



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 31, 2026 – 02:44 PM EDT

PDB ID : 9MSW / pdb_00009msw
Title : anti-EGFR DyAb designed FAB
Authors : Kiefer, J.R.; Lin, J.Y.; Hofmann, J.L.; Watkins, A.M.; Seeger, F.; Frey, N.C.;
Dou, Y.; Tang, Y.
Deposited on : 2025-01-10
Resolution : 2.10 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

<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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

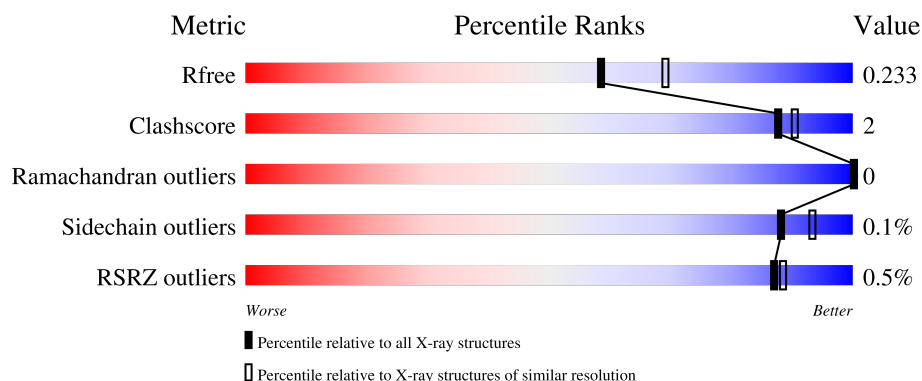
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	225	% 96% ..
1	C	225	% 94% ..
1	H	225	88% 7% 5%
2	B	213	93% 7%
2	D	213	95% ..

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Mol	Chain	Length	Quality of chain
2	L	213	95%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 20563 atoms, of which 9658 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 DyAb Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	214	Total	C	H	N	O	S	0	4	0
			3260	1049	1605	272	326	8			
1	A	222	Total	C	H	N	O	S	0	8	0
			3357	1079	1647	281	342	8			
1	C	218	Total	C	H	N	O	S	0	4	0
			3281	1057	1609	275	332	8			

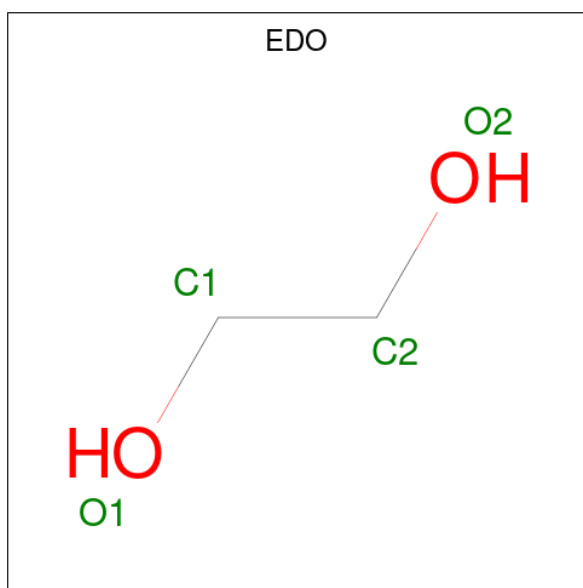
- Molecule 2 is a protein called DyAb Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	210	Total	C	H	N	O	S	0	4	0
			3188	1013	1566	268	337	4			
2	B	212	Total	C	H	N	O	S	0	13	0
			3268	1034	1605	275	350	4			
2	D	210	Total	C	H	N	O	S	0	10	0
			3224	1022	1584	271	343	4			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	3	Total	Cl	0	0
			3	3		
3	L	1	Total	Cl	0	0
			1	1		
3	A	2	Total	Cl	0	0
			2	2		
3	B	2	Total	Cl	0	0
			2	2		
3	C	4	Total	Cl	0	0
			4	4		
3	D	3	Total	Cl	0	0
			3	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	H	1	Total	C	H	O	0	0
			10	2	6	2		
4	L	1	Total	C	H	O	0	0
			10	2	6	2		
4	L	1	Total	C	H	O	0	0
			10	2	6	2		
4	L	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	C	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	130	Total	O	0	1
			130	130		
5	L	127	Total	O	0	0
			127	127		
5	A	156	Total	O	0	2
			157	157		
5	B	144	Total	O	0	1
			145	145		

