



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 11:06 pm BST

PDB ID : 6V8Q
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 Full wwPDB X-ray Structure Validation 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 : 2.11
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) : 2.11

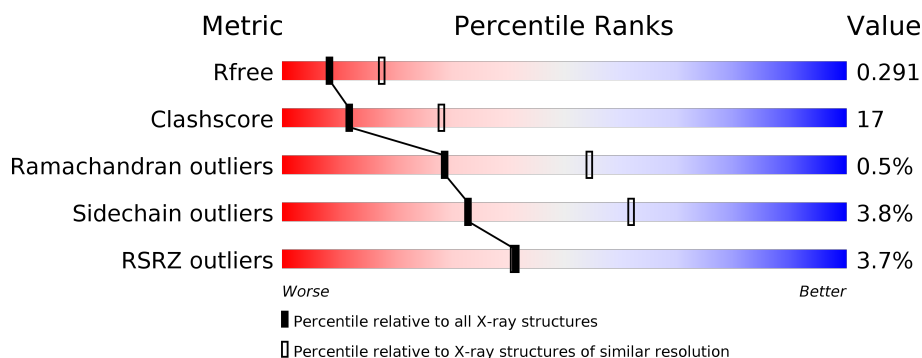
1 Overall quality at a glance

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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 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	592	<div> <div>4%</div> <div> <div></div> <div>60%</div> <div>34%</div> <div>• •</div> </div> </div>
1	B	592	<div> <div>3%</div> <div> <div></div> <div>61%</div> <div>31%</div> <div>• 5%</div> </div> </div>

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 (three-letter code: CA) (formula: Ca).

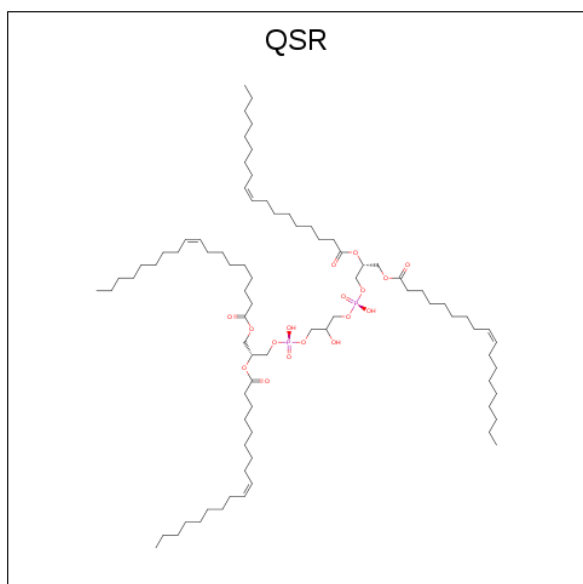
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



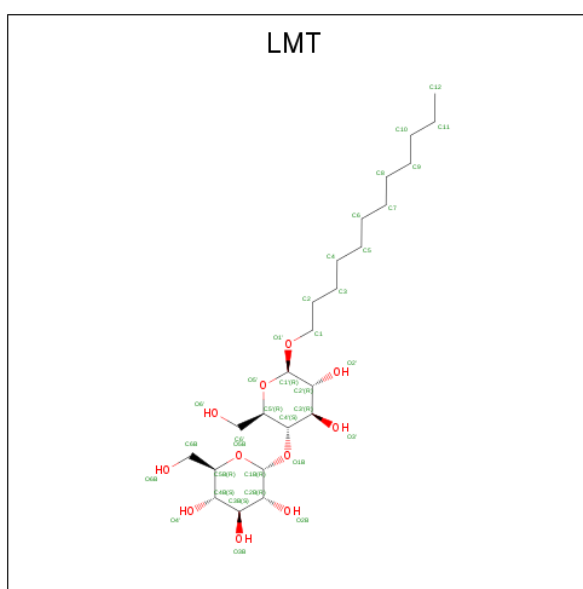
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

- 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 -diphosphatripentaconta-9,44-diene-21,33-diy l (9Z,9'Z)di-octadec-9-enoate (three-letter code: QSR) (formula: C₈₁H₁₅₀O₁₇P₂) (labeled as "Ligand of Interest" by author).



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-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).

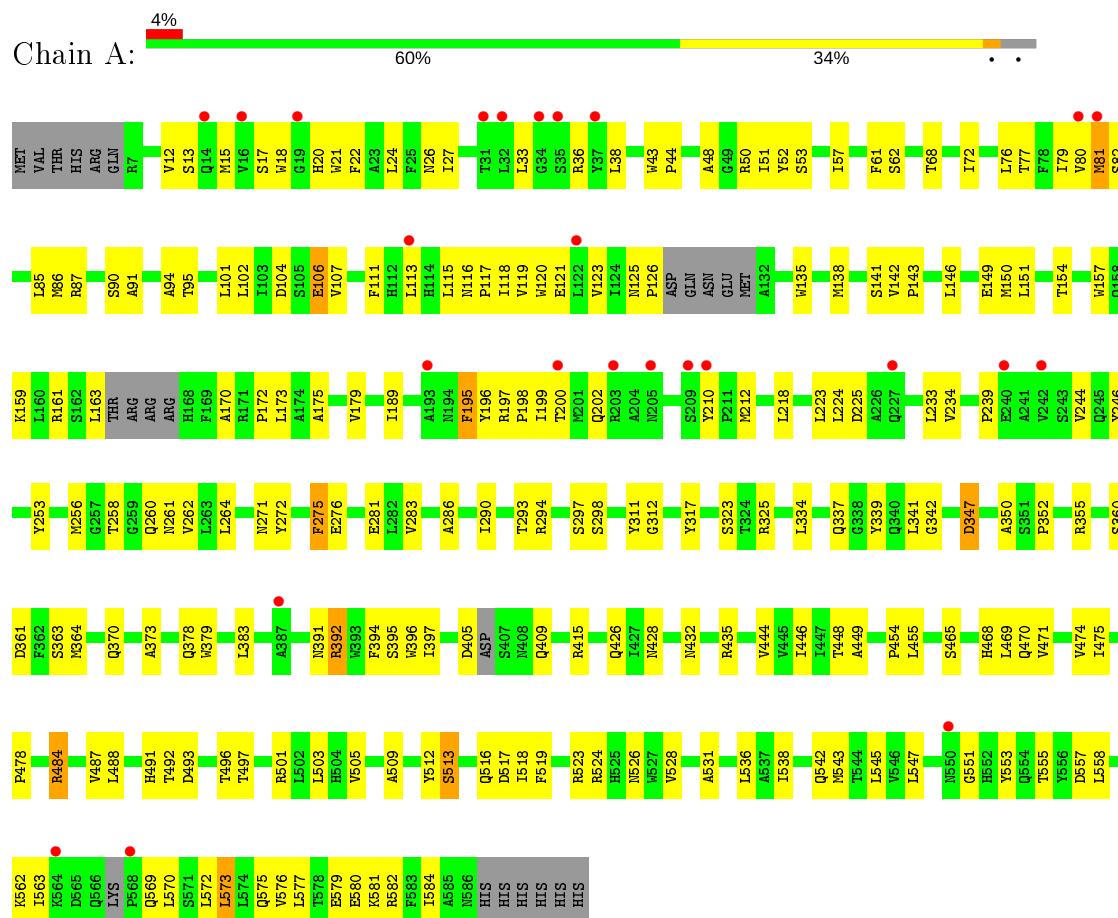


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			24	13	11		
5	B	1	Total	C	O	0	0
			35	24	11		

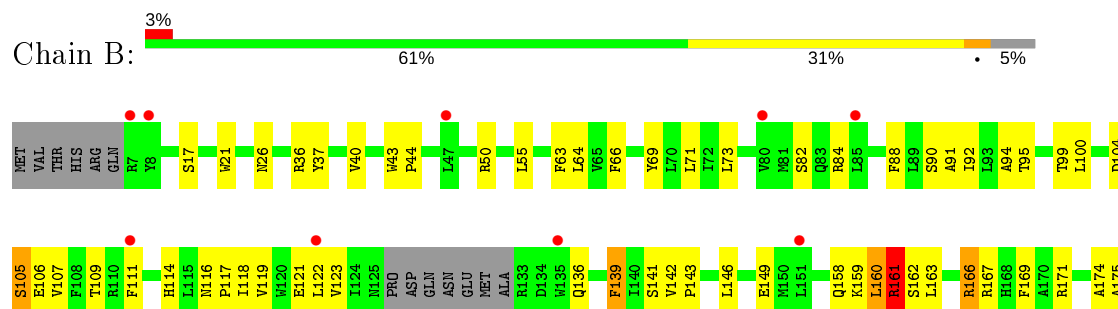
3 Residue-property plots

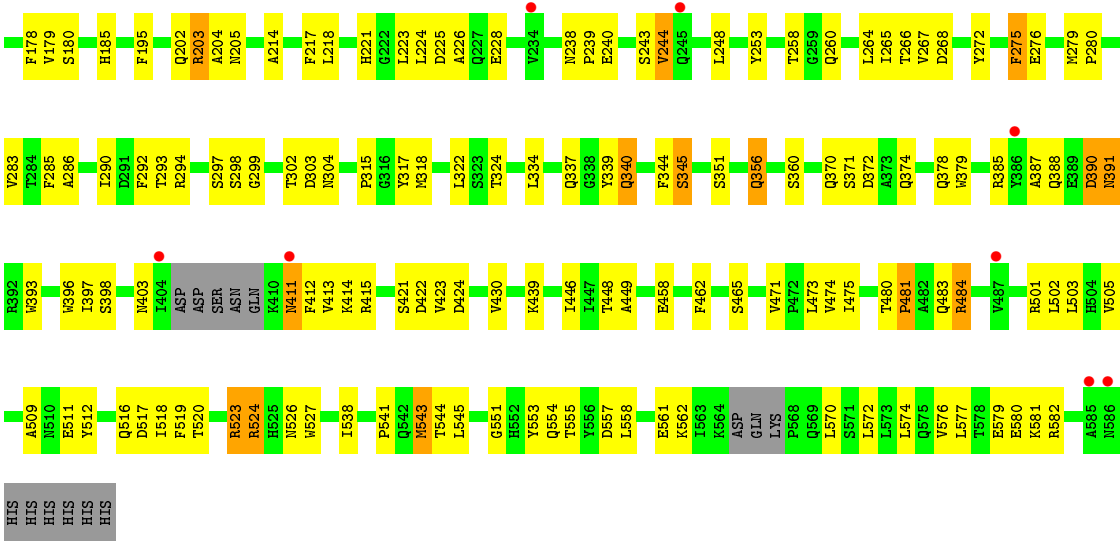
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Inner membrane protein YejM



