



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 11:48 PM UTC

PDB ID : 9BE3 / pdb_00009be3
Title : The pre-condensation state of the dimodular NRPS protein LgrA
Authors : Pistofidis, A.; Schmeing, T.M.
Deposited on : 2024-04-13
Resolution : 2.90 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)
Xtrriage (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

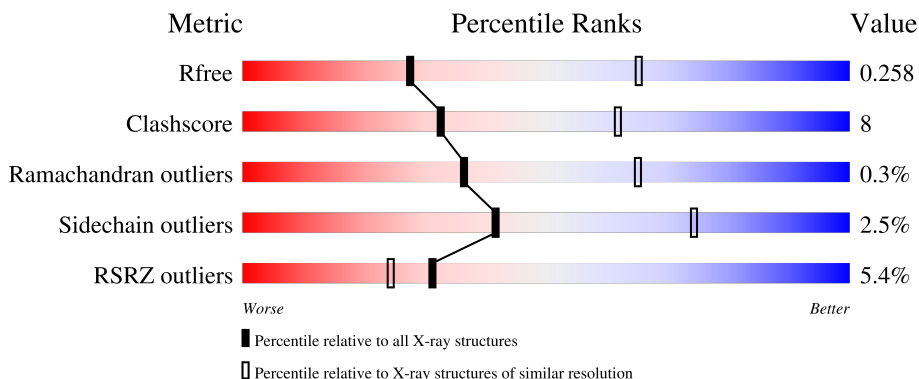
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	1814	 4% 76% 21% ..
1	B	1814	 6% 79% 17% ..

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
5	MN	B	1905	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 28355 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 Linear gramicidin synthase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1774	14120	9015	2413	2634	58	0	1	0
1	B	1746	13627	8719	2307	2544	57	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

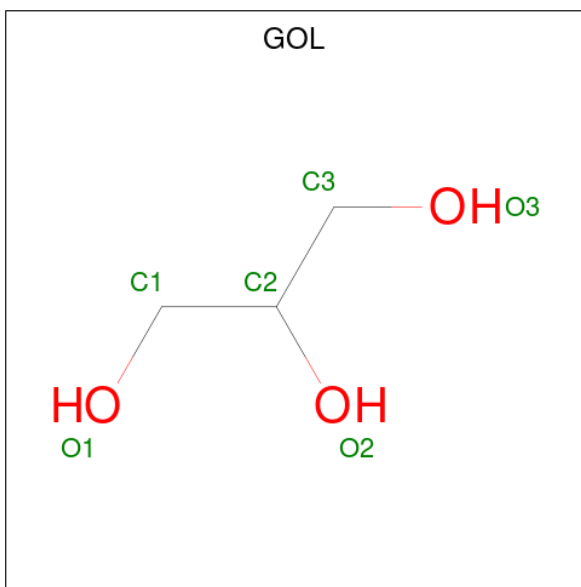
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q70LM7
A	2	GLY	-	expression tag	UNP Q70LM7
A	770A	ASN	SER	conflict	UNP Q70LM7
A	770B	GLY	-	insertion	UNP Q70LM7
A	771	LEU	-	insertion	UNP Q70LM7
A	1804	ALA	-	expression tag	UNP Q70LM7
A	1805	ALA	-	expression tag	UNP Q70LM7
A	1806	ALA	-	expression tag	UNP Q70LM7
A	1807	GLU	-	expression tag	UNP Q70LM7
A	1808	ASN	-	expression tag	UNP Q70LM7
A	1809	LEU	-	expression tag	UNP Q70LM7
A	1810	TYR	-	expression tag	UNP Q70LM7
A	1811	PHE	-	expression tag	UNP Q70LM7
A	1812	GLN	-	expression tag	UNP Q70LM7
B	1	MET	-	initiating methionine	UNP Q70LM7
B	2	GLY	-	expression tag	UNP Q70LM7
B	770A	ASN	SER	conflict	UNP Q70LM7
B	770B	GLY	-	insertion	UNP Q70LM7
B	771	LEU	-	insertion	UNP Q70LM7
B	1804	ALA	-	expression tag	UNP Q70LM7
B	1805	ALA	-	expression tag	UNP Q70LM7
B	1806	ALA	-	expression tag	UNP Q70LM7
B	1807	GLU	-	expression tag	UNP Q70LM7
B	1808	ASN	-	expression tag	UNP Q70LM7
B	1809	LEU	-	expression tag	UNP Q70LM7

