



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 9, 2023 – 03:12 AM EDT

PDB ID : 7KE5  
Title : Heavy chain ferritin with N-terminal EBNA1 epitope  
Authors : Pederick, J.P.; Bruning, J.B.  
Deposited on : 2020-10-10  
Resolution : 2.80 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

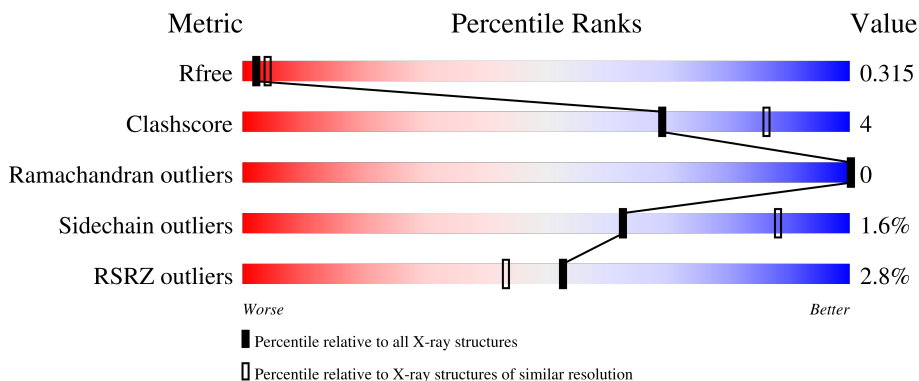
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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.




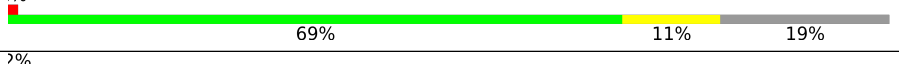
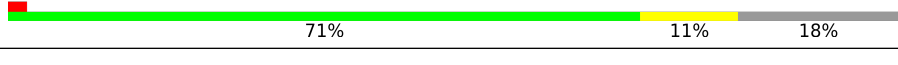
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	209	 2% 73% 9% 18%
1	B	209	 % 70% 12% 18%
1	C	209	 73% 8% 19%
1	D	209	 2% 75% 8% 18%
1	E	209	 2% 73% 8% 19%

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Mol	Chain	Length	Quality of chain
1	F	209	 <p>3% 72% 9% 19%</p>
1	G	209	 <p>3% 72% 10% 18%</p>
1	H	209	 <p>3% 74% 7% 19%</p>
1	I	209	 <p>3% 72% 11% 18%</p>
1	J	209	 <p>2% 74% 7% 19%</p>
1	K	209	 <p>1% 69% 11% 19%</p>
1	L	209	 <p>2% 71% 11% 18%</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16674 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 Epstein-Barr nuclear antigen 1, Ferritin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	172	1380	870	240	264	6	0	0	0
1	B	172	1391	876	246	262	7	0	0	0
1	C	169	1379	868	244	261	6	0	0	0
1	D	172	1396	878	244	267	7	0	0	0
1	E	169	1374	866	240	262	6	0	0	0
1	F	169	1374	866	244	259	5	0	0	0
1	G	172	1398	877	246	268	7	0	0	0
1	H	169	1372	864	243	259	6	0	0	0
1	I	172	1386	869	244	266	7	0	0	0
1	J	169	1368	861	241	260	6	0	0	0
1	K	169	1369	861	241	261	6	0	0	0
1	L	172	1388	868	245	268	7	0	0	0

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	initiating methionine	UNP P03211
A	-14	GLY	-	linker	UNP P03211
A	-13	GLY	-	linker	UNP P03211
A	-12	SER	-	linker	UNP P03211
A	-11	GLY	-	linker	UNP P03211

