

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

#### May 22, 2023 – 10:34 pm BST

PDB ID : 80NO

Title: Modified oligopeptidase B from S. proteamaculans in intermediate conforma-

tion with 5 spermine molecule at 1.65 A resolution

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Deposited on : 2023-04-03

Resolution : 1.65 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.33

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

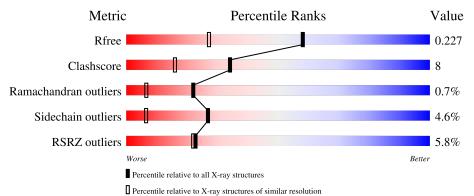
Validation Pipeline (wwPDB-VP) : 2.33

## 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 1.65 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}(\mathring{A}))$
$R_{free}$	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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		
			<u>6%</u>		_
1	A	677	85%	14%	••

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
2	SPM	A	702	-	-	X	-



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6158 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.

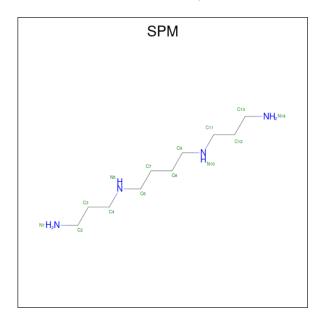
• Molecule 1 is a protein called Oligopeptidase B.

Mol	Chain	Residues	$\mathbf{Atoms}$				ZeroOcc	AltConf	Trace	
1	A	677	Total 5552	C 3526	N 933	O 1080	S 13	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	expression tag	UNP B3VI58
A	71	GLU	ILE	$\operatorname{conflict}$	UNP B3VI58
A	72	ASN	PRO	conflict	UNP B3VI58
A	73	LEU	GLN	conflict	UNP B3VI58
A	74	TYR	GLN	conflict	UNP B3VI58
A	75	PHE	GLU	conflict	UNP B3VI58
A	76	GLN	HIS	conflict	UNP B3VI58

• Molecule 2 is SPERMINE (three-letter code: SPM) (formula:  $C_{10}H_{26}N_4$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
2	A	1	Total C N	0	0	
_		_	14 10 4	Ů		
$\frac{1}{2}$	A	1	Total C N	0	0	
2	Λ	1	14 10 4	0	U	
2	A	1	Total C N	0	0	
2	Λ	1	14 10 4	0	0	
2	A	1	Total C N	0	0	
2	Λ	1	14 10 4	0	U	
2	А	1	Total C N	0	0	
	Α	1	14 10 4		U	

### • Molecule 3 is water.

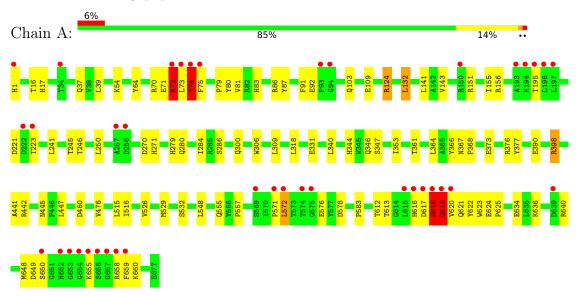
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	536	Total O 536 536	0	0



# 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: Oligopeptidase B





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	73.09Å 100.62Å 108.63Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.59 - 1.65	Depositor
Resolution (A)	29.57 - 1.65	EDS
% Data completeness	98.3 (29.59-1.65)	Depositor
(in resolution range)	98.4 (29.57-1.65)	EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.98 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
D D.	0.186 , 0.220	Depositor
$R, R_{free}$	0.196 , $0.227$	DCC
$R_{free}$ test set	4673 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.4	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 42.0	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6158	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.77% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: SPM

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	Boı	nd lengths	Bo	ond angles
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.77	$1/5698 \; (0.0\%)$	0.94	5/7746 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
1	A	390	GLU	CD-OE1	5.37	1.31	1.25

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	398	ARG	NE-CZ-NH1	-6.81	116.89	120.30
1	A	156	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	A	156	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	A	640	ARG	NE-CZ-NH2	-5.63	117.49	120.30
1	A	70	ARG	NE-CZ-NH1	-5.58	117.51	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	619	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	A	72	ASN	Peptide
1	A	73	LEU	Peptide

## 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	5552	0	5263	85	0
2	A	70	0	130	26	0
3	A	536	0	0	17	0
All	All	6158	0	5393	92	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 8.

The worst 5 of 92 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:132:LEU:CD2	1:A:141:LEU:HD11	1.90	1.02
1:A:132:LEU:HD22	1:A:141:LEU:HD11	1.43	0.98
1:A:376:ARG:HD2	2:A:702:SPM:H42	1.43	0.97
1:A:367:ASN:HD21	1:A:376:ARG:H	1.20	0.89
1:A:221:ASP:OD1	1:A:223:THR:HG22	1.74	0.86

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	676/677 (100%)	648 (96%)	23 (3%)	5 (1%)	22 6	

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	618	SER
1	A	74	TYR
1	A	572	LEU
1	A	649	ASP

#### 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	592/591 (100%)	565 (95%)	27 (5%)	27 6

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	300	GLN
1	A	373	GLU
1	A	655	LYS
1	A	318	LEU
1	A	515	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	445	ASN
1	A	616	HIS
1	A	621	GLN
1	A	619	GLN
1	A	181	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)

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

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

5 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	Chain	Chain	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type		rtes	LillK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2			
2	SPM	A	702	-	13,13,13	0.45	0	12,12,12	0.57	0			
2	SPM	A	703	-	13,13,13	0.18	0	12,12,12	0.70	0			
2	SPM	A	704	_	13,13,13	0.32	0	12,12,12	0.49	0			
2	SPM	A	701	_	13,13,13	0.22	0	12,12,12	0.73	0			
2	SPM	A	705	-	13,13,13	0.39	0	12,12,12	0.81	1 (8%)			

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
2	SPM	A	702	-	-	10/11/11/11	-
2	SPM	A	703	-	-	3/11/11/11	-
2	SPM	A	704	-	-	8/11/11/11	-
2	SPM	A	701	-	-	9/11/11/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SPM	A	705	-	-	9/11/11/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	A	705	SPM	C11-N10-C9	2.17	123.70	113.45

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	705	SPM	N1-C2-C3-C4
2	A	705	SPM	C12-C11-N10-C9
2	A	701	SPM	C2-C3-C4-N5
2	A	704	SPM	N5-C6-C7-C8
2	A	704	SPM	C7-C8-C9-N10

There are no ring outliers.

4 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	702	SPM	20	0
2	A	703	SPM	3	0
2	A	704	SPM	1	0
2	A	705	SPM	2	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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$OWAB(Å^2)$	Q<0.9
1	A	677/677 (100%)	0.13	39 (5%) 23	22	11, 20, 46, 106	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	TYR	12.3
1	A	652	HIS	8.1
1	A	73	LEU	6.5
1	A	618	SER	6.3
1	A	658	ARG	5.4

## 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 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, 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	$\operatorname{B-factors}(\mathrm{\AA}^2)$	Q<0.9
2	SPM	A	705	14/14	0.49	0.24	41,61,68,69	0
2	SPM	A	704	14/14	0.61	0.23	33,54,60,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
2	SPM	A	701	14/14	0.68	0.17	40,46,49,49	0
2	SPM	A	702	14/14	0.76	0.34	29,39,47,50	0
2	SPM	A	703	14/14	0.81	0.11	28,32,38,41	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

