



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:43 PM GMT

PDB ID : 4MBX  
Title : Structure of unliganded B-Lymphotropic Polyomavirus VP1  
Authors : Khan, Z.M.; Neu, U.; Schuch, B.; Stehle, T.  
Deposited on : 2013-08-21  
Resolution : 1.92 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (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

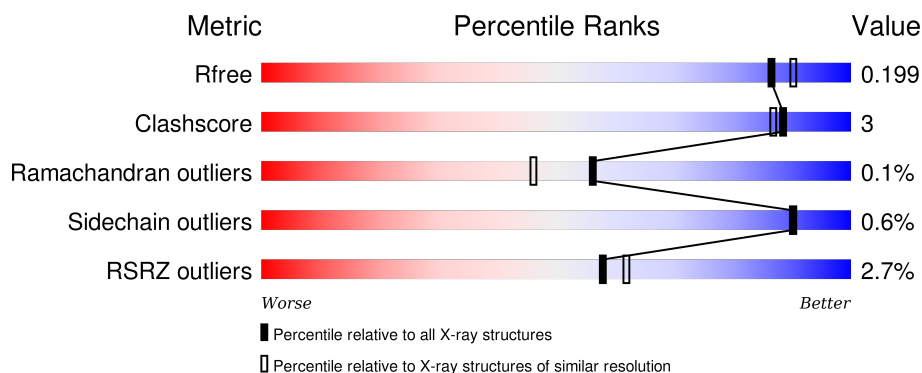
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.92 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.



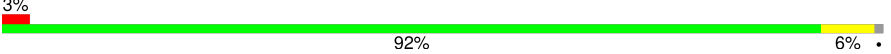

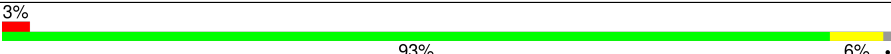
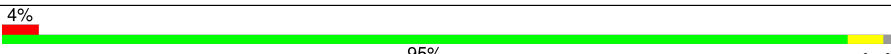
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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. 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	278	<div> <div>97%</div> <div> <div></div> <div>97%</div> <div>5%</div> <div></div> </div> </div>
1	B	278	<div> <div>95%</div> <div> <div></div> <div>95%</div> <div>5%</div> <div></div> </div> </div>
1	C	278	<div> <div>95%</div> <div> <div></div> <div>95%</div> <div>5%</div> <div></div> </div> </div>
1	D	278	<div> <div>95%</div> <div> <div></div> <div>95%</div> <div>5%</div> <div></div> </div> </div>
1	E	278	<div> <div>97%</div> <div> <div></div> <div>97%</div> <div>5%</div> <div></div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	278	
1	G	278	
1	H	278	
1	I	278	
1	J	278	

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	A	403	-	-	-	X
3	EDO	B	403	-	-	X	X
3	EDO	C	402	-	-	X	X
3	EDO	D	402	-	-	-	X
3	EDO	E	402	-	-	-	X
3	EDO	E	403	-	-	X	X
3	EDO	E	404	-	-	-	X
3	EDO	E	405	-	-	X	-
3	EDO	F	403	-	-	-	X
3	EDO	F	404	-	-	-	X
3	EDO	G	402	-	-	-	X
3	EDO	G	404	-	-	-	X
3	EDO	H	402	-	-	-	X
3	EDO	I	402	-	-	-	X
3	EDO	J	402	-	-	-	X
3	EDO	J	403	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23143 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 Major Capsid Protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	2	0
			2118	1339	350	416	13			
1	B	276	Total	C	N	O	S	0	4	0
			2122	1343	350	416	13			
1	C	276	Total	C	N	O	S	0	3	0
			2119	1340	349	417	13			
1	D	275	Total	C	N	O	S	0	4	0
			2108	1333	348	414	13			
1	E	277	Total	C	N	O	S	0	4	0
			2130	1348	351	418	13			
1	F	274	Total	C	N	O	S	0	4	0
			2100	1326	347	413	14			
1	G	270	Total	C	N	O	S	0	7	0
			2087	1325	343	406	13			
1	H	274	Total	C	N	O	S	0	8	0
			2128	1348	348	419	13			
1	I	275	Total	C	N	O	S	0	5	0
			2114	1337	347	417	13			
1	J	276	Total	C	N	O	S	0	4	0
			2122	1343	350	416	13			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Ca	0	0
			1	1		
2	J	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		
2	E	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total 1	Ca 1	0	0
2	B	1	Total 1	Ca 1	0	0
2	I	1	Total 1	Ca 1	0	0
2	C	1	Total 1	Ca 1	0	0
2	A	1	Total 1	Ca 1	0	0
2	F	1	Total 1	Ca 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	J	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	232	Total	O	0	0
			232	232		
4	B	207	Total	O	0	0
			207	207		
4	C	189	Total	O	0	0
			189	189		
4	D	183	Total	O	0	0
			183	183		
4	E	202	Total	O	0	0
			202	202		
4	F	190	Total	O	0	0
			190	190		
4	G	164	Total	O	0	0
			164	164		
4	H	161	Total	O	0	0
			161	161		
4	I	177	Total	O	0	0
			177	177		
4	J	172	Total	O	0	0
			172	172		

