



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:54 PM UTC

PDB ID : 2R5I / pdb_00002r5i
Title : Pentamer Structure of Major Capsid Protein L1 of Human Papilloma Virus type 18
Authors : Bishop, B.; Dasgupta, J.; Chen, X.S.
Deposited on : 2007-09-03
Resolution : 3.40 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 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:

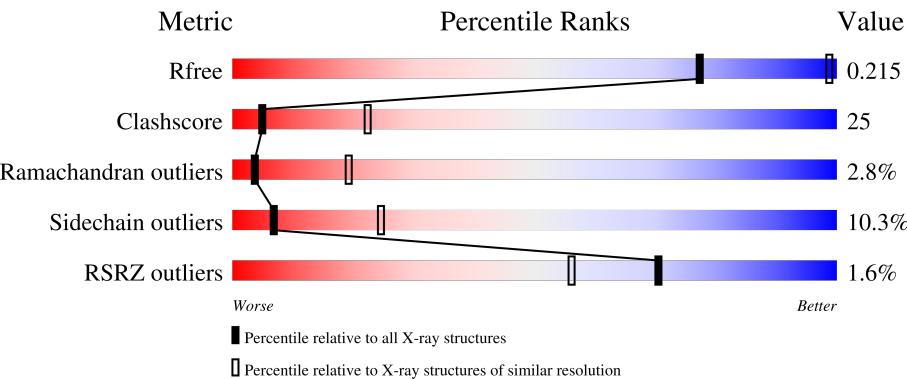
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	428	39%40%17%..
1	B	428	37%43%16%..
1	C	428	43%37%17%..
1	D	428	38%44%15%..
1	E	428	2%38%41%17%..

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Mol	Chain	Length	Quality of chain				
1	F	428		33%	47%	15%	..
1	G	428		32%	45%	19%	..
1	H	428		34%	44%	18%	..
1	I	428		40%	40%	16%	..
1	J	428		36%	45%	15%	..
1	K	428		38%	40%	17%	..
1	L	428		41%	40%	15%	..
1	M	428		38%	43%	16%	..
1	N	428		41%	39%	17%	..
1	O	428		39%	43%	15%	..

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 49845 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 L1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	B	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	C	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	D	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	E	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	F	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	G	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	H	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	I	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	J	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	K	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	L	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	M	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	N	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			
1	O	423	Total	C	N	O	S	0	0	0
			3323	2098	562	643	20			

There are 135 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	ALA	-	expression tag	UNP Q80B70
A	47	ASP	ASN	engineered mutation	UNP Q80B70
A	175	SER	CYS	engineered mutation	UNP Q80B70
A	393	GLN	HIS	engineered mutation	UNP Q80B70
A	405	GLY	-	linker	UNP Q80B70
A	406	GLY	-	linker	UNP Q80B70
A	407	SER	-	linker	UNP Q80B70
A	408	GLY	-	linker	UNP Q80B70
A	409	GLY	-	linker	UNP Q80B70
B	20	ALA	-	expression tag	UNP Q80B70
B	47	ASP	ASN	engineered mutation	UNP Q80B70
B	175	SER	CYS	engineered mutation	UNP Q80B70
B	393	GLN	HIS	engineered mutation	UNP Q80B70
B	405	GLY	-	linker	UNP Q80B70
B	406	GLY	-	linker	UNP Q80B70
B	407	SER	-	linker	UNP Q80B70
B	408	GLY	-	linker	UNP Q80B70
B	409	GLY	-	linker	UNP Q80B70
C	20	ALA	-	expression tag	UNP Q80B70
C	47	ASP	ASN	engineered mutation	UNP Q80B70
C	175	SER	CYS	engineered mutation	UNP Q80B70
C	393	GLN	HIS	engineered mutation	UNP Q80B70
C	405	GLY	-	linker	UNP Q80B70
C	406	GLY	-	linker	UNP Q80B70
C	407	SER	-	linker	UNP Q80B70
C	408	GLY	-	linker	UNP Q80B70
C	409	GLY	-	linker	UNP Q80B70
D	20	ALA	-	expression tag	UNP Q80B70
D	47	ASP	ASN	engineered mutation	UNP Q80B70
D	175	SER	CYS	engineered mutation	UNP Q80B70
D	393	GLN	HIS	engineered mutation	UNP Q80B70
D	405	GLY	-	linker	UNP Q80B70
D	406	GLY	-	linker	UNP Q80B70
D	407	SER	-	linker	UNP Q80B70
D	408	GLY	-	linker	UNP Q80B70
D	409	GLY	-	linker	UNP Q80B70
E	20	ALA	-	expression tag	UNP Q80B70
E	47	ASP	ASN	engineered mutation	UNP Q80B70
E	175	SER	CYS	engineered mutation	UNP Q80B70
E	393	GLN	HIS	engineered mutation	UNP Q80B70
E	405	GLY	-	linker	UNP Q80B70
E	406	GLY	-	linker	UNP Q80B70
E	407	SER	-	linker	UNP Q80B70

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Chain	Residue	Modelled	Actual	Comment	Reference
E	408	GLY	-	linker	UNP Q80B70
E	409	GLY	-	linker	UNP Q80B70
F	20	ALA	-	expression tag	UNP Q80B70
F	47	ASP	ASN	engineered mutation	UNP Q80B70
F	175	SER	CYS	engineered mutation	UNP Q80B70
F	393	GLN	HIS	engineered mutation	UNP Q80B70
F	405	GLY	-	linker	UNP Q80B70
F	406	GLY	-	linker	UNP Q80B70
F	407	SER	-	linker	UNP Q80B70
F	408	GLY	-	linker	UNP Q80B70
F	409	GLY	-	linker	UNP Q80B70
G	20	ALA	-	expression tag	UNP Q80B70
G	47	ASP	ASN	engineered mutation	UNP Q80B70
G	175	SER	CYS	engineered mutation	UNP Q80B70
G	393	GLN	HIS	engineered mutation	UNP Q80B70
G	405	GLY	-	linker	UNP Q80B70
G	406	GLY	-	linker	UNP Q80B70
G	407	SER	-	linker	UNP Q80B70
G	408	GLY	-	linker	UNP Q80B70
G	409	GLY	-	linker	UNP Q80B70
H	20	ALA	-	expression tag	UNP Q80B70
H	47	ASP	ASN	engineered mutation	UNP Q80B70
H	175	SER	CYS	engineered mutation	UNP Q80B70
H	393	GLN	HIS	engineered mutation	UNP Q80B70
H	405	GLY	-	linker	UNP Q80B70
H	406	GLY	-	linker	UNP Q80B70
H	407	SER	-	linker	UNP Q80B70
H	408	GLY	-	linker	UNP Q80B70
H	409	GLY	-	linker	UNP Q80B70
I	20	ALA	-	expression tag	UNP Q80B70
I	47	ASP	ASN	engineered mutation	UNP Q80B70
I	175	SER	CYS	engineered mutation	UNP Q80B70
I	393	GLN	HIS	engineered mutation	UNP Q80B70
I	405	GLY	-	linker	UNP Q80B70
I	406	GLY	-	linker	UNP Q80B70
I	407	SER	-	linker	UNP Q80B70
I	408	GLY	-	linker	UNP Q80B70
I	409	GLY	-	linker	UNP Q80B70
J	20	ALA	-	expression tag	UNP Q80B70
J	47	ASP	ASN	engineered mutation	UNP Q80B70
J	175	SER	CYS	engineered mutation	UNP Q80B70
J	393	GLN	HIS	engineered mutation	UNP Q80B70

