



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:33 PM EDT

PDB ID : 6P1Z / pdb_00006p1z
Title : Bacteriophage phiKZ gp163.1 PAAR repeat protein in complex with the C-terminal part of the T4 gp5 beta-helical domain
Authors : Buth, S.A.; Shneider, M.M.; Leiman, P.G.
Deposited on : 2019-05-20
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

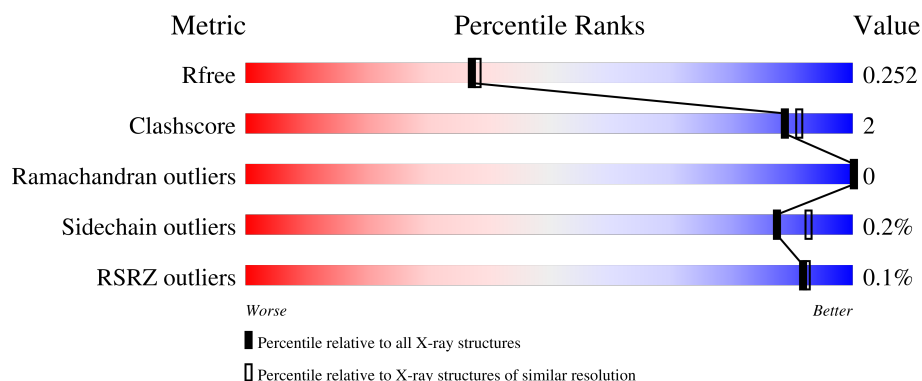
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



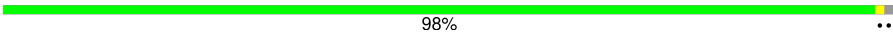
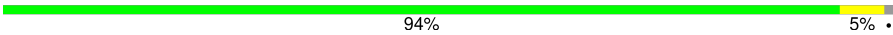
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	96	95%
1	B	96	94%
1	C	96	%
1	E	96	92%
1	F	96	93%

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Mol	Chain	Length	Quality of chain
1	G	96	 91%5% •
2	D	88	 98%5% ••
2	H	88	 94%5% •

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11666 atoms, of which 5342 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 Baseplate central spike complex protein gp5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	92	Total	C	H	N	O	S	0	2	0
			1333	413	656	113	149	2			
1	B	92	Total	C	H	N	O	S	0	0	0
			1316	408	646	112	148	2			
1	C	92	Total	C	H	N	O	S	0	1	0
			1317	408	647	112	148	2			
1	E	92	Total	C	H	N	O	S	0	4	0
			1358	420	668	115	153	2			
1	F	92	Total	C	H	N	O	S	0	2	0
			1329	412	651	113	151	2			
1	G	92	Total	C	H	N	O	S	0	4	0
			1345	416	662	114	151	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	480	GLY	-	expression tag	UNP P16009
A	481	SER	-	expression tag	UNP P16009
A	482	GLY	-	expression tag	UNP P16009
A	483	SER	-	expression tag	UNP P16009
B	480	GLY	-	expression tag	UNP P16009
B	481	SER	-	expression tag	UNP P16009
B	482	GLY	-	expression tag	UNP P16009
B	483	SER	-	expression tag	UNP P16009
C	480	GLY	-	expression tag	UNP P16009
C	481	SER	-	expression tag	UNP P16009
C	482	GLY	-	expression tag	UNP P16009
C	483	SER	-	expression tag	UNP P16009
E	480	GLY	-	expression tag	UNP P16009
E	481	SER	-	expression tag	UNP P16009
E	482	GLY	-	expression tag	UNP P16009
E	483	SER	-	expression tag	UNP P16009
F	480	GLY	-	expression tag	UNP P16009

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Chain	Residue	Modelled	Actual	Comment	Reference
F	481	SER	-	expression tag	UNP P16009
F	482	GLY	-	expression tag	UNP P16009
F	483	SER	-	expression tag	UNP P16009
G	480	GLY	-	expression tag	UNP P16009
G	481	SER	-	expression tag	UNP P16009
G	482	GLY	-	expression tag	UNP P16009
G	483	SER	-	expression tag	UNP P16009

