



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:36 AM UTC

PDB ID : 6KZ8 / pdb_00006kz8
Title : Crystal structure of plant Phospholipase D alpha complex with phosphatidic acid
Authors : Li, J.X.; Yu, F.; Zhang, P.
Deposited on : 2019-09-23
Resolution : 2.29 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

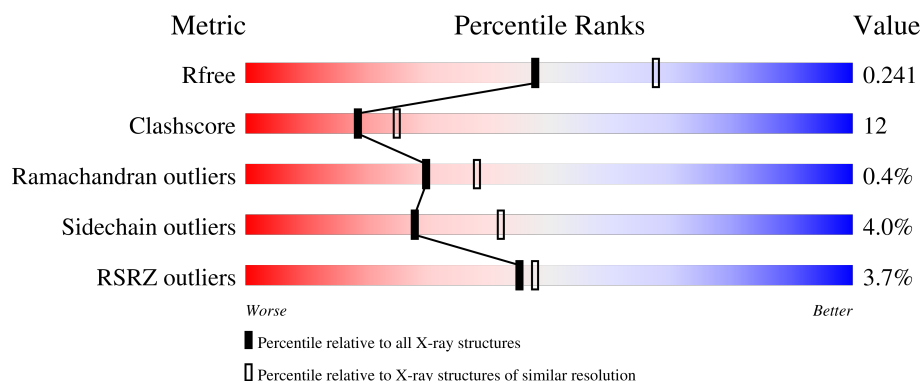
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	810	4% 71% 20% ...
1	B	810	3% 78% 16% ...

2 Entry composition [i](#)

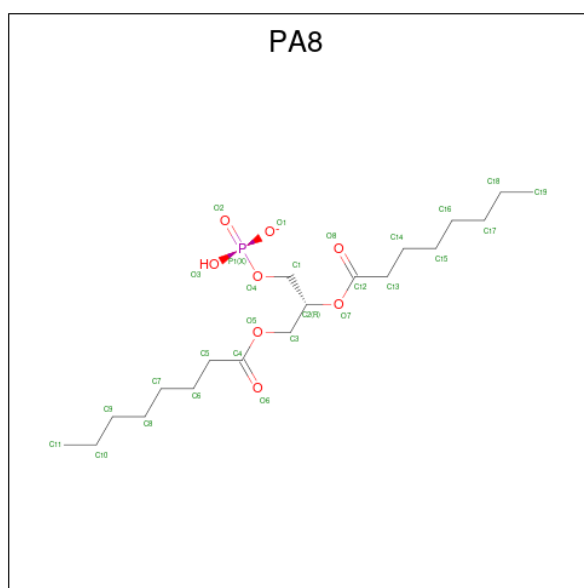
There are 4 unique types of molecules in this entry. The entry contains 13151 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Phospholipase D alpha 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	784	Total	C	N	O	S	0	0	0
			6298	4000	1093	1178	27			
1	B	784	Total	C	N	O	S	0	0	0
			6298	4000	1093	1178	27			

- Molecule 2 is 1,2-DIOCTANOYL-SN-GLYCERO-3-PHOSPHATE (CCD ID: PA8) (formula: $C_{19}H_{36}O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			28	19	8	1		
2	B	1	Total	C	O	P	0	0
			28	19	8	1		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

