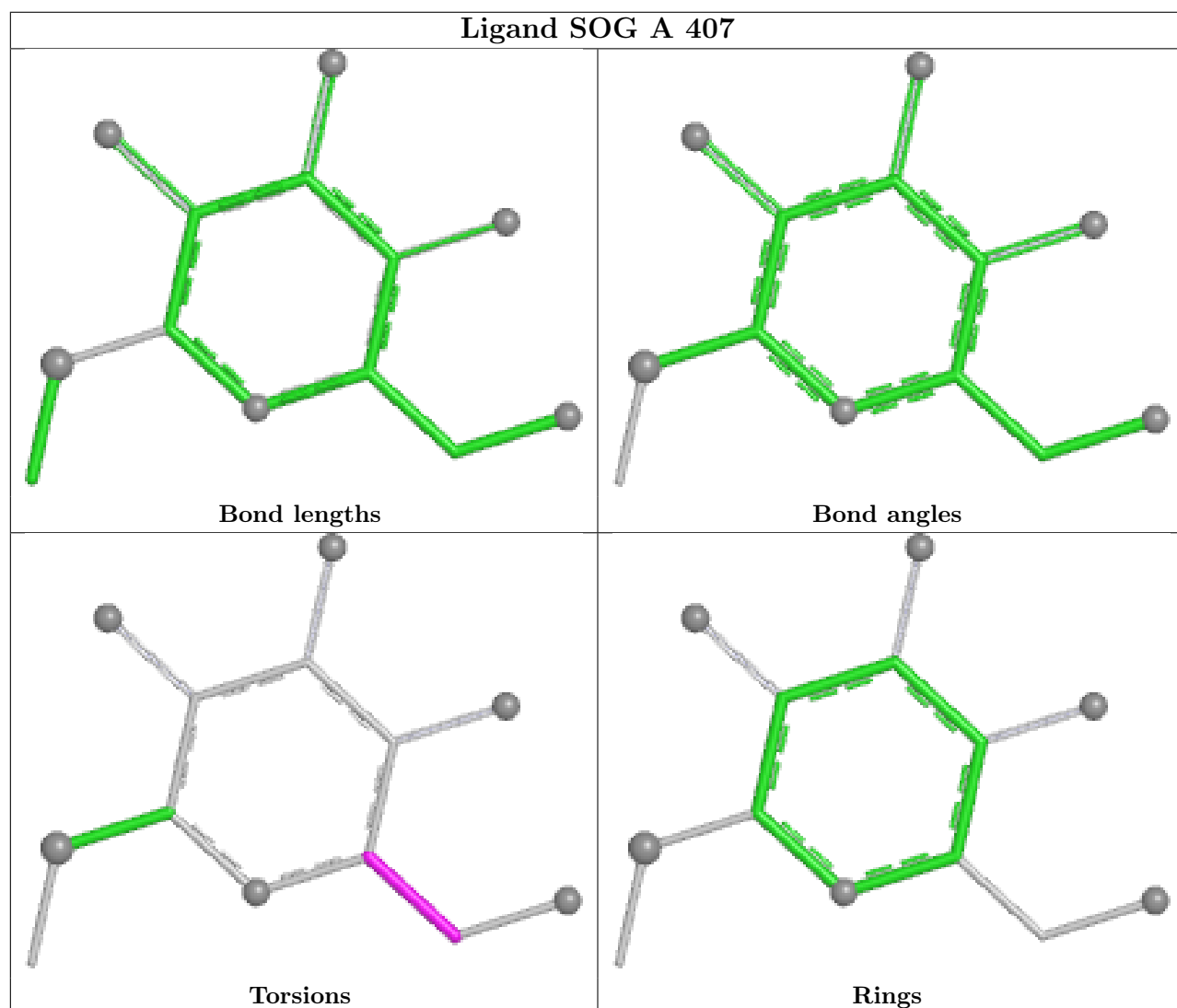
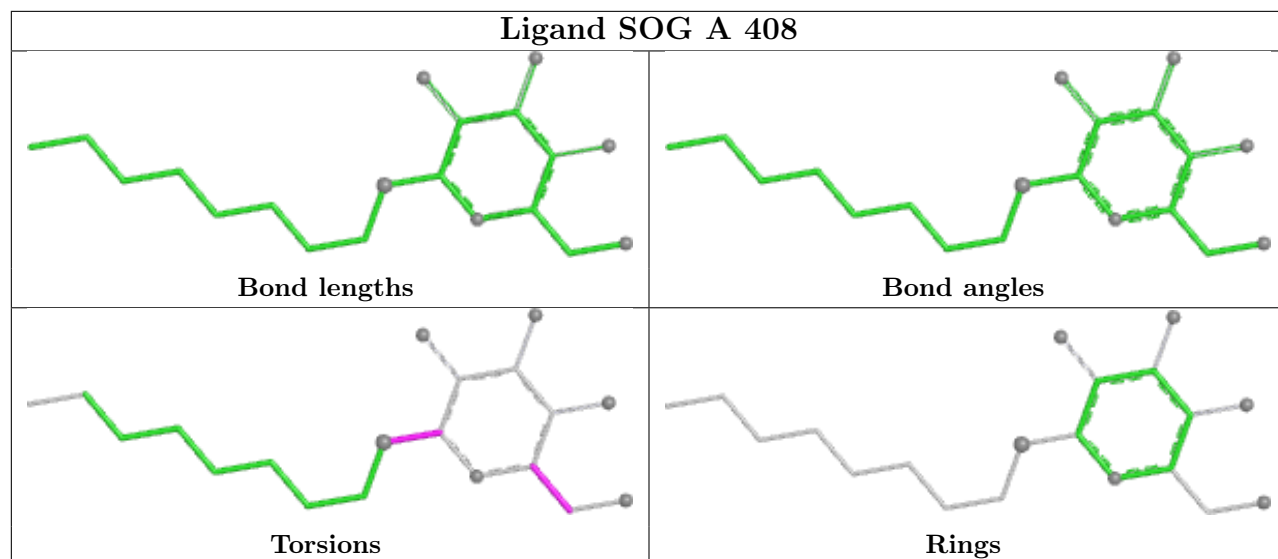
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