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	linker	UNP P03211
A	-9	GLY	-	linker	UNP P03211
A	-8	GLY	-	linker	UNP P03211
A	-7	SER	-	linker	UNP P03211
A	-6	GLY	-	linker	UNP P03211
A	-5	GLY	-	linker	UNP P03211
A	-4	GLY	-	linker	UNP P03211
A	-3	GLY	-	linker	UNP P03211
A	-2	SER	-	linker	UNP P03211
A	-1	GLY	-	linker	UNP P03211
A	0	GLY	-	linker	UNP P03211
B	-26	MET	-	initiating methionine	UNP P03211
B	-14	GLY	-	linker	UNP P03211
B	-13	GLY	-	linker	UNP P03211
B	-12	SER	-	linker	UNP P03211
B	-11	GLY	-	linker	UNP P03211
B	-10	GLY	-	linker	UNP P03211
B	-9	GLY	-	linker	UNP P03211
B	-8	GLY	-	linker	UNP P03211
B	-7	SER	-	linker	UNP P03211
B	-6	GLY	-	linker	UNP P03211
B	-5	GLY	-	linker	UNP P03211
B	-4	GLY	-	linker	UNP P03211
B	-3	GLY	-	linker	UNP P03211
B	-2	SER	-	linker	UNP P03211
B	-1	GLY	-	linker	UNP P03211
B	0	GLY	-	linker	UNP P03211
C	-26	MET	-	initiating methionine	UNP P03211
C	-14	GLY	-	linker	UNP P03211
C	-13	GLY	-	linker	UNP P03211
C	-12	SER	-	linker	UNP P03211
C	-11	GLY	-	linker	UNP P03211
C	-10	GLY	-	linker	UNP P03211
C	-9	GLY	-	linker	UNP P03211
C	-8	GLY	-	linker	UNP P03211
C	-7	SER	-	linker	UNP P03211
C	-6	GLY	-	linker	UNP P03211
C	-5	GLY	-	linker	UNP P03211
C	-4	GLY	-	linker	UNP P03211
C	-3	GLY	-	linker	UNP P03211
C	-2	SER	-	linker	UNP P03211
C	-1	GLY	-	linker	UNP P03211

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	linker	UNP P03211
D	-26	MET	-	initiating methionine	UNP P03211
D	-14	GLY	-	linker	UNP P03211
D	-13	GLY	-	linker	UNP P03211
D	-12	SER	-	linker	UNP P03211
D	-11	GLY	-	linker	UNP P03211
D	-10	GLY	-	linker	UNP P03211
D	-9	GLY	-	linker	UNP P03211
D	-8	GLY	-	linker	UNP P03211
D	-7	SER	-	linker	UNP P03211
D	-6	GLY	-	linker	UNP P03211
D	-5	GLY	-	linker	UNP P03211
D	-4	GLY	-	linker	UNP P03211
D	-3	GLY	-	linker	UNP P03211
D	-2	SER	-	linker	UNP P03211
D	-1	GLY	-	linker	UNP P03211
D	0	GLY	-	linker	UNP P03211
E	-26	MET	-	initiating methionine	UNP P03211
E	-14	GLY	-	linker	UNP P03211
E	-13	GLY	-	linker	UNP P03211
E	-12	SER	-	linker	UNP P03211
E	-11	GLY	-	linker	UNP P03211
E	-10	GLY	-	linker	UNP P03211
E	-9	GLY	-	linker	UNP P03211
E	-8	GLY	-	linker	UNP P03211
E	-7	SER	-	linker	UNP P03211
E	-6	GLY	-	linker	UNP P03211
E	-5	GLY	-	linker	UNP P03211
E	-4	GLY	-	linker	UNP P03211
E	-3	GLY	-	linker	UNP P03211
E	-2	SER	-	linker	UNP P03211
E	-1	GLY	-	linker	UNP P03211
E	0	GLY	-	linker	UNP P03211
F	-26	MET	-	initiating methionine	UNP P03211
F	-14	GLY	-	linker	UNP P03211
F	-13	GLY	-	linker	UNP P03211
F	-12	SER	-	linker	UNP P03211
F	-11	GLY	-	linker	UNP P03211
F	-10	GLY	-	linker	UNP P03211
F	-9	GLY	-	linker	UNP P03211
F	-8	GLY	-	linker	UNP P03211
F	-7	SER	-	linker	UNP P03211

