



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:26 AM UTC

PDB ID : 4AUK / pdb_00004auk
Title : Crystal structure of C2498 2'-O-ribose methyltransferase RlmM from Escherichia coli
Authors : Puneekar, A.S.; Shepherd, T.R.; Liljeruhm, J.; Forster, A.C.; Selmer, M.
Deposited on : 2012-05-18
Resolution : 1.90 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

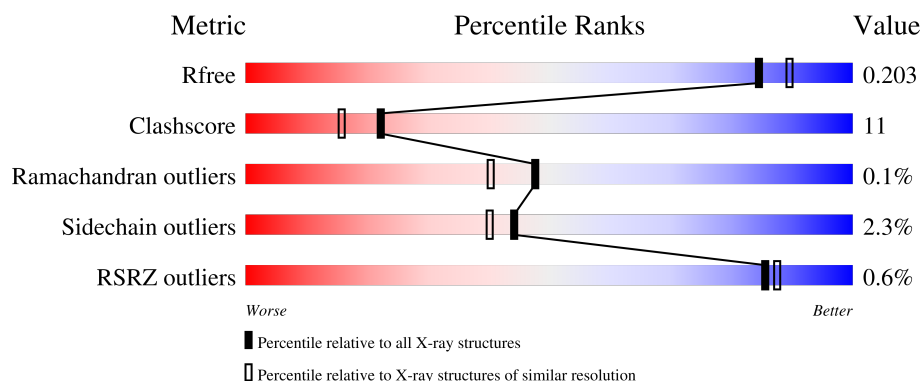
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 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	375	78% 16% • 5%
1	B	375	79% 15% • 5%

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	TRS	A	1362	-	X	X	-
6	PEG	A	1364	-	-	X	-
7	PGE	A	1366	-	-	X	-
8	EDO	A	1368	-	-	X	-
8	EDO	A	1369	-	-	X	-
8	EDO	A	1375	-	-	X	-
8	EDO	B	1361	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6517 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 RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	5	0
			2913	1867	508	516	22			
1	B	355	Total	C	N	O	S	0	6	0
			2895	1855	505	512	23			

There are 18 discrepancies between the modelled and reference sequences:

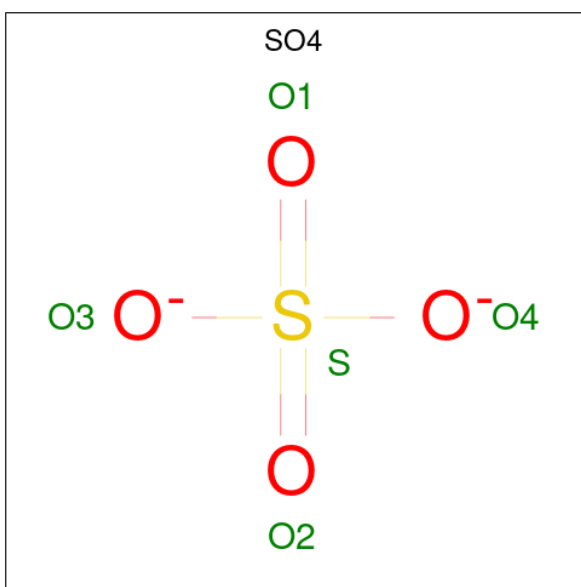
Chain	Residue	Modelled	Actual	Comment	Reference
A	367	SER	-	expression tag	UNP P0ADR6
A	368	LYS	-	expression tag	UNP P0ADR6
A	369	GLY	-	expression tag	UNP P0ADR6
A	370	HIS	-	expression tag	UNP P0ADR6
A	371	HIS	-	expression tag	UNP P0ADR6
A	372	HIS	-	expression tag	UNP P0ADR6
A	373	HIS	-	expression tag	UNP P0ADR6
A	374	HIS	-	expression tag	UNP P0ADR6
A	375	HIS	-	expression tag	UNP P0ADR6
B	367	SER	-	expression tag	UNP P0ADR6
B	368	LYS	-	expression tag	UNP P0ADR6
B	369	GLY	-	expression tag	UNP P0ADR6
B	370	HIS	-	expression tag	UNP P0ADR6
B	371	HIS	-	expression tag	UNP P0ADR6
B	372	HIS	-	expression tag	UNP P0ADR6
B	373	HIS	-	expression tag	UNP P0ADR6
B	374	HIS	-	expression tag	UNP P0ADR6
B	375	HIS	-	expression tag	UNP P0ADR6