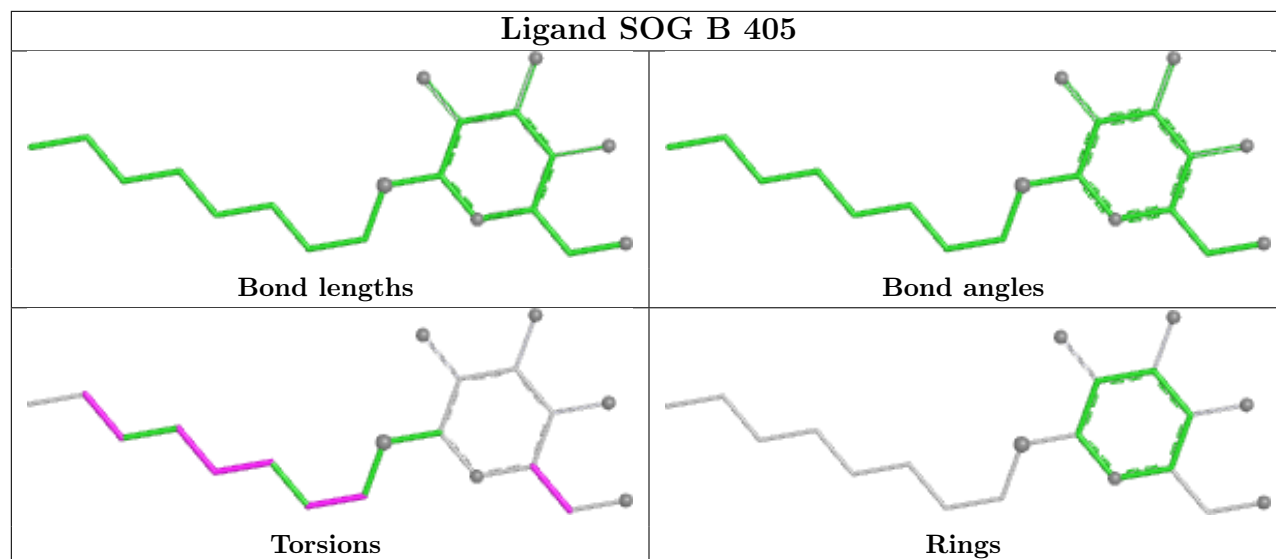












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	305/368 (82%)	0.77	40 (13%) 7 8	38, 65, 135, 179	0
1	B	303/368 (82%)	0.82	38 (12%) 8 9	41, 69, 128, 164	0
All	All	608/736 (82%)	0.80	78 (12%) 7 9	38, 67, 133, 179	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	330	ALA	10.2
1	B	287	VAL	8.7
