



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 2, 2017 – 05:44 PM EDT

PDB ID : 1N4X  
Title : Structure of scFv 1696 at acidic pH  
Authors : Lescar, J.; Brynda, J.; Fabry, M.; Horejsi, M.; Rezacova, P.; Sedlacek, J.; Bentley, G.A.  
Deposited on : unknown  
Resolution : 1.70 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

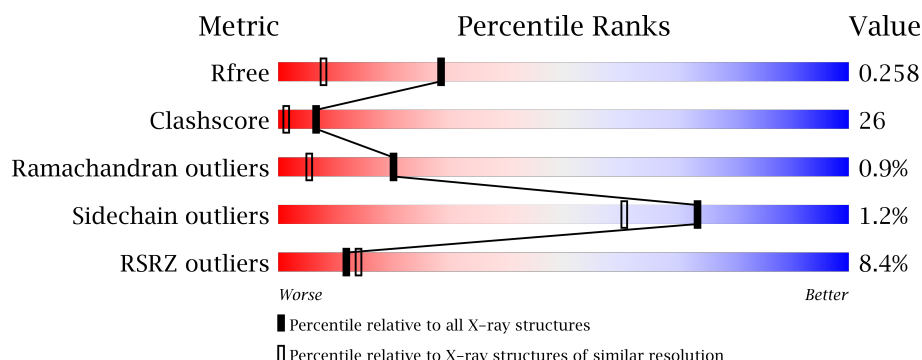
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	100719	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	L	113	<div> <div>16%</div> <div> <div></div> <div>67%</div> <div>33%</div> </div> </div>
1	M	113	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>27%</div> <div>.</div> </div> </div>
2	H	120	<div> <div>10%</div> <div> <div></div> <div>70%</div> <div>27%</div> <div>.</div> </div> </div>
2	I	120	<div> <div>4%</div> <div> <div></div> <div>68%</div> <div>30%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4188 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 immunoglobulin kappa chain variable region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	113	Total	C	N	O	S	0	0	0
			874	556	145	170	3			
1	M	113	Total	C	N	O	S	0	0	0
			874	555	145	170	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	0	MET	-	initiating MET	UNP Q99M37
L	111	ILE	-	CLONING ARTIFACT	UNP Q99M37
L	112	ALA	-	CLONING ARTIFACT	UNP Q99M37
M	0	MET	-	initiating MET	UNP Q99M37
M	111	ILE	-	CLONING ARTIFACT	UNP Q99M37
M	112	ALA	-	CLONING ARTIFACT	UNP Q99M37

- Molecule 2 is a protein called immunoglobulin heavy chain variable region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	120	Total	C	N	O	S	0	0	0
			957	607	155	192	3			
2	I	119	Total	C	N	O	S	0	0	0
			951	604	154	190	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	301	GLU	-	CLONING ARTIFACT	UNP Q921A6
H	302	VAL	-	CLONING ARTIFACT	UNP Q921A6
H	303	GLN	-	CLONING ARTIFACT	UNP Q921A6
H	418	VAL	-	CLONING ARTIFACT	UNP Q921A6
H	419	SER	-	CLONING ARTIFACT	UNP Q921A6
H	420	ALA	-	CLONING ARTIFACT	UNP Q921A6

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Chain	Residue	Modelled	Actual	Comment	Reference
I	301	GLU	-	CLONING ARTIFACT	UNP Q921A6
I	302	VAL	-	CLONING ARTIFACT	UNP Q921A6
I	303	GLN	-	CLONING ARTIFACT	UNP Q921A6
I	418	VAL	-	CLONING ARTIFACT	UNP Q921A6
I	419	SER	-	CLONING ARTIFACT	UNP Q921A6
I	420	ALA	-	CLONING ARTIFACT	UNP Q921A6

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Cl 1 1	0	0
3	I	1	Total Cl 1 1	0	0

