



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:29 PM UTC

PDB ID : 7JVE / pdb_00007jve
Title : Crystal structure of Salmonella enterica Typhimurium BcfH
Authors : Subedi, P.; Heras, B.; Hor, L.; Paxman, J.J.
Deposited on : 2020-08-21
Resolution : 2.31 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

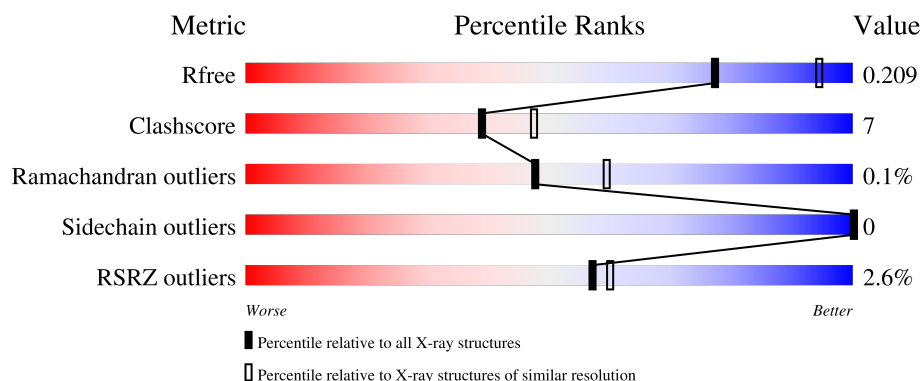
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	254	0% 85% 15%
1	B	254	0% 84% 15%
1	C	254	2% 87% 11%
1	D	254	2% 86% 10%
1	E	254	5% 80% 16%

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Mol	Chain	Length	Quality of chain
1	F	254	

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
4	PGE	A	303	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12630 atoms, of which 114 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 DsbA family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	1	0
			1953	1239	333	373	8			
1	B	251	Total	C	N	O	S	0	1	0
			1937	1231	329	369	8			
1	C	248	Total	C	N	O	S	0	3	0
			1934	1228	327	370	9			
1	D	244	Total	C	N	O	S	0	1	0
			1890	1203	322	357	8			
1	E	245	Total	C	N	O	S	0	0	0
			1890	1204	320	358	8			
1	F	246	Total	C	N	O	S	0	0	0
			1894	1206	321	359	8			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	F	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



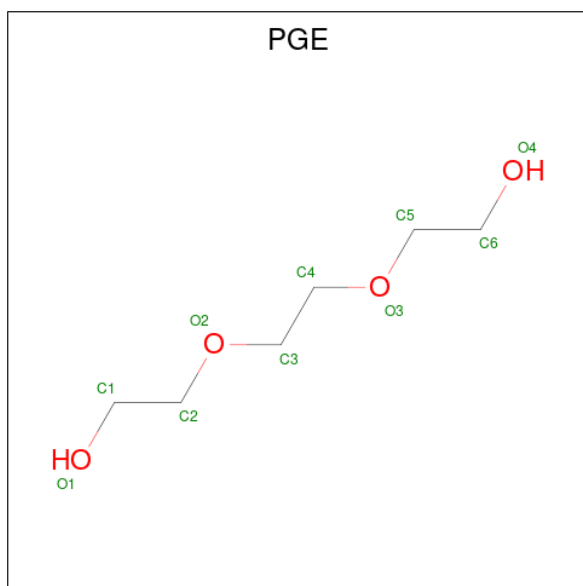
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	C	H	O	0	0
			10	2	6	2		
3	E	1	Total	C	H	O	0	0
			10	2	6	2		
3	F	1	Total	C	H	O	0	0
			10	2	6	2		
3	F	1	Total	C	H	O	0	0
			10	2	6	2		
3	F	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	206	Total	O	0	0
			206	206		
5	B	154	Total	O	0	0
			154	154		
5	C	144	Total	O	0	0
			144	144		

