



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4IF8 / pdb_00004if8
Title : Structure Of Vaspin
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Deposited on : 2012-12-14
Resolution : 2.08 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

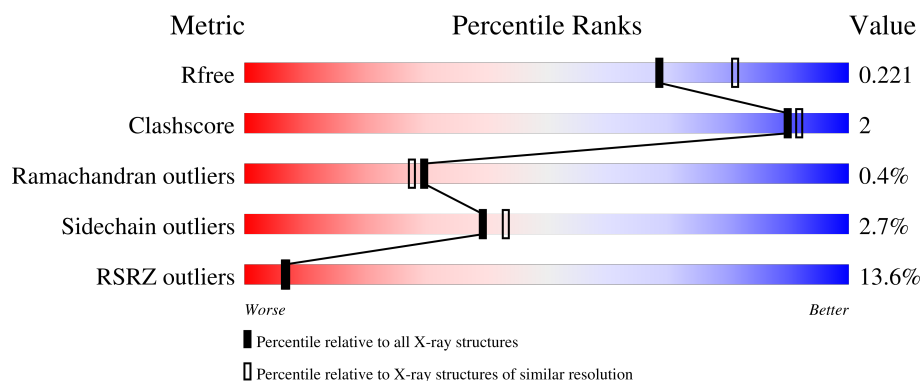
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
Sidechain outliers	187428	8642 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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	414	3% 82% 7% 11%
1	B	414	21% 78% 8% 13%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6275 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 Serpin A12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	7	0
			3008	1938	509	547	14			
1	B	361	Total	C	N	O	S	0	1	0
			2946	1905	498	531	12			

There are 42 discrepancies between the modelled and reference sequences:

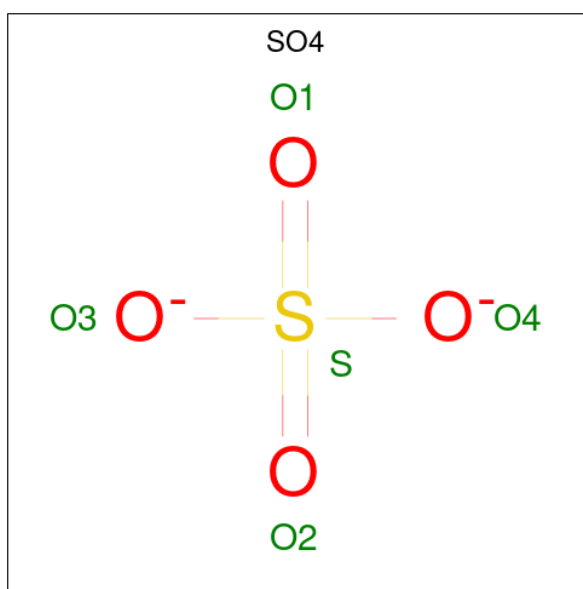
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q8IW75
A	2	HIS	-	expression tag	UNP Q8IW75
A	3	HIS	-	expression tag	UNP Q8IW75
A	4	HIS	-	expression tag	UNP Q8IW75
A	5	HIS	-	expression tag	UNP Q8IW75
A	6	HIS	-	expression tag	UNP Q8IW75
A	7	HIS	-	expression tag	UNP Q8IW75
A	8	HIS	-	expression tag	UNP Q8IW75
A	9	HIS	-	expression tag	UNP Q8IW75
A	10	HIS	-	expression tag	UNP Q8IW75
A	11	HIS	-	expression tag	UNP Q8IW75
A	12	SER	-	expression tag	UNP Q8IW75
A	13	SER	-	expression tag	UNP Q8IW75
A	14	GLY	-	expression tag	UNP Q8IW75
A	15	HIS	-	expression tag	UNP Q8IW75
A	16	ILE	-	expression tag	UNP Q8IW75
A	17	GLU	-	expression tag	UNP Q8IW75
A	18	GLY	-	expression tag	UNP Q8IW75
A	19	ARG	-	expression tag	UNP Q8IW75
A	20	HIS	-	expression tag	UNP Q8IW75
A	21	MET	-	expression tag	UNP Q8IW75
B	1	GLY	-	expression tag	UNP Q8IW75
B	2	HIS	-	expression tag	UNP Q8IW75
B	3	HIS	-	expression tag	UNP Q8IW75
B	4	HIS	-	expression tag	UNP Q8IW75

