



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:47 PM UTC

PDB ID : 6EIG / pdb_00006eig
Title : Crystal structure of N24Q/C128T mutant of Channelrhodopsin 2
Authors : Kovalev, K.; Borshchevskiy, V.; Volkov, O.; Polovinkin, V.; Marin, E.; Balandin, T.; Astashkin, R.; Bamann, C.; Bueldt, G.; Willbold, D.; Popov, A.; Bamberg, E.; Gordeliy, V.
Deposited on : 2017-09-19
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 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

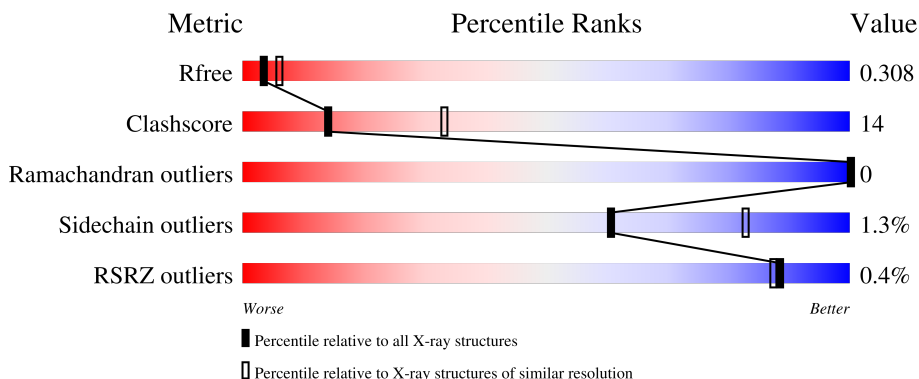
1 Overall quality at a glance

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	315	% 60% 18% • 21%
1	B	315	62% 17% • 21%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4104 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.

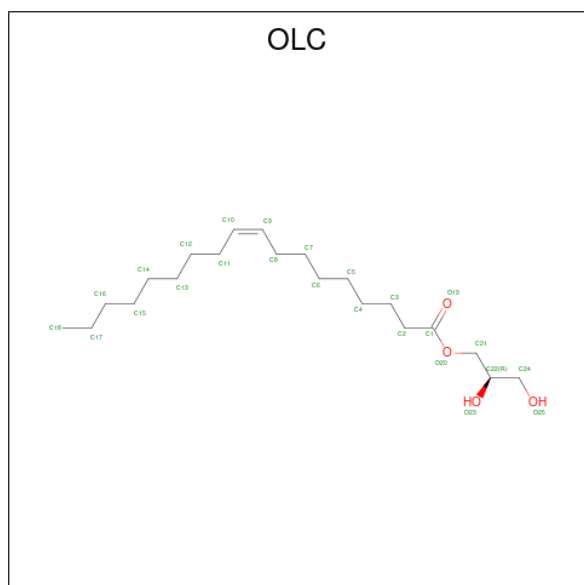
- Molecule 1 is a protein called Archaeal-type opsin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1967	1310	312	330	15			
1	B	250	Total	C	N	O	S	0	0	0
			1971	1310	314	332	15			

There are 4 discrepancies between the modelled and reference sequences:

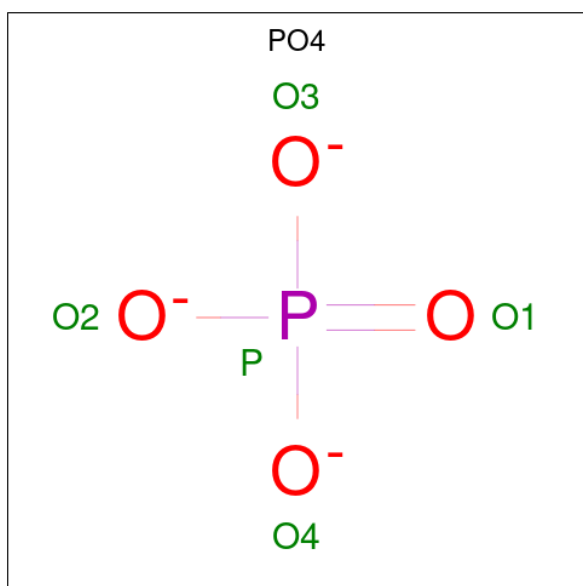
Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLN	ASN	engineered mutation	UNP Q8RUT8
A	128	THR	CYS	engineered mutation	UNP Q8RUT8
B	24	GLN	ASN	engineered mutation	UNP Q8RUT8
B	128	THR	CYS	engineered mutation	UNP Q8RUT8

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



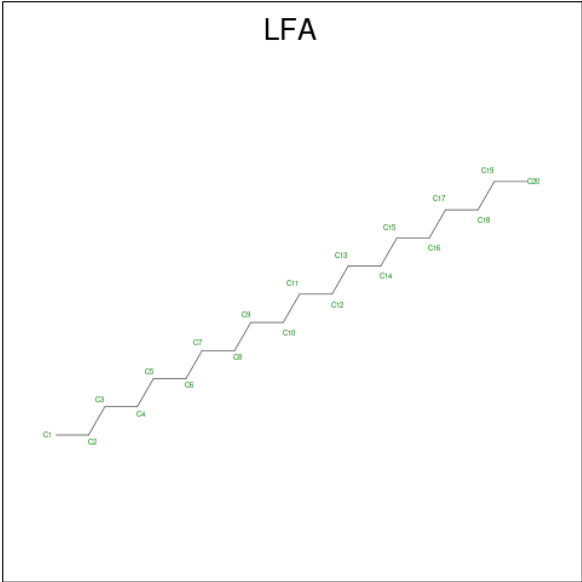
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 16 12 4	0	0
2	A	1	Total C O 17 14 3	0	0
2	A	1	Total C O 15 14 1	0	0
2	A	1	Total C 12 12	0	0
2	B	1	Total C 9 9	0	0
2	B	1	Total C O 16 12 4	0	0
2	B	1	Total C O 19 15 4	0	0

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



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

- Molecule 4 is EICOSANE (CCD ID: LFA) (formula: C₂₀H₄₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 15 15	0	0
4	A	1	Total C 4 4	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	17	Total O 17 17	0	0
5	B	16	Total O 16 16	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	64.51Å 134.06Å 78.47Å 90.00° 90.22° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 20.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.7 (20.00-2.70) 95.1 (20.00-2.70)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.265 , 0.297 0.273 , 0.308	Depositor DCC
R_{free} test set	863 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	53.9	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.408 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4104	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.57% 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: LFA, OLC, PO4, LYR

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	0.30	0/1996	0.69	1/2720 (0.0%)
1	B	0.30	0/1999	0.67	0/2723
All	All	0.30	0/3995	0.68	1/5443 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	GLU	CB-CA-C	-6.26	109.34	116.54

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	1967	0	1918	59	0
1	B	1971	0	1933	56	0
2	A	60	0	85	7	14
2	B	44	0	58	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	19	0	33	0	14
5	A	17	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	16	0	0	4	0
All	All	4104	0	4027	116	14

