



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2N1G / pdb_00002n1g
BMRB ID : 25559
Title : Structure of C-terminal domain of human polymerase Rev1 in complex with PolD3 RIR-motif
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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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

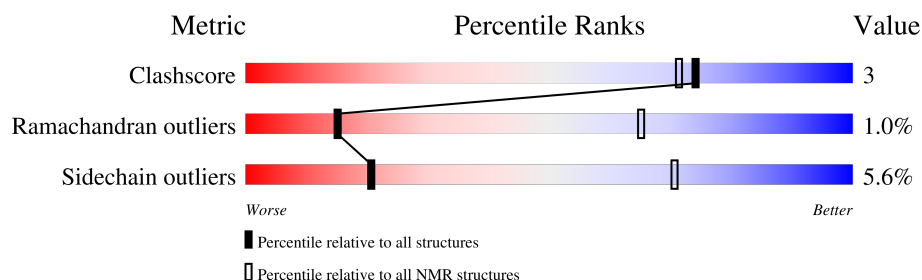
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	94	
2	B	16	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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	A:1158-A:1250, B:237-B:240 (97)	0.77	3

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 10, 11, 12, 15, 18, 19, 20
2	8, 9, 13, 14, 16, 17

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1789 atoms, of which 901 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA repair protein REV1.

Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1544	492	778	119	150	5	

- Molecule 2 is a protein called DNA polymerase delta subunit 3.

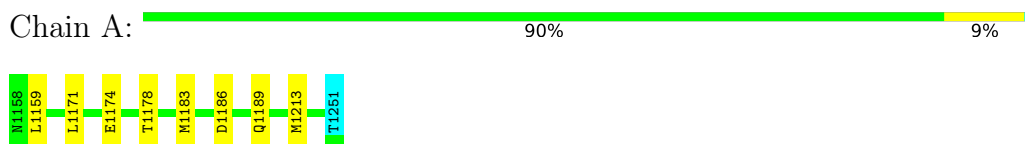
Mol	Chain	Residues	Atoms						Trace
2	B	16	Total	C	H	N	O	S	0
			245	76	123	22	21	3	

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 repair protein REV1



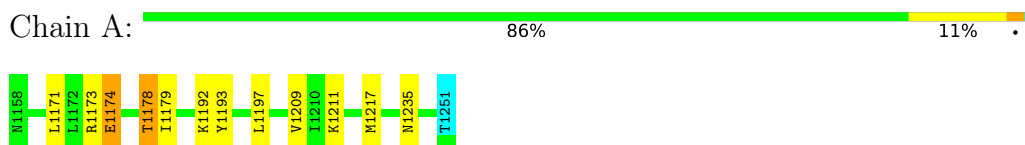
- Molecule 2: DNA polymerase delta subunit 3



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

The representative model is number 3. Colouring as in section 4.1 above.

- Molecule 1: DNA repair protein REV1



- Molecule 2: DNA polymerase delta subunit 3



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	structure solution	2.1
ABACUS (CNS)	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1172
Number of shifts mapped to atoms	1172
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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	A	1.25±0.02	0±0/770 (0.0± 0.0%)	1.10±0.03	0±0/1044 (0.0± 0.0%)
2	B	1.06±0.08	0±0/36 (0.0± 0.0%)	1.14±0.21	0±0/48 (0.1± 0.5%)
All	All	1.24	2/16120 (0.0%)	1.11	3/21840 (0.0%)

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	1209	VAL	CA-CB	6.12	1.60	1.54	19	2

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	A	1174	GLU	N-CA-CB	5.36	117.83	110.07	7	1
2	B	238	PHE	CA-CB-CG	5.28	119.08	113.80	17	1
1	A	1167	ASP	CA-CB-CG	5.10	117.70	112.60	18	1

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	759	771	770	5±3
2	B	34	27	27	2±1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
All	All	15860	15960	15940	103

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.

5 of 70 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1217:MET:SD	1:A:1229:PHE:HB2	0.63	2.32	13	4
1:A:1171:LEU:HD22	2:B:239:PHE:HA	0.60	1.73	15	6
1:A:1213:MET:SD	1:A:1232:ILE:HG21	0.57	2.40	12	9
1:A:1178:THR:HG22	1:A:1179:ILE:HD12	0.57	1.77	17	1
1:A:1159:LEU:HD21	1:A:1168:VAL:HG22	0.54	1.79	9	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	A	92/94 (98%)	87±2 (94±2%)	5±2 (5±2%)	0±1 (0±1%)	31	76
2	B	4/16 (25%)	2±1 (61±20%)	1±1 (24±18%)	1±1 (15±20%)	0	4
All	All	1920/2200 (87%)	1783 (93%)	118 (6%)	19 (1%)	15	65

5 of 7 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	237	ASN	7
1	A	1221	VAL	3
2	B	240	GLY	3
1	A	1161	GLY	2
2	B	239	PHE	2

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	A	88/89 (99%)	83±2 (95±2%)	5±2 (5±2%)	22 72
2	B	3/12 (25%)	3±0 (85±17%)	0±0 (15±17%)	5 42
All	All	1820/2020 (90%)	1718 (94%)	102 (6%)	21 70

5 of 30 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	A	1159	LEU	13
1	A	1186	ASP	7
1	A	1189	GLN	7
1	A	1174	GLU	7
1	A	1178	THR	7

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 oligosaccharides 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](#)

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 75% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1172
Number of shifts mapped to atoms	1172
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	94	-0.86 ± 0.13	Should be checked
$^{13}\text{C}_\beta$	92	0.24 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	2	—	None (insufficient data)
^{15}N	91	0.19 ± 0.34	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 83%, i.e. 1151 atoms were assigned a chemical shift out of a possible 1383. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	369/486 (76%)	184/196 (94%)	95/194 (49%)	90/96 (94%)
Sidechain	732/796 (92%)	500/518 (97%)	222/254 (87%)	10/24 (42%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	50/101 (50%)	30/49 (61%)	18/50 (36%)	2/2 (100%)
Overall	1151/1383 (83%)	714/763 (94%)	335/498 (67%)	102/122 (84%)

7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	1178	THR	HG1	5.34	0.08 – 2.19	19.9
1	A	1177	THR	HG1	5.04	0.08 – 2.19	18.5
1	A	1195	THR	HG1	4.86	0.08 – 2.19	17.6
1	A	1243	THR	HG1	4.86	0.08 – 2.19	17.6
1	A	1170	THR	HG1	4.85	0.08 – 2.19	17.6
1	A	1251	THR	HG1	4.39	0.08 – 2.19	15.4
1	A	1182	PRO	HG2	-0.26	0.41 – 3.45	-7.2
1	A	1169	LYS	HG2	-0.00	0.13 – 2.61	-5.5
1	A	1182	PRO	HD2	1.89	1.93 – 5.38	-5.1

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

