

wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 04:27 am BST

PDB ID	:	$4 \mathrm{JF0}$
Title	:	N79R mutant of N-acetylornithine aminotransferase
Authors	:	Bisht, S.; Bharath, S.R.; Murthy, M.R.N.
Deposited on	:	2013-02-27
Resolution	:	2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

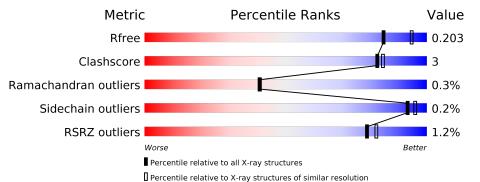
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	5197(2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647(2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	А	422	% 	5%	10%
1	В	422	% 	5%	9%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6144 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	Δ	379	Total	С	Ν	Ο	Р	\mathbf{S}	0	3	0
	I A		2875	1831	492	536	1	15			0
1	р	202	Total	С	Ν	0	Р	S	0	F	0
I B	383	2933	1876	508	532	1	16	0	G	0	

• Molecule 1 is a protein called Acetylornithine/succinyldiaminopimelate aminotransferase.

Chain	Residue	Modelled	Actual	Comment	Reference
А	-14	MET	-	EXPRESSION TAG	UNP P40732
A	-13	ARG	-	EXPRESSION TAG	UNP P40732
А	-12	GLY	_	EXPRESSION TAG	UNP P40732
А	-11	SER	_	EXPRESSION TAG	UNP P40732
А	-10	HIS	-	EXPRESSION TAG	UNP P40732
А	-9	HIS	_	EXPRESSION TAG	UNP P40732
A	-8	HIS	-	EXPRESSION TAG	UNP P40732
A	-7	HIS	-	EXPRESSION TAG	UNP P40732
A	-6	HIS	_	EXPRESSION TAG	UNP P40732
А	-5	HIS	_	EXPRESSION TAG	UNP P40732
A	-4	GLY	_	EXPRESSION TAG	UNP P40732
А	-3	MET	_	EXPRESSION TAG	UNP P40732
А	-2	ALA	_	EXPRESSION TAG	UNP P40732
А	-1	SER	-	EXPRESSION TAG	UNP P40732
А	0	HIS	_	EXPRESSION TAG	UNP P40732
A	79	ARG	ASN	ENGINEERED MUTATION	UNP P40732
А	298	THR	ALA	ENGINEERED MUTATION	UNP P40732
А	406	LEU	_	EXPRESSION TAG	UNP P40732
А	407	GLU	-	EXPRESSION TAG	UNP P40732
В	-14	MET	-	EXPRESSION TAG	UNP P40732
В	-13	ARG	-	EXPRESSION TAG	UNP P40732
В	-12	GLY	-	EXPRESSION TAG	UNP P40732
В	-11	SER	-	EXPRESSION TAG	UNP P40732
В	-10	HIS	-	EXPRESSION TAG	UNP P40732
В	-9	HIS	-	EXPRESSION TAG	UNP P40732

There are 38 discrepancies between the modelled and reference sequences:



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Chain

В

В

В

В

В

В

В

В

В

В

В

В

В

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Actual	Comment	Reference			
_	EXPRESSION TAG	UNP P40732			
-	EXPRESSION TAG	UNP P40732			
-	EXPRESSION TAG	UNP P40732			
_	EXPRESSION TAG	UNP P40732			
-	EXPRESSION TAG	UNP P40732			

EXPRESSION TAG

EXPRESSION TAG

EXPRESSION TAG

EXPRESSION TAG

ENGINEERED MUTATION

ENGINEERED MUTATION

EXPRESSION TAG

EXPRESSION TAG

Continued from previous page...

