



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 21, 2025 – 01:34 PM EDT

PDB ID : 9CB5 / pdb\_00009cb5  
Title : Crystal structure of nucleolin in complex with MYC promoter G-quadruplex  
Authors : Chen, L.; Dickerhoff, J.; Noinaj, N.; Yang, D.  
Deposited on : 2024-06-18  
Resolution : 2.60 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

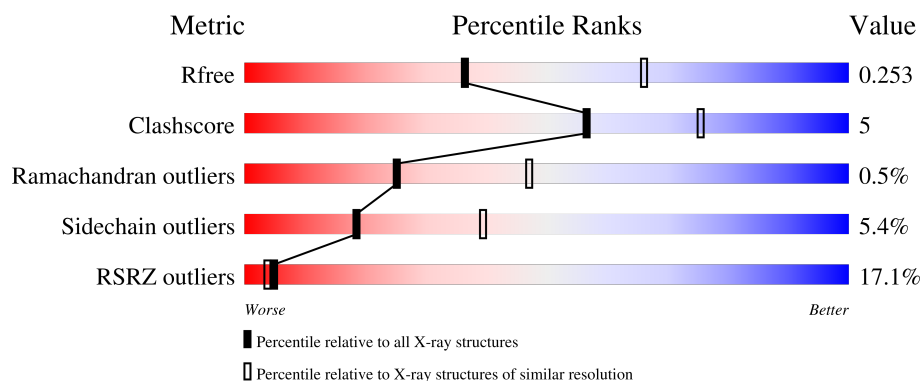
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	A	347	
1	B	347	
2	C	28	
2	F	28	
3	D	246	

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Mol	Chain	Length	Quality of chain
3	G	246	<div><div></div><div>27%</div><div></div><div>80%</div><div></div><div>13%</div><div></div><div>5%</div></div>
4	H	215	<div><div></div><div>6%</div><div></div><div>89%</div><div></div><div>8%</div><div></div><div></div></div>
4	I	215	<div><div></div><div>18%</div><div></div><div>85%</div><div></div><div>13%</div><div></div><div></div></div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10339 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 Nucleolin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	1	0
			1106	687	201	216	2			
1	B	171	Total	C	N	O	S	0	0	0
			1342	848	225	267	2			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	301	GLY	-	expression tag	UNP P19338
A	302	GLY	-	expression tag	UNP P19338
A	303	GLY	-	expression tag	UNP P19338
A	304	GLY	-	expression tag	UNP P19338
A	305	HIS	-	expression tag	UNP P19338
A	306	MET	-	expression tag	UNP P19338
A	543	SER	CYS	conflict	UNP P19338
B	301	GLY	-	expression tag	UNP P19338
B	302	GLY	-	expression tag	UNP P19338
B	303	GLY	-	expression tag	UNP P19338
B	304	GLY	-	expression tag	UNP P19338
B	305	HIS	-	expression tag	UNP P19338
B	306	MET	-	expression tag	UNP P19338
B	543	SER	CYS	conflict	UNP P19338

- Molecule 2 is a DNA chain called MYC promoter G-quadruplex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	28	Total	C	N	O	P	0	0	0
			585	278	109	171	27			
2	F	23	Total	C	N	O	P	0	0	0
			487	230	91	143	23			

- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	234	Total	C	N	O	S	0	0	0
			1749	1114	289	340	6			
3	G	233	Total	C	N	O	S	0	0	0
			1712	1089	284	332	7			

- Molecule 4 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	215	Total	C	N	O	S	0	0	0
			1597	994	269	328	6			
4	I	215	Total	C	N	O	S	0	0	0
			1568	972	266	324	6			

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	K	0	0
			2	2		
5	F	2	Total	K	0	0
			2	2		

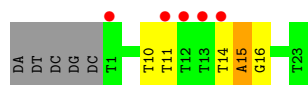
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	7	Total	O	0	0
			7	7		
6	B	34	Total	O	0	0
			34	34		
6	C	12	Total	O	0	0
			12	12		
6	D	35	Total	O	0	0
			35	35		
6	F	5	Total	O	0	0
			5	5		
6	G	21	Total	O	0	0
			21	21		
6	H	55	Total	O	0	0
			55	55		
6	I	20	Total	O	0	0
			20	20		