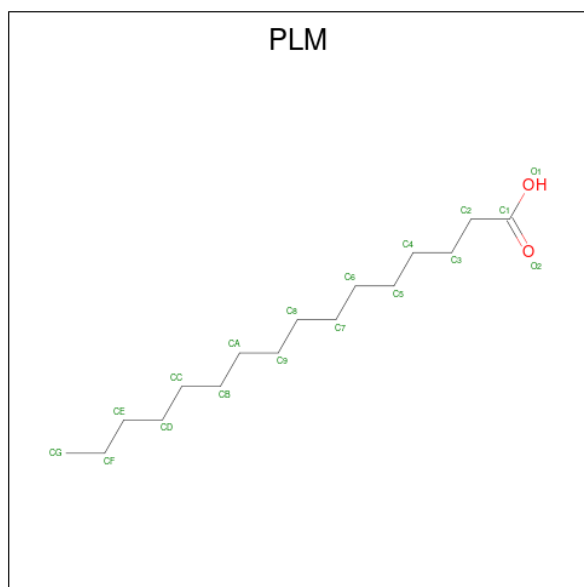
- Molecule 2 is a protein called PAAR-repeat central spike tip protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	D	87	Total	C	H	N	O	S	0	2	0
			1220	375	612	112	110	11			
2	H	87	Total	C	H	N	O	S	0	0	0
			1202	370	602	111	109	10			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

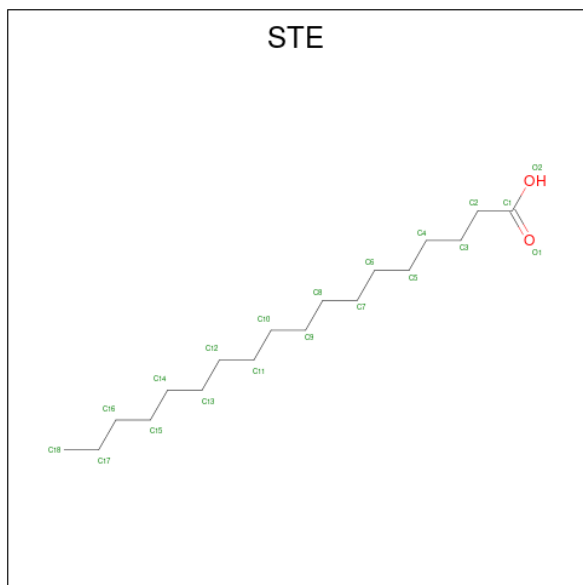
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



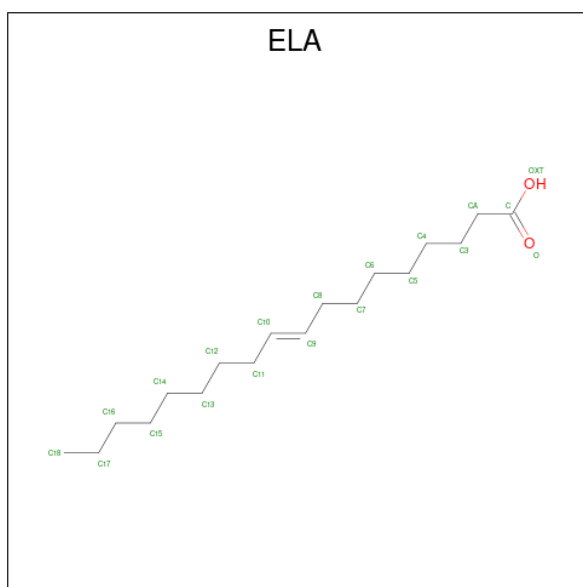
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			49	16	31	2		
4	E	1	Total	C	H	O	0	0
			49	16	31	2		

