



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 05:46 AM UTC

PDB ID : 7FJ3 / pdb_00007fj3
EMDB ID : EMD-31612
Title : Cryo-EM structure of PRV A-capid
Authors : Zheng, Q.; Li, S.; Zha, Z.; Sun, H.
Deposited on : 2021-08-02
Resolution : 4.53 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 : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

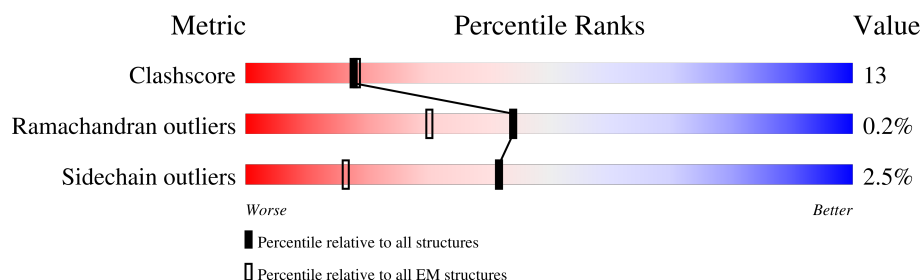
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.53 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.



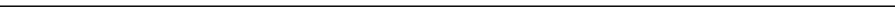
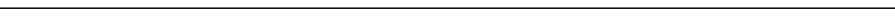
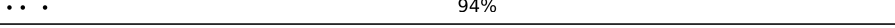
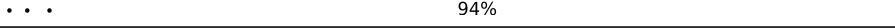
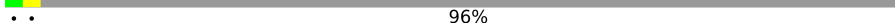
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	1330	73% 25% .
1	A	1330	69% 29% .
1	S	1330	70% 27% .
1	U	1330	76% 22% .
1	a	1330	70% 27% .
1	e	1330	54% 31% 15% .
1	f	1330	78% 21% .
1	g	1330	70% 28% .
1	l	1330	72% 27% .

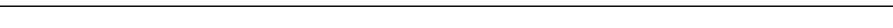
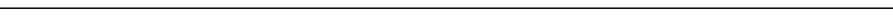
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Mol	Chain	Length	Quality of chain
1	m	1330	 71%28%.
1	n	1330	 73%25%.
1	p	1330	 73%25%.
1	q	1330	 73%26%.
1	u	1330	 75%24%.
1	w	1330	 72%27%.
1	y	1330	 70%28%.
2	1	296	 70%24%6%
2	2	296	 55%38%6%
2	3	296	 67%27%6%
2	j	296	 58%32%10%
2	k	296	 56%38%6%
2	o	296	 74%26%
2	s	296	 73%21%6%
2	v	296	 70%27%.
2	x	296	 64%36%
2	z	296	 70%30%
3	B	368	 94%
3	C	368	 94%
3	D	368	 94%
3	T	368	 57%28%11%
3	W	368	 94%
3	d	368	 96%
3	h	368	 57%28%5%11%
3	i	368	 55%29%11%

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Mol	Chain	Length	Quality of chain
3	r	368	 56% 28% 5% 11%
3	t	368	 56% 29% • 11%
4	E	103	 52% 33% • 12%
4	F	103	 51% 33% • 12%
4	G	103	 50% 36% • 12%
4	H	103	 51% 34% • 12%
4	I	103	 50% 35% • 12%
4	J	103	 54% 30% • 12%
4	K	103	 52% 32% • 12%
4	L	103	 51% 33% • 12%
4	M	103	 50% 33% 5% 12%
4	N	103	 51% 33% • 12%
4	O	103	 52% 32% • 12%
4	P	103	 53% 32% • 12%
4	Q	103	 54% 31% • 12%
4	R	103	 52% 32% • 12%
4	V	103	 50% 34% • 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 205888 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	A	1308	Total	C	N	O	S	0	0
			10112	6393	1820	1837	62		
1	S	1289	Total	C	N	O	S	0	0
			9975	6307	1797	1812	59		
1	U	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	a	1289	Total	C	N	O	S	0	0
			9974	6311	1797	1805	61		
1	e	1126	Total	C	N	O	S	0	0
			8722	5528	1561	1579	54		
1	f	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	g	1310	Total	C	N	O	S	0	0
			10125	6401	1823	1840	61		
1	l	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	m	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	n	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	p	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	q	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	u	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	w	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	y	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		

- Molecule 2 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	2	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	3	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	j	267	Total	C	N	O	S	0	0
			2009	1269	365	364	11		
2	k	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	o	296	Total	C	N	O	S	0	0
			2229	1403	414	401	11		
2	s	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	v	289	Total	C	N	O	S	0	0
			2189	1380	404	394	11		
2	x	296	Total	C	N	O	S	0	0
			2229	1403	414	401	11		
2	z	296	Total	C	N	O	S	0	0
			2229	1403	414	401	11		

- Molecule 3 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	23	Total	C	N	O	S	0	0
			152	96	25	29	2		
3	C	23	Total	C	N	O	S	0	0
			152	96	25	29	2		
3	D	23	Total	C	N	O	S	0	0
			152	96	25	29	2		
3	T	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
3	W	23	Total	C	N	O	S	0	0
			152	96	25	29	2		
3	d	16	Total	C	N	O	S	0	0
			108	69	18	19	2		
3	h	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
3	i	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
3	r	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
3	t	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		

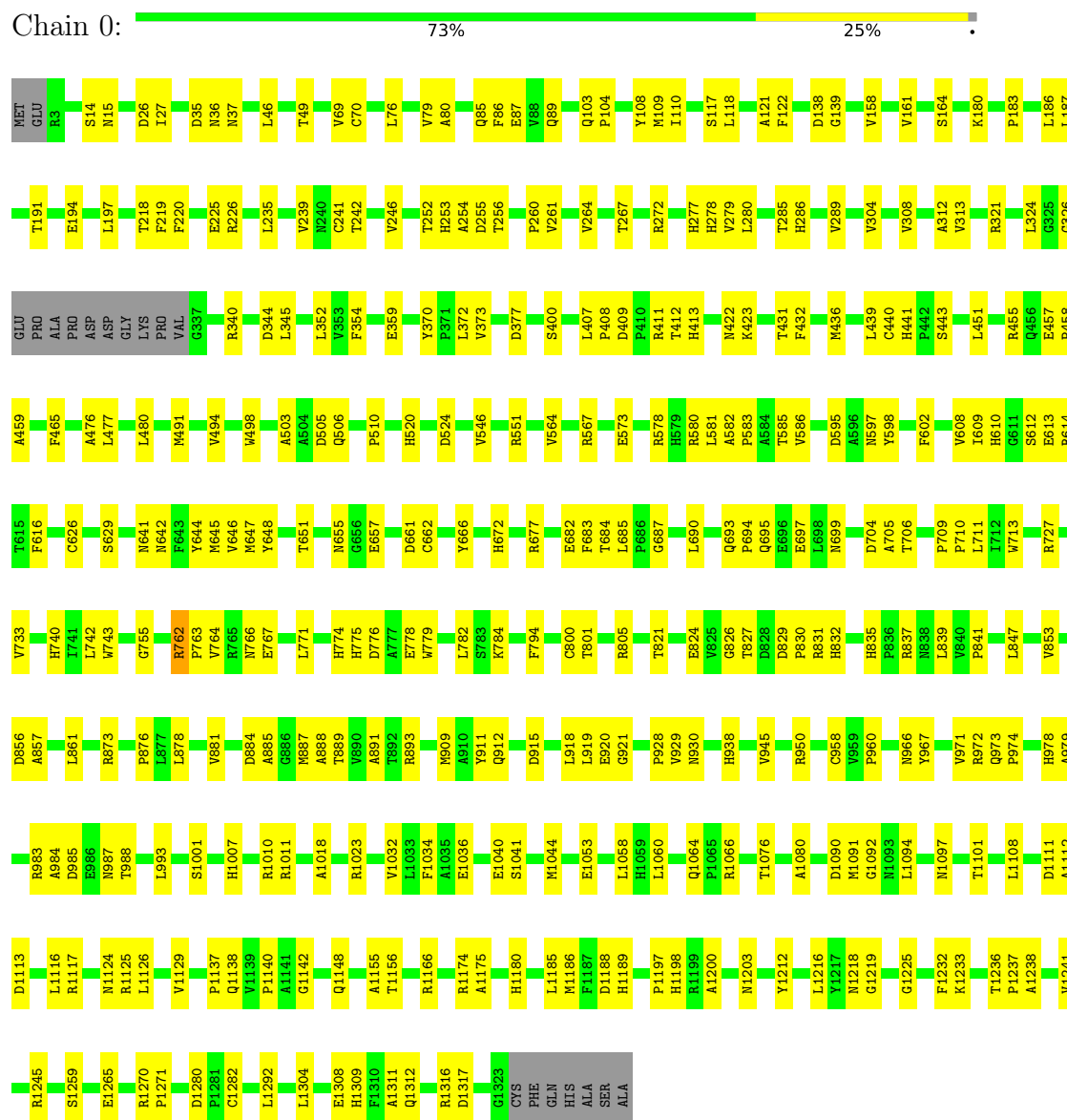
- Molecule 4 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	F	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	G	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	H	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	I	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	J	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	K	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	L	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	M	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	N	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	O	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	P	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	Q	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	R	91	Total 722	C 453	N 139	O 128	S 2	0	0
4	V	91	Total 722	C 453	N 139	O 128	S 2	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. 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: Major capsid protein