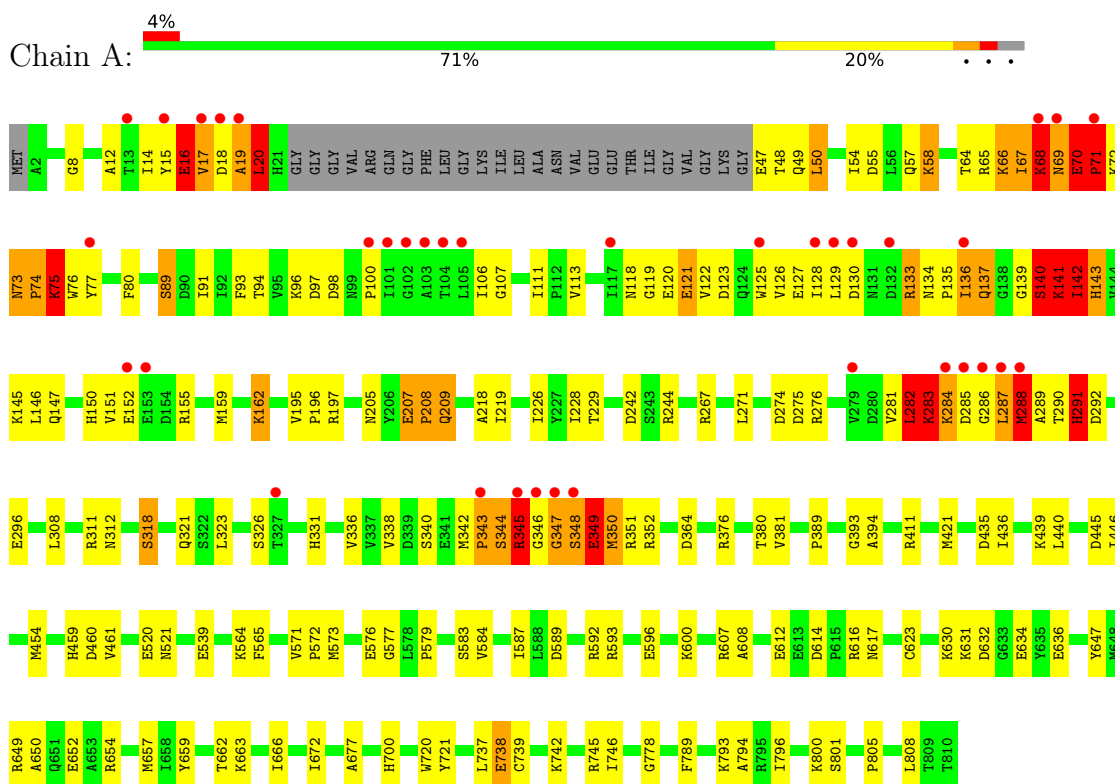
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	227	Total 227	O 227	0	0
4	B	270	Total 270	O 270	0	0

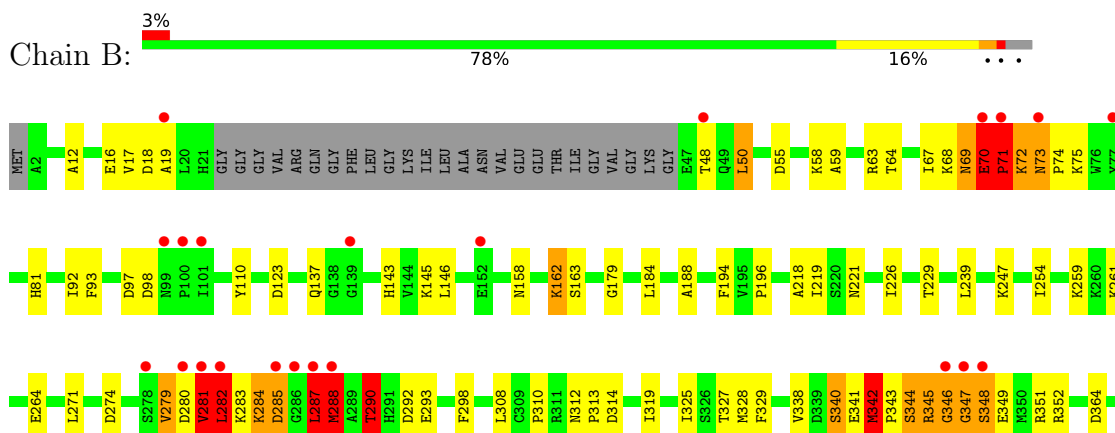
3 Residue-property plots

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: Phospholipase D alpha 1



• Molecule 1: Phospholipase D alpha 1



F371	H372	S373	T380	V381	H387	T392	G393	A394	R402	E403	P404	W405	I408	R411	L412	E413	M421	L440	R441	P452	V453	M454	D460	V461	K514	E520	N521	F524	D534	K558	G562	E563	M573	W574	P579	E580	S583	I587
M598	Y599	K600	Q604	F621	D644	Y647	M657	H661	T662	K663	M664	R682	A687	R688	D689	P689	S703	H704	R705	Q706	Y721	G725	E729	E777	F789	A794	R795	P805	P806	I807	T810							

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.04Å 123.03Å 138.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.89 – 2.29 37.89 – 2.29	Depositor EDS
% Data completeness (in resolution range)	68.6 (37.89-2.29) 88.2 (37.89-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.198 , 0.245 0.197 , 0.241	Depositor DCC
R_{free} test set	1999 reflections (2.60%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13151	wwPDB-VP
Average B, all atoms (Å ²)	15.0	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 50.58 % 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 6.3397e-05. 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: PA8, CA

