



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 01:10 PM UTC

PDB ID : 4H09 / pdb_00004h09
Title : Crystal structure of a leucine-rich repeat protein (EUBVEN_01088) from *Escherichia coli* strain ATCC 27560 at 2.50 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2012-09-07
Resolution : 2.50 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

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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

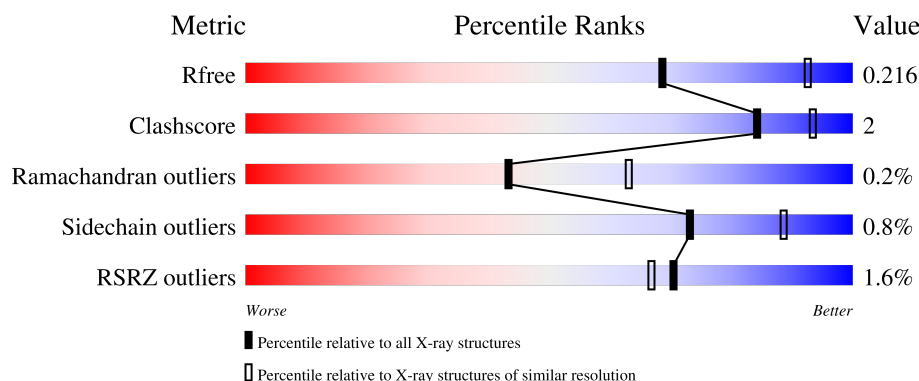
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	379	% 91% 8% .
1	B	379	3% 92% 6% .
1	C	379	3% 92% 6% .
1	D	379	89% 10% .
1	E	379	% 91% 8% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14625 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.

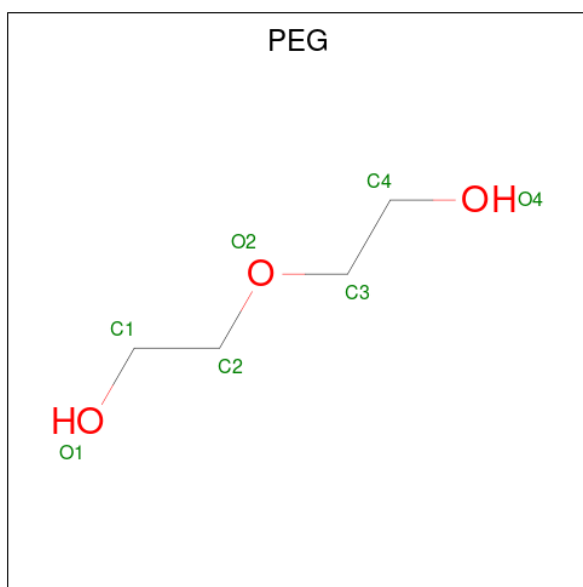
- Molecule 1 is a protein called Hypothetical leucine rich repeat protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	Se	0	1	0
			2832	1808	444	568	6	6			
1	B	372	Total	C	N	O	S	Se	0	0	0
			2778	1768	439	559	6	6			
1	C	373	Total	C	N	O	S	Se	0	0	0
			2780	1768	442	558	6	6			
1	D	377	Total	C	N	O	S	Se	0	2	0
			2849	1818	450	569	6	6			
1	E	373	Total	C	N	O	S	Se	0	0	0
			2807	1791	445	559	6	6			

There are 5 discrepancies between the modelled and reference sequences:

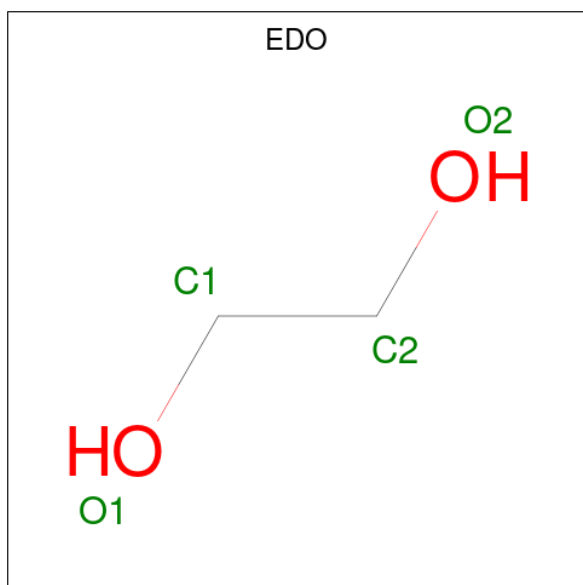
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A5Z5V6
B	0	GLY	-	expression tag	UNP A5Z5V6
C	0	GLY	-	expression tag	UNP A5Z5V6
D	0	GLY	-	expression tag	UNP A5Z5V6
E	0	GLY	-	expression tag	UNP A5Z5V6