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 (116) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:LYR:H192	1:B:257:LYR:H9	1.38	1.01
1:B:235:GLU:OE1	5:B:1201:HOH:O	1.79	1.00
1:A:257:LYR:H192	1:A:257:LYR:H9	1.40	0.98
1:B:257:LYR:H192	1:B:257:LYR:C9	2.06	0.84
1:A:257:LYR:H192	1:A:257:LYR:C9	2.07	0.84
1:B:174:LYS:HE2	1:B:235:GLU:O	1.78	0.83
1:B:36:CYS:SG	1:B:113:GLY:HA2	2.17	0.83
1:B:117:GLN:OE1	5:B:1201:HOH:O	1.99	0.80
1:A:128:THR:OG1	1:A:129:PRO:HD3	1.81	0.80
1:B:128:THR:OG1	1:B:129:PRO:HD3	1.83	0.78
1:A:253:ASP:O	1:A:257:LYR:HB3	1.86	0.74
1:A:166:SER:O	1:A:174:LYS:HE2	1.90	0.71
1:A:48:ALA:HB2	2:A:1102:OLC:H24	1.72	0.70
1:B:97:GLU:O	1:B:101:GLU:HB2	1.93	0.69
1:A:36:CYS:HB3	1:A:39:TRP:CD2	2.28	0.68
1:B:117:GLN:O	1:B:121:TYR:HD2	1.77	0.68
1:B:253:ASP:O	1:B:257:LYR:HB3	1.95	0.66
1:A:237:PHE:CE1	2:A:1101:OLC:H2A	2.31	0.65
1:A:257:LYR:H9	1:A:257:LYR:H183	1.78	0.64
1:B:36:CYS:HB3	1:B:39:TRP:CD2	2.33	0.64
1:A:36:CYS:SG	1:A:113:GLY:HA2	2.39	0.63
1:B:257:LYR:H9	1:B:257:LYR:H183	1.82	0.61
1:A:126:LEU:HD12	2:A:1103:OLC:H11	1.81	0.61
1:A:258:ASN:HD22	1:A:258:ASN:N	1.98	0.61
1:B:28:LEU:C	1:B:28:LEU:HD12	2.26	0.60
1:B:117:GLN:O	1:B:121:TYR:CD2	2.54	0.60
1:A:134:HIS:NE2	5:A:1203:HOH:O	2.32	0.60
1:B:134:HIS:NE2	5:B:1205:HOH:O	2.32	0.59
1:B:272:HIS:O	1:B:276:LEU:HG	2.04	0.57
1:A:155:SER:HB3	1:A:187:ASN:HD22	1.69	0.57
1:B:277:ILE:CG2	1:B:278:HIS:CE1	2.88	0.56
1:A:277:ILE:HG22	1:A:278:HIS:CD2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:LYR:C9	1:A:257:LYR:H183	2.35	0.56
1:A:52:SER:O	1:A:56:GLN:HG2	2.06	0.56
1:B:150:MET:N	1:B:150:MET:HE2	2.21	0.56
1:B:257:LYR:H9	1:B:257:LYR:C19	2.16	0.55
1:B:275:ILE:O	1:B:279:GLY:N	2.37	0.55
1:A:169:ALA:O	1:A:174:LYS:HE3	2.07	0.55
1:B:100:PHE:O	1:B:106:SER:HB3	2.08	0.54
1:B:271:ILE:C	1:B:271:ILE:HD12	2.32	0.54
1:A:237:PHE:CD1	2:A:1101:OLC:H2	2.43	0.54
1:B:277:ILE:HG22	1:B:278:HIS:CE1	2.43	0.54
1:A:129:PRO:O	1:A:133:ILE:HG13	2.09	0.53
1:A:257:LYR:H9	1:A:257:LYR:C19	2.17	0.53
1:B:268:ARG:O	1:B:271:ILE:HG13	2.09	0.53
1:A:226:PHE:N	1:A:227:PRO:HD2	2.24	0.53
1:A:235:GLU:OE1	5:A:1201:HOH:O	2.19	0.52
1:B:257:LYR:C9	1:B:257:LYR:H183	2.38	0.52
1:B:226:PHE:N	1:B:227:PRO:HD2	2.23	0.52
1:A:134:HIS:O	1:A:134:HIS:HD2	1.92	0.52
1:A:117:GLN:O	1:A:121:TYR:HD2	1.93	0.52
1:B:271:ILE:HD12	1:B:272:HIS:N	2.26	0.51
1:A:40:ILE:O	1:A:40:ILE:HG22	2.11	0.51
1:A:241:SER:OG	2:A:1102:OLC:O25	2.26	0.50
1:A:277:ILE:CG2	1:A:278:HIS:CD2	2.94	0.50
1:B:32:ASP:N	1:B:32:ASP:OD1	2.45	0.50
1:A:257:LYR:C9	1:A:257:LYR:C19	2.78	0.50
1:B:128:THR:N	1:B:129:PRO:CD	2.74	0.50
1:A:93:LYS:NZ	1:A:253:ASP:OD2	2.43	0.49
1:A:158:GLY:O	1:A:162:TRP:CD1	2.65	0.49
1:A:28:LEU:HD12	1:A:28:LEU:C	2.38	0.49
1:B:257:LYR:C9	1:B:257:LYR:C19	2.78	0.49
1:A:41:GLU:N	5:A:1208:HOH:O	2.46	0.48
1:A:117:GLN:O	1:A:121:TYR:CD2	2.66	0.48
2:A:1104:OLC:H9	1:B:232:LEU:HD21	1.94	0.48
1:A:100:PHE:O	1:A:106:SER:HB3	2.14	0.47
1:B:235:GLU:H	1:B:235:GLU:CD	2.22	0.47
1:A:237:PHE:CD1	2:A:1101:OLC:C2	2.98	0.47
1:A:128:THR:N	1:A:129:PRO:CD	2.77	0.46
1:B:221:VAL:O	1:B:225:MET:HG2	2.15	0.46
1:B:277:ILE:HB	1:B:278:HIS:HD1	1.80	0.46
1:B:203:VAL:HG23	1:B:209:ARG:HG2	1.98	0.46
1:A:134:HIS:CD2	5:A:1203:HOH:O	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:CYS:HB3	1:A:39:TRP:CE2	2.51	0.45
1:A:267:LEU:O	1:A:271:ILE:HG12	2.17	0.45
1:B:69:PHE:O	1:B:73:GLN:HG2	2.17	0.45
1:B:28:LEU:O	1:B:28:LEU:HG	2.16	0.45
1:B:36:CYS:SG	1:B:113:GLY:CA	2.99	0.45
1:A:128:THR:HG1	1:A:129:PRO:HD3	1.80	0.45
1:B:100:PHE:O	1:B:106:SER:CB	2.65	0.45
1:A:150:MET:N	1:A:150:MET:HE2	2.32	0.44
1:B:134:HIS:HD2	1:B:134:HIS:O	2.00	0.44
1:A:204:PRO:O	1:A:209:ARG:HG3	2.17	0.44
1:B:121:TYR:CD1	1:B:164:ALA:HB2	2.53	0.44
1:A:132:LEU:HD13	1:A:152:LEU:HG	2.00	0.44
1:A:148:ARG:NH1	1:A:195:ALA:HA	2.33	0.44
1:A:232:LEU:O	1:A:239:VAL:N	2.51	0.44
1:B:134:HIS:CD2	1:B:134:HIS:C	2.95	0.44
1:A:215:MET:HG2	1:A:263:LEU:HB3	1.99	0.43
1:B:137:ASN:ND2	1:B:142:SER:O	2.35	0.43
2:B:1101:OLC:H8A	2:B:1101:OLC:H11	1.83	0.43
1:A:97:GLU:O	1:A:101:GLU:HB2	2.18	0.43
1:A:134:HIS:O	1:A:134:HIS:CD2	2.72	0.43
1:B:132:LEU:HD13	1:B:152:LEU:HG	2.00	0.43
1:A:257:LYR:H10	1:A:257:LYR:H81	1.85	0.42
1:B:267:LEU:O	1:B:271:ILE:HG23	2.19	0.42
1:A:36:CYS:SG	1:A:113:GLY:CA	3.08	0.42
1:A:142:SER:HB2	1:A:144:ASP:OD1	2.19	0.42
1:B:257:LYR:H81	1:B:257:LYR:H10	1.85	0.42
1:B:219:PHE:O	1:B:223:TRP:HB2	2.20	0.42
1:B:85:TYR:OH	5:B:1202:HOH:O	2.16	0.41
1:A:104:ASN:CG	1:A:105:PRO:HA	2.46	0.41
1:B:38:GLY:HA3	1:B:113:GLY:O	2.20	0.41
1:B:134:HIS:O	1:B:134:HIS:CD2	2.73	0.41
1:A:181:GLY:C	1:A:257:LYR:H142	2.46	0.41
1:B:158:GLY:O	1:B:162:TRP:CD1	2.74	0.41
1:A:36:CYS:HB3	1:A:39:TRP:CE3	2.55	0.41
1:A:104:ASN:HA	1:A:105:PRO:HA	1.79	0.41
1:A:121:TYR:CD2	1:A:121:TYR:N	2.88	0.41
1:A:169:ALA:O	1:A:174:LYS:CE	2.68	0.41
1:A:266:TYR:CE2	1:A:270:LEU:HD11	2.56	0.41
1:B:148:ARG:NH1	1:B:195:ALA:HA	2.35	0.41
1:B:103:LYS:O	1:B:106:SER:HB3	2.21	0.41
1:B:129:PRO:O	1:B:133:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:LEU:HD21	1:B:271:ILE:HD13	2.03	0.40
1:B:29:VAL:HA	1:B:30:PRO:HD3	1.97	0.40

