



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 2RQO
Title : Solution structure of Polytheonamide B
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This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

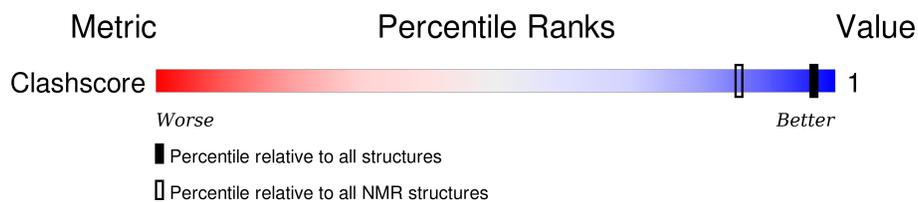
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	114402	11133

WHATHAPPENED

2 Ensemble composition and analysis

This entry contains 20 models. This entry does not contain protein, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 727 atoms, of which 375 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein (with D amino acids) called polytheonamide B.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	49	727	219	375	60	72	1	0

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.2 Score per residue for model 2

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.3 Score per residue for model 3

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.4 Score per residue for model 4

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.5 Score per residue for model 5

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.6 Score per residue for model 6

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.7 Score per residue for model 7

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.8 Score per residue for model 8

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.9 Score per residue for model 9

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.10 Score per residue for model 10

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.11 Score per residue for model 11 (medoid)

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.12 Score per residue for model 12

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.13 Score per residue for model 13

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.14 Score per residue for model 14

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.15 Score per residue for model 15

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.16 Score per residue for model 16

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.17 Score per residue for model 17

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.18 Score per residue for model 18

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.19 Score per residue for model 19

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

4.2.20 Score per residue for model 20

There is no protein, DNA or RNA molecules in this entry to show sequence plots.

5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS*, *distance geometry*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	refinement	3.0
OPALP	refinement	1.4
MolSkop	geometry optimization	1.0

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality i

6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: DAL, 2TL, MHE, TDD, DSN, HVA, DHV, I2M, HTN, DSG, M2S, MND, TBG, LMQ

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	352	375	348	1±1
All	All	7040	7500	6978	14

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:MND:HE22	1:A:22:LMQ:CD	0.53	2.34	3	1
1:A:15:MND:HE22	1:A:21:MND:HB2	0.53	1.80	14	2
1:A:29:HTN:HD22	1:A:35:MND:CE2	0.52	2.18	11	1
1:A:21:MND:HE22	1:A:22:LMQ:CG	0.51	2.35	3	2
1:A:21:MND:HE22	1:A:22:LMQ:HB22	0.49	1.84	2	2
1:A:2:I2M:HD12	1:A:8:TBG:HG12	0.46	1.87	8	1
1:A:21:MND:HE22	1:A:22:LMQ:HG2	0.45	1.89	18	1
1:A:0:MHE:H8B	1:A:0:MHE:C2	0.43	2.44	9	1
1:A:33:MND:HD2	1:A:39:MND:HE22	0.42	1.75	20	1
1:A:15:MND:HE22	1:A:21:MND:CB	0.42	2.44	14	1
1:A:15:MND:HE23	1:A:21:MND:CG	0.42	2.44	8	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

