



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2023 – 08:22 AM EDT

PDB ID : 3PRP
Title : Structural analysis of a viral OTU domain protease from the Crimean-Congo Hemorrhagic Fever virus in complex with human ubiquitin
Authors : Capodagli, G.C.; McKercher, M.A.; Baker, E.A.; Masters, E.M.; Brunzelle, J.S.; Pegan, S.D.
Deposited on : 2010-11-30
Resolution : 1.70 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)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

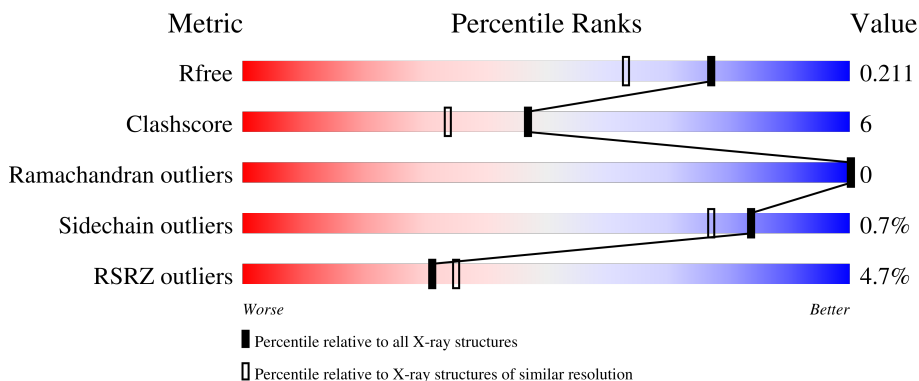
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	178	
1	C	178	
2	B	76	
2	D	76	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4516 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	161	1395	884	239	267	5	0	12	0
1	C	161	1381	874	233	269	5	0	11	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	GLY	-	expression tag	UNP Q6TQR6
A	172	SER	-	expression tag	UNP Q6TQR6
A	173	HIS	-	expression tag	UNP Q6TQR6
A	174	HIS	-	expression tag	UNP Q6TQR6
A	175	HIS	-	expression tag	UNP Q6TQR6
A	176	HIS	-	expression tag	UNP Q6TQR6
A	177	HIS	-	expression tag	UNP Q6TQR6
A	178	HIS	-	expression tag	UNP Q6TQR6
C	171	GLY	-	expression tag	UNP Q6TQR6
C	172	SER	-	expression tag	UNP Q6TQR6
C	173	HIS	-	expression tag	UNP Q6TQR6
C	174	HIS	-	expression tag	UNP Q6TQR6
C	175	HIS	-	expression tag	UNP Q6TQR6
C	176	HIS	-	expression tag	UNP Q6TQR6
C	177	HIS	-	expression tag	UNP Q6TQR6
C	178	HIS	-	expression tag	UNP Q6TQR6

- Molecule 2 is a protein called Polyubiquitin-B (Fragment).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	76	610	384	107	118	1	0	1	0
2	D	76	631	396	110	124	1	0	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	76	4LJ	-	insertion	UNP J3QS39
D	76	4LJ	-	insertion	UNP J3QS39

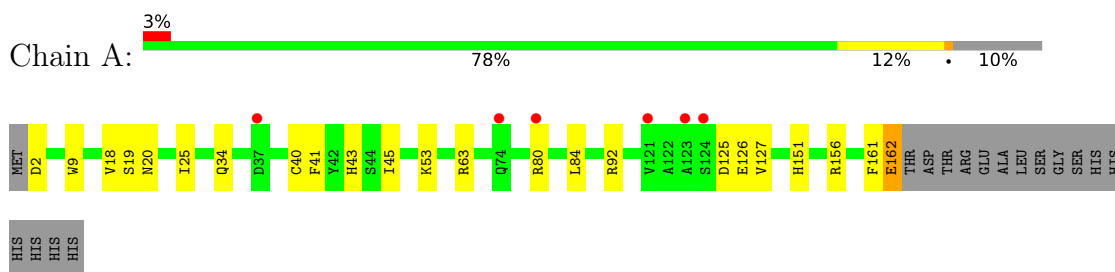
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	183	Total O 186 186	0	3
3	B	80	Total O 81 81	0	1
3	C	162	Total O 165 165	0	3
3	D	67	Total O 67 67	0	0

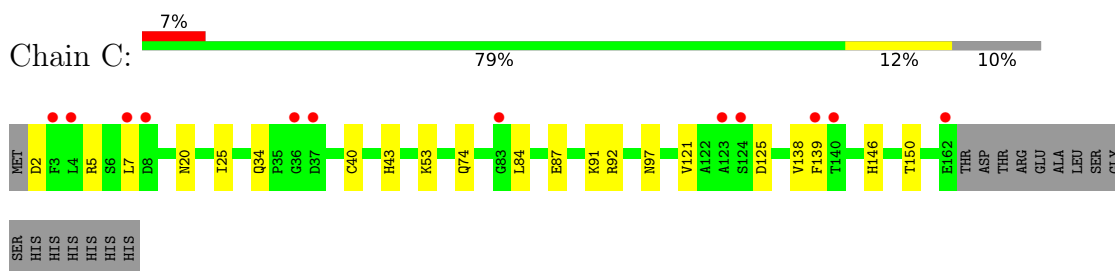
3 Residue-property plots [i](#)

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.

