



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2025 – 02:58 PM JST

PDB ID : 9JYZ / pdb_00009jyz
EMDB ID : EMD-61910
Title : portal-tail complex of mature T7
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2024-10-13
Resolution : 2.70 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : **FAILED**
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

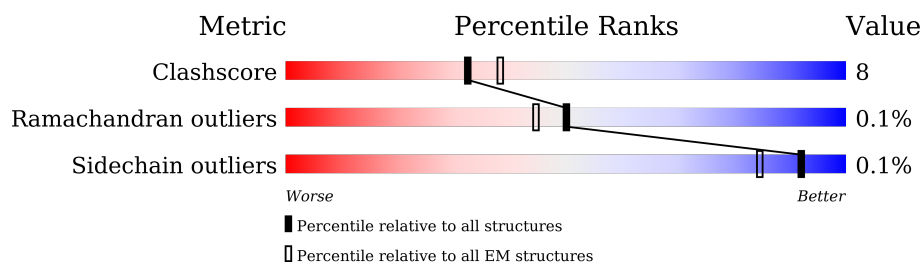
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	88	
1	3	88	
1	4	88	
1	5	88	
1	6	88	
1	7	88	
1	8	88	
1	9	88	
1	AA	88	


























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Mol	Chain	Length	Quality of chain
1	AB	88	 84%
1	AC	88	 84%
1	AD	88	 84%
2	1	99	 85%
2	2	99	 85%
2	v	99	 85%
2	w	99	 85%
2	y	99	 85%
2	z	99	 85%
3	A	553	 75%
3	B	553	 75%
3	C	553	 75%
3	D	553	 75%
3	E	553	 75%
3	F	553	 76%
3	G	553	 76%
3	H	553	 76%
3	I	553	 76%
3	J	553	 76%
3	K	553	 75%
3	L	553	 75%
3	M	553	 75%
3	N	553	 75%
3	O	553	 75%
3	a	553	 75%

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Mol	Chain	Length	Quality of chain
3	b	553	
3	c	553	
4	P	794	
4	Q	794	
4	R	794	
4	S	794	
4	T	794	
4	x	794	
5	U	196	
5	V	196	
5	W	196	
5	X	196	
5	Y	196	
5	Z	196	
5	d	196	
5	e	196	
5	f	196	
5	g	196	
5	h	196	
5	i	196	
6	j	536	
6	k	536	
6	l	536	
6	m	536	
6	n	536	

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Mol	Chain	Length	Quality of chain
6	o	536	 77%21%.
6	p	536	 77%21%.
6	q	536	 79%19%.
6	r	536	 78%20%.
6	s	536	 76%22%.
6	t	536	 77%21%.
6	u	536	 76%22%.

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 126948 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Protein 6.7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	3	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	4	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	5	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	6	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	7	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	8	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	9	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AA	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AB	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AC	14	Total 110	C 70	N 18	O 20	S 2	0	0
1	AD	14	Total 110	C 70	N 18	O 20	S 2	0	0

- Molecule 2 is a protein called Protein 7.3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	15	Total 101	C 60	N 21	O 20	0	0
2	2	15	Total 101	C 60	N 21	O 20	0	0
2	v	15	Total 101	C 60	N 21	O 20	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	w	15	Total 101	C 60	N 21	O 20	0	0
2	y	15	Total 101	C 60	N 21	O 20	0	0
2	z	15	Total 101	C 60	N 21	O 20	0	0

- Molecule 3 is a protein called Tail fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	B	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	C	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	D	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	E	141	Total 1115	C 698	N 201	O 215	S 1	0	0
3	F	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	G	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	H	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	I	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	J	134	Total 1067	C 668	N 192	O 206	S 1	0	0
3	K	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	L	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	M	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	N	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	O	136	Total 1080	C 675	N 195	O 209	S 1	0	0
3	a	141	Total 1115	C 698	N 201	O 215	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	134	Total	C	N	O	S	0	0
			1067	668	192	206	1		
3	c	136	Total	C	N	O	S	0	0
			1080	675	195	209	1		

- Molecule 4 is a protein called Tail tubular protein gp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	Q	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	R	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	S	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	T	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		
4	x	793	Total	C	N	O	S	0	0
			6313	4003	1087	1208	15		

- Molecule 5 is a protein called Tail tubular protein gp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	V	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	W	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	X	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	Y	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	Z	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	d	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	e	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	f	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		
5	h	196	Total	C	N	O	S	0	0
			1565	971	267	318	9		
5	i	195	Total	C	N	O	S	0	0
			1557	966	266	317	8		

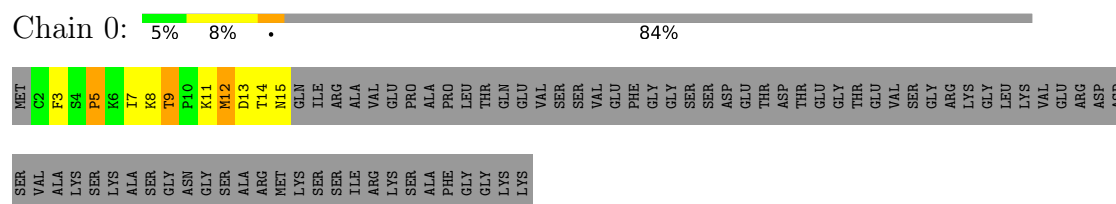
- Molecule 6 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	j	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	k	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	l	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	m	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	n	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	o	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	p	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	q	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	r	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	s	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	t	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		
6	u	526	Total	C	N	O	S	0	0
			4070	2549	692	806	23		

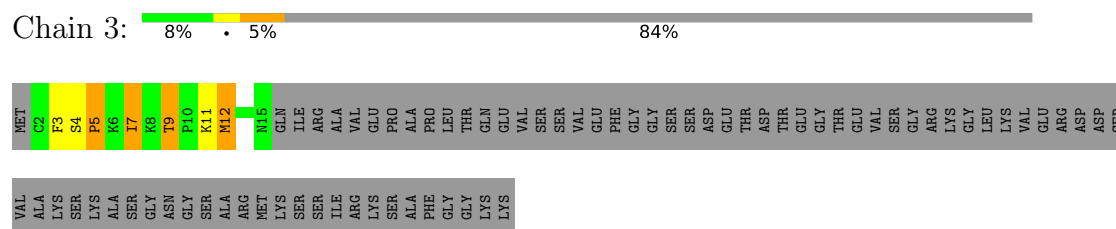
3 Residue-property plots [i](#)

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. 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. 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.

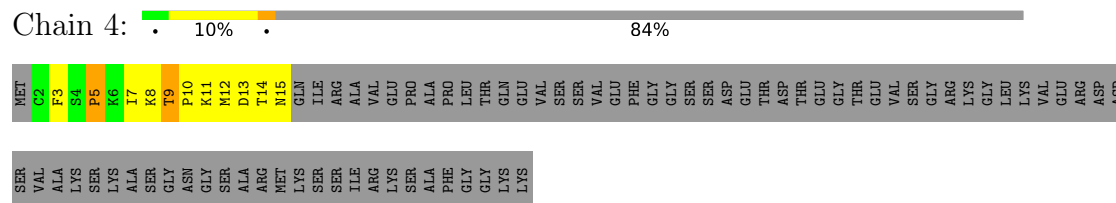
- Molecule 1: Protein 6.7



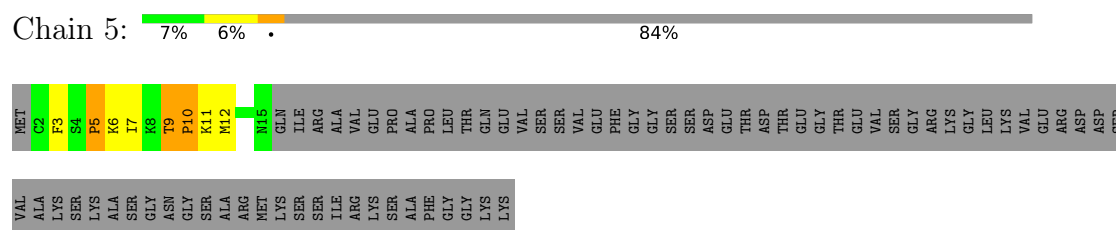
- Molecule 1: Protein 6.7



- Molecule 1: Protein 6.7



- Molecule 1: Protein 6.7



- Molecule 1: Protein 6.7



MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	SER	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP	
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

Chain 7:  84%

MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	SER	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP	
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

Chain 8:  84%

MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	GLU	THR	THR	ASP	THR	THR	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	GLU	THR	THR	THR	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

Chain 9:  84%

MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	SER	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

Chain AA:  84%

MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	SER	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	GLU	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

Chain AB:  84%

MET	C2	F3	S4	P5	K6	I7	K8	T9	P10	K11	M12	D13	T14	M15	GLN	ILE	SER	ARG	ALA	VAL	GLU	PRO	ALA	ALA	ALA	PRO	PHE	LEU	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP
SER	VAL	ALA	LYS	SER	LYS	ALA	SER	GLY	ASN	GLY	SER	ALA	ARG	MET	LYS	SER	SER	ILE	ALA	ARG	LYS	SER	PRO	ALA	ALA	ALA	PHE	GLY	GLY	THR	GLN	VAL	SER	SER	VAL	GLU	PHE	GLY	GLY	SER	SER	ASP	THR	THR	THR	GLU	GLY	THR	GLU	VAL	SER	GLY	ARG	LYS	GLY	LEU	LYS	VAL	GLU	ARG	ASP	ASP