- Molecule 5 is STEARIC ACID (CCD ID: STE) (formula: $C_{18}H_{36}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	H	O	0	0
			55	18	35	2		
5	G	1	Total	C	H	O	0	0
			55	18	35	2		

- Molecule 6 is Elaidic acid (CCD ID: ELA) (formula: $C_{18}H_{34}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	H	O	0	0
			53	18	33	2		
6	E	1	Total	C	H	O	0	0
			53	18	33	2		

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total	Zn	0	0
			1	1		
7	H	1	Total	Zn	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	155	Total	O	0	0
			155	155		
8	B	121	Total	O	0	0
			121	121		
8	C	135	Total	O	0	0
			135	135		
8	D	93	Total	O	0	0
			93	93		
8	E	113	Total	O	0	0
			113	113		

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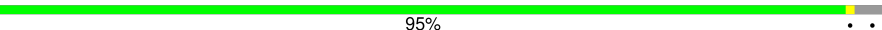
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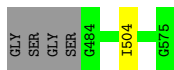
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	F	108	Total 108	O 108	0	0
8	G	114	Total 114	O 114	0	0
8	H	89	Total 89	O 89	0	0

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.

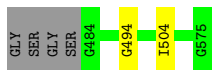
- Molecule 1: Baseplate central spike complex protein gp5

Chain A:  95%

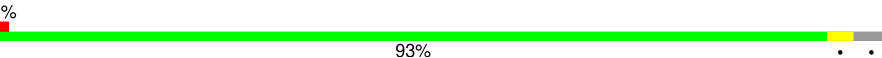


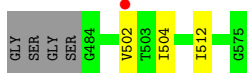
- Molecule 1: Baseplate central spike complex protein gp5

Chain B:  94%



- Molecule 1: Baseplate central spike complex protein gp5

Chain C:  93%



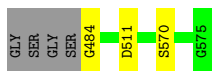
- Molecule 1: Baseplate central spike complex protein gp5

Chain E:  92%



- Molecule 1: Baseplate central spike complex protein gp5

Chain F:  93%



- Molecule 1: Baseplate central spike complex protein gp5

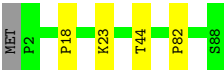
Chain G:  91%



• Molecule 2: PAAR-repeat central spike tip protein



• Molecule 2: PAAR-repeat central spike tip protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.28Å 69.12Å 77.80Å 90.00° 102.48° 90.00°	Depositor
Resolution (Å)	44.60 – 2.10 44.60 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.2 (44.60-2.10) 95.0 (44.60-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.188 , 0.251 0.190 , 0.252	Depositor DCC
R_{free} test set	1529 reflections (3.48%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.567	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 54.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11666	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.35 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.1864e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ELA, STE, MG, PLM, ZN

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	0.07	0/690	0.23	0/937
1	B	0.08	0/676	0.23	0/917
1	C	0.08	0/680	0.23	0/922
1	E	0.07	0/703	0.21	0/955
1	F	0.07	0/692	0.22	0/939
1	G	0.07	0/702	0.21	0/953
2	D	0.11	0/625	0.29	0/843
2	H	0.11	0/612	0.27	0/826
All	All	0.08	0/5380	0.24	0/7292

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 [i](#)

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	677	656	648	1	0
1	B	670	646	646	2	0
1	C	670	647	643	3	0
1	E	690	668	658	3	0
1	F	678	651	639	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	683	662	648	6	0
2	D	608	612	606	0	0
2	H	600	602	602	4	0
3	A	1	0	0	0	0
3	E	1	0	0	0	0
4	B	18	31	31	0	0
4	E	18	31	31	2	0
5	C	20	35	35	2	0
5	G	20	35	35	0	0
6	C	20	33	33	2	0
6	E	20	33	33	0	0
7	D	1	0	0	0	0
7	H	1	0	0	0	0
8	A	155	0	0	0	0
8	B	121	0	0	0	1
8	C	135	0	0	0	0
8	D	93	0	0	0	1
8	E	113	0	0	1	0
8	F	108	0	0	4	0
8	G	114	0	0	1	0
8	H	89	0	0	3	0
All	All	6324	5342	5288	20	1

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 2.

