



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:55 AM UTC

PDB ID : 4Y1K / pdb_00004y1k
Title : PALMITOYLATED OPRM OUTER MEMBRANE FACTOR
Authors : Monlezun, L.; Phan, G.; Broutin, I.
Deposited on : 2015-02-07
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

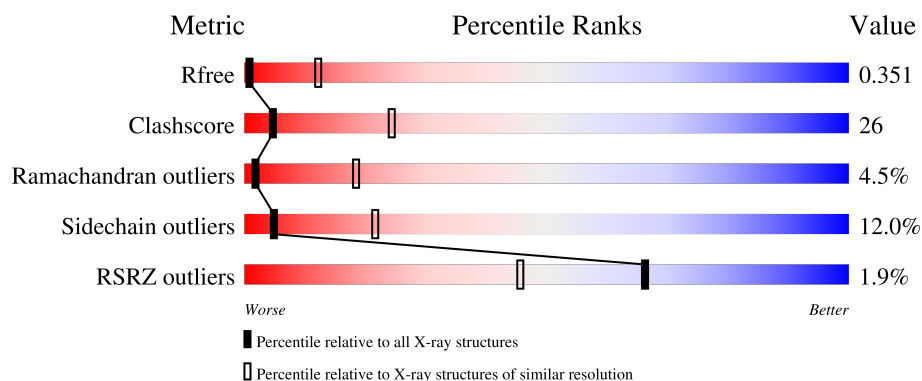
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	474	43% 44% 9% ...
1	B	474	45% 45% 6% ...
1	C	474	45% 43% 8% ...
1	D	474	3% 42% 45% 9% ...
1	E	474	3% 44% 46% 6% ...

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Mol	Chain	Length	Quality of chain
1	F	474	3% 40% 49% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21050 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 Outer membrane protein OprM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3501	2190	624	684	3			
1	B	457	Total	C	N	O	S	0	0	0
			3501	2190	624	684	3			
1	C	457	Total	C	N	O	S	0	0	0
			3503	2191	624	685	3			
1	D	457	Total	C	N	O	S	0	0	0
			3501	2190	624	684	3			
1	E	456	Total	C	N	O	S	0	0	0
			3492	2185	622	682	3			
1	F	457	Total	C	N	O	S	0	0	0
			3501	2190	624	684	3			

There are 36 discrepancies between the modelled and reference sequences:

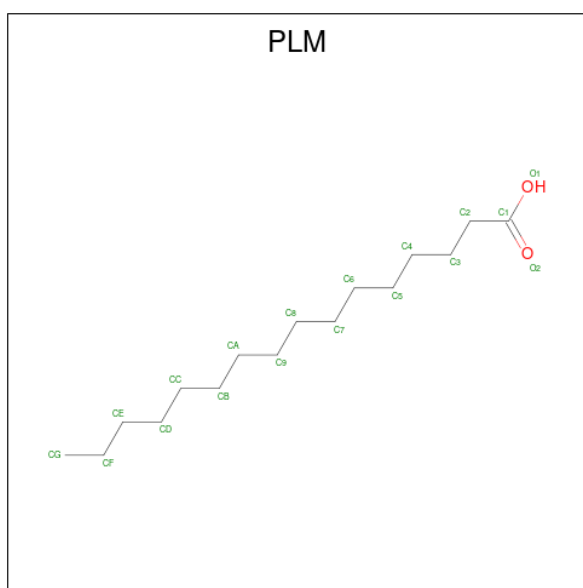
Chain	Residue	Modelled	Actual	Comment	Reference
A	469	HIS	-	expression tag	UNP Q51487
A	470	HIS	-	expression tag	UNP Q51487
A	471	HIS	-	expression tag	UNP Q51487
A	472	HIS	-	expression tag	UNP Q51487
A	473	HIS	-	expression tag	UNP Q51487
A	474	HIS	-	expression tag	UNP Q51487
B	469	HIS	-	expression tag	UNP Q51487
B	470	HIS	-	expression tag	UNP Q51487
B	471	HIS	-	expression tag	UNP Q51487
B	472	HIS	-	expression tag	UNP Q51487
B	473	HIS	-	expression tag	UNP Q51487
B	474	HIS	-	expression tag	UNP Q51487
C	469	HIS	-	expression tag	UNP Q51487
C	470	HIS	-	expression tag	UNP Q51487
C	471	HIS	-	expression tag	UNP Q51487
C	472	HIS	-	expression tag	UNP Q51487
C	473	HIS	-	expression tag	UNP Q51487