- Molecule 1: Protein 6.7

SER VAL ALA LYS SER LYS SER GLY ASN GLY SER SER ALA ARG MET LYS SER SER ILE ARG LYS SER ALA PHE GLY GLY LYS LYS

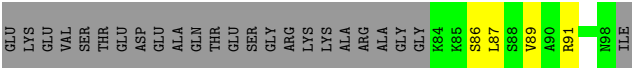
SER VAL ALA LYS SER LYS SER SER GLY ASN GLY SER ALA ARG MET LYS SER SER ILE ARG LYS SER ALA PHE GLY GLY LYS LYS

GLU	LYS	GLU	VAL	SER	THR	GLU	ASP	GLU	ALA	GLN	THR	GLU	SER	GLY	ARG	LYS	ALA	ARG	ALA	GLY	GLY	K94	L87	S98	V99	A90	R91		N96	IIE
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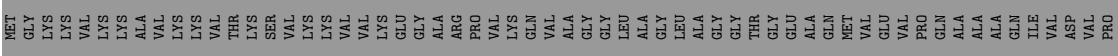
GLU	LYS	GLU	VAL	SER	THR	GLU	ASP	GLU	ALA	GLN	THR	GLU	SER	GLY	ARG	LYS	LYS	ALA	ARG	ALA	GLY	GLY	K64	L67	S68	V69	A90	R91	I97	N98	IIE
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GLU	LYS	GLU	VAL	SER	THR	GLU	ASP	GLU	ALA	GLN	THR	GLU	SER	GLY	ARG	LYS	LYS	ALA	ARG	ALA	GLY	GLY	K34	L87	S38	V89	A90	R91	N98	IIE
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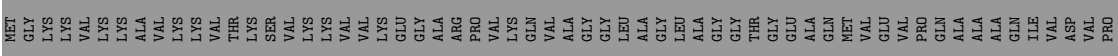
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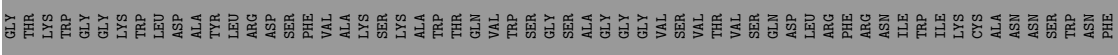
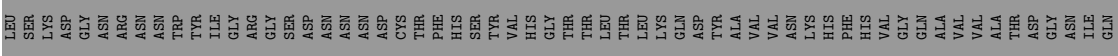
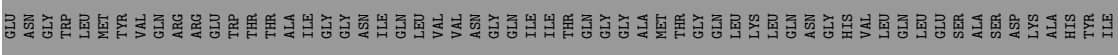
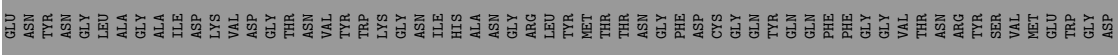
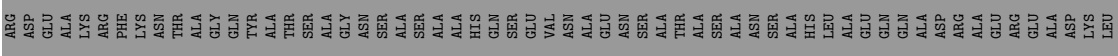
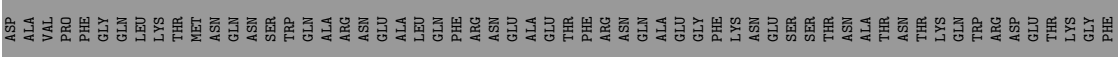
• Molecule 2: Protein 7.3



• Molecule 2: Protein 7.3



• Molecule 3: Tail fiber protein



• Molecule 3: Tail fiber protein



PHE	ILE	ALA	SER	ASP	GLY	GLY	TRP	LEU	ARG	ALA	GLN	ASN	THR	ASP	GLN	GLY	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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● Molecule 3: Tail fiber protein



MET	ALA	N3	V4	I5	V8	L9	T10	I22	P23	F24	E25	Y26	L27	I37	I58	S59	L60	I73	E74	L75	R76	R77	T81	R95	L99	I104	E111	D115	L116	T117	T120	I121	D130	R134	V143	ASP	ASP	ARG	ASP	ALA	VAL	PRO	PHE	GLY		
GLN	LEU	LYS	THR	MET	ASN	GLN	ASN	TRP	ALA	ALA	ASN	GLU	ALA	LEU	PHE	ASN	GLN	GLU	GLU	THR	PHE	ASN	GLN	GLY	PHE	LYS	ASN	GLU	ALA	THR	ASN	THR	LYS	GLN	TRP	ASP	GLU	THR	LYS	GLY	PHE	ARG	ASP	GLY	ASN	
PHE	LYS	ASN	THR	ALA	GLY	GLN	TYR	THR	ALA	VAL	ASN	SER	ALA	ALA	HIS	GLN	SER	VAL	ASN	THR	GLU	ASN	THR	ALA	SER	ALA	SER	LEU	ALA	GLU	GLN	ALA	ARG	GLU	GLY	ALA	ASP	LYS	GLY	LEU	ASP	GLY	ASN	GLU	LEU	
ALA	GLY	ALA	ILE	ARG	LYS	VAL	ASP	THR	THR	TYR	TRP	LYS	GLY	ASN	ILE	ALA	GLY	ARG	THR	MET	THR	THR	GLY	ASP	CYS	GLY	GLN	GLN	PHE	GLY	GLY	THR	ASN	ARG	TYR	VAL	GLU	TRP	GLY	LEU	ASP	GLY	ASN	MET		
TYR	VAL	GLN	ARG	GLY	GLU	THR	THR	ALA	GLY	VAL	TRP	GLN	LEU	VAL	ASN	GLY	ILE	ILE	THR	GLN	GLY	GLY	GLY	ALA	LEU	LYS	VAL	HIS	VAL	LEU	GLN	LEU	GLU	SER	ALA	GLY	HIS	THR	TYR	ILE	GLN	ASN	GLY	GLY		
ARG	ASN	ASN	TRP	TYR	ILE	GLY	GLY	SER	ASN	ASN	ASN	CYS	THR	PHE	SER	THR	VAL	HIS	THR	THR	LEU	THR	LEU	ALA	VAL	VAL	HIS	PHE	HIS	VAL	LEU	GLN	ALA	VAL	ALA	ASN	GLY	ASN	ILE	GLN	GLY	THR	THR	GLY	GLY	
LYS	TRP	LEU	ASP	ALA	LEU	ARG	ASP	PHE	VAL	ALA	LYS	LYS	ALA	THR	THR	VAL	SER	GLY	GLY	ALA	ALA	GLY	GLY	THR	VAL	VAL	VAL	PHE	ARG	HIS	VAL	ASN	VAL	VAL	VAL	ASN	ILE	TRP	ILE	CYS	ALA	ASN	ASN	ASP		
GLY	ILE	TYR	PHE	ILE	SER	ASP	GLY	TRP	LEU	PHE	GLN	ILE	HIS	SER	ASN	GLY	GLY	PHE	LYS	ASN	ILE	ARG	SER	SER	VAL	PRO	ASN	ALA	ILE	VAL	GLU	ASN	ASN	ASN	GLY	ASN	ASN	SER	THR	ASN	PHE	PHE	THR	GLY	PRO	ASP

● Molecule 3: Tail fiber protein



MET	GLN	PHE	ALA	TYR	ARG	ASN	TRP	LYS	THR	ASP	ASN	THR	ILE	GLN	VAL	ASN	GLY	THR	GLY	GLN	ASP	GLY	THR	ASN	GLY	THR	ASN	GLY	GLN	THR	ASP	ARG	GLU	ASP	GLY	THR	LYS	ASP	GLY	THR	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP	GLY	THR	LYS	ASP
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● Molecule 3: Tail fiber protein



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● Molecule 3: Tail fiber protein



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● Molecule 3: Tail fiber protein



MET	ALA	ASN	ASN	VAL	I5	V8	Q12	L13	I22	L36	I37	R41	L44	T45	I46	N47	T48	D49	Y50	A53	T54	T57	I58	S59	L60	W64	T72	R76	T81	R84	V101	M107	L116	T120	I121	M124	H128	L129	D130	N138		
LEU	ALA	ASN	ALA	VAL	ASP	ASP	ARG	ASP	ALA	ASP	GLY	LEU	THR	MET	GLN	ASN	SER	TRP	GLN	ALA	ARG	ASN	ALA	GLN	PHE	ARG	GLU	GLU	THR	PHE	ASN	ALA	GLY	GLY	ASN	SER	SER	THR	THR	LYS	GLY	
TRP	ARG	ASP	GLU	THR	LYS	GLY	PHE	ARG	ASP	ASP	GLY	LYS	ALA	ASP	GLN	TYR	ALA	THR	SER	ALA	GLY	ASN	GLN	ALA	ALA	HIS	GLN	SER	ALA	GLU	ASN	SER	GLY	THR	ALA	HIS	ALA	GLY	GLN	ASP	ARG	
ALA	GLU	ARG	GLU	ALA	ASP	LYS	LEU	GLU	ASN	GLY	GLU	ASN	ILE	ASP	VAL	ASP	THR	THR	ASN	VAL	TYR	TRP	LYS	GLY	ALA	HIS	ASN	THR	MET	THR	GLY	ASP	CYS	GLY	GLN	GLN	GLN	PHE	PHE	GLY	ASN	ARG
TYR	SER	VAL	MET	GLU	TRP	GLY	ASP	GLU	ASN	MET	TYR	VAL	ARG	GLU	TRP	THR	THR	ALA	ILE	GLY	GLY	ASN	GLN	VAL	VAL	ASN	GLN	THR	GLN	GLY	GLY	GLN	GLY	LEU	GLN	ASN	GLY	GLY	ASN	GLU	SER	
ALA	SER	ASP	LYS	ALA	HIS	TYR	ILE	LEU	SER	ASN	ARG	ASN	TRP	ILE	GLY	ARG	GLY	ASP	ASN	ASN	ASN	ASN	THR	PHE	HIS	SER	THR	THR	THR	LEU	THR	GLY	THR	VAL	VAL	LYS	ASN	LYS	HIS	PHE	VAL	
VAL	ALA	THR	ASP	GLY	ASN	ILE	GLN	THR	THR	GLY	TRP	ASP	TYR	ALA	THR	ASP	GLY	SER	PHE	VAL	ALA	THR	THR	GLY	GLY	GLY	THR	THR	ALA	GLY	GLY	VAL	VAL	GLN	ASP	LEU	ARG	PHE	THR	TRP	ILE	
CYS	ALA	ASN	ASN	TRP	ASN	PHE	PHE	THR	GLY	ARG	GLY	ILE	TRP	ALA	TYR	SER	GLY	TRP	LEU	ARG	PHE	ILE	GLN	ASN	GLY	ASN	GLY	ALA	ALA	ASP	ARG	SER	VAL	THR	PRO	ASN	ALA	ILE	VAL	GLU	ASN	

