



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:51 PM UTC

PDB ID : 6V8Q / pdb_00006v8q
Title : Structure of an inner membrane protein required for PhoPQ regulated increases in outer membrane cardiolipin
Authors : Fan, J.; Miller, S.
Deposited on : 2019-12-11
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	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

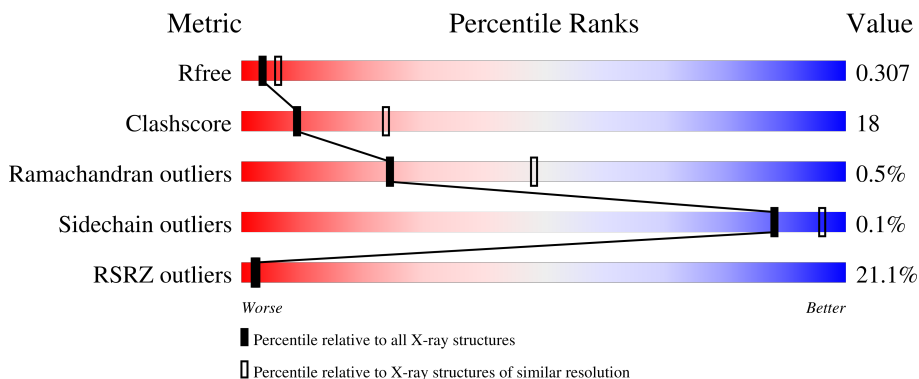
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	592	24% 61% 34% .
1	B	592	16% 61% 32% 5%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9259 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 Inner membrane protein YejM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	569	Total	C	N	O	S	0	0	0
			4473	2894	760	803	16			
1	B	565	Total	C	N	O	S	0	0	0
			4500	2917	765	802	16			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	283	VAL	ALA	conflict	UNP P40709
A	587	HIS	-	expression tag	UNP P40709
A	588	HIS	-	expression tag	UNP P40709
A	589	HIS	-	expression tag	UNP P40709
A	590	HIS	-	expression tag	UNP P40709
A	591	HIS	-	expression tag	UNP P40709
A	592	HIS	-	expression tag	UNP P40709
B	283	VAL	ALA	conflict	UNP P40709
B	587	HIS	-	expression tag	UNP P40709
B	588	HIS	-	expression tag	UNP P40709
B	589	HIS	-	expression tag	UNP P40709
B	590	HIS	-	expression tag	UNP P40709
B	591	HIS	-	expression tag	UNP P40709
B	592	HIS	-	expression tag	UNP P40709

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

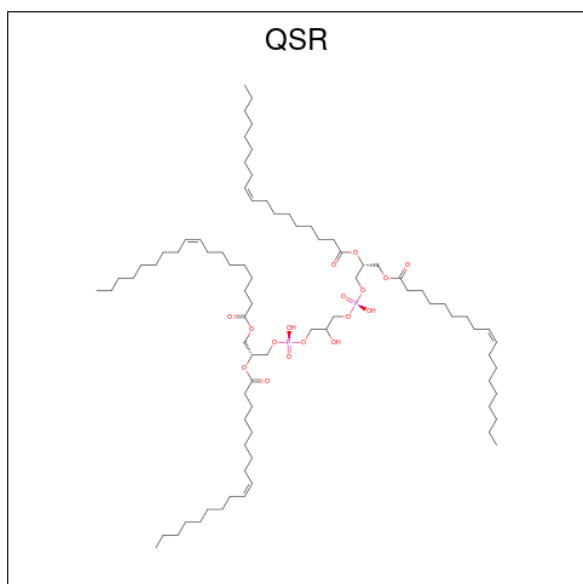
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



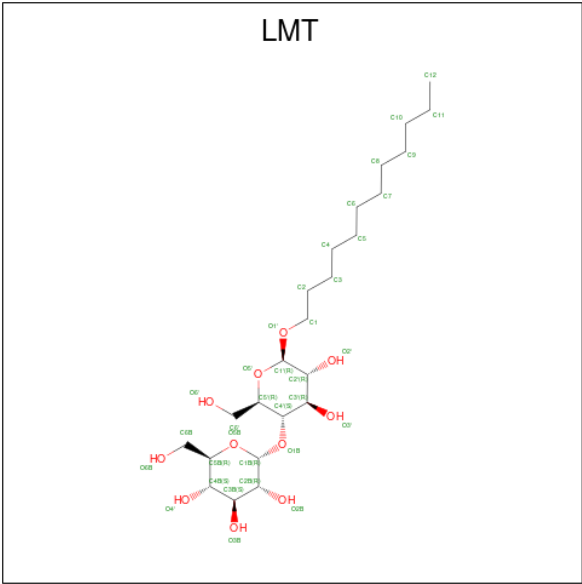
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is (9Z,21R,24R,30R,33R,44Z)-24,27,30-trihydroxy-18,24,30,36-tetraoxo-19,23,25,29,31,35-hexaoxa-24lambda 5 ,30lambda 5 -dip hosphatripentaconta-9,44-diene-21,33-diyl (9Z,9'Z)di-octadec-9-enoate (CCD ID: QSR) (formula: C₈₁H₁₅₀O₁₇P₂) (labeled as "Ligand of Interest" by depositor).