Modelled

HIS

HIS

HIS

HIS

GLY

MET

ALA

SER

HIS

ARG

THR

LEU

GLU

-

-

-

-

ASN

ALA

-

_

Residue

-8

-7

-6

-5

-4

-3

-2

-1

0

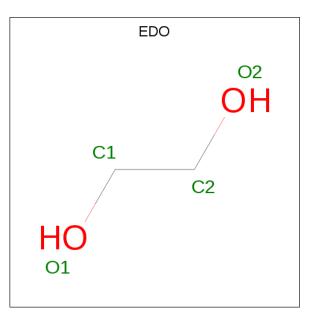
79

298

406

407

• Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

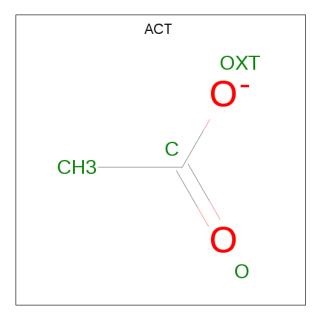


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

UNP P40732





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total Na 1 1	0	0
4	А	1	Total Na 1 1	0	0

• Molecule 5 is water.

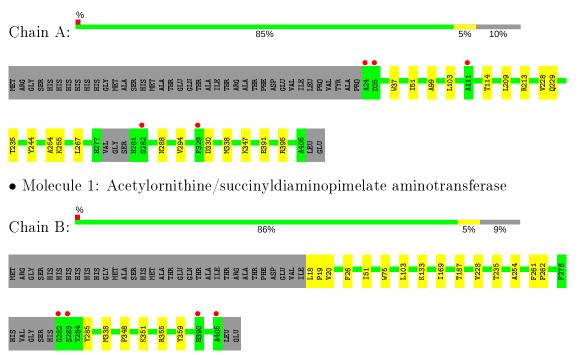
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	151	Total O 151 151	0	0
5	В	159	Total O 159 159	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

 $\bullet \ {\rm Molecule \ 1: \ Acetylornithine/succinyl$ $diaminopimelate \ aminotransferase}$





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	96.91Å 113.60 Å 69.18 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 - 2.10	Depositor
Resolution (A)	37.47 - 2.10	EDS
% Data completeness	99.1 (50.00-2.10)	Depositor
(in resolution range)	99.2(37.47-2.10)	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.27 (at 2.10 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
D D .	0.179 , 0.202	Depositor
R, R_{free}	0.178 , 0.203	DCC
R_{free} test set	2267 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	32.0	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , 45.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6144	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 4.17% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: NA, LLP, EDO, ACT

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	Bo	nd lengths	Bond angles		
	Unam	RMSZ # Z > 5		RMSZ	# Z > 5	
1	А	0.43	1/2924~(0.0%)	0.50	0/3966	
1	В	0.44	0/2990	0.50	0/4048	
All	All	0.43	1/5914~(0.0%)	0.50	0/8014	

All (1) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	А	37	TRP	CD2-CE2	5.20	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	2875	0	2768	12	0
1	В	2933	0	2892	18	0
2	А	8	0	12	0	0
2	В	8	0	12	0	0
3	А	4	0	3	0	0
3	В	4	0	3	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0

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001000										
Mol	Chain	Non-H	${ m H(model)}$	H(added)	Clashes	Symm-Clashes				
5	А	151	0	0	1	0				
5	В	159	0	0	0	0				
All	All	6144	0	5690	29	0				

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 29 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:235:THR:HB	1:A:338:MET:HE2	1.65	0.78
1:B:235:THR:HB	1:B:338:MET:HE2	1.70	0.74
1:B:18:LEU:HB3	1:B:19:PRO:HD3	1.76	0.67
1:B:355[B]:ARG:HH11	1:B:355[B]:ARG:CB	2.07	0.66
1:B:133[B]:LYS:HG3	1:B:169:ILE:HD13	1.78	0.65

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	А	377/422~(89%)	368~(98%)	8 (2%)	1 (0%)	41 41	
1	В	383/422 (91%)	372~(97%)	10 (3%)	1 (0%)	41 41	
All	All	760/844~(90%)	740 (97%)	18 (2%)	2(0%)	41 41	

All (2) Ramachandran outliers are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	51	ILE
1	А	51	ILE



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	А	286/329~(87%)	286~(100%)	0	100 100
1	В	295/329~(90%)	294 (100%)	1 (0%)	92 95
All	All	581/658~(88%)	580~(100%)	1 (0%)	93 96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	26	PHE

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

Mol	Chain	Res	Type
1	А	154	GLN
1	В	321	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)

2 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).



