



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2024 – 09:32 PM EST

PDB ID : 8FWG
EMDB ID : EMD-29504
Title : Structure of neck and portal vertex of Agrobacterium phage Milano, C5 symmetry
Authors : Sonani, R.R.; Wang, F.; Esteves, N.C.; Kelly, R.J.; Sebastian, A.; Kreutzberger, M.A.B.; Leiman, P.G.; Scharf, B.E.; Egelman, E.H.
Deposited on : 2023-01-22
Resolution : 3.45 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:

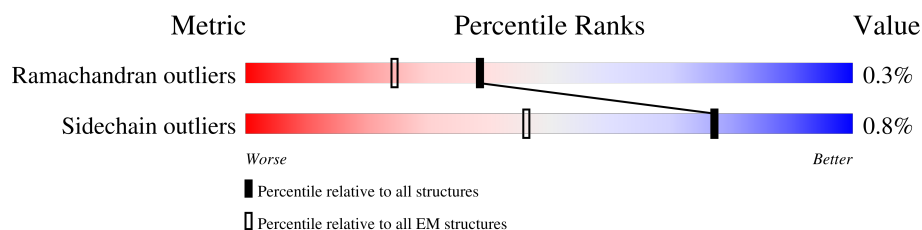
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.45 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.













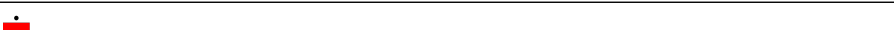

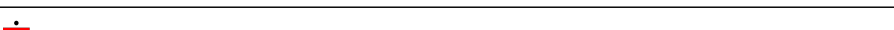
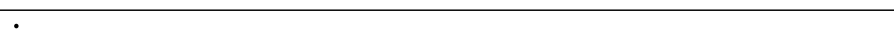











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a1	38	
1	a2	38	
1	a5	38	
1	a6	38	
1	a7	38	
1	b1	38	
1	b2	38	
1	b5	38	
1	b6	38	



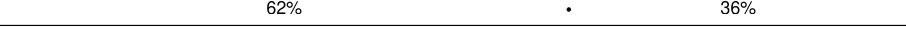
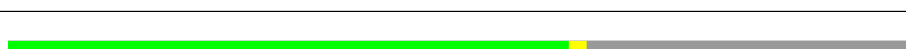



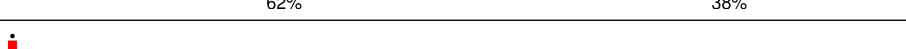



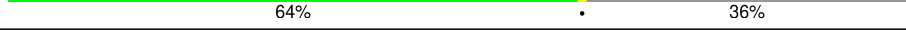

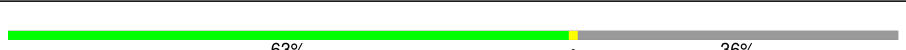


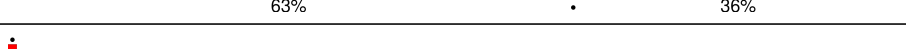







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Mol	Chain	Length	Quality of chain
1	b7	38	
1	c	38	
1	d	38	
1	d1	38	
1	d2	38	
1	d5	38	
1	d6	38	
1	d7	38	
1	e	38	
1	e1	38	
1	e2	38	
1	e5	38	
1	e6	38	
1	e7	38	
1	f	38	
1	g	38	
2	f1	217	
2	f2	217	
2	f5	217	
2	f6	217	
2	f7	217	
3	g1	465	
3	g2	465	
3	g5	465	
3	g6	465	


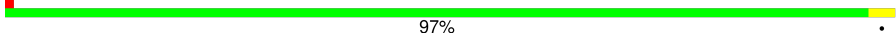
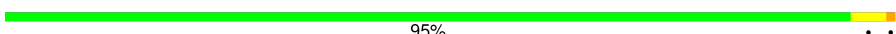
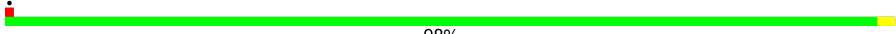


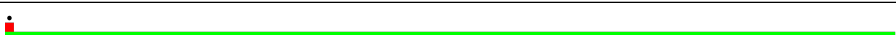
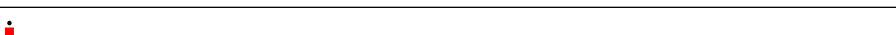
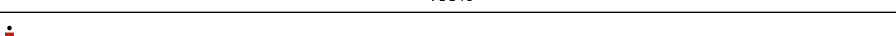
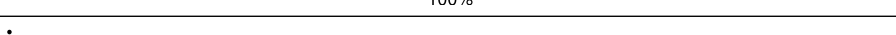
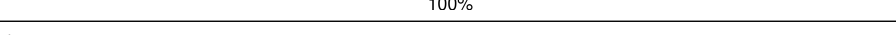
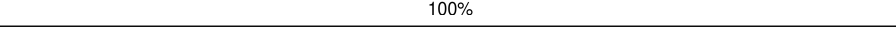
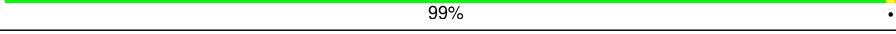
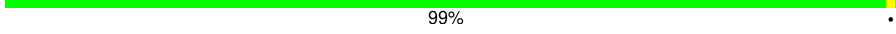
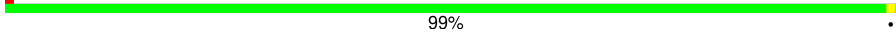
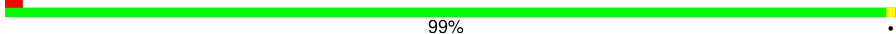
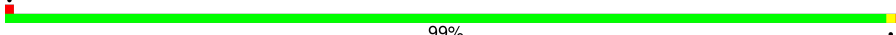
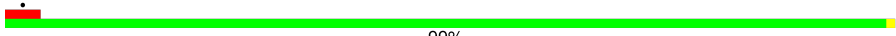





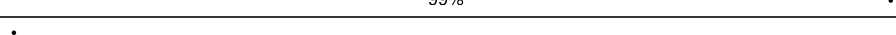
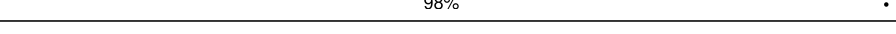
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Mol	Chain	Length	Quality of chain
3	g7	465	
3	h1	465	
3	h2	465	
3	h5	465	
3	h6	465	
3	h7	465	
3	k1	465	
3	k2	465	
3	k5	465	
3	k6	465	
3	k7	465	
3	n1	465	
3	n2	465	
3	n5	465	
3	n6	465	
3	n7	465	
3	o1	465	
3	o2	465	
3	o5	465	
3	o6	465	
3	o7	465	
3	r1	465	
3	r2	465	
3	r5	465	
3	r6	465	

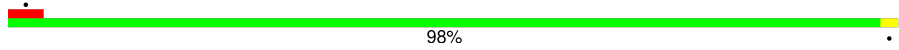
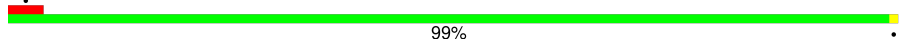
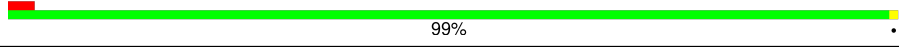
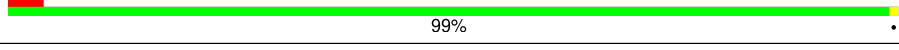
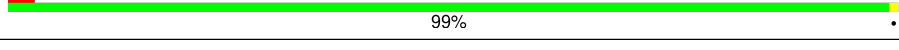
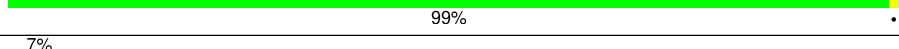
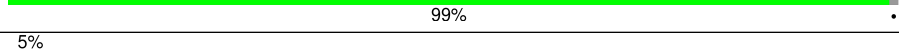
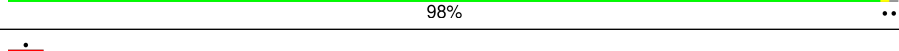
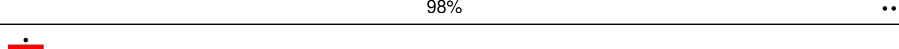
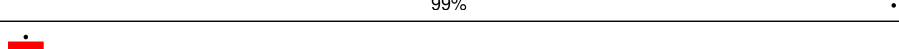
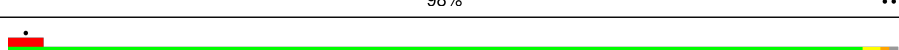
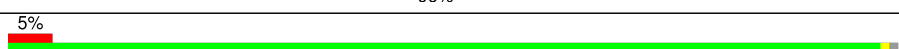
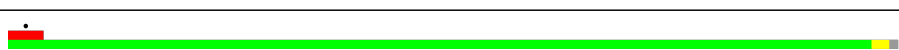
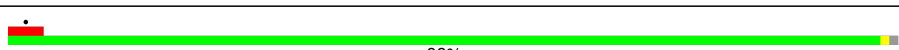
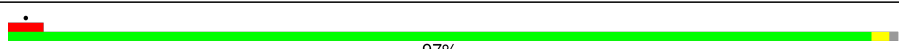
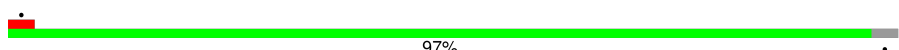

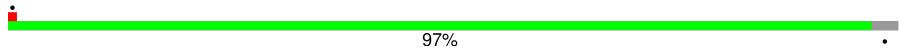
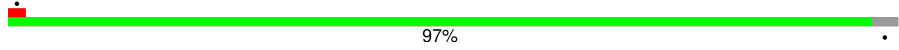
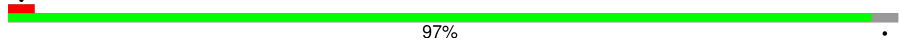
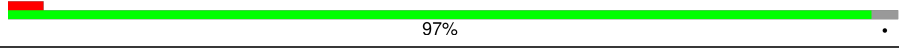
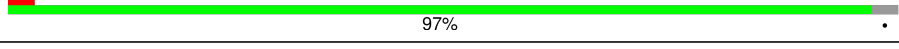
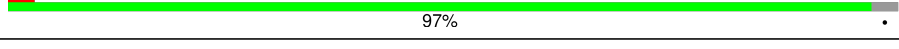
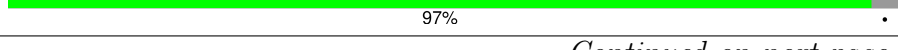

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Mol	Chain	Length	Quality of chain
3	r7	465	
4	l1	137	
4	l2	137	
4	l5	137	
4	l6	137	
4	l7	137	
4	m1	137	
4	m2	137	
4	m5	137	
4	m6	137	
4	m7	137	
4	p1	137	
4	p2	137	
4	p5	137	
4	p6	137	
4	p7	137	
4	q1	137	
4	q2	137	
4	q5	137	
4	q6	137	
4	q7	137	
4	s1	137	
4	s2	137	
4	s5	137	
4	s6	137	

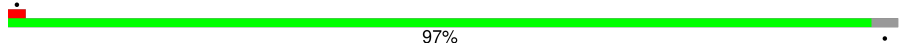
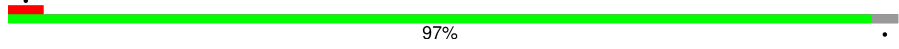
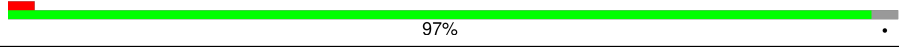
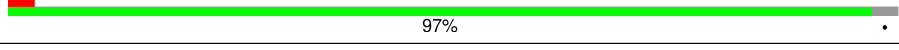
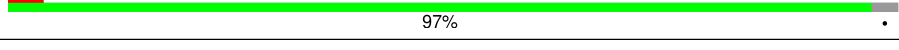
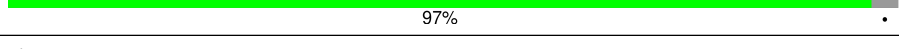
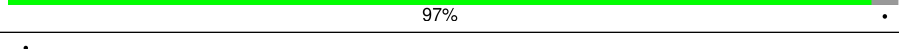
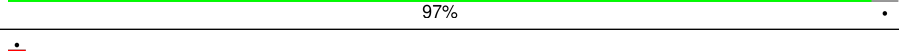
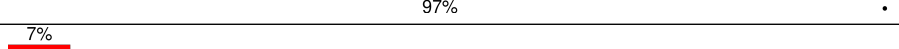
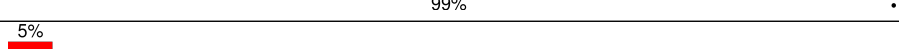
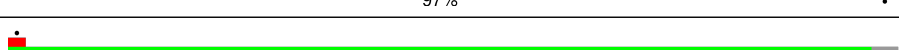
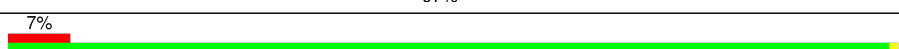
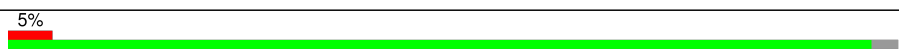
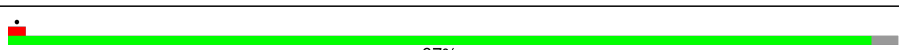
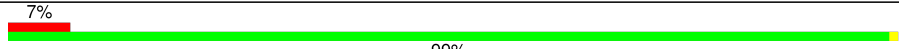
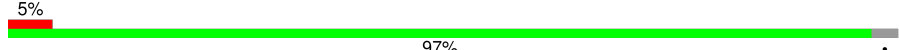

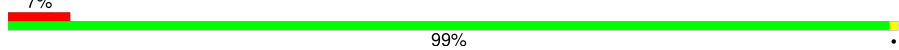
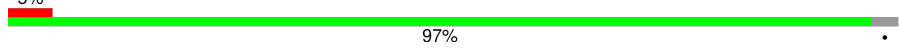
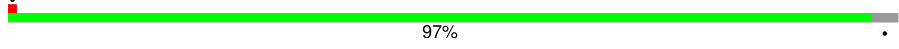
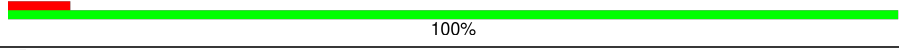
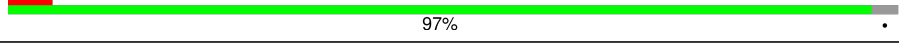
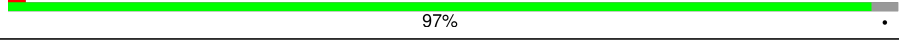
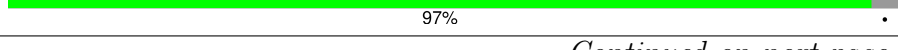

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Mol	Chain	Length	Quality of chain
4	s7	137	 98%
4	t1	137	 99%
4	t2	137	 99%
4	t5	137	 99%
4	t6	137	 99%
4	t7	137	 99%
4	u1	137	 99%
4	u2	137	 98%
4	u5	137	 98%
4	u6	137	 99%
4	u7	137	 98%
4	v1	137	 96%
4	v2	137	 98%
4	v5	137	 97%
4	v6	137	 98%
4	v7	137	 97%
5	03	230	 97%
5	13	230	 97%
5	23	230	 97%
5	33	230	 97%
5	43	230	 97%
5	53	230	 97%
5	63	230	 97%
5	73	230	 97%
5	83	230	 97%

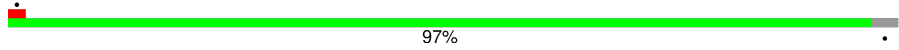
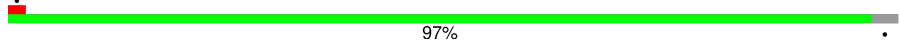
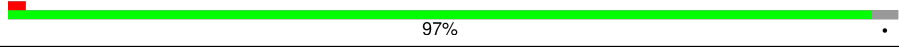
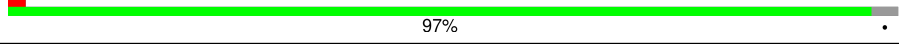
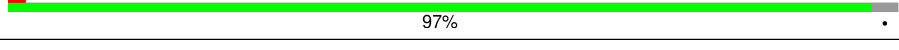
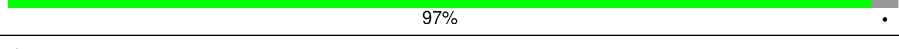
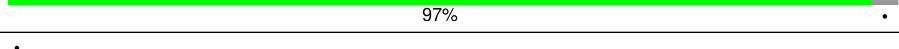
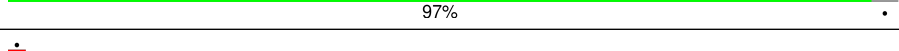
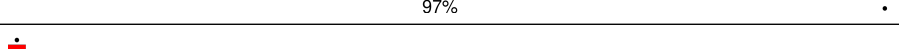
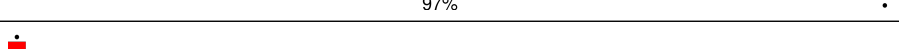
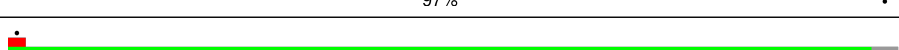
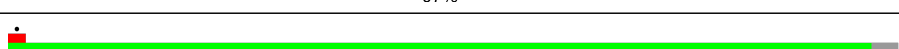
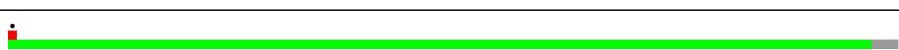
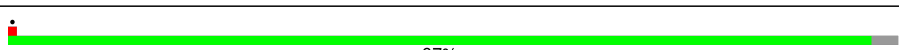
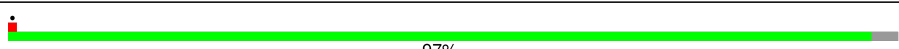
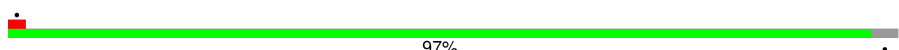

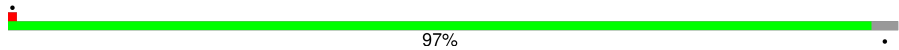
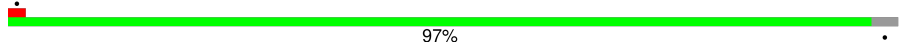
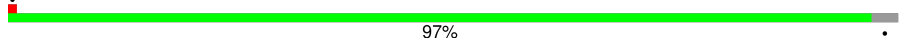
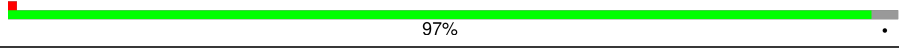
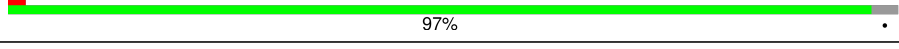
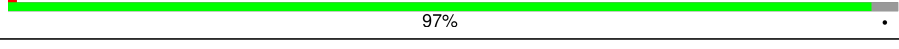
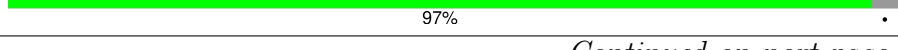

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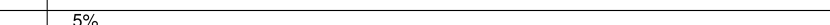




Mol	Chain	Length	Quality of chain
5	93	230	
5	A3	230	
5	B3	230	
5	C3	230	
5	D3	230	
5	E3	230	
5	F3	230	
5	G3	230	
5	J3	230	
5	K3	230	
5	L3	230	
5	M3	230	
5	N3	230	
5	O3	230	
5	P3	230	
5	Q3	230	
5	R3	230	
5	S3	230	
5	T3	230	
5	U3	230	
5	V3	230	
5	W3	230	
5	X3	230	
5	Y3	230	
5	Z3	230	

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Mol	Chain	Length	Quality of chain
5	a3	230	
5	b3	230	
5	c3	230	
5	d3	230	
5	e3	230	
5	f3	230	
5	g3	230	
5	h3	230	
5	i3	230	
5	j3	230	
5	k3	230	
5	l3	230	
5	m3	230	
5	n3	230	
5	o3	230	
5	p3	230	
5	q3	230	
5	r3	230	
5	s3	230	
5	t3	230	
5	u3	230	
5	v3	230	
5	w3	230	
5	x3	230	
5	y3	230	