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	64	Total O 64 64	0	0
4	B	77	Total O 77 77	0	0
4	C	90	Total O 90 90	0	0

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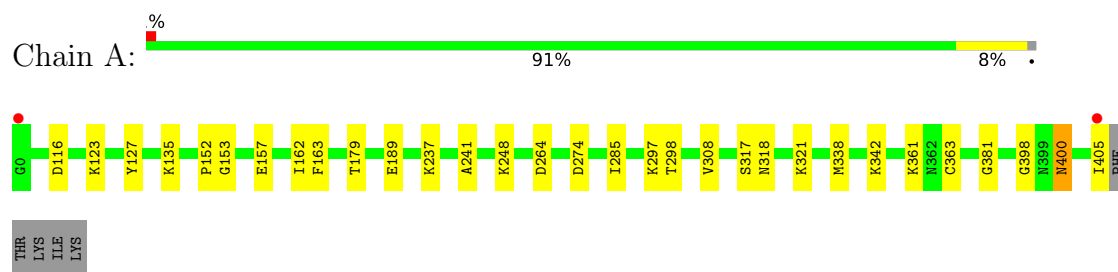
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	93	Total 93	O 93	0	0
4	E	75	Total 75	O 75	0	0

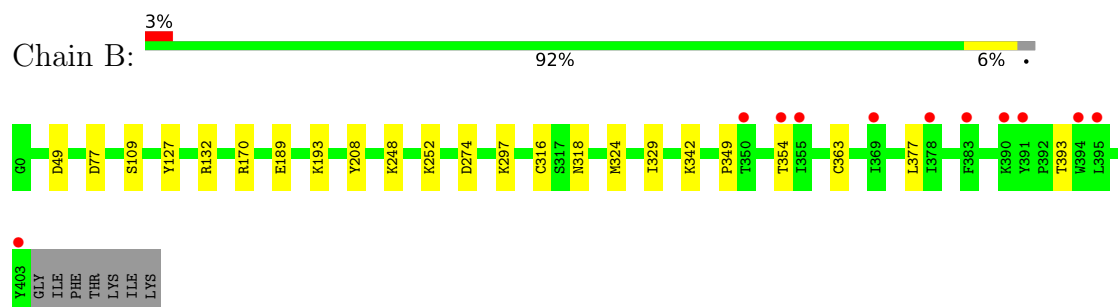
3 Residue-property plots

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.

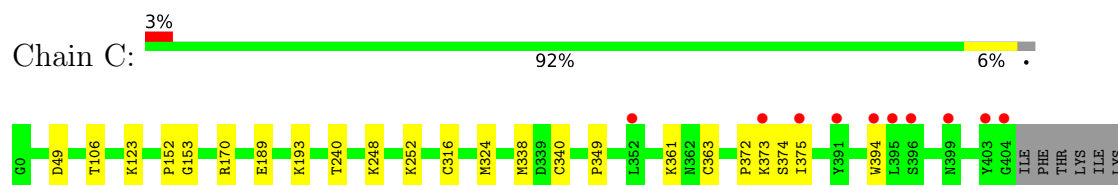
- Molecule 1: Hypothetical leucine rich repeat protein



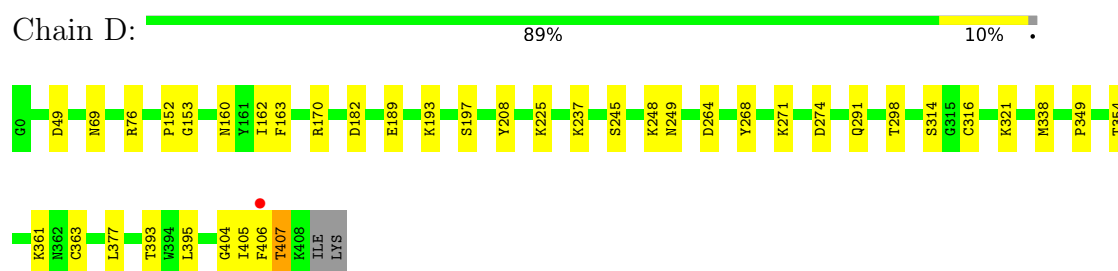
- Molecule 1: Hypothetical leucine rich repeat protein



