Full wwPDB X-ray Structure Validation Report (i)

Aug 7, 2020 – 08:34 AM BST

PDB ID	:	2YGP
Title	:	WIF domain-EGF-like domain 1 Met77Trp of human Wnt inhibitory factor 1 in complex with 1,2-dipalmitoylphosphatidylcholine
Authors	:	Malinauskas, T.; Aricescu, A.R.; Lu, W.; Siebold, C.; Jones, E.Y.
Deposited on	:	2011-04-19
Resolution	:	2.22 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 (i) symbol.

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

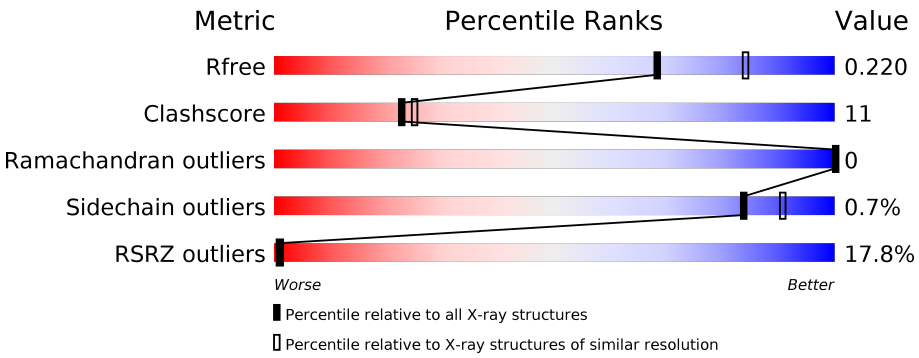
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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}	130704	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 on 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 <=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	188	

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
2	PCF	A	1213	-	-	-	X
5	SPD	A	1216	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1598 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.

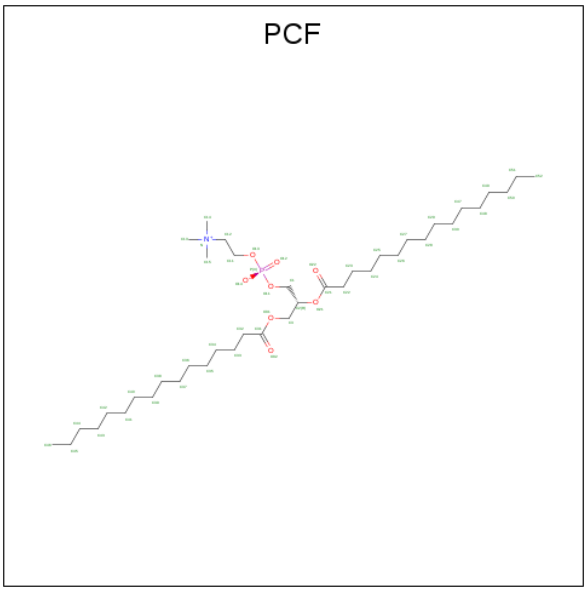
- Molecule 1 is a protein called WNT INHIBITORY FACTOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	180	1412	902	242	256	12	0	1	0

There are 14 discrepancies between the modelled and reference sequences:

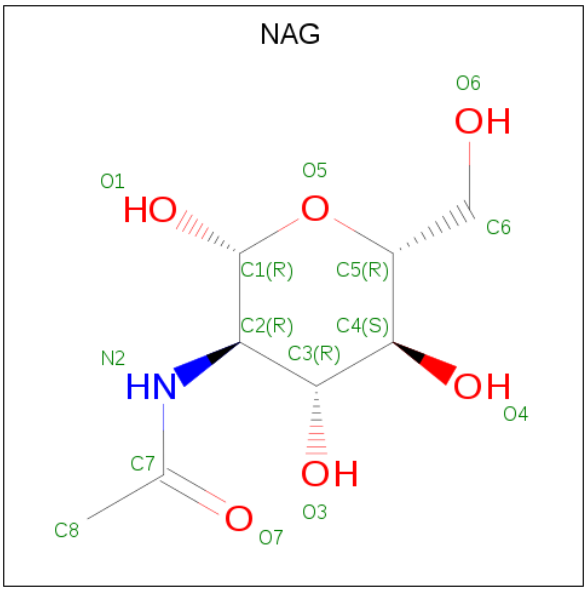
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLU	-	expression tag	UNP Q9Y5W5
A	33	THR	-	expression tag	UNP Q9Y5W5
A	34	GLY	-	expression tag	UNP Q9Y5W5
A	77	TRP	MET	engineered mutation	UNP Q9Y5W5
A	166	MLY	GLN	variant	UNP Q9Y5W5
A	211	GLY	-	expression tag	UNP Q9Y5W5
A	212	THR	-	expression tag	UNP Q9Y5W5
A	213	LYS	-	expression tag	UNP Q9Y5W5
A	214	HIS	-	expression tag	UNP Q9Y5W5
A	215	HIS	-	expression tag	UNP Q9Y5W5
A	216	HIS	-	expression tag	UNP Q9Y5W5
A	217	HIS	-	expression tag	UNP Q9Y5W5
A	218	HIS	-	expression tag	UNP Q9Y5W5
A	219	HIS	-	expression tag	UNP Q9Y5W5

- Molecule 2 is 1,2-DIACYL-SN-GLYCERO-3-PHOSHOCHOLINE (three-letter code: PCF) (formula: $C_{40}H_{80}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	50	40	1	8	1	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

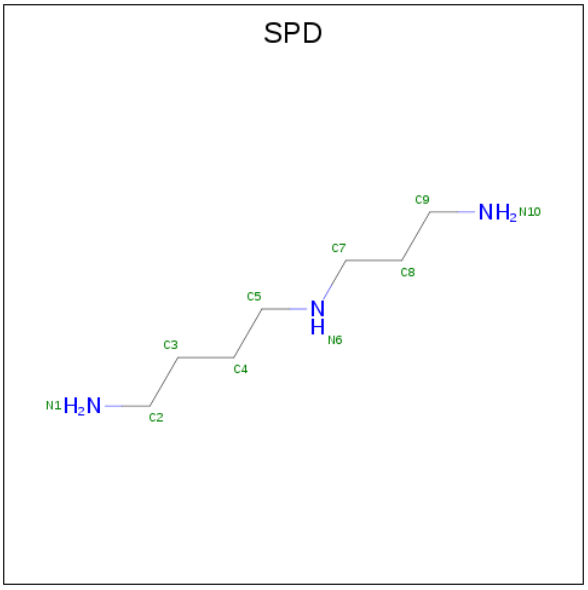


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
5	A	1	10	7	3	0	0

- Molecule 6 is water.

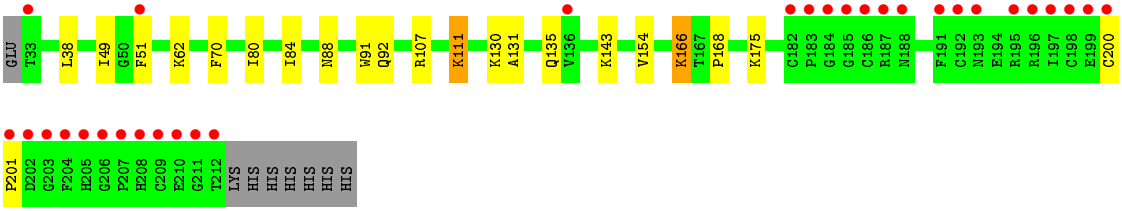
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	111	111	111	0	0

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: WNT INHIBITORY FACTOR 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	50.76Å 134.24Å 60.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.32 – 2.22 29.32 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.32-2.22) 99.2 (29.32-2.22)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.44 (at 2.22Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.185 , 0.229 0.178 , 0.220	Depositor DCC
R_{free} test set	502 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	35.2	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	1598	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SPD, CA, MLY, PCF, NAG

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	0.51	0/1386	0.71	0/1888

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	1412	0	1360	22	0
2	A	50	0	80	8	0
3	A	14	0	13	0	0
4	A	1	0	0	0	0
5	A	10	0	19	20	0
6	A	111	0	0	1	0
All	All	1598	0	1472	34	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 11.