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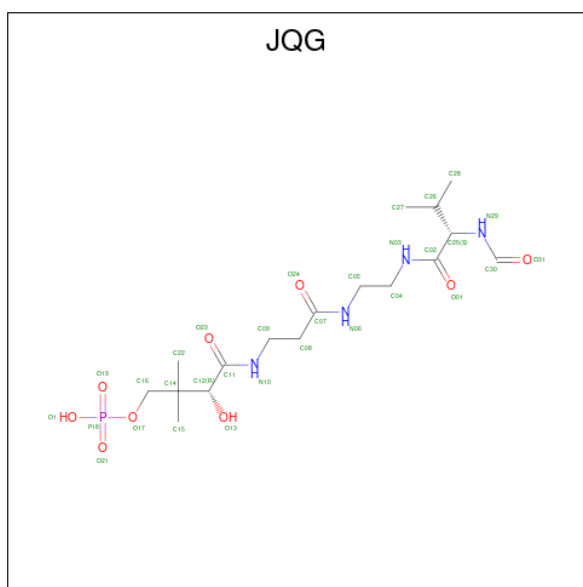
Chain	Residue	Modelled	Actual	Comment	Reference
B	1810	TYR	-	expression tag	UNP Q70LM7
B	1811	PHE	-	expression tag	UNP Q70LM7
B	1812	GLN	-	expression tag	UNP Q70LM7

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



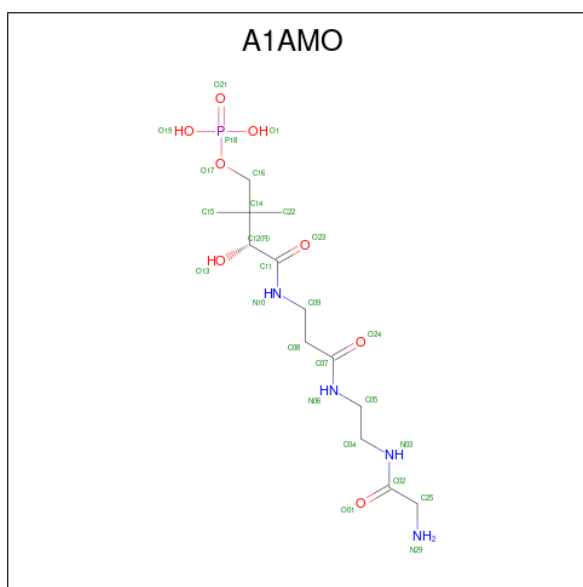
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is (2 {R})- {N}-[3-[2-[(2 {S})-2-formamido-3-methyl-butanoyl]amino]ethylamin o]-3-oxidanylidene-propyl]-3,3-dimethyl-2-oxidanyl-4-[oxidanyl-bis(oxidanylidene)-\$1^{\wedge}\{6\}\$-phosphanyl]oxy-butanamide (CCD ID: JQG) (formula: C₁₇H₃₂N₄O₉P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total	C	N	O	P	0	0
			30	17	4	8	1		
3	B	1	Total	C	N	O	P	0	0
			30	17	4	8	1		

- Molecule 4 is N-[2-(glycylamino)ethyl]-N 3 -(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alaninamide (CCD ID: A1AMO) (formula: $C_{13}H_{27}N_4O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	Total	C	N	O	P	0	0
			25	13	4	7	1		

- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Mn 1	0	0
5	B	3	Total 3	Mn 3	0	0