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

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.

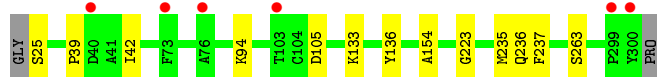
- Molecule 1: Major Capsid Protein VP1



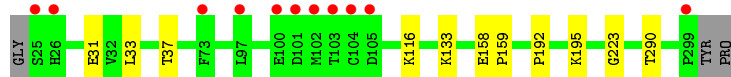
- Molecule 1: Major Capsid Protein VP1



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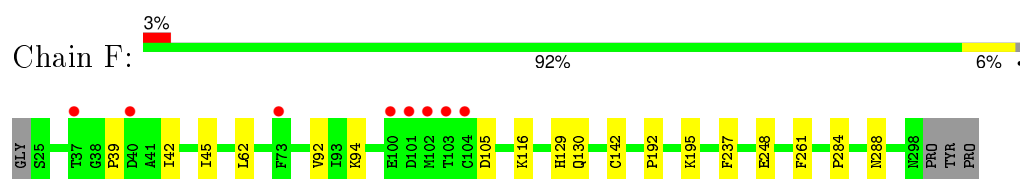


- Molecule 1: Major Capsid Protein VP1

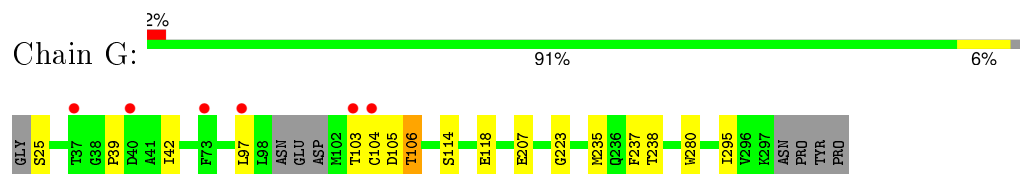


- Molecule 1: Major Capsid Protein VP1

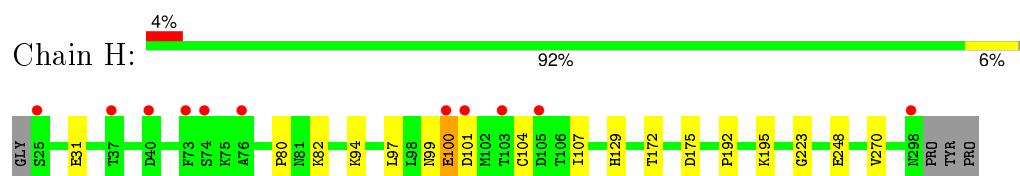




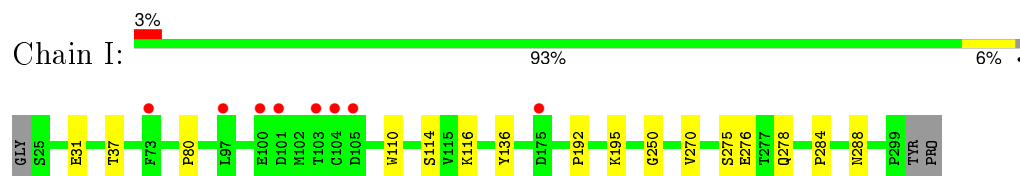
- Molecule 1: Major Capsid Protein VP1



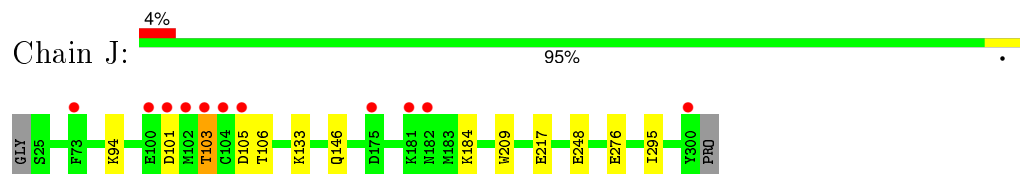
- Molecule 1: Major Capsid Protein VP1



- Molecule 1: Major Capsid Protein VP1



- Molecule 1: Major Capsid Protein VP1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.01Å 95.92Å 231.68Å 90.00° 95.82° 90.00°	Depositor
Resolution (Å)	39.38 – 1.92 39.38 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.8 (39.38-1.92) 98.8 (39.38-1.92)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.01 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.8.0025	Depositor
R, $R_{free}$	0.165 , 0.198 0.166 , 0.199	Depositor DCC
$R_{free}$ test set	12420 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.1	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	9 of 246138 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	23143	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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, 0.375 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: CA, EDO

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	0.52	1/2173 (0.0%)	0.63	0/2962
1	B	0.50	0/2182	0.63	0/2974
1	C	0.50	0/2176	0.61	0/2966
1	D	0.49	0/2167	0.60	0/2954
1	E	0.51	0/2191	0.63	0/2985
1	F	0.51	0/2158	0.62	0/2940
1	G	0.50	1/2153 (0.0%)	0.61	0/2930
1	H	0.49	0/2199	0.61	0/2996
1	I	0.49	1/2176 (0.0%)	0.60	0/2967
1	J	0.49	1/2182 (0.0%)	0.59	0/2973
All	All	0.50	4/21757 (0.0%)	0.61	0/29647

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	209	TRP	CD2-CE2	5.60	1.48	1.41
1	A	209	TRP	CD2-CE2	5.49	1.48	1.41
1	I	110	TRP	CD2-CE2	5.44	1.47	1.41
1	G	280	TRP	CD2-CE2	5.40	1.47	1.41

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	2118	0	2090	9	0
1	B	2122	0	2102	16	0
1	C	2119	0	2090	12	0
1	D	2108	0	2089	10	0
1	E	2130	0	2109	9	0
1	F	2100	0	2078	15	0
1	G	2087	0	2088	11	0
1	H	2128	0	2111	14	4
1	I	2114	0	2093	12	0
1	J	2122	0	2102	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	12	0	18	1	0
3	B	8	0	12	8	0
3	C	4	0	6	4	0
3	D	8	0	12	2	0
3	E	20	0	30	16	0
3	F	16	0	24	5	0
3	G	20	0	30	3	0
3	H	4	0	6	3	0
3	I	8	0	12	3	0
3	J	8	0	12	1	0
4	A	232	0	0	0	0
4	B	207	0	0	2	4
4	C	189	0	0	0	0
4	D	183	0	0	0	0
4	E	202	0	0	1	0
4	F	190	0	0	0	0
4	G	164	0	0	2	0
4	H	161	0	0	0	0
4	I	177	0	0	0	0
4	J	172	0	0	3	0
All	All	23143	0	21114	107	4

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.

