



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 11:17 AM EDT

PDB ID : 2VWE / pdb\_00002vwe  
Title : Crystal Structure of Vascular Endothelial Growth Factor-B in Complex with a Neutralizing Antibody Fab Fragment  
Authors : Leonard, P.; Scotney, P.D.; Jabeen, T.; Iyer, S.; Fabri, L.J.; Nash, A.D.; Acharya, K.R.  
Deposited on : 2008-06-23  
Resolution : 3.40 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

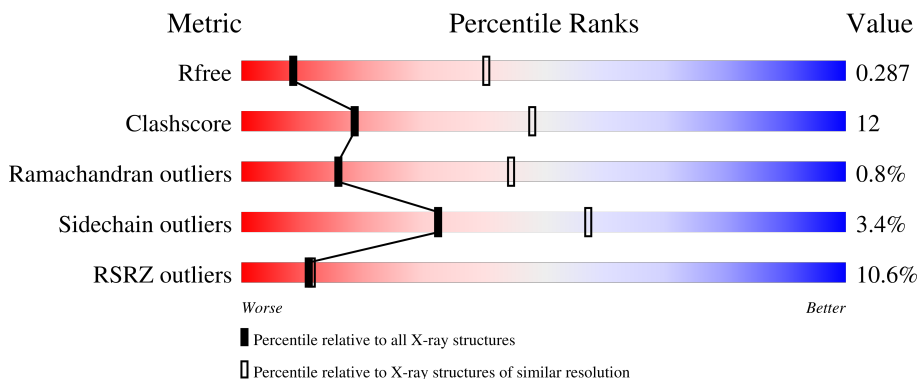
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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.



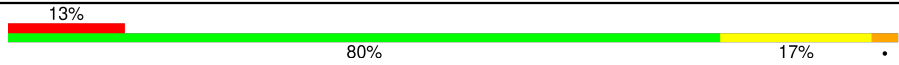
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	167	
1	B	167	
2	C	214	
2	J	214	
3	E	219	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	L	219	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '13%', a large green segment in the middle labeled '80%', and a yellow segment on the right labeled '17%'. A small black dot is visible at the far right end of the bar.</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8109 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 VASCULAR ENDOTHELIAL GROWTH FACTOR B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	98	Total	C	N	O	S	0	0	1
			744	458	135	139	12			
1	B	98	Total	C	N	O	S	0	0	1
			744	458	135	139	12			

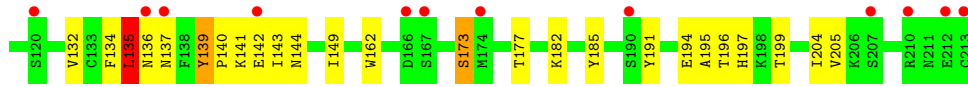
- Molecule 2 is a protein called ANTI-VEGF-B MONOCLONAL ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	214	Total	C	N	O	S	0	0	0
			1659	1029	277	346	7			
2	J	214	Total	C	N	O	S	0	0	0
			1659	1029	277	346	7			

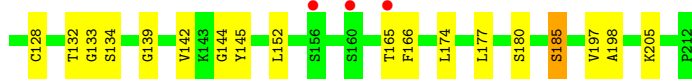
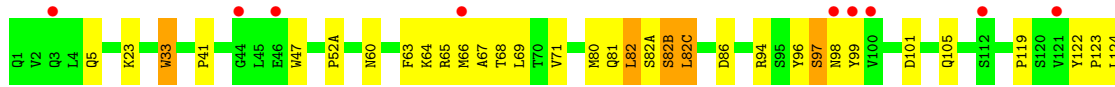
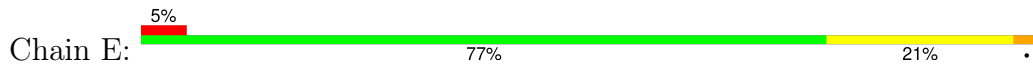
- Molecule 3 is a protein called ANTI-VEGF-B MONOCLONAL ANTIBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	219	Total	C	N	O	S	0	0	0
			1651	1044	275	324	8			
3	L	219	Total	C	N	O	S	0	0	0
			1652	1045	275	324	8			

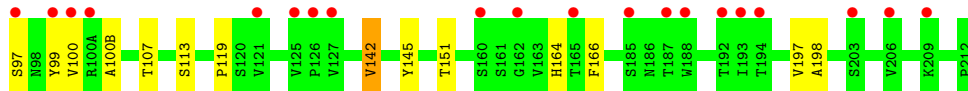
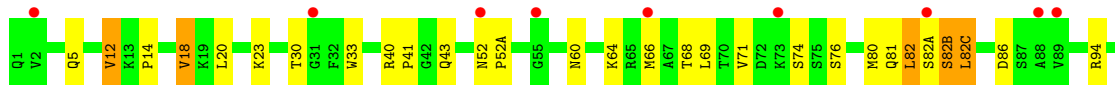
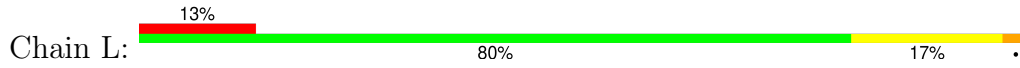




