Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 09:19 pm BST

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PDB ID	:	6MPZ
Title	:	Crystal structure of a double glycine motif protease from AMS/PCAT transporter in complex with the leader peptide
Authors	:	Dong, S.-H.; Nair, S.K.
Deposited on	:	2018-10-09
Resolution	:	2.00 Å(reported)

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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 2.00 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.
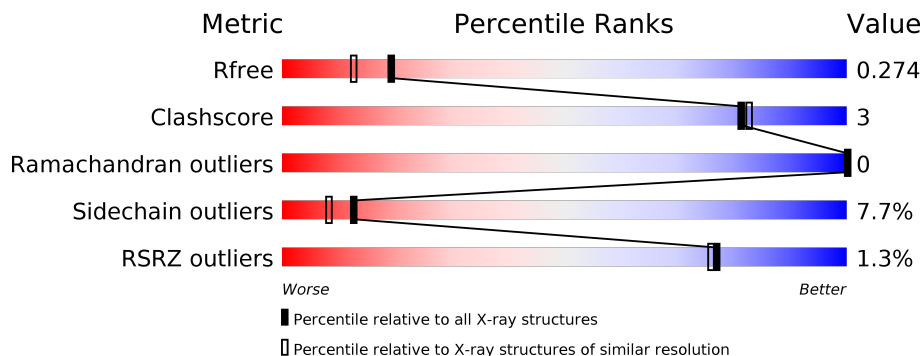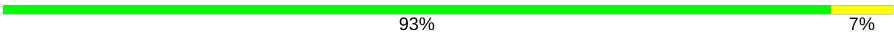
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	147	2% / 82% / 12% / ...
1	B	147	86% / 8% / .. / 5%
1	C	147	% / 84% / 9% / . / 5%
1	D	147	% / 84% / 9% / ..
2	M	14	7% / 93% / 7%
2	N	14	100%

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Mol	Chain	Length	Quality of chain
2	O	14	7% 100%
2	P	14	93% 7%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5010 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 Double Glycine Motif Protease domain from AMS/PCAT Transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	142	Total	C	N	O	S	0	0	0
			1132	731	196	197	8			
1	B	140	Total	C	N	O	S	0	0	0
			1113	721	191	193	8			
1	C	140	Total	C	N	O	S	0	0	0
			1113	721	191	193	8			
1	D	141	Total	C	N	O	S	0	0	0
			1121	725	192	196	8			

- Molecule 2 is a protein called peptide aldehyde inhibitor 1 based on the ProcA2.8 leader peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	14	Total	C	N	O	0	0	0
			92	53	15	24			
2	N	14	Total	C	N	O	0	0	0
			92	53	15	24			
2	O	14	Total	C	N	O	0	0	0
			92	53	15	24			
2	P	14	Total	C	N	O	0	0	0
			92	53	15	24			

- Molecule 3 is 3,6,9,12,15,18-HEXAOXAICOSANE (three-letter code: 16P) (formula: $C_{14}H_{30}O_6$).
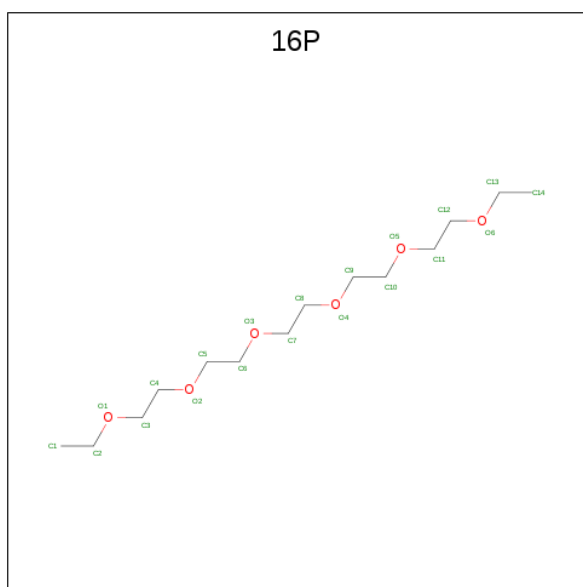
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 20	C 14	O 6	0	0
3	B	1	Total 20	C 14	O 6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total 19	O 19	0	0
4	B	29	Total 29	O 29	0	0
4	C	33	Total 33	O 33	0	0
4	D	27	Total 27	O 27	0	0
4	M	4	Total 4	O 4	0	0
4	N	5	Total 5	O 5	0	0
4	O	2	Total 2	O 2	0	0
4	P	4	Total 4	O 4	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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.
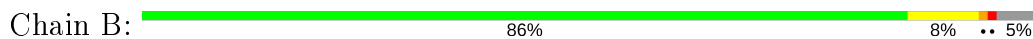
• Molecule 1: Double Glycine Motif Protease domain from AMS/PCAT Transporter
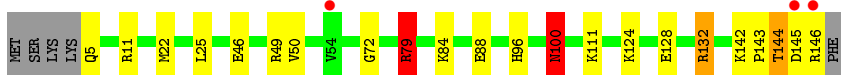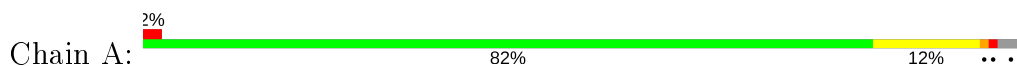
• Molecule 1: Double Glycine Motif Protease domain from AMS/PCAT Transporter