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	0.77	15/6462 (0.2%)	0.98	30/8760 (0.3%)
1	B	0.63	7/6462 (0.1%)	0.78	22/8760 (0.3%)
All	All	0.70	22/12924 (0.2%)	0.89	52/17520 (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	18
1	B	0	8
All	All	0	26

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	745	ARG	C-O	-8.23	1.14	1.24
1	A	209	GLN	C-O	-7.99	1.13	1.23
1	A	207	GLU	C-O	-7.91	1.16	1.24
1	B	81	HIS	C-O	-6.37	1.16	1.24
1	B	351	ARG	C-O	-6.31	1.15	1.23

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	LYS	N-CA-C	21.97	142.98	111.56
1	A	75	LYS	N-CA-C	19.58	135.50	111.02
1	A	381	VAL	N-CA-C	-17.70	96.90	113.71
1	A	71	PRO	CB-CA-C	17.37	140.22	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	69	ASN	N-CA-C	-16.35	84.51	109.86

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	GLU	Peptide
1	A	19	ALA	Peptide
1	A	20	LEU	Peptide
1	A	67	ILE	Peptide
1	A	68	LYS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6298	0	6113	183	2
1	B	6298	0	6113	109	3
2	A	28	0	35	11	0
2	B	28	0	36	7	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	227	0	0	15	1
4	B	270	0	0	16	1
All	All	13151	0	12297	300	4

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 12.

The worst 5 of 300 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:B:70:GLU:HB2	1:B:71:PRO:CD	1.38	1.52
1:B:70:GLU:CB	1:B:71:PRO:HD3	1.28	1.37
1:B:70:GLU:CD	1:B:71:PRO:HD2	1.53	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:MET:O	1:A:344:SER:HB2	1.32	1.29
1:A:576:GLU:O	2:A:1101:PA8:H13	1.37	1.23

All (4) 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:738:GLU:OE2	1:B:281:VAL:CG1[4_548]	2.10	0.10
1:A:349:GLU:OE2	1:B:348:SER:OG[3_448]	2.11	0.09
1:B:348:SER:CA	1:B:777:GLU:OE2[3_448]	2.12	0.08
4:A:1349:HOH:O	4:B:1180:HOH:O[4_448]	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	780/810 (96%)	712 (91%)	63 (8%)	5 (1%)	21	27
1	B	780/810 (96%)	737 (94%)	41 (5%)	2 (0%)	36	46
All	All	1560/1620 (96%)	1449 (93%)	104 (7%)	7 (0%)	30	38

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	71	PRO
1	A	347	GLY
1	B	70	GLU
1	B	71	PRO
1	A	291	HIS

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	680/697 (98%)	649 (95%)	31 (5%)	24	36
1	B	680/697 (98%)	656 (96%)	24 (4%)	32	48
All	All	1360/1394 (98%)	1305 (96%)	55 (4%)	28	42

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	612	GLU
1	B	73	ASN
1	B	777	GLU
1	B	345	ARG
1	A	630	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	542	ASN
1	B	704	HIS
1	B	651	GLN
1	B	156	ASN
1	B	496	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
2	PA8	B	902	-	27,27,27	1.16	4 (14%)	30,32,32	1.03	2 (6%)
2	PA8	A	1101	-	27,27,27	1.51	5 (18%)	30,32,32	1.78	6 (20%)

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	PA8	B	902	-	-	18/29/29/29	-
2	PA8	A	1101	-	-	15/29/29/29	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	PA8	O5-C4	3.52	1.43	1.33
2	A	1101	PA8	O7-C2	-3.40	1.38	1.46
2	A	1101	PA8	O7-C12	3.14	1.43	1.34
2	B	902	PA8	O7-C2	-2.84	1.39	1.46
2	A	1101	PA8	P1-O1	-2.80	1.44	1.54

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	PA8	C2-O7-C12	-4.83	106.24	117.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	PA8	O7-C12-C13	4.32	120.83	111.48
2	B	902	PA8	O7-C12-C13	3.75	119.59	111.48
2	A	1101	PA8	O1-P1-O4	-3.53	97.47	106.67
2	A	1101	PA8	O3-P1-O1	3.22	119.88	107.80