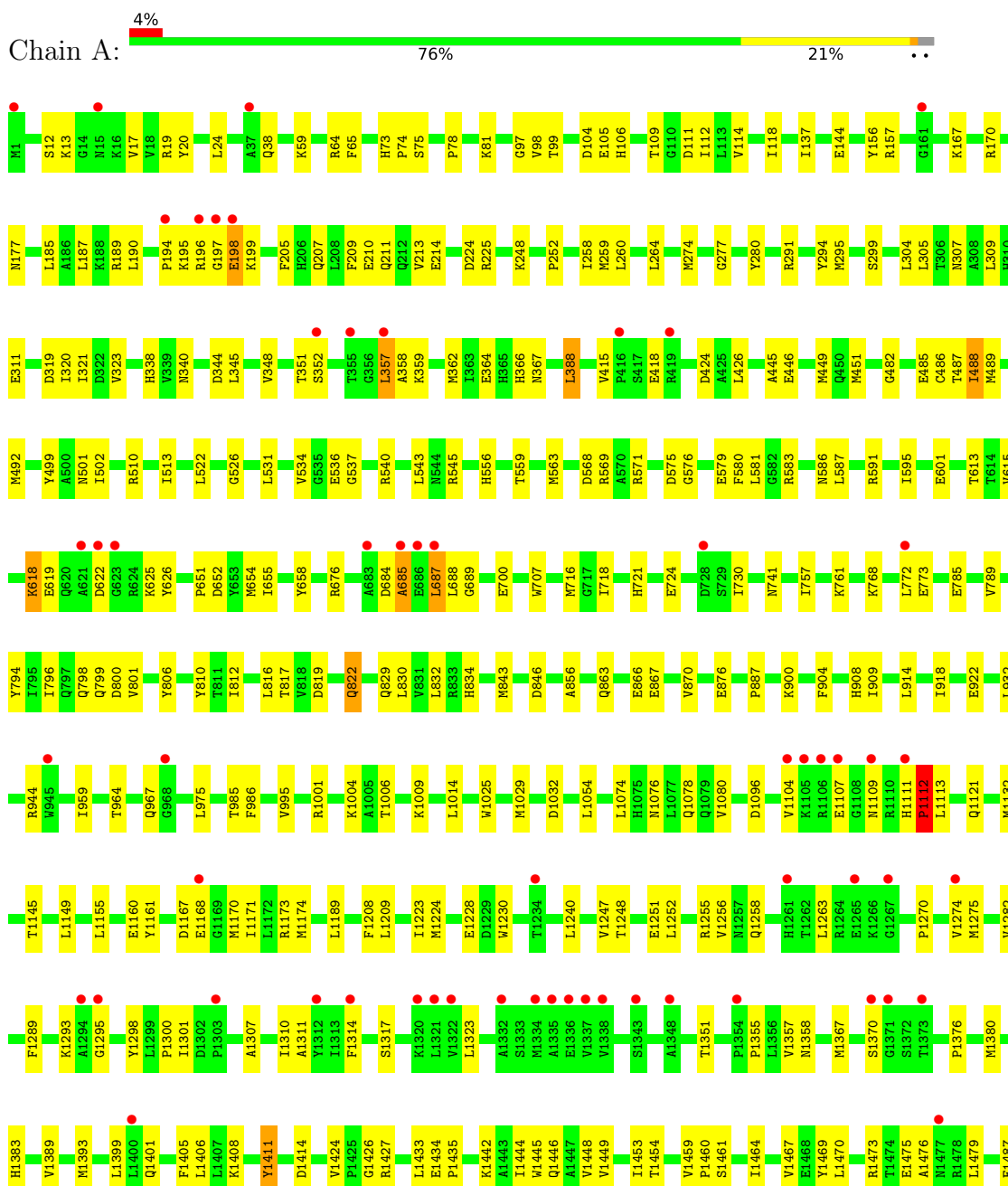
- Molecule 6 is water.

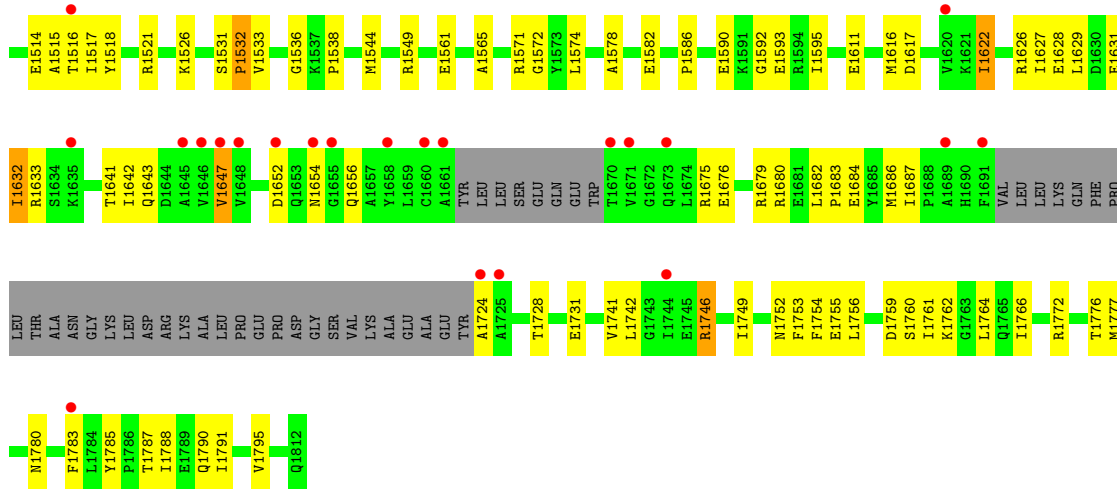
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	277	Total 277	O 277	0	0
6	B	224	Total 224	O 224	0	0