ſ	Mol	Turne	Chain	Res	Dog	Dog	Dog	Dog	Dog	Dog	Dog	Dog	Dec	Dog	Dec	Link	Bond lengths			B	ond ang	les
	WIOI	Type	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2											
	1	LLP	А	255	1	23,24,25	2.52	3 (13%)	25,32,34	1.33	2 (8%)											
	1	LLP	В	255	1	23,24,25	2.38	3 (13%)	25,32,34	1.36	4 (16%)											

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	\mathbf{Link}	Chirals	Torsions	Rings
1	LLP	А	255	1	-	3/16/17/19	0/1/1/1
1	LLP	В	255	1	-	3/16/17/19	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	А	255	LLP	C3-C2	8.27	1.49	1.40
1	В	255	LLP	C3-C2	7.89	1.48	1.40
1	А	255	LLP	C4-C5	6.16	1.49	1.42
1	В	255	LLP	C4-C3	5.45	1.49	1.40
1	В	255	LLP	C4-C5	5.44	1.48	1.42

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
1	А	255	LLP	C3-C4-C5	-3.19	115.81	118.26
1	В	255	LLP	CD-CE-NZ	-2.86	103.93	110.93
1	В	255	LLP	C4-C3-C2	-2.48	118.66	120.19
1	В	255	LLP	C6-N1-C2	2.31	123.44	119.17
1	В	255	LLP	C3-C4-C5	-2.25	116.54	118.26

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	А	255	LLP	O-C-CA-CB
1	А	255	LLP	CG-CD-CE-NZ
1	В	255	LLP	O-C-CA-CB
1	А	255	LLP	C4-C4'-NZ-CE
1	В	255	LLP	C4-C4'-NZ-CE

There are no ring outliers.



1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	А	255	LLP	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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).

Mal	Mol Type Chain R	Chain	Res	Link	B	Bond lengths			Bond angles		
		nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2		
2	EDO	А	501	-	3,3,3	0.45	0	2,2,2	0.32	0	
3	ACT	В	503	-	1,3,3	1.34	0	$_{0,3,3}$	0.00	-	
2	EDO	В	504	-	3,3,3	0.50	0	2,2,2	0.35	0	
2	EDO	В	501	-	3,3,3	0.50	0	$2,\!2,\!2$	0.18	0	
3	ACT	А	503	-	1,3,3	1.57	0	$_{0,3,3}$	0.00	-	
2	EDO	А	502	-	3,3,3	0.49	0	$2,\!2,\!2$	0.20	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	\mathbf{Res}	Link	Chirals	Torsions	Rings
2	EDO	A	501	-	-	0/1/1/1	-
2	EDO	В	501	-	-	0/1/1/1	-
2	EDO	В	504	-	-	0/1/1/1	-
2	EDO	А	502	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.



There are no chirality outliers. There are no torsion outliers. There are no ring outliers.

No monomer is involved in short contacts.

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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	$Q{<}0.9$
1	А	378/422~(89%)	-0.29	5 (1%) 77 80	22, 30, 49, 60	0
1	В	382/422~(90%)	-0.26	4 (1%) 82 85	23, 30, 45, 58	0
All	All	760/844~(90%)	-0.27	9 (1%) 79 82	22, 30, 47, 60	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	282	GLY	4.8
1	А	24	ALA	4.0
1	А	25	ASP	3.6
1	В	283	SER	2.7
1	А	111	ALA	2.4

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, 95^{th} 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	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q<0.9
1	LLP	А	255	24/25	0.96	0.14	$26,\!29,\!31,\!32$	0
1	LLP	В	255	24/25	0.96	0.13	$26,\!30,\!32,\!33$	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.



6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
2	EDO	А	502	4/4	0.90	0.11	$37,\!38,\!38,\!39$	0
4	NA	В	502	1/1	0.92	0.14	32,32,32,32	0
4	NA	А	504	1/1	0.95	0.12	$33,\!33,\!33,\!33$	0
3	ACT	А	503	4/4	0.96	0.09	$30,\!31,\!31,\!32$	0
2	EDO	В	504	4/4	0.97	0.07	32,32,32,33	0
2	EDO	А	501	4/4	0.97	0.08	27,27,27,27	0
2	EDO	В	501	4/4	0.97	0.11	27,28,28,28	0
3	ACT	В	503	4/4	0.98	0.09	34,35,35,36	0

6.5 Other polymers (i)

There are no such residues in this entry.

