



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:46 PM UTC

PDB ID : 6O3C / pdb_00006o3c
Title : Crystal structure of active Smoothened bound to SAG21k, cholesterol, and NbSmo8
Authors : Deshpande, I.S.; Liang, J.; Hedeem, D.; Roberts, K.J.; Zhang, Y.; Ha, B.; Latorraca, N.R.; Faust, B.; Dror, R.O.; Beachy, P.A.; Myers, B.R.; Manglik, A.
Deposited on : 2019-02-26
Resolution : 2.80 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 types of validation reports are described at

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

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)
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

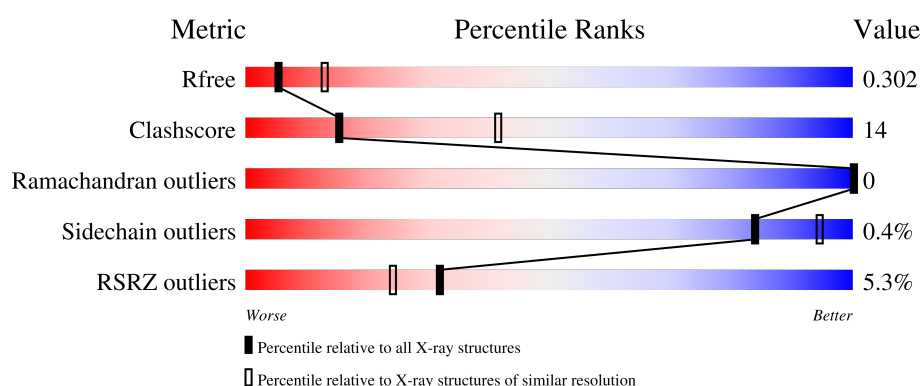
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	525	
2	B	128	

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
3	PO4	A	601	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 4902 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 Smoothened homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3728	2417	622	658	31			

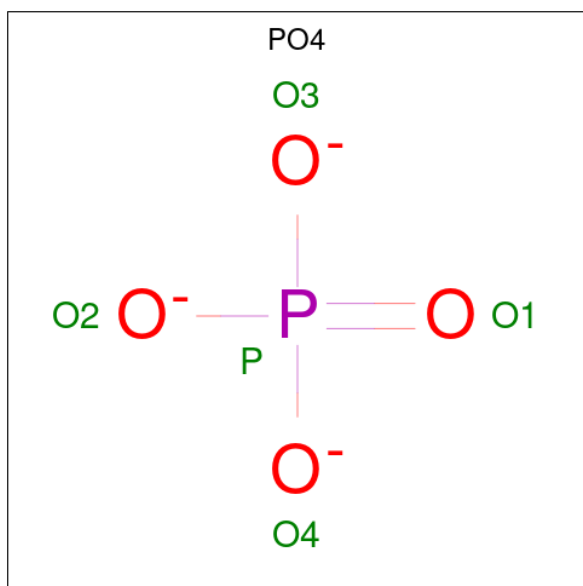
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ASP	-	expression tag	UNP P56726
A	43	TYR	-	expression tag	UNP P56726
A	44	LYS	-	expression tag	UNP P56726
A	45	ASP	-	expression tag	UNP P56726
A	46	ASP	-	expression tag	UNP P56726
A	47	ASP	-	expression tag	UNP P56726
A	48	ASP	-	expression tag	UNP P56726
A	49	ALA	-	expression tag	UNP P56726
A	50	GLY	-	expression tag	UNP P56726
A	51	SER	-	expression tag	UNP P56726
A	52	GLU	-	expression tag	UNP P56726
A	53	ASN	-	expression tag	UNP P56726
A	54	LEU	-	expression tag	UNP P56726
A	55	TYR	-	expression tag	UNP P56726
A	56	PHE	-	expression tag	UNP P56726
A	57	GLN	-	expression tag	UNP P56726
A	58	GLY	-	expression tag	UNP P56726
A	59	SER	-	expression tag	UNP P56726
A	60	GLY	-	expression tag	UNP P56726
A	61	SER	-	expression tag	UNP P56726
A	62	PRO	-	expression tag	UNP P56726
A	63	ARG	-	expression tag	UNP P56726

- Molecule 2 is a protein called NbSmo8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	122	Total	C	N	O	S	0	0	0
			920	585	155	176	4			

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

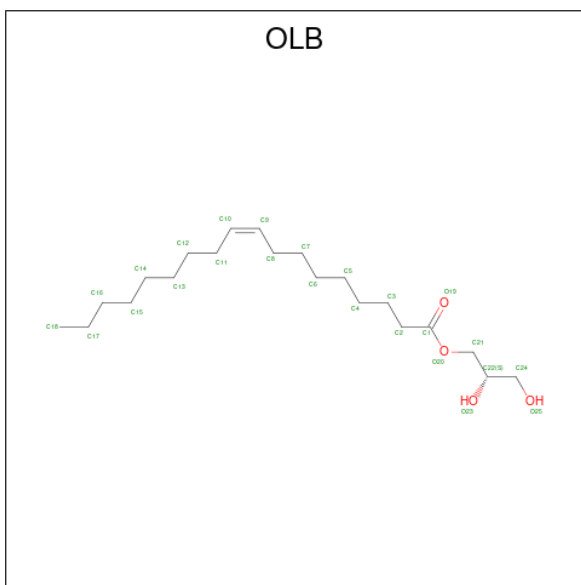


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is (2S)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLB) (formula: $C_{21}H_{40}O_4$).



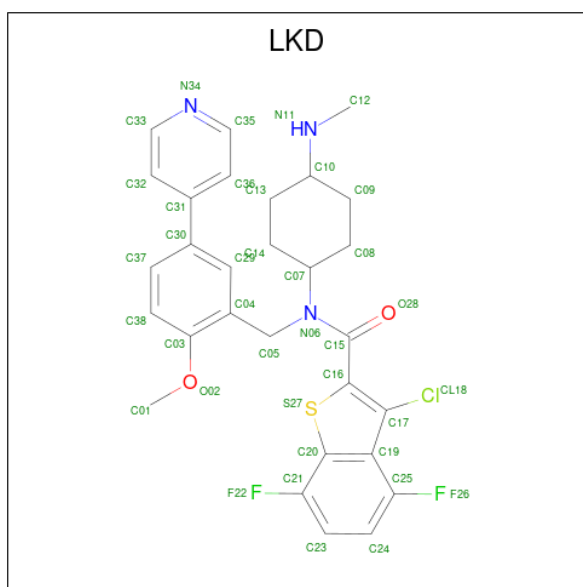
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 18	C 14	O 4	0	0
5	A	1	Total 19	C 15	O 4	0	0
5	A	1	Total 25	C 21	O 4	0	0
5	A	1	Total 19	C 15	O 4	0	0
5	A	1	Total 17	C 13	O 4	0	0
5	A	1	Total 25	C 21	O 4	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$).



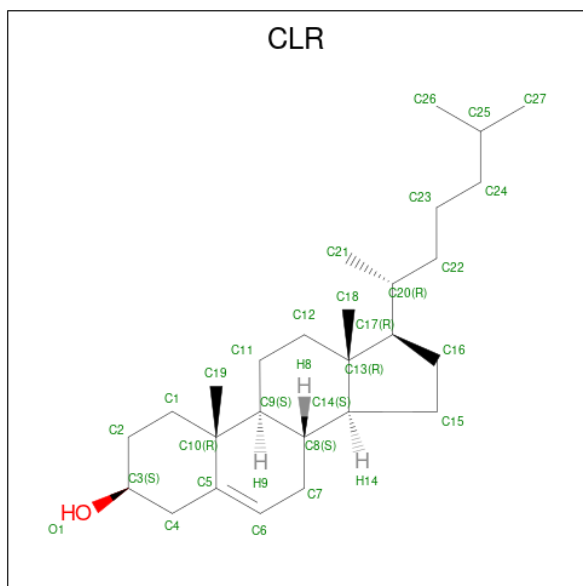
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is 3-chloro-4,7-difluoro-N-{[2-methoxy-5-(pyridin-4-yl)phenyl]methyl}-N-[trans-4-(methylamino)cyclohexyl]-1-benzothiophene-2-carboxamide (CCD ID: LKD) (formula: $C_{29}H_{28}ClF_2N_3O_2S$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
7	A	1	Total	C	Cl	F	N	O	S	0	0
			38	29	1	2	3	2	1		

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			28	27	1		
8	A	1	Total	C	O	0	0
			28	27	1		

