



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 04:15 pm GMT

PDB ID : 1MLC  
Title : MONOCLONAL ANTIBODY FAB D44.1 RAISED AGAINST CHICKEN EGG-WHITE LYSOZYME COMPLEXED WITH LYSOZYME  
Authors : Braden, B.C.; Souchon, H.; Eisele, J.-L.; Bentley, G.A.; Bhat, T.N.; Navaza, J.; Poljak, R.J.  
Deposited on : 1995-03-10  
Resolution : 2.50 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.

---

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

MolProbity : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

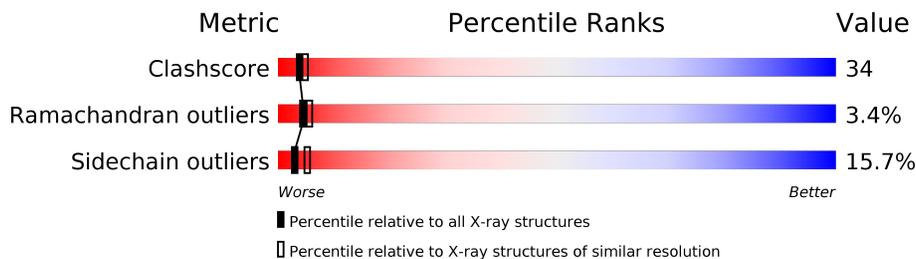
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	214	
1	C	214	
2	B	218	
2	D	218	
3	E	129	
3	F	129	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8792 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 IGG1-KAPPA D44.1 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	214	Total	C	N	O	S	0	0	0
			1658	1023	283	345	7			
1	C	214	Total	C	N	O	S	0	0	0
			1658	1023	283	345	7			

- Molecule 2 is a protein called IGG1-KAPPA D44.1 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	218	Total	C	N	O	S	0	0	0
			1632	1029	266	329	8			
2	D	218	Total	C	N	O	S	0	0	0
			1632	1029	266	329	8			

- Molecule 3 is a protein called HEN EGG WHITE LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	129	Total	C	N	O	S	0	0	0
			1001	613	193	185	10			
3	F	129	Total	C	N	O	S	0	0	0
			1001	613	193	185	10			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	A	47	Total	O	0	0
			47	47		
4	B	48	Total	O	0	0
			48	48		
4	C	35	Total	O	0	0
			35	35		
4	D	35	Total	O	0	0
			35	35		

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	E	22	Total	O	0	0
			22	22		
4	F	23	Total	O	0	0
			23	23		

### 3 Residue-property plots

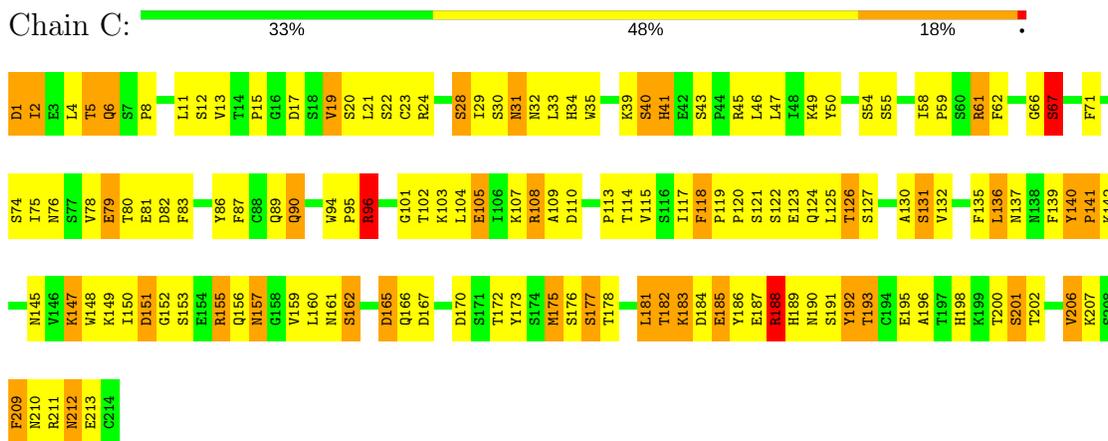
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

- Molecule 1: IGG1-KAPPA D44.1 FAB (LIGHT CHAIN)



- Molecule 1: IGG1-KAPPA D44.1 FAB (LIGHT CHAIN)



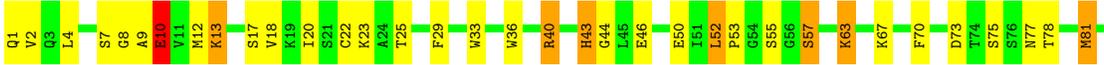
- Molecule 2: IGG1-KAPPA D44.1 FAB (HEAVY CHAIN)