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Chain	Residue	Modelled	Actual	Comment	Reference
C	474	HIS	-	expression tag	UNP Q51487
D	469	HIS	-	expression tag	UNP Q51487
D	470	HIS	-	expression tag	UNP Q51487
D	471	HIS	-	expression tag	UNP Q51487
D	472	HIS	-	expression tag	UNP Q51487
D	473	HIS	-	expression tag	UNP Q51487
D	474	HIS	-	expression tag	UNP Q51487
E	469	HIS	-	expression tag	UNP Q51487
E	470	HIS	-	expression tag	UNP Q51487
E	471	HIS	-	expression tag	UNP Q51487
E	472	HIS	-	expression tag	UNP Q51487
E	473	HIS	-	expression tag	UNP Q51487
E	474	HIS	-	expression tag	UNP Q51487
F	469	HIS	-	expression tag	UNP Q51487
F	470	HIS	-	expression tag	UNP Q51487
F	471	HIS	-	expression tag	UNP Q51487
F	472	HIS	-	expression tag	UNP Q51487
F	473	HIS	-	expression tag	UNP Q51487
F	474	HIS	-	expression tag	UNP Q51487

- Molecule 2 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			17	16	1		
2	B	1	Total	C	O	0	0
			17	16	1		

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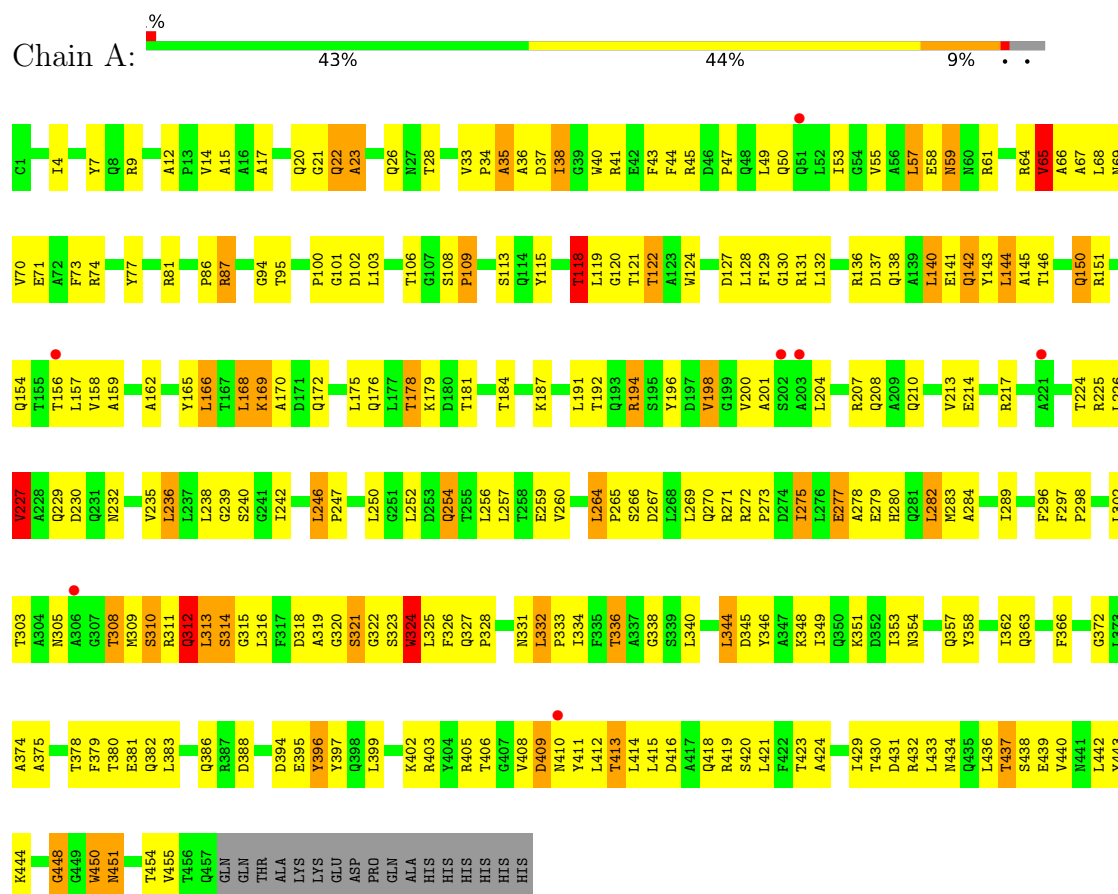
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	C	1	17	16	1	0	0