The worst 5 of 20 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:E:484:GLY:N	8:E:702:HOH:O	2.30	0.64
2:H:18:PRO:O	8:H:201:HOH:O	2.14	0.64
1:F:570:SER:OG	8:F:601:HOH:O	2.17	0.60
1:G:484:GLY:N	8:G:702:HOH:O	2.37	0.57
1:F:484:GLY:N	8:F:605:HOH:O	2.36	0.57

All (1) 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)
8:B:770:HOH:O	8:D:265:HOH:O[2_847]	2.14	0.06

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	92/96 (96%)	92 (100%)	0	0	100	100
1	B	90/96 (94%)	90 (100%)	0	0	100	100
1	C	91/96 (95%)	91 (100%)	0	0	100	100
1	E	94/96 (98%)	94 (100%)	0	0	100	100
1	F	92/96 (96%)	90 (98%)	2 (2%)	0	100	100
1	G	94/96 (98%)	94 (100%)	0	0	100	100
2	D	87/88 (99%)	82 (94%)	5 (6%)	0	100	100
2	H	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
All	All	725/752 (96%)	714 (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	76/76 (100%)	76 (100%)	0	100	100
1	B	74/76 (97%)	74 (100%)	0	100	100
1	C	74/76 (97%)	74 (100%)	0	100	100
1	E	78/76 (103%)	78 (100%)	0	100	100
1	F	76/76 (100%)	76 (100%)	0	100	100
1	G	78/76 (103%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	64/64 (100%)	63 (98%)	1 (2%)	55	64
2	H	63/64 (98%)	63 (100%)	0	100	100
All	All	583/584 (100%)	582 (100%)	1 (0%)	87	93

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

Mol	Chain	Res	Type
2	D	23	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	$\# Z > 2$
4	PLM	B	601	-	17,17,17	0.59	0	17,17,17	1.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	STE	C	601	-	19,19,19	0.57	0	19,19,19	1.09	1 (5%)
4	PLM	E	603	-	17,17,17	0.61	0	17,17,17	1.01	0
5	STE	G	601	-	19,19,19	0.58	0	19,19,19	1.04	0
6	ELA	E	602	-	19,19,19	0.58	0	19,19,19	0.67	0
6	ELA	C	602	-	19,19,19	0.59	0	19,19,19	0.72	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
4	PLM	B	601	-	-	9/15/15/15	-
5	STE	C	601	-	-	9/17/17/17	-
4	PLM	E	603	-	-	11/15/15/15	-
5	STE	G	601	-	-	10/17/17/17	-
6	ELA	E	602	-	-	12/17/17/17	-
6	ELA	C	602	-	-	13/17/17/17	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	601	STE	C3-C2-C1	-2.15	108.90	114.51