1	B	288	LYS	6.7
1	A	332	ASP	6.2
1	B	242	LEU	6.2

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

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

### 6.3 Carbohydrates [i](#)

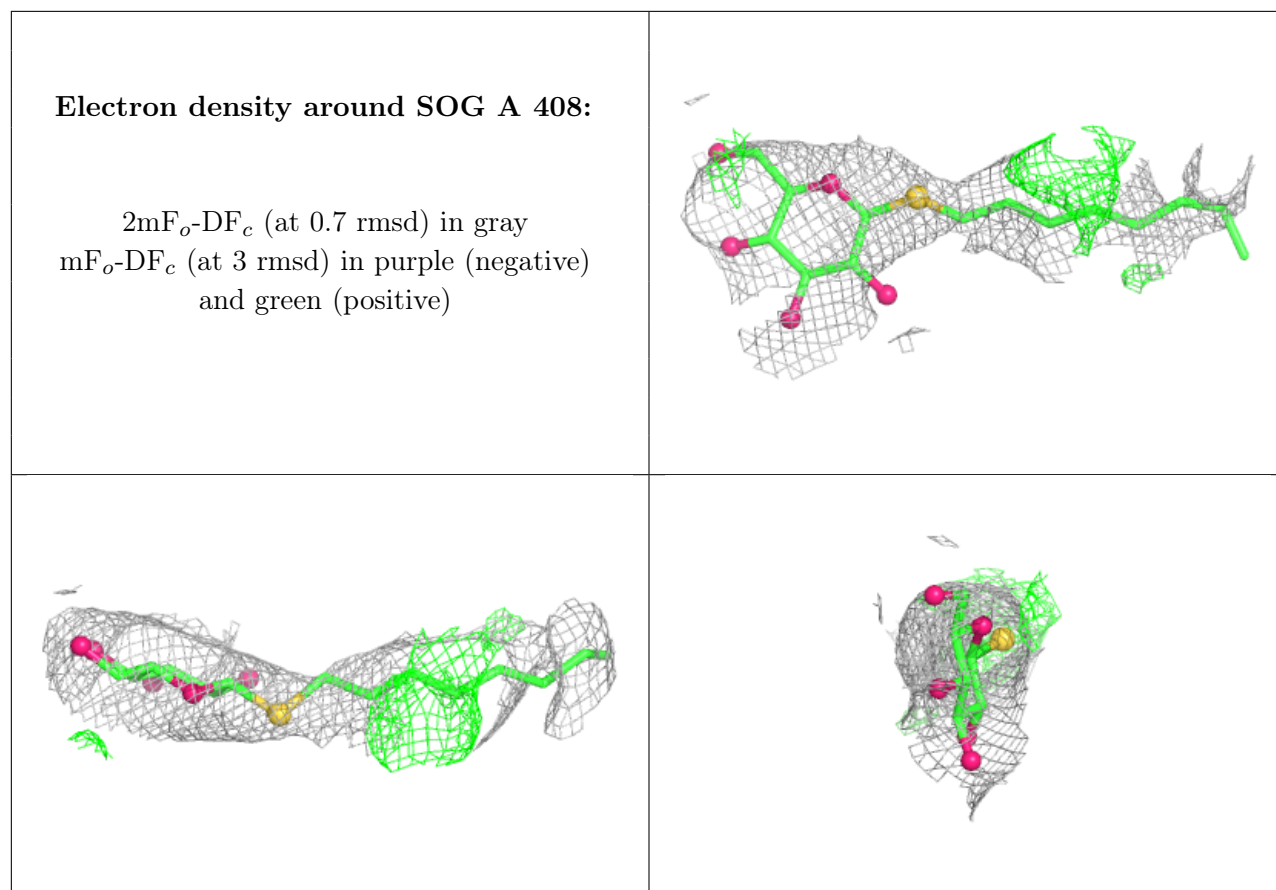
There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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.

