



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:47 PM GMT

PDB ID : 4JHW  
Title : Crystal Structure of Respiratory Syncytial Virus Fusion Glycoprotein Stabilized in the Prefusion Conformation by Human Antibody D25  
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Deposited on : 2013-03-05  
Resolution : 3.60 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

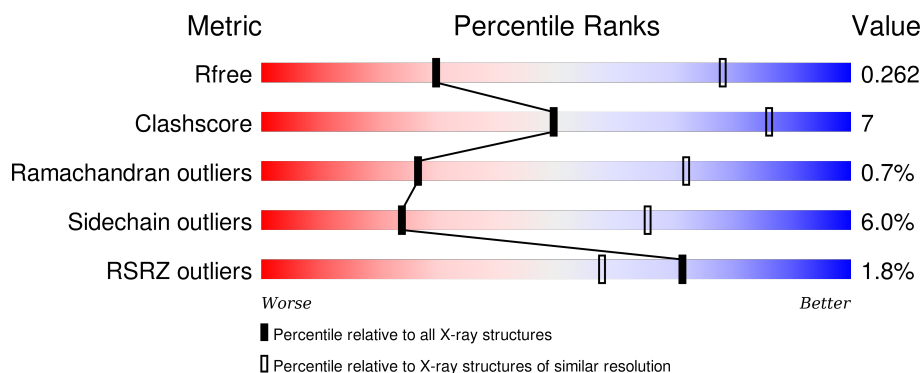
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.60 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))
$R_{free}$	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	230	<div> <div>3%</div> <div>83%</div> <div>14%</div> <div>••</div> </div>
2	L	214	<div> <div>3%</div> <div>84%</div> <div>15%</div> <div>•</div> </div>
3	F	498	<div> <div>%</div> <div>63%</div> <div>24%</div> <div>•</div> <div>10%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6778 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 D25 antigen-binding fragment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	226	Total	C	N	O	S	0	0	0
			1683	1067	279	330	7			

- Molecule 2 is a protein called D25 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			

- Molecule 3 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	449	Total	C	N	O	S	0	0	0
			3476	2195	573	687	21			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	129	ALA	PRO	ENGINEERED MUTATION	UNP P03420
F	379	VAL	ILE	ENGINEERED MUTATION	UNP P03420
F	447	VAL	MET	ENGINEERED MUTATION	UNP P03420
F	514	SER	-	EXPRESSION TAG	UNP P03420
F	515	ALA	-	EXPRESSION TAG	UNP P03420
F	516	ILE	-	EXPRESSION TAG	UNP P03420
F	517	GLY	-	EXPRESSION TAG	UNP P03420
F	518	GLY	-	EXPRESSION TAG	UNP P03420
F	519	TYR	-	EXPRESSION TAG	UNP P03420
F	520	ILE	-	EXPRESSION TAG	UNP P03420
F	521	PRO	-	EXPRESSION TAG	UNP P03420
F	522	GLU	-	EXPRESSION TAG	UNP P03420
F	523	ALA	-	EXPRESSION TAG	UNP P03420
F	524	PRO	-	EXPRESSION TAG	UNP P03420