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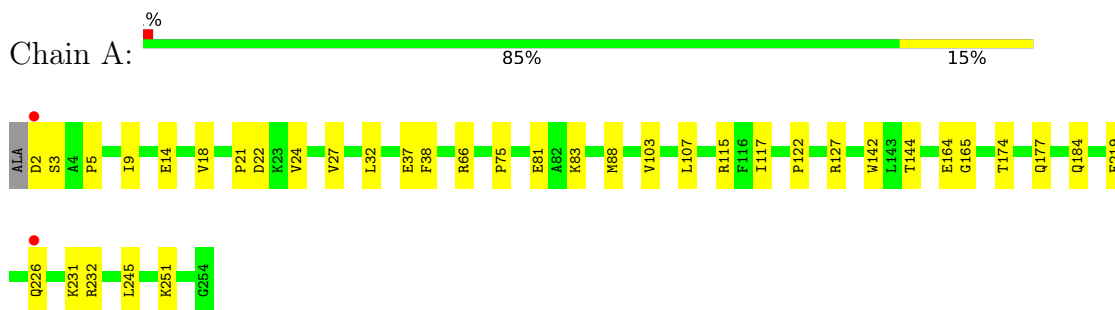
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	158	Total 158	O 158	0	0
5	E	120	Total 120	O 120	0	0
5	F	146	Total 146	O 146	0	0

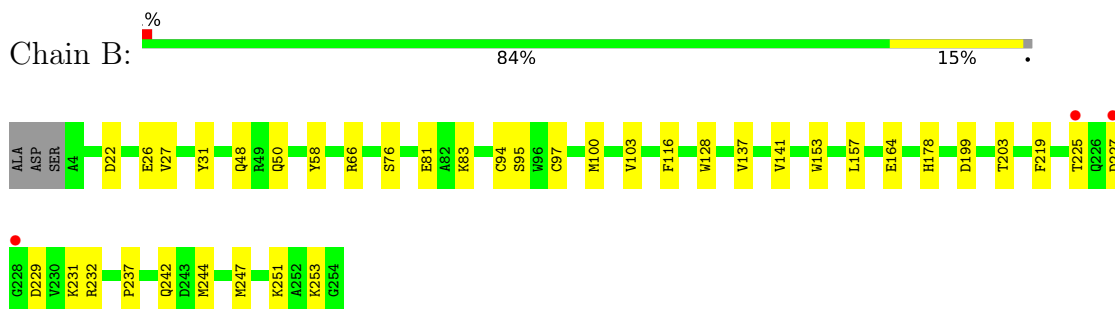
3 Residue-property plots

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.