All (107) 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:B:234:VAL:H	3:B:403:EDO:H22	1.10	1.07
1:D:31:GLU:HG2	3:E:403:EDO:O1	1.60	0.99
1:D:290:THR:OG1	3:D:402:EDO:H22	1.65	0.97
1:B:234:VAL:N	3:B:403:EDO:H22	1.87	0.88
1:B:149:THR:HG21	3:B:403:EDO:H21	1.53	0.88
1:C:235:MET:HA	3:C:402:EDO:H11	1.56	0.86
1:H:100:GLU:HG3	1:H:101:ASP:OD1	1.77	0.83
1:H:31:GLU:HG2	3:H:402:EDO:O2	1.87	0.74
1:B:234:VAL:H	3:B:403:EDO:C2	1.97	0.73
3:E:402:EDO:H21	4:E:603:HOH:O	1.88	0.72
1:H:99:ASN:O	1:H:100:GLU:HB3	1.89	0.71
1:I:31:GLU:HG2	3:J:402:EDO:O1	1.95	0.67
1:E:236[A]:GLN:H	3:E:405:EDO:C1	2.09	0.66
1:D:37:THR:HG22	1:G:25:SER:HB3	1.78	0.65
1:F:62:LEU:CD1	3:F:404:EDO:H21	2.27	0.65
1:E:236[B]:GLN:H	3:E:405:EDO:C1	2.10	0.64
1:C:235:MET:CA	3:C:402:EDO:H11	2.28	0.64
1:A:102:MET:HE3	1:A:107:ILE:HG21	1.80	0.63
1:D:31:GLU:HG2	3:E:403:EDO:HO1	1.60	0.63
1:A:220:ARG:CD	3:E:404:EDO:H22	2.31	0.61
1:F:116:LYS:HG3	3:F:403:EDO:H21	1.83	0.61
1:C:39:PRO:HG2	1:C:42:ILE:HD12	1.82	0.61
1:F:288:ASN:O	3:F:403:EDO:H12	2.01	0.60
1:B:25:SER:HB3	1:I:37:THR:HG22	1.83	0.59
1:I:114:SER:OG	3:I:402:EDO:H12	2.02	0.59
1:C:105:ASP:OD2	1:J:105:ASP:HB3	2.02	0.58
1:G:118[B]:GLU:HG3	4:G:520:HOH:O	2.02	0.58
1:G:104:CYS:C	1:G:106:THR:H	2.07	0.58
1:H:100:GLU:HA	1:H:100:GLU:OE1	2.03	0.58
1:A:102:MET:HE1	1:A:107:ILE:HD13	1.85	0.58
1:J:217[B]:GLU:HA	1:J:217[B]:GLU:OE2	2.04	0.57
1:E:236[A]:GLN:H	3:E:405:EDO:H12	1.70	0.56
1:A:102:MET:HE2	1:A:300:TYR:CD2	2.39	0.56
1:F:116:LYS:HG3	3:F:403:EDO:C2	2.36	0.56
1:E:236[B]:GLN:H	3:E:405:EDO:H12	1.73	0.54
1:I:288:ASN:O	3:I:402:EDO:H21	2.08	0.53
1:G:114:SER:OG	3:G:402:EDO:H22	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:LYS:HG3	3:D:402:EDO:H11	1.91	0.52
1:B:136:TYR:CE1	1:C:133:LYS:HE2	2.45	0.51
1:J:101:ASP:OD1	1:J:103:THR:HB	2.11	0.51
1:G:39:PRO:HG2	1:G:42:ILE:HD12	1.92	0.51
1:I:136:TYR:CE1	1:J:133[A]:LYS:HE2	2.47	0.50
1:H:100:GLU:HG3	1:H:101:ASP:N	2.27	0.49
1:F:192:PRO:O	1:F:195:LYS:HE2	2.13	0.49
1:H:248[A]:GLU:CD	1:H:248[A]:GLU:H	2.15	0.49
1:B:234:VAL:O	3:B:403:EDO:H11	2.12	0.49
1:J:106:THR:CG2	1:J:295:ILE:HG23	2.43	0.49
1:B:233:PRO:HA	3:B:403:EDO:H22	1.95	0.49
1:D:192:PRO:O	1:D:195:LYS:HE2	2.12	0.49
1:B:105:ASP:OD2	1:F:105:ASP:HB2	2.13	0.48
1:D:33:LEU:HD21	3:E:403:EDO:H11	1.96	0.48
