



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:02 PM UTC

PDB ID : 5TQS / pdb_00005tqs
Title : Phospholipase C gamma-1 C-terminal SH2 domain bound to a phosphopeptide
derived from the receptor tyrosine kinase ErbB2
Authors : Wuttke, D.S.; McKercher, M.A.
Deposited on : 2016-10-24
Resolution : 1.88 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 ⓘ 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:

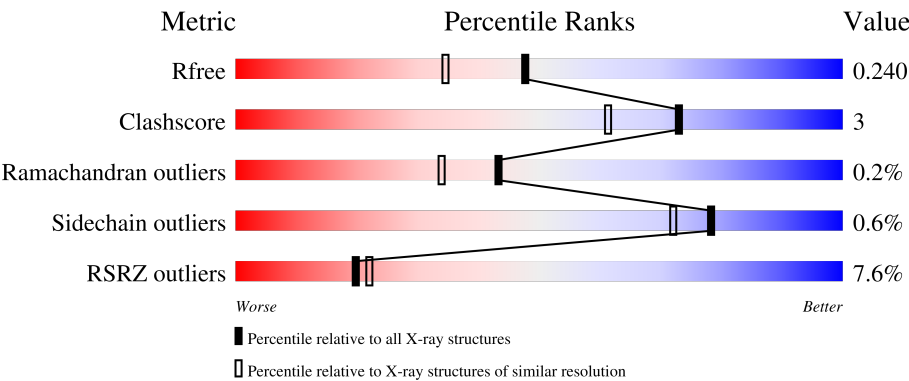
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

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

The reported resolution of this entry is 1.88 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	101	3% 95% 5%
1	B	101	% 93% 5% ..
1	C	101	7% 93% . .
1	D	101	9% 89% 9% .
2	E	11	18% 18% 27% 9% 45%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	11	18% 55% 9% 36%
2	G	11	55% 55% 18% 27%
2	H	11	18% 55% 9% 36%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7137 atoms, of which 3334 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 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	101	Total	C	H	N	O	S	0	1	0
			1640	524	806	155	149	6			
1	B	100	Total	C	H	N	O	S	0	1	0
			1641	520	812	155	149	5			
1	C	98	Total	C	H	N	O	S	0	1	0
			1573	502	773	144	148	6			
1	D	99	Total	C	H	N	O	S	0	1	0
			1592	507	786	148	145	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	659	GLY	-	expression tag	UNP P08487
A	660	SER	-	expression tag	UNP P08487
A	661	HIS	-	expression tag	UNP P08487
A	662	MET	-	expression tag	UNP P08487
B	659	GLY	-	expression tag	UNP P08487
B	660	SER	-	expression tag	UNP P08487
B	661	HIS	-	expression tag	UNP P08487
B	662	MET	-	expression tag	UNP P08487
C	659	GLY	-	expression tag	UNP P08487
C	660	SER	-	expression tag	UNP P08487
C	661	HIS	-	expression tag	UNP P08487
C	662	MET	-	expression tag	UNP P08487
D	659	GLY	-	expression tag	UNP P08487
D	660	SER	-	expression tag	UNP P08487
D	661	HIS	-	expression tag	UNP P08487
D	662	MET	-	expression tag	UNP P08487

- Molecule 2 is a protein called Receptor protein-tyrosine kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	6	Total	C	H	N	O	P	0	0	1
			90	40	30	7	12	1			
2	F	7	Total	C	H	N	O	P	0	0	1
			114	44	46	9	14	1			
2	H	7	Total	C	H	N	O	P	0	0	0
			117	46	46	9	15	1			
2	G	8	Total	C	H	N	O	P	0	0	1
			102	43	35	9	14	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	63	Total	O	0	1
			64	64		
3	B	70	Total	O	0	3
			73	73		
3	C	40	Total	O	0	1
			41	41		
3	D	60	Total	O	0	2
			62	62		
3	E	7	Total	O	0	1
			8	8		
3	F	8	Total	O	0	1
			9	9		
3	H	8	Total	O	0	0
			8	8		
3	G	3	Total	O	0	0
			3	3		

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: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



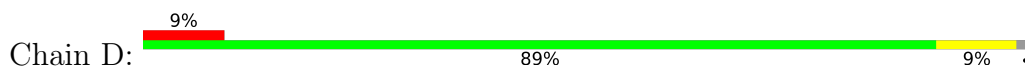
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