• Molecule 1: Inner membrane protein YejM





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 0.240 , 0.291	Depositor DCC
R_{free} test set	2716 reflections (5.05%)	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 , 33.4	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	0.85	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: QSR, PO4, LMT, CA

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	0.46	0/4589	0.72	10/6260 (0.2%)
1	B	0.46	0/4622	0.69	4/6303 (0.1%)
All	All	0.46	0/9211	0.71	14/12563 (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.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	MET	CB-CG-SD	-8.25	87.66	112.40
1	B	411	ASN	CB-CA-C	-7.51	95.37	110.40
1	B	100	LEU	CA-CB-CG	7.35	132.20	115.30
1	A	163	LEU	CB-CG-CD2	6.71	122.41	111.00
1	A	547	LEU	CA-CB-CG	6.66	130.63	115.30
1	B	523	ARG	C-N-CA	-6.31	105.92	121.70
1	A	81	MET	C-N-CA	6.09	136.94	121.70
1	A	81	MET	CA-CB-CG	5.96	123.44	113.30
1	A	151	LEU	CA-CB-CG	5.84	128.73	115.30
1	A	573	LEU	CA-CB-CG	-5.43	102.81	115.30
1	A	126	PRO	N-CA-CB	5.31	109.67	103.30
1	A	163	LEU	CA-CB-CG	5.30	127.49	115.30
1	A	172	PRO	N-CA-CB	5.09	109.40	103.30
1	B	524	ARG	N-CA-CB	5.01	119.61	110.60

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	153	0
1	B	4500	0	4382	156	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	311	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 17.