1:I:192:PRO:O	1:I:195:LYS:HE2	2.14	0.47
1:F:130:GLN:O	1:F:142[B]:CYS:SG	2.71	0.47
1:H:99:ASN:O	1:H:100:GLU:CB	2.59	0.47
1:J:184:LYS:NZ	4:J:662:HOH:O	2.46	0.47
1:C:237:PHE:CZ	1:D:223:GLY:HA3	2.49	0.47
1:C:236[A]:GLN:H	3:C:402:EDO:C1	2.28	0.47
1:A:102:MET:CE	1:A:107:ILE:HD13	2.45	0.46
1:E:275:SER:O	1:E:276:GLU:HB2	2.15	0.46
1:C:236[B]:GLN:H	3:C:402:EDO:C1	2.29	0.45
1:F:129:HIS:HE2	1:G:207:GLU:CD	2.19	0.45
1:E:235:MET:HB3	3:E:405:EDO:H12	1.99	0.45
1:H:31:GLU:HG2	3:H:402:EDO:HO2	1.81	0.45
1:A:102:MET:CE	1:A:300:TYR:CD2	3.00	0.45
1:E:239:ASN:O	3:E:404:EDO:H21	2.16	0.45
1:H:80:PRO:HD2	1:H:172:THR:O	2.17	0.45
1:F:92:VAL:HG22	1:F:261:PHE:CE1	2.52	0.44
1:A:220:ARG:HD3	3:E:404:EDO:H22	2.00	0.44
1:B:45:ILE:HD12	1:B:45:ILE:C	2.38	0.44
1:F:248:GLU:H	1:F:248:GLU:CD	2.21	0.44
1:G:237:PHE:CZ	1:H:223:GLY:HA3	2.53	0.44
1:E:294:ARG:HH22	3:E:403:EDO:C1	2.30	0.44
1:F:284:PRO:HD3	4:G:624:HOH:O	2.18	0.44
1:G:235:MET:HG2	3:G:403:EDO:H11	2.00	0.43
1:I:275:SER:O	1:I:276:GLU:HB2	2.18	0.43
1:B:97:LEU:HD13	4:B:596:HOH:O	2.16	0.43
1:F:39:PRO:HD2	1:F:42:ILE:HD12	2.01	0.43
1:H:82:LYS:HE2	1:H:175[B]:ASP:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:94:LYS:HA	1:H:94:LYS:HD2	1.80	0.43
1:A:48:TYR:CE2	3:A:404:EDO:H22	2.53	0.43
1:F:62:LEU:HD11	3:F:404:EDO:H21	1.99	0.43
1:B:237:PHE:CZ	1:C:223:GLY:HA3	2.54	0.42
1:D:158:GLU:HB2	1:D:159:PRO:CD	2.50	0.42
1:B:233:PRO:CA	3:B:403:EDO:H22	2.50	0.42
1:I:270:VAL:CG1	1:I:278:GLN:HB3	2.50	0.42
1:J:94:LYS:HD2	1:J:94:LYS:HA	1.85	0.42
1:F:237:PHE:CZ	1:G:223:GLY:HA3	2.55	0.42
1:H:129:HIS:CE1	1:I:80:PRO:HG3	2.55	0.41
1:A:237:PHE:CZ	1:B:223:GLY:HA3	2.55	0.41
1:F:45:ILE:HD12	1:F:45:ILE:C	2.40	0.41
3:H:402:EDO:H11	1:I:250:GLY:O	2.20	0.41
1:J:133[B]:LYS:HE2	1:J:276:GLU:HG2	2.02	0.41
1:H:192:PRO:O	1:H:195:LYS:HE2	2.21	0.41
1:G:106:THR:CG2	1:G:295:ILE:CG2	2.99	0.41
1:J:146:GLN:HA	4:J:546:HOH:O	2.21	0.41
1:B:184[A]:LYS:HG2	4:B:584:HOH:O	2.20	0.41
1:I:284:PRO:HD3	4:J:576:HOH:O	2.20	0.40
1:C:136:TYR:CE1	1:D:133:LYS:HE2	2.56	0.40
1:G:118[B]:GLU:OE1	1:G:238:THR:O	2.39	0.40
1:I:116:LYS:NZ	3:I:403:EDO:H21	2.36	0.40
1:C:94:LYS:HA	1:C:94:LYS:HD2	1.89	0.40
1:E:294:ARG:HH12	3:E:403:EDO:H12	1.87	0.40
1:B:233:PRO:HA	3:B:403:EDO:C2	2.51	0.40
1:C:154:ALA:HB3	1:C:263:SER:HB2	2.04	0.40