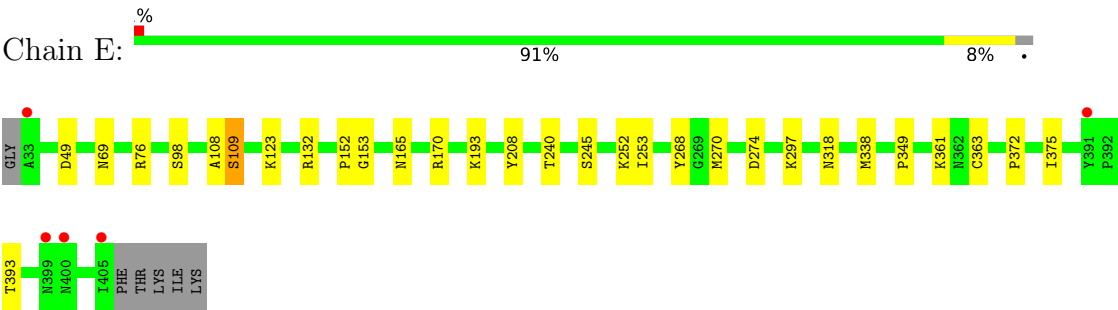
- Molecule 1: Hypothetical leucine rich repeat protein



- Molecule 1: Hypothetical leucine rich repeat protein



● Molecule 1: Hypothetical leucine rich repeat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	105.51Å 105.51Å 361.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.96 – 2.50 29.96 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.96-2.50) 99.9 (29.96-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.51Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.176 , 0.209 0.183 , 0.216	Depositor DCC
R_{free} test set	3933 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.223	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.054 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14625	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, 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	0.82	1/2881 (0.0%)	1.15	8/3907 (0.2%)
1	B	0.81	0/2823	1.16	7/3839 (0.2%)
1	C	0.83	0/2825	1.17	12/3836 (0.3%)
1	D	0.84	0/2901	1.15	12/3937 (0.3%)
1	E	0.80	0/2853	1.13	11/3871 (0.3%)
All	All	0.82	1/14283 (0.0%)	1.15	50/19390 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	400	ASN	CA-C	5.12	1.59	1.53

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	ILE	N-CA-CB	7.08	119.60	111.39
1	B	49	ASP	CA-CB-CG	7.08	119.68	112.60
1	D	153	GLY	N-CA-C	6.58	122.03	113.27
1	A	153	GLY	N-CA-C	6.57	122.01	113.27
1	C	340	CYS	CA-C-N	6.56	131.81	120.86
1	C	340	CYS	C-N-CA	6.56	131.81	120.86
1	E	153	GLY	N-CA-C	6.54	121.97	113.27
1	C	153	GLY	N-CA-C	6.51	121.93	113.27
1	C	316	CYS	CA-C-N	6.25	130.61	120.60
1	C	316	CYS	C-N-CA	6.25	130.61	120.60
1	B	316	CYS	CA-C-N	6.17	129.16	120.28
1	B	316	CYS	C-N-CA	6.17	129.16	120.28
1	C	49	ASP	CA-CB-CG	6.08	118.68	112.60
1	E	49	ASP	CA-CB-CG	6.01	118.61	112.60
1	D	49	ASP	CA-CB-CG	5.93	118.53	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	152	PRO	CA-C-N	5.89	127.55	120.13
1	E	152	PRO	C-N-CA	5.89	127.55	120.13
1	C	152	PRO	CA-C-N	5.80	127.44	120.13
1	C	152	PRO	C-N-CA	5.80	127.44	120.13
1	A	152	PRO	CA-C-N	5.77	127.40	120.13
1	A	152	PRO	C-N-CA	5.77	127.40	120.13
1	D	152	PRO	CA-C-N	5.67	127.28	120.13
1	D	152	PRO	C-N-CA	5.67	127.28	120.13
1	B	274	ASP	CA-CB-CG	5.67	118.27	112.60
1	E	274	ASP	CA-CB-CG	5.61	118.21	112.60
1	A	308	VAL	N-CA-C	-5.53	102.53	107.56
1	D	363	CYS	CA-C-N	5.51	127.93	120.38
1	D	363	CYS	C-N-CA	5.51	127.93	120.38
1	E	123	LYS	N-CA-C	-5.49	106.37	112.57
1	A	274	ASP	CA-CB-CG	5.48	118.08	112.60
1	D	316	CYS	CA-C-N	5.48	129.45	120.63
1	D	316	CYS	C-N-CA	5.48	129.45	120.63
1	C	363	CYS	CA-C-N	5.45	127.85	120.38
1	C	363	CYS	C-N-CA	5.45	127.85	120.38
1	D	249	ASN	N-CA-C	5.40	120.52	113.88
1	E	108	ALA	CA-C-N	5.38	128.03	120.28
1	E	108	ALA	C-N-CA	5.38	128.03	120.28
1	E	363	CYS	CA-C-N	5.37	127.74	120.38
1	E	363	CYS	C-N-CA	5.37	127.74	120.38
1	A	363	CYS	CA-C-N	5.36	127.72	120.38
1	A	363	CYS	C-N-CA	5.36	127.72	120.38
1	B	363	CYS	CA-C-N	5.31	127.65	120.38
1	B	363	CYS	C-N-CA	5.31	127.65	120.38
1	D	69	ASN	CA-CB-CG	5.24	117.84	112.60
1	D	264	ASP	CA-CB-CG	5.21	117.81	112.60
1	C	123	LYS	N-CA-C	-5.18	106.72	112.57
1	D	274	ASP	CA-CB-CG	5.10	117.70	112.60
1	A	123	LYS	N-CA-C	-5.05	106.86	112.57
1	E	69	ASN	CA-CB-CG	5.04	117.64	112.60
1	C	106	THR	CB-CA-C	5.03	118.51	110.16