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

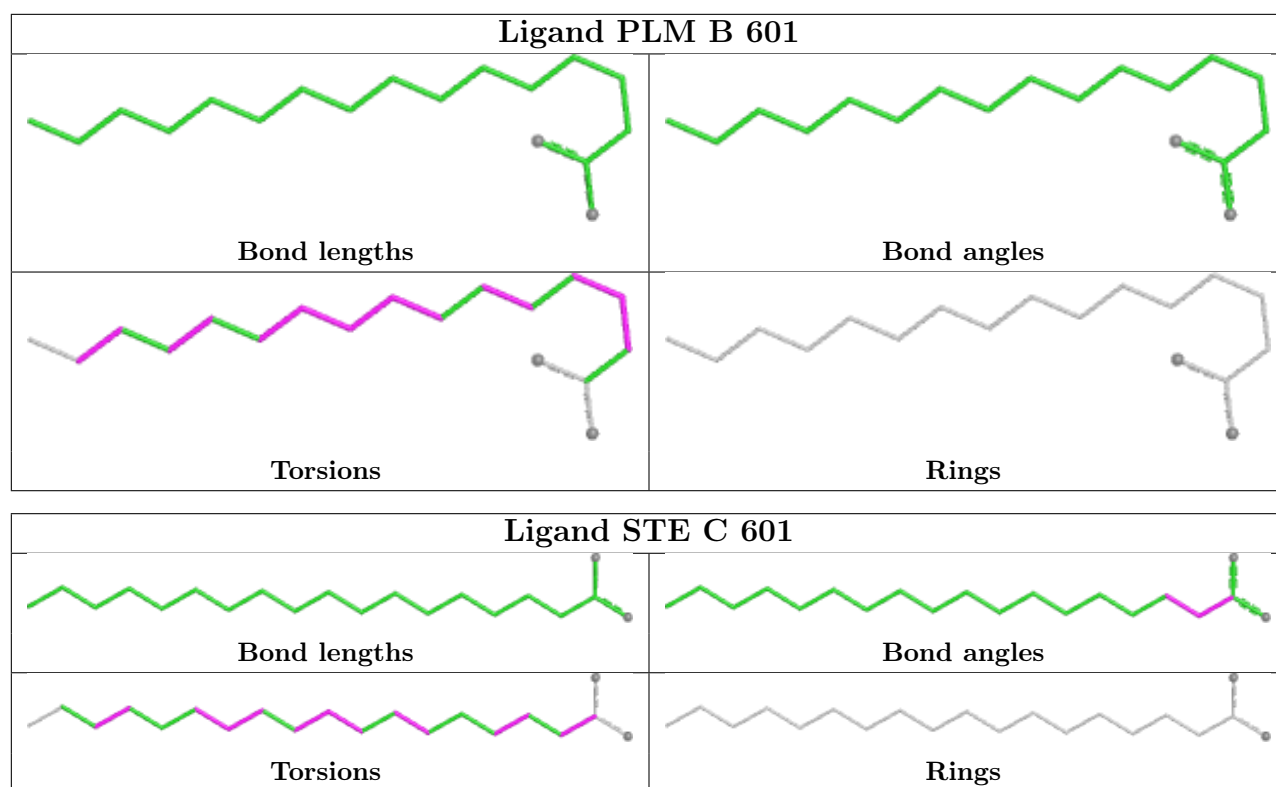
Mol	Chain	Res	Type	Atoms
4	E	603	PLM	C1-C2-C3-C4
4	E	603	PLM	C6-C7-C8-C9
6	E	602	ELA	C4-C3-CA-C
6	E	602	ELA	C5-C6-C7-C8
4	B	601	PLM	C8-C9-CA-CB

