



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:59 PM UTC

PDB ID : 2GLJ / pdb_00002glj
Title : crystal structure of aminopeptidase I from Clostridium acetobutylicum
Authors : Min, T.; Shapiro, L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2006-04-04
Resolution : 3.20 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
Mogul : 2022.3.0, CSD as543be (2022)
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

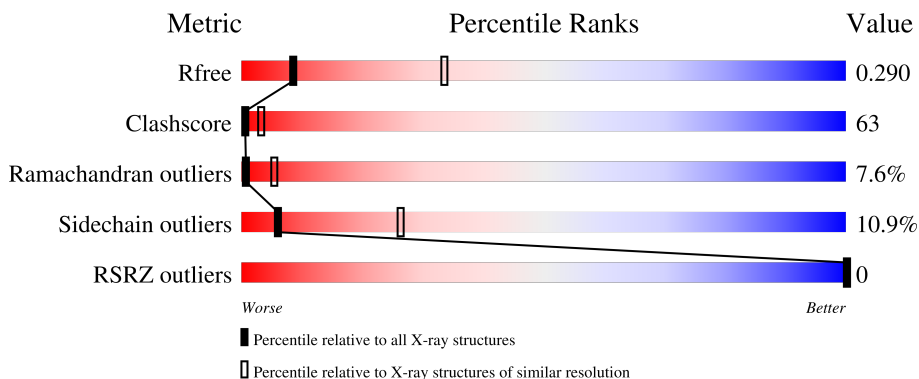
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	461	 36% 47% 14% ..
1	B	461	 37% 48% 12% ..
1	C	461	 34% 48% 14% ..
1	D	461	 36% 48% 13% ..
1	E	461	 35% 48% 14% ..

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Mol	Chain	Length	Quality of chain		
1	F	461	35%	49%	13%
1	G	461	36%	47%	14%
1	H	461	36%	47%	15%
1	I	461	34%	49%	14%
1	J	461	34%	49%	14%
1	K	461	32%	52%	13%
1	L	461	37%	46%	14%
1	M	461	34%	49%	14%
1	N	461	35%	49%	14%
1	O	461	34%	49%	14%
1	P	461	37%	47%	14%
1	Q	461	37%	46%	14%
1	R	461	36%	48%	13%
1	S	461	36%	48%	14%
1	T	461	34%	49%	14%
1	U	461	37%	46%	15%
1	V	461	34%	49%	14%
1	W	461	34%	49%	13%
1	X	461	38%	46%	14%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 91225 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 Probable M18-family aminopeptidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	456	3581	2268	592	701	19	1	0	0	0
1	B	456	3581	2268	592	701	19	1	0	0	0
1	C	456	3581	2268	592	701	19	1	0	0	0
1	D	456	3581	2268	592	701	19	1	0	0	0
1	E	456	3581	2268	592	701	19	1	0	0	0
1	F	456	3581	2268	592	701	19	1	0	0	0
1	G	456	3581	2268	592	701	19	1	0	0	0
1	H	456	3581	2268	592	701	19	1	0	0	0
1	I	456	3581	2268	592	701	19	1	0	0	0
1	J	456	3581	2268	592	701	19	1	0	0	0
1	K	456	3581	2268	592	701	19	1	0	0	0
1	L	456	3581	2268	592	701	19	1	0	0	0
1	M	456	3581	2268	592	701	19	1	0	0	0
1	N	456	3581	2268	592	701	19	1	0	0	0
1	O	456	3581	2268	592	701	19	1	0	0	0
1	P	456	3581	2268	592	701	19	1	0	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	Q	456	3581	2268	592	701	19	1	0	0	0
1	R	456	3581	2268	592	701	19	1	0	0	0
1	S	456	3581	2268	592	701	19	1	0	0	0
1	T	456	3581	2268	592	701	19	1	0	0	0
1	U	456	3581	2268	592	701	19	1	0	0	0
1	V	456	3581	2268	592	701	19	1	0	0	0
1	W	456	3581	2268	592	701	19	1	0	0	0
1	X	456	3581	2268	592	701	19	1	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	440	MSE	MET	modified residue	UNP Q97K30
B	440	MSE	MET	modified residue	UNP Q97K30
C	440	MSE	MET	modified residue	UNP Q97K30
D	440	MSE	MET	modified residue	UNP Q97K30
E	440	MSE	MET	modified residue	UNP Q97K30
F	440	MSE	MET	modified residue	UNP Q97K30
G	440	MSE	MET	modified residue	UNP Q97K30
H	440	MSE	MET	modified residue	UNP Q97K30
I	440	MSE	MET	modified residue	UNP Q97K30
J	440	MSE	MET	modified residue	UNP Q97K30
K	440	MSE	MET	modified residue	UNP Q97K30
L	440	MSE	MET	modified residue	UNP Q97K30
M	440	MSE	MET	modified residue	UNP Q97K30
N	440	MSE	MET	modified residue	UNP Q97K30
O	440	MSE	MET	modified residue	UNP Q97K30
P	440	MSE	MET	modified residue	UNP Q97K30
Q	440	MSE	MET	modified residue	UNP Q97K30
R	440	MSE	MET	modified residue	UNP Q97K30
S	440	MSE	MET	modified residue	UNP Q97K30
T	440	MSE	MET	modified residue	UNP Q97K30
U	440	MSE	MET	modified residue	UNP Q97K30
V	440	MSE	MET	modified residue	UNP Q97K30
W	440	MSE	MET	modified residue	UNP Q97K30

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Chain	Residue	Modelled	Actual	Comment	Reference
X	440	MSE	MET	modified residue	UNP Q97K30

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	B	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0
2	D	2	Total Mn 2 2	0	0
2	E	2	Total Mn 2 2	0	0
2	F	2	Total Mn 2 2	0	0
2	G	2	Total Mn 2 2	0	0
2	H	2	Total Mn 2 2	0	0
2	I	2	Total Mn 2 2	0	0
2	J	2	Total Mn 2 2	0	0
2	K	2	Total Mn 2 2	0	0
2	L	2	Total Mn 2 2	0	0
2	M	2	Total Mn 2 2	0	0
2	N	2	Total Mn 2 2	0	0
2	O	2	Total Mn 2 2	0	0
2	P	2	Total Mn 2 2	0	0
2	Q	2	Total Mn 2 2	0	0
2	R	2	Total Mn 2 2	0	0
2	S	2	Total Mn 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	T	2	Total 2	Mn 2	0	0
2	U	2	Total 2	Mn 2	0	0
2	V	2	Total 2	Mn 2	0	0
2	W	2	Total 2	Mn 2	0	0
2	X	2	Total 2	Mn 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	206	Total 206	O 206	0	0
3	B	187	Total 187	O 187	0	0
3	C	239	Total 239	O 239	0	0
3	D	238	Total 238	O 238	0	0
3	E	210	Total 210	O 210	0	0
3	F	219	Total 219	O 219	0	0
3	G	231	Total 231	O 231	0	0
3	H	215	Total 215	O 215	0	0
3	I	233	Total 233	O 233	0	0
3	J	237	Total 237	O 237	0	0
3	K	219	Total 219	O 219	0	0
3	L	222	Total 222	O 222	0	0
3	M	227	Total 227	O 227	0	0
3	N	246	Total 246	O 246	0	0

