Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 02:34 PM EDT

PDB ID	:	6RRC
Title	:	Crystal structure of the N-terminal region of human cohesin subunit STAG1 in complex with RAD21 peptide
Authors	:	Newman, J.A.; Katis, V.L.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Gileadi, O.
Deposited on	:	2019-05-17
Resolution	:	2.37 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 (i) 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 (i)) were used in the production of this report:

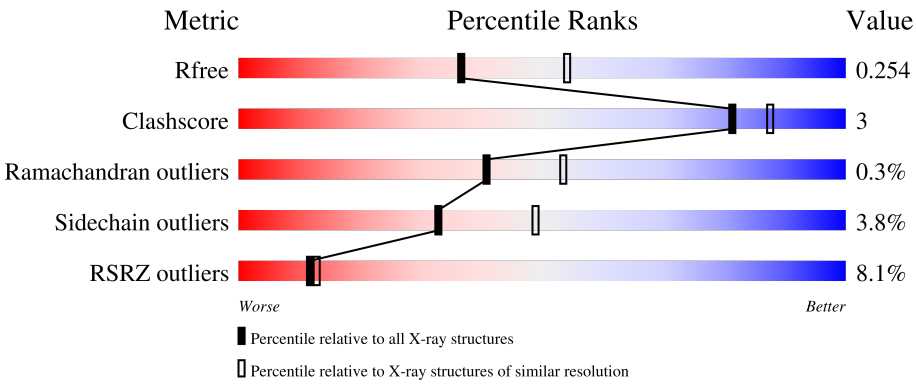
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.37 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 <=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	339	8%, 83%, 10%, • 6%
1	C	339	7%, 91%, 6%, • •
2	B	25	20%, 64%, 8%, 28%
2	D	25	4%, 72%, •, 12%, 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5659 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 Cohesin subunit SA-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	331	2680	1697	453	509	21	0	0	0
1	A	319	2588	1641	437	489	21	0	0	0

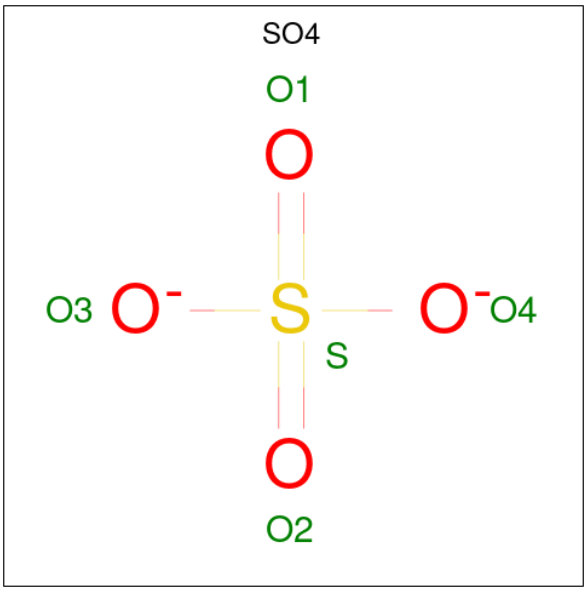
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	82	SER	-	expression tag	UNP Q8WVM7
C	83	MET	-	expression tag	UNP Q8WVM7
C	84	GLY	-	expression tag	UNP Q8WVM7
C	85	GLY	-	expression tag	UNP Q8WVM7
A	82	SER	-	expression tag	UNP Q8WVM7
A	83	MET	-	expression tag	UNP Q8WVM7
A	84	GLY	-	expression tag	UNP Q8WVM7
A	85	GLY	-	expression tag	UNP Q8WVM7

- Molecule 2 is a protein called Double-strand-break repair protein rad21 homolog.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	18	131	81	23	27	0	0	0
2	D	22	175	108	32	35	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

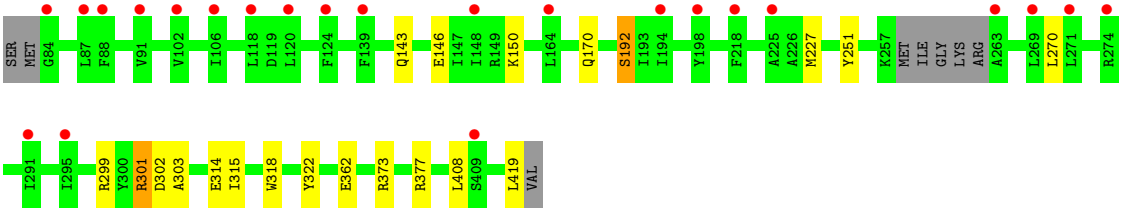
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	42	Total O 42 42	0	0
4	B	2	Total O 2 2	0	0
4	A	20	Total O 20 20	0	0
4	D	1	Total O 1 1	0	0

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.