• Molecule 3: ANTI-VEGF-B MONOCLONAL ANTIBODY



• Molecule 3: ANTI-VEGF-B MONOCLONAL ANTIBODY



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.20Å 94.30Å 91.30Å 90.00° 102.30° 90.00°	Depositor
Resolution (Å)	19.78 – 3.40 19.78 – 3.45	Depositor EDS
% Data completeness (in resolution range)	88.5 (19.78-3.40) 92.5 (19.78-3.45)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 3.44Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.262 , 0.310 0.285 , 0.287	Depositor DCC
$R_{free}$ test set	912 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.5	Xtrriage
Anisotropy	0.331	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 6.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	8109	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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	0.51	1/756 (0.1%)	0.72	1/1026 (0.1%)
1	B	0.49	1/756 (0.1%)	0.70	0/1026
2	C	0.38	0/1693	0.67	2/2296 (0.1%)
2	J	0.38	0/1693	0.69	2/2296 (0.1%)
3	E	0.45	0/1695	0.70	0/2314
3	L	0.42	0/1696	0.69	0/2316
All	All	0.43	2/8289 (0.0%)	0.69	5/11274 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	2
2	J	0	3
3	E	1	0
3	L	1	0
All	All	2	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	107	LYS	C-N	-6.94	1.23	1.33
1	A	107	LYS	C-N	-6.94	1.23	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	43	VAL	N-CA-C	-5.41	108.57	113.71
2	C	117	PHE	CA-C-N	5.05	123.30	119.66
2	C	117	PHE	C-N-CA	5.05	123.30	119.66
2	J	117	PHE	CA-C-N	5.01	123.27	119.66

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	117	PHE	C-N-CA	5.01	123.27	119.66

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	E	66	MET	CA
3	L	64	LYS	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	135	LEU	Peptide
2	C	210	ARG	Peptide
2	J	135	LEU	Peptide
2	J	139	TYR	Peptide
2	J	80	GLN	Peptide

## 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	744	0	737	12	0
1	B	744	0	737	9	0
2	C	1659	0	1591	45	0
2	J	1659	0	1591	61	0
3	E	1651	0	1613	46	0
3	L	1652	0	1617	26	0
All	All	8109	0	7886	190	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 12.

The worst 5 of 190 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)
3:E:132:THR:HG22	3:E:133:GLY:CA	0.99	1.45

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:132:THR:CG2	3:E:133:GLY:HA2	0.98	1.45
2:C:189:ASN:O	2:C:210:ARG:HB3	1.20	1.27
3:E:132:THR:CB	3:E:133:GLY:HA2	1.72	1.18
2:J:31:ASN:HA	2:J:71:TYR:OH	1.49	1.11

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	A	96/167 (58%)	91 (95%)	5 (5%)	0	100	100
1	B	96/167 (58%)	92 (96%)	4 (4%)	0	100	100
2	C	212/214 (99%)	203 (96%)	9 (4%)	0	100	100
2	J	212/214 (99%)	196 (92%)	15 (7%)	1 (0%)	24	54
3	E	217/219 (99%)	199 (92%)	13 (6%)	5 (2%)	5	23
3	L	217/219 (99%)	198 (91%)	17 (8%)	2 (1%)	14	42
All	All	1050/1200 (88%)	979 (93%)	63 (6%)	8 (1%)	16	44

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	67	ALA
3	E	97	SER
3	E	128	CYS
2	J	82	ASP
3	E	41	PRO

### 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	87/154 (56%)	83 (95%)	4 (5%)	24	50
1	B	87/154 (56%)	84 (97%)	3 (3%)	32	57
2	C	192/192 (100%)	187 (97%)	5 (3%)	40	61
2	J	192/192 (100%)	189 (98%)	3 (2%)	55	68
3	E	187/187 (100%)	178 (95%)	9 (5%)	23	50
3	L	187/187 (100%)	179 (96%)	8 (4%)	26	51
All	All	932/1066 (87%)	900 (97%)	32 (3%)	32	57

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	82(B)	SER
3	L	82(C)	LEU
3	E	33	TRP
2	C	210	ARG
3	L	94	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	196	ASN
2	J	38	GLN
3	L	58	ASN
2	J	34	ASN
2	J	80	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 oligosaccharides 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	A	98/167 (58%)	0.79	6 (6%) 27 21	17, 36, 71, 83	0
1	B	98/167 (58%)	0.94	9 (9%) 14 14	18, 38, 69, 80	0
2	C	214/214 (100%)	0.95	25 (11%) 9 10	22, 40, 55, 68	0
2	J	214/214 (100%)	1.13	32 (14%) 5 7	24, 48, 62, 73	0
3	E	219/219 (100%)	0.81	12 (5%) 30 23	13, 38, 59, 72	0
3	L	219/219 (100%)	1.01	29 (13%) 7 8	22, 51, 72, 84	0
All	All	1062/1200 (88%)	0.96	113 (10%) 11 11	13, 44, 68, 84	0

The worst 5 of 113 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	213	CYS	5.0
3	L	125	VAL	4.8
1	A	42	THR	4.5
2	C	101	GLY	4.1
2	J	52	SER	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 oligosaccharides 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.