



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 03:45 AM UTC

PDB ID : 9NO1 / pdb_00009no1
EMDB ID : EMD-49591
Title : Cryo-ET map of the VZV capsid vertex (5-fold axis).
Authors : Oliver, S.L.; Chen, M.
Deposited on : 2025-03-07
Resolution : 8.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

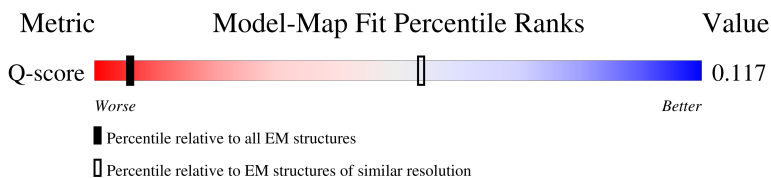
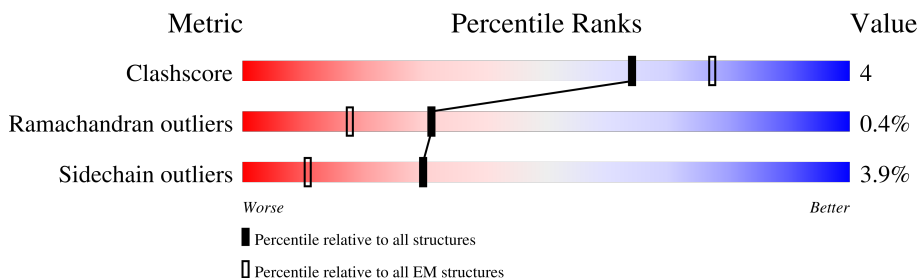
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.30 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	280 (7.82 - 8.80)

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	A	1396	40% 70% 13% 16%
1	B	1396	45% 84% 11% 5%
1	D	1396	42% 83% 12% . .
1	F	1396	43% 85% 10% . .

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Mol	Chain	Length	Quality of chain
1	H	1396	
1	J	1396	
1	L	1396	
2	C	235	
2	E	235	
2	G	235	
2	I	235	
2	K	235	
2	M	235	
3	N	483	
3	Q	483	
4	O	316	
4	P	316	
4	R	316	
4	S	316	
5	T	676	
6	U	579	
6	V	579	
7	W	2763	
7	X	2763	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 102113 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 ORF40.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1166	Total	C	N	O	S	0	0
			9043	5744	1576	1664	59		
1	B	1332	Total	C	N	O	S	0	0
			10283	6529	1786	1900	68		
1	D	1337	Total	C	N	O	S	0	0
			10245	6510	1760	1909	66		
1	F	1337	Total	C	N	O	S	0	0
			10328	6558	1786	1916	68		
1	H	1281	Total	C	N	O	S	0	0
			9821	6246	1690	1819	66		
1	J	1279	Total	C	N	O	S	0	0
			9850	6242	1714	1829	65		
1	L	1314	Total	C	N	O	S	0	0
			10181	6461	1766	1888	66		

- Molecule 2 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	101	Total	C	N	O	S	0	0
			724	461	123	138	2		
2	E	97	Total	C	N	O	S	0	0
			712	452	126	132	2		
2	G	101	Total	C	N	O	S	0	0
			736	467	129	138	2		
2	I	101	Total	C	N	O	S	0	0
			742	470	132	138	2		
2	K	101	Total	C	N	O	S	0	0
			742	470	132	138	2		
2	M	101	Total	C	N	O	S	0	0
			721	459	122	138	2		

- Molecule 3 is a protein called ORF20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	357	Total	C	N	O	S	0	0
			2767	1753	483	515	16		
3	Q	357	Total	C	N	O	S	0	0
			2770	1754	484	516	16		

- Molecule 4 is a protein called ORF41.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	298	Total	C	N	O	S	0	0
			2288	1458	397	422	11		
4	P	275	Total	C	N	O	S	0	0
			2080	1333	354	384	9		
4	R	298	Total	C	N	O	S	0	0
			2288	1458	397	422	11		
4	S	275	Total	C	N	O	S	0	0
			2083	1334	354	386	9		

- Molecule 5 is a protein called ORF43.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	T	593	Total	C	N	O	S	0	0
			4593	2943	782	843	25		

- Molecule 6 is a protein called ORF34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	U	531	Total	C	N	O	S	0	0
			4200	2636	745	799	20		
6	V	531	Total	C	N	O	S	0	0
			4200	2636	745	799	20		

