



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:59 PM UTC

PDB ID : 7Y9H / pdb_00007y9h
Title : Crystal structure of diterpene synthase VenA from *Streptomyces venezuelae* ATCC 15439
Authors : Zhang, L.L.; Xie, Z.Z.; Huang, J.-W.; Hu, Y.C.; Liu, W.D.; Yang, Y.; Chen, C.-C.; Guo, R.-T.
Deposited on : 2022-06-24
Resolution : 2.03 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

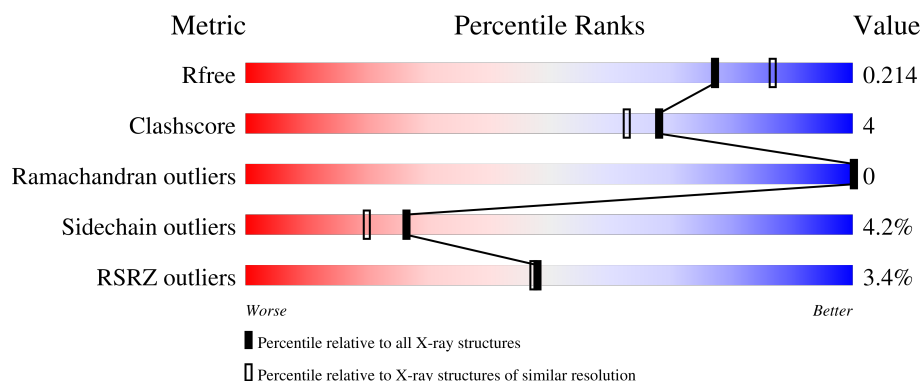
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

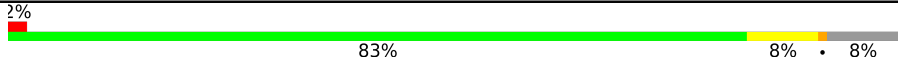
The reported resolution of this entry is 2.03 Å.

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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	377	
1	B	377	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5951 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.

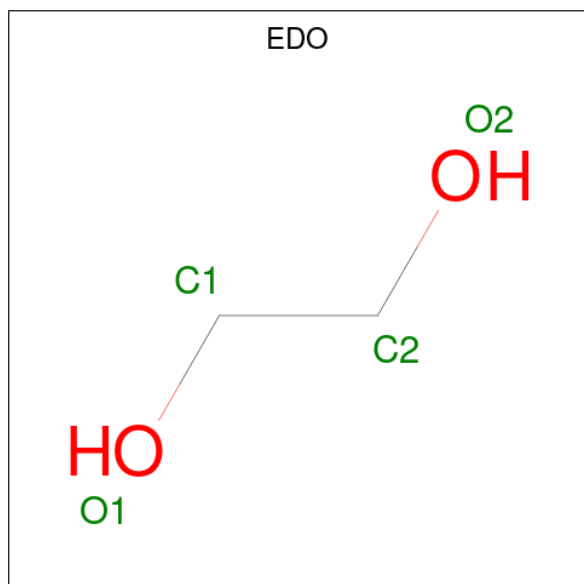
- Molecule 1 is a protein called Diterpene synthase VenA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	1	0
			2688	1694	480	502	12			
1	B	333	Total	C	N	O	S	0	0	0
			2592	1636	459	485	12			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

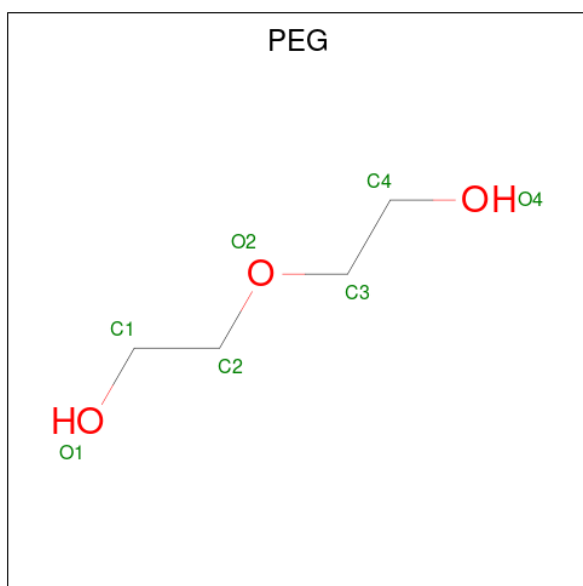
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	B	2	Total	Na	0	0
			2	2		

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



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	B	1	Total C O 4 2 2	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	363	Total O 363 363	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	263	Total 263	O 263	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	94.00Å 94.00Å 80.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.37 – 2.03 36.37 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.37-2.03) 99.9 (36.37-2.03)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.160 , 0.206 0.169 , 0.214	Depositor DCC
R_{free} test set	2578 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.177	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.006 for -h,-k,l 0.023 for h,-h-k,-l 0.014 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5951	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NA, PEG

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	1.03	0/2754	1.37	0/3740
1	B	1.06	0/2652	1.44	3/3600 (0.1%)
All	All	1.04	0/5406	1.41	3/7340 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	HIS	CA-C-N	5.50	127.59	120.44
1	B	203	HIS	C-N-CA	5.50	127.59	120.44
1	B	372	ALA	N-CA-C	5.07	112.78	108.22

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	2688	0	2582	22	0
1	B	2592	0	2479	16	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	24	0	36	2	0
3	B	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	7	0	10	0	0
4	B	7	0	10	0	0
5	A	363	0	0	9	0
5	B	263	0	0	4	0
All	All	5951	0	5123	38	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (38) 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:317:HIS:CD2	5:B:501:HOH:O	2.40	0.73
1:B:271:MET:HE3	1:B:271:MET:HA	1.73	0.69
1:B:247:HIS:HE1	5:B:689:HOH:O	1.75	0.69
1:B:314:PRO:O	5:B:501:HOH:O	2.13	0.66
1:A:247:HIS:HD2	1:A:299:HIS:ND1	1.95	0.65
1:A:164:ARG:HD2	5:A:671:HOH:O	1.96	0.65
1:B:247:HIS:HD2	1:B:299:HIS:ND1	1.97	0.62
1:B:188:GLY:O	1:B:191:GLU:HG2	2.02	0.58
1:B:211:ARG:HD3	1:B:271:MET:O	2.04	0.57
1:B:88:TYR:CZ	1:B:92:THR:HG21	2.41	0.56
1:B:281:GLU:OE2	5:B:502:HOH:O	2.18	0.54
1:A:151:ALA:H	1:A:160:GLN:HE22	1.57	0.52
1:B:123:ALA:HA	1:B:154:LEU:HD21	1.92	0.52
1:A:203:HIS:HD2	3:A:502:EDO:O1	1.92	0.51
1:A:344:ARG:NH1	5:A:613:HOH:O	2.42	0.51
1:A:187:ARG:NH2	5:A:620:HOH:O	2.45	0.50
1:A:151:ALA:H	1:A:160:GLN:NE2	2.09	0.49
1:A:262:ARG:NH1	5:A:615:HOH:O	2.43	0.48
1:B:90:PRO:HD3	1:B:105:ALA:HB2	1.95	0.48
1:B:341:LEU:HD23	1:B:352:TRP:HE3	1.79	0.47
1:A:160:GLN:NE2	5:A:619:HOH:O	2.44	0.47
1:A:262:ARG:CD	1:A:360:ILE:HD11	2.44	0.47
1:B:207:CYS:HB2	1:B:276:VAL:HG21	1.97	0.47
1:A:118:VAL:HA	1:A:124:LEU:HD13	1.97	0.46
1:A:262:ARG:NE	5:A:615:HOH:O	2.45	0.45
1:A:349:GLY:HA2	1:B:82:ARG:HD3	1.99	0.45
1:A:247:HIS:HE1	5:A:601:HOH:O	2.01	0.44
1:A:128:HIS:HE1	1:A:198:ASP:OD1	2.01	0.43
1:A:88:TYR:CD1	1:A:108:TYR:CG	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ARG:O	1:A:238:GLU:HG3	2.19	0.42
1:A:124:LEU:HA	1:A:134:THR:HG21	2.01	0.42
1:B:173:ARG:HD2	1:B:231:ASP:OD2	2.19	0.42
1:A:262:ARG:HD2	1:A:360:ILE:HD11	2.00	0.42
1:A:202:PRO:HG3	1:A:271:MET:SD	2.60	0.42
1:A:243:GLU:OE1	5:A:601:HOH:O	2.22	0.42
1:B:339:GLU:HG2	1:B:345:TYR:HE2	1.84	0.41
1:A:199:LYS:HA	1:A:269:ASP:OD2	2.20	0.41
3:A:504:EDO:O2	5:A:602:HOH:O	2.22	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	344/377 (91%)	343 (100%)	1 (0%)	0	100	100
1	B	327/377 (87%)	323 (99%)	4 (1%)	0	100	100
All	All	671/754 (89%)	666 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	269/297 (91%)	259 (96%)	10 (4%)	30	24
1	B	259/297 (87%)	246 (95%)	13 (5%)	22	15
All	All	528/594 (89%)	505 (96%)	23 (4%)	26	18

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65[A]	ARG
1	A	65[B]	ARG
1	A	87	ILE
1	A	197	LEU
1	A	263	LYS
1	A	271	MET
1	A	272	THR
1	A	291	ARG
1	A	341	LEU
1	A	360	ILE
1	B	43	LEU
1	B	65	ARG
1	B	76	SER
1	B	154	LEU
1	B	173	ARG
1	B	209	ARG
1	B	243	GLU
1	B	244	VAL
1	B	267	GLN
1	B	272	THR
1	B	277	LEU
1	B	295	LEU
1	B	366	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	HIS
1	A	160	GLN
1	A	203	HIS
1	A	247	HIS
1	B	203	HIS
1	B	247	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 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	504	-	3,3,3	0.07	0	2,2,2	0.20	0
3	EDO	A	506	-	3,3,3	0.06	0	2,2,2	0.17	0
3	EDO	A	502	-	3,3,3	0.16	0	2,2,2	0.10	0
3	EDO	B	404	-	3,3,3	0.13	0	2,2,2	0.24	0
3	EDO	A	507	-	3,3,3	0.28	0	2,2,2	0.31	0
4	PEG	B	401	-	6,6,6	0.31	0	5,5,5	0.16	0
3	EDO	A	505	-	3,3,3	0.20	0	2,2,2	0.26	0
3	EDO	A	503	-	3,3,3	0.54	0	2,2,2	0.66	0
4	PEG	A	508	-	6,6,6	0.25	0	5,5,5	0.14	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	504	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	506	-	-	1/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-
3	EDO	B	404	-	-	0/1/1/1	-
3	EDO	A	507	-	-	1/1/1/1	-
4	PEG	B	401	-	-	1/4/4/4	-
3	EDO	A	505	-	-	0/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
4	PEG	A	508	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	508	PEG	O1-C1-C2-O2
3	A	507	EDO	O1-C1-C2-O2
3	A	503	EDO	O1-C1-C2-O2
4	B	401	PEG	C1-C2-O2-C3
4	A	508	PEG	C4-C3-O2-C2
3	A	506	EDO	O1-C1-C2-O2
4	A	508	PEG	C1-C2-O2-C3
3	A	504	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504	EDO	1	0
3	A	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	345/377 (91%)	-0.27	7 (2%) 65 65	13, 25, 51, 81	1 (0%)
1	B	333/377 (88%)	0.10	16 (4%) 35 35	17, 31, 64, 86	0
All	All	678/754 (89%)	-0.09	23 (3%) 48 47	13, 27, 59, 86	1 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	270	THR	3.9
1	B	201	VAL	3.8
1	A	126	ALA	3.7
1	B	193	ILE	3.6
1	B	271	MET	3.5
1	A	125	GLY	3.3
1	A	375	PRO	3.1
1	B	202	PRO	3.0
1	B	154	LEU	3.0
1	B	123	ALA	3.0
1	B	31	GLY	3.0
1	B	372	ALA	2.8
1	B	32	PRO	2.8
1	A	269	ASP	2.7
1	B	317	HIS	2.6
1	B	129	ALA	2.5
1	A	267	GLN	2.5
1	B	373	PRO	2.4
1	B	266	ALA	2.4
1	B	33	GLY	2.2
1	A	268	ARG	2.2
1	B	173	ARG	2.1
1	B	363	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($\text{\AA}^2$)	Q<0.9
3	EDO	A	507	4/4	0.77	0.16	55,58,59,61	0
4	PEG	A	508	7/7	0.78	0.15	57,65,70,70	0
3	EDO	A	504	4/4	0.79	0.15	49,50,51,59	0
3	EDO	B	404	4/4	0.80	0.20	67,71,78,81	0
4	PEG	B	401	7/7	0.80	0.15	54,61,65,67	0
3	EDO	A	503	4/4	0.81	0.23	49,50,51,53	0
3	EDO	A	505	4/4	0.82	0.16	52,56,60,65	0
3	EDO	A	506	4/4	0.84	0.12	68,68,68,70	0
2	NA	B	403	1/1	0.88	0.17	45,45,45,45	0
3	EDO	A	502	4/4	0.96	0.08	29,32,34,34	0
2	NA	B	402	1/1	0.97	0.06	29,29,29,29	0
2	NA	A	501	1/1	0.99	0.11	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.