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

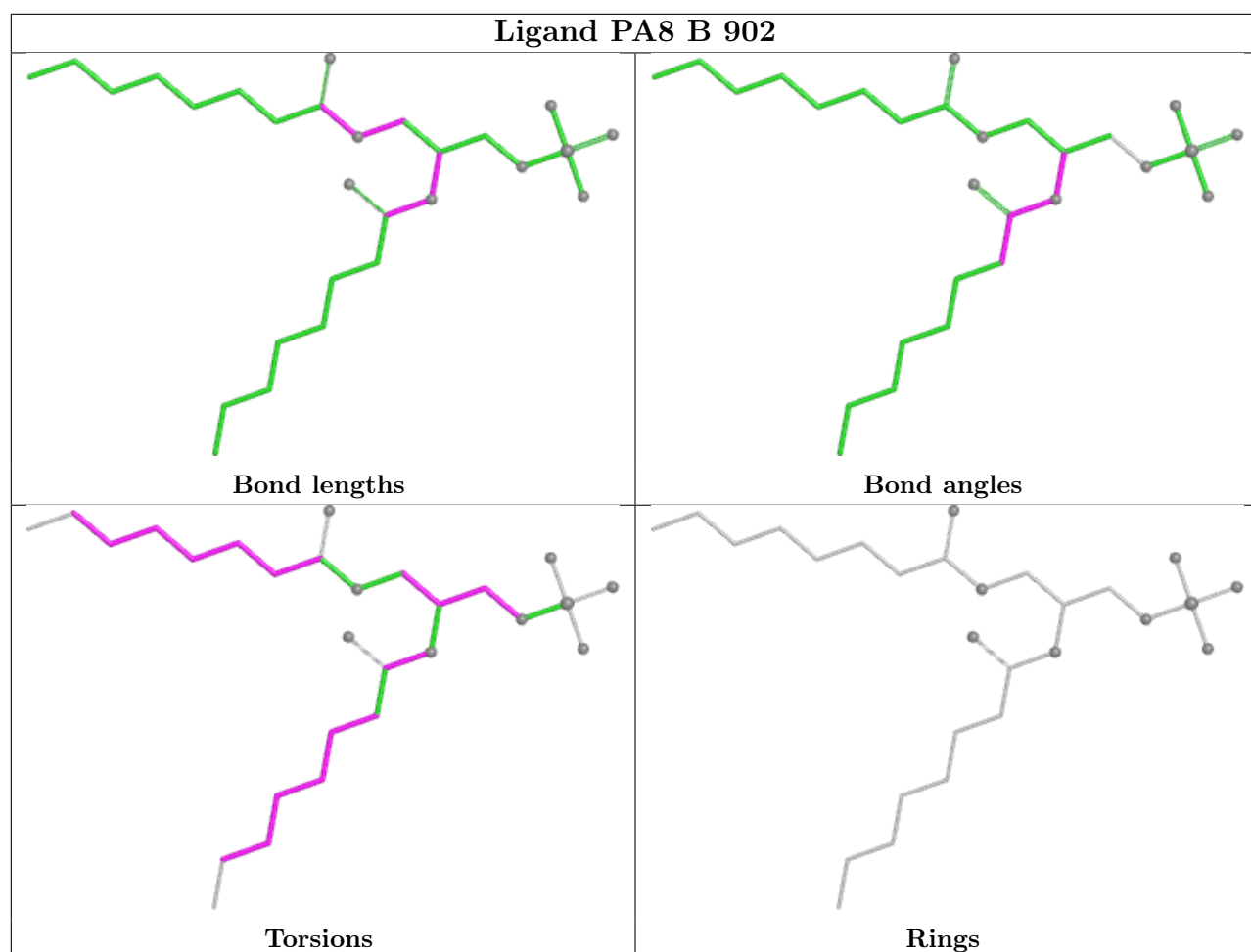
Mol	Chain	Res	Type	Atoms
2	A	1101	PA8	O8-C12-O7-C2
2	B	902	PA8	O8-C12-O7-C2
2	A	1101	PA8	C13-C12-O7-C2
2	B	902	PA8	C13-C12-O7-C2
2	B	902	PA8	C5-C6-C7-C8