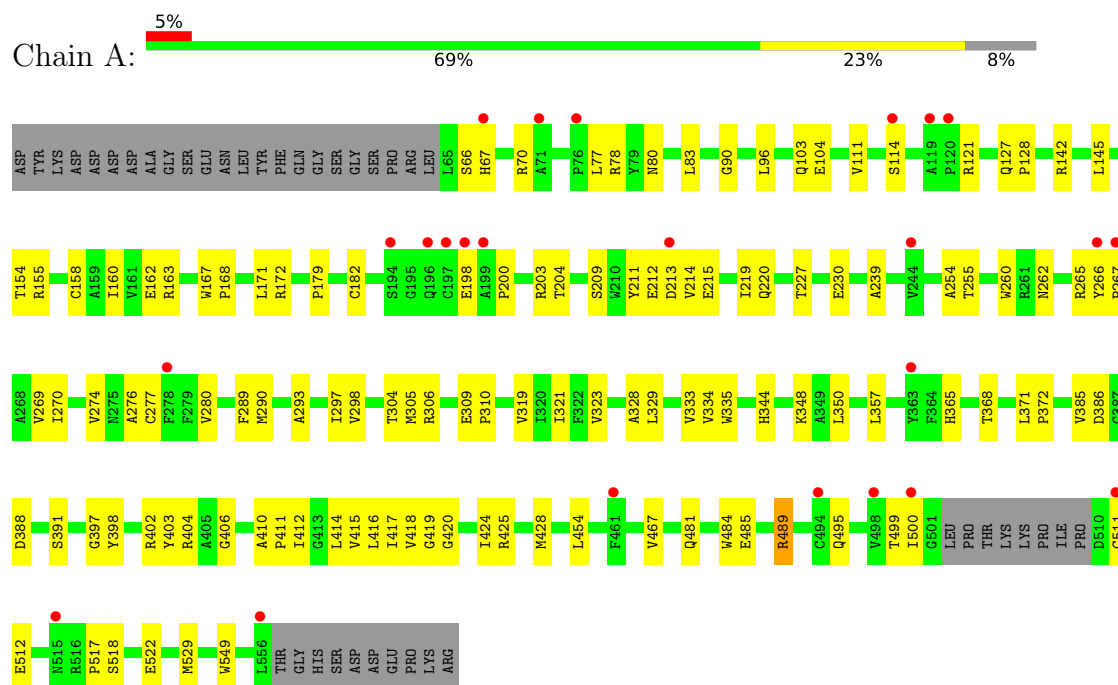
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	3	Total	O	0	0
			3	3		

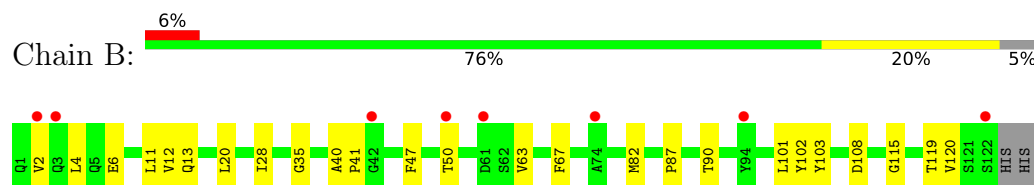
3 Residue-property plots [i](#)

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

• Molecule 1: Smoothened homolog



• Molecule 2: NbSmø8



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	39.01Å 121.09Å 157.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.94 – 2.80 47.94 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.2 (47.94-2.80) 96.3 (47.94-2.80)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.81Å)	Xtriage
Refinement program	BUSTER, PHENIX 1.12 _2829	Depositor
R, R_{free}	0.245 , 0.294 0.257 , 0.302	Depositor DCC
R_{free} test set	926 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	81.4	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 35.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4902	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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: CLR, NAG, LKD, OLB, NA, PO4

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	0.28	0/3834	0.32	0/5234
2	B	0.07	0/943	0.21	0/1282
All	All	0.25	0/4777	0.31	0/6516

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

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	3728	0	3560	109	4
2	B	920	0	852	22	0
3	A	5	0	0	3	2
4	A	1	0	0	0	0
5	A	123	0	175	12	2
6	A	28	0	26	1	0
7	A	38	0	0	1	0
8	A	56	0	92	5	0
9	A	3	0	0	0	0
All	All	4902	0	4705	130	4

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 14.

All (130) 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:425:ARG:NH2	3:A:601:PO4:O4	1.78	1.14
1:A:266:TYR:HA	1:A:269:VAL:HG12	1.39	1.03
1:A:425:ARG:HH22	3:A:601:PO4:P	1.94	0.90
1:A:334:VAL:HG23	1:A:368:THR:HG23	1.53	0.90
1:A:66:SER:HB2	1:A:142:ARG:HH22	1.39	0.88
1:A:267:PRO:HG2	2:B:103:TYR:HB3	1.56	0.87
1:A:386:ASP:HB2	1:A:398:TYR:HB2	1.62	0.81
1:A:428:MET:HE1	5:A:604:OLB:H24	1.62	0.80
1:A:78:ARG:NH1	1:A:104:GLU:OE2	2.16	0.79
1:A:121:ARG:NH1	1:A:215:GLU:OE1	2.16	0.78
1:A:162:GLU:OE2	1:A:172:ARG:NH2	2.20	0.74
1:A:160:ILE:HD12	1:A:213:ASP:OD1	1.88	0.73
1:A:78:ARG:NH1	1:A:103:GLN:HB2	2.04	0.72
1:A:274:VAL:HG22	1:A:335:TRP:HB3	1.71	0.71
1:A:267:PRO:HB2	2:B:103:TYR:O	1.92	0.70
1:A:403:TYR:CE2	5:A:603:OLB:H21A	2.28	0.69
2:B:20:LEU:HD13	2:B:82:MET:HE2	1.76	0.67
1:A:499:THR:OG1	1:A:500:ILE:HD12	1.96	0.65
1:A:66:SER:CB	1:A:142:ARG:HH12	2.08	0.65
1:A:219:ILE:HD12	1:A:219:ILE:H	1.60	0.65
1:A:66:SER:HB2	1:A:142:ARG:NH2	2.11	0.65
1:A:163:ARG:NH1	1:A:213:ASP:OD2	2.31	0.64
2:B:47:PHE:HE1	2:B:50:THR:HG23	1.62	0.64
1:A:262:ASN:O	1:A:265:ARG:NH1	2.31	0.63
1:A:111:VAL:O	1:A:114:SER:OG	2.14	0.62
1:A:155:ARG:NH1	1:A:171:LEU:O	2.32	0.62
1:A:179:PRO:HG2	1:A:182:CYS:SG	2.39	0.62
1:A:200:PRO:HA	1:A:220:GLN:HE21	1.64	0.62
1:A:344:HIS:CE1	1:A:348:LYS:HE3	2.35	0.62
1:A:212:GLU:O	1:A:214:VAL:HG23	2.00	0.61
1:A:297:ILE:HD13	1:A:321:ILE:HG13	1.81	0.61
1:A:344:HIS:CE1	1:A:425:ARG:HG2	2.36	0.60
1:A:306:ARG:HD3	1:A:309:GLU:OE2	2.01	0.60
1:A:77:LEU:HD12	1:A:90:GLY:HA2	1.83	0.60
1:A:155:ARG:HH11	1:A:172:ARG:HA	1.65	0.60
1:A:276:ALA:HB1	5:A:608:OLB:H221	1.84	0.60
1:A:412:ILE:HD12	8:A:612:CLR:H222	1.83	0.60
1:A:267:PRO:HB2	2:B:103:TYR:C	2.27	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ALA:HB3	1:A:411:PRO:HD3	1.85	0.59
1:A:414:LEU:O	1:A:418:VAL:HG22	2.04	0.58
1:A:266:TYR:OH	5:A:607:OLB:H21	2.04	0.58
1:A:162:GLU:CD	1:A:172:ARG:HH22	2.12	0.57
1:A:96:LEU:HD21	1:A:145:LEU:HD22	1.87	0.57
2:B:63:VAL:HG13	2:B:67:PHE:CG	2.39	0.57
1:A:348:LYS:NZ	3:A:601:PO4:O3	2.36	0.57
1:A:481:GLN:O	1:A:485:GLU:HG3	2.04	0.57
1:A:211:TYR:HD1	1:A:219:ILE:HD11	1.71	0.56
1:A:511:CYS:O	1:A:512:GLU:HG3	2.05	0.56
1:A:420:GLY:HA3	5:A:604:OLB:H25	1.86	0.56
1:A:203:ARG:NH1	1:A:204:THR:O	2.39	0.55
2:B:40:ALA:HB1	2:B:41:PRO:HD2	1.88	0.55
1:A:254:ALA:HB1	1:A:549:TRP:HZ2	1.72	0.53
2:B:47:PHE:CE1	2:B:50:THR:HG23	2.44	0.53
1:A:155:ARG:NH2	1:A:167:TRP:CE2	2.77	0.53
1:A:155:ARG:NH2	1:A:167:TRP:CZ2	2.76	0.53
1:A:371:LEU:HB2	1:A:372:PRO:HD3	1.91	0.53
1:A:227:THR:OG1	1:A:230:GLU:HG3	2.09	0.52
1:A:277:CYS:HB3	1:A:328:ALA:O	2.09	0.52
1:A:266:TYR:OH	1:A:365:HIS:NE2	2.40	0.52
1:A:335:TRP:CD2	1:A:368:THR:HG21	2.45	0.52
1:A:500:ILE:HD12	1:A:500:ILE:H	1.74	0.51
1:A:323:VAL:HG12	5:A:608:OLB:H37	1.93	0.50
1:A:350:LEU:HD11	2:B:101:LEU:HD23	1.92	0.50
1:A:416:LEU:HD22	1:A:467:VAL:HG11	1.94	0.50
1:A:270:ILE:O	1:A:274:VAL:HG23	2.12	0.49
1:A:397:GLY:HA3	1:A:404:ARG:HG3	1.95	0.49
2:B:35:GLY:HA3	2:B:50:THR:HG22	1.93	0.49
1:A:66:SER:HB2	1:A:142:ARG:HH12	1.78	0.49
1:A:239:ALA:HB2	1:A:289:PHE:CE1	2.48	0.48
1:A:280:VAL:HG11	5:A:608:OLB:H31	1.94	0.48
1:A:406:GLY:HA3	5:A:603:OLB:H16	1.94	0.48
1:A:80:ASN:HD22	6:A:609:NAG:H61	1.77	0.48
1:A:310:PRO:HB3	1:A:319:VAL:HG11	1.95	0.48
1:A:335:TRP:CE2	1:A:368:THR:HG21	2.48	0.47
2:B:87:PRO:HA	2:B:120:VAL:HB	1.96	0.47
2:B:67:PHE:CE2	2:B:82:MET:HG2	2.49	0.47
1:A:154:THR:O	1:A:158:CYS:HB2	2.15	0.47
1:A:309:GLU:HB2	1:A:385:VAL:HB	1.96	0.47
1:A:298:VAL:O	1:A:306:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:LEU:HD13	1:A:127:GLN:HG2	1.97	0.46
1:A:485:GLU:HA	7:A:611:LKD:F22	2.05	0.46
8:A:612:CLR:H212	8:A:612:CLR:H121	1.98	0.46
1:A:162:GLU:OE1	1:A:167:TRP:HD1	1.99	0.46
1:A:410:ALA:HA	5:A:605:OLB:H16	1.96	0.46
1:A:198:GLU:HG3	1:A:495:GLN:HB3	1.97	0.46
1:A:270:ILE:HG23	1:A:335:TRP:CE3	2.51	0.46
1:A:260:TRP:CD1	5:A:608:OLB:H24	2.52	0.46
1:A:484:TRP:CZ2	1:A:517:PRO:HA	2.51	0.46
5:A:608:OLB:H33	5:A:608:OLB:H39	1.61	0.46
1:A:290:MET:HB2	1:A:293:ALA:HB2	1.98	0.45
1:A:424:ILE:O	1:A:428:MET:HG3	2.17	0.45
1:A:274:VAL:HG22	1:A:335:TRP:CB	2.43	0.45
2:B:6:GLU:OE1	2:B:115:GLY:N	2.50	0.45
1:A:481:GLN:HA	1:A:484:TRP:CE3	2.52	0.45
2:B:12:VAL:HG22	2:B:13:GLN:N	2.32	0.45
1:A:454:LEU:HD23	1:A:454:LEU:C	2.41	0.44
2:B:2:VAL:HG21	2:B:28:ILE:HG13	1.98	0.44
2:B:102:TYR:HA	2:B:108:ASP:HB2	1.99	0.44
1:A:219:ILE:HB	1:A:305:MET:HE2	1.99	0.44
1:A:388:ASP:HB3	1:A:391:SER:OG	2.18	0.44
2:B:11:LEU:HD23	2:B:12:VAL:N	2.33	0.44
8:A:613:CLR:H212	8:A:613:CLR:H121	1.99	0.44
1:A:209:SER:HB3	1:A:304:THR:HG21	2.00	0.44
2:B:63:VAL:HG13	2:B:67:PHE:HB2	2.00	0.44
2:B:12:VAL:HG22	2:B:13:GLN:H	1.83	0.43
1:A:214:VAL:O	1:A:214:VAL:HG12	2.19	0.43
1:A:267:PRO:HG3	1:A:357:LEU:HD12	2.00	0.43
1:A:104:GLU:OE2	1:A:104:GLU:N	2.52	0.43
1:A:266:TYR:O	1:A:270:ILE:HG13	2.19	0.43
1:A:127:GLN:HB2	1:A:128:PRO:HD3	2.00	0.43
1:A:335:TRP:CG	1:A:368:THR:HG21	2.54	0.43
1:A:155:ARG:N	1:A:155:ARG:HD2	2.33	0.42
1:A:333:VAL:CG1	1:A:415:VAL:HG21	2.49	0.42
1:A:255:THR:HG22	1:A:549:TRP:HE1	1.85	0.42
1:A:329:LEU:O	1:A:333:VAL:HG23	2.20	0.42
1:A:424:ILE:HD12	5:A:604:OLB:H17	2.01	0.42
1:A:333:VAL:HG11	1:A:412:ILE:HD13	2.02	0.42
1:A:418:VAL:HG23	1:A:419:GLY:N	2.34	0.41
2:B:11:LEU:HD23	2:B:11:LEU:C	2.45	0.41
2:B:90:THR:HG23	2:B:119:THR:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:518:SER:O	1:A:522:GLU:HG2	2.21	0.41
1:A:529:MET:HG3	8:A:612:CLR:H14	2.01	0.41
1:A:266:TYR:HA	1:A:269:VAL:CG1	2.29	0.41
1:A:160:ILE:HD13	8:A:613:CLR:C27	2.51	0.41
2:B:4:LEU:N	2:B:4:LEU:HD22	2.36	0.41
1:A:266:TYR:N	1:A:267:PRO:CD	2.84	0.40
1:A:213:ASP:CG	1:A:489:ARG:HH22	2.30	0.40
1:A:167:TRP:HA	1:A:168:PRO:HD3	1.94	0.40
1:A:70:ARG:HG2	1:A:145:LEU:HD11	2.03	0.40
1:A:397:GLY:O	1:A:404:ARG:HD3	2.21	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ARG:NH1	3:A:601:PO4:O2[4_555]	1.42	0.78
1:A:417:ILE:CD1	5:A:605:OLB:C10[4_555]	1.49	0.71
1:A:417:ILE:CD1	5:A:605:OLB:C11[4_555]	1.67	0.53
1:A:402:ARG:CZ	3:A:601:PO4:O2[4_555]	1.97	0.23

