



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2017 – 01:30 PM EDT

PDB ID : 5NPI  
Title : Structure of the Hepatitis C virus strain J4 glycoprotein E2 antigenic region 532-540 bound to the single chain variable fragment of the non-neutralizing antibody DAO5  
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Deposited on : 2017-04-16  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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-20029077
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-20029077

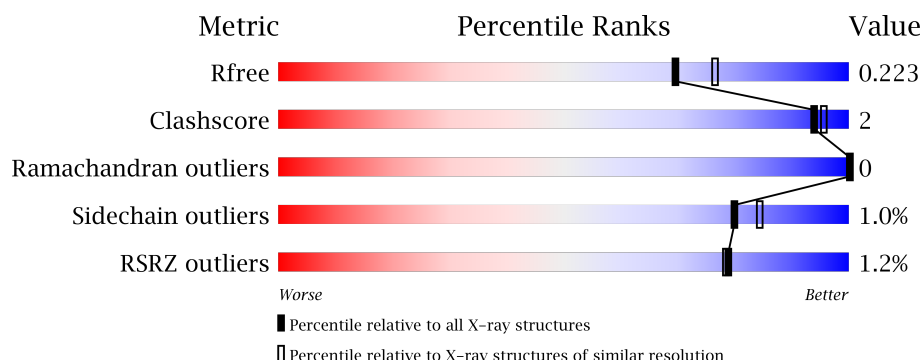
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	A	288	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -10px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>76%</span> <span>5%</span> <span>19%</span> </div> </div>
1	B	288	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -10px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>76%</span> <span>5%</span> <span>19%</span> </div> </div>
2	D	12	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -10px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>75%</span> <span>25%</span> </div> </div>
2	E	12	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -10px; left: 0;">8%</span> </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>92%</span> <span>8%</span> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3996 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 Single chain variable fragment of the non-neutralizing antibody DAO5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1783	1132	296	349	6			
1	B	233	Total	C	N	O	S	0	0	0
			1787	1134	297	350	6			

- Molecule 2 is a protein called Epitope peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	S	0	0	0
			85	50	13	21	1			
2	D	9	Total	C	N	O	S	0	0	0
			72	43	11	17	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	131	Total	O	0	0
			131	131		
3	B	126	Total	O	0	0
			126	126		
3	E	7	Total	O	0	0
			7	7		
3	D	5	Total	O	0	0
			5	5		



- Molecule 1: Single chain variable fragment of the non-neutralizing antibody DAO5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.94Å 155.94Å 61.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.16 – 2.00 48.29 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.4 (20.16-2.00) 97.5 (48.29-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.197 , 0.217 0.199 , 0.223	Depositor DCC
$R_{free}$ test set	2561 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 48.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3996	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 2.86% 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](#)

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	0.52	0/1829	0.65	0/2478
1	B	0.49	0/1833	0.64	0/2483
2	D	0.59	0/71	0.76	0/94
2	E	0.52	0/84	0.67	0/111
All	All	0.51	0/3817	0.65	0/5166

There are no bond length outliers.

There are no bond angle outliers.

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	1783	0	1719	6	0
1	B	1787	0	1722	6	0
2	D	72	0	68	0	0
2	E	85	0	77	0	0
3	A	131	0	0	1	0
3	B	126	0	0	0	0
3	D	5	0	0	0	0
3	E	7	0	0	0	0
All	All	3996	0	3586	12	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 2.

All (12) 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:B:161:LEU:HD22	1:B:242:THR:HG21	1.80	0.64
1:B:43:PRO:HG2	1:B:225:MET:HG3	1.90	0.53
1:A:80:HIS:HD2	3:A:336:HOH:O	1.94	0.51
1:B:231:THR:HA	1:B:236:LEU:HD22	1.98	0.44
1:A:43:PRO:HD2	1:A:225:MET:HE3	2.00	0.44
1:B:171:ASN:O	1:B:190:TYR:HA	2.19	0.43
1:A:171:ASN:O	1:A:190:TYR:HA	2.20	0.42
1:B:177:GLN:HB2	1:B:187:LEU:HD11	2.02	0.41
1:A:231:THR:HA	1:A:236:LEU:HD22	2.02	0.41
1:B:172:TYR:HB2	1:B:232:ASN:HB2	2.03	0.41
1:A:142:ILE:HD12	1:A:167:GLN:HG2	2.03	0.40
1:A:225:MET:HG2	1:A:227:PHE:CZ	2.57	0.40

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	A	228/288 (79%)	220 (96%)	8 (4%)	0	100	100
1	B	229/288 (80%)	221 (96%)	8 (4%)	0	100	100
2	D	7/12 (58%)	7 (100%)	0	0	100	100
2	E	9/12 (75%)	8 (89%)	1 (11%)	0	100	100
All	All	473/600 (79%)	456 (96%)	17 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	197/226 (87%)	194 (98%)	3 (2%)	70	74
1	B	197/226 (87%)	196 (100%)	1 (0%)	91	93
2	D	9/11 (82%)	9 (100%)	0	100	100
2	E	10/11 (91%)	10 (100%)	0	100	100
All	All	413/474 (87%)	409 (99%)	4 (1%)	80	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	67	LYS
1	A	98	ARG
1	B	39	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	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

There are no ligands in this entry.

## 5.7 Other polymers

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	232/288 (80%)	-0.09	2 (0%) 84 83	17, 24, 43, 64	0
1	B	233/288 (80%)	-0.04	3 (1%) 77 77	19, 26, 45, 85	0
2	D	9/12 (75%)	0.16	0 100 100	22, 30, 57, 59	0
2	E	11/12 (91%)	0.47	1 (9%) 10 10	22, 27, 56, 71	0
All	All	485/600 (80%)	-0.05	6 (1%) 79 78	17, 25, 46, 85	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	531	GLU	3.8
1	B	248	ALA	3.0
1	B	216	ASN	2.9
1	A	170	TYR	2.4
1	B	158	ARG	2.3
1	A	66	GLY	2.0

### 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

There are no such residues in this entry.