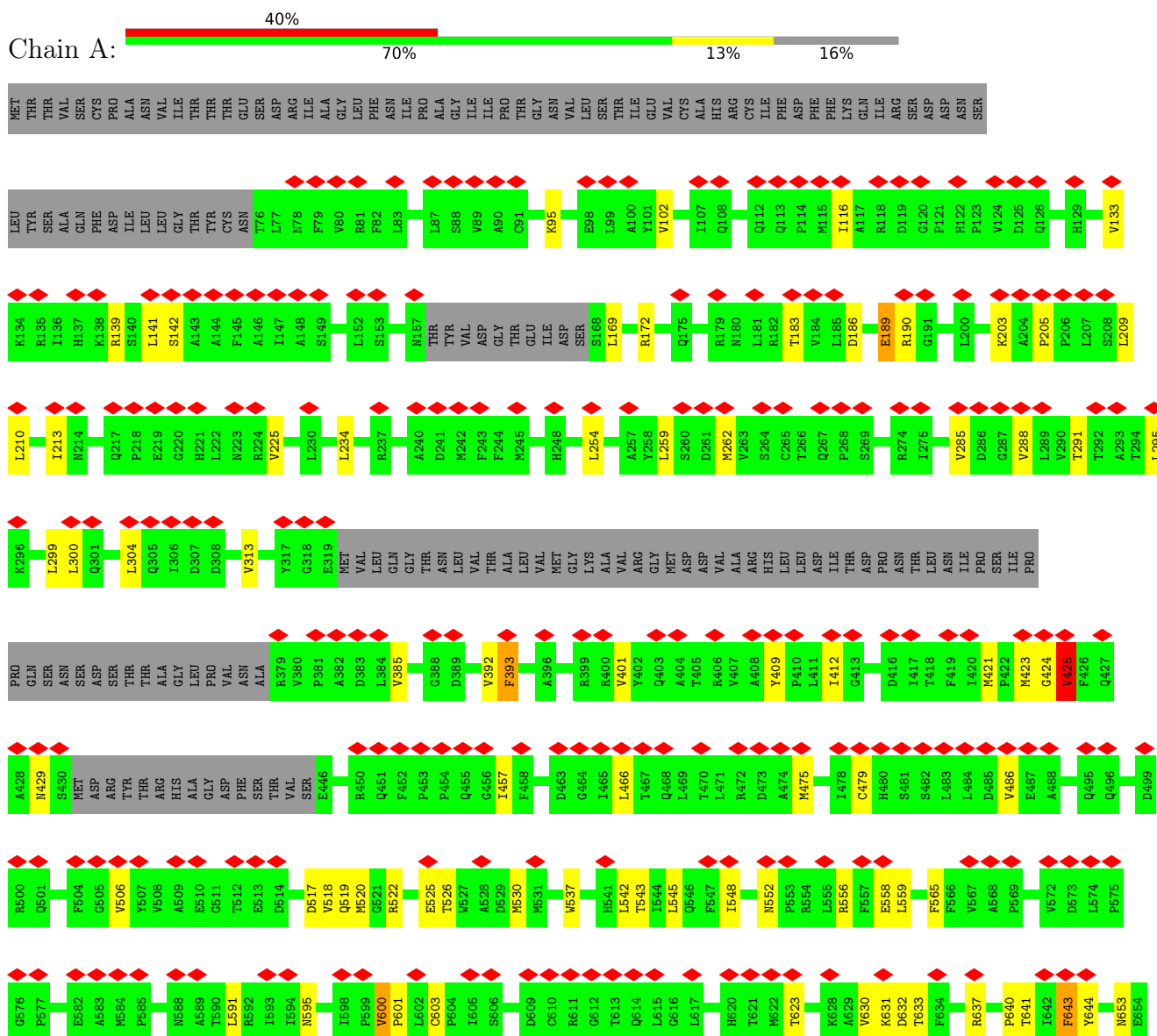
- Molecule 7 is a protein called Large tegument protein deneddylase.

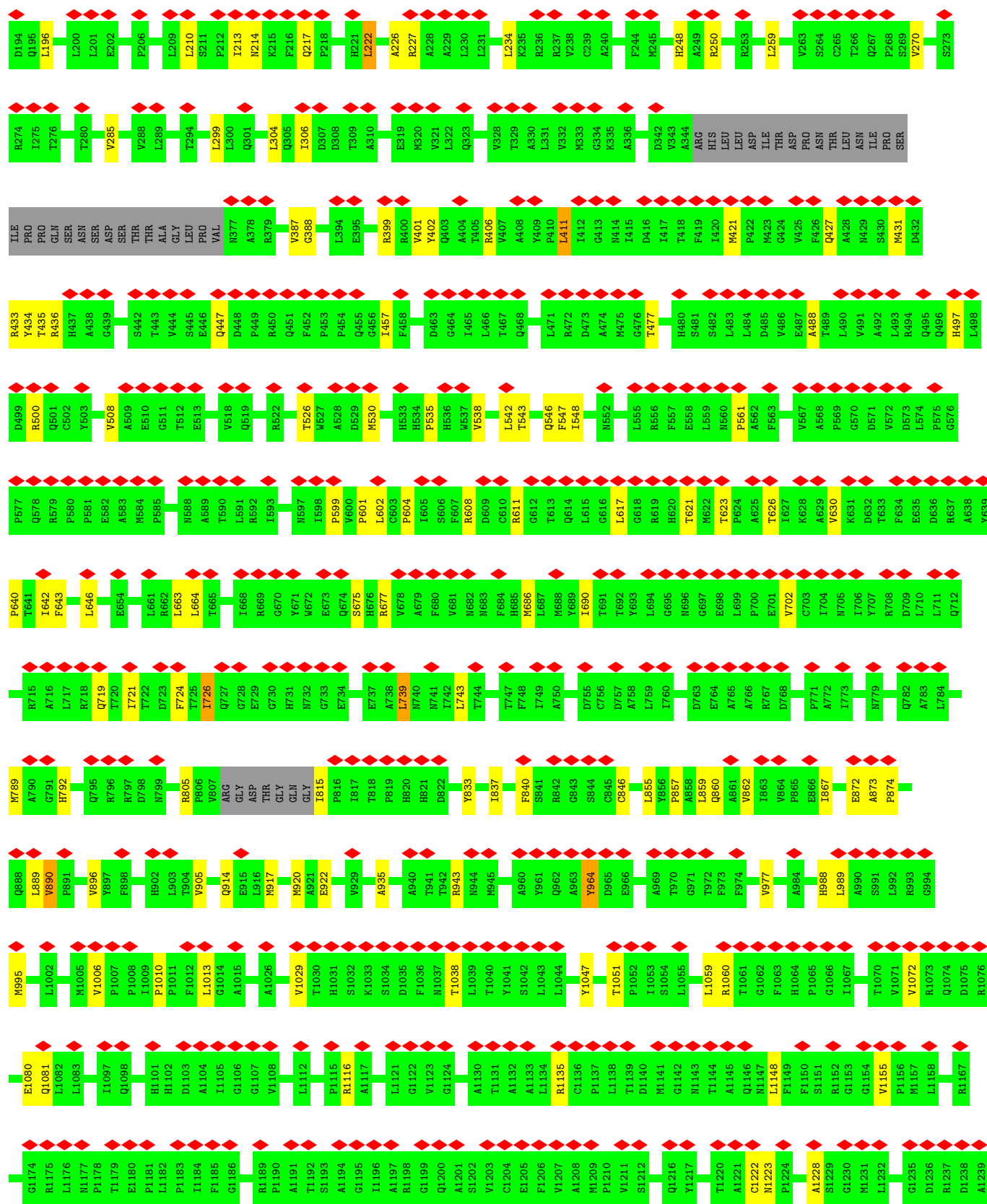
Mol	Chain	Residues	Atoms					AltConf	Trace
7	W	45	Total	C	N	O	S	0	0
			358	228	64	63	3		
7	X	45	Total	C	N	O	S	0	0
			358	228	64	63	3		