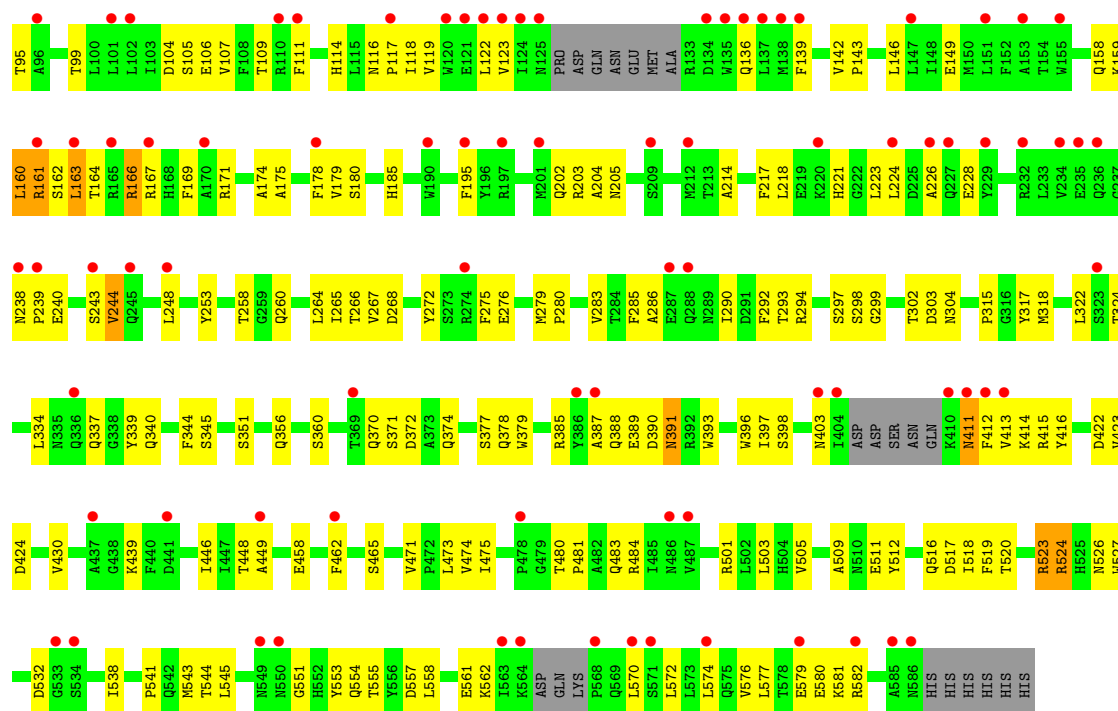


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			52	33	17	2		
4	A	1	Total	C	O	P	0	0
			27	18	8	1		
4	B	1	Total	C	O	P	0	0
			67	48	17	2		
4	B	1	Total	C	O	P	0	0
			70	51	17	2		

- Molecule 5 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			24	13	11		
5	B	1	Total	C	O	0	0
			35	24	11		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.83Å 64.85Å 146.36Å 90.00° 97.66° 90.00°	Depositor
Resolution (Å)	48.34 – 2.70 48.34 – 2.70	Depositor EDS
% Data completeness (in resolution range)	76.7 (48.34-2.70) 76.7 (48.34-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.239 , 0.291 0.262 , 0.307	Depositor DCC
R_{free} test set	2716 reflections (3.73%)	wwPDB-VP
Wilson B-factor (Å ²)	54.0	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 21.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	9259	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PO4, LMT, QSR

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	0.43	0/4589	0.77	7/6260 (0.1%)
1	B	0.43	0/4622	0.72	4/6303 (0.1%)
All	All	0.43	0/9211	0.75	11/12563 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	MET	CB-CG-SD	-8.35	87.66	112.70
1	A	81	MET	CA-C-N	8.23	136.94	121.87
1	A	81	MET	C-N-CA	8.23	136.94	121.87
1	B	411	ASN	CB-CA-C	-7.97	95.37	109.71
1	B	523	ARG	CA-C-N	-6.67	105.92	121.52

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	161	ARG	Peptide
1	B	403	ASN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4473	0	4318	162	0
1	B	4500	0	4382	166	0
2	A	1	0	0	0	0
3	A	5	0	0	1	0
3	B	5	0	0	1	0
4	A	79	0	0	1	0
4	B	137	0	0	5	0
5	A	24	0	21	5	0
5	B	35	0	46	8	0
All	All	9259	0	8767	328	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 18.

The worst 5 of 328 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:197:ARG:HH22	1:A:323:SER:CB	1.69	1.06
1:B:36:ARG:NE	1:B:105:SER:OG	1.92	1.01
1:A:197:ARG:NH2	1:A:323:SER:OG	1.94	1.01
1:A:197:ARG:HH22	1:A:323:SER:HB2	1.40	0.84
1:B:95:THR:HG22	1:B:149:GLU:HG3	1.60	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	559/592 (94%)	526 (94%)	33 (6%)	0	100	100
1	B	557/592 (94%)	526 (94%)	25 (4%)	6 (1%)	11	29
All	All	1116/1184 (94%)	1052 (94%)	58 (5%)	6 (0%)	24	48

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	82	SER
1	B	244	VAL
1	B	391	ASN
1	B	166	ARG
1	B	163	LEU