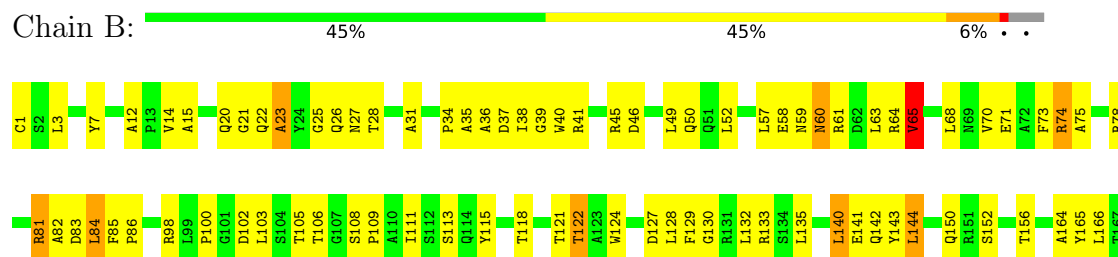
3 Residue-property plots [i](#)

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.

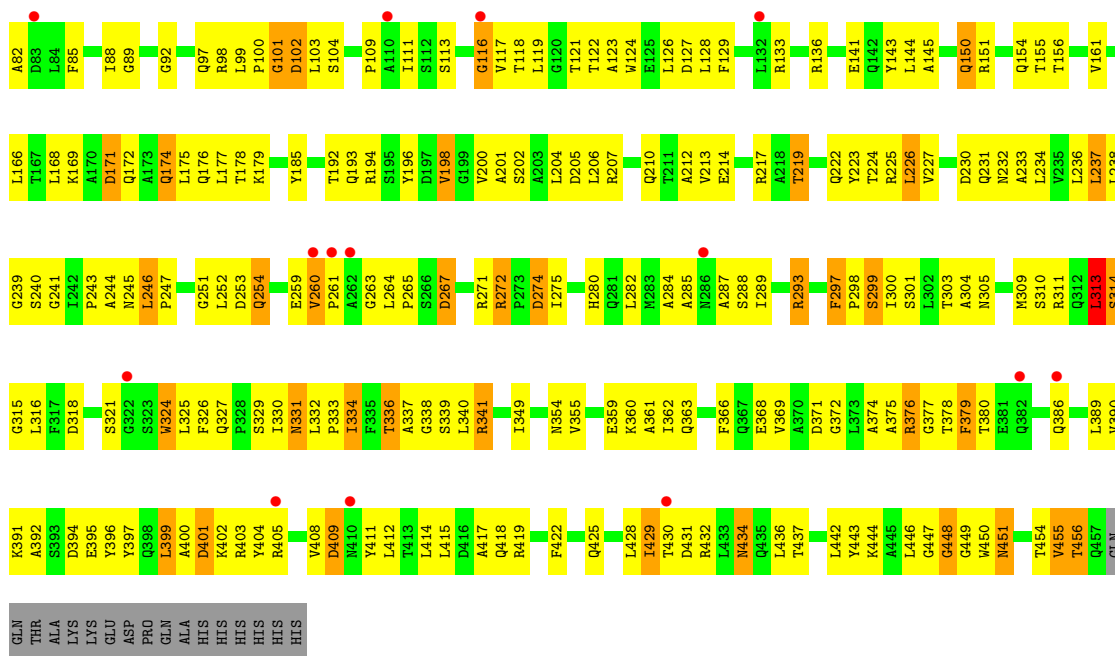
• Molecule 1: Outer membrane protein OprM