- Molecule 1: Major capsid protein

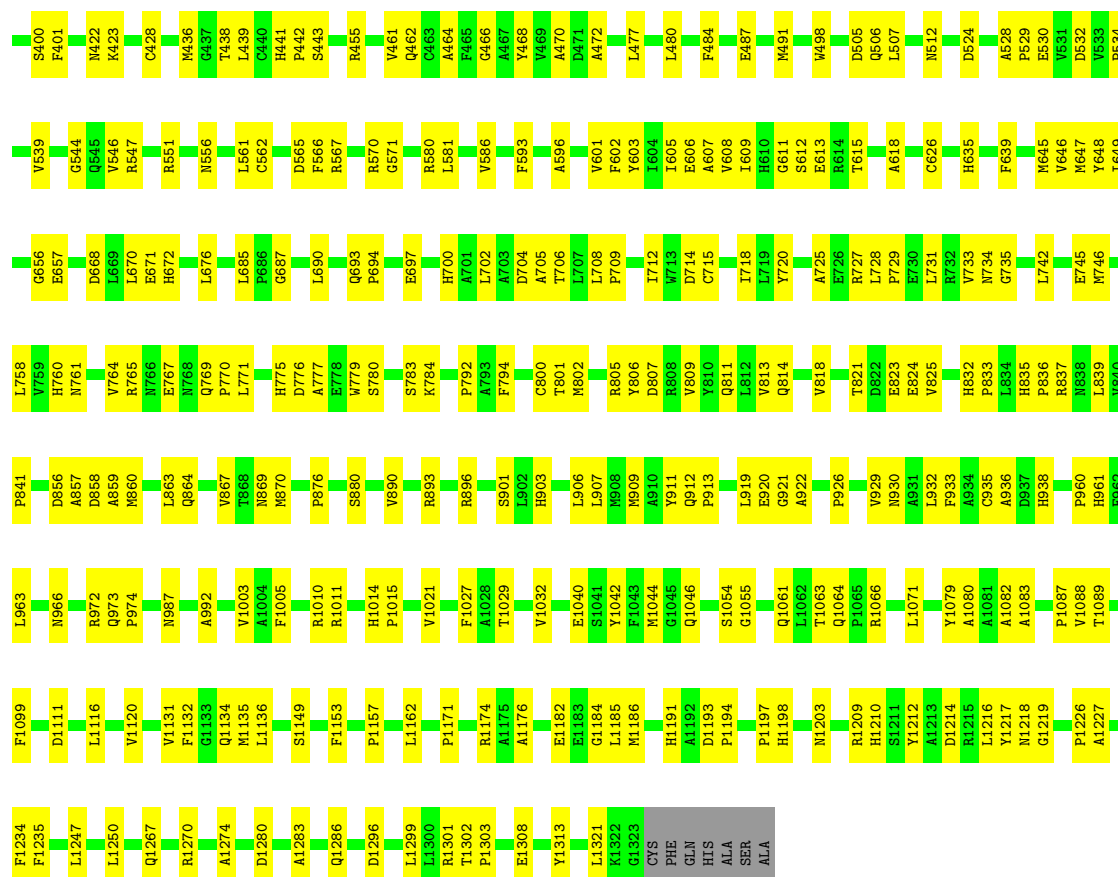


HI	L132	T267	D409	P534	H672	V804	H903	M1031	M1136	F1234	GLN
I6	S133	T268	P410	R551	V673	R805	L906	Y1042	L1136	F1235	HIS
E17	G134	H277	H413	R552	R677	Y806	Q911	F1043	P1137	T1236	ALA
V18	E135	H278	H416	R553	R678	V809	Q912	M1044	G1142	A1238	SER
H19	N136	V279	R419	R554	L679	L812	P913	M1047	L1143	ALA	ALA
R32	L137	Y293	H419	G555	D688	T815	N914	E1053	A1144	VAL	
S33	D138	G294	N422	P563	P689	V818	D915	G1056	R1145	ALA	
E42	H139	E295	K423	E573	L690	L781	A916	G1057	Q1148	ALA	
T49	T140	M296	N423	L574	G693	T821	T917	G1058	E1152	SER	
L60	T145	L303	C428	E573	P694	D822	L918	H1059	F1153	R1245	
L62	R146	V304	H429	L574	G695	E823	L919	L1060	I1154	G1255	
C70	R147	L307	V430	D577	E696	E924	F923	Q1061	A1155	P1260	
F73	L148	V308	T431	R578	E697	V825	F924	L1062	T1156	T1261	
P74	I151	F312	F432	H579	L698	L581	Y925	P926	S1159	S1262	
E75	I154	A312	F433	L581	H699	D829	A927	R1066	L1182	E1265	
L76	A155	V313	H434	V589	H700	P830	A931	A1067	R1172	F1268	
S77	R156	N315	T438	A596	L702	H832	N930	M1068	G1173	K1269	
Y78	V157	G326	C440	N597	L708	L834	H938	Y1079	A1175	R1270	
V79	Q159	ALA	H441	F602	C715	H835	V945	A1080	A1176	P1271	
A80	A160	PRO	P442	E606	D716	P836	E948	L1084	G1177	V1272	
E81	L162	ASP	S443	B611	P717	V840	R948	R1085	L1185	G1273	
V88	S164	ASP	L445	G611	R721	P841	E949	A1086	M1186	V1278	
Q89	F165	GLY	D448	R614	R729	N842	R950	P1087	F1187	V1279	
I93	E166	LYS	A449	T615	P729	S843	N966	V1088	D1188	D1281	
A94	D171	PRO	G466	F616	N734	L844	T970	T1089	H1189	C1282	
R95	P183	V336	G466	C626	L758	F848	Q971	D1090	A1189	Q1286	
D96	L186	L345	Y468	H635	V759	A857	R972	M1091	H1198	P1291	
D102	L192	L352	L477	F639	H760	D858	Q973	G1092	H1198	L1292	
Q103	Y193	F353	W488	V640	N761	L861	R983	M1097	T1201	D1296	
R112	L206	F354	P489	N641	R762	L862	A984	L1098	A1202	L1299	
L113	L210	E359	P489	N642	Q769	N869	D985	F1099	N1203	L1300	
D114	L219	Y363	P493	F643	H772	E872	E986	M1107	P1204	L1304	
R115	F219	Q367	V494	Y644	P773	R873	N987	L1108	W1205		
L118	K228	G374	R495	N645	H774	T874	M994	D1111	Q1208	E1307	
A120	D229	N375	W498	V646	H775	T875	S1001	A1112	S1211	E1308	
A121	A230	L376	Q506	Y648	D776	P876	Y1001	L1116	Y1212	H1309	
F122	V231	D377	N512	I649	W779	A879	R1010	L1120	A1213	F1310	
S123	L232	F380	L519	T651	L782	S880	L1019	V1120	D1214	A1311	
I124	S245	V381	H520	Y652	V791	V881	T1020	Y1217	Y1217	Q1312	
A125	V246	F381	D524	L653	P792	A882	T1021	N1218	G1219	D1317	
V126	D255	V386	V531	P659	R796	M887	V1022	R1125	Q1220	L1321	
L129	V261	F387	D532	C662	C800	V890	R1023	A1127	P1230	K1322	
G130	L131	R388	V533	L669	T801	R896	Q1024	F1027	K1233	G1323	
		P403						Q1134		CYS	
										PHE	

- Molecule 1: Major capsid protein

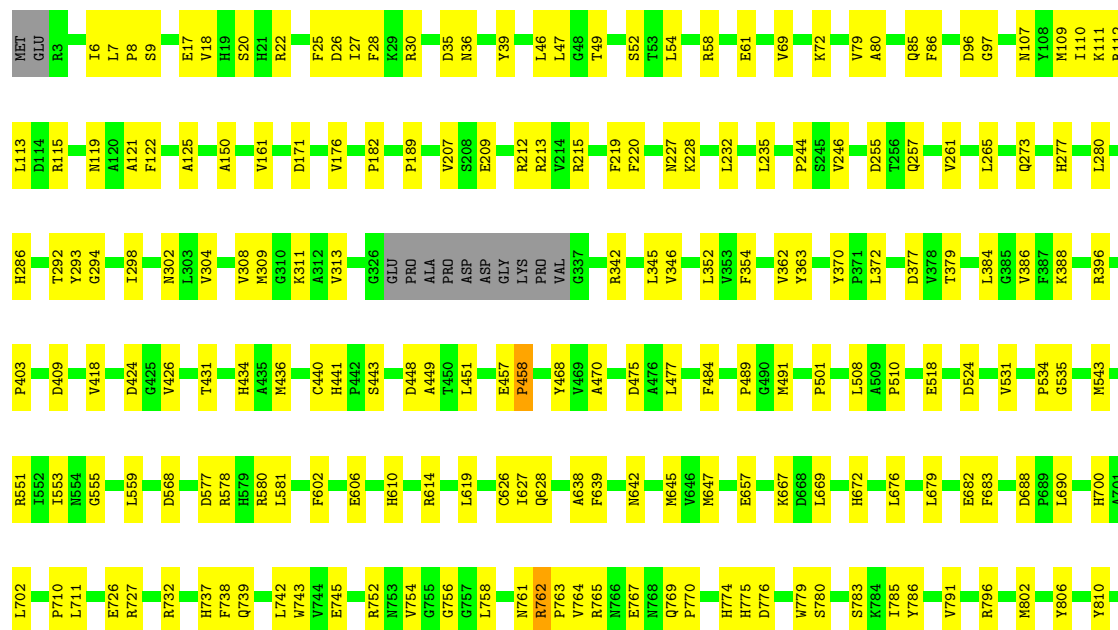
Chain S:  70% 27%

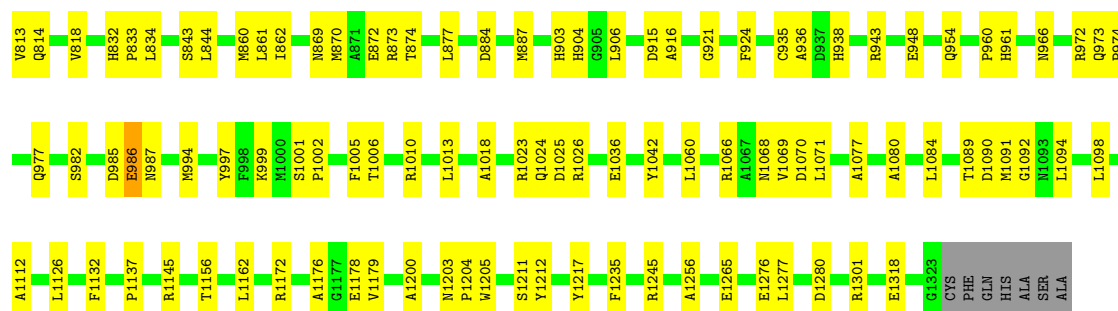
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LVS	P183	VAL	ASN	MET	ASP	ASP	VAL	ALA	ARG	TYR	LEU	LEU	GLY	GLY	PRO	ALA	PRO	VAL	GLY	S338	A339	R340	L345	D350	R351	L352	Y353	F354	Y363	T366	Y370	P371	L372	N375	M382	V386	F387	K388	R393	R396	H397