3 Residue-property plots

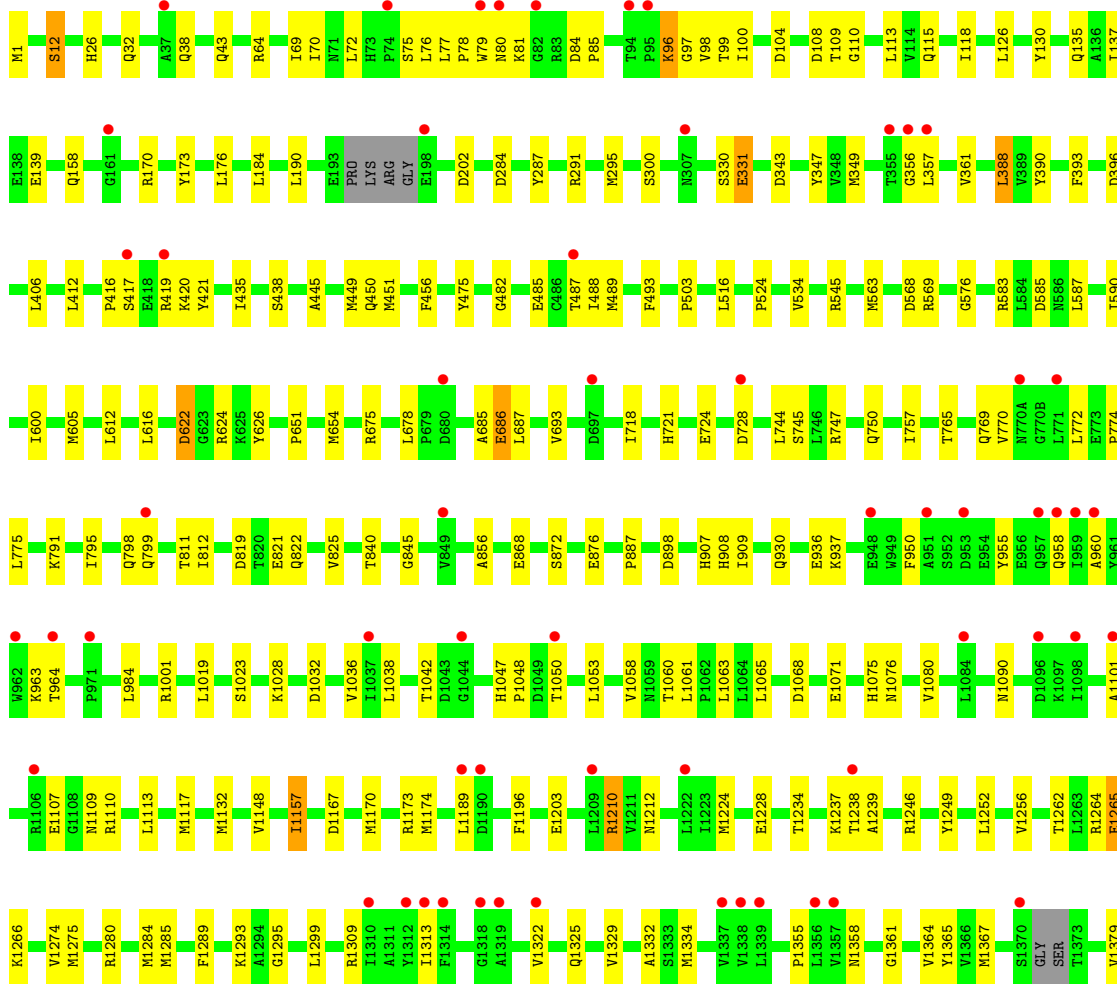
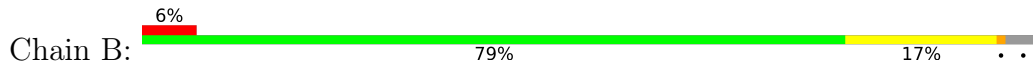
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Linear gramicidin synthase subunit A





● Molecule 1: Linear gramicidin synthase subunit A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	184.82Å 427.90Å 77.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.74 – 2.90 48.74 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.74-2.90) 98.9 (48.74-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.91Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.216 , 0.258 0.216 , 0.258	Depositor DCC
R_{free} test set	3109 reflections (2.15%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtrriage
Anisotropy	0.242	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 67.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	28355	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.17% 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: JQG, GOL, A1AMO, MN

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	0.16	0/14430	0.33	1/19594 (0.0%)
1	B	0.14	0/13926	0.31	0/18947
All	All	0.15	0/28356	0.32	1/38541 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1643	GLN	N-CA-C	-6.04	106.55	114.04

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1746	ARG	Sidechain

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	14120	0	14025	252	2
1	B	13627	0	13332	187	2
2	A	12	0	16	0	0
2	B	6	0	8	0	0
3	A	30	0	0	0	0
3	B	30	0	0	0	0
4	A	25	0	0	0	0
5	A	1	0	0	0	0
5	B	3	0	0	0	0
6	A	277	0	0	6	0
6	B	224	0	0	1	0
All	All	28355	0	27381	438	2

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 8.