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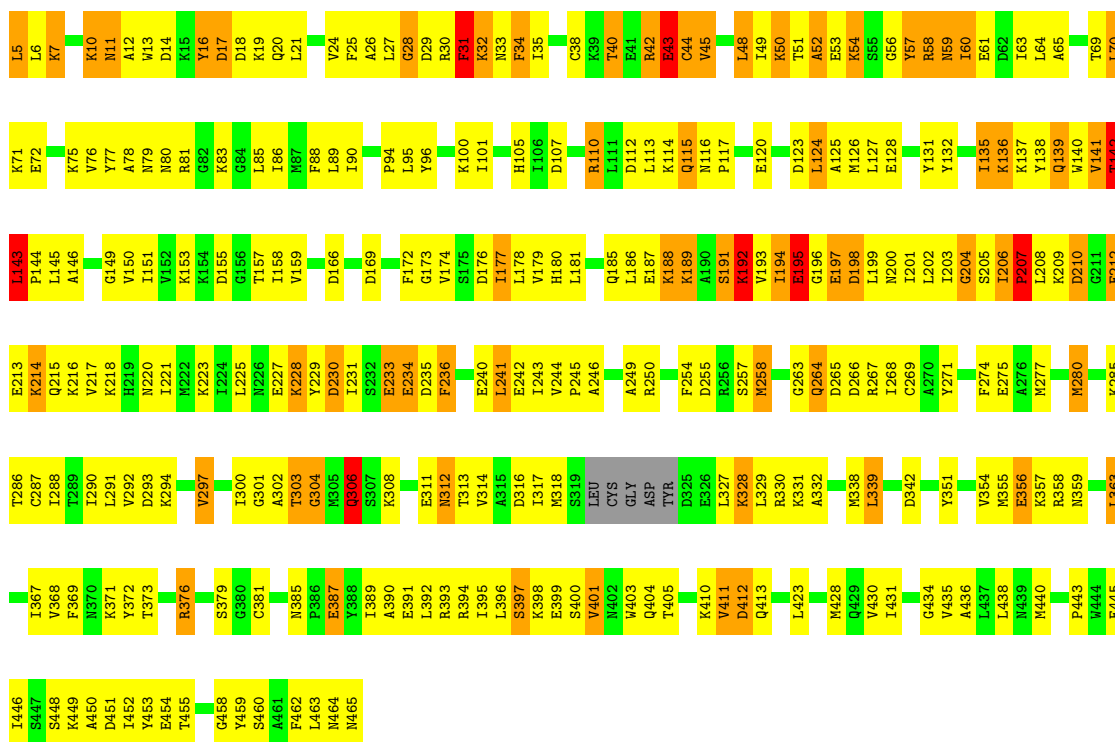
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	O	205	Total 205	O 205	0	0
3	P	208	Total 208	O 208	0	0
3	Q	211	Total 211	O 211	0	0
3	R	200	Total 200	O 200	0	0
3	S	205	Total 205	O 205	0	0
3	T	226	Total 226	O 226	0	0
3	U	214	Total 214	O 214	0	0
3	V	225	Total 225	O 225	0	0
3	W	217	Total 217	O 217	0	0
3	X	193	Total 193	O 193	0	0

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.

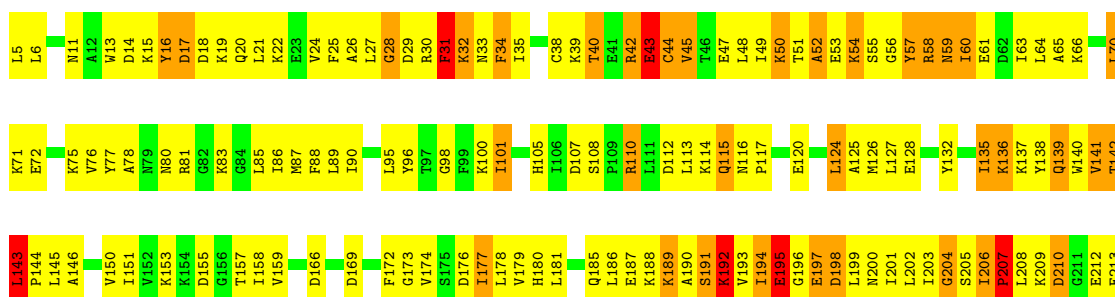
- Molecule 1: Probable M18-family aminopeptidase 1

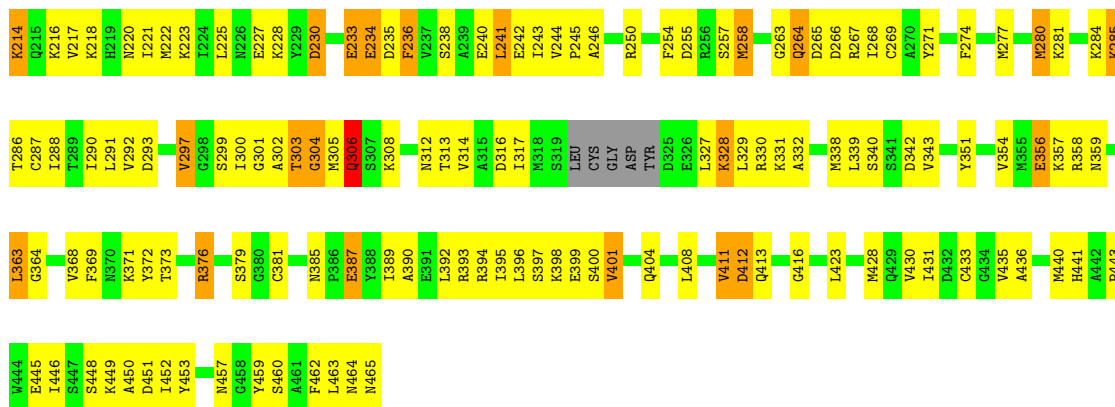
Chain A: 



- Molecule 1: Probable M18-family aminopeptidase 1

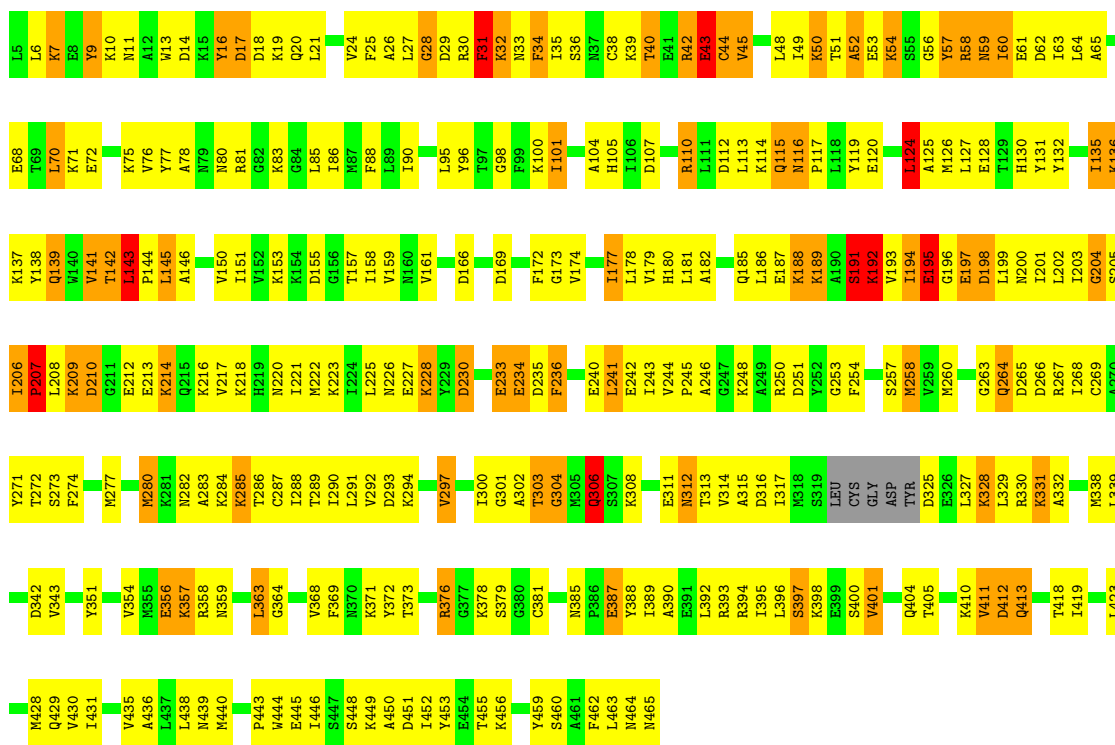
Chain B: 





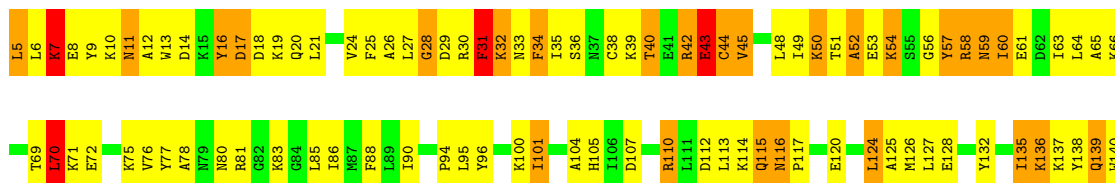
• Molecule 1: Probable M18-family aminopeptidase 1