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Mol	Chain	Length	Quality of chain
5	z3	230	 97%
6	A4	202	 5%43%57%
6	B4	202	 5%42%57%
6	C4	202	 5%42%57%
6	D4	202	 6%40%57%
6	E4	202	 5%42%57%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 221120 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 Linking protein 2, gp128.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a1	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	b1	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	d1	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e1	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	a2	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	b2	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	d2	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e2	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	a5	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	b5	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	d5	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e5	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	a6	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	b6	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	d6	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e6	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	a7	28	Total	C	N	O	S	0	0
			209	131	40	33	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	b7	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	d7	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e7	28	Total	C	N	O	S	0	0
			209	131	40	33	5		
1	c	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	d	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	e	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	f	34	Total	C	N	O	S	0	0
			246	155	46	40	5		
1	g	34	Total	C	N	O	S	0	0
			246	155	46	40	5		

- Molecule 2 is a protein called Linking protein 1, gp16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	f1	20	Total	C	N	O	S	0	0
			140	88	27	23	2		
2	f2	20	Total	C	N	O	S	0	0
			140	88	27	23	2		
2	f5	20	Total	C	N	O	S	0	0
			140	88	27	23	2		
2	f6	20	Total	C	N	O	S	0	0
			140	88	27	23	2		
2	f7	20	Total	C	N	O	S	0	0
			140	88	27	23	2		

- Molecule 3 is a protein called Major capsid protein, gp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	g1	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	h1	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	k1	288	Total	C	N	O	S	0	0
			2257	1430	386	425	16		
3	n1	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	o1	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	r1	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	g2	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	h2	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	k2	288	Total	C	N	O	S	0	0
			2257	1430	386	425	16		
3	n2	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	o2	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	r2	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	g5	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	h5	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	k5	288	Total	C	N	O	S	0	0
			2257	1430	386	425	16		
3	n5	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	o5	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	r5	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	g6	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	h6	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	k6	288	Total	C	N	O	S	0	0
			2257	1430	386	425	16		
3	n6	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	o6	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	r6	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	g7	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	h7	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	k7	288	Total	C	N	O	S	0	0
			2257	1430	386	425	16		
3	n7	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	o7	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		
3	r7	299	Total	C	N	O	S	0	0
			2337	1483	397	441	16		

- Molecule 4 is a protein called Minor capsid protein, gp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	l1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	m1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	p1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	q1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	s1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	t1	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	u1	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	v1	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	l2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	m2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	p2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	q2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	s2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	t2	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	u2	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	v2	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	l5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	m5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	p5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	q5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	s5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	t5	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	u5	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	v5	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	l6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	m6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	p6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	q6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	s6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	t6	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	u6	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	v6	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	l7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	m7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	p7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	q7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	s7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	t7	137	Total	C	N	O	S	0	0
			1023	655	160	201	7		
4	u7	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		
4	v7	136	Total	C	N	O	S	0	0
			1011	649	156	199	7		

- Molecule 5 is a protein called Collar sheath protein, gp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	K3	230	Total	C	N	O	S	0	0
			1723	1090	287	337	9		
5	L3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	M3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	N3	230	Total	C	N	O	S	0	0
			1723	1090	287	337	9		
5	O3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	P3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	Q3	230	Total	C	N	O	S	0	0
			1723	1090	287	337	9		
5	R3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	S3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	T3	230	Total	C	N	O	S	0	0
			1723	1090	287	337	9		
5	U3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	V3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	W3	230	Total	C	N	O	S	0	0
			1723	1090	287	337	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	X3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	Y3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	Z3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	a3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	b3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	c3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	d3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	e3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	f3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	g3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	h3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	i3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	j3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	k3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	l3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	m3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	n3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	o3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	p3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	q3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	r3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	s3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	t3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	u3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	v3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	w3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	x3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	y3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	z3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	13	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	23	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	33	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	43	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	53	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	63	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	73	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	83	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	93	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	03	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	A3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	B3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0
5	C3	223	Total 1679	C 1065	N 279	O 327	S 8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	E3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	F3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		
5	G3	223	Total	C	N	O	S	0	0
			1679	1065	279	327	8		

- Molecule 6 is a protein called Neck 1 protein, gp14.

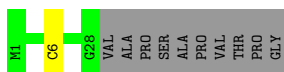
Mol	Chain	Residues	Atoms					AltConf	Trace
6	A4	87	Total	C	N	O	S	0	0
			671	429	120	118	4		
6	B4	87	Total	C	N	O	S	0	0
			671	429	120	118	4		
6	C4	87	Total	C	N	O	S	0	0
			671	429	120	118	4		
6	D4	87	Total	C	N	O	S	0	0
			671	429	120	118	4		
6	E4	87	Total	C	N	O	S	0	0
			671	429	120	118	4		

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 and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

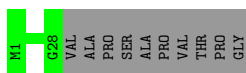
- Molecule 1: Linking protein 2, gp128

Chain a1: 



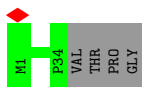
- Molecule 1: Linking protein 2, gp128

Chain b1: 




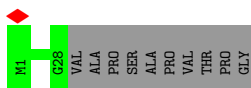
- Molecule 1: Linking protein 2, gp128

Chain d1: 



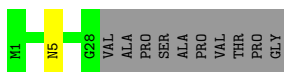
- Molecule 1: Linking protein 2, gp128

Chain e1: 

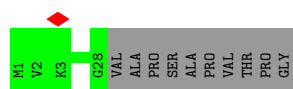
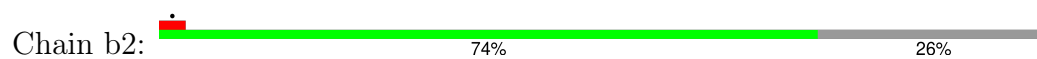


- Molecule 1: Linking protein 2, gp128

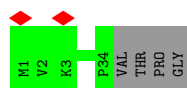
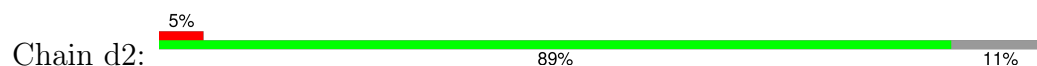
Chain a2: 



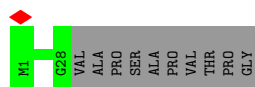
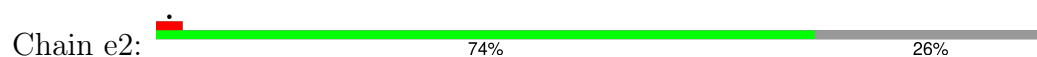
- Molecule 1: Linking protein 2, gp128



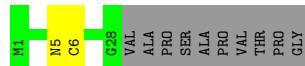
- Molecule 1: Linking protein 2, gp128



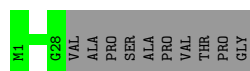
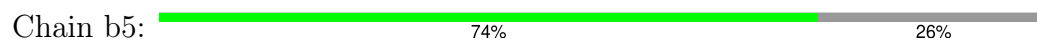
- Molecule 1: Linking protein 2, gp128



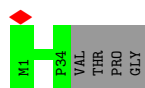
- Molecule 1: Linking protein 2, gp128



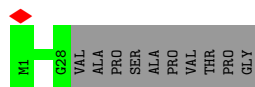
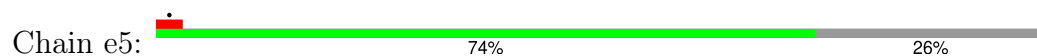
- Molecule 1: Linking protein 2, gp128



- Molecule 1: Linking protein 2, gp128

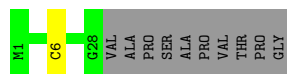


- Molecule 1: Linking protein 2, gp128



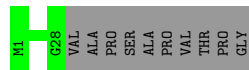
- Molecule 1: Linking protein 2, gp128

Chain a6:  71% 26%



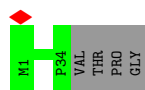
- Molecule 1: Linking protein 2, gp128

Chain b6:  74% 26%



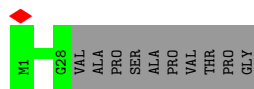
- Molecule 1: Linking protein 2, gp128

Chain d6:  89% 11%



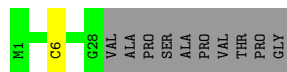
- Molecule 1: Linking protein 2, gp128

Chain e6:  74% 26%



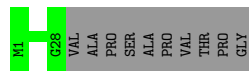
- Molecule 1: Linking protein 2, gp128

Chain a7:  71% 26%



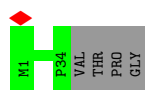
- Molecule 1: Linking protein 2, gp128

Chain b7:  74% 26%




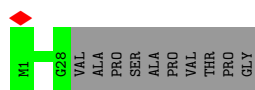
- Molecule 1: Linking protein 2, gp128

Chain d7:  89% 11%




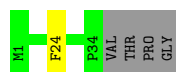
- Molecule 1: Linking protein 2, gp128

Chain e7:  74% 26%




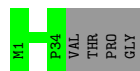
- Molecule 1: Linking protein 2, gp128

Chain c:  87% 11%




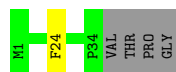
- Molecule 1: Linking protein 2, gp128

Chain d:  89% 11%




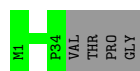
- Molecule 1: Linking protein 2, gp128

Chain e:  87% 11%




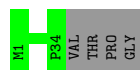
- Molecule 1: Linking protein 2, gp128

Chain f:  89% 11%



- Molecule 1: Linking protein 2, gp128

Chain g:  89% 11%



- Molecule 2: Linking protein 1, gp16

Chain f1:  9% 91%



TYR
LYS
ALA
THR
GLY
LEU
VAL
SER
SER
ILE
SER
ILE
THR
VAL
ASN
THR
THR
TYR
ALA
ASP

- Molecule 2: Linking protein 1, gp16

Chain f7:  9% 91%

MET
ASP
CYS
ARG
ASN
LEU
CYS
GLY
ALA
A10
A11
V28
S29
ILE
PRO
PRO
ALA
ALA
PRO
GLY
GLY
ALA
ALA
THR
SER
VAL
PHE
GLY
ASP
THR
PRO
PRO
SER
THR
PHE
PHE
SER
GLY
LEU
ARG
THR
PRO
ASP
GLY
THR
THR
ILE
ILE
ALA
ALA
GLY
THR
THR
ILE
ILE
ARG
GLY
TYR
TYR
ASP
ASP
HIS
ALA
SER
VAL
SER
VAL
PHE
GLY
THR
ASP
GLY
THR

ILE
GLU
MET
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ILE
GLU
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PHE
ILE
GLY
PRO
GLN
ASP
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SER
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TYR
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THR
GLY
LEU
VAL
SER
SER
SER
ILE
ILE
THR
VAL
ASN
VAL
THR
TYR
ALA
ASP

- Molecule 3: Major capsid protein, gp9

Chain g1:  64% 36%

MET
ALA
ASN
LYS
GLU
TYR
ALA
ASP
GLU
SER
LEU
ASN
GLY
LEU
ASP
ASP
ILE
HIS
SER
ASP
ILE
GLU
HIS
ASP
VAL
HIS
GLU
LEU
SER
MET
LEU
SER
ALA
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GLU
GLY
LYS
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ASP
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VAL
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LYS
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ASP
ASN
ASP
ALA
ILE
GLU
PHE
ARG
MET
HIS
ASP
ARG
GLY
GLY
VAL
ALA
ASP
ALA
ALA

R393
F403
I464
GLY

- Molecule 3: Major capsid protein, gp9

Chain h1:  63% 36%

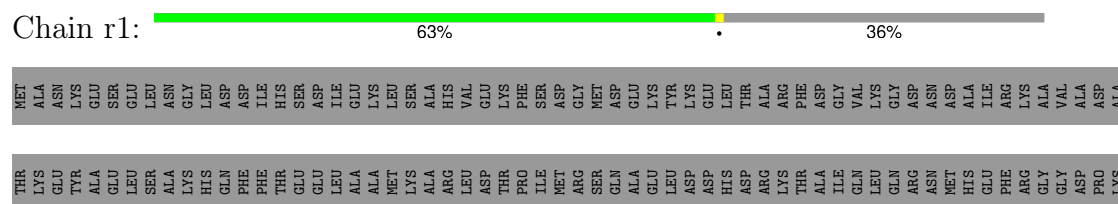
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GLU
TYR
ALA
ASP
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SER
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GLY
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HIS
SER
ASP
ILE
GLU
HIS
ASP
VAL
HIS
GLU
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SER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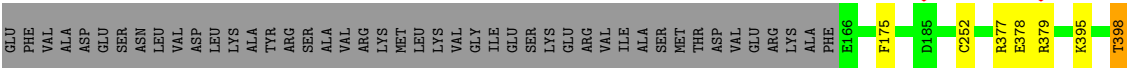
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ASP
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MET
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SER
ALA
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HIS
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GLY
GLY
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THR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

GLU
PHE
VAL
ALA
ASP
GLU
SER
ASN
LEU
VAL
ASP
GLY
LEU
LYS
ALA
TYR
ARG
SER
ALA
VAL
ARG
LYS
MET
LEU
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ALA
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LEU
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ASP
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VAL
GLY
LYS
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ASP
ASN
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VAL
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ASP
ALA
ALA

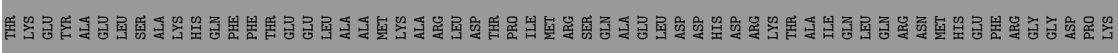
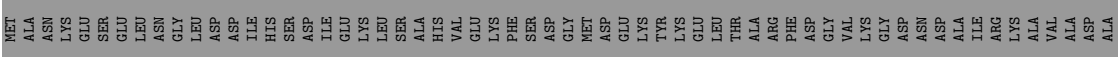
C455
I464
GLY

- Molecule 3: Major capsid protein, gp9

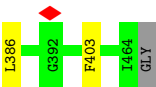
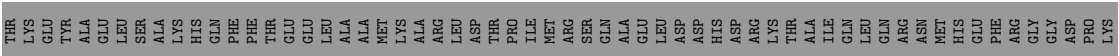
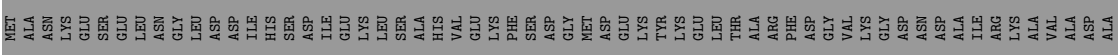




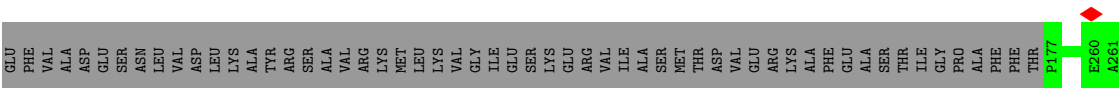
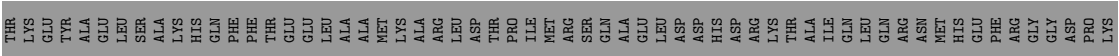
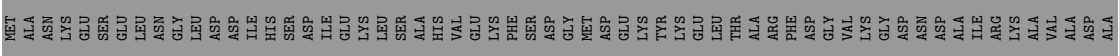
• Molecule 3: Major capsid protein, gp9

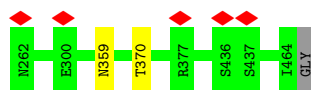


• Molecule 3: Major capsid protein, gp9



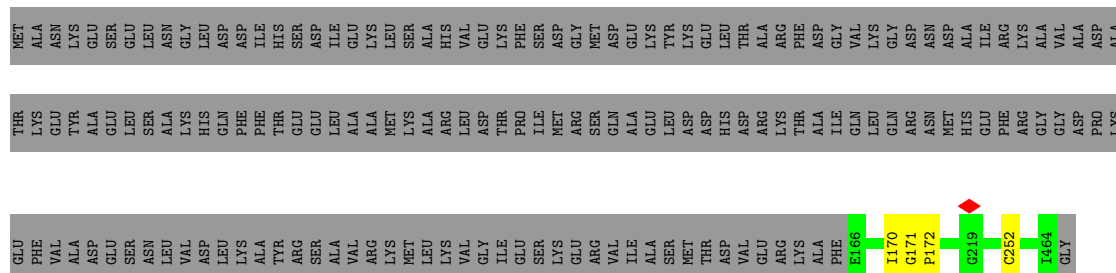
• Molecule 3: Major capsid protein, gp9





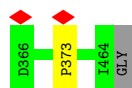
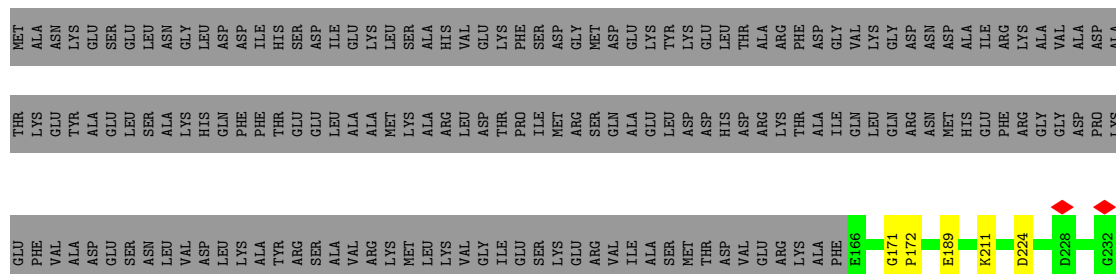
- Molecule 3: Major capsid protein, gp9

Chain n2: 63% 36%



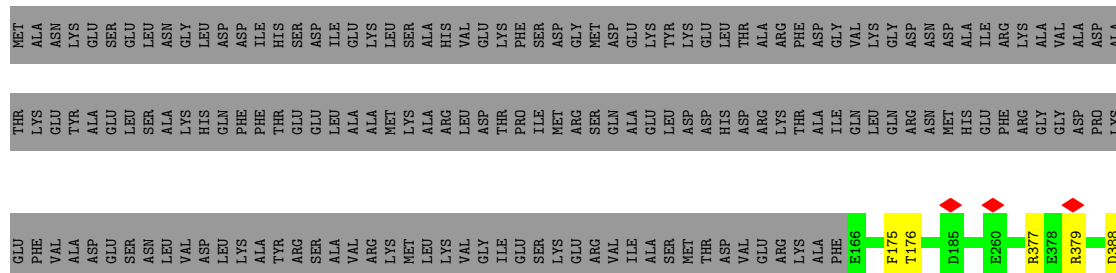
- Molecule 3: Major capsid protein, gp9

Chain o2: 63% 36%

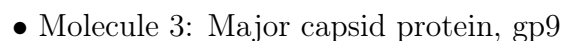


- Molecule 3: Major capsid protein, gp9

Chain r2: 63% 36%



- Molecule 3: Major capsid protein, gp9



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

GLU	PHE
VAL	VAL
ALA	ALA
ASP	ASP
SER	SER
ASN	ASN
LEU	LEU
VAL	VAL
ASP	ASP
GLN	GLN
LYS	LYS
PHE	PHE
ALA	ALA
TYR	TYR
ARG	ARG
SER	SER
SER	SER
VAL	VAL
ARG	ARG
LYS	LYS
VAL	VAL
GLY	GLY
ILE	ILE
THR	THR
ASP	ASP
VAL	VAL
ALA	ALA
LYS	LYS
LEU	LEU
ASP	ASP
GLY	GLY
ARG	ARG
THR	THR
ASP	ASP
VAL	VAL
ALA	ALA
LYS	LYS
THR	THR
ASP	ASP
GLN	GLN
ALA	ALA
LYS	LYS
LEU	LEU
SER	SER
MET	MET
THR	THR
ASP	ASP
GLY	GLY
ARG	ARG
VAL	VAL
ALA	ALA
ILE	ILE
THR	THR
ASP	ASP
GLU	GLU
LYS	LYS
TYR	TYR
LEU	LEU
ASP	ASP
THR	THR
ASP	ASP
HIS	HIS
ASP	ASP
VAL	VAL
ALA	ALA
LYS	LYS
LEU	LEU
ASP	ASP
GLN	GLN
ALA	ALA
LYS	LYS
THR	THR
ASP	ASP
GLY	GLY
ARG	ARG
VAL	VAL
ALA	ALA
ILE	ILE
GLN	GLN
LYS	LYS
GLY	GLY
ASN	ASN
ASP	ASP
ASN	ASN
ASP	ASP
ILE	ILE
GLU	GLU
THR	THR
PHE	PHE
ARG	ARG
LYS	LYS
ALA	ALA
ALA	ALA
PHE	PHE
E166	E166
I170	I170
G171	G171
P172	P172
T464	T464
GLY	GLY