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	2832	0	2816	16	0
1	B	2778	0	2701	10	0
1	C	2780	0	2698	8	0
1	D	2849	0	2823	17	0
1	E	2807	0	2766	13	0
2	A	14	0	20	3	0
2	D	14	0	20	1	0
3	A	48	0	72	4	0
3	B	28	0	42	1	0
3	C	20	0	30	1	0
3	D	32	0	48	2	0
3	E	24	0	36	2	0
4	A	64	0	0	0	0
4	B	77	0	0	0	0
4	C	90	0	0	1	0
4	D	93	0	0	2	0
4	E	75	0	0	1	0
All	All	14625	0	14072	64	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.

All (64) 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:285:ILE:H	3:A:510:EDO:H22	1.40	0.85
1:D:395:LEU:HD22	1:D:404:GLY:O	1.78	0.84
1:E:240:THR:HA	3:E:501:EDO:H12	1.77	0.66
1:C:240:THR:HA	3:C:503:EDO:H12	1.78	0.65
1:A:116:ASP:H	2:A:501:PEG:H12	1.61	0.65
1:E:372:PRO:HD2	1:E:375:ILE:HD11	1.84	0.58
1:D:349:PRO:HB2	4:D:608:HOH:O	2.04	0.57
1:D:160:ASN:OD1	1:D:182:ASP:HB2	2.05	0.56
1:A:157[B]:GLU:HG2	1:A:179:THR:HB	1.87	0.56
1:E:338:MSE:HG3	1:E:361:LYS:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:LYS:HG2	1:A:157[B]:GLU:HB2	1.89	0.54
1:A:127:TYR:CE2	3:A:504:EDO:H21	2.44	0.53
1:D:298:THR:HG22	1:D:321:LYS:HB3	1.89	0.53
1:A:398:GLY:C	1:A:400:ASN:H	2.16	0.52
1:A:298:THR:HG22	1:A:321:LYS:HB3	1.91	0.51
1:D:245:SER:HA	1:D:268:TYR:O	2.11	0.51
1:C:338:MSE:HE1	4:C:630:HOH:O	2.10	0.51
1:E:165:ASN:HD22	3:E:506:EDO:H12	1.75	0.51
1:A:135:LYS:HG2	1:A:157[A]:GLU:HB3	1.93	0.51
3:A:506:EDO:H22	1:B:77:ASP:HB2	1.93	0.50
1:E:245:SER:HA	1:E:268:TYR:O	2.12	0.49
1:C:394:TRP:H	1:C:394:TRP:CD1	2.30	0.49
1:E:297:LYS:HE2	1:E:318:ASN:HB3	1.94	0.48
1:E:253:ILE:HD11	1:E:270:MSE:HE1	1.95	0.48
1:B:127:TYR:CE2	3:B:502:EDO:H12	2.49	0.48
1:A:162:ILE:HG23	1:A:163:PHE:CD2	2.50	0.47
1:A:264:ASP:H	2:A:502:PEG:C2	2.28	0.47
1:E:372:PRO:HD2	1:E:375:ILE:CD1	2.45	0.47
1:A:381:GLY:H	3:A:509:EDO:H11	1.80	0.47
1:C:189:GLU:O	1:C:248:LYS:HE2	2.16	0.46
1:A:297:LYS:HE2	1:A:318:ASN:HB3	1.98	0.45
1:C:372:PRO:C	1:C:374:SER:H	2.24	0.45