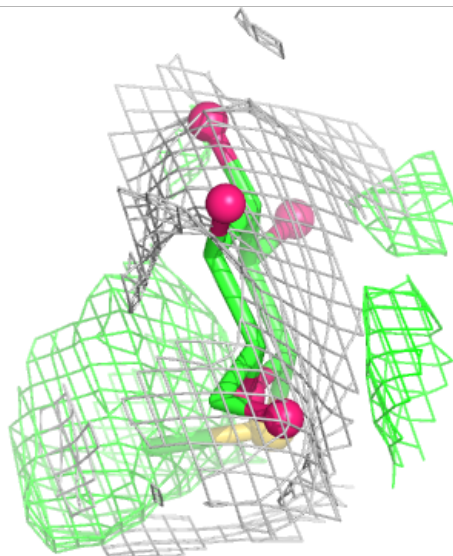
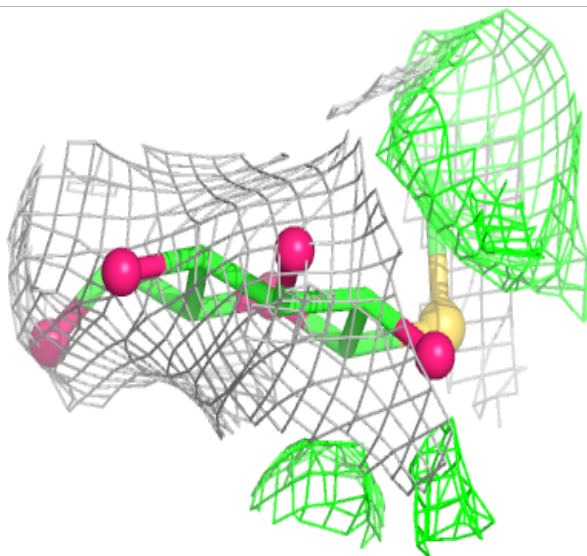
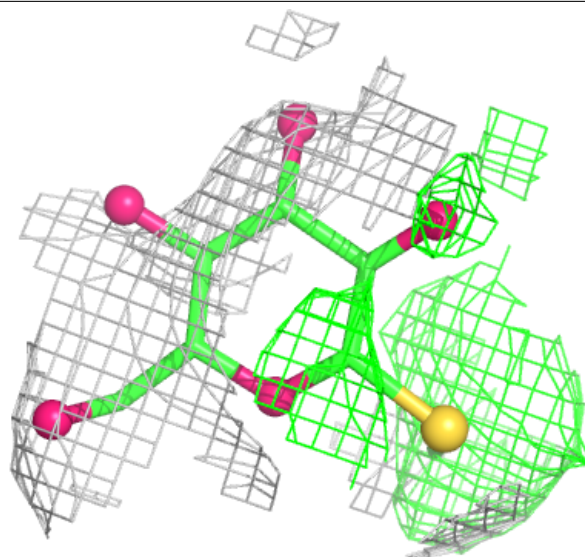
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	SO4	A	404	5/5	0.56	0.13	122,129,133,133	0
5	SOG	A	408	20/20	0.65	0.26	124,138,144,148	0
5	SOG	A	407	13/20	0.66	0.22	134,142,147,151	0
5	SOG	B	407	20/20	0.73	0.20	123,129,140,145	0
4	SO4	B	404	5/5	0.74	0.12	119,122,127,131	0
5	SOG	B	405	20/20	0.75	0.18	80,98,111,112	0
3	PG4	A	402	13/13	0.81	0.26	62,97,110,110	0
5	SOG	B	406	20/20	0.82	0.12	41,98,110,111	0
5	SOG	A	406	20/20	0.82	0.16	49,108,119,126	0
3	PG4	B	402	9/13	0.83	0.24	74,81,83,83	0
5	SOG	B	408	6/20	0.87	0.20	86,89,95,95	0
7	PGW	A	411	51/51	0.87	0.15	47,80,127,131	0
4	SO4	A	403	5/5	0.88	0.09	103,106,112,114	0
5	SOG	A	409	4/20	0.90	0.43	52,62,66,67	0
5	SOG	A	405	20/20	0.90	0.10	42,64,76,88	0
7	PGW	B	409	51/51	0.90	0.15	40,72,132,137	0
4	SO4	B	403	5/5	0.91	0.09	76,81,91,93	0
6	CL	A	410	1/1	0.93	0.15	68,68,68,68	0
2	NT5	B	401	31/31	0.94	0.10	50,66,83,89	0
2	NT5	A	401	31/31	0.95	0.08	40,53,65,72	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.



