



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 12, 2024 – 09:54 AM EDT

PDB ID : 5TDG  
Title : Crystal structure of prefusion-stabilized bovine RSV F (DS-Cav1 variant: strain ATue51908)  
Authors : Chen, L.; Zhang, B.; Kwong, P.D.  
Deposited on : 2016-09-19  
Resolution : 2.65 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>.

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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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

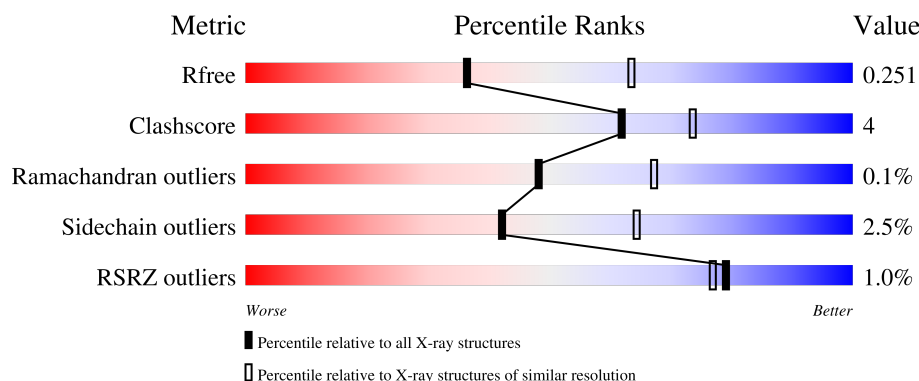
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*




The reported resolution of this entry is 2.65 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))
$R_{free}$	164625	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

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	519	 80% 12% • 8%
1	B	519	 2% 79% 12% • 8%
1	C	519	 % 82% 10% • 8%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11276 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 Fusion glycoprotein F0,Fibritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	480	Total	C	N	O	S	0	0	0
			3732	2355	623	731	23			
1	B	480	Total	C	N	O	S	0	1	0
			3740	2360	626	731	23			
1	C	480	Total	C	N	O	S	0	0	0
			3732	2355	623	731	23			

There are 24 discrepancies between the modelled and reference sequences:

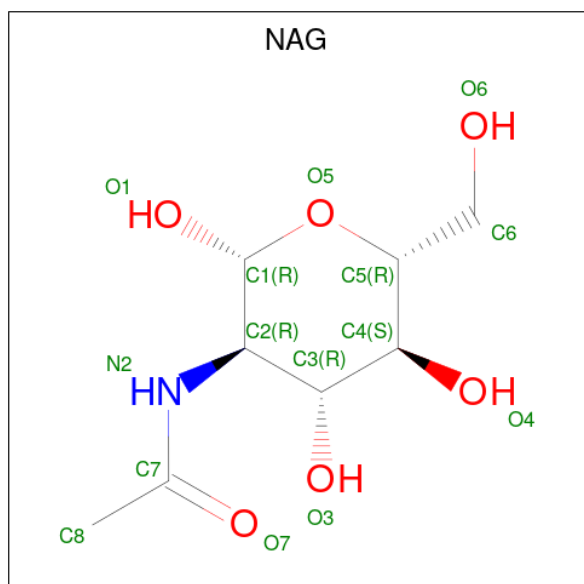
Chain	Residue	Modelled	Actual	Comment	Reference
A	155	CYS	SER	engineered mutation	UNP Q9YS24
A	190	PHE	SER	engineered mutation	UNP Q9YS24
A	207	LEU	VAL	engineered mutation	UNP Q9YS24
A	290	CYS	SER	engineered mutation	UNP Q9YS24
A	514	SER	-	linker	UNP Q9YS24
A	515	ALA	-	linker	UNP Q9YS24
A	516	ILE	-	linker	UNP Q9YS24
A	517	GLY	-	linker	UNP Q9YS24
B	155	CYS	SER	engineered mutation	UNP Q9YS24
B	190	PHE	SER	engineered mutation	UNP Q9YS24
B	207	LEU	VAL	engineered mutation	UNP Q9YS24
B	290	CYS	SER	engineered mutation	UNP Q9YS24
B	514	SER	-	linker	UNP Q9YS24
B	515	ALA	-	linker	UNP Q9YS24
B	516	ILE	-	linker	UNP Q9YS24
B	517	GLY	-	linker	UNP Q9YS24
C	155	CYS	SER	engineered mutation	UNP Q9YS24
C	190	PHE	SER	engineered mutation	UNP Q9YS24
C	207	LEU	VAL	engineered mutation	UNP Q9YS24
C	290	CYS	SER	engineered mutation	UNP Q9YS24
C	514	SER	-	linker	UNP Q9YS24
C	515	ALA	-	linker	UNP Q9YS24
C	516	ILE	-	linker	UNP Q9YS24

