



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 04:28 am BST

PDB ID : 5M4Y  
Title : Crystal structure of the Sec3/Sso2 complex at 2.20 angstrom resolution  
Authors : Zhang, Y.B.; Dong, G.  
Deposited on : 2016-10-19  
Resolution : 2.20 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

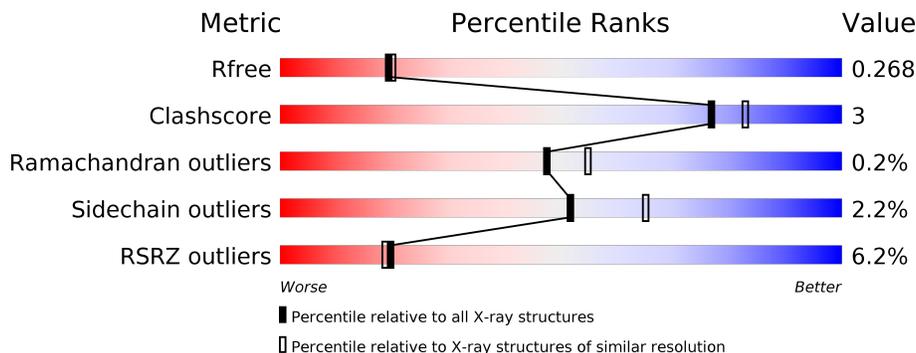
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	210	 9% 74% 10% 16%
1	C	210	 6% 79% 7% 14%
1	E	210	 13% 75% 10% 14%
2	B	250	 2% 65% 31%
2	D	250	 7% 62% 7% 31%
2	F	250	 65% 32%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
3	GOL	D	401	-	-	-	X

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 9010 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 Protein SSO2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	177	1445	888	253	298	6	0	0	0
1	C	181	1476	904	261	305	6	0	0	0
1	E	181	1476	907	258	305	6	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLY	-	expression tag	UNP P39926
A	33	SER	-	expression tag	UNP P39926
A	34	HIS	-	expression tag	UNP P39926
A	35	MET	-	expression tag	UNP P39926
A	228	LEU	-	expression tag	UNP P39926
A	229	THR	-	expression tag	UNP P39926
A	230	GLN	-	expression tag	UNP P39926
A	231	LEU	-	expression tag	UNP P39926
A	232	PHE	-	expression tag	UNP P39926
A	233	ASN	-	expression tag	UNP P39926
A	234	ASP	-	expression tag	UNP P39926
A	235	MET	-	expression tag	UNP P39926
A	236	GLU	-	expression tag	UNP P39926
A	237	GLU	-	expression tag	UNP P39926
A	238	LEU	-	expression tag	UNP P39926
A	239	VAL	-	expression tag	UNP P39926
A	240	ILE	-	expression tag	UNP P39926
A	241	GLU	-	expression tag	UNP P39926
C	32	GLY	-	expression tag	UNP P39926
C	33	SER	-	expression tag	UNP P39926
C	34	HIS	-	expression tag	UNP P39926
C	35	MET	-	expression tag	UNP P39926
C	228	LEU	-	expression tag	UNP P39926

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Chain	Residue	Modelled	Actual	Comment	Reference
C	229	THR	-	expression tag	UNP P39926
C	230	GLN	-	expression tag	UNP P39926
C	231	LEU	-	expression tag	UNP P39926
C	232	PHE	-	expression tag	UNP P39926
C	233	ASN	-	expression tag	UNP P39926
C	234	ASP	-	expression tag	UNP P39926
C	235	MET	-	expression tag	UNP P39926
C	236	GLU	-	expression tag	UNP P39926
C	237	GLU	-	expression tag	UNP P39926
C	238	LEU	-	expression tag	UNP P39926
C	239	VAL	-	expression tag	UNP P39926
C	240	ILE	-	expression tag	UNP P39926
C	241	GLU	-	expression tag	UNP P39926
E	32	GLY	-	expression tag	UNP P39926
E	33	SER	-	expression tag	UNP P39926
E	34	HIS	-	expression tag	UNP P39926
E	35	MET	-	expression tag	UNP P39926
E	228	LEU	-	expression tag	UNP P39926
E	229	THR	-	expression tag	UNP P39926
E	230	GLN	-	expression tag	UNP P39926
E	231	LEU	-	expression tag	UNP P39926
E	232	PHE	-	expression tag	UNP P39926
E	233	ASN	-	expression tag	UNP P39926
E	234	ASP	-	expression tag	UNP P39926
E	235	MET	-	expression tag	UNP P39926
E	236	GLU	-	expression tag	UNP P39926
E	237	GLU	-	expression tag	UNP P39926
E	238	LEU	-	expression tag	UNP P39926
E	239	VAL	-	expression tag	UNP P39926
E	240	ILE	-	expression tag	UNP P39926
E	241	GLU	-	expression tag	UNP P39926