• Molecule 3: Major capsid protein, gp9



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

GLU	PHE
VAL	VAL
ALA	ALA
ASP	ASP
SER	SER
ASN	ASN
LEU	LEU
VAL	ALA
ASP	LYS
ASP	GLN
ILE	ASP
TYR	THR
ARG	GLU
SER	GLU
SER	LEU
ALA	ALA
VAL	VAL
ARG	ARG
LYS	LYS
LEU	LEU
ASP	ASP
THR	THR
ASP	ASP
HIS	HIS
ASP	ASP
VAL	VAL
ALA	ILE
ARG	ALA
GLY	GLU
ASP	LYS
THR	LEU
ASP	ASP
GLN	GLN
ALA	ALA
LYS	LYS
LEU	LEU
SER	SER
MET	MET
THR	THR
ASP	ASP
GLY	GLY
ARG	ARG
VAL	VAL
ALA	ILE
ILE	THR
GLN	ASP
LYS	GLU
GLY	LYS
ASN	ASN
ASP	ASP
ASN	ASN
ASP	ASP
ILE	ILE
GLU	GLU
THR	THR
PHE	PHE
ARG	ARG
LYS	LYS
ALA	ALA
ALA	ALA
PHE	PHE
E166	E166
G171	G171
P172	P172
E189	E189
K211	K211
D224	D224
G232	G232
P373	P373
GLY	GLY

• Molecule 3: Major capsid protein, gp9



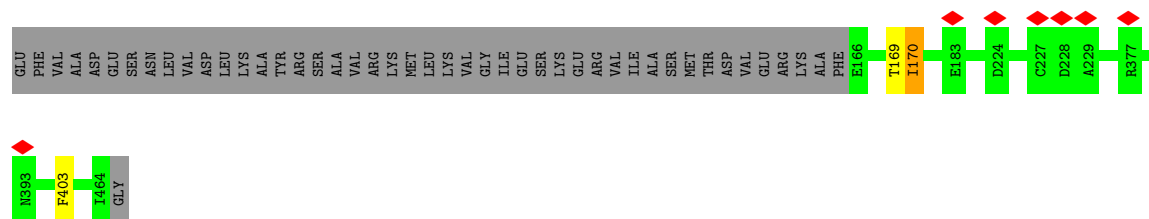
MET	THR
ALA	LYS
ASN	GLU
LYS	TYR
GLU	ALA
SER	GLU
GLU	LEU
LEU	SER
ASN	LEU
GLY	ALA
LEU	LYS
ASP	GLN
ASP	HIS
ILE	PHE
HIS	PHE
ASP	THR
ASP	GLU
ASP	GLU
ILE	LEU
ILE	ALA
GLU	ALA
LYS	ALA
LEU	MET
VAL	LYS
VAL	ARG
GLY	HIS
ILE	ASP
THR	THR
ASP	ASP
THR	ASP
ASP	HIS
GLU	ASP
VAL	VAL
ALA	ILE
ARG	ALA
GLY	GLU
ASP	LYS
THR	LEU
ASP	ASP
GLN	GLN
ALA	ALA
LYS	LYS
LEU	LEU
SER	SER
MET	MET
THR	THR
ASP	ASP
GLY	GLY
ARG	ARG
VAL	VAL
ALA	ILE
ILE	THR
GLN	ASP
LYS	GLU
GLY	LYS
ASN	ASN
ASP	ASP
ASN	ASN
ASP	ASP
ILE	ILE
GLU	GLU
THR	THR
PHE	PHE
ARG	ARG
LYS	LYS
ALA	ALA
ALA	ALA
PHE	PHE
E166	E166
P172	P172
F175	F175
T176	T176
D185	D185
R379	R379
G392	G392
K395	K395
G396	G396
GLY	GLY

G397	T398
I464	I464
GLY	GLY

• Molecule 3: Major capsid protein, gp9

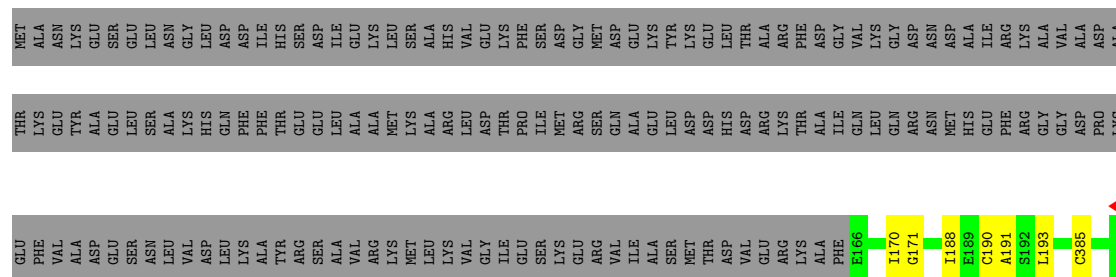


MET	THR
ALA	LYS
ASN	GLU
LYS	TYR
GLU	ALA
SER	GLU
GLU	LEU
LEU	SER
ASN	LEU
GLY	ALA
LEU	LYS
ASP	GLN
ASP	HIS
ILE	PHE
HIS	PHE
ASP	THR
ASP	GLU
ASP	GLU
ILE	LEU
ILE	ALA
GLU	ALA
LYS	ALA
LEU	MET
VAL	LYS
VAL	ARG
GLY	HIS
ILE	ASP
THR	THR
ASP	ASP
THR	ASP
ASP	HIS
GLU	ASP
VAL	VAL
ALA	ILE
ARG	ALA
GLY	GLU
ASP	LYS
THR	LEU
ASP	ASP
GLN	GLN
ALA	ALA
LYS	LYS
LEU	LEU
SER	SER
MET	MET
THR	THR
ASP	ASP
GLY	GLY
ARG	ARG
VAL	VAL
ALA	ALA
ILE	ILE
GLN	GLN
LYS	LYS
GLY	GLY
ASN	ASN
ASP	ASP
ASN	ASN
ASP	ASP
ILE	ILE
GLU	GLU
THR	THR
PHE	PHE
ARG	ARG
LYS	LYS
ALA	ALA
ALA	ALA
PHE	PHE
E166	E166
P172	P172
F175	F175
T176	T176
D185	D185
R379	R379
G392	G392
K395	K395
G396	G396
GLY	GLY



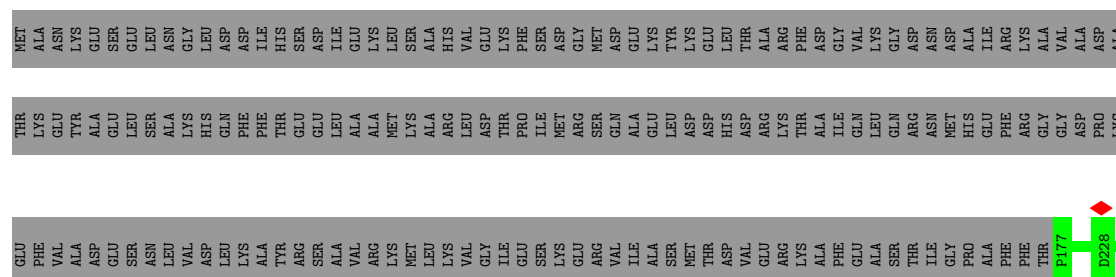
- Molecule 3: Major capsid protein, gp9

Chain h6:



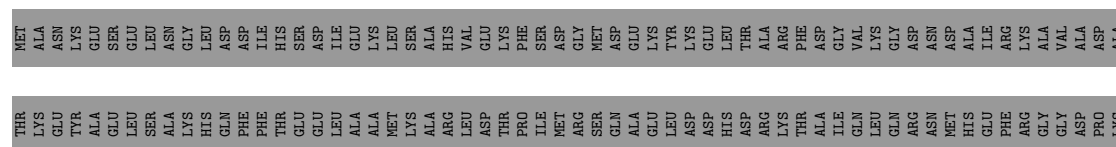
- Molecule 3: Major capsid protein, gp9

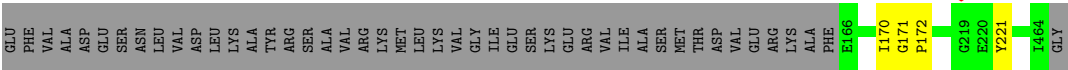
Chain k6:



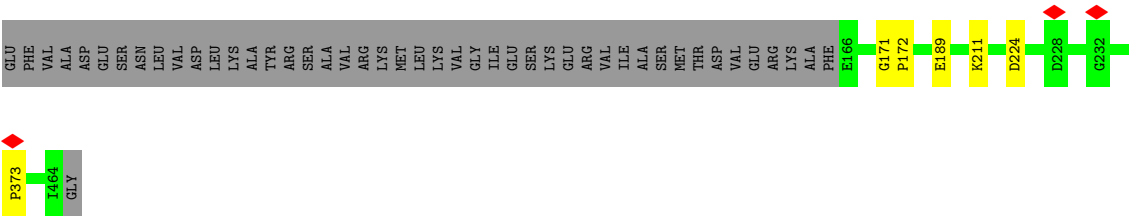
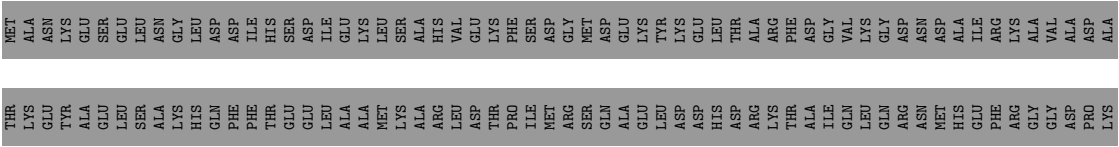
- Molecule 3: Major capsid protein, gp9

Chain n6:

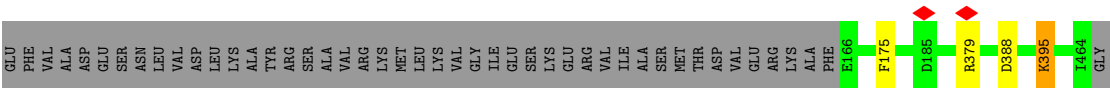
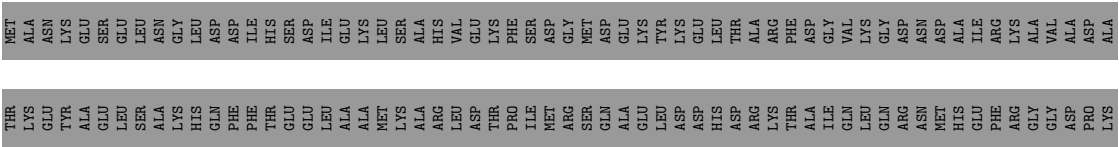




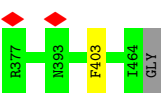
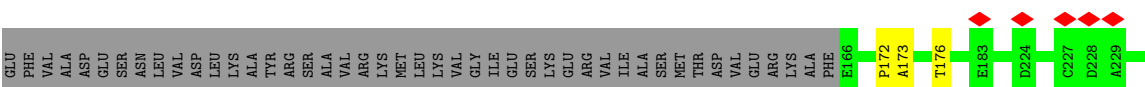
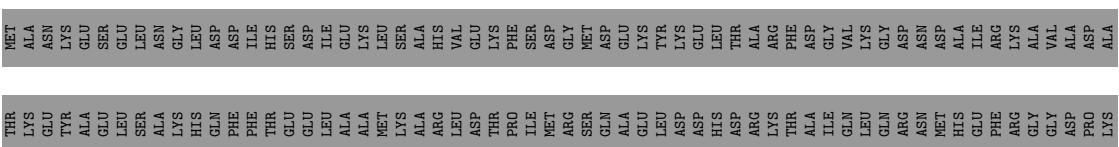
• Molecule 3: Major capsid protein, gp9



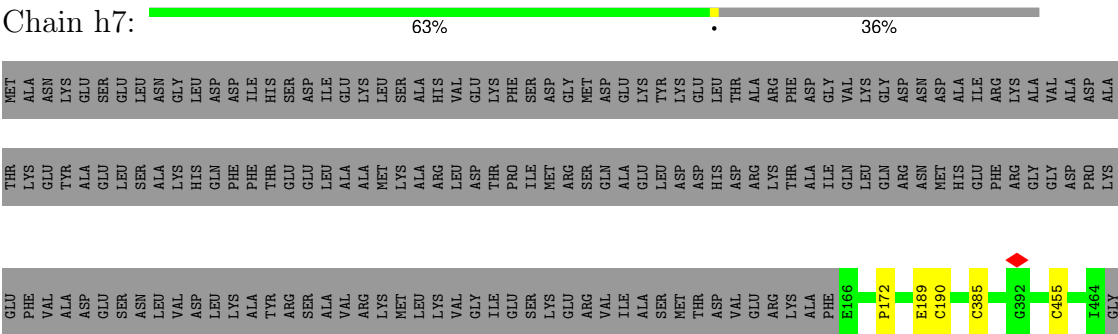
• Molecule 3: Major capsid protein, gp9



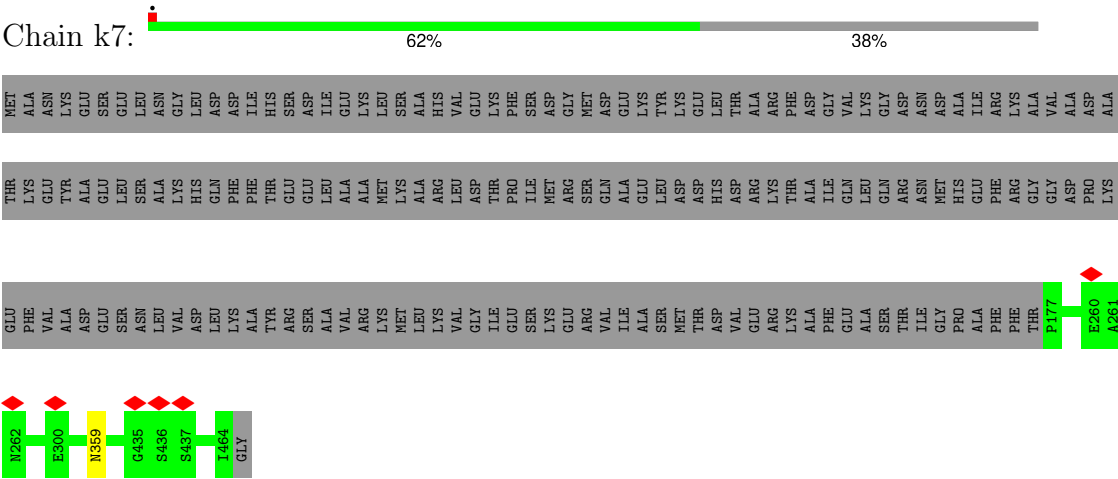
• Molecule 3: Major capsid protein, gp9



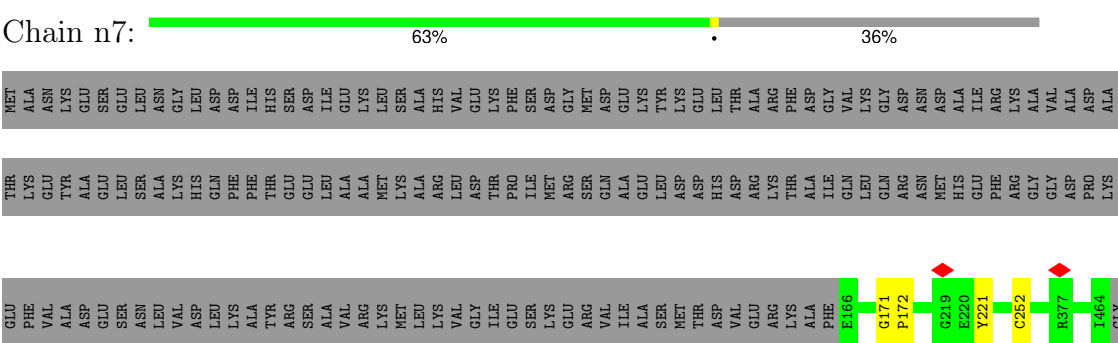
• Molecule 3: Major capsid protein, gp9



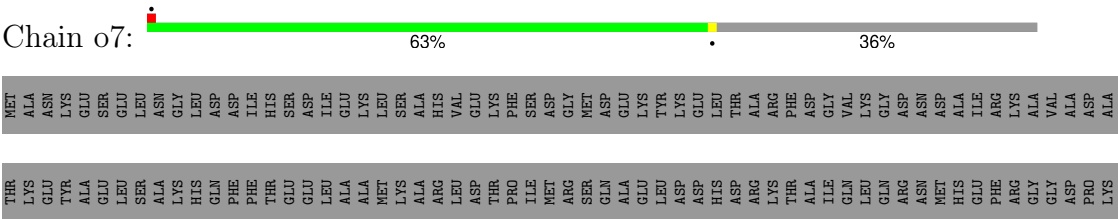
• Molecule 3: Major capsid protein, gp9

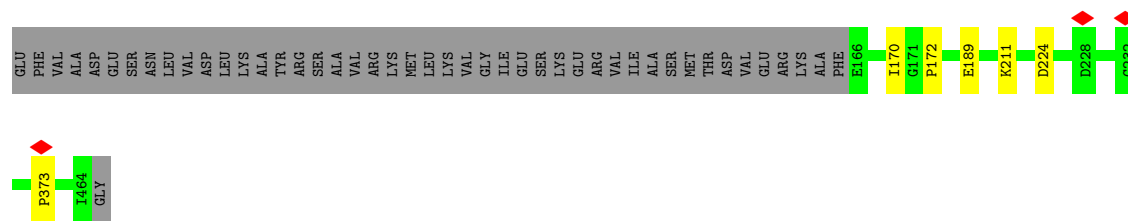


• Molecule 3: Major capsid protein, gp9



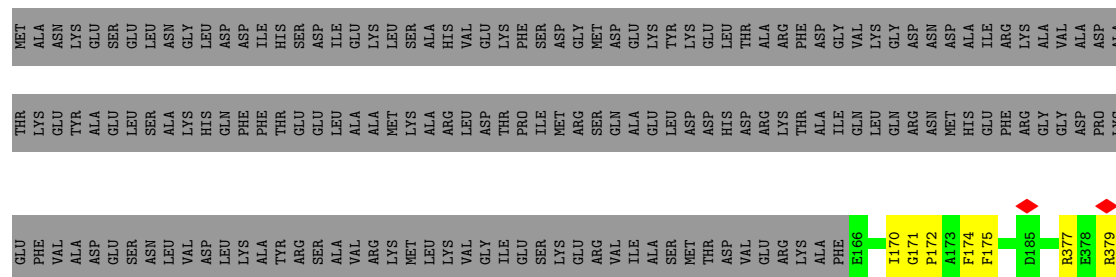
• Molecule 3: Major capsid protein, gp9





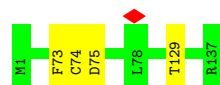
- Molecule 3: Major capsid protein, gp9

Chain r7: 62% 36%



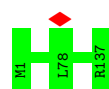
- Molecule 4: Minor capsid protein, gp10

Chain l1: 97%



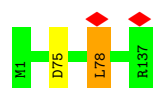
- Molecule 4: Minor capsid protein, gp10

Chain m1: 100%



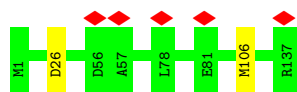
- Molecule 4: Minor capsid protein, gp10

Chain p1: 99%

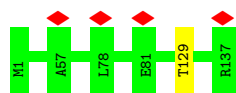


- Molecule 4: Minor capsid protein, gp10

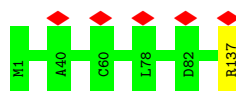
Chain q1: 99%



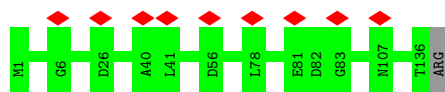
- Molecule 4: Minor capsid protein, gp10



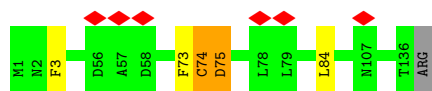
- Molecule 4: Minor capsid protein, gp10



- Molecule 4: Minor capsid protein, gp10



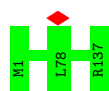
- Molecule 4: Minor capsid protein, gp10



- Molecule 4: Minor capsid protein, gp10

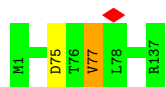


- Molecule 4: Minor capsid protein, gp10



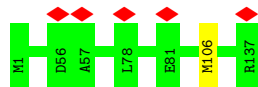
- Molecule 4: Minor capsid protein, gp10

