



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 6QN9
Title : Structure of bovine anti-RSV Fab B4
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Deposited on : 2019-02-10
Resolution : 1.89 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

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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

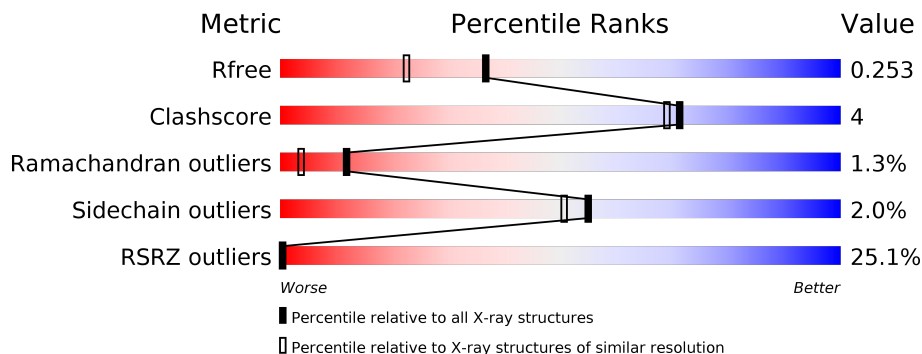
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	H	239	
2	L	214	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3072 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 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	193	1418	886	234	288	10	0	0	0

- Molecule 2 is a protein called light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	210	1565	973	262	325	5	0	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	L	1	6	3	3	0	0
3	L	1	6	3	3	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	O	S	0	0
			5	4	1		

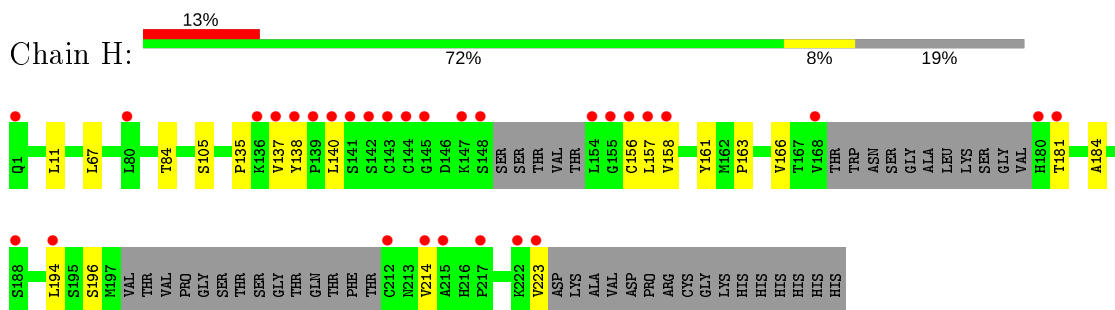
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	48	Total	O	0	0
			48	48		
5	L	24	Total	O	0	0
			24	24		

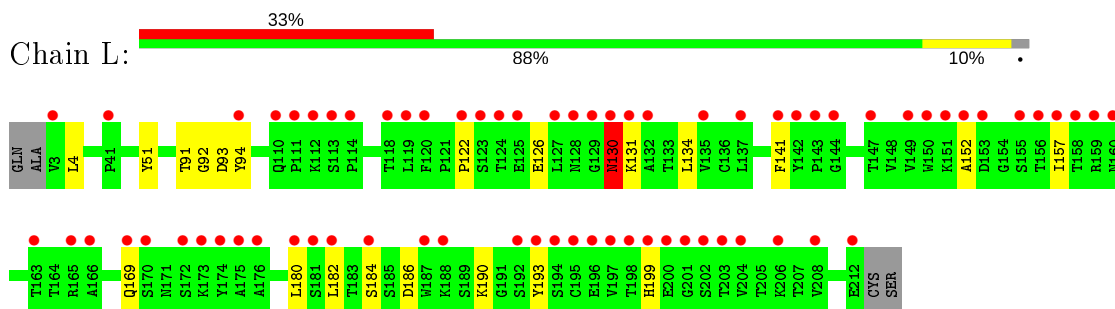
3 Residue-property plots [i](#)

