Full wwPDB X-ray Structure Validation Report ⓘ

Nov 5, 2023 – 05:19 PM EST

PDB ID	:	6VJO
Title	:	Human parainfluenza virus type 3 fusion glycoprotein N-terminal heptad repeat domain+alpha/beta-VI
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Deposited on	:	2020-01-16
Resolution	:	2.00 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:

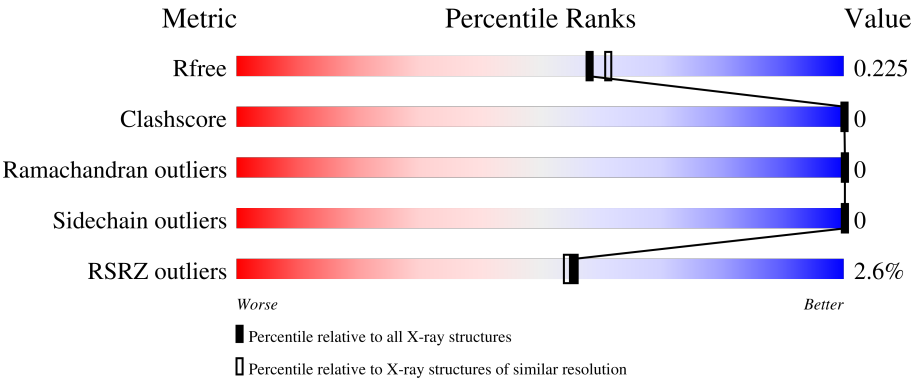
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	38	3% 63% 32% 5%
2	B	53	2% 92% 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1394 atoms, of which 694 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
1	A	38	609	193	312	48	56	0	0	1

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	448	ACE	-	acetylation	UNP A0A1X9QNY3
A	458	XCP	ILE	engineered mutation	UNP A0A1X9QNY3
A	459	VAL	GLU	engineered mutation	UNP A0A1X9QNY3
A	462	XPC	LYS	engineered mutation	UNP A0A1X9QNY3
A	463	ILE	ALA	engineered mutation	UNP A0A1X9QNY3
A	465	XCP	SER	engineered mutation	UNP A0A1X9QNY3
A	476	XPC	ARG	engineered mutation	UNP A0A1X9QNY3
A	479	XCP	GLN	engineered mutation	UNP A0A1X9QNY3
A	483	XCP	SER	engineered mutation	UNP A0A1X9QNY3
A	485	NH2	-	amidation	UNP A0A1X9QNY3

- Molecule 2 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	B	49	750	230	382	63	75	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	138	ACE	-	acetylation	UNP Q84193
B	190	NH2	-	amidation	UNP Q84193

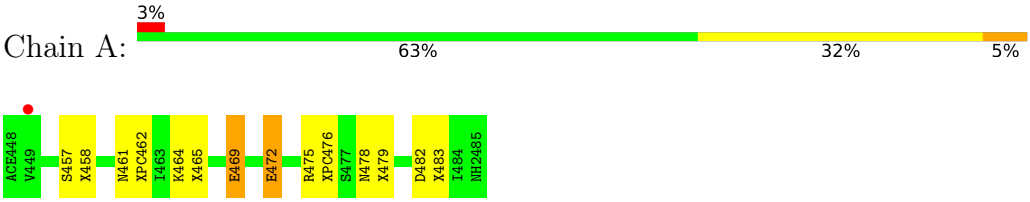
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	17	Total O 17 17	0	0
3	B	18	Total O 18 18	0	0

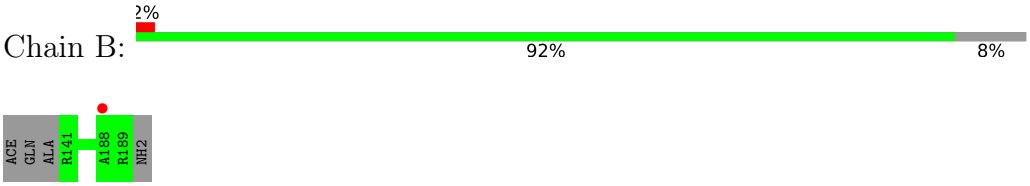
3 Residue-property plots (i)

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



• Molecule 2: Fusion glycoprotein F0



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	48.34Å 48.34Å 134.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.55 – 2.00 35.55 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.7 (35.55-2.00) 94.4 (35.55-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.200 , 0.226 0.199 , 0.225	Depositor DCC
R_{free} test set	776 reflections (10.11%)	wwPDB-VP
Wilson B-factor (Å^2)	15.2	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 64.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.106 for -h-k,k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1394	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.28% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: B3E, XCP, ACE, NH2, XPC

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	0.20	0/220	0.39	0/285
2	B	0.22	0/369	0.34	0/498
All	All	0.21	0/589	0.36	0/783

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	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	457	SER	Peptide
1	A	461	ASN	Peptide
1	A	464	LYS	Peptide
1	A	469	B3E	Mainchain,Peptide
1	A	472	B3E	Mainchain,Peptide
1	A	475	ARG	Peptide
1	A	478	ASN	Peptide
1	A	482	ASP	Peptide

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	297	312	297	0	0
2	B	368	382	382	0	0
3	A	17	0	0	0	0
3	B	18	0	0	0	0
All	All	700	694	679	0	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 0.

There are no clashes within the asymmetric unit.

