



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:54 PM UTC

PDB ID : 6QPN / pdb_00006qpn
Title : Adenovirus species D serotype 49 Fiber-Knob
Authors : Baker, A.T.; Rizkallah, P.J.
Deposited on : 2019-02-14
Resolution : 2.74 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
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

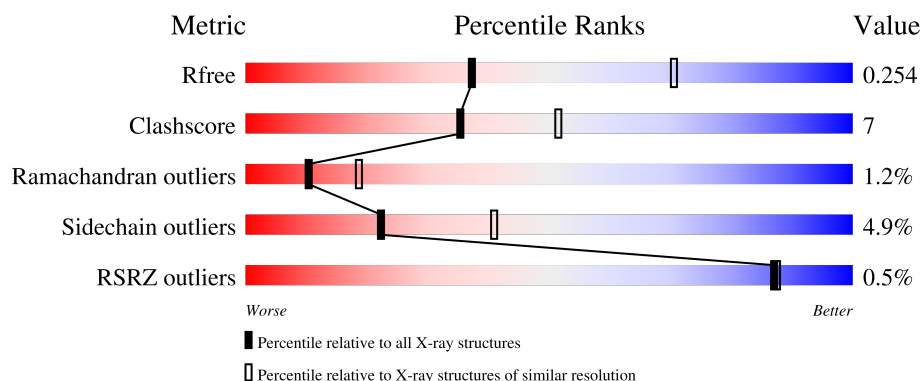
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

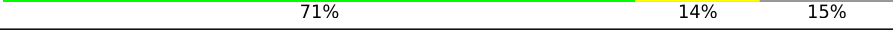
The reported resolution of this entry is 2.74 Å.

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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	226	
1	B	226	
1	C	226	
1	D	226	
1	E	226	

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Mol	Chain	Length	Quality of chain
1	F	226	% 69% 14% • 15%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9083 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 Fiber.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	199	Total	C	N	O	S	0	0	0
			1542	979	252	307	4			
1	B	184	Total	C	N	O	S	0	0	0
			1439	919	234	282	4			
1	C	196	Total	C	N	O	S	0	0	0
			1523	968	247	304	4			
1	D	193	Total	C	N	O	S	0	0	0
			1502	956	244	298	4			
1	E	200	Total	C	N	O	S	0	0	0
			1551	984	253	310	4			
1	F	193	Total	C	N	O	S	0	0	0
			1502	956	244	298	4			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	MET	-	initiating methionine	UNP Q09TX9
A	374	ARG	-	expression tag	UNP Q09TX9
A	375	GLY	-	expression tag	UNP Q09TX9
A	376	SER	-	expression tag	UNP Q09TX9
A	377	HIS	-	expression tag	UNP Q09TX9
A	378	HIS	-	expression tag	UNP Q09TX9
A	379	HIS	-	expression tag	UNP Q09TX9
A	380	HIS	-	expression tag	UNP Q09TX9
A	381	HIS	-	expression tag	UNP Q09TX9
A	382	HIS	-	expression tag	UNP Q09TX9
A	383	GLY	-	expression tag	UNP Q09TX9
A	384	SER	-	expression tag	UNP Q09TX9
B	373	MET	-	initiating methionine	UNP Q09TX9
B	374	ARG	-	expression tag	UNP Q09TX9
B	375	GLY	-	expression tag	UNP Q09TX9
B	376	SER	-	expression tag	UNP Q09TX9
B	377	HIS	-	expression tag	UNP Q09TX9