All (14) 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)
2:A:1103:OLC:C3	4:A:1106:LFA:C6[2_555]	1.01	1.19
2:A:1103:OLC:C7	4:A:1106:LFA:C10[2_555]	1.04	1.16
2:A:1103:OLC:C5	4:A:1106:LFA:C7[2_555]	1.81	0.39
2:A:1103:OLC:C7	4:A:1106:LFA:C12[2_555]	1.81	0.39
2:A:1103:OLC:C8	4:A:1106:LFA:C11[2_555]	1.85	0.35
2:A:1103:OLC:C8	4:A:1106:LFA:C12[2_555]	1.85	0.35
2:A:1103:OLC:C9	4:A:1106:LFA:C11[2_555]	1.91	0.29
2:A:1103:OLC:C10	4:A:1106:LFA:C12[2_555]	1.99	0.21
2:A:1103:OLC:C12	4:A:1106:LFA:C15[2_555]	2.12	0.08
2:A:1103:OLC:C10	4:A:1106:LFA:C13[2_555]	2.12	0.08
2:A:1103:OLC:C9	4:A:1106:LFA:C13[2_555]	2.13	0.07
2:A:1103:OLC:C4	4:A:1106:LFA:C6[2_555]	2.14	0.06
2:A:1103:OLC:C7	4:A:1106:LFA:C9[2_555]	2.14	0.06
2:A:1103:OLC:C8	4:A:1106:LFA:C10[2_555]	2.18	0.02

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	245/315 (78%)	239 (98%)	6 (2%)	0	100	100
1	B	245/315 (78%)	240 (98%)	5 (2%)	0	100	100
All	All	490/630 (78%)	479 (98%)	11 (2%)	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	196/258 (76%)	193 (98%)	3 (2%)	57	81
1	B	199/258 (77%)	197 (99%)	2 (1%)	68	86
All	All	395/516 (77%)	390 (99%)	5 (1%)	61	83

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	66	LEU
1	A	258	ASN
1	B	28	LEU
1	B	66	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	49	GLN
1	A	73	GLN
1	A	114	HIS
1	A	117	GLN
1	A	134	HIS
1	A	187	ASN
1	A	258	ASN
1	A	265	HIS
1	A	278	HIS
1	B	33	GLN
1	B	46	ASN
1	B	49	GLN
1	B	114	HIS
1	B	134	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	LYR	B	257	1	27,29,30	0.61	0	30,37,39	1.94	7 (23%)
1	LYR	A	257	1	27,29,30	0.62	0	30,37,39	1.94	7 (23%)

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
1	LYR	B	257	1	-	4/22/40/42	0/1/1/1
1	LYR	A	257	1	-	4/22/40/42	0/1/1/1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	257	LYR	C13-C12-C11	-5.30	118.70	124.48
1	A	257	LYR	C13-C12-C11	-5.26	118.75	124.48
1	A	257	LYR	C1-NZ-CE	4.21	121.39	112.85
1	B	257	LYR	C1-NZ-CE	4.18	121.33	112.85
1	B	257	LYR	C6-C7-C80	-3.56	122.28	127.28
1	A	257	LYR	C6-C7-C80	-3.51	122.35	127.28
1	B	257	LYR	C10-C9-C80	-3.36	121.26	126.23
1	A	257	LYR	C10-C9-C80	-3.33	121.31	126.23
1	A	257	LYR	C9-C10-C11	-2.80	119.51	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	257	LYR	C9-C10-C11	-2.76	119.62	127.00
1	A	257	LYR	C13-C12-C14	2.28	118.45	113.60
1	B	257	LYR	C13-C12-C14	2.26	118.42	113.60
1	A	257	LYR	C15-C14-C12	-2.13	110.26	114.06
1	B	257	LYR	C15-C14-C12	-2.10	110.31	114.06

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	257	LYR	N-CA-CB-CG
1	A	257	LYR	C-CA-CB-CG
1	A	257	LYR	CD-CE-NZ-C1
1	B	257	LYR	N-CA-CB-CG
1	B	257	LYR	C-CA-CB-CG
1	B	257	LYR	CD-CE-NZ-C1
1	A	257	LYR	CE-CD-CG-CB
1	B	257	LYR	CE-CD-CG-CB