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



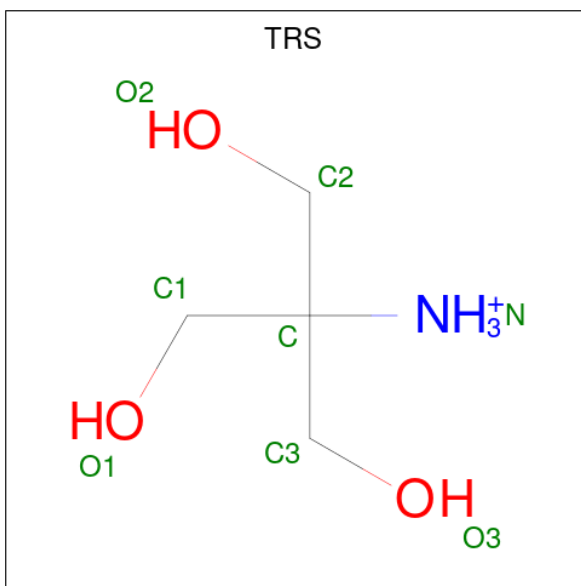
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



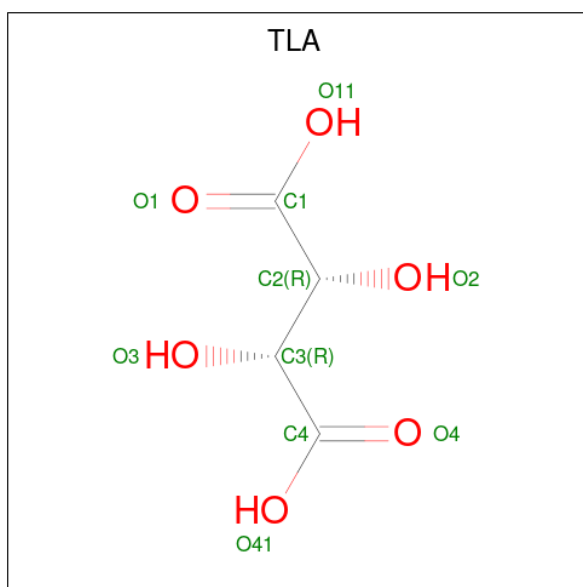
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



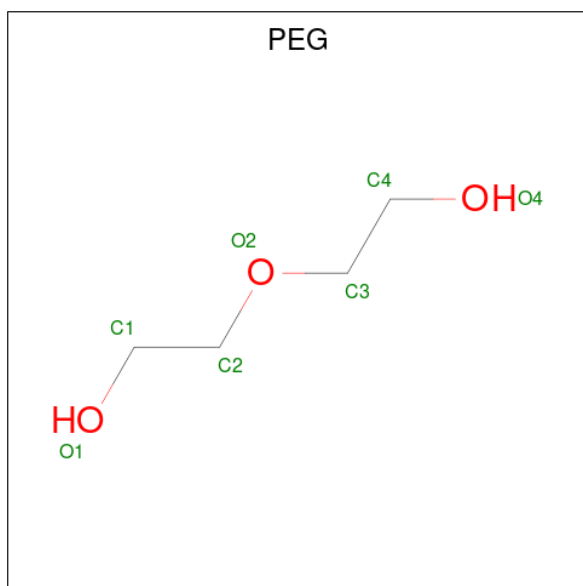
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C₄H₆O₆).



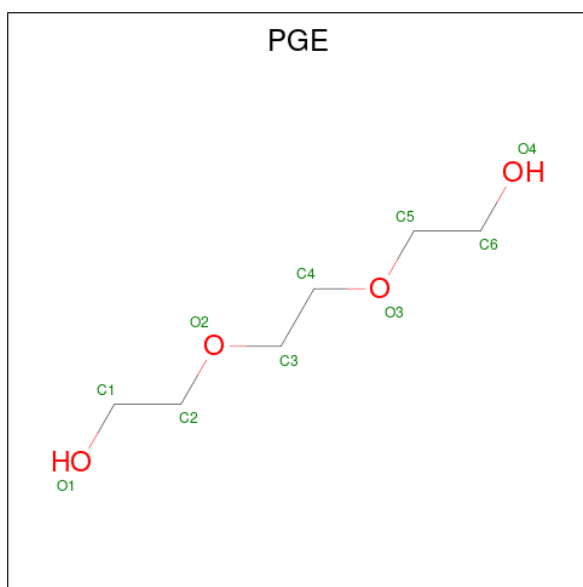
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	4	6		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



