



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6WMH  
Title : Next generation monomeric IgG4 Fc  
Authors : Oganessian, V.Y.; Shan, L.; van Dyk, N.; Dall'Acqua, W.F.  
Deposited on : 2020-04-21  
Resolution : 2.30 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.

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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)	:	1.13
EDS	:	2.23.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

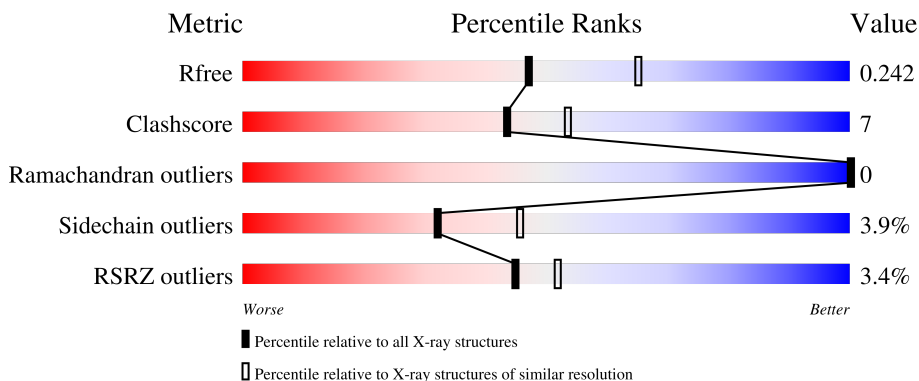
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	207	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>.</div> </div> </div>
1	H	207	<div> <div></div> <div> <div>84%</div> <div>14%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3496 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 heavy constant gamma 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	207	Total	C	N	O	S	0	0	0
			1674	1058	283	327	6			
1	A	206	Total	C	N	O	S	0	0	0
			1668	1055	282	325	6			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	252	TYR	MET	engineered mutation	UNP P01861
H	254	THR	SER	engineered mutation	UNP P01861
H	256	GLU	THR	engineered mutation	UNP P01861
H	297	ASP	ASN	engineered mutation	UNP P01861
H	351	PHE	LEU	engineered mutation	UNP P01861
H	354	GLU	SER	engineered mutation	UNP P01861
H	366	ARG	THR	engineered mutation	UNP P01861
H	395	LYS	PRO	engineered mutation	UNP P01861
H	405	ARG	PHE	engineered mutation	UNP P01861
H	407	GLU	TYR	engineered mutation	UNP P01861
A	252	TYR	MET	engineered mutation	UNP P01861
A	254	THR	SER	engineered mutation	UNP P01861
A	256	GLU	THR	engineered mutation	UNP P01861
A	297	ASP	ASN	engineered mutation	UNP P01861
A	351	PHE	LEU	engineered mutation	UNP P01861
A	354	GLU	SER	engineered mutation	UNP P01861
A	366	ARG	THR	engineered mutation	UNP P01861
A	395	LYS	PRO	engineered mutation	UNP P01861
A	405	ARG	PHE	engineered mutation	UNP P01861
A	407	GLU	TYR	engineered mutation	UNP P01861

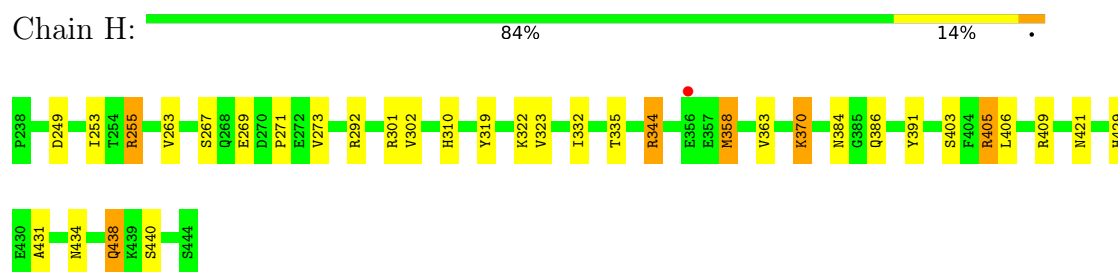
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	98	Total 98	O 98	0	0
2	A	56	Total 56	O 56	0	0