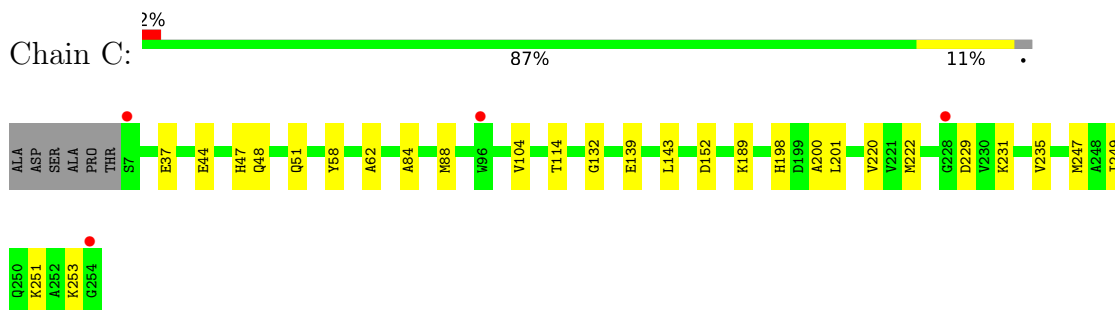
- Molecule 1: DsbA family protein



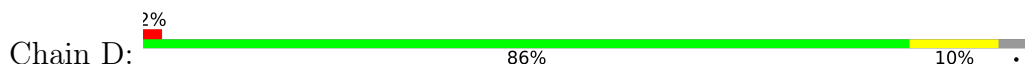
- Molecule 1: DsbA family protein

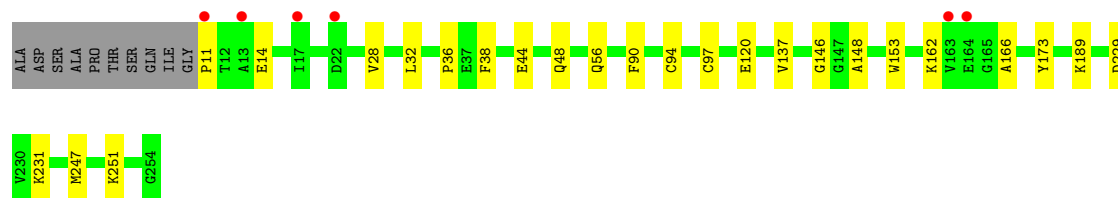


- Molecule 1: DsbA family protein

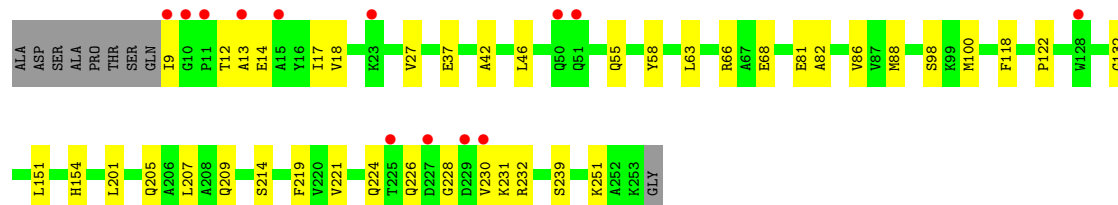
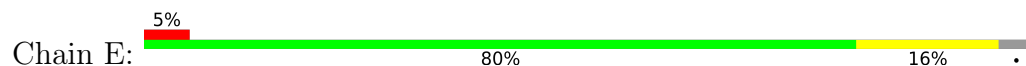


- Molecule 1: DsbA family protein

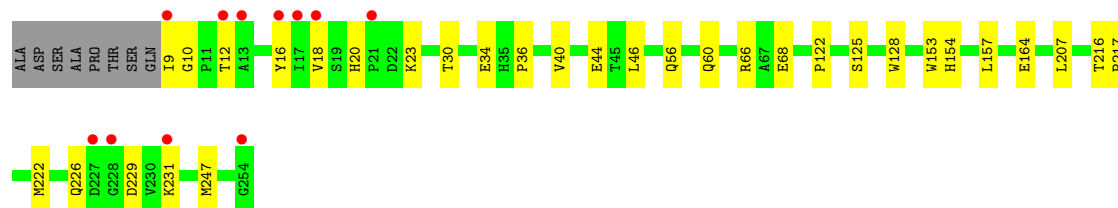
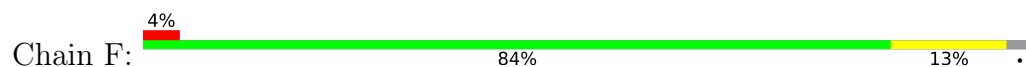




- Molecule 1: DsbA family protein



- Molecule 1: DsbA family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.01Å 133.73Å 146.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.65 – 2.31 42.65 – 2.31	Depositor EDS
% Data completeness (in resolution range)	97.2 (42.65-2.31) 97.2 (42.65-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.167 , 0.208 0.167 , 0.209	Depositor DCC
R_{free} test set	4312 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12630	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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: EDO, MG, PGE

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	0.38	0/2000	0.58	0/2727
1	B	0.36	0/1984	0.54	1/2706 (0.0%)
1	C	0.34	0/1980	0.53	0/2698
1	D	0.35	0/1939	0.52	0/2642
1	E	0.32	0/1936	0.49	0/2640
1	F	0.33	0/1940	0.52	0/2645
All	All	0.35	0/11779	0.53	1/16058 (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	B	81	GLU	CA-CB-CG	-5.49	103.11	114.10

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	1953	0	1911	32	0
1	B	1937	0	1897	25	0
1	C	1934	0	1885	20	0
1	D	1890	0	1858	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1890	0	1853	36	0
1	F	1894	0	1858	36	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	F	1	0	0	0	0
3	A	24	36	36	0	0
3	C	8	12	12	0	0
3	D	12	18	18	3	0
3	E	20	30	30	2	0
3	F	12	18	18	0	0
4	A	10	0	14	10	0
5	A	206	0	0	2	0
5	B	154	0	0	1	0
5	C	144	0	0	0	0
5	D	158	0	0	2	0
5	E	120	0	0	2	0
5	F	146	0	0	1	0
All	All	12516	114	11390	155	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 7.