1:E:76:ARG:HD2	1:E:98:SER:O	2.16	0.45
1:B:297:LYS:HE2	1:B:318:ASN:HB3	1.99	0.44
1:D:162:ILE:HG23	1:D:163:PHE:CD2	2.53	0.44
1:A:241:ALA:HB2	2:A:502:PEG:H21	2.00	0.44
1:A:318:ASN:HA	1:A:342:LYS:HD2	2.00	0.44
1:D:291:GLN:HG3	1:D:314:SER:HB3	2.00	0.44
1:D:76:ARG:HH22	3:D:506:EDO:H12	1.83	0.43
1:A:189:GLU:O	1:A:248:LYS:HE2	2.19	0.43
1:E:170:ARG:HG3	1:E:193:LYS:HB2	2.01	0.43
1:C:338:MSE:HG3	1:C:361:LYS:HB3	2.01	0.42
1:B:354:THR:HG23	1:B:377:LEU:HD23	2.02	0.42
1:E:349:PRO:HB2	4:E:635:HOH:O	2.18	0.42
1:D:225:LYS:HG3	3:D:510:EDO:H21	2.02	0.42
1:C:324:MSE:HB3	1:C:349:PRO:HG3	2.02	0.42
1:D:170:ARG:HG3	1:D:193:LYS:HB2	2.02	0.42
1:D:193:LYS:HA	1:D:208:TYR:HB3	2.02	0.41
1:B:318:ASN:HA	1:B:342:LYS:HD2	2.02	0.41
1:D:197:SER:HA	2:D:502:PEG:H11	2.02	0.41
1:C:170:ARG:HG3	1:C:193:LYS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:MSE:HG3	1:A:361:LYS:HB3	2.03	0.41
1:E:109:SER:O	1:E:132:ARG:HB2	2.20	0.41
1:B:109:SER:O	1:B:132:ARG:HB2	2.21	0.41
1:D:271:LYS:NZ	4:D:646:HOH:O	2.48	0.41
1:D:338:MSE:HG3	1:D:361:LYS:HB3	2.03	0.41
1:B:193:LYS:HA	1:B:208:TYR:HB3	2.03	0.41
1:D:354:THR:HG23	1:D:377:LEU:HD23	2.03	0.41
1:B:170:ARG:HG3	1:B:193:LYS:HB2	2.02	0.40
1:B:189:GLU:O	1:B:248:LYS:HE3	2.20	0.40
1:B:324:MSE:HB3	1:B:349:PRO:HG3	2.03	0.40
1:D:189:GLU:O	1:D:248:LYS:HE3	2.21	0.40
1:D:405:ILE:C	1:D:407:THR:H	2.28	0.40
1:E:193:LYS:HA	1:E:208:TYR:HB3	2.02	0.40

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	373/379 (98%)	360 (96%)	13 (4%)	0	100	100
1	B	370/379 (98%)	359 (97%)	11 (3%)	0	100	100
1	C	371/379 (98%)	358 (96%)	11 (3%)	2 (0%)	24	43
1	D	377/379 (100%)	365 (97%)	11 (3%)	1 (0%)	36	55
1	E	371/379 (98%)	358 (96%)	13 (4%)	0	100	100
All	All	1862/1895 (98%)	1800 (97%)	59 (3%)	3 (0%)	43	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	406	PHE

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Mol	Chain	Res	Type
1	C	373	LYS
1	C	375	ILE