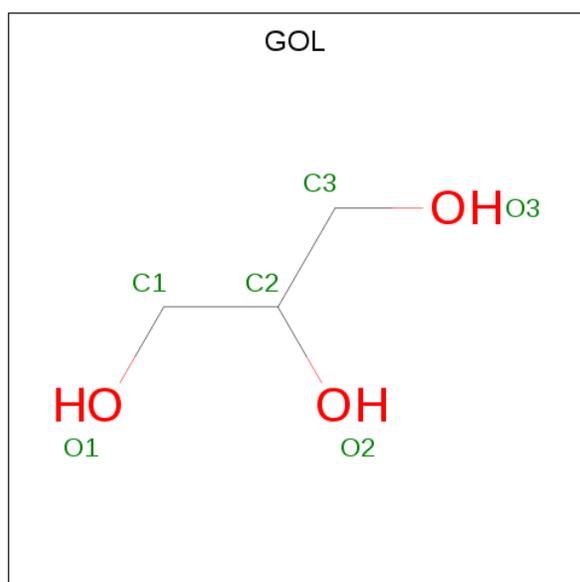
- Molecule 2 is a protein called Exocyst complex component SEC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1433	914	250	266	3			
2	D	173	Total	C	N	O	S	0	0	0
			1433	914	250	266	3			
2	F	171	Total	C	N	O	S	0	0	0
			1416	904	246	263	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	71	GLN	-	expression tag	UNP P33332
B	72	GLY	-	expression tag	UNP P33332
B	73	HIS	-	expression tag	UNP P33332
B	74	MET	-	expression tag	UNP P33332
D	71	GLN	-	expression tag	UNP P33332
D	72	GLY	-	expression tag	UNP P33332
D	73	HIS	-	expression tag	UNP P33332
D	74	MET	-	expression tag	UNP P33332
F	71	GLN	-	expression tag	UNP P33332
F	72	GLY	-	expression tag	UNP P33332
F	73	HIS	-	expression tag	UNP P33332
F	74	MET	-	expression tag	UNP P33332

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	C O	0	0
			6	3 3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	B	80	Total	O	0	0
			80	80		
4	C	29	Total	O	0	0
			29	29		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	D	76	Total O 76 76	0	0
4	E	20	Total O 20 20	0	0
4	F	78	Total O 78 78	0	0



PHE  
SER  
SER  
ALA  
PRO  
THR  
GLU  
ARG  
THR  
ARG  
ARG  
SER  
SER  
GLU  
THR  
GLU  
SER  
VAL  
VAL  
ASN  
PRO  
VAL  
SER  
SER  
ALA  
SER  
VAL  
GLU  
TYR

- Molecule 2: Exocyst complex component SEC3



GLN  
GLY  
HIS  
MET  
S75  
R86  
H99  
LYS  
THR  
G102  
Y108  
D117  
K130  
I131  
E132  
M133  
K134  
M146  
W170  
E179  
K180  
I184  
S185  
E186  
M192  
K211  
E222  
S234  
Y237  
Y243  
V247  
I248  
T249  
ASN  
ARG  
PRO  
GLY  
SER  
VAL  
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PHE  
ILE  
SER