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-6	GLY	-	linker	UNP P03211
F	-5	GLY	-	linker	UNP P03211
F	-4	GLY	-	linker	UNP P03211
F	-3	GLY	-	linker	UNP P03211
F	-2	SER	-	linker	UNP P03211
F	-1	GLY	-	linker	UNP P03211
F	0	GLY	-	linker	UNP P03211
G	-26	MET	-	initiating methionine	UNP P03211
G	-14	GLY	-	linker	UNP P03211
G	-13	GLY	-	linker	UNP P03211
G	-12	SER	-	linker	UNP P03211
G	-11	GLY	-	linker	UNP P03211
G	-10	GLY	-	linker	UNP P03211
G	-9	GLY	-	linker	UNP P03211
G	-8	GLY	-	linker	UNP P03211
G	-7	SER	-	linker	UNP P03211
G	-6	GLY	-	linker	UNP P03211
G	-5	GLY	-	linker	UNP P03211
G	-4	GLY	-	linker	UNP P03211
G	-3	GLY	-	linker	UNP P03211
G	-2	SER	-	linker	UNP P03211
G	-1	GLY	-	linker	UNP P03211
G	0	GLY	-	linker	UNP P03211
H	-26	MET	-	initiating methionine	UNP P03211
H	-14	GLY	-	linker	UNP P03211
H	-13	GLY	-	linker	UNP P03211
H	-12	SER	-	linker	UNP P03211
H	-11	GLY	-	linker	UNP P03211
H	-10	GLY	-	linker	UNP P03211
H	-9	GLY	-	linker	UNP P03211
H	-8	GLY	-	linker	UNP P03211
H	-7	SER	-	linker	UNP P03211
H	-6	GLY	-	linker	UNP P03211
H	-5	GLY	-	linker	UNP P03211
H	-4	GLY	-	linker	UNP P03211
H	-3	GLY	-	linker	UNP P03211
H	-2	SER	-	linker	UNP P03211
H	-1	GLY	-	linker	UNP P03211
H	0	GLY	-	linker	UNP P03211
I	-26	MET	-	initiating methionine	UNP P03211
I	-14	GLY	-	linker	UNP P03211
I	-13	GLY	-	linker	UNP P03211

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-12	SER	-	linker	UNP P03211
I	-11	GLY	-	linker	UNP P03211
I	-10	GLY	-	linker	UNP P03211
I	-9	GLY	-	linker	UNP P03211
I	-8	GLY	-	linker	UNP P03211
I	-7	SER	-	linker	UNP P03211
I	-6	GLY	-	linker	UNP P03211
I	-5	GLY	-	linker	UNP P03211
I	-4	GLY	-	linker	UNP P03211
I	-3	GLY	-	linker	UNP P03211
I	-2	SER	-	linker	UNP P03211
I	-1	GLY	-	linker	UNP P03211
I	0	GLY	-	linker	UNP P03211
J	-26	MET	-	initiating methionine	UNP P03211
J	-14	GLY	-	linker	UNP P03211
J	-13	GLY	-	linker	UNP P03211
J	-12	SER	-	linker	UNP P03211
J	-11	GLY	-	linker	UNP P03211
J	-10	GLY	-	linker	UNP P03211
J	-9	GLY	-	linker	UNP P03211
J	-8	GLY	-	linker	UNP P03211
J	-7	SER	-	linker	UNP P03211
J	-6	GLY	-	linker	UNP P03211
J	-5	GLY	-	linker	UNP P03211
J	-4	GLY	-	linker	UNP P03211
J	-3	GLY	-	linker	UNP P03211
J	-2	SER	-	linker	UNP P03211
J	-1	GLY	-	linker	UNP P03211
J	0	GLY	-	linker	UNP P03211
K	-26	MET	-	initiating methionine	UNP P03211
K	-14	GLY	-	linker	UNP P03211
K	-13	GLY	-	linker	UNP P03211
K	-12	SER	-	linker	UNP P03211
K	-11	GLY	-	linker	UNP P03211
K	-10	GLY	-	linker	UNP P03211
K	-9	GLY	-	linker	UNP P03211
K	-8	GLY	-	linker	UNP P03211
K	-7	SER	-	linker	UNP P03211
K	-6	GLY	-	linker	UNP P03211
K	-5	GLY	-	linker	UNP P03211
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K	-3	GLY	-	linker	UNP P03211

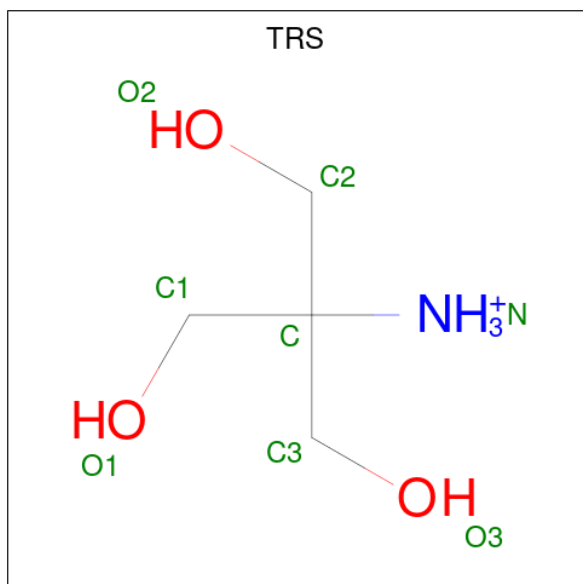
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Chain	Residue	Modelled	Actual	Comment	Reference
K	-2	SER	-	linker	UNP P03211
K	-1	GLY	-	linker	UNP P03211
K	0	GLY	-	linker	UNP P03211
L	-26	MET	-	initiating methionine	UNP P03211
L	-14	GLY	-	linker	UNP P03211
L	-13	GLY	-	linker	UNP P03211
L	-12	SER	-	linker	UNP P03211
L	-11	GLY	-	linker	UNP P03211
L	-10	GLY	-	linker	UNP P03211
L	-9	GLY	-	linker	UNP P03211
L	-8	GLY	-	linker	UNP P03211
L	-7	SER	-	linker	UNP P03211
L	-6	GLY	-	linker	UNP P03211
L	-5	GLY	-	linker	UNP P03211
L	-4	GLY	-	linker	UNP P03211
L	-3	GLY	-	linker	UNP P03211
L	-2	SER	-	linker	UNP P03211
L	-1	GLY	-	linker	UNP P03211
L	0	GLY	-	linker	UNP P03211