● Molecule 3: Tail fiber protein



ARG	THR	SER	ASN	GLY	THR	ASP	GLY	THR	ASP	ASN	TYR	ASN	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY	THR	ASP	GLY
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● Molecule 3: Tail fiber protein



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● Molecule 3: Tail fiber protein



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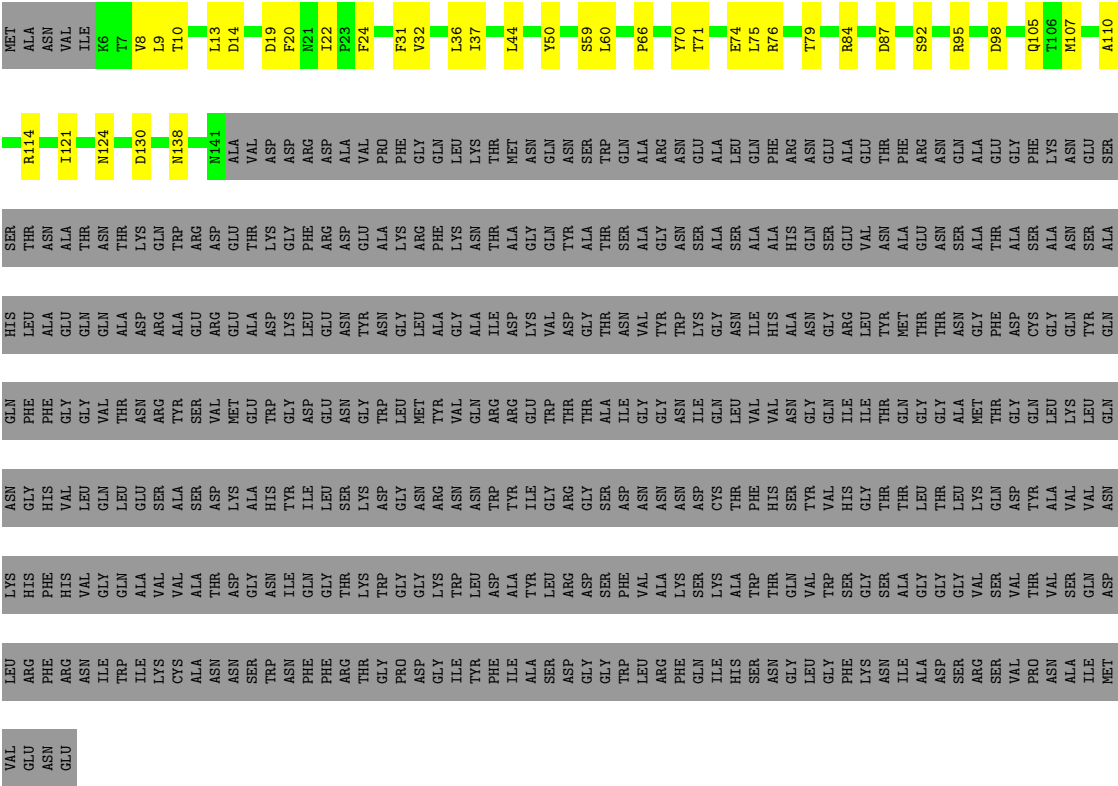
● Molecule 3: Tail fiber protein



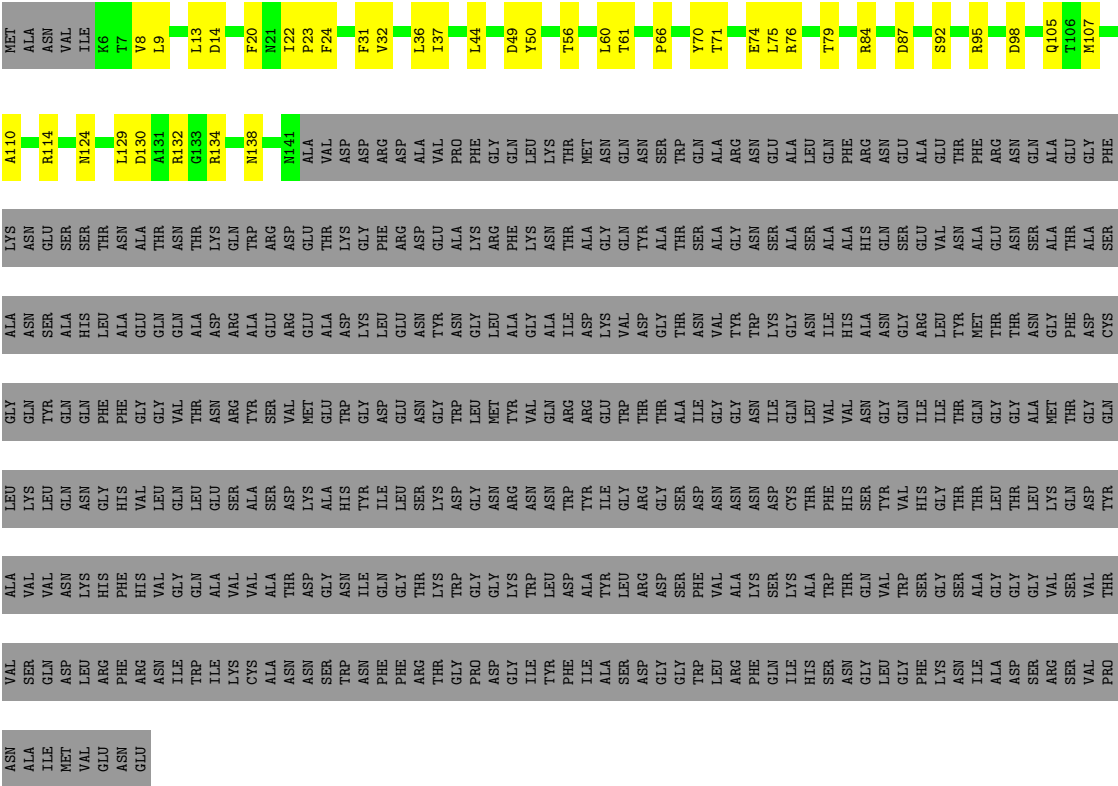
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● Molecule 3: Tail fiber protein

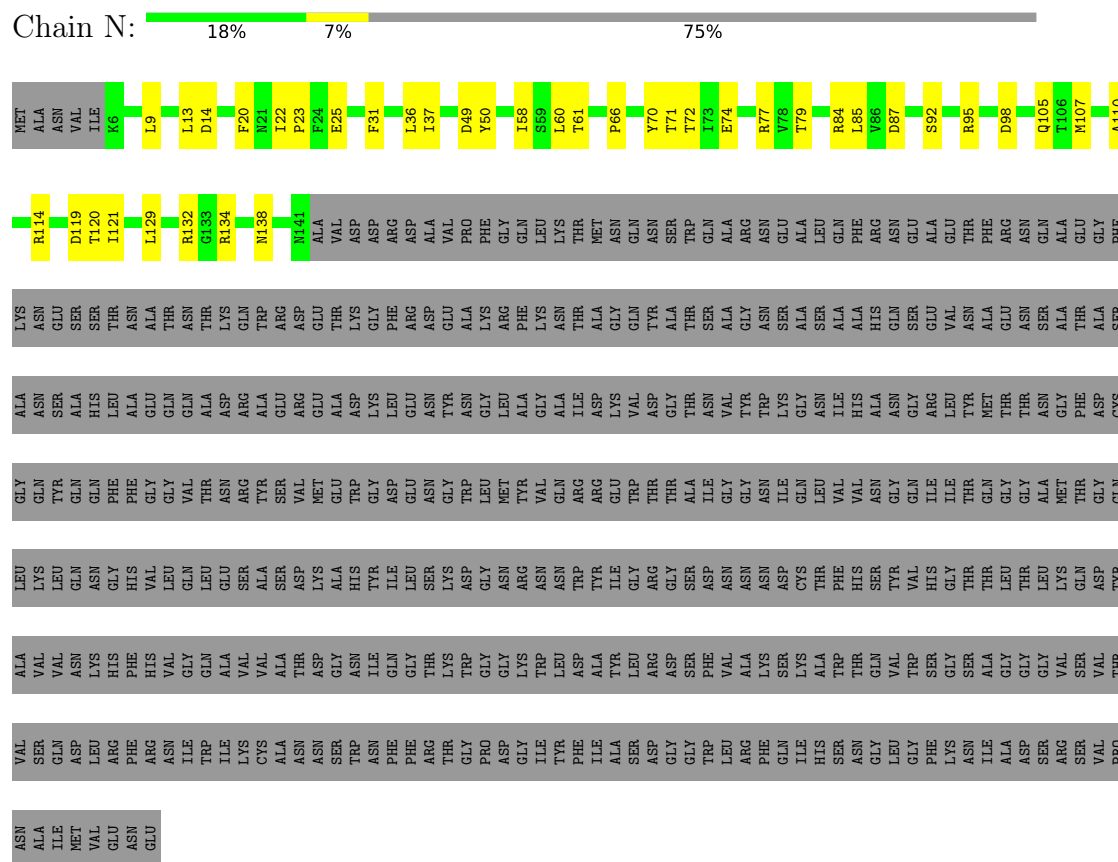




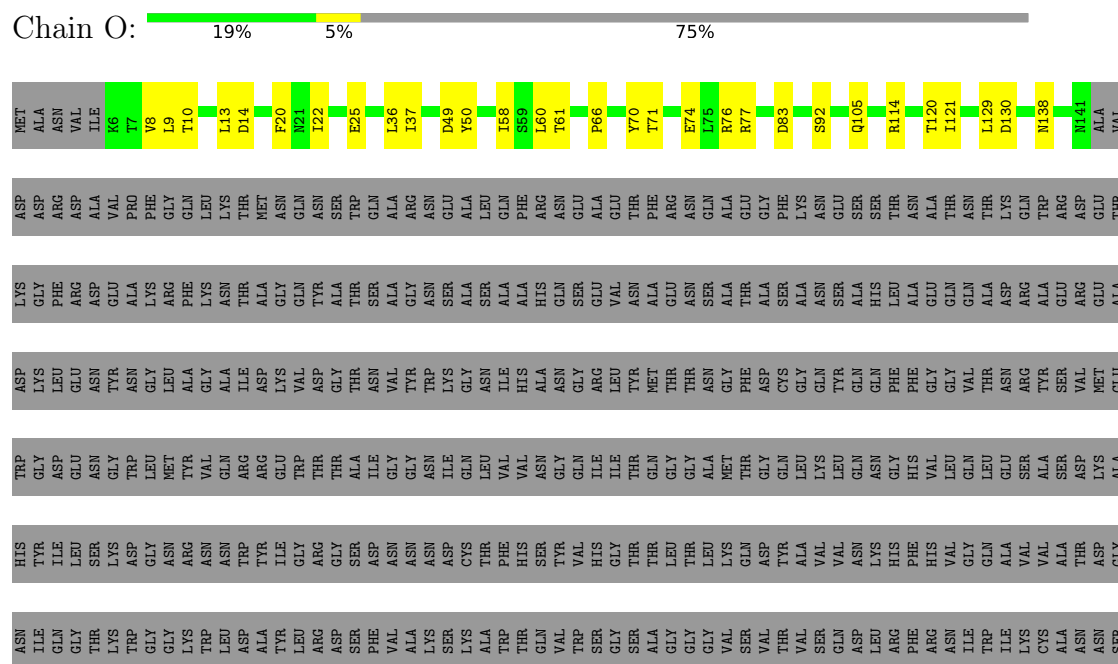
● Molecule 3: Tail fiber protein

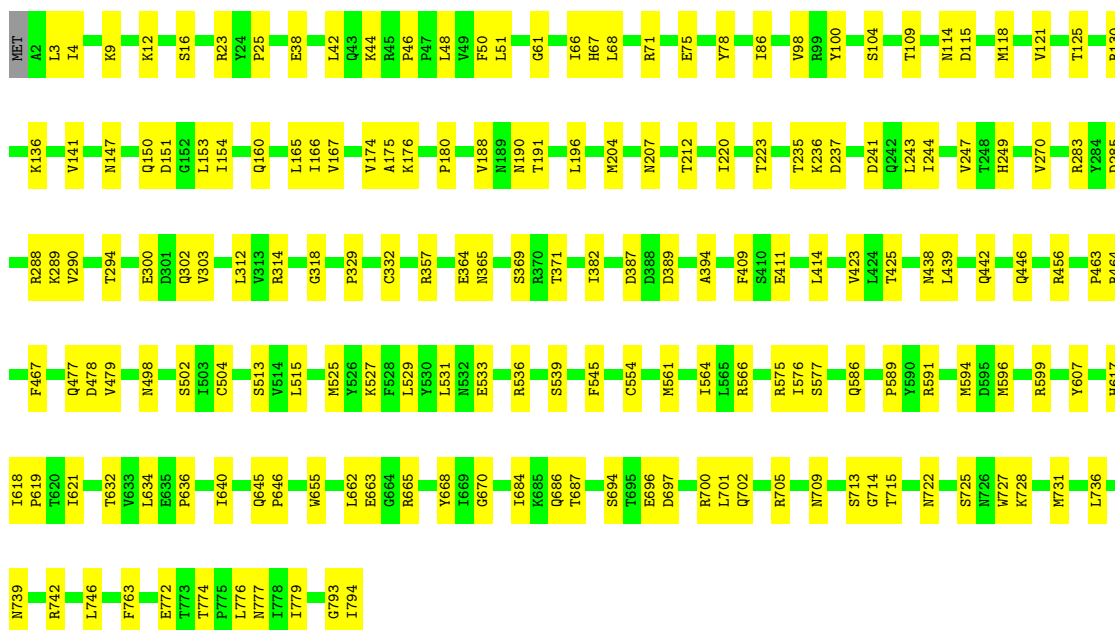


- Molecule 3: Tail fiber protein



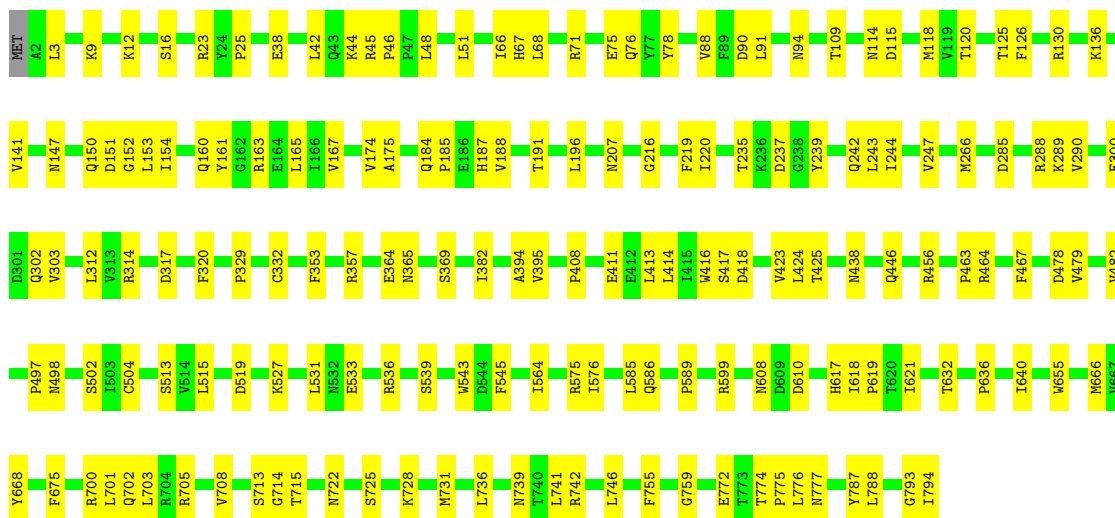
- Molecule 3: Tail fiber protein





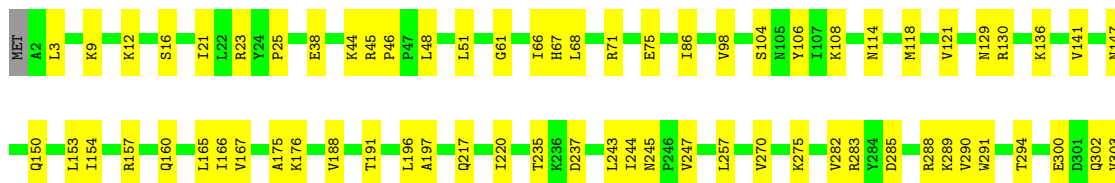
• Molecule 4: Tail tubular protein gp12

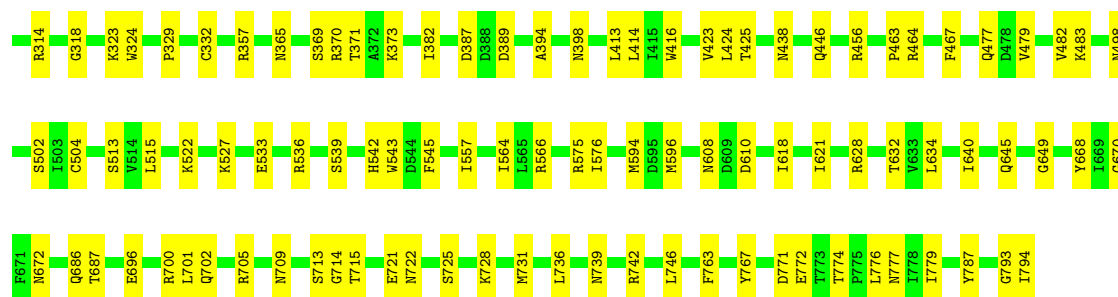
Chain R: 79% 21%



• Molecule 4: Tail tubular protein gp12

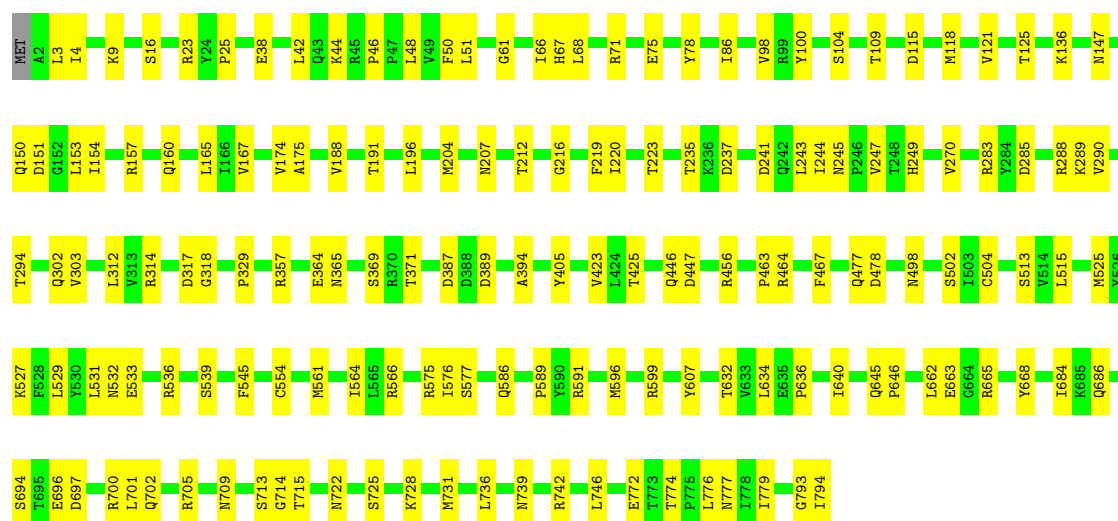
Chain S: 79% 21%





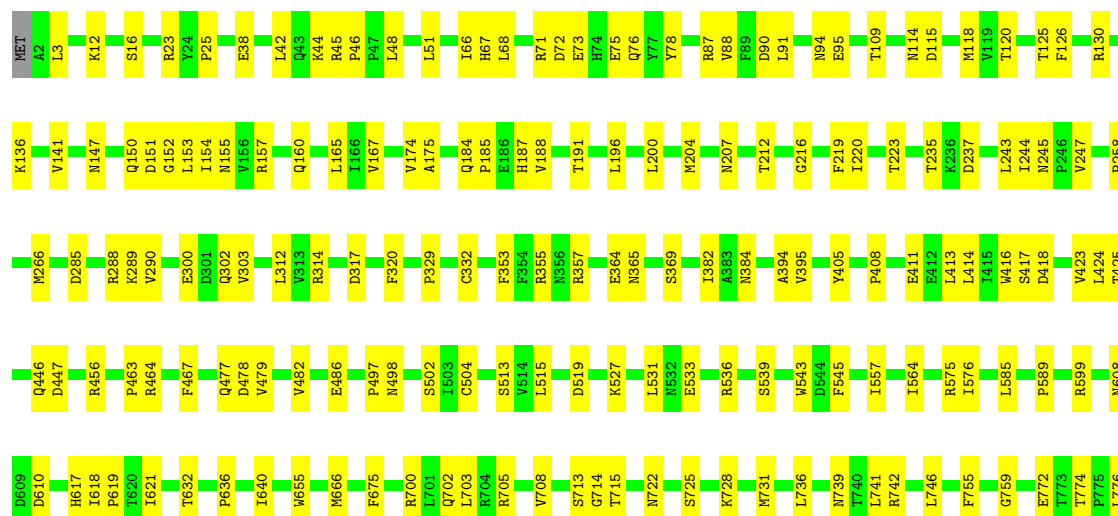
• Molecule 4: Tail tubular protein gp12

Chain T: 80% 20%



• Molecule 4: Tail tubular protein gp12

Chain x: 78% 22%





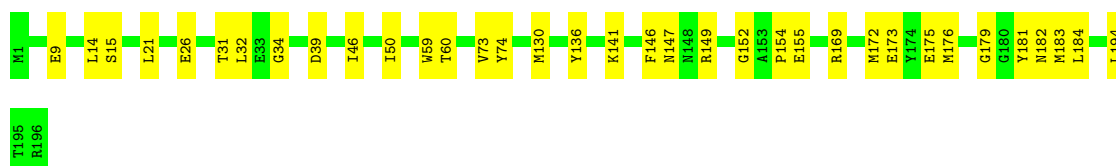
- Molecule 5: Tail tubular protein gp11