Chain p2:  99%



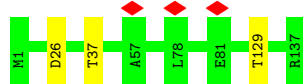
- Molecule 4: Minor capsid protein, gp10

Chain q2:  99%



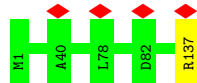
- Molecule 4: Minor capsid protein, gp10

Chain s2:  98%



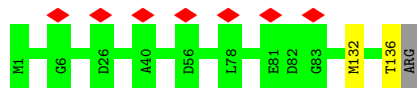
- Molecule 4: Minor capsid protein, gp10

Chain t2:  99%



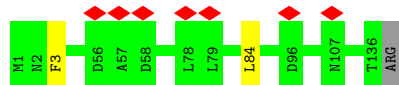
- Molecule 4: Minor capsid protein, gp10

Chain u2:  5% 98%



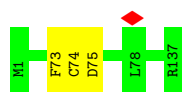
- Molecule 4: Minor capsid protein, gp10

Chain v2:  5% 98%

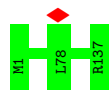


- Molecule 4: Minor capsid protein, gp10

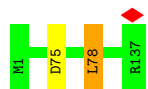
Chain l5:  98%



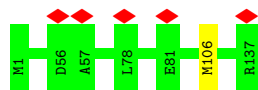
- Molecule 4: Minor capsid protein, gp10



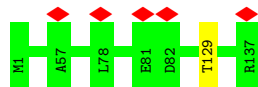
- Molecule 4: Minor capsid protein, gp10



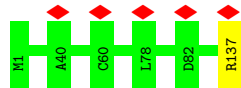
- Molecule 4: Minor capsid protein, gp10



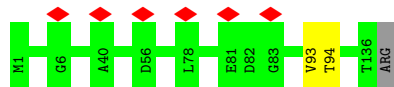
- Molecule 4: Minor capsid protein, gp10



- Molecule 4: Minor capsid protein, gp10



- Molecule 4: Minor capsid protein, gp10



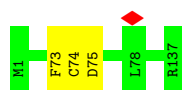
- Molecule 4: Minor capsid protein, gp10

Chain v5:  97%



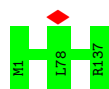
- Molecule 4: Minor capsid protein, gp10

Chain l6:  98%



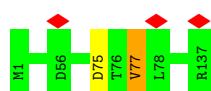
- Molecule 4: Minor capsid protein, gp10

Chain m6:  100%



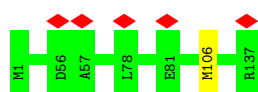
- Molecule 4: Minor capsid protein, gp10

Chain p6:  99%



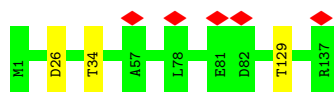
- Molecule 4: Minor capsid protein, gp10

Chain q6:  99%



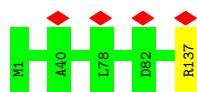
- Molecule 4: Minor capsid protein, gp10

Chain s6:  98%

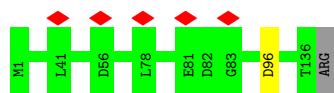
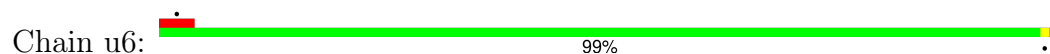


- Molecule 4: Minor capsid protein, gp10

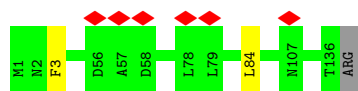
Chain t6:  99%



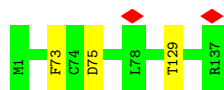
- Molecule 4: Minor capsid protein, gp10



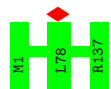
- Molecule 4: Minor capsid protein, gp10



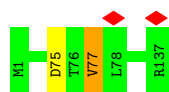
- Molecule 4: Minor capsid protein, gp10



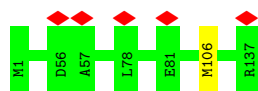
- Molecule 4: Minor capsid protein, gp10



- Molecule 4: Minor capsid protein, gp10

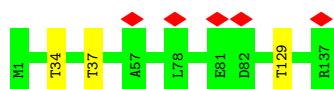


- Molecule 4: Minor capsid protein, gp10



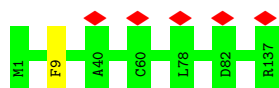
- Molecule 4: Minor capsid protein, gp10

Chain s7:  98%



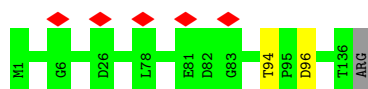
- Molecule 4: Minor capsid protein, gp10

Chain t7:  99%



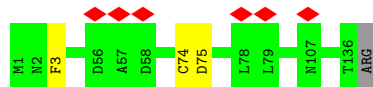
- Molecule 4: Minor capsid protein, gp10

Chain u7:  98%



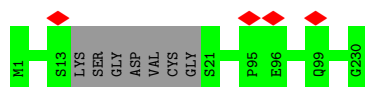
- Molecule 4: Minor capsid protein, gp10

Chain v7:  97%



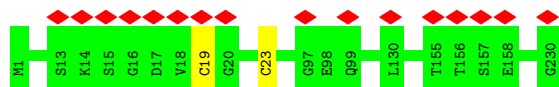
- Molecule 5: Collar sheath protein, gp13

Chain J3:  97%



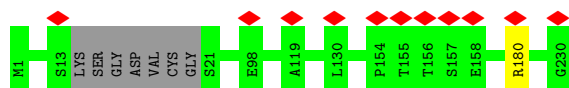
- Molecule 5: Collar sheath protein, gp13

Chain K3:  99%



- Molecule 5: Collar sheath protein, gp13

Chain L3:  97%



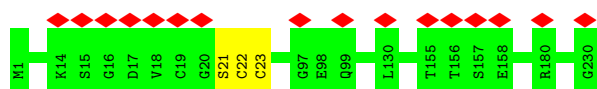
- Molecule 5: Collar sheath protein, gp13

Chain M3:  97%



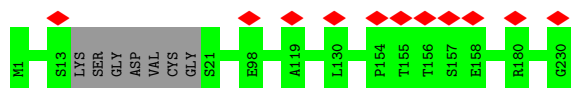
- Molecule 5: Collar sheath protein, gp13

Chain N3:  99%



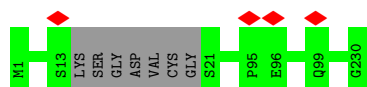
- Molecule 5: Collar sheath protein, gp13

Chain O3:  97%



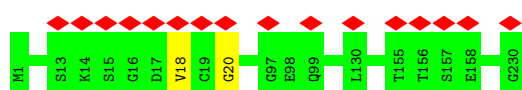
- Molecule 5: Collar sheath protein, gp13

Chain P3:  97%



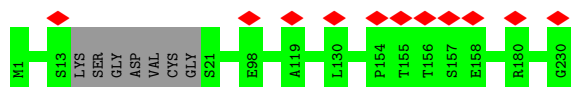
- Molecule 5: Collar sheath protein, gp13

Chain Q3:  99%



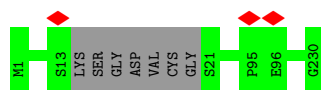
- Molecule 5: Collar sheath protein, gp13

Chain R3:  97%

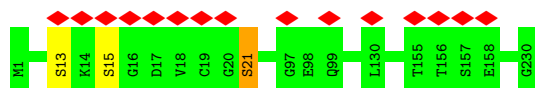


- Molecule 5: Collar sheath protein, gp13

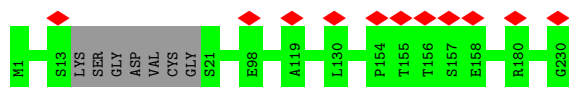
Chain S3:  97%



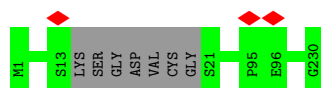
- Molecule 5: Collar sheath protein, gp13



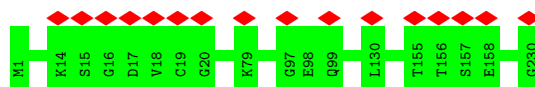
- Molecule 5: Collar sheath protein, gp13



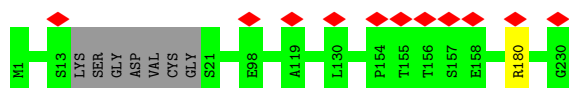
- Molecule 5: Collar sheath protein, gp13



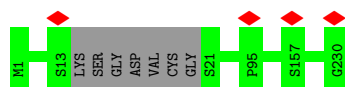
- Molecule 5: Collar sheath protein, gp13



- Molecule 5: Collar sheath protein, gp13

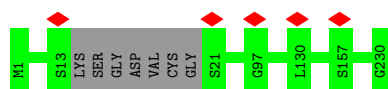


- Molecule 5: Collar sheath protein, gp13



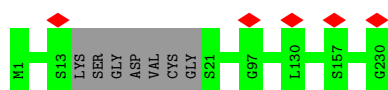
- Molecule 5: Collar sheath protein, gp13

Chain Z3:  97%



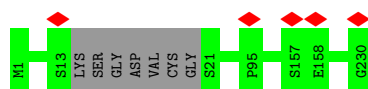
- Molecule 5: Collar sheath protein, gp13

Chain a3:  97%



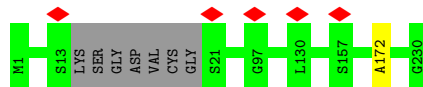
- Molecule 5: Collar sheath protein, gp13

Chain b3:  97%



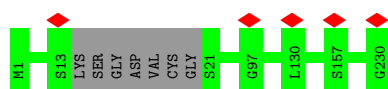
- Molecule 5: Collar sheath protein, gp13

Chain c3:  97%



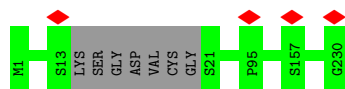
- Molecule 5: Collar sheath protein, gp13

Chain d3:  97%



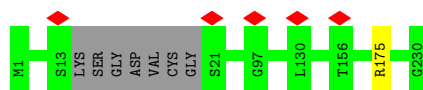
- Molecule 5: Collar sheath protein, gp13

Chain e3:  97%



- Molecule 5: Collar sheath protein, gp13

Chain f3:  97%



- Molecule 5: Collar sheath protein, gp13

Chain g3:  97%



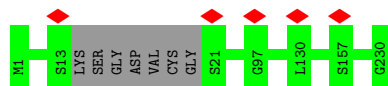
- Molecule 5: Collar sheath protein, gp13

Chain h3:  97%



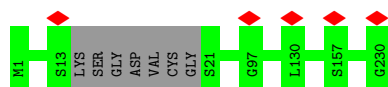
- Molecule 5: Collar sheath protein, gp13

Chain i3:  97%



- Molecule 5: Collar sheath protein, gp13

Chain j3:  97%



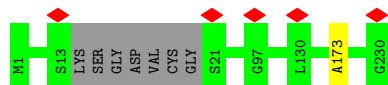
- Molecule 5: Collar sheath protein, gp13

Chain k3:  97%



- Molecule 5: Collar sheath protein, gp13

Chain l3:  97%

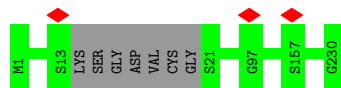


- Molecule 5: Collar sheath protein, gp13

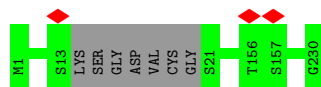
Chain m3:  97%



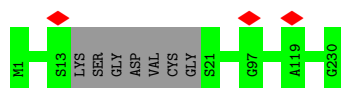
- Molecule 5: Collar sheath protein, gp13



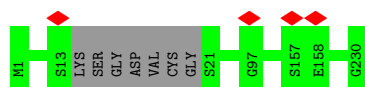
- Molecule 5: Collar sheath protein, gp13



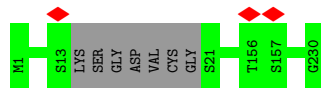
- Molecule 5: Collar sheath protein, gp13



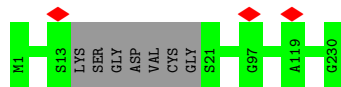
- Molecule 5: Collar sheath protein, gp13



- Molecule 5: Collar sheath protein, gp13

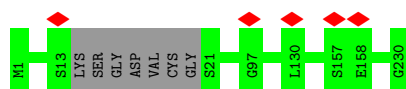


- Molecule 5: Collar sheath protein, gp13



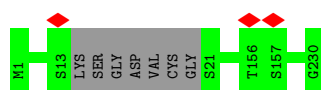
- Molecule 5: Collar sheath protein, gp13

Chain t3:  97%



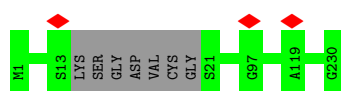
- Molecule 5: Collar sheath protein, gp13

Chain u3:  97%



- Molecule 5: Collar sheath protein, gp13

Chain v3:  97%



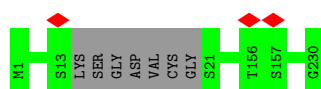
- Molecule 5: Collar sheath protein, gp13

Chain w3:  97%



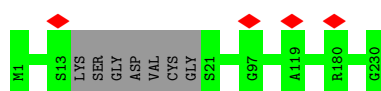
- Molecule 5: Collar sheath protein, gp13

Chain x3:  97%



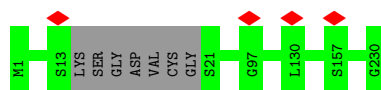
- Molecule 5: Collar sheath protein, gp13

Chain y3:  97%



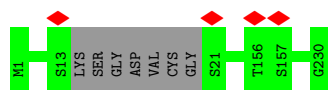
- Molecule 5: Collar sheath protein, gp13

Chain z3:  97%



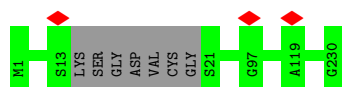
- Molecule 5: Collar sheath protein, gp13

Chain 13:  97%



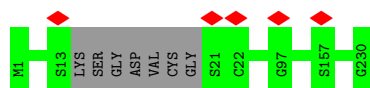
- Molecule 5: Collar sheath protein, gp13

Chain 23:  97%



- Molecule 5: Collar sheath protein, gp13

Chain 33:  97%



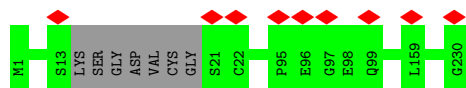
- Molecule 5: Collar sheath protein, gp13

Chain 43:  97%



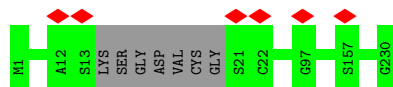
- Molecule 5: Collar sheath protein, gp13

Chain 53:  97%



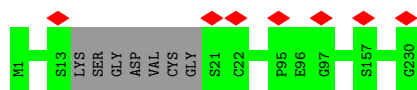
- Molecule 5: Collar sheath protein, gp13

Chain 63:  97%



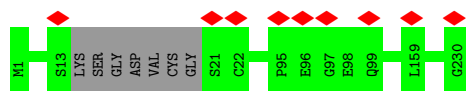
- Molecule 5: Collar sheath protein, gp13

Chain 73:  97%



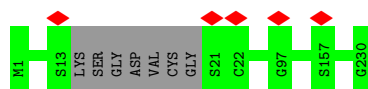
- Molecule 5: Collar sheath protein, gp13

Chain 83: 97%



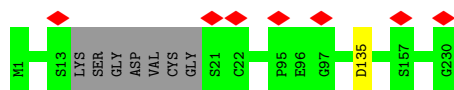
- Molecule 5: Collar sheath protein, gp13

Chain 93: 97%



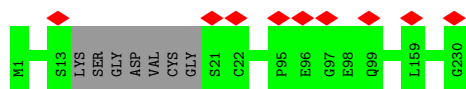
- Molecule 5: Collar sheath protein, gp13

Chain 03: 97%



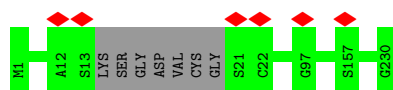
- Molecule 5: Collar sheath protein, gp13

Chain A3: 97%



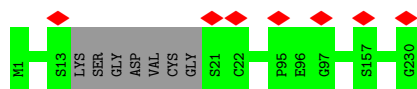
- Molecule 5: Collar sheath protein, gp13

Chain B3: 97%



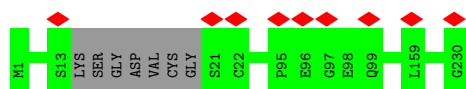
- Molecule 5: Collar sheath protein, gp13

Chain C3: 97%



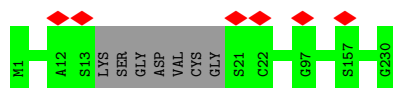
- Molecule 5: Collar sheath protein, gp13

Chain D3:  97%



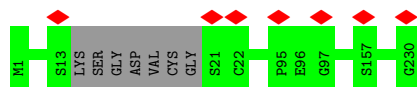
- Molecule 5: Collar sheath protein, gp13

Chain E3:  97%



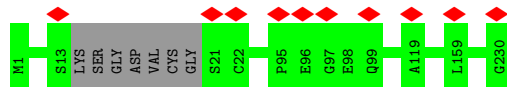
- Molecule 5: Collar sheath protein, gp13

Chain F3:  97%



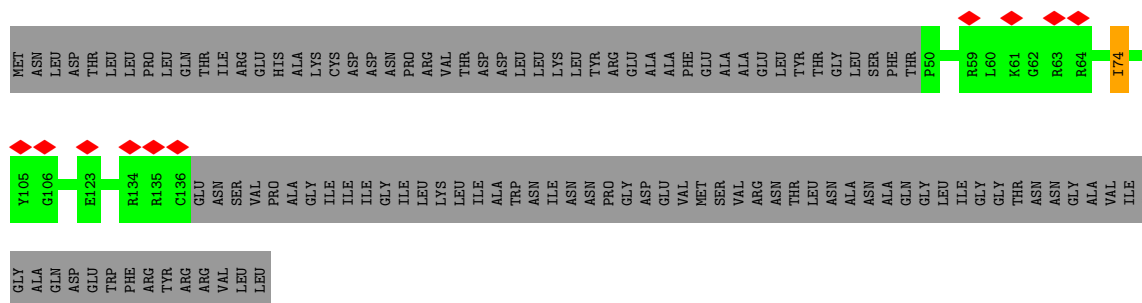
- Molecule 5: Collar sheath protein, gp13

Chain G3:  97%



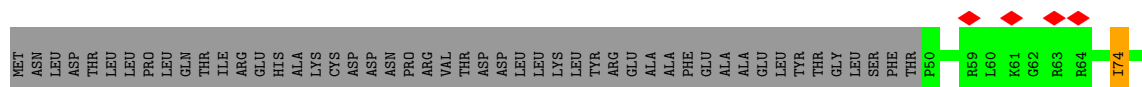
- Molecule 6: Neck 1 protein, gp14

Chain A4:  5% 43% 57%

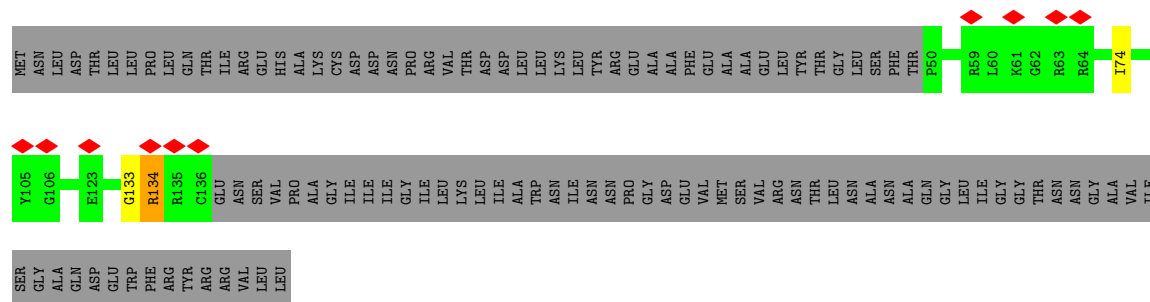


- Molecule 6: Neck 1 protein, gp14

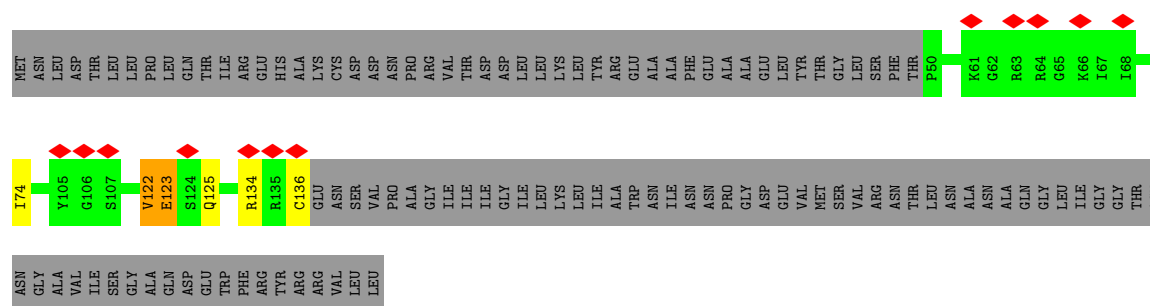
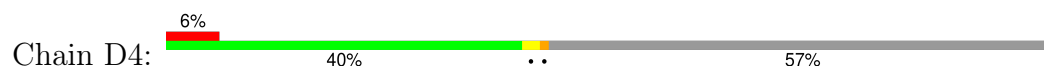
Chain B4:  5% 42% 57%