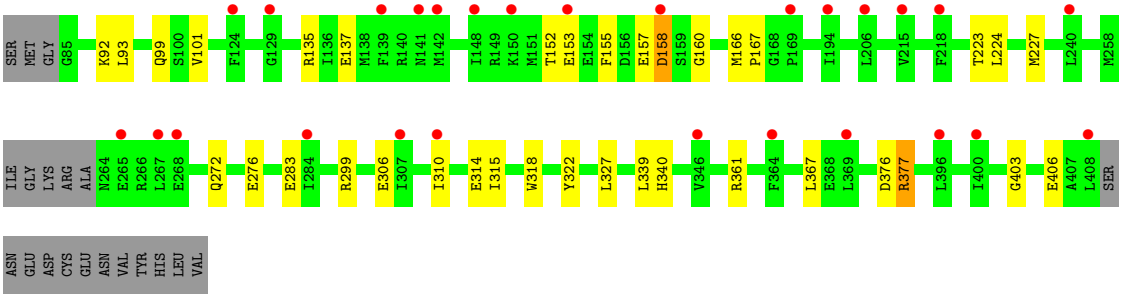
- Molecule 1: Cohesin subunit SA-1

Chain C:



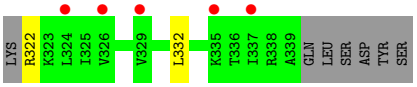
- Molecule 1: Cohesin subunit SA-1

Chain A:



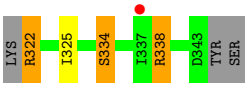
- Molecule 2: Double-strand-break repair protein rad21 homolog

Chain B:



- Molecule 2: Double-strand-break repair protein rad21 homolog

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	117.08Å 151.66Å 126.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.79 – 2.37 74.79 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.8 (74.79-2.37) 99.7 (74.79-2.37)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.46 (at 2.37Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.214 , 0.248 0.221 , 0.254	Depositor DCC
R_{free} test set	2295 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	66.0	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 63.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5659	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: 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	0.23	0/2630	0.37	0/3545
1	C	0.23	0/2724	0.37	0/3672
2	B	0.22	0/130	0.42	0/174
2	D	0.21	0/174	0.38	0/231
All	All	0.23	0/5658	0.37	0/7622

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	2588	0	2546	19	0
1	C	2680	0	2633	9	0
2	B	131	0	131	1	0
2	D	175	0	190	4	0
3	C	20	0	0	1	0
4	A	20	0	0	0	0
4	B	2	0	0	0	0
4	C	42	0	0	0	0
4	D	1	0	0	0	0
All	All	5659	0	5500	29	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 (29) 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:A:227:MET:HB3	1:A:314:GLU:HG2	1.80	0.64
1:C:227:MET:HB3	1:C:314:GLU:HG2	1.81	0.63
1:A:152:THR:O	2:D:322:ARG:NH1	2.36	0.59
1:C:301:ARG:NH2	2:B:332:LEU:O	2.37	0.57
1:C:373:ARG:NH2	3:C:503:SO4:O4	2.34	0.57
1:A:272:GLN:NE2	1:A:276:GLU:OE1	2.38	0.56
1:A:155:PHE:HD1	1:A:157:GLU:HB3	1.72	0.55
1:A:361:ARG:HG2	1:A:403:GLY:HA2	1.92	0.52
2:D:334:SER:O	2:D:338:ARG:N	2.36	0.51
1:C:251:TYR:HA	1:C:270:LEU:HD13	1.94	0.49
1:A:153:GLU:HA	2:D:322:ARG:HH11	1.80	0.47
1:A:339:LEU:O	1:A:377:ARG:NH1	2.50	0.45
1:A:224:LEU:HD13	1:A:310:ILE:HD12	1.98	0.45
1:A:135:ARG:NH1	1:A:137:GLU:OE2	2.49	0.45
1:C:302:ASP:OD1	1:C:303:ALA:N	2.49	0.45
1:C:299:ARG:NH1	1:C:302:ASP:OD2	2.42	0.45
1:A:340:HIS:CE1	1:A:377:ARG:HG3	2.52	0.44
1:A:327:LEU:HD11	1:A:367:LEU:HD21	2.00	0.44
1:C:419:LEU:HD23	1:C:419:LEU:HA	1.90	0.44
1:A:155:PHE:CD1	1:A:157:GLU:HB3	2.53	0.43
1:A:361:ARG:NH1	1:A:406:GLU:OE1	2.49	0.43
1:C:315:ILE:HA	1:C:318:TRP:CE3	2.54	0.43
1:A:223:THR:O	1:A:227:MET:HG2	2.19	0.42
1:C:146:GLU:O	1:C:150:LYS:HG2	2.20	0.42
1:A:135:ARG:HB3	1:A:135:ARG:HH11	1.85	0.42
1:A:160:GLY:HA3	2:D:325:ILE:HG13	2.02	0.41
1:A:166:MET:HA	1:A:167:PRO:HD3	1.94	0.41
1:A:315:ILE:HA	1:A:318:TRP:CE3	2.56	0.41
1:A:135:ARG:NH1	1:A:135:ARG:HB3	2.36	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	315/339 (93%)	306 (97%)	8 (2%)	1 (0%)	41	53
1	C	327/339 (96%)	321 (98%)	5 (2%)	1 (0%)	41	53
2	B	16/25 (64%)	15 (94%)	1 (6%)	0	100	100
2	D	20/25 (80%)	20 (100%)	0	0	100	100
All	All	678/728 (93%)	662 (98%)	14 (2%)	2 (0%)	41	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	192	SER
1	A	158	ASP