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Chain	Residue	Modelled	Actual	Comment	Reference
J	405	GLY	-	linker	UNP Q80B70
J	406	GLY	-	linker	UNP Q80B70
J	407	SER	-	linker	UNP Q80B70
J	408	GLY	-	linker	UNP Q80B70
J	409	GLY	-	linker	UNP Q80B70
K	20	ALA	-	expression tag	UNP Q80B70
K	47	ASP	ASN	engineered mutation	UNP Q80B70
K	175	SER	CYS	engineered mutation	UNP Q80B70
K	393	GLN	HIS	engineered mutation	UNP Q80B70
K	405	GLY	-	linker	UNP Q80B70
K	406	GLY	-	linker	UNP Q80B70
K	407	SER	-	linker	UNP Q80B70
K	408	GLY	-	linker	UNP Q80B70
K	409	GLY	-	linker	UNP Q80B70
L	20	ALA	-	expression tag	UNP Q80B70
L	47	ASP	ASN	engineered mutation	UNP Q80B70
L	175	SER	CYS	engineered mutation	UNP Q80B70
L	393	GLN	HIS	engineered mutation	UNP Q80B70
L	405	GLY	-	linker	UNP Q80B70
L	406	GLY	-	linker	UNP Q80B70
L	407	SER	-	linker	UNP Q80B70
L	408	GLY	-	linker	UNP Q80B70
L	409	GLY	-	linker	UNP Q80B70
M	20	ALA	-	expression tag	UNP Q80B70
M	47	ASP	ASN	engineered mutation	UNP Q80B70
M	175	SER	CYS	engineered mutation	UNP Q80B70
M	393	GLN	HIS	engineered mutation	UNP Q80B70
M	405	GLY	-	linker	UNP Q80B70
M	406	GLY	-	linker	UNP Q80B70
M	407	SER	-	linker	UNP Q80B70
M	408	GLY	-	linker	UNP Q80B70
M	409	GLY	-	linker	UNP Q80B70
N	20	ALA	-	expression tag	UNP Q80B70
N	47	ASP	ASN	engineered mutation	UNP Q80B70
N	175	SER	CYS	engineered mutation	UNP Q80B70
N	393	GLN	HIS	engineered mutation	UNP Q80B70
N	405	GLY	-	linker	UNP Q80B70
N	406	GLY	-	linker	UNP Q80B70
N	407	SER	-	linker	UNP Q80B70
N	408	GLY	-	linker	UNP Q80B70
N	409	GLY	-	linker	UNP Q80B70
O	20	ALA	-	expression tag	UNP Q80B70

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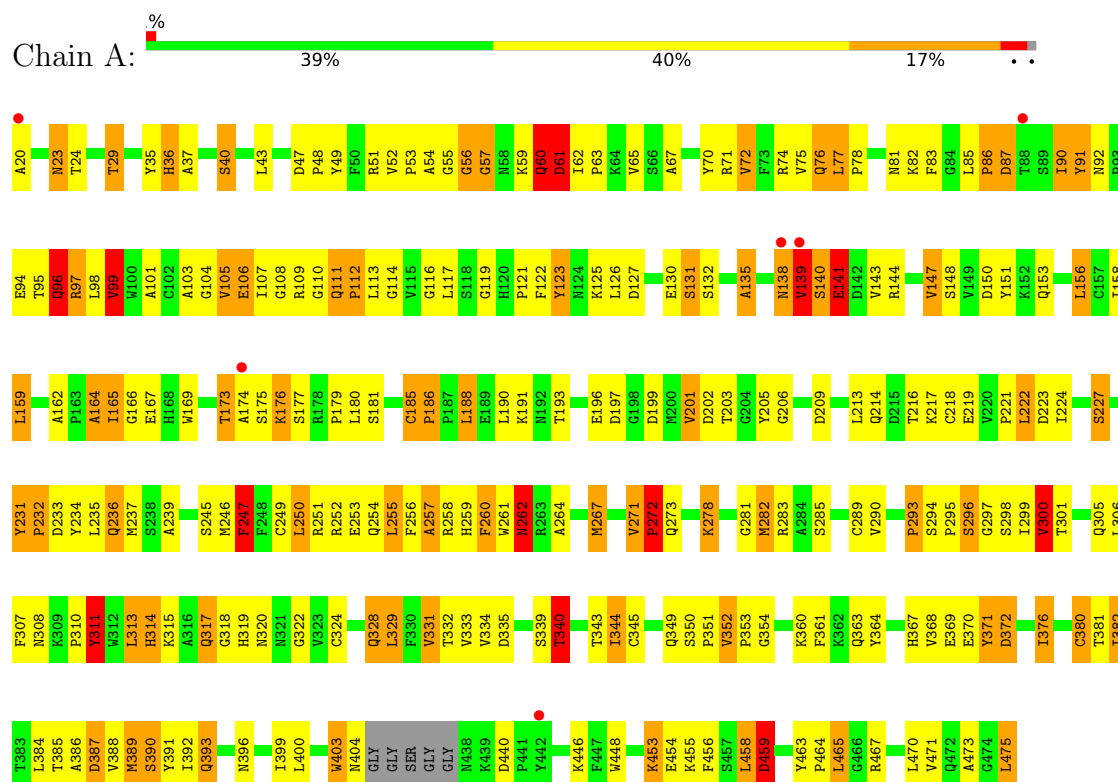
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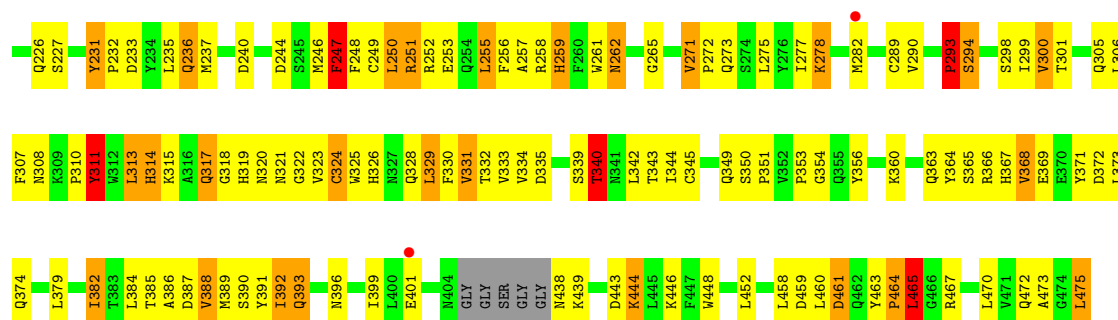
Chain	Residue	Modelled	Actual	Comment	Reference
O	47	ASP	ASN	engineered mutation	UNP Q80B70
O	175	SER	CYS	engineered mutation	UNP Q80B70
O	393	GLN	HIS	engineered mutation	UNP Q80B70
O	405	GLY	-	linker	UNP Q80B70
O	406	GLY	-	linker	UNP Q80B70
O	407	SER	-	linker	UNP Q80B70
O	408	GLY	-	linker	UNP Q80B70
O	409	GLY	-	linker	UNP Q80B70

3 Residue-property plots

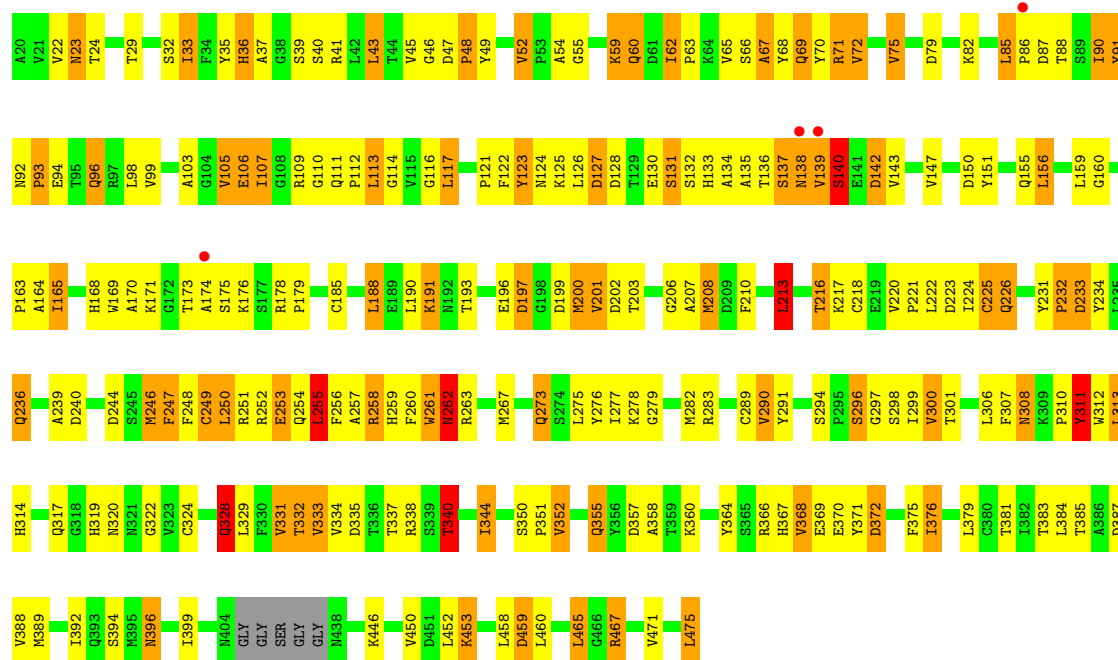
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: L1 protein

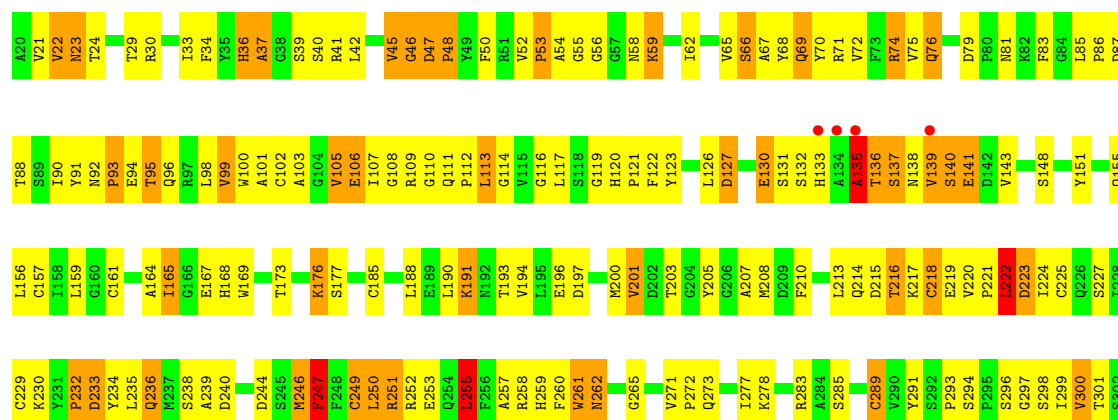


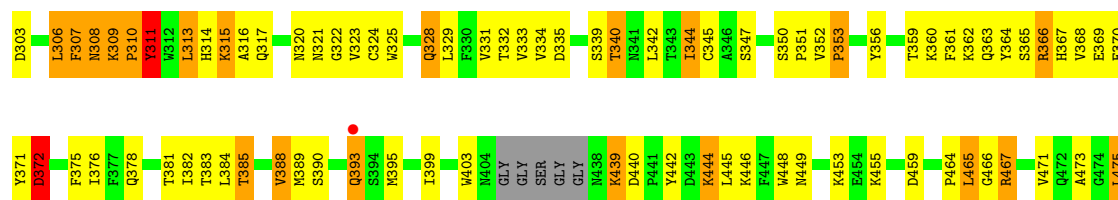


• Molecule 1: L1 protein

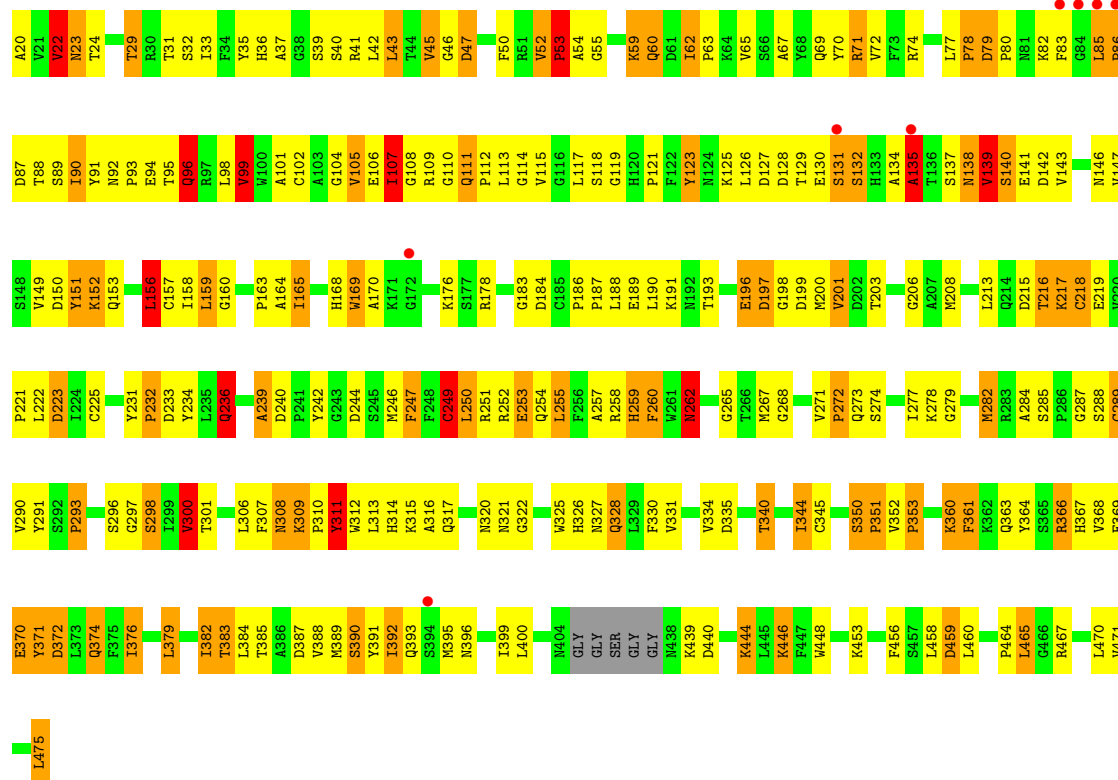


• Molecule 1: L1 protein

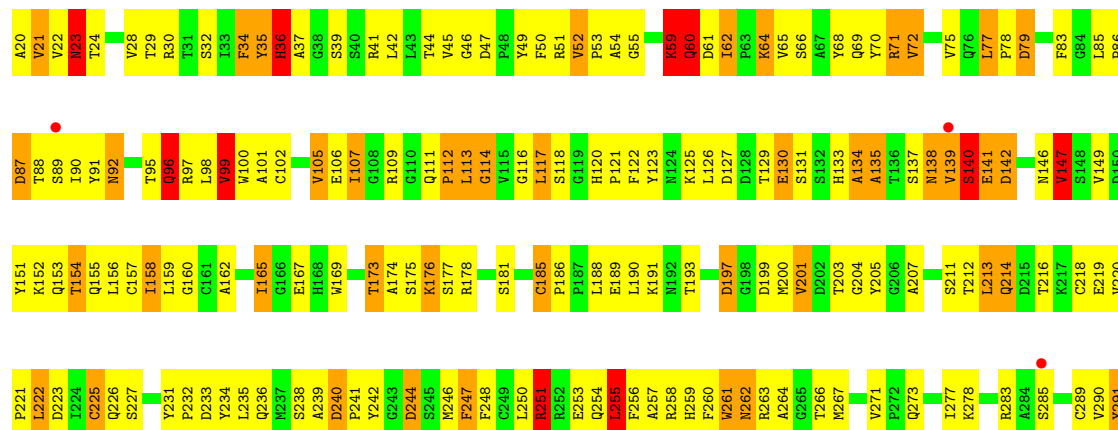




• Molecule 1: L1 protein

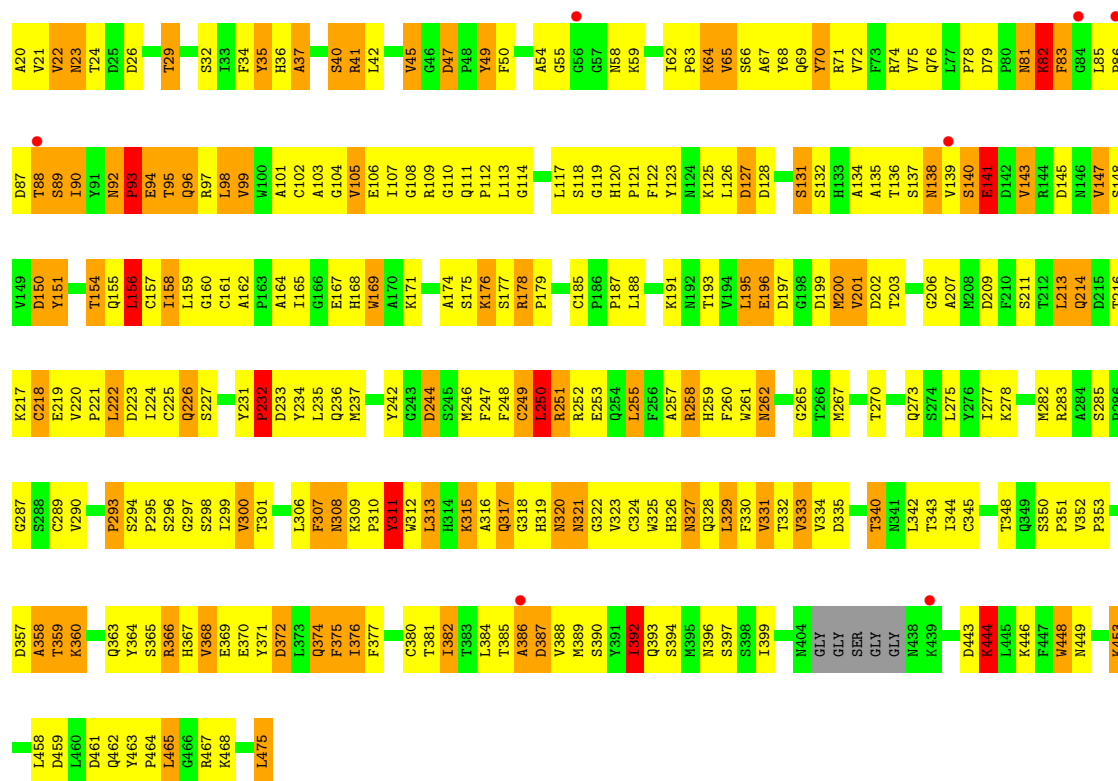


• Molecule 1: L1 protein

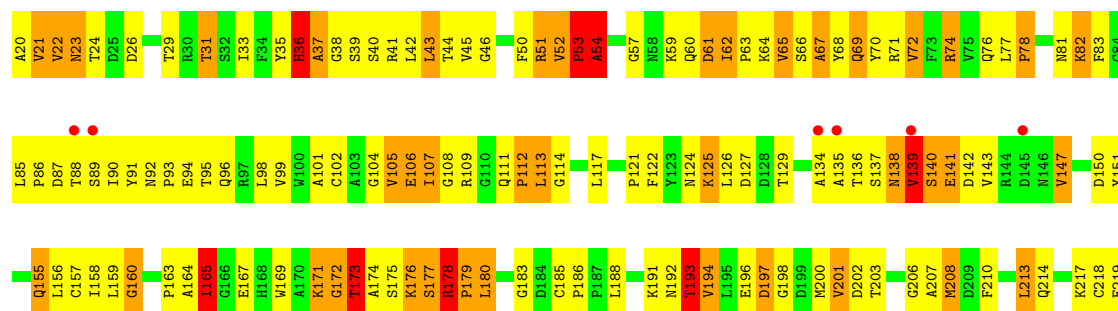


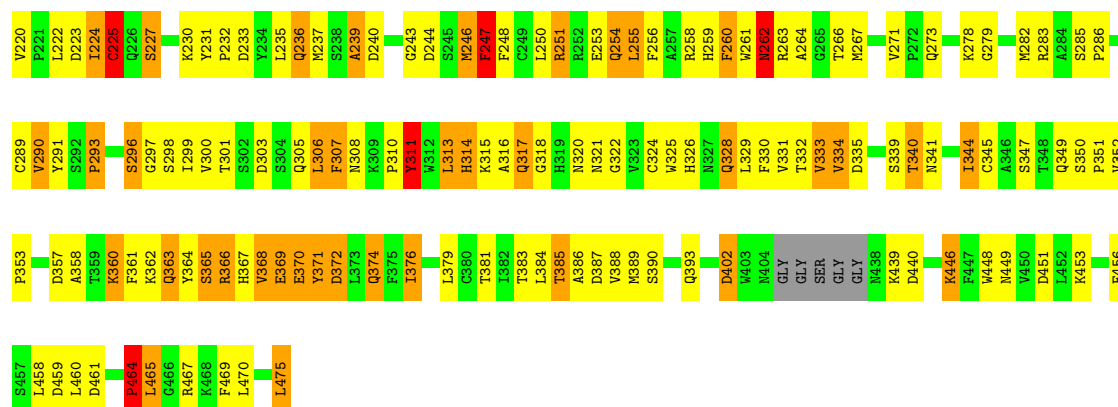


• Molecule 1: L1 protein

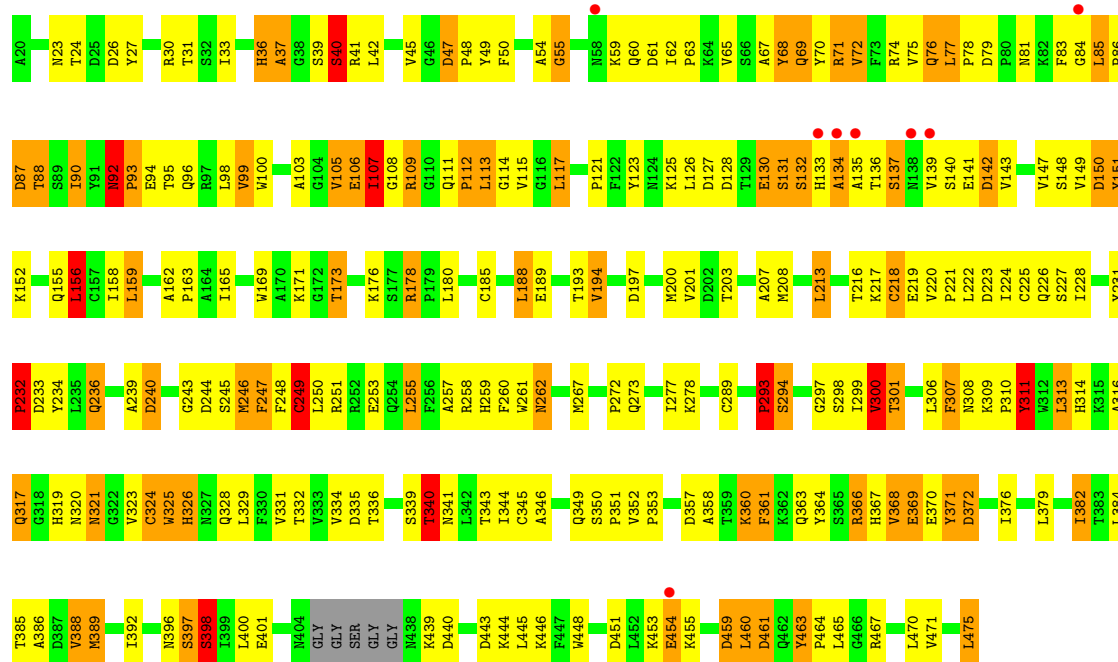


• Molecule 1: L1 protein

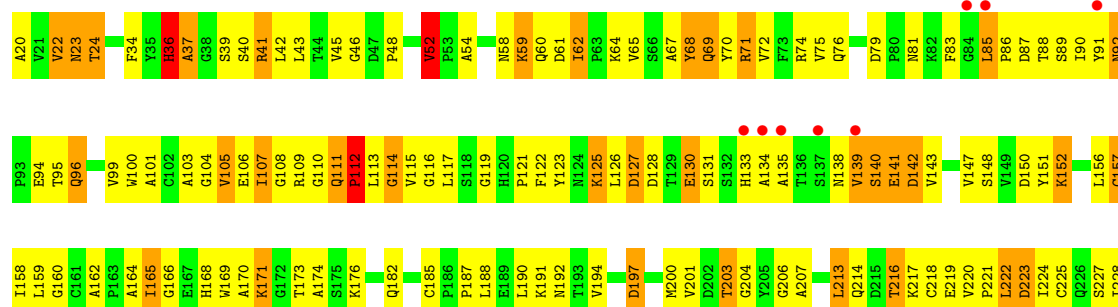


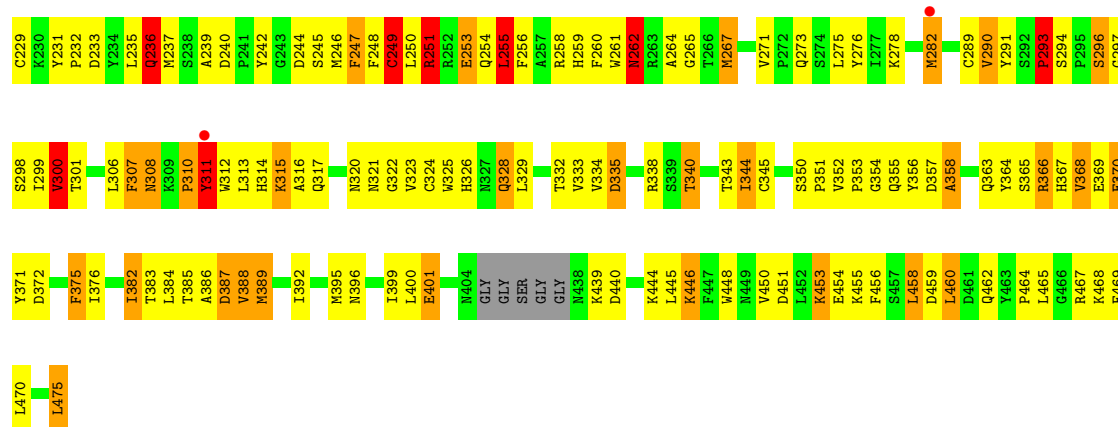


• Molecule 1: L1 protein

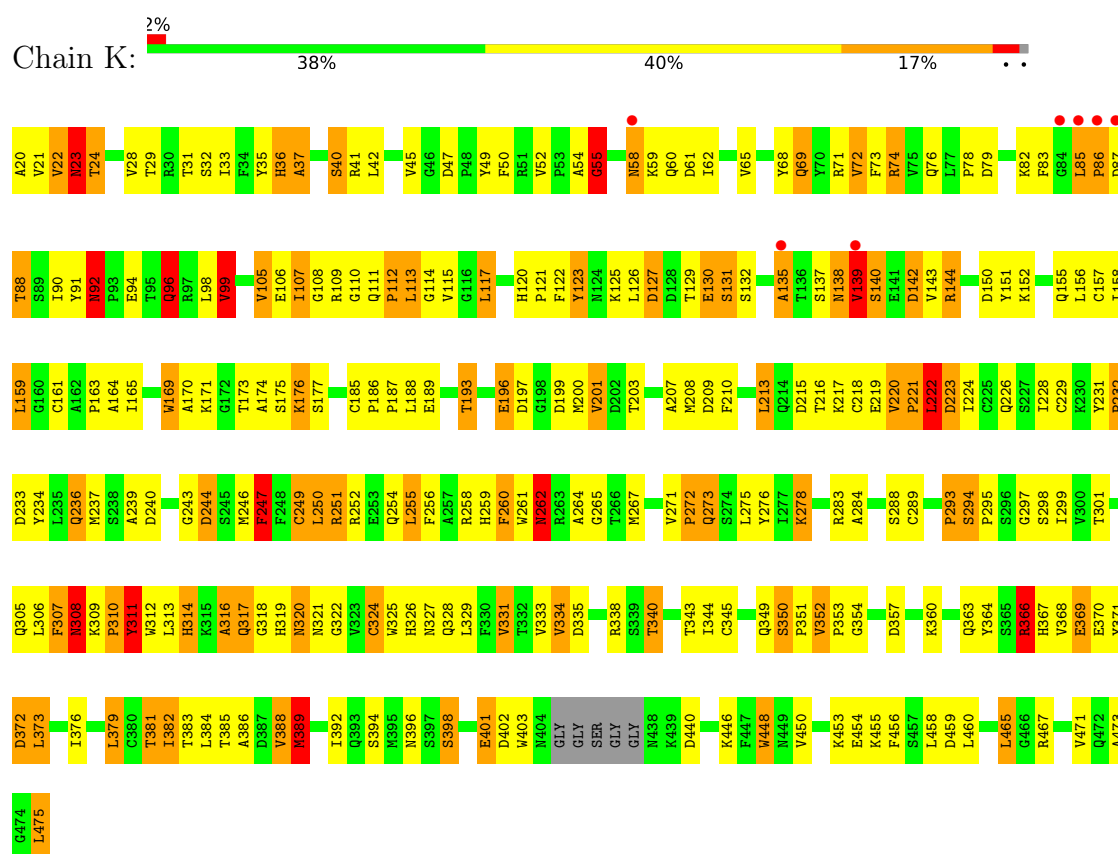


• Molecule 1: L1 protein

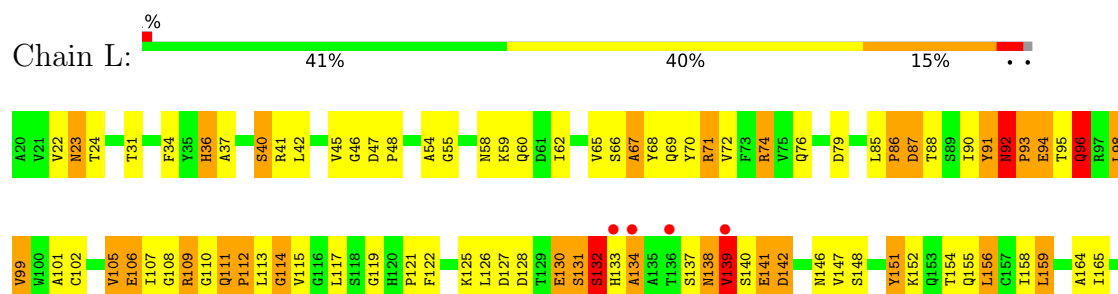


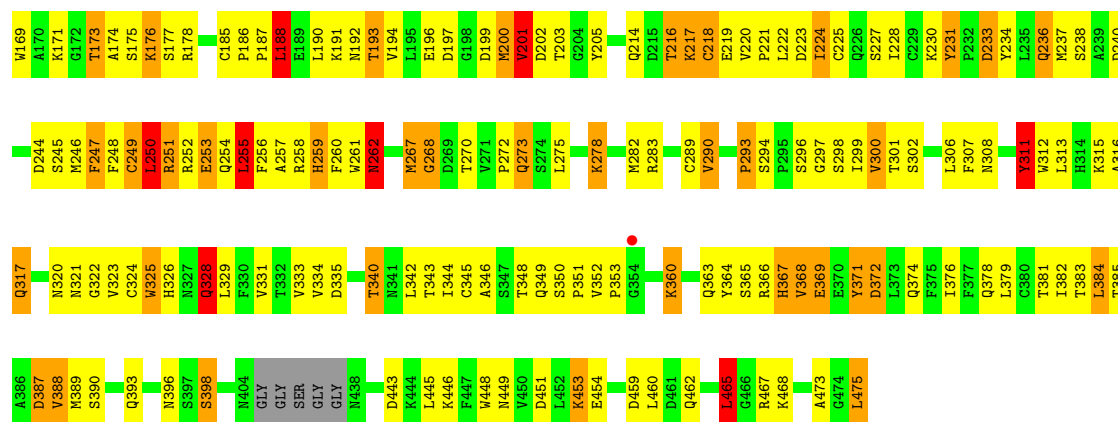


• Molecule 1: L1 protein

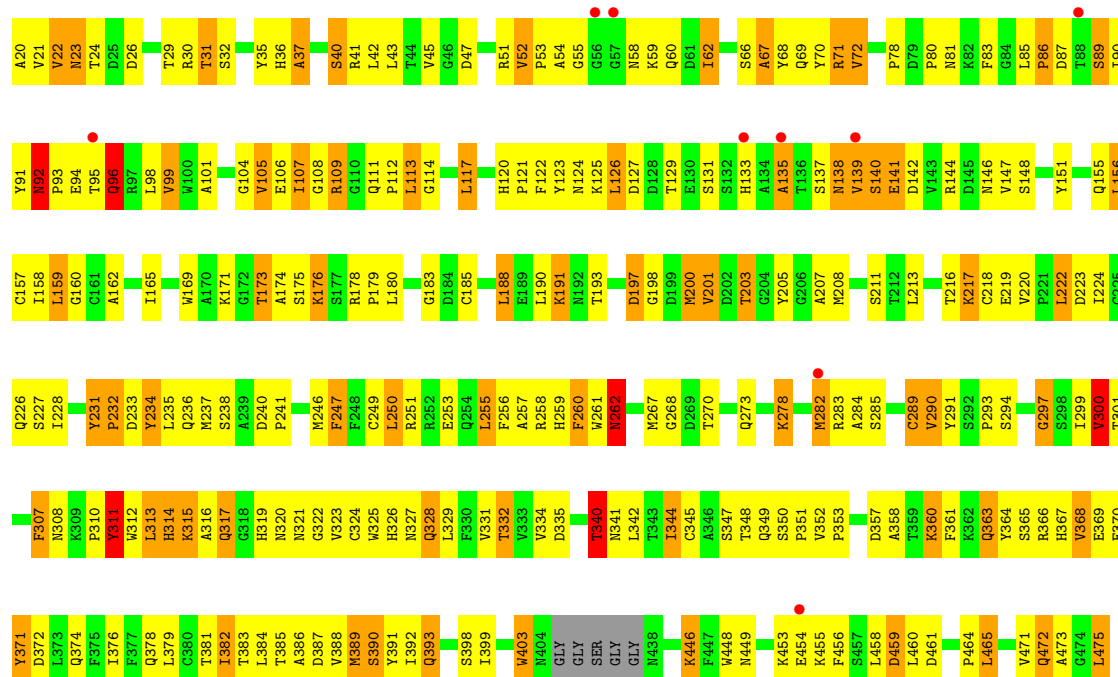
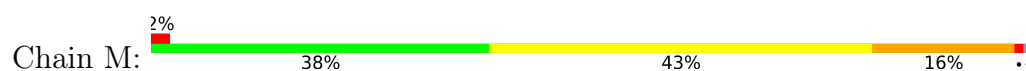


• Molecule 1: L1 protein

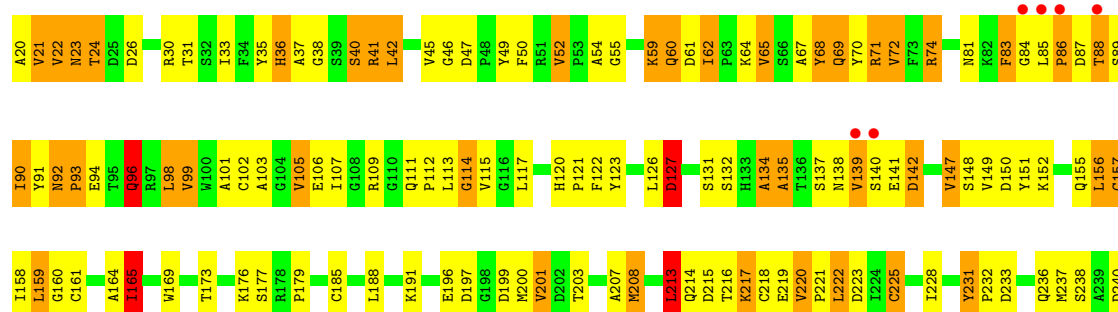
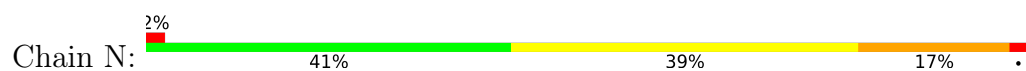


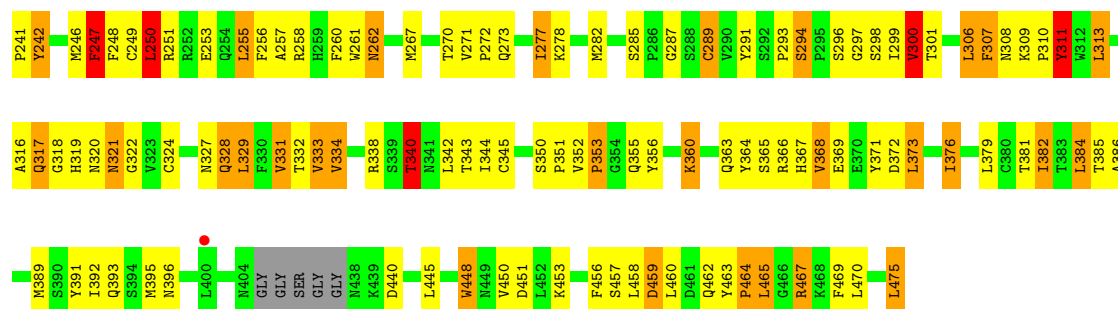


• Molecule 1: L1 protein

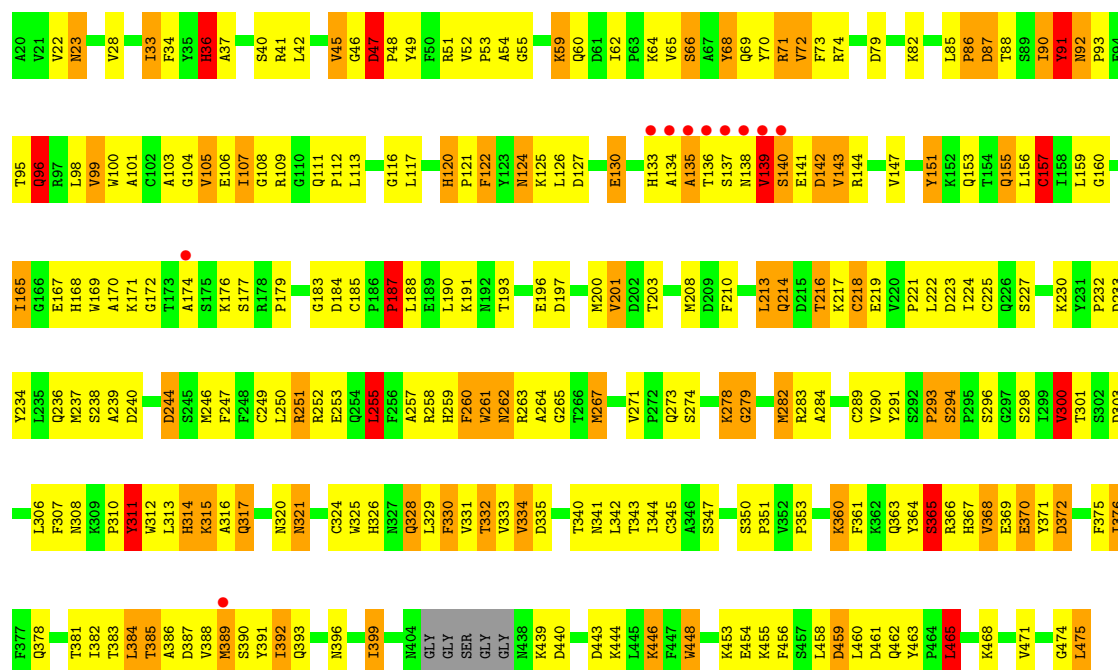


• Molecule 1: L1 protein





• Molecule 1: L1 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	81.16Å 105.04Å 235.75Å 87.56° 85.66° 68.16°	Depositor
Resolution (Å)	40.00 – 3.40 40.00 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.00-3.40) 99.6 (40.00-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	19.60	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.260 0.204 , 0.215	Depositor DCC
R_{free} test set	11857 reflections (7.47%)	wwPDB-VP
Wilson B-factor (Å ²)	63.4	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,-h+k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	49845	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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 ⓘ

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	2.21	109/3408 (3.2%)	1.81	74/4633 (1.6%)
1	B	2.25	113/3408 (3.3%)	1.72	53/4633 (1.1%)
1	C	2.20	99/3408 (2.9%)	1.75	59/4633 (1.3%)
1	D	2.30	118/3408 (3.5%)	1.76	49/4633 (1.1%)
1	E	2.33	139/3408 (4.1%)	1.75	51/4633 (1.1%)
1	F	2.28	130/3408 (3.8%)	1.73	58/4633 (1.3%)
1	G	2.32	131/3408 (3.8%)	1.82	67/4633 (1.4%)
1	H	2.22	127/3408 (3.7%)	1.82	84/4633 (1.8%)
1	I	2.17	104/3408 (3.1%)	1.69	46/4633 (1.0%)
1	J	2.25	118/3408 (3.5%)	1.75	56/4633 (1.2%)
1	K	2.26	121/3408 (3.6%)	1.78	74/4633 (1.6%)
1	L	2.23	117/3408 (3.4%)	1.77	56/4633 (1.2%)
1	M	2.26	117/3408 (3.4%)	1.75	51/4633 (1.1%)
1	N	2.23	102/3408 (3.0%)	1.70	47/4633 (1.0%)
1	O	2.24	112/3408 (3.3%)	1.77	54/4633 (1.2%)
All	All	2.25	1757/51120 (3.4%)	1.76	879/69495 (1.3%)

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	D	0	1

The worst 5 of 1757 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	207	ALA	CA-CB	-15.49	1.32	1.53
1	M	257	ALA	CA-CB	-14.13	1.34	1.52
1	G	160	GLY	C-O	13.29	1.38	1.23
1	D	439	LYS	CE-NZ	13.26	1.89	1.49
1	F	89	SER	C-O	13.11	1.38	1.24

The worst 5 of 879 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	141	GLU	N-CA-C	13.91	122.11	108.75
1	G	140	SER	CA-C-N	-13.31	96.11	121.54
1	G	140	SER	C-N-CA	-13.31	96.11	121.54
1	D	54	ALA	N-CA-C	13.20	127.31	111.33
1	K	314	HIS	N-CA-C	-10.48	100.34	113.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	53	PRO	Peptide

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	3323	0	3192	200	1
1	B	3323	0	3192	184	0
1	C	3323	0	3192	157	1
1	D	3323	0	3192	159	0
1	E	3323	0	3192	173	0
1	F	3323	0	3192	207	0
1	G	3323	0	3192	216	0
1	H	3323	0	3192	211	0
1	I	3323	0	3192	181	0
1	J	3323	0	3192	171	0
1	K	3323	0	3192	164	0
1	L	3323	0	3192	183	0
1	M	3323	0	3192	168	0
1	N	3323	0	3192	179	0
1	O	3323	0	3192	168	0
All	All	49845	0	47880	2464	1

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 25.

The worst 5 of 2464 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:J:446:LYS:CG	1:J:446:LYS:CD	1.75	1.63
1:B:141:GLU:CB	1:B:141:GLU:CG	1.75	1.63
1:C:191:LYS:CE	1:C:191:LYS:CD	1.76	1.62
1:L:360:LYS:CD	1:L:360:LYS:CE	1.78	1.61
1:F:465:LEU:CG	1:F:465:LEU:CD1	1.74	1.61

All (1) 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:A:387:ASP:OD2	1:C:360:LYS:NZ[1_565]	2.12	0.08

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	419/428 (98%)	372 (89%)	34 (8%)	13 (3%)	3	18
1	B	419/428 (98%)	370 (88%)	34 (8%)	15 (4%)	2	16
1	C	419/428 (98%)	372 (89%)	36 (9%)	11 (3%)	4	21
1	D	419/428 (98%)	373 (89%)	38 (9%)	8 (2%)	6	26
1	E	419/428 (98%)	373 (89%)	34 (8%)	12 (3%)	3	19
1	F	419/428 (98%)	367 (88%)	43 (10%)	9 (2%)	5	24
1	G	419/428 (98%)	366 (87%)	42 (10%)	11 (3%)	4	21
1	H	419/428 (98%)	362 (86%)	46 (11%)	11 (3%)	4	21
1	I	419/428 (98%)	373 (89%)	32 (8%)	14 (3%)	3	17
1	J	419/428 (98%)	369 (88%)	39 (9%)	11 (3%)	4	21
1	K	419/428 (98%)	370 (88%)	39 (9%)	10 (2%)	4	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	419/428 (98%)	369 (88%)	36 (9%)	14 (3%)	3	17
1	M	419/428 (98%)	367 (88%)	37 (9%)	15 (4%)	2	16
1	N	419/428 (98%)	376 (90%)	30 (7%)	13 (3%)	3	18
1	O	419/428 (98%)	372 (89%)	38 (9%)	9 (2%)	5	24
All	All	6285/6420 (98%)	5551 (88%)	558 (9%)	176 (3%)	4	19

5 of 176 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	ASP
1	A	131	SER
1	A	135	ALA
1	B	59	LYS
1	B	131	SER

5.3.2 Protein sidechains ⓘ

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	370/371 (100%)	330 (89%)	40 (11%)	6	22
1	B	370/371 (100%)	336 (91%)	34 (9%)	8	29
1	C	370/371 (100%)	337 (91%)	33 (9%)	9	31
1	D	370/371 (100%)	334 (90%)	36 (10%)	8	28
1	E	370/371 (100%)	328 (89%)	42 (11%)	5	21
1	F	370/371 (100%)	334 (90%)	36 (10%)	8	28
1	G	370/371 (100%)	325 (88%)	45 (12%)	5	19
1	H	370/371 (100%)	334 (90%)	36 (10%)	8	28
1	I	370/371 (100%)	333 (90%)	37 (10%)	7	26
1	J	370/371 (100%)	333 (90%)	37 (10%)	7	26
1	K	370/371 (100%)	329 (89%)	41 (11%)	6	21
1	L	370/371 (100%)	329 (89%)	41 (11%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	370/371 (100%)	334 (90%)	36 (10%)	8	28
1	N	370/371 (100%)	333 (90%)	37 (10%)	7	26
1	O	370/371 (100%)	331 (90%)	39 (10%)	6	23
All	All	5550/5565 (100%)	4980 (90%)	570 (10%)	7	24

5 of 570 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	96	GLN
1	M	247	PHE
1	M	92	ASN
1	N	311	TYR
1	F	133	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 230 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	254	GLN
1	O	262	ASN
1	J	23	ASN
1	O	138	ASN
1	M	341	ASN

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 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](#)

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	423/428 (98%)	-0.17	6 (1%) 73 59	16, 46, 103, 121	0
1	B	423/428 (98%)	-0.13	6 (1%) 73 59	19, 45, 101, 127	0
1	C	423/428 (98%)	-0.16	4 (0%) 81 68	15, 45, 103, 123	0
1	D	423/428 (98%)	-0.13	5 (1%) 76 63	14, 44, 102, 126	0
1	E	423/428 (98%)	-0.18	8 (1%) 66 51	15, 45, 104, 123	0
1	F	423/428 (98%)	-0.10	3 (0%) 84 73	19, 50, 105, 123	0
1	G	423/428 (98%)	0.02	7 (1%) 69 54	22, 50, 103, 127	0
1	H	423/428 (98%)	-0.14	6 (1%) 73 59	19, 46, 103, 124	0
1	I	423/428 (98%)	-0.15	8 (1%) 66 51	17, 45, 101, 123	0
1	J	423/428 (98%)	-0.06	10 (2%) 59 45	18, 46, 103, 123	0
1	K	423/428 (98%)	-0.15	7 (1%) 69 54	18, 44, 103, 122	0
1	L	423/428 (98%)	-0.13	5 (1%) 76 63	16, 46, 103, 122	0
1	M	423/428 (98%)	-0.08	9 (2%) 63 48	18, 46, 102, 126	0
1	N	423/428 (98%)	-0.12	7 (1%) 69 54	19, 45, 103, 125	0
1	O	423/428 (98%)	-0.11	10 (2%) 59 45	17, 46, 103, 126	0
All	All	6345/6420 (98%)	-0.12	101 (1%) 70 56	14, 46, 104, 127	0

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	86	PRO	5.4
1	O	139	VAL	5.4
1	D	135	ALA	4.8
1	J	84	GLY	4.7
1	F	139	VAL	4.5

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 oligosaccharides 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.