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	480/525 (91%)	459 (96%)	21 (4%)	0	100	100
2	B	120/128 (94%)	112 (93%)	8 (7%)	0	100	100
All	All	600/653 (92%)	571 (95%)	29 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	385/443 (87%)	383 (100%)	2 (0%)	81	93
2	B	89/102 (87%)	89 (100%)	0	100	100
All	All	474/545 (87%)	472 (100%)	2 (0%)	84	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	HIS
1	A	489	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	HIS
1	A	220	GLN
1	A	222	GLN
1	A	384	GLN
1	A	450	ASN
1	A	481	GLN
1	A	515	ASN
1	A	525	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	OLB	A	604	-	18,18,24	0.67	0	19,19,25	0.99	1 (5%)
3	PO4	A	601	-	4,4,4	1.56	0	6,6,6	0.61	0
6	NAG	A	610	1	14,14,15	0.26	0	17,19,21	0.53	0
5	OLB	A	607	-	16,16,24	0.71	0	17,17,25	1.02	1 (5%)
5	OLB	A	608	-	24,24,24	0.60	0	25,25,25	0.92	1 (4%)
5	OLB	A	603	-	17,17,24	0.70	0	18,18,25	1.05	1 (5%)
8	CLR	A	613	-	31,31,31	2.05	4 (12%)	48,48,48	1.63	10 (20%)
8	CLR	A	612	-	31,31,31	3.09	16 (51%)	48,48,48	2.08	15 (31%)
7	LKD	A	611	-	42,42,42	2.24	12 (28%)	54,60,60	1.82	11 (20%)
6	NAG	A	609	1	14,14,15	0.56	0	17,19,21	0.81	1 (5%)
5	OLB	A	606	-	18,18,24	0.68	0	19,19,25	1.00	1 (5%)
5	OLB	A	605	-	24,24,24	0.59	0	25,25,25	0.94	1 (4%)

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	OLB	A	604	-	-	6/18/18/24	-
6	NAG	A	610	1	-	4/6/23/26	0/1/1/1
5	OLB	A	607	-	-	9/16/16/24	-
5	OLB	A	608	-	-	16/24/24/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OLB	A	603	-	-	4/17/17/24	-
8	CLR	A	613	-	-	4/10/68/68	0/4/4/4
8	CLR	A	612	-	-	6/10/68/68	0/4/4/4
7	LKD	A	611	-	-	6/24/34/34	0/5/5/5
6	NAG	A	609	1	-	1/6/23/26	0/1/1/1
5	OLB	A	606	-	-	9/18/18/24	-
5	OLB	A	605	-	-	14/24/24/24	-

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	611	LKD	C15-N06	9.26	1.48	1.34
8	A	612	CLR	C10-C5	-8.29	1.37	1.52
8	A	612	CLR	C4-C5	-6.82	1.38	1.51
8	A	613	CLR	C10-C5	-5.99	1.41	1.52
8	A	613	CLR	C4-C5	-5.79	1.40	1.51
8	A	612	CLR	C7-C6	-5.76	1.38	1.50
8	A	613	CLR	C7-C6	-5.35	1.39	1.50
8	A	612	CLR	C10-C9	-4.75	1.48	1.56
7	A	611	LKD	C05-C04	4.47	1.59	1.51
8	A	612	CLR	C13-C14	-4.31	1.47	1.55
7	A	611	LKD	C15-C16	3.73	1.55	1.49
8	A	613	CLR	C6-C5	3.60	1.40	1.33
8	A	612	CLR	C13-C17	-3.52	1.48	1.55
8	A	612	CLR	C7-C8	-3.50	1.47	1.53
7	A	611	LKD	C17-C16	3.30	1.43	1.36
8	A	612	CLR	C12-C13	-3.29	1.48	1.54
7	A	611	LKD	C16-S27	-3.26	1.68	1.74
8	A	612	CLR	C8-C9	-3.22	1.47	1.53
7	A	611	LKD	C20-S27	-3.15	1.68	1.74
7	A	611	LKD	C31-C30	3.12	1.56	1.49
8	A	612	CLR	C11-C9	-2.80	1.49	1.53
7	A	611	LKD	C05-N06	2.80	1.51	1.46
8	A	612	CLR	C15-C14	-2.78	1.48	1.54
8	A	612	CLR	C8-C14	-2.67	1.48	1.53
7	A	611	LKD	O02-C03	2.66	1.41	1.37
8	A	612	CLR	C6-C5	2.45	1.38	1.33
8	A	612	CLR	C4-C3	-2.41	1.47	1.52
8	A	612	CLR	C19-C10	-2.29	1.50	1.54
7	A	611	LKD	C17-CL18	2.24	1.79	1.74
8	A	612	CLR	C1-C10	-2.12	1.50	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	611	LKD	C19-C17	2.11	1.50	1.44
7	A	611	LKD	O28-C15	-2.02	1.18	1.23