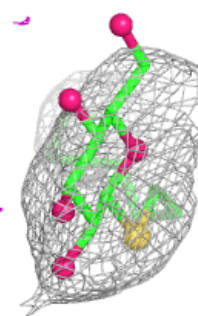
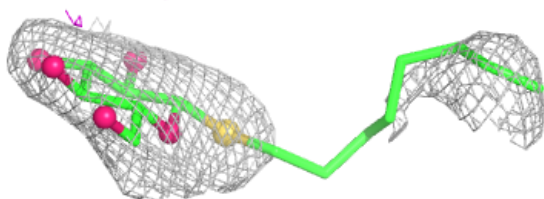
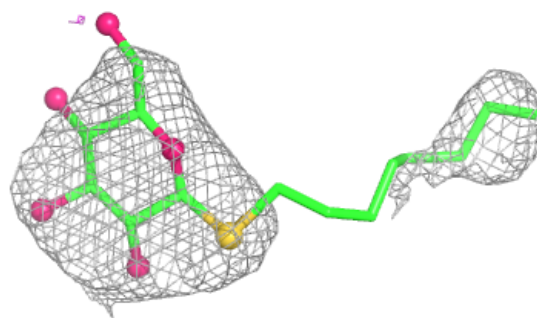
**Electron density around SOG A 407:**

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

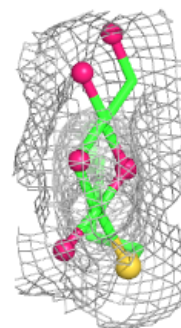
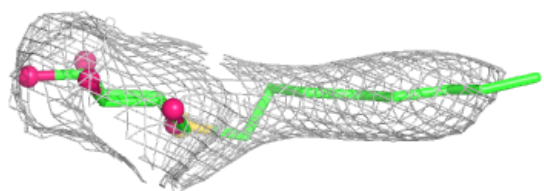
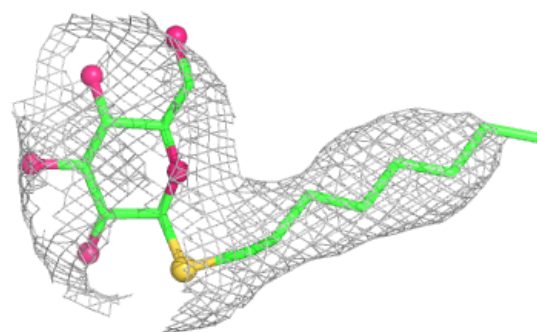