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	257	LYR	8	0
1	A	257	LYR	9	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OLC	A	1101	-	15,15,24	1.16	1 (6%)	16,16,25	1.00	1 (6%)
2	OLC	A	1104	-	11,11,24	0.28	0	10,10,25	0.64	0
4	LFA	A	1107	-	3,3,19	0.37	0	2,2,18	0.64	0
3	PO4	A	1105	-	4,4,4	0.96	0	6,6,6	0.47	0
3	PO4	B	1104	-	4,4,4	0.96	0	6,6,6	0.47	0
4	LFA	A	1106	2	14,14,19	0.25	0	13,13,18	0.58	0
2	OLC	A	1102	-	16,16,24	0.37	0	16,16,25	0.85	0
2	OLC	B	1102	-	15,15,24	1.17	1 (6%)	16,16,25	1.02	1 (6%)
2	OLC	B	1101	-	8,8,24	0.27	0	7,7,25	0.51	0
2	OLC	A	1103	4	14,14,24	0.53	0	13,13,25	0.87	0
2	OLC	B	1103	-	18,18,24	1.07	1 (5%)	19,19,25	0.99	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OLC	A	1101	-	-	7/15/15/24	-
2	OLC	A	1104	-	-	4/9/9/24	-
4	LFA	A	1107	-	-	1/1/1/17	-
4	LFA	A	1106	2	-	8/12/12/17	-
2	OLC	A	1102	-	-	9/15/15/24	-
2	OLC	B	1102	-	-	7/15/15/24	-
2	OLC	B	1101	-	-	2/6/6/24	-
2	OLC	A	1103	4	-	5/12/12/24	-
2	OLC	B	1103	-	-	7/18/18/24	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	OLC	O20-C1	4.32	1.45	1.33
2	B	1102	OLC	O20-C1	4.31	1.45	1.33
2	B	1103	OLC	O20-C1	4.29	1.45	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1103	OLC	O20-C1-C2	2.77	120.29	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1102	OLC	O20-C1-C2	2.76	120.27	111.83
2	A	1101	OLC	O20-C1-C2	2.72	120.12	111.83

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1102	OLC	C21-C22-C24-O25
4	A	1107	LFA	C10-C11-C12-C13
2	B	1102	OLC	C2-C1-O20-C21
2	B	1102	OLC	O19-C1-O20-C21
2	A	1101	OLC	C2-C1-O20-C21
2	A	1101	OLC	O20-C21-C22-O23
2	A	1101	OLC	O19-C1-O20-C21
2	B	1103	OLC	C1-C2-C3-C4
2	A	1102	OLC	O20-C1-C2-C3
2	A	1102	OLC	O23-C22-C24-O25
2	A	1101	OLC	C4-C5-C6-C7
2	A	1103	OLC	C1-C2-C3-C4
2	A	1104	OLC	C10-C11-C12-C13
2	B	1103	OLC	C4-C5-C6-C7
2	B	1103	OLC	C9-C10-C11-C12
4	A	1106	LFA	C5-C6-C7-C8
4	A	1106	LFA	C3-C4-C5-C6
2	A	1102	OLC	C2-C3-C4-C5
2	B	1102	OLC	C4-C5-C6-C7
2	A	1103	OLC	C6-C7-C8-C9
2	A	1102	OLC	C6-C7-C8-C9
2	B	1103	OLC	C3-C4-C5-C6
4	A	1106	LFA	C7-C8-C9-C10
2	B	1103	OLC	C2-C1-O20-C21
2	A	1102	OLC	C22-C21-O20-C1
2	B	1102	OLC	C3-C4-C5-C6
2	A	1104	OLC	C12-C13-C14-C15
2	B	1103	OLC	O23-C22-C24-O25
4	A	1106	LFA	C9-C10-C11-C12
2	B	1103	OLC	O19-C1-O20-C21
2	A	1103	OLC	C9-C10-C11-C12
4	A	1106	LFA	C11-C12-C13-C14
2	A	1102	OLC	C3-C4-C5-C6
2	A	1101	OLC	C2-C3-C4-C5
2	A	1101	OLC	C5-C6-C7-C8

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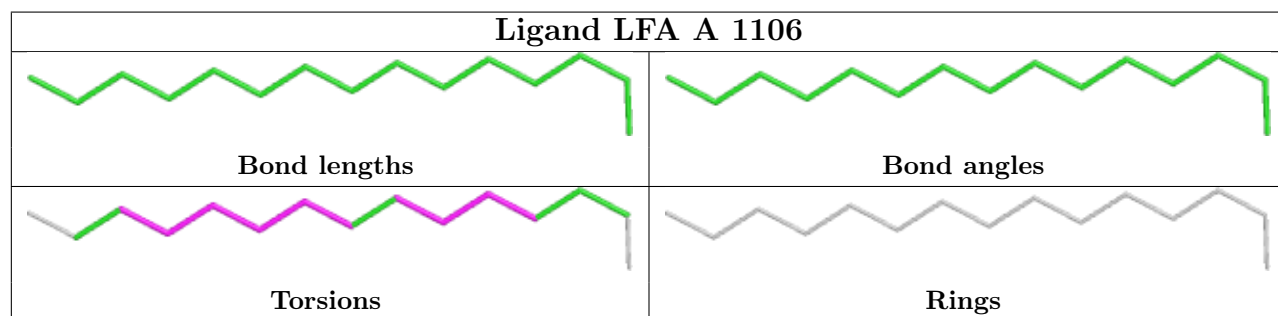
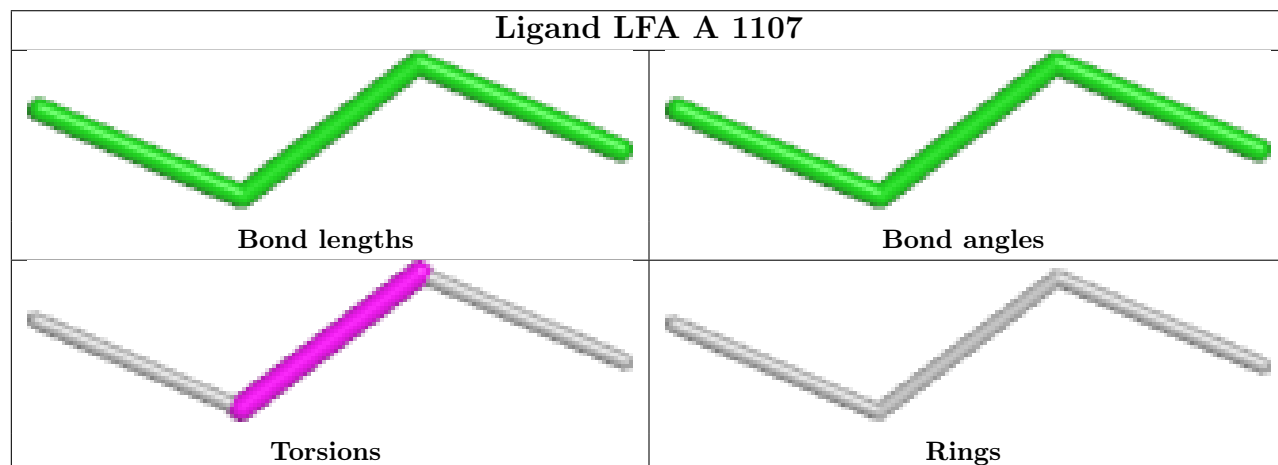
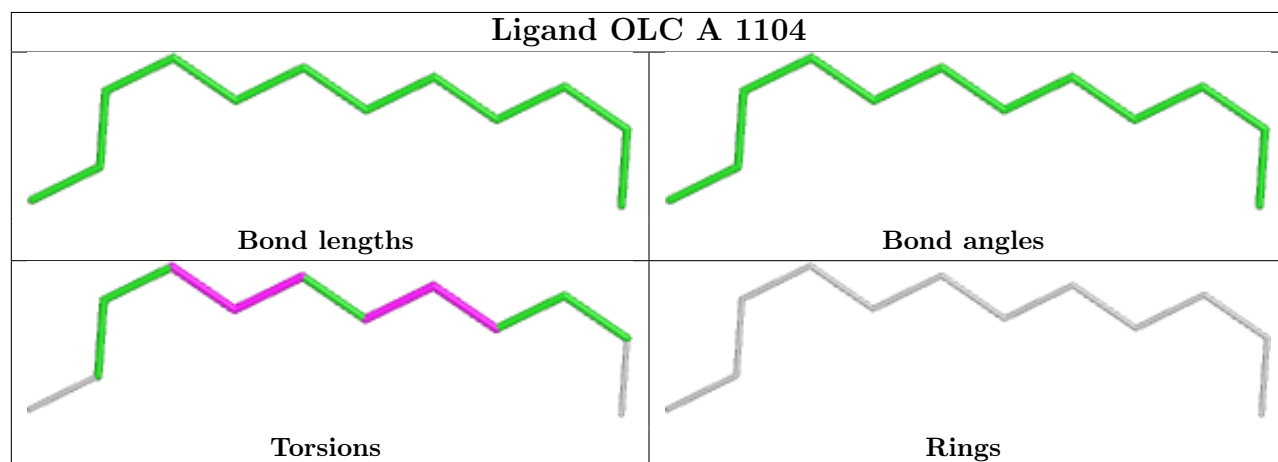
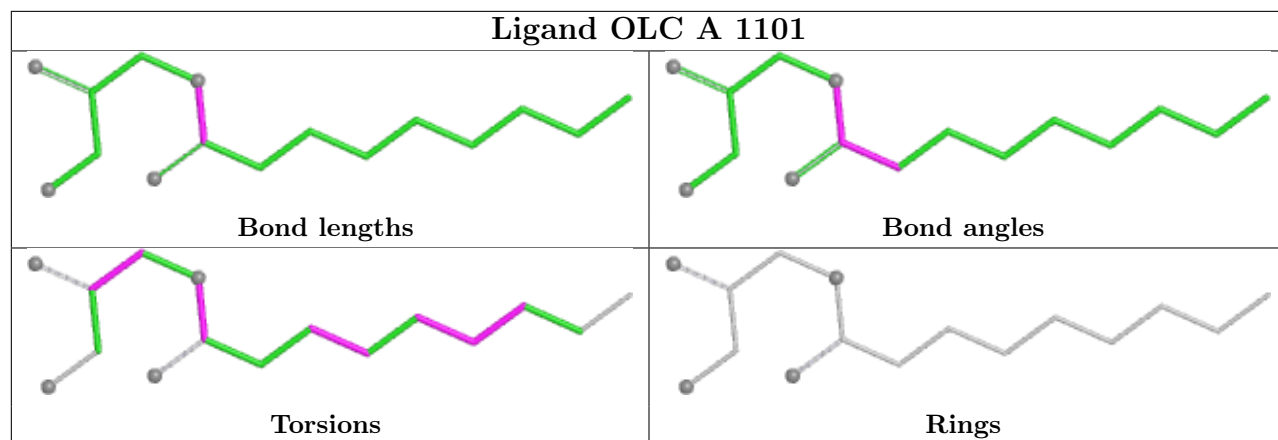
Mol	Chain	Res	Type	Atoms
4	A	1106	LFA	C11-C10-C9-C8
2	A	1104	OLC	C13-C14-C15-C16
2	B	1101	OLC	C6-C7-C8-C9
2	A	1101	OLC	O20-C21-C22-C24
2	B	1102	OLC	O20-C21-C22-C24
2	A	1104	OLC	C9-C10-C11-C12
4	A	1106	LFA	C10-C11-C12-C13
2	A	1103	OLC	C22-C21-O20-C1
2	B	1102	OLC	O20-C21-C22-O23
2	B	1102	OLC	C6-C7-C8-C9
2	A	1102	OLC	C2-C1-O20-C21
4	A	1106	LFA	C4-C5-C6-C7
2	A	1103	OLC	O20-C1-C2-C3
2	A	1102	OLC	C4-C5-C6-C7
2	B	1101	OLC	C7-C8-C9-C10

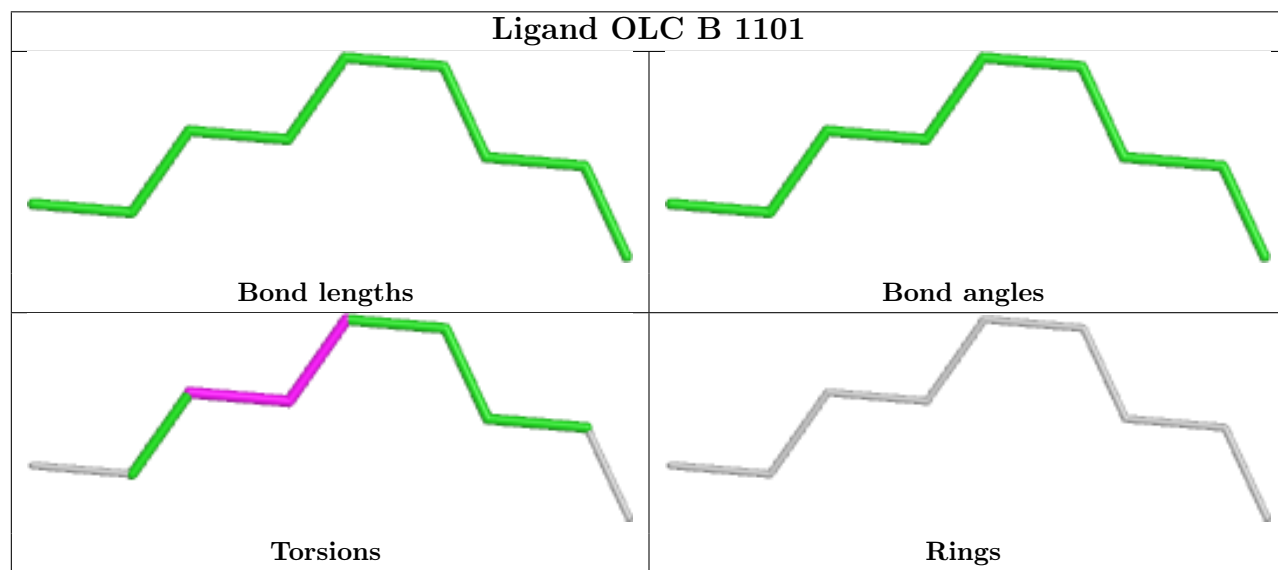
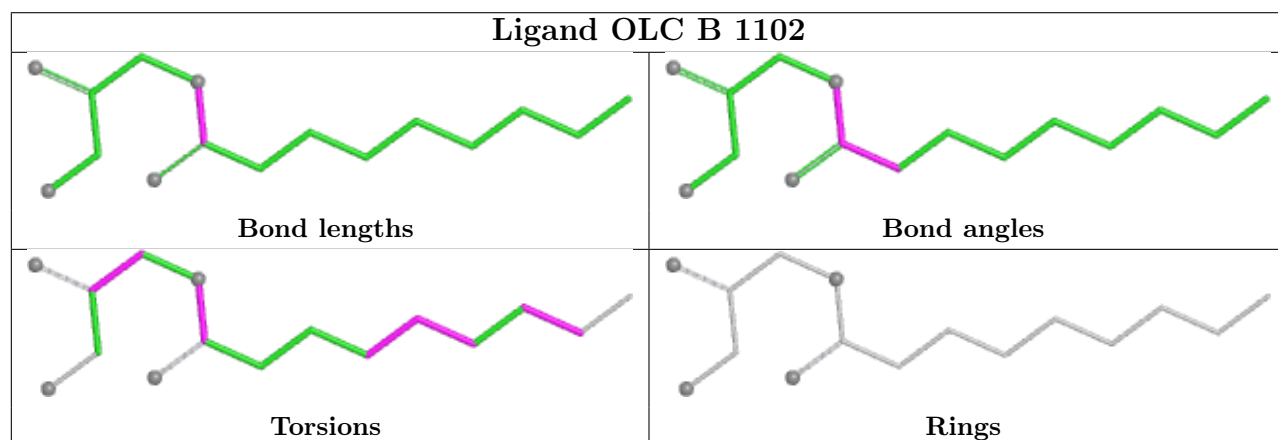
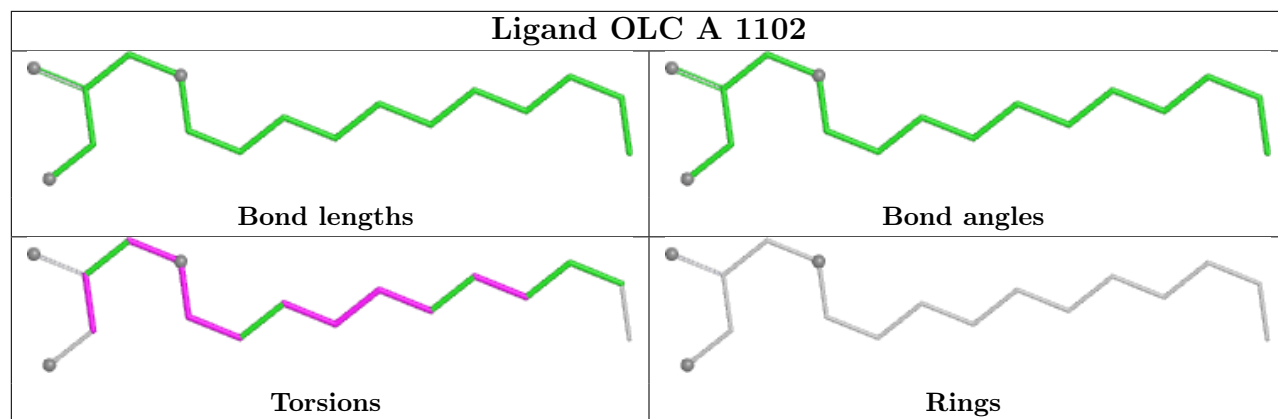
There are no ring outliers.

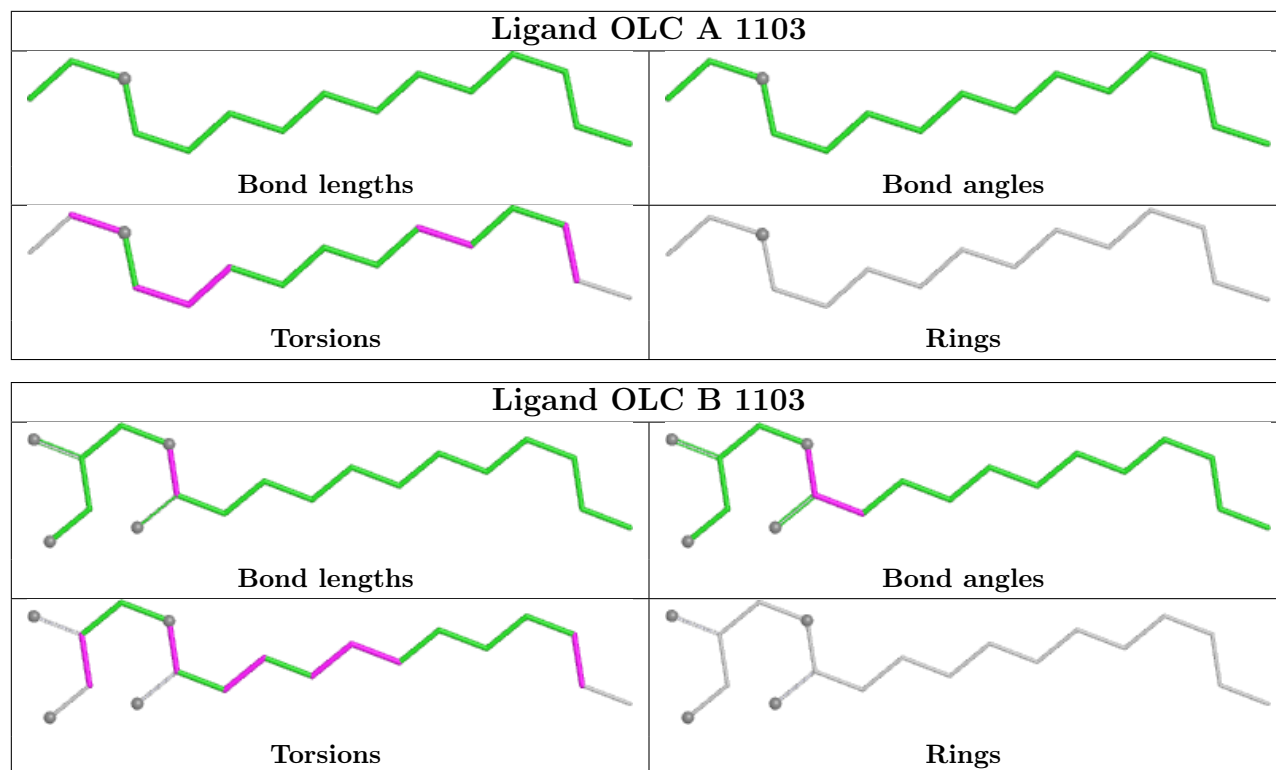
6 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	OLC	3	0
2	A	1104	OLC	1	0
4	A	1106	LFA	0	14
2	A	1102	OLC	2	0
2	B	1101	OLC	1	0
2	A	1103	OLC	1	14

