

# Full wwPDB X-ray Structure Validation Report (i)

#### Feb 20, 2021 – 08:22 AM GMT

PDB ID	:	6SQX
Title	:	Insights into a novel NlpC/P60 Endopeptidase from Photobacterium damselae
		subsp. piscicida
Authors	:	Lisboa, J.; Pereira, P.J.B.; dos Santos, N.M.S.
Deposited on	:	2019-09-04
Resolution	:	1.40  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 (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
$\mathrm{EDS}$	:	$2.17.1.  m{dev1}$
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	7.0.044  (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	$2.17.1.  m{dev1}$

# 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 1.40 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.



Motrio	Whole archive	Similar resolution
	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
$R_{free}$	130704	1714(1.40-1.40)
Clashscore	141614	1812(1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762(1.40-1.40)
RSRZ outliers	127900	1674(1.40-1.40)

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 <=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	499	85%	6% • 8%
1	В	499	86%	5% 8%

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
3	EDO	В	518	-	-	Х	-
4	PEG	А	521	-	-	-	Х



#### 6SQX

## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8870 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 Peptide-binding protein.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	457	Total 3817	C 2449	N 627	О 726	S 15	0	25	0
1	В	457	Total 3829	C 2452	N 631	O 730	S 16	0	25	0

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	3	Total Cl 3 3	0	0
2	В	3	Total Cl 3 3	0	0

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





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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	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	В	1	$\begin{array}{c cc} Total & C & O \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{c cc} Total & C & O \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{c cc} Total & C & O \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
3	В	1	$\begin{array}{c cc} Total & C & O \\ 4 & 2 & 2 \end{array}$	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	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
3	В	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
3	В	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
3	В	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
3	В	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
3	В	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
3	В	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
3	В	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 DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{c cc} Total & C & O \\ \hline 7 & 4 & 3 \end{array}$	0	0

• Molecule 5 is BICARBONATE ION (three-letter code: BCT) (formula:  $CHO_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	В	1	Total 4	С 1	O 3	0	0

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	507	Total O 508 508	0	1
6	В	547	Total O 547 547	0	0



## 3 Residue-property plots (i)

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: Peptide-binding protein



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	76.58Å $109.97$ Å $130.94$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{Bosolution} \left( \overset{\circ}{\mathbf{A}} \right)$	38.29 - 1.40	Depositor
Resolution (A)	45.34 - 1.40	EDS
% Data completeness	99.7 (38.29-1.40)	Depositor
(in resolution range $)$	99.8 (45.34 - 1.40)	EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.22 (at 1.40 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D .	0.147 , $0.175$	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.147 , $0.176$	DCC
$R_{free}$ test set	10708 reflections $(4.94%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	19.3	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.32 , $45.5$	EDS
L-test for $twinning^2$	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	8870	wwPDB-VP
Average B, all atoms $(Å^2)$	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: EDO, BCT, OCS, CL, 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	
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.53	0/3960	0.66	0/5387
1	В	0.53	0/3969	0.67	1/5395~(0.0%)
All	All	0.53	0/7929	0.66	1/10782~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	237	ARG	NE-CZ-NH2	6.17	123.38	120.30

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	3817	0	3754	21	0
1	В	3829	0	3757	18	0
2	А	3	0	0	0	0
2	В	3	0	0	0	0
3	А	68	0	102	3	0
3	В	84	0	126	8	0
4	А	7	0	10	3	0
5	В	4	0	1	0	0