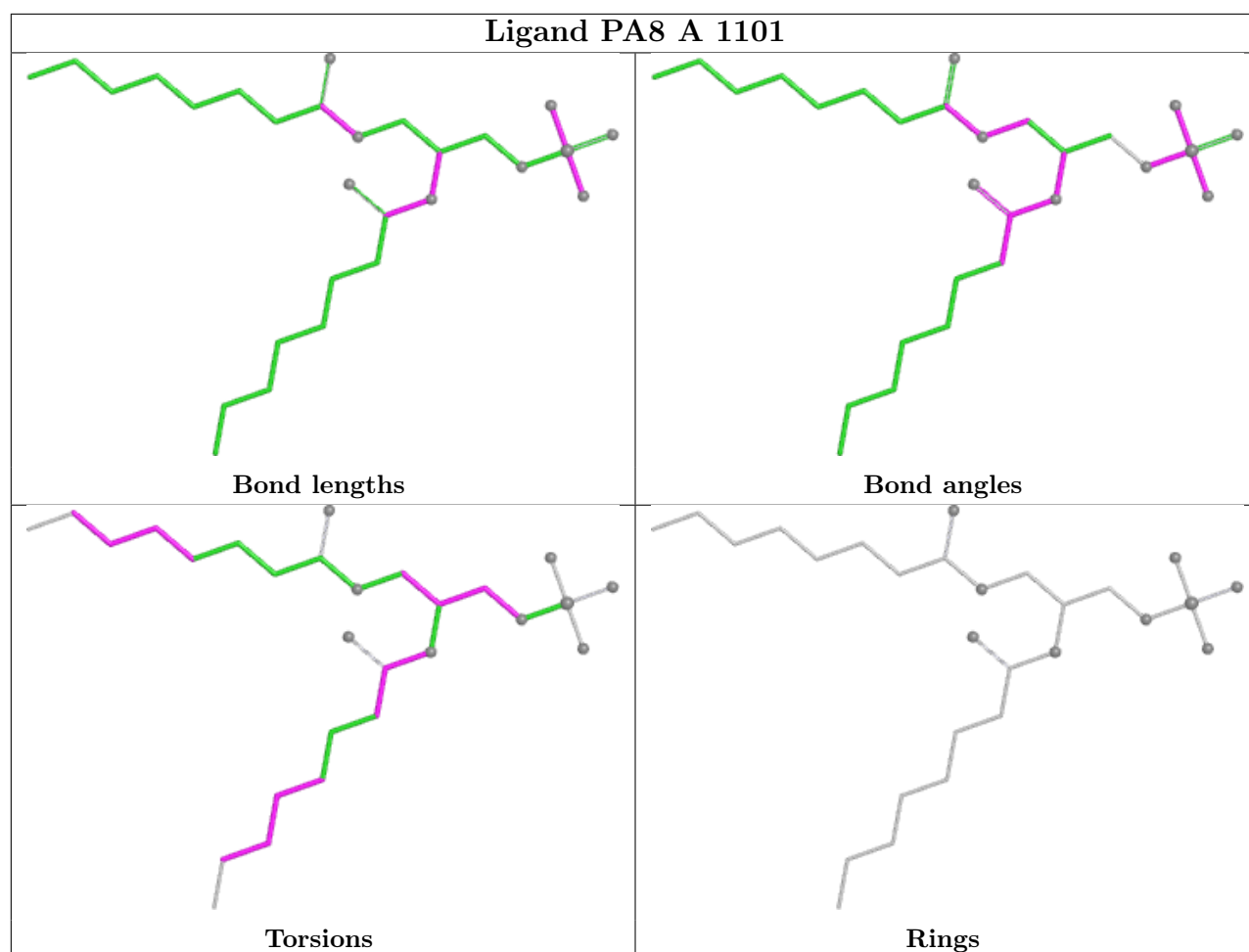
There are no ring outliers.

2 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	902	PA8	7	0
2	A	1101	PA8	11	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	784/810 (96%)	-0.07	36 (4%) 37 39	5, 14, 42, 53	0
1	B	784/810 (96%)	-0.24	22 (2%) 55 57	4, 12, 32, 54	0
All	All	1568/1620 (96%)	-0.15	58 (3%) 45 48	4, 13, 37, 54	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	281	VAL	6.8
1	B	347	GLY	4.3
1	B	285	ASP	4.1
1	B	100	PRO	4.0
1	B	346	GLY	4.0