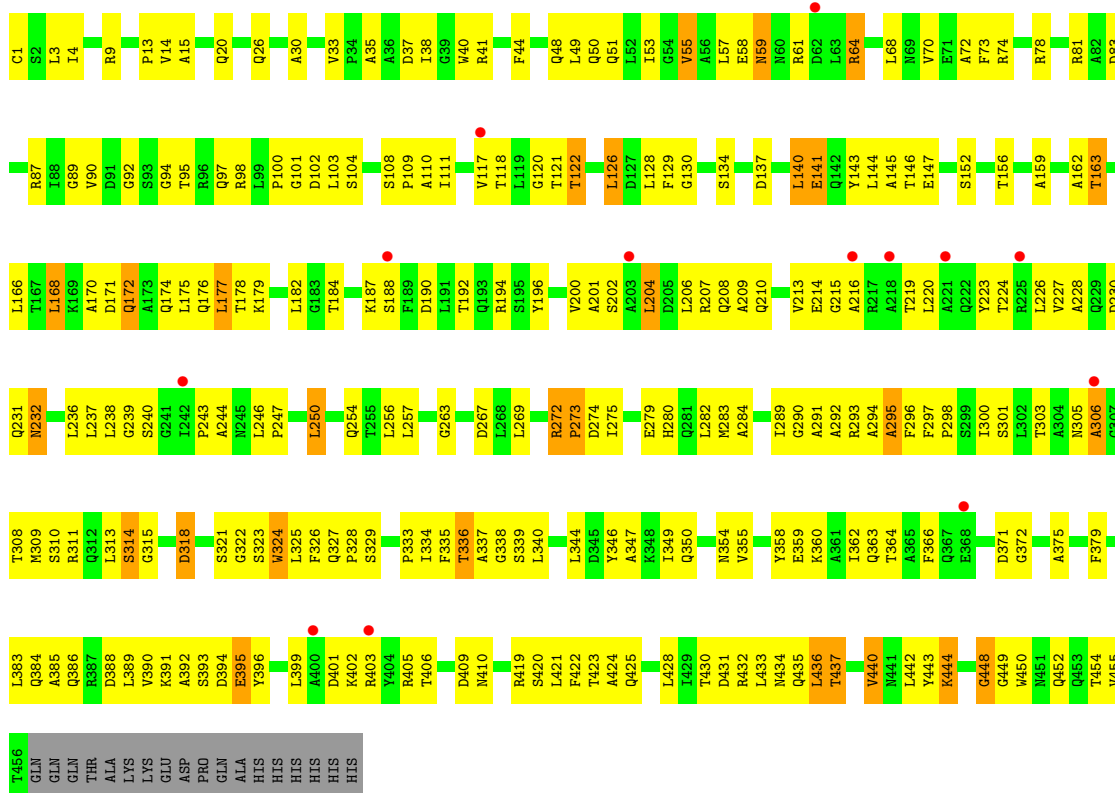
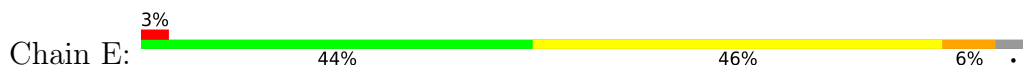
• Molecule 1: Outer membrane protein OprM







• Molecule 1: Outer membrane protein OprM



• Molecule 1: Outer membrane protein OprM



W441	F366	R293	A221	R151	C1
L442	Q367	F297	Q222	S152	S2
Y443	E368	P298	Y223	A153	L3
K444	D371	S299	L226	D83	
L445	G372	T300	V227	T155	Q8
L446	A375	S301	D230	T156	R9
G447	R376	L302	Q231	L157	P10
G448	F379	N303	N232	G89	E11
W450	F379	A304	A233	V90	A12
N451	L383	N305	A234	G92	D91
Q452	L383	A306	V235	G97	P13
Q453	Q386	G307	L236	R98	V14
T454	Q386	T308	L237	L166	A15
V455	T456	N309	L238	T167	P19
T456	L389	S310	G239	L168	Q20
Q457	V390	R311	S240	K169	
GLN	D394	Q312	G241	A170	T28
GLN	E395	L313	T242	D171	Q29
THR	Y396	G315	P243	Q172	A30
ALA	Y397	L316	L246	A173	A31
LYS	Q398	F317		L174	A32
GLU	L399	D318	L250	L175	P34
ASP	K402	S321	G251	Q176	A35
PRO	R403	G322	L252	L177	A36
GLN	A404	S323	D253	T178	D37
ALA	Y405	W324	Q254	K179	I38
HIS		L325	T255	D180	G39
HIS	V408	F326	L256	T181	W40
HIS	D409	Q327	E259	L182	R41
HIS	N410	P328	V260	G183	F44
HIS	Y411	S329	P261	T192	
	L412	I330	A262	Q193	L49
	T413	N331	G263	R194	Q50
	L414	L332	L264	S195	Q51
	A417	P333	P265	Y196	L52
		I334	S266	D197	I53
	F422	F335	D267	V198	G54
	A424	A337	L269	A201	V55
Q425	Q426	G338		S202	A56
Q427	Q427	S339	R272	A203	L57
L428	L428	L340	D273	L204	E58
T429	T430	A342	I275	D205	N59
	D431	I349	A278	R207	N60
R432	L433	N354	E279	Q210	R61
L434		V355	H280	T211	D62
R434			Q281	A212	L63
Q435	L436	Y358	L282	V213	R64
L436	Q437	E359	N283	E214	V65
T437	S438	Q363	A284	Q215	
E439	T364	I289		A216	L68
V440		G290	S288	R217	N69
			T219	A218	V70
			L220	T219	E71
				A149	A72
				Q150	F73
					R74
					Y77

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.64Å 87.86Å 355.94Å 90.00° 98.94° 90.00°	Depositor
Resolution (Å)	87.91 – 3.80 87.91 – 3.80	Depositor EDS
% Data completeness (in resolution range)	86.8 (87.91-3.80) 84.4 (87.91-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 3.78Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.297 , 0.346 0.302 , 0.351	Depositor DCC
R_{free} test set	1992 reflections (4.29%)	wwPDB-VP
Wilson B-factor (Å ²)	96.7	Xtriage
Anisotropy	0.934	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 321.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.378 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.339 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	21050	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.23% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PLM

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	0.73	0/3557	1.09	22/4838 (0.5%)
1	B	0.76	3/3557 (0.1%)	1.07	13/4838 (0.3%)
1	C	0.75	0/3559	1.08	16/4841 (0.3%)
1	D	0.56	0/3557	1.03	14/4838 (0.3%)
1	E	0.57	0/3548	1.01	9/4826 (0.2%)
1	F	0.56	0/3557	1.02	11/4838 (0.2%)
All	All	0.66	3/21335 (0.0%)	1.05	85/29019 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	280	HIS	CG-ND1	-7.22	1.30	1.38
1	B	280	HIS	CG-CD2	6.67	1.43	1.35
1	B	280	HIS	ND1-CE1	5.32	1.37	1.32

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	272	ARG	CA-C-N	8.25	130.15	119.84
1	E	272	ARG	C-N-CA	8.25	130.15	119.84
1	C	272	ARG	CA-C-N	8.08	129.94	119.84
1	C	272	ARG	C-N-CA	8.08	129.94	119.84
1	B	81	ARG	N-CA-C	-7.98	102.17	111.03

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	3501	0	3475	195	0
1	B	3501	0	3475	182	0
1	C	3503	0	3480	185	0
1	D	3501	0	3476	195	0
1	E	3492	0	3468	196	0
1	F	3501	0	3476	217	0
2	A	17	0	31	0	0
2	B	17	0	31	0	0
2	C	17	0	31	1	0
All	All	21050	0	20943	1082	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 26.

The worst 5 of 1082 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:D:177:LEU:HD21	1:D:425:GLN:HB3	1.48	0.95
1:D:372:GLY:HA3	1:D:442:LEU:HD22	1.55	0.88
1:E:210:GLN:HE21	1:E:214:GLU:HG3	1.39	0.87
1:A:81:ARG:HA	1:A:136:ARG:HG3	1.57	0.87
1:E:98:ARG:HA	1:E:111:ILE:HG12	1.55	0.86

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	455/474 (96%)	363 (80%)	74 (16%)	18 (4%)	2	20
1	B	455/474 (96%)	368 (81%)	68 (15%)	19 (4%)	2	19
1	C	455/474 (96%)	365 (80%)	67 (15%)	23 (5%)	1	17
1	D	455/474 (96%)	371 (82%)	60 (13%)	24 (5%)	1	16
1	E	454/474 (96%)	380 (84%)	51 (11%)	23 (5%)	1	17
1	F	455/474 (96%)	385 (85%)	54 (12%)	16 (4%)	3	23
All	All	2729/2844 (96%)	2232 (82%)	374 (14%)	123 (4%)	2	18

5 of 123 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	23	ALA
1	A	69	ASN
1	A	314	SER
1	B	22	GLN

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	359/375 (96%)	313 (87%)	46 (13%)	4	21
1	B	359/375 (96%)	317 (88%)	42 (12%)	5	22
1	C	360/375 (96%)	311 (86%)	49 (14%)	3	18
1	D	359/375 (96%)	316 (88%)	43 (12%)	5	21
1	E	358/375 (96%)	321 (90%)	37 (10%)	7	27
1	F	359/375 (96%)	317 (88%)	42 (12%)	5	22
All	All	2154/2250 (96%)	1895 (88%)	259 (12%)	5	21

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	152	SER

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Mol	Chain	Res	Type
1	F	220	LEU
1	C	71	GLU
1	C	57	LEU
1	F	266	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	386	GLN
1	E	270	GLN
1	D	425	GLN
1	E	172	GLN
1	E	452	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 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	PLM	C	1001	1	15,16,17	0.36	0	14,15,17	1.03	0
2	PLM	B	1001	1	15,16,17	0.53	0	14,15,17	0.94	0
2	PLM	A	1001	1	15,16,17	1.66	3 (20%)	14,15,17	0.89	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLM	C	1001	1	-	7/14/14/15	-
2	PLM	B	1001	1	-	9/14/14/15	-
2	PLM	A	1001	1	-	7/14/14/15	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	PLM	C3-C2	4.49	1.71	1.52
2	A	1001	PLM	C5-C4	-2.74	1.38	1.51
2	A	1001	PLM	C7-C6	2.35	1.63	1.51

There are no bond angle outliers.