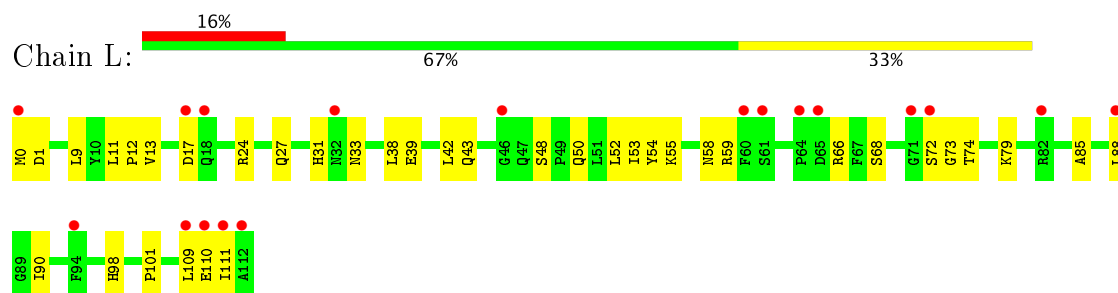
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	L	106	Total O 106 106	0	0
4	H	156	Total O 156 156	0	0
4	M	114	Total O 114 114	0	0
4	I	154	Total O 154 154	0	0

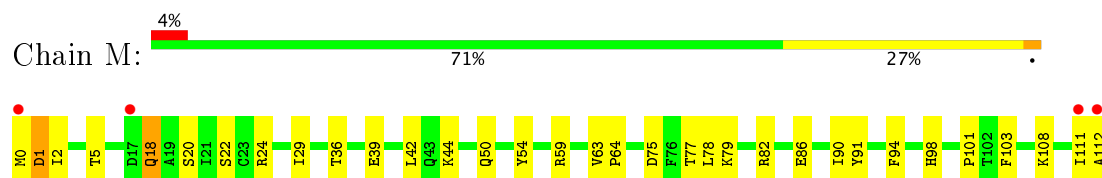
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

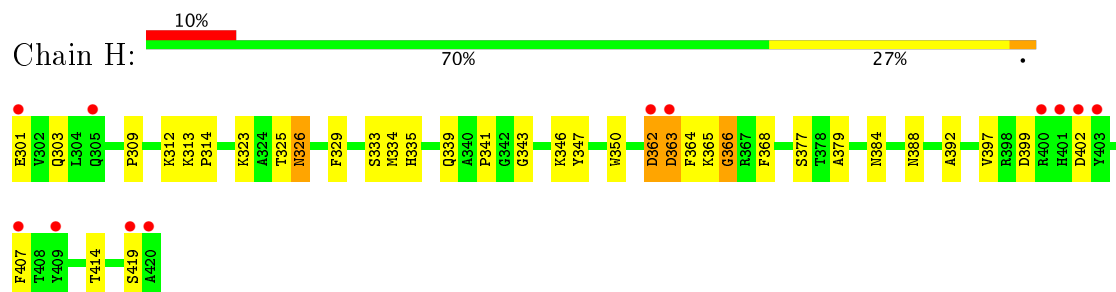
- Molecule 1: immunoglobulin kappa chain variable region



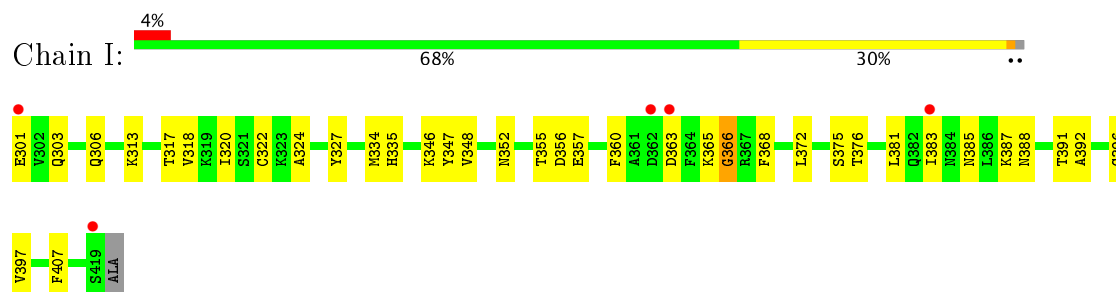
- Molecule 1: immunoglobulin kappa chain variable region