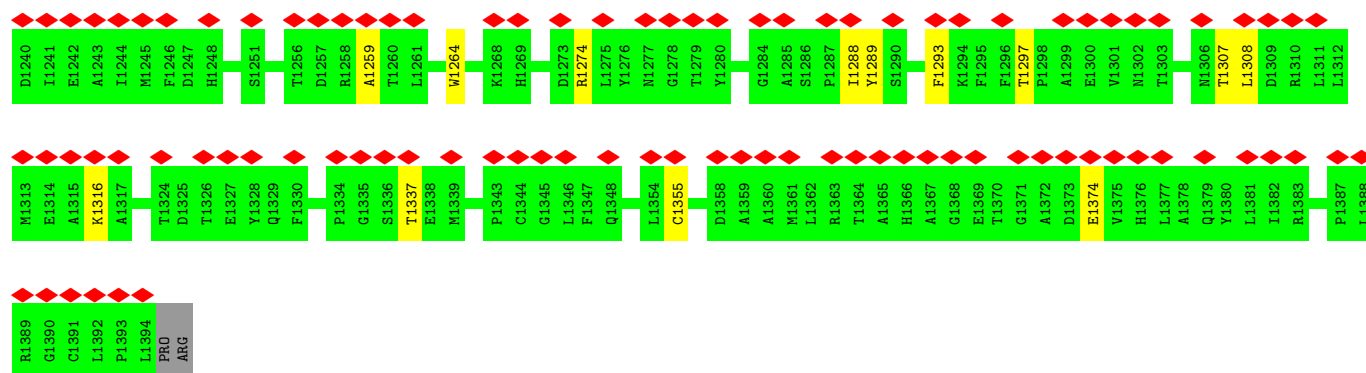
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

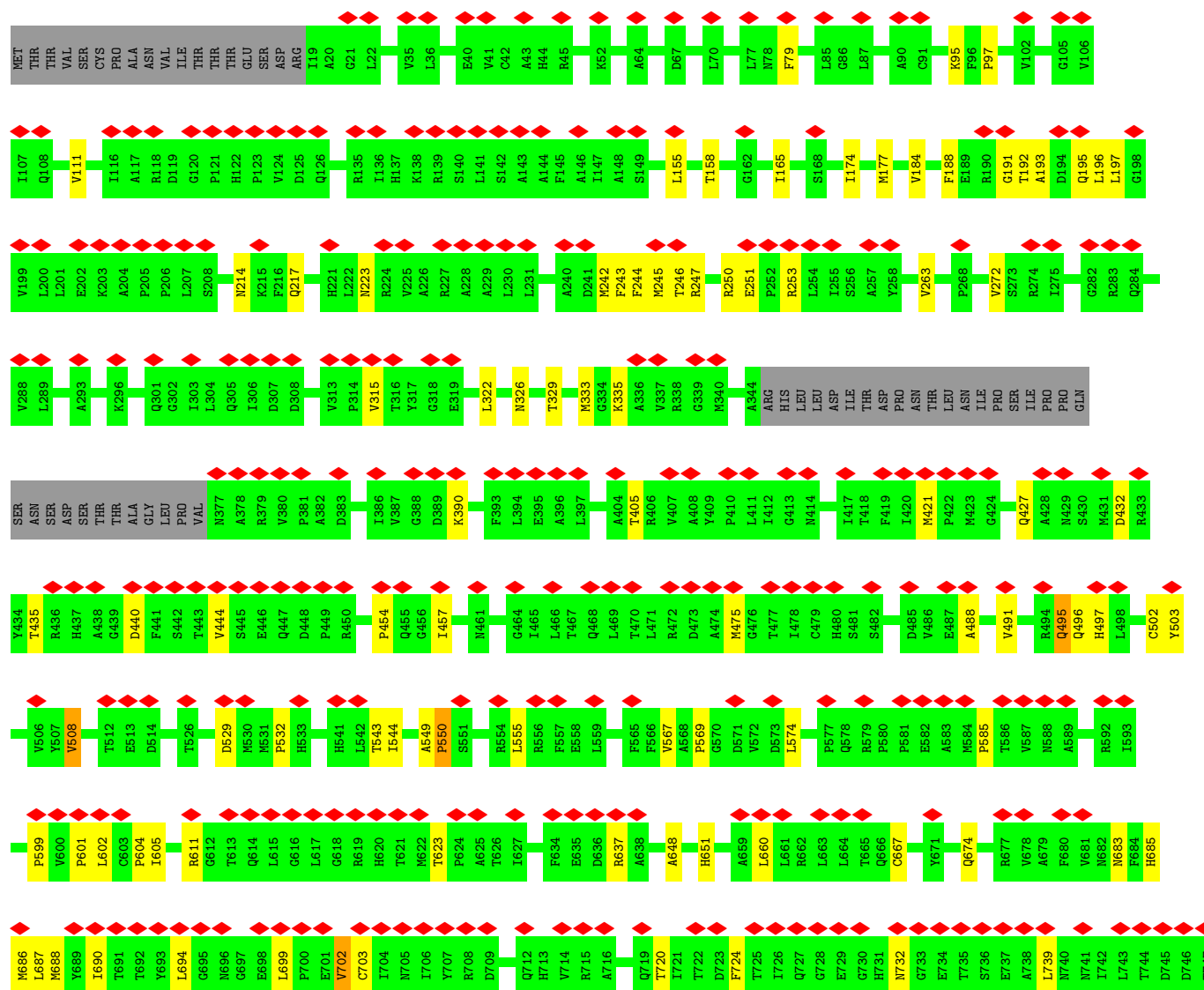
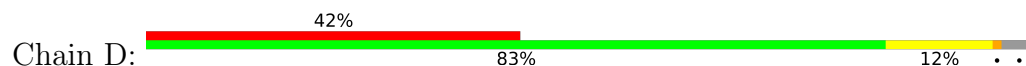
• Molecule 1: ORF40