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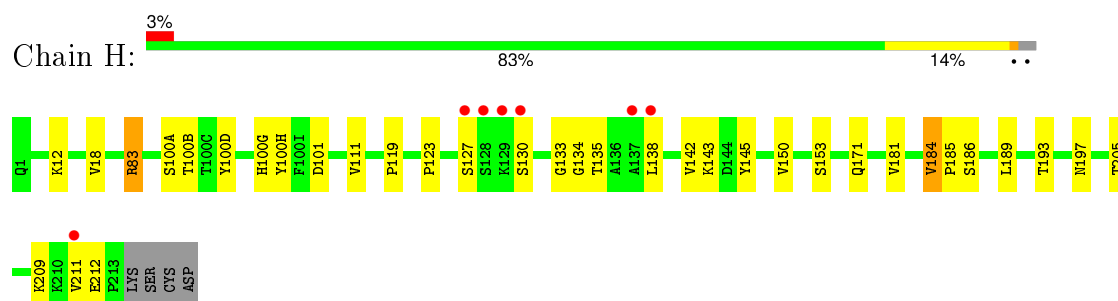
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Chain	Residue	Modelled	Actual	Comment	Reference
F	525	ARG	-	EXPRESSION TAG	UNP P03420
F	526	ASP	-	EXPRESSION TAG	UNP P03420
F	527	GLY	-	EXPRESSION TAG	UNP P03420
F	528	GLN	-	EXPRESSION TAG	UNP P03420
F	529	ALA	-	EXPRESSION TAG	UNP P03420
F	530	TYR	-	EXPRESSION TAG	UNP P03420
F	531	VAL	-	EXPRESSION TAG	UNP P03420
F	532	ARG	-	EXPRESSION TAG	UNP P03420
F	533	LYS	-	EXPRESSION TAG	UNP P03420
F	534	ASP	-	EXPRESSION TAG	UNP P03420
F	535	GLY	-	EXPRESSION TAG	UNP P03420
F	536	GLU	-	EXPRESSION TAG	UNP P03420
F	537	TRP	-	EXPRESSION TAG	UNP P03420
F	538	VAL	-	EXPRESSION TAG	UNP P03420
F	539	LEU	-	EXPRESSION TAG	UNP P03420
F	540	LEU	-	EXPRESSION TAG	UNP P03420
F	541	SER	-	EXPRESSION TAG	UNP P03420
F	542	THR	-	EXPRESSION TAG	UNP P03420
F	543	PHE	-	EXPRESSION TAG	UNP P03420
F	544	LEU	-	EXPRESSION TAG	UNP P03420
F	545	GLY	-	EXPRESSION TAG	UNP P03420
F	546	GLY	-	EXPRESSION TAG	UNP P03420
F	547	LEU	-	EXPRESSION TAG	UNP P03420
F	548	VAL	-	EXPRESSION TAG	UNP P03420
F	549	PRO	-	EXPRESSION TAG	UNP P03420
F	550	ARG	-	EXPRESSION TAG	UNP P03420

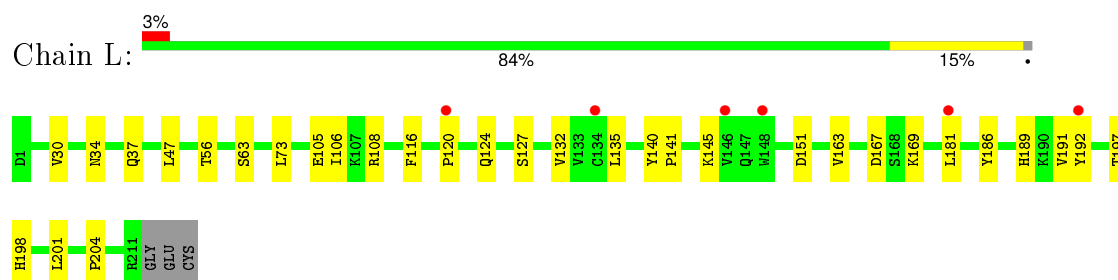
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

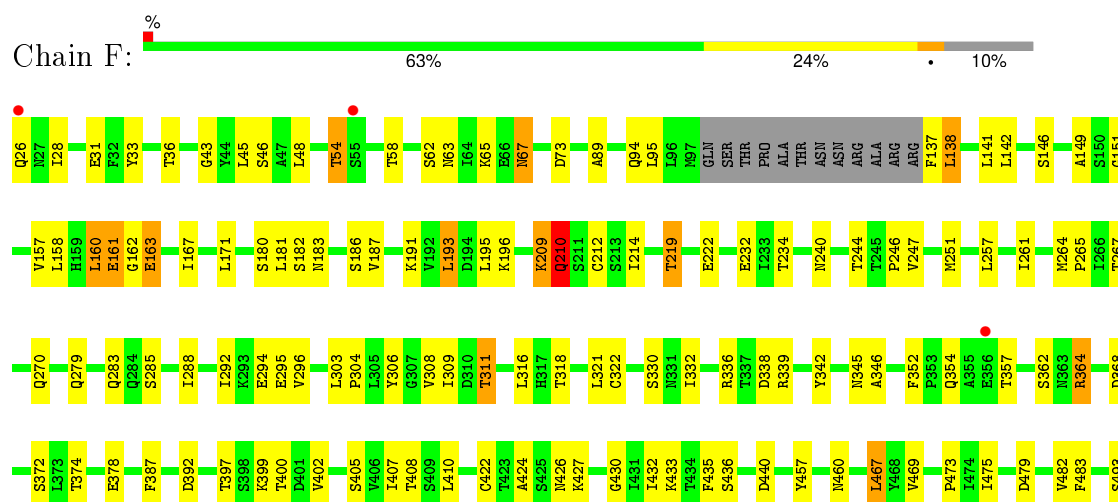
- Molecule 1: D25 antigen-binding fragment heavy chain



