wwPDB X-ray Structure Validation Summary Report (i)

Jun 13, 2024 – 12:27 AM EDT

PDB ID	:	1KCW
Title	:	X-RAY CRYSTAL STRUCTURE OF HUMAN CERULOPLASMIN AT 3.0 ANGSTROMS
Authors	:	Card, G.L.; Zaitsev, V.N.; Lindley, P.F.
Deposited on	:	1996-09-25
Resolution	:	3.00 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 (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:

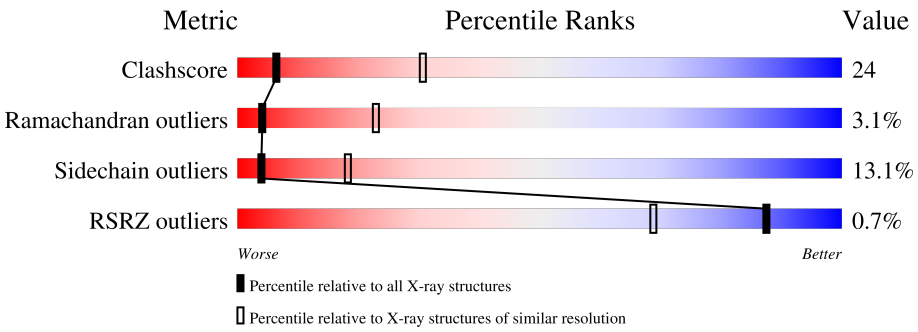
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.00 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))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	1046	

2 Entry composition (i)

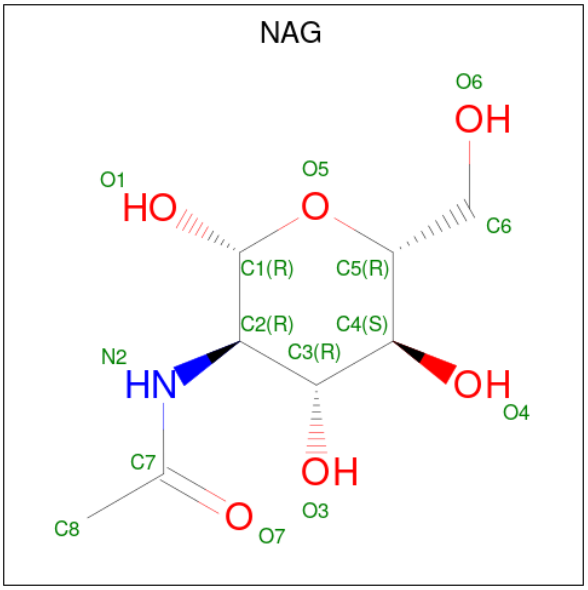
There are 4 unique types of molecules in this entry. The entry contains 8228 atoms, of which 3 are hydrogens and 0 are deuteriums.

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 CERULOPLASMIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	1017	8190	5225	3	1361	1563	38	0	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	14	8	1	5	0	0
2	A	1	14	8	1	5	0	0

- Molecule 3 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cu		
3	A	8	8	8	0	0

- Molecule 4 is OXYGEN ATOM (three-letter code: O) (formula: O).