All (4) 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:H:100:GLU:OE2	4:B:697:HOH:O[3_445]	0.40	1.80
1:H:100:GLU:CD	4:B:697:HOH:O[3_445]	1.09	1.11
1:H:100:GLU:OE1	4:B:702:HOH:O[3_445]	1.86	0.34
1:H:100:GLU:OE1	4:B:697:HOH:O[3_445]	1.91	0.29

## 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	277/278 (100%)	271 (98%)	6 (2%)	0	100	100
1	B	278/278 (100%)	272 (98%)	6 (2%)	0	100	100
1	C	277/278 (100%)	272 (98%)	5 (2%)	0	100	100
1	D	277/278 (100%)	271 (98%)	6 (2%)	0	100	100
1	E	279/278 (100%)	273 (98%)	6 (2%)	0	100	100
1	F	276/278 (99%)	269 (98%)	7 (2%)	0	100	100
1	G	273/278 (98%)	267 (98%)	5 (2%)	1 (0%)	39	27
1	H	280/278 (101%)	269 (96%)	10 (4%)	1 (0%)	39	27
1	I	278/278 (100%)	271 (98%)	7 (2%)	0	100	100
1	J	278/278 (100%)	270 (97%)	8 (3%)	0	100	100
All	All	2773/2780 (100%)	2705 (98%)	66 (2%)	2 (0%)	56	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	105	ASP
1	H	100	GLU