● Molecule 1: Major capsid protein

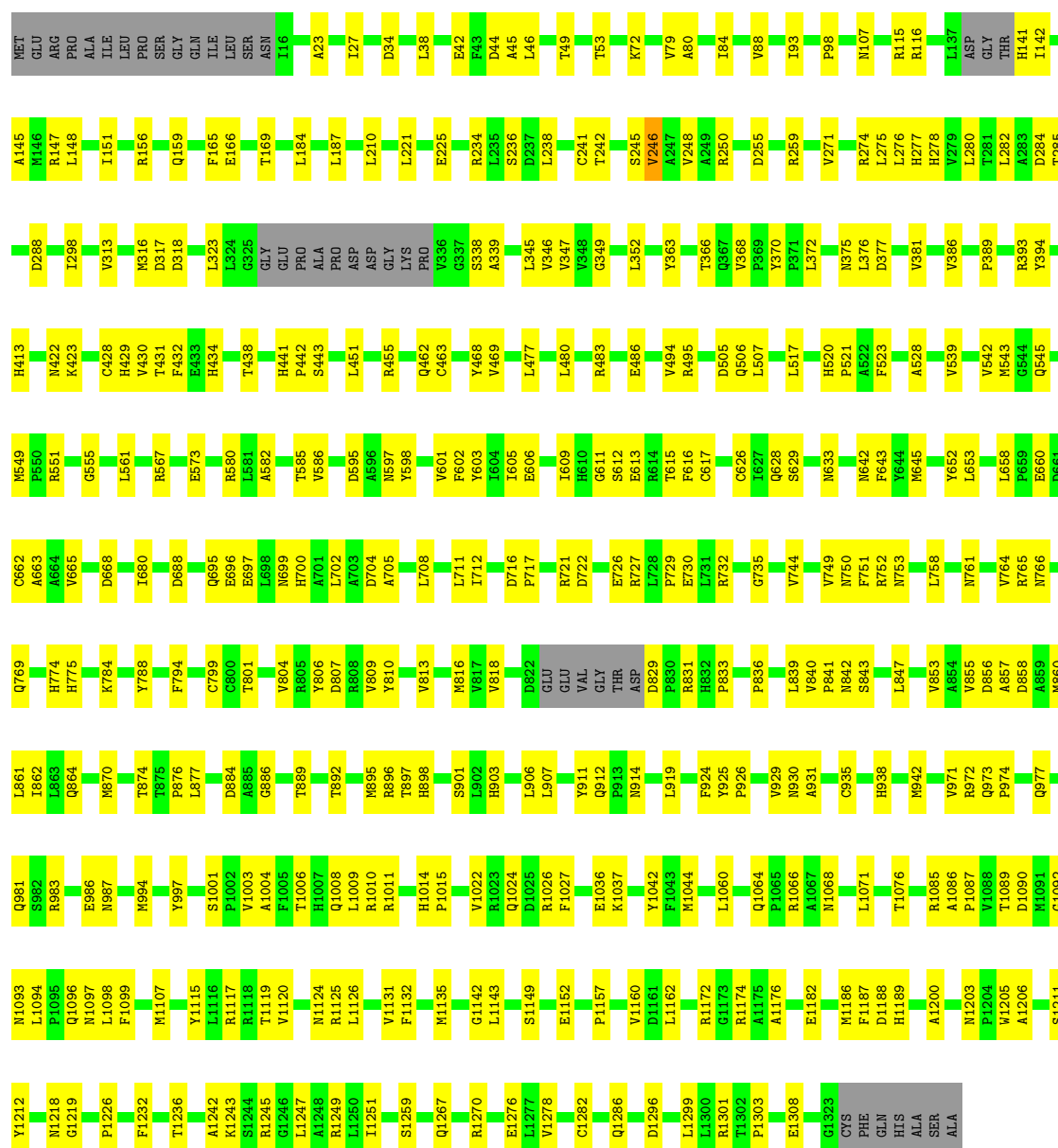
Chain U: 76% 22%





• Molecule 1: Major capsid protein

Chain a: 70% 27%



• Molecule 1: Major capsid protein

Response	Percentage
Yes	54%
No	31%
Don't know	15%



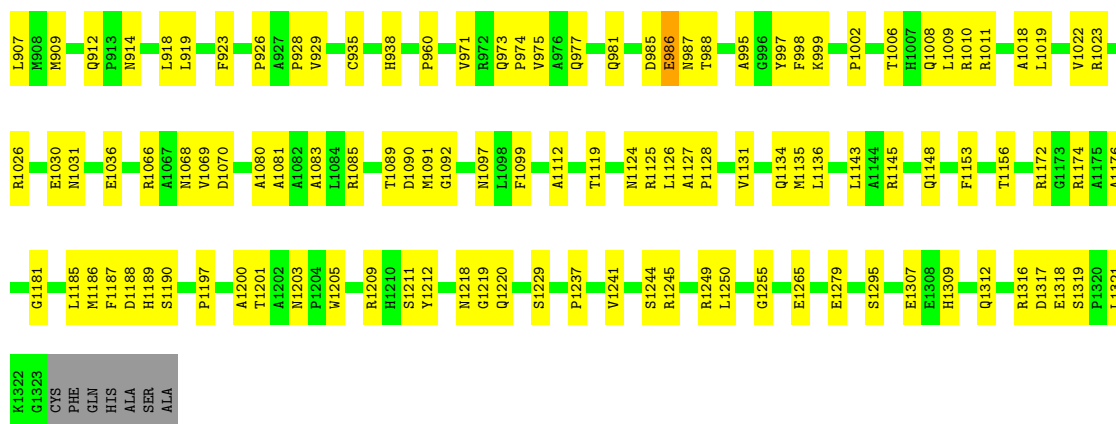
Chain f: 78% 21%





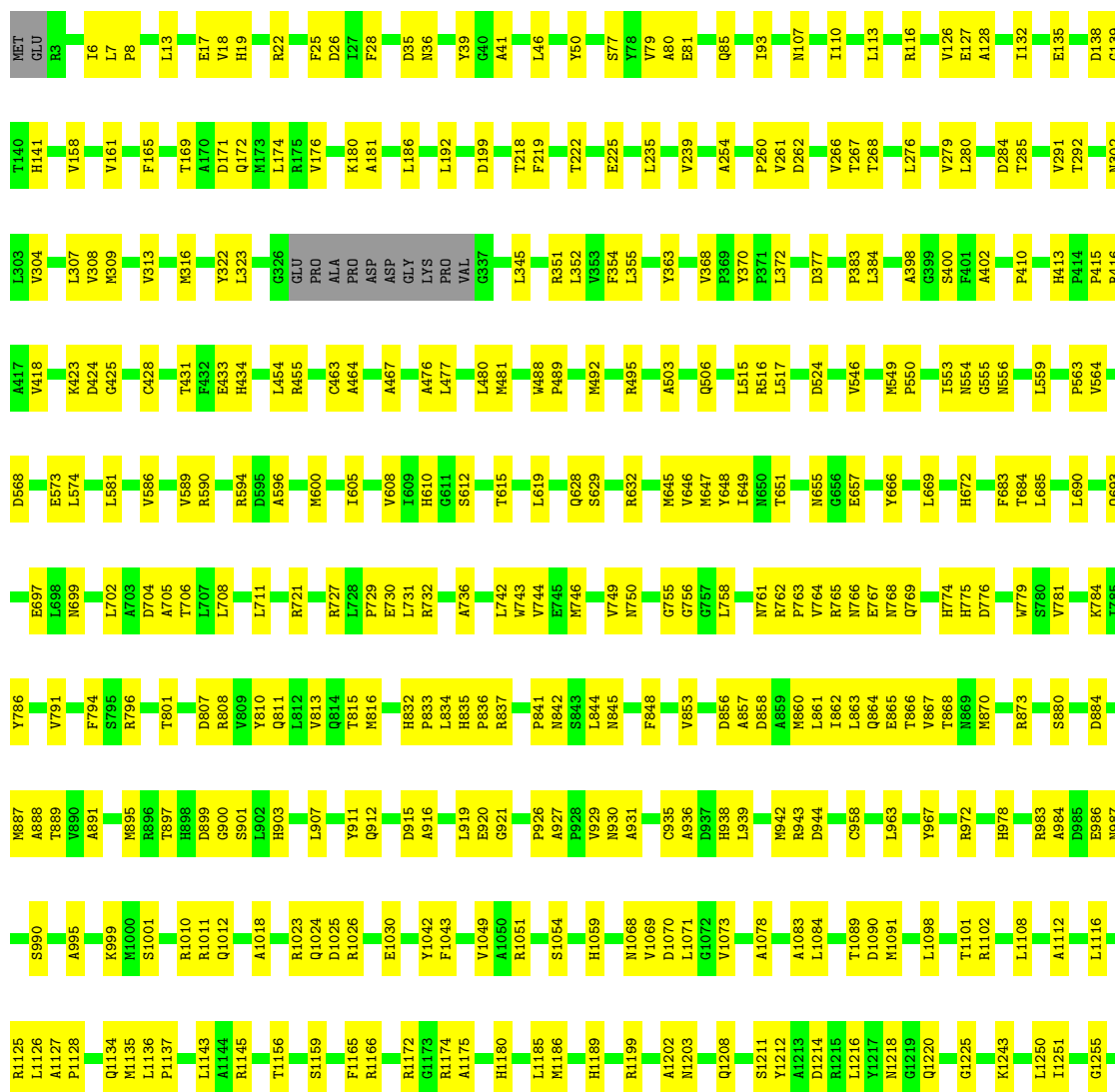
Response	Percentage
Democracy	72%
Dictatorship	27%