Chain U: 86% 14%



- Molecule 5: Tail tubular protein gp11

Chain V: 82% 18%



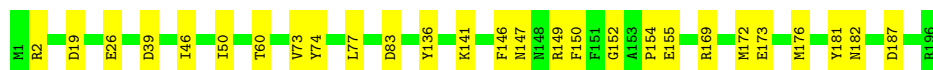
- Molecule 5: Tail tubular protein gp11

Chain W: 85% 15%



- Molecule 5: Tail tubular protein gp11

Chain X: 86% 14%



- Molecule 5: Tail tubular protein gp11

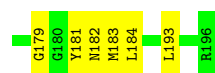
Chain Y: 88% 12%



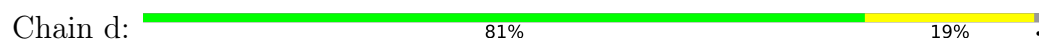
- Molecule 5: Tail tubular protein gp11

Chain Z: 80% 19%

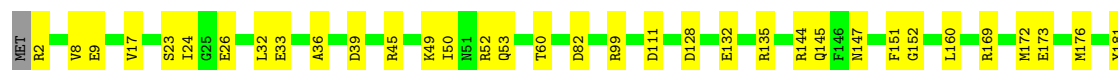
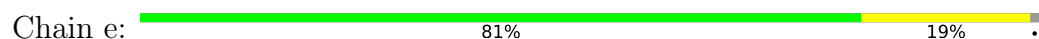




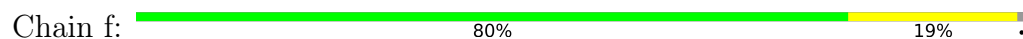
- Molecule 5: Tail tubular protein gp11



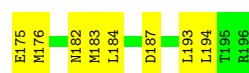
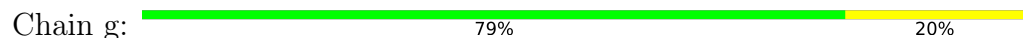
- Molecule 5: Tail tubular protein gp11