### 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	239/237 (101%)	239 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	240/237 (101%)	239 (100%)	1 (0%)	93	94
1	C	239/237 (101%)	238 (100%)	1 (0%)	93	94
1	D	239/237 (101%)	239 (100%)	0	100	100
1	E	241/237 (102%)	240 (100%)	1 (0%)	93	94
1	F	238/237 (100%)	237 (100%)	1 (0%)	93	94
1	G	237/237 (100%)	234 (99%)	3 (1%)	76	73
1	H	242/237 (102%)	238 (98%)	4 (2%)	68	63
1	I	240/237 (101%)	240 (100%)	0	100	100
1	J	240/237 (101%)	238 (99%)	2 (1%)	86	85
All	All	2395/2370 (101%)	2382 (100%)	13 (0%)	90	92

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	94	LYS
1	C	25	SER
1	E	284	PRO
1	F	94	LYS
1	G	97	LEU
1	G	103	THR
1	G	106	THR
1	H	97	LEU
1	H	104	CYS
1	H	107	ILE
1	H	270	VAL
1	J	103	THR
1	J	248	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	182	ASN
1	J	182	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 37 ligands modelled in this entry, 10 are monoatomic - leaving 27 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	$\# Z  > 2$
3	EDO	A	402	-	3,3,3	0.45	0	2,2,2	0.73	0
3	EDO	A	403	-	3,3,3	0.29	0	2,2,2	0.88	0
3	EDO	A	404	-	3,3,3	0.51	0	2,2,2	0.33	0
3	EDO	B	402	-	3,3,3	0.41	0	2,2,2	0.72	0
3	EDO	B	403	-	3,3,3	0.52	0	2,2,2	0.53	0
3	EDO	C	402	-	3,3,3	0.44	0	2,2,2	0.70	0
3	EDO	D	402	-	3,3,3	0.42	0	2,2,2	0.40	0
3	EDO	D	403	-	3,3,3	0.41	0	2,2,2	0.71	0
3	EDO	E	402	-	3,3,3	0.42	0	2,2,2	0.62	0
3	EDO	E	403	-	3,3,3	0.38	0	2,2,2	0.72	0
3	EDO	E	404	-	3,3,3	0.57	0	2,2,2	0.29	0
3	EDO	E	405	-	3,3,3	0.38	0	2,2,2	0.31	0
3	EDO	E	406	-	3,3,3	0.47	0	2,2,2	0.58	0
3	EDO	F	402	-	3,3,3	0.48	0	2,2,2	0.46	0
3	EDO	F	403	-	3,3,3	0.39	0	2,2,2	0.42	0
3	EDO	F	404	-	3,3,3	0.39	0	2,2,2	0.58	0
3	EDO	F	405	-	3,3,3	0.44	0	2,2,2	0.67	0
3	EDO	G	402	-	3,3,3	0.40	0	2,2,2	0.57	0
3	EDO	G	403	-	3,3,3	0.47	0	2,2,2	0.28	0
3	EDO	G	404	-	3,3,3	0.51	0	2,2,2	0.48	0
3	EDO	G	405	-	3,3,3	0.45	0	2,2,2	0.56	0
3	EDO	G	406	-	3,3,3	0.52	0	2,2,2	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	H	402	-	3,3,3	0.46	0	2,2,2	0.65	0
3	EDO	I	402	-	3,3,3	0.55	0	2,2,2	0.14	0
3	EDO	I	403	-	3,3,3	0.53	0	2,2,2	0.36	0
3	EDO	J	402	-	3,3,3	0.45	0	2,2,2	0.73	0
3	EDO	J	403	-	3,3,3	0.44	0	2,2,2	0.51	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	EDO	A	402	-	-	0/1/1/1	0/0/0/0
3	EDO	A	403	-	-	0/1/1/1	0/0/0/0
3	EDO	A	404	-	-	0/1/1/1	0/0/0/0
3	EDO	B	402	-	-	0/1/1/1	0/0/0/0
3	EDO	B	403	-	-	0/1/1/1	0/0/0/0
3	EDO	C	402	-	-	0/1/1/1	0/0/0/0
3	EDO	D	402	-	-	0/1/1/1	0/0/0/0
3	EDO	D	403	-	-	0/1/1/1	0/0/0/0
3	EDO	E	402	-	-	0/1/1/1	0/0/0/0
3	EDO	E	403	-	-	0/1/1/1	0/0/0/0
3	EDO	E	404	-	-	0/1/1/1	0/0/0/0
3	EDO	E	405	-	-	0/1/1/1	0/0/0/0
3	EDO	E	406	-	-	0/1/1/1	0/0/0/0
3	EDO	F	402	-	-	0/1/1/1	0/0/0/0
3	EDO	F	403	-	-	0/1/1/1	0/0/0/0
3	EDO	F	404	-	-	0/1/1/1	0/0/0/0
3	EDO	F	405	-	-	0/1/1/1	0/0/0/0
3	EDO	G	402	-	-	0/1/1/1	0/0/0/0
3	EDO	G	403	-	-	0/1/1/1	0/0/0/0
3	EDO	G	404	-	-	0/1/1/1	0/0/0/0
3	EDO	G	405	-	-	0/1/1/1	0/0/0/0
3	EDO	G	406	-	-	0/1/1/1	0/0/0/0
3	EDO	H	402	-	-	0/1/1/1	0/0/0/0
3	EDO	I	402	-	-	0/1/1/1	0/0/0/0
3	EDO	I	403	-	-	0/1/1/1	0/0/0/0
3	EDO	J	402	-	-	0/1/1/1	0/0/0/0
3	EDO	J	403	-	-	0/1/1/1	0/0/0/0