- Molecule 2: IGG1-KAPPA D44.1 FAB (HEAVY CHAIN)

Chain D: 45% 45% 8%



- Molecule 3: HEN EGG WHITE LYSOZYME

Chain E: 35% 43% 17% 5%



- Molecule 3: HEN EGG WHITE LYSOZYME

Chain F: 50% 37% 8% 5%



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.70Å 167.30Å 84.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-2.50)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.184 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8792	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

## 5 Model quality i

### 5.1 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 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	1.00	0/1695	1.93	38/2298 (1.7%)
1	C	0.98	0/1695	1.87	35/2298 (1.5%)
2	B	1.10	1/1676 (0.1%)	1.95	29/2290 (1.3%)
2	D	1.01	1/1676 (0.1%)	1.74	20/2290 (0.9%)
3	E	0.89	0/1021	1.87	25/1379 (1.8%)
3	F	0.97	1/1021 (0.1%)	2.01	29/1379 (2.1%)
All	All	1.00	3/8784 (0.0%)	1.89	176/11934 (1.5%)

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 outliers	#Planarity outliers
1	A	0	1
3	E	0	1
3	F	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	101	GLY	N-CA	7.17	1.56	1.46
2	B	101	GLY	N-CA	6.57	1.55	1.46
3	F	35	GLU	CD-OE2	-5.20	1.20	1.25

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	40	ARG	NE-CZ-NH1	20.44	130.52	120.30
3	E	68	ARG	NE-CZ-NH1	19.01	129.80	120.30
1	A	211	ARG	NE-CZ-NH2	-16.75	111.93	120.30
3	E	68	ARG	NE-CZ-NH2	-16.17	112.22	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	68	ARG	NE-CZ-NH1	15.51	128.06	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ARG	Sidechain
3	E	68	ARG	Sidechain
3	F	5	ARG	Sidechain

## 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	1658	0	1572	93	0
1	C	1658	0	1572	165	0
2	B	1632	0	1576	67	0
2	D	1632	0	1576	110	0
3	E	1001	0	959	98	0
3	F	1001	0	959	49	0
4	A	47	0	0	3	0
4	B	48	0	0	3	0
4	C	35	0	0	2	0
4	D	35	0	0	3	0
4	E	22	0	0	0	0
4	F	23	0	0	2	0
All	All	8792	0	8214	560	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 34.

The worst 5 of 560 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)
1:C:187:GLU:HA	1:C:211:ARG:NH1	1.60	1.15

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:GLU:HG2	1:A:206:VAL:HG22	1.29	1.09
1:A:115:VAL:HG12	1:A:207:LYS:HG3	1.25	1.08
3:E:121:GLN:HA	3:E:124:ILE:HD11	1.38	1.05
2:D:187:PRO:HD2	2:D:190:PRO:HG2	1.37	1.04

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	212/214 (99%)	199 (94%)	7 (3%)	6 (3%)	6	8
1	C	212/214 (99%)	180 (85%)	26 (12%)	6 (3%)	6	8
2	B	216/218 (99%)	194 (90%)	19 (9%)	3 (1%)	13	23
2	D	216/218 (99%)	175 (81%)	30 (14%)	11 (5%)	2	2
3	E	127/129 (98%)	99 (78%)	18 (14%)	10 (8%)	1	1
3	F	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	11	19
All	All	1110/1122 (99%)	958 (86%)	114 (10%)	38 (3%)	4	5

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
2	B	134	GLN
1	C	67	SER
1	C	213	GLU
2	D	160	GLY

### 5.3.2 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 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	194/194 (100%)	163 (84%)	31 (16%)	3	5
1	C	194/194 (100%)	160 (82%)	34 (18%)	2	4
2	B	184/184 (100%)	159 (86%)	25 (14%)	4	8
2	D	184/184 (100%)	155 (84%)	29 (16%)	3	5
3	E	105/105 (100%)	85 (81%)	20 (19%)	2	3
3	F	105/105 (100%)	92 (88%)	13 (12%)	5	10
All	All	966/966 (100%)	814 (84%)	152 (16%)	3	5

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	67	SER
1	C	185	GLU
3	F	25	LEU
1	C	96	ARG
1	C	141	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	137	ASN
1	C	161	ASN
3	E	113	ASN
1	C	145	ASN
1	C	198	HIS

### 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](#)

There are no ligands in this entry.

## 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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.