



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2016 – 02:07 PM EDT

PDB ID : 5I5O
Title : Crystal Structure of N-terminal Domain of Matrix Protein of Thogoto Virus at Neutral pH.
Authors : Liu, Y.; Liang, H.; Yang, M.
Deposited on : 2016-02-15
Resolution : 2.68 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

i

X-RAY DIFFRACTION

A.

Metric	Percentile Banks	Value
Mean	0.0000	0.0000
Median	0.0000	0.0000
Mode	0.0000	0.0000
Standard Deviation	0.0000	0.0000
Skewness	0.0000	0.0000
Kurtosis	0.0000	0.0000
Minimum	0.0000	0.0000
Maximum	0.0000	0.0000
Range	0.0000	0.0000
Interquartile Range	0.0000	0.0000
5th Percentile	0.0000	0.0000
95th Percentile	0.0000	0.0000

Ramachandran outliers

electron density. The numeric value is given above the bar.

1	A	154
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2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2066 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 Matrix protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	130	Total	C	N	O	S	0	0	0
			1026	639	184	192	11			
1	B	130	Total	C	N	O	S	0	0	0
			1026	639	184	192	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9E781
A	-1	PRO	-	expression tag	UNP Q9E781
A	0	LEU	-	expression tag	UNP Q9E781
A	1	GLY	-	expression tag	UNP Q9E781
A	2	SER	-	expression tag	UNP Q9E781
B	-2	GLY	-	expression tag	UNP Q9E781
B	-1	PRO	-	expression tag	UNP Q9E781
B	0	LEU	-	expression tag	UNP Q9E781
B	1	GLY	-	expression tag	UNP Q9E781
B	2	SER	-	expression tag	UNP Q9E781

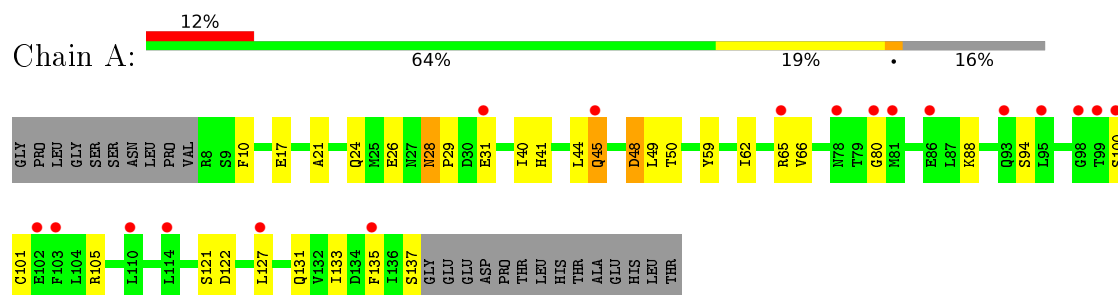
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	10	Total	O	0	0
			10	10		

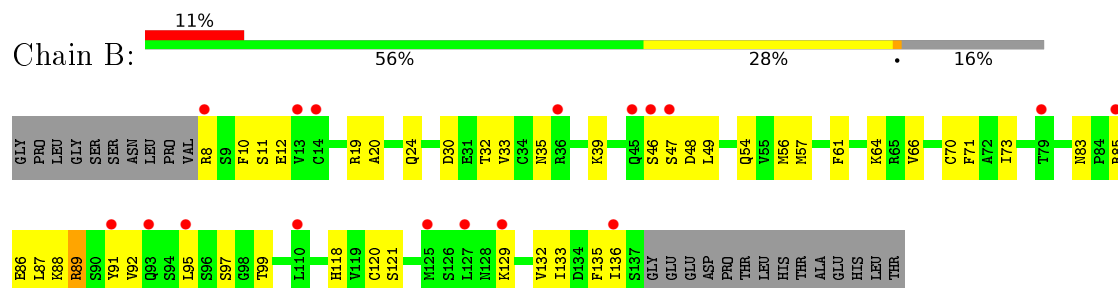
3 Residue-property plots [i](#)

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: Matrix protein



• Molecule 1: Matrix protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	37.04Å 73.30Å 94.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.16 – 2.68 39.63 – 2.68	Depositor EDS
% Data completeness (in resolution range)	96.6 (34.16-2.68) 96.8 (39.63-2.68)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.57 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.271 , 0.285 0.268 , 0.284	Depositor DCC
R_{free} test set	737 reflections (9.99%)	DCC
Wilson B-factor (Å ²)	55.6	Xtriage
Anisotropy	0.984	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 68.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	2066	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.15% 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	0.50	0/1040	0.67	3/1400 (0.2%)
1	B	0.49	0/1040	0.64	0/1400
All	All	0.50	0/2080	0.66	3/2800 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	45	GLN	CB-CA-C	-7.02	96.36	110.40
1	A	45	GLN	N-CA-C	6.27	127.92	111.00
1	A	44	LEU	CB-CA-C	6.21	122.01	110.20

There are no chirality outliers.