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.

16 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	404	EDO	1	0
3	B	403	EDO	8	0
3	C	402	EDO	4	0
3	D	402	EDO	2	0
3	E	402	EDO	1	0
3	E	403	EDO	5	0
3	E	404	EDO	3	0
3	E	405	EDO	7	0
3	F	403	EDO	3	0
3	F	404	EDO	2	0
3	G	402	EDO	1	0
3	G	403	EDO	2	0
3	H	402	EDO	3	0
3	I	402	EDO	2	0
3	I	403	EDO	1	0
3	J	402	EDO	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	277/278 (99%)	-0.32	3 (1%) 82 84	16, 23, 44, 67	0
1	B	276/278 (99%)	-0.11	4 (1%) 78 80	16, 23, 51, 74	0
1	C	276/278 (99%)	-0.09	6 (2%) 65 69	17, 24, 49, 88	0
1	D	275/278 (98%)	-0.15	11 (4%) 42 46	19, 26, 53, 83	0
1	E	277/278 (99%)	-0.12	5 (1%) 71 74	17, 25, 44, 73	0
1	F	274/278 (98%)	-0.27	8 (2%) 55 59	19, 25, 55, 72	0
1	G	270/278 (97%)	-0.23	6 (2%) 65 69	18, 25, 47, 92	0
1	H	274/278 (98%)	-0.14	11 (4%) 42 46	19, 27, 54, 90	0
1	I	275/278 (98%)	-0.17	8 (2%) 55 59	20, 27, 50, 78	0
1	J	276/278 (99%)	-0.06	11 (3%) 42 46	19, 27, 60, 76	0
All	All	2750/2780 (98%)	-0.17	73 (2%) 58 62	16, 25, 51, 92	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	300	TYR	10.6
1	B	300	TYR	6.6
1	H	100	GLU	5.3
1	H	105	ASP	5.1
1	J	73	PHE	5.0
1	F	73	PHE	4.7
1	G	103	THR	4.6
1	J	104	CYS	4.4
1	J	300	TYR	4.3
1	C	299	PRO	4.2
1	D	73	PHE	4.0
1	D	103	THR	4.0
1	J	103	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	I	101	ASP	4.0
1	C	73	PHE	4.0
1	H	73	PHE	4.0
1	G	37	THR	3.9
1	I	100	GLU	3.9
1	J	182	ASN	3.8
1	I	103	THR	3.6
1	D	299	PRO	3.6
1	I	104	CYS	3.5
1	F	103	THR	3.5
1	H	37	THR	3.5
1	A	38	GLY	3.4
1	I	73	PHE	3.4
1	D	104	CYS	3.3
1	B	37	THR	3.3
1	B	73	PHE	3.2
1	E	37	THR	3.2
1	C	76	ALA	3.1
1	E	97	LEU	3.1
1	E	73	PHE	3.1
1	J	100	GLU	3.1
1	J	101	ASP	3.0
1	F	102	MET	2.9
1	F	100	GLU	2.9
1	D	105	ASP	2.9
1	I	105	ASP	2.9
1	G	73	PHE	2.8
1	G	104	CYS	2.8
1	D	102	MET	2.8
1	A	73	PHE	2.8
1	H	76	ALA	2.8
1	I	97	LEU	2.7
1	J	181	LYS	2.7
1	E	40	ASP	2.6
1	J	102	MET	2.6
1	F	37	THR	2.6
1	C	103	THR	2.6
1	D	97	LEU	2.5
1	G	97	LEU	2.5
1	G	40	ASP	2.4
1	F	104	CYS	2.4
1	H	40	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	100	GLU	2.4
1	H	103	THR	2.3
1	J	175	ASP	2.3
1	D	101	ASP	2.2
1	F	101	ASP	2.2
1	B	299	PRO	2.2
1	E	100	GLU	2.2
1	H	101	ASP	2.2
1	H	74	SER	2.2
1	J	105	ASP	2.2
1	F	40	ASP	2.1
1	H	25	SER	2.1
1	A	97	LEU	2.1
1	D	26	HIS	2.1
1	H	298	ASN	2.1
1	D	25	SER	2.0
1	C	40	ASP	2.0
1	I	175[A]	ASP	2.0