All (155) 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:E:46:LEU:HD11	1:F:36:PRO:HB2	1.50	0.92
1:E:82:ALA:O	1:E:224:GLN:HG3	1.70	0.91
1:C:229:ASP:OD1	1:C:231:LYS:HG2	1.77	0.83
4:A:303:PGE:H22	1:C:152[B]:ASP:OD1	1.79	0.82
1:A:164:GLU:OE1	4:A:303:PGE:H3	1.85	0.77
1:F:40:VAL:O	1:F:44:GLU:HG3	1.85	0.77
1:E:231:LYS:O	1:E:251:LYS:HD3	1.85	0.76
1:E:118:PHE:CE2	1:E:151:LEU:HD21	2.22	0.75
1:E:118:PHE:CZ	1:E:151:LEU:HD21	2.24	0.73
1:B:247:MET:HE2	1:F:247:MET:HB3	1.70	0.73
1:A:127:ARG:HH21	4:A:303:PGE:H42	1.54	0.73
1:A:231:LYS:O	1:A:251:LYS:HE3	1.88	0.72
1:B:199:ASP:O	1:B:203:THR:HG23	1.88	0.72
1:E:66:ARG:NH1	1:E:224:GLN:O	2.21	0.71
1:F:30:THR:O	1:F:34:GLU:HG3	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66[A]:ARG:CD	1:A:226:GLN:HG3	2.21	0.70
1:A:14:GLU:O	1:A:18:VAL:HG23	1.91	0.69
1:D:44:GLU:OE2	1:D:48:GLN:NE2	2.26	0.68
1:C:220:VAL:HG11	1:C:222:MET:HE3	1.76	0.67
1:E:9:ILE:HA	1:F:9:ILE:HD11	1.78	0.66
1:E:228:GLY:HA3	1:E:232:ARG:HH21	1.61	0.65
1:E:46:LEU:CD1	1:F:36:PRO:HB2	2.26	0.65
1:D:146:GLY:HA3	3:D:301:EDO:H12	1.80	0.63
1:B:58:TYR:CE2	1:B:237:PRO:HG3	2.34	0.62
1:A:66[B]:ARG:HD2	1:A:226:GLN:HG3	1.82	0.61
1:A:66[A]:ARG:HD2	1:A:226:GLN:HG3	1.83	0.59
1:E:42:ALA:O	1:E:46:LEU:HD12	2.03	0.59
1:A:127:ARG:NH2	4:A:303:PGE:H42	2.17	0.59
1:B:48:GLN:HE21	1:F:56:GLN:NE2	2.00	0.59
1:B:153:TRP:CZ2	1:B:157:LEU:HD22	2.38	0.59
1:B:229:ASP:OD2	1:B:231:LYS:HB2	2.03	0.58
1:F:154:HIS:HE1	5:F:524:HOH:O	1.85	0.58
1:D:94:CYS:SG	1:D:97:CYS:SG	3.00	0.58
1:A:88:MET:HG2	1:A:219:PHE:CD2	2.39	0.58
1:A:103:VAL:HG23	5:A:459:HOH:O	2.03	0.57
1:B:178:HIS:HD2	5:B:538:HOH:O	1.86	0.57
1:C:220:VAL:CG1	1:C:222:MET:HE3	2.34	0.57
1:E:132:GLY:HA2	1:E:201:LEU:HD22	1.87	0.57
1:E:201:LEU:HD23	3:E:303:EDO:H11	1.87	0.57
1:B:94:CYS:HG	1:B:97:CYS:HG	1.53	0.57
1:D:173:TYR:CZ	1:D:189:LYS:HG3	2.40	0.57
1:E:86:VAL:HG22	1:E:221:VAL:HG22	1.87	0.56
1:E:88:MET:HG3	1:E:219:PHE:CE2	2.41	0.56
1:E:100:MET:HB2	3:E:304:EDO:O2	2.06	0.56
1:A:83:LYS:HE2	1:A:232:ARG:HH12	1.70	0.56
1:E:46:LEU:HD22	1:E:214:SER:OG	2.06	0.55
1:D:32:LEU:HB3	1:D:38:PHE:CE1	2.42	0.55
1:A:127:ARG:HH21	4:A:303:PGE:C4	2.20	0.54
1:D:247:MET:HE3	1:D:247:MET:HA	1.90	0.54
1:F:153:TRP:CZ2	1:F:157:LEU:HD22	2.41	0.54
1:A:88:MET:HG2	1:A:219:PHE:CE2	2.43	0.54
1:F:23:LYS:N	1:F:23:LYS:HD3	2.23	0.53
1:E:228:GLY:HA3	1:E:232:ARG:HE	1.73	0.53
1:D:229:ASP:OD1	1:D:231:LYS:HB2	2.08	0.53