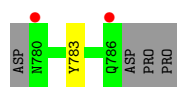
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



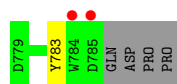
- Molecule 2: Receptor protein-tyrosine kinase



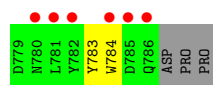
- Molecule 2: Receptor protein-tyrosine kinase



- Molecule 2: Receptor protein-tyrosine kinase



- Molecule 2: Receptor protein-tyrosine kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.32Å 30.62Å 104.57Å 90.00° 100.12° 90.00°	Depositor
Resolution (Å)	51.47 – 1.88 51.47 – 1.88	Depositor EDS
% Data completeness (in resolution range)	98.6 (51.47-1.88) 95.1 (51.47-1.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 1.88Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.189 , 0.237 0.194 , 0.240	Depositor DCC
R_{free} test set	1685 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7137	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.12% 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: PTR

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	0.36	0/859	0.50	0/1152
1	B	0.34	0/854	0.51	0/1146
1	C	0.28	0/823	0.39	0/1106
1	D	0.28	0/829	0.44	0/1111
2	E	0.29	0/45	0.39	0/60
2	F	0.29	0/53	0.34	0/71
2	G	0.16	0/52	0.41	0/70
2	H	0.16	0/56	0.32	0/75
All	All	0.31	0/3571	0.46	0/4791

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	834	806	815	5	0
1	B	829	812	810	5	0
1	C	800	773	768	4	0
1	D	806	786	782	6	0
2	E	60	30	41	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	68	46	47	0	0
2	G	67	35	36	1	0
2	H	71	46	48	0	0
3	A	64	0	0	1	0
3	B	73	0	0	0	0
3	C	41	0	0	0	0
3	D	62	0	0	1	0
3	E	8	0	0	1	0
3	F	9	0	0	0	0
3	G	3	0	0	0	0
3	H	8	0	0	0	0
All	All	3803	3334	3347	22	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 3.

All (22) 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)
2:E:785:ASP:OD1	3:E:801:HOH:O	2.05	0.73
1:A:757:ASN:N	1:A:759:GLU:OE1	2.26	0.69
2:E:781:LEU:HD12	2:E:781:LEU:O	1.94	0.66
1:D:698:GLU:N	1:D:698:GLU:OE1	2.33	0.61
2:E:781:LEU:HD22	2:E:784:TRP:HA	1.91	0.53
1:B:682:LEU:HD23	1:B:756:ILE:HD12	1.96	0.48
1:B:715:CYS:SG	1:B:726:LEU:HD11	2.54	0.48
1:A:758:GLU:HA	1:A:758:GLU:OE1	2.14	0.46
1:D:670:HIS:CE1	1:D:758:GLU:HA	2.52	0.45
1:A:737:LEU:C	1:A:737:LEU:HD23	2.41	0.45
1:A:711:LYS:NZ	3:A:803:HOH:O	2.43	0.43
1:B:681:MET:HE3	1:B:758:GLU:C	2.44	0.43
1:D:684:ARG:NH2	3:D:801:HOH:O	2.45	0.42
1:A:759:GLU:CD	1:D:753:ARG:HH22	2.28	0.42
1:C:707:ARG:HG2	1:C:712:ILE:HD13	2.01	0.42
1:C:715:CYS:SG	2:G:784:TRP:HE3	2.43	0.42
1:B:715:CYS:SG	1:B:726:LEU:CD1	3.07	0.41
1:C:737:LEU:C	1:C:737:LEU:HD23	2.45	0.41
1:D:709:GLU:OE1	1:D:748:ARG:NH2	2.53	0.41
1:D:737:LEU:C	1:D:737:LEU:HD23	2.46	0.41
1:C:707:ARG:HG2	1:C:712:ILE:CD1	2.51	0.41
1:B:726:LEU:HD12	1:B:726:LEU:C	2.46	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	100/101 (99%)	96 (96%)	4 (4%)	0	100	100
1	B	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
1	C	97/101 (96%)	93 (96%)	4 (4%)	0	100	100
1	D	98/101 (97%)	93 (95%)	4 (4%)	1 (1%)	12	3
2	E	3/11 (27%)	3 (100%)	0	0	100	100
2	F	4/11 (36%)	4 (100%)	0	0	100	100
2	G	5/11 (46%)	3 (60%)	2 (40%)	0	100	100
2	H	4/11 (36%)	4 (100%)	0	0	100	100
All	All	410/448 (92%)	393 (96%)	16 (4%)	1 (0%)	43	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	721	GLY