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	611	LKD	C20-S27-C16	6.49	99.04	90.42
8	A	612	CLR	C16-C17-C13	-4.34	98.74	103.84
8	A	612	CLR	C15-C14-C8	-4.30	112.24	119.10
8	A	612	CLR	C4-C5-C10	4.28	121.91	116.42
7	A	611	LKD	C12-N11-C10	-4.22	109.52	114.33
8	A	612	CLR	C13-C17-C20	-4.02	113.29	119.50
8	A	613	CLR	C15-C14-C8	-3.90	112.87	119.10
8	A	612	CLR	C15-C14-C13	-3.84	99.33	103.84
7	A	611	LKD	C23-C21-C20	-3.77	119.85	122.87
8	A	612	CLR	C11-C9-C10	-3.77	108.43	113.08
8	A	612	CLR	C7-C8-C14	-3.65	105.76	110.93
8	A	613	CLR	C1-C2-C3	-3.54	105.80	110.48
8	A	613	CLR	C10-C9-C8	-3.25	107.96	112.71
8	A	613	CLR	C17-C13-C14	-3.19	96.44	100.10
8	A	612	CLR	C13-C14-C8	-3.18	109.90	114.41
8	A	612	CLR	C11-C9-C8	-3.17	107.36	111.78
8	A	612	CLR	C11-C12-C13	-3.14	107.45	112.74
6	A	609	NAG	C1-O5-C5	2.96	116.16	112.19
7	A	611	LKD	O02-C03-C04	2.95	120.35	115.96
8	A	613	CLR	C4-C5-C6	-2.91	116.62	120.57
8	A	613	CLR	C13-C14-C8	-2.86	110.35	114.41
7	A	611	LKD	C01-O02-C03	-2.84	113.35	117.51
7	A	611	LKD	C14-C07-N06	-2.82	107.91	111.83
7	A	611	LKD	O02-C03-C38	-2.81	119.57	124.30
8	A	612	CLR	C19-C10-C9	-2.80	108.52	111.66
8	A	613	CLR	C4-C5-C10	2.78	119.98	116.42
8	A	612	CLR	C14-C8-C9	-2.67	105.59	109.09
7	A	611	LKD	C20-C19-C17	2.65	115.10	110.57
7	A	611	LKD	F22-C21-C20	2.58	119.89	118.03
8	A	612	CLR	C21-C20-C17	-2.49	109.14	112.88
7	A	611	LKD	C19-C20-S27	-2.48	107.74	112.59
8	A	613	CLR	C18-C13-C14	2.48	116.18	111.68
5	A	603	OLB	C3-C2-C1	-2.46	104.68	113.69
5	A	605	OLB	C3-C2-C1	-2.44	104.75	113.69
5	A	608	OLB	C3-C2-C1	-2.43	104.81	113.69
8	A	612	CLR	C12-C11-C9	-2.42	109.02	113.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	604	OLB	C3-C2-C1	-2.41	104.85	113.69
5	A	606	OLB	C3-C2-C1	-2.41	104.88	113.69
8	A	612	CLR	C4-C5-C6	-2.25	117.52	120.57
5	A	607	OLB	C3-C2-C1	-2.25	105.46	113.69
8	A	613	CLR	C11-C12-C13	-2.24	108.96	112.74
7	A	611	LKD	C21-C20-S27	2.22	132.16	125.93
8	A	613	CLR	C13-C17-C20	-2.01	116.39	119.50

There are no chirality outliers.

All (79) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	603	OLB	C21-C22-C24-O25
5	A	603	OLB	O23-C22-C24-O25
5	A	606	OLB	C21-C22-C24-O25
5	A	608	OLB	O20-C21-C22-O23
5	A	608	OLB	O23-C22-C24-O25
8	A	612	CLR	C21-C20-C22-C23
5	A	608	OLB	C2-C1-O20-C21
8	A	612	CLR	C17-C20-C22-C23
5	A	608	OLB	O19-C1-O20-C21
6	A	610	NAG	O5-C5-C6-O6
5	A	604	OLB	C2-C1-O20-C21
5	A	606	OLB	C2-C1-O20-C21
5	A	604	OLB	O19-C1-O20-C21
8	A	612	CLR	C20-C22-C23-C24
5	A	606	OLB	O19-C1-O20-C21
5	A	605	OLB	O20-C21-C22-O23
5	A	603	OLB	C2-C1-O20-C21
5	A	605	OLB	O20-C21-C22-C24
5	A	608	OLB	O20-C21-C22-C24
8	A	612	CLR	C13-C17-C20-C21
6	A	610	NAG	C4-C5-C6-O6
5	A	607	OLB	C2-C1-O20-C21
5	A	607	OLB	C1-C2-C3-C4
5	A	607	OLB	O20-C21-C22-O23
5	A	607	OLB	C21-C22-C24-O25
5	A	608	OLB	C21-C22-C24-O25
8	A	613	CLR	C20-C22-C23-C24
5	A	606	OLB	C1-C2-C3-C4
5	A	606	OLB	O23-C22-C24-O25
5	A	607	OLB	O23-C22-C24-O25

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Mol	Chain	Res	Type	Atoms
5	A	605	OLB	C12-C13-C14-C15
5	A	603	OLB	O19-C1-O20-C21
8	A	612	CLR	C22-C23-C24-C25
5	A	607	OLB	O19-C1-O20-C21
7	A	611	LKD	C13-C10-N11-C12
5	A	608	OLB	C4-C5-C6-C7
5	A	608	OLB	C5-C6-C7-C8
5	A	605	OLB	C1-C2-C3-C4
5	A	605	OLB	C13-C14-C15-C16
5	A	608	OLB	C12-C13-C14-C15
5	A	604	OLB	C5-C6-C7-C8
8	A	612	CLR	C13-C17-C20-C22
6	A	609	NAG	O5-C5-C6-O6
5	A	607	OLB	C6-C7-C8-C9
5	A	608	OLB	C6-C7-C8-C9
5	A	608	OLB	C11-C12-C13-C14
5	A	607	OLB	O20-C21-C22-C24
5	A	605	OLB	C4-C5-C6-C7
5	A	605	OLB	C10-C11-C12-C13
5	A	608	OLB	C14-C15-C16-C17
5	A	606	OLB	C2-C3-C4-C5
5	A	605	OLB	C2-C3-C4-C5
5	A	606	OLB	C5-C6-C7-C8
7	A	611	LKD	O28-C15-C16-S27
5	A	604	OLB	C4-C5-C6-C7
5	A	605	OLB	C5-C6-C7-C8
5	A	605	OLB	C11-C12-C13-C14
5	A	605	OLB	C3-C4-C5-C6
7	A	611	LKD	N06-C15-C16-S27
5	A	605	OLB	C14-C15-C16-C17
5	A	605	OLB	C6-C7-C8-C9
5	A	608	OLB	C15-C16-C17-C18
6	A	610	NAG	C3-C2-N2-C7
7	A	611	LKD	C09-C10-N11-C12
5	A	604	OLB	C1-C2-C3-C4
8	A	613	CLR	C23-C24-C25-C27
8	A	613	CLR	C23-C24-C25-C26
5	A	608	OLB	C1-C2-C3-C4
6	A	610	NAG	C1-C2-N2-C7
7	A	611	LKD	O28-C15-C16-C17
5	A	608	OLB	C7-C8-C9-C10
5	A	608	OLB	C9-C10-C11-C12