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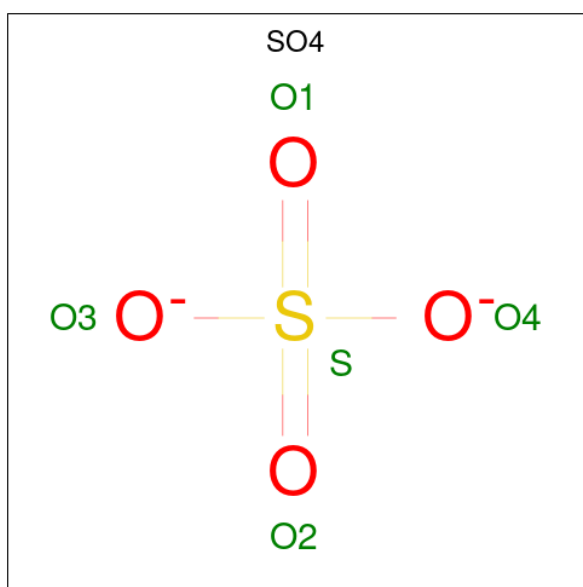
Chain	Residue	Modelled	Actual	Comment	Reference
B	378	HIS	-	expression tag	UNP Q09TX9
B	379	HIS	-	expression tag	UNP Q09TX9
B	380	HIS	-	expression tag	UNP Q09TX9
B	381	HIS	-	expression tag	UNP Q09TX9
B	382	HIS	-	expression tag	UNP Q09TX9
B	383	GLY	-	expression tag	UNP Q09TX9
B	384	SER	-	expression tag	UNP Q09TX9
C	373	MET	-	initiating methionine	UNP Q09TX9
C	374	ARG	-	expression tag	UNP Q09TX9
C	375	GLY	-	expression tag	UNP Q09TX9
C	376	SER	-	expression tag	UNP Q09TX9
C	377	HIS	-	expression tag	UNP Q09TX9
C	378	HIS	-	expression tag	UNP Q09TX9
C	379	HIS	-	expression tag	UNP Q09TX9
C	380	HIS	-	expression tag	UNP Q09TX9
C	381	HIS	-	expression tag	UNP Q09TX9
C	382	HIS	-	expression tag	UNP Q09TX9
C	383	GLY	-	expression tag	UNP Q09TX9
C	384	SER	-	expression tag	UNP Q09TX9
D	373	MET	-	initiating methionine	UNP Q09TX9
D	374	ARG	-	expression tag	UNP Q09TX9
D	375	GLY	-	expression tag	UNP Q09TX9
D	376	SER	-	expression tag	UNP Q09TX9
D	377	HIS	-	expression tag	UNP Q09TX9
D	378	HIS	-	expression tag	UNP Q09TX9
D	379	HIS	-	expression tag	UNP Q09TX9
D	380	HIS	-	expression tag	UNP Q09TX9
D	381	HIS	-	expression tag	UNP Q09TX9
D	382	HIS	-	expression tag	UNP Q09TX9
D	383	GLY	-	expression tag	UNP Q09TX9
D	384	SER	-	expression tag	UNP Q09TX9
E	373	MET	-	initiating methionine	UNP Q09TX9
E	374	ARG	-	expression tag	UNP Q09TX9
E	375	GLY	-	expression tag	UNP Q09TX9
E	376	SER	-	expression tag	UNP Q09TX9
E	377	HIS	-	expression tag	UNP Q09TX9
E	378	HIS	-	expression tag	UNP Q09TX9
E	379	HIS	-	expression tag	UNP Q09TX9
E	380	HIS	-	expression tag	UNP Q09TX9
E	381	HIS	-	expression tag	UNP Q09TX9
E	382	HIS	-	expression tag	UNP Q09TX9
E	383	GLY	-	expression tag	UNP Q09TX9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	384	SER	-	expression tag	UNP Q09TX9
F	373	MET	-	initiating methionine	UNP Q09TX9
F	374	ARG	-	expression tag	UNP Q09TX9
F	375	GLY	-	expression tag	UNP Q09TX9
F	376	SER	-	expression tag	UNP Q09TX9
F	377	HIS	-	expression tag	UNP Q09TX9
F	378	HIS	-	expression tag	UNP Q09TX9
F	379	HIS	-	expression tag	UNP Q09TX9
F	380	HIS	-	expression tag	UNP Q09TX9
F	381	HIS	-	expression tag	UNP Q09TX9
F	382	HIS	-	expression tag	UNP Q09TX9
F	383	GLY	-	expression tag	UNP Q09TX9
F	384	SER	-	expression tag	UNP Q09TX9

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



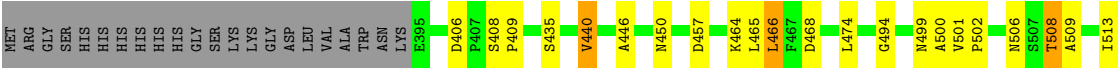
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

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



• Molecule 1: Fiber



• Molecule 1: Fiber



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.83Å 56.28Å 115.70Å 90.00° 112.95° 90.00°	Depositor
Resolution (Å)	106.54 – 2.74 106.54 – 2.74	Depositor EDS
% Data completeness (in resolution range)	98.7 (106.54-2.74) 98.7 (106.54-2.74)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.211 , 0.259 0.212 , 0.254	Depositor DCC
R_{free} test set	1609 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	66.7	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.8	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	9083	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.01	0/1576	1.48	7/2141 (0.3%)
1	B	1.01	1/1470 (0.1%)	1.40	4/1991 (0.2%)
1	C	1.00	0/1556	1.42	6/2112 (0.3%)
1	D	0.99	0/1535	1.40	3/2083 (0.1%)
1	E	1.00	0/1585	1.40	2/2153 (0.1%)
1	F	0.98	0/1535	1.39	3/2083 (0.1%)
All	All	1.00	1/9257 (0.0%)	1.42	25/12563 (0.2%)