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	315/320 (98%)	312 (99%)	3 (1%)	68	86
1	B	301/320 (94%)	299 (99%)	2 (1%)	76	89
1	C	298/320 (93%)	297 (100%)	1 (0%)	86	94
1	D	314/320 (98%)	311 (99%)	3 (1%)	68	86
1	E	307/320 (96%)	304 (99%)	3 (1%)	68	86
All	All	1535/1600 (96%)	1523 (99%)	12 (1%)	73	88

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	237	LYS
1	A	317	SER
1	A	405	ILE
1	B	252	LYS
1	B	393	THR
1	C	252	LYS
1	D	237	LYS
1	D	393	THR
1	D	407	THR
1	E	109	SER
1	E	252	LYS
1	E	393	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	142	GLN
1	A	160	ASN
1	A	318	ASN
1	B	69	ASN
1	B	326	ASN
1	C	69	ASN
1	C	142	GLN
1	C	160	ASN
1	C	190	ASN
1	C	292	ASN
1	C	318	ASN
1	D	142	GLN
1	E	142	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](#)

42 ligands are modelled in this entry.

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	505	-	3,3,3	0.58	0	2,2,2	0.40	0
2	PEG	A	502	-	6,6,6	0.19	0	5,5,5	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	507	-	3,3,3	0.77	0	2,2,2	0.26	0
3	EDO	A	509	-	3,3,3	0.70	0	2,2,2	0.13	0
3	EDO	D	503	-	3,3,3	0.52	0	2,2,2	0.51	0
3	EDO	D	504	-	3,3,3	0.38	0	2,2,2	0.36	0
3	EDO	E	502	-	3,3,3	0.41	0	2,2,2	0.44	0
3	EDO	A	513	-	3,3,3	0.48	0	2,2,2	0.40	0
3	EDO	E	505	-	3,3,3	0.48	0	2,2,2	0.38	0
3	EDO	A	508	-	3,3,3	0.99	0	2,2,2	0.16	0
2	PEG	D	501	-	6,6,6	0.19	0	5,5,5	0.10	0
3	EDO	A	504	-	3,3,3	0.62	0	2,2,2	0.11	0
3	EDO	A	506	-	3,3,3	0.93	0	2,2,2	0.16	0
3	EDO	A	511	-	3,3,3	0.70	0	2,2,2	0.09	0
3	EDO	E	504	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	E	506	-	3,3,3	0.44	0	2,2,2	0.66	0
3	EDO	B	505	-	3,3,3	0.60	0	2,2,2	0.26	0
3	EDO	C	504	-	3,3,3	0.65	0	2,2,2	0.07	0
3	EDO	C	505	-	3,3,3	0.67	0	2,2,2	0.17	0
3	EDO	B	503	-	3,3,3	0.69	0	2,2,2	0.13	0
3	EDO	E	501	-	3,3,3	0.34	0	2,2,2	0.46	0
3	EDO	B	507	-	3,3,3	0.53	0	2,2,2	0.31	0
3	EDO	B	506	-	3,3,3	0.63	0	2,2,2	0.14	0
3	EDO	A	514	-	3,3,3	0.53	0	2,2,2	0.38	0
3	EDO	D	505	-	3,3,3	0.45	0	2,2,2	0.43	0
2	PEG	D	502	-	6,6,6	0.19	0	5,5,5	0.11	0
3	EDO	A	510	-	3,3,3	0.60	0	2,2,2	0.21	0
3	EDO	C	503	-	3,3,3	0.45	0	2,2,2	0.49	0
3	EDO	D	509	-	3,3,3	0.67	0	2,2,2	0.11	0
3	EDO	B	504	-	3,3,3	0.86	0	2,2,2	0.05	0
3	EDO	D	508	-	3,3,3	0.51	0	2,2,2	0.29	0
3	EDO	D	510	-	3,3,3	0.55	0	2,2,2	0.17	0
3	EDO	D	506	-	3,3,3	0.59	0	2,2,2	0.17	0
3	EDO	E	503	-	3,3,3	0.61	0	2,2,2	0.35	0
2	PEG	A	501	-	6,6,6	0.37	0	5,5,5	0.28	0
3	EDO	D	507	-	3,3,3	0.62	0	2,2,2	0.15	0
3	EDO	A	512	-	3,3,3	0.32	0	2,2,2	0.51	0