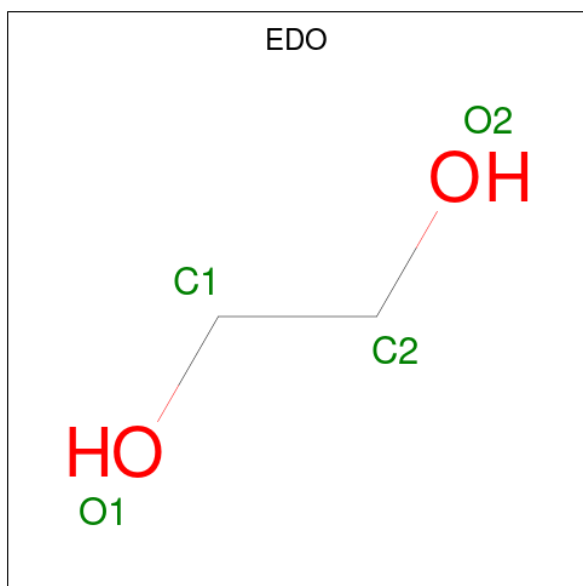
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



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

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	336	Total O 336 336	0	0
9	B	216	Total O 216 216	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	132.80Å 132.80Å 41.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.12 – 1.90 20.12 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.12-1.90) 99.6 (20.12-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.91Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.164 , 0.206 0.160 , 0.203	Depositor DCC
R_{free} test set	3215 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 46.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l 0.025 for h,-h-k,-l 0.018 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6517	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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: TLA, EDO, PEG, TRS, SO4, GOL, CSS, 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	0.90	1/2988 (0.0%)	0.98	5/4047 (0.1%)
1	B	0.81	0/2971	0.94	4/4022 (0.1%)
All	All	0.85	1/5959 (0.0%)	0.96	9/8069 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	34	ARG	CB-CG	-5.80	1.35	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	242	GLY	CA-C-N	8.66	129.18	119.83
1	B	242	GLY	C-N-CA	8.66	129.18	119.83
1	A	267	THR	N-CA-C	-6.52	99.40	109.24
1	A	48	GLN	CA-C-N	6.37	126.86	119.47
1	A	48	GLN	C-N-CA	6.37	126.86	119.47
1	A	78	GLN	CA-C-N	-5.72	113.98	123.37
1	A	78	GLN	C-N-CA	-5.72	113.98	123.37
1	B	211	ASN	CB-CA-C	5.66	119.12	109.72
1	B	254	VAL	N-CA-C	5.17	115.35	108.11

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	2913	0	2890	75	0
1	B	2895	0	2883	47	0
2	A	18	0	24	2	0
2	B	24	0	32	4	0
3	A	5	0	0	0	0
4	A	8	0	12	7	0
5	A	10	0	4	0	0
6	A	14	0	20	8	0
7	A	10	0	14	9	0
8	A	44	0	66	33	0
8	B	24	0	36	7	0
9	A	336	0	0	6	0
9	B	216	0	0	5	0
All	All	6517	0	5981	126	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 11.

