



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 06:35 AM EDT

PDB ID : 6NRO
Title : Human parainfluenza virus type 3 fusion protein N-terminal heptad repeat domain+VIQKI
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Deposited on : 2019-01-23
Resolution : 1.75 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	:	2.36.2
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)	:	2.36.2

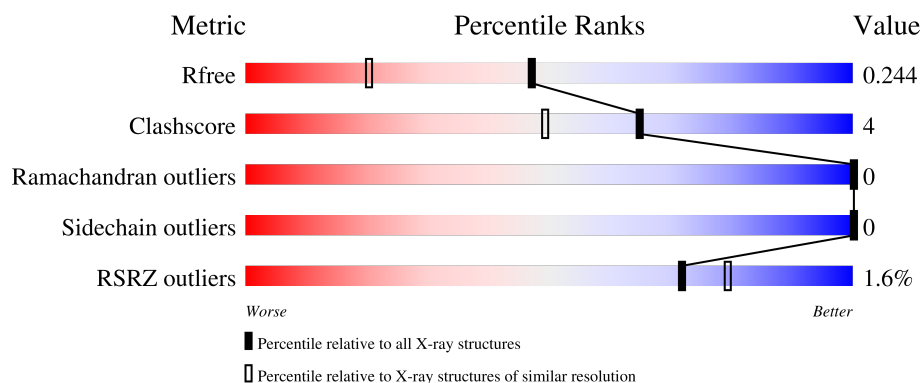
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	53	
1	C	53	
1	E	53	
2	B	38	
2	D	38	

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Mol	Chain	Length	Quality of chain
2	F	38	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a green segment representing 68%, a yellow segment representing 21%, and a grey segment representing 11%. The percentages are labeled below the corresponding segments.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4017 atoms, of which 2003 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 Human parainfluenza virus type 3 fusion glycoprotein N-terminal heptad repeat domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	50	Total	C	H	N	O	0	0	1
			745	230	379	63	73			
1	E	49	Total	C	H	N	O	0	0	0
			710	222	356	61	71			
1	C	49	Total	C	H	N	O	0	0	0
			750	230	382	63	75			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	138	ACE	-	acetylation	UNP A0A1V0E102
A	165	ILE	VAL	engineered mutation	UNP A0A1V0E102
A	190	NH2	-	amidation	UNP A0A1V0E102
E	138	ACE	-	acetylation	UNP A0A1V0E102
E	165	ILE	VAL	engineered mutation	UNP A0A1V0E102
E	190	NH2	-	amidation	UNP A0A1V0E102
C	138	ACE	-	acetylation	UNP A0A1V0E102
C	165	ILE	VAL	engineered mutation	UNP A0A1V0E102
C	190	NH2	-	amidation	UNP A0A1V0E102

- Molecule 2 is a protein called Human parainfluenza virus type 3 fusion glycoprotein C-terminal heptad repeat domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	34	Total	C	H	N	O	0	0	0
			568	176	291	47	54			
2	B	35	Total	C	H	N	O	0	0	0
			590	181	305	49	55			
2	F	34	Total	C	H	N	O	0	0	0
			553	173	280	46	54			