The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
	Atom-2	distance (Å)	overlap (Å)
1:A:243[A]:ILE:HD11	1:A:250:ASN:HA	1.56	0.88
1:B:75:ASN:HB3	3:B:518:EDO:H22	1.58	0.84
1:A:367:LEU:HD13	1:A:373:GLY:HA3	1.67	0.76
1:B:89:ASN:HD21	3:B:518:EDO:H21	1.55	0.70
1:A:243[A]:ILE:HD11	1:A:250:ASN:CA	2.22	0.70
1:A:291[B]:THR:HG21	6:A:911:HOH:O	1.97	0.65
1:B:89:ASN:ND2	3:B:518:EDO:H21	2.13	0.64
1:B:194:THR:HB	3:B:522:EDO:H22	1.82	0.61
1:B:356:MET:CE	1:B:470:THR:HG23	2.34	0.56
1:B:356:MET:HE1	1:B:470:THR:HG23	1.86	0.56
1:A:456:ASP:HB3	3:A:515:EDO:H21	1.89	0.54
1:A:427:ASN:HD21	4:A:521:PEG:H21	1.73	0.54
1:A:285:LYS:HD3	1:A:285:LYS:H	1.74	0.53
1:B:421:LYS:NZ	1:B:429[A]:GLN:HE21	2.08	0.52
6:A:750:HOH:O	3:B:516:EDO:H21	2.09	0.51
1:B:384[B]:VAL:HG12	1:B:470:THR:HG22	1.93	0.50
1:B:299:LYS:HD3	6:B:862:HOH:O	2.11	0.50
1:A:371:GLN:HB3	6:A:709:HOH:O	2.12	0.49
1:A:97:THR:HA	3:A:520:EDO:H22	1.94	0.49
1:A:46:ASN:HA	1:A:297:SER:HA	1.94	0.48
1:B:190[B]:ILE:HD11	1:B:202:LYS:HE3	1.95	0.48
1:A:423:VAL:HG21	4:A:521:PEG:H12	1.95	0.48
1:B:48:ILE:HD11	1:B:53:ILE:HD13	1.94	0.48
1:B:367:LEU:HB2	6:B:982:HOH:O	2.15	0.46
1:A:242:PRO:HG2	1:A:283:ASN:O	2.16	0.46
1:A:243[B]:ILE:HD13	3:B:521:EDO:H11	1.99	0.45
1:B:89:ASN:HD21	3:B:518:EDO:C2	2.26	0.44
1:A:190[B]:ILE:HD11	1:A:202:LYS:HE3	1.99	0.44
1:A:429[B]:GLN:NE2	4:A:521:PEG:O4	2.48	0.43
1:A:24[B]:ILE:HG22	1:A:25:THR:O	2.19	0.43
1:B:456:ASP:OD1	3:B:511:EDO:H12	2.18	0.43



Chain Non-H H(added) Clashes Symm-Clashes Mol H(model) 6 508 3 А 0 0 0 6 В 547 0 0 2 0 All All 0 8870 0775039

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:LEU:HD11	1:B:243:ILE:HG21	2.00	0.43
1:A:243[A]:ILE:HD13	1:A:243[A]:ILE:HA	1.70	0.43
1:B:312:PRO:O	1:B:321:ASN:HB3	2.18	0.43
1:A:312:PRO:O	1:A:321:ASN:HB3	2.18	0.43
1:A:248:ILE:O	1:A:249:ASN:ND2	2.53	0.42
1:B:421:LYS:HE3	1:B:429[A]:GLN:HG2	2.02	0.41
1:A:211:PRO:HG3	3:A:511:EDO:H22	2.04	0.40
1:B:120:ASN:O	1:B:124[A]:GLU:HG3	2.21	0.40

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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	479/499~(96%)	474 (99%)	4 (1%)	1 (0%)	47 21
1	В	479/499~(96%)	474 (99%)	5(1%)	0	100 100
All	All	958/998~(96%)	948~(99%)	9 (1%)	1 (0%)	51 23

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	22	ASN

#### 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	433/447~(97%)	425~(98%)	8 (2%)	59 28
1	В	434/447~(97%)	430 (99%)	4 (1%)	78 58
All	All	867/894 (97%)	855~(99%)	12 (1%)	65 40

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

Mol	Chain	Res	Type
1	А	22	ASN
1	А	48	ILE
1	А	248	ILE
1	А	285	LYS
1	А	371	GLN
1	А	372	GLU
1	А	408	ASN
1	А	415	ASN
1	В	22	ASN
1	В	376	GLN
1	В	407	HIS
1	В	415	ASN

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

Mol	Chain	Res	Type
1	А	225	GLN
1	А	249	ASN
1	А	406	ASN
1	А	408	ASN
1	В	22	ASN
1	В	406	ASN