All (311) 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:77:THR:O	1:A:81:MET:HE1	1.76	0.86
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
1:B:317:TYR:OH	1:B:580:GLU:O	1.98	0.82
1:A:95:THR:HG22	1:A:149:GLU:HG3	1.62	0.81
1:A:557:ASP:HB3	1:A:563:ILE:HD11	1.63	0.81
1:A:444:VAL:HG12	1:A:478:PRO:HD2	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:THR:O	1:A:81:MET:CE	2.31	0.77
1:A:121:GLU:OE1	1:A:121:GLU:N	2.17	0.76
1:A:135:TRP:HA	1:A:138:MET:HB3	1.68	0.76
1:B:543:MET:HG3	1:B:555:THR:HG23	1.69	0.74
1:A:142:VAL:HG13	1:A:143:PRO:HD3	1.69	0.74
1:A:36:ARG:HH12	1:A:106:GLU:HG2	1.51	0.74
1:B:258:THR:HG23	1:B:260:GLN:H	1.53	0.74
1:B:458:GLU:OE2	1:B:458:GLU:N	2.19	0.72
1:B:294:ARG:HG2	1:B:294:ARG:HH11	1.54	0.72
4:B:603:QSR:O1	4:B:603:QSR:O9	2.08	0.72
1:A:91:ALA:O	1:A:95:THR:HG23	1.91	0.71
1:B:446:ILE:HG12	1:B:475:ILE:HG12	1.72	0.71
1:B:449:ALA:HB3	1:B:471:VAL:HB	1.72	0.71
1:B:387:ALA:HB1	1:B:439:LYS:NZ	2.07	0.70
4:B:603:QSR:O5	4:B:603:QSR:O9	2.10	0.69
1:A:493:ASP:HB3	1:A:518:ILE:HG23	1.74	0.69
1:B:95:THR:HG21	1:B:146:LEU:HA	1.75	0.69
1:B:292:PHE:HB2	1:B:473:LEU:HB3	1.72	0.69
5:B:604:LMT:O2B	5:B:604:LMT:O4'	2.10	0.68
1:A:38:LEU:HD13	1:A:57:ILE:HD11	1.75	0.68
1:A:487:VAL:HG11	1:A:523:ARG:HD3	1.76	0.68
1:A:76:LEU:HA	1:A:79:ILE:HG22	1.76	0.68
1:A:150:MET:O	1:A:154:THR:HG22	1.93	0.67
1:A:82:SER:HB3	1:A:85:LEU:HB3	1.76	0.67
1:B:36:ARG:NE	1:B:105:SER:HG	1.89	0.67
1:B:40:VAL:HG11	1:B:109:THR:HA	1.76	0.67
1:B:119:VAL:O	1:B:123:VAL:HG23	1.95	0.67
1:B:243:SER:O	1:B:244:VAL:HG22	1.95	0.67
1:B:114:HIS:NE2	1:B:204:ALA:O	2.29	0.66
1:B:345:SER:HB2	1:B:398:SER:HB3	1.78	0.65
1:B:178:PHE:HA	5:B:604:LMT:H81	1.79	0.64
1:A:15:MET:HE1	1:A:86:MET:HB3	1.78	0.64
1:A:195:PHE:CE1	1:A:239:PRO:HG3	2.33	0.64
1:A:373:ALA:HA	1:A:426:GLN:OE1	1.98	0.64
1:B:91:ALA:O	1:B:95:THR:HG23	1.96	0.63
1:A:170:ALA:HB3	5:A:605:LMT:H6E	1.80	0.63
1:A:17:SER:OG	5:A:605:LMT:O6B	2.14	0.63
1:A:576:VAL:HG12	1:A:577:LEU:HD23	1.80	0.63
1:B:579:GLU:HB2	1:B:582:ARG:HH21	1.63	0.63
1:B:387:ALA:HB1	1:B:439:LYS:HZ3	1.63	0.63
1:B:520:THR:O	1:B:523:ARG:NH1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:543:MET:HG2	1:B:544:THR:N	2.14	0.62
1:B:36:ARG:HH22	1:B:106:GLU:CG	2.12	0.62
1:B:118:ILE:HD12	1:B:118:ILE:H	1.64	0.62
1:B:122:LEU:HD22	1:B:574:LEU:HD13	1.81	0.62
1:B:279:MET:O	1:B:283:VAL:HG23	1.99	0.62
1:A:27:ILE:HG12	1:A:62:SER:HA	1.82	0.62
1:A:197:ARG:NH2	1:A:323:SER:CB	2.50	0.62
1:A:575:GLN:O	1:A:579:GLU:HG2	2.00	0.61
1:B:554:GLN:HE22	1:B:562:LYS:HD2	1.65	0.61
1:B:36:ARG:CZ	1:B:105:SER:OG	2.48	0.61
1:B:411:ASN:CG	1:B:413:VAL:HG23	2.21	0.61
1:A:272:TYR:CB	1:A:470:GLN:HG2	2.31	0.60
1:A:347:ASP:O	1:A:350:ALA:HB2	2.01	0.60
1:A:276:GLU:HA	1:A:283:VAL:CG2	2.31	0.60
1:A:496:THR:OG1	1:A:513:SER:OG	2.18	0.60
1:A:12:VAL:HG22	1:A:81:MET:SD	2.41	0.60
1:B:290:ILE:HG21	1:B:519:PHE:HE1	1.66	0.60
1:B:265:ILE:HD11	1:B:430:VAL:HG11	1.84	0.59
1:A:405:ASP:O	1:A:415:ARG:NH1	2.34	0.59
1:B:340:GLN:HG2	1:B:393:TRP:HB3	1.84	0.59
1:A:262:VAL:HG13	1:A:444:VAL:HG23	1.83	0.58
1:A:17:SER:HG	5:A:605:LMT:H6B	1.47	0.58
1:A:496:THR:HG1	1:A:513:SER:HG	1.52	0.58
1:B:36:ARG:HH22	1:B:106:GLU:HG2	1.69	0.58
1:B:390:ASP:O	1:B:391:ASN:HB2	2.04	0.58
1:A:262:VAL:HB	1:A:394:PHE:CD2	2.39	0.57
1:A:33:LEU:HD23	1:A:101:LEU:HD23	1.86	0.57
1:A:391:ASN:OD1	1:A:392:ARG:N	2.34	0.57
1:A:538:ILE:HG21	1:A:572:LEU:HD11	1.87	0.56
1:A:258:THR:OG1	1:A:260:GLN:HG3	2.05	0.56
1:B:379:TRP:CG	1:B:397:ILE:HD11	2.40	0.56
1:B:379:TRP:CD2	1:B:397:ILE:HD11	2.41	0.56
1:B:114:HIS:HE1	1:B:205:ASN:O	1.90	0.55
1:A:379:TRP:CG	1:A:397:ILE:HD11	2.41	0.55
1:A:119:VAL:O	1:A:123:VAL:HG23	2.07	0.55
1:A:360:SER:O	1:B:415:ARG:HD2	2.06	0.55
1:B:118:ILE:HD11	1:B:551:GLY:O	2.07	0.55
1:B:238:ASN:ND2	1:B:240:GLU:HG3	2.22	0.54
1:A:189:ILE:HD11	1:A:212:MET:SD	2.48	0.54
1:B:370:GLN:NE2	1:B:378:GLN:OE1	2.34	0.54
1:B:337:GLN:NE2	1:B:503:LEU:O	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:SER:HB2	1:B:324:THR:HG21	1.89	0.54
1:B:36:ARG:NH2	1:B:106:GLU:HG2	2.23	0.54
1:B:501:ARG:NH2	1:B:517:ASP:OD1	2.40	0.53
1:A:117:PRO:O	1:A:121:GLU:OE1	2.26	0.53
1:B:272:TYR:CE1	1:B:275:PHE:HE2	2.27	0.53
1:A:116:ASN:HB2	1:A:117:PRO:HD2	1.91	0.53
1:A:432:ASN:OD1	1:A:435:ARG:NH1	2.40	0.53
1:B:293:THR:HG21	1:B:484:ARG:NH1	2.24	0.53
1:A:111:PHE:O	1:A:113:LEU:HD12	2.07	0.53
1:A:355:ARG:CZ	1:A:364:MET:HE3	2.38	0.53
1:A:276:GLU:HA	1:A:283:VAL:HG21	1.90	0.53
1:B:541:PRO:O	1:B:558:LEU:HD21	2.08	0.53
1:A:61:PHE:CE1	1:A:101:LEU:HD11	2.44	0.52
1:A:142:VAL:CG1	1:A:143:PRO:HD3	2.39	0.52
1:B:36:ARG:HH22	1:B:106:GLU:HA	1.74	0.52
1:B:570:LEU:HB2	1:B:572:LEU:HB3	1.90	0.52
1:B:294:ARG:HG2	1:B:294:ARG:NH1	2.23	0.52
1:A:253:TYR:CD1	1:A:505:VAL:HG22	2.45	0.52
1:B:318:MET:HG3	1:B:322:LEU:HD13	1.92	0.52
1:B:114:HIS:CE1	1:B:205:ASN:O	2.62	0.52
1:A:175:ALA:O	1:A:179:VAL:HG23	2.10	0.51
1:A:118:ILE:HD11	1:A:573:LEU:HD13	1.91	0.51
1:B:167:ARG:O	1:B:171:ARG:HB2	2.10	0.51
1:A:262:VAL:HG13	1:A:444:VAL:CG2	2.40	0.51
1:B:579:GLU:HB2	1:B:582:ARG:NH2	2.24	0.51
1:A:581:LYS:HE2	1:A:584:ILE:HD11	1.91	0.51
1:B:226:ALA:HB3	1:B:228:GLU:HG3	1.91	0.51
1:A:253:TYR:CE1	1:A:505:VAL:HG22	2.45	0.51
1:B:36:ARG:NH2	1:B:105:SER:OG	2.44	0.51
1:A:18:TRP:CE2	1:A:87:ARG:HG2	2.45	0.51
1:B:160:LEU:O	1:B:160:LEU:HD23	2.10	0.51
1:B:572:LEU:O	1:B:576:VAL:HG13	2.10	0.51
1:B:411:ASN:OD1	1:B:411:ASN:O	2.29	0.51
1:B:303:ASP:OD2	1:B:351:SER:OG	2.20	0.51
1:A:543:MET:CG	1:A:555:THR:HG23	2.42	0.50
1:B:171:ARG:HH22	5:B:604:LMT:H6'1	1.75	0.50
1:A:449:ALA:HB3	1:A:471:VAL:HB	1.93	0.50
1:A:516:GLN:HB3	1:A:524:ARG:NH2	2.26	0.50
1:B:159:LYS:C	1:B:161:ARG:H	2.14	0.50
1:B:334:LEU:HD23	1:B:503:LEU:HD21	1.93	0.50
1:A:256:MET:HE1	1:B:374:GLN:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:PHE:HB3	1:A:113:LEU:HD12	1.93	0.50
1:A:379:TRP:CH2	1:A:383:LEU:HD22	2.47	0.50
1:B:37:TYR:OH	1:B:104:ASP:OD2	2.13	0.49
1:B:371:SER:HB2	1:B:374:GLN:H	1.76	0.49
1:A:361:ASP:O	1:B:415:ARG:HG3	2.12	0.49
1:B:248:LEU:HB2	1:B:511:GLU:HG2	1.94	0.49
1:B:526:ASN:OD1	1:B:541:PRO:HD2	2.12	0.49
1:B:545:LEU:HD11	1:B:553:TYR:CD2	2.46	0.49
1:A:18:TRP:CZ2	1:A:87:ARG:HG2	2.48	0.49
1:B:411:ASN:OD1	1:B:413:VAL:HG23	2.12	0.49
1:B:253:TYR:CE2	1:B:505:VAL:HG22	2.48	0.49
1:A:497:THR:OG1	1:A:518:ILE:HG12	2.13	0.49
1:A:197:ARG:NH2	1:A:323:SER:HB2	2.19	0.49
1:A:272:TYR:CE1	1:A:275:PHE:HE2	2.31	0.49
1:A:469:LEU:HA	1:A:469:LEU:HD23	1.57	0.49
1:B:481:PRO:HD2	1:B:483:GLN:NE2	2.27	0.49
1:A:197:ARG:N	1:A:198:PRO:CD	2.76	0.48
1:B:299:GLY:HA3	1:B:304:ASN:HB2	1.95	0.48
1:B:36:ARG:NH2	1:B:106:GLU:HA	2.28	0.48
1:A:118:ILE:HD12	1:A:121:GLU:HB2	1.95	0.48
1:A:77:THR:C	1:A:81:MET:CE	2.82	0.48
1:B:166:ARG:HA	1:B:169:PHE:HB2	1.94	0.48
1:B:292:PHE:CE1	1:B:475:ILE:HD12	2.48	0.48
1:B:538:ILE:HD11	1:B:576:VAL:HG21	1.94	0.48
1:B:298:SER:O	1:B:315:PRO:HG2	2.13	0.48
1:B:174:ALA:HB1	5:B:604:LMT:H51	1.95	0.48
1:A:17:SER:O	1:A:21:TRP:HD1	1.97	0.48
1:A:370:GLN:NE2	1:A:378:GLN:OE1	2.44	0.48
1:B:136:GLN:HA	1:B:139:PHE:HB2	1.94	0.48
1:A:77:THR:C	1:A:81:MET:HE1	2.34	0.47
1:B:260:GLN:O	1:B:339:TYR:OH	2.17	0.47
1:B:276:GLU:HA	1:B:283:VAL:HG22	1.96	0.47
1:A:542:GLN:O	1:A:558:LEU:HD13	2.15	0.47
1:A:196:TYR:O	1:A:200:THR:HG23	2.14	0.47
1:B:509:ALA:HA	1:B:512:TYR:CZ	2.50	0.47
1:A:446:ILE:HG12	1:A:475:ILE:HG12	1.96	0.47
1:B:116:ASN:HB2	1:B:117:PRO:HD2	1.96	0.47
1:B:111:PHE:O	1:B:581:LYS:HD2	2.15	0.47
1:A:264:LEU:O	1:A:396:TRP:HA	2.15	0.47
1:B:268:ASP:OD1	1:B:302:THR:HG21	2.14	0.47
1:A:272:TYR:O	1:A:275:PHE:HD2	1.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:603:QSR:O9	4:A:603:QSR:O2	2.32	0.47
1:B:36:ARG:NH2	1:B:106:GLU:CA	2.78	0.47
1:A:342:GLY:O	1:A:395:SER:HA	2.14	0.47
1:A:290:ILE:HD13	1:A:519:PHE:CE1	2.49	0.47
1:B:185:HIS:NE2	3:B:601:PO4:O4	2.48	0.46
1:B:73:LEU:HD13	1:B:90:SER:HB3	1.96	0.46
1:A:26:ASN:OD1	1:A:94:ALA:HB1	2.15	0.46
1:A:43:TRP:HE1	1:A:50:ARG:HE	1.62	0.46
1:A:334:LEU:O	1:A:339:TYR:HB2	2.16	0.46
1:B:171:ARG:HH12	5:B:604:LMT:H6'1	1.80	0.46
1:A:531:ALA:HB2	1:A:536:LEU:HD12	1.97	0.46
1:B:458:GLU:CD	1:B:458:GLU:H	2.13	0.46
1:B:111:PHE:HZ	1:B:574:LEU:HD11	1.81	0.46
1:B:267:VAL:O	1:B:449:ALA:HA	2.16	0.46
1:A:293:THR:HG21	1:A:484:ARG:NH1	2.31	0.45
1:B:17:SER:O	1:B:21:TRP:HD1	1.99	0.45
1:A:43:TRP:CE3	1:A:44:PRO:HD2	2.51	0.45
1:A:173:LEU:HD12	1:A:173:LEU:HA	1.84	0.45
1:A:297:SER:OG	1:A:298:SER:N	2.50	0.45
1:A:261:ASN:OD1	1:A:392:ARG:HA	2.16	0.45
1:B:104:ASP:HA	1:B:107:VAL:HG22	1.98	0.45
1:A:545:LEU:HD11	1:A:553:TYR:HB2	1.97	0.45
1:B:248:LEU:HD23	1:B:248:LEU:HA	1.56	0.45
1:A:488:LEU:HB3	1:A:528:VAL:HG13	1.98	0.45
1:B:412:PHE:CD1	1:B:412:PHE:N	2.85	0.45
1:B:43:TRP:CE2	1:B:50:ARG:HG2	2.52	0.45
1:A:117:PRO:HB2	1:A:551:GLY:O	2.17	0.45
1:A:68:THR:O	1:A:72:ILE:HD12	2.16	0.45
1:B:290:ILE:HD11	1:B:480:THR:OG1	2.17	0.45
1:A:337:GLN:NE2	1:A:503:LEU:O	2.50	0.45
1:A:290:ILE:HD13	1:A:519:PHE:HE1	1.82	0.45
1:B:297:SER:OG	1:B:298:SER:N	2.49	0.45
1:B:50:ARG:NH2	4:B:603:QSR:O11	2.50	0.45
1:A:210:TYR:N	3:A:602:PO4:O4	2.35	0.45
1:B:63:PHE:HA	5:B:604:LMT:H101	1.99	0.44
1:B:88:PHE:O	1:B:92:ILE:HG12	2.17	0.44
1:B:142:VAL:HB	1:B:143:PRO:HD3	1.99	0.44
1:B:175:ALA:O	1:B:179:VAL:HG13	2.18	0.44
1:A:121:GLU:HB3	1:A:570:LEU:HD21	2.00	0.44
1:A:135:TRP:CA	1:A:138:MET:HB3	2.45	0.44
1:A:22:PHE:HE2	1:A:90:SER:O	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:ASP:HA	1:B:107:VAL:CG2	2.48	0.44
1:B:26:ASN:OD1	1:B:94:ALA:HB1	2.18	0.44
1:B:509:ALA:HA	1:B:512:TYR:CE2	2.53	0.44
1:A:509:ALA:HA	1:A:512:TYR:CE2	2.53	0.44
1:B:379:TRP:CZ3	1:B:430:VAL:HG13	2.53	0.44
1:A:223:LEU:HA	1:A:224:LEU:HA	1.65	0.44
1:B:95:THR:O	1:B:99:THR:HG22	2.18	0.44
1:A:38:LEU:HD22	1:A:57:ILE:CD1	2.48	0.43
1:B:36:ARG:HH22	1:B:106:GLU:CA	2.31	0.43
1:A:218:LEU:HD23	1:A:218:LEU:HA	1.78	0.43
1:A:256:MET:HE2	1:A:256:MET:HB2	1.88	0.43
1:B:462:PHE:O	1:B:465:SER:HB3	2.19	0.43
1:B:524:ARG:NH1	1:B:524:ARG:HG2	2.32	0.43
1:A:293:THR:HG21	1:A:484:ARG:HH12	1.83	0.43
1:B:292:PHE:CZ	1:B:518:ILE:HD12	2.53	0.43
1:A:125:ASN:CB	1:A:570:LEU:HD13	2.48	0.43
1:B:385:ARG:O	1:B:388:GLN:HG2	2.18	0.43
1:A:272:TYR:HB2	1:A:470:GLN:HG2	2.01	0.43
1:A:312:GLY:O	1:A:492:THR:HB	2.19	0.43
1:A:286:ALA:HB2	1:A:474:VAL:HG21	2.00	0.43
1:B:238:ASN:HD21	1:B:240:GLU:HG3	1.83	0.43
1:A:44:PRO:HG3	1:A:202:GLN:NE2	2.33	0.43
1:A:294:ARG:HB3	1:A:488:LEU:HD23	2.01	0.43
1:A:159:LYS:C	1:A:161:ARG:H	2.20	0.43
1:B:276:GLU:HA	1:B:283:VAL:CG2	2.49	0.43
1:B:481:PRO:O	1:B:483:GLN:HG2	2.19	0.43
1:A:562:LYS:HB2	1:A:562:LYS:HE3	1.78	0.42
1:B:285:PHE:HD2	1:B:474:VAL:HG11	1.83	0.42
1:B:66:PHE:O	1:B:69:TYR:HB3	2.18	0.42
1:A:579:GLU:HB3	1:A:582:ARG:HH12	1.83	0.42
1:B:577:LEU:HD23	1:B:577:LEU:HA	1.83	0.42
1:B:63:PHE:CD1	1:B:64:LEU:HD23	2.54	0.42
1:A:33:LEU:HD21	1:A:102:LEU:HG	2.01	0.42
1:A:244:VAL:HG11	1:A:317:TYR:HB3	2.01	0.42
1:B:118:ILE:CD1	1:B:551:GLY:O	2.67	0.42
1:B:414:LYS:NZ	1:B:422:ASP:OD2	2.33	0.42
1:B:286:ALA:HB2	1:B:474:VAL:CG2	2.49	0.42
1:A:38:LEU:CD2	1:A:53:SER:HB3	2.49	0.42
1:B:217:PHE:CE1	1:B:221:HIS:CE1	3.08	0.42
1:A:286:ALA:HA	1:A:474:VAL:CG1	2.49	0.42
1:B:161:ARG:HG2	1:B:161:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:TYR:OH	1:A:580:GLU:O	2.22	0.42
1:B:55:LEU:HD23	1:B:180:SER:HB3	2.00	0.42
1:B:214:ALA:O	1:B:218:LEU:HG	2.19	0.42
1:B:44:PRO:HG3	1:B:202:GLN:NE2	2.34	0.42
1:B:40:VAL:HG21	1:B:109:THR:OG1	2.20	0.42
1:B:557:ASP:OD1	1:B:561:GLU:N	2.52	0.42
1:A:102:LEU:HD23	1:A:102:LEU:HA	1.87	0.42
1:A:454:PRO:HG2	1:A:468:HIS:NE2	2.35	0.42
1:A:135:TRP:CD1	1:A:135:TRP:N	2.86	0.41
1:A:233:LEU:HD12	1:A:239:PRO:HD3	2.02	0.41
1:A:95:THR:HG21	1:A:146:LEU:HA	2.01	0.41
1:B:178:PHE:CA	5:B:604:LMT:H81	2.46	0.41
1:A:20:HIS:HB3	5:A:605:LMT:H3'	2.02	0.41
1:A:48:ALA:HA	1:A:51:ILE:HD12	2.02	0.41
1:A:61:PHE:HE1	1:A:101:LEU:HD11	1.84	0.41
1:A:341:LEU:HA	1:A:341:LEU:HD23	1.80	0.41
1:A:281:GLU:HG3	1:A:428:ASN:HB2	2.02	0.41
1:A:493:ASP:HB3	1:A:518:ILE:CG2	2.47	0.41
1:A:509:ALA:HA	1:A:512:TYR:CZ	2.56	0.41
1:A:79:ILE:HG23	1:A:80:VAL:N	2.35	0.41
1:A:135:TRP:HA	1:A:138:MET:CB	2.44	0.41
1:A:234:VAL:HG22	1:A:352:PRO:HG2	2.02	0.41
1:A:272:TYR:O	1:A:275:PHE:CD2	2.73	0.41
1:B:290:ILE:HD13	1:B:519:PHE:CE1	2.55	0.41
1:A:246:TYR:OH	1:A:311:TYR:O	2.32	0.41
1:B:195:PHE:CZ	1:B:239:PRO:HG3	2.55	0.41
1:B:372:ASP:OD2	1:B:423:VAL:HG12	2.19	0.41
4:B:602:QSR:O1	4:B:602:QSR:O9	2.39	0.41
1:B:66:PHE:CD1	5:B:604:LMT:H22	2.56	0.41
1:A:104:ASP:HA	1:A:107:VAL:HG22	2.02	0.41
1:A:20:HIS:HB3	5:A:605:LMT:C3'	2.51	0.41
1:A:115:LEU:HD22	1:A:120:TRP:CZ2	2.56	0.41
1:B:158:GLN:HG2	1:B:159:LYS:HG2	2.03	0.41
1:B:527:TRP:CZ3	1:B:576:VAL:HG12	2.56	0.41
1:B:203:ARG:HD2	1:B:240:GLU:OE2	2.21	0.41
1:B:162:SER:O	1:B:166:ARG:N	2.54	0.41
1:B:223:LEU:HA	1:B:224:LEU:HA	1.71	0.41
1:A:87:ARG:CZ	1:A:157:TRP:CD1	3.04	0.41
1:A:448:THR:OG1	1:A:491:HIS:HE1	2.04	0.41
1:A:82:SER:O	1:A:85:LEU:N	2.53	0.41
1:B:50:ARG:CZ	4:B:603:QSR:O11	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:GLN:OE1	1:A:524:ARG:N	2.34	0.40
1:B:344:PHE:CE2	1:B:378:GLN:HB3	2.56	0.40
1:B:356:GLN:O	1:B:360:SER:HB3	2.21	0.40
1:A:52:TYR:CD2	1:A:199:ILE:HG23	2.56	0.40
1:B:264:LEU:O	1:B:396:TRP:HA	2.21	0.40
1:B:387:ALA:HB1	1:B:439:LYS:HZ1	1.81	0.40
1:A:271:ASN:ND2	1:A:455:LEU:HG	2.37	0.40
1:A:543:MET:HG2	1:A:555:THR:HG23	2.03	0.40
1:B:37:TYR:CE1	1:B:105:SER:HA	2.56	0.40
1:B:516:GLN:HE21	1:B:520:THR:HG21	1.87	0.40
1:B:266:THR:HA	1:B:448:THR:O	2.22	0.40
1:A:501:ARG:NH2	1:A:517:ASP:OD2	2.55	0.40
1:B:280:PRO:HD2	1:B:424:ASP:OD2	2.21	0.40
1:B:462:PHE:CZ	1:B:465:SER:HA	2.57	0.40