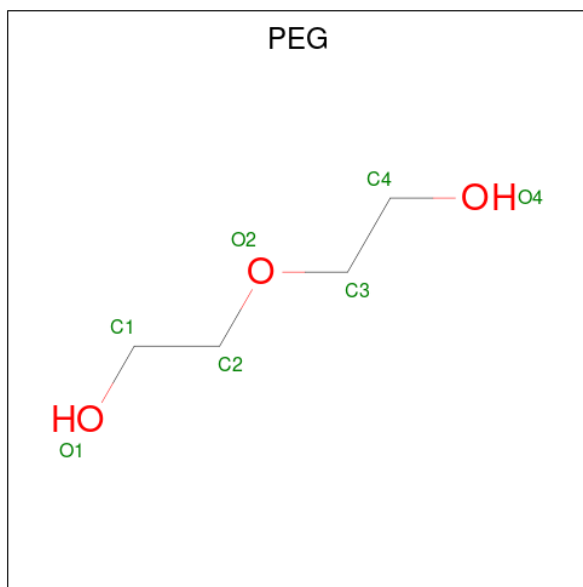
There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	448	ACE	-	acetylation	UNP A0A023PHT3
D	459	VAL	GLU	engineered mutation	UNP A0A023PHT3
D	463	ILE	ALA	engineered mutation	UNP A0A023PHT3
D	466	GLN	ASP	engineered mutation	UNP A0A023PHT3
D	479	LYS	GLN	engineered mutation	UNP A0A023PHT3
D	480	ILE	LYS	engineered mutation	UNP A0A023PHT3
D	485	NH2	-	amidation	UNP A0A023PHT3
B	448	ACE	-	acetylation	UNP A0A023PHT3
B	459	VAL	GLU	engineered mutation	UNP A0A023PHT3
B	463	ILE	ALA	engineered mutation	UNP A0A023PHT3
B	466	GLN	ASP	engineered mutation	UNP A0A023PHT3
B	479	LYS	GLN	engineered mutation	UNP A0A023PHT3
B	480	ILE	LYS	engineered mutation	UNP A0A023PHT3
B	485	NH2	-	amidation	UNP A0A023PHT3
F	448	ACE	-	acetylation	UNP A0A023PHT3
F	459	VAL	GLU	engineered mutation	UNP A0A023PHT3
F	463	ILE	ALA	engineered mutation	UNP A0A023PHT3
F	466	GLN	ASP	engineered mutation	UNP A0A023PHT3
F	479	LYS	GLN	engineered mutation	UNP A0A023PHT3
F	480	ILE	LYS	engineered mutation	UNP A0A023PHT3
F	485	NH2	-	amidation	UNP A0A023PHT3

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	F	1	Total	C	H	O	0	0
			17	4	10	3		


- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	E	10	Total	O	0	0
			10	10		
5	C	16	Total	O	0	0
			16	16		
5	D	16	Total	O	0	0
			16	16		
5	B	16	Total	O	0	0
			16	16		
5	F	11	Total	O	0	0
			11	11		

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: Human parainfluenza virus type 3 fusion glycoprotein N-terminal heptad repeat domain

Chain A: 




- Molecule 1: Human parainfluenza virus type 3 fusion glycoprotein N-terminal heptad repeat domain

Chain E: 



- Molecule 1: Human parainfluenza virus type 3 fusion glycoprotein N-terminal heptad repeat domain

Chain C: 




- Molecule 2: Human parainfluenza virus type 3 fusion glycoprotein C-terminal heptad repeat domain

Chain D: 



- Molecule 2: Human parainfluenza virus type 3 fusion glycoprotein C-terminal heptad repeat domain

Chain B: 



- Molecule 2: Human parainfluenza virus type 3 fusion glycoprotein C-terminal heptad repeat domain

Chain F: 68% 21% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.97Å 52.25Å 54.11Å 90.00° 100.56° 90.00°	Depositor
Resolution (Å)	39.29 – 1.75 39.29 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.29-1.75) 99.5 (39.29-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.217 , 0.244 0.217 , 0.244	Depositor DCC
R_{free} test set	1997 reflections (9.03%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4017	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.61% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NH2, CA, PEG

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	0.71	0/366	0.57	0/494
1	C	0.85	1/369 (0.3%)	0.58	0/498
1	E	0.69	0/355	0.63	0/482
2	B	0.85	0/287	0.60	0/385
2	D	0.77	0/279	0.64	0/375
2	F	0.65	0/275	0.58	0/371
All	All	0.76	1/1931 (0.1%)	0.60	0/2605

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	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	151	ILE	C-N	6.27	1.48	1.34

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	152	ARG	Sidechain

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	366	379	377	3	0
1	C	368	382	382	3	0
1	E	354	356	356	6	0
2	B	285	305	304	3	3
2	D	277	291	290	5	3
2	F	273	280	279	6	0
3	A	1	0	0	0	0
4	F	7	10	10	0	0
5	A	14	0	0	0	0
5	B	16	0	0	0	0
5	C	16	0	0	0	0
5	D	16	0	0	0	0
5	E	10	0	0	0	0
5	F	11	0	0	0	0
All	All	2014	2003	1998	16	3

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.