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	8	4	1	3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			8	4	1	3		
2	E	1	Total	C	N	O	0	0
			8	4	1	3		
2	H	1	Total	C	N	O	0	0
			8	4	1	3		
2	I	1	Total	C	N	O	0	0
			8	4	1	3		
2	L	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Fe	0	0
			2	2		
3	B	1	Total	Fe	0	0
			1	1		
3	C	2	Total	Fe	0	0
			2	2		
3	D	2	Total	Fe	0	0
			2	2		
3	E	2	Total	Fe	0	0
			2	2		
3	F	1	Total	Fe	0	0
			1	1		
3	G	1	Total	Fe	0	0
			1	1		
3	H	1	Total	Fe	0	0
			1	1		
3	I	1	Total	Fe	0	0
			1	1		
3	J	1	Total	Fe	0	0
			1	1		
3	K	1	Total	Fe	0	0
			1	1		
3	L	1	Total	Fe	0	0
			1	1		

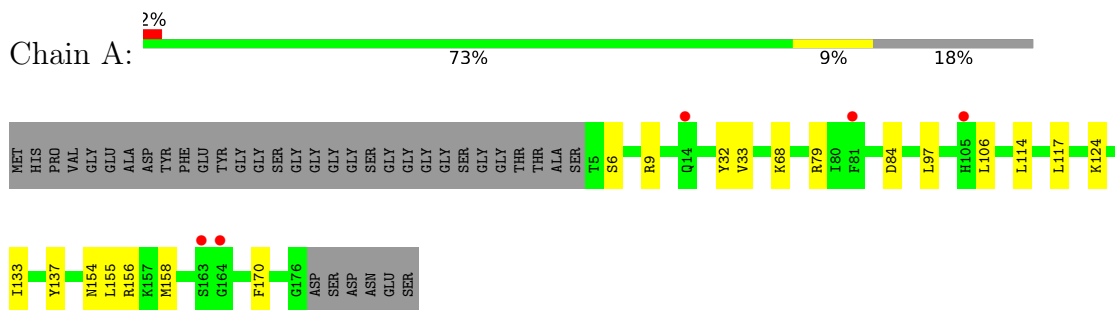
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total O 2 2	0	0
4	B	6	Total O 6 6	0	0
4	C	2	Total O 2 2	0	0
4	D	3	Total O 3 3	0	0
4	E	4	Total O 4 4	0	0
4	F	5	Total O 5 5	0	0
4	G	3	Total O 3 3	0	0
4	H	1	Total O 1 1	0	0
4	J	2	Total O 2 2	0	0
4	K	2	Total O 2 2	0	0
4	L	5	Total O 5 5	0	0

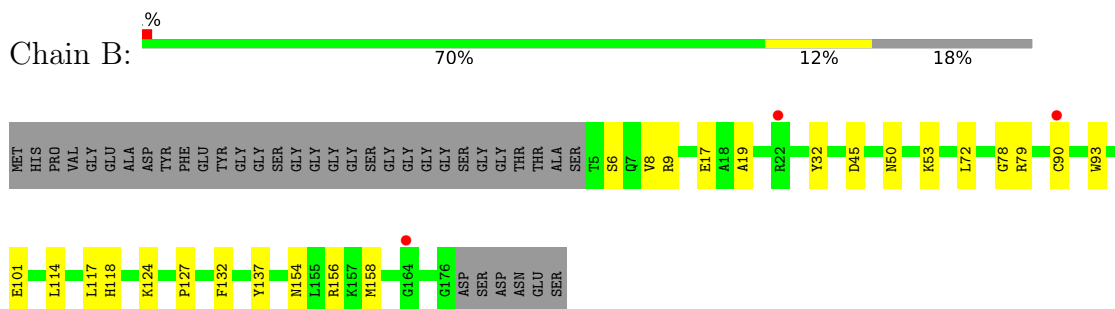
### 3 Residue-property plots [i](#)

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.