#### 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 length (or angle).

Mal	Turne	Chain	Pog Link		B	ond leng	$_{ m gths}$	Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	OCS	В	324	1	7,8,9	1.08	1 (14%)	6, 11, 13	1.36	1(16%)
1	OCS	А	324	1	7,8,9	1.28	1 (14%)	6,11,13	1.74	1(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	OCS	В	324	1	-	1/4/7/9	-
1	OCS	А	324	1	-	1/4/7/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	А	324	OCS	CB-SG	2.10	1.85	1.77
1	В	324	OCS	OD2-SG	-2.02	1.40	1.47

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	324	OCS	OD2-SG-CB	3.44	111.23	105.74
1	В	324	OCS	OD3-SG-CB	2.83	110.31	106.94

All (2) bond angle outliers are listed below:

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	А	324	OCS	N-CA-CB-SG
1	В	324	OCS	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.



#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 46 ligands modelled in this entry, 6 are monoatomic - leaving 40 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	Tune	Chain	Dog	Tink	B	Bond lengths			Bond angles		
	туре	Ullalli	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
3	EDO	В	513	-	3,3,3	0.54	0	$^{2,2,2}$	0.11	0	
3	EDO	В	507	-	3,3,3	0.48	0	$^{2,2,2}$	0.07	0	
3	EDO	В	515	-	3,3,3	0.73	0	$^{2,2,2}$	0.02	0	
3	EDO	В	509	-	3,3,3	0.40	0	$^{2,2,2}$	0.49	0	
3	EDO	A	510	-	3,3,3	0.46	0	$^{2,2,2}$	0.33	0	
3	EDO	В	519	-	3,3,3	0.45	0	$^{2,2,2}$	0.35	0	
3	EDO	А	508	-	3,3,3	0.51	0	$^{2,2,2}$	0.38	0	
3	EDO	A	519	-	3,3,3	0.42	0	$^{2,2,2}$	0.41	0	
3	EDO	А	520	-	3,3,3	0.50	0	$^{2,2,2}$	0.29	0	
3	EDO	В	504	-	3,3,3	0.62	0	$^{2,2,2}$	0.20	0	
3	EDO	В	516	-	3,3,3	0.63	0	$^{2,2,2}$	0.14	0	
3	EDO	В	517	-	3,3,3	0.37	0	$2,\!2,\!2$	0.49	0	
3	EDO	А	517	-	3,3,3	0.46	0	$^{2,2,2}$	0.51	0	
3	EDO	В	524	-	3,3,3	0.52	0	$2,\!2,\!2$	0.35	0	
3	EDO	А	506	-	3,3,3	0.57	0	$^{2,2,2}$	0.39	0	
3	EDO	А	504	-	3,3,3	0.44	0	$^{2,2,2}$	0.19	0	
3	EDO	В	506	-	3,3,3	0.70	0	$^{2,2,2}$	0.41	0	
3	EDO	A	511	-	$^{3,3,3}$	0.49	0	$^{2,2,2}$	0.37	0	
3	EDO	А	518	-	3,3,3	0.59	0	$^{2,2,2}$	0.23	0	
3	EDO	В	522	-	$^{3,3,3}$	0.41	0	$^{2,2,2}$	0.25	0	
3	EDO	A	509	-	3, 3, 3	0.48	0	$^{2,2,2}$	0.56	0	
3	EDO	В	505	-	3,3,3	0.20	0	$^{2,2,2}$	0.36	0	
3	EDO	В	508	-	3,3,3	0.74	0	$^{2,2,2}$	0.34	0	
3	EDO	В	521	-	3,3,3	0.42	0	2,2,2	0.82	0	
5	BCT	В	525	-	0,3,3	0.00	-	$_{0,3,3}$	0.00	-	
3	EDO	A	514	-	3,3,3	0.36	0	2,2,2	0.73	0	
3	EDO	A	505	-	3,3,3	0.49	0	$^{2,2,2}$	0.16	0	