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	465/518 (90%)	464 (100%)	1 (0%)	87	95
1	B	474/518 (92%)	474 (100%)	0	100	100
All	All	939/1036 (91%)	938 (100%)	1 (0%)	88	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	363	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	428	ASN
1	B	483	GLN
1	B	575	GLN
1	B	525	HIS
1	A	476	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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
5	LMT	B	604	-	36,36,36	1.30	3 (8%)	47,47,47	1.23	4 (8%)
5	LMT	A	605	-	25,25,36	1.28	3 (12%)	36,36,47	1.66	6 (16%)
3	PO4	B	601	-	4,4,4	0.96	0	6,6,6	0.63	0
4	QSR	B	603	-	69,69,99	1.56	9 (13%)	75,81,111	1.25	8 (10%)
4	QSR	A	603	-	51,51,99	1.68	6 (11%)	57,63,111	1.63	7 (12%)
4	QSR	A	604	-	26,26,99	1.65	4 (15%)	29,31,111	1.26	4 (13%)
4	QSR	B	602	-	66,66,99	1.56	9 (13%)	72,78,111	1.35	9 (12%)
3	PO4	A	602	-	4,4,4	0.93	0	6,6,6	0.82	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	LMT	B	604	-	-	9/21/61/61	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	LMT	A	605	-	-	5/10/50/61	0/2/2/2
4	QSR	B	603	-	-	46/80/80/110	-
4	QSR	A	604	-	-	15/28/28/110	-
4	QSR	A	603	-	-	36/61/61/110	-
4	QSR	B	602	-	-	45/77/77/110	-

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	QSR	O14-C35	4.95	1.47	1.33
4	A	603	QSR	O16-C46	4.86	1.48	1.34
4	B	603	QSR	O2-C14	4.74	1.47	1.34
4	A	604	QSR	O2-C14	4.71	1.47	1.34
4	B	603	QSR	C44-C43	4.69	1.58	1.31

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	QSR	O2-C14-C13	6.08	121.92	111.09
4	A	603	QSR	O16-C46-C47	4.55	121.32	111.48
5	A	605	LMT	O5B-C5B-C4B	4.31	117.47	109.70
4	B	602	QSR	O3-C17-C18	4.28	124.90	111.83
4	A	603	QSR	O14-C35-C36	4.26	124.08	111.15

There are no chirality outliers.

5 of 156 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	603	QSR	C28-O5-P1-O6
4	A	603	QSR	C28-O5-P1-O8
4	A	603	QSR	O1-C14-O2-C15
4	A	603	QSR	C13-C14-O2-C15
4	A	603	QSR	C32-O13-P2-O10

There are no ring outliers.

7 monomers are involved in 21 short contacts:

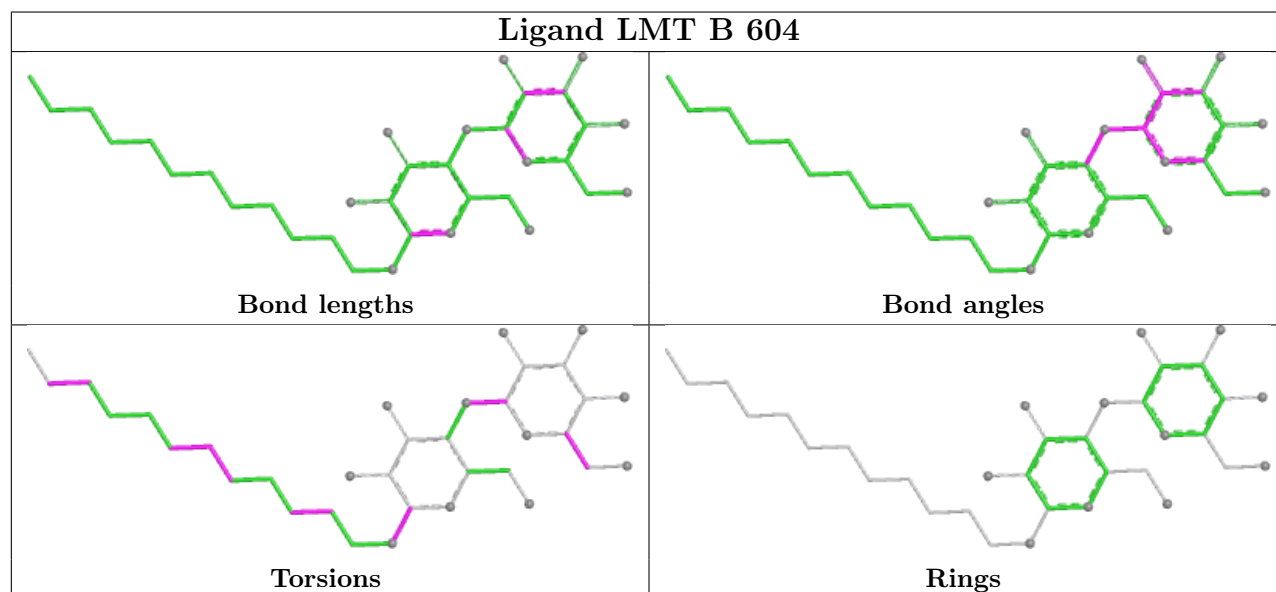
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	604	LMT	8	0
5	A	605	LMT	5	0