• Molecule 1: Double Glycine Motif Protease domain from AMS/PCAT Transporter
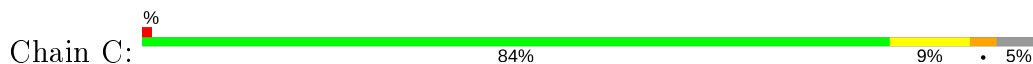
• Molecule 1: Double Glycine Motif Protease domain from AMS/PCAT Transporter
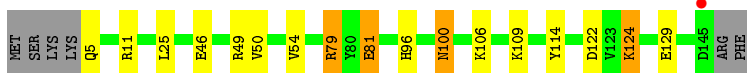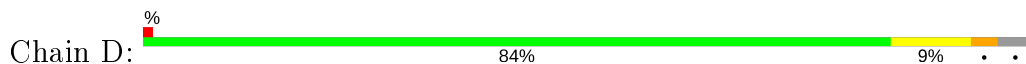
• Molecule 2: peptide aldehyde inhibitor 1 based on the ProcA2.8 leader peptide
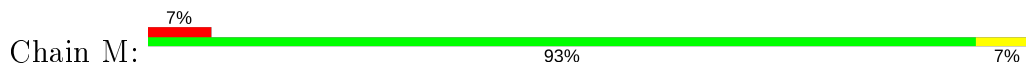
• Molecule 2: peptide aldehyde inhibitor 1 based on the ProcA2.8 leader peptide

Chain N:

100%

There are no outlier residues recorded for this chain.

• Molecule 2: peptide aldehyde inhibitor 1 based on the ProcA2.8 leader peptide

Chain O:

7%

100%

• Molecule 2: peptide aldehyde inhibitor 1 based on the ProcA2.8 leader peptide

Chain P:

93%

7%

Full wwPDB X-ray Structure Validation Report

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	37.89Å 119.43Å 76.52Å 90.00° 93.84° 90.00°	Depositor
Resolution (Å)	50.01 – 2.00 76.35 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.01-2.00) 99.8 (76.35-1.98)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.75 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.234 , 0.268 0.243 , 0.274	Depositor DCC
R_{free} test set	2378 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	1.026	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 42.5	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	0.95	EDS
Total number of atoms	5010	wwPDB-VP
Average B, all atoms (Å^2)	37.0	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 64.11 % 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 8.7201e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[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: GLZ, 16P

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	0.76	0/1159	0.96	6/1562 (0.4%)
1	B	0.76	0/1140	0.93	5/1537 (0.3%)
1	C	0.76	0/1140	0.93	4/1537 (0.3%)
1	D	0.81	1/1148 (0.1%)	0.92	5/1548 (0.3%)
2	M	0.87	0/87	0.74	0/116
2	N	0.82	0/87	0.71	0/116
2	O	0.78	0/87	0.82	0/116
2	P	0.86	0/87	0.77	0/116
All	All	0.78	1/4935 (0.0%)	0.93	20/6648 (0.3%)