The worst 5 of 438 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:248:LYS:NZ	1:A:319:ASP:OD2	2.05	0.88
1:B:130:TYR:OH	1:B:170:ARG:NH2	2.08	0.86
1:B:1759:ASP:OD1	1:B:1760:SER:N	2.09	0.84
1:B:1264:ARG:NH2	1:B:1355:PRO:O	2.11	0.83
1:B:1751:ASP:HB3	1:B:1756:LEU:HD21	1.61	0.82

All (2) 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:38:GLN:NE2	1:B:43:GLN:OE1[1_456]	2.12	0.08
1:A:38:GLN:NE2	1:B:43:GLN:NE2[1_456]	2.17	0.03

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	1769/1814 (98%)	1693 (96%)	67 (4%)	9 (0%)	24	54
1	B	1734/1814 (96%)	1640 (95%)	92 (5%)	2 (0%)	48	77
All	All	3503/3628 (97%)	3333 (95%)	159 (4%)	11 (0%)	36	65

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	685	ALA
1	A	1112	PRO
1	A	194	PRO
1	A	198	GLU
1	A	687	LEU

5.3.2 Protein sidechains [i](#)

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	1515/1563 (97%)	1485 (98%)	30 (2%)	48	78
1	B	1429/1563 (91%)	1385 (97%)	44 (3%)	35	69
All	All	2944/3126 (94%)	2870 (98%)	74 (2%)	42	74

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1210	ARG
1	B	1749	ILE
1	B	1274	VAL
1	B	1504	VAL
1	A	1642	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1191	GLN
1	B	1550	HIS
1	B	1736	HIS
1	A	1134	HIS
1	A	1131	ASN

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	$\# Z > 2$
3	JQG	B	1902	1	24,29,30	2.39	7 (29%)	30,38,41	1.19	3 (10%)
2	GOL	B	1901	-	5,5,5	0.08	0	5,5,5	0.39	0
2	GOL	A	1902	-	5,5,5	0.08	0	5,5,5	0.33	0
3	JQG	A	1903	1	24,29,30	2.41	7 (29%)	30,38,41	1.37	4 (13%)
2	GOL	A	1901	-	5,5,5	0.10	0	5,5,5	0.29	0
4	A1AMO	A	1904	1	18,24,25	2.57	6 (33%)	21,31,34	1.10	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
3	JQG	B	1902	1	-	16/38/40/41	-
2	GOL	B	1901	-	-	0/4/4/4	-
2	GOL	A	1902	-	-	0/4/4/4	-
3	JQG	A	1903	1	-	8/38/40/41	-
2	GOL	A	1901	-	-	0/4/4/4	-
4	A1AMO	A	1904	1	-	9/29/31/32	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1902	JQG	C07-N06	5.88	1.47	1.33
3	A	1903	JQG	C07-N06	5.75	1.47	1.33
4	A	1904	A1AMO	C02-N03	5.74	1.47	1.33
4	A	1904	A1AMO	C07-N06	5.68	1.46	1.33
3	A	1903	JQG	C11-N10	5.66	1.46	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1903	JQG	C25-C02-N03	3.90	122.81	116.38
3	B	1902	JQG	C25-C02-N03	3.20	121.66	116.38
3	A	1903	JQG	C02-C25-N29	2.30	116.58	110.31
3	A	1903	JQG	C04-N03-C02	-2.16	118.66	122.55
3	A	1903	JQG	O01-C02-N03	-2.09	118.57	122.98