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	89/90 (99%)	89 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	89/90 (99%)	88 (99%)	1 (1%)	65	56
1	C	85/90 (94%)	85 (100%)	0	100	100
1	D	84/90 (93%)	84 (100%)	0	100	100
2	E	4/10 (40%)	3 (75%)	1 (25%)	0	0
2	F	5/10 (50%)	5 (100%)	0	100	100
2	G	3/10 (30%)	3 (100%)	0	100	100
2	H	5/10 (50%)	5 (100%)	0	100	100
All	All	364/400 (91%)	362 (100%)	2 (0%)	78	76

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	726	LEU
2	E	781	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	719	GLN
1	B	661	HIS
1	B	719	GLN
1	C	744	HIS
1	C	757	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	PTR	G	783	2	15,16,17	1.22	1 (6%)	17,22,24	0.64	1 (5%)
2	PTR	H	783	2	15,16,17	1.43	1 (6%)	17,22,24	0.46	0
2	PTR	F	783	2	15,16,17	1.39	1 (6%)	17,22,24	0.50	0
2	PTR	E	783	2	15,16,17	1.36	1 (6%)	17,22,24	0.59	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
2	PTR	G	783	2	-	0/10/11/13	0/1/1/1
2	PTR	H	783	2	-	0/10/11/13	0/1/1/1
2	PTR	F	783	2	-	1/10/11/13	0/1/1/1
2	PTR	E	783	2	-	1/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	783	PTR	OH-CZ	-4.88	1.29	1.40
2	E	783	PTR	OH-CZ	-4.67	1.30	1.40
2	F	783	PTR	OH-CZ	-4.49	1.30	1.40
2	G	783	PTR	OH-CZ	-4.30	1.31	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	783	PTR	O3P-P-OH	2.28	112.07	105.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	783	PTR	O-C-CA-CB
2	E	783	PTR	CZ-OH-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	101/101 (100%)	0.05	3 (2%)	52	57	13, 27, 51, 66	1 (0%)
1	B	100/101 (99%)	0.04	1 (1%)	79	83	16, 29, 48, 55	1 (1%)
1	C	98/101 (97%)	0.71	7 (7%)	22	24	17, 45, 74, 99	1 (1%)
1	D	99/101 (98%)	0.51	9 (9%)	15	16	19, 38, 61, 67	1 (1%)
2	E	5/11 (45%)	1.67	2 (40%)	1	0	30, 31, 45, 47	0
2	F	6/11 (54%)	1.10	2 (33%)	1	1	27, 32, 47, 62	0
2	G	7/11 (63%)	2.75	6 (85%)	0	0	30, 56, 73, 77	0
2	H	6/11 (54%)	1.82	2 (33%)	1	1	41, 47, 57, 61	0
All	All	422/448 (94%)	0.42	32 (7%)	20	22	13, 36, 65, 99	4 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	785	ASP	4.3
1	C	662	MET	4.2
1	C	685	VAL	3.7
2	G	785	ASP	3.5
2	G	780	ASN	3.5
1	D	663	HIS	3.4
1	A	659	GLY	3.2
1	C	663	HIS	3.1
2	E	781	LEU	2.9
1	B	659	GLY	2.9
2	G	782	TYR	2.8
1	C	678	ALA	2.8
1	C	686	PRO	2.7
2	H	784	TRP	2.7
2	G	786	GLN	2.6
2	G	784	TRP	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	661	HIS	2.5
2	G	781	LEU	2.4
1	D	759	GLU	2.4
1	D	728	ASN	2.3
1	D	685	VAL	2.3
1	D	662	MET	2.3
1	D	698	GLU	2.2
1	A	759	GLU	2.2
2	F	786	GLN	2.2
1	D	723	THR	2.2
2	E	782	TYR	2.1
1	A	758	GLU	2.0
1	D	722	GLN	2.0
1	C	715	CYS	2.0
1	C	710	GLY	2.0
2	F	780	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
2	PTR	H	783	16/17	0.94	0.09	26,33,39,45	0
2	PTR	G	783	16/17	0.95	0.09	38,48,58,61	0
2	PTR	E	783	16/17	0.97	0.06	19,25,28,30	0
2	PTR	F	783	16/17	0.97	0.06	17,22,27,28	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.