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	282/306 (92%)	271 (96%)	11 (4%)	32	48
1	C	293/306 (96%)	285 (97%)	8 (3%)	44	62
2	B	14/24 (58%)	13 (93%)	1 (7%)	14	21
2	D	21/24 (88%)	18 (86%)	3 (14%)	3	3
All	All	610/660 (92%)	587 (96%)	23 (4%)	33	49

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	143	GLN
1	C	170	GLN
1	C	192	SER
1	C	301	ARG
1	C	322	TYR
1	C	362	GLU
1	C	377	ARG
1	C	408	LEU
2	B	322	ARG
1	A	92	LYS
1	A	93	LEU
1	A	99	GLN
1	A	101	VAL
1	A	158	ASP
1	A	283	GLU
1	A	299	ARG
1	A	306	GLU
1	A	322	TYR
1	A	376	ASP
1	A	377	ARG
2	D	322	ARG
2	D	334	SER
2	D	338	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	SO4	C	501	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	C	504	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	C	503	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	C	502	-	4,4,4	0.23	0	6,6,6	0.09	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	503	SO4	1	0

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	319/339 (94%)	0.89	27 (8%)	10	12	60, 87, 149, 200	0
1	C	331/339 (97%)	0.80	23 (6%)	16	18	59, 78, 120, 156	0
2	B	18/25 (72%)	1.45	5 (27%)	0	0	92, 121, 162, 177	0
2	D	22/25 (88%)	0.48	1 (4%)	33	36	107, 129, 148, 165	0
All	All	690/728 (94%)	0.85	56 (8%)	12	13	59, 85, 140, 200	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	335	LYS	5.2
1	A	148	ILE	5.0
1	A	150	LYS	4.6
1	A	139	PHE	4.4
1	C	87	LEU	4.3
1	A	408	LEU	4.3
1	A	218	PHE	4.2
1	A	158	ASP	4.2
1	C	120	LEU	3.8
1	A	141	ASN	3.8
1	C	139	PHE	3.7
1	A	307	ILE	3.7
1	C	91	VAL	3.7
1	A	267	LEU	3.6
1	C	88	PHE	3.2
1	C	198	TYR	3.1
1	A	265	GLU	3.1
1	C	263	ALA	3.1
1	C	194	ILE	3.0
1	A	124	PHE	3.0
1	C	218	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	324	LEU	2.9
1	A	129	GLY	2.8
1	A	268	GLU	2.8
1	C	164	LEU	2.8
1	C	124	PHE	2.8
1	A	369	LEU	2.7
1	A	169	PRO	2.6
2	D	337	ILE	2.6
2	B	329	VAL	2.6
1	A	153	GLU	2.5
1	C	106	ILE	2.5
1	C	409	SER	2.4
1	A	284	ILE	2.4
1	C	118	LEU	2.4
1	C	148	ILE	2.4
1	A	240	LEU	2.4
1	C	102	VAL	2.3
1	C	295	ILE	2.3
1	C	84	GLY	2.2
1	C	269	LEU	2.2
1	A	396	LEU	2.2
1	C	291	ILE	2.2
1	A	310	ILE	2.2
1	A	346	VAL	2.2
1	A	400	ILE	2.1
2	B	326	VAL	2.1
1	A	364	PHE	2.1
1	C	274	ARG	2.1
2	B	337	ILE	2.1
1	C	225	ALA	2.1
1	A	194	ILE	2.1
1	A	215	VAL	2.0
1	A	142	MET	2.0
1	C	271	LEU	2.0
1	A	206	LEU	2.0

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 monosaccharides 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	SO4	C	503	5/5	0.78	0.28	217,217,218,219	0
3	SO4	C	504	5/5	0.87	0.18	183,183,184,184	0
3	SO4	C	501	5/5	0.92	0.22	129,129,133,141	0
3	SO4	C	502	5/5	0.93	0.13	106,108,111,111	0

6.5 Other polymers (i)

There are no such residues in this entry.