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	PLM	C4-C5-C6-C7
2	A	1001	PLM	CA-CB-CC-CD
2	B	1001	PLM	C2-C3-C4-C5
2	C	1001	PLM	C2-C3-C4-C5
2	A	1001	PLM	C2-C3-C4-C5

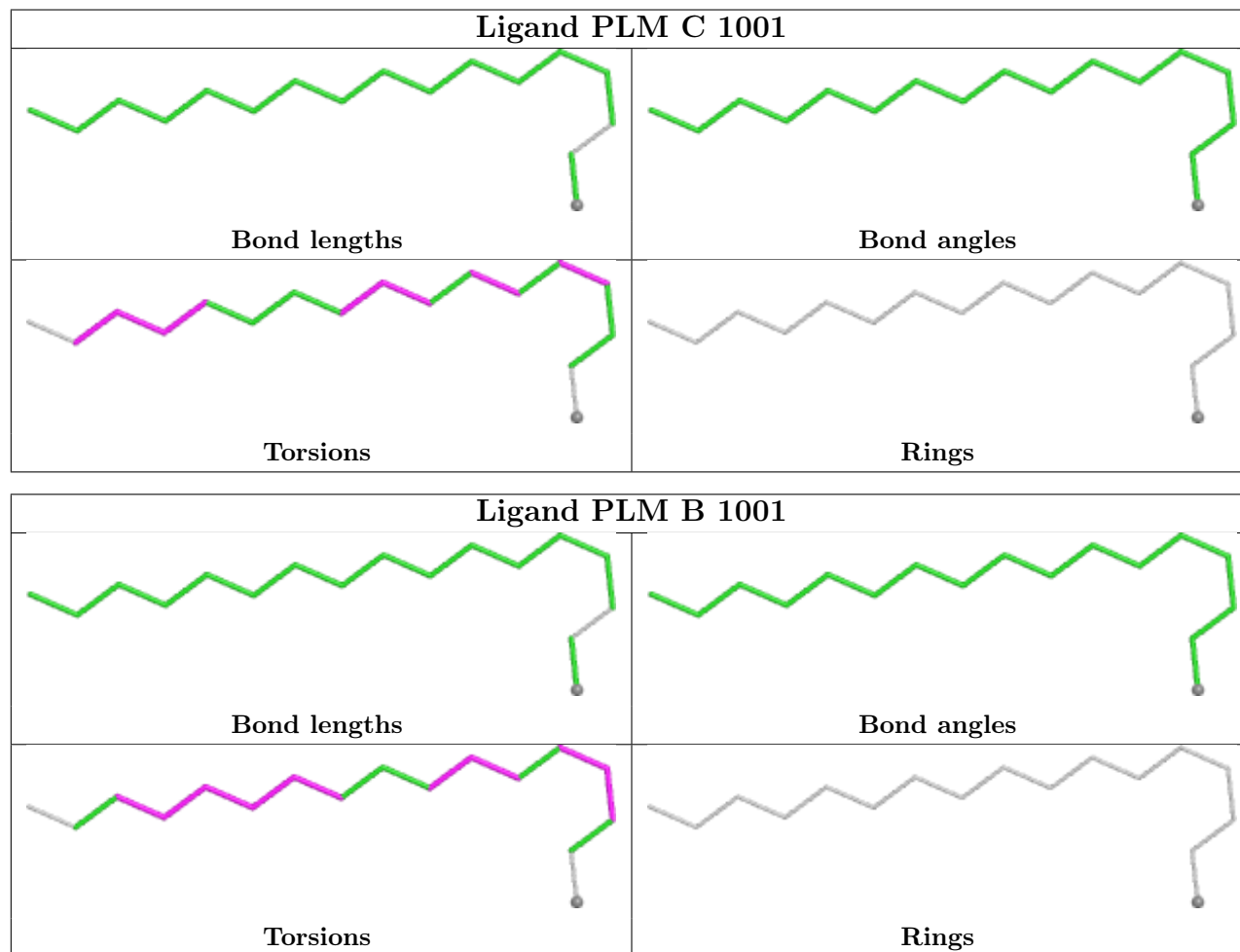
There are no ring outliers.