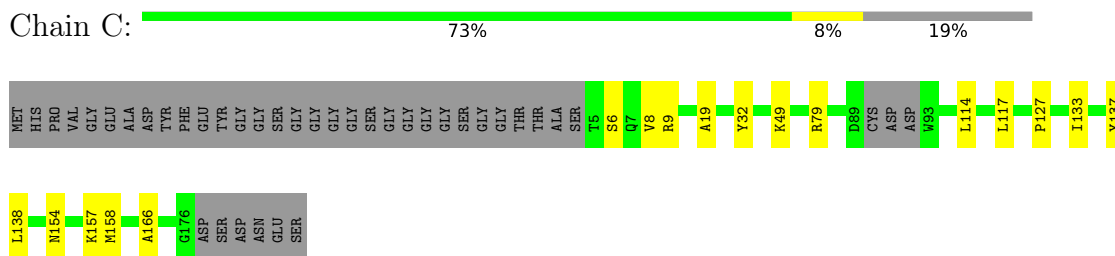
- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



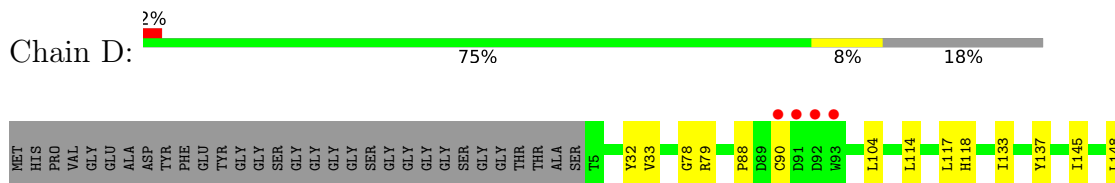
- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

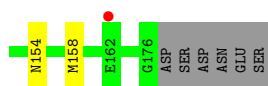


- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

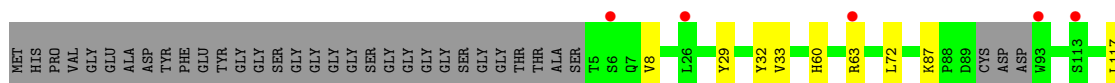
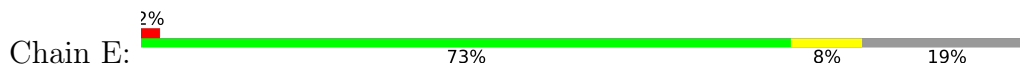


- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

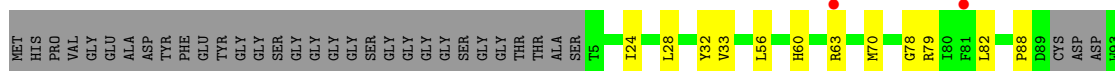




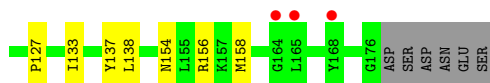
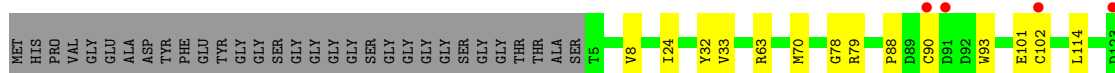
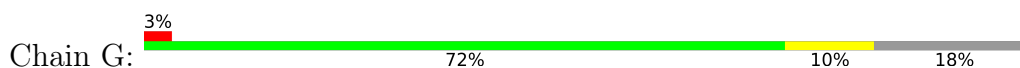
- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



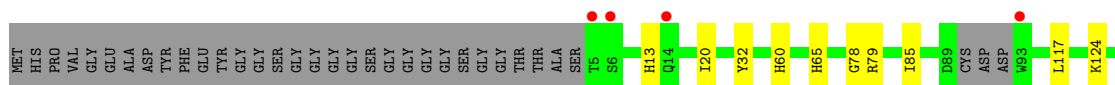
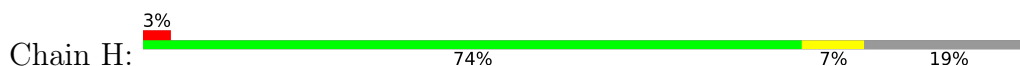
- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