Mal	Tune	Chain	Dec	Tink	B	ond leng	$_{ m gths}$	Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	В	518	-	3,3,3	0.57	0	2,2,2	0.27	0
3	EDO	В	510	-	3,3,3	0.49	0	2,2,2	0.57	0
3	EDO	В	520	-	3,3,3	0.45	0	2,2,2	0.22	0
3	EDO	А	512	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	В	511	-	3,3,3	0.49	0	2,2,2	0.33	0
3	EDO	В	514	-	3,3,3	0.53	0	2,2,2	0.20	0
3	EDO	А	513	-	3,3,3	0.39	0	2,2,2	0.63	0
3	EDO	А	507	-	3,3,3	0.43	0	2,2,2	0.61	0
3	EDO	А	516	-	3,3,3	0.42	0	2,2,2	0.74	0
4	PEG	А	521	-	6,6,6	0.11	0	$5,\!5,\!5$	0.09	0
3	EDO	В	512	-	3,3,3	0.46	0	2,2,2	0.46	0
3	EDO	A	515	-	3,3,3	0.45	0	2,2,2	0.37	0
3	EDO	В	523	-	3,3,3	0.52	0	2,2,2	0.29	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
3	EDO	В	513	-	-	1/1/1/1	-
3	EDO	В	507	-	-	0/1/1/1	-
3	EDO	В	515	-	-	0/1/1/1	-
3	EDO	В	509	-	-	0/1/1/1	-
3	EDO	А	510	-	-	0/1/1/1	-
3	EDO	В	519	-	-	0/1/1/1	-
3	EDO	А	508	-	-	0/1/1/1	-
3	EDO	А	519	-	-	1/1/1/1	-
3	EDO	А	520	-	-	0/1/1/1	-
3	EDO	В	504	-	-	0/1/1/1	-
3	EDO	В	516	-	-	0/1/1/1	-
3	EDO	В	517	-	-	0/1/1/1	-
3	EDO	А	517	-	-	0/1/1/1	-
3	EDO	В	524	-	-	0/1/1/1	-
3	EDO	А	506	-	-	0/1/1/1	-
3	EDO	А	504	-	-	0/1/1/1	-
3	EDO	В	506	-	-	0/1/1/1	-
3	EDO	А	511	-	-	0/1/1/1	-
3	EDO	А	518	-	-	1/1/1/1	-
3	EDO	B	522	-	-	0/1/1/1	-
3	EDO	A	509	-	-	0/1/1/1	_
3	EDO	В	505	-	-	0/1/1/1	-
3	EDO	В	508	-	-	0/1/1/1	-



Mol	Type	Chain	<b>R</b> og	Link	Chirola	Torsions	Bings
	туре	Chain	nes		Omrais	101510115	Trings
3	EDO	В	521	-	_	1/1/1/1	-
3	EDO	А	514	-	-	0/1/1/1	-
3	EDO	А	505	-	-	0/1/1/1	-
3	EDO	В	518	-	-	1/1/1/1	-
3	EDO	В	510	-	-	0/1/1/1	-
3	EDO	В	520	-	-	1/1/1/1	-
3	EDO	А	512	-	-	0/1/1/1	-
3	EDO	В	511	-	-	0/1/1/1	-
3	EDO	В	514	-	-	0/1/1/1	-
3	EDO	А	513	-	-	1/1/1/1	-
3	EDO	А	507	-	-	1/1/1/1	-
3	EDO	А	516	-	-	1/1/1/1	-
4	PEG	А	521	-	-	1/4/4/4	-
3	EDO	В	512	-	-	0/1/1/1	-
3	EDO	А	515	-	-	0/1/1/1	-
3	EDO	В	523	-	_	1/1/1/1	-

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There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	513	EDO	O1-C1-C2-O2
3	А	518	EDO	O1-C1-C2-O2
3	В	518	EDO	O1-C1-C2-O2
3	В	520	EDO	O1-C1-C2-O2
4	А	521	PEG	C4-C3-O2-C2
3	А	516	EDO	O1-C1-C2-O2
3	А	519	EDO	O1-C1-C2-O2
3	В	513	EDO	O1-C1-C2-O2
3	В	521	EDO	O1-C1-C2-O2
3	А	507	EDO	O1-C1-C2-O2
3	В	523	EDO	O1-C1-C2-O2

There are no ring outliers.