All (126) 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:312:ARG:HH12	8:A:1374:EDO:H12	1.25	0.96
1:A:282:PRO:HG2	8:A:1375:EDO:H21	1.57	0.86
4:A:1362:TRS:H21	1:B:48:GLN:HE21	1.41	0.83
1:B:26:GLN:HE22	8:B:1361:EDO:H21	1.43	0.83
1:A:308:PRO:HG3	1:A:315:GLU:HG3	1.62	0.81
1:A:26:GLN:HE22	8:A:1367:EDO:H21	1.46	0.80
1:B:337:GLN:HA	2:B:1357:GOL:H12	1.63	0.80
1:B:140:TYR:H	2:B:1358:GOL:H11	1.51	0.74
1:B:34:ARG:NH2	9:B:2033:HOH:O	2.21	0.72
1:A:14:LYS:HB2	8:A:1369:EDO:H12	1.72	0.71
1:A:319:ASN:HD21	8:A:1375:EDO:H12	1.57	0.70
1:B:140:TYR:HD1	2:B:1358:GOL:H12	1.56	0.68
1:B:211:ASN:HB2	1:B:233:ASN:HB2	1.76	0.68
1:A:283:ALA:HB2	8:A:1375:EDO:H11	1.76	0.68
1:A:34:ARG:NH1	1:B:34:ARG:NH2	2.41	0.67
1:A:34:ARG:NH1	1:B:34:ARG:HH22	1.94	0.66
8:A:1374:EDO:H11	9:A:2322:HOH:O	1.95	0.65
1:A:282:PRO:CG	8:A:1375:EDO:H21	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1362:TRS:H21	1:B:48:GLN:NE2	2.12	0.65
1:A:14:LYS:H	8:A:1369:EDO:C1	2.10	0.64
1:A:337:GLN:HB2	8:A:1368:EDO:H22	1.78	0.64
1:A:109:ASP:OD1	8:A:1371:EDO:H11	1.98	0.64
1:B:214:TRP:CG	1:B:268:ARG:HH22	2.16	0.64
4:A:1362:TRS:H32	9:A:2017:HOH:O	1.99	0.63
1:A:315:GLU:OE1	8:A:1375:EDO:O1	2.17	0.63
4:A:1362:TRS:C2	1:B:48:GLN:HE21	2.11	0.62
1:A:23:LYS:NZ	7:A:1366:PGE:H4	2.15	0.62
1:A:312:ARG:NH1	8:A:1374:EDO:H12	2.06	0.61
1:A:335:GLN:HG3	1:A:355:ILE:HD11	1.82	0.61
1:A:14:LYS:HE3	1:A:37:GLU:OE2	2.00	0.61
1:B:14:LYS:HG3	8:B:1364:EDO:H11	1.81	0.61
1:A:259:GLU:HB3	6:A:1365:PEG:H12	1.83	0.60
1:A:104:ARG:HA	8:A:1377:EDO:H21	1.84	0.60
1:B:125:VAL:HB	1:B:126:PRO:HD3	1.85	0.59
1:A:241:ASN:HD21	6:A:1365:PEG:H41	1.68	0.58
1:B:77:LEU:HD11	1:B:92:MET:SD	2.44	0.57
1:A:14:LYS:HG3	8:A:1369:EDO:H22	1.85	0.57
1:A:13:GLU:HB2	8:A:1369:EDO:H21	1.86	0.57
1:B:77:LEU:HD11	1:B:92:MET:HG3	1.86	0.56
1:B:59:LEU:HD12	1:B:60:PRO:HD2	1.86	0.56
1:A:65:ILE:HG12	7:A:1366:PGE:H6	1.88	0.56
1:A:77:LEU:HD21	1:A:92:MET:HE3	1.87	0.56
1:B:117:LEU:HA	1:B:120[B]:CYS:SG	2.46	0.56
8:B:1361:EDO:O1	9:B:2025:HOH:O	2.16	0.56
1:B:63:SER:HA	2:B:1357:GOL:H11	1.88	0.55
1:A:2:ASN:HD22	1:A:2:ASN:H	1.55	0.55
1:A:103:LEU:O	8:A:1377:EDO:H21	2.07	0.55
1:A:333[B]:ASN:ND2	9:A:2308:HOH:O	2.36	0.55
1:A:23:LYS:HE2	8:A:1367:EDO:H22	1.88	0.54
1:B:335:GLN:HG3	1:B:355:ILE:HD11	1.90	0.54
1:A:172:TYR:N	8:A:1372:EDO:H21	2.22	0.54
1:A:14:LYS:H	8:A:1369:EDO:C2	2.20	0.54
1:B:256:TRP:CE2	1:B:258:ARG:HG2	2.43	0.54
1:B:26:GLN:HE22	8:B:1361:EDO:C2	2.17	0.53
1:B:111:ASN:HA	1:B:114:LYS:HE2	1.91	0.53
1:A:282:PRO:CD	8:A:1375:EDO:H21	2.38	0.53
1:B:90:VAL:HG22	1:B:131:LEU:HD23	1.91	0.52
1:A:14:LYS:H	8:A:1369:EDO:H21	1.74	0.52
1:A:26:GLN:HE22	8:A:1367:EDO:C2	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:LYS:HD3	9:B:2128:HOH:O	2.11	0.51
1:A:263:LYS:HB2	6:A:1365:PEG:H21	1.93	0.50
1:B:77:LEU:HD21	1:B:92:MET:HG3	1.94	0.50
1:A:59[B]:LEU:HD22	1:A:60:PRO:HD2	1.94	0.50
1:A:283:ALA:HB2	8:A:1375:EDO:C1	2.40	0.49
