



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1U6G
Title : Crystal Structure of The Cand1-Cul1-Roc1 Complex
Authors : Goldenberg, S.J.; Shumway, S.D.; Cascio, T.C.; Garbutt, K.C.; Liu, J.; Xiong, Y.; Zheng, N.
Deposited on : 2004-07-29
Resolution : 3.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

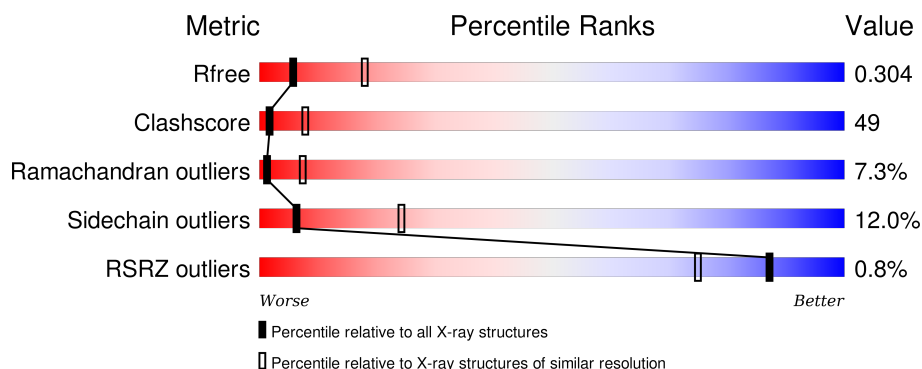
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	776	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 10%, yellow 40%, green 41%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 41% 40% 10% 8% </div> </div>
2	B	108	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 11%, yellow 38%, green 31%, grey 19%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 31% 38% 11% 19% </div> </div>
3	C	1230	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 30%, yellow 50%, orange 11%, red 7%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 30% 50% 11% 7% </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 15511 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 Cullin homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	715	Total	C	N	O	S	0	0	0
			5855	3719	998	1109	29			

- Molecule 2 is a protein called RING-box protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			731	464	133	125	9			

- Molecule 3 is a protein called TIP120 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	1146	Total	C	N	O	S	0	0	0
			8904	5667	1509	1672	56			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Zn	0	0
			3	3		

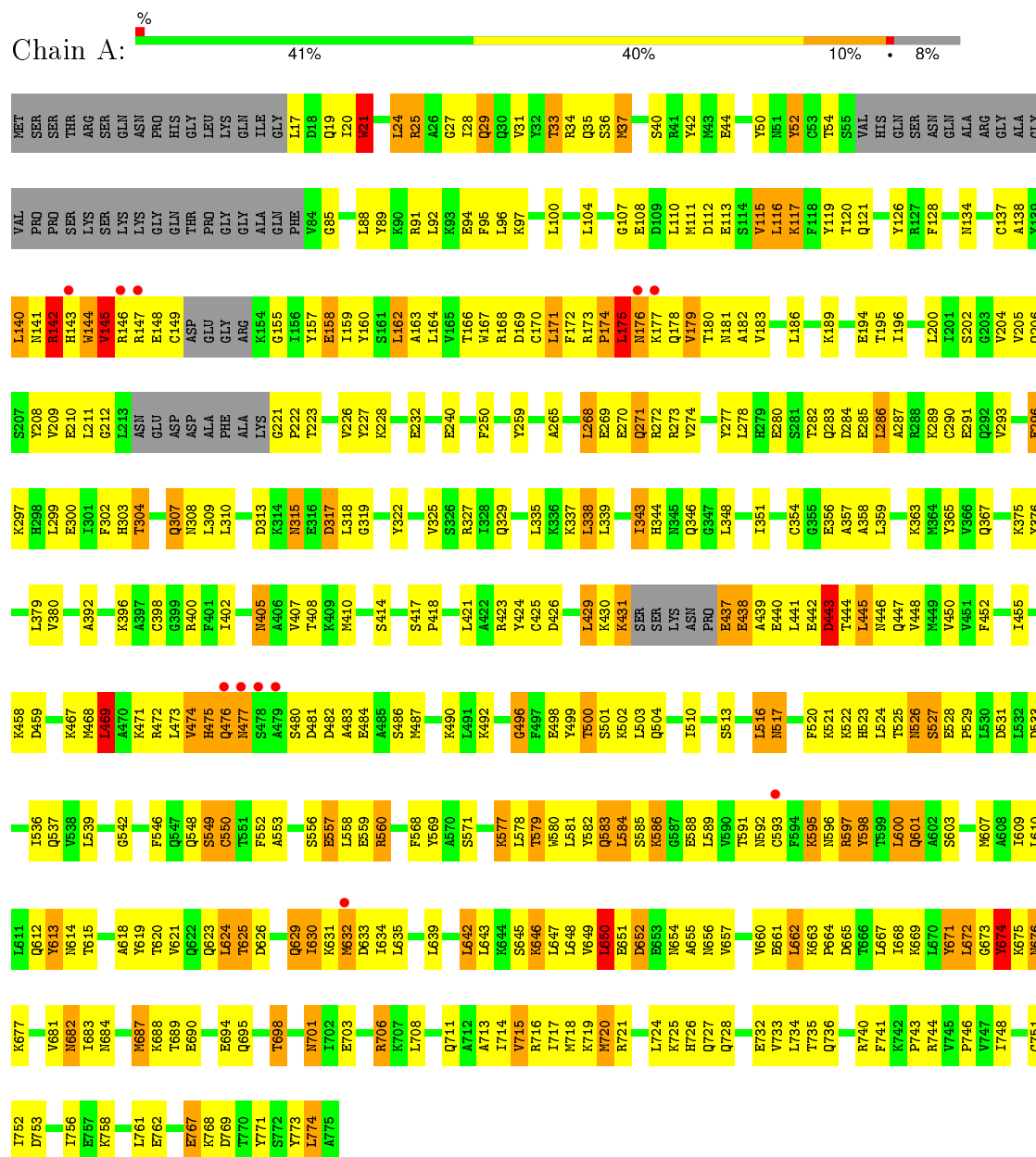
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	0
			10	10		
5	B	3	Total	O	0	0
			3	3		
5	C	5	Total	O	0	0
			5	5		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Cullin homolog 1