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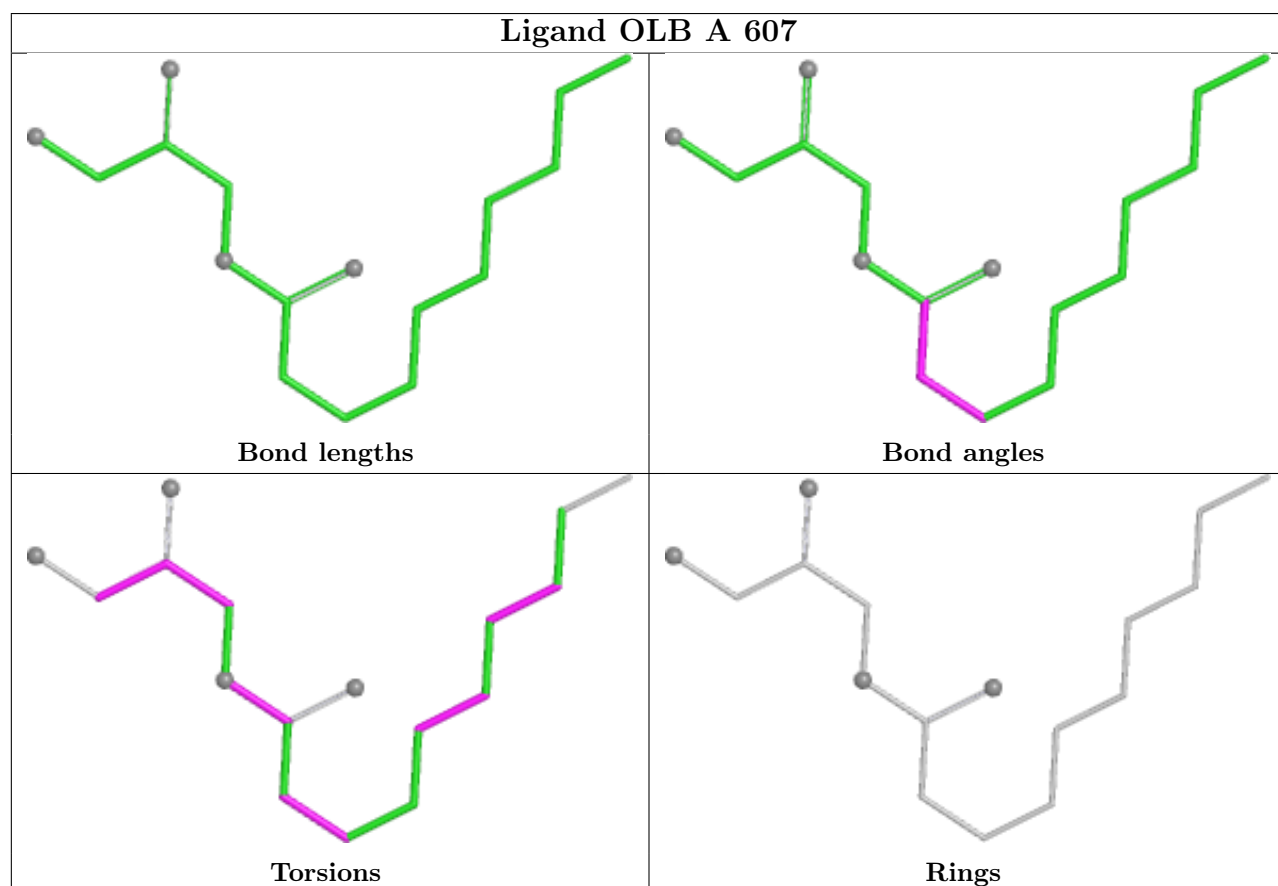
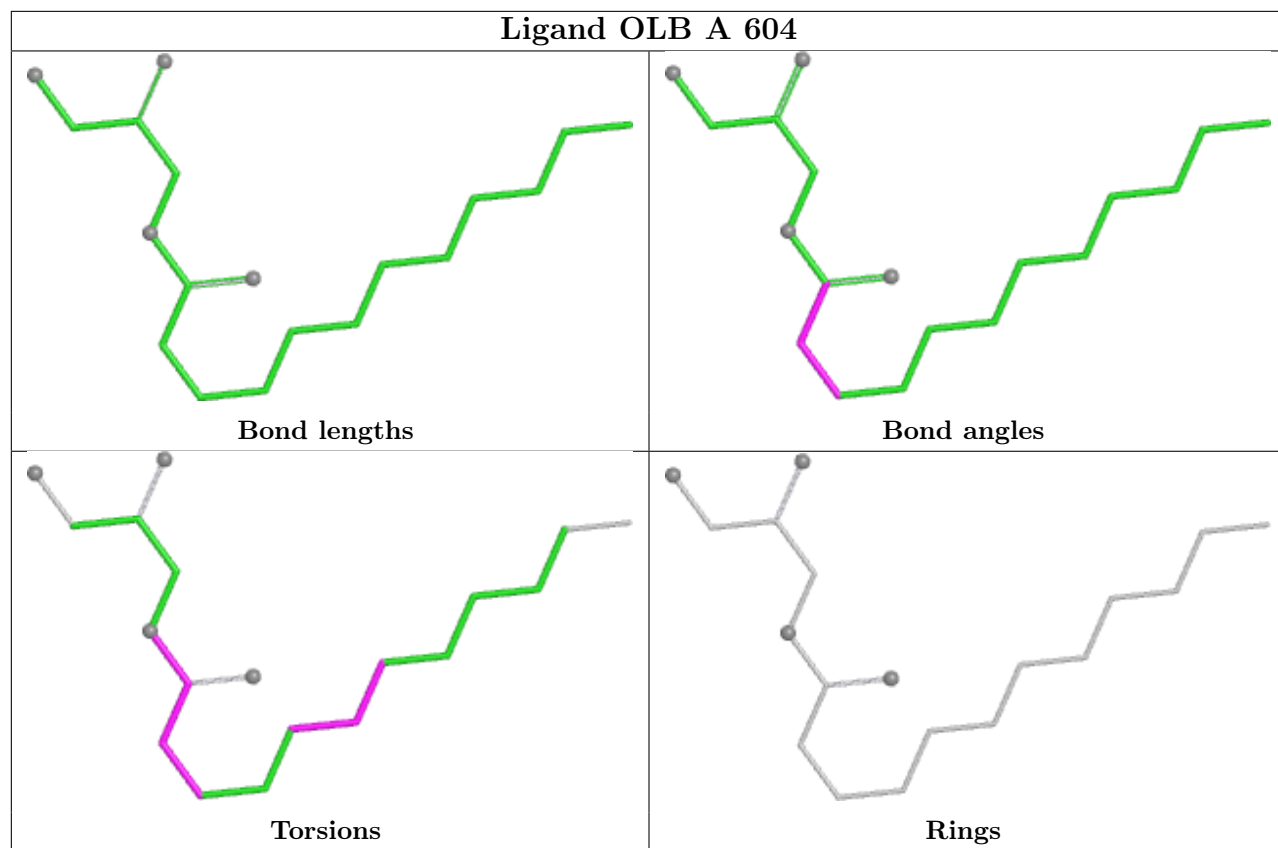
Mol	Chain	Res	Type	Atoms
5	A	607	OLB	C4-C5-C6-C7
5	A	606	OLB	C7-C8-C9-C10
7	A	611	LKD	C04-C05-N06-C15
5	A	606	OLB	C6-C7-C8-C9
5	A	604	OLB	O20-C1-C2-C3
5	A	605	OLB	C15-C16-C17-C18
8	A	613	CLR	C22-C23-C24-C25

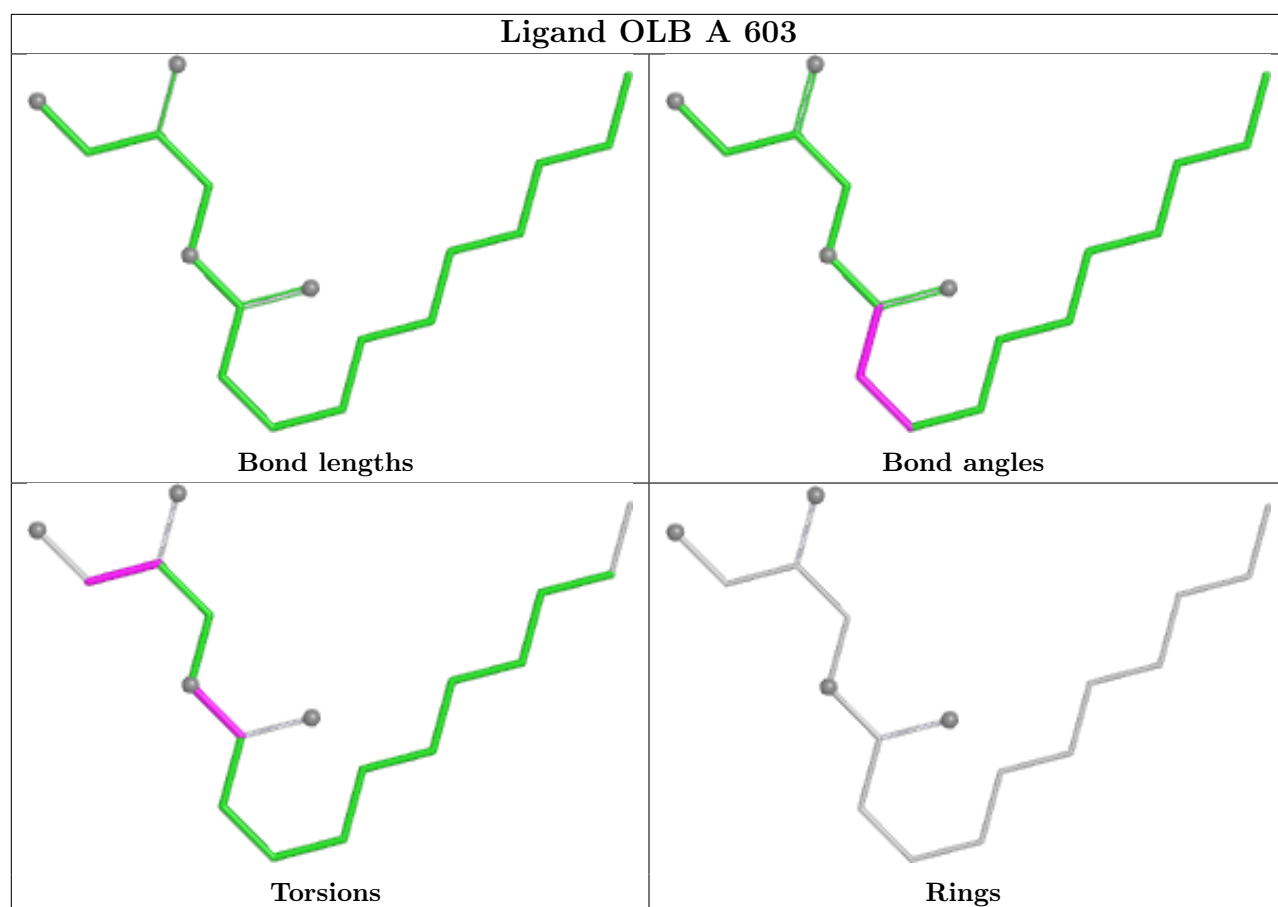
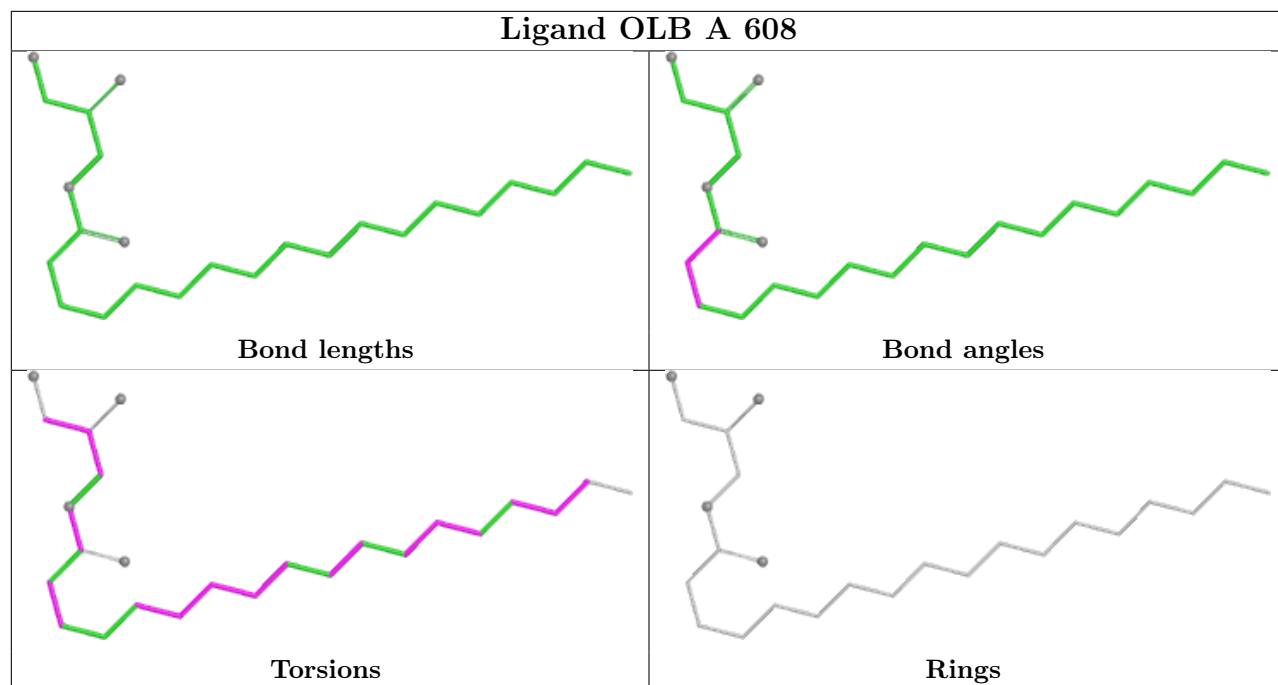
There are no ring outliers.