9 monomers are involved in 14 short contacts:

$\mathbb{N}$	/lol	Chain	Res	Type	Clashes	Symm-Clashes
	3	А	520	EDO	1	0



Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	516	EDO	1	0
3	А	511	EDO	1	0
3	В	522	EDO	1	0
3	В	521	EDO	1	0
3	В	518	EDO	4	0
3	В	511	EDO	1	0
4	А	521	PEG	3	0
3	А	515	EDO	1	0

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## 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, 95<sup>th</sup> 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	А	456/499~(91%)	0.80	51 (11%) 5 4	16, 24, 50, 95	0
1	В	456/499~(91%)	0.55	35 (7%) 13 12	15, 22, 45, 81	0
All	All	912/998~(91%)	0.68	86 (9%) 8 7	15, 23, 47, 95	0

All (86) RSRZ outliers are listed below:

Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	А	373	GLY	16.0
1	А	374	SER	11.1
1	А	246	TYR	11.1
1	В	246	TYR	10.3
1	А	372	GLU	9.6
1	А	116	SER	8.4
1	А	375	ILE	8.1
1	А	243[A]	ILE	7.8
1	А	248	ILE	6.7
1	В	116	SER	6.5
1	В	375	ILE	6.0
1	А	407	HIS	5.9
1	А	249	ASN	5.7
1	А	358	ASP	5.7
1	В	248	ILE	5.6
1	А	371	GLN	5.5
1	А	476	THR	5.5
1	В	245	LYS	5.5
1	В	407	HIS	5.3
1	В	374	SER	5.2
1	A	21	GLY	5.1
1	В	117	ASN	5.1
1	A	115	THR	4.9
1	В	373	GLY	4.7



Mol	Chain	Res	Type	RSRZ
1	А	51	TYR	4.5
1	В	372	GLU	4.4
1	В	478	LYS	4.4
1	А	118	TRP	4.3
1	А	474	THR	4.3
1	А	44	ASP	4.1
1	В	406	ASN	4.0
1	В	118	TRP	3.9
1	А	477	PRO	3.9
1	А	376	GLN	3.7
1	А	40	HIS	3.7
1	А	245	LYS	3.6
1	В	22	ASN	3.6
1	А	283	ASN	3.5
1	A	305	ILE	3.4
1	A	309	ILE	3.3
1	В	24[A]	ILE	3.3
1	В	376	GLN	3.3
1	A	354	TYR	3.3
1	В	228	ARG	3.3
1	В	51	TYR	3.2
1	В	283	ASN	3.2
1	В	249	ASN	3.2
1	A	475	GLU	3.2
1	A	274	ASN	3.2
1	В	285	LYS	3.1
1	A	367	LEU	3.0
1	В	286	ASN	3.0
1	В	367	LEU	3.0
1	A	138	ASN	3.0
1	A	22	ASN	2.9
1	A	308	TYR	2.9
1	В	115	THR	2.8
1	В	137	ASP	2.8
1	A	41	LYS	2.8
1	A	117	ASN	2.8
1	B	274	ASN	2.7
1	B	230	ARG	2.6
1	A	327	LEU	2.5
1	A	50	LYS	2.5
1	A	416	ALA	2.5
1	B	309	ILE	2.5

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6S	QX
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Mol	Chain	Res	Type	RSRZ
1	В	305	ILE	2.4
1	А	369	VAL	2.4
1	А	129	LYS	2.3
1	А	438	LEU	2.3
1	В	262	HIS	2.3
1	В	40	HIS	2.3
1	А	273	LYS	2.2
1	А	103	GLU	2.2
1	А	408	ASN	2.2
1	В	225	GLN	2.2
1	В	327	LEU	2.2
1	А	54	ARG	2.2
1	В	136	CYS	2.1
1	В	280	LEU	2.1
1	А	285	LYS	2.1
1	А	71	ASP	2.1
1	А	272	ASP	2.0
1	A	48	ILE	2.0
1	А	313	TYR	2.0
1	А	439	ILE	2.0

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#### 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	OCS	А	324	9/10	0.97	0.11	$16,\!17,\!23,\!25$	0
1	OCS	В	324	9/10	0.98	0.08	14, 16, 20, 23	0

#### 6.3 Carbohydrates (i)

There are no monosaccharides 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,



