



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2021 – 10:02 PM EDT

PDB ID : 7KEZ  
Title : Crystal structure of bH1 Fab variant (CDR H3 loop design 16\_0325) in complex with VEGF  
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Deposited on : 2020-10-13  
Resolution : 2.31 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

<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	:	2.23.2
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)	:	2.23.2

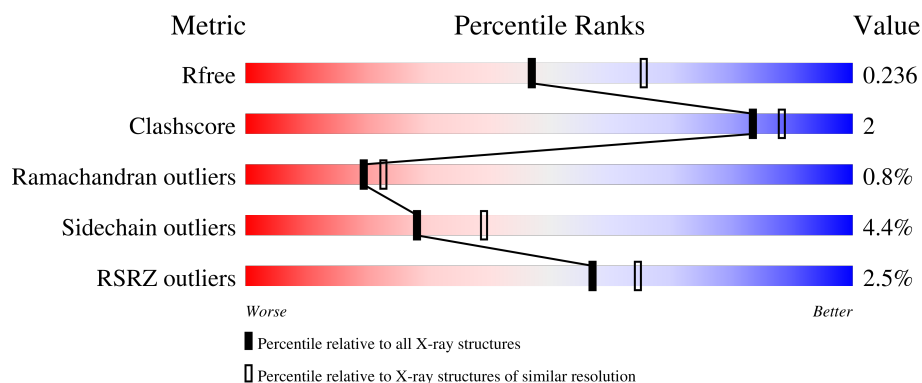
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.31 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	H	239	<div> <div>83%</div> <div>8%</div> <div>8%</div> </div>
2	L	218	<div> <div>3%</div> <div>90%</div> <div>7%</div> <div>..</div> </div>
3	V	116	<div> <div>3%</div> <div>73%</div> <div>5%</div> <div>19%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4328 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 anti-VEGF-A Fab bH1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	220	Total	C	N	O	S	0	0	0
			1642	1041	277	319	5			

- Molecule 2 is a protein called anti-VEGF-A Fab bH1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	216	Total	C	N	O	S	0	1	0
			1678	1056	282	335	5			

- Molecule 3 is a protein called Isoform L-VEGF206 of Vascular endothelial growth factor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	94	Total	C	N	O	S	0	0	0
			761	477	127	144	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	111	HIS	-	expression tag	UNP P15692-14
V	112	HIS	-	expression tag	UNP P15692-14
V	113	HIS	-	expression tag	UNP P15692-14
V	114	HIS	-	expression tag	UNP P15692-14
V	115	HIS	-	expression tag	UNP P15692-14
V	116	HIS	-	expression tag	UNP P15692-14

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total	Cl	0	0
			1	1		

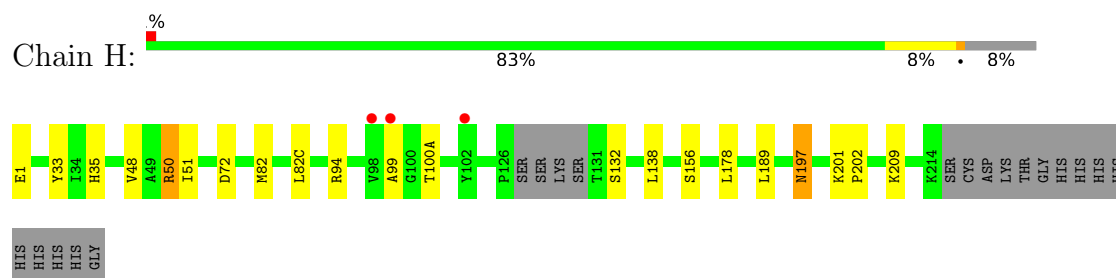
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	120	Total 120	O 120	0	0
5	L	120	Total 120	O 120	0	0
5	V	6	Total 6	O 6	0	0

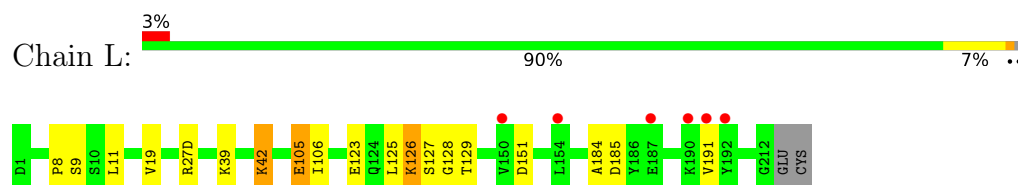
### 3 Residue-property plots

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.