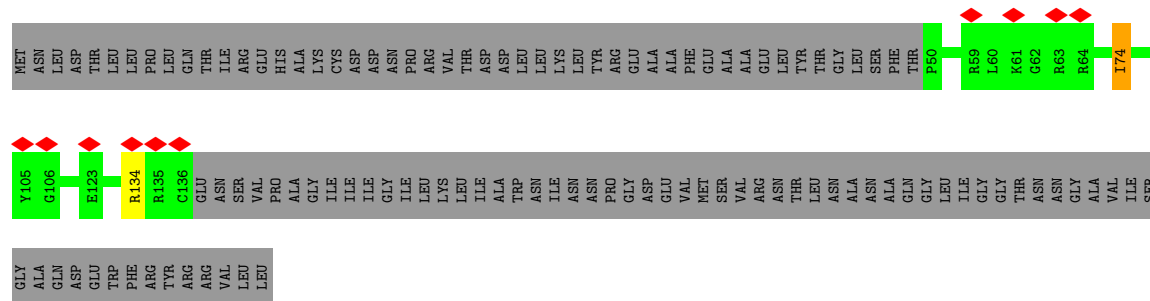
- Molecule 6: Neck 1 protein, gp14



- Molecule 6: Neck 1 protein, gp14



- Molecule 6: Neck 1 protein, gp14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	10086	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.857	Depositor
Minimum map value	-0.549	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	648.0, 648.0, 648.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a1	0.36	0/213	0.54	0/288
1	a2	0.30	0/213	0.53	0/288
1	a5	0.37	0/213	0.54	0/288
1	a6	0.35	0/213	0.53	0/288
1	a7	0.34	0/213	0.53	0/288
1	b1	0.31	0/213	0.52	0/288
1	b2	0.31	0/213	0.49	0/288
1	b5	0.30	0/213	0.50	0/288
1	b6	0.30	0/213	0.50	0/288
1	b7	0.33	0/213	0.46	0/288
1	c	0.33	0/252	0.55	0/344
1	d	0.37	0/252	0.54	0/344
1	d1	0.31	0/252	0.58	0/344
1	d2	0.31	0/252	0.59	0/344
1	d5	0.31	0/252	0.60	0/344
1	d6	0.30	0/252	0.57	0/344
1	d7	0.31	0/252	0.59	0/344
1	e	0.34	0/252	0.53	0/344
1	e1	0.32	0/213	0.54	0/288
1	e2	0.31	0/213	0.55	0/288
1	e5	0.32	0/213	0.56	0/288
1	e6	0.31	0/213	0.55	0/288
1	e7	0.31	0/213	0.56	0/288
1	f	0.42	0/252	0.57	0/344
1	g	0.44	0/252	0.55	0/344
2	f1	0.39	0/142	0.53	0/192
2	f2	0.38	0/142	0.52	0/192
2	f5	0.41	0/142	0.57	0/192
2	f6	0.38	0/142	0.54	0/192
2	f7	0.39	0/142	0.54	0/192
3	g1	0.33	0/2396	0.49	0/3243
3	g2	0.34	0/2396	0.49	0/3243
3	g5	0.33	0/2396	0.48	0/3243
3	g6	0.34	0/2396	0.49	0/3243

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	g7	0.33	0/2396	0.49	0/3243
3	h1	0.38	0/2396	0.53	0/3243
3	h2	0.38	0/2396	0.54	0/3243
3	h5	0.38	0/2396	0.52	0/3243
3	h6	0.38	0/2396	0.52	0/3243
3	h7	0.37	0/2396	0.54	2/3243 (0.1%)
3	k1	0.34	0/2313	0.48	0/3128
3	k2	0.34	0/2313	0.49	0/3128
3	k5	0.34	0/2313	0.49	0/3128
3	k6	0.34	0/2313	0.49	0/3128
3	k7	0.35	0/2313	0.51	0/3128
3	n1	0.35	0/2396	0.52	0/3243
3	n2	0.34	0/2396	0.52	0/3243
3	n5	0.34	0/2396	0.52	0/3243
3	n6	0.34	0/2396	0.51	0/3243
3	n7	0.34	0/2396	0.51	0/3243
3	o1	0.31	0/2396	0.49	0/3243
3	o2	0.31	0/2396	0.48	0/3243
3	o5	0.31	0/2396	0.49	0/3243
3	o6	0.31	0/2396	0.49	0/3243
3	o7	0.31	0/2396	0.48	0/3243
3	r1	0.33	0/2396	0.51	0/3243
3	r2	0.33	0/2396	0.52	1/3243 (0.0%)
3	r5	0.34	0/2396	0.51	0/3243
3	r6	0.33	0/2396	0.52	1/3243 (0.0%)
3	r7	0.34	0/2396	0.52	0/3243
4	l1	0.32	0/1052	0.52	0/1443
4	l2	0.33	0/1052	0.51	0/1443
4	l5	0.33	0/1052	0.51	0/1443
4	l6	0.33	0/1052	0.51	0/1443
4	l7	0.32	0/1052	0.52	0/1443
4	m1	0.34	0/1052	0.50	0/1443
4	m2	0.34	0/1052	0.48	0/1443
4	m5	0.34	0/1052	0.49	0/1443
4	m6	0.34	0/1052	0.50	0/1443
4	m7	0.34	0/1052	0.51	0/1443
4	p1	0.31	0/1052	0.50	0/1443
4	p2	0.31	0/1052	0.51	0/1443
4	p5	0.31	0/1052	0.51	0/1443
4	p6	0.30	0/1052	0.51	0/1443
4	p7	0.31	0/1052	0.52	0/1443
4	q1	0.31	0/1052	0.50	0/1443
4	q2	0.31	0/1052	0.50	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	q5	0.31	0/1052	0.49	0/1443
4	q6	0.31	0/1052	0.49	0/1443
4	q7	0.31	0/1052	0.49	0/1443
4	s1	0.31	0/1052	0.50	0/1443
4	s2	0.32	0/1052	0.50	0/1443
4	s5	0.31	0/1052	0.49	0/1443
4	s6	0.31	0/1052	0.50	0/1443
4	s7	0.30	0/1052	0.49	0/1443
4	t1	0.29	0/1052	0.50	0/1443
4	t2	0.29	0/1052	0.50	0/1443
4	t5	0.29	0/1052	0.49	0/1443
4	t6	0.30	0/1052	0.47	0/1443
4	t7	0.32	0/1052	0.54	0/1443
4	u1	0.28	0/1040	0.52	0/1429
4	u2	0.30	0/1040	0.53	0/1429
4	u5	0.28	0/1040	0.51	0/1429
4	u6	0.29	0/1040	0.53	0/1429
4	u7	0.28	0/1040	0.52	0/1429
4	v1	0.29	0/1040	0.50	0/1429
4	v2	0.31	0/1040	0.53	0/1429
4	v5	0.30	0/1040	0.51	0/1429
4	v6	0.30	0/1040	0.52	0/1429
4	v7	0.29	0/1040	0.51	0/1429
5	03	0.30	0/1723	0.47	0/2353
5	13	0.33	0/1723	0.48	0/2353
5	23	0.32	0/1723	0.49	0/2353
5	33	0.30	0/1723	0.46	0/2353
5	43	0.30	0/1723	0.46	0/2353
5	53	0.31	0/1723	0.48	0/2353
5	63	0.30	0/1723	0.47	0/2353
5	73	0.30	0/1723	0.46	0/2353
5	83	0.30	0/1723	0.48	0/2353
5	93	0.30	0/1723	0.47	0/2353
5	A3	0.31	0/1723	0.47	0/2353
5	B3	0.30	0/1723	0.47	0/2353
5	C3	0.30	0/1723	0.47	0/2353
5	D3	0.31	0/1723	0.48	0/2353
5	E3	0.30	0/1723	0.47	0/2353
5	F3	0.30	0/1723	0.47	0/2353
5	G3	0.32	0/1723	0.50	0/2353
5	J3	0.35	0/1723	0.47	0/2353
5	K3	0.33	0/1768	0.47	0/2414
5	L3	0.32	0/1723	0.47	0/2353

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
5	M3	0.35	0/1723	0.48	0/2353
5	N3	0.35	0/1768	0.49	0/2414
5	O3	0.32	0/1723	0.47	0/2353
5	P3	0.35	0/1723	0.47	0/2353
5	Q3	0.33	0/1768	0.48	1/2414 (0.0%)
5	R3	0.32	0/1723	0.47	0/2353
5	S3	0.35	0/1723	0.47	0/2353
5	T3	0.34	0/1768	0.49	0/2414
5	U3	0.33	0/1723	0.47	0/2353
5	V3	0.35	0/1723	0.48	0/2353
5	W3	0.33	0/1768	0.50	0/2414
5	X3	0.32	0/1723	0.47	0/2353
5	Y3	0.33	0/1723	0.46	0/2353
5	Z3	0.34	0/1723	0.47	0/2353
5	a3	0.33	0/1723	0.47	0/2353
5	b3	0.34	0/1723	0.47	0/2353
5	c3	0.34	0/1723	0.48	0/2353
5	d3	0.33	0/1723	0.47	0/2353
5	e3	0.34	0/1723	0.47	0/2353
5	f3	0.35	0/1723	0.48	0/2353
5	g3	0.33	0/1723	0.48	0/2353
5	h3	0.33	0/1723	0.46	0/2353
5	i3	0.35	0/1723	0.49	0/2353
5	j3	0.33	0/1723	0.47	0/2353
5	k3	0.34	0/1723	0.47	0/2353
5	l3	0.35	0/1723	0.49	0/2353
5	m3	0.33	0/1723	0.47	0/2353
5	n3	0.33	0/1723	0.47	0/2353
5	o3	0.33	0/1723	0.47	0/2353
5	p3	0.32	0/1723	0.48	0/2353
5	q3	0.33	0/1723	0.47	0/2353
5	r3	0.33	0/1723	0.48	0/2353
5	s3	0.33	0/1723	0.48	0/2353
5	t3	0.33	0/1723	0.47	0/2353
5	u3	0.33	0/1723	0.47	0/2353
5	v3	0.32	0/1723	0.47	0/2353
5	w3	0.33	0/1723	0.46	0/2353
5	x3	0.32	0/1723	0.47	0/2353
5	y3	0.32	0/1723	0.47	0/2353
5	z3	0.33	0/1723	0.47	0/2353
6	A4	0.31	0/689	0.50	0/934
6	B4	0.31	0/689	0.53	0/934
6	C4	0.31	0/689	0.51	0/934

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	D4	0.29	0/689	0.50	0/934
6	E4	0.31	0/689	0.53	0/934
All	All	0.33	0/226900	0.49	5/309170 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	r6	388	ASP	CB-CG-OD1	5.26	123.04	118.30
3	h7	189	GLU	N-CA-C	-5.25	96.83	111.00
3	h7	385	CYS	CB-CA-C	-5.15	100.09	110.40
5	Q3	20	GLY	N-CA-C	5.12	125.90	113.10
3	r2	388	ASP	CB-CG-OD1	5.05	122.85	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	a1	26/38 (68%)	24 (92%)	2 (8%)	0	100	100
1	a2	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	a5	26/38 (68%)	24 (92%)	2 (8%)	0	100	100
1	a6	26/38 (68%)	24 (92%)	2 (8%)	0	100	100
1	a7	26/38 (68%)	24 (92%)	2 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b1	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	b2	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	b5	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	b6	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	b7	26/38 (68%)	25 (96%)	1 (4%)	0	100	100
1	c	32/38 (84%)	29 (91%)	3 (9%)	0	100	100
1	d	32/38 (84%)	29 (91%)	3 (9%)	0	100	100
1	d1	32/38 (84%)	24 (75%)	8 (25%)	0	100	100
1	d2	32/38 (84%)	26 (81%)	6 (19%)	0	100	100
1	d5	32/38 (84%)	25 (78%)	7 (22%)	0	100	100
1	d6	32/38 (84%)	25 (78%)	7 (22%)	0	100	100
1	d7	32/38 (84%)	24 (75%)	8 (25%)	0	100	100
1	e	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
1	e1	26/38 (68%)	19 (73%)	7 (27%)	0	100	100
1	e2	26/38 (68%)	22 (85%)	4 (15%)	0	100	100
1	e5	26/38 (68%)	21 (81%)	5 (19%)	0	100	100
1	e6	26/38 (68%)	19 (73%)	7 (27%)	0	100	100
1	e7	26/38 (68%)	18 (69%)	8 (31%)	0	100	100
1	f	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
1	g	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
2	f1	18/217 (8%)	15 (83%)	3 (17%)	0	100	100
2	f2	18/217 (8%)	16 (89%)	2 (11%)	0	100	100
2	f5	18/217 (8%)	12 (67%)	6 (33%)	0	100	100
2	f6	18/217 (8%)	15 (83%)	3 (17%)	0	100	100
2	f7	18/217 (8%)	16 (89%)	2 (11%)	0	100	100
3	g1	297/465 (64%)	253 (85%)	43 (14%)	1 (0%)	37	69
3	g2	297/465 (64%)	251 (84%)	44 (15%)	2 (1%)	19	53
3	g5	297/465 (64%)	250 (84%)	46 (16%)	1 (0%)	37	69
3	g6	297/465 (64%)	250 (84%)	46 (16%)	1 (0%)	37	69
3	g7	297/465 (64%)	252 (85%)	43 (14%)	2 (1%)	19	53
3	h1	297/465 (64%)	243 (82%)	51 (17%)	3 (1%)	13	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	h2	297/465 (64%)	242 (82%)	50 (17%)	5 (2%)	7	36
3	h5	297/465 (64%)	242 (82%)	53 (18%)	2 (1%)	19	53
3	h6	297/465 (64%)	241 (81%)	54 (18%)	2 (1%)	19	53
3	h7	297/465 (64%)	247 (83%)	48 (16%)	2 (1%)	19	53
3	k1	286/465 (62%)	251 (88%)	35 (12%)	0	100	100
3	k2	286/465 (62%)	248 (87%)	37 (13%)	1 (0%)	37	69
3	k5	286/465 (62%)	248 (87%)	38 (13%)	0	100	100
3	k6	286/465 (62%)	251 (88%)	34 (12%)	1 (0%)	37	69
3	k7	286/465 (62%)	249 (87%)	36 (13%)	1 (0%)	37	69
3	n1	297/465 (64%)	247 (83%)	49 (16%)	1 (0%)	37	69
3	n2	297/465 (64%)	243 (82%)	52 (18%)	2 (1%)	19	53
3	n5	297/465 (64%)	245 (82%)	50 (17%)	2 (1%)	19	53
3	n6	297/465 (64%)	246 (83%)	49 (16%)	2 (1%)	19	53
3	n7	297/465 (64%)	249 (84%)	46 (16%)	2 (1%)	19	53
3	o1	297/465 (64%)	248 (84%)	45 (15%)	4 (1%)	10	41
3	o2	297/465 (64%)	245 (82%)	47 (16%)	5 (2%)	7	36
3	o5	297/465 (64%)	245 (82%)	47 (16%)	5 (2%)	7	36
3	o6	297/465 (64%)	242 (82%)	50 (17%)	5 (2%)	7	36
3	o7	297/465 (64%)	248 (84%)	45 (15%)	4 (1%)	10	41
3	r1	297/465 (64%)	254 (86%)	42 (14%)	1 (0%)	37	69
3	r2	297/465 (64%)	251 (84%)	45 (15%)	1 (0%)	37	69
3	r5	297/465 (64%)	250 (84%)	44 (15%)	3 (1%)	13	46
3	r6	297/465 (64%)	252 (85%)	44 (15%)	1 (0%)	37	69
3	r7	297/465 (64%)	255 (86%)	37 (12%)	5 (2%)	7	36
4	l1	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
4	l2	135/137 (98%)	117 (87%)	15 (11%)	3 (2%)	5	32
4	l5	135/137 (98%)	120 (89%)	14 (10%)	1 (1%)	19	53
4	l6	135/137 (98%)	119 (88%)	15 (11%)	1 (1%)	19	53
4	l7	135/137 (98%)	121 (90%)	13 (10%)	1 (1%)	19	53
4	m1	135/137 (98%)	117 (87%)	18 (13%)	0	100	100
4	m2	135/137 (98%)	119 (88%)	16 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	m5	135/137 (98%)	118 (87%)	17 (13%)	0	100	100
4	m6	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
4	m7	135/137 (98%)	117 (87%)	18 (13%)	0	100	100
4	p1	135/137 (98%)	112 (83%)	22 (16%)	1 (1%)	19	53
4	p2	135/137 (98%)	111 (82%)	23 (17%)	1 (1%)	19	53
4	p5	135/137 (98%)	110 (82%)	24 (18%)	1 (1%)	19	53
4	p6	135/137 (98%)	111 (82%)	23 (17%)	1 (1%)	19	53
4	p7	135/137 (98%)	112 (83%)	22 (16%)	1 (1%)	19	53
4	q1	135/137 (98%)	120 (89%)	15 (11%)	0	100	100
4	q2	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
4	q5	135/137 (98%)	117 (87%)	18 (13%)	0	100	100
4	q6	135/137 (98%)	122 (90%)	13 (10%)	0	100	100
4	q7	135/137 (98%)	120 (89%)	15 (11%)	0	100	100
4	s1	135/137 (98%)	125 (93%)	10 (7%)	0	100	100
4	s2	135/137 (98%)	124 (92%)	10 (7%)	1 (1%)	19	53
4	s5	135/137 (98%)	125 (93%)	10 (7%)	0	100	100
4	s6	135/137 (98%)	124 (92%)	10 (7%)	1 (1%)	19	53
4	s7	135/137 (98%)	125 (93%)	10 (7%)	0	100	100
4	t1	135/137 (98%)	121 (90%)	14 (10%)	0	100	100
4	t2	135/137 (98%)	123 (91%)	12 (9%)	0	100	100
4	t5	135/137 (98%)	122 (90%)	13 (10%)	0	100	100
4	t6	135/137 (98%)	124 (92%)	11 (8%)	0	100	100
4	t7	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
4	u1	134/137 (98%)	119 (89%)	15 (11%)	0	100	100
4	u2	134/137 (98%)	118 (88%)	16 (12%)	0	100	100
4	u5	134/137 (98%)	118 (88%)	16 (12%)	0	100	100
4	u6	134/137 (98%)	119 (89%)	15 (11%)	0	100	100
4	u7	134/137 (98%)	119 (89%)	15 (11%)	0	100	100
4	v1	134/137 (98%)	113 (84%)	19 (14%)	2 (2%)	8	38
4	v2	134/137 (98%)	111 (83%)	23 (17%)	0	100	100
4	v5	134/137 (98%)	113 (84%)	21 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	v6	134/137 (98%)	114 (85%)	20 (15%)	0	100	100
4	v7	134/137 (98%)	113 (84%)	20 (15%)	1 (1%)	19	53
5	03	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	13	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
5	23	219/230 (95%)	192 (88%)	27 (12%)	0	100	100
5	33	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
5	43	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	53	219/230 (95%)	206 (94%)	13 (6%)	0	100	100
5	63	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	73	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	83	219/230 (95%)	206 (94%)	13 (6%)	0	100	100
5	93	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	A3	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
5	B3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	C3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	D3	219/230 (95%)	204 (93%)	15 (7%)	0	100	100
5	E3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	F3	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
5	G3	219/230 (95%)	203 (93%)	16 (7%)	0	100	100
5	J3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	K3	228/230 (99%)	210 (92%)	18 (8%)	0	100	100
5	L3	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
5	M3	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
5	N3	228/230 (99%)	207 (91%)	20 (9%)	1 (0%)	30	64
5	O3	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	P3	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
5	Q3	228/230 (99%)	206 (90%)	21 (9%)	1 (0%)	30	64
5	R3	219/230 (95%)	203 (93%)	16 (7%)	0	100	100
5	S3	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
5	T3	228/230 (99%)	206 (90%)	20 (9%)	2 (1%)	14	48
5	U3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	V3	219/230 (95%)	202 (92%)	17 (8%)	0	100	100
5	W3	228/230 (99%)	206 (90%)	22 (10%)	0	100	100
5	X3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	Y3	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
5	Z3	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	a3	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	b3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	c3	219/230 (95%)	196 (90%)	22 (10%)	1 (0%)	25	59
5	d3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	e3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	f3	219/230 (95%)	195 (89%)	24 (11%)	0	100	100
5	g3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	h3	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
5	i3	219/230 (95%)	196 (90%)	23 (10%)	0	100	100
5	j3	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
5	k3	219/230 (95%)	198 (90%)	21 (10%)	0	100	100
5	l3	219/230 (95%)	196 (90%)	22 (10%)	1 (0%)	25	59
5	m3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	n3	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
5	o3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	p3	219/230 (95%)	192 (88%)	27 (12%)	0	100	100
5	q3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	r3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	s3	219/230 (95%)	192 (88%)	27 (12%)	0	100	100
5	t3	219/230 (95%)	197 (90%)	22 (10%)	0	100	100
5	u3	219/230 (95%)	201 (92%)	18 (8%)	0	100	100
5	v3	219/230 (95%)	191 (87%)	28 (13%)	0	100	100
5	w3	219/230 (95%)	200 (91%)	19 (9%)	0	100	100
5	x3	219/230 (95%)	199 (91%)	20 (9%)	0	100	100
5	y3	219/230 (95%)	192 (88%)	27 (12%)	0	100	100
5	z3	219/230 (95%)	197 (90%)	22 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A4	85/202 (42%)	66 (78%)	18 (21%)	1 (1%)	11	43
6	B4	85/202 (42%)	72 (85%)	12 (14%)	1 (1%)	11	43
6	C4	85/202 (42%)	67 (79%)	15 (18%)	3 (4%)	3	24
6	D4	85/202 (42%)	71 (84%)	11 (13%)	3 (4%)	3	24
6	E4	85/202 (42%)	71 (84%)	13 (15%)	1 (1%)	11	43
All	All	28655/36275 (79%)	25176 (88%)	3381 (12%)	98 (0%)	38	69