There are no planarity outliers.

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	1026	0	1040	27	0
1	B	1026	0	1041	60	3
2	A	4	0	0	7	0
2	B	10	0	0	32	0
All	All	2066	0	2081	86	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 21.

All (86) 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:B:89:ARG:HB2	1:B:89:ARG:NH1	1.56	1.18
1:A:17:GLU:HG3	2:A:202:HOH:O	1.46	1.13
1:B:56:MET:SD	2:B:210:HOH:O	2.06	1.12
1:A:48:ASP:OD1	1:A:49:LEU:N	1.80	1.12
1:B:118:HIS:ND1	2:B:203:HOH:O	1.85	1.09
1:B:86:GLU:HA	2:B:201:HOH:O	1.64	0.98
1:B:85:ARG:O	2:B:201:HOH:O	1.82	0.96
1:B:89:ARG:CG	2:B:202:HOH:O	2.12	0.95
1:B:89:ARG:NH1	1:B:89:ARG:CB	2.30	0.95
1:B:89:ARG:HH11	1:B:89:ARG:CG	1.80	0.94
1:B:89:ARG:O	2:B:202:HOH:O	1.84	0.93
1:B:46:SER:C	2:B:205:HOH:O	2.11	0.88
1:B:89:ARG:HH11	1:B:89:ARG:HG3	1.39	0.86
1:B:89:ARG:CZ	1:B:89:ARG:HB2	2.04	0.86
1:B:11:SER:O	1:B:19:ARG:NH2	2.08	0.86
1:B:47:SER:N	2:B:205:HOH:O	2.09	0.84
1:B:19:ARG:HB3	2:B:204:HOH:O	1.80	0.82
1:B:85:ARG:C	2:B:201:HOH:O	2.14	0.81
1:A:17:GLU:N	2:A:202:HOH:O	2.11	0.80
1:B:20:ALA:N	2:B:204:HOH:O	2.00	0.79
1:B:89:ARG:HH11	1:B:89:ARG:CB	1.93	0.77
1:B:89:ARG:CA	2:B:202:HOH:O	2.31	0.77
1:B:56:MET:CG	2:B:210:HOH:O	2.29	0.75
1:B:89:ARG:C	2:B:202:HOH:O	2.22	0.74
1:B:56:MET:HG2	2:B:210:HOH:O	1.87	0.72
1:B:57:MET:HG3	1:B:136:ILE:HD11	1.72	0.71
1:B:89:ARG:HG2	2:B:202:HOH:O	1.84	0.70
1:A:40:ILE:O	2:A:201:HOH:O	2.09	0.69
1:B:86:GLU:CA	2:B:201:HOH:O	2.30	0.69
1:A:48:ASP:OD1	1:A:48:ASP:C	2.30	0.69
1:B:92:VAL:HA	1:B:95:LEU:HD12	1.73	0.69
1:A:31:GLU:HG2	1:A:65:ARG:HH12	1.58	0.68
1:B:120:CYS:CB	2:B:210:HOH:O	2.41	0.68
1:A:17:GLU:CG	2:A:202:HOH:O	2.19	0.65
1:A:101:CYS:O	1:A:105:ARG:HG3	1.97	0.65
1:A:17:GLU:CB	2:A:202:HOH:O	2.44	0.63
1:A:80:GLY:N	1:B:46:SER:OG	2.32	0.63
1:B:89:ARG:CZ	1:B:89:ARG:CB	2.70	0.62
1:B:89:ARG:HG3	2:B:202:HOH:O	1.85	0.61
1:B:129:LYS:O	1:B:133:ILE:HD12	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:HIS:HB3	2:B:203:HOH:O	2.00	0.60
1:B:19:ARG:CB	2:B:204:HOH:O	2.44	0.60
1:B:97:SER:OG	1:B:99:THR:OG1	2.17	0.60
1:A:31:GLU:CG	1:A:65:ARG:HH12	2.14	0.59
1:A:24:GLN:OE1	2:A:203:HOH:O	2.17	0.58
1:A:133:ILE:O	1:A:137:SER:OG	2.18	0.58
1:A:31:GLU:CB	1:A:65:ARG:HH12	2.17	0.58
1:A:31:GLU:HB3	1:A:65:ARG:HH12	1.67	0.57
1:B:33:VAL:HB	2:B:209:HOH:O	2.03	0.57
1:B:56:MET:CE	2:B:210:HOH:O	2.45	0.57
1:A:31:GLU:HG2	1:A:65:ARG:NH1	2.20	0.56
1:B:66:VAL:HG13	1:B:121:SER:HA	1.87	0.56
1:B:70:CYS:O	1:B:73:ILE:HG12	2.07	0.55
1:A:59:TYR:OH	1:A:65:ARG:NH2	2.39	0.55
1:B:118:HIS:CG	2:B:203:HOH:O	2.50	0.55
1:A:24:GLN:HB2	2:A:203:HOH:O	2.07	0.55
1:B:30:ASP:OD2	1:B:32:THR:HB	2.07	0.55
1:B:10:PHE:CZ	1:B:129:LYS:HD2	2.43	0.54
1:B:48:ASP:OD1	1:B:49:LEU:N	2.41	0.53
1:B:19:ARG:CA	2:B:204:HOH:O	2.57	0.52
1:B:89:ARG:HA	2:B:202:HOH:O	2.02	0.52
1:B:132:VAL:O	1:B:136:ILE:HG12	2.09	0.52
1:B:71:PHE:HB2	2:B:207:HOH:O	2.10	0.51
1:B:8:ARG:N	2:B:208:HOH:O	2.43	0.51
1:B:120:CYS:HB2	2:B:210:HOH:O	2.10	0.51
1:A:88:LYS:NZ	1:A:122:ASP:OD2	2.41	0.50
1:B:118:HIS:CB	2:B:203:HOH:O	2.60	0.49
1:B:83:ASN:OD1	1:B:85:ARG:HB2	2.12	0.48
1:B:91:TYR:CE2	1:B:95:LEU:HD11	2.50	0.47
1:A:29:PRO:HB3	1:A:62:ILE:HG23	1.97	0.46
1:B:33:VAL:CG1	2:B:209:HOH:O	2.64	0.46
1:B:61:PHE:O	1:B:64:LYS:HE2	2.17	0.45
1:A:10:PHE:HB2	1:A:26:GLU:OE2	2.15	0.45
1:B:24:GLN:HB2	2:B:206:HOH:O	2.17	0.45
1:B:54:GLN:HA	1:B:136:ILE:HD12	2.00	0.44
1:A:48:ASP:OD1	1:A:50:THR:N	2.51	0.44
1:A:24:GLN:O	1:A:28:ASN:HB2	2.17	0.44
1:A:21:ALA:HB2	1:A:41:HIS:NE2	2.33	0.43
1:A:66:VAL:HG13	1:A:121:SER:HA	2.00	0.42
1:B:89:ARG:CG	1:B:89:ARG:NH1	2.48	0.42
1:B:54:GLN:HG2	1:B:136:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:LEU:HD23	1:B:87:LEU:HA	1.73	0.42
1:A:127:LEU:HA	1:A:131:GLN:OE1	2.20	0.41
1:B:88:LYS:O	1:B:92:VAL:HG23	2.21	0.41
1:B:35:ASN:OD1	1:B:39:LYS:HE3	2.21	0.41
1:A:94:SER:OG	1:A:100:SER:HA	2.22	0.40