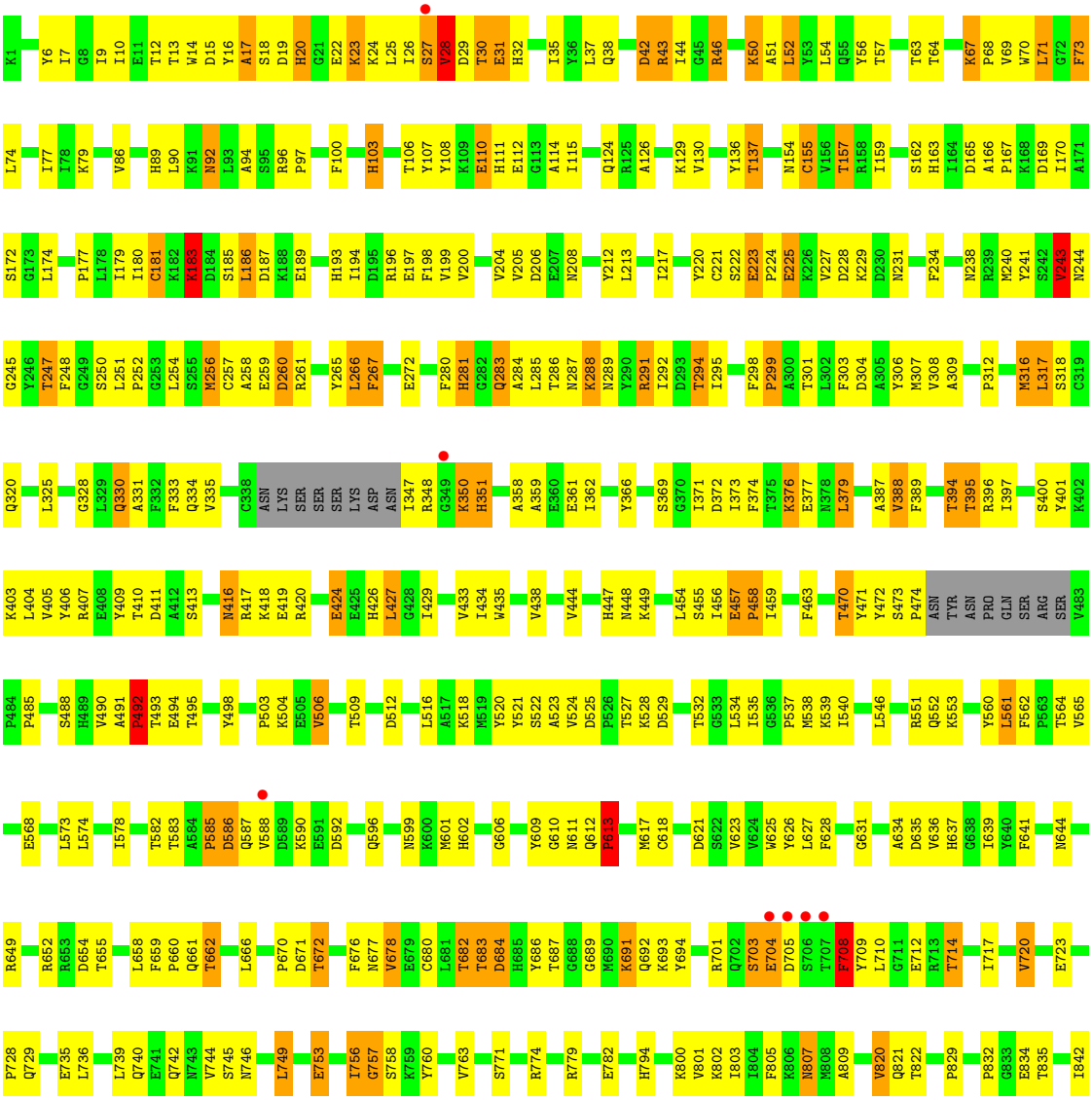
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	2	2	2	0	0

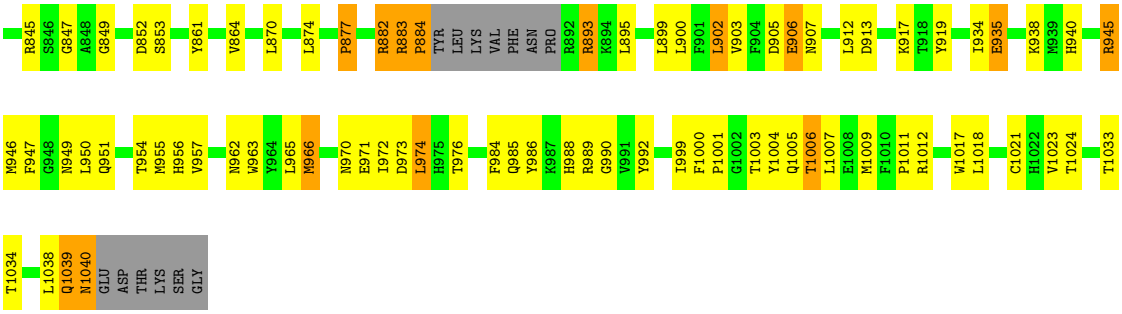
3 Residue-property plots (i)

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: CERULOPLASMIN

Chain A:




R845
S846
G847
A848
G849
D852
S853
Y861
V864
L870
L874
P877
R882
R883
P884
TYR
LEU
LYS
VAL
PHE
ASN
PRO
R892
R893
K894
L895
L899
L900
F901
L902
V903
F904
D905
E906
N907
L912
D913
K917
T918
Y919
I934
E935
K938
M939
H940
R945
M946
F947
G948
N949
L950
Q951
T954
M955
H956
V957
N962
W963
Y964
L965
M966
N970
E971
I972
D973
L974
H975
T976
F984
Q985
Y986
K987
H988
R989
G990
V991
Y992
I999
F1000
P1001
G1002
T1003
Y1004
Q1005
T1006
L1007
E1008
M1009
F1010
P1011
R1012
W1017
L1018
C1021
H1022
V1023
T1024
T1033
T1034
L1038
Q1039
N1040
GLU
ASP
THR
LYS
SER
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	213.92Å 213.92Å 85.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.00 – 3.00 42.50 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (12.00-3.00) 98.3 (42.50-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.96 (at 3.01Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.220 , 0.286 0.206 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	65.3	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 93.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.010 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8228	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.24% 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: O, NAG, CU