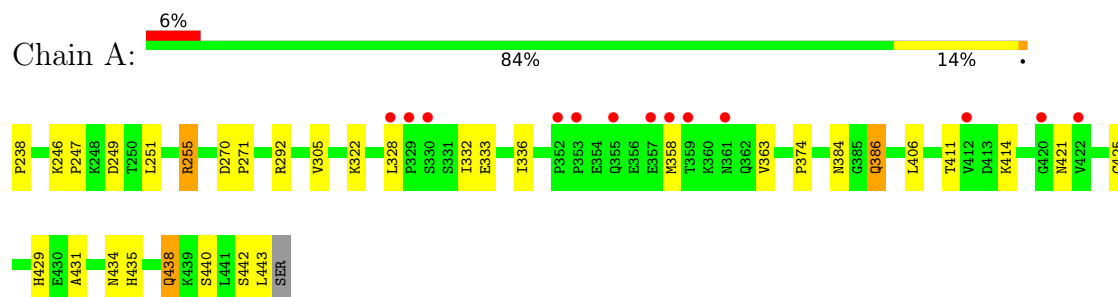
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 heavy constant gamma 4



- Molecule 1: Immunoglobulin heavy constant gamma 4



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.97Å 110.92Å 87.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 2.30 37.74 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.0 (35.00-2.30) 99.0 (37.74-2.30)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.201 , 0.243 0.208 , 0.242	Depositor DCC
$R_{free}$ test set	1047 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.4	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 24.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3496	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.76% 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

### 5.1 Standard geometry

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	0.84	0/1711	1.02	0/2324
1	H	0.86	0/1717	0.97	0/2332
All	All	0.85	0/3428	1.00	0/4656

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

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	1668	0	1620	21	0
1	H	1674	0	1625	23	0
2	A	56	0	0	1	0
2	H	98	0	0	1	1
All	All	3496	0	3245	44	1

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 7.

The worst 5 of 44 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:A:384:ASN:HD21	1:A:421:ASN:ND2	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:GLN:HB3	2:A:514:HOH:O	1.87	0.72
1:A:384:ASN:HD21	1:A:421:ASN:HD22	1.36	0.72
1:H:370:LYS:HE3	1:H:405:ARG:HH21	1.62	0.63
1:H:384:ASN:HD21	1:H:421:ASN:ND2	2.01	0.58

All (1) 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)
2:H:596:HOH:O	2:H:597:HOH:O[6_555]	2.00	0.20

## 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	204/207 (99%)	201 (98%)	3 (2%)	0	100	100
1	H	205/207 (99%)	201 (98%)	4 (2%)	0	100	100
All	All	409/414 (99%)	402 (98%)	7 (2%)	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	194/195 (100%)	188 (97%)	6 (3%)	40	55
1	H	195/195 (100%)	186 (95%)	9 (5%)	27	38
All	All	389/390 (100%)	374 (96%)	15 (4%)	32	46

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	405	ARG
1	A	386	GLN
1	H	438	GLN
1	A	438	GLN
1	A	305	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	434	ASN
1	A	435	HIS
1	A	438	GLN
1	H	434	ASN
1	H	438	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	A	206/207 (99%)	0.20	13 (6%) 20 25	25, 47, 99, 173	0
1	H	207/207 (100%)	-0.23	1 (0%) 91 94	26, 38, 64, 113	0
All	All	413/414 (99%)	-0.02	14 (3%) 45 52	25, 42, 89, 173	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	357	GLU	7.0
1	A	329	PRO	6.4
1	A	358	MET	6.2
1	A	359	THR	4.3
1	A	361	ASN	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 monosaccharides 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.