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	A	28/38 (74%)	27 (96%)	1 (4%)	0	100	100
2	B	47/53 (89%)	47 (100%)	0	0	100	100
All	All	75/91 (82%)	74 (99%)	1 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	A	27/27 (100%)	27 (100%)	0	100	100
2	B	42/45 (93%)	42 (100%)	0	100	100
All	All	69/72 (96%)	69 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

8 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	XCP	A	458	1	8,8,9	3.58	2 (25%)	4,10,12	1.97	2 (50%)
1	XCP	A	465	1	8,8,9	3.52	2 (25%)	4,10,12	1.93	2 (50%)
1	XPC	A	462	1	6,8,9	4.42	3 (50%)	4,10,12	2.58	2 (50%)
1	XCP	A	479	1	8,8,9	3.72	2 (25%)	4,10,12	1.64	1 (25%)
1	XPC	A	476	1	6,8,9	4.40	3 (50%)	4,10,12	2.73	3 (75%)
1	B3E	A	469	1	9,9,10	2.11	4 (44%)	9,10,12	1.45	1 (11%)
1	XCP	A	483	1	8,8,9	3.39	2 (25%)	4,10,12	1.88	1 (25%)
1	B3E	A	472	1	9,9,10	2.22	3 (33%)	9,10,12	1.59	1 (11%)

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
1	XCP	A	458	1	-	1/1/12/14	0/1/1/1
1	XCP	A	465	1	-	1/1/12/14	0/1/1/1
1	XPC	A	462	1	-	1/1/12/14	0/1/1/1
1	XCP	A	479	1	-	1/1/12/14	0/1/1/1
1	XPC	A	476	1	-	1/1/12/14	0/1/1/1
1	B3E	A	469	1	-	2/8/8/9	-
1	XCP	A	483	1	-	1/1/12/14	0/1/1/1
1	B3E	A	472	1	-	1/8/8/9	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	462	XPC	CA-C	9.93	1.65	1.50
1	A	476	XPC	CA-C	9.91	1.65	1.50
1	A	479	XCP	CA-C	8.21	1.63	1.50
1	A	458	XCP	CA-C	8.13	1.63	1.50
1	A	465	XCP	CA-C	8.01	1.62	1.50
1	A	483	XCP	CA-C	7.33	1.61	1.50
1	A	479	XCP	CG-CB	6.10	1.64	1.53
1	A	483	XCP	CG-CB	5.81	1.63	1.53
1	A	458	XCP	CG-CB	5.49	1.63	1.53
1	A	465	XCP	CG-CB	5.35	1.63	1.53
1	A	472	B3E	CB-CA	-4.70	1.47	1.53
1	A	469	B3E	CB-CA	-4.48	1.47	1.53
1	A	462	XPC	CE-ND	3.14	1.56	1.46
1	A	476	XPC	CE-ND	3.11	1.56	1.46
1	A	472	B3E	CG-CA	2.62	1.57	1.53
1	A	462	XPC	CG-ND	2.31	1.54	1.46
1	A	476	XPC	CG-ND	2.28	1.53	1.46
1	A	472	B3E	CB-C	2.20	1.55	1.49
1	A	469	B3E	CA-N	2.16	1.53	1.46
1	A	469	B3E	CG-CA	2.02	1.56	1.53
1	A	469	B3E	CB-C	2.00	1.55	1.49

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	472	B3E	CA-CB-C	4.22	118.46	112.25
1	A	462	XPC	O-C-CA	-3.96	115.91	125.16
1	A	476	XPC	O-C-CA	-3.93	115.99	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	469	B3E	CA-CB-C	3.68	117.66	112.25
1	A	483	XCP	O-C-CA	-2.91	118.36	125.16
1	A	458	XCP	O-C-CA	-2.84	118.53	125.16
1	A	465	XCP	O-C-CA	-2.84	118.54	125.16
1	A	462	XPC	CE-CA-C	2.74	117.69	113.17
1	A	476	XPC	CG-CB-CA	2.70	106.53	104.14
1	A	479	XCP	O-C-CA	-2.70	118.87	125.16
1	A	476	XPC	CE-CA-C	2.67	117.58	113.17
1	A	465	XCP	CD-CE-CA	2.36	110.95	105.09
1	A	458	XCP	CD-CE-CA	2.32	110.87	105.09

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	465	XCP	O-C-CA-CB
1	A	476	XPC	O-C-CA-CB
1	A	458	XCP	O-C-CA-CB
1	A	469	B3E	O-C-CB-CA
1	A	462	XPC	O-C-CA-CB
1	A	469	B3E	N-CA-CB-C
1	A	472	B3E	N-CA-CB-C
1	A	479	XCP	O-C-CA-CB
1	A	483	XCP	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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

6.1 Protein, DNA and RNA chains

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^{th} 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	28/38 (73%)	-0.10	1 (3%)	42	42	16, 33, 57, 59	0
2	B	49/53 (92%)	-0.23	1 (2%)	65	63	12, 20, 64, 83	0
All	All	77/91 (84%)	-0.18	2 (2%)	56	54	12, 24, 63, 83	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	449	VAL	2.7
2	B	188	ALA	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

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^{th} 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(Å^2)	Q<0.9
1	B3E	A	469	10/11	0.88	0.14	19,27,51,51	0
1	XCP	A	479	8/9	0.88	0.19	20,27,41,41	0
1	XCP	A	483	8/9	0.90	0.13	45,52,63,63	0
1	XPC	A	462	8/9	0.91	0.13	17,31,43,43	0
1	B3E	A	472	10/11	0.92	0.12	13,20,77,97	0
1	XPC	A	476	8/9	0.92	0.12	15,21,31,32	0
1	XCP	A	458	8/9	0.93	0.16	18,51,72,72	0
1	XCP	A	465	8/9	0.94	0.11	20,29,52,52	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.