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	2
1	B	0	1
1	D	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	81	GLU	CD-OE2	6.54	1.32	1.25

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	100	ASN	CB-CA-C	-7.50	95.40	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	100	ASN	CB-CA-C	-7.42	95.56	110.40
1	A	79	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	A	100	ASN	CB-CA-C	-7.21	95.97	110.40
1	B	49	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	D	49	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	C	79	ARG	NE-CZ-NH1	6.31	123.45	120.30
1	B	49	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	C	49	ARG	NE-CZ-NH2	-6.15	117.23	120.30
1	A	22	MET	CG-SD-CE	6.11	109.97	100.20
1	C	49	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	D	79	ARG	NE-CZ-NH2	-5.79	117.40	120.30
1	D	49	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	B	79	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	C	132	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	49	ARG	NE-CZ-NH1	5.47	123.04	120.30
1	D	79	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	79	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	B	79	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	A	49	ARG	NE-CZ-NH2	-5.14	117.73	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100	ASN	Peptide
1	A	143	PRO	Peptide
1	B	100	ASN	Peptide
1	D	100	ASN	Peptide

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	1132	0	1149	7	0
1	B	1113	0	1132	3	0
1	C	1113	0	1132	10	1
1	D	1121	0	1136	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	92	0	80	1	0
2	N	92	0	80	0	0
2	O	92	0	80	0	0
2	P	92	0	80	1	0
3	A	20	0	30	2	0
3	B	20	0	30	1	0
4	A	19	0	0	0	0
4	B	29	0	0	1	0
4	C	33	0	0	7	0
4	D	27	0	0	2	0
4	M	4	0	0	0	0
4	N	5	0	0	0	0
4	O	2	0	0	0	0
4	P	4	0	0	0	0
All	All	5010	0	4929	25	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 3.

All (25) 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:54:VAL:HB	4:D:223:HOH:O	1.62	0.98
1:C:47:GLN:NE2	4:C:201:HOH:O	2.01	0.94
1:C:34:MET:SD	4:C:220:HOH:O	2.43	0.76
1:B:20:MET:O	4:B:401:HOH:O	2.08	0.71
1:C:34:MET:CE	4:C:220:HOH:O	2.43	0.67
1:C:50:VAL:CG1	4:C:201:HOH:O	2.44	0.66
1:A:128:GLU:OE1	1:A:132:ARG:NH2	2.31	0.64
1:C:50:VAL:HG12	4:C:201:HOH:O	2.00	0.61
1:D:114:TYR:CE2	1:D:124:LYS:HD3	2.36	0.61
1:D:106:LYS:NZ	1:D:122:ASP:OD1	2.37	0.58
1:A:72:GLY:O	1:A:144:THR:HG22	2.04	0.57
1:A:84:LYS:HG3	1:A:88:GLU:HG3	1.85	0.57
1:A:144:THR:OG1	1:A:145:ASP:N	2.37	0.57
1:A:79:ARG:HD2	3:A:300:16P:H51	1.92	0.50
1:C:100:ASN:HD22	1:C:100:ASN:C	2.16	0.48
1:B:79:ARG:HD2	3:B:300:16P:H51	1.96	0.48
1:C:34:MET:HE2	4:C:220:HOH:O	2.09	0.47
1:B:114:TYR:CE2	1:B:124:LYS:HG2	2.51	0.45
1:C:117:ASP:OD2	1:C:120:LYS:HE3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ARG:HG2	3:A:300:16P:H91	2.00	0.43
1:A:96:HIS:HE1	2:M:12:ALA:O	2.02	0.43
1:D:81:GLU:HB3	4:D:207:HOH:O	2.19	0.42
1:C:128:GLU:HB3	4:C:216:HOH:O	2.20	0.41
1:C:128:GLU:OE2	1:C:132:ARG:NH2	2.52	0.41
1:D:96:HIS:HE1	2:P:12:ALA:O	2.04	0.41

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)
1:C:112:TYR:OH	1:D:129:GLU:OE2[1_554]	2.19	0.01