10 monomers are involved in 26 short contacts:

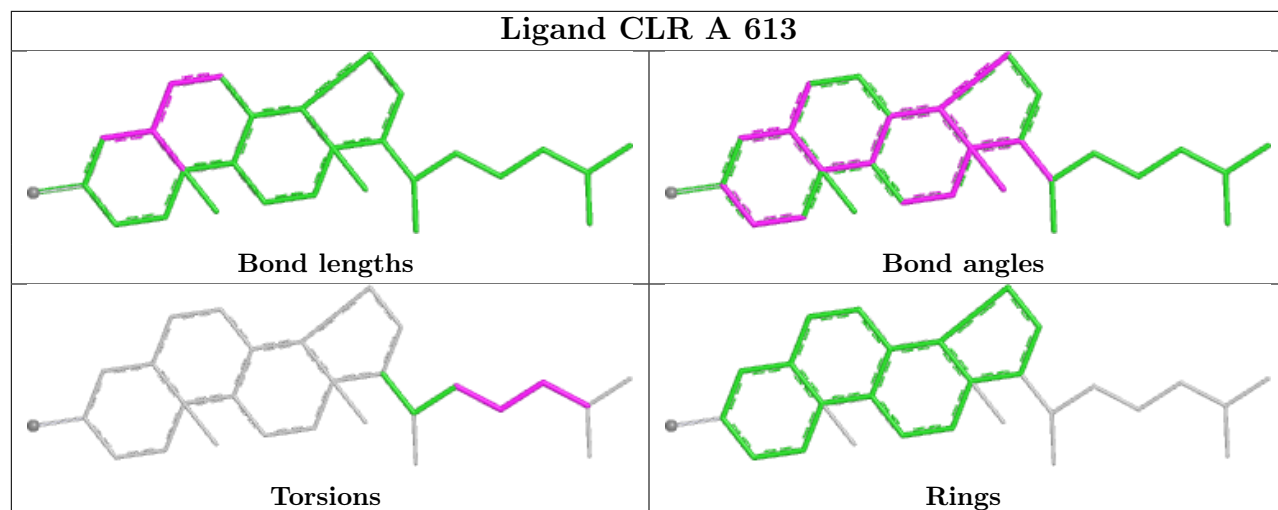
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	604	OLB	3	0
3	A	601	PO4	3	2
5	A	607	OLB	1	0
5	A	608	OLB	5	0
5	A	603	OLB	2	0
8	A	613	CLR	2	0
8	A	612	CLR	3	0
7	A	611	LKD	1	0
6	A	609	NAG	1	0
5	A	605	OLB	1	2