• Molecule 2: RING-box protein 1



GLU SER MET ASP THR SER	Q1164	D1098	D1019	C954	I883
	E1165	R1099	L1020	L958	S884
	F1166	L1100	M1021	T959	
	E1167	D1101	V1022	T959	N887
	K1168	T1102	R1023	L960	L888
	Q1169	F1103	R1024	I961	P889
	D1170	E1104	N1025	D962	F890
	E1171		A1026	P963	T891
		M1107	L1027	E964	L892
	R1174	H1108	V1028	T965	F893
	S1175	V1109	T1029	L966	F894
	A1176	E1110	F1030	L967	V895
	M1177	D1111	M1031	P868	L896
	R1178	G1112	S1032	R969	Q897
	A1179	L1113	A1033	L970	E898
	V1180		A1034	R971	L899
	A1181	Y1117	N1035	G972	T900
	A1182		H1036	V973	S901
	L1183	K1120	K1037	L974	Q902
	L1184	H1121	P1038	T975	P903
	T1185	L1122	S1039	S976	R904
	I1186	T1123	L1040	G977	R905
	P1187		I1041	S978	Q906
	E1188	M1126		S979	
	A1189	L1127	L1044	V980	L913
	E1190	H1128		L981	K914
	K1191	R1129	T1047	R982	E915
	P1193	L1130	V1048		I916
	L1194	S1192	L1049	V985	I917
	K1195	T1132	P1050	V986	S918
	S1196	L1133	H1051	T987	S919
	E1197	C1134	L1052	L988	L920
	F1198	P1135	Y1053	V989	S921
	Q1199		M1054	R990	R922
	S1200	V1138	E1055	F991	V923
	Q1201	L1139	T1056	T992	G924
	T1202	Q1140		T993	L925
	S1203	R1141	R1064	S994	I926
	S1204	L1142	E1065	D995	P927
	N1205	D1143	V1066	H996	Y928
	P1206	R1144	E1067		
	E1207	L1145	M1068	P999	I932
	L1208	V1146		I1000	V933
	A1209	E1147	H1073	D1001	L934
	A1210	P1148	L1079	P1002	L935
	ILE	R1150	D1080	L1003	L936
	PHE	A1151	I1081	K1005	L937
	GLU	T1152	R1082		
	SER	C1153	K1083	I1008	E941
	ILE	T1154		G1009	C942
	GLN	T1155	C1088	L1010	A943
	LYS	K1156	M1089	F1011	E944
	ASP	V1157	Y1090	L1012	E945
	SER	K1158		K1013	G946
	SER	A1159	L1093	T1014	T947
	SER	M1160	D1094	L1015	R948
	THR	S1161	S1095	L1016	
	ASN	V1162	C1096	D1017	V951
	LEU	K1163	L1097	P1018	E953