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

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

6.3 Carbohydrates [i](#)

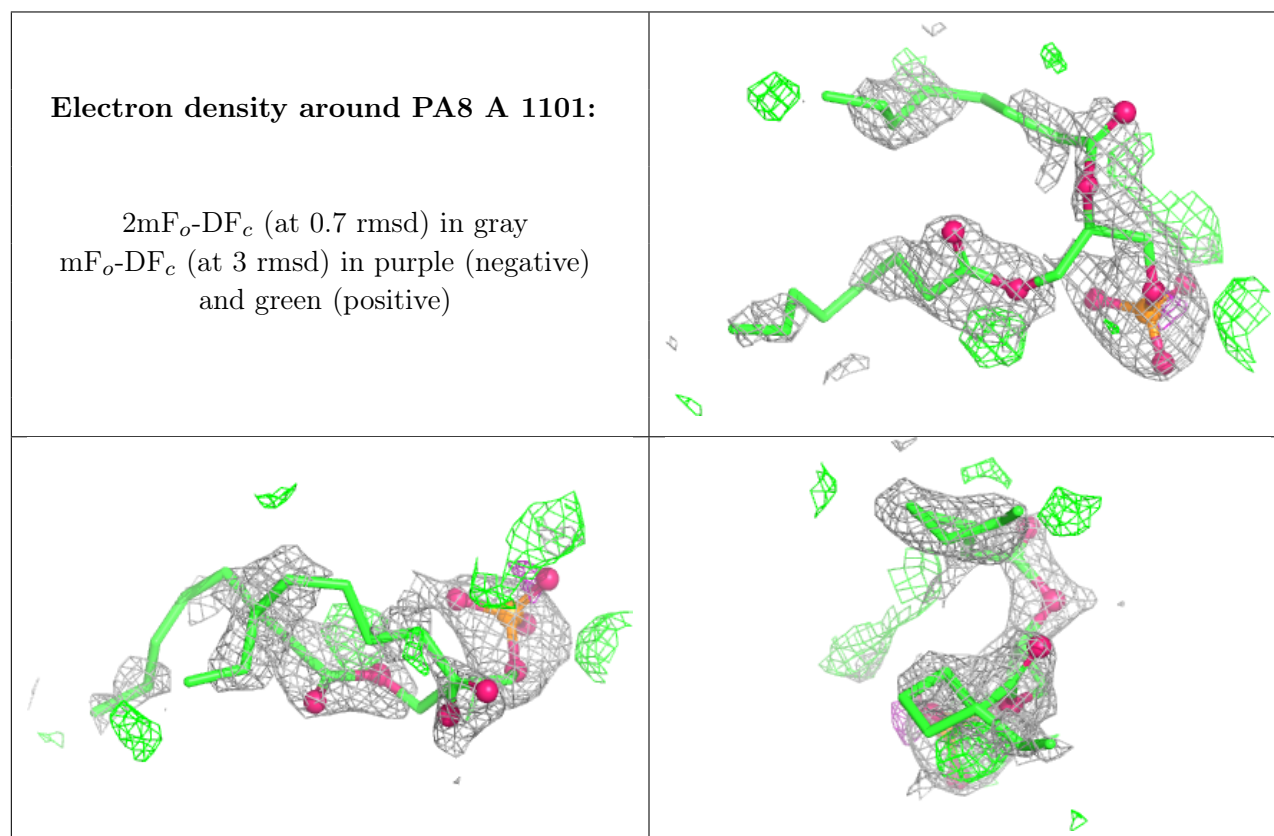
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