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	h1	172	PRO
4	p1	78	LEU
3	g2	457	GLU
3	h2	191	ALA
4	l2	75	ASP

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	a1	25/32 (78%)	24 (96%)	1 (4%)	27	57
1	a2	25/32 (78%)	24 (96%)	1 (4%)	27	57
1	a5	25/32 (78%)	23 (92%)	2 (8%)	10	34
1	a6	25/32 (78%)	24 (96%)	1 (4%)	27	57
1	a7	25/32 (78%)	24 (96%)	1 (4%)	27	57
1	b1	25/32 (78%)	25 (100%)	0	100	100
1	b2	25/32 (78%)	25 (100%)	0	100	100
1	b5	25/32 (78%)	25 (100%)	0	100	100
1	b6	25/32 (78%)	25 (100%)	0	100	100
1	b7	25/32 (78%)	25 (100%)	0	100	100
1	c	29/32 (91%)	28 (97%)	1 (3%)	32	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	d	29/32 (91%)	29 (100%)	0	100	100
1	d1	29/32 (91%)	29 (100%)	0	100	100
1	d2	29/32 (91%)	29 (100%)	0	100	100
1	d5	29/32 (91%)	29 (100%)	0	100	100
1	d6	29/32 (91%)	29 (100%)	0	100	100
1	d7	29/32 (91%)	29 (100%)	0	100	100
1	e	29/32 (91%)	28 (97%)	1 (3%)	32	61
1	e1	25/32 (78%)	25 (100%)	0	100	100
1	e2	25/32 (78%)	25 (100%)	0	100	100
1	e5	25/32 (78%)	25 (100%)	0	100	100
1	e6	25/32 (78%)	25 (100%)	0	100	100
1	e7	25/32 (78%)	25 (100%)	0	100	100
1	f	29/32 (91%)	29 (100%)	0	100	100
1	g	29/32 (91%)	29 (100%)	0	100	100
2	f1	15/175 (9%)	15 (100%)	0	100	100
2	f2	15/175 (9%)	15 (100%)	0	100	100
2	f5	15/175 (9%)	15 (100%)	0	100	100
2	f6	15/175 (9%)	15 (100%)	0	100	100
2	f7	15/175 (9%)	15 (100%)	0	100	100
3	g1	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	g2	240/379 (63%)	234 (98%)	6 (2%)	42	69
3	g5	240/379 (63%)	240 (100%)	0	100	100
3	g6	240/379 (63%)	237 (99%)	3 (1%)	65	81
3	g7	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	h1	240/379 (63%)	234 (98%)	6 (2%)	42	69
3	h2	240/379 (63%)	234 (98%)	6 (2%)	42	69
3	h5	240/379 (63%)	233 (97%)	7 (3%)	37	65
3	h6	240/379 (63%)	234 (98%)	6 (2%)	42	69
3	h7	240/379 (63%)	239 (100%)	1 (0%)	89	94
3	k1	232/379 (61%)	231 (100%)	1 (0%)	89	94
3	k2	232/379 (61%)	231 (100%)	1 (0%)	89	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	k5	232/379 (61%)	232 (100%)	0	100	100
3	k6	232/379 (61%)	232 (100%)	0	100	100
3	k7	232/379 (61%)	232 (100%)	0	100	100
3	n1	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	n2	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	n5	240/379 (63%)	239 (100%)	1 (0%)	89	94
3	n6	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	n7	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	o1	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	o2	240/379 (63%)	239 (100%)	1 (0%)	89	94
3	o5	240/379 (63%)	239 (100%)	1 (0%)	89	94
3	o6	240/379 (63%)	239 (100%)	1 (0%)	89	94
3	o7	240/379 (63%)	238 (99%)	2 (1%)	79	87
3	r1	240/379 (63%)	233 (97%)	7 (3%)	37	65
3	r2	240/379 (63%)	234 (98%)	6 (2%)	42	69
3	r5	240/379 (63%)	235 (98%)	5 (2%)	48	72
3	r6	240/379 (63%)	237 (99%)	3 (1%)	65	81
3	r7	240/379 (63%)	233 (97%)	7 (3%)	37	65
4	l1	112/112 (100%)	108 (96%)	4 (4%)	30	60
4	l2	112/112 (100%)	107 (96%)	5 (4%)	23	54
4	l5	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	l6	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	l7	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	m1	112/112 (100%)	112 (100%)	0	100	100
4	m2	112/112 (100%)	112 (100%)	0	100	100
4	m5	112/112 (100%)	112 (100%)	0	100	100
4	m6	112/112 (100%)	112 (100%)	0	100	100
4	m7	112/112 (100%)	112 (100%)	0	100	100
4	p1	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	p2	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	p5	112/112 (100%)	110 (98%)	2 (2%)	54	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	p6	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	p7	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	q1	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	q2	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	q5	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	q6	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	q7	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	s1	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	s2	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	s5	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	s6	112/112 (100%)	110 (98%)	2 (2%)	54	75
4	s7	112/112 (100%)	109 (97%)	3 (3%)	40	67
4	t1	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	t2	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	t5	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	t6	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	t7	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	u1	111/112 (99%)	111 (100%)	0	100	100
4	u2	111/112 (99%)	109 (98%)	2 (2%)	54	75
4	u5	111/112 (99%)	109 (98%)	2 (2%)	54	75
4	u6	111/112 (99%)	110 (99%)	1 (1%)	75	86
4	u7	111/112 (99%)	109 (98%)	2 (2%)	54	75
4	v1	111/112 (99%)	106 (96%)	5 (4%)	23	54
4	v2	111/112 (99%)	109 (98%)	2 (2%)	54	75
4	v5	111/112 (99%)	108 (97%)	3 (3%)	40	67
4	v6	111/112 (99%)	109 (98%)	2 (2%)	54	75
4	v7	111/112 (99%)	109 (98%)	2 (2%)	54	75
5	03	186/191 (97%)	185 (100%)	1 (0%)	86	92
5	13	186/191 (97%)	186 (100%)	0	100	100
5	23	186/191 (97%)	186 (100%)	0	100	100
5	33	186/191 (97%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	43	186/191 (97%)	185 (100%)	1 (0%)	86	92
5	53	186/191 (97%)	186 (100%)	0	100	100
5	63	186/191 (97%)	186 (100%)	0	100	100
5	73	186/191 (97%)	186 (100%)	0	100	100
5	83	186/191 (97%)	186 (100%)	0	100	100
5	93	186/191 (97%)	186 (100%)	0	100	100
5	A3	186/191 (97%)	186 (100%)	0	100	100
5	B3	186/191 (97%)	186 (100%)	0	100	100
5	C3	186/191 (97%)	186 (100%)	0	100	100
5	D3	186/191 (97%)	186 (100%)	0	100	100
5	E3	186/191 (97%)	186 (100%)	0	100	100
5	F3	186/191 (97%)	186 (100%)	0	100	100
5	G3	186/191 (97%)	186 (100%)	0	100	100
5	J3	186/191 (97%)	186 (100%)	0	100	100
5	K3	191/191 (100%)	189 (99%)	2 (1%)	73	84
5	L3	186/191 (97%)	185 (100%)	1 (0%)	86	92
5	M3	186/191 (97%)	186 (100%)	0	100	100
5	N3	191/191 (100%)	189 (99%)	2 (1%)	73	84
5	O3	186/191 (97%)	186 (100%)	0	100	100
5	P3	186/191 (97%)	186 (100%)	0	100	100
5	Q3	191/191 (100%)	191 (100%)	0	100	100
5	R3	186/191 (97%)	186 (100%)	0	100	100
5	S3	186/191 (97%)	186 (100%)	0	100	100
5	T3	191/191 (100%)	189 (99%)	2 (1%)	73	84
5	U3	186/191 (97%)	186 (100%)	0	100	100
5	V3	186/191 (97%)	186 (100%)	0	100	100
5	W3	191/191 (100%)	191 (100%)	0	100	100
5	X3	186/191 (97%)	185 (100%)	1 (0%)	86	92
5	Y3	186/191 (97%)	186 (100%)	0	100	100
5	Z3	186/191 (97%)	186 (100%)	0	100	100
5	a3	186/191 (97%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	b3	186/191 (97%)	186 (100%)	0	100	100
5	c3	186/191 (97%)	186 (100%)	0	100	100
5	d3	186/191 (97%)	186 (100%)	0	100	100
5	e3	186/191 (97%)	186 (100%)	0	100	100
5	f3	186/191 (97%)	185 (100%)	1 (0%)	86	92
5	g3	186/191 (97%)	186 (100%)	0	100	100
5	h3	186/191 (97%)	186 (100%)	0	100	100
5	i3	186/191 (97%)	186 (100%)	0	100	100
5	j3	186/191 (97%)	186 (100%)	0	100	100
5	k3	186/191 (97%)	186 (100%)	0	100	100
5	l3	186/191 (97%)	186 (100%)	0	100	100
5	m3	186/191 (97%)	186 (100%)	0	100	100
5	n3	186/191 (97%)	186 (100%)	0	100	100
5	o3	186/191 (97%)	186 (100%)	0	100	100
5	p3	186/191 (97%)	186 (100%)	0	100	100
5	q3	186/191 (97%)	186 (100%)	0	100	100
5	r3	186/191 (97%)	186 (100%)	0	100	100
5	s3	186/191 (97%)	186 (100%)	0	100	100
5	t3	186/191 (97%)	186 (100%)	0	100	100
5	u3	186/191 (97%)	186 (100%)	0	100	100
5	v3	186/191 (97%)	186 (100%)	0	100	100
5	w3	186/191 (97%)	186 (100%)	0	100	100
5	x3	186/191 (97%)	186 (100%)	0	100	100
5	y3	186/191 (97%)	186 (100%)	0	100	100
5	z3	186/191 (97%)	186 (100%)	0	100	100
6	A4	73/168 (44%)	72 (99%)	1 (1%)	62	79
6	B4	73/168 (44%)	70 (96%)	3 (4%)	26	56
6	C4	73/168 (44%)	72 (99%)	1 (1%)	62	79
6	D4	73/168 (44%)	68 (93%)	5 (7%)	13	41
6	E4	73/168 (44%)	71 (97%)	2 (3%)	40	67
All	All	23920/29825 (80%)	23738 (99%)	182 (1%)	77	87

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	r5	379	ARG
3	r6	175	PHE
4	t5	137	ARG
3	h6	188	ILE
4	v6	3	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 260 such sidechains are listed below:

Mol	Chain	Res	Type
3	k7	324	GLN
3	n7	283	GLN
5	m3	99	GLN
5	h3	55	ASN
3	o7	384	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 ⓘ

There are no chain breaks in this entry.

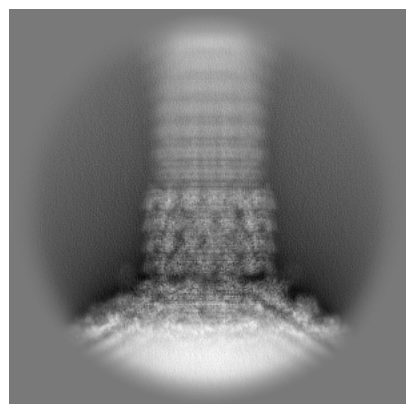
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29504. These allow visual inspection of the internal detail of the map and identification of artifacts.

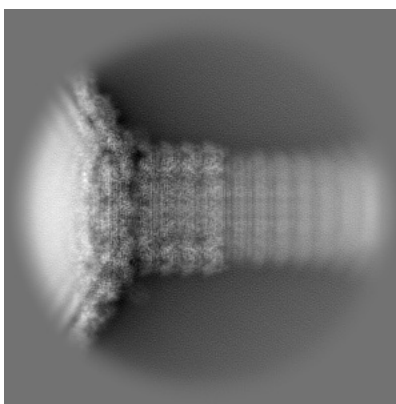
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

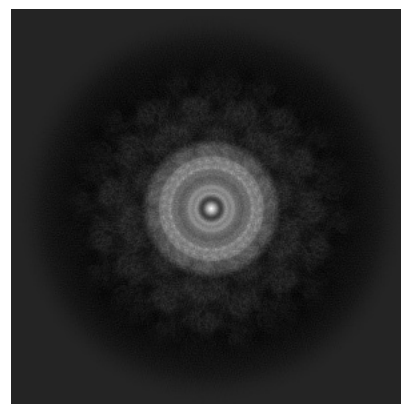
6.1.1 Primary map



X

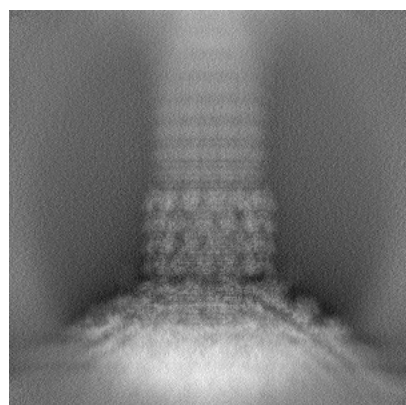


Y

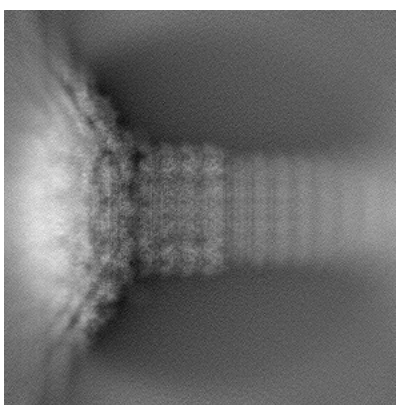


Z

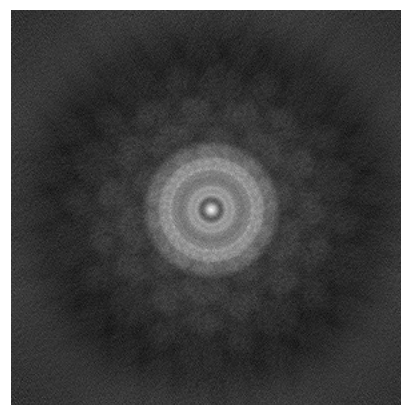
6.1.2 Raw map



X



Y

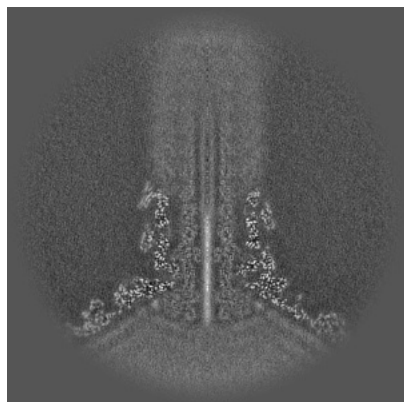


Z

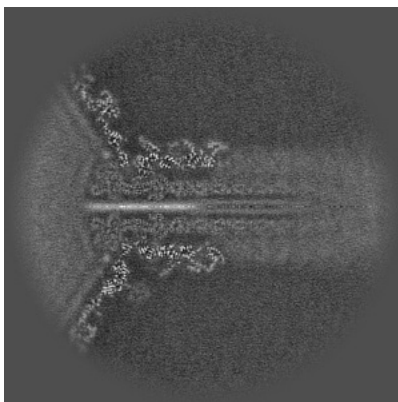
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

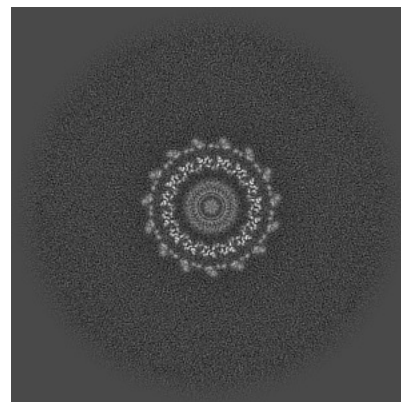
6.2.1 Primary map



X Index: 300

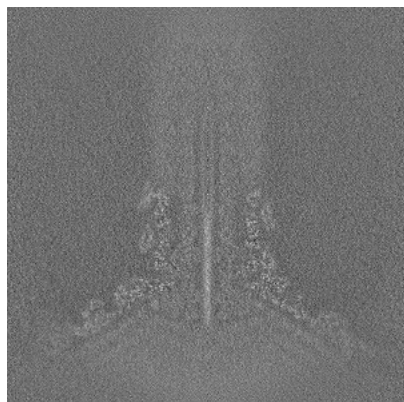


Y Index: 300

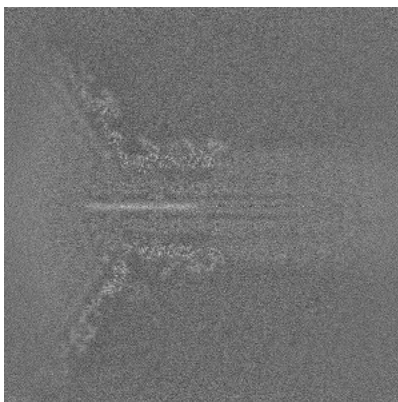


Z Index: 300

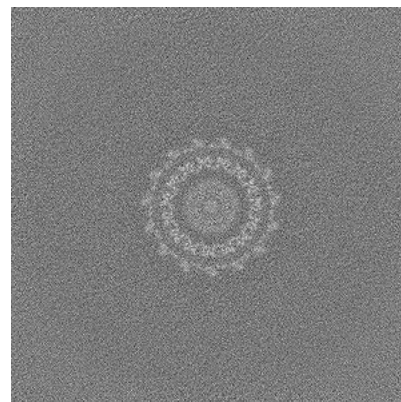
6.2.2 Raw map



X Index: 300



Y Index: 300

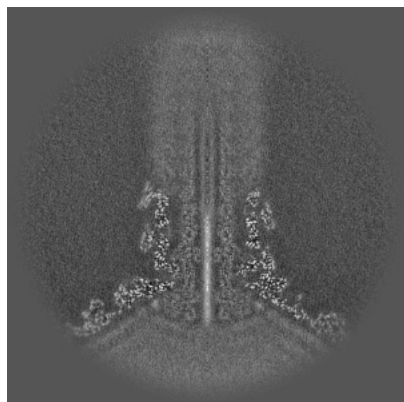


Z Index: 300

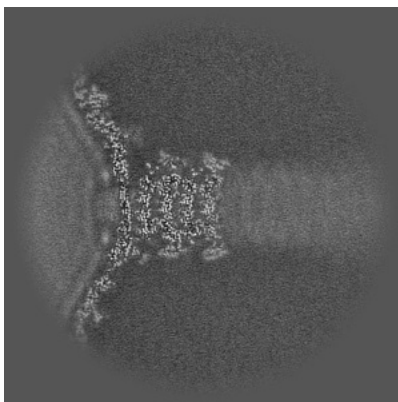
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