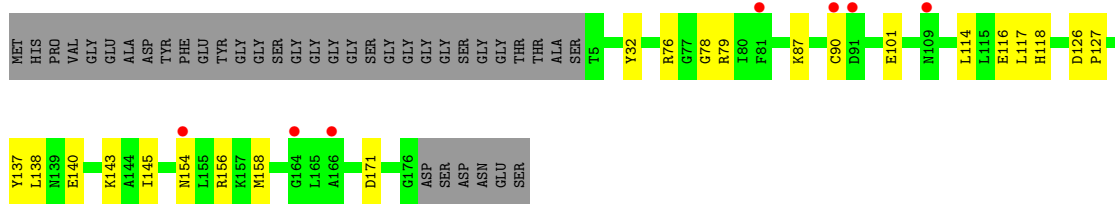


- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

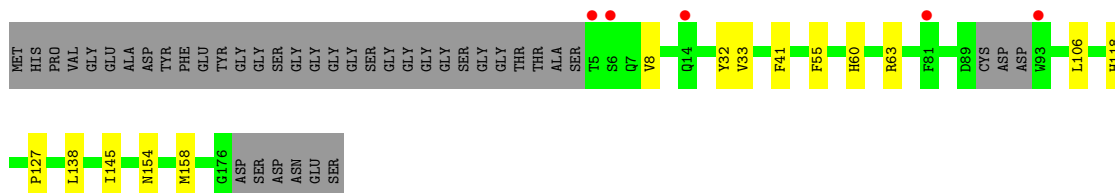
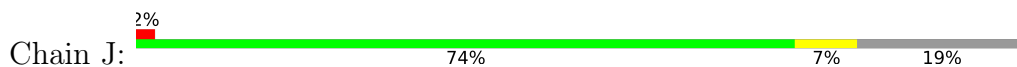


- Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain

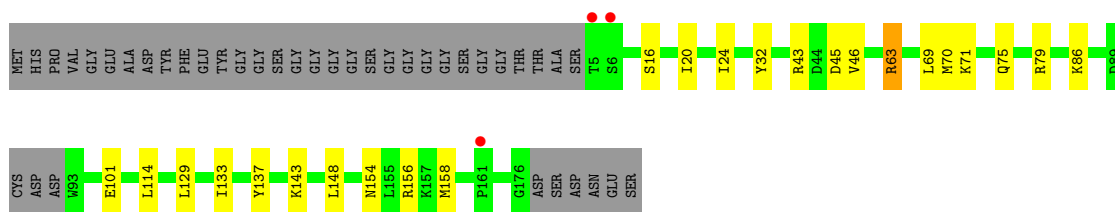




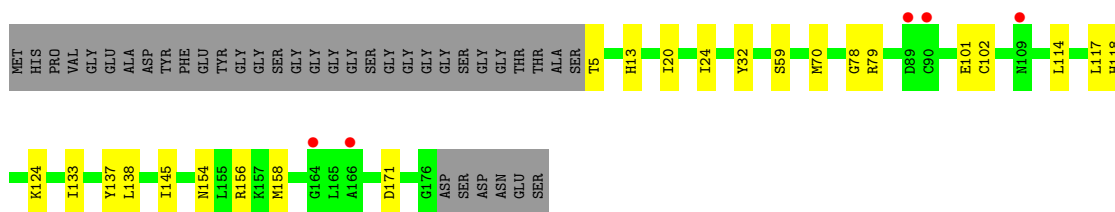
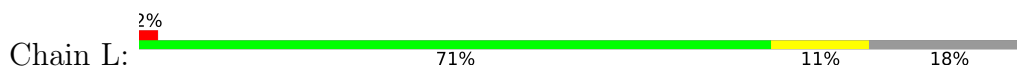
● Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



● Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



● Molecule 1: Epstein-Barr nuclear antigen 1,Ferritin heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	219.32Å 219.32Å 148.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.82 – 2.80 48.82 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.0 (48.82-2.80) 92.8 (48.82-2.80)	Depositor EDS
$R_{merge}$	0.25	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.70 (at 2.81Å)	Xtrriage
Refinement program	PHENIX 1.18.2-3874	Depositor
R, $R_{free}$	0.274 , 0.317 0.273 , 0.315	Depositor DCC
$R_{free}$ test set	4320 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.9	Xtrriage
Anisotropy	0.290	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 28.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	16674	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.2217e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