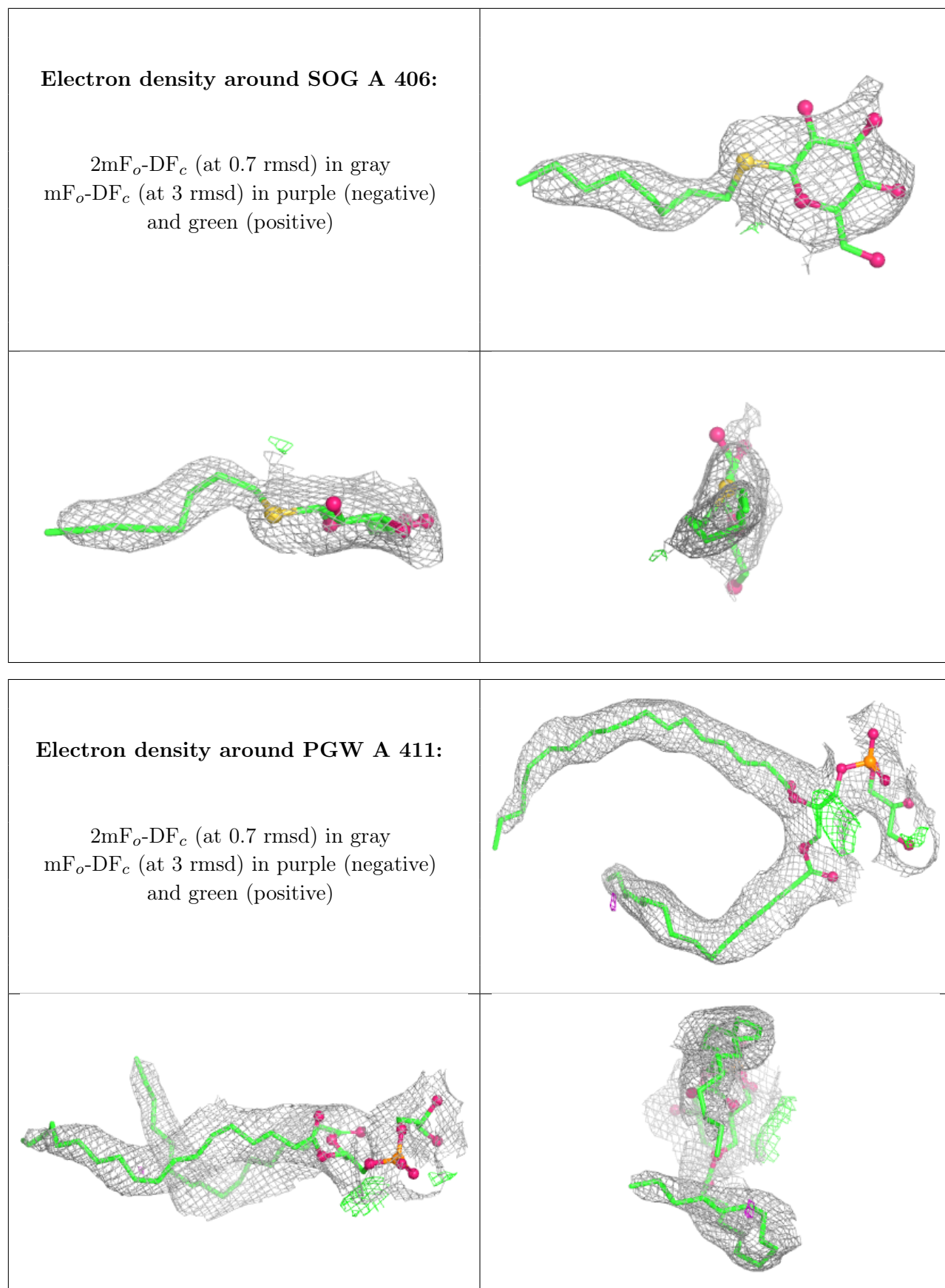
**Electron density around SOG B 405:**