All (34) 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)
5:A:1216:SPD:H51	5:A:1216:SPD:H91	1.40	1.00
5:A:1216:SPD:C9	5:A:1216:SPD:C5	2.44	0.96
2:A:1213:PCF:H121	2:A:1213:PCF:O12	1.66	0.93
5:A:1216:SPD:H52	5:A:1216:SPD:H92	1.49	0.93
1:A:168:PRO:HA	5:A:1216:SPD:H91	1.57	0.85
5:A:1216:SPD:C9	5:A:1216:SPD:H51	2.05	0.84
5:A:1216:SPD:C9	5:A:1216:SPD:H52	2.11	0.76
1:A:80:ILE:HD11	2:A:1213:PCF:H361	1.72	0.71
1:A:168:PRO:HG3	5:A:1216:SPD:H42	1.83	0.61
1:A:166:MLY:HG2	5:A:1216:SPD:H82	1.85	0.58
2:A:1213:PCF:O12	2:A:1213:PCF:C12	2.37	0.58
1:A:166:MLY:HE3	5:A:1216:SPD:C8	2.34	0.57
1:A:168:PRO:HA	5:A:1216:SPD:H51	1.86	0.56
1:A:49:ILE:HG21	2:A:1213:PCF:H12	1.88	0.56
1:A:168:PRO:HB3	5:A:1216:SPD:H21	1.91	0.52
5:A:1216:SPD:H92	5:A:1216:SPD:C5	2.17	0.51
5:A:1216:SPD:H71	6:A:2099:HOH:O	2.09	0.51
1:A:166:MLY:HE3	5:A:1216:SPD:H82	1.92	0.51
1:A:166:MLY:O	5:A:1216:SPD:H72	2.11	0.49
1:A:166:MLY:HE3	5:A:1216:SPD:H81	1.95	0.49
5:A:1216:SPD:H91	5:A:1216:SPD:C5	2.12	0.48
1:A:92:GLN:HB3	1:A:131:ALA:HA	1.97	0.47
1:A:70:PHE:HB2	5:A:1216:SPD:H32	1.97	0.47
1:A:49:ILE:HD12	1:A:51:PHE:H	1.80	0.46
1:A:84:ILE:O	1:A:175:LYS:HE2	2.16	0.45
1:A:154:VAL:HG13	2:A:1213:PCF:H491	1.99	0.45
1:A:107:ARG:HG3	1:A:111:MLY:HH12	1.99	0.44
1:A:200:CYS:HA	1:A:201:PRO:HD3	1.95	0.44
5:A:1216:SPD:H91	5:A:1216:SPD:H21	2.00	0.43
1:A:154:VAL:HG11	2:A:1213:PCF:H441	2.00	0.43
1:A:38:LEU:HD22	2:A:1213:PCF:H501	2.00	0.43
1:A:166:MLY:CE	5:A:1216:SPD:H82	2.49	0.41
1:A:88:ASN:OD1	1:A:135:GLN:HG2	2.21	0.41
2:A:1213:PCF:H472	2:A:1213:PCF:H501	1.94	0.40

There are no symmetry-related clashes.

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	173/188 (92%)	166 (96%)	7 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	144/151 (95%)	143 (99%)	1 (1%)	84 91

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

Mol	Chain	Res	Type
1	A	91	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

6 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	MLY	A	111	1	9,10,11	1.02	0	6,11,13	1.41	1 (16%)
1	MLY	A	72	1	9,10,11	1.01	0	6,11,13	1.11	0
1	MLY	A	130	1	9,10,11	1.13	1 (11%)	6,11,13	1.42	0
1	MLY	A	143	1	9,10,11	0.99	0	6,11,13	1.22	1 (16%)
1	MLY	A	62	1	9,10,11	0.71	0	6,11,13	1.28	1 (16%)
1	MLY	A	166	1	9,10,11	0.99	0	6,11,13	1.11	1 (16%)

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	MLY	A	111	1	-	1/8/9/11	-
1	MLY	A	72	1	-	3/8/9/11	-
1	MLY	A	130	1	-	1/8/9/11	-
1	MLY	A	143	1	-	1/8/9/11	-
1	MLY	A	62	1	-	5/8/9/11	-
1	MLY	A	166	1	-	2/8/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	MLY	CB-CA	2.11	1.56	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	111	MLY	CD-CE-NZ	-3.12	105.33	113.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	143	MLY	CD-CG-CB	-2.39	105.16	113.62
1	A	166	MLY	CD-CE-NZ	2.22	119.79	113.79
1	A	62	MLY	CD-CG-CB	-2.02	106.49	113.62

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	62	MLY	N-CA-CB-CG
1	A	62	MLY	C-CA-CB-CG
1	A	166	MLY	CD-CE-NZ-CH2
1	A	62	MLY	CG-CD-CE-NZ
1	A	111	MLY	CG-CD-CE-NZ
1	A	62	MLY	CE-CD-CG-CB
1	A	62	MLY	CA-CB-CG-CD
1	A	72	MLY	CE-CD-CG-CB
1	A	143	MLY	CE-CD-CG-CB
1	A	72	MLY	CD-CE-NZ-CH1
1	A	130	MLY	CA-CB-CG-CD
1	A	166	MLY	CE-CD-CG-CB
1	A	72	MLY	CG-CD-CE-NZ

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	111	MLY	1	0
1	A	166	MLY	6	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	NAG	A	1214	1	14,14,15	0.54	0	17,19,21	1.00	2 (11%)
5	SPD	A	1216	-	9,9,9	0.64	0	8,8,8	1.29	1 (12%)
2	PCF	A	1213	-	49,49,49	0.93	3 (6%)	55,57,57	1.58	7 (12%)

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	NAG	A	1214	1	-	2/6/23/26	0/1/1/1
5	SPD	A	1216	-	-	3/7/7/7	-
2	PCF	A	1213	-	-	34/53/53/53	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1213	PCF	O21-C21	3.36	1.43	1.34
2	A	1213	PCF	O31-C31	2.94	1.41	1.33
2	A	1213	PCF	O31-C3	-2.26	1.40	1.45

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1213	PCF	O21-C21-C22	6.14	124.72	111.50
2	A	1213	PCF	C2-O21-C21	-5.57	104.08	117.79
2	A	1213	PCF	O21-C21-O22	-4.33	113.24	123.70
5	A	1216	SPD	C8-C7-N6	3.34	121.16	112.14
2	A	1213	PCF	O31-C31-O32	-2.96	116.12	123.59
2	A	1213	PCF	O31-C31-C32	2.66	120.26	111.91
3	A	1214	NAG	C4-C3-C2	-2.45	107.42	111.02
2	A	1213	PCF	O13-P-O12	-2.22	100.38	109.07
3	A	1214	NAG	C8-C7-N2	2.16	119.76	116.10
2	A	1213	PCF	C11-C12-N	-2.08	108.82	115.78