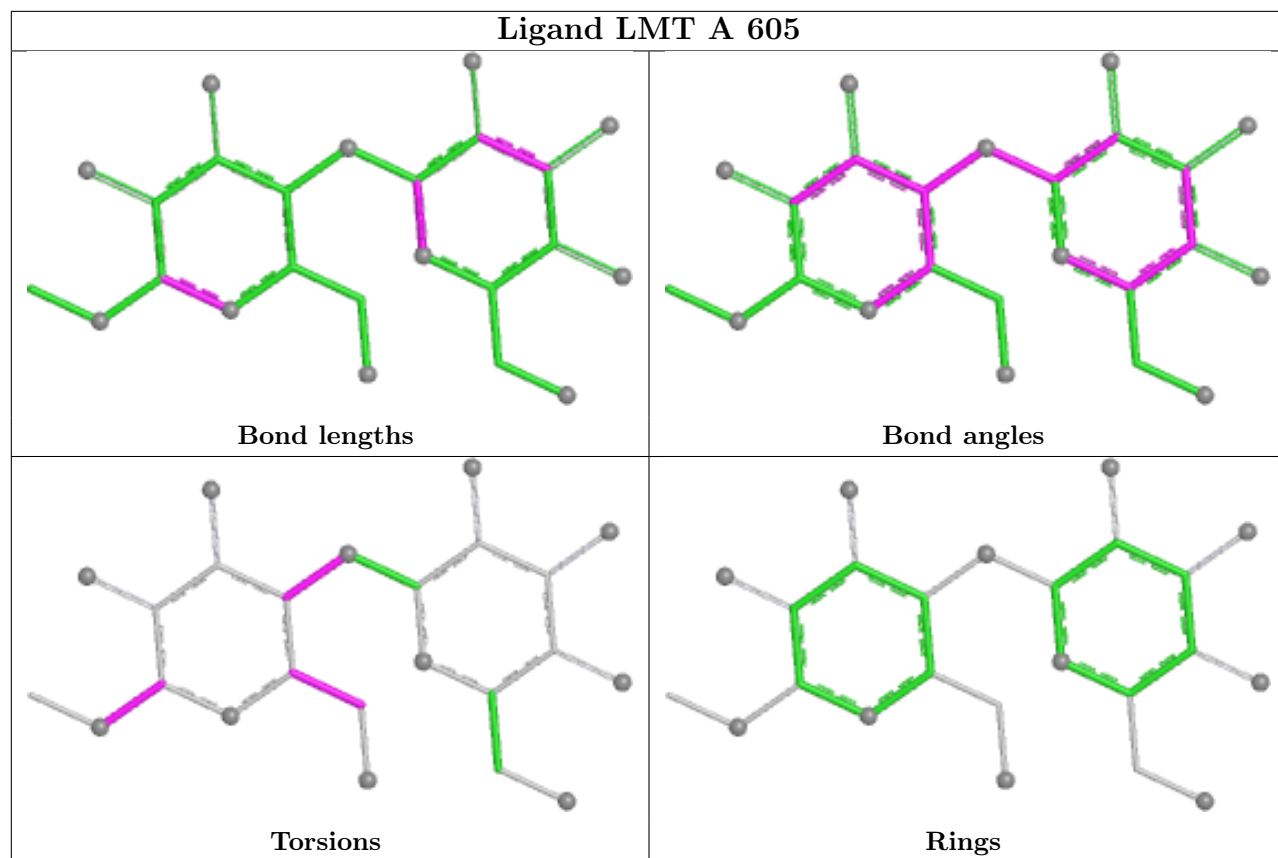
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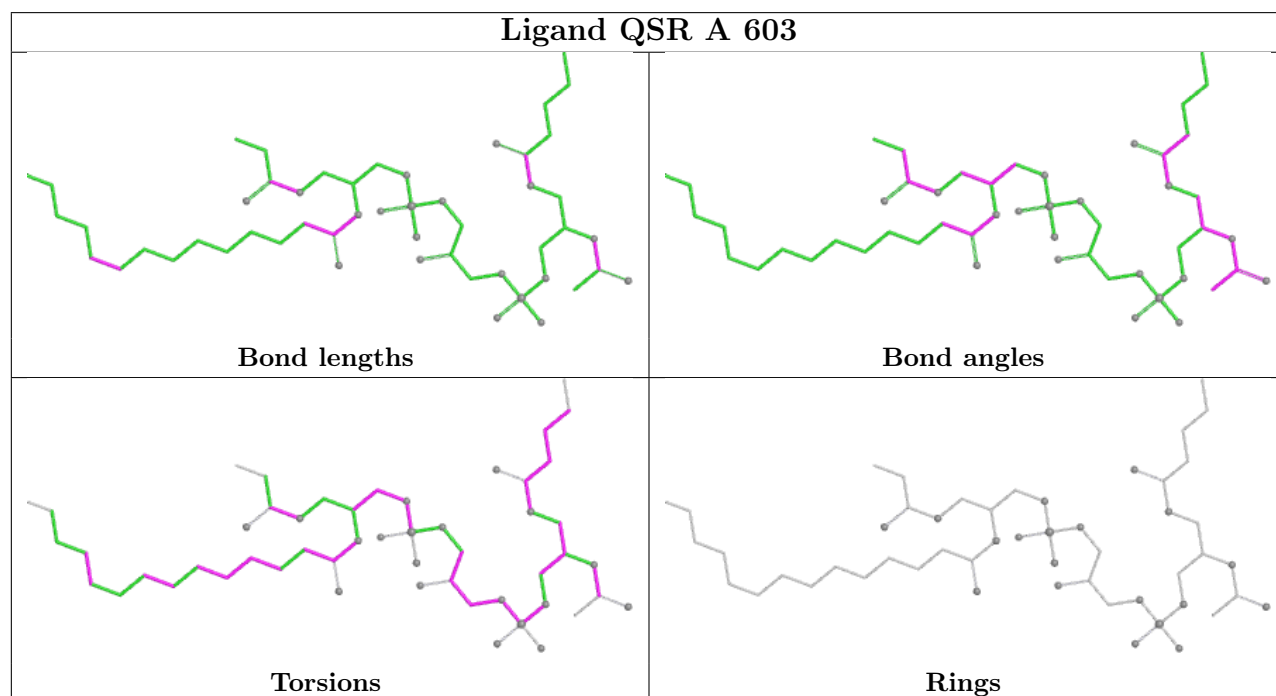
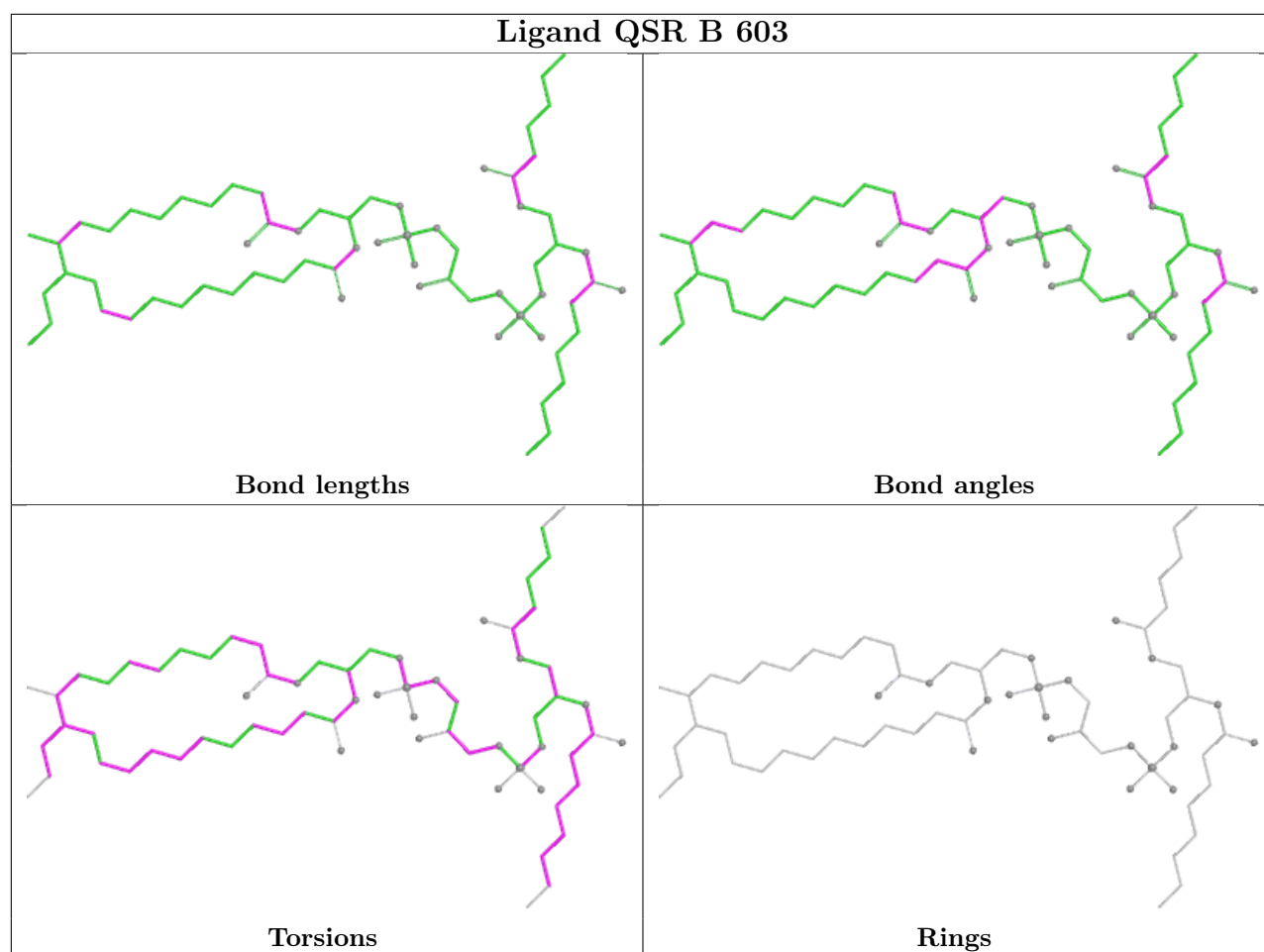