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	expression tag	UNP Q8IW75
B	6	HIS	-	expression tag	UNP Q8IW75
B	7	HIS	-	expression tag	UNP Q8IW75
B	8	HIS	-	expression tag	UNP Q8IW75
B	9	HIS	-	expression tag	UNP Q8IW75
B	10	HIS	-	expression tag	UNP Q8IW75
B	11	HIS	-	expression tag	UNP Q8IW75
B	12	SER	-	expression tag	UNP Q8IW75
B	13	SER	-	expression tag	UNP Q8IW75
B	14	GLY	-	expression tag	UNP Q8IW75
B	15	HIS	-	expression tag	UNP Q8IW75
B	16	ILE	-	expression tag	UNP Q8IW75
B	17	GLU	-	expression tag	UNP Q8IW75
B	18	GLY	-	expression tag	UNP Q8IW75
B	19	ARG	-	expression tag	UNP Q8IW75
B	20	HIS	-	expression tag	UNP Q8IW75
B	21	MET	-	expression tag	UNP Q8IW75

- 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		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	214	Total 214	O 214	0	0
3	B	97	Total 97	O 97	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.55Å 152.10Å 61.45Å 90.00° 97.52° 90.00°	Depositor
Resolution (Å)	29.80 – 2.08 29.80 – 2.08	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.80-2.08) 99.9 (29.80-2.08)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 2.08Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.197 , 0.221 0.200 , 0.221	Depositor DCC
R_{free} test set	1069 reflections (1.47%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6275	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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	0.85	0/3105	1.16	8/4176 (0.2%)
1	B	0.76	0/3012	1.18	7/4053 (0.2%)
All	All	0.81	0/6117	1.17	15/8229 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	PHE	CA-CB-CG	-7.08	106.72	113.80
1	A	382	LEU	N-CA-C	-5.93	102.88	110.53
1	B	92	ASP	N-CA-C	5.71	116.99	108.31
1	A	41	GLN	CA-C-N	5.64	127.84	120.28
1	A	41	GLN	C-N-CA	5.64	127.84	120.28
1	A	52	ASN	CA-CB-CG	5.62	118.22	112.60
1	A	104	PHE	CA-CB-CG	5.54	119.33	113.80
1	A	201	VAL	N-CA-C	-5.36	107.90	113.10
1	B	83	PHE	CA-CB-CG	-5.29	108.52	113.80
1	B	290	ASP	CA-C-N	5.22	127.23	120.44
1	B	290	ASP	C-N-CA	5.22	127.23	120.44
1	B	104	PHE	CA-C-N	5.15	127.44	120.38
1	B	104	PHE	C-N-CA	5.15	127.44	120.38
1	B	124	THR	CB-CA-C	5.14	117.98	110.26
1	A	341	ILE	N-CA-C	-5.13	106.07	110.74

There are no chirality outliers.

There are no planarity outliers.

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	3008	0	3071	8	0
1	B	2946	0	3011	14	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	214	0	0	1	0
3	B	97	0	0	0	0
All	All	6275	0	6082	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 2.

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)
1:B:82:ALA:HB1	1:B:204:LEU:HD21	1.83	0.60
1:A:131:LYS:HB2	1:A:211:ARG:HB2	1.88	0.54
1:B:148:ARG:HA	1:B:151:LEU:HD12	1.90	0.53
1:B:135:GLY:HA3	1:B:207[B]:TYR:CE2	2.43	0.53
1:A:82:ALA:HB1	1:A:204:LEU:HD21	1.93	0.50
1:A:141:ASP:OD2	1:A:143:ARG:HD3	2.12	0.49
1:B:211:ARG:HE	1:B:359:LYS:HD2	1.78	0.48
1:B:238:VAL:HG12	1:B:412:ILE:HG12	1.96	0.48
1:A:243:ARG:NH2	3:A:692:HOH:O	2.48	0.46
1:A:122:GLU:HB3	1:A:399:ILE:HG13	1.99	0.45
1:B:249:VAL:HG22	1:B:260:LEU:HD12	1.98	0.45
1:B:214:TRP:HA	1:B:264:TYR:HA	1.99	0.45
1:A:280:LEU:HD21	1:A:407:LYS:HE3	1.98	0.44
1:B:75:SER:HB2	1:B:208:ILE:HG21	2.00	0.43
1:A:137:THR:HG23	1:A:161:GLU:HG2	2.00	0.43
1:B:99:LYS:HA	1:B:104:PHE:HB2	2.00	0.42
1:B:151:LEU:HD23	1:B:162:THR:HB	2.02	0.42
1:A:273:ILE:HD11	1:A:393:LEU:HD13	2.00	0.42
1:B:247:TYR:HE2	1:B:262:ILE:HG23	1.85	0.42
1:B:308:VAL:HG22	1:B:386:ILE:HD12	2.02	0.42
1:B:249:VAL:HG21	1:B:304:VAL:HG21	2.04	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	370/414 (89%)	361 (98%)	7 (2%)	2 (0%)	24	21
1	B	356/414 (86%)	343 (96%)	12 (3%)	1 (0%)	36	36
All	All	726/828 (88%)	704 (97%)	19 (3%)	3 (0%)	30	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	344	HIS
1	A	267	ASN
1	B	267	ASN