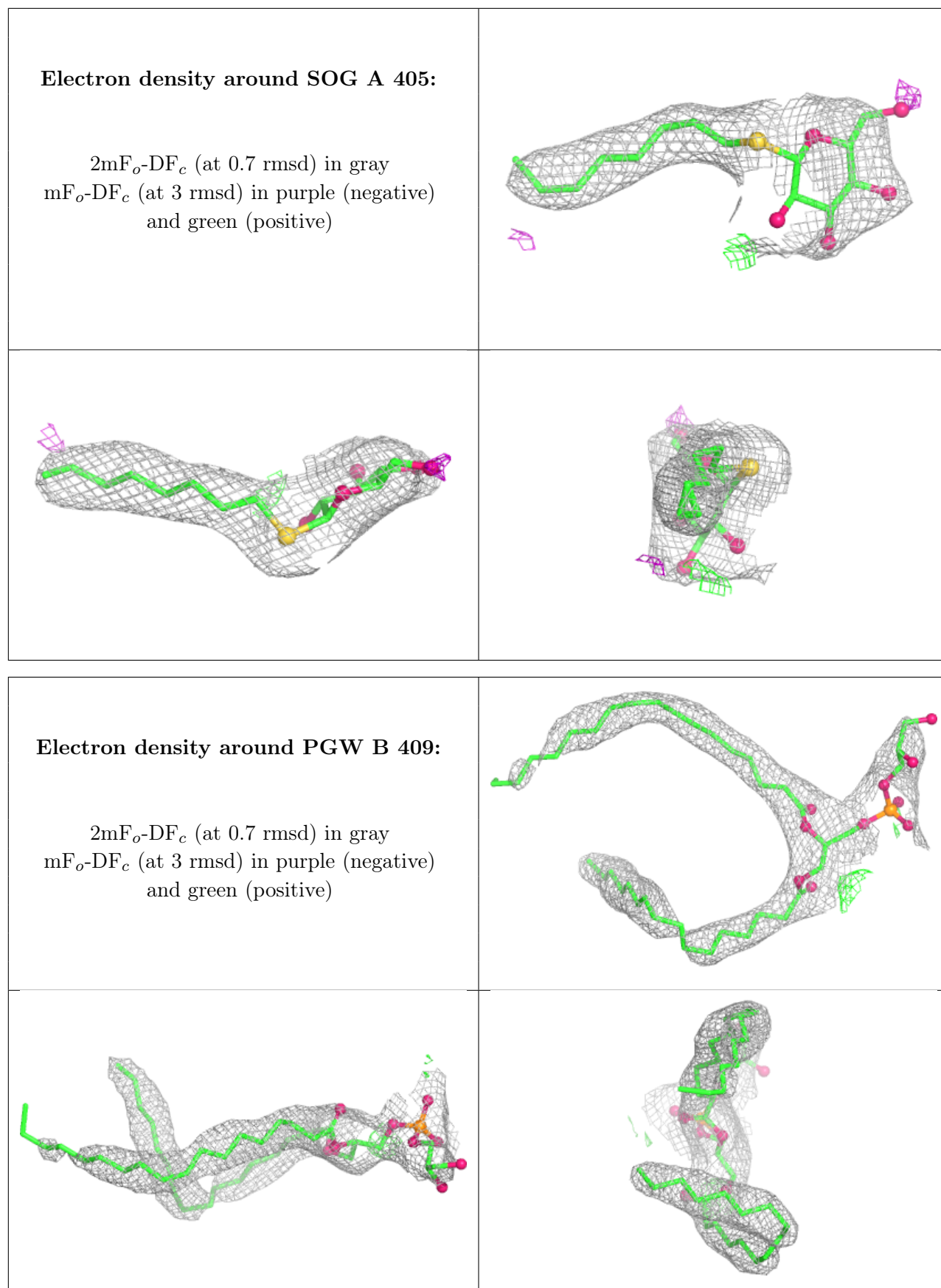
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around SOG B 406:**