- Molecule 2: D25 light chain



- Molecule 3: Fusion glycoprotein F0



E497	R498	I499	N500	D501	R502	L503	A504	F505	L513	SER	ALA	ILE	GLY	GLY	TYR	ILE	PRO	GLU	ALA	PRO	ARG	ASP	GLY	GLN	ALA	TYR	VAL	ARG	LYS	ASP	GLY	GLU	TRP	VAL	LEU	LEU	SER	THR	PHE	LEU	GLY	GLY	LEU	VAL	PRO	ARG
------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	152.29 Å   152.29 Å   152.29 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	42.24 – 3.60 42.24 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (42.24-3.60) 99.6 (42.24-3.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.03 (at 3.57 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.213   ,   0.267 0.212   ,   0.262	Depositor DCC
$R_{free}$ test set	670 reflections (4.84%)	DCC
Wilson B-factor (Å <sup>2</sup> )	156.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 80.4	EDS
Estimated twinning fraction	0.039 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 13879 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6778	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.85% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	H	0.22	0/1726	0.48	0/2363
2	L	0.24	0/1652	0.48	0/2247
3	F	0.25	0/3525	0.50	0/4775
All	All	0.24	0/6903	0.49	0/9385

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	H	1683	0	1662	17	0
2	L	1619	0	1579	16	0
3	F	3476	0	3522	67	0
All	All	6778	0	6763	96	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 96 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:56:THR:HG21	3:F:210:GLN:HE21	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:167:ILE:HD11	3:F:181:LEU:HD11	1.70	0.74
2:L:120:PRO:HD3	2:L:132:VAL:HG22	1.71	0.73
3:F:45:LEU:HB3	3:F:364:ARG:HH21	1.51	0.72
3:F:407:ILE:HD11	3:F:457:TYR:HB3	1.73	0.69

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	224/230 (97%)	219 (98%)	5 (2%)	0	100	100
2	L	209/214 (98%)	202 (97%)	6 (3%)	1 (0%)	34	77
3	F	445/498 (89%)	387 (87%)	53 (12%)	5 (1%)	17	64
All	All	878/942 (93%)	808 (92%)	64 (7%)	6 (1%)	26	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	182	SER
3	F	210	GLN
3	F	212	CYS
3	F	505	PHE
2	L	30	VAL

### 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	191/195 (98%)	184 (96%)	7 (4%)	41	77
2	L	186/188 (99%)	182 (98%)	4 (2%)	60	86
3	F	410/448 (92%)	374 (91%)	36 (9%)	12	50
All	All	787/831 (95%)	740 (94%)	47 (6%)	24	65

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	160	LEU
3	F	186	SER
3	F	436	SER
3	F	163	GLU
3	F	193	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	210	GLN
3	F	354	GLN
3	F	270	GLN
2	L	137	ASN
3	F	302	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 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, 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	226/230 (98%)	0.09	7 (3%) 52 38	77, 151, 223, 256	0
2	L	211/214 (98%)	0.13	6 (2%) 56 42	62, 126, 222, 251	0
3	F	449/498 (90%)	-0.06	3 (0%) 89 81	66, 107, 166, 225	0
All	All	886/942 (94%)	0.02	16 (1%) 71 58	62, 120, 214, 256	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	211	VAL	4.5
1	H	130	SER	4.1
1	H	138	LEU	3.4
1	H	129	LYS	2.8
3	F	356	GLU	2.7

### 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.