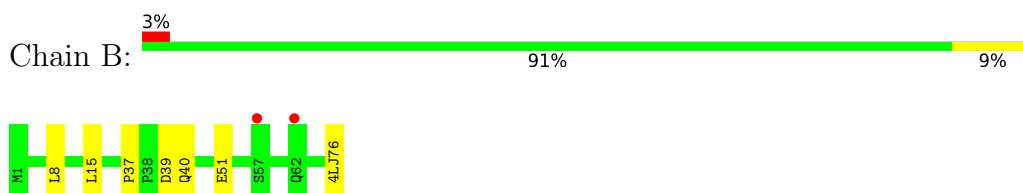
- Molecule 1: RNA-directed RNA polymerase L



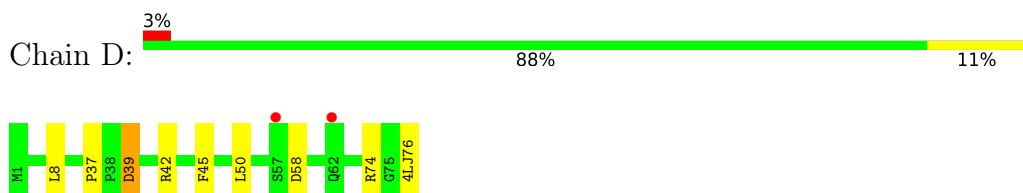
- Molecule 1: RNA-directed RNA polymerase L



- Molecule 2: Polyubiquitin-B (Fragment)



- Molecule 2: Polyubiquitin-B (Fragment)



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	79.32Å 105.84Å 113.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.26 – 1.70 42.21 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.5 (77.26-1.70) 96.5 (42.21-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 1.70Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.172 , 0.212 0.171 , 0.211	Depositor DCC
R_{free} test set	2581 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtrriage
Anisotropy	0.532	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4516	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.05% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 4LJ

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	0.64	0/1427	0.73	1/1933 (0.1%)
1	C	0.56	0/1412	0.62	0/1913
2	B	0.56	0/612	0.72	1/823 (0.1%)
2	D	0.53	0/633	0.69	1/852 (0.1%)
All	All	0.58	0/4084	0.69	3/5521 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	42	ARG	NE-CZ-NH2	-5.70	117.45	120.30
2	B	15	LEU	CA-CB-CG	5.51	127.97	115.30
1	A	63	ARG	NE-CZ-NH1	-5.02	117.79	120.30

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	1395	0	1339	26	0
1	C	1381	0	1319	21	0
2	B	610	0	638	8	0
2	D	631	0	653	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	186	0	0	8	0
3	B	81	0	0	1	0
3	C	165	0	0	3	0
3	D	67	0	0	1	0
All	All	4516	0	3949	50	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 6.

