



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:15 AM UTC

PDB ID : 4HJC / pdb_00004hjc
Title : Crystal structure of glycoprotein C from Rift Valley Fever Virus (non-glycosylated)
Authors : Dessau, M.; Modis, Y.
Deposited on : 2012-10-12
Resolution : 4.15 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 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

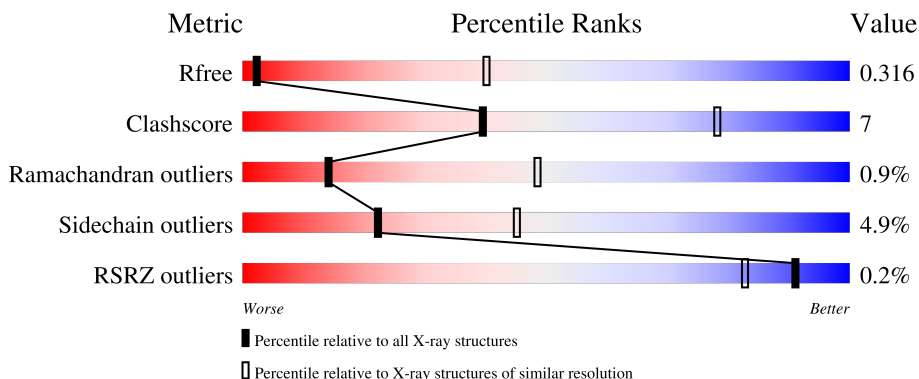
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.15 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	1077 (4.50-3.82)
Clashscore	190562	1019 (4.48-3.84)
Ramachandran outliers	187476	1035 (4.50-3.82)
Sidechain outliers	187428	1022 (4.50-3.82)
RSRZ outliers	180081	1074 (4.50-3.82)

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 ≥ 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	428	 90% 8% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3257 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 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3252	2019	558	646	29			

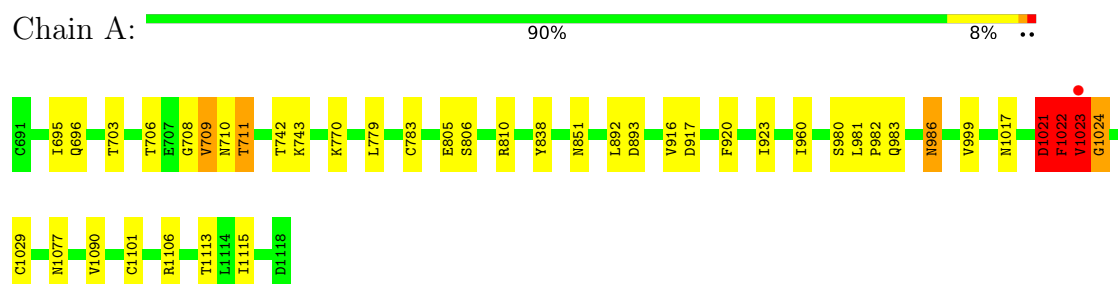
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		

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: ENVELOPE GLYCOPROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	114.35Å 114.35Å 170.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.99 – 4.15 19.99 – 4.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.99-4.15) 98.6 (19.99-4.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 4.21Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.259 , 0.311 0.276 , 0.316	Depositor DCC
R_{free} test set	245 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	200.5	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 91.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3257	wwPDB-VP
Average B, all atoms (Å ²)	158.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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](#)

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	0.34	0/3311	0.67	4/4475 (0.1%)

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
1	A	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1023	VAL	N-CA-C	6.25	122.33	109.34
1	A	1021	ASP	CA-C-N	5.44	131.93	121.54
1	A	1021	ASP	C-N-CA	5.44	131.93	121.54
1	A	1024	GLY	N-CA-C	5.17	121.50	112.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1021	ASP	Peptide
1	A	1022	PHE	Peptide
1	A	980	SER	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	3252	0	3129	43	0
2	A	5	0	0	0	0
All	All	3257	0	3129	43	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.