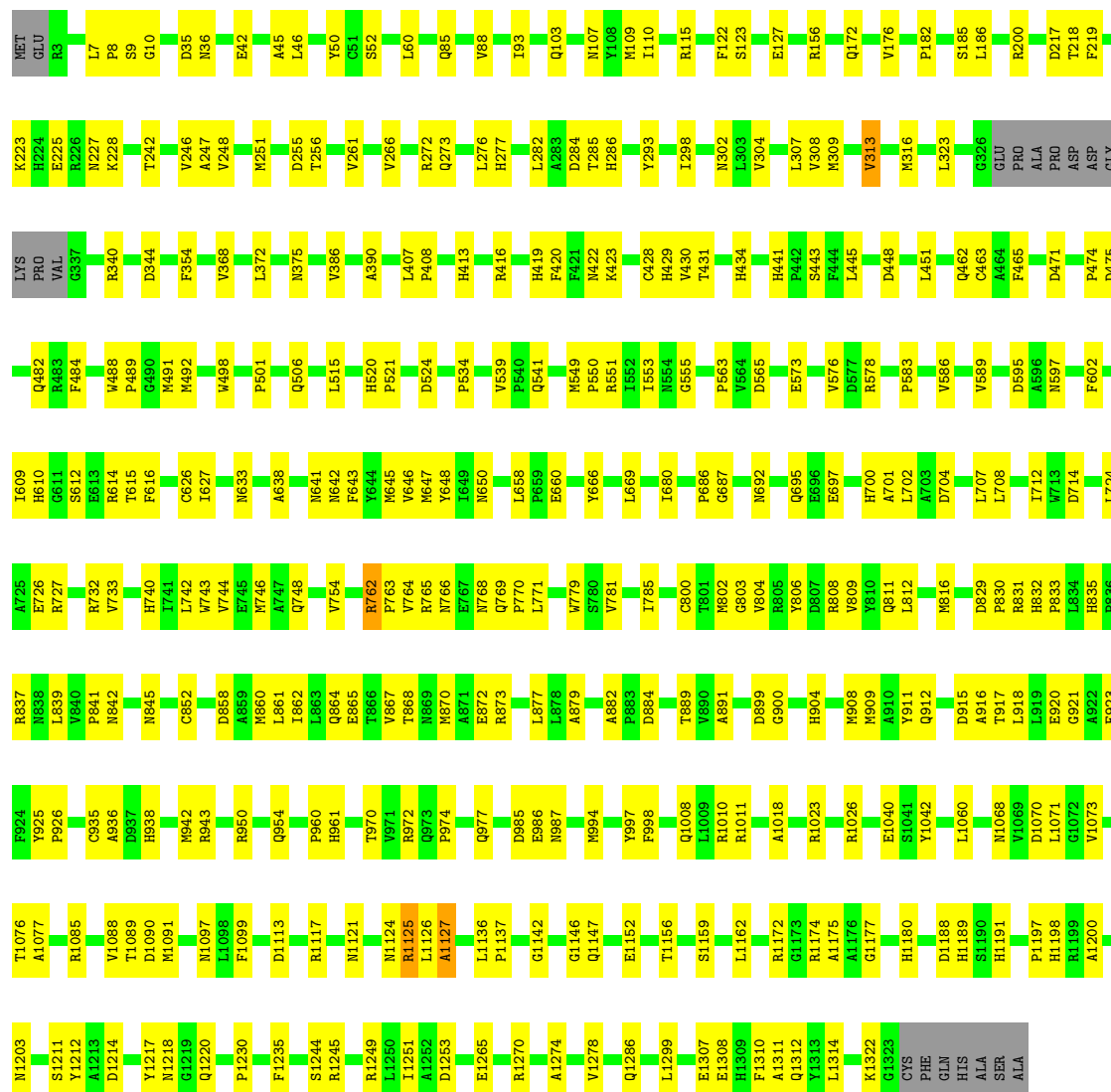
• Molecule 1: Major capsid protein

Chain m: 71% 28%

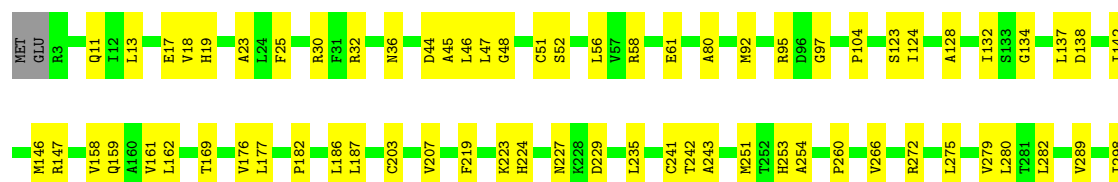


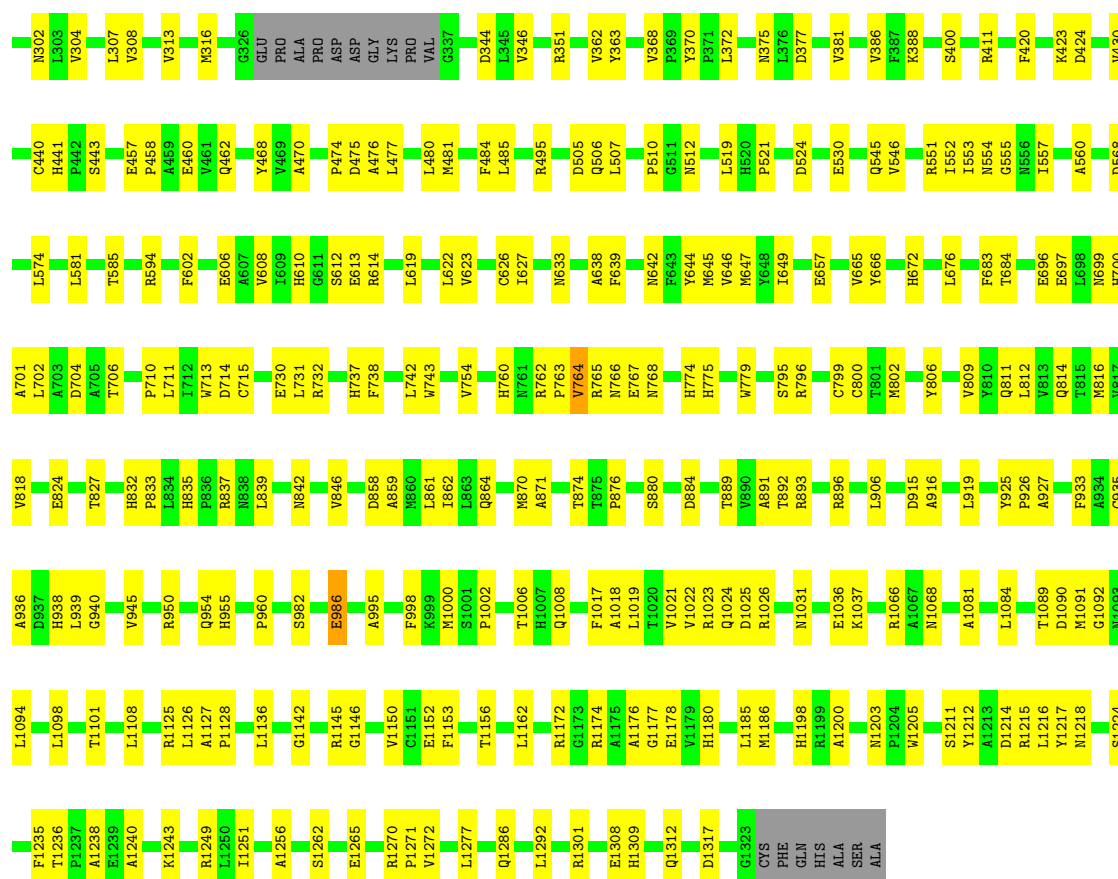


• Molecule 1: Major capsid protein

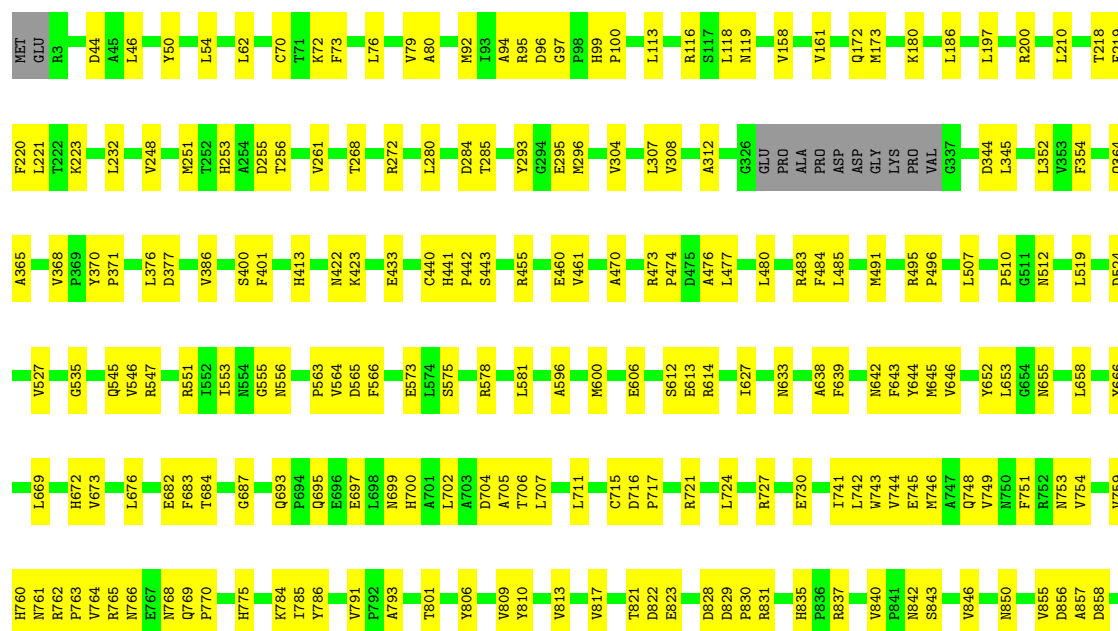


• Molecule 1: Major capsid protein



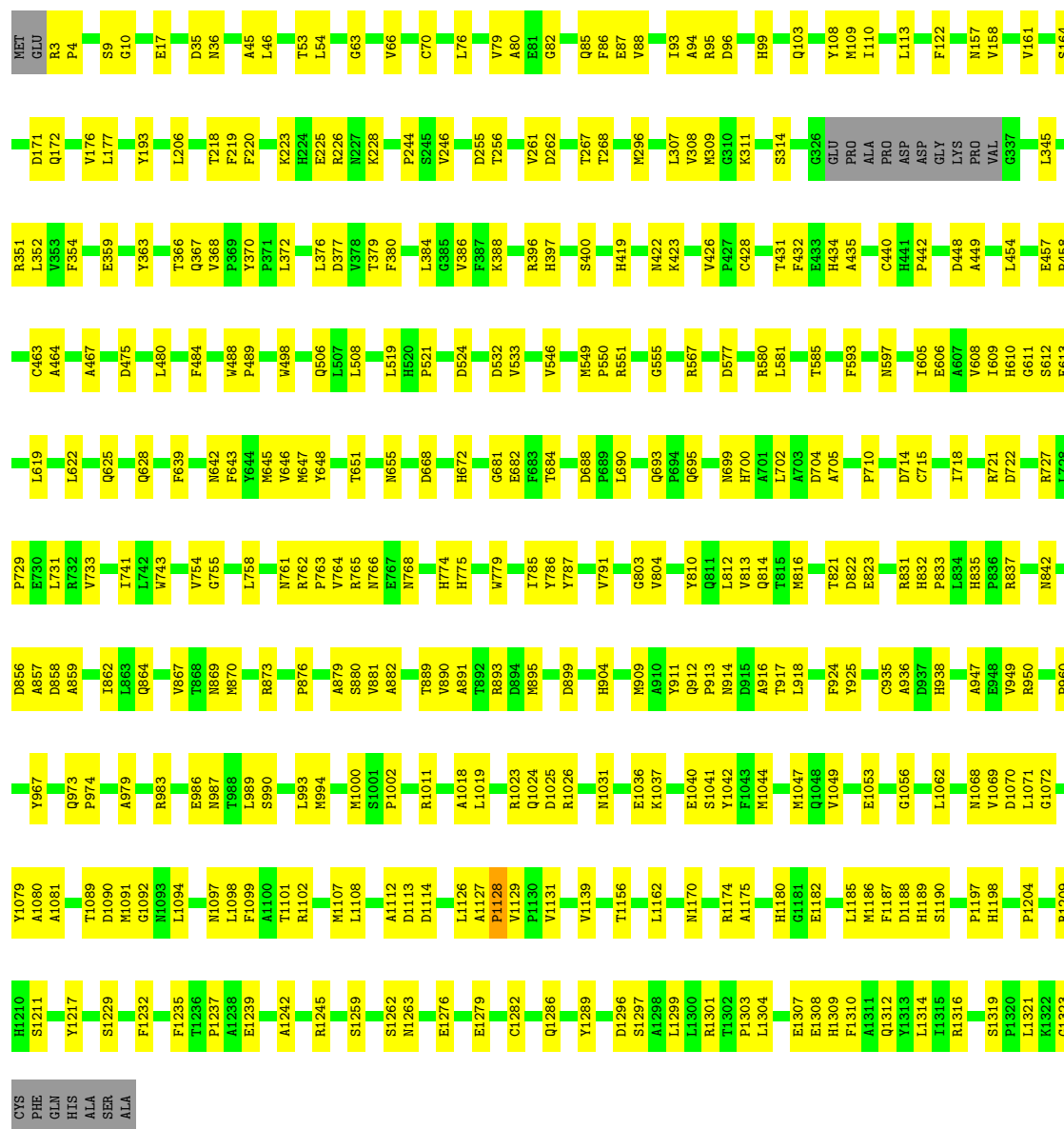


● Molecule 1: Major capsid protein



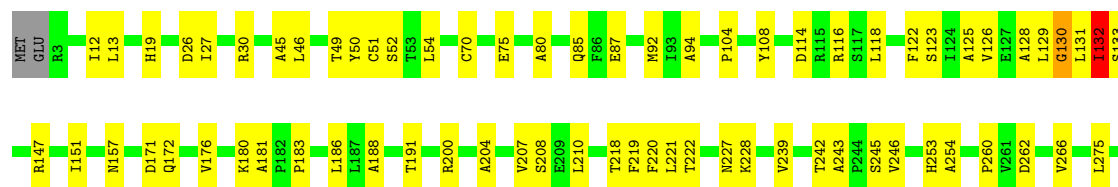
• Molecule 1: Major capsid protein

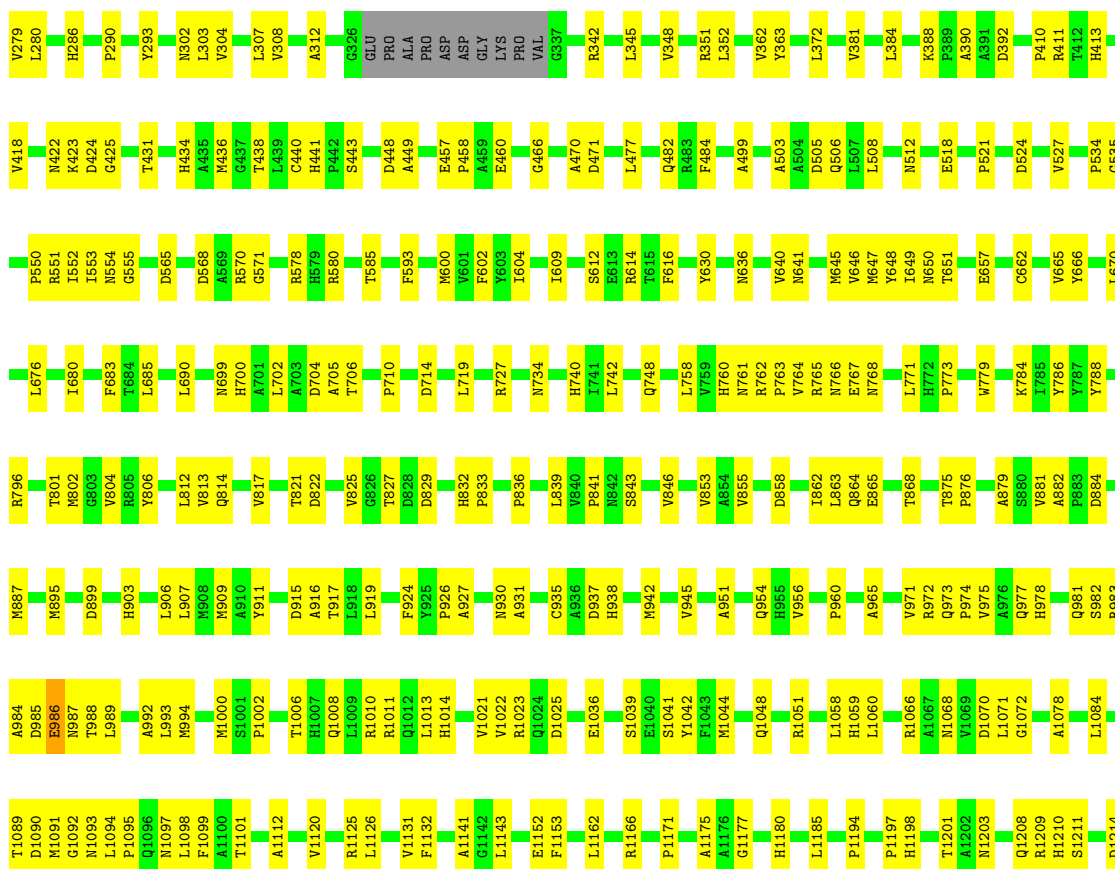
Chain w:  72% 27%



• Molecule 1: Major capsid protein

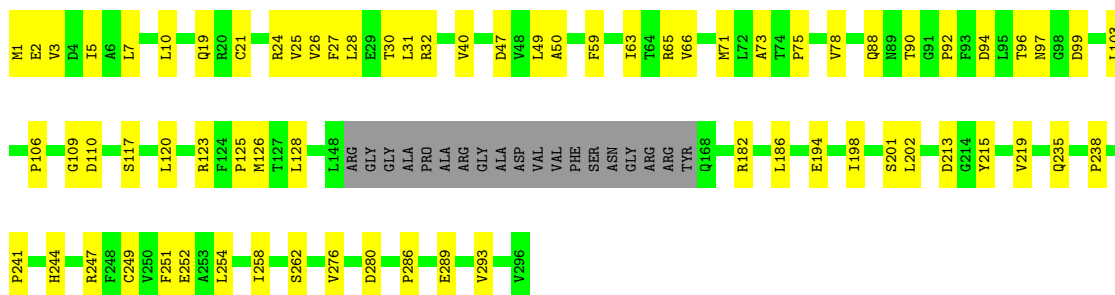
Chain y:  70% 28%





• Molecule 2: Triplex capsid protein 2

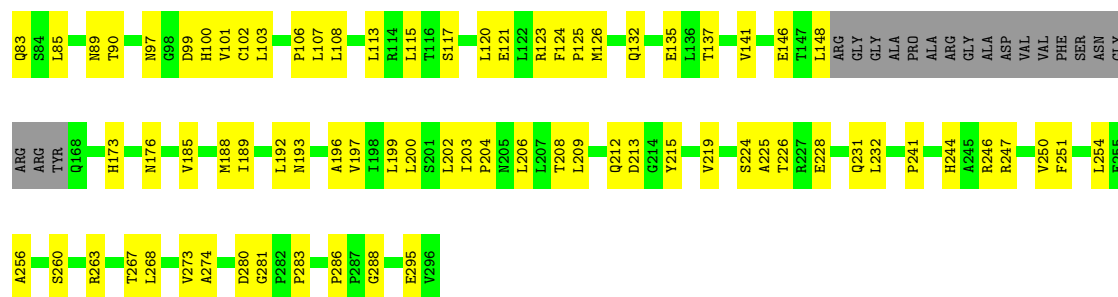
Chain 1: 70% 24% 6%



• Molecule 2: Triplex capsid protein 2

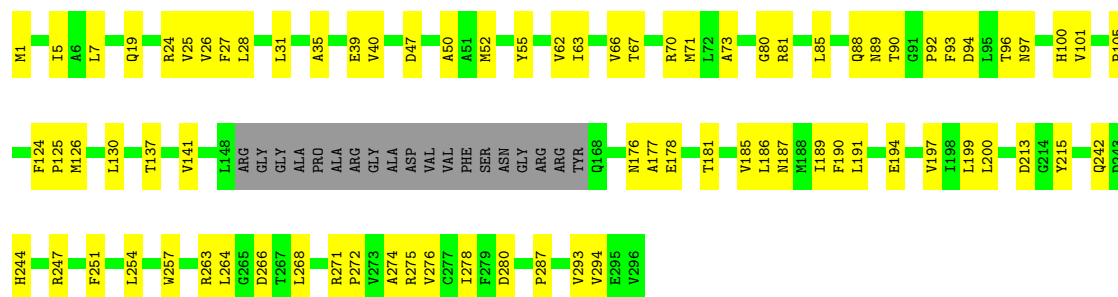
Chain 2: 55% 38% 6%





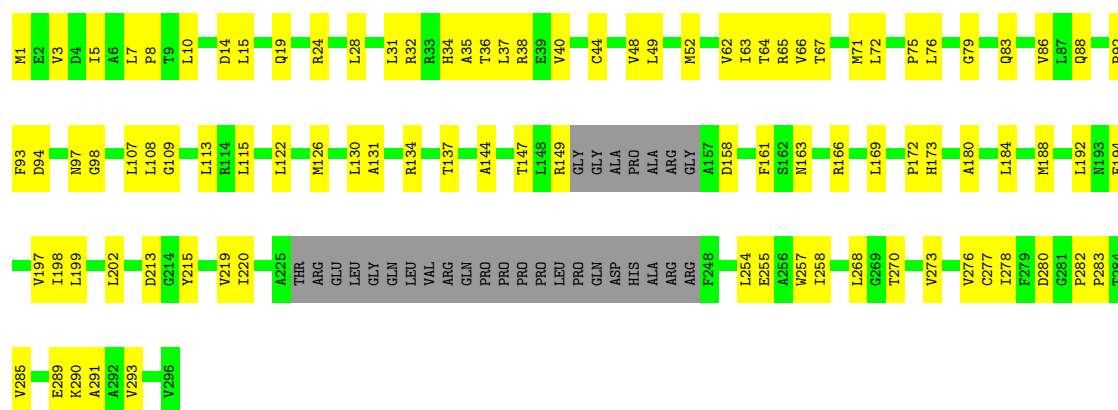
• Molecule 2: Triplex capsid protein 2

Chain 3: 67% 27% 6%



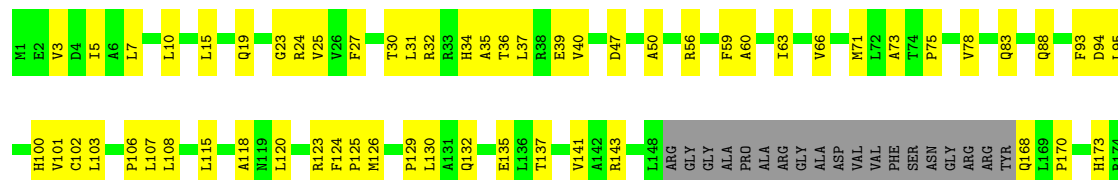
• Molecule 2: Triplex capsid protein 2

Chain j: 58% 32% 10%



• Molecule 2: Triplex capsid protein 2

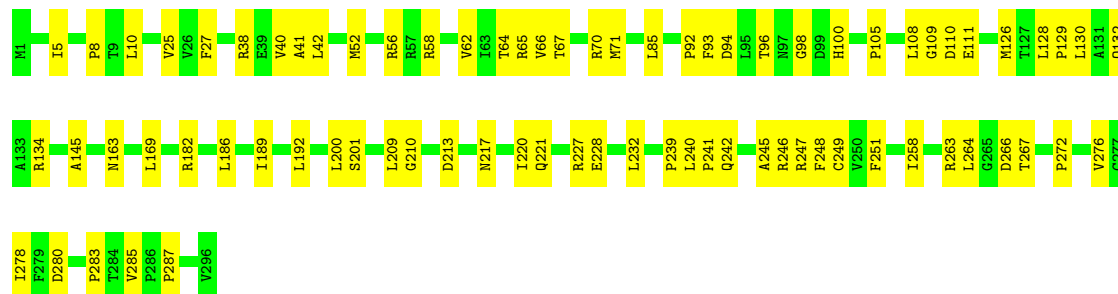
Chain k: 56% 38% 6%





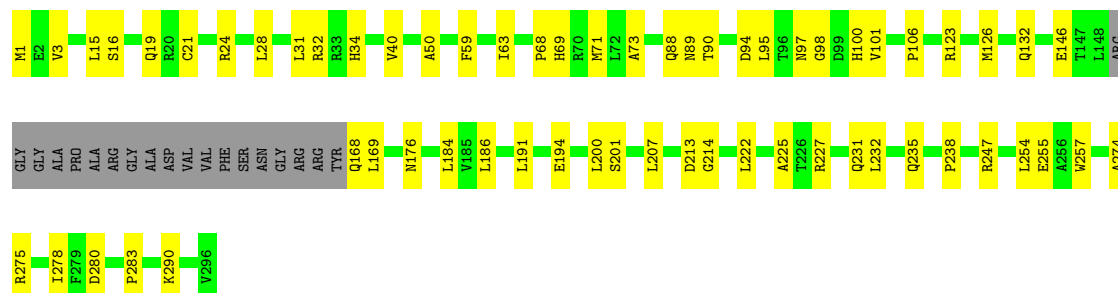
• Molecule 2: Triplex capsid protein 2

Chain o: 74% 26%



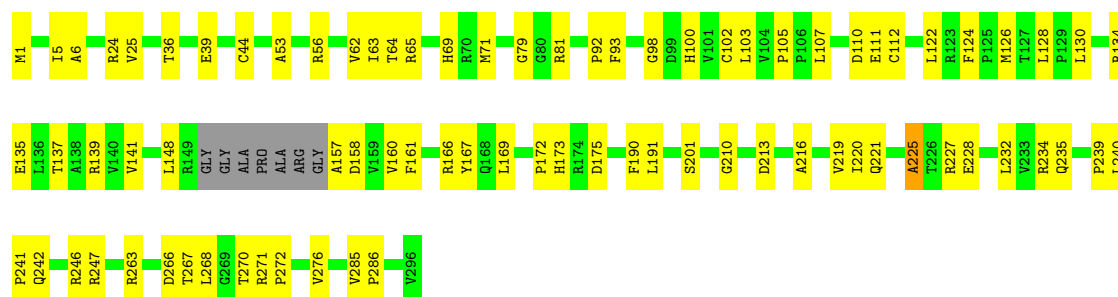
• Molecule 2: Triplex capsid protein 2

Chain s: 73% 21% 6%



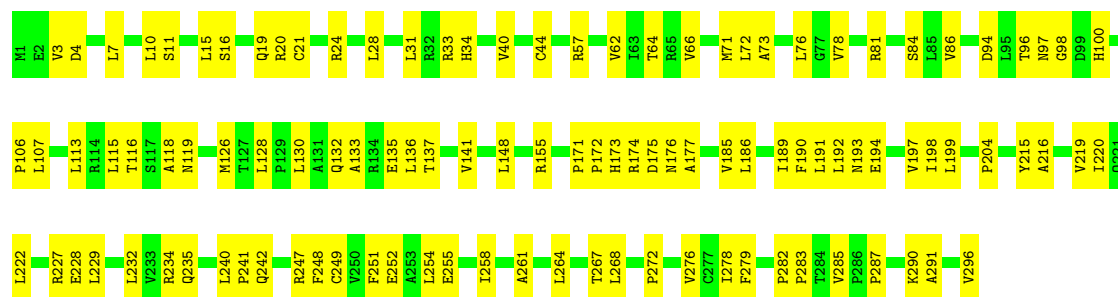
• Molecule 2: Triplex capsid protein 2

Chain v: 70% 27%

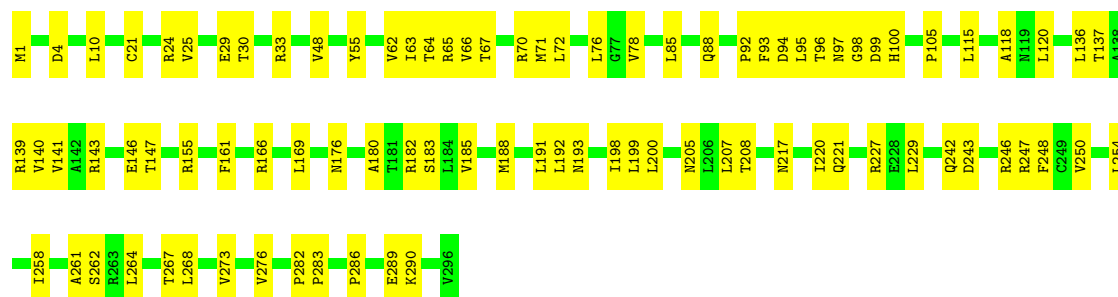


• Molecule 2: Triplex capsid protein 2

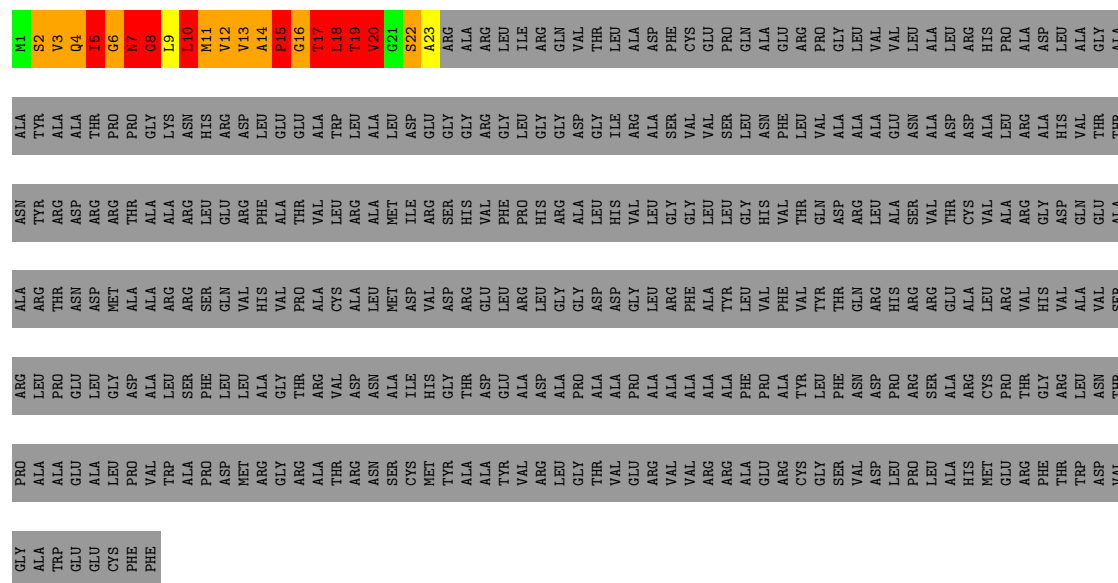
Chain x: 64% 36%



• Molecule 2: Triplex capsid protein 2



• Molecule 3: Triplex capsid protein 1



• Molecule 3: Triplex capsid protein 1



GLY	PRO	ARG	ALA	ASN	ALA	ASN	ALA	TYR	ALA
ALA	ALA	LEU	ARG	THR	THR	ARG	THR	TYR	ALA