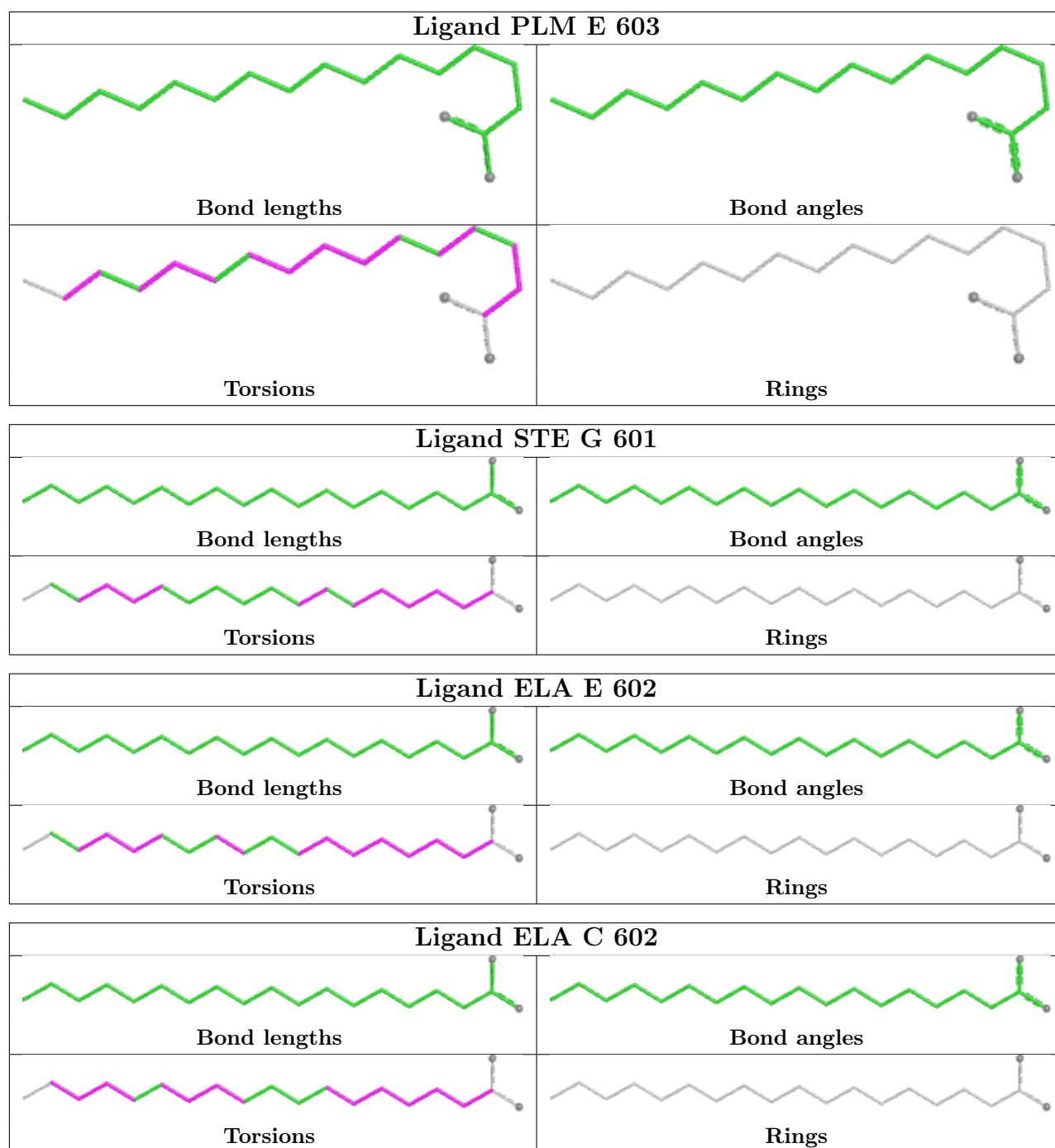
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	601	STE	2	0
4	E	603	PLM	2	0
6	C	602	ELA	2	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	92/96 (95%)	-0.27	0	100	100	11, 24, 40, 56	1 (1%)
1	B	92/96 (95%)	-0.32	0	100	100	17, 24, 35, 51	0
1	C	92/96 (95%)	-0.31	1 (1%)	78	80	18, 24, 40, 51	0
1	E	92/96 (95%)	0.19	0	100	100	16, 32, 47, 71	3 (3%)
1	F	92/96 (95%)	0.16	0	100	100	14, 32, 47, 74	1 (1%)
1	G	92/96 (95%)	0.11	0	100	100	13, 31, 52, 66	2 (2%)
2	D	87/88 (98%)	-0.45	0	100	100	15, 22, 37, 101	1 (1%)
2	H	87/88 (98%)	0.04	0	100	100	22, 32, 52, 94	0
All	All	726/752 (96%)	-0.10	1 (0%)	92	92	11, 28, 46, 101	8 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	502	VAL	2.3

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.