All (43) 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:A:1021:ASP:OD1	1:A:1022:PHE:CD1	1.84	1.30
1:A:1021:ASP:C	1:A:1022:PHE:CD1	2.14	1.24
1:A:1021:ASP:O	1:A:1022:PHE:CD1	1.90	1.24
1:A:711:THR:N	1:A:1023:VAL:HG21	1.55	1.19
1:A:742:THR:O	1:A:743:LYS:HE2	1.45	1.16
1:A:710:ASN:HA	1:A:1023:VAL:CG1	1.75	1.15
1:A:710:ASN:CA	1:A:1023:VAL:HG11	1.72	1.14
1:A:711:THR:H	1:A:1023:VAL:CG2	1.67	1.06
1:A:1021:ASP:C	1:A:1022:PHE:HD1	1.52	1.04
1:A:711:THR:H	1:A:1023:VAL:HG21	0.88	1.03
1:A:1021:ASP:OD1	1:A:1022:PHE:CE1	2.17	0.96
1:A:710:ASN:HA	1:A:1023:VAL:HG11	0.95	0.93
1:A:1023:VAL:HG12	1:A:1024:GLY:N	1.85	0.90
1:A:709:VAL:O	1:A:1023:VAL:CG1	2.23	0.87
1:A:1021:ASP:OD1	1:A:1022:PHE:HD1	1.55	0.86
1:A:709:VAL:O	1:A:1023:VAL:HG11	1.76	0.84
1:A:1023:VAL:CG1	1:A:1024:GLY:H	1.94	0.80
1:A:1021:ASP:O	1:A:1022:PHE:CE1	2.36	0.77
1:A:1023:VAL:CG1	1:A:1024:GLY:N	2.47	0.76
1:A:1023:VAL:HG12	1:A:1024:GLY:H	1.46	0.75
1:A:710:ASN:CA	1:A:1023:VAL:HG21	2.27	0.64
1:A:710:ASN:C	1:A:1023:VAL:HG21	2.21	0.63
1:A:710:ASN:HA	1:A:1023:VAL:CB	2.28	0.63
1:A:1021:ASP:CA	1:A:1022:PHE:HD1	2.14	0.60
1:A:1021:ASP:CG	1:A:1022:PHE:CD1	2.77	0.58
1:A:709:VAL:C	1:A:1023:VAL:HG11	2.29	0.58
1:A:710:ASN:HA	1:A:1023:VAL:HG21	1.85	0.57
1:A:710:ASN:HA	1:A:1023:VAL:CG2	2.37	0.54
1:A:779:LEU:N	1:A:783:CYS:O	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:SER:O	1:A:810:ARG:NH1	2.45	0.50
1:A:1029:CYS:SG	1:A:1101:CYS:N	2.85	0.50
1:A:1021:ASP:CG	1:A:1022:PHE:HD1	2.15	0.49
1:A:1021:ASP:CB	1:A:1022:PHE:HD1	2.26	0.48
1:A:892:LEU:HD23	1:A:893:ASP:N	2.31	0.46
1:A:710:ASN:N	1:A:1023:VAL:HG11	2.28	0.44
1:A:1021:ASP:C	1:A:1022:PHE:CG	2.80	0.44
1:A:711:THR:HG22	1:A:1023:VAL:HG22	1.99	0.43
1:A:708:GLY:O	1:A:710:ASN:N	2.50	0.43
1:A:986:ASN:OD1	1:A:986:ASN:N	2.52	0.42
1:A:917:ASP:N	1:A:917:ASP:OD1	2.53	0.42
1:A:770:LYS:HB2	1:A:838:TYR:CZ	2.55	0.41
1:A:982:PRO:O	1:A:983:GLN:NE2	2.53	0.41
1:A:851:ASN:HB3	1:A:920:PHE:HB2	2.03	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	A	426/428 (100%)	395 (93%)	27 (6%)	4 (1%)	14 48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1022	PHE
1	A	1023	VAL
1	A	960	ILE
1	A	1077	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	A	369/369 (100%)	351 (95%)	18 (5%)	22	45

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	695	ILE
1	A	696	GLN
1	A	703	THR
1	A	706	THR
1	A	709	VAL
1	A	711	THR
1	A	805	GLU
1	A	916	VAL
1	A	923	ILE
1	A	981	LEU
1	A	986	ASN
1	A	999	VAL
1	A	1017	ASN
1	A	1022	PHE
1	A	1090	VAL
1	A	1106	ARG
1	A	1113	THR
1	A	1115	ILE

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

Mol	Chain	Res	Type
1	A	840	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, 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	A	428/428 (100%)	-0.68	1 (0%) 91 83	26, 149, 258, 366	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1023	VAL	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.