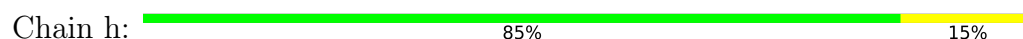
- Molecule 5: Tail tubular protein gp11



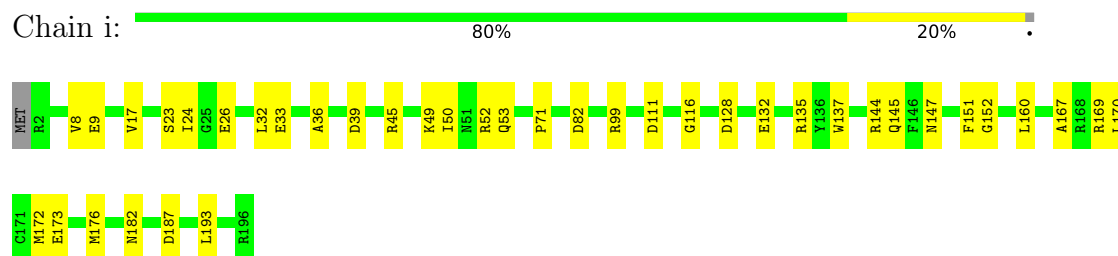
- Molecule 5: Tail tubular protein gp11



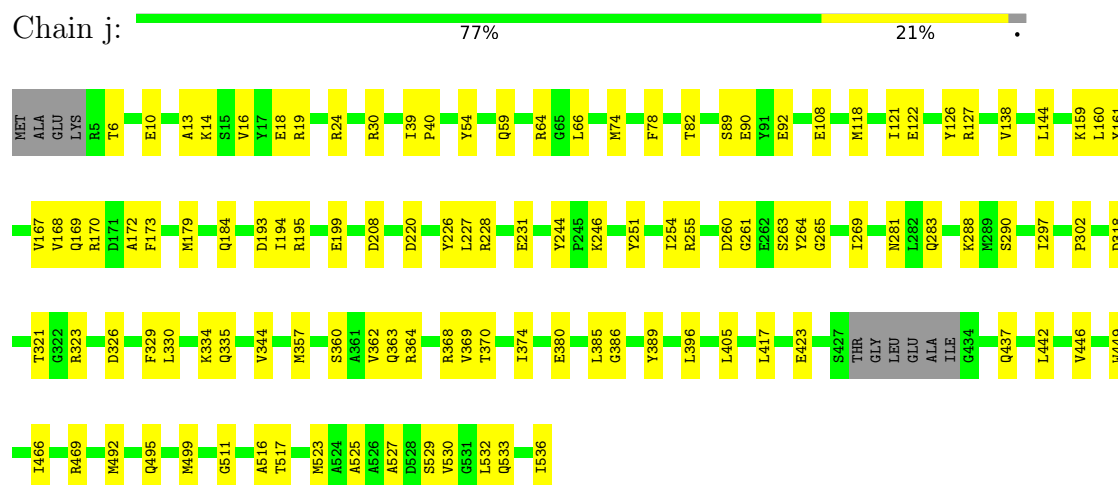
- Molecule 5: Tail tubular protein gp11



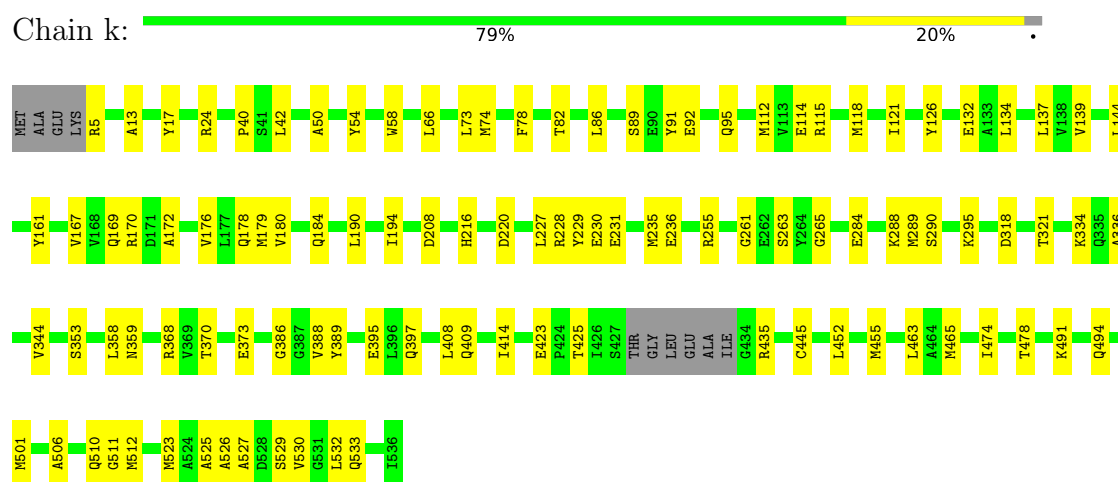
- Molecule 5: Tail tubular protein gp11



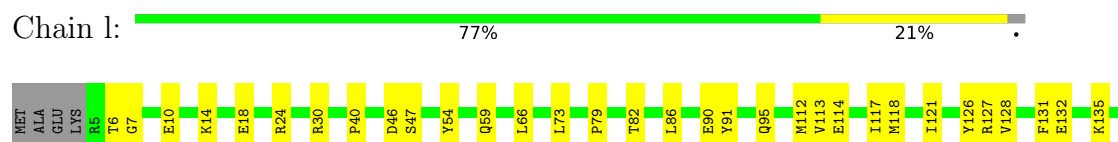
- Molecule 6: Portal protein



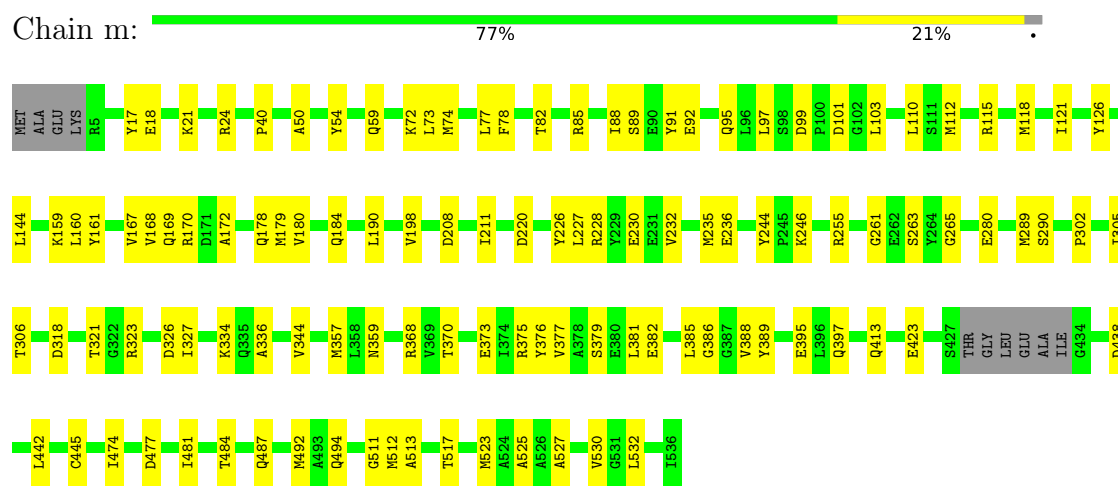
- Molecule 6: Portal protein



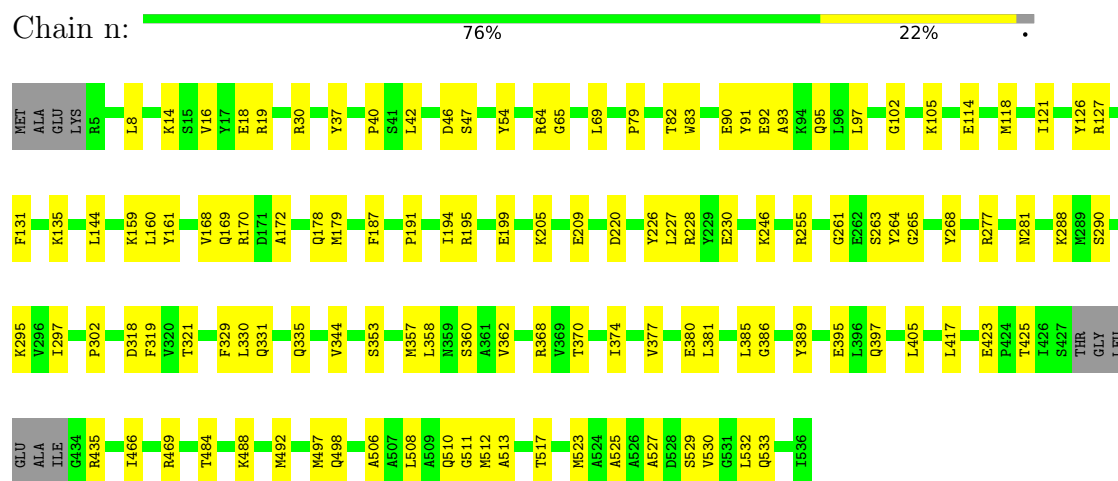
- Molecule 6: Portal protein



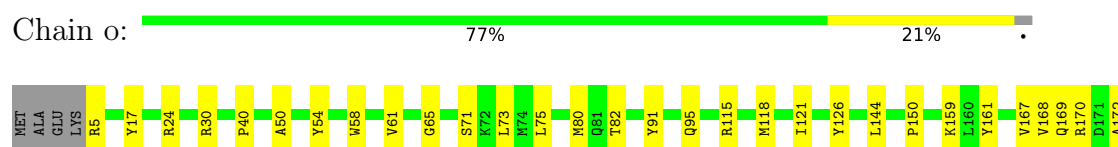
- Molecule 6: Portal protein

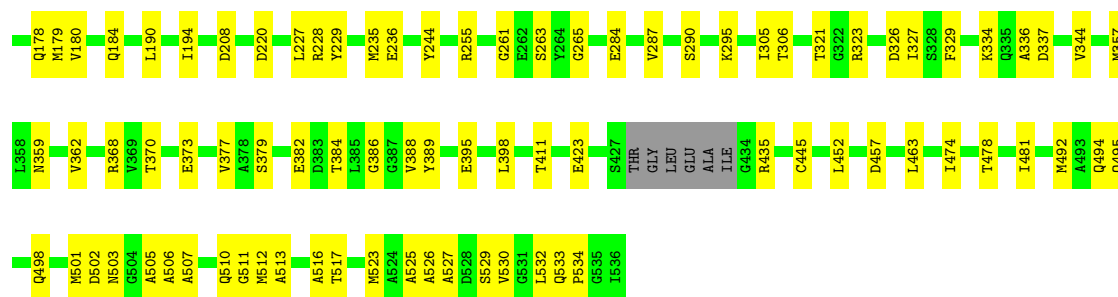


- Molecule 6: Portal protein



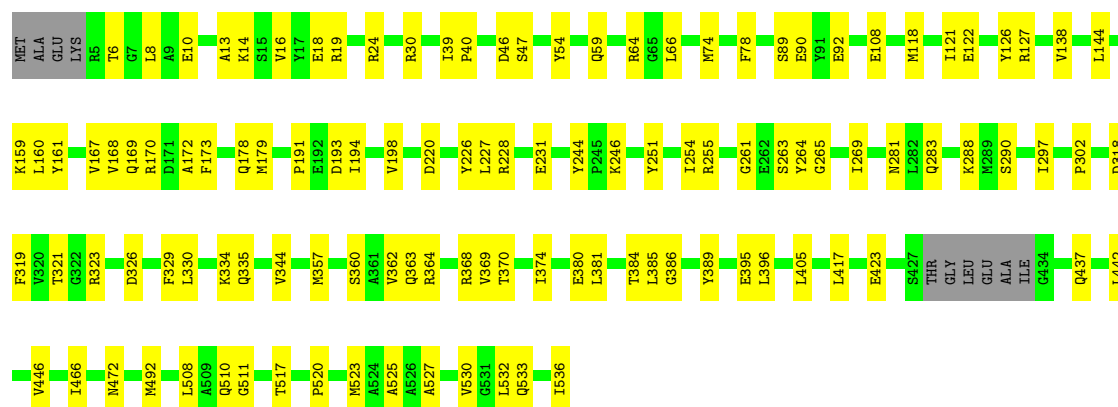
- Molecule 6: Portal protein





• Molecule 6: Portal protein

Chain p: 77% 21%



• Molecule 6: Portal protein

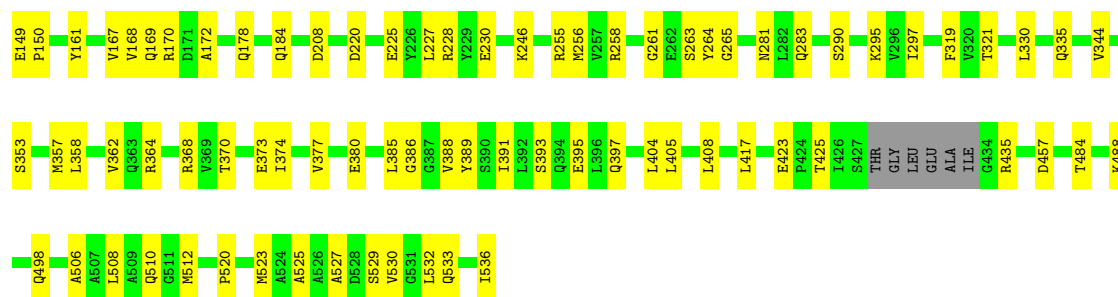
Chain q: 79% 19%



• Molecule 6: Portal protein

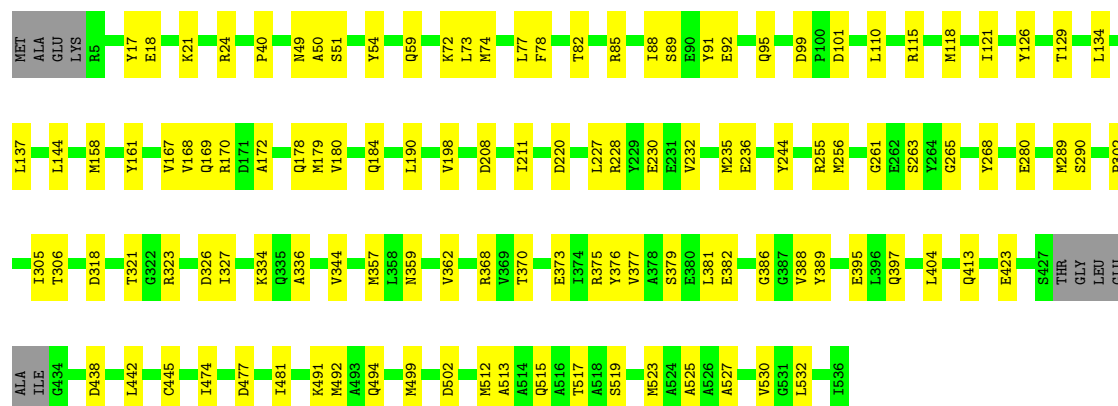
Chain r: 78% 20%





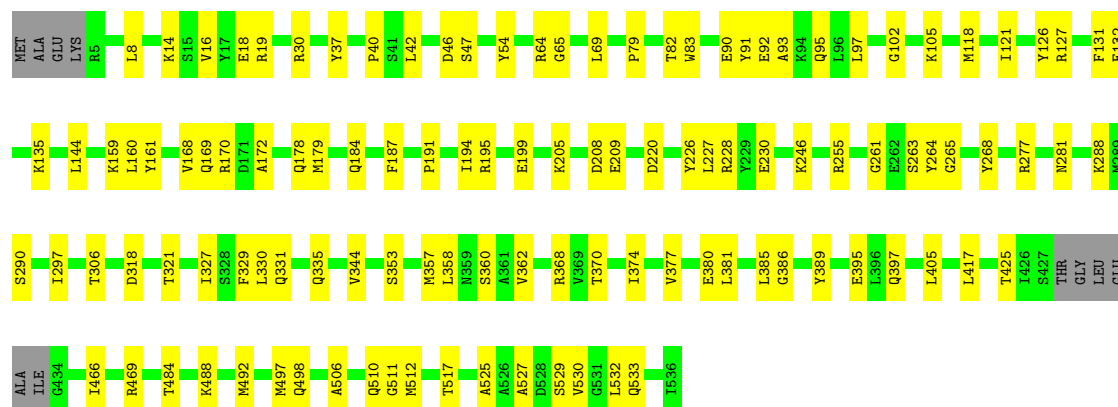
• Molecule 6: Portal protein

Chain s: 76% 22%



• Molecule 6: Portal protein

Chain t: 77% 21%



• Molecule 6: Portal protein

Chain u: 76% 22%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	65620	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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	0	0.61	0/112	1.38	2/149 (1.3%)
1	3	0.55	0/112	1.44	2/149 (1.3%)
1	4	0.60	0/112	1.40	3/149 (2.0%)
1	5	0.55	0/112	1.45	3/149 (2.0%)
1	6	0.63	0/112	1.40	4/149 (2.7%)
1	7	0.55	0/112	1.54	2/149 (1.3%)
1	8	0.58	0/112	1.41	5/149 (3.4%)
1	9	0.23	0/112	0.63	0/149
1	AA	0.53	0/112	1.47	4/149 (2.7%)
1	AB	0.63	0/112	1.39	4/149 (2.7%)
1	AC	0.52	0/112	1.50	4/149 (2.7%)
1	AD	0.58	0/112	1.32	3/149 (2.0%)
2	1	0.12	0/100	0.30	0/130
2	2	0.13	0/100	0.31	0/130
2	v	0.13	0/100	0.32	0/130
2	w	0.12	0/100	0.30	0/130
2	y	0.13	0/100	0.32	0/130
2	z	0.14	0/100	0.32	0/130
3	A	0.13	0/1130	0.30	0/1538
3	B	0.13	0/1130	0.28	0/1538
3	C	0.13	0/1130	0.28	0/1538
3	D	0.13	0/1130	0.30	0/1538
3	E	0.13	0/1130	0.30	0/1538
3	F	0.12	0/1082	0.30	0/1471
3	G	0.13	0/1082	0.31	0/1471
3	H	0.13	0/1082	0.30	0/1471
3	I	0.13	0/1082	0.32	0/1471
3	J	0.12	0/1082	0.29	0/1471
3	K	0.14	0/1095	0.38	0/1489
3	L	0.14	0/1095	0.38	0/1489
3	M	0.13	0/1095	0.37	0/1489
3	N	0.14	0/1095	0.37	0/1489
3	O	0.13	0/1095	0.38	0/1489
3	a	0.14	0/1130	0.30	0/1538

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	b	0.13	0/1082	0.32	0/1471
3	c	0.14	0/1095	0.37	0/1489
4	P	0.16	0/6473	0.31	0/8804
4	Q	0.15	0/6473	0.31	0/8804
4	R	0.15	0/6473	0.32	0/8804
4	S	0.16	0/6473	0.32	0/8804
4	T	0.15	0/6473	0.31	0/8804
4	x	0.15	0/6473	0.32	0/8804
5	U	0.16	0/1592	0.31	0/2153
5	V	0.17	0/1592	0.30	0/2153
5	W	0.15	0/1592	0.29	0/2153
5	X	0.15	0/1592	0.30	0/2153
5	Y	0.17	0/1592	0.32	0/2153
5	Z	0.17	0/1584	0.32	0/2143
5	d	0.16	0/1584	0.33	0/2143
5	e	0.16	0/1584	0.33	0/2143
5	f	0.16	0/1584	0.31	0/2143
5	g	0.16	0/1584	0.32	0/2143
5	h	0.15	0/1592	0.28	0/2153
5	i	0.16	0/1584	0.34	0/2143
6	j	0.14	0/4131	0.32	0/5590
6	k	0.14	0/4131	0.31	0/5590
6	l	0.14	0/4131	0.31	0/5590
6	m	0.15	0/4131	0.31	0/5590
6	n	0.15	0/4131	0.33	0/5590
6	o	0.14	0/4131	0.31	0/5590
6	p	0.14	0/4131	0.32	0/5590
6	q	0.14	0/4131	0.31	0/5590
6	r	0.14	0/4131	0.32	0/5590
6	s	0.15	0/4131	0.32	0/5590
6	t	0.15	0/4131	0.33	0/5590
6	u	0.16	0/4131	0.32	0/5590
All	All	0.16	0/129252	0.34	36/175236 (0.0%)

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AC	14	THR	N-CA-C	8.22	120.25	111.28
1	7	14	THR	N-CA-C	7.26	119.19	111.28
1	AD	10	PRO	N-CA-C	7.16	123.71	113.47
1	4	5	PRO	N-CA-C	6.67	122.33	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	5	PRO	N-CA-C	6.64	122.75	113.53

There are no chirality outliers.

There are no planarity outliers.