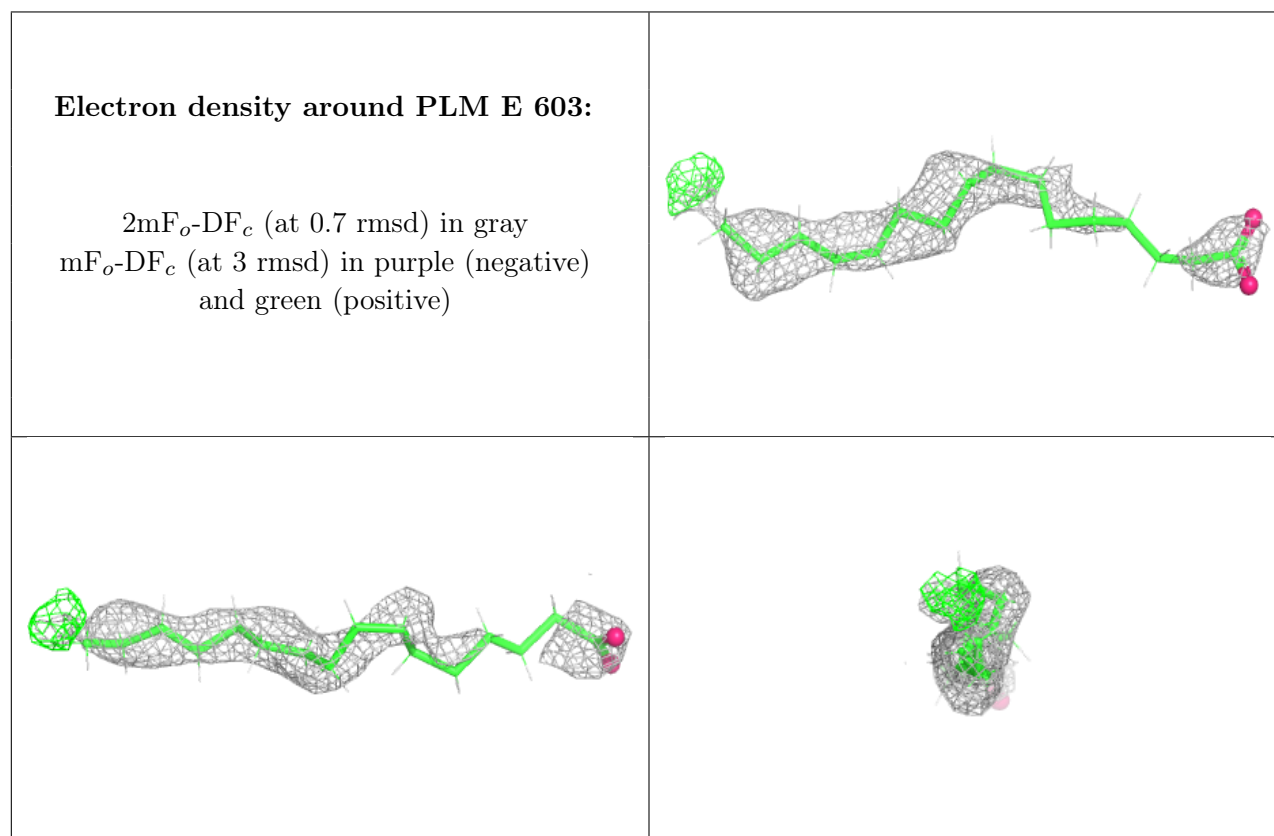
6.4 Ligands [i](#)

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.

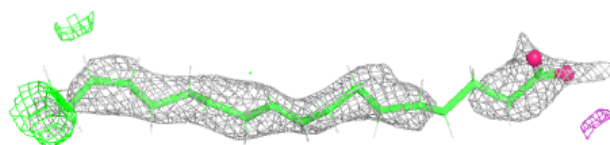
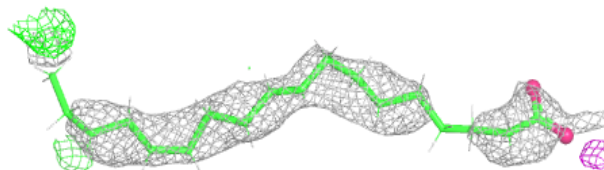
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PLM	E	603	18/18	0.81	0.18	48,70,87,88	0
6	ELA	C	602	20/20	0.81	0.16	44,63,94,102	0
6	ELA	E	602	20/20	0.81	0.18	43,69,91,98	0
5	STE	G	601	20/20	0.83	0.20	38,64,94,96	0
4	PLM	B	601	18/18	0.85	0.17	38,65,91,96	0
5	STE	C	601	20/20	0.90	0.14	31,63,80,88	0
3	MG	E	601	1/1	0.95	0.03	18,18,18,18	0
3	MG	A	601	1/1	0.98	0.03	15,15,15,15	0
7	ZN	D	101	1/1	0.99	0.11	14,14,14,14	0
7	ZN	H	101	1/1	0.99	0.06	24,24,24,24	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.