3	EDO	A	503	-	3,3,3	0.76	0	2,2,2	0.01	0
3	EDO	B	502	-	3,3,3	0.43	0	2,2,2	0.46	0
3	EDO	C	502	-	3,3,3	0.68	0	2,2,2	0.19	0
3	EDO	B	501	-	3,3,3	0.72	0	2,2,2	0.17	0
3	EDO	C	501	-	3,3,3	0.69	0	2,2,2	0.12	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	505	-	-	0/1/1/1	-
2	PEG	A	502	-	-	0/4/4/4	-
3	EDO	A	507	-	-	0/1/1/1	-
3	EDO	A	509	-	-	1/1/1/1	-
3	EDO	D	503	-	-	0/1/1/1	-
3	EDO	D	504	-	-	0/1/1/1	-
3	EDO	E	502	-	-	0/1/1/1	-
3	EDO	A	513	-	-	1/1/1/1	-
3	EDO	E	505	-	-	0/1/1/1	-
3	EDO	A	508	-	-	1/1/1/1	-
2	PEG	D	501	-	-	0/4/4/4	-
3	EDO	A	504	-	-	1/1/1/1	-
3	EDO	A	506	-	-	0/1/1/1	-
3	EDO	A	511	-	-	1/1/1/1	-
3	EDO	E	504	-	-	0/1/1/1	-
3	EDO	E	506	-	-	0/1/1/1	-
3	EDO	B	505	-	-	0/1/1/1	-
3	EDO	C	504	-	-	0/1/1/1	-
3	EDO	C	505	-	-	0/1/1/1	-
3	EDO	B	503	-	-	1/1/1/1	-
3	EDO	E	501	-	-	0/1/1/1	-
3	EDO	B	507	-	-	0/1/1/1	-
3	EDO	B	506	-	-	0/1/1/1	-
3	EDO	A	514	-	-	1/1/1/1	-
3	EDO	D	505	-	-	1/1/1/1	-
2	PEG	D	502	-	-	0/4/4/4	-
3	EDO	A	510	-	-	0/1/1/1	-
3	EDO	C	503	-	-	1/1/1/1	-
3	EDO	D	509	-	-	0/1/1/1	-
3	EDO	B	504	-	-	0/1/1/1	-
3	EDO	D	508	-	-	0/1/1/1	-
3	EDO	D	510	-	-	0/1/1/1	-
3	EDO	D	506	-	-	0/1/1/1	-
3	EDO	E	503	-	-	0/1/1/1	-
2	PEG	A	501	-	-	2/4/4/4	-
3	EDO	D	507	-	-	0/1/1/1	-
3	EDO	A	512	-	-	0/1/1/1	-
3	EDO	A	503	-	-	0/1/1/1	-
3	EDO	B	502	-	-	1/1/1/1	-
3	EDO	C	502	-	-	1/1/1/1	-
3	EDO	B	501	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	503	EDO	O1-C1-C2-O2
3	A	508	EDO	O1-C1-C2-O2
3	C	502	EDO	O1-C1-C2-O2
2	A	501	PEG	C1-C2-O2-C3
3	A	509	EDO	O1-C1-C2-O2
3	D	505	EDO	O1-C1-C2-O2
3	A	511	EDO	O1-C1-C2-O2
3	B	502	EDO	O1-C1-C2-O2
2	A	501	PEG	O1-C1-C2-O2
3	A	504	EDO	O1-C1-C2-O2
3	A	513	EDO	O1-C1-C2-O2
3	A	514	EDO	O1-C1-C2-O2
3	C	503	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	PEG	2	0
3	A	509	EDO	1	0
3	A	504	EDO	1	0
3	A	506	EDO	1	0
3	E	506	EDO	1	0
3	E	501	EDO	1	0
2	D	502	PEG	1	0
3	A	510	EDO	1	0
3	C	503	EDO	1	0
3	D	510	EDO	1	0
3	D	506	EDO	1	0
2	A	501	PEG	1	0
3	B	502	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, 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	368/379 (97%)	-0.31	2 (0%) 87 85	36, 63, 89, 121	1 (0%)
1	B	366/379 (96%)	-0.03	11 (3%) 52 48	39, 67, 122, 146	0
1	C	367/379 (96%)	-0.14	10 (2%) 56 51	40, 59, 116, 153	0
1	D	371/379 (97%)	-0.25	1 (0%) 90 87	29, 58, 99, 129	2 (0%)
1	E	367/379 (96%)	-0.23	5 (1%) 73 70	38, 60, 105, 134	0
All	All	1839/1895 (97%)	-0.19	29 (1%) 70 67	29, 61, 107, 153	3 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	396	SER	4.0