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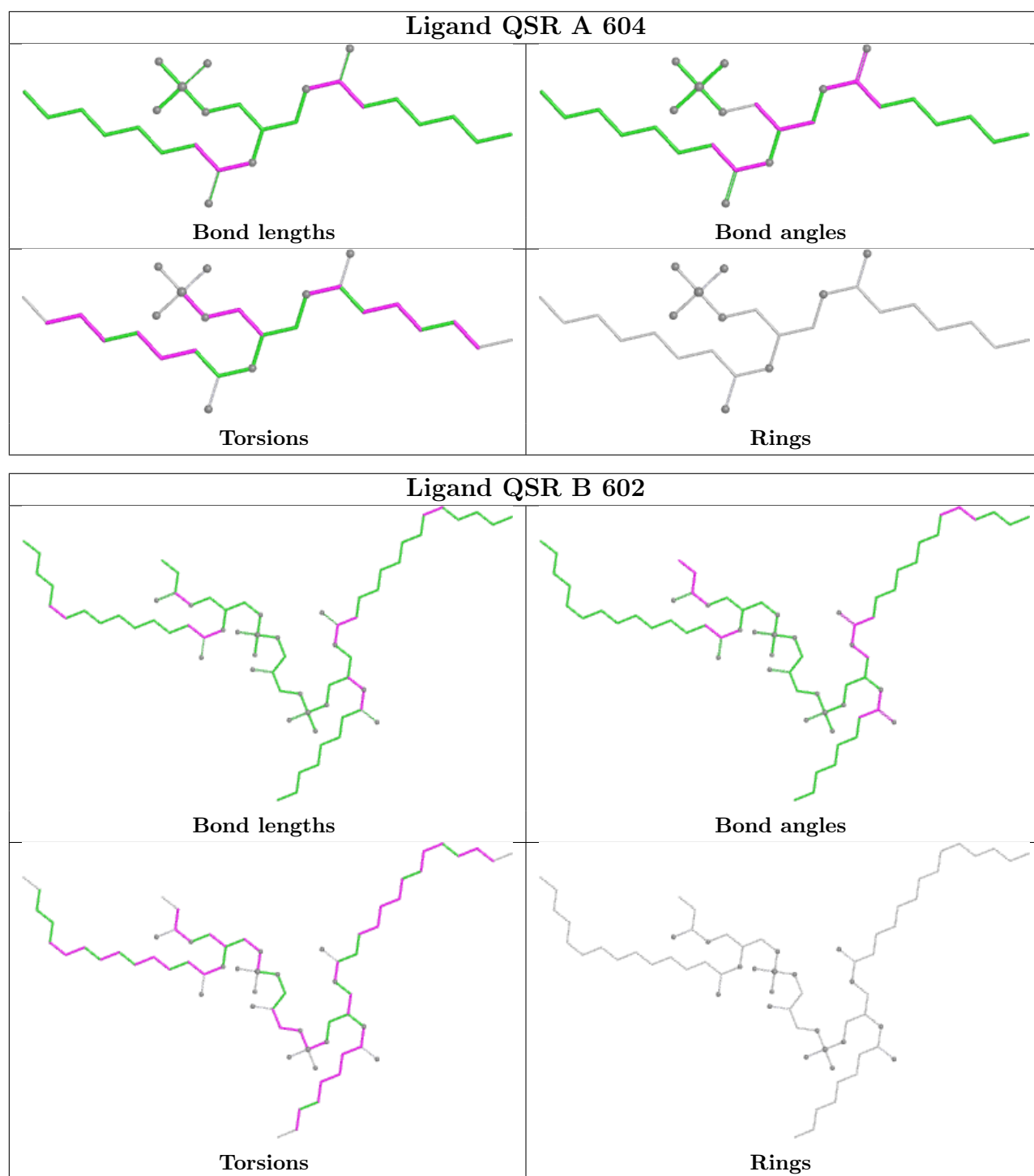
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	601	PO4	1	0
4	B	603	QSR	4	0
4	A	603	QSR	1	0
4	B	602	QSR	1	0
3	A	602	PO4	1	0