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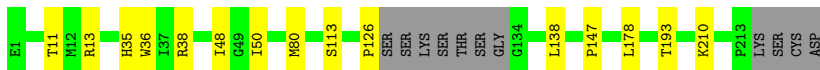
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	137	Total 140	O 140	0	3
5	D	200	Total 201	O 201	0	3

3 Residue-property plots [i](#)

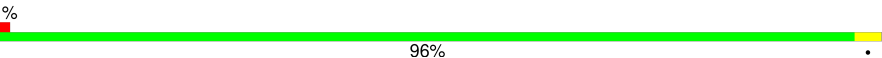
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

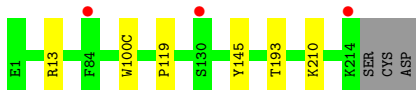
- Molecule 1: DyAb Fab heavy chain

Chain H: 

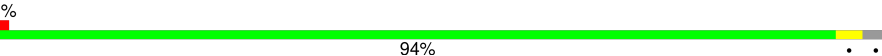


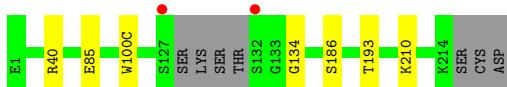
- Molecule 1: DyAb Fab heavy chain

Chain A: 

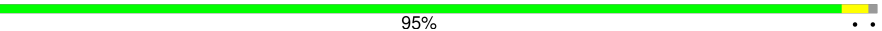


- Molecule 1: DyAb Fab heavy chain

Chain C: 



- Molecule 2: DyAb Fab light chain

Chain L: 

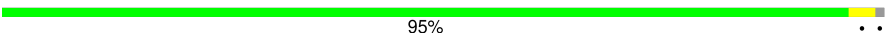


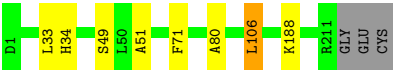
- Molecule 2: DyAb Fab light chain

Chain B: 



- Molecule 2: DyAb Fab light chain

Chain D:  95% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	77.91Å 77.91Å 202.29Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.73 – 2.10 33.73 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (33.73-2.10) 99.7 (33.73-2.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.179 , 0.232 0.180 , 0.233	Depositor DCC
R_{free} test set	3986 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.033 for h,-h-k,-l 0.013 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20563	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.83% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, CL

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	0.18	0/1778	0.35	0/2424
1	C	0.17	0/1731	0.34	0/2359
1	H	0.17	0/1711	0.34	0/2332
2	B	0.17	0/1737	0.37	0/2367
2	D	0.18	0/1710	0.38	0/2329
2	L	0.16	0/1672	0.36	0/2277
All	All	0.17	0/10339	0.36	0/14088

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	1710	1647	1617	6	0
1	C	1672	1609	1587	5	0
1	H	1655	1605	1589	8	0
2	B	1663	1605	1555	11	0
2	D	1640	1584	1538	6	0
2	L	1622	1566	1551	4	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
3	C	4	0	0	0	0
3	D	3	0	0	0	0
3	H	3	0	0	1	0
3	L	1	0	0	0	0
4	A	4	6	6	0	0
4	C	4	6	6	0	0
4	D	4	6	6	0	0
4	H	4	6	6	0	0
4	L	12	18	18	0	0
5	A	157	0	0	0	0
5	B	145	0	0	1	0
5	C	140	0	0	0	0
5	D	201	0	0	2	0
5	H	130	0	0	0	0
5	L	127	0	0	0	0
All	All	10905	9658	9479	38	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.

The worst 5 of 38 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:13:ARG:HG2	1:A:13:ARG:HH11	1.33	0.93
3:H:301:CL:CL	5:D:547:HOH:O	2.36	0.80
2:B:33:LEU:HD22	2:B:71:PHE:CG	2.27	0.69
1:H:36:TRP:CE3	1:H:80:MET:HE2	2.32	0.65
1:A:193:THR:HG23	1:A:210:LYS:HE3	1.80	0.63