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: Heavy chain



- Molecule 2: light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	78.33Å 134.87Å 42.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.70 – 1.89 67.74 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.4 (67.70-1.89) 99.9 (67.74-1.89)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 1.88Å)	Xtrriage
Refinement program	PHENIX (dev_3386: ???)	Depositor
R, R_{free}	0.228 , 0.254 0.227 , 0.253	Depositor DCC
R_{free} test set	1828 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtrriage
Anisotropy	1.157	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 65.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3072	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4

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	0.28	0/1445	0.52	0/1966
2	L	0.28	0/1599	0.47	0/2179
All	All	0.28	0/3044	0.50	0/4145

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	H	1418	0	1393	12	0
2	L	1565	0	1518	10	0
3	L	12	0	16	0	0
4	L	5	0	0	0	0
5	H	48	0	0	0	0
5	L	24	0	0	0	0
All	All	3072	0	2927	21	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 4.

All (21) 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:186:ASP:O	2:L:193:TYR:OH	2.05	0.75
1:H:135:PRO:HB3	1:H:161:TYR:HB3	1.77	0.66
1:H:184:ALA:HB2	1:H:194:LEU:HD23	1.84	0.60
1:H:184:ALA:HA	1:H:194:LEU:HB3	1.87	0.56
1:H:137:VAL:HG11	1:H:223:VAL:HG11	1.88	0.55
2:L:134:LEU:HB2	2:L:180:LEU:HB3	1.89	0.54
1:H:140:LEU:HD21	1:H:157:LEU:HD22	1.91	0.53
2:L:130:ASN:HA	2:L:184:SER:HB2	1.90	0.53
1:H:214:VAL:HG22	1:H:223:VAL:HB	1.91	0.53
1:H:11:LEU:HB2	1:H:163:PRO:HG3	1.90	0.52
1:H:138:TYR:HB2	1:H:157:LEU:HD23	1.92	0.51
2:L:180:LEU:HG	2:L:182:LEU:HD23	1.92	0.51
2:L:152:ALA:HB2	2:L:157:ILE:HD11	1.97	0.47
2:L:4:LEU:HD11	2:L:91:THR:HG22	1.95	0.47
2:L:190:LYS:HB2	2:L:193:TYR:CZ	2.50	0.46
1:H:166:VAL:HG12	1:H:194:LEU:HD21	1.98	0.45
1:H:105:SER:OG	2:L:92:GLY:HA3	2.19	0.43
1:H:137:VAL:HA	1:H:157:LEU:O	2.19	0.42
1:H:181:THR:HA	1:H:196:SER:HA	2.01	0.41
2:L:131:LYS:HD2	2:L:131:LYS:HA	1.95	0.41
2:L:141:PHE:HB2	2:L:199:HIS:NE2	2.36	0.41

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	H	185/239 (77%)	176 (95%)	9 (5%)	0	100	100
2	L	208/214 (97%)	191 (92%)	12 (6%)	5 (2%)	6	1
All	All	393/453 (87%)	367 (93%)	21 (5%)	5 (1%)	12	4

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	122	PRO
2	L	51	TYR
2	L	94	TYR
2	L	169	GLN
2	L	130	ASN

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	H	165/204 (81%)	161 (98%)	4 (2%)	49 43
2	L	181/184 (98%)	178 (98%)	3 (2%)	60 57
All	All	346/388 (89%)	339 (98%)	7 (2%)	55 51

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	67	LEU
1	H	84	THR
1	H	156	CYS
1	H	158	VAL
2	L	93	ASP
2	L	126	GLU
2	L	130	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	L	303	-	4,4,4	0.14	0	6,6,6	0.07	0
3	GOL	L	302	-	5,5,5	0.93	0	5,5,5	0.95	0
3	GOL	L	301	-	5,5,5	0.91	0	5,5,5	0.98	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	L	302	-	-	0/4/4/4	-
3	GOL	L	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	301	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	L	301	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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