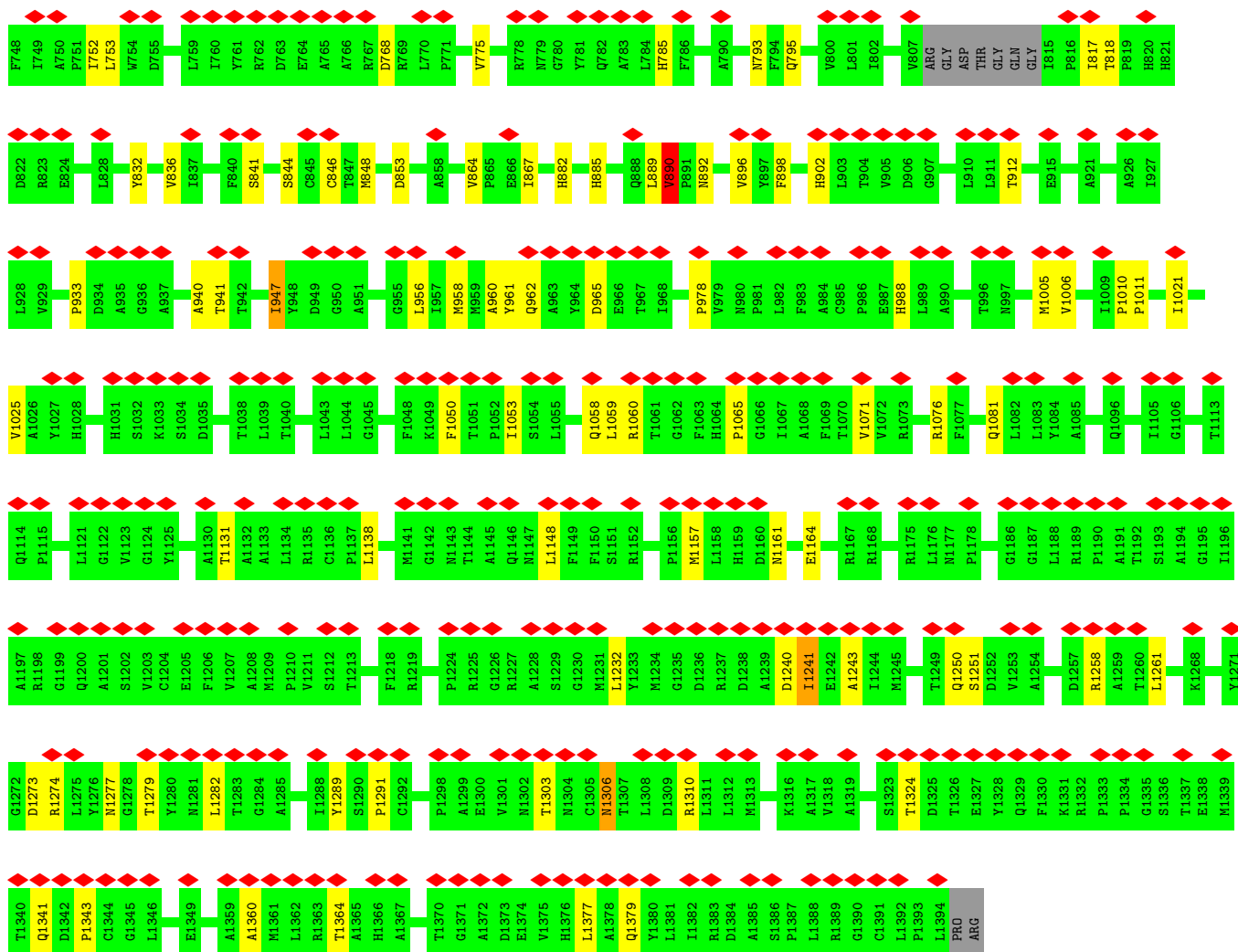




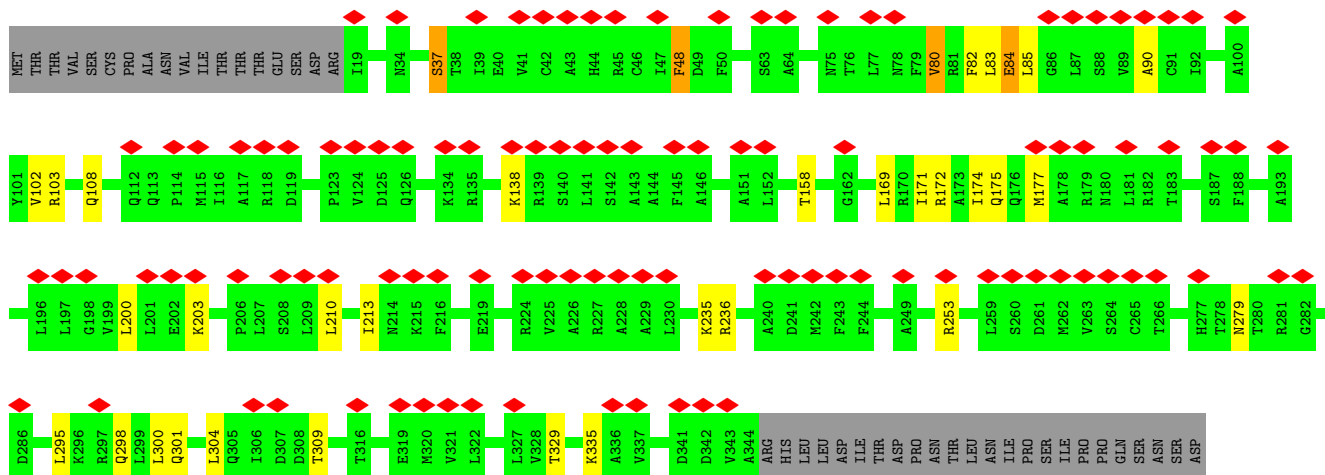
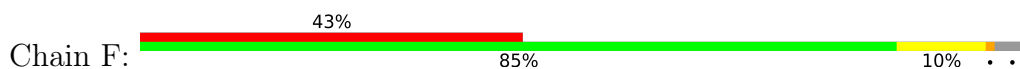