1:A:165:GLY:HA2	4:A:303:PGE:H6	1.89	0.53
1:B:22:ASP:O	1:B:26:GLU:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:ALA:O	1:E:17:ILE:HG12	2.09	0.53
1:D:14:GLU:OE2	1:F:23:LYS:HE3	2.10	0.52
1:A:5:PRO:O	1:A:9:ILE:HG13	2.09	0.51
1:B:232:ARG:HG2	1:B:251:LYS:O	2.10	0.51
1:D:189:LYS:NZ	5:D:402:HOH:O	2.37	0.51
1:E:228:GLY:CA	1:E:232:ARG:HH21	2.23	0.51
1:C:229:ASP:CG	1:C:231:LYS:HG2	2.35	0.51
1:B:100:MET:HE2	1:B:219:PHE:CZ	2.46	0.51
1:C:198:HIS:CE1	1:C:200:ALA:HB3	2.45	0.51
1:E:66:ARG:CZ	1:E:226:GLN:HG3	2.41	0.50
1:D:137:VAL:HG11	1:D:153:TRP:CH2	2.46	0.50
1:E:55:GLN:O	1:E:58:TYR:N	2.45	0.50
1:C:88[B]:MET:HE1	1:C:104:VAL:HG21	1.93	0.50
4:A:303:PGE:O1	4:A:303:PGE:H32	2.10	0.50
1:A:165:GLY:CA	4:A:303:PGE:H6	2.42	0.50
1:B:50:GLN:NE2	1:B:50:GLN:HA	2.27	0.49
1:A:24:VAL:HA	1:A:27:VAL:HG12	1.95	0.49
1:D:90:PHE:CZ	1:D:120:GLU:HG2	2.48	0.49
1:E:98:SER:CB	1:E:239:SER:HB3	2.42	0.49
1:F:128:TRP:CH2	1:F:164:GLU:HA	2.48	0.49
1:C:231:LYS:O	1:C:251:LYS:CE	2.60	0.49
1:C:62:ALA:HB1	1:C:222:MET:CE	2.42	0.49
1:C:58:TYR:CD1	1:C:235:VAL:HG11	2.48	0.49
1:D:36:PRO:HG2	1:F:46:LEU:CD2	2.43	0.49
1:A:127:ARG:HE	4:A:303:PGE:H62	1.78	0.48
1:F:23:LYS:H	1:F:23:LYS:CE	2.27	0.48
1:A:2:ASP:CG	1:A:3:SER:H	2.22	0.48
1:E:228:GLY:HA3	1:E:232:ARG:NH2	2.27	0.48
1:B:83:LYS:HE3	1:B:253:LYS:O	2.13	0.47
1:B:66:ARG:HB3	1:B:66:ARG:HH11	1.79	0.47
1:E:14:GLU:O	1:E:18:VAL:HG23	2.15	0.47
1:E:205:GLN:O	1:E:209:GLN:HG3	2.13	0.47
1:F:9:ILE:HG23	1:F:10:GLY:H	1.79	0.47
1:D:28:VAL:O	1:D:32:LEU:HG	2.15	0.47
1:C:132:GLY:HA2	1:C:201:LEU:HD22	1.97	0.46
1:E:46:LEU:HD11	1:F:36:PRO:CB	2.33	0.46
1:E:46:LEU:CD1	1:F:36:PRO:CB	2.93	0.46
1:A:81:GLU:HA	1:A:81:GLU:OE1	2.15	0.46
1:D:56:GLN:HB3	5:D:546:HOH:O	2.14	0.46
1:F:20:HIS:C	1:F:23:LYS:HZ1	2.24	0.46
1:E:37:GLU:HG2	5:E:485:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66[A]:ARG:HD3	1:A:226:GLN:HG3	1.96	0.45
1:E:27:VAL:O	5:E:401:HOH:O	2.21	0.45
1:F:226:GLN:HG2	1:F:226:GLN:O	2.16	0.45
1:A:174:THR:O	1:A:177:GLN:HG2	2.16	0.45
1:B:50:GLN:HA	1:B:50:GLN:HE21	1.82	0.45
1:C:249:ILE:HG22	1:C:253:LYS:HE2	1.99	0.45
1:F:68:GLU:HG3	1:F:207:LEU:HD22	1.98	0.44
1:E:63:LEU:HD11	1:E:230:VAL:HG12	1.99	0.44
1:F:23:LYS:H	1:F:23:LYS:CD	2.30	0.44
1:B:128:TRP:CH2	1:B:164:GLU:HA	2.52	0.44
1:E:27:VAL:HG11	1:F:18:VAL:HA	1.98	0.44
1:F:23:LYS:H	1:F:23:LYS:HE2	1.82	0.44
1:F:56:GLN:O	1:F:60:GLN:HG2	2.17	0.44
