wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2AXD
Title	:	solution structure of the theta subunit of escherichia coli DNA polymerase III in complex with the epsilon subunit
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This is a wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

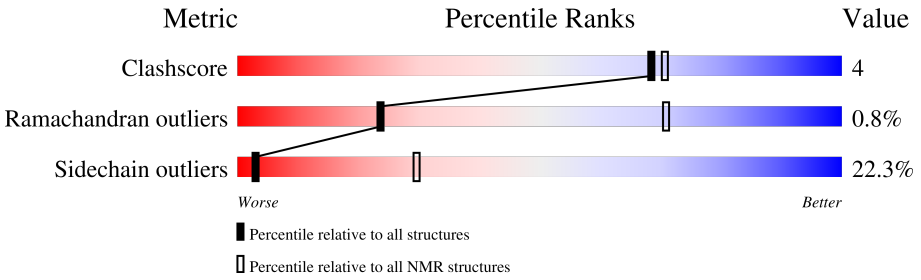
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain
1	S	76	49% 21% 30%

2 Ensemble composition and analysis (i)

This entry contains 12 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	S:13-S:65 (53)	0.44	12

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models in file

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1276 atoms, of which 655 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA polymerase III, theta subunit.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	S	76	1276	394	655	114	110	3	0

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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.

- Molecule 1: DNA polymerase III, theta subunit

Chain S: 49% 21% 30%

M1 L2 K3 N4 L5 A6 K7 L8 D9 Q10 T11 E12 M13 D14 D19 L20 V25 E29 V35 E38 A39 V40 E41 R42 E43 E46 H47 L48 E54 R55 L56 N65 L66 S67 R68 L69 P70 Y71 E72 P73 K74 L75 K76

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 12. Colouring as in section 4.1 above.

- Molecule 1: DNA polymerase III, theta subunit

Chain S: 42% 26% • 30%

M1 L2 K3 N4 L5 A6 K7 L8 D9 Q10 T11 E12 M13 D14 D19 V25 K28 E29 V35 E38 A39 V40 E41 R42 E43 Q44 P45 E46 H47 L48 R49 R53 E54 R55 L56 L61 V64 N65 L66 S67 R68 L69 P70 Y71 E72 P73 K74 L75 K76

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 200 calculated structures, 12 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
DYANA	refinement	1.5
XPLOR-NIH	refinement	2.9.7

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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 (average) 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	S	1.41±0.01	12±1/440 (2.6± 0.2%)	1.15±0.03	4±1/595 (0.6± 0.1%)
All	All	1.41	139/5280 (2.6%)	1.15	46/7140 (0.6%)

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 mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	S	0.0±0.0	0.1±0.3
All	All	0	1

5 of 12 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	S	41	GLU	CD-OE2	9.15	1.35	1.25	2	12
1	S	54	GLU	CD-OE2	9.01	1.35	1.25	11	12
1	S	29	GLU	CD-OE2	8.86	1.35	1.25	6	12
1	S	43	GLU	CD-OE2	8.82	1.35	1.25	8	12
1	S	46	GLU	CD-OE2	8.81	1.35	1.25	4	12

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	S	19	ASP	CB-CG-OD1	9.04	126.43	118.30	7	11
1	S	19	ASP	CB-CG-OD2	-8.46	110.69	118.30	7	10
1	S	14	ASP	CB-CG-OD2	-7.59	111.46	118.30	6	12
1	S	14	ASP	CB-CG-OD1	7.49	125.04	118.30	10	12
1	S	49	ARG	NE-CZ-NH2	-5.29	117.66	120.30	8	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	S	30	ARG	Sidechain	1

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	S	431	440	430	3±2
All	All	5172	5280	5160	39

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.

5 of 25 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:S:25:VAL:HG22	1:S:40:VAL:HG21	0.76	1.55	3	6
1:S:25:VAL:CG2	1:S:40:VAL:HG21	0.59	2.27	5	4
1:S:18:VAL:HG21	1:S:48:LEU:HD22	0.57	1.77	2	1
1:S:25:VAL:HG22	1:S:40:VAL:CG2	0.56	2.29	10	2
1:S:14:ASP:O	1:S:18:VAL:HG23	0.55	2.01	2	1

6.3 Torsion angles (i)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	S	53/76 (70%)	49±2 (93±3%)	3±1 (6±2%)	0±1 (1±1%)	24	71
All	All	636/912 (70%)	590 (93%)	41 (6%)	5 (1%)	24	71

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	S	30	ARG	2
1	S	33	MET	2
1	S	31	TYR	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	S	44/66 (67%)	34±3 (78±7%)	10±3 (22±7%)	3 29
All	All	528/792 (67%)	410 (78%)	118 (22%)	3 29

5 of 32 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	S	56	LEU	8
1	S	48	LEU	7
1	S	55	ARG	7
1	S	35	VAL	6
1	S	53	ARG	6

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides 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 (i)

No chemical shift data were provided