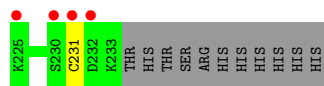
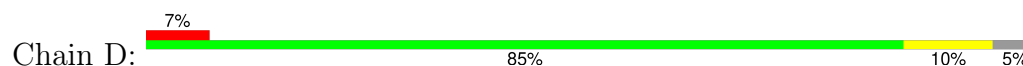




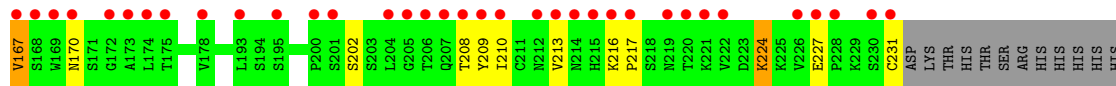
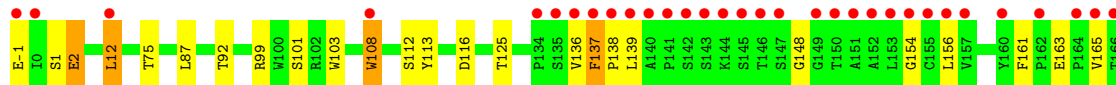
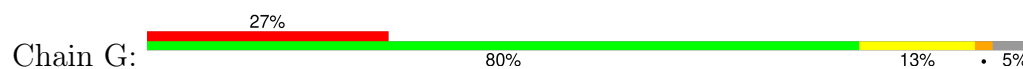
- Molecule 2: MYC promoter G-quadruplex



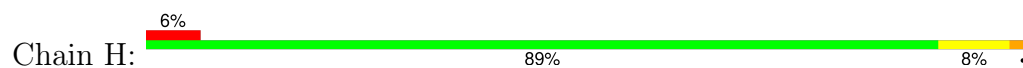
- Molecule 3: Fab heavy chain



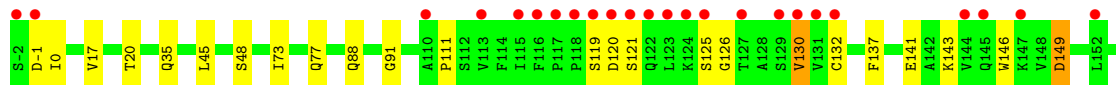
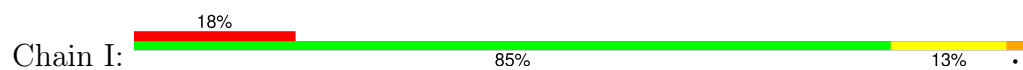
- Molecule 3: Fab heavy chain

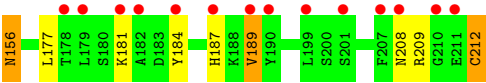


- Molecule 4: Fab light chain



- Molecule 4: Fab light chain







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.25Å 134.66Å 185.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.43 – 2.60 48.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.8 (48.43-2.60) 96.7 (48.43-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.23	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, $R_{free}$	0.232 , 0.254 0.232 , 0.253	Depositor DCC
$R_{free}$ test set	56399 reflections (3.54%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.396	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 43.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	10339	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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:  
K

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	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.26	0/1117	0.48	0/1514
1	B	0.25	0/1360	0.45	0/1818
2	C	0.49	0/657	0.90	0/1017
2	F	0.54	0/547	0.99	1/847 (0.1%)
3	D	0.25	0/1799	0.50	0/2460
3	G	0.26	0/1761	0.50	0/2408
4	H	0.25	0/1630	0.49	0/2216
4	I	0.27	0/1600	0.50	0/2179
All	All	0.30	0/10471	0.57	1/14459 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	15	DA	O4'-C1'-N9	5.32	111.73	108.00

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	A	1106	0	906	16	0
1	B	1342	0	1342	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	585	0	319	3	0
2	F	487	0	262	6	0
3	D	1749	0	1652	12	0
3	G	1712	0	1578	28	0
4	H	1597	0	1532	10	0
4	I	1568	0	1458	19	0
5	C	2	0	0	0	0
5	F	2	0	0	0	0
6	A	7	0	0	0	0
6	B	34	0	0	0	0
6	C	12	0	0	0	0
6	D	35	0	0	0	0
6	F	5	0	0	0	0
6	G	21	0	0	0	0
6	H	55	0	0	0	0
6	I	20	0	0	0	0
All	All	10339	0	9049	86	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 5.