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	249/315 (79%)	-0.98	2 (0%) 82 81	32, 62, 90, 126	0
1	B	249/315 (79%)	-1.04	0 100 100	33, 63, 100, 122	0
All	All	498/630 (79%)	-1.01	2 (0%) 88 87	32, 63, 95, 126	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	40	ILE	2.1
1	A	275	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LYR	A	257	29/30	0.99	0.06	52,67,78,85	0
1	LYR	B	257	29/30	0.99	0.06	56,64,76,76	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

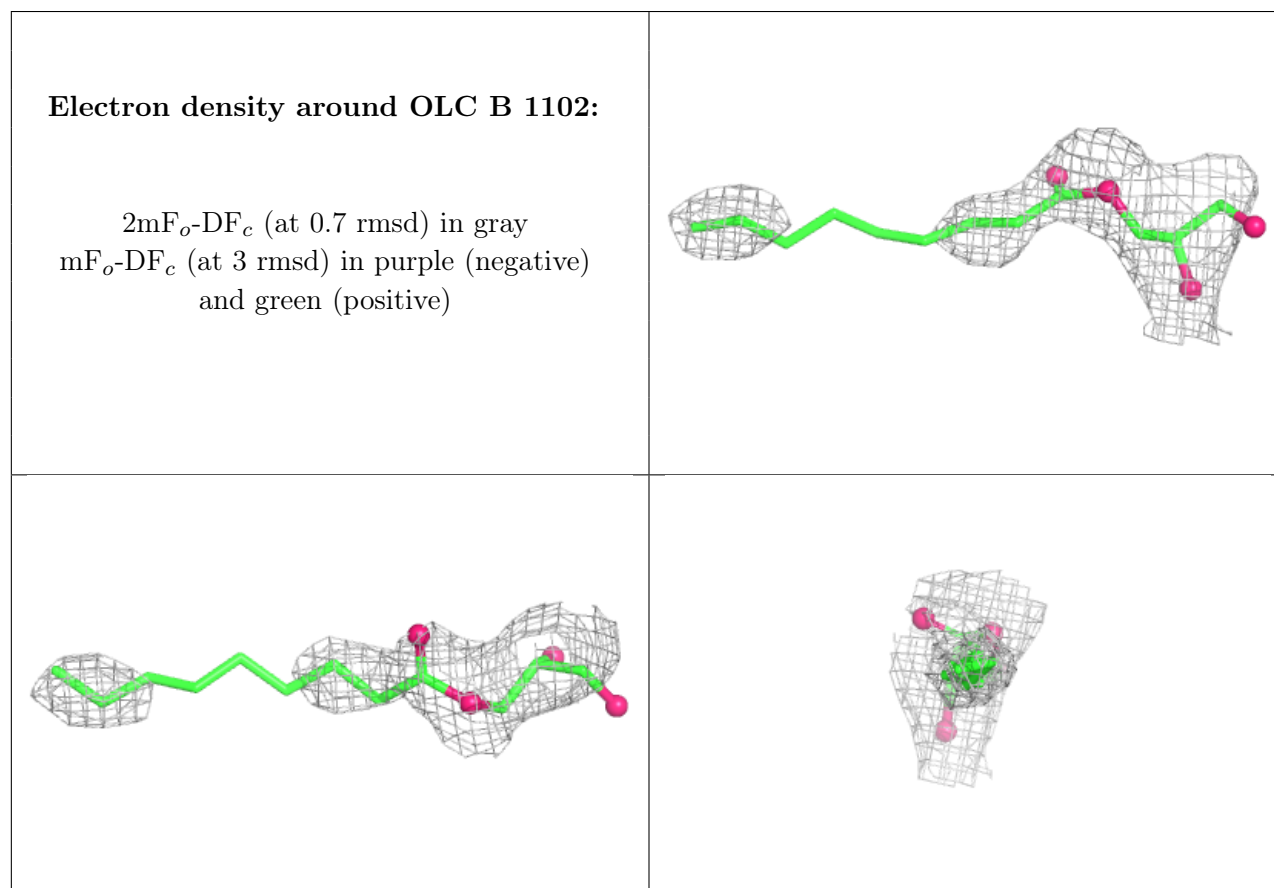
6.4 Ligands [i](#)

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.

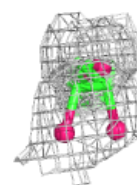
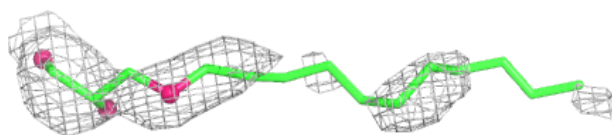
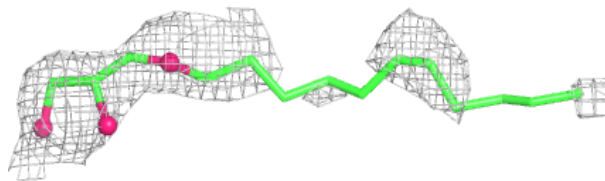
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	OLC	B	1102	16/25	0.97	0.08	65,89,96,101	0
2	OLC	A	1102	17/25	0.98	0.08	69,77,89,91	0
2	OLC	A	1103	15/25	0.98	0.09	93,112,162,170	0
2	OLC	A	1104	12/25	0.98	0.11	69,74,92,94	0
2	OLC	A	1101	16/25	0.98	0.07	57,83,119,131	0
3	PO4	B	1104	5/5	0.98	0.04	102,102,114,115	0
4	LFA	A	1107	4/20	0.98	0.06	28,28,29,31	0
3	PO4	A	1105	5/5	0.99	0.04	94,102,107,119	0
2	OLC	B	1101	9/25	0.99	0.06	37,57,63,65	0
4	LFA	A	1106	15/20	0.99	0.08	166,222,263,270	0
2	OLC	B	1103	19/25	0.99	0.07	59,70,104,115	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.

