



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 05:00 pm BST

PDB ID : 5WNA
Title : Structure of antibody 3D3 bound to the central conserved region of RSV G
Authors : Fedechkin, S.O.; George, N.L.; Wolff, J.T.; Kauvar, L.M.; DuBois, R.M.
Deposited on : 2017-07-31
Resolution : 2.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

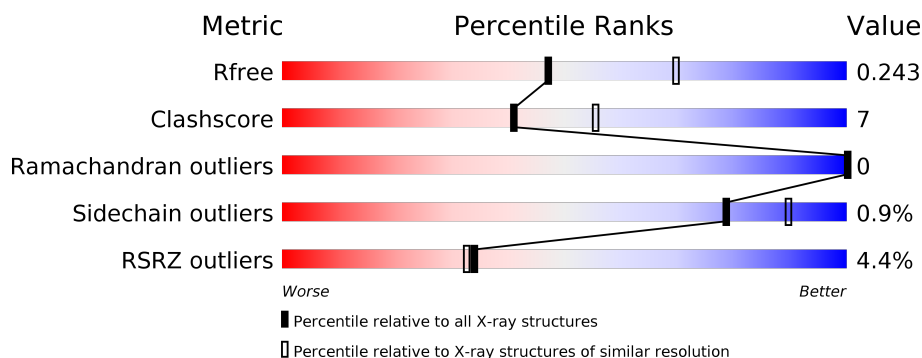
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 ≥ 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	C	231	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div></div> </div> </div>
1	H	231	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div></div> </div> </div>
2	D	213	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>17%</div> <div></div> </div> </div>
2	L	213	<div> <div>0%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div></div> </div> </div>
3	A	45	<div> <div>9%</div> <div> <div></div> <div>56%</div> <div>9%</div> <div>33%</div> </div> </div>
3	B	45	<div> <div>11%</div> <div> <div></div> <div>58%</div> <div>9%</div> <div>33%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7256 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 mAb 3D3 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	227	Total	C	N	O	S	0	0	0
			1692	1066	286	332	8			
1	C	225	Total	C	N	O	S	0	0	0
			1683	1059	288	329	7			

- Molecule 2 is a protein called mAb 3D3 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	1	0
			1628	1020	277	327	4			
2	D	211	Total	C	N	O	S	0	0	0
			1636	1024	281	327	4			

- Molecule 3 is a protein called Major surface glycoprotein G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	30	Total	C	N	O	S	0	0	0
			238	155	38	41	4			
3	A	30	Total	C	N	O	S	0	0	0
			244	158	41	41	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	159	MET	-	initiating methionine	UNP P03423
B	160	GLY	-	expression tag	UNP P03423
B	198	HIS	-	expression tag	UNP P03423
B	199	HIS	-	expression tag	UNP P03423
B	200	HIS	-	expression tag	UNP P03423
B	201	HIS	-	expression tag	UNP P03423
B	202	HIS	-	expression tag	UNP P03423
B	203	HIS	-	expression tag	UNP P03423

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Chain	Residue	Modelled	Actual	Comment	Reference
A	159	MET	-	initiating methionine	UNP P03423
A	160	GLY	-	expression tag	UNP P03423
A	198	HIS	-	expression tag	UNP P03423
A	199	HIS	-	expression tag	UNP P03423
A	200	HIS	-	expression tag	UNP P03423
A	201	HIS	-	expression tag	UNP P03423
A	202	HIS	-	expression tag	UNP P03423
A	203	HIS	-	expression tag	UNP P03423

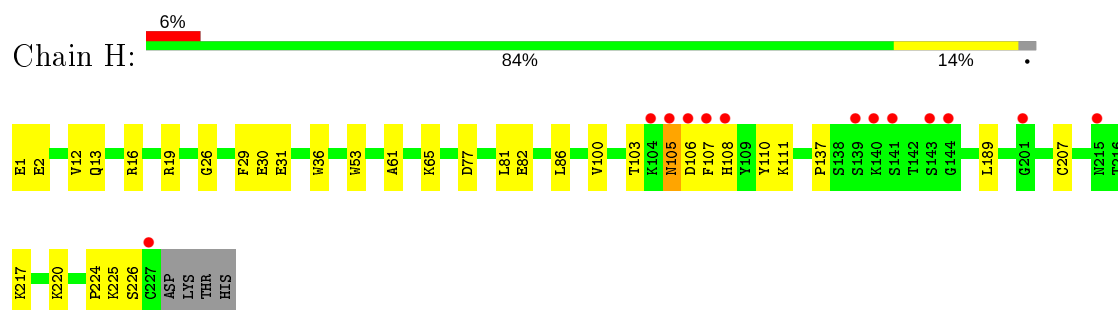
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	28	Total 28	O 28	0	0
4	L	31	Total 31	O 31	0	0
4	B	2	Total 2	O 2	0	0
4	C	32	Total 32	O 32	0	0
4	D	40	Total 40	O 40	0	0
4	A	2	Total 2	O 2	0	0