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

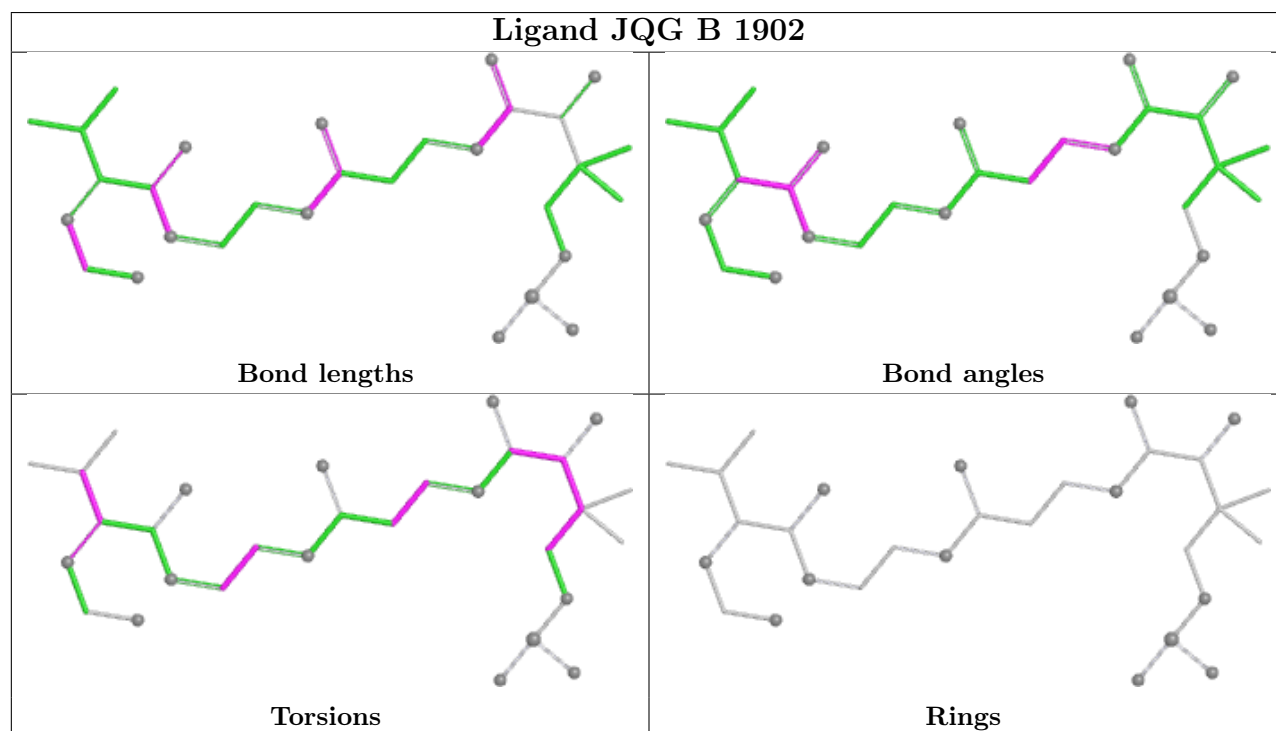
Mol	Chain	Res	Type	Atoms
3	A	1903	JQG	C12-C14-C16-O17
3	A	1903	JQG	C15-C14-C16-O17
3	A	1903	JQG	C22-C14-C16-O17
3	A	1903	JQG	C02-C25-N29-C30
3	B	1902	JQG	C07-C08-C09-N10

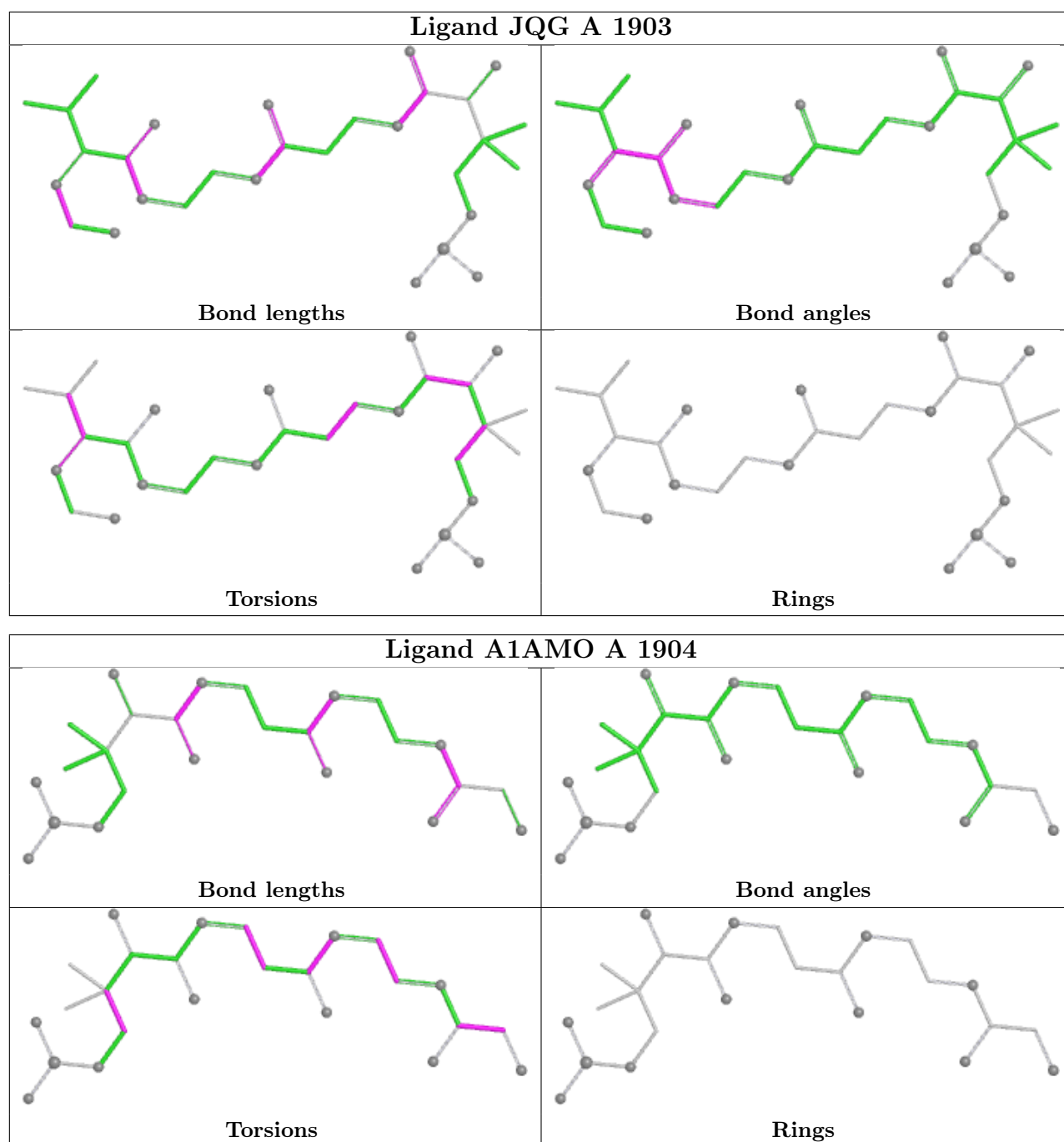
There are no ring outliers.