TRP	ALA	PRO	GLU	ASN	ASN	ASP	ARG	ARG	ALA
GLU	GLU	LEU	LEU	ASP	ASP	MET	ASP	THR	THR
CYS	LEU	GLY	ASP	GLY	ALA	ALA	PRO	PRO	PRO
PHE	PRO	ASP	ALA	ALA	ARG	ALA	ALA	GLY	GLY
PHE	TRP	LEU	LEU	LEU	ARG	ARG	LYS	ASN	ASN
	ALA	SER	PHE	PHE	ARG	ARG	ASN	HIS	HIS
	PRO	LEU	LEU	GLN	VAL	GLN	LEU	ASP	ARG
	MET	LEU	ALA	HIS	VAL	PHE	GLU	ASP	ASP
	GLY	GLY	THR	PRO	VAL	ALA	ALA	GLU	GLU
	ARG	THR	ARG	ALA	VAL	VAL	ALA	TRP	ALA
	ALA	VAL	VAL	CYS	CYS	LEU	TRP	ALA	TRP
	THR	ASP	ASP	ALA	ALA	ALA	ALA	ALA	ALA
	ARG	ASP	ASN	ASP	ALA	ALA	ALA	LEU	LEU
	ASN	ASN	ASP	LEU	ALA	ALA	ALA	ASP	ASP
	SER	ILE	ILE	MET	MET	ILE	ILE	ASP	ASP
	CYS	ILE	ASP	ASP	ASP	ASP	ASP	GLY	GLY
	MET	HIS	GLY	VAL	ARG	HIS	HIS	GLY	GLY
	TYR	GLY	THR	ASP	ASP	HIS	ASP	GLY	GLY
	ALA	THR	ALA	ASP	GLU	VAL	ASP	GLY	GLY
	ALA	GLU	GLU	GLU	LEU	PHE	PHE	GLY	GLY
	VAL	ALA	ALA	ALA	LEU	PRO	ILE	ILE	ILE
	ARG	GLU	PRO	GLY	GLY	VAL	ARG	ARG	ALA
	VAL	ALA	ALA	ALA	LEU	LEU	ALA	SER	ALA
	VAL	ALA	ALA	ALA	PHE	GLY	GLY	VAL	SER
	ARG	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
	ARG	ALA	PHE	ALA	LEU	HIS	ASN	PHE	ASN
	GLU	PRO	PRO	PRO	VAL	VAL	GLY	LEU	ASN
	ALA	ALA	LEU	LEU	TYR	VAL	VAL	LEU	PHE
	GLY	LEU	LEU	LEU	TYR	THR	GLN	VAL	VAL
	SER	PHE	PHE	ASN	THR	ARG	ALA	ALA	ALA
	VAL	VAL	ASN	GLN	GLN	ARG	ARG	ALA	ALA
	ASP	ASP	ASP	THR	LEU	CYS	VAL	ALA	ALA
	LEU	PRO	PRO	HIS	ALA	LEU	VAL	ASP	ASP
	PRO	ARG	ARG	ARG	ARG	ALA	ALA	LEU	LEU
	LEU	SER	SER	THR	THR	ARG	ARG	ASP	ASP
	ALA	ALA	ALA	GLU	GLU	GLY	GLY	ALA	ALA
	ALA	HIS	HIS	ALA	VAL	HIS	VAL	HIS	HIS
	MET	MET	CYS	PRO	ARG	ALA	VAL	VAL	VAL
	GLU	ARG	THR	THR	THR	THR	VAL	LEU	LEU
	PHE	PHE	PHE	GLY	GLY	HIS	VAL	ASP	ASP
	THR	THR	ARG	VAL	VAL	ALA	GLN	THR	HIS
	TRP	TRP	LEU	LEU	ALA	ALA	ALA	THR	VAL
	VAL	VAL	ASN	THR	VAL	SER	ALA	THR	THR

- Molecule 3: Triplex capsid protein 1

Chain D: 94%

GLY ALA TRP GLU GLU CYS PHE PHE	PRO	ARG	ALA	ASN	ALA
	ALA	LEU	ARG	TYR	ALA
	ALA	PRO	THR	ARG	TYR
	GLU	GLU	ASN	ASP	ALA
	ALA	LEU	ASN	ARG	THR
	LEU	GLY	MET	ARG	PRO