The worst 5 of 86 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:231:CYS:SG	4:I:212:CYS:N	2.46	0.87
1:A:342:ARG:NH2	2:F:10:DT:O4	2.19	0.75
1:A:309:LEU:HD21	1:A:364:LEU:HG	1.72	0.70
1:A:308:ASN:HD21	2:F:10:DT:H3	1.40	0.69
1:A:324:LYS:HA	1:A:341:VAL:HG11	1.75	0.68

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	168/347 (48%)	147 (88%)	20 (12%)	1 (1%)	22	43
1	B	169/347 (49%)	168 (99%)	1 (1%)	0	100	100
3	D	232/246 (94%)	219 (94%)	12 (5%)	1 (0%)	30	52
3	G	231/246 (94%)	208 (90%)	21 (9%)	2 (1%)	14	31
4	H	213/215 (99%)	201 (94%)	11 (5%)	1 (0%)	25	47
4	I	213/215 (99%)	193 (91%)	19 (9%)	1 (0%)	25	47
All	All	1226/1616 (76%)	1136 (93%)	84 (7%)	6 (0%)	25	47

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	401	PRO
3	D	231	CYS
3	G	137	PHE
3	G	208	THR
4	H	149	ASP

### 5.3.2 Protein sidechains ⓘ

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	78/289 (27%)	74 (95%)	4 (5%)	20	42
1	B	142/289 (49%)	134 (94%)	8 (6%)	17	38
3	D	185/208 (89%)	181 (98%)	4 (2%)	47	72
3	G	174/208 (84%)	163 (94%)	11 (6%)	15	32
4	H	180/187 (96%)	170 (94%)	10 (6%)	17	38
4	I	169/187 (90%)	156 (92%)	13 (8%)	10	22
All	All	928/1368 (68%)	878 (95%)	50 (5%)	18	39

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	72	THR
4	H	178	THR
4	I	212	CYS
4	H	120	ASP
4	H	148	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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 <sup>2</sup> )	Q<0.9
1	A	169/347 (48%)	1.77	76 (44%) <b>1</b> <b>1</b>	31, 106, 144, 151	1 (0%)
1	B	171/347 (49%)	0.07	3 (1%) 67 62	33, 49, 72, 83	0
2	C	28/28 (100%)	-0.09	1 (3%) 46 40	35, 48, 70, 112	0
2	F	23/28 (82%)	0.56	5 (21%) <b>3</b> <b>2</b>	51, 60, 128, 148	0
3	D	234/246 (95%)	0.43	18 (7%) <b>21</b> <b>17</b>	30, 50, 111, 134	0
3	G	233/246 (94%)	1.06	67 (28%) <b>1</b> <b>1</b>	38, 62, 140, 153	0
4	H	215/215 (100%)	0.27	12 (5%) 31 25	30, 47, 95, 119	0
4	I	215/215 (100%)	0.95	38 (17%) <b>4</b> <b>3</b>	39, 70, 127, 153	0
All	All	1288/1672 (77%)	0.72	220 (17%) <b>5</b> <b>4</b>	30, 58, 134, 153	1 (0%)

The worst 5 of 220 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	145	SER	5.9
2	C	-4	DA	5.8
3	G	209	TYR	5.6
3	G	138	PRO	5.5
1	A	458	SER	5.3

### 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<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
5	K	F	101	1/1	0.91	0.06	56,56,56,56	0
5	K	F	102	1/1	0.97	0.03	41,41,41,41	0
5	K	C	101	1/1	0.99	0.02	35,35,35,35	0
5	K	C	102	1/1	0.99	0.05	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.