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)
1:B:12:GLU:OE1	1:B:85:ARG:CZ[1_655]	1.88	0.32
1:B:8:ARG:CB	1:B:85:ARG:NH2[1_655]	2.03	0.17
1:B:12:GLU:OE1	1:B:85:ARG:NH2[1_655]	2.04	0.16

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	128/154 (83%)	124 (97%)	4 (3%)	0	100	100
1	B	128/154 (83%)	123 (96%)	5 (4%)	0	100	100
All	All	256/308 (83%)	247 (96%)	9 (4%)	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	119/139 (86%)	115 (97%)	4 (3%)	44	73
1	B	119/139 (86%)	117 (98%)	2 (2%)	68	89
All	All	238/278 (86%)	232 (98%)	6 (2%)	55	83

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	45	GLN
1	A	48	ASP
1	A	135	PHE
1	B	89	ARG
1	B	135	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	GLN
1	B	93	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 ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	130/154 (84%)	0.86	18 (13%) 4 3	47, 63, 80, 95	0
1	B	130/154 (84%)	0.79	17 (13%) 5 3	47, 65, 84, 96	0
All	All	260/308 (84%)	0.83	35 (13%) 4 3	47, 65, 84, 96	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	31	GLU	6.5
1	A	100	SER	5.2
1	B	8	ARG	5.1
1	A	99	THR	5.0
1	B	125	MET	4.6
1	B	47	SER	3.9
1	B	85	ARG	3.9
1	B	127	LEU	3.9
1	A	81	MET	3.8
1	A	127	LEU	3.8
1	A	110	LEU	3.4
1	B	79	THR	3.4
1	B	45	GLN	3.2
1	A	80	GLY	3.1
1	B	13	VAL	3.1
1	B	46	SER	3.0
1	A	45	GLN	2.9
1	A	86	GLU	2.9
1	A	135	PHE	2.7
1	A	98	GLY	2.7
1	B	129	LYS	2.7
1	B	95	LEU	2.6
1	B	36	ARG	2.4
1	B	110	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	93	GLN	2.4
1	B	91	TYR	2.3
1	A	114	LEU	2.3
1	B	136	ILE	2.3
1	B	93	GLN	2.2
1	A	78	ASN	2.2
1	A	103	PHE	2.2
1	A	102	GLU	2.2
1	A	65	ARG	2.2
1	B	14	CYS	2.1
1	A	95	LEU	2.0

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 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.