6	S	QX
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B$ -factors( $Å^2$ )	Q<0.9
5	BCT	В	525	4/4	0.13	0.28	27,36,56,66	0
4	PEG	А	521	7/7	0.51	0.40	29,29,30,30	7
3	EDO	В	523	4/4	0.52	0.24	$50,\!52,\!61,\!67$	0
3	EDO	В	516	4/4	0.57	0.26	$35,\!41,\!44,\!44$	0
3	EDO	А	518	4/4	0.62	0.28	$40,\!40,\!53,\!55$	0
3	EDO	В	504	4/4	0.62	0.28	40,41,42,45	0
3	EDO	В	518	4/4	0.64	0.23	41,48,49,60	0
3	EDO	А	517	4/4	0.64	0.18	42,43,48,55	0
3	EDO	В	519	4/4	0.67	0.21	$57,\!58,\!59,\!64$	0
3	EDO	В	524	4/4	0.68	0.18	$35,\!49,\!51,\!52$	0
3	EDO	В	506	4/4	0.74	0.13	32,33,37,38	0
3	EDO	В	511	4/4	0.77	0.23	$45,\!47,\!55,\!57$	0
3	EDO	А	520	4/4	0.78	0.13	$50,\!56,\!56,\!62$	0
3	EDO	А	516	4/4	0.79	0.23	$52,\!52,\!55,\!58$	0
3	EDO	А	509	4/4	0.81	0.19	$46,\!46,\!49,\!52$	0
3	EDO	А	515	4/4	0.81	0.25	$48,\!54,\!55,\!59$	0
3	EDO	А	510	4/4	0.83	0.13	$43,\!50,\!50,\!54$	0
3	EDO	В	522	4/4	0.83	0.36	$48,\!53,\!55,\!64$	0
3	EDO	В	521	4/4	0.84	0.17	38,43,44,60	0
3	EDO	А	506	4/4	0.85	0.13	$29,\!30,\!31,\!37$	0
3	EDO	А	511	4/4	0.86	0.13	$50,\!52,\!54,\!60$	0
3	EDO	В	513	4/4	0.87	0.17	$36,\!37,\!52,\!57$	0
3	EDO	А	508	4/4	0.88	0.14	$34,\!35,\!35,\!39$	0
3	EDO	А	519	4/4	0.88	0.16	42,48,52,66	0
3	EDO	В	520	4/4	0.88	0.19	$42,\!43,\!56,\!63$	0
3	EDO	А	513	4/4	0.89	0.19	$30,\!34,\!37,\!50$	0
3	EDO	В	515	4/4	0.89	0.12	$24,\!37,\!43,\!44$	0
3	EDO	В	514	4/4	0.90	0.08	$45,\!49,\!52,\!67$	0
3	EDO	А	512	4/4	0.91	0.15	$21,\!31,\!32,\!34$	0
3	EDO	А	505	4/4	0.91	0.09	$29,\!32,\!34,\!36$	0
3	EDO	В	510	4/4	0.93	0.13	$31,\!31,\!37,\!38$	0
3	EDO	A	514	4/4	0.93	0.16	$37,\!43,\!52,\!54$	0
3	EDO	В	517	4/4	0.93	0.09	$28,\!33,\!49,\!52$	0
3	EDO	А	507	4/4	0.94	0.15	$28,\!34,\!37,\!46$	0
3	EDO	В	512	4/4	0.94	0.20	$43,\!49,\!53,\!55$	0
3	EDO	В	508	4/4	0.94	0.09	24,27,30,33	0
3	EDO	B	$50\overline{5}$	4/4	0.94	0.07	26,27,27,30	0
3	EDO	В	509	4/4	0.96	0.12	23,30,33,37	0
3	EDO	В	507	4/4	0.96	0.09	28,33,40,44	0
2	CL	А	503	1/1	0.96	0.07	$29,\!29,\!29,\!29$	0
3	EDO	A	504	4/4	0.98	0.07	27,32,34,39	0

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
2	CL	А	502	1/1	0.98	0.12	$23,\!23,\!23,\!23$	0
2	CL	А	501	1/1	0.98	0.10	21,21,21,21	0
2	CL	В	503	1/1	0.98	0.12	$23,\!23,\!23,\!23$	0
2	CL	В	502	1/1	0.99	0.09	21,21,21,21	0
2	CL	В	501	1/1	0.99	0.09	20,20,20,20	0

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## 6.5 Other polymers (i)

There are no such residues in this entry.