1:B:103:VAL:HG13	1:B:242:GLN:HB2	1.99	0.44
1:C:44:GLU:O	1:C:48:GLN:HG3	2.18	0.44
1:F:23:LYS:N	1:F:23:LYS:CD	2.80	0.44
1:A:22:ASP:OD1	1:B:31:TYR:HE2	2.00	0.44
1:A:107:LEU:HD11	1:A:245:LEU:HB2	1.99	0.44
1:C:47:HIS:O	1:C:51:GLN:HG2	2.18	0.44
1:D:146:GLY:CA	3:D:301:EDO:H12	2.45	0.44
1:B:225:THR:HG23	1:B:227:ASP:O	2.16	0.44
1:A:37:GLU:OE1	5:A:402:HOH:O	2.21	0.44
1:E:151:LEU:HD23	1:E:151:LEU:HA	1.85	0.44
1:A:21:PRO:HB3	1:B:27:VAL:HG13	2.00	0.43
1:D:148:ALA:H	3:D:301:EDO:HO2	1.61	0.43
1:F:9:ILE:N	1:F:12:THR:HG22	2.33	0.43
1:F:30:THR:HG22	1:F:34:GLU:OE2	2.18	0.43
1:A:115:ARG:NH1	1:A:117:ILE:HD11	2.33	0.43
1:F:229:ASP:OD1	1:F:231:LYS:HG2	2.17	0.43
1:D:162:LYS:HD3	1:D:166:ALA:HB1	2.00	0.43
1:E:81:GLU:OE1	1:E:81:GLU:HA	2.18	0.43
1:F:122:PRO:HB2	1:F:125:SER:HB3	2.00	0.43
1:C:84:ALA:O	1:C:114:THR:HG23	2.19	0.42
1:A:32:LEU:HB3	1:A:38:PHE:CE1	2.55	0.42
1:B:244:MET:HE1	1:F:231:LYS:O	2.19	0.42
1:B:95:SER:HB2	1:B:164:GLU:OE1	2.19	0.42
1:E:12:THR:HB	1:F:9:ILE:HD11	2.01	0.42
1:B:137:VAL:O	1:B:141:VAL:HG23	2.20	0.42
1:A:37:GLU:H	1:A:37:GLU:CD	2.28	0.42
1:D:11:PRO:HG3	1:F:16:TYR:CE2	2.55	0.42
1:A:144:THR:HG21	1:A:184:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:151:LEU:O	1:E:154:HIS:HB3	2.19	0.41
4:A:303:PGE:C2	1:C:152[B]:ASP:OD1	2.60	0.41
1:C:189:LYS:HB2	1:C:189:LYS:HE3	1.94	0.41
1:E:68:GLU:HG3	1:E:207:LEU:HD22	2.03	0.41
1:B:58:TYR:HE2	1:B:237:PRO:HG3	1.83	0.41
1:B:76:SER:HA	1:B:116:PHE:O	2.20	0.41
1:F:9:ILE:HG23	1:F:10:GLY:N	2.36	0.41
1:A:107:LEU:HD11	1:A:245:LEU:CB	2.51	0.41
1:C:37[A]:GLU:CD	1:C:37[A]:GLU:H	2.29	0.41
1:D:231:LYS:O	1:D:251:LYS:HE3	2.21	0.41
1:D:162:LYS:HA	1:D:162:LYS:HE2	2.02	0.40
1:A:75:PRO:HA	1:A:142:TRP:CE2	2.56	0.40
1:C:139:GLU:O	1:C:143:LEU:HG	2.22	0.40
1:F:66:ARG:HG3	1:F:222:MET:HE2	2.02	0.40
1:C:247:MET:HE3	1:C:247:MET:HB2	1.92	0.40
1:D:36:PRO:HG2	1:F:46:LEU:HD23	2.04	0.40
1:F:216:THR:HB	1:F:217:PRO:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	252/254 (99%)	250 (99%)	1 (0%)	1 (0%)	30	37
1	B	250/254 (98%)	248 (99%)	2 (1%)	0	100	100
1	C	249/254 (98%)	245 (98%)	4 (2%)	0	100	100
1	D	243/254 (96%)	240 (99%)	3 (1%)	0	100	100
1	E	243/254 (96%)	236 (97%)	6 (2%)	1 (0%)	30	37
1	F	244/254 (96%)	240 (98%)	4 (2%)	0	100	100
All	All	1481/1524 (97%)	1459 (98%)	20 (1%)	2 (0%)	48	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	122	PRO
1	A	122	PRO