● Molecule 1: ORF40

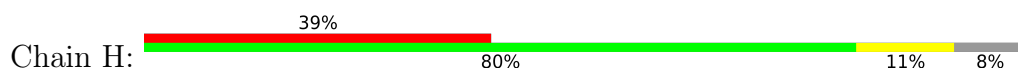




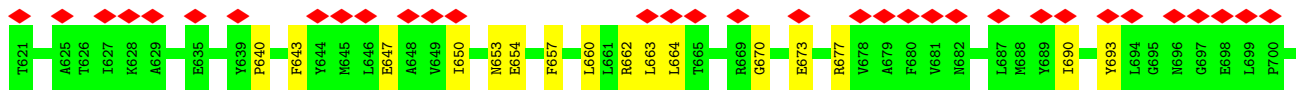
• Molecule 1: ORF40

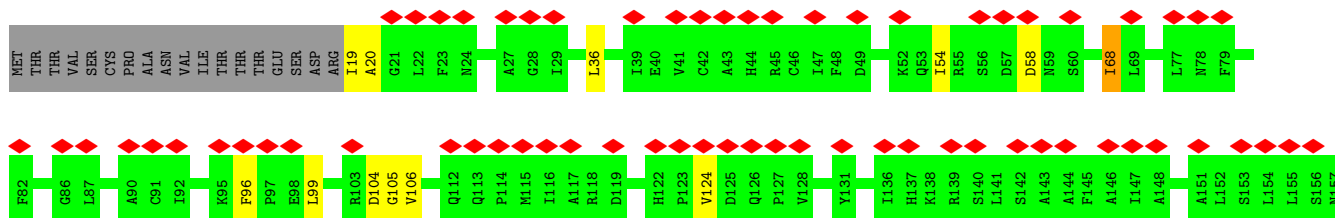






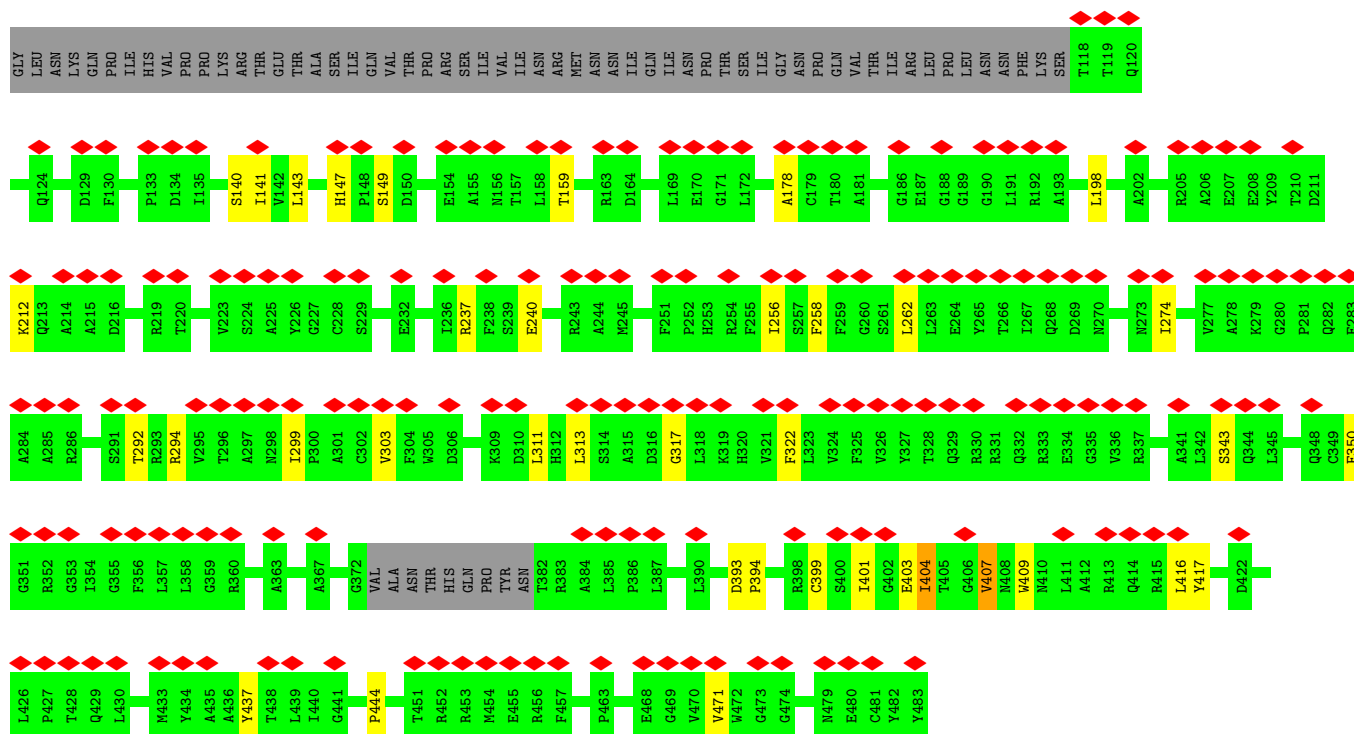
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LEU	TYR	SER	SER	ALA		Q65		T68	L69	L70	G71	T72		T76	L77	N78	F79	V80	R81	F82	L83	E84	L85	G86	S88	V89	A90	C91	T92		R103		V111		F114		R118	D119	G120		V124	D125		R135	I136	H137	K138	R139	S140	L141	S142	A143	A144		I147	A148		A151	L152	S153																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
L154	L155	S156	N157	THR	TYR	VAL	ASP	GLY	T163	E164	I165	D166		V263	S264	C265	T266	Q267	P268	S269	V270	M271	V272		T276		D194	Q195	L196	L197		L201	E202		P205	P206	L207	S208	L209	L210		I213	N214	K215	F216	Q217	P218		R135	I136	H137	K138	R139	S140	L141	S142	A143	A144		I147	A148		A151	L152	S153																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
D241	M242	F243	R247	R250	E251	P252	R253	V263	S264	I171	I174	Q175	L181	R182	T183	V184		D194	Q195	L196	L197		L201	E202		P205	P206	L207	S208	L209	L210		I213	N214	K215	F216	Q217	P218		R135	I136	H137	K138	R139	S140	L141	S142	A143	A144		I147	A148		A151	L152	S153																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
K335	A336	V337	R338	G339	M340	A344	ARG	HIS	LEU	ASP	PRO	ASN	THR	THR	LEU	ASN	ILE	PRO	PRO	ILE	PRO	GLN	SER	ASN	ASP	THR	THR	ALA	GLY	LEU	PRO	VAL	N377	A378	R379	V380	P381	A382	D383	L384	V385	L386	V387	G388	D389	K390		L394	E395	A396	Q397	E398																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
R399	Q403	A404	R405	R406	V407		L411	H412	G413	L414	I415	D416	I417	T418	F419	I420	M421	P422	M423	G424	V425	F426	Q427	A428	N429	S430	ASP	M431	D432	R433	Y434	T435	R436	H437	A438	Q439	D440	G441	F442	S442	T443	V444	S445	E446		P449	R450		P453	P454	Q455	G456	I457	F458	F459		K462		I465	L466																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