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1216	SPD	C8-C7-N6-C5
5	A	1216	SPD	N6-C7-C8-C9
2	A	1213	PCF	C1-O11-P-O12
2	A	1213	PCF	C1-O11-P-O14
2	A	1213	PCF	C11-O13-P-O12
2	A	1213	PCF	C12-C11-O13-P
2	A	1213	PCF	O21-C2-C3-O31
3	A	1214	NAG	C4-C5-C6-O6
5	A	1216	SPD	C2-C3-C4-C5
3	A	1214	NAG	O5-C5-C6-O6
2	A	1213	PCF	C47-C48-C49-C50
2	A	1213	PCF	C1-O11-P-O13
2	A	1213	PCF	C22-C23-C24-C25
2	A	1213	PCF	C31-C32-C33-C34
2	A	1213	PCF	C33-C34-C35-C36
2	A	1213	PCF	C26-C27-C28-C29
2	A	1213	PCF	C24-C25-C26-C27
2	A	1213	PCF	C38-C39-C40-C41
2	A	1213	PCF	C34-C35-C36-C37
2	A	1213	PCF	C30-C47-C48-C49
2	A	1213	PCF	C40-C41-C42-C43
2	A	1213	PCF	C36-C37-C38-C39
2	A	1213	PCF	C32-C31-O31-C3
2	A	1213	PCF	C37-C38-C39-C40
2	A	1213	PCF	C11-O13-P-O11
2	A	1213	PCF	O32-C31-O31-C3
2	A	1213	PCF	C39-C40-C41-C42
2	A	1213	PCF	O31-C31-C32-C33
2	A	1213	PCF	C23-C24-C25-C26
2	A	1213	PCF	C2-C1-O11-P
2	A	1213	PCF	C11-O13-P-O14
2	A	1213	PCF	O13-C11-C12-N
2	A	1213	PCF	C1-C2-C3-O31
2	A	1213	PCF	C32-C33-C34-C35
2	A	1213	PCF	O32-C31-C32-C33
2	A	1213	PCF	C49-C50-C51-C52
2	A	1213	PCF	O21-C21-C22-C23
2	A	1213	PCF	O22-C21-C22-C23
2	A	1213	PCF	C43-C44-C45-C46

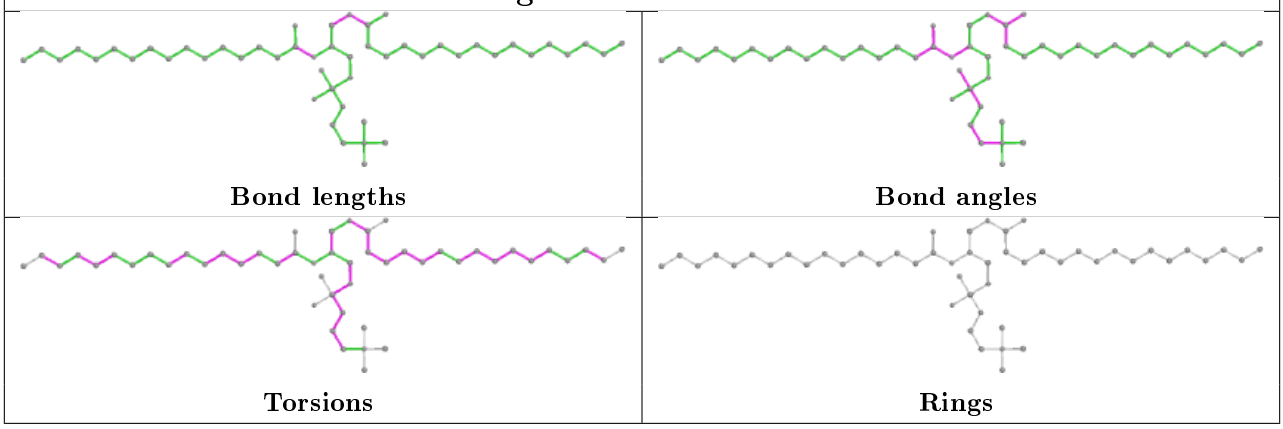
There are no ring outliers.