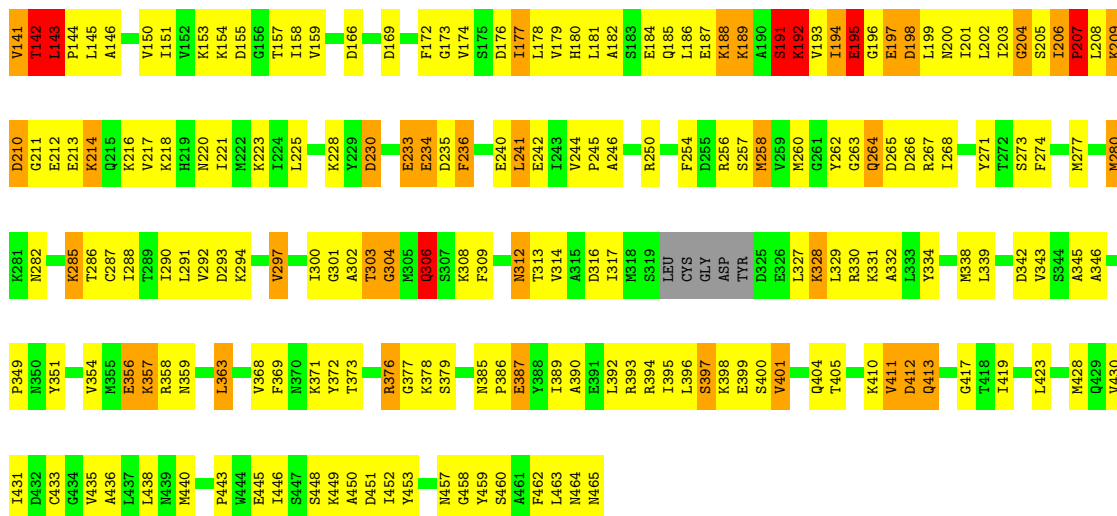
Chain C: 34% 48% 14% ..



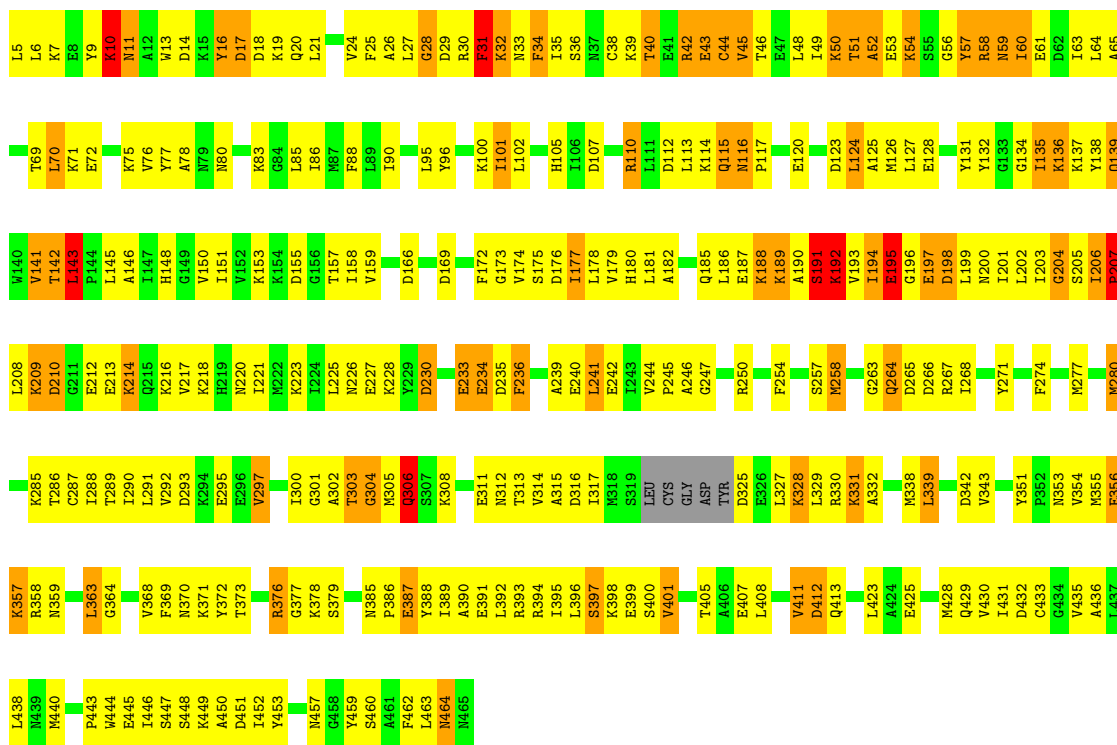
• Molecule 1: Probable M18-family aminopeptidase 1

Chain D: 36% 48% 13% ..

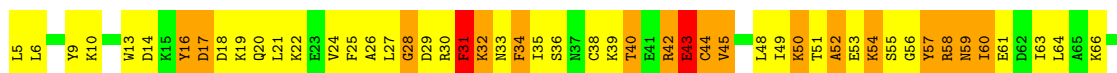


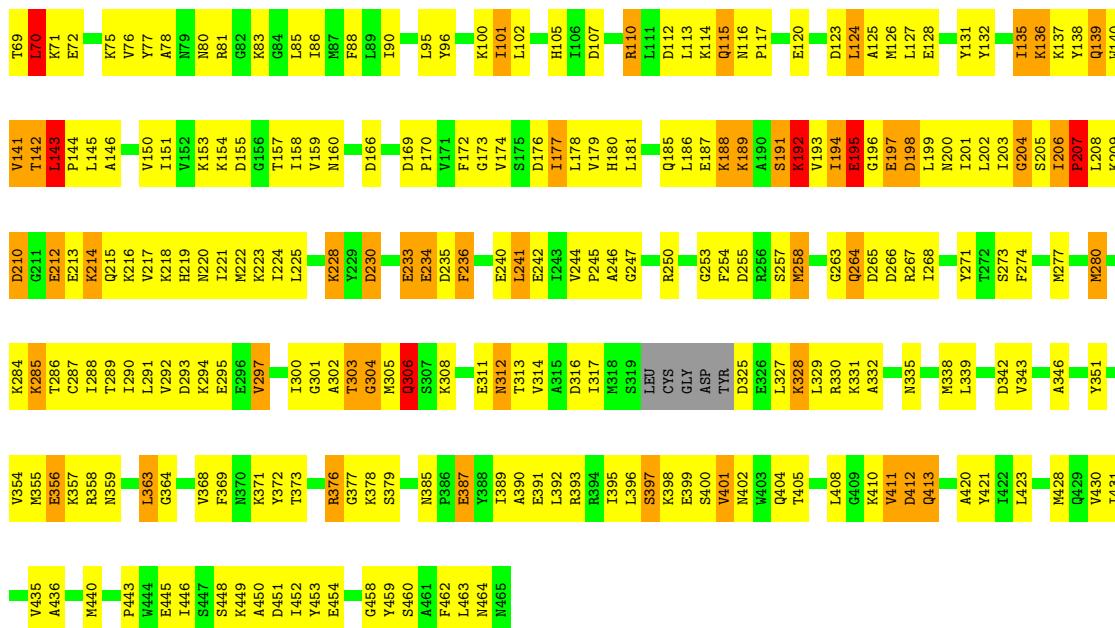


• Molecule 1: Probable M18-family aminopeptidase 1



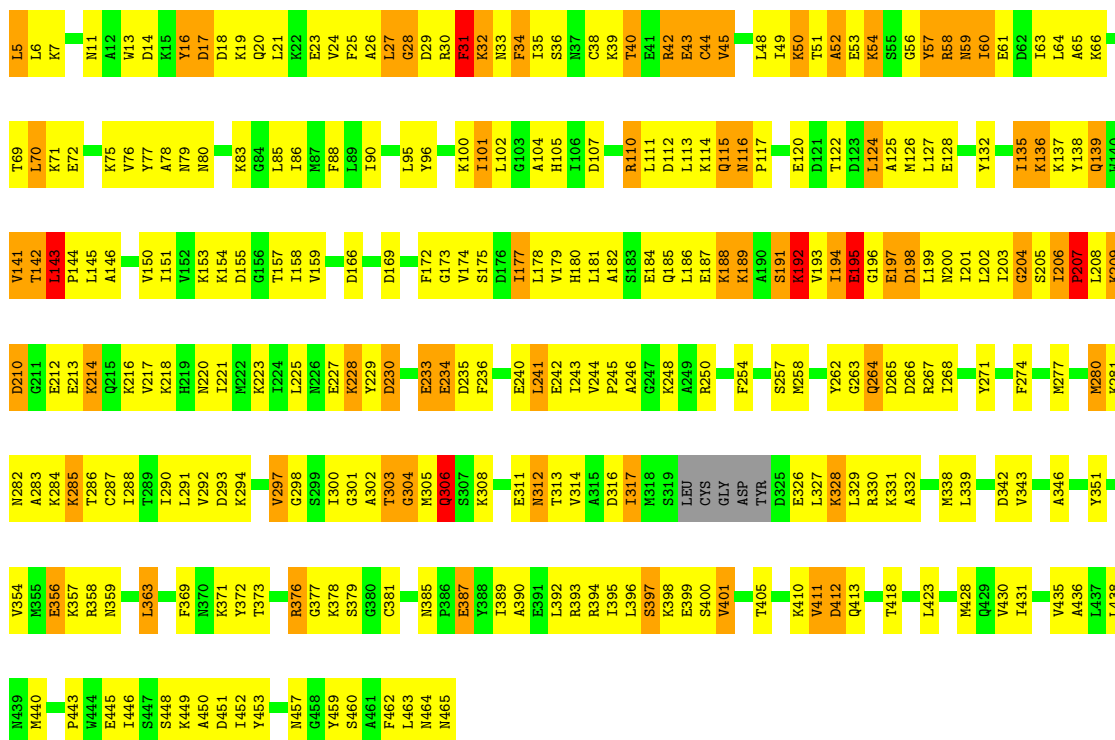
• Molecule 1: Probable M18-family aminopeptidase 1





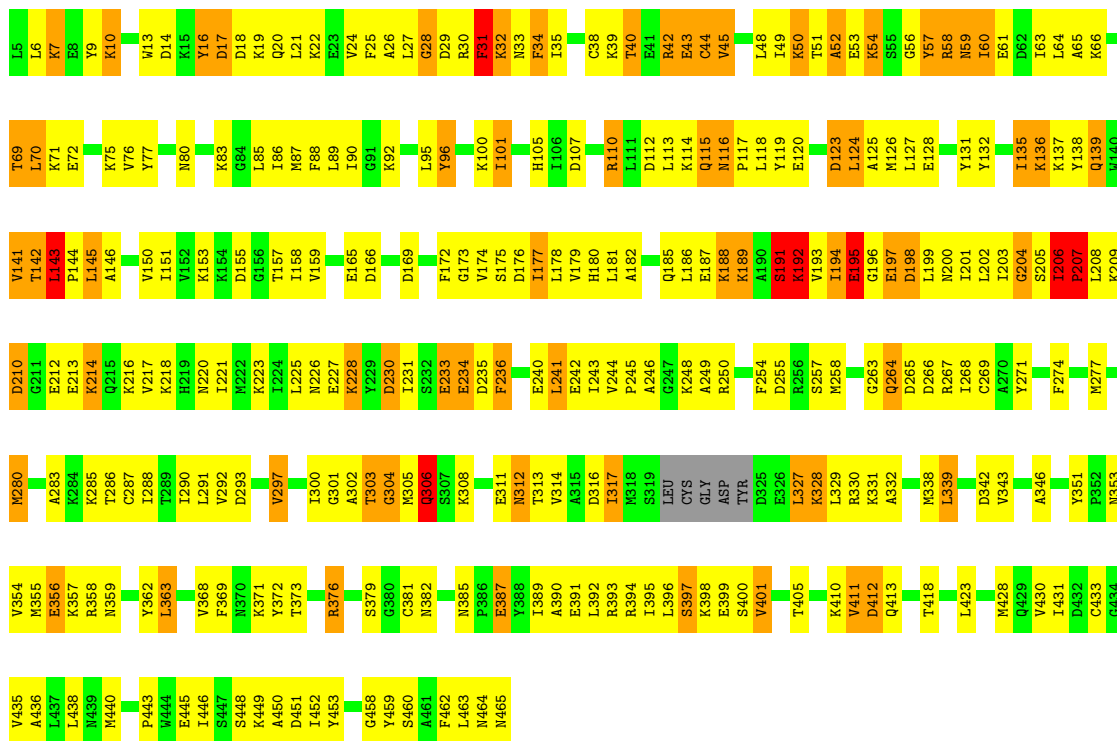
- Molecule 1: Probable M18-family aminopeptidase 1

Chain G: 36% 47% 14% ..



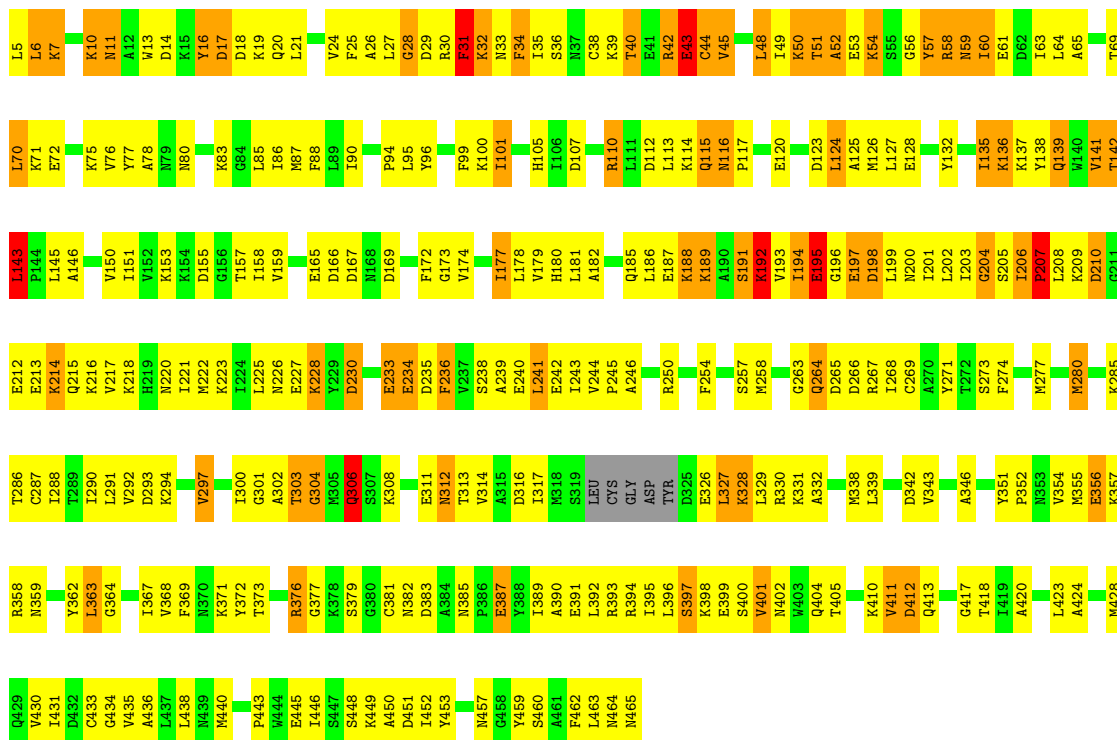
- Molecule 1: Probable M18-family aminopeptidase 1

Chain H: 36% 47% 15% ..

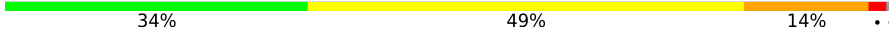


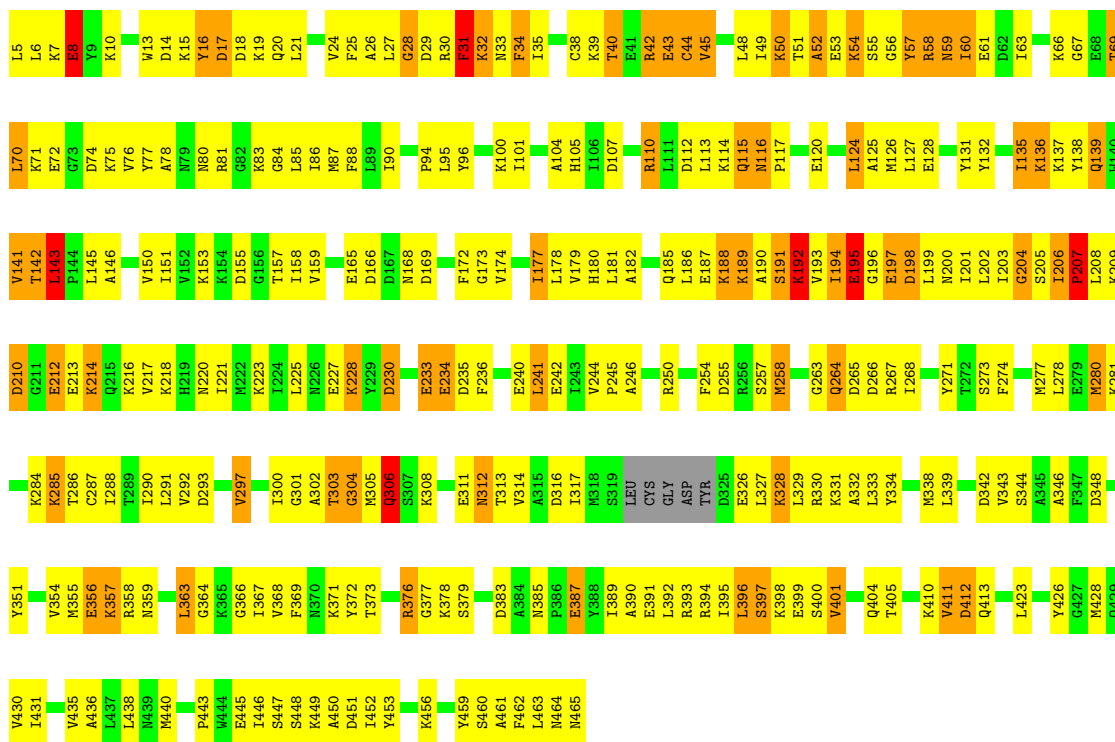
• Molecule 1: Probable M18-family aminopeptidase 1

Chain I: 34% 49% 14% ..



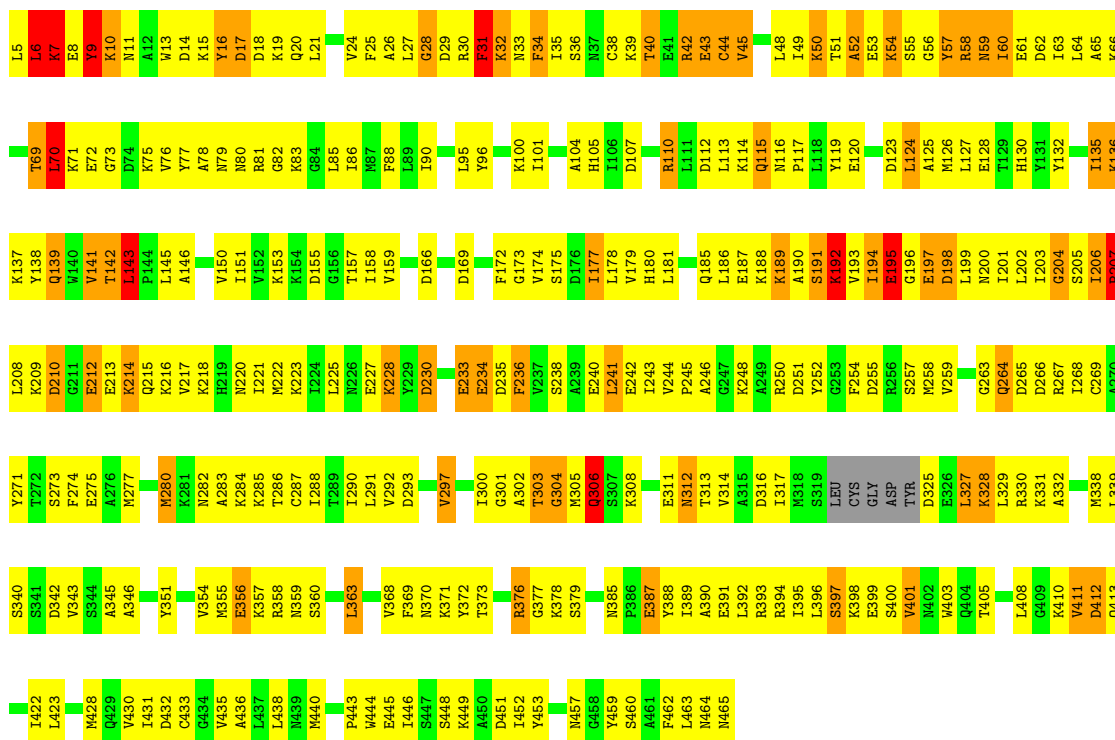
• Molecule 1: Probable M18-family aminopeptidase 1

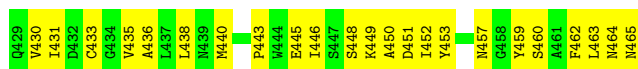
Chain J:  34% 49% 14% ..



• Molecule 1: Probable M18-family aminopeptidase 1

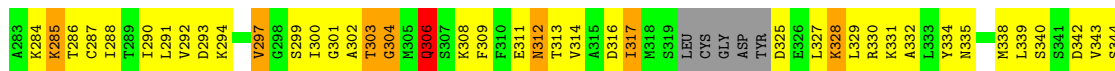
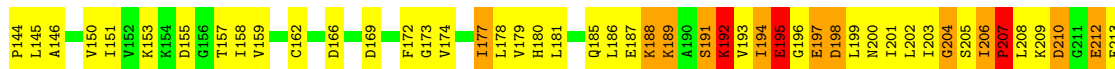
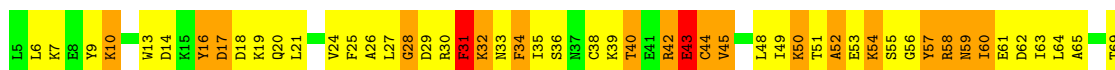
Chain K:  32% 52% 13% ..





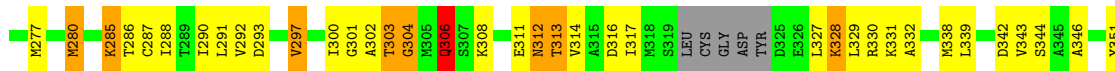
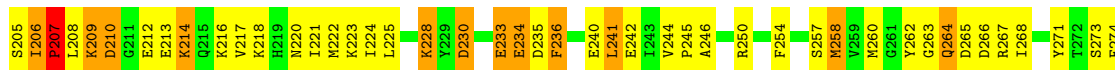
● Molecule 1: Probable M18-family aminopeptidase 1

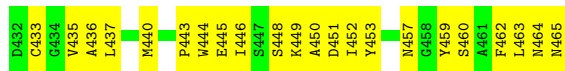
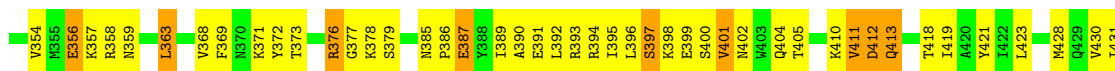
Chain N: 35% 49% 14% ..



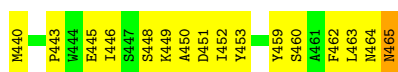
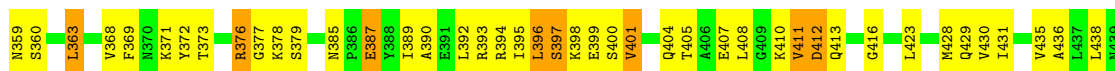
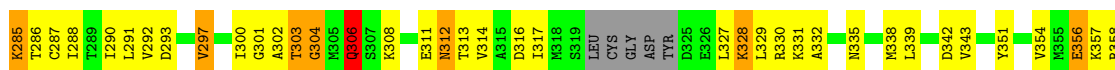
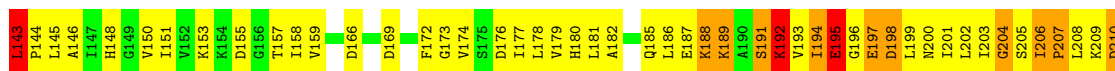
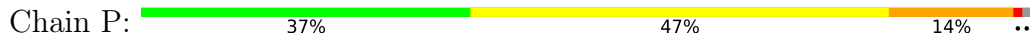
● Molecule 1: Probable M18-family aminopeptidase 1

Chain O: 34% 49% 14% ..

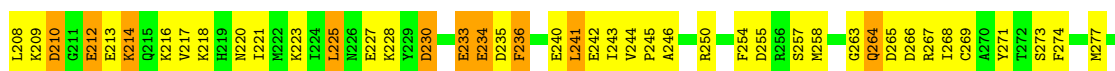
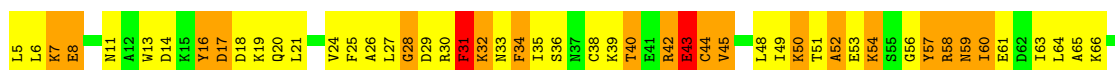
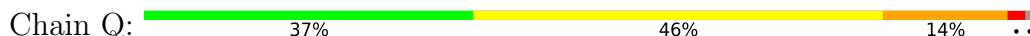


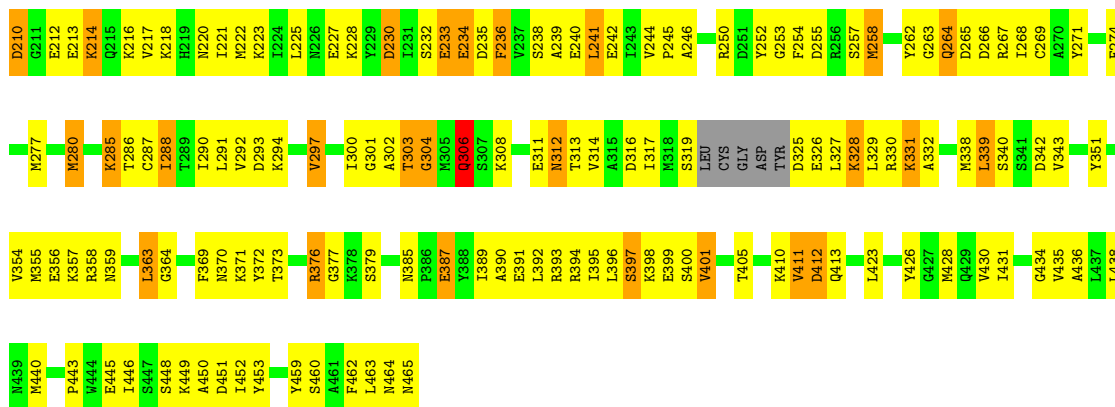


• Molecule 1: Probable M18-family aminopeptidase 1

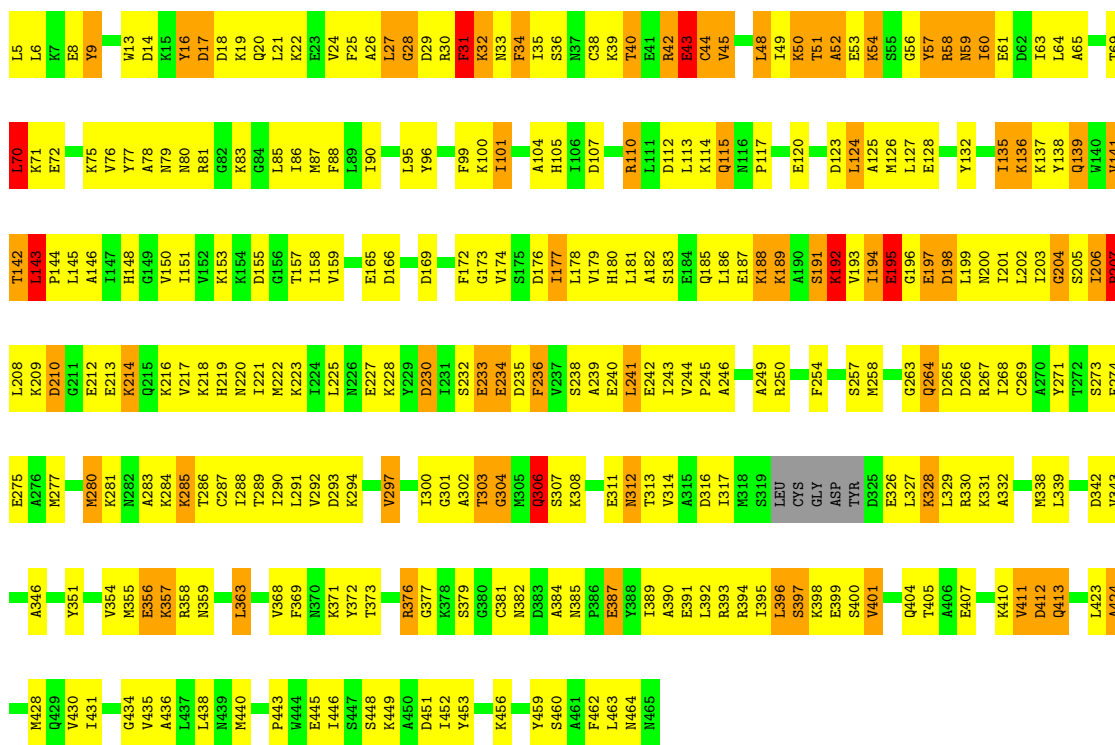


• Molecule 1: Probable M18-family aminopeptidase 1

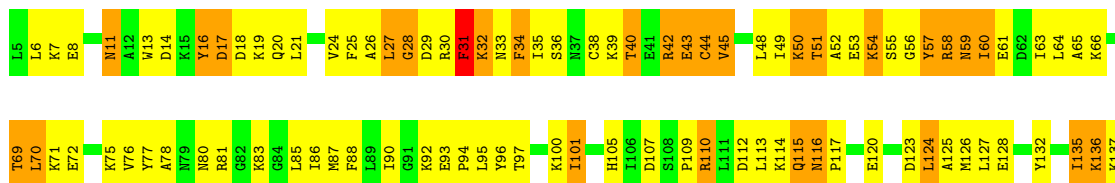
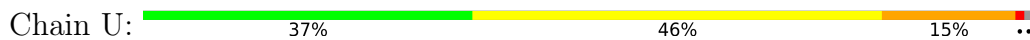


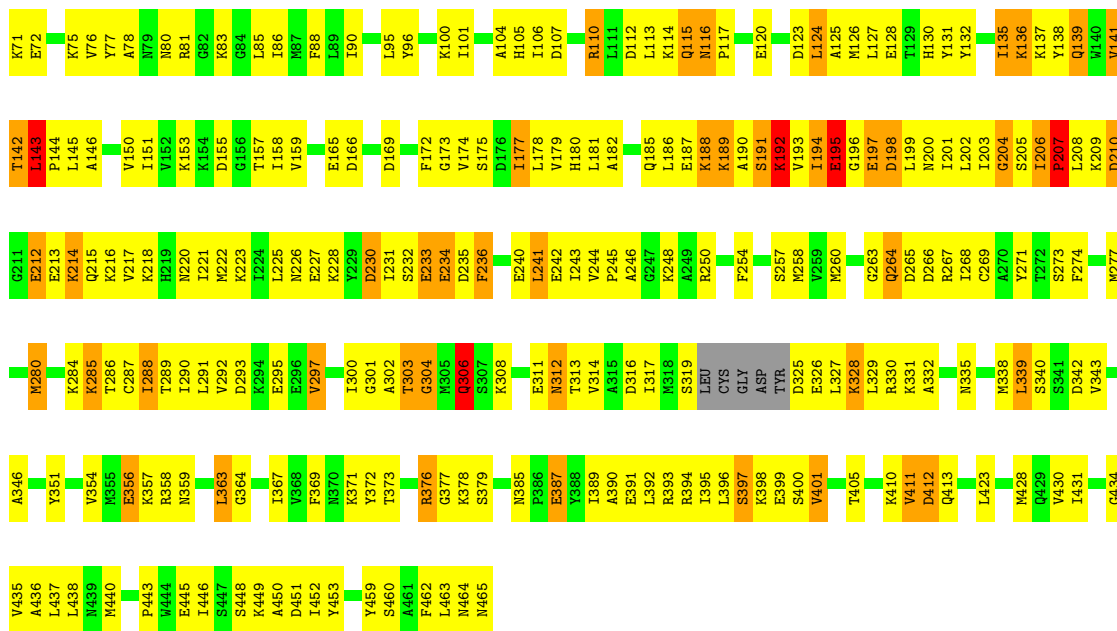


• Molecule 1: Probable M18-family aminopeptidase 1

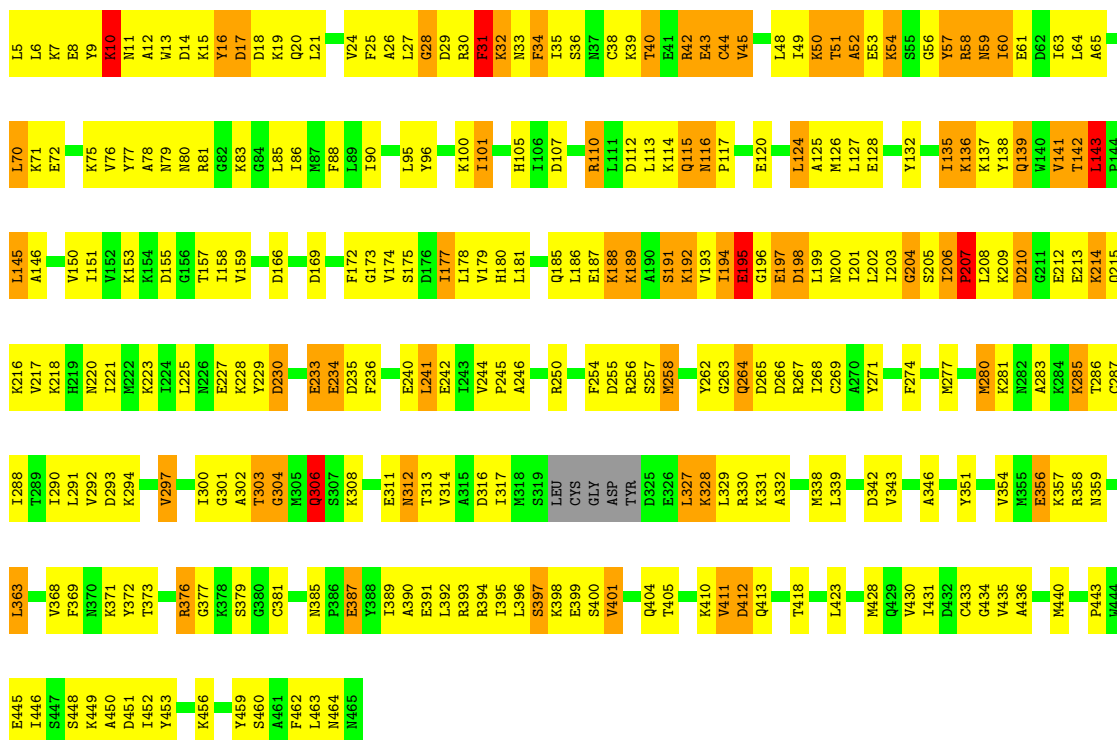
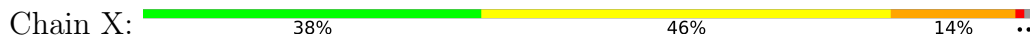


• Molecule 1: Probable M18-family aminopeptidase 1





• Molecule 1: Probable M18-family aminopeptidase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	121.71Å 129.68Å 222.73Å 89.88° 90.00° 116.68°	Depositor
Resolution (Å)	19.95 – 3.20 19.95 – 3.20	Depositor EDS
% Data completeness (in resolution range)	60.1 (19.95-3.20) 90.5 (19.95-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.22Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.250 , 0.297 0.249 , 0.290	Depositor DCC
R_{free} test set	10245 reflections (3.29%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtrriage
Anisotropy	0.197	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.012 for h,-h-k,-l 0.357 for -h,-k,l 0.008 for -h,h+k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	91225	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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: MN

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	0.52	0/3639	0.97	19/4893 (0.4%)
1	B	0.51	0/3639	0.96	18/4893 (0.4%)
1	C	0.52	0/3639	0.96	21/4893 (0.4%)
1	D	0.52	0/3639	0.97	22/4893 (0.4%)
1	E	0.53	0/3639	0.97	19/4893 (0.4%)
1	F	0.54	0/3639	0.97	20/4893 (0.4%)
1	G	0.53	0/3639	0.97	18/4893 (0.4%)
1	H	0.55	1/3639 (0.0%)	0.98	20/4893 (0.4%)
1	I	0.52	0/3639	0.97	19/4893 (0.4%)
1	J	0.53	0/3639	0.97	19/4893 (0.4%)
1	K	0.53	0/3639	0.96	20/4893 (0.4%)
1	L	0.52	0/3639	0.96	19/4893 (0.4%)
1	M	0.53	0/3639	0.96	21/4893 (0.4%)
1	N	0.51	0/3639	0.96	19/4893 (0.4%)
1	O	0.53	0/3639	0.97	20/4893 (0.4%)
1	P	0.52	0/3639	0.97	18/4893 (0.4%)
1	Q	0.53	0/3639	0.96	20/4893 (0.4%)
1	R	0.54	0/3639	0.97	21/4893 (0.4%)
1	S	0.53	0/3639	0.96	20/4893 (0.4%)
1	T	0.53	0/3639	0.96	19/4893 (0.4%)
1	U	0.54	0/3639	0.97	21/4893 (0.4%)
1	V	0.53	0/3639	0.97	19/4893 (0.4%)
1	W	0.52	0/3639	0.96	20/4893 (0.4%)
1	X	0.54	0/3639	0.97	17/4893 (0.3%)
All	All	0.53	1/87336 (0.0%)	0.97	469/117432 (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	K	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	206	ILE	N-CA	-5.05	1.42	1.46

The worst 5 of 469 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	313	THR	N-CA-C	-9.41	100.91	111.82
1	I	313	THR	N-CA-C	-9.17	101.18	111.82
1	F	313	THR	N-CA-C	-9.13	101.23	111.82
1	T	313	THR	N-CA-C	-9.03	101.35	111.82
1	W	313	THR	N-CA-C	-8.98	101.41	111.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	9	TYR	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	3581	0	3567	496	0
1	B	3581	0	3567	485	0
1	C	3581	0	3567	525	0
1	D	3581	0	3567	495	1
1	E	3581	0	3567	502	1
1	F	3581	0	3567	503	0
1	G	3581	0	3567	482	0
1	H	3581	0	3567	494	0
1	I	3581	0	3567	519	0
1	J	3581	0	3567	501	0
1	K	3581	0	3567	520	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	3581	0	3567	506	0
1	M	3581	0	3567	512	0
1	N	3581	0	3567	528	0
1	O	3581	0	3567	522	0
1	P	3581	0	3567	492	0
1	Q	3581	0	3567	492	0
1	R	3581	0	3567	519	0
1	S	3581	0	3567	515	0
1	T	3581	0	3567	517	0
1	U	3581	0	3567	491	0
1	V	3581	0	3567	506	0
1	W	3581	0	3567	510	1
1	X	3581	0	3567	461	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
2	Q	2	0	0	0	0
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	2	0	0	0	0
2	U	2	0	0	0	0
2	V	2	0	0	0	0
2	W	2	0	0	0	0
2	X	2	0	0	0	0
3	A	206	0	0	50	0
3	B	187	0	0	42	0
3	C	239	0	0	88	0
3	D	238	0	0	67	0
3	E	210	0	0	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	219	0	0	75	0
3	G	231	0	0	65	0
3	H	215	0	0	65	0
3	I	233	0	0	81	0
3	J	237	0	0	78	0
3	K	219	0	0	70	0
3	L	222	0	0	60	0
3	M	227	0	0	65	0
3	N	246	0	0	89	0
3	O	205	0	0	69	0
3	P	208	0	0	53	0
3	Q	211	0	0	55	0
3	R	200	0	0	63	0
3	S	205	0	0	72	0
3	T	226	0	0	75	0
3	U	214	0	0	69	0
3	V	225	0	0	66	0
3	W	217	0	0	73	0
3	X	193	0	0	42	0
All	All	91225	0	85608	10854	2

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 63.

The worst 5 of 10854 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:M:317:ILE:HD13	3:M:6168:HOH:O	1.38	1.20
1:T:87:MET:HE3	3:T:6087:HOH:O	1.45	1.15
1:T:87:MET:HB2	3:T:6087:HOH:O	1.52	1.08
1:F:54:LYS:HA	3:F:6039:HOH:O	1.52	1.07
1:R:235:ASP:HA	1:S:393:ARG:HH12	1.19	1.07

All (2) 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:D:66:LYS:NZ	1:W:284:LYS:NZ[1_654]	2.11	0.09
1:E:400:SER:OG	1:K:325:ASP:OD1[1_665]	2.17	0.03

5.3 Torsion angles

5.3.1 Protein backbone

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	452/461 (98%)	316 (70%)	103 (23%)	33 (7%)	1	6
1	B	452/461 (98%)	314 (70%)	106 (24%)	32 (7%)	1	6
1	C	452/461 (98%)	315 (70%)	102 (23%)	35 (8%)	1	5
1	D	452/461 (98%)	312 (69%)	105 (23%)	35 (8%)	1	5
1	E	452/461 (98%)	312 (69%)	105 (23%)	35 (8%)	1	5
1	F	452/461 (98%)	317 (70%)	102 (23%)	33 (7%)	1	6
1	G	452/461 (98%)	319 (71%)	100 (22%)	33 (7%)	1	6
1	H	452/461 (98%)	316 (70%)	101 (22%)	35 (8%)	1	5
1	I	452/461 (98%)	315 (70%)	103 (23%)	34 (8%)	1	5
1	J	452/461 (98%)	316 (70%)	101 (22%)	35 (8%)	1	5
1	K	452/461 (98%)	316 (70%)	101 (22%)	35 (8%)	1	5
1	L	452/461 (98%)	314 (70%)	102 (23%)	36 (8%)	1	4
1	M	452/461 (98%)	314 (70%)	103 (23%)	35 (8%)	1	5
1	N	452/461 (98%)	315 (70%)	102 (23%)	35 (8%)	1	5
1	O	452/461 (98%)	316 (70%)	102 (23%)	34 (8%)	1	5
1	P	452/461 (98%)	314 (70%)	103 (23%)	35 (8%)	1	5
1	Q	452/461 (98%)	316 (70%)	102 (23%)	34 (8%)	1	5
1	R	452/461 (98%)	317 (70%)	101 (22%)	34 (8%)	1	5
1	S	452/461 (98%)	319 (71%)	100 (22%)	33 (7%)	1	6
1	T	452/461 (98%)	317 (70%)	100 (22%)	35 (8%)	1	5
1	U	452/461 (98%)	313 (69%)	105 (23%)	34 (8%)	1	5
1	V	452/461 (98%)	315 (70%)	102 (23%)	35 (8%)	1	5
1	W	452/461 (98%)	316 (70%)	103 (23%)	33 (7%)	1	6
1	X	452/461 (98%)	316 (70%)	102 (23%)	34 (8%)	1	5
All	All	10848/11064 (98%)	7570 (70%)	2456 (23%)	822 (8%)	1	5

5 of 822 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	TYR
1	A	43	GLU
1	A	60	ILE
1	A	136	LYS
1	A	141	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	387/390 (99%)	341 (88%)	46 (12%)	5 23
1	B	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	C	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	D	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	E	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	F	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	G	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	H	387/390 (99%)	345 (89%)	42 (11%)	6 26
1	I	387/390 (99%)	345 (89%)	42 (11%)	6 26
1	J	387/390 (99%)	346 (89%)	41 (11%)	6 27
1	K	387/390 (99%)	343 (89%)	44 (11%)	5 24
1	L	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	M	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	N	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	O	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	P	387/390 (99%)	345 (89%)	42 (11%)	6 26
1	Q	387/390 (99%)	344 (89%)	43 (11%)	6 25
1	R	387/390 (99%)	347 (90%)	40 (10%)	7 28
1	S	387/390 (99%)	343 (89%)	44 (11%)	5 24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T	387/390 (99%)	347 (90%)	40 (10%)	7	28
1	U	387/390 (99%)	346 (89%)	41 (11%)	6	27
1	V	387/390 (99%)	345 (89%)	42 (11%)	6	26
1	W	387/390 (99%)	346 (89%)	41 (11%)	6	27
1	X	387/390 (99%)	345 (89%)	42 (11%)	6	26
All	All	9288/9360 (99%)	8278 (89%)	1010 (11%)	6	26

5 of 1010 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	LYS
1	V	32	LYS
1	N	207	PRO
1	U	297	VAL
1	W	195	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 261 such sidechains are listed below:

Mol	Chain	Res	Type
1	V	219	HIS
1	V	465	ASN
1	X	464	ASN
1	J	402	ASN
1	J	160	ASN

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](#)

Of 48 ligands modelled in this entry, 48 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	455/461 (98%)	-1.69	0 100 100	4, 27, 72, 106	0
1	B	455/461 (98%)	-1.69	0 100 100	3, 27, 73, 106	0
1	C	455/461 (98%)	-1.68	0 100 100	3, 27, 73, 105	0
1	D	455/461 (98%)	-1.68	0 100 100	4, 26, 72, 107	0
1	E	455/461 (98%)	-1.69	0 100 100	3, 26, 72, 104	0
1	F	455/461 (98%)	-1.68	0 100 100	4, 27, 72, 105	0
1	G	455/461 (98%)	-1.69	0 100 100	3, 26, 73, 105	0
1	H	455/461 (98%)	-1.70	0 100 100	3, 26, 72, 106	0
1	I	455/461 (98%)	-1.69	0 100 100	3, 27, 72, 108	0
1	J	455/461 (98%)	-1.68	0 100 100	3, 26, 72, 103	0
1	K	455/461 (98%)	-1.69	0 100 100	3, 26, 72, 105	0
1	L	455/461 (98%)	-1.70	0 100 100	4, 26, 72, 101	0
1	M	455/461 (98%)	-1.68	0 100 100	4, 26, 74, 106	0
1	N	455/461 (98%)	-1.66	0 100 100	4, 27, 74, 106	0
1	O	455/461 (98%)	-1.69	0 100 100	4, 27, 73, 103	0
1	P	455/461 (98%)	-1.69	0 100 100	3, 27, 74, 103	0
1	Q	455/461 (98%)	-1.69	0 100 100	2, 27, 72, 104	0
1	R	455/461 (98%)	-1.68	0 100 100	4, 27, 73, 107	0
1	S	455/461 (98%)	-1.69	0 100 100	3, 27, 73, 102	0
1	T	455/461 (98%)	-1.68	0 100 100	2, 27, 73, 104	0
1	U	455/461 (98%)	-1.70	0 100 100	4, 26, 73, 102	0
1	V	455/461 (98%)	-1.69	0 100 100	2, 26, 72, 104	0
1	W	455/461 (98%)	-1.70	0 100 100	4, 26, 73, 104	0
1	X	455/461 (98%)	-1.68	0 100 100	5, 26, 72, 105	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	10920/11064 (98%)	-1.69	0 100 100	2, 27, 73, 108	0

There are no RSRZ outliers to report.

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MN	J	6020	1/1	0.99	0.01	8,8,8,8	0
2	MN	T	6039	1/1	0.99	0.01	21,21,21,21	0
2	MN	W	6045	1/1	0.99	0.02	31,31,31,31	0
2	MN	B	6004	1/1	1.00	0.01	7,7,7,7	0
2	MN	C	6005	1/1	1.00	0.01	44,44,44,44	0
2	MN	C	6006	1/1	1.00	0.01	6,6,6,6	0
2	MN	D	6007	1/1	1.00	0.01	0,0,0,0	0
2	MN	D	6008	1/1	1.00	0.01	16,16,16,16	0
2	MN	E	6009	1/1	1.00	0.02	35,35,35,35	0
2	MN	E	6010	1/1	1.00	0.01	12,12,12,12	0
2	MN	F	6011	1/1	1.00	0.02	21,21,21,21	0
2	MN	F	6012	1/1	1.00	0.01	1,1,1,1	0
2	MN	G	6013	1/1	1.00	0.02	40,40,40,40	0
2	MN	G	6014	1/1	1.00	0.01	5,5,5,5	0
2	MN	H	6015	1/1	1.00	0.01	16,16,16,16	0
2	MN	H	6016	1/1	1.00	0.01	4,4,4,4	0
2	MN	I	6017	1/1	1.00	0.02	43,43,43,43	0
2	MN	I	6018	1/1	1.00	0.01	15,15,15,15	0
2	MN	J	6019	1/1	1.00	0.01	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MN	A	6001	1/1	1.00	0.01	31,31,31,31	0
2	MN	K	6021	1/1	1.00	0.01	20,20,20,20	0
2	MN	K	6022	1/1	1.00	0.01	16,16,16,16	0
2	MN	L	6023	1/1	1.00	0.01	25,25,25,25	0
2	MN	L	6024	1/1	1.00	0.01	34,34,34,34	0
2	MN	M	6025	1/1	1.00	0.01	29,29,29,29	0
2	MN	M	6026	1/1	1.00	0.01	15,15,15,15	0
2	MN	N	6027	1/1	1.00	0.02	39,39,39,39	0
2	MN	N	6028	1/1	1.00	0.01	12,12,12,12	0
2	MN	O	6029	1/1	1.00	0.01	14,14,14,14	0
2	MN	O	6030	1/1	1.00	0.02	28,28,28,28	0
2	MN	P	6031	1/1	1.00	0.01	33,33,33,33	0
2	MN	P	6032	1/1	1.00	0.01	22,22,22,22	0
2	MN	Q	6033	1/1	1.00	0.01	25,25,25,25	0
2	MN	Q	6034	1/1	1.00	0.01	38,38,38,38	0
2	MN	R	6035	1/1	1.00	0.01	35,35,35,35	0
2	MN	R	6036	1/1	1.00	0.01	2,2,2,2	0
2	MN	S	6037	1/1	1.00	0.03	26,26,26,26	0
2	MN	S	6038	1/1	1.00	0.01	0,0,0,0	0
2	MN	A	6002	1/1	1.00	0.01	1,1,1,1	0
2	MN	T	6040	1/1	1.00	0.01	8,8,8,8	0
2	MN	U	6041	1/1	1.00	0.01	29,29,29,29	0
2	MN	U	6042	1/1	1.00	0.01	9,9,9,9	0
2	MN	V	6043	1/1	1.00	0.01	11,11,11,11	0
2	MN	V	6044	1/1	1.00	0.01	0,0,0,0	0
2	MN	B	6003	1/1	1.00	0.02	31,31,31,31	0
2	MN	W	6046	1/1	1.00	0.01	0,0,0,0	0
2	MN	X	6047	1/1	1.00	0.01	30,30,30,30	0
2	MN	X	6048	1/1	1.00	0.01	0,0,0,0	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.