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.47Å 151.33Å 215.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 49.68 – 2.49	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.10) 73.1 (49.68-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.84 (at 2.48Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.317 0.236 , 0.304	Depositor DCC
R_{free} test set	3108 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 53.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 105510 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15511	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	0.49	3/5949 (0.1%)	1.14	14/8007 (0.2%)
2	B	0.51	0/752	0.86	1/1020 (0.1%)
3	C	0.45	1/9041 (0.0%)	0.86	31/12243 (0.3%)
All	All	0.47	4/15742 (0.0%)	0.97	46/21270 (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	A	0	1
3	C	0	2
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	437	GLU	C-N	-8.90	1.13	1.34
1	A	443	ASP	C-N	7.93	1.52	1.34
3	C	601	GLY	C-N	-6.35	1.19	1.34
1	A	630	ILE	CG1-CD1	5.03	1.85	1.50

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	437	GLU	O-C-N	-72.37	6.91	122.70
3	C	117	LEU	C-N-CD	-20.01	76.58	120.60
3	C	117	LEU	C-N-CA	13.74	179.69	122.00
3	C	487	LYS	CB-CA-C	12.45	135.31	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	377	PRO	CA-N-CD	-10.61	96.64	111.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	437	GLU	Mainchain
3	C	599	ASN	Mainchain
3	C	601	GLY	Mainchain

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	5855	0	5900	502	0
2	B	731	0	689	76	0
3	C	8904	0	9248	998	0
4	B	3	0	0	0	0
5	A	10	0	0	0	0
5	B	3	0	0	0	0
5	C	5	0	0	0	0
All	All	15511	0	15837	1525	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 49.

The worst 5 of 1525 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)
3:C:373:LYS:CE	3:C:427:MET:HE1	1.31	1.56
3:C:373:LYS:HE3	3:C:427:MET:CE	1.36	1.54
1:A:630:ILE:CD1	1:A:630:ILE:CG1	1.85	1.51
3:C:373:LYS:CE	3:C:427:MET:CE	1.84	1.48
3:C:373:LYS:CD	3:C:427:MET:HE1	1.53	1.37

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	705/776 (91%)	584 (83%)	91 (13%)	30 (4%)	3	19
2	B	86/108 (80%)	68 (79%)	13 (15%)	5 (6%)	2	12
3	C	1134/1230 (92%)	793 (70%)	236 (21%)	105 (9%)	1	4
All	All	1925/2114 (91%)	1445 (75%)	340 (18%)	140 (7%)	1	7

5 of 140 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	TRP
1	A	145	VAL
1	A	646	LYS
1	A	652	ASP
1	A	674	TYR

5.3.2 Protein sidechains

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	650/698 (93%)	575 (88%)	75 (12%)	7	27
2	B	78/90 (87%)	65 (83%)	13 (17%)	3	11
3	C	1022/1098 (93%)	900 (88%)	122 (12%)	6	25
All	All	1750/1886 (93%)	1540 (88%)	210 (12%)	6	24

5 of 210 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	96	LEU
3	C	298	LEU
3	C	1102	ILE
3	C	144	LYS
3	C	228	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	676	ASN
3	C	66	ASN
3	C	1036	ASN
1	A	682	ASN
1	A	736	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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	715/776 (92%)	-0.56	11 (1%) 76 58	13, 46, 129, 197	0
2	B	88/108 (81%)	-0.61	2 (2%) 64 40	3, 38, 76, 151	0
3	C	1146/1230 (93%)	-0.67	2 (0%) 95 91	14, 61, 122, 190	0
All	All	1949/2114 (92%)	-0.63	15 (0%) 87 75	3, 55, 124, 197	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	478	SER	16.5
1	A	477	ASN	10.9
1	A	479	ALA	4.7
1	A	176	ASN	4.1
2	B	20	LYS	3.8

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	ZN	B	1230	1/1	0.93	0.14	-0.61	56,56,56,56	0
4	ZN	B	1229	1/1	0.95	0.12	-1.25	42,42,42,42	0
4	ZN	B	1231	1/1	0.97	0.10	-2.00	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.