



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 05:33 pm BST

PDB ID : 1Z0E
Title : Crystal Structure of *A. fulgidus* Lon proteolytic domain
Authors : Botos, I.; Melnikov, E.E.; Cherry, S.; Kozlov, S.; Makhovskaya, O.V.; Tropea, J.E.; Gustchina, A.; Rotanova, T.V.; Wlodawer, A.
Deposited on : 2005-03-01
Resolution : 2.05 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

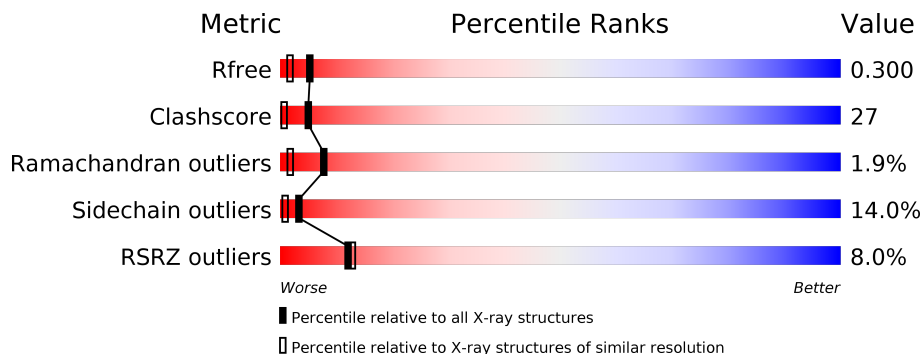
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 on 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	205	
1	B	205	
1	C	205	
1	D	205	
1	E	205	
1	F	205	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9285 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 Putative protease La homolog type.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	195	1457	921	247	284	5	0	0	0
1	B	195	1457	921	247	284	5	0	0	0
1	C	194	1448	915	245	283	5	0	0	0
1	D	195	1457	921	247	284	5	0	0	0
1	E	195	1457	921	247	284	5	0	0	0
1	F	195	1457	921	247	284	5	0	0	0

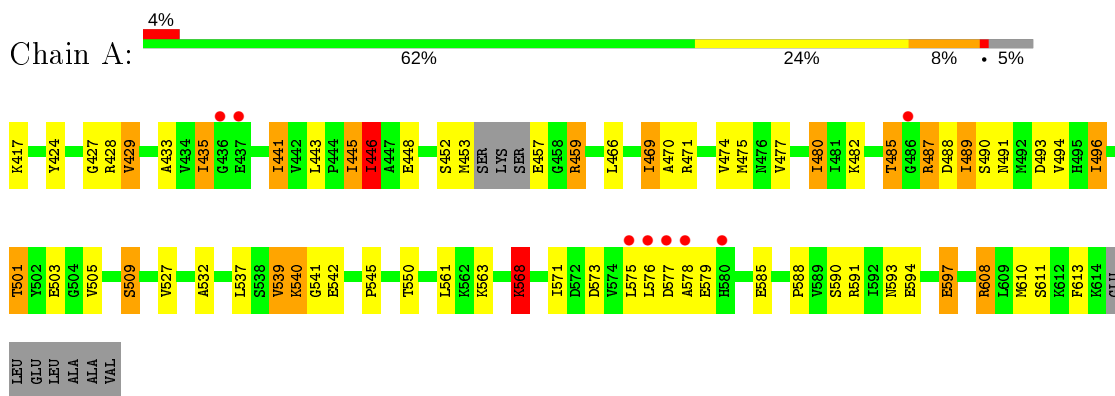
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	89	Total 89	O 89	0	0
2	B	65	Total 65	O 65	0	0
2	C	121	Total 121	O 121	0	0
2	D	106	Total 106	O 106	0	0
2	E	67	Total 67	O 67	0	0
2	F	104	Total 104	O 104	0	0

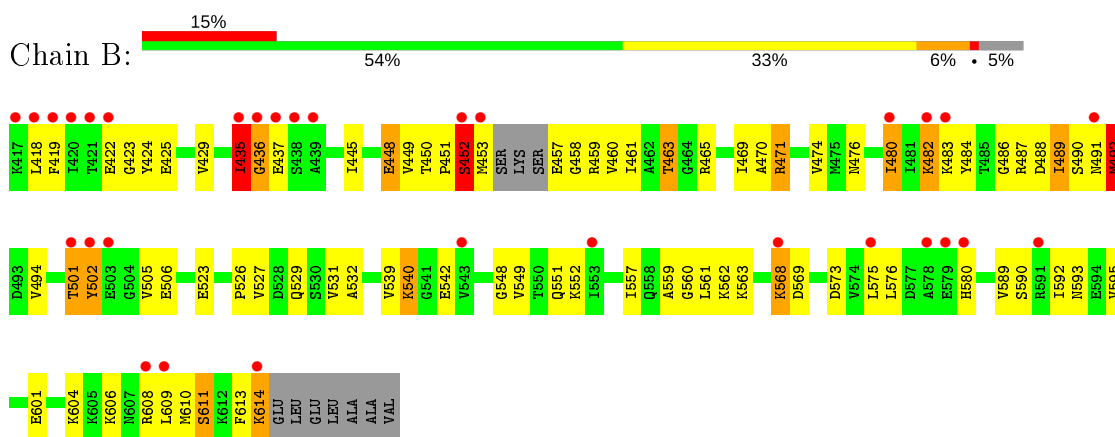
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

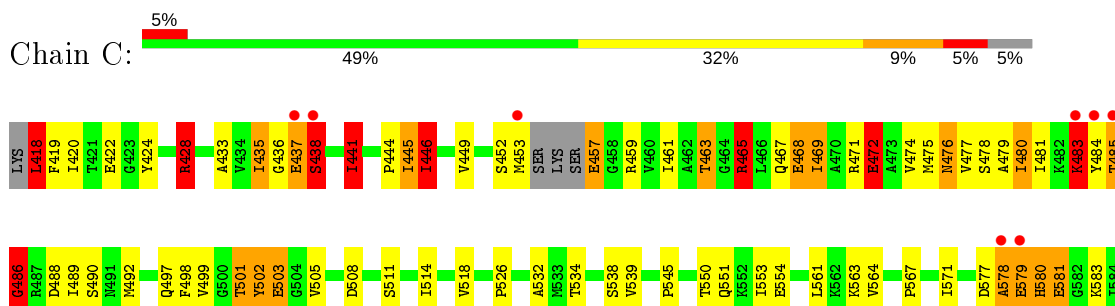
- Molecule 1: Putative protease La homolog type

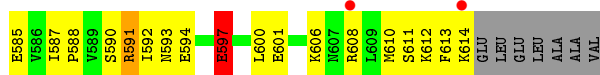


- Molecule 1: Putative protease La homolog type

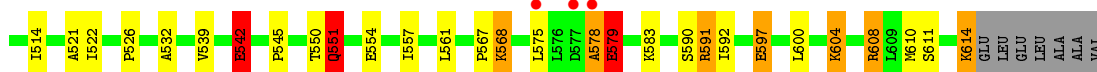


- Molecule 1: Putative protease La homolog type

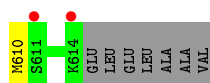
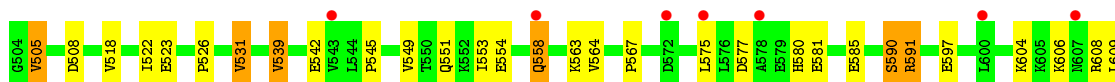




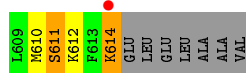
- Molecule 1: Putative protease La homolog type



- Molecule 1: Putative protease La homolog type



- Molecule 1: Putative protease La homolog type



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.68Å 86.11Å 135.61Å 90.00° 94.70° 90.00°	Depositor
Resolution (Å)	15.00 – 2.05 14.92 – 2.05	Depositor EDS
% Data completeness (in resolution range)	100.0 (15.00-2.05) 96.7 (14.92-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.05Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.213 , 0.299 0.211 , 0.300	Depositor DCC
R_{free} test set	1009 reflections (1.49%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtrriage
Anisotropy	0.135	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.3	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	0.95	EDS
Total number of atoms	9285	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.77% 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	1.35	7/1470 (0.5%)	1.21	8/1983 (0.4%)
1	B	1.17	2/1470 (0.1%)	1.07	3/1983 (0.2%)
1	C	1.49	12/1461 (0.8%)	1.30	12/1972 (0.6%)
1	D	1.51	14/1470 (1.0%)	1.23	6/1983 (0.3%)
1	E	1.22	5/1470 (0.3%)	1.13	5/1983 (0.3%)
1	F	1.37	7/1470 (0.5%)	1.27	12/1983 (0.6%)
All	All	1.36	47/8811 (0.5%)	1.20	46/11887 (0.4%)

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	C	0	1
1	F	0	2
All	All	0	3

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	542	GLU	CB-CG	13.16	1.77	1.52
1	C	597	GLU	CD-OE2	10.30	1.36	1.25
1	D	542	GLU	CG-CD	9.28	1.65	1.51
1	C	468	GLU	CD-OE2	9.08	1.35	1.25
1	F	597	GLU	CG-CD	9.05	1.65	1.51

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	600	LEU	CB-CG-CD1	-8.91	95.86	111.00
1	C	446	ILE	CB-CA-C	-8.87	93.86	111.60
1	A	591	ARG	NE-CZ-NH1	8.35	124.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	597	GLU	OE1-CD-OE2	8.22	133.17	123.30
1	F	441	ILE	CB-CA-C	-7.51	96.58	111.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	438	SER	Peptide
1	F	579	GLU	Peptide
1	F	580	HIS	Peptide

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	1457	0	1523	78	0
1	B	1457	0	1523	85	0
1	C	1448	0	1510	128	1
1	D	1457	0	1523	68	2
1	E	1457	0	1523	54	0
1	F	1457	0	1523	93	1
2	A	89	0	0	25	0
2	B	65	0	0	17	0
2	C	121	0	0	36	1
2	D	106	0	0	22	0
2	E	67	0	0	17	0
2	F	104	0	0	23	0
All	All	9285	0	9125	485	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 27.

The worst 5 of 485 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:D:542:GLU:CB	1:D:542:GLU:CG	1.77	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:ILE:HG21	2:A:691:HOH:O	1.11	1.27
1:B:480:ILE:HG21	2:B:682:HOH:O	1.37	1.24
1:C:418:LEU:N	2:C:725:HOH:O	1.62	1.23
1:C:502:TYR:HB2	2:C:726:HOH:O	1.12	1.22

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:F:486:GLY:O	1:F:578:ALA:CB[1_455]	1.82	0.38
1:C:585:GLU:OE2	1:D:597:GLU:OE1[2_546]	2.13	0.07
1:D:568:LYS:CD	2:C:738:HOH:O[2_556]	2.16	0.04

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	191/205 (93%)	183 (96%)	8 (4%)	0	100	100
1	B	191/205 (93%)	181 (95%)	5 (3%)	5 (3%)	5	1
1	C	190/205 (93%)	179 (94%)	5 (3%)	6 (3%)	4	0
1	D	191/205 (93%)	183 (96%)	6 (3%)	2 (1%)	15	6
1	E	191/205 (93%)	181 (95%)	9 (5%)	1 (0%)	29	18
1	F	191/205 (93%)	177 (93%)	6 (3%)	8 (4%)	3	0
All	All	1145/1230 (93%)	1084 (95%)	39 (3%)	22 (2%)	8	2

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	436	GLY
1	B	452	SER

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Mol	Chain	Res	Type
1	C	579	GLU
1	F	476	ASN
1	F	477	VAL

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	160/168 (95%)	142 (89%)	18 (11%)	6	1
1	B	160/168 (95%)	140 (88%)	20 (12%)	4	1
1	C	159/168 (95%)	131 (82%)	28 (18%)	2	0
1	D	160/168 (95%)	139 (87%)	21 (13%)	4	1
1	E	160/168 (95%)	138 (86%)	22 (14%)	3	1
1	F	160/168 (95%)	135 (84%)	25 (16%)	2	0
All	All	959/1008 (95%)	825 (86%)	134 (14%)	3	1

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	538	SER
1	D	480	ILE
1	F	513	SER
1	C	581	GLU
1	D	428	ARG

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	491	ASN
1	F	558	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 carbohydrates 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 [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	195/205 (95%)	0.29	8 (4%) 37 40	26, 33, 52, 60	0
1	B	195/205 (95%)	0.91	31 (15%) 1 1	29, 39, 60, 78	0
1	C	194/205 (94%)	0.18	10 (5%) 27 29	23, 30, 54, 65	0
1	D	195/205 (95%)	0.10	7 (3%) 42 46	24, 31, 48, 60	0
1	E	195/205 (95%)	0.88	24 (12%) 4 3	30, 38, 57, 77	0
1	F	195/205 (95%)	0.33	14 (7%) 15 17	26, 33, 56, 60	0
All	All	1169/1230 (95%)	0.45	94 (8%) 12 13	23, 35, 56, 78	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	419	PHE	8.7
1	E	418	LEU	8.3
1	E	502	TYR	7.5
1	E	501	THR	7.1
1	E	578	ALA	6.8

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

There are no such residues in this entry.