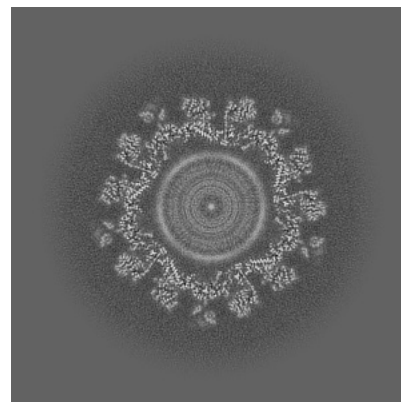
6.3.1 Primary map



X Index: 300

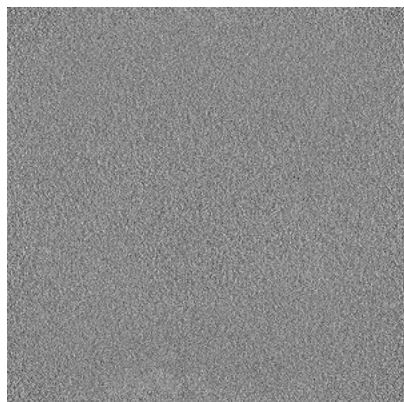


Y Index: 239

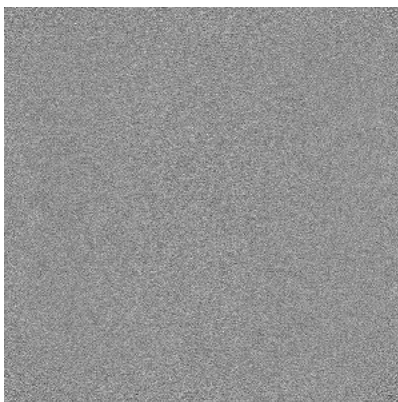


Z Index: 156

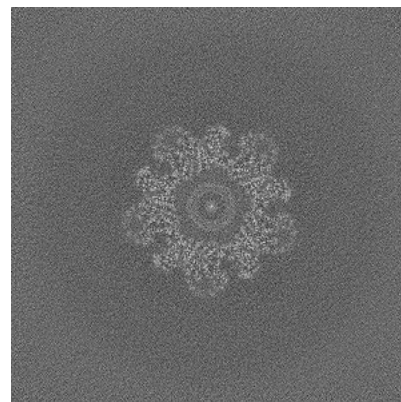
6.3.2 Raw map



X Index: 0



Y Index: 0

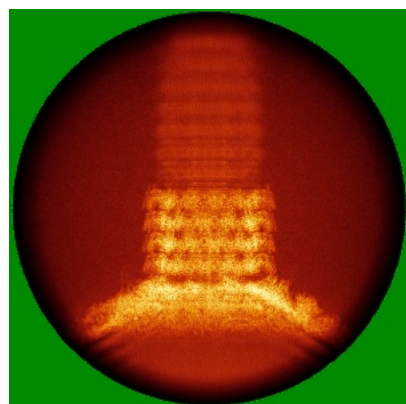


Z Index: 179

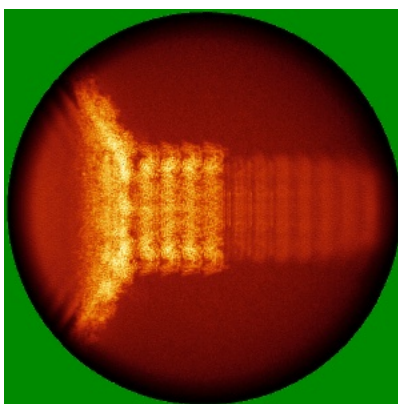
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

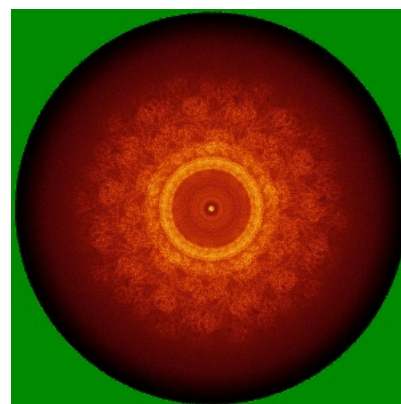
6.4.1 Primary map



X

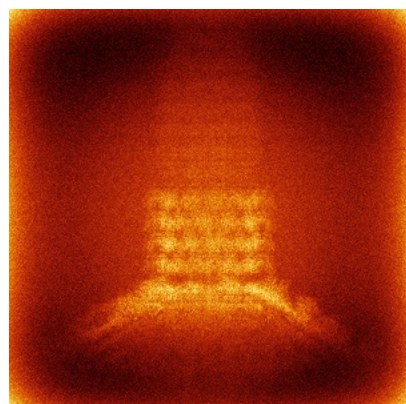


Y

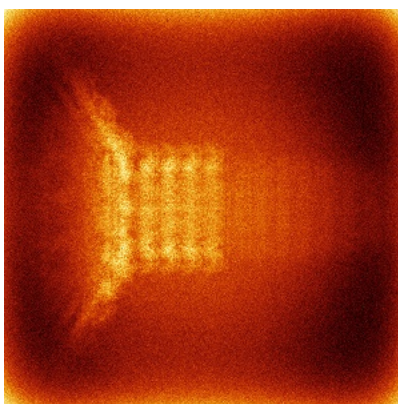


Z

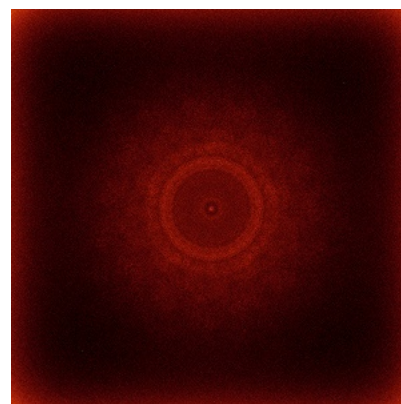
6.4.2 Raw map



X



Y

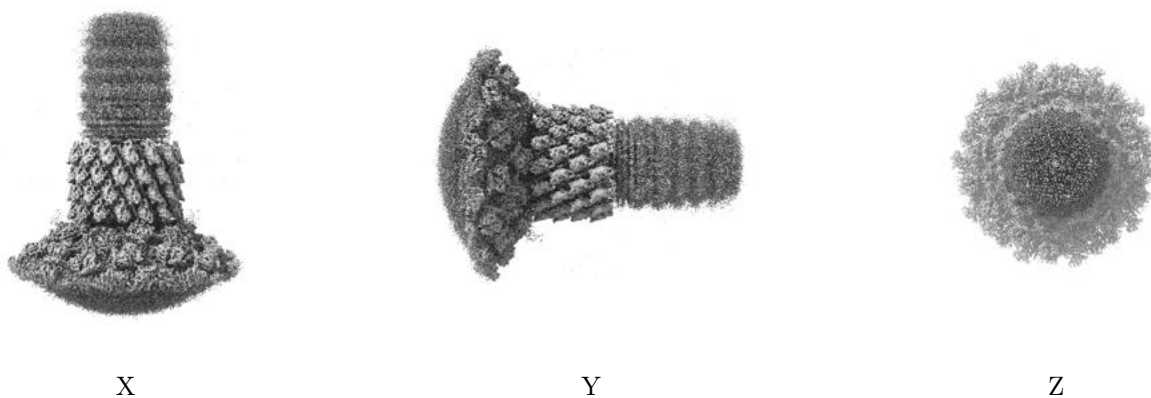


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

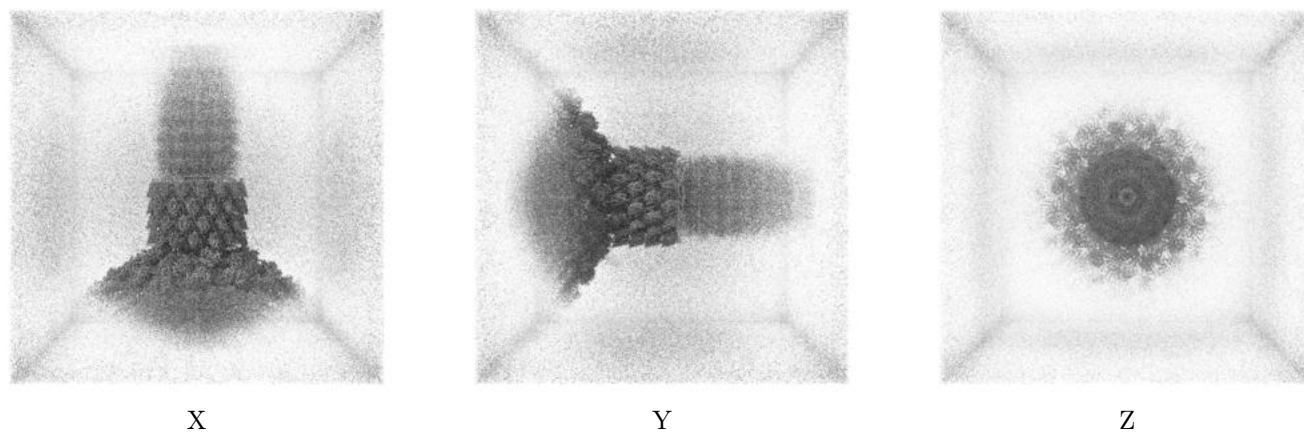
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

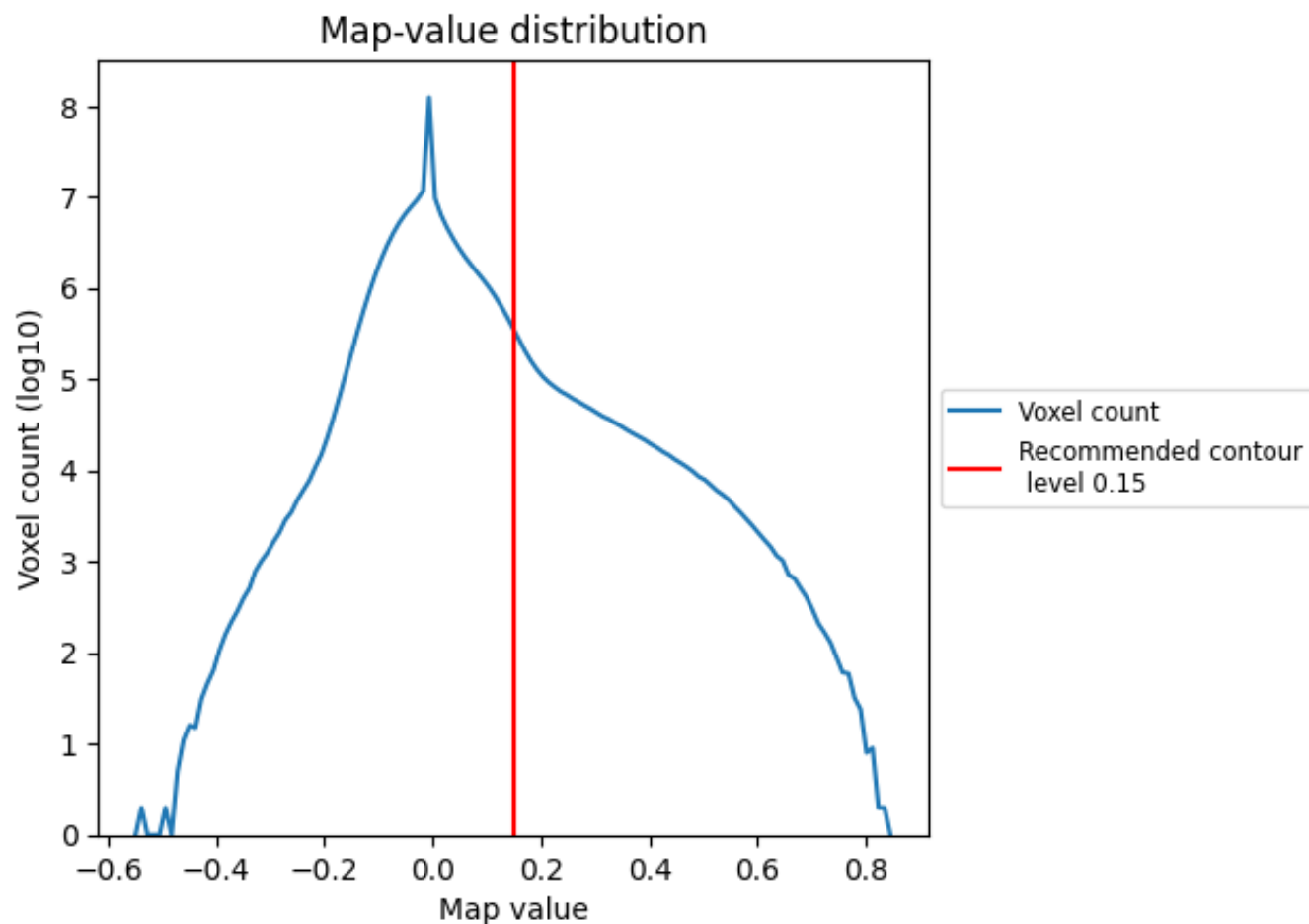
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

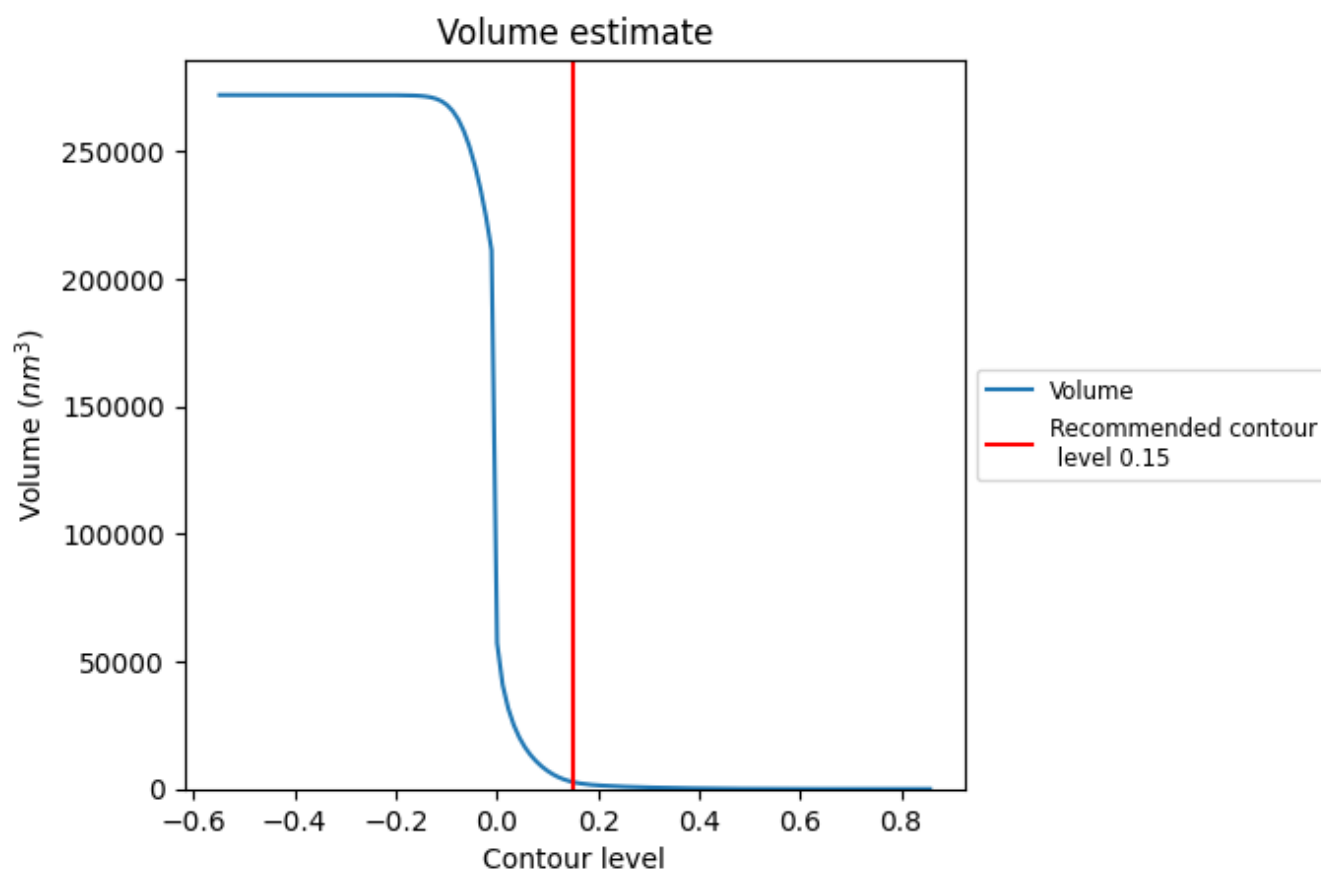
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

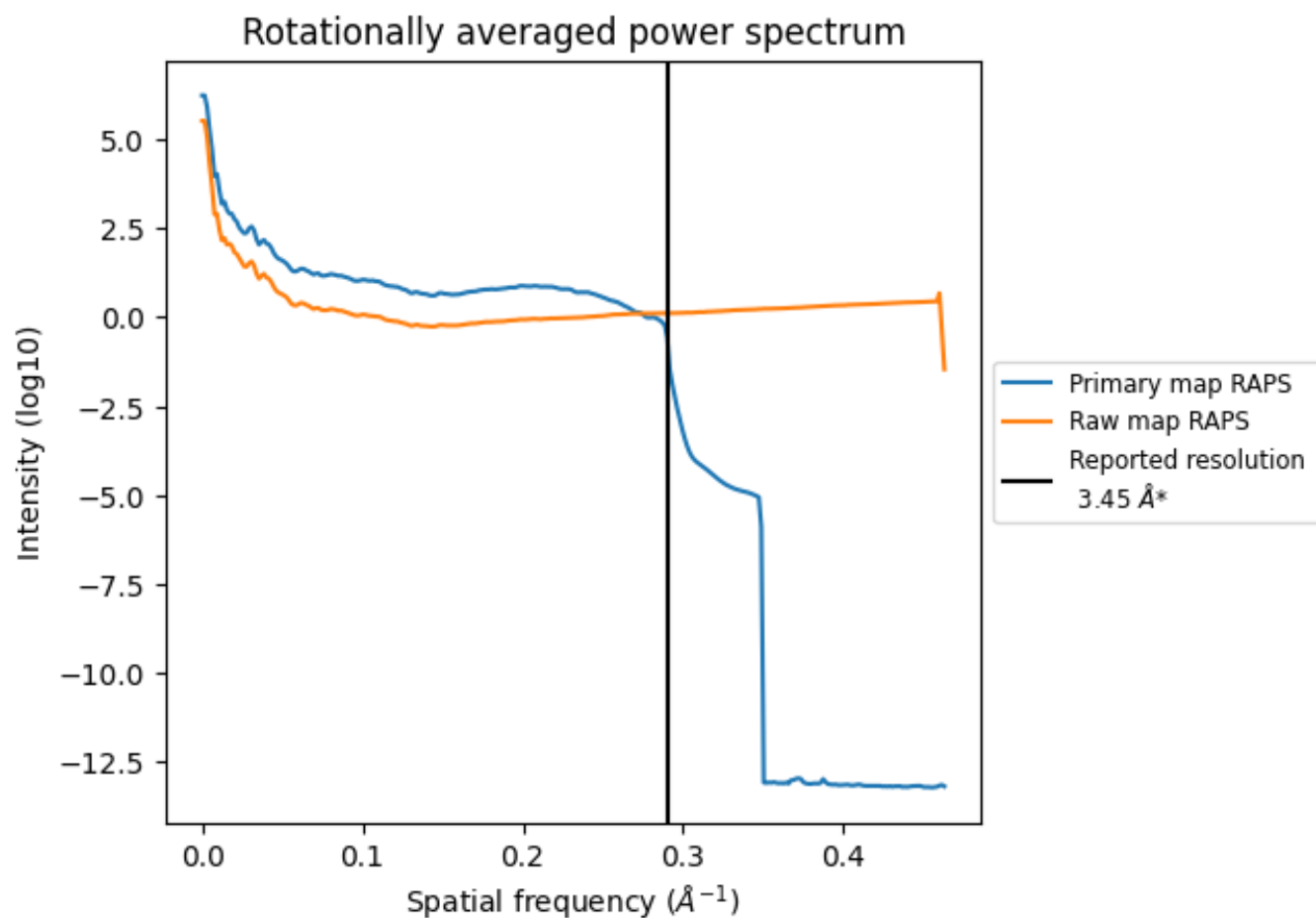
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2752 nm³; this corresponds to an approximate mass of 2486 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