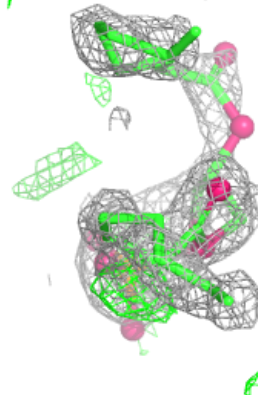
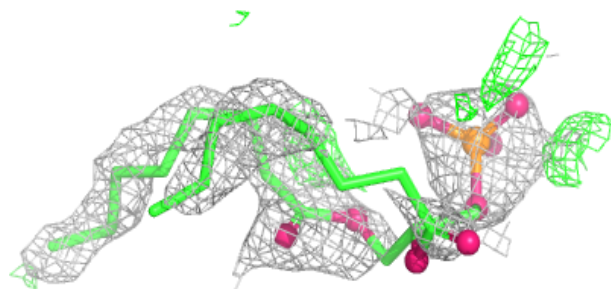
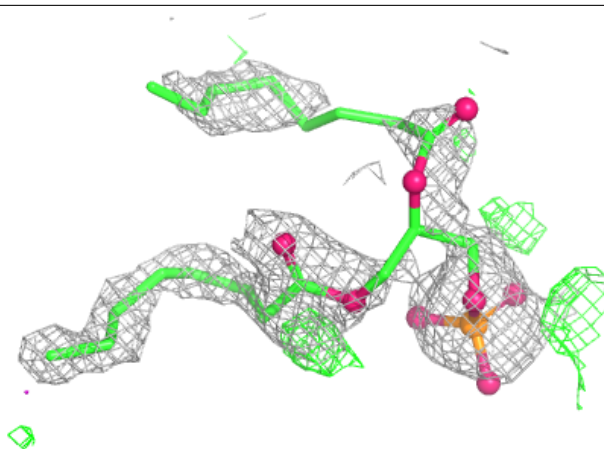
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PA8	A	1101	28/28	0.80	0.17	7,15,21,21	28
2	PA8	B	902	28/28	0.81	0.17	4,16,22,24	28
3	CA	A	1102	1/1	0.98	0.10	4,4,4,4	0
3	CA	B	901	1/1	0.98	0.11	5,5,5,5	0

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.



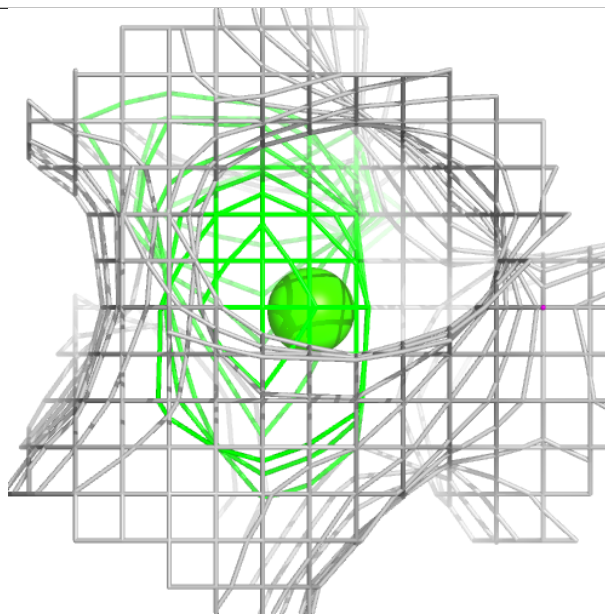
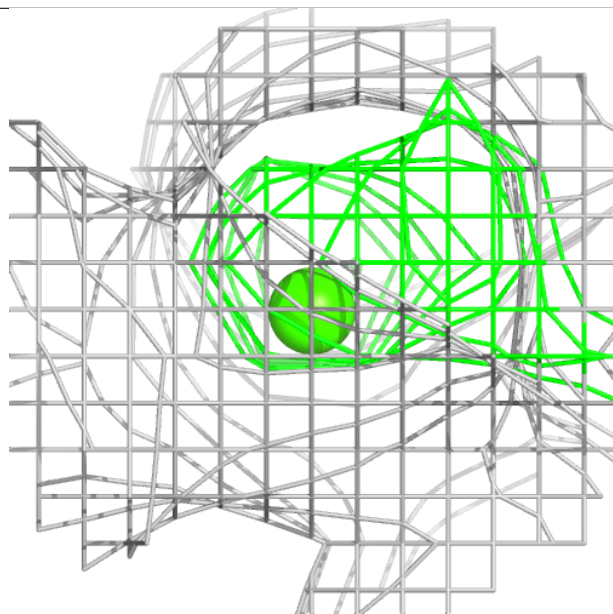
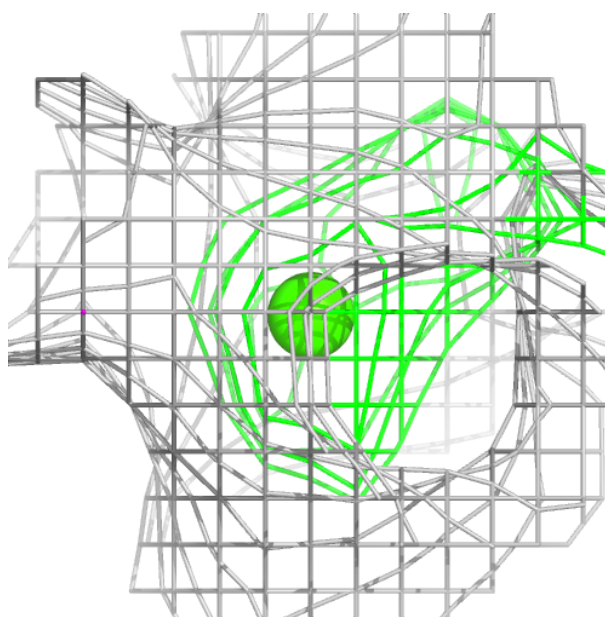
Electron density around PA8 B 902:

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



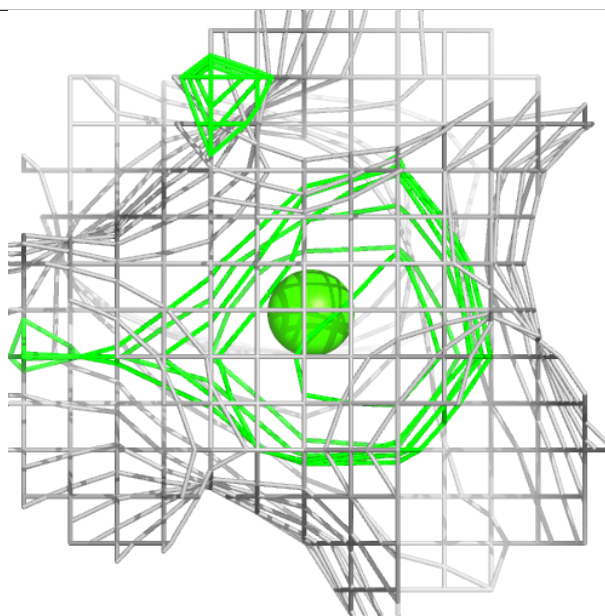
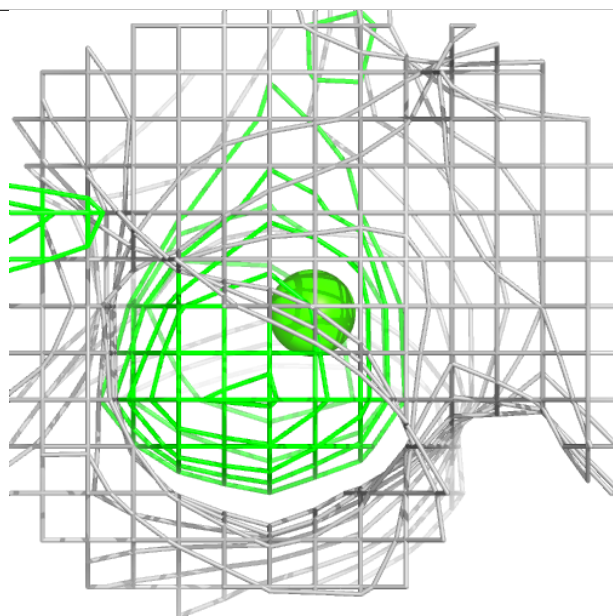
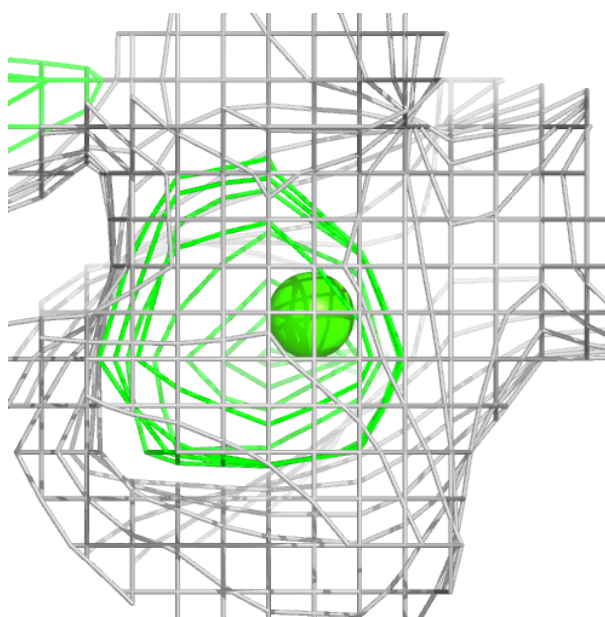
Electron density around CA A 1102:

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



Electron density around CA B 901:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.