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

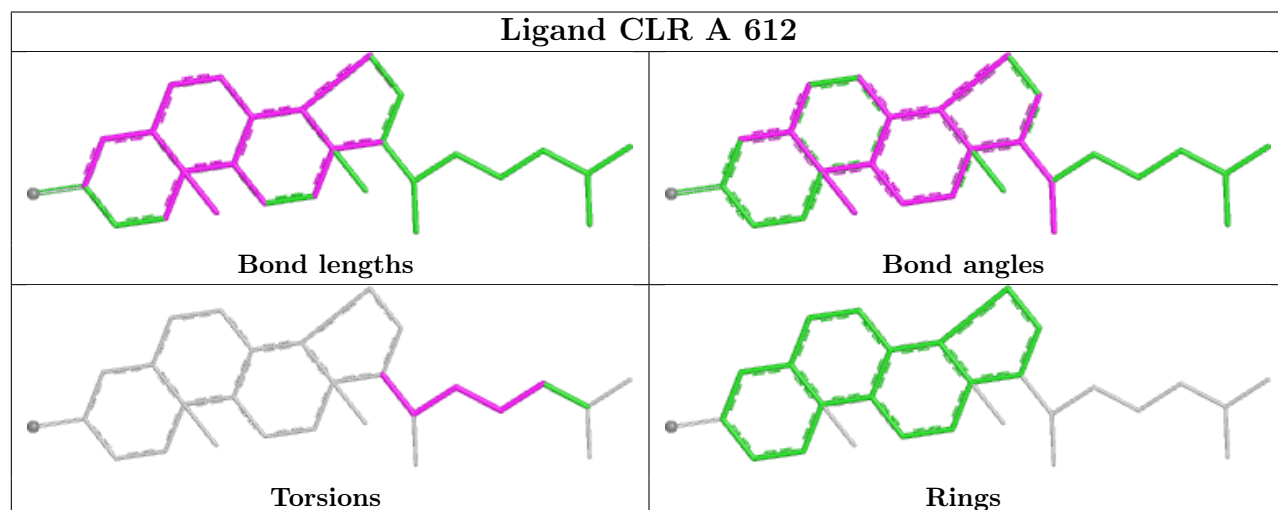


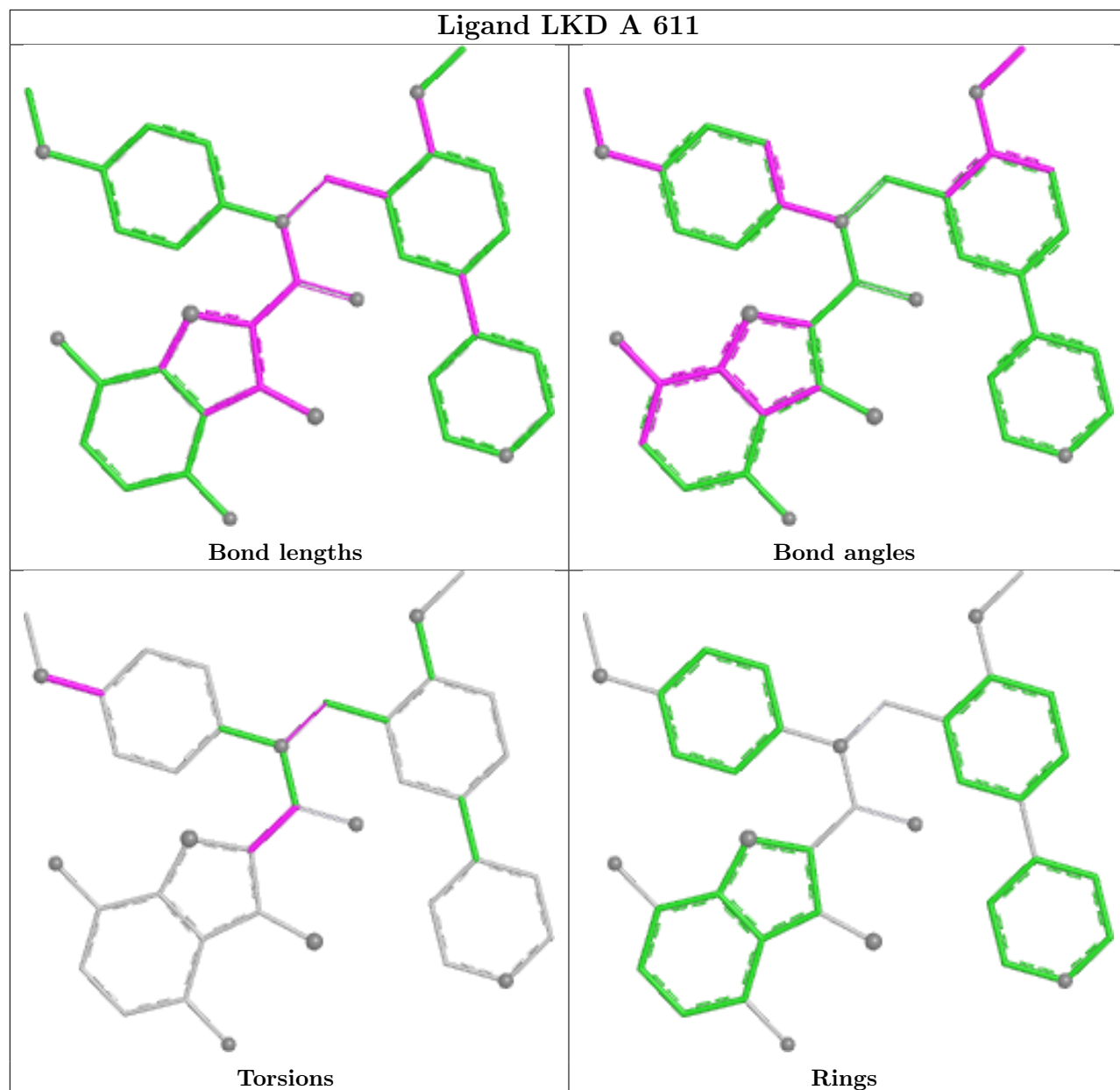


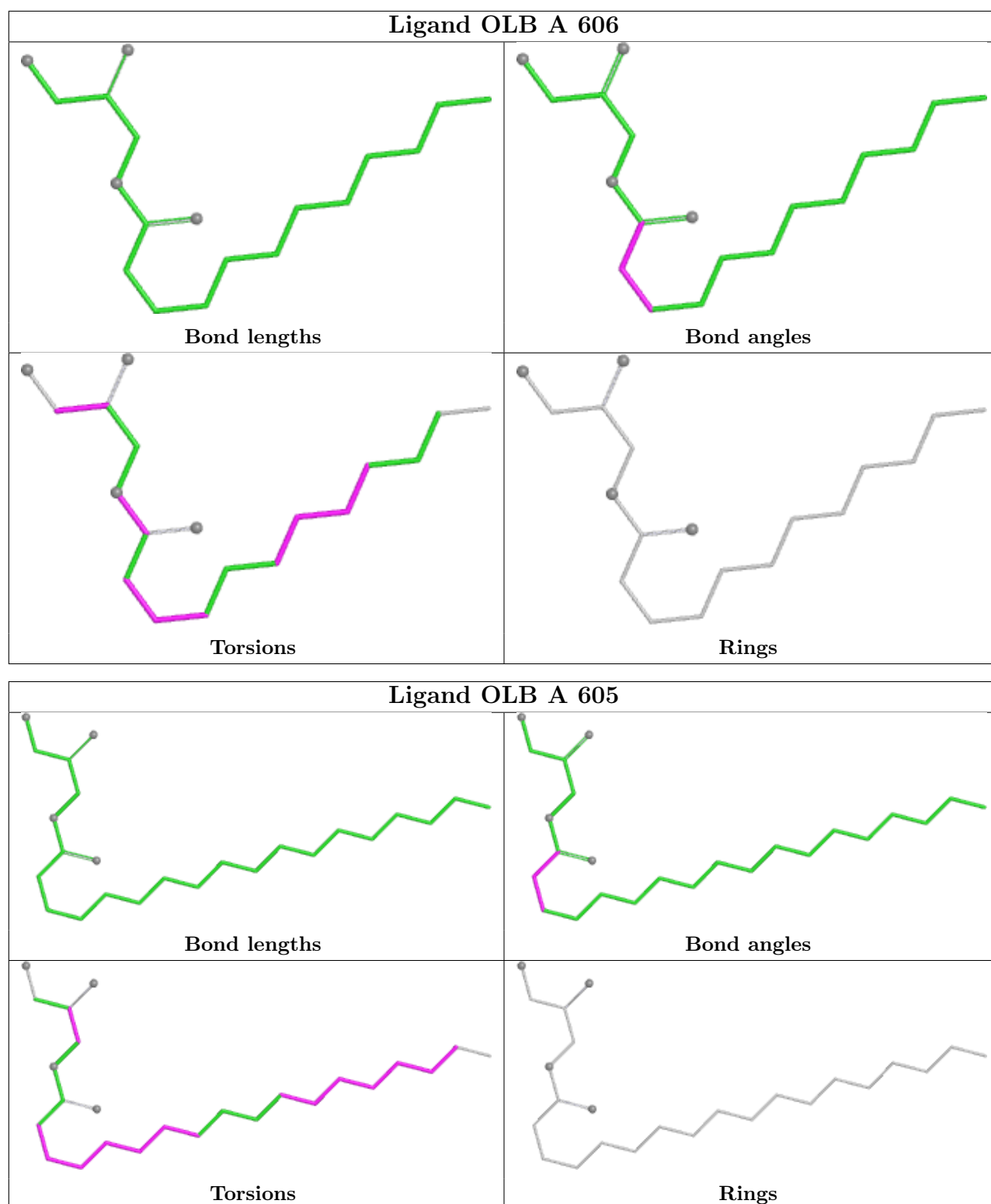
Ligand CLR A 613



Ligand CLR A 612







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	484/525 (92%)	0.40	24 (4%) 34 26	45, 68, 108, 142	0
2	B	122/128 (95%)	0.57	8 (6%) 24 18	49, 78, 115, 130	0
All	All	606/653 (92%)	0.43	32 (5%) 32 24	45, 71, 110, 142	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	CYS	4.1
1	A	196	GLN	3.8
1	A	266	TYR	3.6
1	A	244	VAL	3.5
1	A	120	PRO	3.4
1	A	278	PHE	3.3
1	A	199	ALA	3.2
1	A	194	SER	3.1
1	A	461	PHE	3.0
1	A	498	VAL	3.0
1	A	198	GLU	2.8
1	A	119	ALA	2.8
2	B	50	THR	2.8
1	A	515	ASN	2.7
1	A	76	PRO	2.6
1	A	114	SER	2.6
1	A	213	ASP	2.6
2	B	2	VAL	2.5
2	B	94	TYR	2.5
1	A	500	ILE	2.4
1	A	556	LEU	2.3
2	B	61	ASP	2.3
1	A	71	ALA	2.3
1	A	67	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	267	PRO	2.3
1	A	511	CYS	2.2
2	B	3	GLN	2.2
2	B	122	SER	2.1
2	B	42	GLY	2.1
2	B	74	ALA	2.1
1	A	363	TYR	2.1
1	A	494	CYS	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 oligosaccharides in this entry.

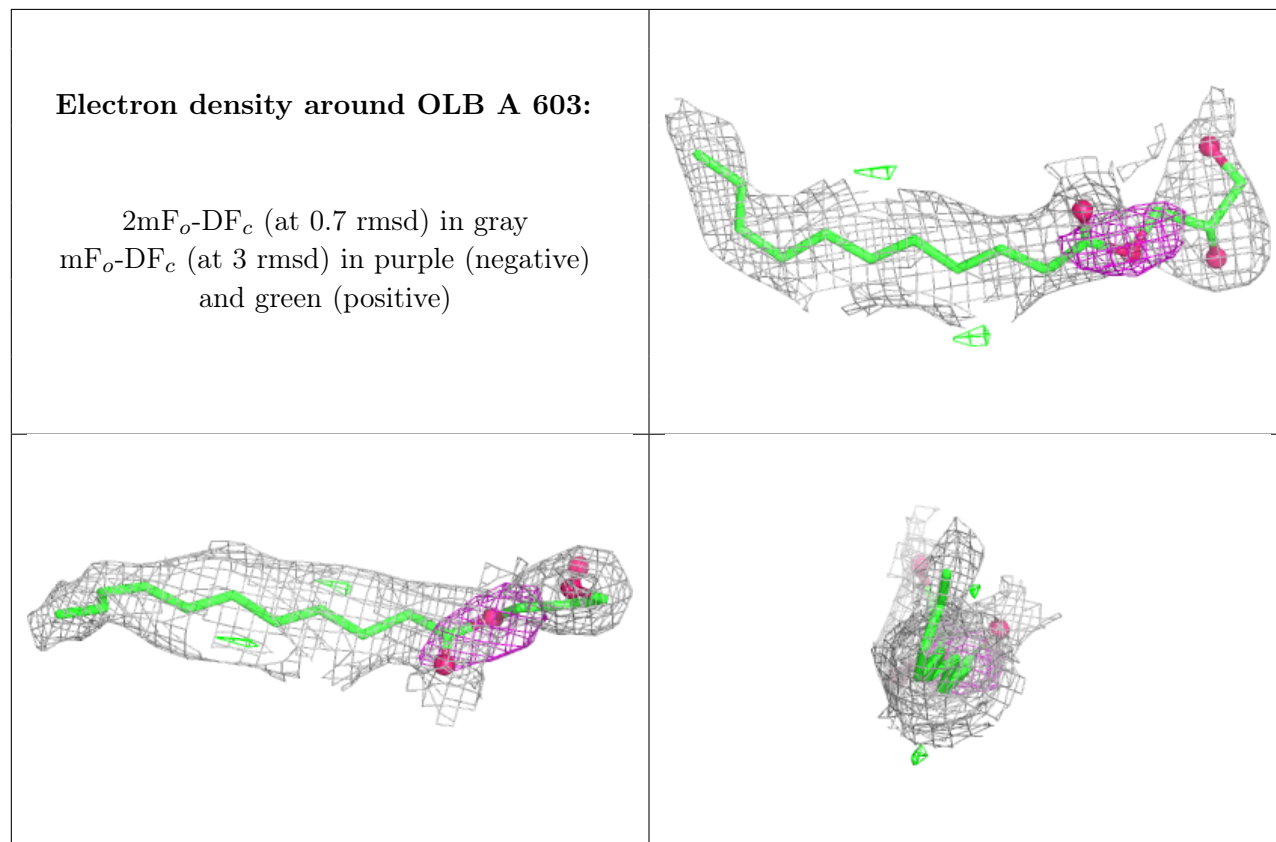
6.4 Ligands [i](#)