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	0	110	0	115	13	0
1	3	110	0	115	11	0
1	4	110	0	115	17	0
1	5	110	0	115	10	0
1	6	110	0	115	11	0
1	7	110	0	115	12	0
1	8	110	0	115	11	0
1	9	110	0	115	13	0
1	AA	110	0	115	11	0
1	AB	110	0	115	12	0
1	AC	110	0	115	14	0
1	AD	110	0	115	11	0
2	1	101	0	109	5	0
2	2	101	0	109	5	0
2	v	101	0	109	4	0
2	w	101	0	109	5	0
2	y	101	0	109	6	0
2	z	101	0	109	5	0
3	A	1115	0	1122	26	0
3	B	1115	0	1122	21	0
3	C	1115	0	1122	21	0
3	D	1115	0	1122	25	0
3	E	1115	0	1122	25	0
3	F	1067	0	1071	20	0
3	G	1067	0	1071	21	0
3	H	1067	0	1071	18	0
3	I	1067	0	1071	23	0
3	J	1067	0	1071	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	1080	0	1082	24	0
3	L	1080	0	1082	24	0
3	M	1080	0	1082	26	0
3	N	1080	0	1082	23	0
3	O	1080	0	1082	19	0
3	a	1115	0	1122	22	0
3	b	1067	0	1071	22	0
3	c	1080	0	1082	19	0
4	P	6313	0	6075	114	0
4	Q	6313	0	6075	122	0
4	R	6313	0	6075	111	0
4	S	6313	0	6075	108	0
4	T	6313	0	6075	110	0
4	x	6313	0	6075	119	0
5	U	1565	0	1485	26	0
5	V	1565	0	1485	28	0
5	W	1565	0	1485	26	0
5	X	1565	0	1485	25	0
5	Y	1565	0	1485	22	0
5	Z	1557	0	1473	33	0
5	d	1557	0	1473	28	0
5	e	1557	0	1473	29	0
5	f	1557	0	1473	31	0
5	g	1557	0	1473	31	0
5	h	1565	0	1485	25	0
5	i	1557	0	1473	30	0
6	j	4070	0	4060	80	0
6	k	4070	0	4060	76	0
6	l	4070	0	4060	84	0
6	m	4070	0	4060	85	0
6	n	4070	0	4060	95	0
6	o	4070	0	4060	83	0
6	p	4070	0	4060	84	0
6	q	4070	0	4060	73	0
6	r	4070	0	4060	81	0
6	s	4070	0	4060	89	0
6	t	4070	0	4060	91	0
6	u	4070	0	4060	87	0
All	All	126948	0	124602	2088	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 8.

The worst 5 of 2088 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)
1:0:7:ILE:HA	6:n:530:VAL:HG21	1.39	1.01
1:4:7:ILE:HA	6:t:530:VAL:HG21	1.45	0.99
1:6:7:ILE:HA	6:r:530:VAL:HG21	1.46	0.97
1:AB:7:ILE:HA	6:l:530:VAL:HG21	1.49	0.93
1:AD:7:ILE:HA	6:j:530:VAL:HG21	1.51	0.90

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 PDB entries followed by that with respect to all EM entries.

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	0	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	3	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	4	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	5	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	6	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	7	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
1	8	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	9	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
1	AA	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AB	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AC	12/88 (14%)	11 (92%)	0	1 (8%)	0	1
1	AD	12/88 (14%)	10 (83%)	1 (8%)	1 (8%)	0	1
2	1	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	2	13/99 (13%)	12 (92%)	1 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	v	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	w	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	y	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
2	z	13/99 (13%)	12 (92%)	1 (8%)	0	100	100
3	A	139/553 (25%)	135 (97%)	4 (3%)	0	100	100
3	B	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	C	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	D	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	E	139/553 (25%)	135 (97%)	4 (3%)	0	100	100
3	F	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	G	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	H	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	I	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	J	132/553 (24%)	129 (98%)	3 (2%)	0	100	100
3	K	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	L	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	M	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	N	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	O	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
3	a	139/553 (25%)	134 (96%)	5 (4%)	0	100	100
3	b	132/553 (24%)	128 (97%)	4 (3%)	0	100	100
3	c	134/553 (24%)	127 (95%)	7 (5%)	0	100	100
4	P	791/794 (100%)	773 (98%)	18 (2%)	0	100	100
4	Q	791/794 (100%)	775 (98%)	16 (2%)	0	100	100
4	R	791/794 (100%)	776 (98%)	15 (2%)	0	100	100
4	S	791/794 (100%)	774 (98%)	17 (2%)	0	100	100
4	T	791/794 (100%)	775 (98%)	16 (2%)	0	100	100
4	x	791/794 (100%)	774 (98%)	17 (2%)	0	100	100
5	U	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	V	194/196 (99%)	192 (99%)	2 (1%)	0	100	100
5	W	194/196 (99%)	193 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	X	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	Y	194/196 (99%)	193 (100%)	1 (0%)	0	100	100
5	Z	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	d	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	e	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	f	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	g	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
5	h	194/196 (99%)	192 (99%)	2 (1%)	0	100	100
5	i	193/196 (98%)	191 (99%)	2 (1%)	0	100	100
6	j	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	k	522/536 (97%)	513 (98%)	9 (2%)	0	100	100
6	l	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	m	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	n	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	o	522/536 (97%)	513 (98%)	9 (2%)	0	100	100
6	p	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	q	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	r	522/536 (97%)	515 (99%)	7 (1%)	0	100	100
6	s	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	t	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
6	u	522/536 (97%)	514 (98%)	8 (2%)	0	100	100
All	All	15984/25152 (64%)	15660 (98%)	312 (2%)	12 (0%)	50	73

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	9	9	THR
1	0	9	THR
1	6	9	THR
1	AB	9	THR
1	AC	9	THR

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 PDB entries followed by that with respect to all EM entries.

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	0	14/73 (19%)	12 (86%)	2 (14%)	2	7
1	3	14/73 (19%)	12 (86%)	2 (14%)	2	7
1	4	14/73 (19%)	13 (93%)	1 (7%)	12	30
1	5	14/73 (19%)	14 (100%)	0	100	100
1	6	14/73 (19%)	14 (100%)	0	100	100
1	7	14/73 (19%)	13 (93%)	1 (7%)	12	30
1	8	14/73 (19%)	13 (93%)	1 (7%)	12	30
1	9	14/73 (19%)	14 (100%)	0	100	100
1	AA	14/73 (19%)	12 (86%)	2 (14%)	2	7
1	AB	14/73 (19%)	14 (100%)	0	100	100
1	AC	14/73 (19%)	12 (86%)	2 (14%)	2	7
1	AD	14/73 (19%)	13 (93%)	1 (7%)	12	30
2	1	11/72 (15%)	11 (100%)	0	100	100
2	2	11/72 (15%)	11 (100%)	0	100	100
2	v	11/72 (15%)	11 (100%)	0	100	100
2	w	11/72 (15%)	11 (100%)	0	100	100
2	y	11/72 (15%)	11 (100%)	0	100	100
2	z	11/72 (15%)	11 (100%)	0	100	100
3	A	122/451 (27%)	122 (100%)	0	100	100
3	B	122/451 (27%)	122 (100%)	0	100	100
3	C	122/451 (27%)	122 (100%)	0	100	100
3	D	122/451 (27%)	122 (100%)	0	100	100
3	E	122/451 (27%)	122 (100%)	0	100	100
3	F	117/451 (26%)	117 (100%)	0	100	100
3	G	117/451 (26%)	117 (100%)	0	100	100
3	H	117/451 (26%)	117 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	117/451 (26%)	117 (100%)	0	100	100
3	J	117/451 (26%)	117 (100%)	0	100	100
3	K	118/451 (26%)	118 (100%)	0	100	100
3	L	118/451 (26%)	118 (100%)	0	100	100
3	M	118/451 (26%)	118 (100%)	0	100	100
3	N	118/451 (26%)	118 (100%)	0	100	100
3	O	118/451 (26%)	118 (100%)	0	100	100
3	a	122/451 (27%)	122 (100%)	0	100	100
3	b	117/451 (26%)	117 (100%)	0	100	100
3	c	118/451 (26%)	118 (100%)	0	100	100
4	P	687/688 (100%)	687 (100%)	0	100	100
4	Q	687/688 (100%)	687 (100%)	0	100	100
4	R	687/688 (100%)	686 (100%)	1 (0%)	92	98
4	S	687/688 (100%)	687 (100%)	0	100	100
4	T	687/688 (100%)	687 (100%)	0	100	100
4	x	687/688 (100%)	686 (100%)	1 (0%)	92	98
5	U	169/169 (100%)	169 (100%)	0	100	100
5	V	169/169 (100%)	168 (99%)	1 (1%)	84	94
5	W	169/169 (100%)	169 (100%)	0	100	100
5	X	169/169 (100%)	169 (100%)	0	100	100
5	Y	169/169 (100%)	169 (100%)	0	100	100
5	Z	168/169 (99%)	168 (100%)	0	100	100
5	d	168/169 (99%)	168 (100%)	0	100	100
5	e	168/169 (99%)	168 (100%)	0	100	100
5	f	168/169 (99%)	168 (100%)	0	100	100
5	g	168/169 (99%)	168 (100%)	0	100	100
5	h	169/169 (100%)	169 (100%)	0	100	100
5	i	168/169 (99%)	168 (100%)	0	100	100
6	j	435/442 (98%)	435 (100%)	0	100	100
6	k	435/442 (98%)	435 (100%)	0	100	100
6	l	435/442 (98%)	435 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	m	435/442 (98%)	435 (100%)	0	100	100
6	n	435/442 (98%)	434 (100%)	1 (0%)	92	98
6	o	435/442 (98%)	434 (100%)	1 (0%)	92	98
6	p	435/442 (98%)	435 (100%)	0	100	100
6	q	435/442 (98%)	435 (100%)	0	100	100
6	r	435/442 (98%)	435 (100%)	0	100	100
6	s	435/442 (98%)	435 (100%)	0	100	100
6	t	435/442 (98%)	435 (100%)	0	100	100
6	u	435/442 (98%)	433 (100%)	2 (0%)	86	95
All	All	13740/20886 (66%)	13721 (100%)	19 (0%)	92	98

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	n	423	GLU
6	u	519	SER
4	x	71	ARG
6	u	30	ARG
1	AA	12	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
5	h	93	GLN
6	t	359	ASN
6	k	487	GLN
6	t	335	GLN
6	u	498	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

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.