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	H	193/239 (80%)	1.26	30 (15%) 2 2	38, 56, 135, 155	0
2	L	210/214 (98%)	1.87	71 (33%) 0 0	38, 101, 155, 180	0
All	All	403/453 (88%)	1.58	101 (25%) 0 0	38, 65, 152, 180	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	127	LEU	13.9
2	L	124	THR	10.2
2	L	152	ALA	10.1
2	L	128	ASN	9.4
2	L	173	LYS	7.9
2	L	114	PRO	7.8
1	H	137	VAL	7.6
2	L	208	VAL	6.9
2	L	130	ASN	6.6
1	H	155	GLY	6.4
1	H	212	CYS	6.4
1	H	168	VAL	6.1
2	L	113	SER	6.1
2	L	166	ALA	5.7
2	L	143	PRO	5.5
1	H	154	LEU	5.3
2	L	193	TYR	5.2
1	H	156	CYS	5.1
2	L	147	THR	5.0
2	L	155	SER	5.0
2	L	170	SER	4.8
1	H	188	SER	4.7
2	L	150	TRP	4.6
1	H	222	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
2	L	132	ALA	4.5
2	L	129	GLY	4.4
2	L	157	ILE	4.4
2	L	188	LYS	4.3
2	L	159	ARG	4.2
2	L	120	PHE	4.2
2	L	156	THR	4.2
2	L	187	TRP	4.2
2	L	180	LEU	4.2
2	L	158	THR	4.2
2	L	175	ALA	4.1
1	H	139	PRO	4.1
1	H	1	GLN	4.0
1	H	138	TYR	4.0
2	L	141	PHE	4.0
2	L	195	CYS	4.0
2	L	3	VAL	3.9
2	L	174	TYR	3.9
1	H	140	LEU	3.8
1	H	148	SER	3.7
2	L	123	SER	3.7
2	L	192	SER	3.7
1	H	147	LYS	3.6
1	H	217	PRO	3.6
1	H	142	SER	3.6
2	L	144	GLY	3.6
1	H	157	LEU	3.6
1	H	194	LEU	3.6
1	H	180	HIS	3.5
2	L	182	LEU	3.4
2	L	125	GLU	3.4
1	H	215	ALA	3.4
2	L	204	VAL	3.4
1	H	181	THR	3.3
1	H	144	CYS	3.3
2	L	137	LEU	3.2
2	L	160	ASN	3.2
2	L	94	TYR	3.1
2	L	199	HIS	3.1
2	L	119	LEU	3.0
1	H	145	GLY	3.0
2	L	151	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
2	L	131	LYS	3.0
1	H	214	VAL	2.9
2	L	181	SER	2.9
2	L	41	PRO	2.9
2	L	149	VAL	2.8
2	L	200	GLU	2.8
2	L	163	THR	2.7
2	L	153	ASP	2.7
1	H	223	VAL	2.7
2	L	201	GLY	2.6
2	L	172	SER	2.6
2	L	194	SER	2.5
2	L	122	PRO	2.5
2	L	112	LYS	2.5
2	L	198	THR	2.4
2	L	197	VAL	2.4
1	H	143	CYS	2.4
2	L	176	ALA	2.3
2	L	111	PRO	2.3
2	L	202	SER	2.3
1	H	141	SER	2.3
1	H	136	LYS	2.2
2	L	165	ARG	2.2
2	L	184	SER	2.2
2	L	203	THR	2.2
2	L	118	THR	2.2
2	L	196	GLU	2.1
1	H	158	VAL	2.1
2	L	169	GLN	2.1
2	L	206	LYS	2.1
2	L	212	GLU	2.1
2	L	110	GLN	2.1
2	L	135	VAL	2.1
1	H	80	LEU	2.1
2	L	142	TYR	2.0

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

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	L	302	6/6	0.47	0.24	97,98,98,98	0
3	GOL	L	301	6/6	0.69	0.18	79,80,80,80	0
4	SO4	L	303	5/5	0.73	0.31	155,155,155,155	0

6.5 Other polymers [i](#)

There are no such residues in this entry.