	PRO	ASP	ALA	THR	PRO
	VAL	ALA	ALA	THR	GLY
	TRP	LEU	ARG	ARG	LYS
	ALA	SER	ARG	ARG	L10
ASP	PHE	SER	LEU	M11	
MET	LEU	GLN	GLU	M12	
GLY	ALA	VAL	ARG	V13	
ARG	ALA	HIS	PHE	A14	
GLY	THR	VAL	ALA	P15	
ALA	THR	PRO	THR	G16	
ALA	ARG	ALA	VAL	T17	
THR	VAL	CYS	LEU	L18	
ARG	ASP	ALA	ARG	T19	
ASN	ASN	LEU	ALA	V20	
SER	ILE	MET	ILE	G21	
CYS	ILE	ASP	ASP	S22	
MET	VAL	VAL	ARG	A23	
TYR	GLY	ASP	SER	ARG	
ALA	THR	GLU	HIS	ALA	
ALA	ASP	GLU	VAL	ARG	
TYR	GLU	LEU	PHE	GLY	
VAL	ALA	ARG	PRO	ILE	
ARG	ASP	LEU	HIS	GLY	
LEU	ALA	GLY	ARG	GLN	
GLY	PRO	ALA	LEU	ASP	
VAL	ALA	ARG	GLY	VAL	
VAL	ALA	PHE	GLY	CYS	
ARG	ALA	ALA	LEU	GLU	
ARG	ALA	TYR	LEU	SER	
ALA	PHE	LEU	GLY	GLN	
GLU	PRO	VAL	HIS	ASN	
ARG	ALA	PHE	VAL	PHE	
CYS	TYR	VAL	THR	GLU	
GLY	LEU	TYR	GLN	VAL	
SER	PHE	THR	ASP	ALA	
VAL	ASN	GLN	ARG	LEU	
ASP	ASP	ARG	LEU	ALA	
LEU	PRO	HIS	ALA	GLU	
PRO	ARG	ARG	SER	ASN	
LEU	SER	ARG	VAL	ALA	
ALA	ALA	GLU	THR	LEU	
HIS	ARG	ALA	CYS	ASP	
MET	CYS	LEU	VAL	HIS	
GLU	PRO	ARG	ALA	PRO	
ARG	THR	VAL	VAL	ARG	
PHE	GLY	HIS	GLY	ALA	
THR	ARG	VAL	ASP	HIS	
TRP	LEU	ALA	GLN	VAL	
ASP	ASN	VAL	GLU	GLY	
VAL	THR	SER	ALA	THR	

- Molecule 3: Triplex capsid protein 1

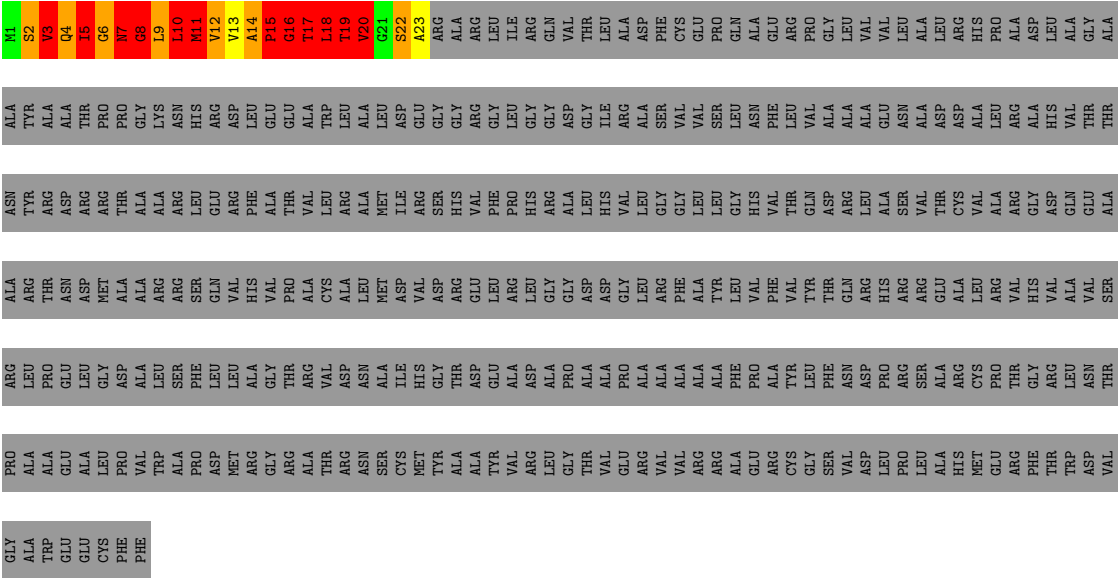
Chain T: 57% 28% 0 11%

L159	G160	H161	V162	T163	Q164	V170	T171	C172	V173	A174	D177	Q178	M186	C198	D204	R205	E206	L209	D213	F217	L220	V221	F222	Z223	Z224	T225	Q226	R227	R230	R234	V235	H236	S240	E241	L242	P243	E244	L245	L249	L252	T256	P257	C258						
D73	L74	E75	W78	L81	D82	GLU	GLY	GLY	ARG	GLY	LEU	GLY	GLY	ASP	GLY	ILE	R94	A95	S96	V97	V98	S99	N109	A110	D111	A113	L114	R115	A116	H117	V118	T119	T120	N121	Y122	R123	D124	R126	R130	R133	F134	A135	T136	V137	L138	R139	I142	V154	C155
MET	SER	VAL	ILE	GLY	ASN	LEU	MET	VAL	VAL	ALA	PRO	GLY	THR	LEU	THR	VAL	SER	ALA	R24	A25	R26	L27	I28	T32	L33	A34	D35	F36	C37	E38	P39	Q40	A41	E42	R43	P44	V47	V48	H53	P54	A55	A58	A61	T65	P66	P67	H71	D72	