2 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1216	SPD	20	0
2	A	1213	PCF	8	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PCF A 1213



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	174/188 (92%)	0.53	31 (17%) 1 1	21, 34, 132, 165	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	CYS	7.1
1	A	207	PRO	6.4
1	A	205	HIS	6.2
1	A	184	GLY	6.0
1	A	186	CYS	6.0
1	A	212	THR	5.8
1	A	211	GLY	5.7
1	A	204	PHE	5.7
1	A	185	GLY	5.6
1	A	209	CYS	5.5
1	A	201	PRO	5.4
1	A	187	ARG	5.3
1	A	208	HIS	5.2
1	A	202	ASP	5.2
1	A	199	GLU	5.1
1	A	206	GLY	4.5
1	A	192	CYS	4.1
1	A	188	ASN	4.1
1	A	210	GLU	4.0
1	A	191	PHE	3.9
1	A	33	THR	3.5
1	A	197	ILE	3.3
1	A	183	PRO	3.2
1	A	182	CYS	2.8
1	A	195	ARG	2.7
1	A	198	CYS	2.5
1	A	51	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	136	VAL	2.2
1	A	203	GLY	2.1
1	A	196	ARG	2.0
1	A	193	ASN	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	MLY	A	72	11/12	0.90	0.21	29,41,74,75	0
1	MLY	A	143	11/12	0.90	0.17	47,52,97,101	0
1	MLY	A	111	11/12	0.94	0.16	32,45,73,78	0
1	MLY	A	62	11/12	0.95	0.15	30,39,77,77	0
1	MLY	A	166	11/12	0.95	0.15	26,30,67,68	0
1	MLY	A	130	11/12	0.97	0.09	25,33,50,54	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

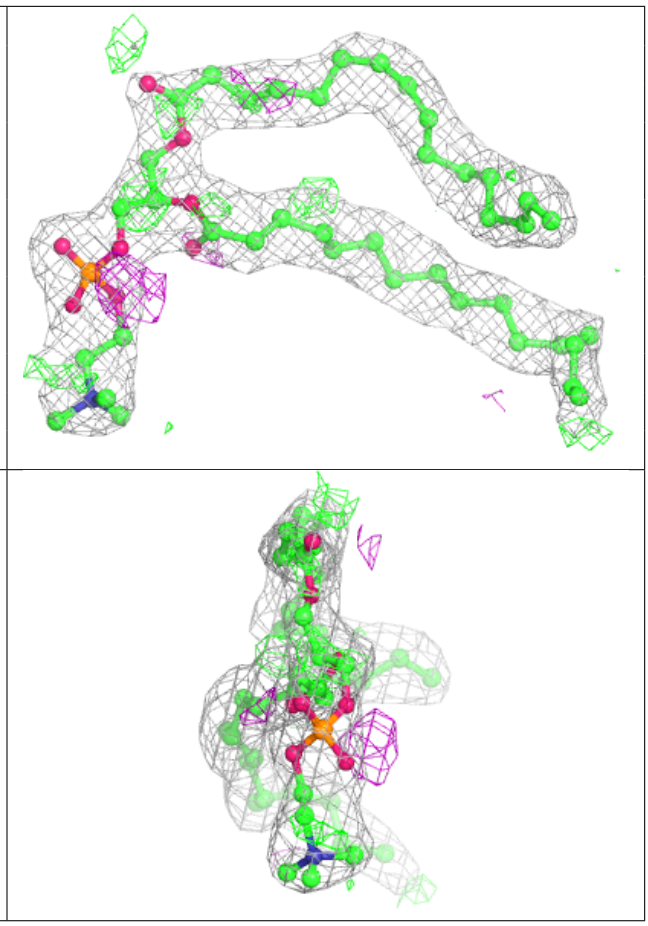
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	SPD	A	1216	10/10	0.65	0.31	42,58,61,63	0
2	PCF	A	1213	50/50	0.75	0.44	28,53,161,182	0
4	CA	A	1215	1/1	0.76	0.06	108,108,108,108	0
3	NAG	A	1214	14/15	0.93	0.21	28,49,63,65	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 PCF A 1213:

$2mF_o$-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.