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	207/206 (100%)	207 (100%)	0	100	100
1	B	205/206 (100%)	205 (100%)	0	100	100
1	C	205/206 (100%)	205 (100%)	0	100	100
1	D	200/206 (97%)	200 (100%)	0	100	100
1	E	200/206 (97%)	200 (100%)	0	100	100
1	F	200/206 (97%)	200 (100%)	0	100	100
All	All	1217/1236 (98%)	1217 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	A	246	GLN
1	B	48	GLN
1	B	178	HIS
1	C	51	GLN
1	C	111	ASN
1	C	246	GLN
1	C	250	GLN
1	D	170	HIS
1	D	205	GLN
1	D	209	GLN
1	E	111	ASN
1	E	155	ASN

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Mol	Chain	Res	Type
1	E	246	GLN
1	E	250	GLN
1	F	111	ASN
1	F	154	HIS
1	F	246	GLN
1	F	250	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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	302	-	3,3,3	0.46	0	2,2,2	0.50	0
4	PGE	A	303	-	9,9,9	0.59	0	8,8,8	0.72	0
3	EDO	A	306	-	3,3,3	0.58	0	2,2,2	0.13	0
3	EDO	D	303	-	3,3,3	0.57	0	2,2,2	0.35	0
3	EDO	A	308	-	3,3,3	0.57	0	2,2,2	0.30	0
3	EDO	F	304	-	3,3,3	0.53	0	2,2,2	0.51	0
3	EDO	F	302	-	3,3,3	0.48	0	2,2,2	0.43	0
3	EDO	F	303	-	3,3,3	0.53	0	2,2,2	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	E	304	-	3,3,3	0.42	0	2,2,2	0.15	0
3	EDO	C	303	-	3,3,3	0.53	0	2,2,2	0.19	0
3	EDO	A	307	-	3,3,3	0.54	0	2,2,2	0.43	0
3	EDO	D	301	-	3,3,3	0.39	0	2,2,2	0.50	0
3	EDO	E	301	-	3,3,3	0.47	0	2,2,2	0.65	0
3	EDO	D	302	-	3,3,3	0.45	0	2,2,2	0.46	0
3	EDO	E	305	-	3,3,3	0.42	0	2,2,2	0.49	0
3	EDO	E	302	-	3,3,3	0.42	0	2,2,2	0.51	0
3	EDO	A	304	-	3,3,3	0.46	0	2,2,2	0.84	0
3	EDO	A	305	-	3,3,3	0.58	0	2,2,2	0.35	0
3	EDO	E	303	-	3,3,3	0.52	0	2,2,2	0.12	0
3	EDO	C	302	-	3,3,3	0.44	0	2,2,2	0.70	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	302	-	-	0/1/1/1	-
4	PGE	A	303	-	-	3/7/7/7	-
3	EDO	A	306	-	-	0/1/1/1	-
3	EDO	D	303	-	-	1/1/1/1	-
3	EDO	A	308	-	-	0/1/1/1	-
3	EDO	F	304	-	-	1/1/1/1	-
3	EDO	F	302	-	-	0/1/1/1	-
3	EDO	F	303	-	-	0/1/1/1	-
3	EDO	E	304	-	-	0/1/1/1	-
3	EDO	C	303	-	-	0/1/1/1	-
3	EDO	A	307	-	-	1/1/1/1	-
3	EDO	D	301	-	-	0/1/1/1	-
3	EDO	E	301	-	-	0/1/1/1	-
3	EDO	D	302	-	-	1/1/1/1	-
3	EDO	E	305	-	-	0/1/1/1	-
3	EDO	E	302	-	-	0/1/1/1	-
3	EDO	A	304	-	-	0/1/1/1	-
3	EDO	A	305	-	-	0/1/1/1	-
3	EDO	E	303	-	-	1/1/1/1	-
3	EDO	C	302	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	PGE	O2-C3-C4-O3
4	A	303	PGE	O3-C5-C6-O4
3	D	303	EDO	O1-C1-C2-O2
3	E	303	EDO	O1-C1-C2-O2
3	A	307	EDO	O1-C1-C2-O2
3	C	302	EDO	O1-C1-C2-O2
3	D	302	EDO	O1-C1-C2-O2
3	F	304	EDO	O1-C1-C2-O2
4	A	303	PGE	C1-C2-O2-C3