All (50) 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:40:CYS:SG	2:B:76:4LJ:C1	2.02	1.46
1:C:40:CYS:SG	2:D:76:4LJ:C1	2.13	1.36
1:A:20[B]:ASN:ND2	3:A:412:HOH:O	1.72	1.21
1:C:25[B]:ILE:HD11	1:C:121:VAL:HG11	1.53	0.91
1:A:92[B]:ARG:HH22	1:C:97:ASN:HD22	1.20	0.86
3:A:292:HOH:O	2:D:39:ASP:HB3	1.74	0.86
1:A:18[B]:VAL:HG12	3:A:412:HOH:O	1.85	0.74
2:B:40[B]:GLN:N	2:B:40[B]:GLN:OE1	2.23	0.71
1:C:34:GLN:HE21	1:C:43:HIS:HB3	1.56	0.71
1:C:5:ARG:HG3	1:C:139:PHE:HE2	1.55	0.70
1:C:125[B]:ASP:O	3:C:217:HOH:O	2.07	0.70
1:A:34:GLN:HE22	1:A:53:LYS:NZ	1.92	0.67
1:C:5:ARG:HG3	1:C:139:PHE:CE2	2.30	0.67
2:B:40[B]:GLN:NE2	1:C:150:THR:OG1	2.30	0.63
1:C:125[B]:ASP:OD1	1:C:125[B]:ASP:C	2.38	0.62
1:C:125[B]:ASP:O	1:C:125[B]:ASP:OD1	2.18	0.62
1:A:20[B]:ASN:OD1	2:B:8:LEU:O	2.18	0.60
1:A:34:GLN:HE22	1:A:53:LYS:HZ1	1.51	0.57
1:A:25:ILE:HG12	1:A:127:VAL:HG23	1.88	0.56
1:C:34:GLN:HE22	1:C:53:LYS:NZ	2.04	0.56
1:A:41:PHE:CZ	1:A:45[B]:ILE:HD11	2.42	0.55
1:A:80:ARG:HD2	3:B:399:HOH:O	2.07	0.55
1:A:161:PHE:O	1:A:162:GLU:HB2	2.08	0.53
1:A:84:LEU:HD11	1:A:92[B]:ARG:CZ	2.38	0.53
1:A:34:GLN:HE21	1:A:43:HIS:HB3	1.74	0.52
1:A:151:HIS:HB2	2:D:37:PRO:HB3	1.95	0.49
1:C:20[B]:ASN:OD1	2:D:8:LEU:O	2.30	0.49
2:B:37:PRO:HB2	2:B:40[B]:GLN:OE1	2.12	0.48
1:A:125:ASP:O	3:A:378[A]:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92[B]:ARG:HH22	1:C:97:ASN:ND2	1.99	0.47
1:A:92[B]:ARG:NH2	1:C:97:ASN:HD22	2.00	0.46
1:C:34:GLN:HE22	1:C:53:LYS:HZ1	1.63	0.46
2:D:74:ARG:CZ	3:D:306:HOH:O	2.64	0.45
1:C:146:HIS:HE1	2:D:74:ARG:O	2.00	0.45
1:C:2:ASP:HA	1:C:5:ARG:HD2	1.99	0.45
1:C:74[A]:GLN:HG2	3:C:215:HOH:O	2.17	0.44
1:A:9:TRP:CE3	1:A:19[B]:SER:HB2	2.53	0.44
1:C:84:LEU:HD11	1:C:92:ARG:CZ	2.48	0.44
2:B:39:ASP:HB2	3:C:345:HOH:O	2.17	0.43
1:C:7:LEU:HD12	1:C:138:VAL:HG21	1.99	0.43
1:A:156[B]:ARG:NH1	3:A:373:HOH:O	2.38	0.42
1:A:2:ASP:HB3	3:A:392:HOH:O	2.20	0.42
1:A:126:GLU:HA	3:A:378[A]:HOH:O	2.18	0.42
2:D:45:PHE:HB3	2:D:50:LEU:HD21	2.01	0.42
1:A:25:ILE:CD1	1:A:127:VAL:CG2	2.98	0.42
1:A:80:ARG:NH1	2:B:51:GLU:OE2	2.53	0.42
1:A:156[B]:ARG:NH2	3:A:373:HOH:O	2.44	0.41
1:A:25:ILE:HD11	1:A:127:VAL:CG2	2.50	0.41
1:C:87:GLU:O	1:C:91[A]:LYS:HG3	2.20	0.41
1:A:40:CYS:SG	2:B:76:4LJ:H5	2.61	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	171/178 (96%)	166 (97%)	5 (3%)	0	100	100
1	C	170/178 (96%)	168 (99%)	2 (1%)	0	100	100
2	B	74/76 (97%)	74 (100%)	0	0	100	100
2	D	77/76 (101%)	77 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	492/508 (97%)	485 (99%)	7 (1%)	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	151/154 (98%)	150 (99%)	1 (1%)	84	77
1	C	150/154 (97%)	150 (100%)	0	100	100
2	B	69/68 (102%)	69 (100%)	0	100	100
2	D	72/68 (106%)	70 (97%)	2 (3%)	43	25
All	All	442/444 (100%)	439 (99%)	3 (1%)	84	77

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	162	GLU
2	D	39	ASP
2	D	58	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	97	ASN
2	B	25	ASN
1	C	34	GLN
1	C	97	ASN
1	C	146	HIS

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](#)

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, 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	161/178 (90%)	0.02	6 (3%) 41 46	11, 18, 37, 77	0
1	C	161/178 (90%)	-0.04	12 (7%) 14 16	12, 21, 59, 86	0
2	B	75/76 (98%)	-0.03	2 (2%) 54 58	14, 23, 40, 43	0
2	D	75/76 (98%)	0.01	2 (2%) 54 58	16, 24, 44, 49	0
All	All	472/508 (92%)	-0.01	22 (4%) 31 35	11, 21, 44, 86	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	123	ALA	8.8
1	A	124	SER	5.0
1	A	74	GLN	4.1
1	C	123	ALA	3.7
1	C	4	LEU	3.0
1	C	139	PHE	3.0
1	A	37	ASP	3.0
1	C	7	LEU	3.0
1	C	8	ASP	2.7
1	C	124	SER	2.6
1	A	121	VAL	2.5
1	C	3	PHE	2.4
2	D	57	SER	2.4
1	C	162	GLU	2.3
2	B	62	GLN	2.2
2	D	62	GLN	2.2
1	C	83	GLY	2.2
1	A	80	ARG	2.1
1	C	36	GLY	2.1
2	B	57	SER	2.0
1	C	140	THR	2.0
1	C	37	ASP	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 monosaccharides 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.