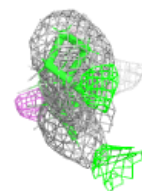
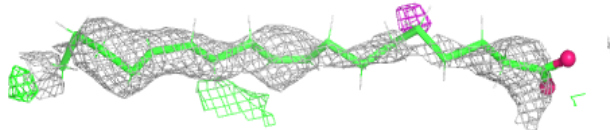
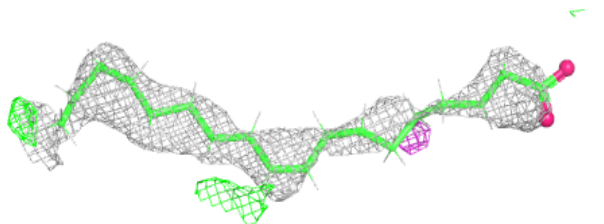


Electron density around ELA C 602:

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

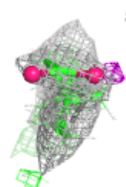
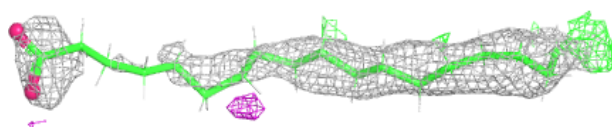
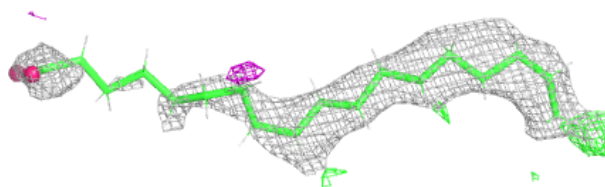
**Electron density around ELA E 602:**

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

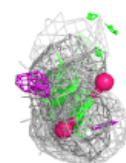
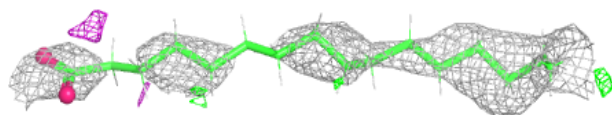
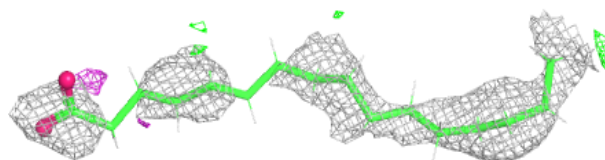


Electron density around STE G 601:

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

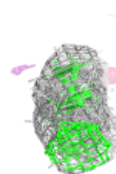
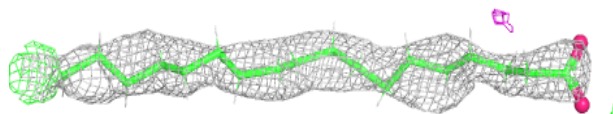
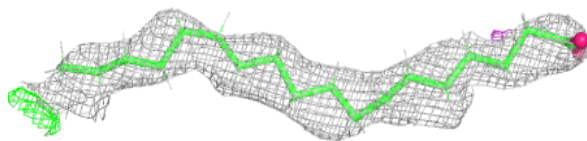
**Electron density around PLM B 601:**

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



Electron density around STE C 601:

$2mF_o-DF_c$ (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.