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, 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	569/592 (96%)	1.39	144 (25%) 1 1	26, 62, 102, 124	0
1	B	565/592 (95%)	1.13	95 (16%) 4 3	28, 56, 84, 108	0
All	All	1134/1184 (95%)	1.26	239 (21%) 2 2	26, 57, 96, 124	0

The worst 5 of 239 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	586	ASN	10.0
1	A	387	ALA	9.9
1	A	209	SER	9.0
1	A	35	SER	8.9
1	A	240	GLU	8.7

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

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

6.3 Carbohydrates [i](#)

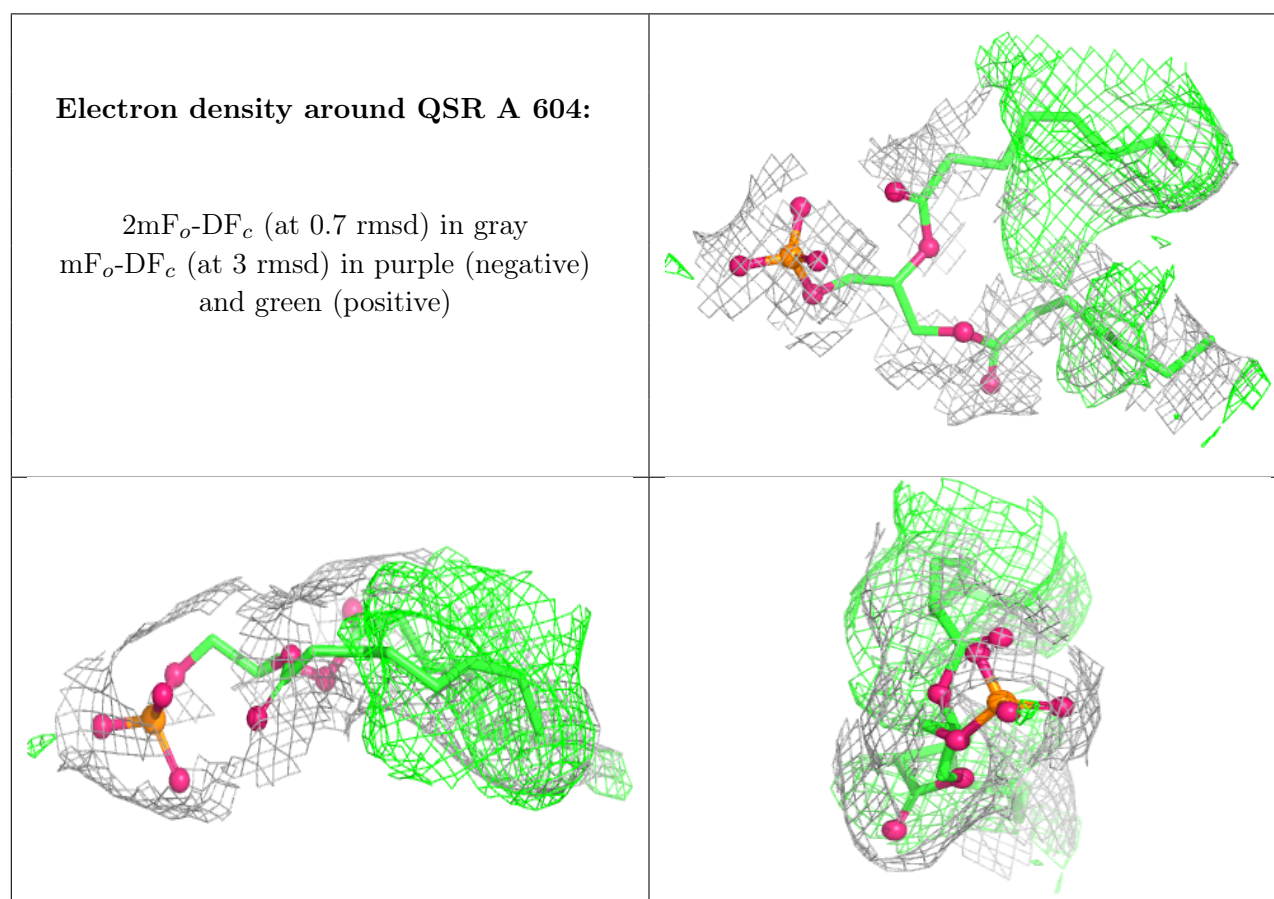
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