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	339/369 (92%)	332 (98%)	7 (2%)	47	52
1	B	328/369 (89%)	317 (97%)	11 (3%)	32	34
All	All	667/738 (90%)	649 (97%)	18 (3%)	39	43

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	MET
1	A	126	LYS
1	A	161	GLU
1	A	192	LEU
1	A	294	ARG
1	A	344	HIS
1	A	401	SER
1	B	168	GLN
1	B	188	LYS
1	B	243	ARG
1	B	260	LEU
1	B	266	LYS
1	B	269	THR
1	B	289	VAL
1	B	294	ARG
1	B	304	VAL
1	B	306	VAL
1	B	412	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	HIS
1	A	216	HIS
1	A	248	GLN
1	B	51	GLN
1	B	117	HIS
1	B	168	GLN
1	B	174	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	$\# Z > 2$
2	SO4	B	501	-	4,4,4	0.35	0	6,6,6	0.10	0
2	SO4	A	501	-	4,4,4	0.39	0	6,6,6	0.31	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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	367/414 (88%)	-0.04	13 (3%)	47 49	17, 34, 63, 92	7 (1%)
1	B	361/414 (87%)	1.07	86 (23%)	2 2	20, 59, 122, 143	1 (0%)
All	All	728/828 (87%)	0.51	99 (13%)	7 7	17, 42, 118, 143	8 (1%)

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	246	ILE	6.3
1	B	382	LEU	5.9
1	B	242	PHE	5.8
1	B	413	GLY	5.6
1	B	218	PHE	5.6
1	B	222	VAL	5.6
1	B	365	THR	5.1
1	B	36	VAL	5.0
1	B	289	VAL	4.5
1	B	237	LYS	4.5
1	B	247	TYR	4.4
1	A	399	ILE	4.3
1	B	51	GLN	4.3
1	B	298	LEU	4.2
1	B	232	LYS	4.1
1	B	221	ASN	4.0
1	B	220	PRO	4.0
1	B	260	LEU	3.9
1	A	378	MET	3.9
1	A	414	LYS	3.9
1	B	389	PRO	3.9
1	B	224	LYS	3.9
1	B	219	ASP	3.8
1	B	233	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	289	VAL	3.8
1	B	306	VAL	3.8
1	B	215	LYS	3.8
1	A	126	LYS	3.6
1	B	229	PHE	3.6
1	B	251	TYR	3.6
1	B	277	GLU	3.5
1	B	230	LEU	3.5
1	B	244	SER	3.4
1	B	303	VAL	3.3
1	B	412	ILE	3.3
1	B	383	VAL	3.3
1	B	386	ILE	3.3
1	B	216	HIS	3.2
1	B	259	ILE	3.2
1	B	127	THR	3.2
1	B	214	TRP	3.1
1	B	299	LEU	3.1
1	B	297	THR	3.1
1	B	236	VAL	3.1
1	B	274	LEU	3.1
1	B	240	MET	3.1
1	B	234	SER	3.1
1	B	296	LYS	3.0
1	B	223	THR	3.0
1	B	235	SER	3.0
1	A	125	GLN	3.0
1	B	287	LEU	3.0
1	B	249	VAL	2.9
1	B	37	GLN	2.9
1	B	314	THR	2.9
1	B	228	PHE	2.9
1	A	297	THR	2.8
1	B	262	ILE	2.8
1	B	267	ASN	2.8
1	B	212	ALA	2.7
1	B	290	ASP	2.7
1	B	280	LEU	2.7
1	B	103	ASN	2.7
1	B	395	TYR	2.7
1	B	363	ARG	2.6
1	B	385	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	366	GLU	2.6
1	B	217	GLU	2.6
1	A	233	ASN	2.6
1	B	226	GLU	2.6
1	B	364	GLY	2.6
1	B	209	PHE	2.5
1	B	292	PHE	2.5
1	B	311	LEU	2.5
1	A	232	LYS	2.5
1	B	308	VAL	2.5
1	B	310	ARG	2.4
1	A	344	HIS	2.4
1	B	305	ASP	2.4
1	B	254	LYS	2.4
1	B	35	GLU	2.3
1	A	345	ARG	2.3
1	B	398	LYS	2.3
1	B	225	GLU	2.3
1	B	253	ASP	2.3
1	B	239	PRO	2.3
1	B	388	LYS	2.3
1	B	390	TYR	2.2
1	B	255	LEU	2.2
1	B	300	SER	2.2
1	B	302	ARG	2.2
1	A	400	PRO	2.2
1	B	46	LYS	2.2
1	B	129	ASP	2.2
1	B	384	VAL	2.1
1	B	362	GLU	2.1
1	B	263	PRO	2.1
1	B	264	TYR	2.1
1	B	282	HIS	2.0

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

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

6.3 Carbohydrates ⓘ

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	SO4	B	501	5/5	0.81	0.26	66,70,71,71	5
2	SO4	A	501	5/5	0.91	0.10	60,63,65,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.