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	140/147 (95%)	137 (98%)	3 (2%)	0	100	100
1	B	138/147 (94%)	136 (99%)	2 (1%)	0	100	100
1	C	138/147 (94%)	135 (98%)	3 (2%)	0	100	100
1	D	139/147 (95%)	137 (99%)	2 (1%)	0	100	100
2	M	12/14 (86%)	12 (100%)	0	0	100	100
2	N	12/14 (86%)	12 (100%)	0	0	100	100
2	O	12/14 (86%)	12 (100%)	0	0	100	100
2	P	12/14 (86%)	12 (100%)	0	0	100	100
All	All	603/644 (94%)	593 (98%)	10 (2%)	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	119/124 (96%)	106 (89%)	13 (11%)	6	3
1	B	117/124 (94%)	108 (92%)	9 (8%)	13	8
1	C	117/124 (94%)	108 (92%)	9 (8%)	13	8
1	D	118/124 (95%)	110 (93%)	8 (7%)	16	11
2	M	9/9 (100%)	9 (100%)	0	100	100
2	N	9/9 (100%)	9 (100%)	0	100	100
2	O	9/9 (100%)	9 (100%)	0	100	100
2	P	9/9 (100%)	9 (100%)	0	100	100
All	All	507/532 (95%)	468 (92%)	39 (8%)	13	8

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	11	ARG
1	A	25	LEU
1	A	46	GLU
1	A	50	VAL
1	A	79	ARG
1	A	100	ASN
1	A	111	LYS
1	A	124	LYS
1	A	132	ARG
1	A	142	LYS
1	A	144	THR
1	A	146	ARG
1	B	5	GLN
1	B	11	ARG
1	B	25	LEU
1	B	46	GLU
1	B	50	VAL
1	B	79	ARG

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Mol	Chain	Res	Type
1	B	109	LYS
1	B	111	LYS
1	B	127	MET
1	C	11	ARG
1	C	15	LYS
1	C	25	LEU
1	C	46	GLU
1	C	50	VAL
1	C	79	ARG
1	C	100	ASN
1	C	124	LYS
1	C	142	LYS
1	D	5	GLN
1	D	11	ARG
1	D	25	LEU
1	D	46	GLU
1	D	50	VAL
1	D	79	ARG
1	D	109	LYS
1	D	124	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	96	HIS
1	B	5	GLN
1	B	70	ASN
1	B	96	HIS
1	C	70	ASN
1	C	96	HIS
1	C	100	ASN
1	D	70	ASN
1	D	96	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	#$|Z| > 2$
2	GLZ	O	14	1,2	3,3,3	0.43	0	0,2,2	0.00	-
2	GLZ	P	14	1,2	3,3,3	0.50	0	0,2,2	0.00	-
2	GLZ	M	14	1,2	3,3,3	0.46	0	0,2,2	0.00	-
2	GLZ	N	14	1,2	3,3,3	0.47	0	0,2,2	0.00	-

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	GLZ	O	14	1,2	-	0/0/1/1	-
2	GLZ	P	14	1,2	-	0/0/1/1	-
2	GLZ	M	14	1,2	-	0/0/1/1	-
2	GLZ	N	14	1,2	-	0/0/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	#$|Z| > 2$
3	16P	B	300	-	19,19,19	0.59	0	18,18,18	0.98	1 (5%)
3	16P	A	300	-	19,19,19	0.74	0	18,18,18	0.92	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	16P	B	300	-	-	9/17/17/17	-
3	16P	A	300	-	-	8/17/17/17	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	300	16P	O3-C6-C5	-2.31	99.98	110.39
3	A	300	16P	O2-C5-C6	2.02	119.52	110.39

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	300	16P	O2-C5-C6-O3
3	B	300	16P	O1-C3-C4-O2
3	A	300	16P	O2-C5-C6-O3
3	A	300	16P	O1-C3-C4-O2
3	A	300	16P	O5-C11-C12-O6
3	B	300	16P	O3-C7-C8-O4