L471	R472	M475	L478	C479	H480	S481	S482	L483	L484	D485	V486	E487	V491	R494	H497	L498	D499	C502	V506	Y507	Y508		T512	E513	D514	L515	L516	D517	V518	Q519	M520	G521	R522	F523	M524	E525	T526	W527	A528	D529	M530	M531		H534	P535	H536		N539	E540	H541	L542		T626																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
L545	Q546	F547	I548	A549	P550	S551	N552	P553	R554	L555	R556	F557	E558	L559	N560	F565	G570	D571	V572	D573	F577	Q578	R579	P580	P581	E582	A583	H584		I593	I596	P599	V600	P601	L602	C603	F607	R608	D609	C610	Q614	L615	G616	L617	G618	R619	H620	T621	M622	T623		T626																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
T627	K628	A629	V630	K631	D632	T633	F634	E635	D636	H637	A638	V639	P640	T641	L642	F643	V644	H645	L646		L660		H669	G670		H677	V678	A679	F680	V681	N682	H683		N686	L687	M688	Y689	L690	T691	T692	V693	L694	C695	M696	G697	E698		E701	V702	C703	I704	N705	I706	Y707	R708	D709	L710	L711	Q712																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
A716	L717	R718	Q719	I726	Q727	G728	E729	G730	H731	N732	G733	E734	T735	S736	E737	A738	L739	N740	N741	L742	L743	T744	D745	D746	T747	F748	I749	W754	D755	C756	D757	A758	L759	R762	D763	E764	A765		V775		L801		V807	ARG	GLY	ASP	THR	GLY	GLN	GLY	I815	R816	I817	T818	P819																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
H820	H821	K830	Y834	P838	R842	G843	A861	V862	I863	V864	P865	E866	T867	P868	A869	D870	E871	E872	T876	P883	P891	H902	V905	A909	L910	L913	L916	D919	A926	I927	D934	A935	Q936	A937	A938	T939	A940	T941	T942	R943	N944		A951																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								



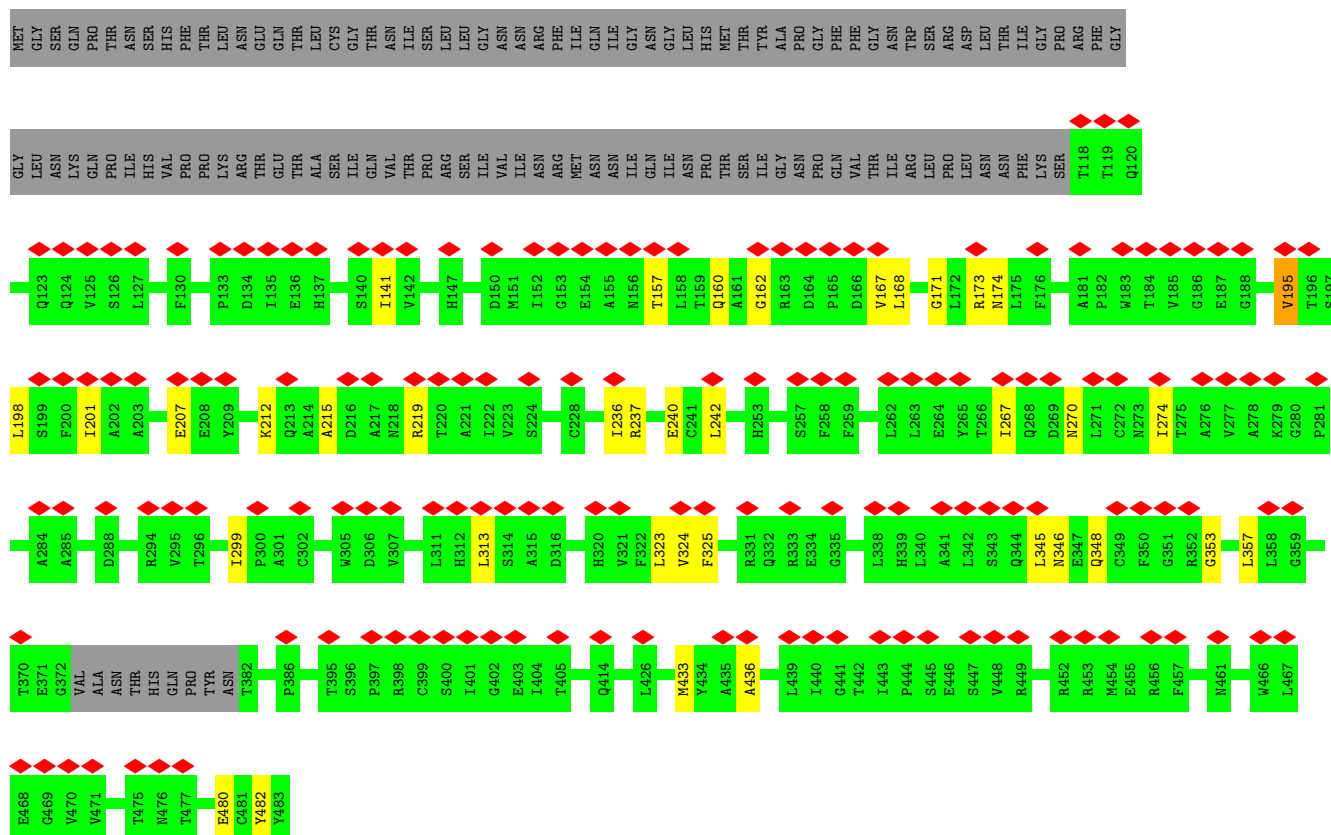




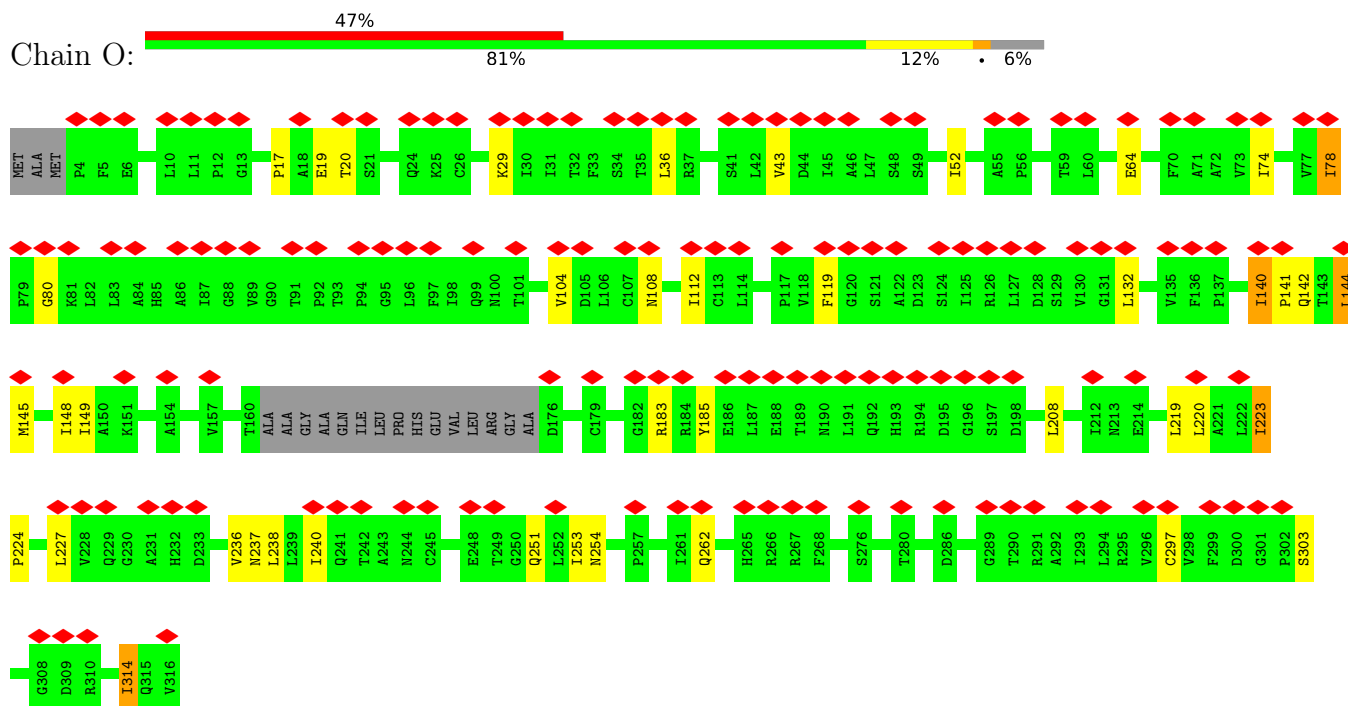
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