1:A:2:ASN:HD21	1:A:3:LYS:NZ	2.09	0.49
1:A:172:TYR:H	8:A:1372:EDO:H21	1.76	0.49
1:B:176:PRO:HG2	1:B:194:GLU:HG3	1.94	0.49
1:B:196:PHE:HB3	1:B:205:TRP:CZ2	2.48	0.48
1:A:132:ARG:HD3	1:A:139:ASN:HA	1.96	0.48
1:A:63:SER:O	7:A:1366:PGE:H62	2.13	0.47
1:A:62:SER:O	8:A:1368:EDO:H21	2.14	0.47
1:A:23:LYS:HZ3	7:A:1366:PGE:H4	1.79	0.47
1:A:308:PRO:HG3	1:A:315:GLU:CG	2.38	0.47
1:A:282:PRO:HD2	8:A:1375:EDO:H21	1.97	0.47
1:A:34:ARG:CZ	1:B:34:ARG:NH2	2.78	0.47
1:A:314:GLU:CD	4:A:1362:TRS:H12	2.40	0.46
1:A:244:MET:HE3	1:A:244:MET:HB3	1.76	0.46
1:B:72:VAL:O	1:B:161:GLY:HA3	2.16	0.46
1:A:23:LYS:HZ1	7:A:1366:PGE:H4	1.80	0.46
1:A:294:VAL:HA	1:A:332:ILE:HD13	1.98	0.45
1:B:166:ASN:HD21	8:B:1362:EDO:H12	1.81	0.45
1:A:36:LYS:HD2	2:A:1358:GOL:H31	1.98	0.45
1:A:57:ARG:HA	6:A:1364:PEG:H42	1.99	0.45
7:A:1366:PGE:H12	9:A:2029:HOH:O	2.16	0.45
1:B:77:LEU:HD11	1:B:92:MET:CG	2.46	0.45
1:A:48:GLN:HA	1:A:49:PRO:HD3	1.82	0.45
1:A:166:ASN:OD1	6:A:1364:PEG:H31	2.16	0.45
1:A:72:VAL:O	1:A:161:GLY:HA3	2.17	0.44
1:A:199:PHE:CD1	8:A:1368:EDO:H11	2.53	0.44
1:B:312:ARG:O	1:B:316[B]:VAL:HG22	2.18	0.44
1:A:177:ARG:NH2	8:A:1371:EDO:O1	2.39	0.44
1:A:319:ASN:HD21	8:A:1375:EDO:C1	2.28	0.44
1:A:333[B]:ASN:ND2	1:A:355:ILE:HB	2.33	0.44
1:B:296:GLY:HA2	1:B:354[A]:ARG:NH1	2.34	0.43
1:B:93:LEU:O	1:B:96:VAL:HG12	2.19	0.43
1:A:63:SER:C	7:A:1366:PGE:H62	2.43	0.43
1:A:309:MET:SD	2:A:1360:GOL:H11	2.59	0.43
1:A:57:ARG:O	6:A:1364:PEG:H42	2.19	0.43
1:B:76:LEU:HB2	1:B:159:TYR:CE1	2.52	0.43
1:A:81:PRO:HB3	1:A:83[B]:GLU:OE2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:GLU:OE2	4:A:1362:TRS:H12	2.19	0.42
1:B:354[B]:ARG:HE	1:B:354[B]:ARG:HB3	1.62	0.42
1:A:274:MET:HE1	1:A:289:MET:SD	2.58	0.42
1:B:327:LEU:HD13	1:B:334:ALA:HB3	2.01	0.42
1:A:282:PRO:HG3	1:A:306:LYS:O	2.18	0.42
1:B:294[A]:VAL:HA	1:B:332:ILE:HD13	2.01	0.42
1:B:282:PRO:HG2	9:B:2177:HOH:O	2.18	0.42
1:A:79:HIS:O	1:A:81:PRO:HD3	2.20	0.42
7:A:1366:PGE:H42	9:A:2333:HOH:O	2.18	0.42
1:B:37:GLU:HA	8:B:1364:EDO:O1	2.19	0.42
1:A:2:ASN:HD22	1:A:2:ASN:N	2.15	0.41
1:A:240:ASP:OD2	8:A:1373:EDO:H22	2.20	0.41
1:A:314:GLU:OE1	4:A:1362:TRS:H12	2.20	0.41
1:B:79:HIS:HD2	9:B:2067:HOH:O	2.03	0.41
1:A:199:PHE:CE1	8:A:1368:EDO:H11	2.55	0.41
1:A:167:ASN:CB	6:A:1364:PEG:H41	2.50	0.41
1:B:140:TYR:O	1:B:142:THR:HG22	2.21	0.41
1:B:59:LEU:HD12	1:B:60:PRO:CD	2.50	0.41
1:A:274:MET:O	1:A:301:THR:HA	2.20	0.41
1:B:211:ASN:CB	1:B:233:ASN:HB2	2.48	0.41
1:A:65:ILE:CG1	7:A:1366:PGE:H6	2.51	0.40
1:A:167:ASN:HB2	6:A:1364:PEG:H41	2.03	0.40
8:A:1370:EDO:H11	9:A:2220:HOH:O	2.21	0.40
1:B:123:PHE:O	1:B:126:PRO:HD2	2.20	0.40
8:B:1361:EDO:O2	8:B:1365:EDO:O2	2.33	0.40
1:B:77:LEU:O	1:B:157:CSS:HA	2.21	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	358/375 (96%)	348 (97%)	9 (2%)	1 (0%)	36	29
1	B	357/375 (95%)	346 (97%)	11 (3%)	0	100	100
All	All	715/750 (95%)	694 (97%)	20 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	ARG