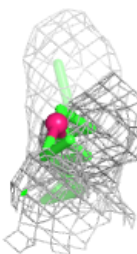
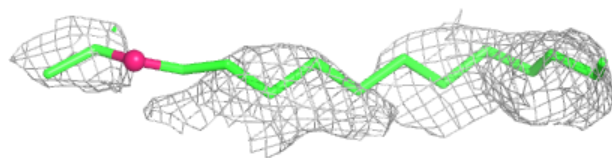
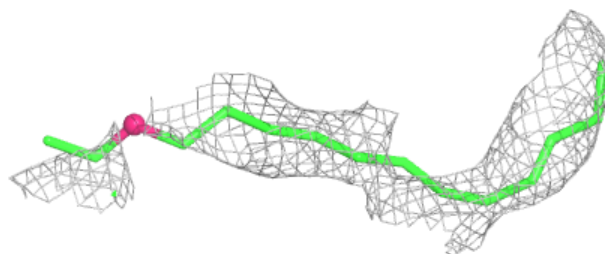


Electron density around OLC A 1102:

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

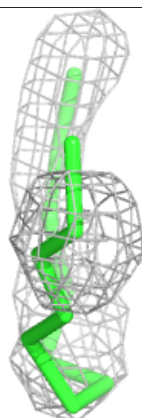
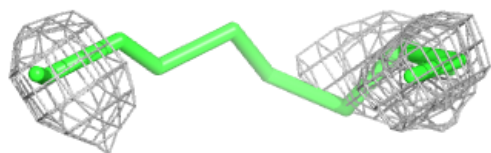
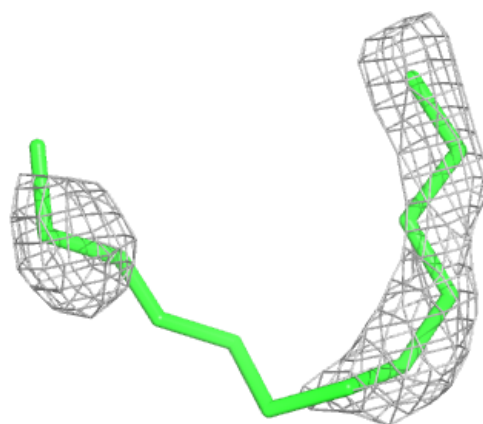
**Electron density around OLC A 1103:**

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and green (positive)

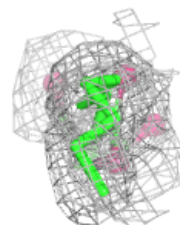
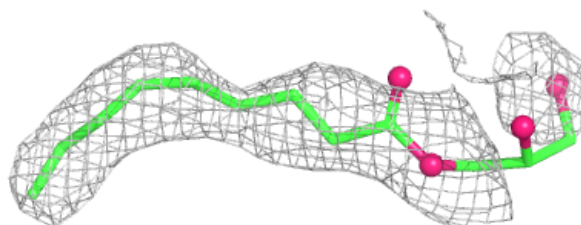


Electron density around OLC A 1104:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

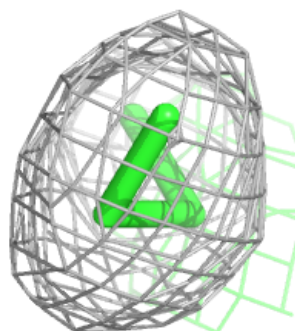
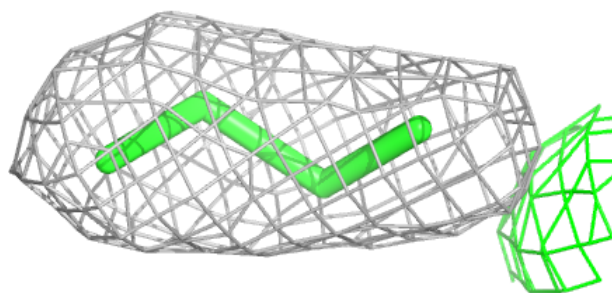
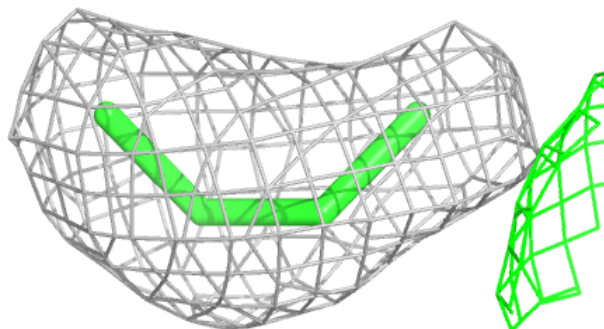
**Electron density around OLC A 1101:**

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

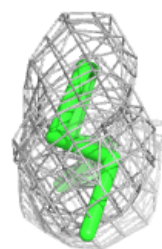
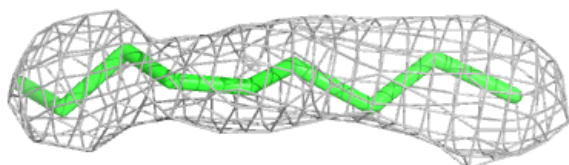
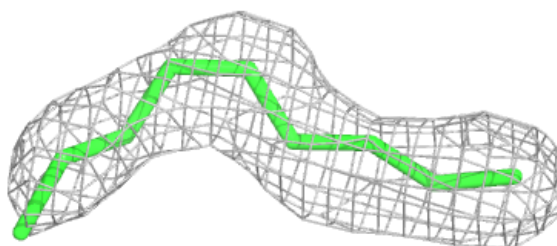


Electron density around LFA A 1107:

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

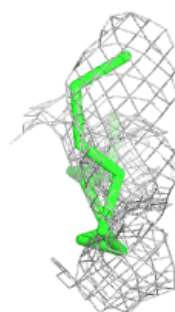
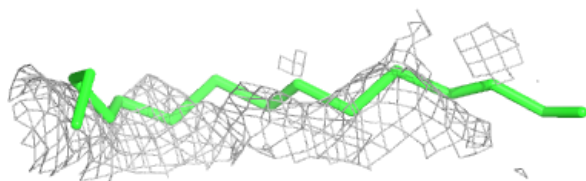
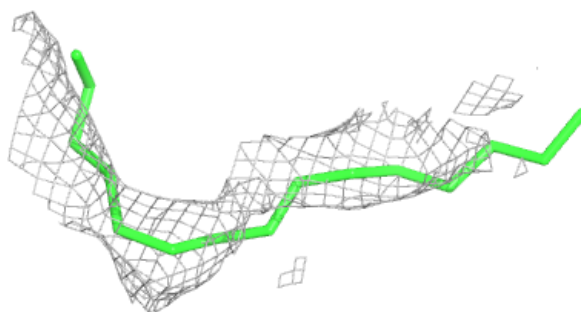
**Electron density around OLC B 1101:**

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

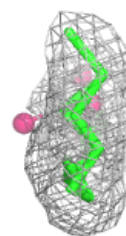
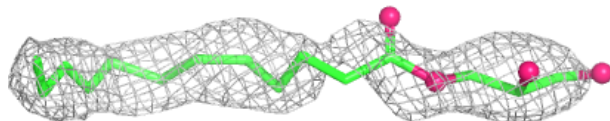
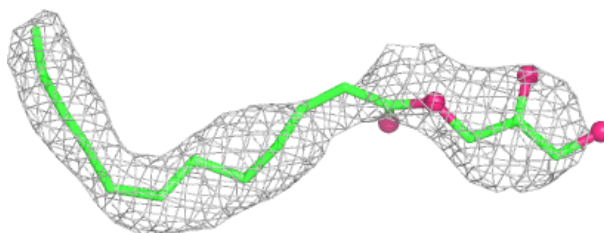


Electron density around LFA A 1106:

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

**Electron density around OLC B 1103:**

$2mF_o-DF_c$ (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.