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

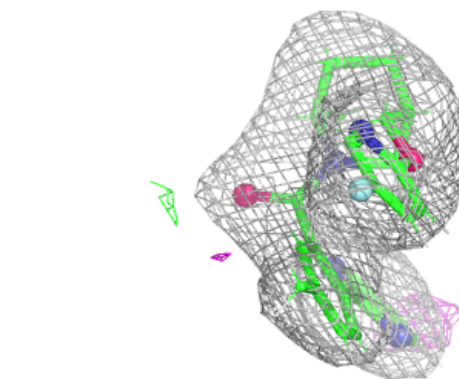
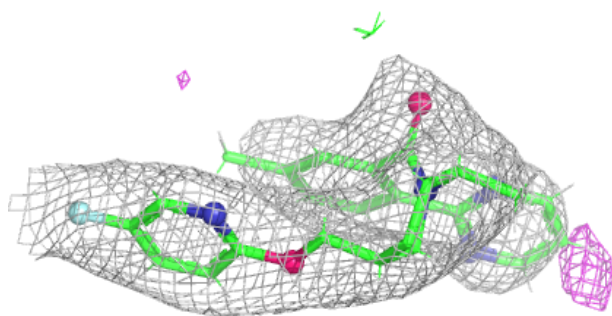
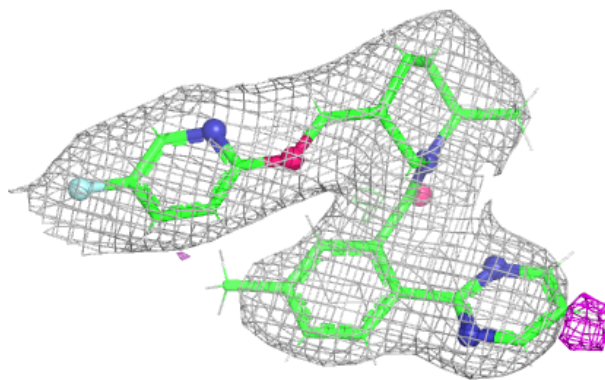




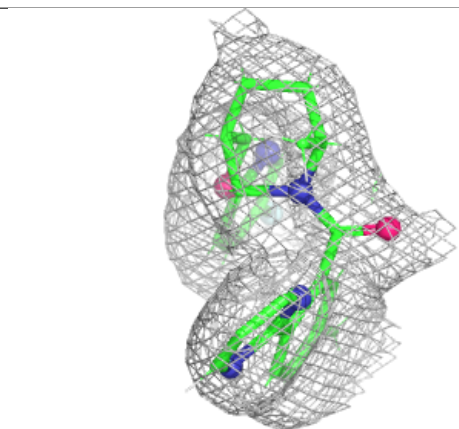
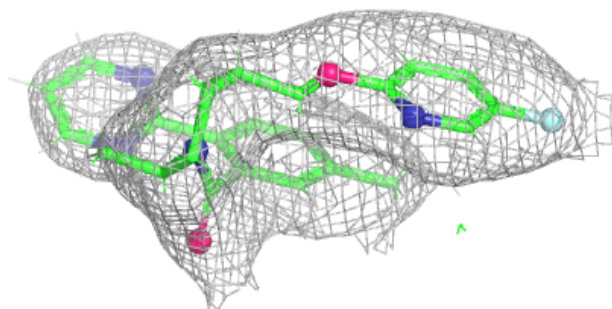
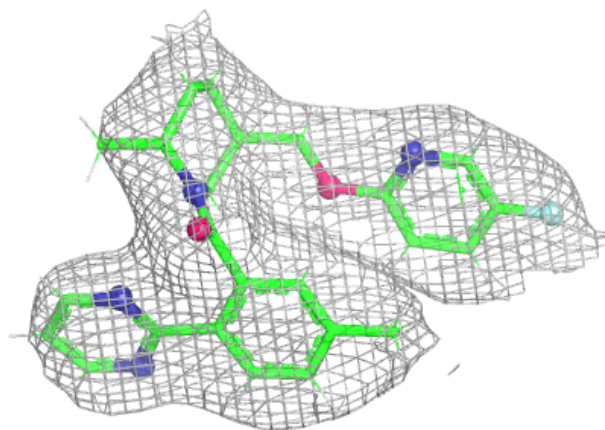


**Electron density around NT5 B 401:**

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

**Electron density around NT5 A 401:**

$2mF_o-DF_c$  (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.