6.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

28 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	MHE	A	0	1	9,9,10	0.65±0.05	0±0 (0±0%)
1	TDD	A	13	1	4,7,8	0.66±0.04	0±0 (0±0%)
1	MND	A	15	1	6,8,9	0.58±0.11	0±0 (0±0%)
1	HVA	A	16	1	4,7,8	1.07±0.08	0±0 (0±0%)
1	I2M	A	2	1	5,8,9	0.68±0.09	0±0 (0±0%)
1	TBG	A	20	1	4,7,8	0.58±0.03	0±0 (0±0%)
1	MND	A	21	1	6,8,9	0.60±0.07	0±0 (0±0%)
1	LMQ	A	22	1	8,9,10	0.47±0.04	0±0 (0±0%)
1	DHV	A	23	1	4,7,8	1.06±0.10	0±0 (0±0%)
1	MND	A	27	1	6,8,9	0.53±0.06	0±0 (0±0%)
1	HTN	A	29	1	8,9,10	0.51±0.05	0±0 (0±0%)
1	TBG	A	30	1	4,7,8	0.60±0.05	0±0 (0±0%)
1	DHV	A	31	1	4,7,8	1.05±0.08	0±0 (0±0%)
1	MND	A	33	1	6,8,9	0.49±0.07	0±0 (0±0%)
1	MND	A	35	1	6,8,9	0.46±0.05	0±0 (0±0%)
1	HTN	A	37	1	8,9,10	0.54±0.06	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Counts	Bond lengths	
						RMSZ	#Z>2
1	MND	A	39	1	6,8,9	0.54±0.06	0±0 (0±0%)
1	TBG	A	4	1	4,7,8	0.63±0.03	0±0 (0±0%)
1	DSN	A	41	1	3,5,6	0.59±0.04	0±0 (0±0%)
1	DSG	A	43	1	5,7,8	0.44±0.02	0±0 (0±0%)
1	M2S	A	44	1	6,10,11	5.54±0.12	1±0 (16±0%)
1	DSG	A	45	1	5,7,8	0.46±0.04	0±0 (0±0%)
1	2TL	A	47	1	5,6,7	0.61±0.06	0±0 (0±0%)
1	TDD	A	5	1	4,7,8	0.59±0.03	0±0 (0±0%)
1	TBG	A	6	1	4,7,8	0.63±0.04	0±0 (0±0%)
1	DAL	A	7	1	1,4,5	0.89±0.04	0±0 (0±0%)
1	TBG	A	8	1	4,7,8	0.60±0.03	0±0 (0±0%)
1	TDD	A	9	1	4,7,8	0.58±0.04	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Counts	Bond angles	
						RMSZ	#Z>2
1	MHE	A	0	1	10,12,14	0.58±0.12	0±0 (0±0%)
1	TDD	A	13	1	7,10,12	1.23±0.09	0±0 (0±0%)
1	MND	A	15	1	6,9,11	0.97±0.21	0±0 (0±0%)
1	HVA	A	16	1	3,10,12	1.25±0.38	0±0 (0±0%)
1	I2M	A	2	1	5,11,13	1.20±0.18	0±0 (0±0%)
1	TBG	A	20	1	7,10,12	0.92±0.13	0±0 (0±0%)
1	MND	A	21	1	6,9,11	1.16±0.11	0±0 (0±0%)
1	LMQ	A	22	1	8,11,13	1.01±0.12	0±0 (0±0%)
1	DHV	A	23	1	3,10,12	1.25±0.39	0±0 (0±0%)
1	MND	A	27	1	6,9,11	1.38±0.22	0±0 (0±0%)
1	HTN	A	29	1	8,11,13	1.45±0.15	0±0 (0±0%)
1	TBG	A	30	1	7,10,12	0.99±0.17	0±0 (0±0%)
1	DHV	A	31	1	3,10,12	1.50±0.40	0±0 (0±0%)
1	MND	A	33	1	6,9,11	1.22±0.15	0±0 (0±0%)
1	MND	A	35	1	6,9,11	1.30±0.29	0±0 (0±0%)
1	HTN	A	37	1	8,11,13	1.43±0.25	0±0 (0±0%)
1	MND	A	39	1	6,9,11	1.22±0.20	0±0 (0±0%)
1	TBG	A	4	1	7,10,12	0.78±0.07	0±0 (0±0%)
1	DSN	A	41	1	3,5,7	1.21±0.19	0±0 (0±0%)
1	DSG	A	43	1	6,8,10	1.26±0.13	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	M2S	A	44	1	6,14,16	1.79±0.43	0±0 (0±0%)
1	DSG	A	45	1	6,8,10	1.20±0.13	0±0 (0±0%)
1	2TL	A	47	1	5,7,9	1.24±0.16	0±0 (0±0%)
1	TDD	A	5	1	7,10,12	0.86±0.08	0±0 (0±0%)
1	TBG	A	6	1	7,10,12	0.86±0.13	0±0 (0±0%)
1	DAL	A	7	1	1,4,6	0.50±0.09	0±0 (0±0%)
1	TBG	A	8	1	7,10,12	0.85±0.19	0±0 (0±0%)
1	TDD	A	9	1	7,10,12	0.94±0.12	0±0 (0±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	MHE	A	0	1	-	0±0,6,8,10	0±0,0,0,0
1	TDD	A	13	1	-	0±0,6,8,10	0±0,0,0,0
1	MND	A	15	1	-	0±0,6,8,10	0±0,0,0,0
1	HVA	A	16	1	-	0±0,4,8,10	0±0,0,0,0
1	I2M	A	2	1	-	0±0,7,11,13	0±0,0,0,0
1	TBG	A	20	1	-	0±0,6,8,10	0±0,0,0,0
1	MND	A	21	1	-	0±0,6,8,10	0±0,0,0,0
1	LMQ	A	22	1	-	0±0,8,10,12	0±0,0,0,0
1	DHV	A	23	1	-	0±0,4,8,10	0±0,0,0,0
1	MND	A	27	1	-	0±0,6,8,10	0±0,0,0,0
1	HTN	A	29	1	-	0±0,9,12,14	0±0,0,0,0
1	TBG	A	30	1	-	0±0,6,8,10	0±0,0,0,0
1	DHV	A	31	1	-	0±0,4,8,10	0±0,0,0,0
1	MND	A	33	1	-	0±0,6,8,10	0±0,0,0,0
1	MND	A	35	1	-	0±0,6,8,10	0±0,0,0,0
1	HTN	A	37	1	-	0±0,9,12,14	0±0,0,0,0
1	MND	A	39	1	-	0±0,6,8,10	0±0,0,0,0
1	TBG	A	4	1	-	0±0,6,8,10	0±0,0,0,0
1	DSN	A	41	1	-	0±0,2,4,6	0±0,0,0,0
1	DSG	A	43	1	-	0±0,4,6,8	0±0,0,0,0
1	M2S	A	44	1	-	0±0,9,13,15	0±0,0,0,0
1	DSG	A	45	1	-	0±0,4,6,8	0±0,0,0,0
1	2TL	A	47	1	-	0±0,4,6,8	0±0,0,0,0
1	TDD	A	5	1	-	0±0,6,8,10	0±0,0,0,0
1	TBG	A	6	1	-	0±0,6,8,10	0±0,0,0,0
1	DAL	A	7	1	-	0±0,0,2,4	0±0,0,0,0
1	TBG	A	8	1	-	0±0,6,8,10	0±0,0,0,0
1	TDD	A	9	1	-	0±0,6,8,10	0±0,0,0,0

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	44	M2S	OE-SD	13.98	1.84	1.50	5	20

There are no bond-angle outliers.

There are no chirality outliers.

All unique torsion outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	37	HTN	CB-CG-ND2-CE	5
1	A	37	HTN	OD1-CG-ND2-CE	5

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided