



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 12:41 AM UTC

PDB ID : 6Z7N / pdb_00006z7n
EMDB ID : EMD-11108
Title : The atomic structure of HAdV-F41 at pH 7.4
Authors : Carlson, L.-A.; Rafie, K.
Deposited on : 2020-05-31
Resolution : 3.77 Å(reported)
Based on initial model : 5TX1

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

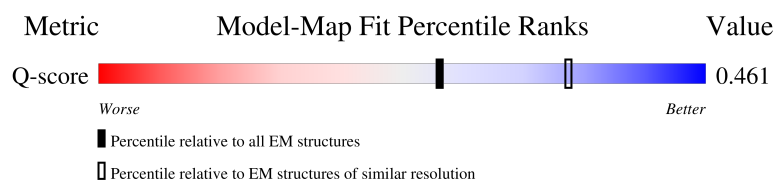
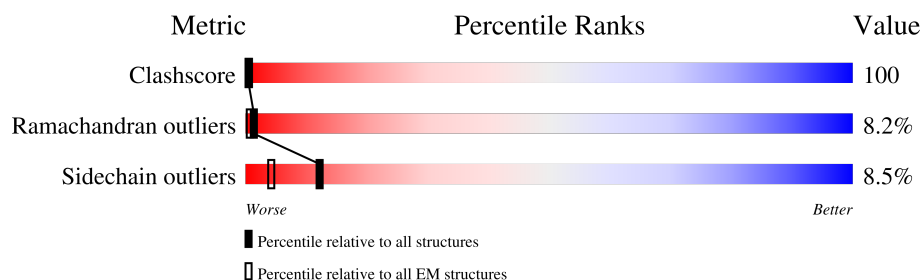
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.77 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10146 (3.27 - 4.27)

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	0	266	 95%
1	1	266	 94%
1	2	266	 98%
1	3	266	 95%

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Mol	Chain	Length	Quality of chain
1	4	266	93%
1	5	266	94%
1	6	266	99%
1	7	266	99%
1	8	266	90%
1	9	266	99%
2	A	925	25% 16% 55% 8% 7% 15%
2	B	925	31% 12% 42% 24% 14% 8%
2	C	925	29% 11% 42% 23% 17% 7%
2	D	925	25% 16% 62% 11% 8% .
2	E	925	25% 17% 63% 7% 7% 5%
2	F	925	20% 14% 59% 13% 10% .
2	G	925	19% 17% 54% 15% 9% 5%
2	H	925	22% 18% 63% 10% 7% .
2	I	925	22% 25% 66% . . .
2	J	925	25% 17% 59% 14% 8% .
2	K	925	22% 22% 61% 5% . 9%
2	L	925	22% 22% 62% . . 8%
3	M	508	64% 37% 49% . . 10%
4	N	348	93%
5	O	579	15% 14% 25% . . 54%
6	P	133	17% 14% 25% . . 56%
6	Q	133	14% 10% 23% . . 62%
6	R	133	6% 12% . . 77%
6	S	133	13% 14% 19% 8% 56%

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Mol	Chain	Length	Quality of chain
7	T	233	9% 24% 48% 24%
7	U	233	7% 25% 48% 23%
8	X	7	100% 43% 57%
9	V	10	10% 90% 10%
9	W	10	50% 40% 10%
9	Z	10	20% 80% 10% 10%
10	Y	6	17% 50% 50%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 94362 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 Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	12	Total	C	N	O	S	0	0
			94	59	20	14	1		
1	1	16	Total	C	N	O	S	0	0
			124	79	25	19	1		
1	2	6	Total	C	N	O	S	0	0
			48	31	9	7	1		
1	3	12	Total	C	N	O	S	0	0
			98	63	17	17	1		
1	4	19	Total	C	N	O	S	0	0
			147	91	29	26	1		
1	5	16	Total	C	N	O	S	0	0
			123	76	22	24	1		
1	6	3	Total	C	N	O		0	0
			28	17	8	3			
1	7	3	Total	C	N	O		0	0
			28	17	8	3			
1	8	26	Total	C	N	O	S	0	0
			197	122	38	36	1		
1	9	3	Total	C	N	O		0	0
			28	17	8	3			

- Molecule 2 is a protein called Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	788	Total	C	N	O	S	0	0
			6307	4029	1063	1180	35		
2	B	847	Total	C	N	O	S	0	0
			6761	4305	1146	1277	33		
2	C	860	Total	C	N	O	S	0	0
			6862	4368	1163	1296	35		
2	D	887	Total	C	N	O	S	0	0
			7057	4493	1194	1335	35		
2	E	878	Total	C	N	O	S	0	0
			6988	4451	1180	1321	36		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	889	Total	C	N	O	S	0	0
			7070	4499	1196	1339	36		
2	G	880	Total	C	N	O	S	0	0
			7008	4462	1183	1328	35		
2	H	894	Total	C	N	O	S	0	0
			7095	4513	1202	1344	36		
2	I	908	Total	C	N	O	S	0	0
			7212	4584	1222	1370	36		
2	J	907	Total	C	N	O	S	0	0
			7203	4577	1219	1371	36		
2	K	840	Total	C	N	O	S	0	0
			6702	4271	1130	1265	36		
2	L	855	Total	C	N	O	S	0	0
			6831	4358	1155	1283	35		

- Molecule 3 is a protein called Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	458	Total	C	N	O	S	0	0
			3659	2322	630	696	11		

- Molecule 4 is a protein called Core-capsid bridging protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	24	Total	C	N	O	S	0	0
			198	124	34	37	3		

- Molecule 5 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	O	267	Total	C	N	O	S	0	0
			2088	1309	371	404	4		

- Molecule 6 is a protein called Hexon-interlacing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	58	Total	C	N	O	S	0	0
			419	262	74	80	3		
6	Q	50	Total	C	N	O	S	0	0
			366	233	65	67	1		
6	R	30	Total	C	N	O	S	0	0
			228	147	41	39	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	S	58	Total	C	N	O	S	0	0
			419	262	74	80	3		

- Molecule 7 is a protein called Pre-hexon-linking protein VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	178	Total	C	N	O	S	0	0
			1368	859	234	270	5		
7	U	179	Total	C	N	O	S	0	0
			1372	861	235	271	5		

- Molecule 8 is a protein called Fiber protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	X	7	Total	C	N	O	0	0
			64	46	8	10		

- Molecule 9 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	W	9	Total	C	N	O	0	0
			45	27	9	9		
9	V	10	Total	C	N	O	0	0
			50	30	10	10		
9	Z	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 10 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	Y	6	Total	C	N	O	0	0
			30	18	6	6		



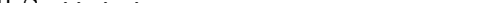
- Molecule 1: Pre-protein VI

Chain 6:

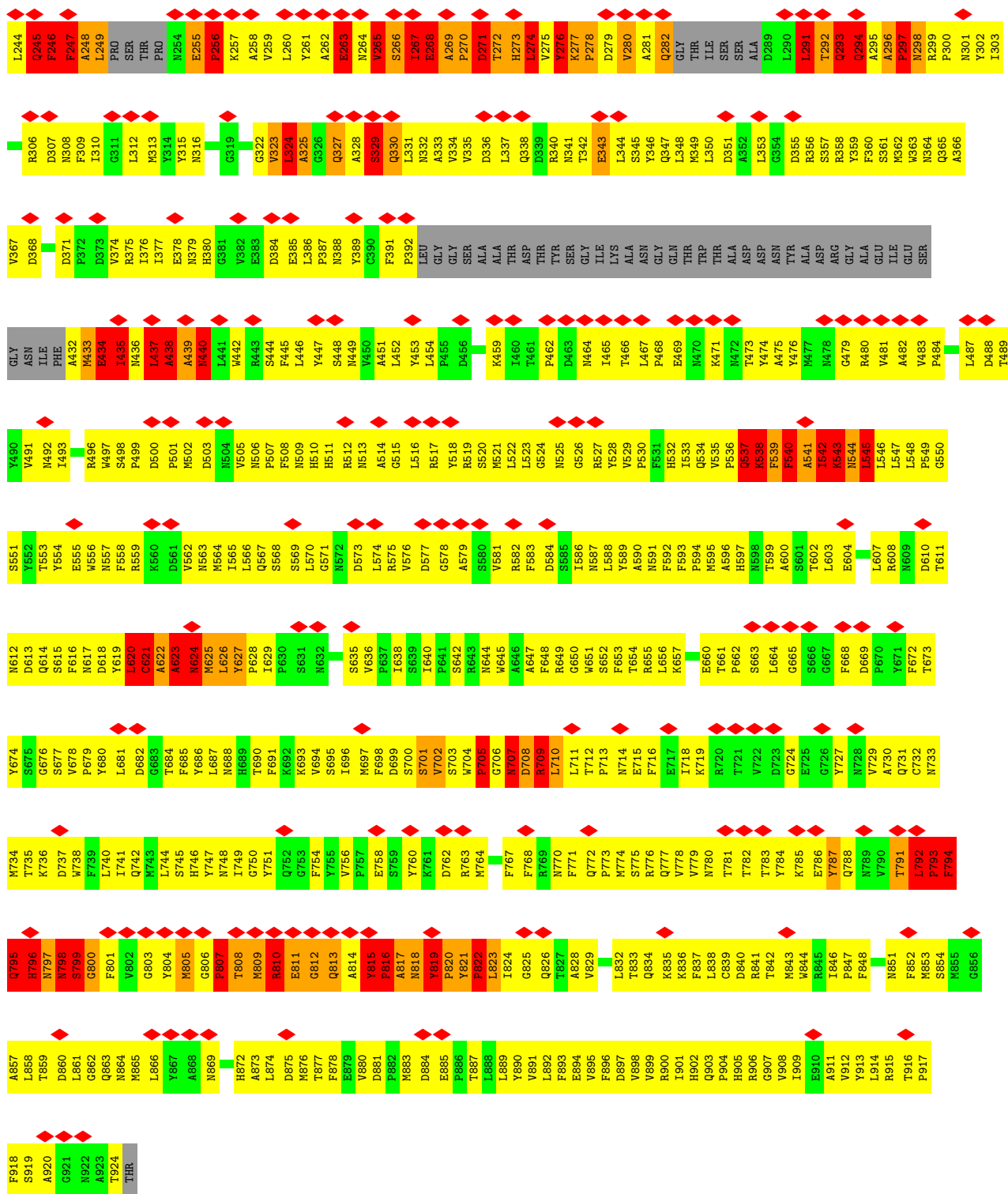
- Molecule 1: Pre-protein VI

Chain 7:

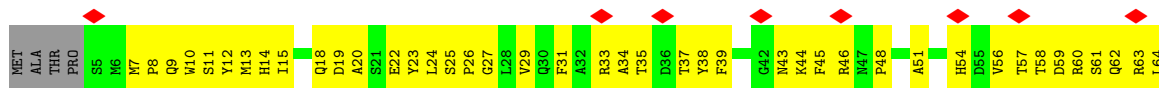
- Molecule 1: Pre-protein VI

Chain 8:  90%





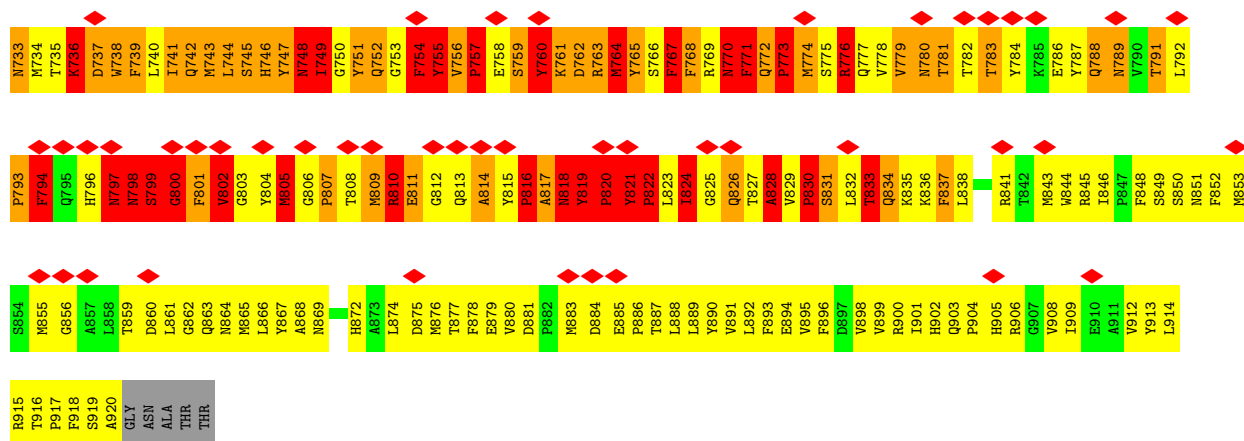
• Molecule 2: Hexon protein



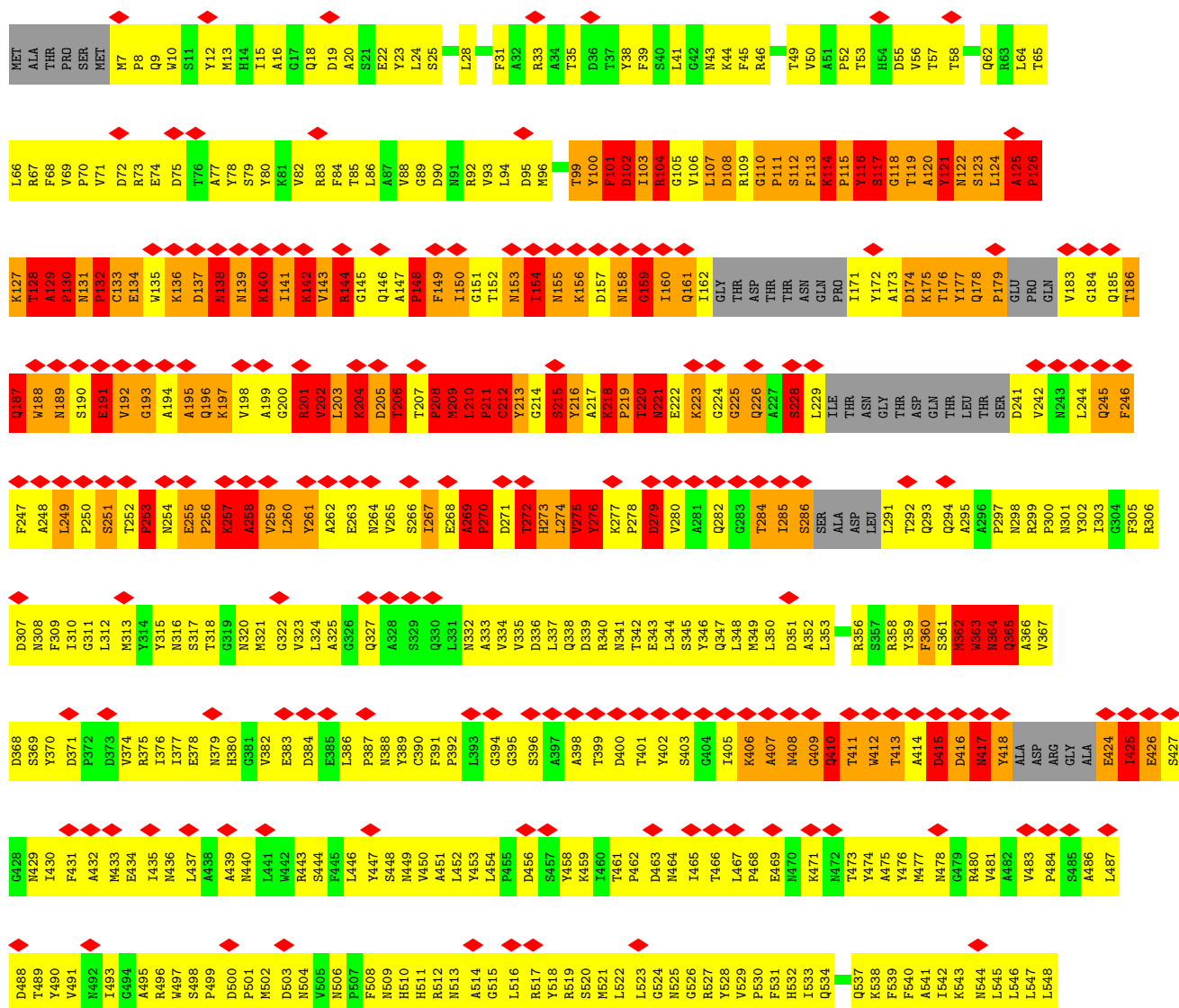
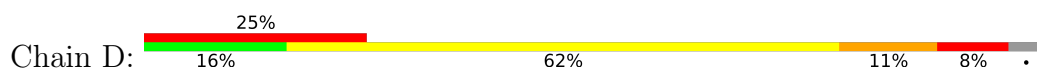
G856	H786	K736	G676	F616	P549	D488	GLY	D368	N308	A248	V188	T128	T65
A857	N797	D737	S677	M617	Y552	T489	N429	S369	F309	L249	N189	A129	L66
L858	W798	W738	V678	D618	T553	V490	I430	Y370	G311	P250	S190	P130	R67
T859	GLY	F739	P679	Y619	Y554	V491	I430	D371	G311	P250	S190	P130	
D860	PHE	L740	Y680	L620	E555	N492	A432	P372	M312	S251	E191	P131	D72
L861	VAL	I741	L681	C621	E556	N493	M433	D373	M313	T252	E192	P132	R73
G862	GLY	Q742	D682	A622	Y557	N494	M433	Y374	Y314	P253	G193	C133	E74
Q863	TYR	H743	D683	A623	F558	N495	E434	E375	N315	N254	A194	E134	D75
M864	MET	L744	T684	M624	R559	N496	I435	I376	N316	E255	A195	M135	T76
M865	GLY	S745	F685	M625	K560	N497	M436	I377	T318	P256	K196	K136	A77
L866	PRO	L626	Y686	L626	K560	S498	L437	E378	G319	K257	Q197	D137	T78
Y867	THR	Y747	D687	Y627	D561	P499	A438	N379	G319	K257	Q197	D137	Y78
A868	MET	N748	N688	P628	V562	D500	A439	H380	N320	A258	H380	M138	S79
N869	ARG	I749	H689	L629	N563	P501	M440	G381	M321	V259	V198	M139	Y80
S870	GLU	Q750	P501	P630	M564	N502	L441	V382	G322	A199	K140	K140	K81
A871	GLY	Y751	S631	S631	M565	D503	R442	E383	V323	G200	I141	I141	V82
H872	GLN	Q752	L566	M632	L566	D504	R443	D384	L324	L260	K142	K142	R83
A873	ALA	G753	D567	A633	D567	N505	S444	E385	A328	N264	F84	F84	F84
L874	TYR	F754	L570	L634	L570	V505	F445	L386	S329	V265	V202	V202	T85
D875	P816	F755	G571	T634	G571	P507	F446	L386	Q330	S266	K144	K144	L86
T877	A817	Y756	N572	Y636	N572	F508	Y447	PRO	Q330	I267	A147	A147	A87
F878	N818	W757	N573	P637	N573	N509	S448	ASN	V335	E268	G89	G89	V88
Y879	Y819	P757	D573	L638	D573	H510	M449	TYR	V335	E268	T207	T207	D90
E878	F698	E758	L574	L640	L574	H511	V450	PHE	N332	A269	P148	P148	N91
S759	D699	S759	R575	P641	R575	H512	A451	PRO	A333	A269	F149	F149	R92
K761	S701	K761	V576	P641	V576	N513	Y453	LEU	V334	P270	M209	M209	R92
D762	V702	D762	G577	S642	G577	A514	L454	GLY	V335	D271	I150	I150	V93
R763	S703	R763	G577	R643	G577	O515	P455	GLY	V335	T272	G151	G151	L94
M764	W704	M764	G578	M644	G578	L516	D456	SER	D336	H273	T152	T152	D95
Y765	P705	Y765	A579	M645	A579	R517	D456	ALA	Q338	Y213	M153	M153	M96
S766	G706	S766	S580	A646	S580	R518	S457	ALA	D339	G214	I154	I154	A97
F767	N707	F767	Y581	A647	Y581	V518	Y458	THR	R340	S215	M155	M155	S98
F768	D708	F768	R582	F648	R582	R519	K459	ASP	N341	Y216	K156	K156	T99
R769	R709	R769	F583	S649	F583	S520	K459	THR	K242	K277	K157	K157	F101
N770	L710	N770	G580	G650	G580	N521	T460	TYR	E343	A217	D157	D157	F101
L711	L711	L711	D584	G650	D584	L522	T461	GLY	L344	D279	N158	N158	D102
T712	T712	T712	S585	S652	S585	L523	P462	GLY	L344	V280	G159	G159	R104
P713	P713	P713	L586	L586	L586	L523	D463	ILE	S345	I160	I160	I160	G105
N714	N714	N714	L588	L588	L588	N525	M464	LYS	Q347	N221	Q161	Q161	L106
E715	E715	E715	Y589	L656	Y589	G526	I465	ALA	L348	ASN	I162	I162	L107
F716	F716	F716	K657	L656	K657	V528	L466	GLY	M349	THR	G163	G163	D108
E717	E717	E717	T658	T658	T658	V529	L467	GLN	D351	G225	T164	T164	R109
I718	I718	I718	E660	E660	E660	V530	P468	THR	A352	Q226	D165	D165	G110
K719	K719	K719	T661	T661	T661	F531	E469	THR	L353	A227	P111	P111	P111
R720	R720	R720	P662	P662	P662	H532	M470	ALA	G354	A288	T166	T166	S112
T721	T721	T721	L533	L533	L533	I533	K471	ASP	R355	D289	T167	T167	F113
V722	V722	V722	Q534	Q534	Q534	Q534	M472	ASP	R356	L290	M168	M168	K114
D723	D723	D723	Q537	Q537	Q537	Q537	T473	ASN	S357	L291	Q169	Q169	P115
E725	E725	E725	K538	K538	K538	V539	Y474	ALA	R358	T292	ASN	ASN	Y116
G726	G726	G726	F539	F539	F539	F540	Y475	ASP	Y359	Q293	P170	P170	S117
N727	N727	N727	F540	F540	F540	A541	Y476	ARG	F360	Q294	I171	I171	G118
M728	M728	M728	A541	A541	A541	I542	M477	GLY	S361	A295	Y172	Y172	T119
Y729	Y729	Y729	I542	I542	I542	I542	G479	ALA	M362	GLN	ASP	ASP	A120
A730	A730	A730	K543	K543	K543	N544	R480	GLU	W363	A296	D174	D174	Y121
Q731	Q731	Q731	N544	N544	N544	L545	B480	ILE	W363	N297	K175	K175	M122
L732	L732	L732	L546	L546	L546	L547	B480	GLU	Q365	N298	T176	T176	S123
F733	F733	F733	L547	L547	L547	L548	V481	GLU	A366	R299	Y177	Y177	L124
F794	F794	F794	L548	L548	L548	L548	V483	GLU	A366	P300	S240	S240	A125
Q795	Q795	Q795	L548	L548	L548	L548	P484	GLU	A366	N301	Q178	Q178	P126
							A486	GLU	A366	Y302	F179	F179	K127
							L487	GLU	A366	S303	E180	E180	
								SER	A366	G304	P181	P181	
									A366	F305	Q182	Q182	
									A366	R306	V183	V183	
									A366	D307	G184	G184	
									A366		T186	T186	
									A366		Q187	Q187	

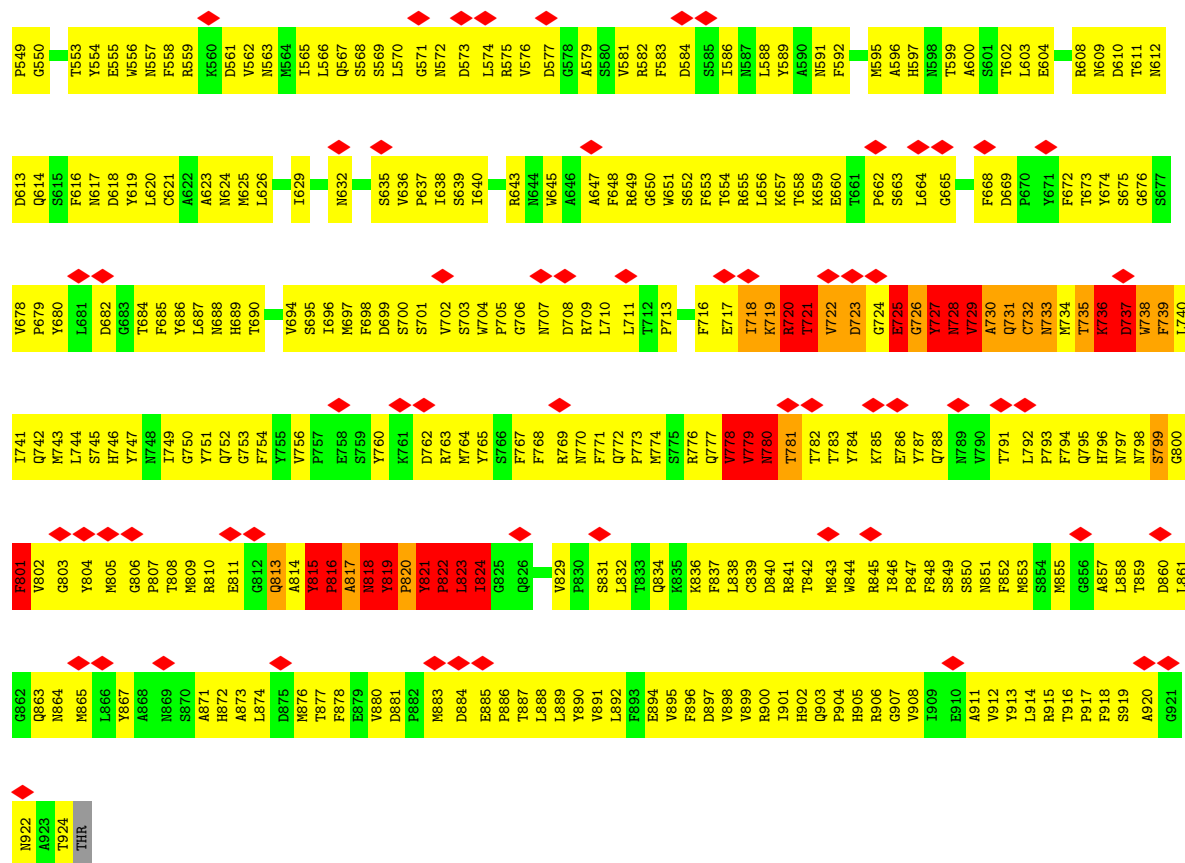
Chain C: 11% 29% 42% 23% 17% 7%



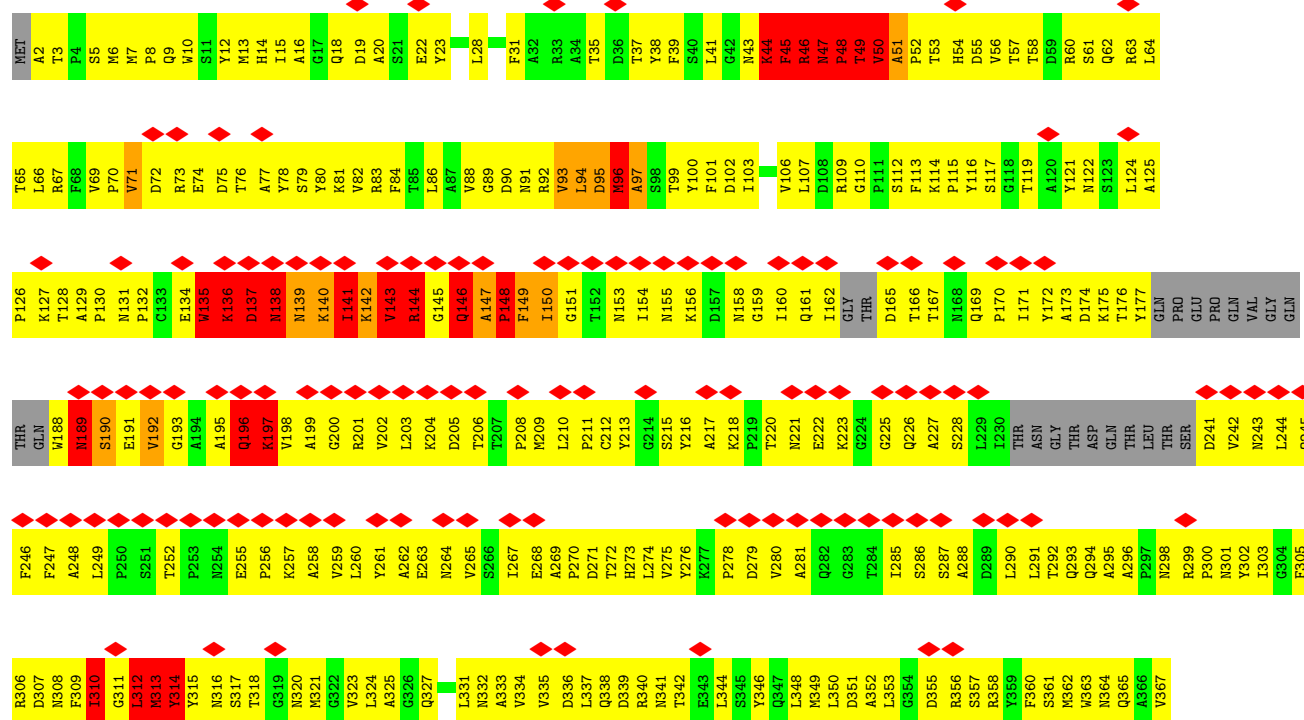


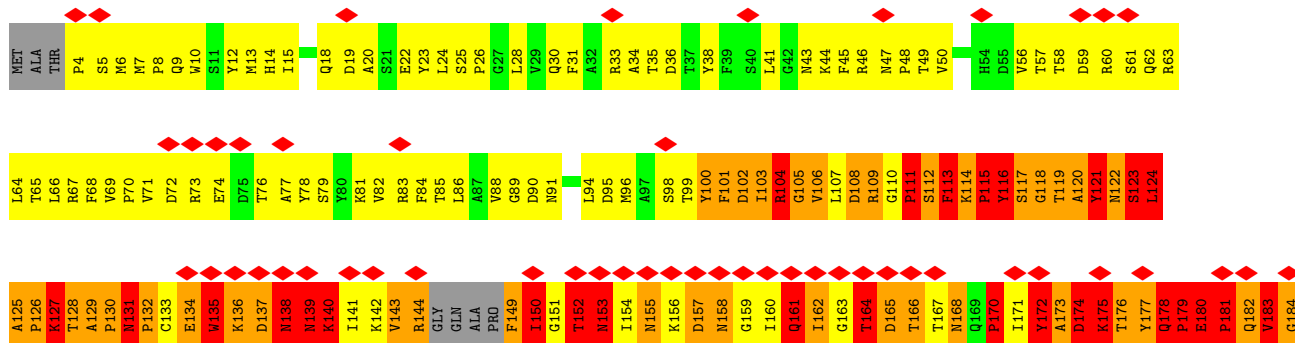
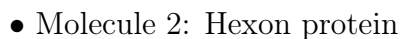
• Molecule 2: Hexon protein

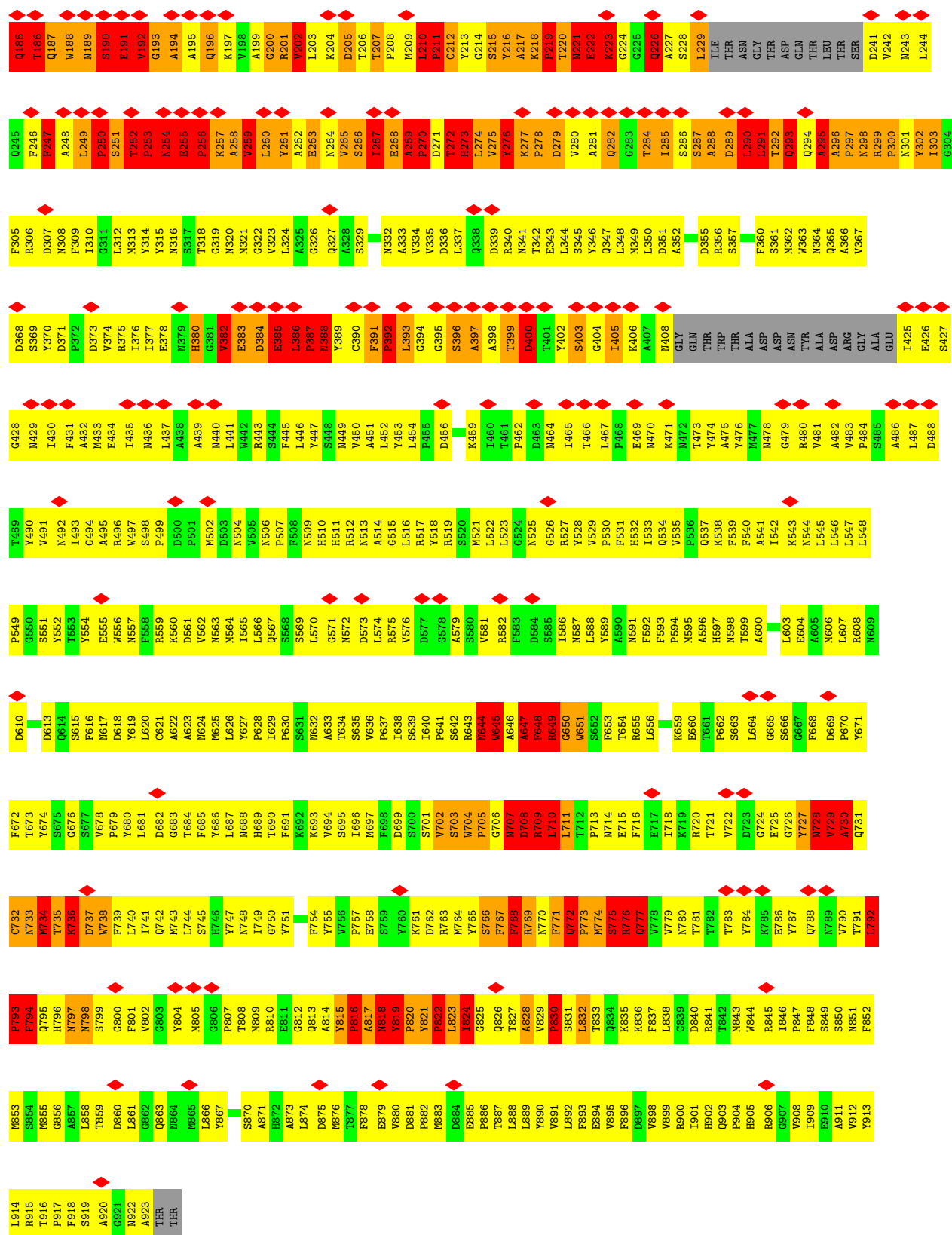




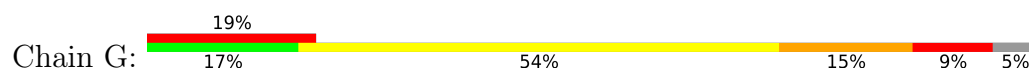
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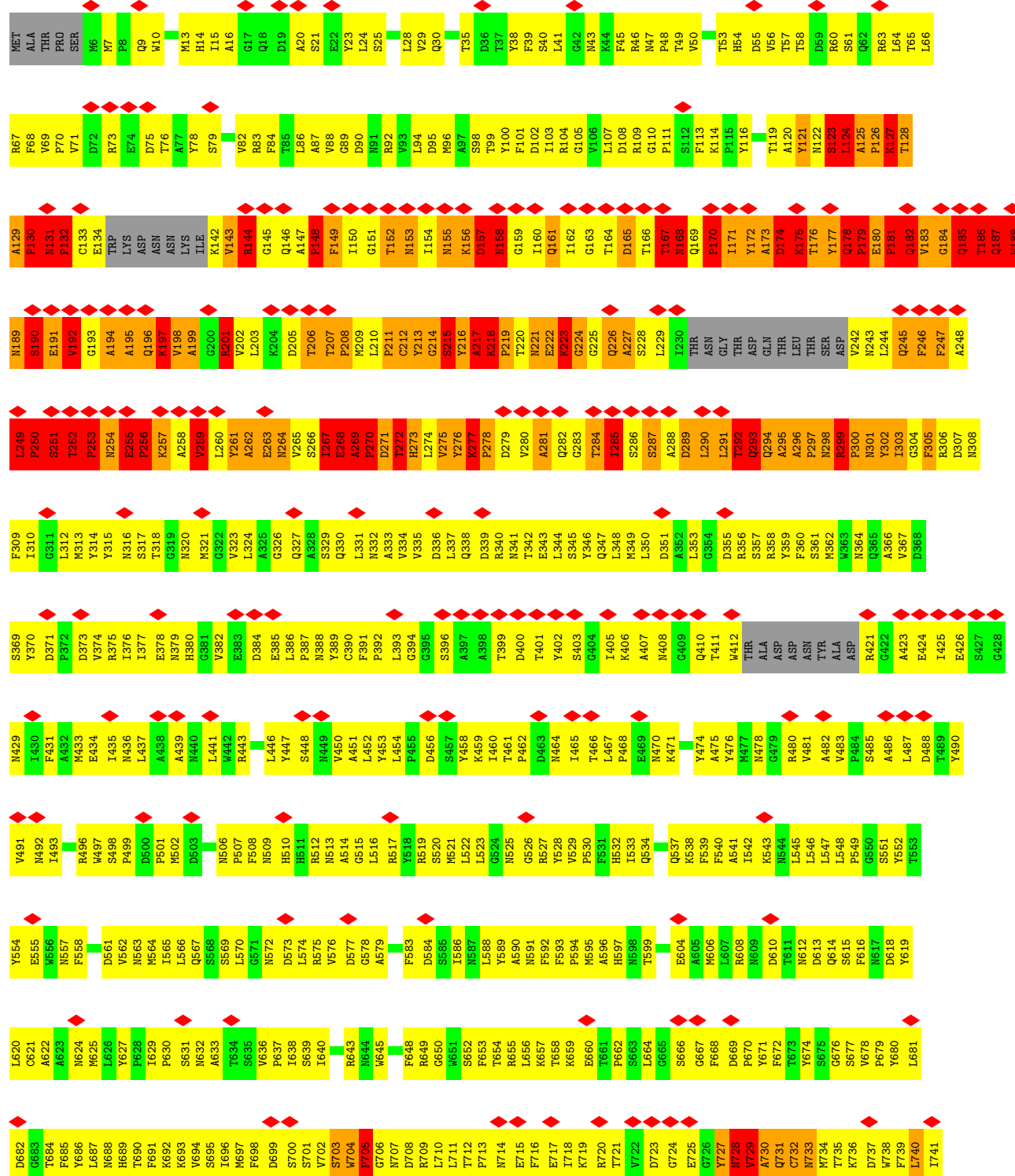
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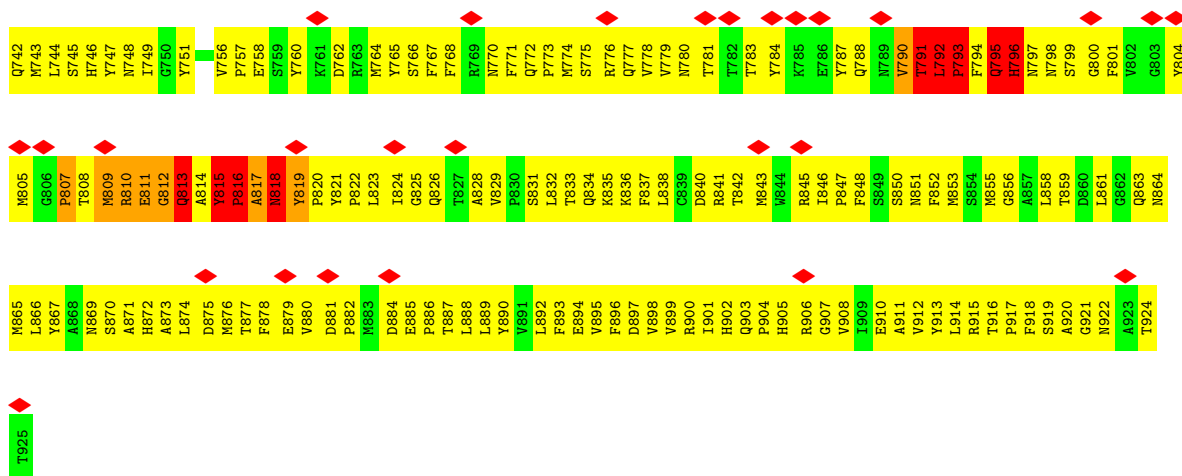


E811	Y751	F691	A623	N557	I493	F431	D371	G311	S251	N189	P130	L66	MET
G812	Q752	K692	M624	F558	G494	A432	P372	L312	T252	S190	M131	R67	ALA
Q813	G753	K693	M625	R559	R496	M433	D373	M313	P253	E191	P132	F68	THR
A814	Y755	K694	L626	K560	R496	E434	R374	Y314	M254	A194	C133	V70	PRO
Y815	Y756	S695	I629	D61	S498	T435	R375	Y315	E255	A195	E134	D72	SER
P816	P757	M697		F682	P499	A436	L376	S317	P256	A196	W135	W10	MET
A817	E758	F698	A633	N563	D500	A438	L377	S318	K257	Q196	W136	Q8	
N818	S759	D699	T634	M564	P501	A439	E378	G319	K258	K197	K136	P9	
Y819	Y760	S700	S635	L566	M502	N440	R379	N320	A258	G200	D137	W11	
P820	K761	S701	S636	S567	D503	L441	H380	G321	V259	G201	N138	D75	
Y821	D762	Y702		S688	N504	W442	G381	G322		R201	W139	T76	
P822	R763	S703	I640	S689	V505	R443	V382	G323		V202	K140	A77	
L823	W641	W704	S642	L570	N506		E383	L324	A262	L203	Y78	Y78	
I824	S643	P705	R643	G571	P507	L446	D384	A325	E263	K204	I141	S79	
Q826	W644	N572	W645	D573	F508	Y447	E385	G326	M264	D205	K142	K81	
T827	W645	N509		L574	N509	Y448	L386	Q327	W266	T206	V143	V82	
A828	A646	H510		F683	H510	W449	R387	A328	S266	T207	R444	R83	
W829	A647	H511		L575	H511	W450	N388	Q329	I267	P208	G145	T85	
P830	F648	H512		V576	H512	A451	Y389	L331	E268	M209	Q146	L86	
S831	W770	L710		D577	H513	L452	C390	N332	A269	L210	A147	A87	
L832	Q772	W712		G578	A514	Y453	F391	A333	D271	P211	P148	V88	
T833	P773	W713				L454	P392	W334	C212	C212	F149	G89	
K836	W774	W714		V581	L516	P455	L393	Y335	Y213	Y213	I150	D90	
F837	W775	E715		R582	R517	D456	G394	D386	G214	G214	G151	N91	
L838	Q777	F716		F583	Y518	S457	G395	L337	L274	S215	T152	R92	
C839	W778	E717		D584	R519	Y458	S396	Q338	V275	Y216	N153	W93	
D840	W779	K719		S585	S520	K459	A397	D339	Y276	A217	K154	L94	
R841	W780	W720		L586	N521	L460	A398	R340	K277	K218	N155	D95	
T842	T781	W721		W587	L522	W461	A399	N341	P278	P219	K156	M96	
W843	W782	W722		L588	L523	P462	T399	T342	D279	T220	K157	A97	
M844	T783	D723		F589	G524	D463	D400	E343	W280	N221	S98	F99	
W844	W784	W724		N591	N525	W464	T401	L344	A281	K222	T99	S40	
R845	G724	P662		P662	G526	L465	Y402	S345	Q282	K223	Y100	L41	
L846	E786	E725		F593	R527	L466	Y403	Y346	G283	G224	G159	F101	
P847	W787	W726		P594	W528	L467	GLY	Q347	T284	G225	I160	G105	
S850	Q788	W727		M595	P530	E469	ILE	L348	I285	Q226	Q161	V106	
F851	W789	W729		N598	I533	W470	LYS	M349	S287	A227	I162	L107	
P852	W790	A730		E604	O534	K471	ALA	D351	S286	S228	GLY	D108	
M853	Q791	W731		A605		W472	ASN	A352	A288	THR	THR	P48	
Y854	L792	W732		M606	K538	T473	GLN	L353	D289	L229	D165	G110	
L858	W793	W733		L607	F539	Y474	THR	D355	L290	THR	T166	P111	
T859	W794	W734		R608	A541	Y475	THR	R356	L291	ASN	T167	V50	
D860	W795	W735		W609	I542	W477	ALA	S357	T292	THR	N168	F113	
W861	W796	K736		D610	K543	W478	ASP	R358	Q293	GLY	Q169	K114	
L862	W797	W737		T611	N544	G479	ASP	Y359	Q294	THR	P170	Y116	
Q863	W798	F739		N612	L545	R480	ASN	F360	A296	GLN	I171	S117	
W864	W799	L740		D613	L546	W481	THR	S361	A296	THR	Y172	G118	
M865	F801	L741		O614	L547	W482	ALA	W362	P297	LEU	A173	T119	
L866	W802	Q742		S615	L548	W483	ASP	W363	N298	THR	D174	A120	
A868	W803	W743		F616	P549	P484	ARG	N364	R299	SER	K175	Y121	
N869	L744	W744		N617			GLY	Q365	P300	D241	T176	N122	
W870	W805	S745		D618	Y552	L487	ALA	A366	N301	V242	Y177	S123	
S871	W806	T563		T553	Y564	D488	E424	D368	Y302	N243	Q178	L124	
T872	W807	W747		L620	E555	T489	I425	S369	G304	L244	P179	A125	
W873	W808	C621		A622		W491	E426	Y370	F305	Q245	E180	P126	
H874	W809	W748					S427		R306	F246	PRO	K127	
W875	W810	G750				W492	G428		D307	F247	GLN		
							N429		N308	A248	GLN		
							I430		F309	L249	THR		
										P250	GLN		
											W188		

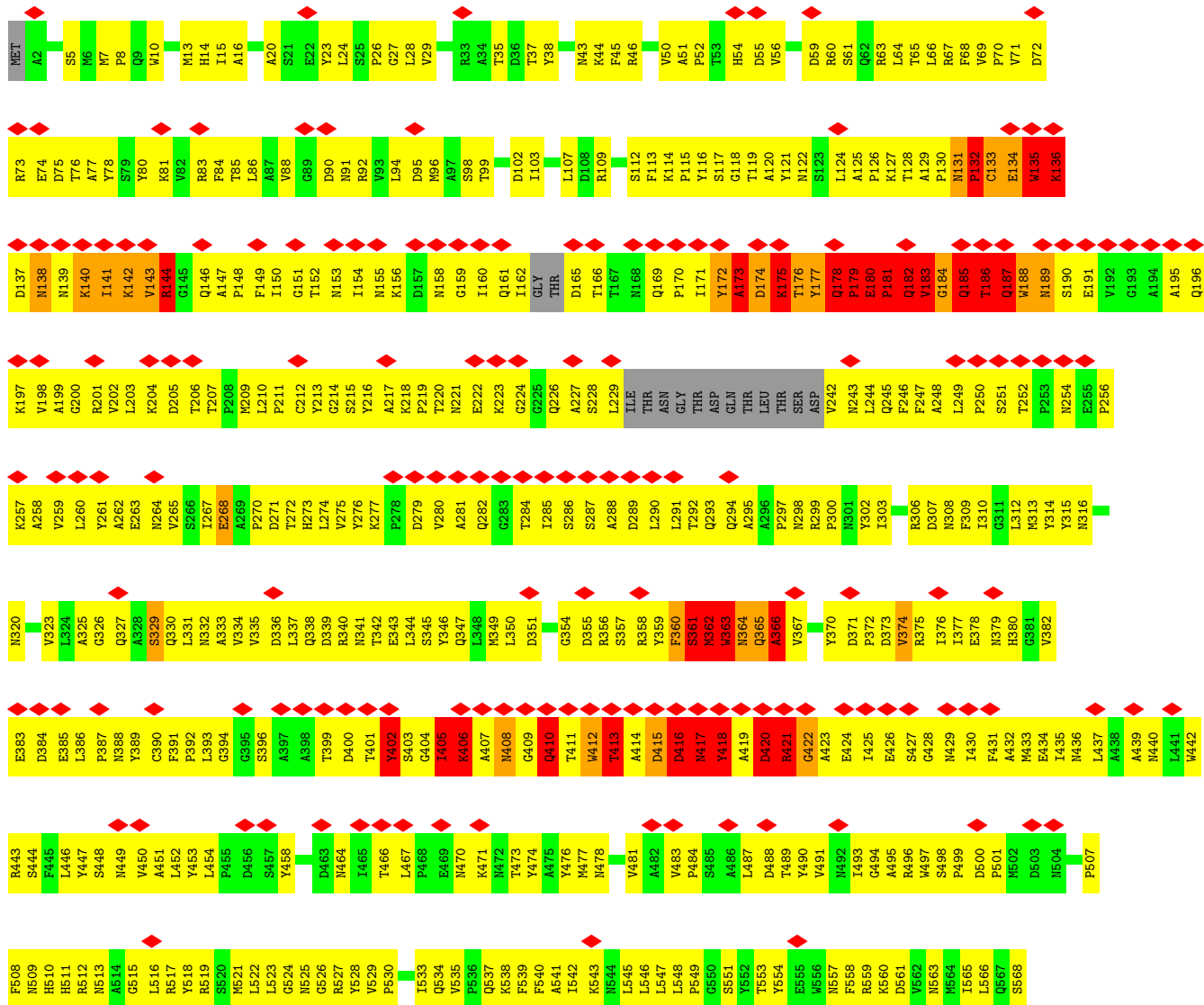


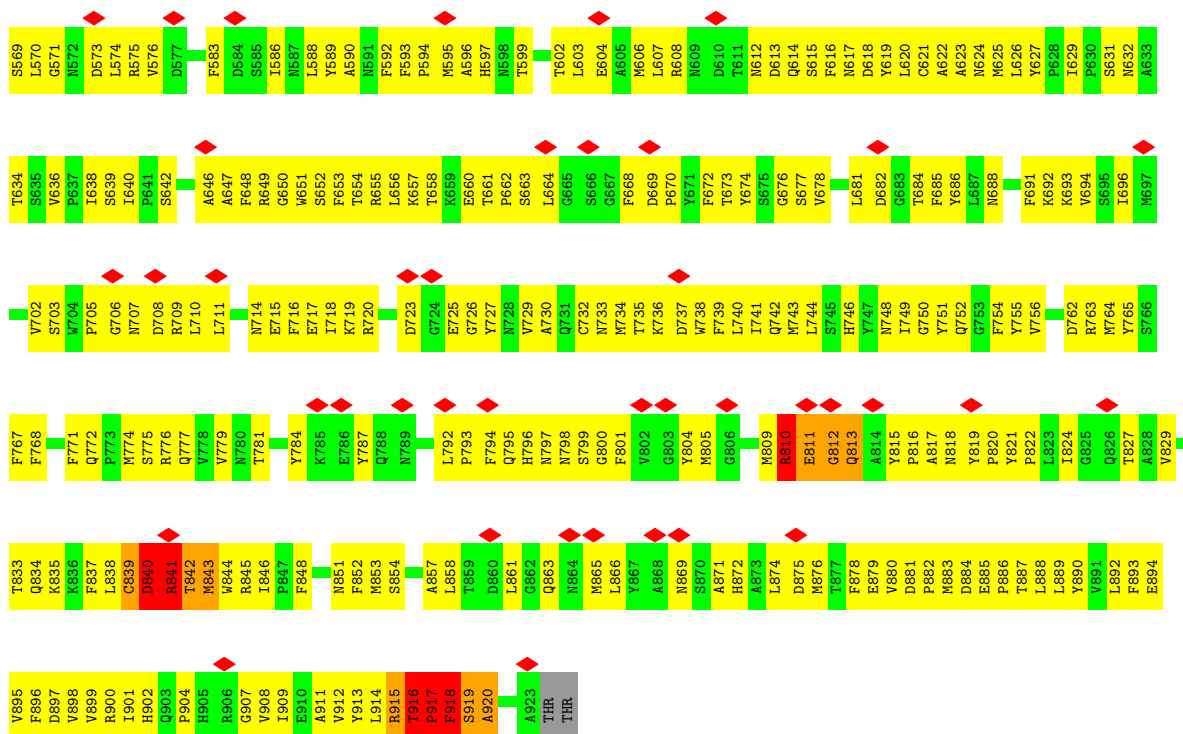
• Molecule 2: Hexon protein



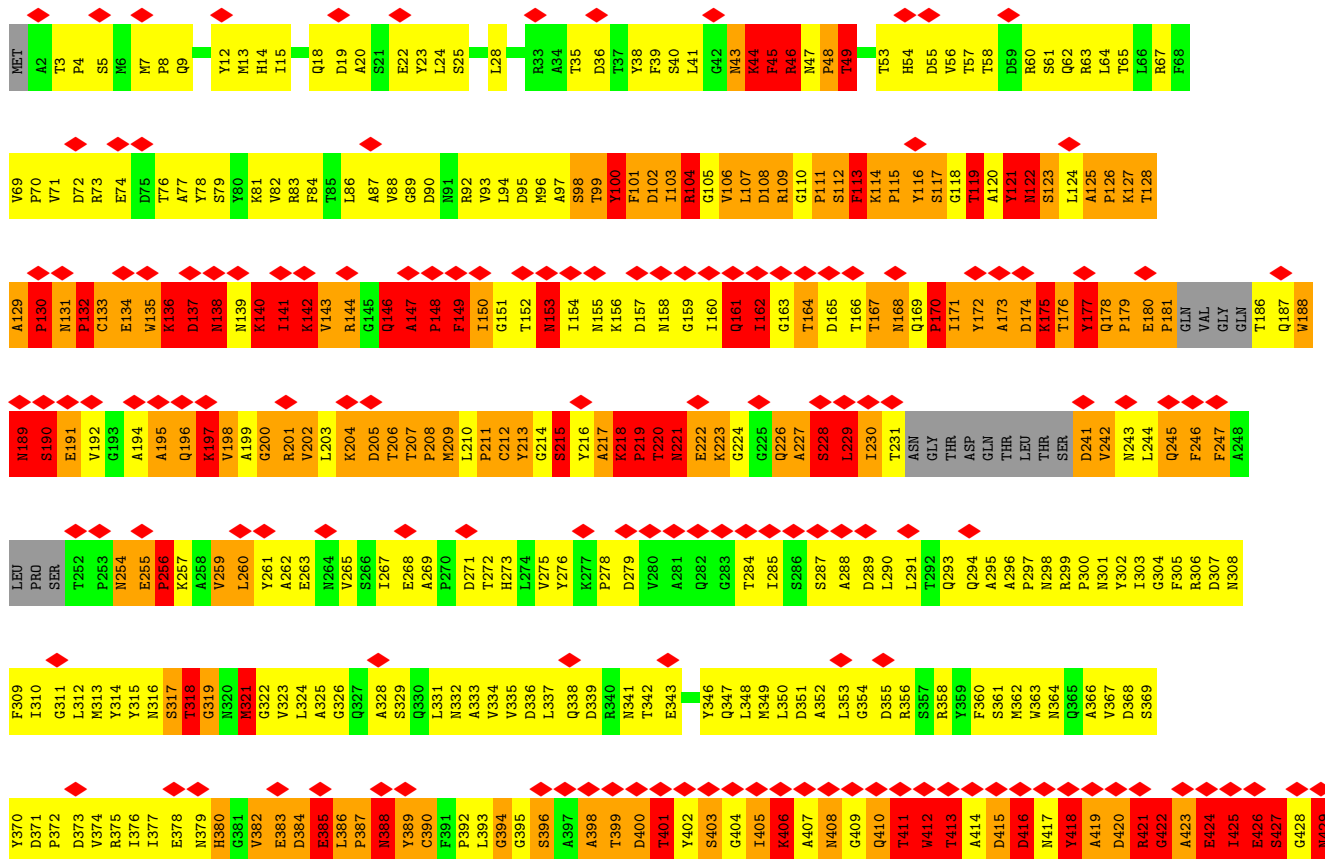
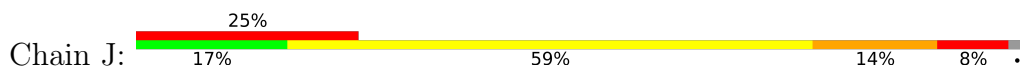


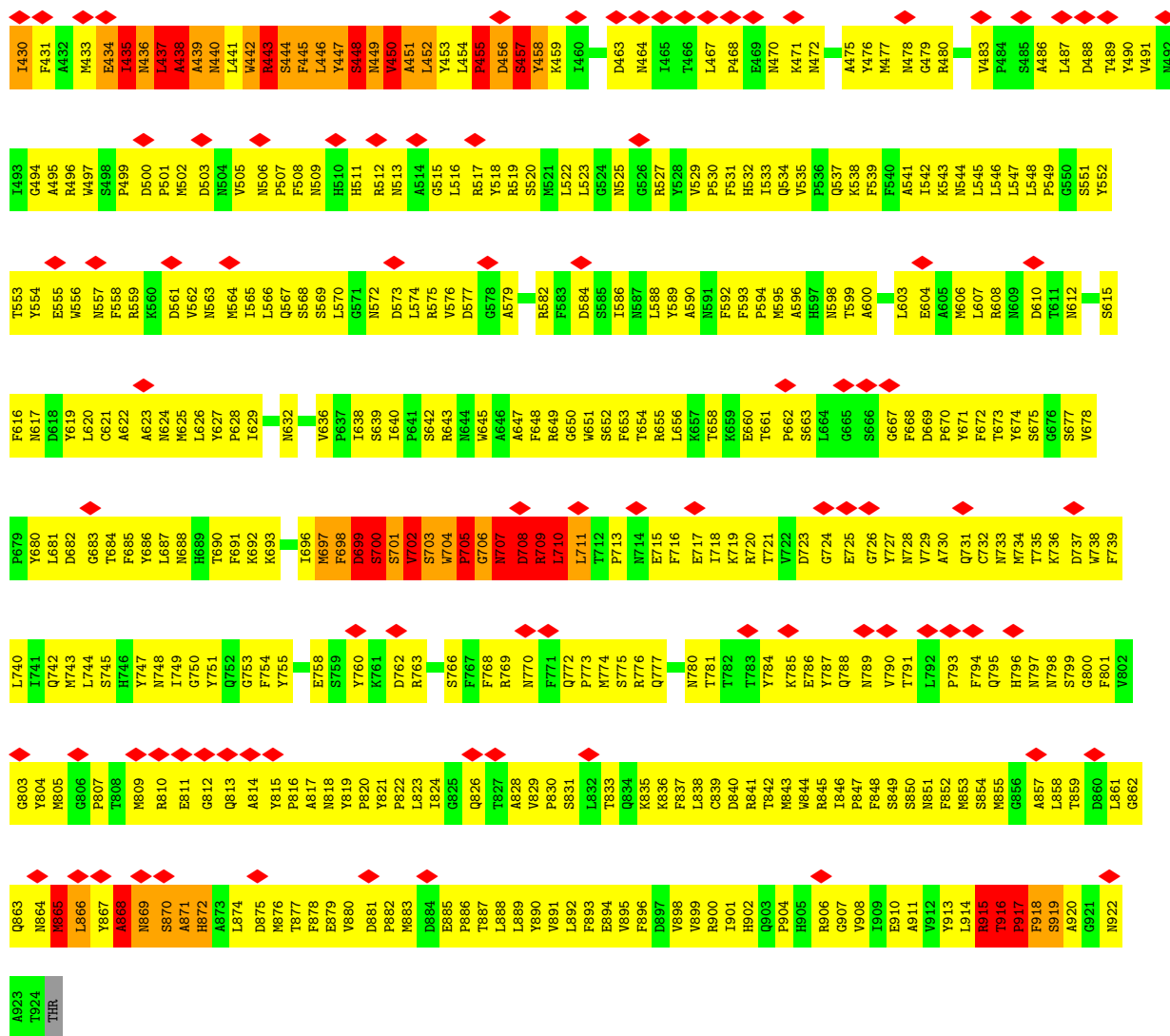
• Molecule 2: Hexon protein



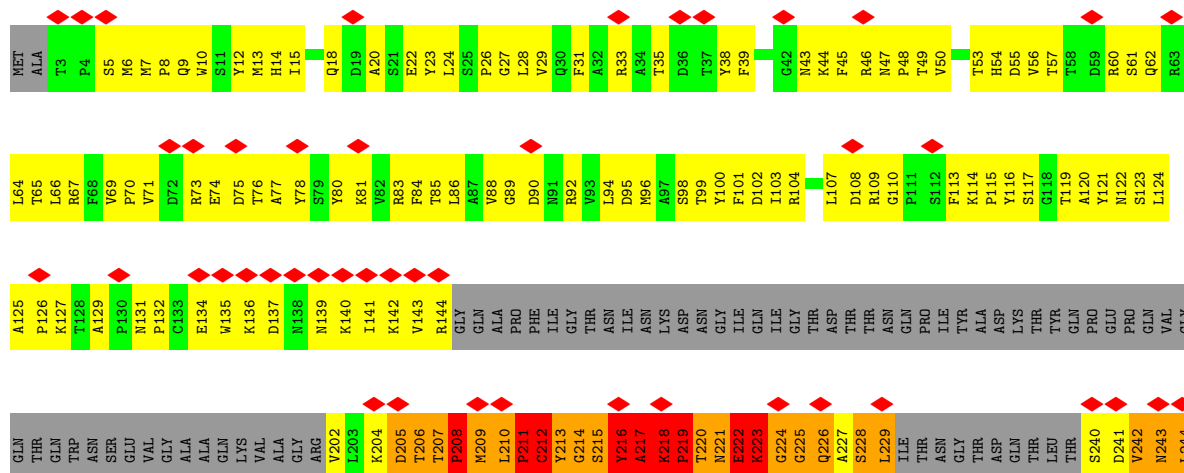


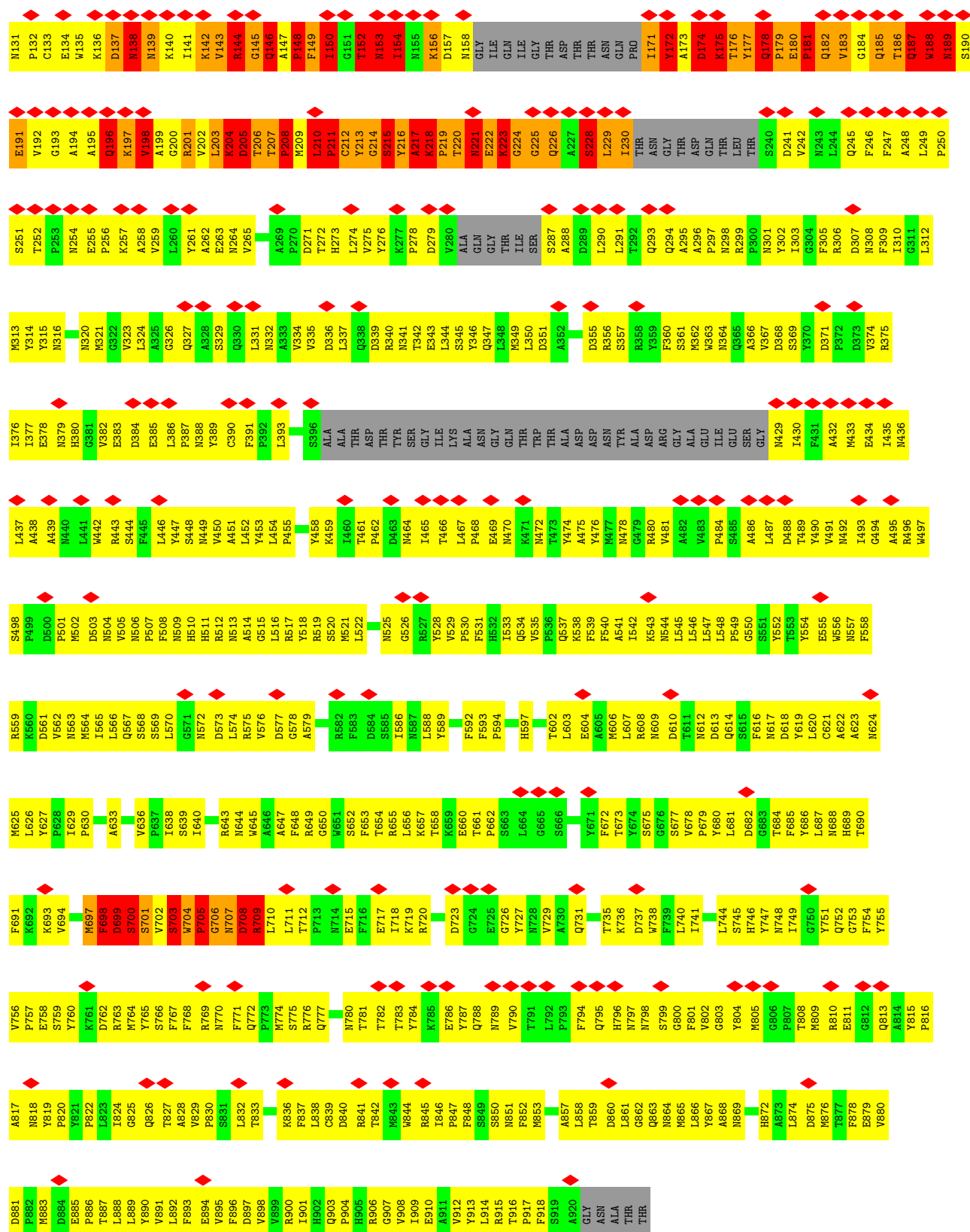
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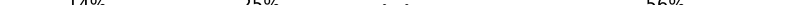
• Molecule 2: Hexon protein

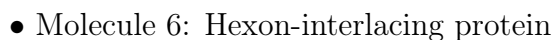


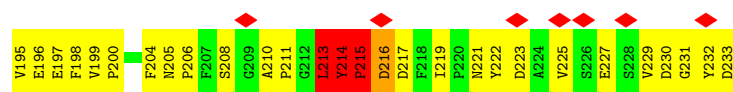


[illegible]

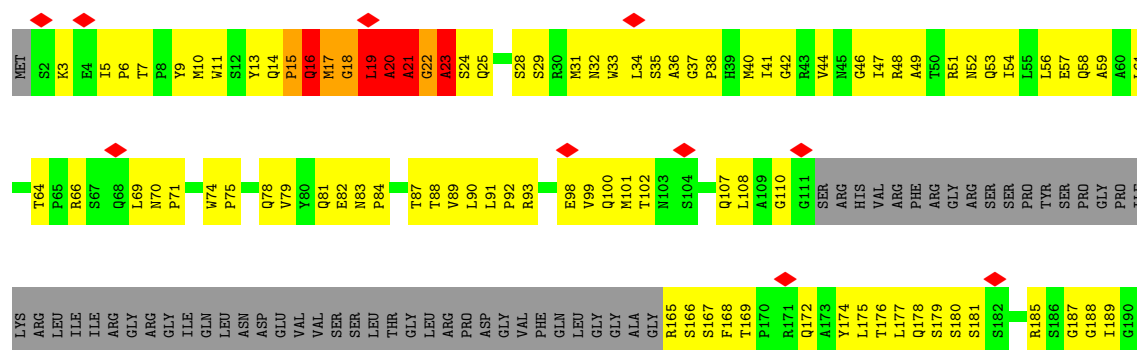
Category	Percentage
14%	14%
25%	25%
54%	54%

Chain P: 

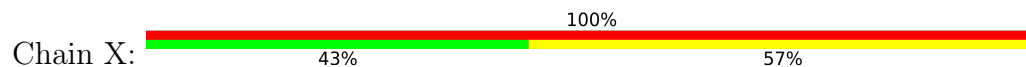




• Molecule 7: Pre-hexon-linking protein VIII



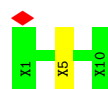
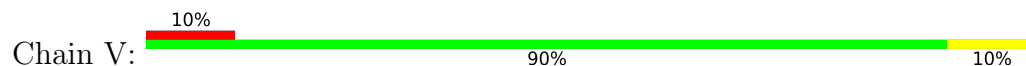
• Molecule 8: Fiber protein



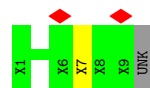
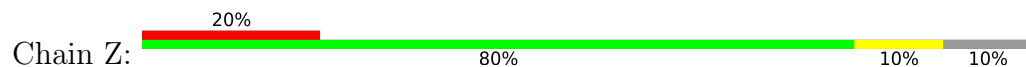
• Molecule 9: Unknown



• Molecule 9: Unknown



• Molecule 9: Unknown



- Molecule 10: Unknown

Chain Y: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	19472	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.03	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	936.9, 936.9, 936.9	wwPDB
Map dimensions	900, 900, 900	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.041, 1.041, 1.041	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	1.90	2/97 (2.1%)	2.57	9/129 (7.0%)
1	1	2.39	8/129 (6.2%)	2.63	10/174 (5.7%)
1	2	1.45	0/49	2.61	6/64 (9.4%)
1	3	1.40	0/101	1.57	2/136 (1.5%)
1	4	2.01	9/152 (5.9%)	2.18	8/205 (3.9%)
1	5	2.32	7/126 (5.6%)	3.09	11/169 (6.5%)
1	6	0.78	0/29	2.00	2/37 (5.4%)
1	7	1.40	1/29 (3.4%)	1.69	1/37 (2.7%)
1	8	2.09	10/203 (4.9%)	2.80	12/272 (4.4%)
1	9	1.13	0/29	1.53	1/37 (2.7%)
2	A	1.02	64/6485 (1.0%)	1.41	132/8832 (1.5%)
2	B	1.66	173/6946 (2.5%)	2.03	338/9461 (3.6%)
2	C	1.75	222/7052 (3.1%)	2.13	394/9608 (4.1%)
2	D	1.14	94/7250 (1.3%)	1.45	146/9872 (1.5%)
2	E	1.09	89/7181 (1.2%)	1.45	149/9781 (1.5%)
2	F	1.36	128/7265 (1.8%)	1.72	235/9895 (2.4%)
2	G	1.53	174/7201 (2.4%)	1.70	247/9809 (2.5%)
2	H	1.16	100/7290 (1.4%)	1.48	175/9931 (1.8%)
2	I	0.70	28/7412 (0.4%)	0.99	70/10100 (0.7%)
2	J	1.26	103/7401 (1.4%)	1.58	203/10084 (2.0%)
2	K	0.83	43/6891 (0.6%)	1.04	71/9387 (0.8%)
2	L	0.84	32/7023 (0.5%)	1.11	99/9565 (1.0%)
3	M	0.57	6/3744 (0.2%)	0.94	28/5099 (0.5%)
4	N	2.31	11/199 (5.5%)	2.68	17/265 (6.4%)
5	O	1.03	22/2120 (1.0%)	1.41	56/2882 (1.9%)
6	P	1.16	5/428 (1.2%)	1.24	8/583 (1.4%)
6	Q	1.10	7/375 (1.9%)	1.31	9/514 (1.8%)
6	R	1.91	9/234 (3.8%)	2.15	11/317 (3.5%)
6	S	1.89	13/428 (3.0%)	2.32	21/583 (3.6%)
7	T	0.68	7/1406 (0.5%)	0.95	13/1922 (0.7%)
7	U	0.83	14/1410 (1.0%)	0.83	9/1927 (0.5%)
8	X	0.21	0/68	0.34	0/94
All	All	1.22	1381/96753 (1.4%)	1.53	2493/131771 (1.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	2	0
1	3	1	0
1	5	1	0
1	8	3	0
2	A	4	1
2	B	5	3
2	C	12	2
2	D	4	3
2	E	2	6
2	F	3	1
2	G	0	4
2	H	1	1
2	I	4	0
2	J	6	1
2	K	1	0
2	L	1	2
3	M	2	1
5	O	2	2
6	P	1	0
6	R	1	0
6	S	1	0
7	T	0	1
7	U	0	1
All	All	57	29

The worst 5 of 1381 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	886	PRO	N-CD	-37.89	0.94	1.47
2	L	179	PRO	N-CD	-21.82	1.17	1.47
2	G	392	PRO	N-CD	-20.32	1.19	1.47
2	H	208	PRO	N-CD	-19.64	1.20	1.47
2	J	181	PRO	N-CD	-18.34	1.22	1.47

The worst 5 of 2493 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	816	PRO	N-CA-CB	-27.54	80.19	103.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	816	PRO	N-CA-CB	-25.96	75.99	103.25
2	E	917	PRO	N-CA-CB	-25.31	76.67	103.25
2	B	886	PRO	CA-N-CD	23.94	145.51	112.00
2	H	220	THR	CB-CA-C	-23.50	69.60	109.07

5 of 57 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	2	17	PRO	CA
1	2	21	THR	CA
1	3	23	ASN	CA
1	5	27	THR	CA
1	8	16	ARG	CA

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	323	VAL	Mainchain
2	B	180	GLU	Mainchain
2	B	431	PHE	Mainchain
2	B	822	PRO	Mainchain
2	C	125	ALA	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	94	0	93	20	0
1	1	124	0	118	32	0
1	2	48	0	47	10	0
1	3	98	0	90	14	0
1	4	147	0	135	41	0
1	5	123	0	111	52	0
1	6	28	0	27	6	0
1	7	28	0	27	10	0
1	8	197	0	181	68	0
1	9	28	0	27	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	6307	0	6043	1355	0
2	B	6761	0	6493	1725	0
2	C	6862	0	6575	1775	0
2	D	7057	0	6749	1609	0
2	E	6988	0	6702	1742	0
2	F	7070	0	6781	1733	0
2	G	7008	0	6715	1594	0
2	H	7095	0	6803	1635	0
2	I	7212	0	6900	1427	0
2	J	7203	0	6888	1633	0
2	K	6702	0	6413	1401	0
2	L	6831	0	6550	1349	0
3	M	3659	0	3605	502	0
4	N	198	0	209	94	0
5	O	2088	0	2087	338	0
6	P	419	0	414	88	0
6	Q	366	0	365	96	0
6	R	228	0	227	64	0
6	S	419	0	413	90	0
7	T	1368	0	1297	234	0
7	U	1372	0	1300	195	0
8	X	64	0	55	3	0
9	V	50	0	14	1	0
9	W	45	0	12	8	0
9	Z	45	0	13	1	0
10	Y	30	0	10	3	0
All	All	94362	0	90489	18531	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 100.

The worst 5 of 18531 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:885:GLU:HG2	2:E:886:PRO:CD	1.24	1.68
2:A:704:TRP:CG	2:A:705:PRO:HD2	1.14	1.65
2:L:136:LYS:CG	2:L:140:LYS:HG2	1.25	1.63
3:M:221:LEU:HD11	3:M:336:ASN:CB	1.14	1.62
3:M:221:LEU:CD1	3:M:336:ASN:HB3	1.30	1.61

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	10/266 (4%)	3 (30%)	3 (30%)	4 (40%)	0	0
1	1	14/266 (5%)	6 (43%)	2 (14%)	6 (43%)	0	0
1	2	4/266 (2%)	2 (50%)	0	2 (50%)	0	0
1	3	10/266 (4%)	3 (30%)	5 (50%)	2 (20%)	0	1
1	4	17/266 (6%)	7 (41%)	8 (47%)	2 (12%)	0	4
1	5	14/266 (5%)	7 (50%)	4 (29%)	3 (21%)	0	1
1	6	1/266 (0%)	1 (100%)	0	0	100	100
1	7	1/266 (0%)	1 (100%)	0	0	100	100
1	8	24/266 (9%)	10 (42%)	9 (38%)	5 (21%)	0	1
1	9	1/266 (0%)	1 (100%)	0	0	100	100
2	A	776/925 (84%)	555 (72%)	163 (21%)	58 (8%)	1	11
2	B	837/925 (90%)	534 (64%)	178 (21%)	125 (15%)	0	2
2	C	852/925 (92%)	513 (60%)	186 (22%)	153 (18%)	0	1
2	D	875/925 (95%)	604 (69%)	202 (23%)	69 (8%)	1	10
2	E	868/925 (94%)	576 (66%)	230 (26%)	62 (7%)	1	12
2	F	881/925 (95%)	599 (68%)	185 (21%)	97 (11%)	0	5
2	G	870/925 (94%)	611 (70%)	184 (21%)	75 (9%)	0	9
2	H	886/925 (96%)	682 (77%)	146 (16%)	58 (6%)	1	13
2	I	902/925 (98%)	737 (82%)	137 (15%)	28 (3%)	3	24
2	J	899/925 (97%)	639 (71%)	183 (20%)	77 (9%)	0	9
2	K	830/925 (90%)	662 (80%)	138 (17%)	30 (4%)	2	21
2	L	845/925 (91%)	683 (81%)	127 (15%)	35 (4%)	2	19
3	M	452/508 (89%)	365 (81%)	81 (18%)	6 (1%)	9	38
4	N	22/348 (6%)	9 (41%)	6 (27%)	7 (32%)	0	0
5	O	259/579 (45%)	190 (73%)	53 (20%)	16 (6%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	P	56/133 (42%)	41 (73%)	12 (21%)	3 (5%)	1	16
6	Q	48/133 (36%)	34 (71%)	12 (25%)	2 (4%)	2	19
6	R	28/133 (21%)	13 (46%)	11 (39%)	4 (14%)	0	3
6	S	56/133 (42%)	17 (30%)	16 (29%)	23 (41%)	0	0
7	T	174/233 (75%)	139 (80%)	33 (19%)	2 (1%)	11	40
7	U	175/233 (75%)	139 (79%)	31 (18%)	5 (3%)	3	25
8	X	5/7 (71%)	1 (20%)	4 (80%)	0	100	100
All	All	11692/16200 (72%)	8384 (72%)	2349 (20%)	959 (8%)	1	9

5 of 959 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	20	ALA
1	0	23	HIS
1	0	25	SER
1	1	10	ALA
1	1	12	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	10/227 (4%)	7 (70%)	3 (30%)	0	2
1	1	12/227 (5%)	8 (67%)	4 (33%)	0	1
1	2	5/227 (2%)	2 (40%)	3 (60%)	0	0
1	3	10/227 (4%)	7 (70%)	3 (30%)	0	2
1	4	15/227 (7%)	13 (87%)	2 (13%)	4	19
1	5	13/227 (6%)	9 (69%)	4 (31%)	0	1
1	6	3/227 (1%)	2 (67%)	1 (33%)	0	1
1	7	3/227 (1%)	2 (67%)	1 (33%)	0	1
1	8	20/227 (9%)	11 (55%)	9 (45%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	9	3/227 (1%)	2 (67%)	1 (33%)	0	1
2	A	687/797 (86%)	631 (92%)	56 (8%)	10	34
2	B	739/797 (93%)	606 (82%)	133 (18%)	2	12
2	C	748/797 (94%)	624 (83%)	124 (17%)	2	13
2	D	764/797 (96%)	688 (90%)	76 (10%)	7	29
2	E	761/797 (96%)	710 (93%)	51 (7%)	15	40
2	F	770/797 (97%)	691 (90%)	79 (10%)	7	27
2	G	763/797 (96%)	698 (92%)	65 (8%)	10	33
2	H	770/797 (97%)	715 (93%)	55 (7%)	13	39
2	I	782/797 (98%)	756 (97%)	26 (3%)	33	55
2	J	781/797 (98%)	710 (91%)	71 (9%)	9	32
2	K	731/797 (92%)	707 (97%)	24 (3%)	33	55
2	L	744/797 (93%)	714 (96%)	30 (4%)	28	51
3	M	408/447 (91%)	402 (98%)	6 (2%)	57	69
4	N	24/307 (8%)	22 (92%)	2 (8%)	10	34
5	O	228/501 (46%)	218 (96%)	10 (4%)	25	48
6	P	44/97 (45%)	42 (96%)	2 (4%)	24	48
6	Q	38/97 (39%)	35 (92%)	3 (8%)	11	36
6	R	24/97 (25%)	22 (92%)	2 (8%)	10	34
6	S	44/97 (45%)	26 (59%)	18 (41%)	0	0
7	T	148/192 (77%)	143 (97%)	5 (3%)	32	54
7	U	148/192 (77%)	147 (99%)	1 (1%)	76	77
8	X	7/7 (100%)	6 (86%)	1 (14%)	3	17
All	All	10247/13868 (74%)	9376 (92%)	871 (8%)	12	33

5 of 871 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	883	MET
2	G	299	ARG
2	L	171	ILE
2	F	121	TYR
2	E	820	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 291 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	347	GLN
7	T	81	GLN
2	K	707	ASN
2	L	795	GLN
2	E	189	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

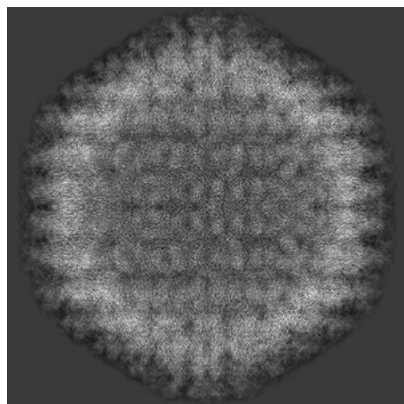
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11108. These allow visual inspection of the internal detail of the map and identification of artifacts.

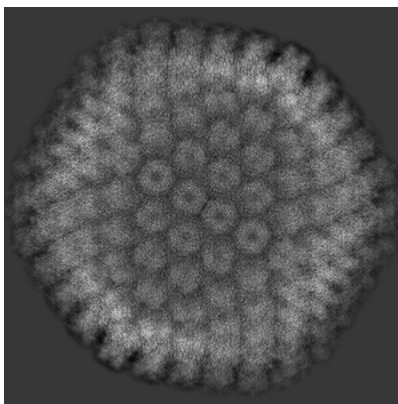
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

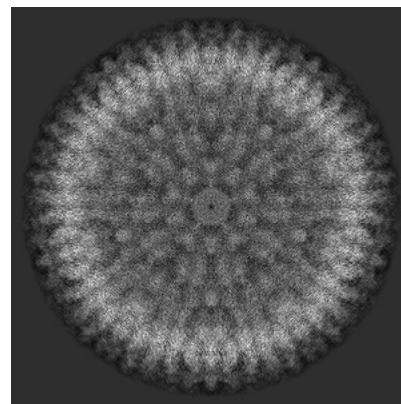
6.1.1 Primary map



X

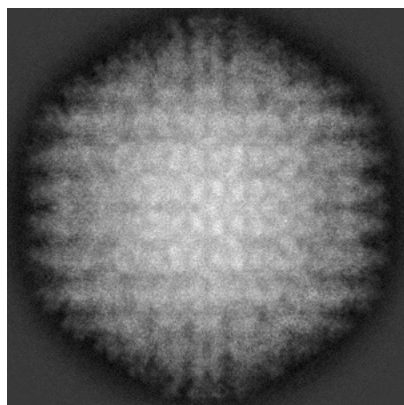


Y

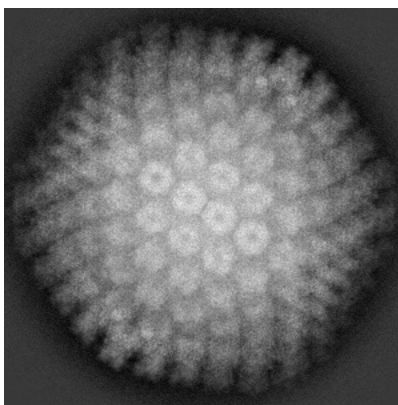


Z

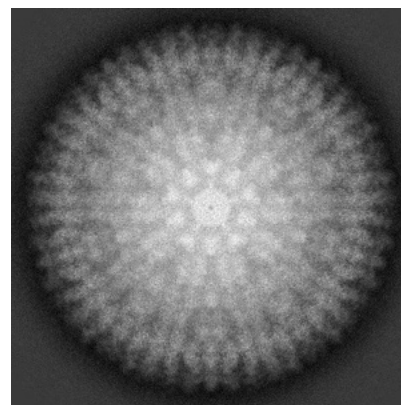
6.1.2 Raw map



X



Y

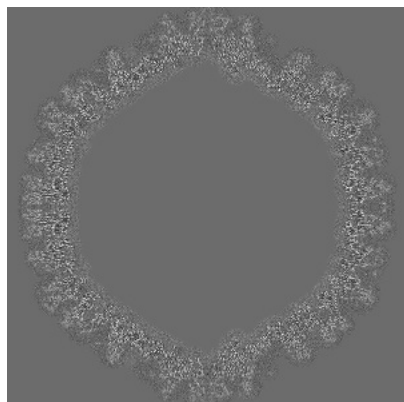


Z

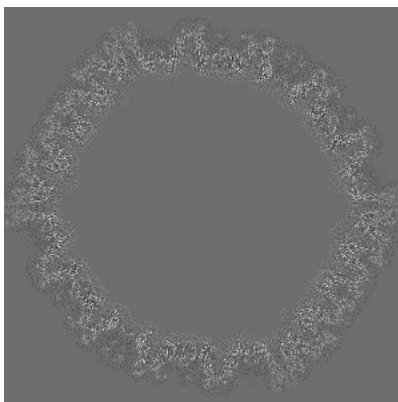
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

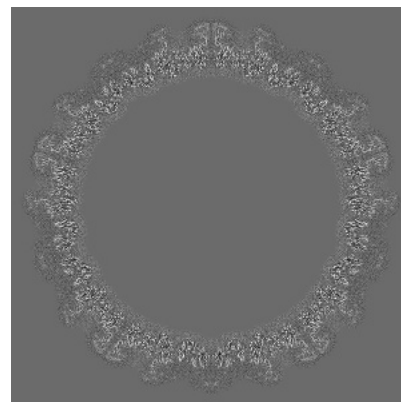
6.2.1 Primary map



X Index: 450

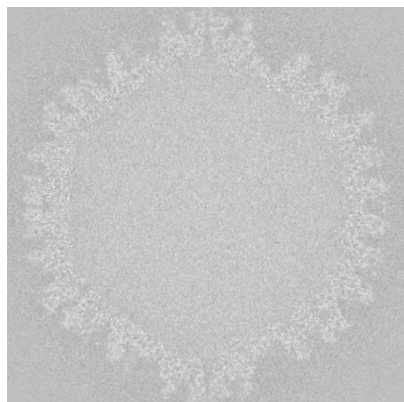


Y Index: 450

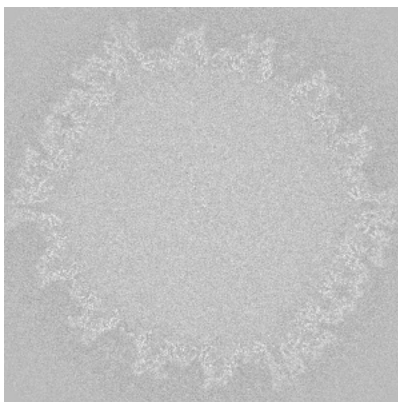


Z Index: 450

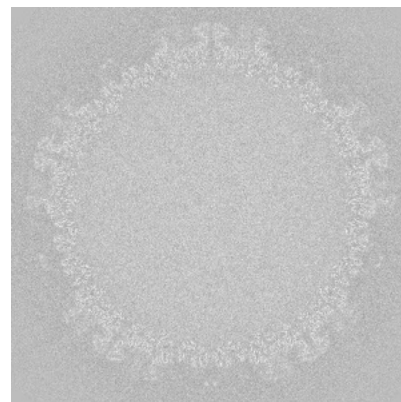
6.2.2 Raw map



X Index: 450



Y Index: 450

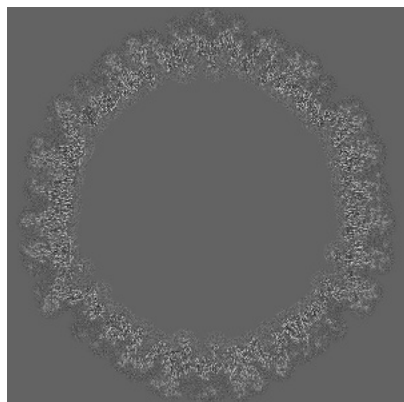


Z Index: 450

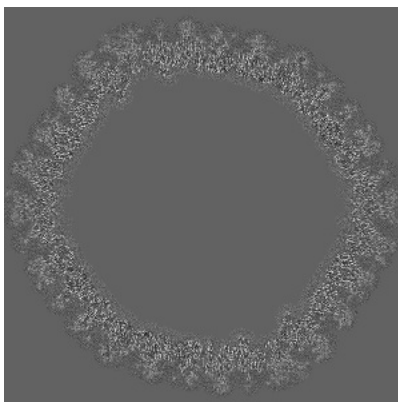
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

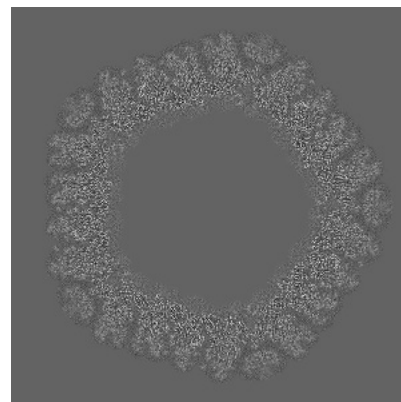
6.3.1 Primary map



X Index: 492

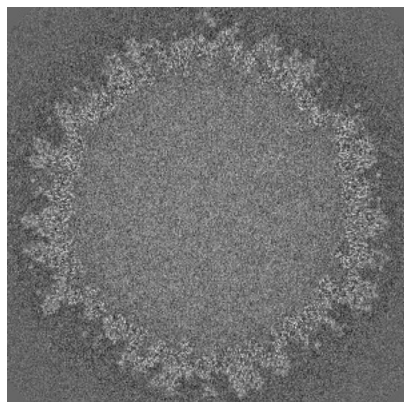


Y Index: 431

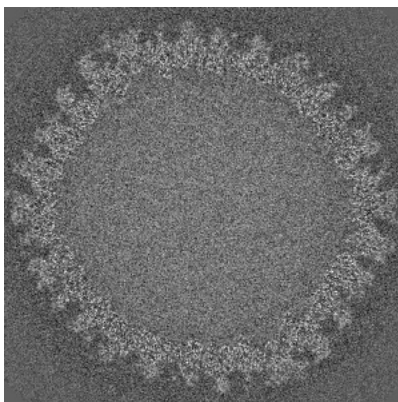


Z Index: 249

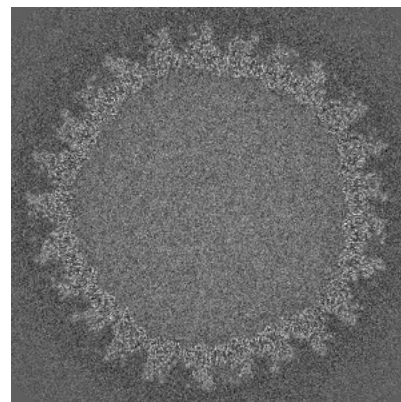
6.3.2 Raw map



X Index: 490



Y Index: 431

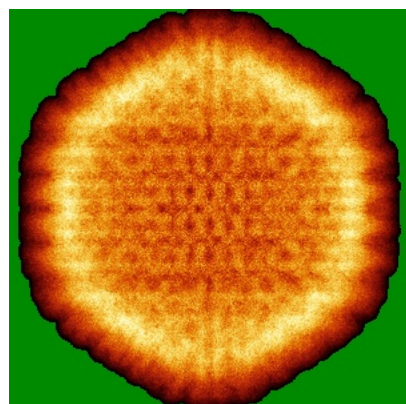


Z Index: 504

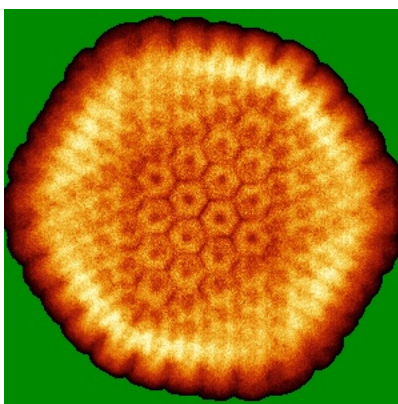
The images above show the largest variance slices of the map in three orthogonal directions.

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

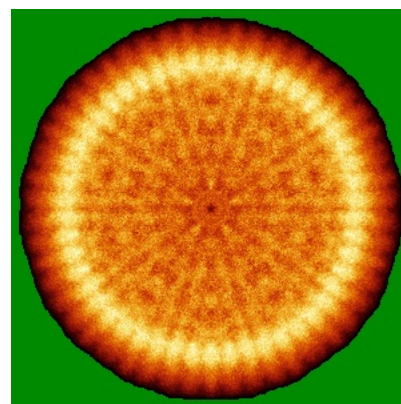
6.4.1 Primary map



X

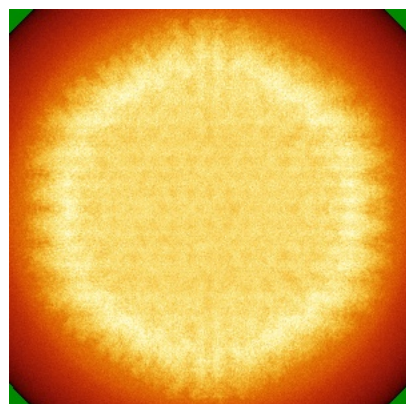


Y

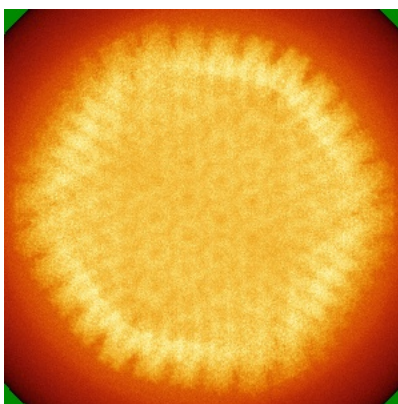


Z

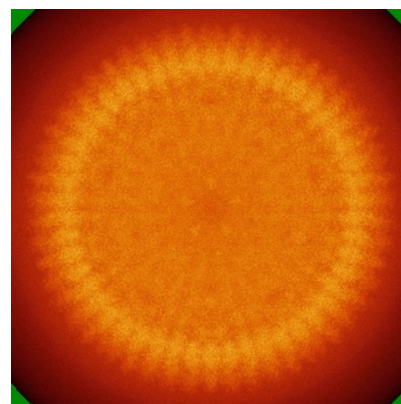
6.4.2 Raw map



X



Y

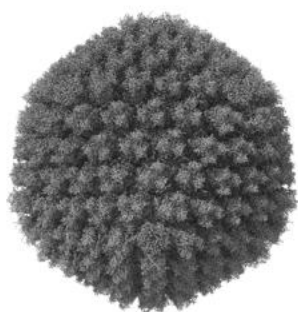


Z

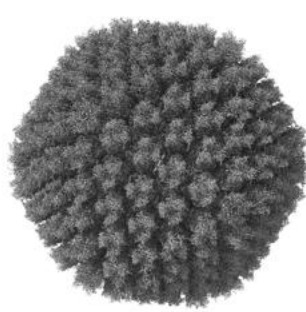
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

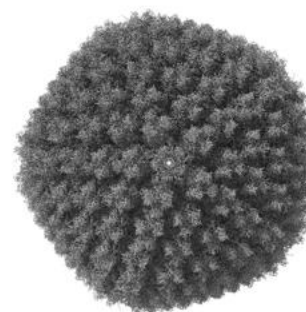
6.5.1 Primary map



X



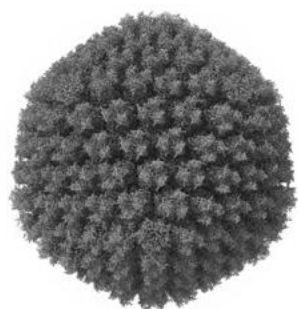
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. 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



X



Y



Z

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.

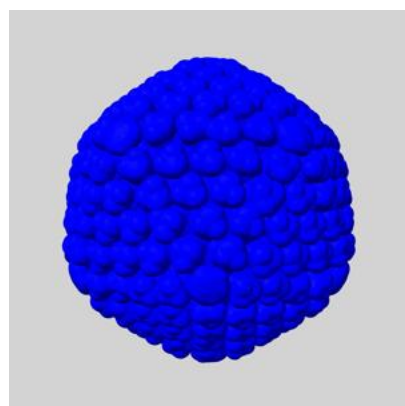
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

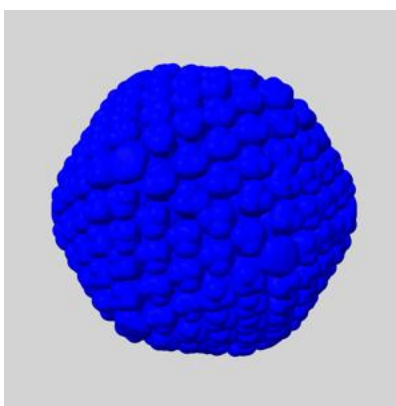
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

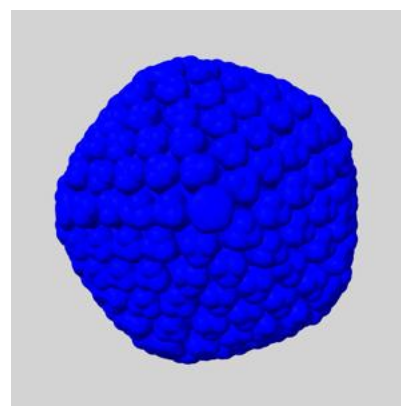
6.6.1 emd_11108_msk_1.map [i](#)



X



Y

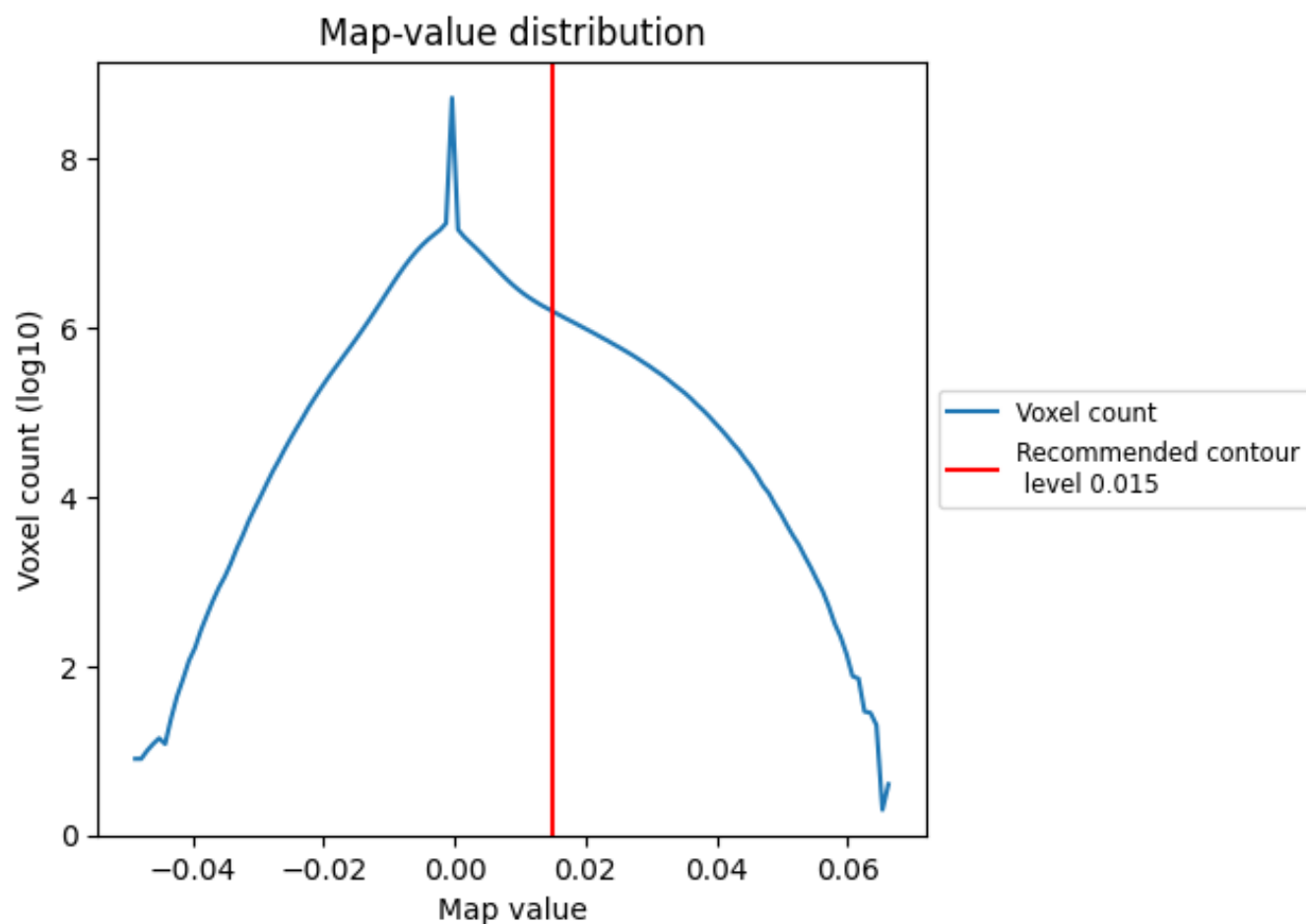


Z

7 Map analysis [i](#)

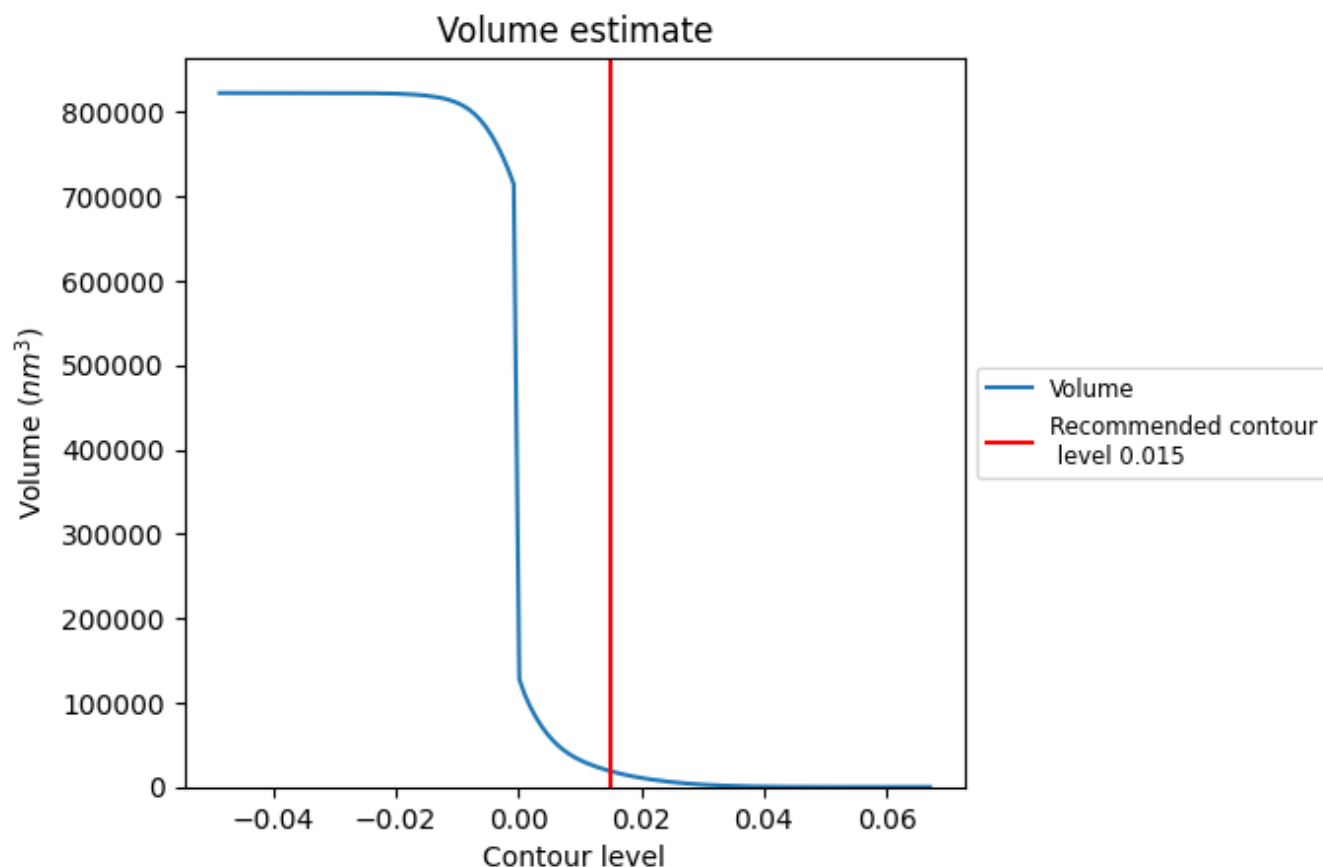
This section contains the results of statistical analysis of the map.

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.

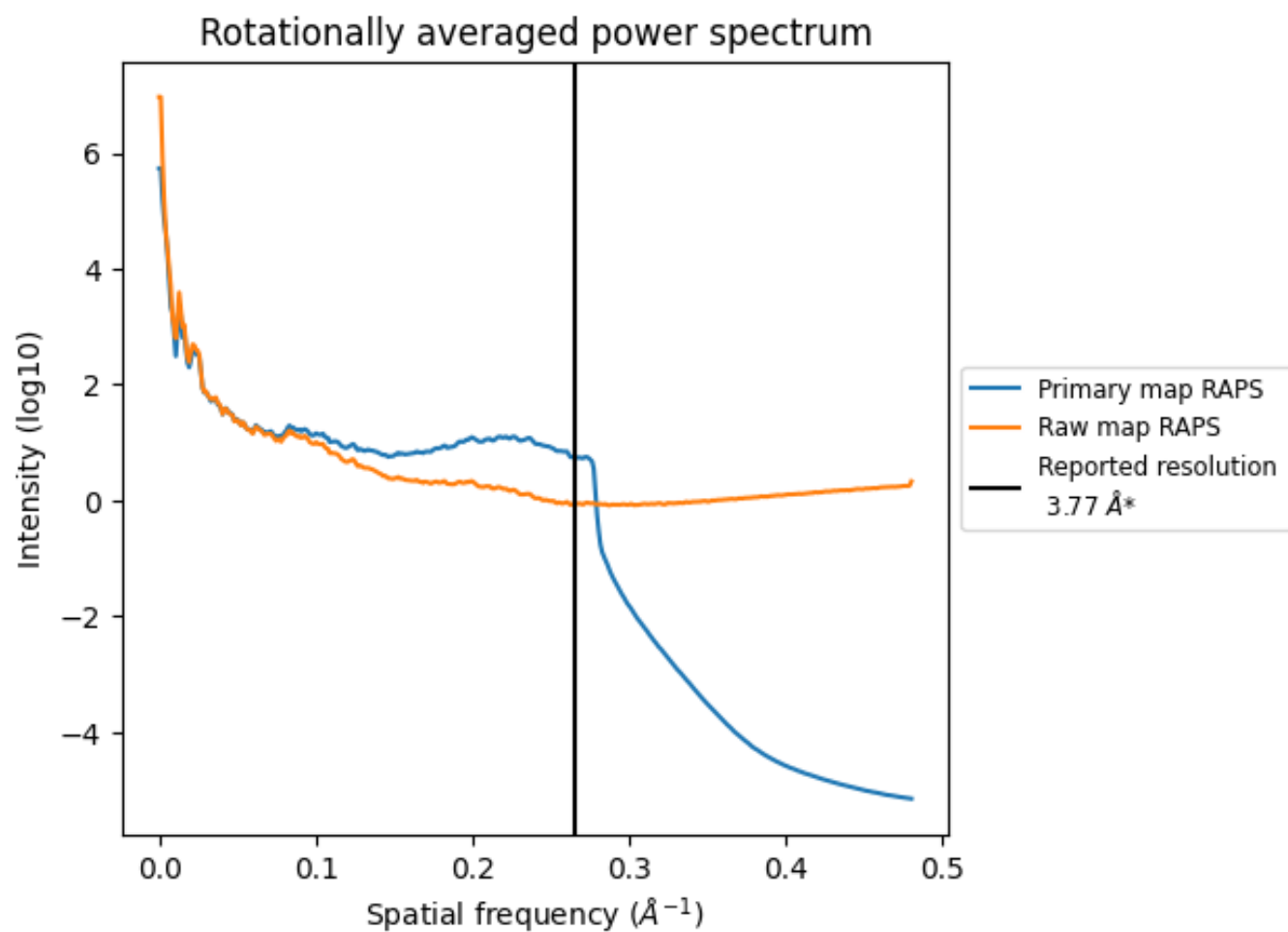
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 18776 nm^3 ; this corresponds to an approximate mass of 16961 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 ⓘ

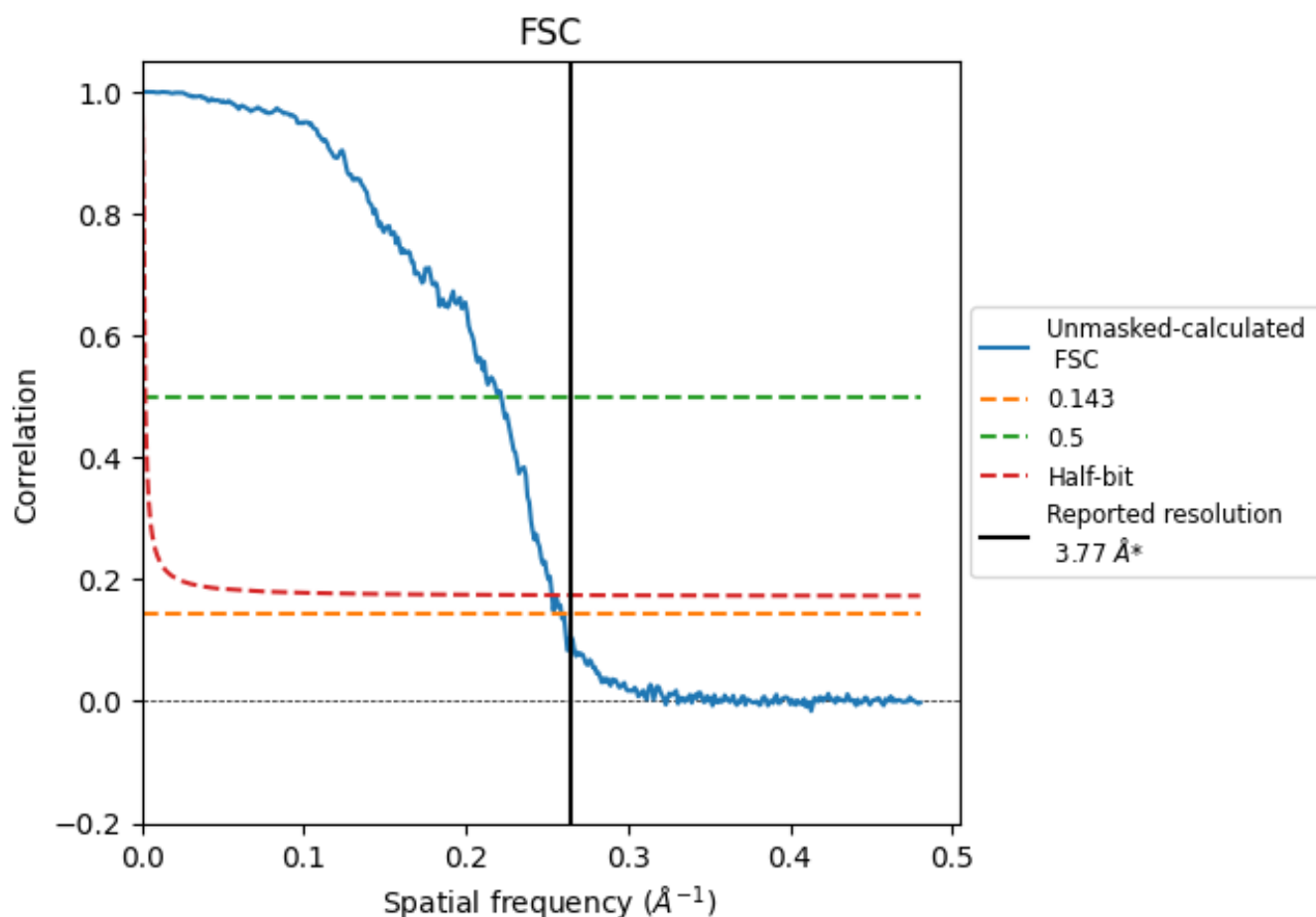


*Reported resolution corresponds to spatial frequency of 0.265 Å⁻¹

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 0.265 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.77	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.86	4.51	3.95

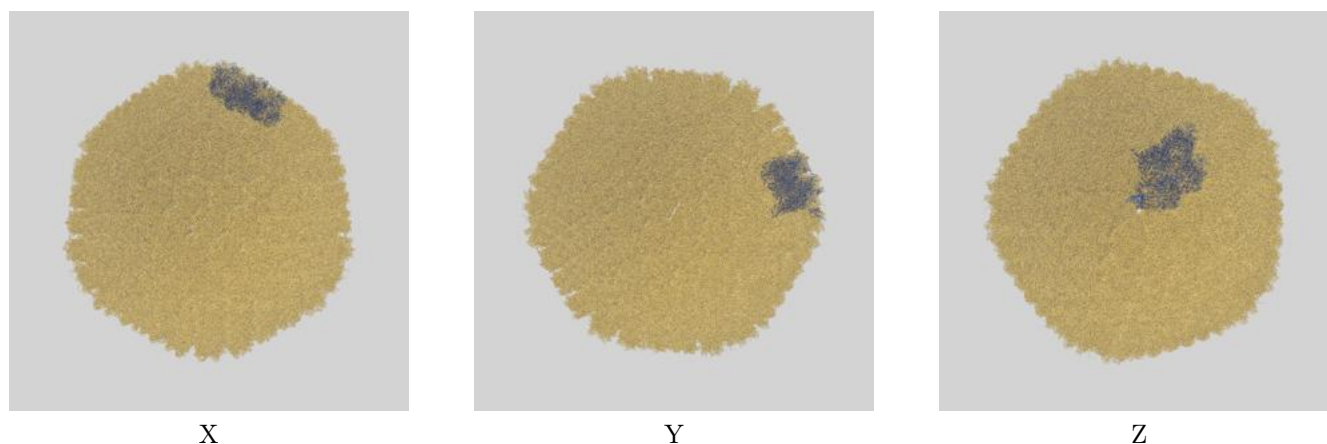
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

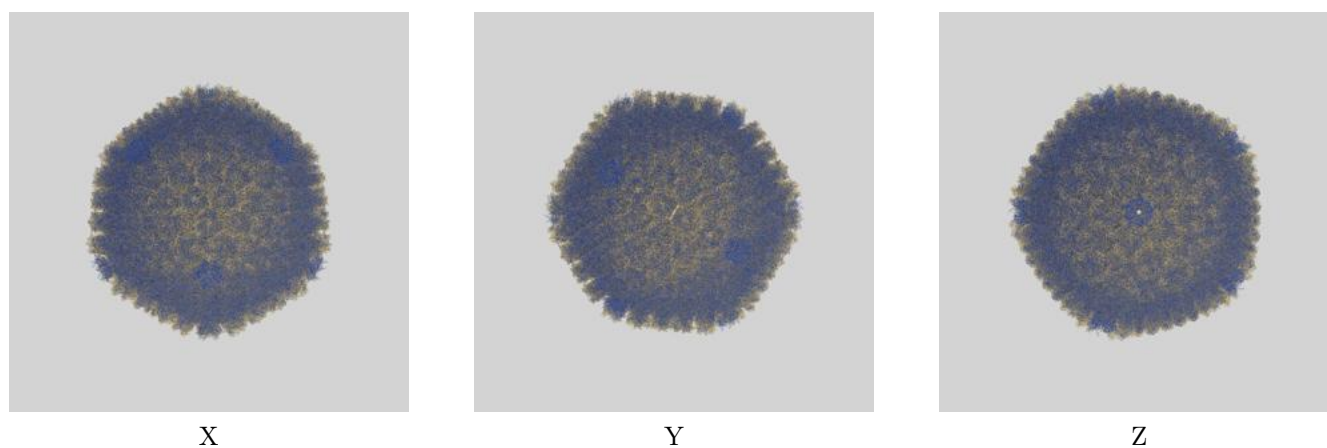
This section contains information regarding the fit between EMDB map EMD-11108 and PDB model 6Z7N. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

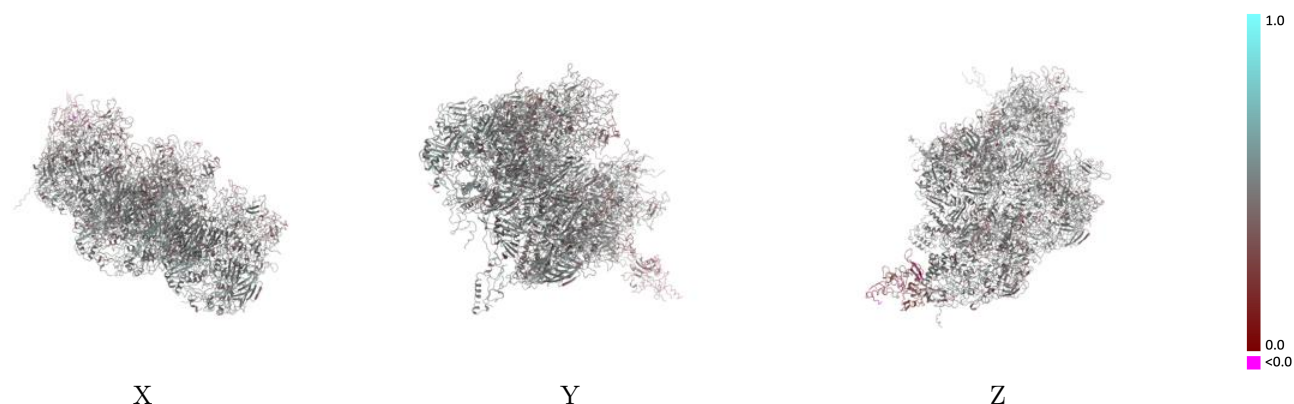


9.1.2 Map-model assembly overlay [i](#)



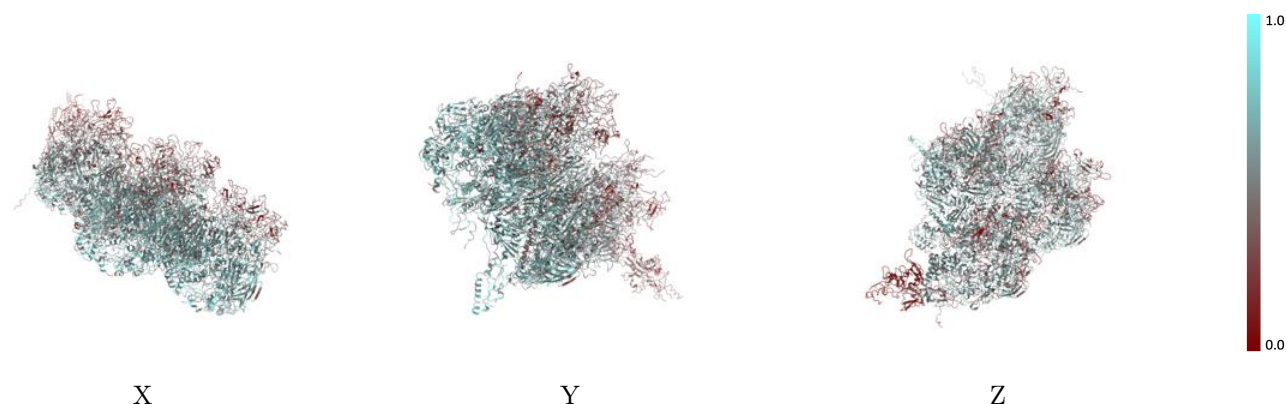
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



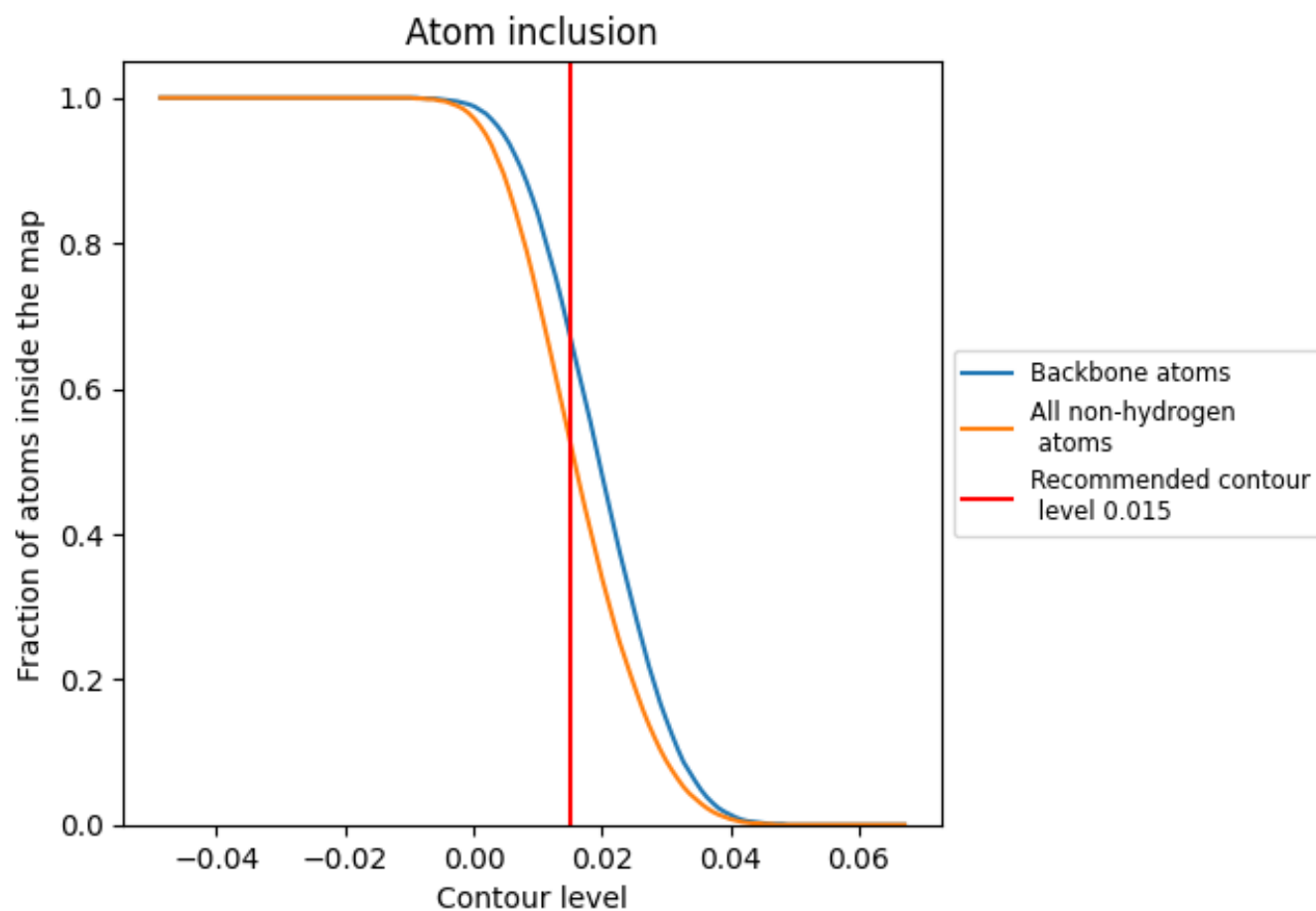
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 53% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5290	 0.4610
0	 0.2440	 0.4680
1	 0.6220	 0.5020
2	 0.4350	 0.4980
3	 0.3900	 0.4510
4	 0.5000	 0.4060
5	 0.5420	 0.4650
6	 0.6150	 0.5350
7	 0.5770	 0.4950
8	 0.5100	 0.4680
9	 0.5770	 0.5150
A	 0.5140	 0.4630
B	 0.4800	 0.4610
C	 0.5110	 0.4660
D	 0.5410	 0.4650
E	 0.5330	 0.4640
F	 0.5610	 0.4760
G	 0.5750	 0.4760
H	 0.5610	 0.4720
I	 0.5580	 0.4650
J	 0.5380	 0.4650
K	 0.5430	 0.4590
L	 0.5490	 0.4680
M	 0.2800	 0.3230
N	 0.5770	 0.4360
O	 0.4840	 0.4540
P	 0.4560	 0.4440
Q	 0.4710	 0.4460
R	 0.5000	 0.4750
S	 0.5270	 0.4830
T	 0.5990	 0.4750
U	 0.6330	 0.4950
V	 0.7800	 0.5380
W	 0.7780	 0.4850
X	 0.0000	 0.0520



Continued on next page...

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Chain	Atom inclusion	Q-score
Y	 0.6000	 0.5160
Z	 0.5780	 0.4700