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(Å ²)	Q<0.9
6	NAG	A	609	14/15	0.24	0.15	121,137,142,143	0
5	OLB	A	603	18/25	0.49	0.18	51,64,72,73	0
6	NAG	A	610	14/15	0.67	0.16	124,143,150,153	0
5	OLB	A	606	19/25	0.68	0.15	54,62,71,72	0
5	OLB	A	604	19/25	0.71	0.14	51,61,76,89	0
5	OLB	A	608	25/25	0.76	0.15	53,68,79,84	0
5	OLB	A	607	17/25	0.80	0.13	56,70,82,94	0
5	OLB	A	605	25/25	0.82	0.12	44,55,65,77	0
4	NA	A	602	1/1	0.82	0.13	72,72,72,72	0
3	PO4	A	601	5/5	0.83	0.14	95,104,108,110	0
7	LKD	A	611	38/38	0.89	0.12	48,65,81,84	0
8	CLR	A	612	28/28	0.91	0.11	61,75,80,82	0
8	CLR	A	613	28/28	0.95	0.10	59,71,82,84	0

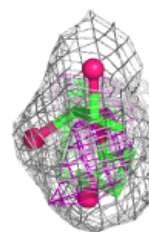
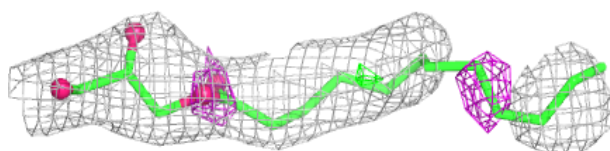
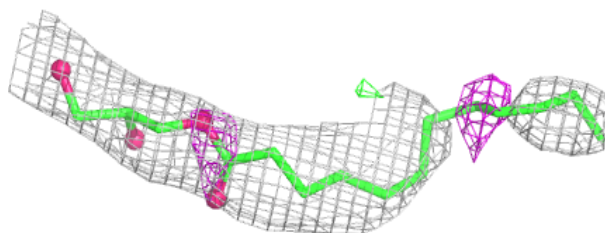
The following is a graphical depiction of the model fit to experimental electron density of all

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.

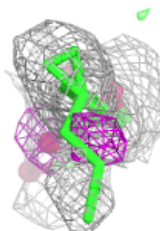
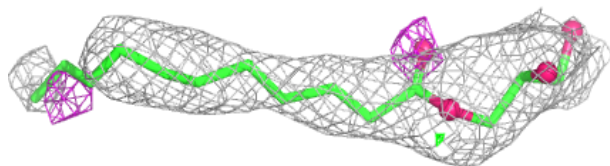
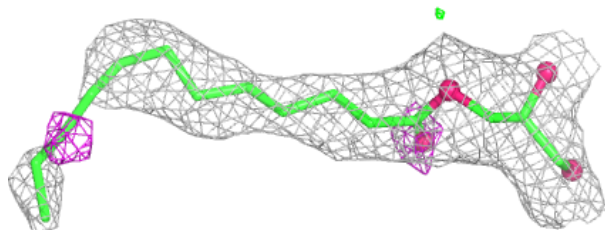


Electron density around OLB A 606:

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

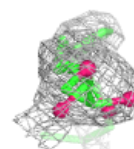
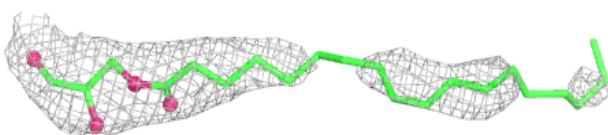
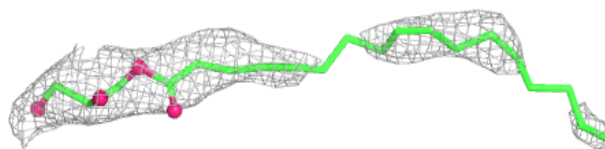
**Electron density around OLB A 604:**

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

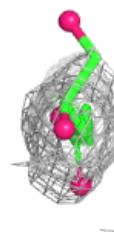
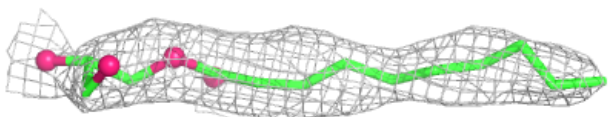
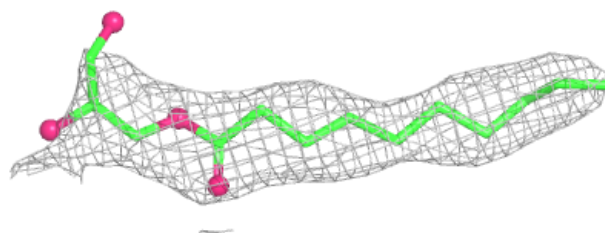


Electron density around OLB A 608:

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

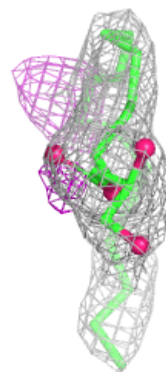
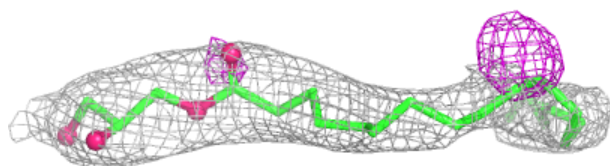
**Electron density around OLB A 607:**

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

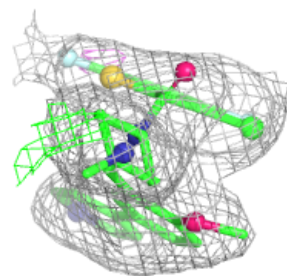
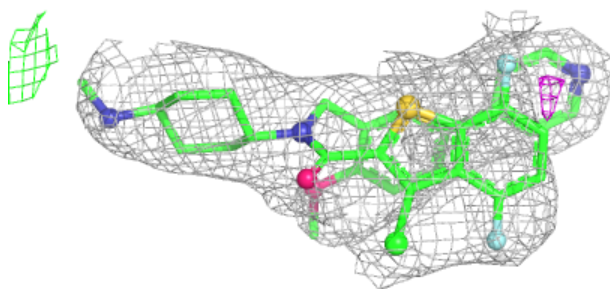
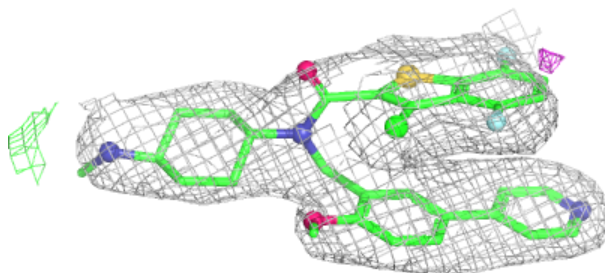


Electron density around OLB A 605:

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

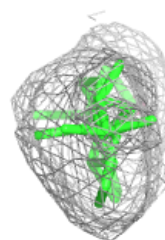
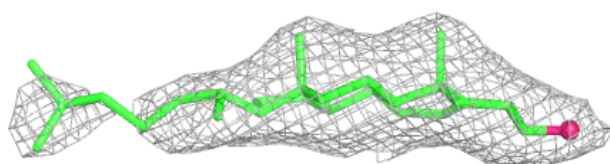
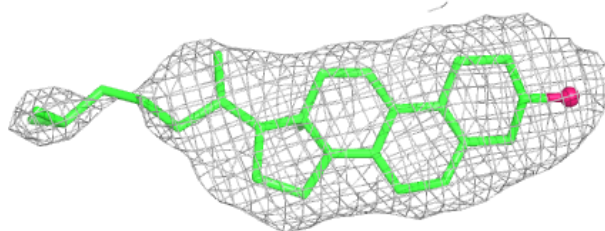
**Electron density around LKD A 611:**

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

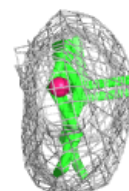
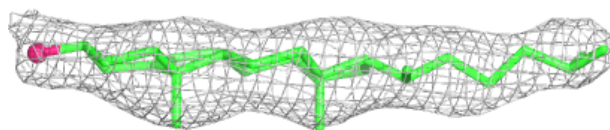
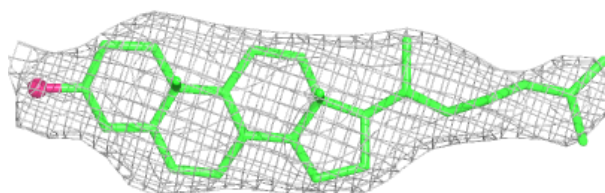


Electron density around CLR A 612:

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

**Electron density around CLR A 613:**

$2mF_o-DF_c$ (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.