All (16) 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:176:GLN:HG3	2:B:454:ILE:HG23	1.75	0.69
1:E:169:ILE:HD11	2:F:463:ILE:HG22	1.81	0.63
1:A:182:GLU:HB3	2:F:451:LEU:HD22	1.82	0.61
1:C:176:GLN:HG3	2:D:454:ILE:HG23	1.84	0.57
1:A:169:ILE:HD11	2:B:463:ILE:HG22	1.87	0.56
2:F:472:GLU:OE1	2:F:475:ARG:NH1	2.39	0.55
2:B:456:ILE:O	2:B:459:VAL:HG12	2.14	0.47
1:E:176:GLN:HG3	2:F:454:ILE:HG23	1.99	0.44
1:E:181:LYS:O	1:E:185:PRO:HG2	2.17	0.44
2:D:467:LEU:HD12	2:D:467:LEU:HA	1.89	0.43
1:E:168:LEU:HD11	1:C:165:ILE:HG23	2.01	0.42
2:F:473:TRP:HA	2:F:473:TRP:CE3	2.53	0.42
2:F:456:ILE:O	2:F:459:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:169:ILE:HD11	2:D:463:ILE:HG22	2.00	0.42
1:E:146:LYS:HE2	2:D:483:SER:OG	2.20	0.41
1:E:182:GLU:HB3	2:D:451:LEU:HD13	2.02	0.41

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:462:LYS:NZ	2:B:455:ASP:OD2[2_554]	1.65	0.55
2:D:462:LYS:HZ1	2:B:455:ASP:OD2[2_554]	1.44	0.16
2:D:462:LYS:HZ3	2:B:455:ASP:OD2[2_554]	1.50	0.10

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	48/53 (91%)	48 (100%)	0	0	100	100
1	C	47/53 (89%)	47 (100%)	0	0	100	100
1	E	47/53 (89%)	47 (100%)	0	0	100	100
2	B	33/38 (87%)	33 (100%)	0	0	100	100
2	D	32/38 (84%)	32 (100%)	0	0	100	100
2	F	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
All	All	239/273 (88%)	238 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	40/45 (89%)	40 (100%)	0	100	100
1	C	42/45 (93%)	42 (100%)	0	100	100
1	E	38/45 (84%)	38 (100%)	0	100	100
2	B	34/35 (97%)	34 (100%)	0	100	100
2	D	33/35 (94%)	33 (100%)	0	100	100
2	F	32/35 (91%)	32 (100%)	0	100	100
All	All	219/240 (91%)	219 (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](#)

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 [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
4	PEG	F	501	-	6,6,6	0.65	0	5,5,5	0.37	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
4	PEG	F	501	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	501	PEG	O2-C3-C4-O4
4	F	501	PEG	O1-C1-C2-O2
4	F	501	PEG	C1-C2-O2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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	49/53 (92%)	0.04	0	100	100	31, 42, 65, 84	0
1	C	49/53 (92%)	0.16	0	100	100	28, 41, 60, 70	0
1	E	49/53 (92%)	0.36	3 (6%)	21	26	31, 43, 83, 117	0
2	B	35/38 (92%)	0.11	1 (2%)	51	57	32, 46, 59, 70	0
2	D	34/38 (89%)	0.09	0	100	100	35, 47, 62, 70	0
2	F	34/38 (89%)	0.42	0	100	100	41, 52, 69, 87	0
All	All	250/273 (91%)	0.20	4 (1%)	72	79	28, 46, 68, 117	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	183	ILE	3.4
1	E	188	ALA	3.1
1	E	187	ILE	3.0
2	B	450	ALA	2.2

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, 95th 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(\AA^2)	Q<0.9
4	PEG	F	501	7/7	0.51	0.28	73,87,93,98	0
3	CA	A	201	1/1	0.85	0.10	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.