No monomer is involved in short contacts.

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	1774/1814 (97%)	0.34	80 (4%) 38 30	29, 56, 102, 162	1 (0%)
1	B	1746/1814 (96%)	0.42	109 (6%) 26 21	24, 61, 99, 130	0
All	All	3520/3628 (97%)	0.38	189 (5%) 31 24	24, 58, 100, 162	1 (0%)

The worst 5 of 189 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	683	ALA	7.2
1	A	1724	ALA	6.5
1	A	1646	VAL	5.9
1	B	1726	PRO	5.5
1	B	357	LEU	5.4

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](#)

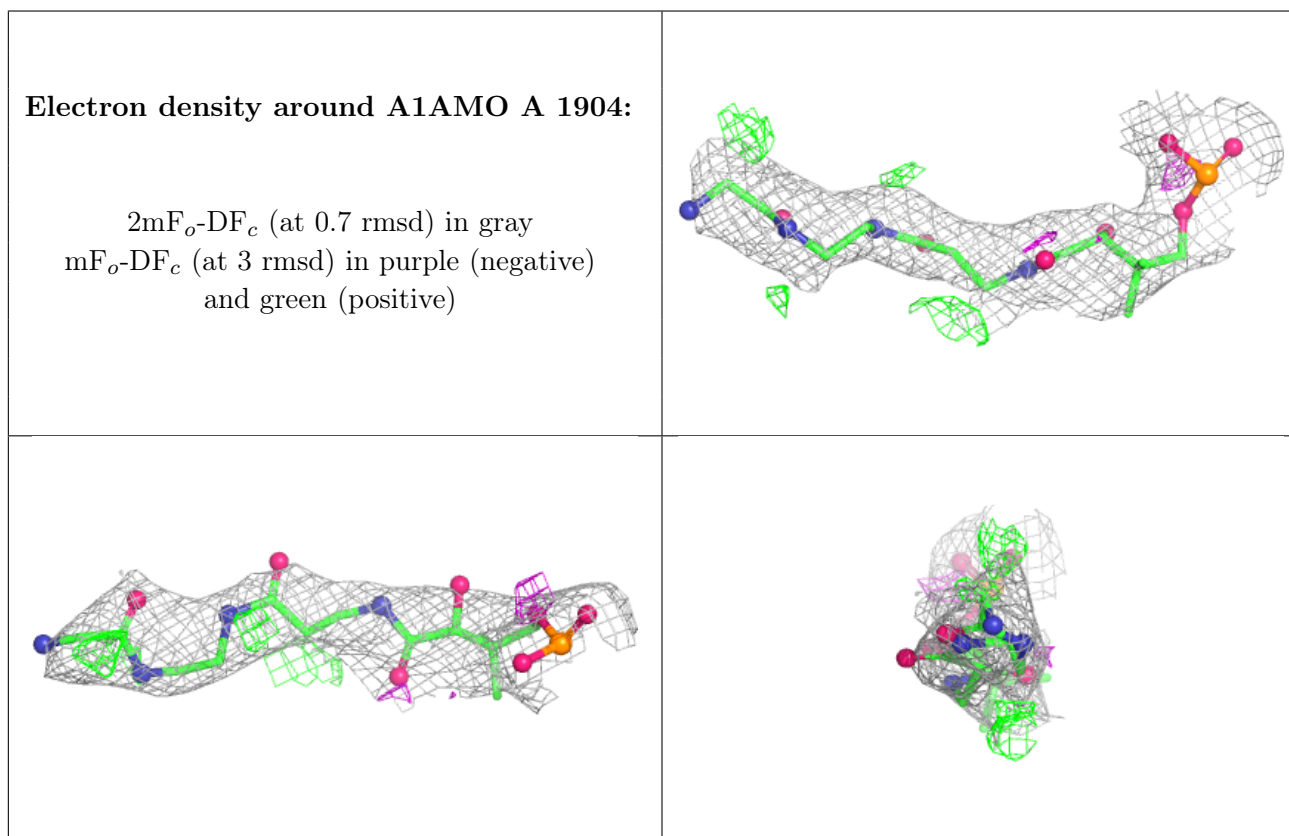
There are no oligosaccharides in this entry.