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

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	0.44	0/1409	0.58	0/1903
1	B	0.43	0/1420	0.57	0/1914
1	C	0.43	0/1407	0.55	0/1895
1	D	0.44	0/1425	0.57	0/1921
1	E	0.47	0/1402	0.57	0/1889
1	F	0.46	0/1402	0.58	0/1889
1	G	0.49	0/1427	0.59	0/1925
1	H	0.44	0/1400	0.56	0/1887
1	I	0.43	0/1415	0.60	1/1912 (0.1%)
1	J	0.47	0/1396	0.56	0/1883
1	K	0.45	0/1397	0.55	0/1885
1	L	0.46	0/1416	0.58	0/1912
All	All	0.45	0/16916	0.57	1/22815 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	117	LEU	CA-CB-CG	7.49	132.52	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	1380	0	1302	9	0
1	B	1391	0	1333	16	0
1	C	1379	0	1324	10	0
1	D	1396	0	1334	9	0
1	E	1374	0	1313	13	0
1	F	1374	0	1317	11	0
1	G	1398	0	1329	14	0
1	H	1372	0	1311	11	0
1	I	1386	0	1303	11	0
1	J	1368	0	1298	9	0
1	K	1369	0	1295	14	0
1	L	1388	0	1311	13	0
2	A	8	0	12	0	0
2	C	8	0	12	0	0
2	E	8	0	12	1	0
2	H	8	0	12	1	0
2	I	8	0	12	0	0
2	L	8	0	12	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	2	0	0	0	0
4	B	6	0	0	0	0
4	C	2	0	0	0	0
4	D	3	0	0	0	0
4	E	4	0	0	0	0
4	F	5	0	0	1	0
4	G	3	0	0	0	0
4	H	1	0	0	0	0
4	J	2	0	0	0	0
4	K	2	0	0	0	0
4	L	5	0	0	0	0
All	All	16674	0	15842	121	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 4.

The worst 5 of 121 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:117:LEU:HD22	1:A:133:ILE:HD11	1.55	0.89
1:D:117:LEU:HD22	1:D:133:ILE:HD11	1.58	0.86
1:E:60:HIS:HD2	1:E:63:ARG:HH22	1.32	0.77
1:G:78:GLY:O	1:G:79:ARG:NH1	2.20	0.74
1:I:154:ASN:O	1:I:158:MET:HG3	1.89	0.72

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	170/209 (81%)	167 (98%)	3 (2%)	0	100	100
1	B	170/209 (81%)	166 (98%)	4 (2%)	0	100	100
1	C	165/209 (79%)	163 (99%)	2 (1%)	0	100	100
1	D	170/209 (81%)	168 (99%)	2 (1%)	0	100	100
1	E	165/209 (79%)	164 (99%)	1 (1%)	0	100	100
1	F	165/209 (79%)	162 (98%)	3 (2%)	0	100	100
1	G	170/209 (81%)	167 (98%)	3 (2%)	0	100	100
1	H	165/209 (79%)	163 (99%)	2 (1%)	0	100	100
1	I	170/209 (81%)	168 (99%)	2 (1%)	0	100	100
1	J	165/209 (79%)	163 (99%)	2 (1%)	0	100	100
1	K	165/209 (79%)	163 (99%)	2 (1%)	0	100	100
1	L	170/209 (81%)	168 (99%)	2 (1%)	0	100	100
All	All	2010/2508 (80%)	1982 (99%)	28 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	144/175 (82%)	141 (98%)	3 (2%)	53	84
1	B	147/175 (84%)	146 (99%)	1 (1%)	84	95
1	C	147/175 (84%)	145 (99%)	2 (1%)	67	90
1	D	149/175 (85%)	147 (99%)	2 (1%)	69	91
1	E	146/175 (83%)	145 (99%)	1 (1%)	84	95
1	F	145/175 (83%)	143 (99%)	2 (1%)	67	90
1	G	149/175 (85%)	147 (99%)	2 (1%)	69	91
1	H	145/175 (83%)	144 (99%)	1 (1%)	84	95
1	I	146/175 (83%)	141 (97%)	5 (3%)	37	71
1	J	144/175 (82%)	143 (99%)	1 (1%)	84	95
1	K	144/175 (82%)	140 (97%)	4 (3%)	43	77
1	L	147/175 (84%)	143 (97%)	4 (3%)	44	78
All	All	1753/2100 (84%)	1725 (98%)	28 (2%)	62	88

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	32	TYR
1	L	171	ASP
1	I	116	GLU
1	L	5	THR
1	I	90	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	60	HIS

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Mol	Chain	Res	Type
1	F	139	ASN
1	G	60	HIS
1	H	60	HIS
1	J	60	HIS