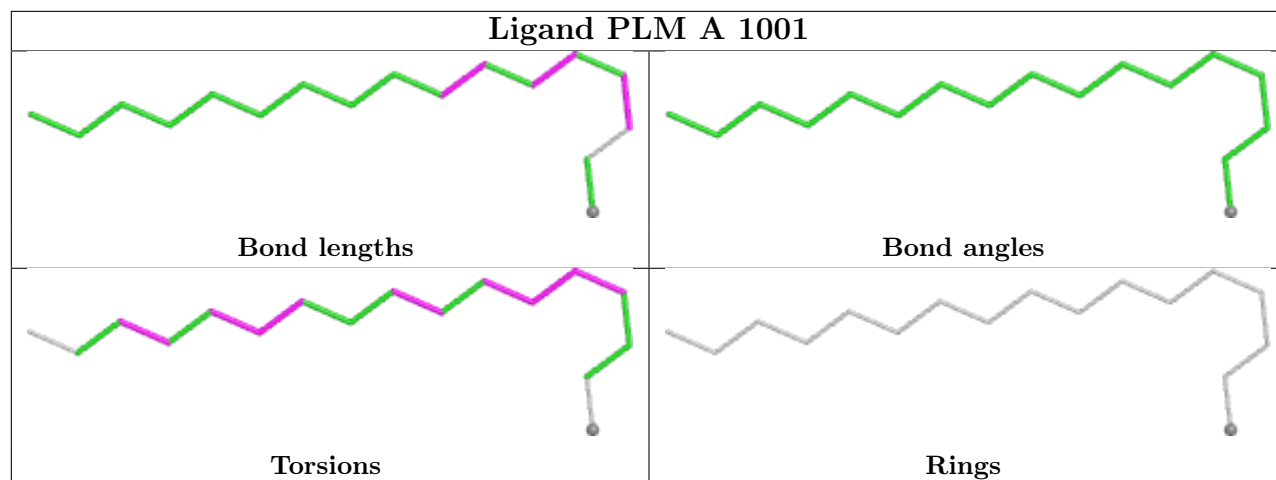
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	PLM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	457/474 (96%)	-0.35	7 (1%) 72 50	57, 72, 105, 105	0
1	B	457/474 (96%)	-0.42	1 (0%) 91 81	54, 69, 102, 102	0
1	C	457/474 (96%)	-0.41	6 (1%) 75 53	54, 69, 102, 102	0
1	D	457/474 (96%)	-0.01	14 (3%) 51 35	81, 121, 121, 121	0
1	E	456/474 (96%)	0.02	13 (2%) 53 37	109, 120, 120, 120	0
1	F	457/474 (96%)	0.01	12 (2%) 57 39	79, 119, 119, 119	0
All	All	2741/2844 (96%)	-0.19	53 (1%) 66 45	54, 105, 121, 121	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	203	ALA	5.5
1	E	368	GLU	5.0
1	D	260	VAL	4.7
1	F	156	THR	4.7
1	A	202	SER	4.5

