



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:18 PM UTC

PDB ID : 2G3P / pdb_00002g3p
Title : STRUCTURE OF THE N-TERMINAL TWO DOMAINS OF THE INFECTIVITY PROTEIN G3P OF FILAMENTOUS PHAGE FD
Authors : Holliger, P.; Williams, R.L.
Deposited on : 1998-10-27
Resolution : 1.90 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

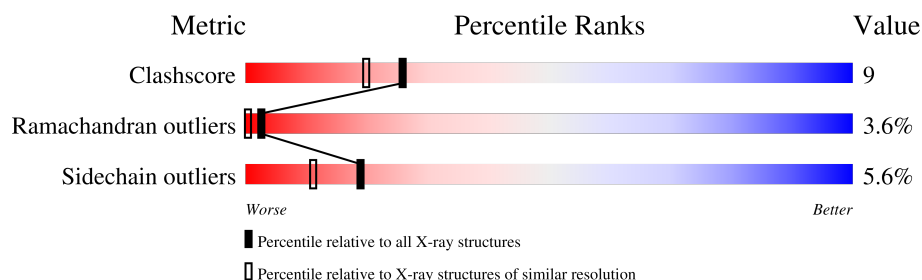
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	225	 70% 15% 6% 11%
1	B	225	 65% 17% 6% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3463 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 INFECTIVITY PROTEIN G3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	75	0	0
			1580	994	265	313	8			
1	B	201	Total	C	N	O	S	142	0	0
			1580	994	265	313	8			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	163	Total	O	0	0
			163	163		
2	B	140	Total	O	0	0
			140	140		

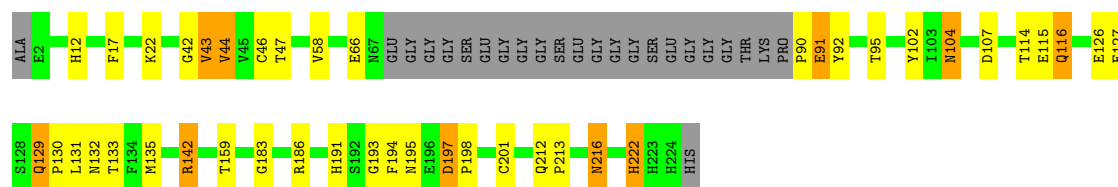
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

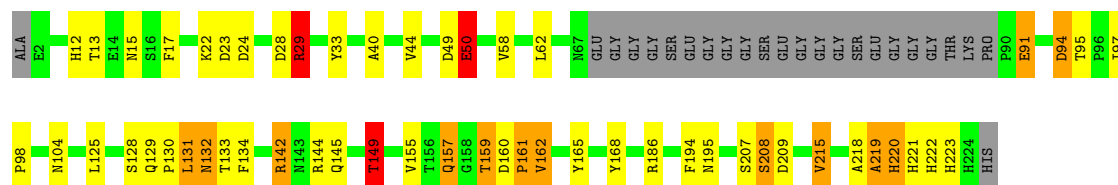
• Molecule 1: INFECTIVITY PROTEIN G3P

Chain A: 



• Molecule 1: INFECTIVITY PROTEIN G3P

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	125.22Å 78.25Å 62.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	13.00 – 1.90	Depositor
% Data completeness (in resolution range)	99.7 (13.00-1.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.260 , 0.298	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3463	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

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	A	0.65	2/1632 (0.1%)	1.26	8/2235 (0.4%)
1	B	1.21	10/1633 (0.6%)	1.59	30/2238 (1.3%)
All	All	0.97	12/3265 (0.4%)	1.43	38/4473 (0.8%)

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	1
1	B	0	3
All	All	0	4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	161	PRO	C-N	-26.91	0.97	1.33
1	B	91	GLU	C-N	23.40	1.67	1.33
1	A	90	PRO	N-CA	8.99	1.60	1.47
1	A	195	ASN	C-N	8.87	1.46	1.33
1	B	50	GLU	CG-CD	8.64	1.73	1.52
1	B	145	GLN	CG-CD	-8.47	1.30	1.52
1	B	208	SER	C-N	-8.44	1.21	1.33
1	B	162	VAL	CA-CB	-8.23	1.43	1.54
1	B	222	HIS	C-N	7.99	1.44	1.33
1	B	24	ASP	CA-CB	-7.51	1.40	1.53
1	B	209	ASP	C-N	-7.07	1.22	1.33
1	B	91	GLU	CA-C	5.25	1.59	1.52