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	559/592 (94%)	526 (94%)	33 (6%)	0	100	100
1	B	557/592 (94%)	526 (94%)	25 (4%)	6 (1%)	14	34
All	All	1116/1184 (94%)	1052 (94%)	58 (5%)	6 (0%)	29	54

All (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

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Mol	Chain	Res	Type
1	B	163	LEU
1	B	160	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%)	448 (96%)	17 (4%)	34	63
1	B	474/518 (92%)	455 (96%)	19 (4%)	31	60
All	All	939/1036 (91%)	903 (96%)	36 (4%)	33	62

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	24	LEU
1	A	106	GLU
1	A	141	SER
1	A	195	PHE
1	A	225	ASP
1	A	275	PHE
1	A	325	ARG
1	A	347	ASP
1	A	363	SER
1	A	392	ARG
1	A	409	GLN
1	A	465	SER
1	A	484	ARG
1	A	513	SER
1	A	526	ASN
1	A	569	GLN
1	B	71	LEU
1	B	84	ARG
1	B	105	SER
1	B	121	GLU

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Mol	Chain	Res	Type
1	B	139	PHE
1	B	141	SER
1	B	161	ARG
1	B	203	ARG
1	B	225	ASP
1	B	275	PHE
1	B	340	GLN
1	B	345	SER
1	B	356	GLN
1	B	390	ASP
1	B	421	SER
1	B	481	PRO
1	B	484	ARG
1	B	502	LEU
1	B	543	MET

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

Mol	Chain	Res	Type
1	A	340	GLN
1	A	368	GLN
1	B	238	ASN
1	B	340	GLN
1	B	554	GLN

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 carbohydrates 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	1.31	3 (8%)	47,47,47	1.22	4 (8%)
3	PO4	B	601	-	4,4,4	0.92	0	6,6,6	0.60	0
4	QSR	B	602	-	66,66,99	1.54	9 (13%)	72,78,111	1.34	8 (11%)
3	PO4	A	602	-	4,4,4	0.88	0	6,6,6	0.78	0
4	QSR	A	604	-	26,26,99	1.63	4 (15%)	30,31,111	1.23	4 (13%)
5	LMT	A	605	-	25,25,36	1.31	3 (12%)	36,36,47	1.64	6 (16%)
4	QSR	A	603	-	51,51,99	1.66	6 (11%)	57,63,111	1.63	6 (10%)
4	QSR	B	603	-	69,69,99	1.54	9 (13%)	75,81,111	1.24	7 (9%)

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
4	QSR	B	602	-	-	45/77/77/110	-
4	QSR	A	604	-	-	15/28/28/110	-
5	LMT	A	605	-	-	5/10/50/61	0/2/2/2
4	QSR	A	603	-	-	38/61/61/110	-
4	QSR	B	603	-	-	46/80/80/110	-

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	QSR	O14-C35	4.94	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

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	604	QSR	O2-C14	4.71	1.47	1.34
4	B	603	QSR	C44-C43	4.58	1.58	1.31
4	B	602	QSR	O16-C46	4.54	1.47	1.34
4	B	602	QSR	C70-C69	4.54	1.58	1.31
4	A	604	QSR	O3-C17	4.52	1.46	1.33
4	B	603	QSR	O3-C17	4.45	1.46	1.33
4	B	603	QSR	O14-C35	4.10	1.45	1.33
4	B	603	QSR	C55-C54	4.10	1.55	1.31
4	A	603	QSR	O2-C14	4.07	1.44	1.35
4	A	603	QSR	O3-C17	4.05	1.45	1.33
4	A	603	QSR	C55-C54	3.96	1.54	1.31
5	B	604	LMT	O5B-C1B	3.92	1.51	1.41
4	B	602	QSR	O3-C17	3.91	1.44	1.33
4	B	602	QSR	C55-C54	3.78	1.53	1.31
4	B	602	QSR	O14-C35	3.77	1.44	1.33
4	B	603	QSR	O16-C46	3.36	1.43	1.34
5	B	604	LMT	O5'-C1'	3.26	1.50	1.41
4	B	602	QSR	O2-C14	3.22	1.43	1.34
5	A	605	LMT	O5'-C1'	3.07	1.49	1.41
5	A	605	LMT	O5B-C1B	3.06	1.49	1.41
5	B	604	LMT	C3B-C2B	-2.87	1.45	1.52
4	A	604	QSR	C13-C14	2.65	1.58	1.50
4	A	603	QSR	C47-C46	2.59	1.58	1.50
4	B	602	QSR	C47-C46	2.49	1.58	1.50
4	B	603	QSR	C13-C14	2.42	1.57	1.50
4	B	602	QSR	O2-C15	-2.37	1.40	1.46
5	A	605	LMT	C3B-C2B	-2.31	1.46	1.52
4	A	604	QSR	C18-C17	2.24	1.57	1.50
4	B	603	QSR	C18-C17	2.14	1.57	1.50
4	B	603	QSR	C36-C35	2.07	1.56	1.50
4	B	602	QSR	C18-C17	2.01	1.56	1.50