• Molecule 3: Triplex capsid protein 1

Chain W:  94%



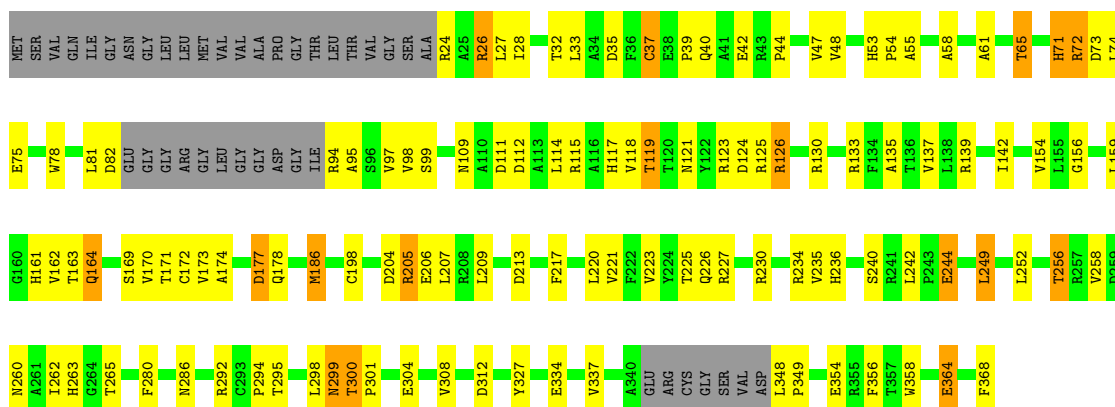
• Molecule 3: Triplex capsid protein 1

Chain d:  96%



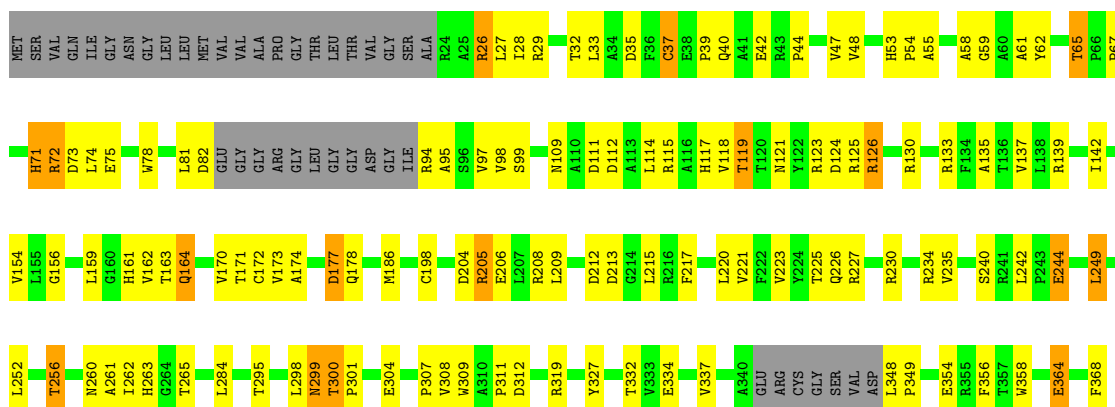
• Molecule 3: Triplex capsid protein 1

Chain h:  57% 28% 5% 11%



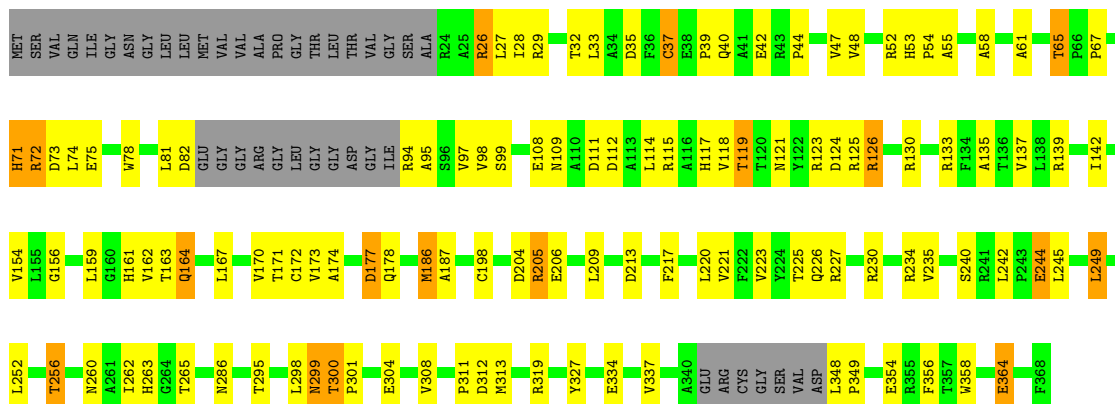
• Molecule 3: Triplex capsid protein 1

Chain i: 55% 29% 11%



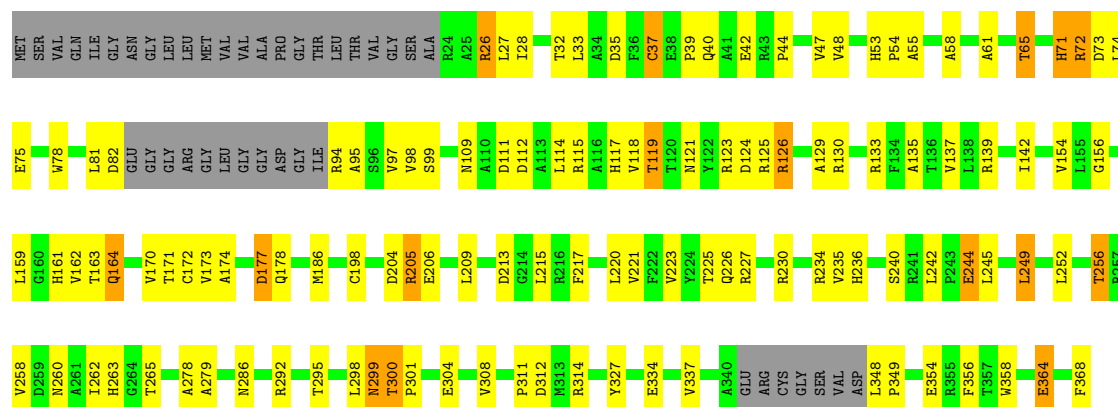
• Molecule 3: Triplex capsid protein 1

Chain r: 56% 28% 5% 11%

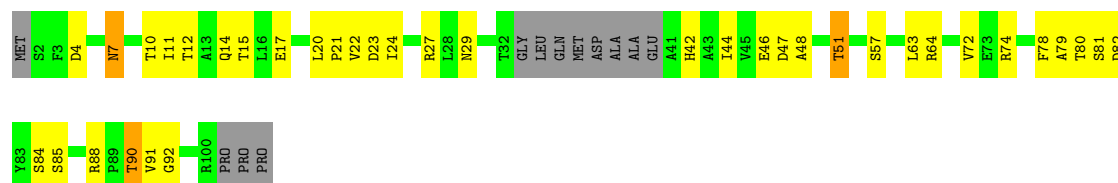


• Molecule 3: Triplex capsid protein 1

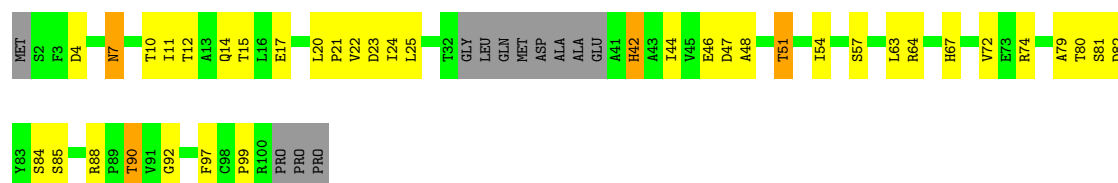
Chain t: 56% 29% 11%



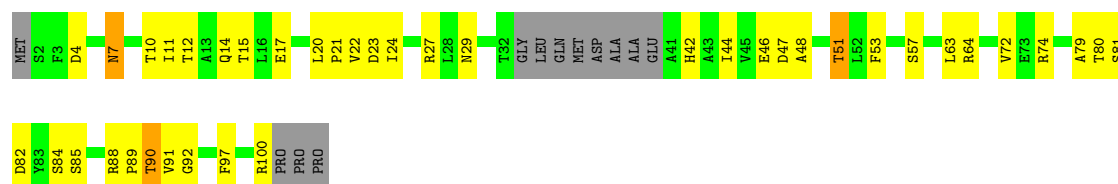
• Molecule 4: Small capsomere-interacting protein



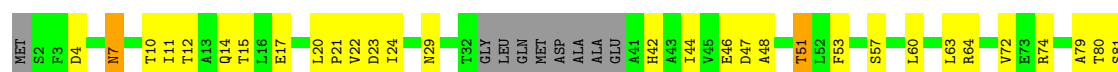
• Molecule 4: Small capsomere-interacting protein



• Molecule 4: Small capsomere-interacting protein



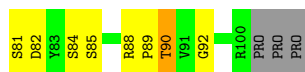
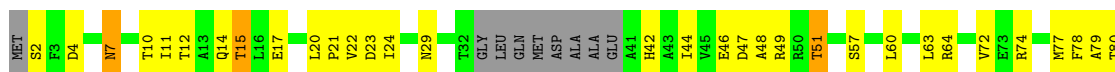
• Molecule 4: Small capsomere-interacting protein





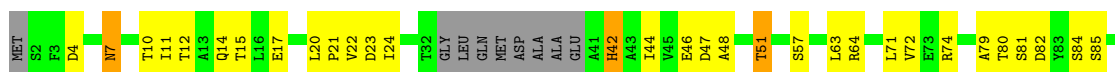
- Molecule 4: Small capsomere-interacting protein

Chain I: 50% 35% 12%



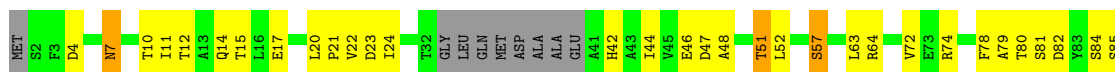
- Molecule 4: Small capsomere-interacting protein

Chain J: 54% 30% 12%



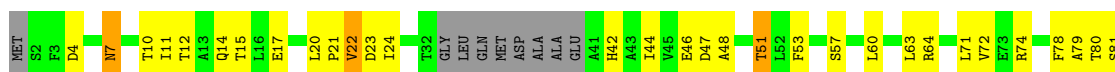
- Molecule 4: Small capsomere-interacting protein

Chain K: 52% 32% 12%



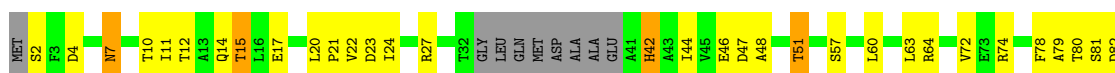
- Molecule 4: Small capsomere-interacting protein

Chain L: 51% 33% 12%



- Molecule 4: Small capsomere-interacting protein

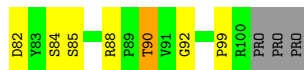
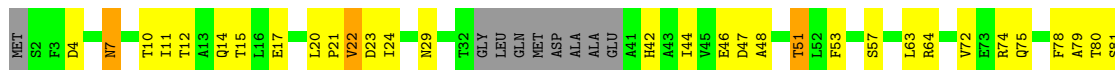
Chain M: 50% 33% 5% 12%





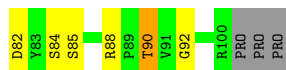
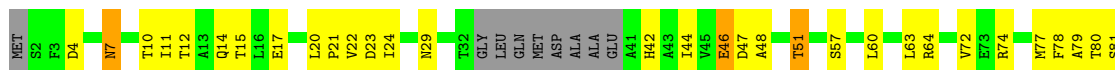
- Molecule 4: Small capsomere-interacting protein

Chain N: 51% 33% 12%



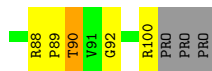
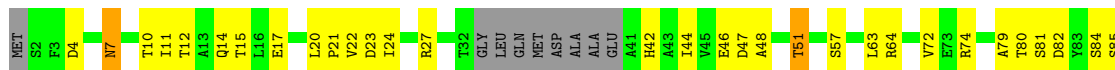
- Molecule 4: Small capsomere-interacting protein

Chain O: 52% 32% 12%



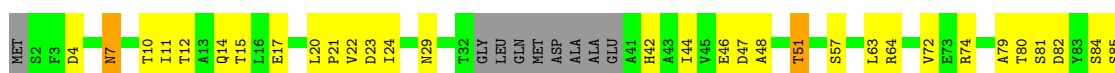
- Molecule 4: Small capsomere-interacting protein

Chain P: 53% 32% 12%



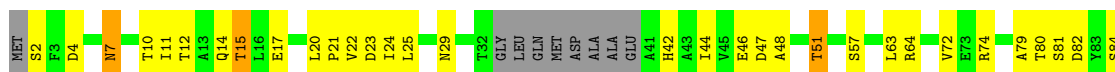
- Molecule 4: Small capsomere-interacting protein

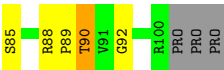
Chain Q: 54% 31% 12%



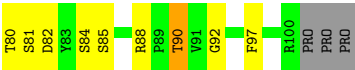
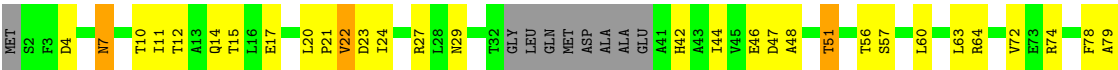
- Molecule 4: Small capsomere-interacting protein