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.

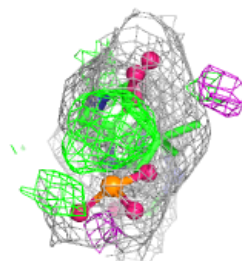
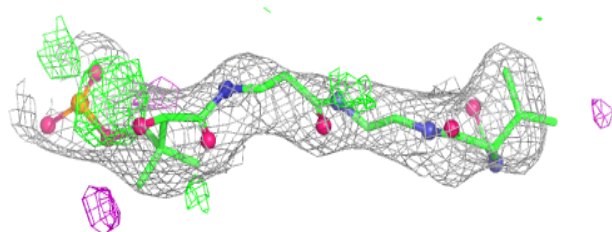
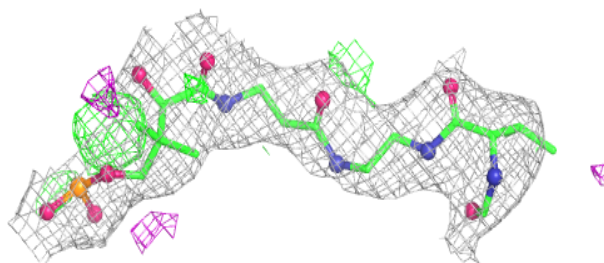
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MN	B	1905	1/1	0.63	0.41	224,224,224,224	0
5	MN	A	1905	1/1	0.78	0.15	107,107,107,107	0
2	GOL	A	1902	6/6	0.81	0.18	36,52,77,84	0
2	GOL	B	1901	6/6	0.84	0.12	34,39,55,76	0
5	MN	B	1904	1/1	0.88	0.12	140,140,140,140	0
4	A1AMO	A	1904	25/26	0.88	0.18	71,83,104,111	0
5	MN	B	1903	1/1	0.93	0.08	79,79,79,79	0
2	GOL	A	1901	6/6	0.93	0.13	38,49,59,62	0
3	JQG	B	1902	30/31	0.93	0.14	42,61,77,86	0
3	JQG	A	1903	30/31	0.97	0.10	30,43,73,77	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.

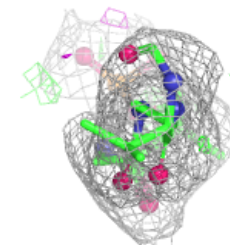
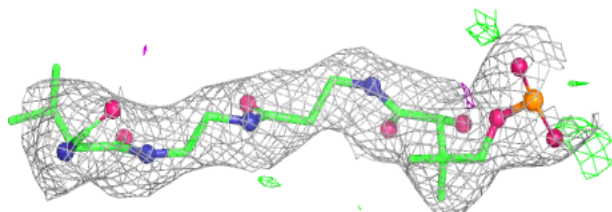
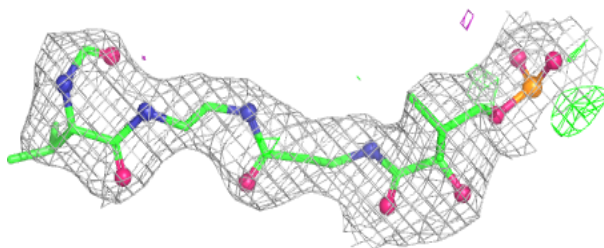


Electron density around JQG B 1902:

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

**Electron density around JQG A 1903:**

$2mF_o-DF_c$ (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.