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Mol	Chain	Res	Type	Atoms
3	B	300	16P	O5-C11-C12-O6
3	B	300	16P	O5-C10-C9-O4
3	A	300	16P	C12-C11-O5-C10
3	A	300	16P	O5-C10-C9-O4
3	A	300	16P	C7-C8-O4-C9
3	B	300	16P	C10-C9-O4-C8
3	B	300	16P	C12-C11-O5-C10
3	B	300	16P	C7-C8-O4-C9
3	B	300	16P	C3-C4-O2-C5
3	A	300	16P	O3-C7-C8-O4
3	A	300	16P	C10-C9-O4-C8

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	300	16P	1	0
3	A	300	16P	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 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 16P B 300

Ligand 16P A 300

Bond lengths

Bond angles

Torsions

Rings
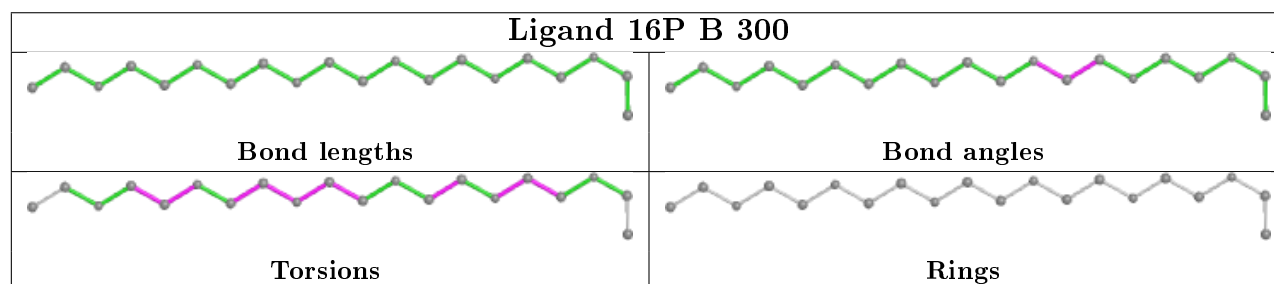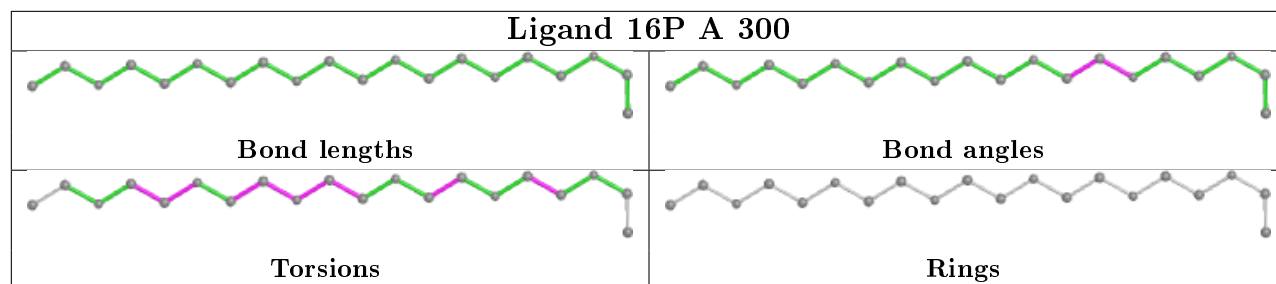
5.7 Other polymers (i)

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(Å²)	Q<0.9
1	A	142/147 (96%)	0.21	3 (2%)	63	62	23, 38, 58, 119	0
1	B	140/147 (95%)	0.07	0	100	100	21, 34, 52, 67	0
1	C	140/147 (95%)	0.13	2 (1%)	75	74	24, 34, 53, 70	0
1	D	141/147 (95%)	0.06	1 (0%)	87	87	22, 32, 51, 85	0
2	M	13/14 (92%)	0.12	1 (7%)	13	12	31, 35, 48, 48	0
2	N	13/14 (92%)	-0.05	0	100	100	28, 31, 41, 48	0
2	O	13/14 (92%)	0.34	1 (7%)	13	12	30, 34, 40, 42	0
2	P	13/14 (92%)	-0.15	0	100	100	28, 29, 41, 43	0
All	All	615/644 (95%)	0.11	8 (1%)	77	76	21, 34, 54, 119	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	ARG	4.9
2	O	1	GLY	4.5
1	A	145	ASP	3.6
1	C	54	VAL	2.8
1	C	42	TRP	2.6
1	D	145	ASP	2.3
1	A	54	VAL	2.2
2	M	1	GLY	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
2	GLZ	P	14	4/4	0.94	0.13	23,28,28,29	0
2	GLZ	O	14	4/4	0.95	0.10	31,32,33,33	0
2	GLZ	N	14	4/4	0.95	0.09	33,33,35,36	0
2	GLZ	M	14	4/4	0.96	0.12	32,33,34,37	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.

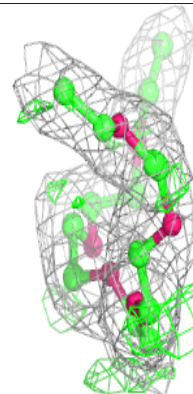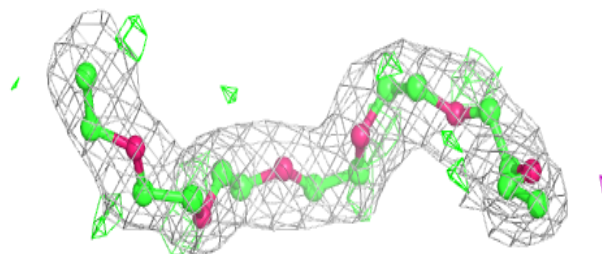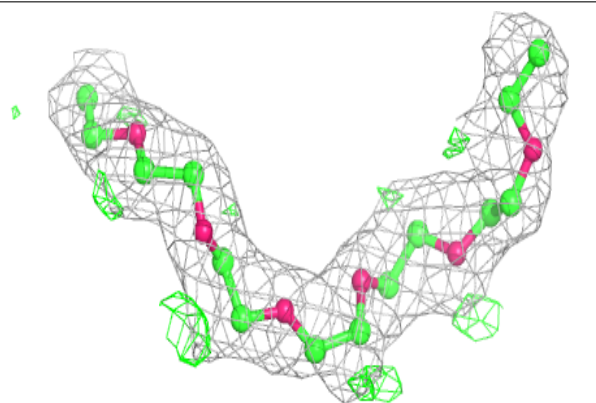| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	16P	A	300	20/20	0.87	0.15	31,39,47,47	0
3	16P	B	300	20/20	0.92	0.15	26,34,44,46	0

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 16P A 300:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
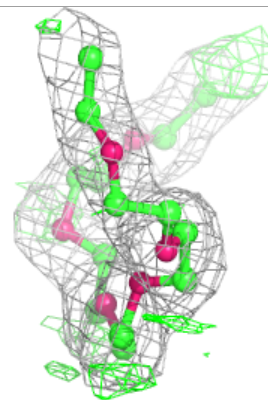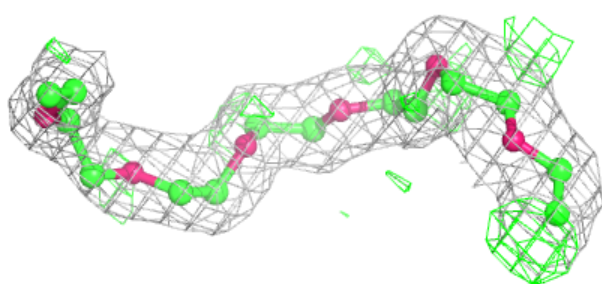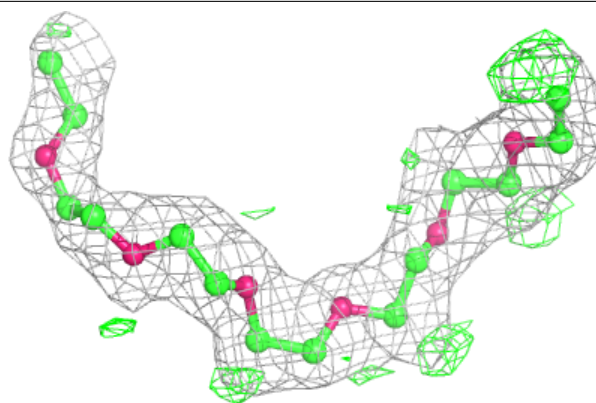
Electron density around 16P B 300:

$2mF_o$-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.