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	308/317 (97%)	301 (98%)	7 (2%)	44	40
1	B	308/317 (97%)	301 (98%)	7 (2%)	44	40
All	All	616/634 (97%)	602 (98%)	14 (2%)	44	40

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	34	ARG
1	A	35	VAL
1	A	36	LYS
1	A	142	THR
1	A	207	GLU
1	A	306	LYS
1	B	86	ILE
1	B	92	MET
1	B	142	THR
1	B	211	ASN
1	B	299	ARG
1	B	304	ASN
1	B	345	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	26	GLN
1	A	139	ASN
1	A	319	ASN
1	B	26	GLN
1	B	38	ASN
1	B	48	GLN
1	B	79	HIS
1	B	304	ASN
1	B	337	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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
1	CSS	B	157	1	4,6,7	0.87	0	2,6,8	0.93	0
1	CSS	A	221	1	4,6,7	1.15	1 (25%)	2,6,8	1.09	0
1	CSS	B	221	1	4,6,7	1.25	1 (25%)	2,6,8	0.96	0
1	CSS	A	157	1	4,6,7	0.48	0	2,6,8	1.18	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
1	CSS	B	157	1	-	0/1/5/7	-
1	CSS	A	221	1	-	0/1/5/7	-
1	CSS	B	221	1	-	1/1/5/7	-
1	CSS	A	157	1	-	0/1/5/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	221	CSS	CB-SG	-2.23	1.74	1.81
1	A	221	CSS	CB-SG	-2.18	1.74	1.81

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	221	CSS	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	157	CSS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