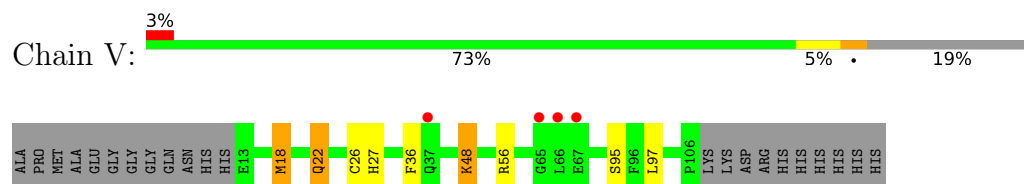
- Molecule 1: anti-VEGF-A Fab bH1 heavy chain



- Molecule 2: anti-VEGF-A Fab bH1 light chain



- Molecule 3: Isoform L-VEGF206 of Vascular endothelial growth factor A



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.80Å 193.84Å 76.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	96.92 – 2.31 48.46 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.9 (96.92-2.31) 99.9 (48.46-2.31)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.178 , 0.235 0.184 , 0.236	Depositor DCC
$R_{free}$ test set	1654 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.1	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	0.96	EDS
Total number of atoms	4328	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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](#)

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

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	0.87	0/1682	0.92	3/2294 (0.1%)
2	L	0.93	1/1722 (0.1%)	0.87	0/2341
3	V	0.67	0/779	0.85	0/1051
All	All	0.86	1/4183 (0.0%)	0.89	3/5686 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	9	SER	CB-OG	-8.20	1.31	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	50	ARG	NE-CZ-NH1	-9.95	115.32	120.30
1	H	50	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	H	72	ASP	CB-CG-OD2	-5.40	113.44	118.30

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	1642	0	1609	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	1678	0	1632	8	0
3	V	761	0	721	3	0
4	H	1	0	0	0	0
5	H	120	0	0	2	0
5	L	120	0	0	1	0
5	V	6	0	0	0	0
All	All	4328	0	3962	19	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 (19) 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:126:LYS:O	2:L:128:GLY:N	2.24	0.71
1:H:156:SER:H	1:H:197:ASN:HD21	1.43	0.66
1:H:82:MET:HB3	1:H:82(C):LEU:HD21	1.81	0.62
1:H:35:HIS:CE1	1:H:50:ARG:HG3	2.36	0.60
1:H:50:ARG:HD2	5:H:467:HOH:O	2.05	0.56
2:L:39:LYS:HB2	2:L:42:LYS:HE3	1.90	0.54
2:L:125:LEU:O	2:L:126:LYS:O	2.28	0.52
2:L:105:GLU:HG3	2:L:106:ILE:N	2.28	0.49
1:H:33:TYR:CD1	1:H:50:ARG:HD3	2.48	0.48
2:L:151:ASP:HA	2:L:191:VAL:HG12	1.97	0.47
2:L:39:LYS:HD3	5:L:302:HOH:O	2.14	0.46
3:V:56:ARG:NH2	3:V:97:LEU:O	2.48	0.46
1:H:209:LYS:NZ	2:L:123:GLU:OE2	2.49	0.46
1:H:201:LYS:N	1:H:202:PRO:CD	2.83	0.42
2:L:8:PRO:HG2	2:L:11:LEU:HD23	2.02	0.42
1:H:100(A):THR:CG2	5:H:413:HOH:O	2.69	0.41
3:V:18:MET:O	3:V:22:GLN:HB2	2.21	0.41
1:H:178:LEU:C	1:H:178:LEU:HD12	2.41	0.41
1:H:99:ALA:HB1	3:V:48:LYS:HD3	2.04	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	H	216/239 (90%)	208 (96%)	8 (4%)	0	100	100
2	L	215/218 (99%)	206 (96%)	6 (3%)	3 (1%)	11	10
3	V	92/116 (79%)	84 (91%)	7 (8%)	1 (1%)	14	15
All	All	523/573 (91%)	498 (95%)	21 (4%)	4 (1%)	19	23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	126	LYS
2	L	127	SER
3	V	26	CYS
2	L	184	ALA

### 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	H	178/195 (91%)	170 (96%)	8 (4%)	27	38
2	L	191/192 (100%)	185 (97%)	6 (3%)	40	55
3	V	89/106 (84%)	83 (93%)	6 (7%)	16	21
All	All	458/493 (93%)	438 (96%)	20 (4%)	28	39

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	1	GLU
1	H	48	VAL
1	H	51	ILE
1	H	94	ARG
1	H	132	SER
1	H	138	LEU
1	H	189	LEU
1	H	197	ASN
2	L	19	VAL
2	L	27(D)	ARG
2	L	42	LYS
2	L	105	GLU
2	L	129	THR
2	L	185	ASP
3	V	18	MET
3	V	22	GLN
3	V	27	HIS
3	V	36	PHE
3	V	48	LYS
3	V	95	SER

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

Mol	Chain	Res	Type
1	H	197	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	H	220/239 (92%)	-0.27	3 (1%) 75 80	29, 49, 80, 117	0
2	L	216/218 (99%)	0.06	6 (2%) 53 60	26, 45, 90, 108	0
3	V	94/116 (81%)	0.42	4 (4%) 35 42	49, 77, 111, 123	0
All	All	530/573 (92%)	-0.01	13 (2%) 57 64	26, 52, 99, 123	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	99	ALA	4.9
2	L	191	VAL	4.8
2	L	190	LYS	3.6
3	V	65	GLY	3.5
3	V	37	GLN	3.5
2	L	154	LEU	2.8
2	L	187	GLU	2.8
2	L	192	TYR	2.5
1	H	98	VAL	2.4
1	H	102	TYR	2.4
3	V	67	GLU	2.3
2	L	150	VAL	2.1
3	V	66	LEU	2.1

### 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 monosaccharides 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	CL	H	300	1/1	0.97	0.08	46,46,46,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.