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	QSR	O2-C14-C13	5.89	121.92	111.09
4	A	603	QSR	O14-C35-C36	4.84	124.08	111.38
4	A	603	QSR	O16-C46-C47	4.56	121.32	111.50
5	A	605	LMT	O5B-C5B-C4B	4.28	117.47	109.69
5	A	605	LMT	C3B-C4B-C5B	4.27	117.86	110.24
4	B	602	QSR	O3-C17-C18	4.14	124.90	111.91
5	A	605	LMT	C1B-O1B-C4'	-3.93	108.25	117.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	602	QSR	O2-C14-C13	3.87	119.83	111.50
4	B	603	QSR	O2-C14-C13	3.81	119.71	111.50
4	B	603	QSR	C33-O16-C46	3.55	126.53	117.79
5	B	604	LMT	O2B-C2B-C3B	-3.46	102.35	110.35
4	A	604	QSR	O2-C14-C13	3.33	118.68	111.50
4	B	602	QSR	O16-C46-C47	3.18	118.36	111.50
4	A	603	QSR	O3-C17-C18	3.08	121.58	111.91
4	B	602	QSR	O3-C17-O4	-3.03	115.96	123.59
4	B	602	QSR	O14-C35-C36	3.02	119.30	111.38
4	B	603	QSR	C48-C47-C46	-2.92	102.99	113.62
4	A	604	QSR	O3-C17-C18	2.77	120.59	111.91
5	B	604	LMT	O5B-C1B-C2B	2.71	116.08	110.35
5	A	605	LMT	O5'-C5'-C4'	2.65	115.33	109.75
5	B	604	LMT	C1B-O5B-C5B	2.62	118.84	113.69
4	B	602	QSR	C16-O3-C17	-2.61	107.45	117.12
4	A	603	QSR	C34-C33-C32	-2.58	105.69	111.79
5	A	605	LMT	C2'-C3'-C4'	2.57	115.55	109.68
5	A	605	LMT	O1B-C1B-C2B	2.26	113.95	108.10
4	B	603	QSR	O14-C35-C36	2.23	118.91	111.91
4	A	604	QSR	C28-C15-C16	-2.21	106.57	111.79
4	A	603	QSR	O2-C14-O1	-2.20	118.60	122.96
4	B	603	QSR	C42-C43-C44	-2.18	107.97	124.73
4	B	603	QSR	O16-C46-C47	2.14	116.12	111.50
4	B	602	QSR	C71-C70-C69	-2.14	108.32	124.73
5	B	604	LMT	C1B-O1B-C4'	-2.08	112.82	117.96
4	B	603	QSR	O16-C33-C32	2.06	115.86	108.40
4	B	602	QSR	C37-C36-C35	-2.06	104.20	114.15
4	A	604	QSR	O3-C17-O4	-2.04	118.45	123.59

There are no chirality outliers.

All (158) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	602	QSR	C28-O5-P1-O6
4	B	602	QSR	O1-C14-O2-C15
4	B	602	QSR	C32-O13-P2-O10
4	B	602	QSR	C32-O13-P2-O11
4	B	602	QSR	C32-O13-P2-O12
4	B	602	QSR	C33-C32-O13-P2
4	B	602	QSR	O8-C29-C30-C31
4	A	604	QSR	C28-O5-P1-O7
4	A	604	QSR	C28-O5-P1-O8

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Mol	Chain	Res	Type	Atoms
5	A	605	LMT	C2'-C1'-O1'-C1
4	A	603	QSR	C28-O5-P1-O6
4	A	603	QSR	O1-C14-O2-C15
4	A	603	QSR	C13-C14-O2-C15
4	A	603	QSR	C32-O13-P2-O11
4	A	603	QSR	C32-O13-P2-O12
4	A	603	QSR	O17-C46-O16-C33
4	A	603	QSR	C47-C46-O16-C33
4	A	603	QSR	O8-C29-C30-C31
4	B	603	QSR	C28-O5-P1-O6
4	B	603	QSR	C28-O5-P1-O8
4	B	603	QSR	O1-C14-O2-C15
4	B	603	QSR	C13-C14-O2-C15
4	B	603	QSR	C31-O10-P2-O12
4	B	603	QSR	C31-O10-P2-O13
4	B	603	QSR	C32-O13-P2-O10
4	B	603	QSR	C32-O13-P2-O11
4	B	603	QSR	C32-O13-P2-O12
4	B	603	QSR	C30-C31-O10-P2
4	B	603	QSR	O17-C46-O16-C33
4	B	603	QSR	C47-C46-O16-C33
4	B	602	QSR	O15-C35-O14-C34
4	A	603	QSR	O15-C35-O14-C34
5	B	604	LMT	O5B-C1B-O1B-C4'
4	B	602	QSR	C36-C35-O14-C34
4	A	603	QSR	C36-C35-O14-C34
4	B	602	QSR	C13-C14-O2-C15
4	B	602	QSR	C53-C54-C55-C09
4	B	603	QSR	C53-C54-C55-C09
4	B	602	QSR	C47-C46-O16-C33
4	A	603	QSR	C30-C29-O8-P1
4	B	603	QSR	C30-C29-O8-P1
5	B	604	LMT	O5B-C5B-C6B-O6B
4	B	602	QSR	O17-C46-O16-C33
5	A	605	LMT	C4'-C5'-C6'-O6'
4	A	604	QSR	C18-C17-O3-C16
4	B	603	QSR	C18-C17-O3-C16
5	B	604	LMT	C4B-C5B-C6B-O6B
4	B	602	QSR	O8-C29-C30-O9
4	A	603	QSR	O8-C29-C30-O9
4	B	603	QSR	O8-C29-C30-O9
4	B	602	QSR	C50-C51-C52-C53

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Mol	Chain	Res	Type	Atoms
5	A	605	LMT	O5'-C5'-C6'-O6'
4	A	604	QSR	O4-C17-O3-C16
4	B	603	QSR	O4-C17-O3-C16
4	B	603	QSR	C36-C35-O14-C34
4	B	602	QSR	C28-O5-P1-O8
4	A	603	QSR	C29-O8-P1-O5
4	A	603	QSR	C32-O13-P2-O10
4	A	603	QSR	C51-C52-C53-C54
4	B	603	QSR	C51-C52-C53-C54
4	B	602	QSR	C9-C10-C11-C12
4	B	602	QSR	C30-C29-O8-P1
4	A	603	QSR	C33-C32-O13-P2
4	B	603	QSR	C47-C48-C49-C50
4	B	603	QSR	C50-C51-C52-C53
5	B	604	LMT	C2'-C1'-O1'-C1
4	B	602	QSR	C48-C49-C50-C51
4	B	602	QSR	C20-C21-C22-C67
4	B	603	QSR	C11-C10-C9-C8
4	B	603	QSR	O15-C35-O14-C34
4	A	603	QSR	C48-C49-C50-C51
4	B	602	QSR	C68-C69-C70-C71
4	B	603	QSR	C55-C09-C23-C24
4	B	603	QSR	C39-C40-C41-C42
4	B	603	QSR	C42-C43-C44-C01
4	A	603	QSR	C23-C09-C55-C54
4	B	603	QSR	C46-C47-C48-C49
5	B	604	LMT	C1-C2-C3-C4
4	B	603	QSR	C11-C12-C13-C14
4	B	602	QSR	C29-O8-P1-O5
4	A	603	QSR	C28-O5-P1-O8
4	A	604	QSR	C17-C18-C19-C20
4	B	603	QSR	O8-C29-C30-C31
4	B	602	QSR	C28-C15-C16-O3
4	B	602	QSR	C71-C72-C73-C74
4	B	602	QSR	C70-C71-C72-C73
4	B	603	QSR	C44-C01-C02-C03
4	A	604	QSR	C28-O5-P1-O6
4	A	604	QSR	C15-C28-O5-P1
4	B	602	QSR	C21-C22-C67-C68
4	B	603	QSR	O3-C17-C18-C19
4	B	603	QSR	C01-C02-C03-C04
4	B	603	QSR	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
4	B	603	QSR	C35-C36-C37-C38
4	A	603	QSR	O13-C32-C33-C34
4	A	604	QSR	C11-C12-C13-C14
4	A	604	QSR	C7-C8-C9-C10
4	B	603	QSR	C28-C15-C16-O3
4	A	604	QSR	C20-C21-C22-C67
5	B	604	LMT	C4-C5-C6-C7
4	B	602	QSR	O2-C15-C16-O3
4	B	603	QSR	C09-C23-C24-C25
5	B	604	LMT	O5'-C1'-O1'-C1
5	B	604	LMT	C5-C6-C7-C8
4	A	604	QSR	C18-C19-C20-C21
4	B	602	QSR	C19-C20-C21-C22
4	A	603	QSR	O2-C15-C16-O3
4	B	603	QSR	C9-C10-C11-C12
4	A	604	QSR	C10-C11-C12-C13
4	B	602	QSR	C18-C19-C20-C21
4	B	602	QSR	C28-O5-P1-O7
4	B	602	QSR	C29-O8-P1-O6
4	A	603	QSR	C28-O5-P1-O7
4	A	603	QSR	C29-O8-P1-O6
4	A	603	QSR	C29-O8-P1-O7
4	B	603	QSR	C31-O10-P2-O11
4	A	603	QSR	C18-C17-O3-C16
4	B	602	QSR	C7-C8-C9-C10
4	A	603	QSR	O4-C17-O3-C16
4	A	603	QSR	C17-C18-C19-C20
4	A	604	QSR	O2-C15-C28-O5
4	A	603	QSR	C28-C15-C16-O3
4	B	603	QSR	O2-C15-C16-O3
5	A	605	LMT	O5'-C1'-O1'-C1
4	B	603	QSR	C52-C53-C54-C55
5	B	604	LMT	C9-C10-C11-C12
4	B	603	QSR	C10-C11-C12-C13
4	B	602	QSR	C11-C12-C13-C14
4	A	604	QSR	C16-C15-C28-O5
4	B	602	QSR	O4-C17-O3-C16
4	B	602	QSR	C31-O10-P2-O13
4	A	603	QSR	C31-O10-P2-O13
4	B	602	QSR	C47-C48-C49-C50
4	B	602	QSR	C18-C17-O3-C16
4	B	602	QSR	C52-C53-C54-C55