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Chain	Residue	Modelled	Actual	Comment	Reference
C	517	GLY	-	linker	UNP Q9YS24

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

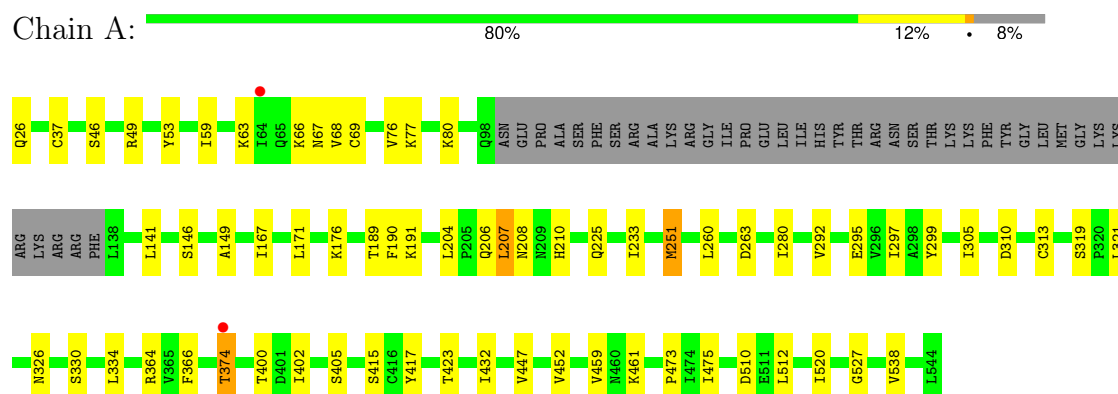
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total	O	0	0
			7	7		
3	B	15	Total	O	0	0
			15	15		
3	C	8	Total	O	0	0
			8	8		

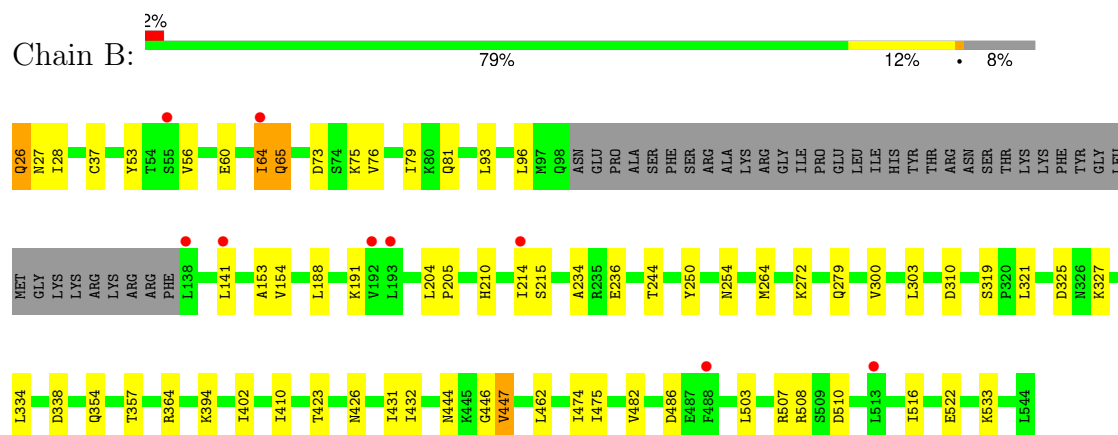
### 3 Residue-property plots [i](#)

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.