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SER

- Molecule 2: Exocyst complex component SEC3



GLN  
GLY  
HIS  
MET  
S75  
E83  
K87  
D98  
HIS  
LYS  
THR  
G102  
I114  
S122  
L139  
V176  
M192  
S193  
E222  
I248  
THR  
ASN  
ARG  
PRO  
GLY  
SER  
VAL  
SER  
PRO  
ILE  
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PRO  
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.14Å 135.80Å 185.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.20 49.22 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.98-2.20) 99.7 (49.22-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.96 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, $R_{free}$	0.229 , 0.264 0.232 , 0.268	Depositor DCC
$R_{free}$ test set	2000 reflections (2.68%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.3	Xtrriage
Anisotropy	0.114	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 39.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9010	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.24% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: GOL

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	0/1458	0.33	0/1958
1	C	0.22	0/1489	0.33	0/1998
1	E	0.23	0/1489	0.35	0/2000
2	B	0.24	0/1465	0.42	0/1978
2	D	0.24	0/1465	0.42	0/1978
2	F	0.24	0/1447	0.41	0/1953
All	All	0.23	0/8813	0.38	0/11865

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	1445	0	1408	10	0
1	C	1476	0	1434	7	0
1	E	1476	0	1438	11	0
2	B	1433	0	1433	7	0
2	D	1433	0	1433	13	0
2	F	1416	0	1419	5	0
3	D	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	42	0	0	1	0
4	B	80	0	0	2	0
4	C	29	0	0	0	0
4	D	76	0	0	3	0
4	E	20	0	0	1	0
4	F	78	0	0	2	0
All	All	9010	0	8573	51	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.

The worst 5 of 51 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:170:ASP:HB2	1:A:171:VAL:HG13	1.67	0.76
2:F:193:SER:OG	4:F:401:HOH:O	2.06	0.74
2:D:179:GLU:OE1	4:D:501:HOH:O	2.06	0.73
2:B:146:ASN:OD1	4:B:401:HOH:O	2.06	0.73
2:D:211:LYS:NZ	4:D:503:HOH:O	2.23	0.71

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	173/210 (82%)	169 (98%)	3 (2%)	1 (1%)	25	26
1	C	177/210 (84%)	174 (98%)	3 (2%)	0	100	100
1	E	177/210 (84%)	171 (97%)	6 (3%)	0	100	100
2	B	169/250 (68%)	165 (98%)	4 (2%)	0	100	100
2	D	169/250 (68%)	164 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	F	167/250 (67%)	162 (97%)	4 (2%)	1 (1%)	25 26
All	All	1032/1380 (75%)	1005 (97%)	25 (2%)	2 (0%)	47 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
2	F	222	GLU

### 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	159/187 (85%)	152 (96%)	7 (4%)	28 35
1	C	161/187 (86%)	158 (98%)	3 (2%)	57 71
1	E	162/187 (87%)	155 (96%)	7 (4%)	29 36
2	B	161/230 (70%)	161 (100%)	0	100 100
2	D	161/230 (70%)	159 (99%)	2 (1%)	71 83
2	F	159/230 (69%)	157 (99%)	2 (1%)	69 81
All	All	963/1251 (77%)	942 (98%)	21 (2%)	52 65

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	174	GLN
2	D	247	VAL
1	E	205	LEU
1	C	172	ASN
1	E	218	PHE

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	GOL	D	401	-	5,5,5	0.36	0	5,5,5	0.22	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
3	GOL	D	401	-	-	0/4/4/4	-

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	D	401	GOL	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	177/210 (84%)	0.53	18 (10%) 6 6	35, 54, 99, 112	0
1	C	181/210 (86%)	0.35	12 (6%) 18 17	34, 52, 99, 112	0
1	E	181/210 (86%)	0.64	28 (15%) 2 1	37, 56, 120, 130	0
2	B	173/250 (69%)	0.12	5 (2%) 51 49	34, 43, 74, 117	0
2	D	173/250 (69%)	-0.07	2 (1%) 79 77	29, 40, 63, 116	0
2	F	171/250 (68%)	-0.10	1 (0%) 89 88	30, 40, 62, 81	0
All	All	1056/1380 (76%)	0.25	66 (6%) 20 19	29, 46, 100, 130	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	197	VAL	5.9
1	A	35	MET	5.6
1	E	191	LYS	5.6
1	E	156	GLN	5.5
1	A	171	VAL	5.3

### 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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GOL	D	401	6/6	0.54	0.42	61,64,67,75	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.