### 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 22 ligands modelled in this entry, 16 are monoatomic - leaving 6 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	TRS	L	201	-	7,7,7	0.36	0	9,9,9	0.57	0
2	TRS	A	201	-	7,7,7	0.44	0	9,9,9	0.63	0
2	TRS	I	201	-	7,7,7	0.40	0	9,9,9	0.75	0
2	TRS	E	201	-	7,7,7	0.36	0	9,9,9	0.81	0
2	TRS	C	201	-	7,7,7	0.40	0	9,9,9	1.28	1 (11%)
2	TRS	H	201	-	7,7,7	0.75	0	9,9,9	1.49	3 (33%)

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	TRS	L	201	-	-	3/9/9/9	-
2	TRS	A	201	-	-	4/9/9/9	-
2	TRS	I	201	-	-	0/9/9/9	-
2	TRS	E	201	-	-	4/9/9/9	-
2	TRS	C	201	-	-	0/9/9/9	-
2	TRS	H	201	-	-	6/9/9/9	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	201	TRS	O2-C2-C	-2.91	101.77	111.00
2	H	201	TRS	O1-C1-C	-2.70	102.42	111.00
2	H	201	TRS	O2-C2-C	-2.10	104.35	111.00
2	H	201	TRS	C3-C-C1	2.02	117.08	110.81

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	201	TRS	N-C-C1-O1
2	H	201	TRS	C2-C-C1-O1
2	H	201	TRS	C3-C-C1-O1
2	L	201	TRS	C2-C-C1-O1
2	L	201	TRS	C3-C-C1-O1

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	201	TRS	1	0
2	H	201	TRS	1	0

## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	172/209 (82%)	0.27	5 (2%) 51 41	17, 23, 45, 70	0
1	B	172/209 (82%)	0.23	3 (1%) 70 63	18, 24, 40, 76	0
1	C	169/209 (80%)	0.09	0 100 100	17, 24, 39, 64	0
1	D	172/209 (82%)	0.22	5 (2%) 51 41	18, 25, 46, 87	0
1	E	169/209 (80%)	0.27	5 (2%) 50 40	17, 25, 44, 70	0
1	F	169/209 (80%)	0.40	7 (4%) 37 27	15, 24, 40, 61	0
1	G	172/209 (82%)	0.40	7 (4%) 37 27	16, 24, 45, 84	0
1	H	169/209 (80%)	0.22	6 (3%) 42 32	17, 24, 41, 78	0
1	I	172/209 (82%)	0.39	7 (4%) 37 27	18, 24, 45, 77	0
1	J	169/209 (80%)	0.23	5 (2%) 50 40	18, 24, 40, 56	0
1	K	169/209 (80%)	0.20	3 (1%) 68 61	19, 24, 40, 57	0
1	L	172/209 (82%)	0.37	5 (2%) 51 41	19, 24, 47, 82	0
All	All	2046/2508 (81%)	0.27	58 (2%) 53 43	15, 24, 43, 87	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	93	TRP	3.9
1	A	14	GLN	3.8
1	I	90	CYS	3.7
1	I	91	ASP	3.6
1	G	102	CYS	3.6

### 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, 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
2	TRS	C	201	8/8	0.78	0.24	30,32,37,42	0
2	TRS	I	201	8/8	0.81	0.34	22,26,28,31	8
2	TRS	H	201	8/8	0.85	0.34	23,30,33,34	8
2	TRS	E	201	8/8	0.85	0.30	24,30,37,39	0
2	TRS	A	201	8/8	0.87	0.29	22,25,28,29	0
2	TRS	L	201	8/8	0.87	0.39	23,28,36,37	8
3	FE	E	203	1/1	0.88	0.11	40,40,40,40	1
3	FE	J	201	1/1	0.90	0.13	15,15,15,15	0
3	FE	A	203	1/1	0.91	0.08	36,36,36,36	1
3	FE	C	203	1/1	0.91	0.12	42,42,42,42	1
3	FE	D	202	1/1	0.92	0.08	38,38,38,38	0
3	FE	E	202	1/1	0.92	0.14	18,18,18,18	0
3	FE	H	202	1/1	0.95	0.13	18,18,18,18	0
3	FE	I	202	1/1	0.96	0.11	7,7,7,7	0
3	FE	F	201	1/1	0.96	0.17	13,13,13,13	0
3	FE	K	201	1/1	0.96	0.11	16,16,16,16	0
3	FE	D	201	1/1	0.97	0.11	11,11,11,11	0
3	FE	G	201	1/1	0.97	0.19	25,25,25,25	0
3	FE	A	202	1/1	0.98	0.09	9,9,9,9	0
3	FE	C	202	1/1	0.99	0.05	9,9,9,9	0
3	FE	B	201	1/1	0.99	0.10	16,16,16,16	0
3	FE	L	202	1/1	0.99	0.11	15,15,15,15	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.