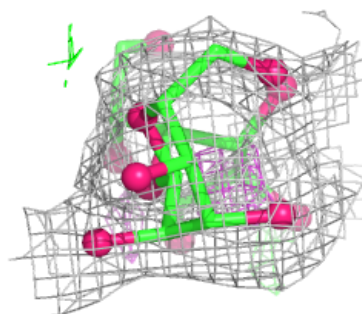
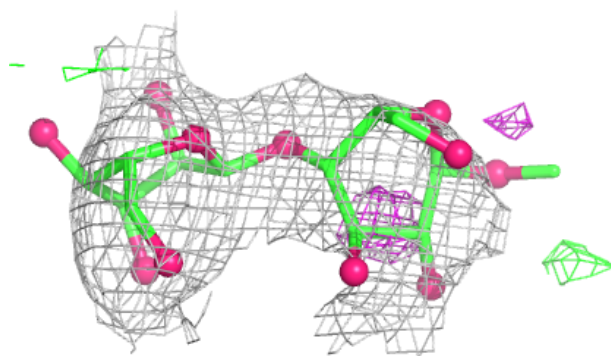
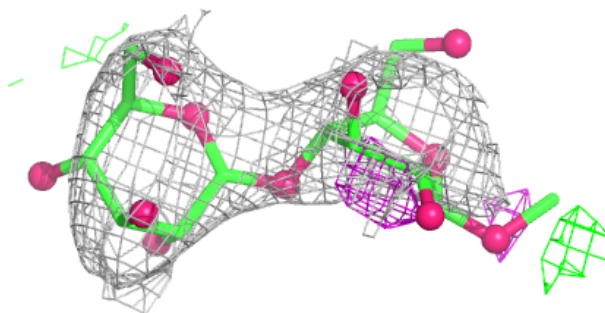
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	QSR	A	604	27/100	0.57	0.28	76,88,95,96	0
5	LMT	A	605	24/35	0.69	0.20	96,105,113,123	0
3	PO4	B	601	5/5	0.74	0.32	81,81,83,86	0
4	QSR	A	603	52/100	0.78	0.23	68,90,107,115	0
2	CA	A	601	1/1	0.81	0.23	86,86,86,86	0
4	QSR	B	602	67/100	0.81	0.24	47,66,82,88	0
3	PO4	A	602	5/5	0.81	0.46	86,93,94,98	0
4	QSR	B	603	70/100	0.83	0.20	48,68,79,94	0
5	LMT	B	604	35/35	0.84	0.16	56,75,89,92	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.

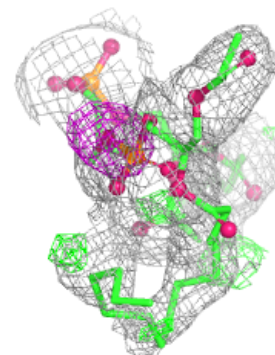
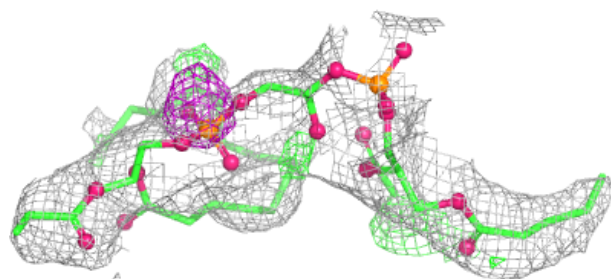
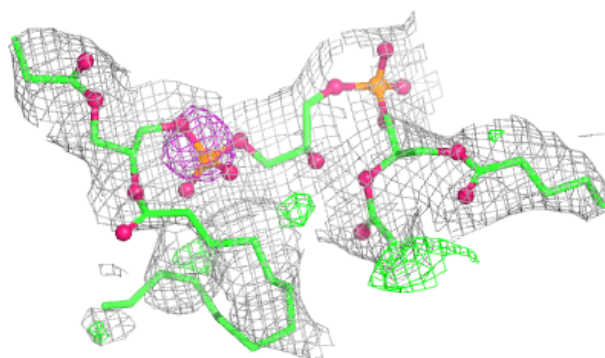