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	161	PRO	CA-C-N	20.27	158.45	121.97
1	B	161	PRO	C-N-CA	20.27	158.45	121.97
1	B	91	GLU	O-C-N	-15.25	102.31	122.59
1	B	208	SER	O-C-N	-11.92	110.92	123.56
1	A	191	HIS	CA-CB-CG	-11.78	102.02	113.80
1	B	91	GLU	CA-C-N	10.14	139.87	122.64
1	B	91	GLU	C-N-CA	10.14	139.87	122.64
1	B	209	ASP	CA-C-N	10.08	137.56	121.83
1	B	209	ASP	C-N-CA	10.08	137.56	121.83
1	B	145	GLN	CB-CG-CD	10.00	129.60	112.60
1	B	157	GLN	O-C-N	-8.58	114.25	123.26
1	B	162	VAL	N-CA-CB	-8.04	97.96	111.23
1	B	222	HIS	O-C-N	7.12	131.74	123.41
1	B	15	ASN	CA-CB-CG	6.88	119.48	112.60
1	B	161	PRO	O-C-N	-6.87	108.04	121.10
1	B	17	PHE	CA-CB-CG	6.53	120.33	113.80
1	B	149	THR	N-CA-CB	-6.44	99.66	111.37
1	B	134	PHE	CA-CB-CG	6.03	119.83	113.80
1	B	50	GLU	CB-CG-CD	-5.98	102.43	112.60
1	A	104	ASN	N-CA-CB	5.97	118.85	110.07
1	B	220	HIS	CA-C-O	5.95	126.14	119.41
1	B	220	HIS	CA-CB-CG	5.80	119.60	113.80
1	A	216	ASN	N-CA-CB	-5.68	102.24	110.47
1	B	145	GLN	CG-CD-NE2	5.66	124.89	116.40
1	A	222	HIS	CA-CB-CG	-5.61	108.19	113.80
1	A	104	ASN	CA-CB-CG	-5.59	107.01	112.60
1	B	94	ASP	CA-CB-CG	5.59	118.19	112.60
1	A	17	PHE	CA-CB-CG	5.58	119.38	113.80
1	B	219	ALA	CA-C-N	5.45	131.84	122.09
1	B	219	ALA	C-N-CA	5.45	131.84	122.09
1	B	142	ARG	NE-CZ-NH2	5.42	124.08	119.20
1	A	142	ARG	CD-NE-CZ	5.35	131.89	124.40
1	B	186	ARG	NE-CZ-NH2	5.35	124.02	119.20
1	B	23	ASP	CA-CB-CG	5.33	117.93	112.60
1	B	144	ARG	NE-CZ-NH2	5.29	123.96	119.20
1	A	47	THR	CA-C-O	-5.28	116.47	122.01
1	B	24	ASP	N-CA-CB	5.21	118.35	110.28
1	B	29	ARG	CA-CB-CG	5.07	124.23	114.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	GLU	Sidechain
1	B	157	GLN	Mainchain
1	B	208	SER	Mainchain
1	B	50	GLU	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	1580	0	1419	28	0
1	B	1580	0	1418	25	0
2	A	163	0	0	4	0
2	B	140	0	0	1	0
All	All	3463	0	2837	53	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 9.