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Mol	Chain	Res	Type	Atoms
4	A	603	QSR	C47-C48-C49-C50
4	A	603	QSR	C16-C15-C28-O5
4	A	604	QSR	C11-C10-C9-C8
4	B	603	QSR	C32-C33-O16-C46
4	B	603	QSR	O14-C35-C36-C37
4	B	602	QSR	O14-C35-C36-C37
4	B	603	QSR	O4-C17-C18-C19
4	A	603	QSR	C18-C19-C20-C21
4	A	603	QSR	O16-C46-C47-C48
4	B	602	QSR	C67-C68-C69-C70
4	B	602	QSR	O15-C35-C36-C37
4	B	602	QSR	O16-C46-C47-C48
4	B	603	QSR	C02-C01-C44-C43
4	B	602	QSR	C12-C13-C14-O2
5	A	605	LMT	C3'-C4'-O1B-C1B
4	A	603	QSR	O17-C46-C47-C48
4	B	602	QSR	C10-C11-C12-C13
4	A	603	QSR	C29-C30-C31-O10
4	B	602	QSR	O17-C46-C47-C48
4	A	603	QSR	C49-C50-C51-C52
4	A	603	QSR	O3-C17-C18-C19
4	B	603	QSR	C12-C13-C14-O2
4	A	603	QSR	O4-C17-C18-C19

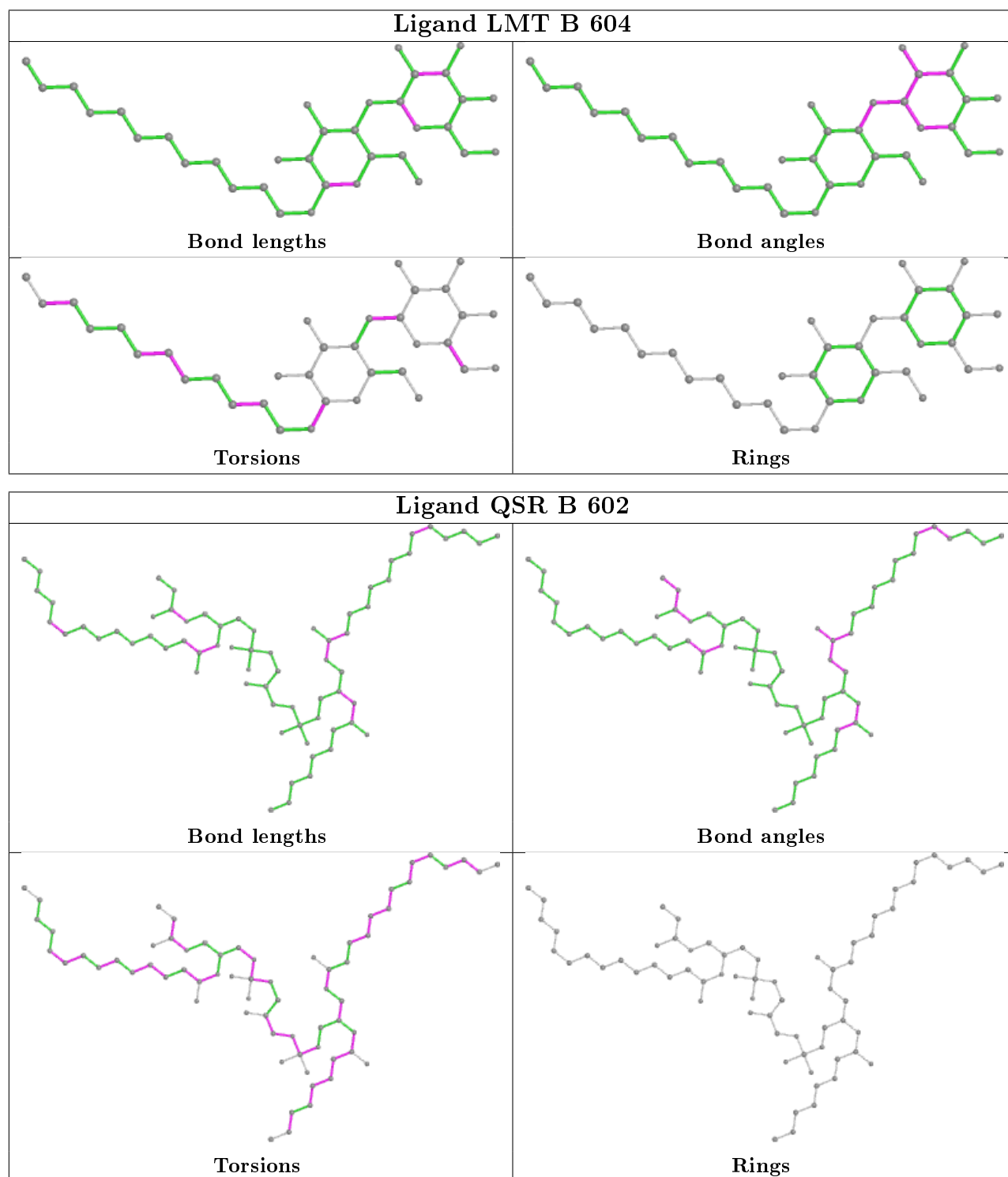
There are no ring outliers.

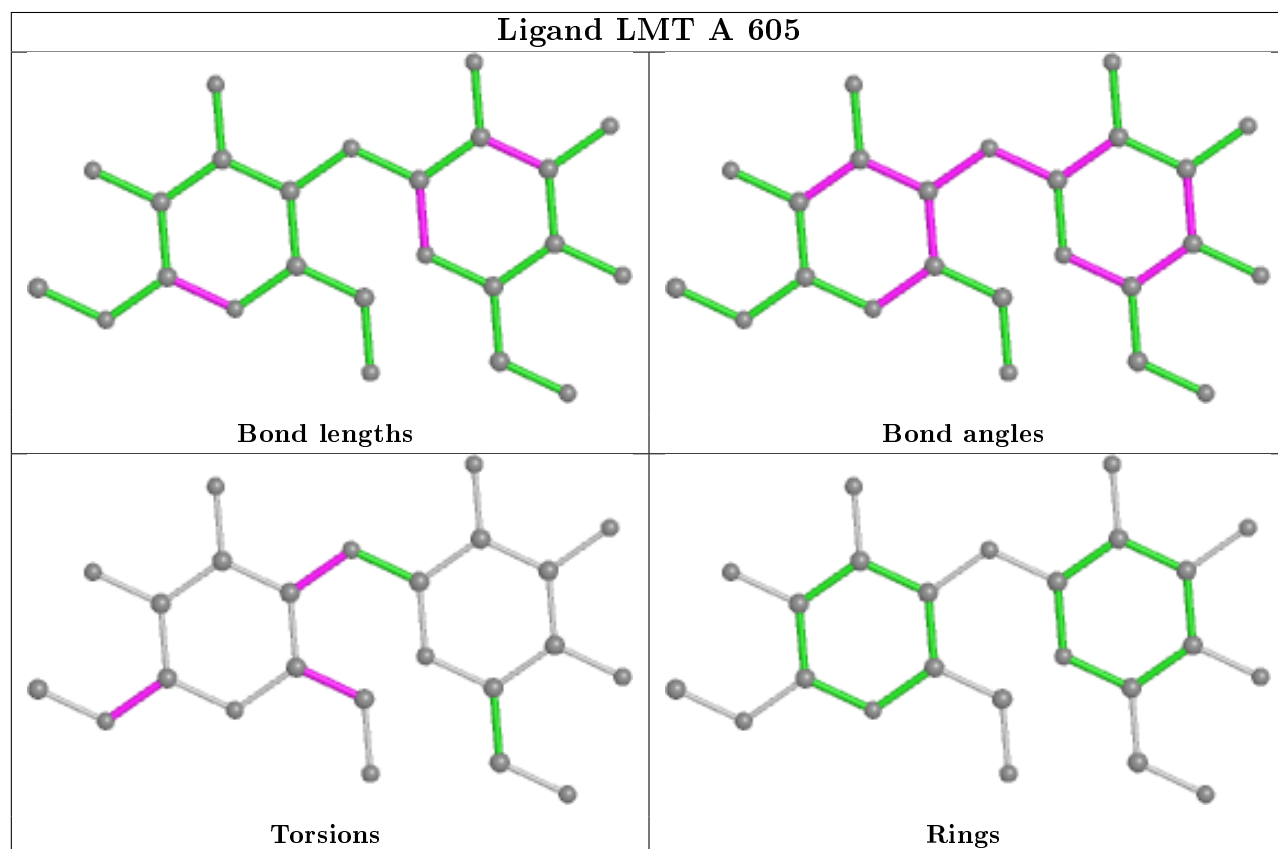
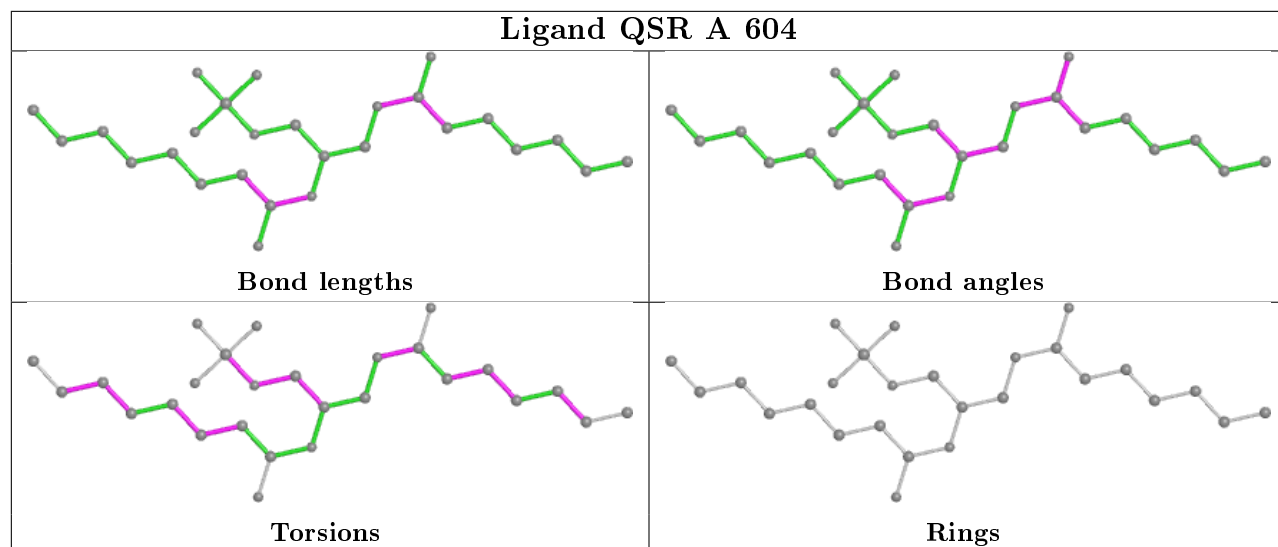
7 monomers are involved in 21 short contacts:

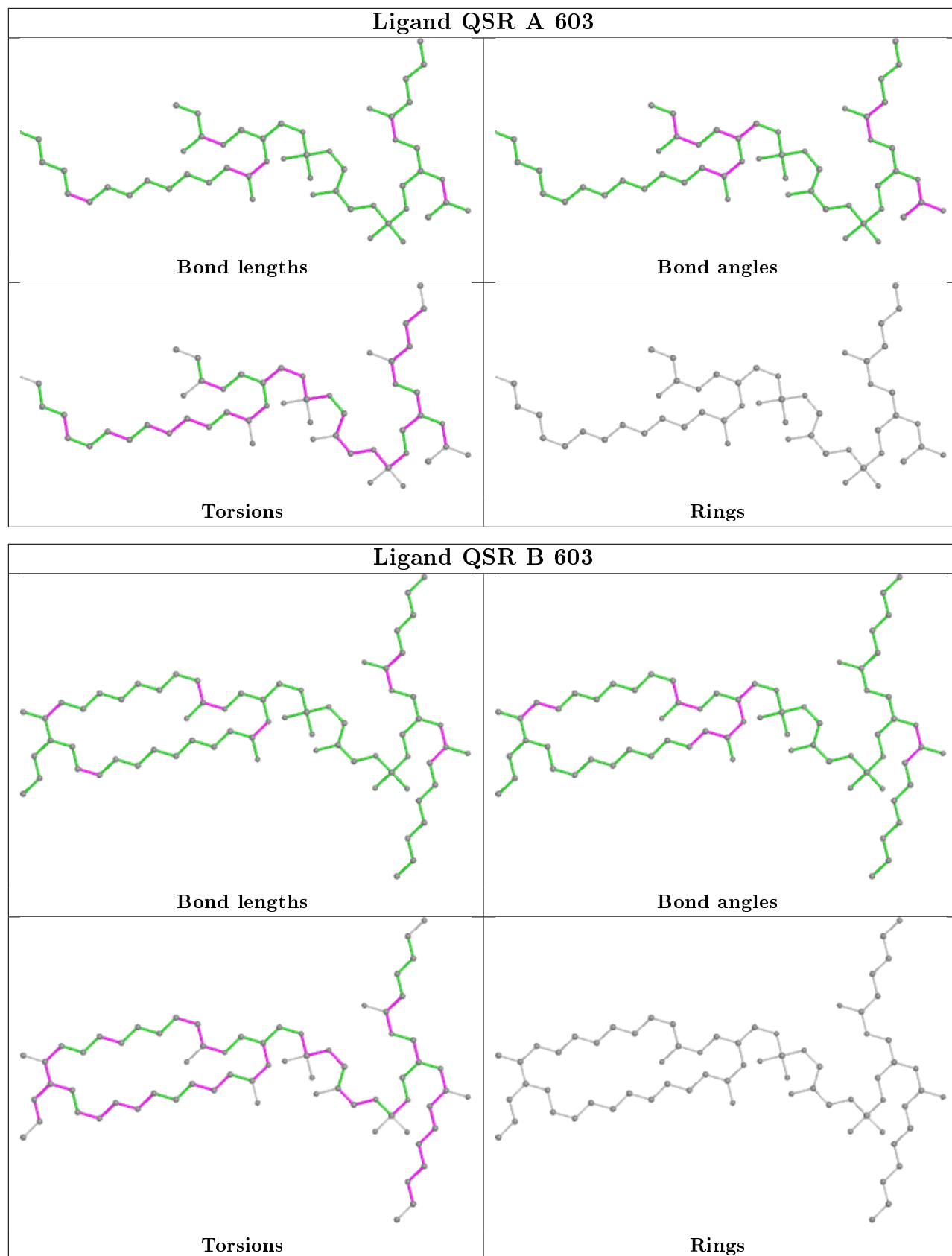
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	604	LMT	8	0
3	B	601	PO4	1	0
4	B	602	QSR	1	0
3	A	602	PO4	1	0
5	A	605	LMT	5	0
4	A	603	QSR	1	0
4	B	603	QSR	4	0

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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%)	0.11	25 (4%) 34 33	26, 62, 102, 124	0
1	B	565/592 (95%)	0.06	17 (3%) 50 51	28, 56, 84, 108	0
All	All	1134/1184 (95%)	0.08	42 (3%) 41 41	26, 57, 96, 124	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	586	ASN	8.1
1	A	80	VAL	6.6
1	A	387	ALA	6.1
1	A	113	LEU	5.6
1	B	404	ILE	4.7
1	A	16	VAL	4.7
1	B	122	LEU	4.0
1	A	14	GLN	4.0
1	A	122	LEU	4.0
1	B	411	ASN	3.9
1	B	151	LEU	3.9
1	B	585	ALA	3.8
1	A	568	PRO	3.7
1	B	7	ARG	3.5
1	B	234	VAL	3.4
1	A	31	THR	3.3
1	A	209	SER	3.3
1	B	487	VAL	3.3
1	A	203	ARG	3.2
1	A	240	GLU	3.2
1	A	550	ASN	3.1
1	B	8	TYR	3.1
1	B	135	TRP	3.0
1	B	245	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	564	LYS	2.8
1	A	37	TYR	2.7
1	A	200	THR	2.7
1	B	80	VAL	2.5
1	B	47	LEU	2.4
1	A	19	GLY	2.4
1	A	81	MET	2.4
1	A	193	ALA	2.4
1	B	111	PHE	2.4
1	A	35	SER	2.3
1	A	34	GLY	2.3
1	A	32	LEU	2.3
1	B	85	LEU	2.2
1	B	386	TYR	2.2
1	A	205	ASN	2.1
1	A	227	GLN	2.0
1	A	242	VAL	2.0
1	A	210	TYR	2.0

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 carbohydrates 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.

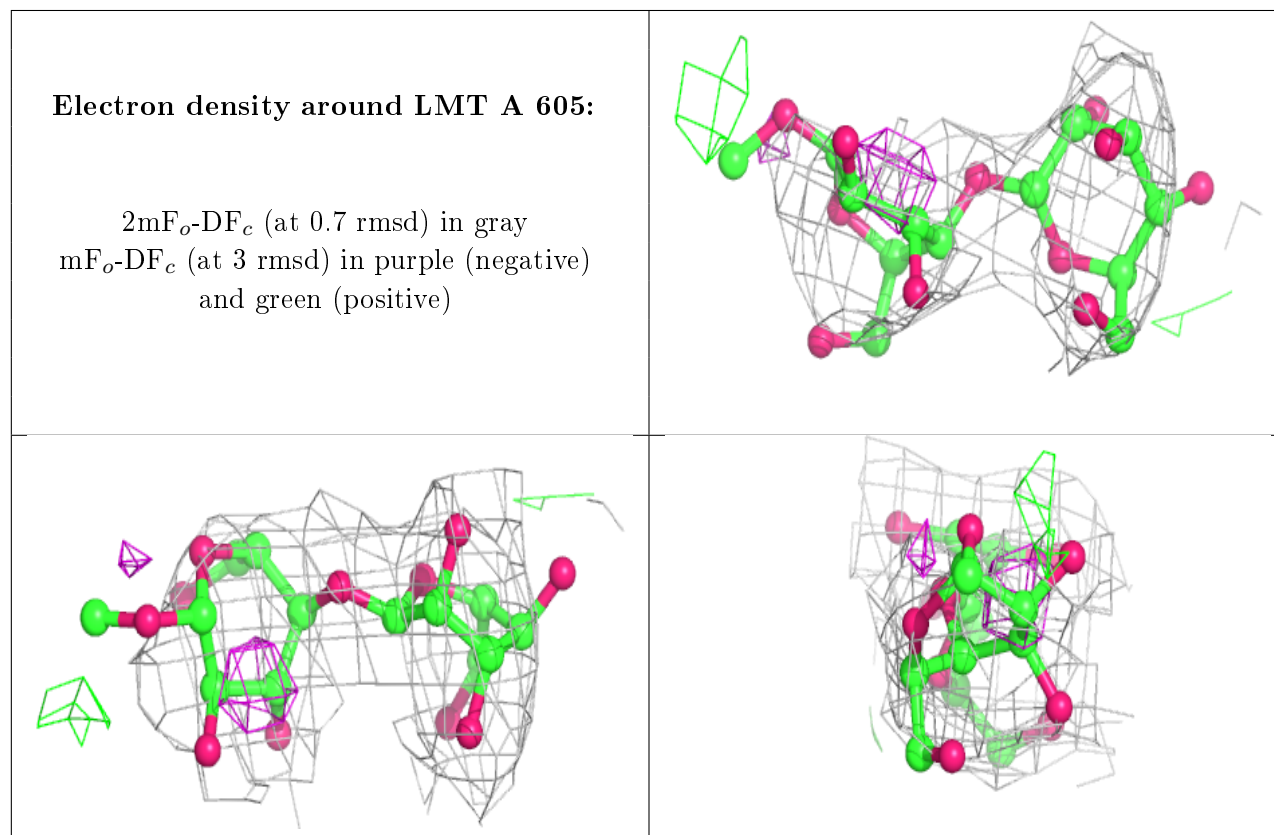
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	A	601	1/1	0.83	0.22	86,86,86,86	0
3	PO4	B	601	5/5	0.84	0.28	81,81,83,86	0
5	LMT	A	605	24/35	0.85	0.41	96,105,113,123	0
4	QSR	A	603	52/100	0.85	0.19	68,90,107,115	0
4	QSR	A	604	27/100	0.86	0.15	76,88,95,96	0