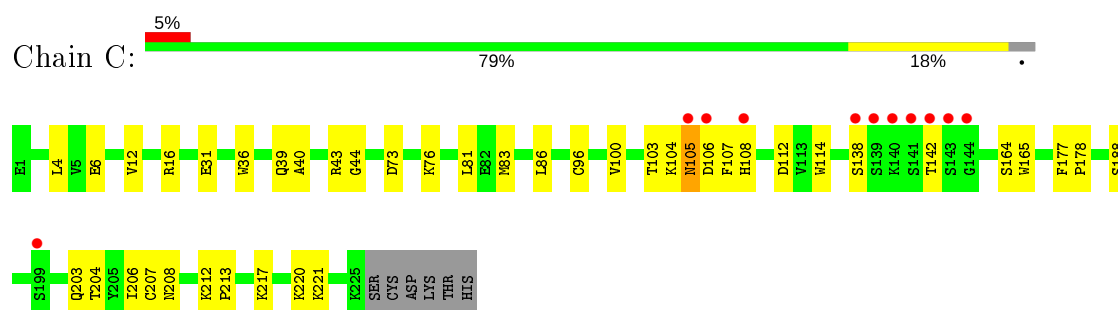
3 Residue-property plots [i](#)

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.

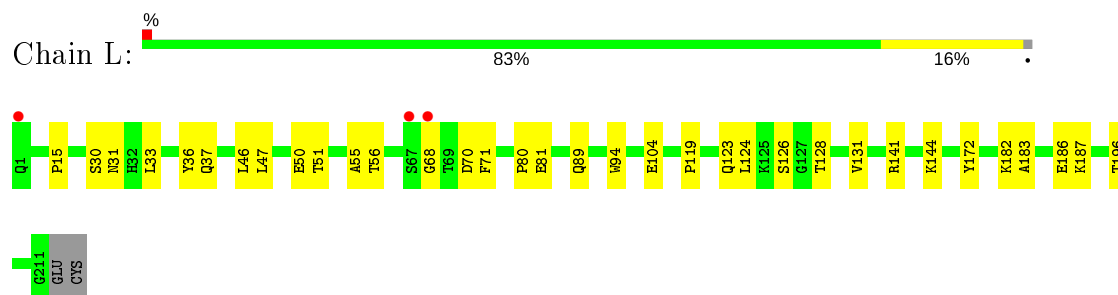
- Molecule 1: mAb 3D3 Fab heavy chain



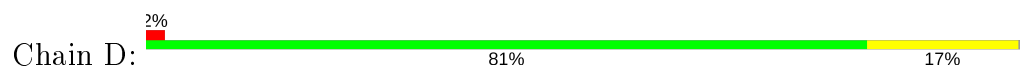
- Molecule 1: mAb 3D3 Fab heavy chain

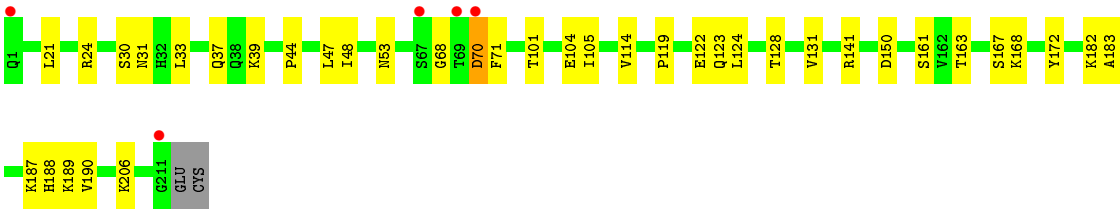


- Molecule 2: mAb 3D3 Fab light chain

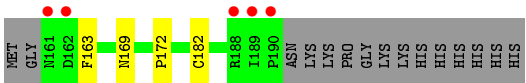


- Molecule 2: mAb 3D3 Fab light chain

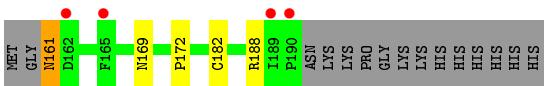




● Molecule 3: Major surface glycoprotein G



● Molecule 3: Major surface glycoprotein G



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.62Å 135.01Å 73.78Å 90.00° 107.45° 90.00°	Depositor
Resolution (Å)	48.72 – 2.40 48.72 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.72-2.40) 94.8 (48.72-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, R_{free}	0.192 , 0.245 0.196 , 0.243	Depositor DCC
R_{free} test set	2000 reflections (4.27%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7256	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	C	0.38	0/1723	0.57	0/2345
1	H	0.34	0/1731	0.54	0/2355
2	D	0.38	0/1673	0.58	0/2275
2	L	0.41	0/1670	0.56	0/2274
3	A	0.37	0/253	0.51	0/345
3	B	0.39	0/247	0.60	0/338
All	All	0.38	0/7297	0.56	0/9932

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	C	1683	0	1639	29	0
1	H	1692	0	1646	22	0
2	D	1636	0	1587	27	0
2	L	1628	0	1572	24	0
3	A	244	0	222	8	0
3	B	238	0	211	5	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	32	0	0	0	0
4	D	40	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	28	0	0	0	0
4	L	31	0	0	1	0
All	All	7256	0	6877	99	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 7.

The worst 5 of 99 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:H:19:ARG:HG3	1:H:82:GLU:HG2	1.70	0.73