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	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	454	PRO	C-O	-5.93	1.17	1.24

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	404	THR	CA-CB-OG1	-12.78	90.43	109.60
1	B	499	ASN	CA-CB-CG	-9.21	103.39	112.60
1	A	403	THR	CA-C-O	-7.18	112.66	120.92
1	C	531	THR	CA-CB-OG1	-6.70	99.55	109.60
1	B	531	THR	CA-CB-OG1	-6.51	99.83	109.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	497	TYR	Peptide
1	B	499	ASN	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	1542	0	1524	32	0
1	B	1439	0	1429	29	0
1	C	1523	0	1503	35	1
1	D	1502	0	1485	16	1
1	E	1551	0	1530	28	0
1	F	1502	0	1485	19	1
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	D	5	0	0	0	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	F	2	0	0	0	0
All	All	9083	0	8956	134	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 134 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:403:THR:O	1:B:404:THR:HG22	1.59	1.03
1:A:424:VAL:HG21	1:C:589:ILE:HD12	1.56	0.85
1:E:502:PRO:HG3	1:E:593:ALA:HB2	1.57	0.85
1:E:518:THR:CG2	1:E:518:THR:O	2.27	0.82
1:C:401:LEU:HD11	1:C:486:TYR:CE1	2.16	0.80

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:482:ASN:ND2	1:D:482:ASN:ND2[2_655]	1.99	0.21
1:C:498:GLU:OE1	1:F:475:THR:OG1[2_656]	2.08	0.12

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	197/226 (87%)	179 (91%)	15 (8%)	3 (2%)	8	14
1	B	178/226 (79%)	168 (94%)	9 (5%)	1 (1%)	21	36
1	C	192/226 (85%)	179 (93%)	11 (6%)	2 (1%)	12	22
1	D	189/226 (84%)	174 (92%)	13 (7%)	2 (1%)	11	20
1	E	198/226 (88%)	181 (91%)	14 (7%)	3 (2%)	8	14
1	F	189/226 (84%)	171 (90%)	15 (8%)	3 (2%)	7	13
All	All	1143/1356 (84%)	1052 (92%)	77 (7%)	14 (1%)	10	19

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	518	THR
1	A	557	GLU
1	C	557	GLU
1	D	521	PRO
1	F	521	PRO

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	175/198 (88%)	170 (97%)	5 (3%)	37	59
1	B	163/198 (82%)	152 (93%)	11 (7%)	15	27
1	C	173/198 (87%)	164 (95%)	9 (5%)	21	38
1	D	171/198 (86%)	165 (96%)	6 (4%)	32	54
1	E	176/198 (89%)	169 (96%)	7 (4%)	28	49
1	F	171/198 (86%)	159 (93%)	12 (7%)	14	26
All	All	1029/1188 (87%)	979 (95%)	50 (5%)	22	41

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	523	ASP
1	E	508	THR
1	F	563	SER
1	D	525	LYS
1	E	440	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	450	ASN
1	E	447	ASN
1	F	535	ASN
1	D	482	ASN
1	D	506	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

3 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	$\# Z > 2$
2	SO4	A	601	-	4,4,4	0.33	0	6,6,6	0.09	0
2	SO4	D	601	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	B	601	-	4,4,4	0.34	0	6,6,6	0.13	0

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.

5.7 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	199/226 (88%)	-0.37	0 100 100	51, 81, 131, 143	0
1	B	184/226 (81%)	-0.19	1 (0%) 87 87	51, 90, 164, 194	0
1	C	196/226 (86%)	0.13	3 (1%) 72 69	75, 127, 173, 211	0
1	D	193/226 (85%)	-0.43	0 100 100	48, 75, 128, 190	0
1	E	200/226 (88%)	-0.23	0 100 100	65, 106, 152, 180	0
1	F	193/226 (85%)	-0.05	2 (1%) 79 79	67, 99, 150, 205	0
All	All	1165/1356 (85%)	-0.19	6 (0%) 87 87	48, 95, 160, 211	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	469	ALA	2.7
1	C	401	LEU	2.6
1	B	593	ALA	2.5
1	C	405	PRO	2.4
1	C	479	LEU	2.2

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(Å ²)	Q<0.9
2	SO4	B	601	5/5	0.67	0.11	154,154,166,174	0
2	SO4	D	601	5/5	0.89	0.07	112,119,122,124	5
2	SO4	A	601	5/5	0.93	0.11	144,145,148,161	0

6.5 Other polymers [i](#)

There are no such residues in this entry.