Electron density around LMT A 605:

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

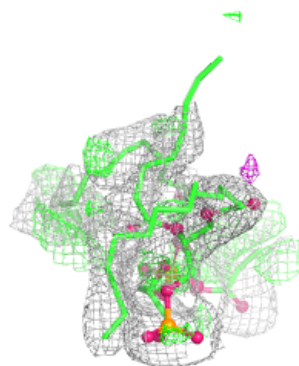
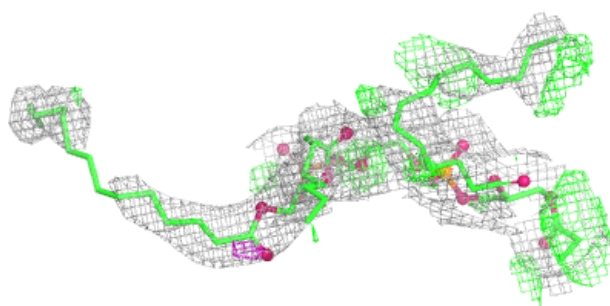
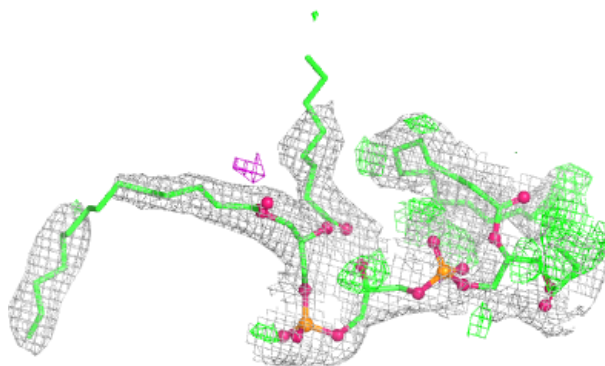
**Electron density around QSR A 603:**

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



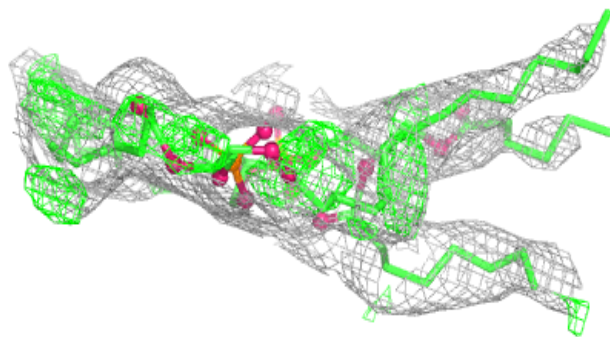
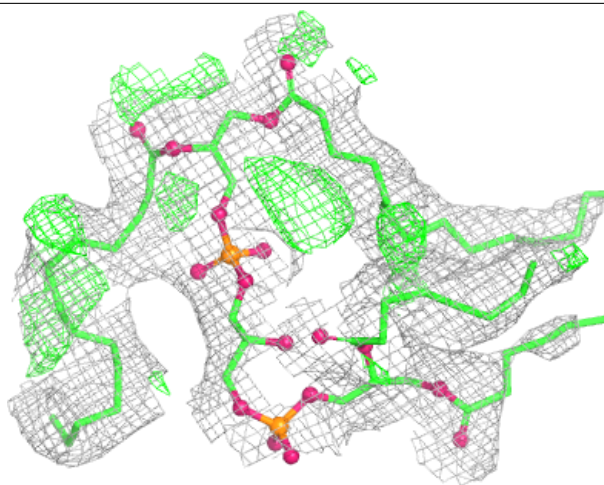
Electron density around QSR B 602:

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



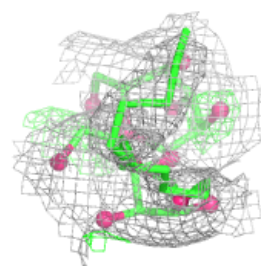
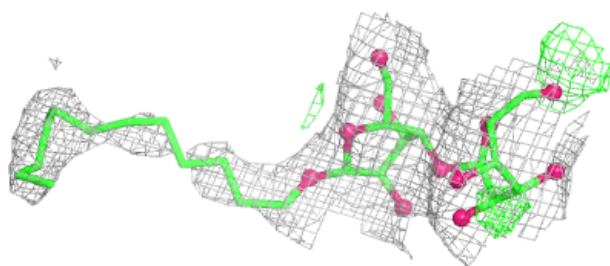
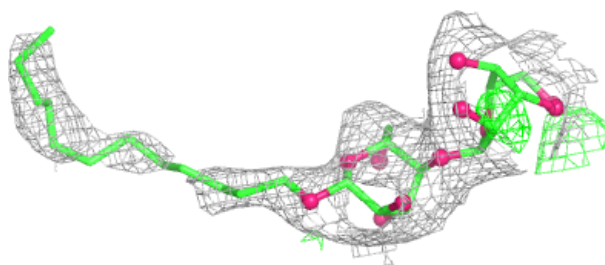
Electron density around QSR B 603:

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



Electron density around LMT B 604:

$2mF_o-DF_c$ (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.