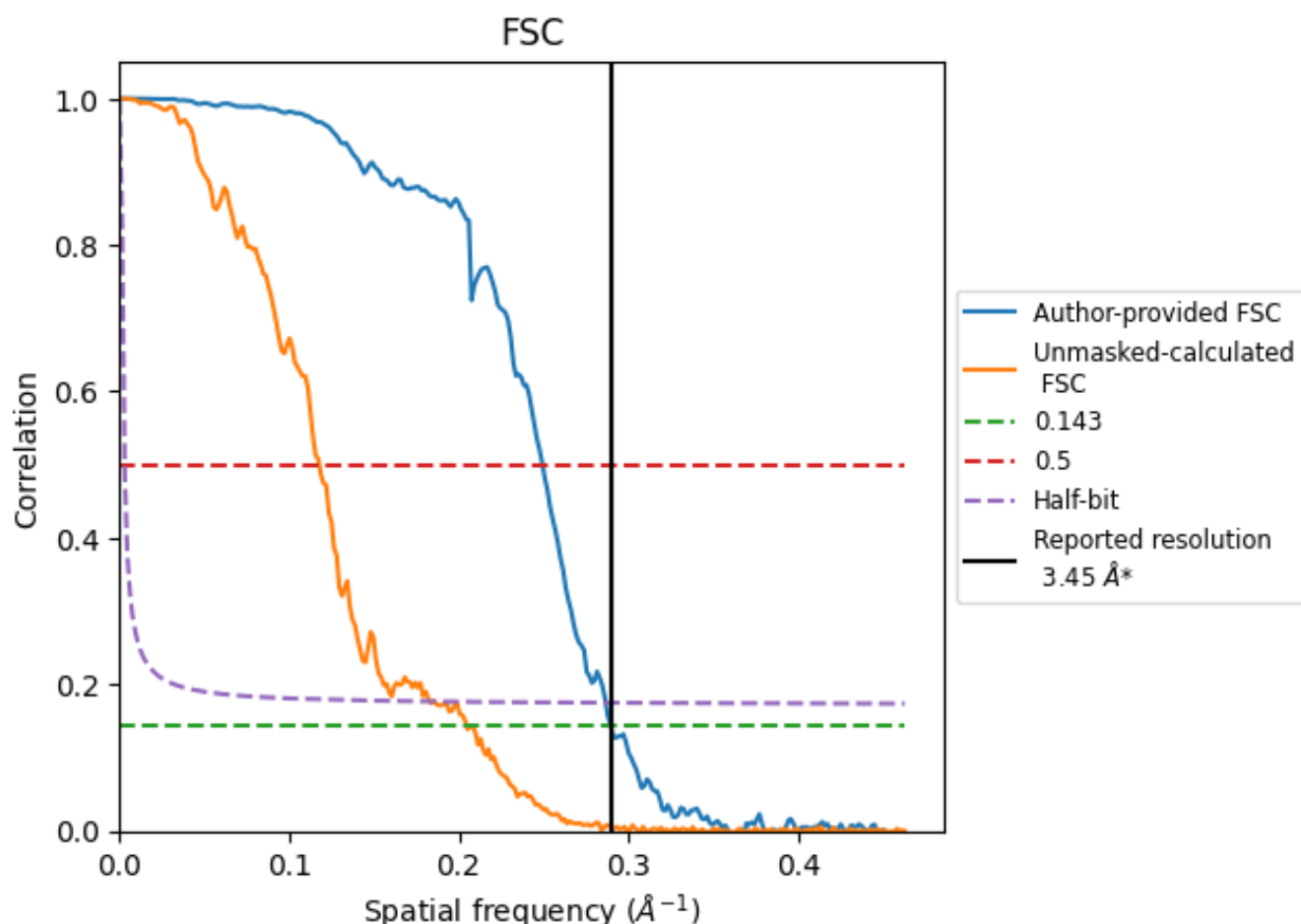


*Reported resolution corresponds to spatial frequency of 0.290 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.290 \AA^{-1}

8.2 Resolution estimates [i](#)

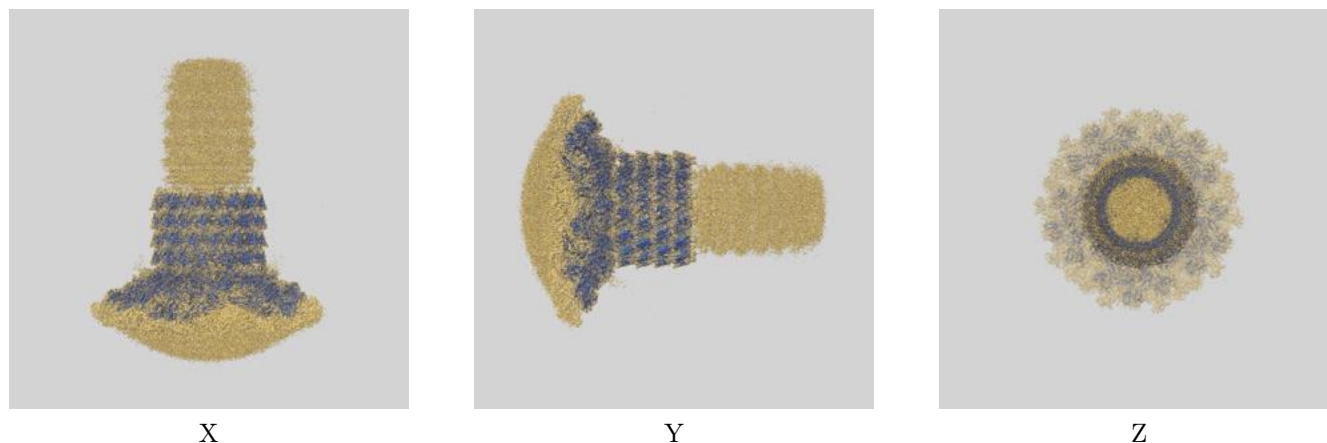
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.45	-	-
Author-provided FSC curve	3.45	4.01	3.49
Unmasked-calculated*	4.89	8.49	5.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.89 differs from the reported value 3.45 by more than 10 %

9 Map-model fit [i](#)

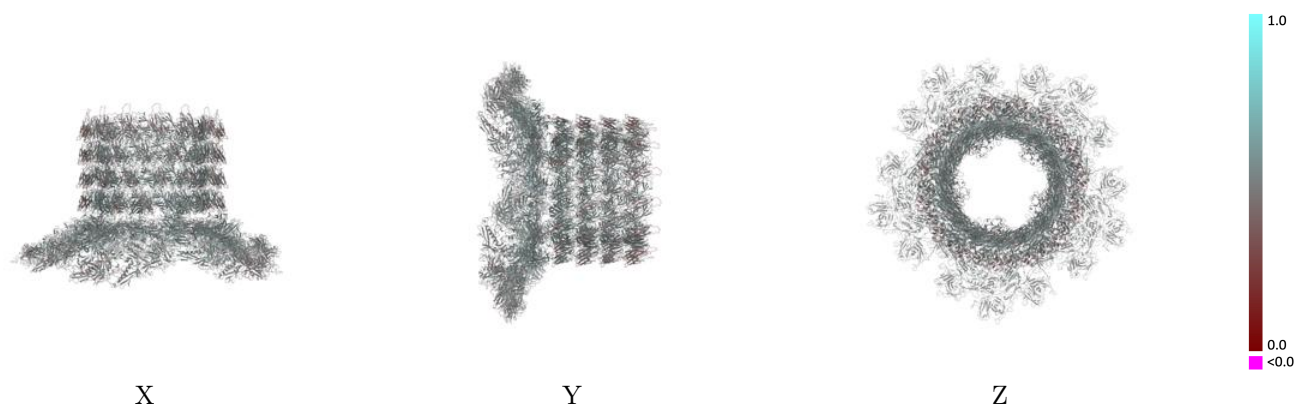
This section contains information regarding the fit between EMDB map EMD-29504 and PDB model 8FWG. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



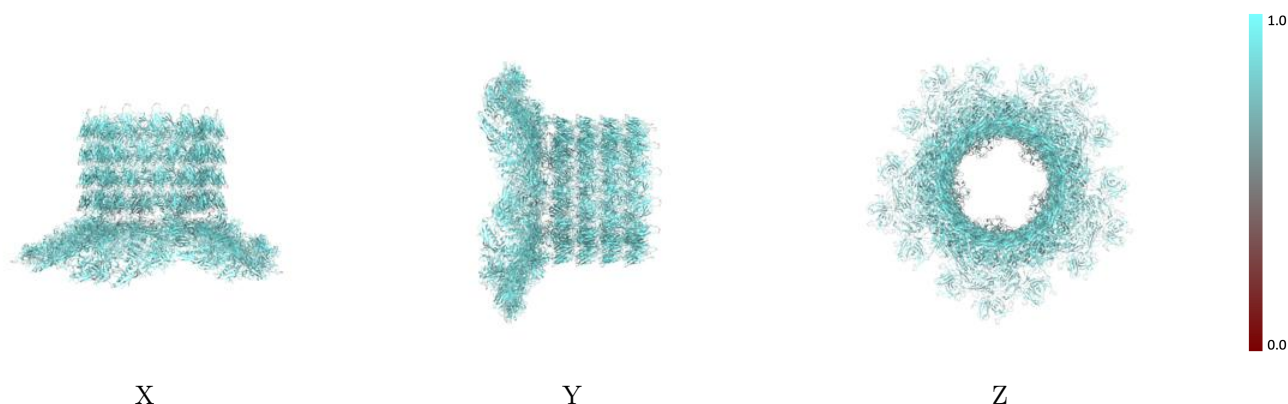
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



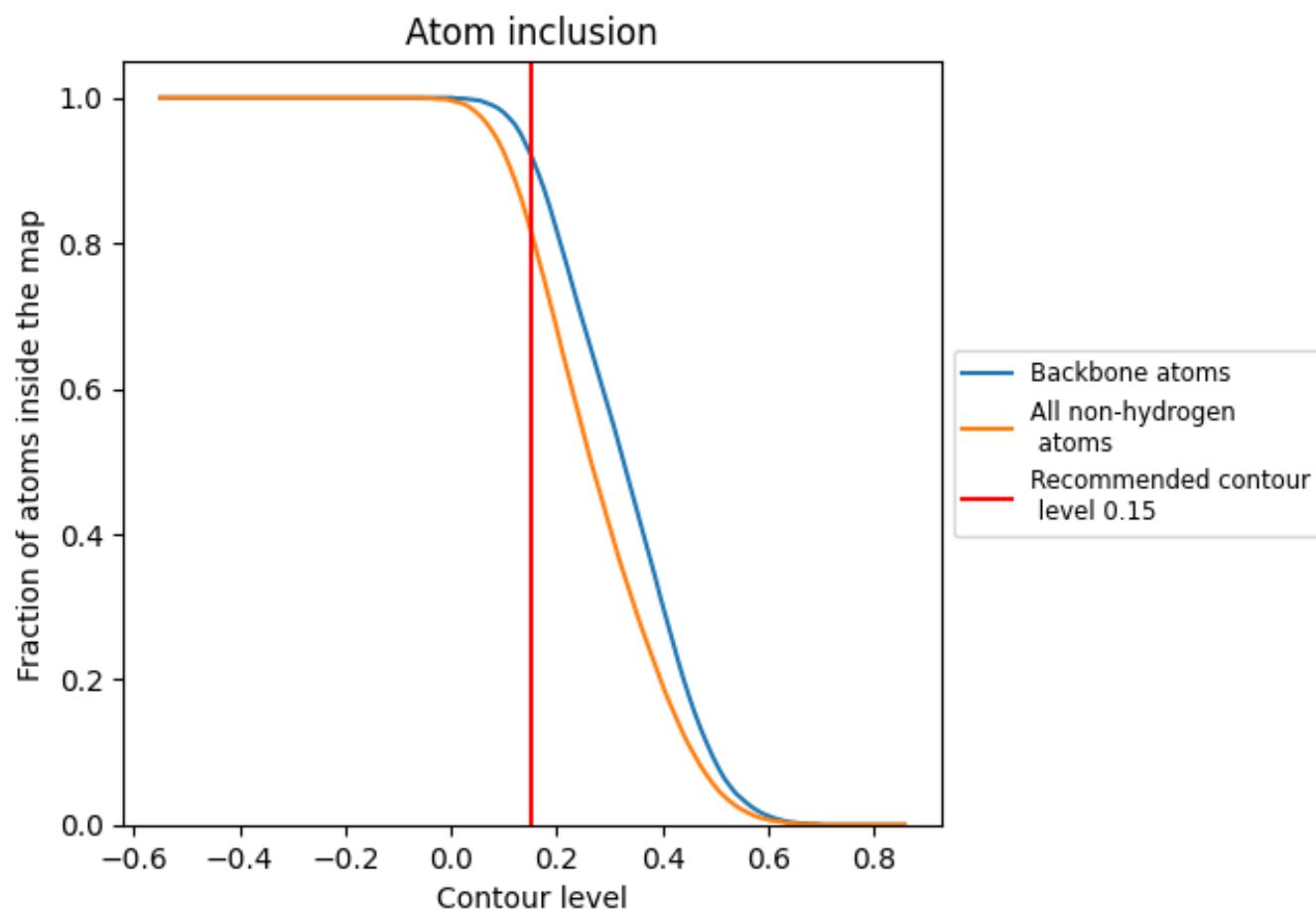
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8190	 0.4910
03	 0.8310	 0.4670
13	 0.8610	 0.4970
23	 0.8580	 0.4900
33	 0.8270	 0.4600
43	 0.8280	 0.4650
53	 0.8440	 0.4610
63	 0.8330	 0.4570
73	 0.8290	 0.4680
83	 0.8360	 0.4610
93	 0.8310	 0.4590
A3	 0.8390	 0.4630
A4	 0.6250	 0.4810
B3	 0.8320	 0.4590
B4	 0.6270	 0.4770
C3	 0.8310	 0.4670
C4	 0.6300	 0.4730
D3	 0.8390	 0.4630
D4	 0.6040	 0.4550
E3	 0.8300	 0.4630
E4	 0.6220	 0.4700
F3	 0.8330	 0.4670
G3	 0.8220	 0.4520
J3	 0.8550	 0.5110
K3	 0.8010	 0.4930
L3	 0.8050	 0.4920
M3	 0.8470	 0.5120
N3	 0.7990	 0.4960
O3	 0.8050	 0.4920
P3	 0.8560	 0.5130
Q3	 0.8060	 0.4960
R3	 0.8100	 0.4950
S3	 0.8590	 0.5120
T3	 0.8070	 0.4930
U3	 0.8020	 0.4950























































































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Chain	Atom inclusion	Q-score
V3	 0.8560	 0.5120
W3	 0.7950	 0.4910
X3	 0.8100	 0.4930
Y3	 0.8490	 0.4960
Z3	 0.8550	 0.4910
a1	 0.8330	 0.5290
a2	 0.8370	 0.5290
a3	 0.8420	 0.4930
a5	 0.8330	 0.5250
a6	 0.8180	 0.5270
a7	 0.8470	 0.5270
b1	 0.7680	 0.5240
b2	 0.7540	 0.5130
b3	 0.8500	 0.4960
b5	 0.7830	 0.5170
b6	 0.7680	 0.5170
b7	 0.7730	 0.5190
c	 0.8000	 0.5160
c3	 0.8480	 0.4890
d	 0.7920	 0.4970
d1	 0.8000	 0.5020
d2	 0.7790	 0.4870
d3	 0.8500	 0.4960
d5	 0.7920	 0.5040
d6	 0.7870	 0.5010
d7	 0.7920	 0.4990
e	 0.7960	 0.5000
e1	 0.7390	 0.4810
e2	 0.7630	 0.4870
e3	 0.8520	 0.4960
e5	 0.7630	 0.4830
e6	 0.7490	 0.4860
e7	 0.7590	 0.4840
f	 0.8000	 0.5090
f1	 0.6990	 0.5180
f2	 0.7130	 0.5200
f3	 0.8480	 0.4900
f5	 0.6990	 0.5120
f6	 0.7130	 0.5170
f7	 0.7060	 0.5150
g	 0.7960	 0.5010
g1	 0.8200	 0.5060








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Chain	Atom inclusion	Q-score
g2	 0.8250	 0.5060
g3	 0.8450	 0.4950
g5	 0.8200	 0.5040
g6	 0.8240	 0.5040
g7	 0.8190	 0.5030
h1	 0.8380	 0.5170
h2	 0.8410	 0.5190
h3	 0.8480	 0.4970
h5	 0.8410	 0.5180
h6	 0.8420	 0.5170
h7	 0.8400	 0.5160
i3	 0.8530	 0.4920
j3	 0.8500	 0.4930
k1	 0.8150	 0.5140
k2	 0.8170	 0.5160
k3	 0.8480	 0.4960
k5	 0.8160	 0.5150
k6	 0.8160	 0.5170
k7	 0.8140	 0.5100
l1	 0.8530	 0.5170
l2	 0.8540	 0.5160
l3	 0.8530	 0.4890
l5	 0.8530	 0.5170
l6	 0.8570	 0.5170
l7	 0.8490	 0.5140
m1	 0.8420	 0.5130
m2	 0.8430	 0.5140
m3	 0.8490	 0.4950
m5	 0.8450	 0.5170
m6	 0.8510	 0.5140
m7	 0.8500	 0.5150
n1	 0.8400	 0.5090
n2	 0.8390	 0.5090
n3	 0.8620	 0.4890
n5	 0.8410	 0.5100
n6	 0.8450	 0.5120
n7	 0.8410	 0.5100
o1	 0.8010	 0.4790
o2	 0.8030	 0.4790
o3	 0.8650	 0.4960
o5	 0.8000	 0.4800
o6	 0.8040	 0.4790











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Chain	Atom inclusion	Q-score
o7	 0.7990	 0.4820
p1	 0.8030	 0.4890
p2	 0.8030	 0.4860
p3	 0.8550	 0.4890
p5	 0.8050	 0.4860
p6	 0.8010	 0.4870
p7	 0.8030	 0.4840
q1	 0.7660	 0.4690
q2	 0.7640	 0.4680
q3	 0.8590	 0.4890
q5	 0.7620	 0.4660
q6	 0.7580	 0.4690
q7	 0.7680	 0.4690
r1	 0.8030	 0.4940
r2	 0.8010	 0.4920
r3	 0.8630	 0.4960
r5	 0.8090	 0.4930
r6	 0.8110	 0.4920
r7	 0.8060	 0.4870
s1	 0.7940	 0.4890
s2	 0.7970	 0.4890
s3	 0.8550	 0.4910
s5	 0.7940	 0.4900
s6	 0.7950	 0.4900
s7	 0.7930	 0.4890
t1	 0.7860	 0.4690
t2	 0.7860	 0.4710
t3	 0.8590	 0.4890
t5	 0.7880	 0.4700
t6	 0.7850	 0.4720
t7	 0.7730	 0.4670
u1	 0.7160	 0.4480
u2	 0.7170	 0.4490
u3	 0.8660	 0.4960
u5	 0.7180	 0.4520
u6	 0.7170	 0.4490
u7	 0.7190	 0.4490
v1	 0.7040	 0.4500
v2	 0.7160	 0.4490
v3	 0.8600	 0.4890
v5	 0.7180	 0.4540
v6	 0.7090	 0.4530

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Chain	Atom inclusion	Q-score
v7	 0.6980	 0.4460
w3	 0.8670	 0.4900
x3	 0.8640	 0.4960
y3	 0.8530	 0.4880
z3	 0.8630	 0.4910