- Molecule 2: immunoglobulin heavy chain variable region



- Molecule 2: immunoglobulin heavy chain variable region



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.93 Å 61.21 Å 57.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.70 19.86 – 1.70	Depositor EDS
% Data completeness (in resolution range)	91.0 (20.00-1.70) 91.1 (19.86-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.08 (at 1.70 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.227 , 0.256 0.228 , 0.258	Depositor DCC
$R_{free}$ test set	2280 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.3	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 52.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4188	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.16% 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: CL

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	L	0.31	0/896	0.59	0/1215
1	M	0.34	0/896	0.64	0/1214
2	H	0.34	0/982	0.64	0/1333
2	I	0.35	0/976	0.68	1/1326 (0.1%)
All	All	0.34	0/3750	0.64	1/5088 (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	I	366	GLY	N-CA-C	5.63	127.19	113.10

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	L	874	0	845	49	0
1	M	874	0	843	40	0
2	H	957	0	893	50	0
2	I	951	0	888	51	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	156	0	0	42	1
4	I	154	0	0	39	2
4	L	106	0	0	31	1
4	M	114	0	0	26	0
All	All	4188	0	3469	187	2

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 26.

The worst 5 of 187 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)
2:H:325:THR:HB	4:H:1086:HOH:O	1.46	1.14
2:H:303:GLN:HB2	4:H:1086:HOH:O	1.48	1.11
1:M:0:MET:HB2	4:I:1119:HOH:O	1.54	1.07
4:L:211:HOH:O	2:I:375:SER:HB3	1.58	1.01
2:I:306:GLN:HB3	4:I:1122:HOH:O	1.64	0.96

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:1127:HOH:O	4:I:1118:HOH:O[2_564]	2.17	0.03
4:L:119:HOH:O	4:I:1127:HOH:O[2_564]	2.18	0.02

## 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	L	111/113 (98%)	106 (96%)	5 (4%)	0	100	100
1	M	111/113 (98%)	107 (96%)	3 (3%)	1 (1%)	20	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	118/120 (98%)	112 (95%)	3 (2%)	3 (2%)	6	1
2	I	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
All	All	457/466 (98%)	438 (96%)	15 (3%)	4 (1%)	20	5

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	362	ASP
1	M	1	ASP
2	H	363	ASP
2	H	366	GLY

### 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	L	97/98 (99%)	97 (100%)	0	100	100
1	M	97/98 (99%)	95 (98%)	2 (2%)	59	40
2	H	103/103 (100%)	102 (99%)	1 (1%)	80	71
2	I	103/103 (100%)	101 (98%)	2 (2%)	62	45
All	All	400/402 (100%)	395 (99%)	5 (1%)	73	60

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	326	ASN
1	M	18	GLN
1	M	75	ASP
2	I	303	GLN
2	I	313	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	388	ASN
1	M	18	GLN
2	I	335	HIS
2	H	335	HIS
2	I	305	GLN

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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 [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<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	L	113/113 (100%)	1.20	18 (15%) 2 2	18, 31, 47, 54	0
1	M	113/113 (100%)	0.49	4 (3%) 44 50	15, 23, 36, 55	0
2	H	120/120 (100%)	0.63	12 (10%) 8 9	14, 22, 45, 52	0
2	I	119/120 (99%)	0.39	5 (4%) 37 42	15, 21, 36, 40	0
All	All	465/466 (99%)	0.68	39 (8%) 12 14	14, 24, 43, 55	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	0	MET	8.7
1	L	0	MET	8.5
1	M	112	ALA	8.4
2	H	420	ALA	8.3
1	L	112	ALA	7.9

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	I	1001	1/1	0.99	0.15	1.13	7,7,7,7	0
3	CL	H	1002	1/1	0.98	0.26	0.93	17,17,17,17	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.