30 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
8	EDO	B	1364	-	3,3,3	0.30	0	2,2,2	0.89	0
2	GOL	B	1357	-	5,5,5	0.67	0	5,5,5	1.05	0
2	GOL	A	1358	-	5,5,5	0.79	0	5,5,5	0.69	0
2	GOL	B	1359	-	5,5,5	0.33	0	5,5,5	0.87	0
8	EDO	B	1362	-	3,3,3	0.90	0	2,2,2	0.20	0
8	EDO	B	1363	-	3,3,3	0.59	0	2,2,2	0.08	0
6	PEG	A	1365	-	6,6,6	0.57	0	5,5,5	1.56	0
8	EDO	A	1368	-	3,3,3	0.18	0	2,2,2	0.81	0
5	TLA	A	1363	-	9,9,9	1.34	0	12,12,12	1.51	3 (25%)
6	PEG	A	1364	-	6,6,6	0.54	0	5,5,5	1.57	0
4	TRS	A	1362	-	7,7,7	0.73	0	9,9,9	2.60	5 (55%)
8	EDO	A	1375	-	3,3,3	0.42	0	2,2,2	0.38	0
3	SO4	A	1361	-	4,4,4	1.04	0	6,6,6	0.22	0
8	EDO	A	1371	-	3,3,3	0.61	0	2,2,2	0.61	0
8	EDO	A	1370	-	3,3,3	0.45	0	2,2,2	0.60	0
8	EDO	A	1377	-	3,3,3	0.46	0	2,2,2	0.32	0
8	EDO	A	1369	-	3,3,3	0.43	0	2,2,2	0.42	0
2	GOL	B	1358	-	5,5,5	0.39	0	5,5,5	0.54	0
8	EDO	A	1372	-	3,3,3	0.50	0	2,2,2	0.14	0
7	PGE	A	1366	-	9,9,9	0.66	0	8,8,8	1.88	4 (50%)
8	EDO	A	1376	-	3,3,3	0.52	0	2,2,2	0.34	0
8	EDO	A	1374	-	3,3,3	0.25	0	2,2,2	1.00	0
2	GOL	A	1359	-	5,5,5	0.50	0	5,5,5	0.94	0
8	EDO	B	1360	-	3,3,3	0.69	0	2,2,2	0.47	0
8	EDO	A	1367	-	3,3,3	0.48	0	2,2,2	0.48	0
8	EDO	B	1361	-	3,3,3	0.29	0	2,2,2	0.46	0
8	EDO	B	1365	-	3,3,3	0.25	0	2,2,2	0.57	0
2	GOL	B	1356	-	5,5,5	0.50	0	5,5,5	0.69	0
8	EDO	A	1373	-	3,3,3	0.50	0	2,2,2	0.35	0
2	GOL	A	1360	-	5,5,5	0.21	0	5,5,5	0.64	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
8	EDO	B	1364	-	-	1/1/1/1	-
2	GOL	B	1357	-	-	2/4/4/4	-
2	GOL	A	1358	-	-	0/4/4/4	-
2	GOL	B	1359	-	-	0/4/4/4	-
8	EDO	B	1362	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	EDO	B	1363	-	-	0/1/1/1	-
6	PEG	A	1365	-	-	1/4/4/4	-
8	EDO	A	1368	-	-	1/1/1/1	-
5	TLA	A	1363	-	-	0/12/12/12	-
6	PEG	A	1364	-	-	1/4/4/4	-
4	TRS	A	1362	-	-	5/9/9/9	-
8	EDO	A	1375	-	-	1/1/1/1	-
8	EDO	A	1371	-	-	1/1/1/1	-
8	EDO	A	1370	-	-	1/1/1/1	-
8	EDO	A	1377	-	-	1/1/1/1	-
8	EDO	A	1369	-	-	1/1/1/1	-
2	GOL	B	1358	-	-	1/4/4/4	-
8	EDO	A	1372	-	-	0/1/1/1	-
7	PGE	A	1366	-	-	2/7/7/7	-
8	EDO	A	1376	-	-	1/1/1/1	-
8	EDO	A	1374	-	-	0/1/1/1	-
2	GOL	A	1359	-	-	0/4/4/4	-
8	EDO	B	1360	-	-	1/1/1/1	-
8	EDO	A	1367	-	-	1/1/1/1	-
8	EDO	B	1361	-	-	1/1/1/1	-
8	EDO	B	1365	-	-	0/1/1/1	-
2	GOL	B	1356	-	-	0/4/4/4	-
8	EDO	A	1373	-	-	0/1/1/1	-
2	GOL	A	1360	-	-	0/4/4/4	-

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1362	TRS	C3-C-C2	4.55	122.78	110.66
4	A	1362	TRS	C1-C-N	3.72	117.66	108.17
4	A	1362	TRS	C3-C-N	-3.08	100.32	108.17
7	A	1366	PGE	O2-C2-C1	2.67	121.90	110.11
4	A	1362	TRS	C2-C-C1	-2.56	103.83	110.66
5	A	1363	TLA	O11-C1-C2	2.52	120.32	113.31
5	A	1363	TLA	O41-C4-C3	2.48	120.22	113.31
4	A	1362	TRS	C2-C-N	-2.46	101.90	108.17
7	A	1366	PGE	O1-C1-C2	2.28	125.24	111.82
7	A	1366	PGE	O3-C4-C3	2.17	120.22	110.35
7	A	1366	PGE	O2-C3-C4	2.16	120.20	110.35
5	A	1363	TLA	O11-C1-O1	-2.05	119.44	124.08

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1357	GOL	O1-C1-C2-C3
4	A	1362	TRS	C1-C-C2-O2
4	A	1362	TRS	N-C-C2-O2
2	B	1357	GOL	O1-C1-C2-O2
7	A	1366	PGE	O3-C5-C6-O4
8	A	1371	EDO	O1-C1-C2-O2
6	A	1365	PEG	O1-C1-C2-O2
8	A	1368	EDO	O1-C1-C2-O2
8	A	1376	EDO	O1-C1-C2-O2
8	B	1361	EDO	O1-C1-C2-O2
8	B	1362	EDO	O1-C1-C2-O2
8	B	1364	EDO	O1-C1-C2-O2
4	A	1362	TRS	C3-C-C2-O2
7	A	1366	PGE	O1-C1-C2-O2
6	A	1364	PEG	C1-C2-O2-C3
8	A	1375	EDO	O1-C1-C2-O2
8	A	1367	EDO	O1-C1-C2-O2
8	A	1370	EDO	O1-C1-C2-O2
8	A	1377	EDO	O1-C1-C2-O2
4	A	1362	TRS	C1-C-C3-O3
4	A	1362	TRS	N-C-C3-O3
8	B	1360	EDO	O1-C1-C2-O2
2	B	1358	GOL	O1-C1-C2-O2
8	A	1369	EDO	O1-C1-C2-O2

There are no ring outliers.