## 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	EDO	F	403	4/4	0.96	0.36	16.22	38,38,47,48	0
3	EDO	D	402	4/4	0.94	0.28	10.98	39,42,46,56	0
3	EDO	A	403	4/4	0.92	0.27	10.40	28,35,38,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	B	403	4/4	0.87	0.26	10.00	34,36,37,42	0
3	EDO	F	404	4/4	0.96	0.18	9.67	33,34,37,41	0
3	EDO	E	402	4/4	0.91	0.25	7.28	40,43,50,56	0
3	EDO	J	402	4/4	0.82	0.27	6.16	52,62,65,67	0
3	EDO	G	402	4/4	0.95	0.32	6.14	35,37,44,54	0
3	EDO	I	402	4/4	0.87	0.21	5.73	39,40,51,52	0
3	EDO	J	403	4/4	0.97	0.14	5.53	25,29,30,33	0
3	EDO	G	404	4/4	0.67	0.25	5.20	49,53,57,57	0
3	EDO	E	403	4/4	0.92	0.21	4.03	43,46,47,54	0
3	EDO	H	402	4/4	0.74	0.21	3.82	50,56,58,58	0
3	EDO	E	404	4/4	0.84	0.16	2.24	38,41,45,50	0
3	EDO	C	402	4/4	0.91	0.13	2.16	34,42,42,48	0
3	EDO	B	402	4/4	0.95	0.12	1.04	32,40,40,43	0
3	EDO	A	402	4/4	0.95	0.12	1.02	32,35,36,36	0
3	EDO	G	403	4/4	0.93	0.13	0.88	36,36,42,44	0
3	EDO	I	403	4/4	0.82	0.16	0.61	45,49,52,55	0
3	EDO	F	402	4/4	0.95	0.11	0.59	35,39,40,42	0
3	EDO	D	403	4/4	0.91	0.15	0.54	48,50,54,55	0
3	EDO	F	405	4/4	0.89	0.14	0.38	40,42,44,52	0
3	EDO	G	405	4/4	0.96	0.09	0.08	38,42,45,49	0
3	EDO	E	406	4/4	0.94	0.10	-0.06	38,44,48,51	0
3	EDO	E	405	4/4	0.93	0.10	-1.09	33,36,36,42	0
2	CA	I	401	1/1	0.97	0.06	-1.23	27,27,27,27	1
2	CA	D	401	1/1	0.94	0.06	-1.61	29,29,29,29	1
2	CA	J	401	1/1	0.95	0.05	-1.83	31,31,31,31	1
2	CA	H	401	1/1	0.96	0.05	-2.20	30,30,30,30	1
2	CA	B	401	1/1	0.98	0.06	-2.69	23,23,23,23	1
3	EDO	A	404	4/4	0.89	0.17	-	26,35,42,47	0
2	CA	A	401	1/1	0.98	0.04	-	24,24,24,24	1
2	CA	G	401	1/1	0.95	0.05	-	24,24,24,24	1
2	CA	C	401	1/1	0.97	0.05	-	24,24,24,24	1
2	CA	F	401	1/1	0.97	0.04	-	25,25,25,25	1
3	EDO	G	406	4/4	0.88	0.13	-	37,39,45,48	0
2	CA	E	401	1/1	0.98	0.06	-	25,25,25,25	1

## 6.5 Other polymers ⓘ

There are no such residues in this entry.