



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 05:44 am GMT

PDB ID : 2VXU  
Title : CRYSTAL STRUCTURE OF MURINE REFERENCE ANTIBODY 125-2H  
FAB FRAGMENT  
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Deposited on : 2008-07-10  
Resolution : 2.36 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 : trunk28620  
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) : recalc28949

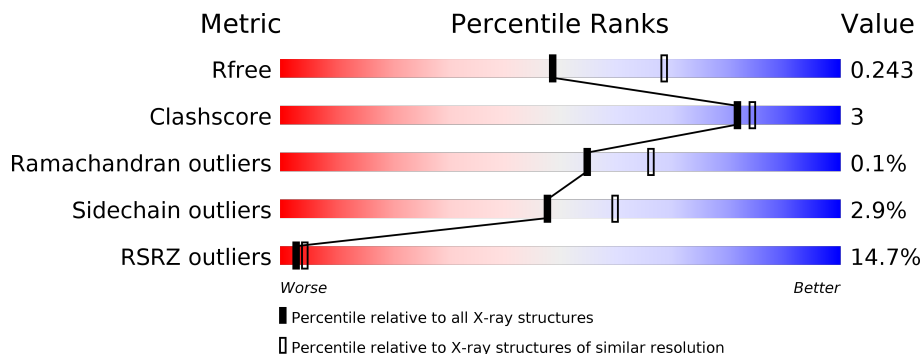
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.36 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	1522 (2.38-2.34)
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)
RSRZ outliers	101464	1528 (2.38-2.34)

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	H	216	<div> <div>19%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	I	216	<div> <div>13%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
2	L	214	<div> <div>12%</div> <div> <div></div> <div>88%</div> <div>11%</div> <div>.</div> </div> </div>
2	M	214	<div> <div>14%</div> <div> <div></div> <div>91%</div> <div>8%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7186 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 MURINE IGG 125-2H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	216	Total	C	N	O	S	0	5	0
			1673	1060	276	329	8			
1	I	216	Total	C	N	O	S	0	5	0
			1671	1059	276	329	7			

- Molecule 2 is a protein called MURINE IGG 125-2H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	5	0
			1696	1049	283	355	9			
2	M	214	Total	C	N	O	S	0	0	0
			1658	1029	277	345	7			

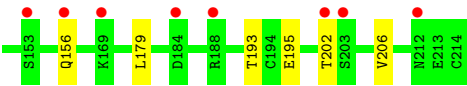
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	135	Total	O	0	0
			135	135		
3	I	121	Total	O	0	0
			121	121		
3	L	109	Total	O	0	0
			109	109		
3	M	123	Total	O	0	0
			123	123		



- Molecule 1: MURINE IGG 125-2H





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.06Å 92.49Å 137.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.42 – 2.36 17.42 – 2.37	Depositor EDS
% Data completeness (in resolution range)	98.2 (17.42-2.36) 97.6 (17.42-2.37)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.57 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.184 , 0.242 0.189 , 0.243	Depositor DCC
$R_{free}$ test set	2065 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.3	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 39.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7186	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.63 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7828e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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](#)

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	H	0.99	13/1718 (0.8%)	0.90	5/2347 (0.2%)
1	I	0.56	0/1716	0.70	0/2344
2	L	0.71	4/1731 (0.2%)	0.69	0/2345
2	M	0.54	0/1693	0.68	1/2294 (0.0%)
All	All	0.72	17/6858 (0.2%)	0.75	6/9330 (0.1%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	74	SER	C-N	12.67	1.63	1.34
1	H	74	SER	CB-OG	12.11	1.57	1.42
2	L	14	SER	CA-CB	10.66	1.69	1.52
2	L	107	LYS	CD-CE	10.12	1.76	1.51
1	H	72	ASP	CB-CG	9.16	1.71	1.51

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	31	ASP	CB-CG-OD1	13.24	130.22	118.30
1	H	72	ASP	CB-CG-OD2	-12.54	107.01	118.30
1	H	72	ASP	CB-CG-OD1	8.19	125.67	118.30
2	M	104	LEU	CA-CB-CG	6.37	129.94	115.30
1	H	31	ASP	CB-CG-OD2	-5.56	113.30	118.30

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	H	1673	0	1623	7	0
1	I	1671	0	1624	9	0
2	L	1696	0	1604	17	0
2	M	1658	0	1583	9	0
3	H	135	0	0	1	0
3	I	121	0	0	0	0
3	L	109	0	0	1	0
3	M	123	0	0	0	0
All	All	7186	0	6434	39	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 3.

The worst 5 of 39 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:L:107:LYS:CE	2:L:107:LYS:CD	1.76	1.63
2:L:21:LEU:HD22	2:L:102:THR:HG21	1.54	0.86
1:H:96[A]:LEU:HD13	2:L:89:LEU:HD21	1.59	0.84
2:L:107:LYS:CE	2:L:107:LYS:CG	2.61	0.79
1:I:95[B]:GLY:O	1:I:96[B]:LEU:HB2	1.97	0.65

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	H	219/216 (101%)	211 (96%)	6 (3%)	2 (1%)	20	21
1	I	219/216 (101%)	211 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	217/214 (101%)	212 (98%)	5 (2%)	0	100	100
2	M	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
All	All	867/860 (101%)	842 (97%)	23 (3%)	2 (0%)	55	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	41[A]	HIS
1	H	41[B]	HIS

### 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	H	191/187 (102%)	181 (95%)	10 (5%)	27	33
1	I	190/187 (102%)	186 (98%)	4 (2%)	59	72
2	L	196/191 (103%)	193 (98%)	3 (2%)	70	81
2	M	191/191 (100%)	185 (97%)	6 (3%)	45	56
All	All	768/756 (102%)	745 (97%)	23 (3%)	48	58

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	28	SER
1	I	71	VAL
2	M	156	GLN
1	I	44	SER
1	I	82(B)	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	131	GLN
2	M	190	ASN
2	L	212	ASN
1	I	73	GLN
2	M	156	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](#)

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 [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	H	216/216 (100%)	1.12	42 (19%) <b>1</b> <b>2</b>	40, 49, 58, 64	0
1	I	216/216 (100%)	0.95	27 (12%) <b>4</b> <b>7</b>	39, 48, 55, 60	0
2	L	214/214 (100%)	0.95	26 (12%) <b>5</b> <b>8</b>	43, 50, 55, 61	0
2	M	214/214 (100%)	1.01	31 (14%) <b>3</b> <b>5</b>	41, 48, 53, 56	0
All	All	860/860 (100%)	1.01	126 (14%) <b>3</b> <b>4</b>	39, 49, 55, 64	0

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	42	GLY	5.7
2	M	202	THR	5.1
1	H	132	THR	4.7
1	H	1	GLU	4.5
2	L	33	LEU	4.0

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.