Chain R: 52% 32% 12%





- Molecule 4: Small capsomere-interacting protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8899	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k 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	0.25	0/10384	0.40	0/14158
1	A	0.30	0/10366	0.50	10/14132 (0.1%)
1	S	0.22	0/10229	0.40	0/13950
1	U	0.29	0/10384	0.42	1/14158 (0.0%)
1	a	0.24	0/10225	0.42	1/13938 (0.0%)
1	e	0.19	1/8938 (0.0%)	0.43	4/12175 (0.0%)
1	f	0.29	0/10384	0.42	0/14158
1	g	0.27	0/10379	0.42	0/14150
1	l	0.27	0/10384	0.41	0/14158
1	m	0.27	0/10384	0.42	0/14158
1	n	0.26	0/10384	0.41	0/14158
1	p	0.25	0/10384	0.40	0/14158
1	q	0.25	0/10384	0.40	0/14158
1	u	0.28	0/10384	0.42	0/14158
1	w	0.27	0/10384	0.42	0/14158
1	y	0.26	0/10384	0.42	1/14158 (0.0%)
2	1	0.22	0/2127	0.42	0/2903
2	2	0.20	0/2127	0.44	0/2903
2	3	0.21	0/2127	0.44	0/2903
2	j	0.22	0/2043	0.50	1/2783 (0.0%)
2	k	0.19	0/2127	0.43	0/2903
2	o	0.25	0/2272	0.44	0/3099
2	s	0.25	0/2127	0.42	0/2903
2	v	0.23	0/2230	0.43	0/3041
2	x	0.23	0/2272	0.45	0/3099
2	z	0.19	0/2272	0.44	1/3099 (0.0%)
3	B	2.47	9/152 (5.9%)	3.39	28/206 (13.6%)
3	C	2.47	9/152 (5.9%)	3.39	28/206 (13.6%)
3	D	2.47	9/152 (5.9%)	3.39	28/206 (13.6%)
3	T	0.27	0/2591	0.60	2/3521 (0.1%)
3	W	2.47	9/152 (5.9%)	3.39	28/206 (13.6%)
3	d	0.17	0/108	0.45	0/145
3	h	0.27	0/2591	0.60	2/3521 (0.1%)
3	i	0.26	0/2591	0.60	2/3521 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	r	0.26	0/2591	0.60	2/3521 (0.1%)
3	t	0.27	0/2591	0.60	2/3521 (0.1%)
4	E	0.23	0/736	0.52	0/999
4	F	0.23	0/736	0.52	0/999
4	G	0.23	0/736	0.52	0/999
4	H	0.23	0/736	0.52	0/999
4	I	0.22	0/736	0.52	0/999
4	J	0.23	0/736	0.52	0/999
4	K	0.23	0/736	0.52	0/999
4	L	0.23	0/736	0.52	0/999
4	M	0.23	0/736	0.52	0/999
4	N	0.23	0/736	0.52	0/999
4	O	0.23	0/736	0.52	0/999
4	P	0.23	0/736	0.52	0/999
4	Q	0.23	0/736	0.52	0/999
4	R	0.23	0/736	0.52	0/999
4	V	0.23	0/736	0.52	0/999
All	All	0.29	37/210796 (0.0%)	0.48	141/287278 (0.0%)

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	0	0	2
1	A	0	1
1	U	0	1
1	n	0	3
1	u	0	1
1	y	0	1
2	v	0	1
3	B	0	6
3	C	0	6
3	D	0	6
3	W	0	6
All	All	0	34

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	16	GLY	C-N	10.27	1.48	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	W	16	GLY	C-N	10.24	1.48	1.33
3	C	16	GLY	C-N	10.20	1.48	1.33
3	D	16	GLY	C-N	10.18	1.48	1.33
3	C	8	GLY	N-CA	9.59	1.59	1.45

The worst 5 of 141 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	17	THR	N-CA-CB	13.49	130.37	110.53
3	B	17	THR	N-CA-CB	13.47	130.34	110.53
3	D	17	THR	N-CA-CB	13.47	130.33	110.53
3	W	17	THR	N-CA-CB	13.45	130.30	110.53
1	A	162	LEU	CB-CG-CD2	-12.31	73.78	110.70

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	762	ARG	Peptide
1	0	984	ALA	Peptide
1	A	163	ASP	Peptide
3	B	5	ILE	Peptide
3	B	6	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	10129	0	9939	241	0
1	A	10112	0	9922	389	0
1	S	9975	0	9780	250	0
1	U	10129	0	9939	226	0
1	a	9974	0	9791	274	0
1	e	8722	0	8537	301	0
1	f	10129	0	9939	195	0
1	g	10125	0	9935	298	0
1	l	10129	0	9939	261	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	m	10129	0	9939	272	0
1	n	10129	0	9939	267	0
1	p	10129	0	9939	271	0
1	q	10129	0	9939	258	0
1	u	10129	0	9939	242	0
1	w	10129	0	9939	252	0
1	y	10129	0	9939	306	0
2	1	2088	0	2157	50	0
2	2	2088	0	2157	98	0
2	3	2088	0	2157	67	0
2	j	2009	0	2067	72	0
2	k	2088	0	2157	93	0
2	o	2229	0	2293	59	0
2	s	2088	0	2157	55	0
2	v	2189	0	2253	59	0
2	x	2229	0	2293	85	0
2	z	2229	0	2293	74	0
3	B	152	0	167	28	0
3	C	152	0	167	175	0
3	D	152	0	167	49	0
3	T	2538	0	2514	67	0
3	W	152	0	166	197	0
3	d	108	0	120	7	0
3	h	2538	0	2514	68	0
3	i	2538	0	2514	79	0
3	r	2538	0	2514	71	0
3	t	2538	0	2514	72	0
4	E	722	0	734	22	0
4	F	722	0	734	25	0
4	G	722	0	734	30	0
4	H	722	0	734	30	0
4	I	722	0	734	32	0
4	J	722	0	734	25	0
4	K	722	0	734	25	0
4	L	722	0	734	27	0
4	M	722	0	734	26	0
4	N	722	0	734	26	0
4	O	722	0	734	28	0
4	P	722	0	734	24	0
4	Q	722	0	734	20	0
4	R	722	0	734	23	0
4	V	722	0	734	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	205888	0	203645	5490	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 13.

The worst 5 of 5490 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)
3:C:17:THR:HA	3:W:6:GLY:N	1.05	1.36
3:C:16:GLY:N	3:W:8:GLY:C	1.91	1.29
3:C:17:THR:CA	3:W:6:GLY:N	1.98	1.26
3:C:16:GLY:O	3:W:5:ILE:C	1.79	1.25
3:C:16:GLY:N	3:W:8:GLY:CA	1.95	1.25

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	1307/1330 (98%)	1171 (90%)	135 (10%)	1 (0%)	48	83
1	A	1302/1330 (98%)	1159 (89%)	138 (11%)	5 (0%)	30	67
1	S	1285/1330 (97%)	1146 (89%)	136 (11%)	3 (0%)	43	77
1	U	1307/1330 (98%)	1168 (89%)	137 (10%)	2 (0%)	43	77
1	a	1281/1330 (96%)	1137 (89%)	144 (11%)	0	100	100
1	e	1102/1330 (83%)	987 (90%)	114 (10%)	1 (0%)	48	83
1	f	1307/1330 (98%)	1162 (89%)	142 (11%)	3 (0%)	43	77
1	g	1304/1330 (98%)	1158 (89%)	146 (11%)	0	100	100
1	l	1307/1330 (98%)	1168 (89%)	138 (11%)	1 (0%)	48	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	m	1307/1330 (98%)	1163 (89%)	144 (11%)	0	100	100
1	n	1307/1330 (98%)	1163 (89%)	140 (11%)	4 (0%)	36	71
1	p	1307/1330 (98%)	1167 (89%)	139 (11%)	1 (0%)	48	83
1	q	1307/1330 (98%)	1183 (90%)	124 (10%)	0	100	100
1	u	1307/1330 (98%)	1156 (88%)	150 (12%)	1 (0%)	48	83
1	w	1307/1330 (98%)	1174 (90%)	132 (10%)	1 (0%)	48	83
1	y	1307/1330 (98%)	1168 (89%)	138 (11%)	1 (0%)	48	83
2	1	273/296 (92%)	252 (92%)	21 (8%)	0	100	100
2	2	273/296 (92%)	252 (92%)	21 (8%)	0	100	100
2	3	273/296 (92%)	250 (92%)	23 (8%)	0	100	100
2	j	261/296 (88%)	236 (90%)	25 (10%)	0	100	100
2	k	273/296 (92%)	252 (92%)	21 (8%)	0	100	100
2	o	294/296 (99%)	263 (90%)	31 (10%)	0	100	100
2	s	273/296 (92%)	248 (91%)	25 (9%)	0	100	100
2	v	285/296 (96%)	257 (90%)	28 (10%)	0	100	100
2	x	294/296 (99%)	258 (88%)	36 (12%)	0	100	100
2	z	294/296 (99%)	262 (89%)	32 (11%)	0	100	100
3	B	21/368 (6%)	11 (52%)	6 (29%)	4 (19%)	0	2
3	C	21/368 (6%)	11 (52%)	6 (29%)	4 (19%)	0	2
3	D	21/368 (6%)	11 (52%)	6 (29%)	4 (19%)	0	2
3	T	321/368 (87%)	293 (91%)	28 (9%)	0	100	100
3	W	21/368 (6%)	11 (52%)	6 (29%)	4 (19%)	0	2
3	d	14/368 (4%)	12 (86%)	2 (14%)	0	100	100
3	h	321/368 (87%)	292 (91%)	29 (9%)	0	100	100
3	i	321/368 (87%)	292 (91%)	29 (9%)	0	100	100
3	r	321/368 (87%)	293 (91%)	28 (9%)	0	100	100
3	t	321/368 (87%)	293 (91%)	28 (9%)	0	100	100
4	E	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	F	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	G	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	H	87/103 (84%)	81 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	I	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	J	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	K	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	L	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	M	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	N	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	O	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	P	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	Q	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	R	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	V	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
All	All	26452/29465 (90%)	23694 (90%)	2718 (10%)	40 (0%)	44	77

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	SER
3	B	13	VAL
3	B	16	GLY
3	B	20	VAL
3	C	13	VAL

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	1057/1072 (99%)	1057 (100%)	0	100	100
1	A	1056/1072 (98%)	1051 (100%)	5 (0%)	81	81
1	S	1042/1072 (97%)	1042 (100%)	0	100	100
1	U	1057/1072 (99%)	1057 (100%)	0	100	100
1	a	1040/1072 (97%)	1039 (100%)	1 (0%)	88	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	e	909/1072 (85%)	909 (100%)	0	100	100
1	f	1057/1072 (99%)	1057 (100%)	0	100	100
1	g	1057/1072 (99%)	1057 (100%)	0	100	100
1	l	1057/1072 (99%)	1057 (100%)	0	100	100
1	m	1057/1072 (99%)	1057 (100%)	0	100	100
1	n	1057/1072 (99%)	1056 (100%)	1 (0%)	88	88
1	p	1057/1072 (99%)	1056 (100%)	1 (0%)	88	88
1	q	1057/1072 (99%)	1057 (100%)	0	100	100
1	u	1057/1072 (99%)	1057 (100%)	0	100	100
1	w	1057/1072 (99%)	1057 (100%)	0	100	100
1	y	1057/1072 (99%)	1056 (100%)	1 (0%)	88	88
2	1	223/235 (95%)	223 (100%)	0	100	100
2	2	223/235 (95%)	223 (100%)	0	100	100
2	3	223/235 (95%)	223 (100%)	0	100	100
2	j	213/235 (91%)	212 (100%)	1 (0%)	81	81
2	k	223/235 (95%)	223 (100%)	0	100	100
2	o	235/235 (100%)	235 (100%)	0	100	100
2	s	223/235 (95%)	223 (100%)	0	100	100
2	v	233/235 (99%)	233 (100%)	0	100	100
2	x	235/235 (100%)	234 (100%)	1 (0%)	84	82
2	z	235/235 (100%)	235 (100%)	0	100	100
3	B	17/279 (6%)	6 (35%)	11 (65%)	0	0
3	C	17/279 (6%)	6 (35%)	11 (65%)	0	0
3	D	17/279 (6%)	6 (35%)	11 (65%)	0	0
3	T	251/279 (90%)	195 (78%)	56 (22%)	1	6
3	W	17/279 (6%)	6 (35%)	11 (65%)	0	0
3	d	12/279 (4%)	12 (100%)	0	100	100
3	h	251/279 (90%)	195 (78%)	56 (22%)	1	6
3	i	251/279 (90%)	195 (78%)	56 (22%)	1	6
3	r	251/279 (90%)	194 (77%)	57 (23%)	1	6
3	t	251/279 (90%)	195 (78%)	56 (22%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	F	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	G	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	H	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	I	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	J	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	K	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	L	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	M	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	N	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	O	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	P	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	Q	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	R	78/87 (90%)	64 (82%)	14 (18%)	2	10
4	V	78/87 (90%)	64 (82%)	14 (18%)	2	10
All	All	21502/23597 (91%)	20956 (98%)	546 (2%)	42	62

5 of 546 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	r	177	ASP
3	r	265	THR
3	r	172	CYS
3	t	186	MET
4	P	17	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 536 such sidechains are listed below:

Mol	Chain	Res	Type
2	v	69	HIS
1	w	462	GLN
1	u	1208	GLN
1	y	898	HIS
1	e	1170	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](#)

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-31612. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.