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	303	PGE	10	0
3	E	304	EDO	1	0
3	D	301	EDO	3	0
3	E	303	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	253/254 (99%)	-0.50	2 (0%) 82 84	20, 29, 58, 91	1 (0%)
1	B	251/254 (98%)	-0.42	3 (1%) 76 78	13, 34, 58, 118	1 (0%)
1	C	248/254 (97%)	-0.25	4 (1%) 70 72	14, 36, 69, 130	3 (1%)
1	D	244/254 (96%)	-0.30	6 (2%) 58 61	20, 34, 79, 108	1 (0%)
1	E	245/254 (96%)	-0.05	13 (5%) 32 34	22, 39, 93, 145	0
1	F	246/254 (96%)	-0.19	11 (4%) 38 40	20, 40, 95, 112	0
All	All	1487/1524 (97%)	-0.28	39 (2%) 57 60	13, 35, 79, 145	6 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	228	GLY	4.9
1	D	11	PRO	3.8
1	C	96	TRP	3.5
1	C	228	GLY	3.1
1	E	9	ILE	3.0
1	F	9	ILE	3.0
1	F	254	GLY	3.0
1	E	230	VAL	3.0
1	E	128	TRP	2.9
1	E	50	GLN	2.9
1	C	7	SER	2.9
1	F	13	ALA	2.8
1	E	227	ASP	2.8
1	F	17	ILE	2.7
1	D	13	ALA	2.7
1	F	16	TYR	2.6
1	E	225	THR	2.6
1	E	51	GLN	2.6
1	D	163	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	11	PRO	2.5
1	B	227	ASP	2.4
1	A	226	GLN	2.3
1	E	229	ASP	2.3
1	C	254	GLY	2.3
1	D	164	GLU	2.3
1	F	18	VAL	2.3
1	A	2	ASP	2.2
1	F	228	GLY	2.2
1	E	15	ALA	2.2
1	B	225	THR	2.1
1	E	10	GLY	2.1
1	E	23	LYS	2.1
1	F	231	LYS	2.1
1	D	17	ILE	2.1
1	D	22	ASP	2.1
1	F	21	PRO	2.1
1	E	13	ALA	2.1
1	F	227	ASP	2.1
1	F	12	THR	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	F	302	4/4	0.57	0.20	58,70,75,75	0
3	EDO	E	302	4/4	0.73	0.20	55,66,72,72	0
3	EDO	A	308	4/4	0.76	0.18	46,55,60,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	D	303	4/4	0.83	0.20	48,58,63,65	0
3	EDO	E	303	4/4	0.84	0.17	38,51,62,62	0
3	EDO	E	304	4/4	0.84	0.17	39,47,52,62	0
2	MG	A	301	1/1	0.84	0.15	54,54,54,54	0
4	PGE	A	303	10/10	0.84	0.12	33,43,48,51	0
3	EDO	A	306	4/4	0.87	0.14	44,53,59,59	0
3	EDO	C	303	4/4	0.87	0.20	45,54,60,60	0
3	EDO	C	302	4/4	0.88	0.15	39,48,58,59	0
3	EDO	E	305	4/4	0.89	0.27	40,48,50,56	0
3	EDO	A	305	4/4	0.89	0.15	26,37,48,49	0
3	EDO	D	301	4/4	0.89	0.17	41,49,53,58	0
3	EDO	A	307	4/4	0.90	0.21	26,36,44,48	0
3	EDO	F	304	4/4	0.90	0.21	32,39,47,56	0
3	EDO	A	302	4/4	0.90	0.13	35,43,51,52	0
3	EDO	A	304	4/4	0.91	0.15	29,36,38,44	0
3	EDO	E	301	4/4	0.93	0.13	28,34,39,47	0
3	EDO	F	303	4/4	0.94	0.11	42,51,59,61	0
2	MG	B	301	1/1	0.95	0.05	41,41,41,41	0
3	EDO	D	302	4/4	0.95	0.09	37,46,55,59	0
2	MG	F	301	1/1	0.97	0.08	36,36,36,36	0
2	MG	C	301	1/1	0.98	0.11	38,38,38,38	0

6.5 Other polymers ⓘ

There are no such residues in this entry.