All (53) 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:197:ASP:HB3	1:A:198:PRO:CD	1.86	1.04
1:A:197:ASP:HB3	1:A:198:PRO:HD2	1.45	0.98
1:B:142:ARG:HB3	1:B:149:THR:HG22	1.68	0.76
1:B:149:THR:HG23	1:B:168:TYR:HB3	1.66	0.76
1:B:132:ASN:HD21	1:B:195:ASN:HD22	1.38	0.71
1:A:44:VAL:HG12	1:A:102:TYR:HB2	1.73	0.69
1:A:197:ASP:HB3	1:A:198:PRO:HD3	1.75	0.67
1:B:129:GLN:HE21	1:B:130:PRO:HD2	1.59	0.67
1:A:131:LEU:HD13	1:A:194:PHE:HB3	1.79	0.65
1:B:29:ARG:HH12	1:B:104:ASN:HD22	1.43	0.64
1:B:132:ASN:ND2	1:B:195:ASN:HD22	1.95	0.63
1:A:133:THR:HG22	1:A:142:ARG:HG2	1.82	0.60
1:A:129:GLN:HE21	1:A:129:GLN:HA	1.65	0.60
1:B:29:ARG:HH11	1:B:29:ARG:HG2	1.66	0.60
1:B:12:HIS:CD2	1:B:58:VAL:HG22	2.41	0.55
1:A:197:ASP:CB	1:A:198:PRO:HD2	2.27	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:ALA:O	1:B:220:HIS:N	2.41	0.54
1:B:12:HIS:HD2	1:B:58:VAL:HG22	1.72	0.54
1:B:49:ASP:O	1:B:50:GLU:HB2	2.08	0.53
1:A:135:MET:HG2	2:A:258:HOH:O	2.09	0.53
1:A:12:HIS:CG	1:A:58:VAL:HG22	2.45	0.52
1:A:129:GLN:HE21	1:A:130:PRO:HD2	1.75	0.52
1:A:42:GLY:O	1:A:43:VAL:C	2.53	0.51
1:B:155:VAL:CG2	1:B:165:TYR:HB2	2.41	0.51
1:B:97:ILE:HB	1:B:98:PRO:HD2	1.94	0.50
1:B:149:THR:HB	2:B:264:HOH:O	2.11	0.49
1:A:43:VAL:HA	2:A:381:HOH:O	2.12	0.49
1:B:221:HIS:H	1:B:221:HIS:CD2	2.30	0.49
1:A:216:ASN:HD21	1:A:222:HIS:CE1	2.31	0.48
1:A:183:GLY:O	1:A:186:ARG:HG3	2.15	0.47
1:A:193:GLY:O	1:A:194:PHE:C	2.57	0.47
1:A:114:THR:OG1	1:A:116:GLN:HG3	2.15	0.47
1:B:129:GLN:NE2	1:B:168:TYR:OH	2.47	0.47
1:A:43:VAL:O	1:A:43:VAL:HG23	2.16	0.46
1:A:216:ASN:ND2	1:A:222:HIS:CE1	2.83	0.46
1:A:201:CYS:HB3	2:A:232:HOH:O	2.16	0.46
1:A:126:GLU:HG3	1:A:130:PRO:HG3	1.98	0.46
1:B:125:LEU:HD22	1:B:155:VAL:HG21	1.98	0.45
1:A:44:VAL:HG13	1:A:46:CYS:SG	2.55	0.45
1:B:149:THR:CG2	1:B:168:TYR:HB3	2.41	0.45
1:B:29:ARG:HH12	1:B:104:ASN:ND2	2.13	0.45
1:B:131:LEU:O	1:B:133:THR:N	2.49	0.45
1:A:212:GLN:HB3	1:A:213:PRO:HA	1.99	0.44
1:B:29:ARG:HG2	1:B:29:ARG:NH1	2.31	0.44
1:B:33:TYR:CE1	1:B:215:VAL:HG13	2.52	0.44
1:A:132:ASN:HB3	2:A:379:HOH:O	2.18	0.43
1:B:40:ALA:HB1	1:B:44:VAL:HG11	2.00	0.43
1:A:130:PRO:HG2	1:A:142:ARG:HD3	2.01	0.42
1:B:129:GLN:NE2	1:B:130:PRO:HD2	2.30	0.42
1:B:22:LYS:HA	1:B:28:ASP:O	2.20	0.41
1:A:216:ASN:ND2	1:A:216:ASN:O	2.53	0.41
1:A:104:ASN:HB3	1:A:107:ASP:HB3	2.02	0.41
1:A:133:THR:HG22	1:A:142:ARG:CG	2.51	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	195/225 (87%)	184 (94%)	6 (3%)	5 (3%)	4	1
1	B	197/225 (88%)	186 (94%)	2 (1%)	9 (5%)	2	0
All	All	392/450 (87%)	370 (94%)	8 (2%)	14 (4%)	2	0

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	VAL
1	A	66	GLU
1	A	91	GLU
1	A	197	ASP
1	B	131	LEU
1	B	132	ASN
1	B	159	THR
1	B	160	ASP
1	B	162	VAL
1	A	92	TYR
1	B	219	ALA
1	B	223	HIS
1	B	91	GLU
1	B	161	PRO

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	171/185 (92%)	163 (95%)	8 (5%)	23	15
1	B	171/185 (92%)	160 (94%)	11 (6%)	16	8
All	All	342/370 (92%)	323 (94%)	19 (6%)	19	11

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	44	VAL
1	A	91	GLU
1	A	95	THR
1	A	115	GLU
1	A	116	GLN
1	A	129	GLN
1	A	159	THR
1	B	13	THR
1	B	29	ARG
1	B	62	LEU
1	B	94	ASP
1	B	95	THR
1	B	128	SER
1	B	149	THR
1	B	159	THR
1	B	194	PHE
1	B	207	SER
1	B	215	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	19	ASN
1	A	52	GLN
1	A	116	GLN
1	A	129	GLN
1	A	206	GLN
1	A	212	GLN
1	A	216	ASN
1	A	220	HIS
1	B	19	ASN
1	B	52	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	104	ASN
1	B	116	GLN
1	B	129	GLN
1	B	132	ASN
1	B	138	ASN
1	B	191	HIS
1	B	195	ASN
1	B	212	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	194:PHE	C	195:ASN	N	2.97
1	B	91:GLU	C	92:TYR	N	1.67
1	B	161:PRO	C	162:VAL	N	0.97

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.