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	0.64	2/8417 (0.0%)	0.94	18/11429 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	VAL	N-CA	-5.64	1.35	1.46
1	A	586	ASP	N-CA	-5.42	1.35	1.46

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	708	PHE	CB-CA-C	-16.61	77.17	110.40
1	A	28	VAL	CB-CA-C	12.93	135.96	111.40
1	A	705	ASP	CB-CA-C	-9.15	92.11	110.40
1	A	28	VAL	N-CA-C	-9.13	86.35	111.00
1	A	684	ASP	O-C-N	7.59	134.84	122.70

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	8187	3	7732	383	1

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	28	0	26	1	0
3	A	8	0	0	0	0
4	A	2	0	0	0	0
All	All	8225	3	7758	384	1

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 24.

The worst 5 of 384 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:24:LYS:HA	1:A:474:PRO:CG	1.79	1.12
1:A:24:LYS:HA	1:A:474:PRO:HG3	1.29	1.12
1:A:23:LYS:O	1:A:474:PRO:HG3	1.55	1.05
1:A:294:THR:HG21	1:A:661:GLN:HG2	1.39	1.04
1:A:288:LYS:HG3	1:A:303:PHE:CZ	1.99	0.98

All (1) 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:A:553:LYS:O	1:A:712:GLU:OE2[2_654]	1.93	0.27

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	1009/1046 (96%)	836 (83%)	142 (14%)	31 (3%)	4 23

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	27	SER
1	A	243	VAL
1	A	492	PRO
1	A	506	VAL

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	880/921 (96%)	765 (87%)	115 (13%)	4 18

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	427	LEU
1	A	1000	PHE
1	A	662	THR
1	A	976	THR
1	A	900	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	729	GLN
1	A	1005	GLN
1	A	1040	ASN
1	A	1039	GLN
1	A	336	GLN

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)

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 for Mogul analysis.

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	NAG	A	1047	1	14,14,15	0.97	1 (7%)	17,19,21	1.53	3 (17%)
2	NAG	A	1048	1	14,14,15	0.80	1 (7%)	17,19,21	0.98	1 (5%)

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	NAG	A	1047	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1048	1	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1047	NAG	C1-C2	3.25	1.57	1.52
2	A	1048	NAG	C1-C2	2.18	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1047	NAG	C1-O5-C5	3.66	117.15	112.19
2	A	1047	NAG	O5-C1-C2	3.13	116.24	111.29
2	A	1048	NAG	O7-C7-C8	-2.60	117.23	122.06
2	A	1047	NAG	C1-C2-N2	-2.33	106.51	110.49

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1047	NAG	O5-C5-C6-O6
2	A	1047	NAG	C4-C5-C6-O6
2	A	1048	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1048	NAG	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	1017/1046 (97%)	-0.54	7 (0%) 87 69	6, 39, 108, 241	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	349	GLY	7.2
1	A	706	SER	5.0
1	A	705	ASP	5.0
1	A	704	GLU	4.2
1	A	27	SER	3.3

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 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
2	NAG	A	1048	14/15	0.57	0.32	284,284,284,284	0
3	CU	A	1054	1/1	0.73	0.26	61,61,61,61	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	A	1047	14/15	0.85	0.21	143,143,143,143	0
3	CU	A	1050	1/1	0.97	0.15	46,46,46,46	0
3	CU	A	1055	1/1	0.97	0.15	33,33,33,33	0
4	O	A	1057	1/1	0.97	0.19	6,6,6,6	0
3	CU	A	1049	1/1	0.98	0.15	34,34,34,34	0
3	CU	A	1052	1/1	0.98	0.14	31,31,31,31	0
3	CU	A	1053	1/1	0.98	0.11	34,34,34,34	0
3	CU	A	1056	1/1	0.99	0.12	27,27,27,27	0
3	CU	A	1051	1/1	0.99	0.20	44,44,44,44	0
4	O	A	1058	1/1	0.99	0.29	2,2,2,2	0

6.5 Other polymers (i)

There are no such residues in this entry.