2:L:123:GLN:O	2:L:126:SER:OG	2.06	0.71
2:D:21:LEU:HD22	2:D:101:THR:HG21	1.73	0.71
1:H:107:PHE:CE1	3:B:182:CYS:HB2	2.29	0.67
3:A:161:ASN:N	3:A:161:ASN:HD22	1.90	0.67

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	C	223/231 (96%)	218 (98%)	5 (2%)	0	100	100
1	H	225/231 (97%)	219 (97%)	6 (3%)	0	100	100
2	D	209/213 (98%)	205 (98%)	4 (2%)	0	100	100
2	L	210/213 (99%)	206 (98%)	4 (2%)	0	100	100
3	A	28/45 (62%)	27 (96%)	1 (4%)	0	100	100
3	B	28/45 (62%)	26 (93%)	2 (7%)	0	100	100
All	All	923/978 (94%)	901 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	C	187/196 (95%)	184 (98%)	3 (2%)	62	79
1	H	188/196 (96%)	187 (100%)	1 (0%)	88	95
2	D	184/187 (98%)	183 (100%)	1 (0%)	88	95
2	L	183/187 (98%)	182 (100%)	1 (0%)	88	95
3	A	29/42 (69%)	28 (97%)	1 (3%)	37	56
3	B	28/42 (67%)	28 (100%)	0	100	100
All	All	799/850 (94%)	792 (99%)	7 (1%)	78	90

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	112	ASP
3	A	161	ASN
1	C	188	SER
2	L	70	ASP
2	D	70	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	105	ASN
2	D	198	GLN
2	D	92	ASN
2	L	136	ASN
1	C	108	HIS

5.3.3 RNA ⓘ

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, 95th 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 ²)	Q<0.9
1	C	225/231 (97%)	0.28	11 (4%) 29 28	24, 38, 79, 104	0
1	H	227/231 (98%)	0.28	13 (5%) 23 22	25, 38, 82, 116	0
2	D	211/213 (99%)	0.24	5 (2%) 59 57	25, 38, 57, 76	0
2	L	211/213 (99%)	0.25	3 (1%) 75 73	26, 38, 59, 82	0
3	A	30/45 (66%)	0.90	4 (13%) 3 3	26, 52, 81, 84	0
3	B	30/45 (66%)	1.08	5 (16%) 1 1	41, 55, 77, 92	0
All	All	934/978 (95%)	0.31	41 (4%) 34 33	24, 39, 69, 116	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	144	GLY	7.1
3	A	190	PRO	5.2
1	C	139	SER	4.4
2	L	67	SER	4.3
1	H	141	SER	4.1

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.