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	228/225 (101%)	225 (99%)	3 (1%)	0	100	100
1	C	218/225 (97%)	213 (98%)	5 (2%)	0	100	100
1	H	214/225 (95%)	212 (99%)	2 (1%)	0	100	100
2	B	223/213 (105%)	217 (97%)	6 (3%)	0	100	100
2	D	218/213 (102%)	213 (98%)	5 (2%)	0	100	100
2	L	212/213 (100%)	207 (98%)	5 (2%)	0	100	100
All	All	1313/1314 (100%)	1287 (98%)	26 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	193/193 (100%)	193 (100%)	0	100	100
1	C	188/193 (97%)	188 (100%)	0	100	100
1	H	187/193 (97%)	187 (100%)	0	100	100
2	B	197/186 (106%)	197 (100%)	0	100	100
2	D	194/186 (104%)	193 (100%)	1 (0%)	81	88
2	L	188/186 (101%)	188 (100%)	0	100	100
All	All	1147/1137 (101%)	1146 (100%)	1 (0%)	88	93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	106	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	43	GLN
1	C	39	GLN
2	D	38	GLN
1	C	61	GLN
2	L	160	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 15 are monoatomic - leaving 7 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	$\# Z > 2$
4	EDO	C	304	-	3,3,3	0.24	0	2,2,2	0.35	0
4	EDO	D	303	-	3,3,3	0.26	0	2,2,2	0.28	0
4	EDO	L	302	-	3,3,3	0.24	0	2,2,2	0.30	0
4	EDO	A	303	-	3,3,3	0.23	0	2,2,2	0.37	0
4	EDO	H	303	-	3,3,3	0.27	0	2,2,2	0.35	0
4	EDO	L	301	-	3,3,3	0.24	0	2,2,2	0.29	0
4	EDO	L	303	-	3,3,3	0.26	0	2,2,2	0.28	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
4	EDO	C	304	-	-	0/1/1/1	-
4	EDO	D	303	-	-	0/1/1/1	-
4	EDO	L	302	-	-	0/1/1/1	-
4	EDO	A	303	-	-	0/1/1/1	-
4	EDO	H	303	-	-	0/1/1/1	-
4	EDO	L	301	-	-	1/1/1/1	-
4	EDO	L	303	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	301	EDO	O1-C1-C2-O2

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	222/225 (98%)	-0.38	3 (1%) 73 75	13, 30, 48, 73	4 (1%)
1	C	218/225 (96%)	-0.33	2 (0%) 81 83	12, 32, 59, 80	2 (0%)
1	H	214/225 (95%)	-0.20	0 100 100	13, 36, 56, 70	2 (0%)
2	B	212/213 (99%)	-0.29	1 (0%) 87 88	13, 34, 49, 63	7 (3%)
2	D	210/213 (98%)	-0.60	0 100 100	10, 28, 40, 57	5 (2%)
2	L	210/213 (98%)	-0.29	0 100 100	13, 37, 51, 71	2 (0%)
All	All	1286/1314 (97%)	-0.35	6 (0%) 87 88	10, 33, 52, 80	22 (1%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	114[A]	SER	6.2
1	C	132	SER	3.1
1	A	130	SER	2.9
1	C	127	SER	2.7
1	A	84	PHE	2.5

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 oligosaccharides in this entry.

6.4 Ligands

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
4	EDO	L	303	4/4	0.88	0.10	47,56,63,66	0
4	EDO	L	301	4/4	0.89	0.12	38,46,51,55	0
3	CL	C	303	1/1	0.90	0.10	55,55,55,55	0
4	EDO	A	303	4/4	0.90	0.14	30,37,49,53	0
3	CL	C	305	1/1	0.91	0.10	49,49,49,49	0
4	EDO	L	302	4/4	0.92	0.09	30,37,52,54	0
3	CL	D	304	1/1	0.92	0.12	61,61,61,61	0
3	CL	L	304	1/1	0.92	0.09	55,55,55,55	0
4	EDO	C	304	4/4	0.92	0.09	25,36,43,51	0
3	CL	A	301	1/1	0.93	0.07	55,55,55,55	0
3	CL	H	302	1/1	0.94	0.10	65,65,65,65	0
3	CL	C	302	1/1	0.94	0.07	45,45,45,45	0
4	EDO	H	303	4/4	0.95	0.09	30,36,42,51	0
4	EDO	D	303	4/4	0.95	0.09	29,38,50,56	0
3	CL	B	302	1/1	0.96	0.07	54,54,54,54	0
3	CL	H	301	1/1	0.97	0.05	38,38,38,38	0
3	CL	H	304	1/1	0.97	0.04	43,43,43,43	0
3	CL	C	301	1/1	0.98	0.03	27,27,27,27	0
3	CL	B	301	1/1	0.98	0.04	32,32,32,32	0
3	CL	A	302	1/1	0.98	0.05	42,42,42,42	0
3	CL	D	301	1/1	0.99	0.03	20,20,20,20	0
3	CL	D	302	1/1	0.99	0.05	15,15,15,15	0

6.5 Other polymers

There are no such residues in this entry.