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

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

6.3 Carbohydrates [i](#)

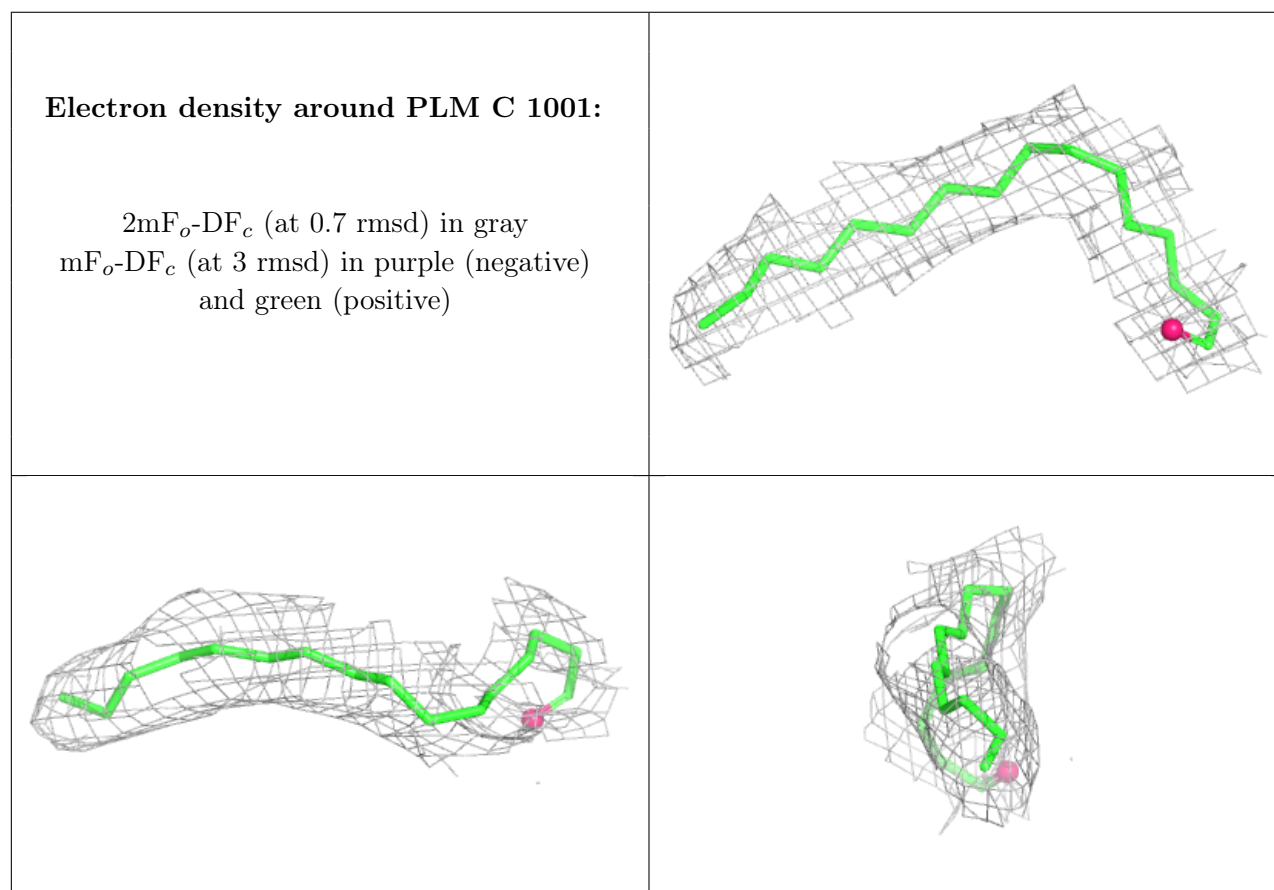
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

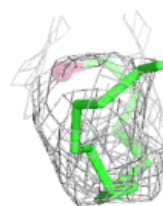
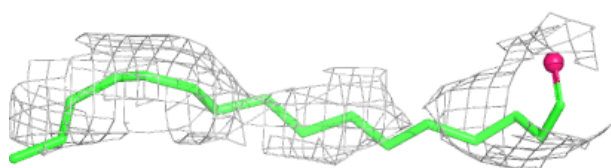
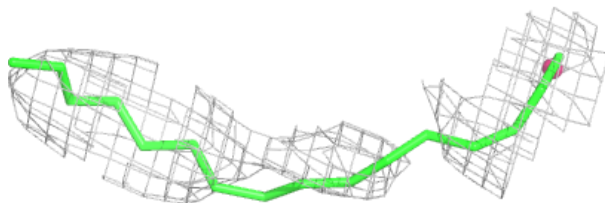
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PLM	C	1001	17/18	0.96	0.07	58,58,58,58	0
2	PLM	B	1001	17/18	0.97	0.09	72,72,72,72	0
2	PLM	A	1001	17/18	0.98	0.08	72,72,76,76	0

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.

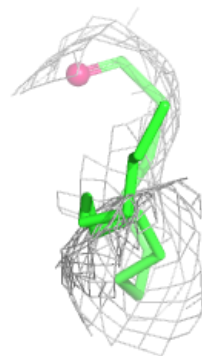
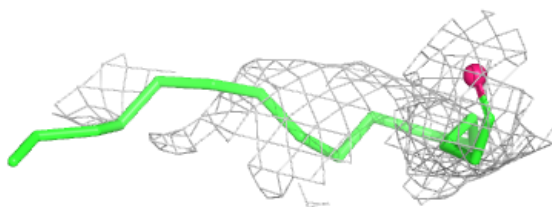
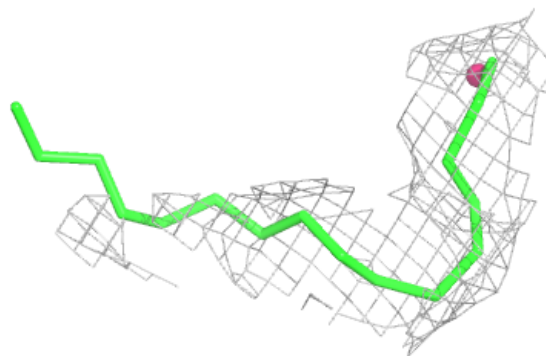


Electron density around PLM B 1001:

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

**Electron density around PLM A 1001:**

$2mF_o-DF_c$ (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.