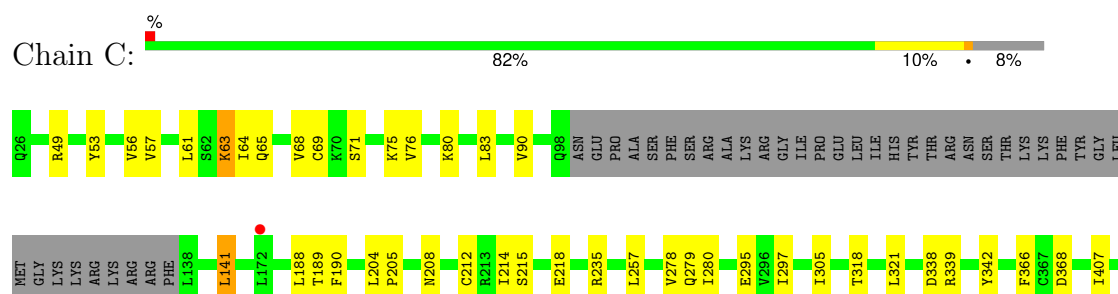
#### • Molecule 1: Fusion glycoprotein F0,Fibritin



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.07Å 127.03Å 92.43Å 90.00° 93.91° 90.00°	Depositor
Resolution (Å)	92.21 – 2.65 92.21 – 2.65	Depositor EDS
% Data completeness (in resolution range)	96.5 (92.21-2.65) 96.8 (92.21-2.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, $R_{free}$	0.205 , 0.249 0.207 , 0.251	Depositor DCC
$R_{free}$ test set	2430 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.3	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11276	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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

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

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	0.27	0/3788	0.47	0/5136
1	B	0.27	0/3799	0.47	0/5150
1	C	0.27	0/3788	0.47	0/5136
All	All	0.27	0/11375	0.47	0/15422

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	3732	0	3757	36	0
1	B	3740	0	3770	37	0
1	C	3732	0	3757	31	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
3	A	7	0	0	0	0
3	B	15	0	0	2	0
3	C	8	0	0	0	0
All	All	11276	0	11323	91	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.

The worst 5 of 91 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:B:250:TYR:OH	1:C:235:ARG:NH1	2.23	0.71
1:A:374:THR:HG21	1:C:453:GLY:HA3	1.73	0.69
1:B:334:LEU:HD23	1:B:475:ILE:HD13	1.76	0.66
1:C:321:LEU:HD11	1:C:473:PRO:HB3	1.76	0.65
1:A:400:THR:HG21	1:B:141:LEU:HD21	1.79	0.64

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	476/519 (92%)	449 (94%)	26 (6%)	1 (0%)	44	61
1	B	477/519 (92%)	453 (95%)	23 (5%)	1 (0%)	44	61
1	C	476/519 (92%)	447 (94%)	29 (6%)	0	100	100
All	All	1429/1557 (92%)	1349 (94%)	78 (6%)	2 (0%)	48	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	B	64	ILE

### 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	433/467 (93%)	422 (98%)	11 (2%)	42	64
1	B	434/467 (93%)	420 (97%)	14 (3%)	34	54
1	C	433/467 (93%)	425 (98%)	8 (2%)	54	73
All	All	1300/1401 (93%)	1267 (98%)	33 (2%)	42	64

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	141	LEU
1	C	188	LEU
1	C	508	ARG
1	B	27	ASN
1	B	26	GLN

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

Mol	Chain	Res	Type
1	B	26	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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	$\# Z  > 2$
2	NAG	C	5001	1	14,14,15	0.44	0	17,19,21	0.53	0
2	NAG	A	5001	1	14,14,15	0.30	0	17,19,21	0.52	0
2	NAG	B	5001	1	14,14,15	0.30	0	17,19,21	0.43	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
2	NAG	C	5001	1	-	2/6/23/26	0/1/1/1
2	NAG	A	5001	1	-	2/6/23/26	0/1/1/1
2	NAG	B	5001	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	5001	NAG	O5-C5-C6-O6
2	C	5001	NAG	C4-C5-C6-O6
2	A	5001	NAG	O5-C5-C6-O6
2	A	5001	NAG	C4-C5-C6-O6

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	A	480/519 (92%)	-0.14	2 (0%) 89 88	46, 73, 125, 191	0
1	B	480/519 (92%)	-0.07	9 (1%) 66 64	42, 73, 127, 197	1 (0%)
1	C	480/519 (92%)	-0.11	3 (0%) 85 83	48, 77, 133, 172	0
All	All	1440/1557 (92%)	-0.10	14 (0%) 79 77	42, 74, 129, 197	1 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	514	SER	3.2
1	B	141	LEU	2.8
1	B	192	VAL	2.7
1	B	55	SER	2.6
1	B	193	LEU	2.5

### 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
2	NAG	B	5001	14/15	0.57	0.16	135,136,143,143	0
2	NAG	C	5001	14/15	0.65	0.11	105,116,124,125	0
2	NAG	A	5001	14/15	0.67	0.11	131,145,150,150	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.