1	B	369	ILE	3.6
1	C	404	GLY	3.5
1	E	405	ILE	3.3
1	E	400	ASN	3.2
1	B	403	TYR	3.2
1	E	33	ALA	3.1
1	C	399	ASN	3.1
1	D	406	PHE	2.6
1	C	391	TYR	2.4
1	C	394	TRP	2.4
1	A	0	GLY	2.4
1	B	378	ILE	2.3
1	C	373	LYS	2.3
1	C	403	TYR	2.3
1	B	395	LEU	2.3
1	C	352	LEU	2.3
1	B	391	TYR	2.3
1	E	391	TYR	2.2
1	B	390	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	375	ILE	2.2
1	B	350	THR	2.2
1	B	354	THR	2.1
1	B	355	ILE	2.1
1	B	383	PHE	2.1
1	B	394	TRP	2.1
1	E	399	ASN	2.1
1	C	395	LEU	2.0
1	A	405	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	C	502	4/4	0.56	0.19	88,90,90,91	0
3	EDO	B	505	4/4	0.61	0.18	80,82,84,85	0
3	EDO	B	506	4/4	0.73	0.12	80,81,84,85	0
3	EDO	A	504	4/4	0.75	0.17	71,71,74,75	0
2	PEG	D	502	7/7	0.75	0.11	96,99,100,100	0
2	PEG	A	502	7/7	0.78	0.18	71,72,75,77	0
3	EDO	A	507	4/4	0.79	0.23	83,83,83,84	0
3	EDO	D	509	4/4	0.79	0.15	79,82,84,85	0
3	EDO	A	508	4/4	0.80	0.16	61,64,68,70	0
3	EDO	C	504	4/4	0.80	0.17	73,76,78,79	0
3	EDO	B	503	4/4	0.80	0.20	71,71,73,73	0
3	EDO	C	505	4/4	0.83	0.18	70,72,75,76	0
3	EDO	A	509	4/4	0.83	0.17	74,76,76,77	0
2	PEG	D	501	7/7	0.84	0.16	95,97,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	D	510	4/4	0.84	0.12	73,76,80,84	0
3	EDO	B	507	4/4	0.85	0.14	81,81,83,83	0
3	EDO	A	505	4/4	0.85	0.15	58,62,66,66	0
3	EDO	B	504	4/4	0.85	0.16	60,61,62,64	0
3	EDO	A	513	4/4	0.86	0.21	63,65,69,76	0
3	EDO	A	514	4/4	0.86	0.12	69,71,71,71	0
3	EDO	A	506	4/4	0.86	0.18	65,66,67,68	0
3	EDO	A	510	4/4	0.88	0.13	67,67,70,76	0
3	EDO	D	506	4/4	0.88	0.12	73,75,77,77	0
3	EDO	A	511	4/4	0.89	0.15	66,66,69,69	0
3	EDO	E	503	4/4	0.89	0.15	56,57,58,60	0
3	EDO	E	505	4/4	0.89	0.16	84,84,84,86	0
3	EDO	D	507	4/4	0.90	0.10	78,78,78,78	0
3	EDO	E	502	4/4	0.91	0.10	56,56,58,58	0
2	PEG	A	501	7/7	0.91	0.11	64,66,70,71	0
3	EDO	D	503	4/4	0.91	0.11	62,63,63,63	0
3	EDO	E	506	4/4	0.91	0.14	64,64,65,67	0
3	EDO	B	502	4/4	0.92	0.09	54,55,55,56	0
3	EDO	D	508	4/4	0.92	0.15	63,65,66,66	0
3	EDO	C	503	4/4	0.93	0.10	64,64,64,65	0
3	EDO	E	504	4/4	0.93	0.12	44,47,50,56	0
3	EDO	E	501	4/4	0.94	0.11	54,56,56,60	0
3	EDO	C	501	4/4	0.94	0.10	54,55,56,56	0
3	EDO	D	505	4/4	0.95	0.08	54,55,56,59	0
3	EDO	B	501	4/4	0.95	0.11	45,47,49,51	0
3	EDO	D	504	4/4	0.95	0.10	59,59,60,61	0
3	EDO	A	503	4/4	0.97	0.07	38,39,42,45	0
3	EDO	A	512	4/4	0.97	0.09	55,57,62,67	0

6.5 Other polymers

There are no such residues in this entry.