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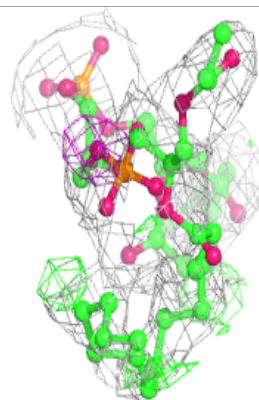
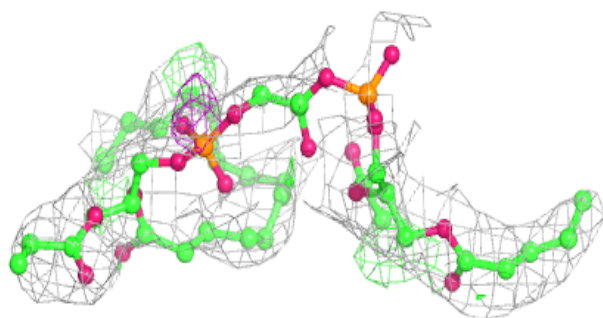
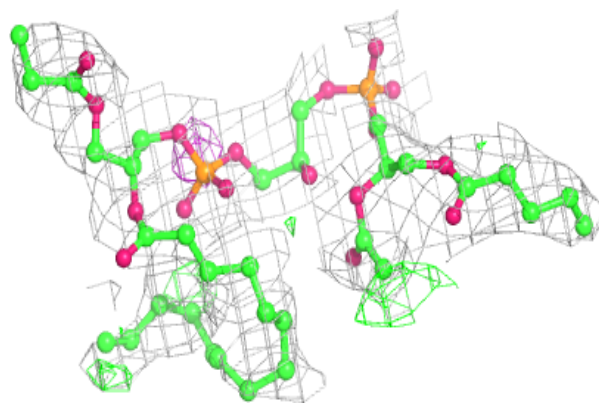
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	QSR	B	602	67/100	0.87	0.22	47,66,82,88	0
4	QSR	B	603	70/100	0.88	0.19	48,68,79,94	0
3	PO4	A	602	5/5	0.89	0.56	86,93,94,98	0
5	LMT	B	604	35/35	0.90	0.23	56,75,89,92	0

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.

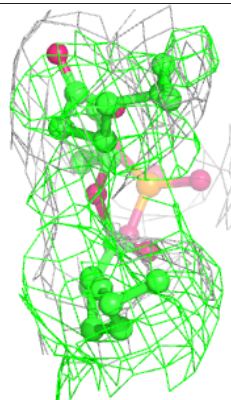
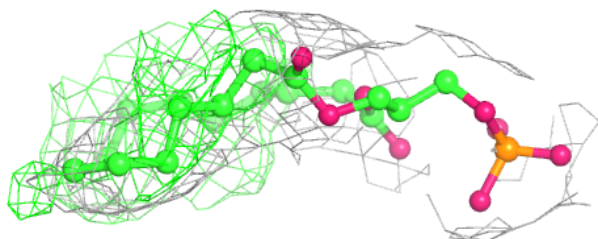
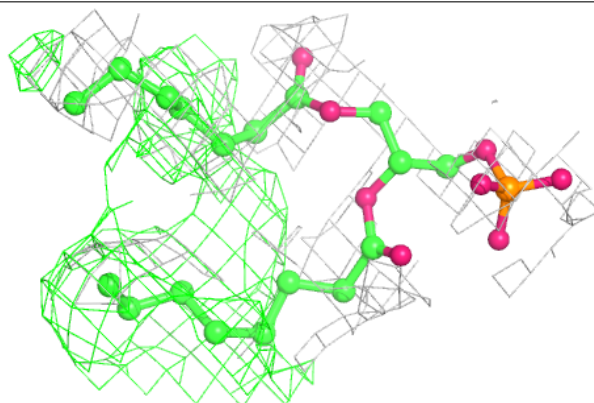


Electron density around QSR A 603:

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

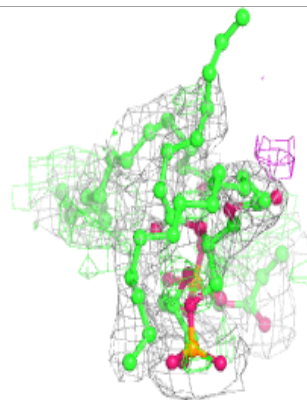
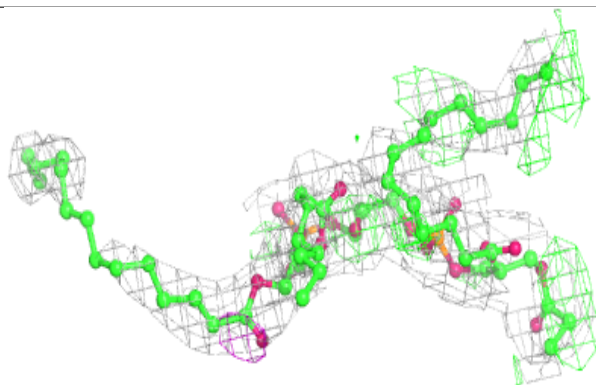
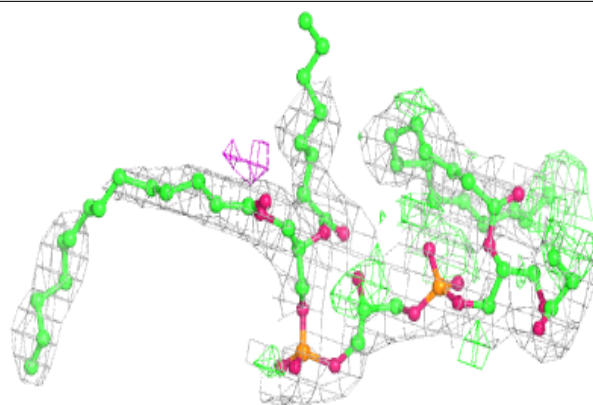
**Electron density around QSR A 604:**

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



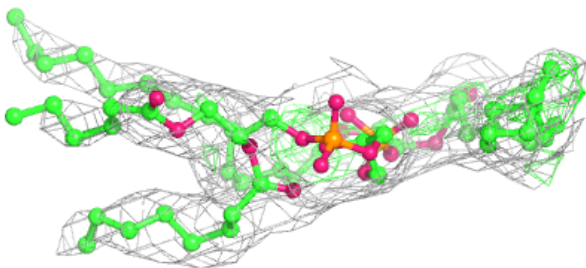
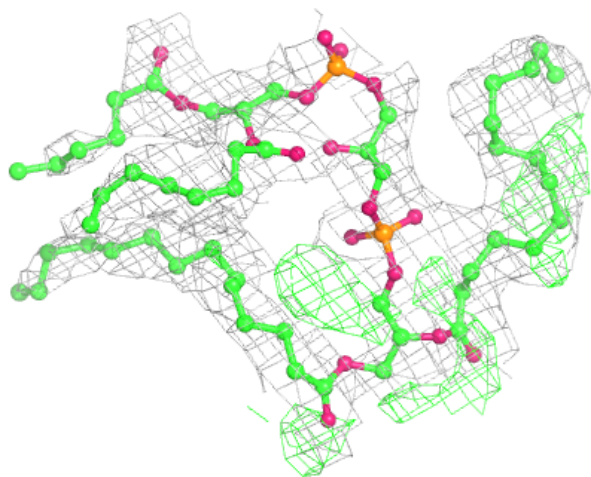
Electron density around QSR B 602:

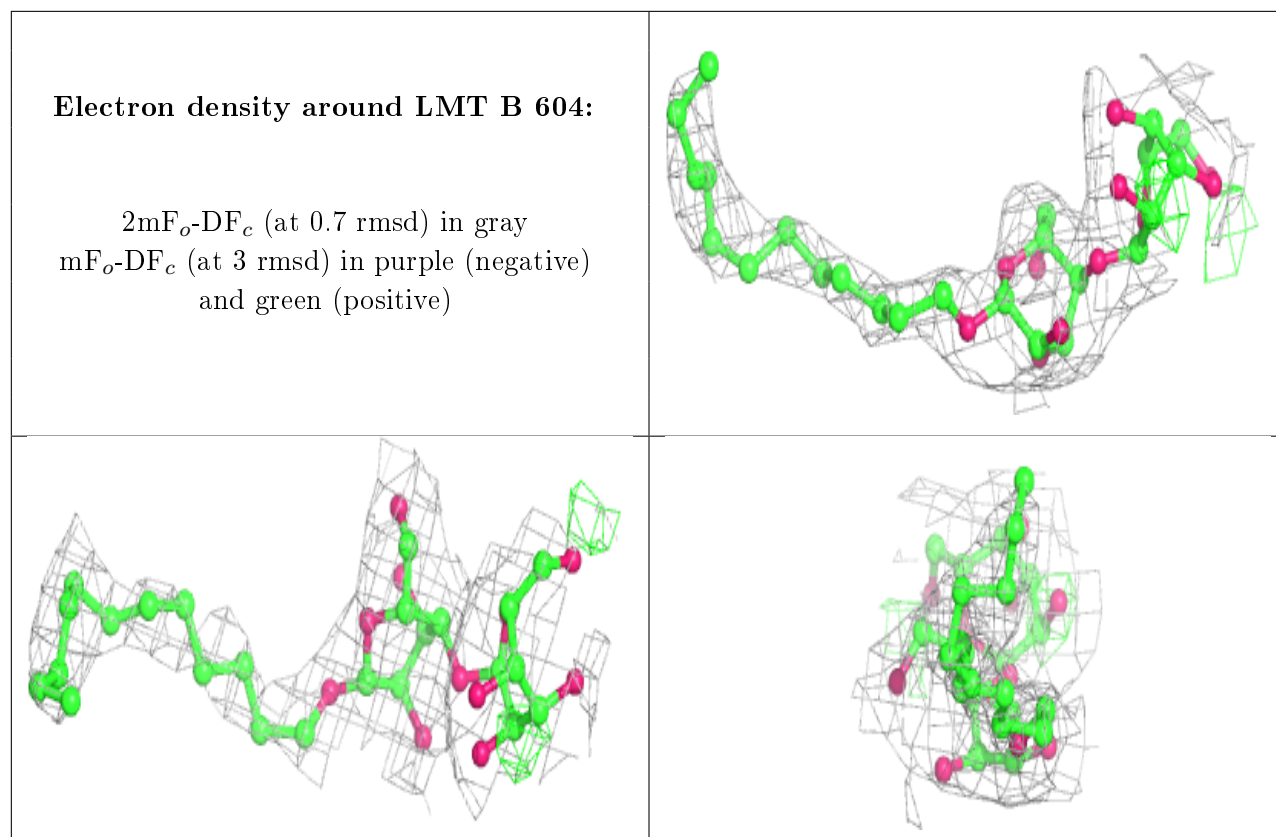
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.5 Other polymers [i](#)

There are no such residues in this entry.