22 monomers are involved in 70 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	1364	EDO	2	0
2	B	1357	GOL	2	0
2	A	1358	GOL	1	0
8	B	1362	EDO	1	0
6	A	1365	PEG	3	0
8	A	1368	EDO	4	0
6	A	1364	PEG	5	0
4	A	1362	TRS	7	0
8	A	1375	EDO	9	0
8	A	1371	EDO	2	0
8	A	1370	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1377	EDO	2	0
8	A	1369	EDO	6	0
2	B	1358	GOL	2	0
8	A	1372	EDO	2	0
7	A	1366	PGE	9	0
8	A	1374	EDO	3	0
8	A	1367	EDO	3	0
8	B	1361	EDO	4	0
8	B	1365	EDO	1	0
8	A	1373	EDO	1	0
2	A	1360	GOL	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	355/375 (94%)	-0.66	3 (0%) 82 85	7, 16, 32, 47	5 (1%)
1	B	353/375 (94%)	-0.32	1 (0%) 90 91	9, 22, 41, 58	6 (1%)
All	All	708/750 (94%)	-0.49	4 (0%) 85 87	7, 19, 37, 58	11 (1%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	357	ALA	3.0
1	A	79	HIS	2.3
1	B	355	ILE	2.1
1	A	268	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSS	B	157	7/8	0.89	0.10	20,29,40,58	0
1	CSS	A	221	7/8	0.94	0.09	16,18,43,61	0
1	CSS	A	157	7/8	0.94	0.07	13,17,33,52	0
1	CSS	B	221	7/8	0.95	0.07	21,25,39,60	0

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($\text{\AA}^2$)	Q<0.9
2	GOL	B	1358	6/6	0.74	0.14	30,33,44,44	0
8	EDO	A	1370	4/4	0.79	0.13	31,34,37,48	0
8	EDO	B	1362	4/4	0.80	0.12	25,32,35,36	0
8	EDO	A	1376	4/4	0.81	0.12	33,38,41,43	0
8	EDO	A	1368	4/4	0.84	0.28	22,25,28,31	0
8	EDO	A	1375	4/4	0.84	0.17	25,30,31,33	0
8	EDO	B	1361	4/4	0.85	0.14	28,29,34,35	0
6	PEG	A	1364	7/7	0.85	0.11	23,31,42,43	0
8	EDO	A	1371	4/4	0.86	0.14	21,33,42,43	0
8	EDO	A	1374	4/4	0.86	0.14	21,30,32,37	0
8	EDO	A	1373	4/4	0.87	0.17	28,33,43,49	0
8	EDO	A	1369	4/4	0.88	0.22	12,24,30,42	0
8	EDO	B	1364	4/4	0.88	0.23	24,25,31,34	0
8	EDO	A	1372	4/4	0.90	0.17	25,29,32,35	0
6	PEG	A	1365	7/7	0.90	0.15	34,36,38,43	0
8	EDO	A	1367	4/4	0.90	0.13	23,28,33,41	0
2	GOL	A	1360	6/6	0.90	0.16	26,28,37,46	0
7	PGE	A	1366	10/10	0.91	0.10	19,26,38,44	0
4	TRS	A	1362	8/8	0.91	0.14	12,29,32,33	0
2	GOL	B	1357	6/6	0.92	0.10	20,25,30,33	0
8	EDO	B	1360	4/4	0.93	0.09	24,26,27,28	0
2	GOL	B	1359	6/6	0.93	0.09	22,25,26,32	0
5	TLA	A	1363	10/10	0.93	0.07	26,30,36,37	0
8	EDO	B	1363	4/4	0.93	0.09	31,31,33,37	0
3	SO4	A	1361	5/5	0.93	0.13	27,33,46,50	0
8	EDO	B	1365	4/4	0.93	0.13	24,28,33,35	0
2	GOL	A	1359	6/6	0.94	0.09	18,20,23,28	0
8	EDO	A	1377	4/4	0.94	0.14	14,18,31,47	0
2	GOL	A	1358	6/6	0.97	0.07	12,19,29,29	0
2	GOL	B	1356	6/6	0.98	0.05	16,19,22,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.