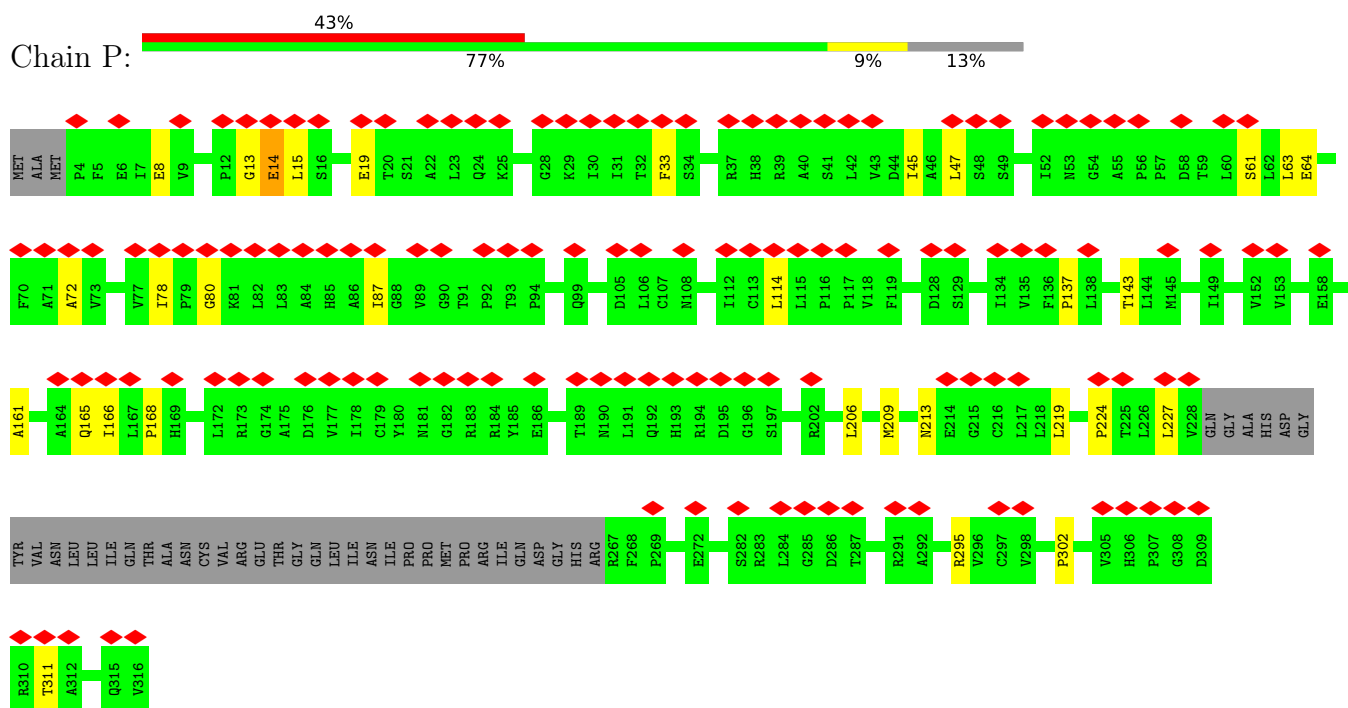
• Molecule 3: ORF20



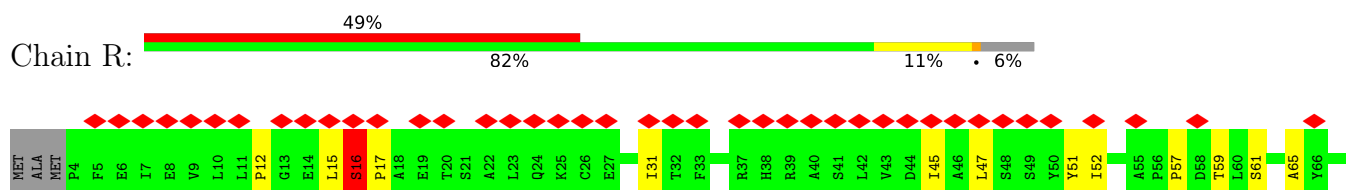
- Molecule 4: ORF41

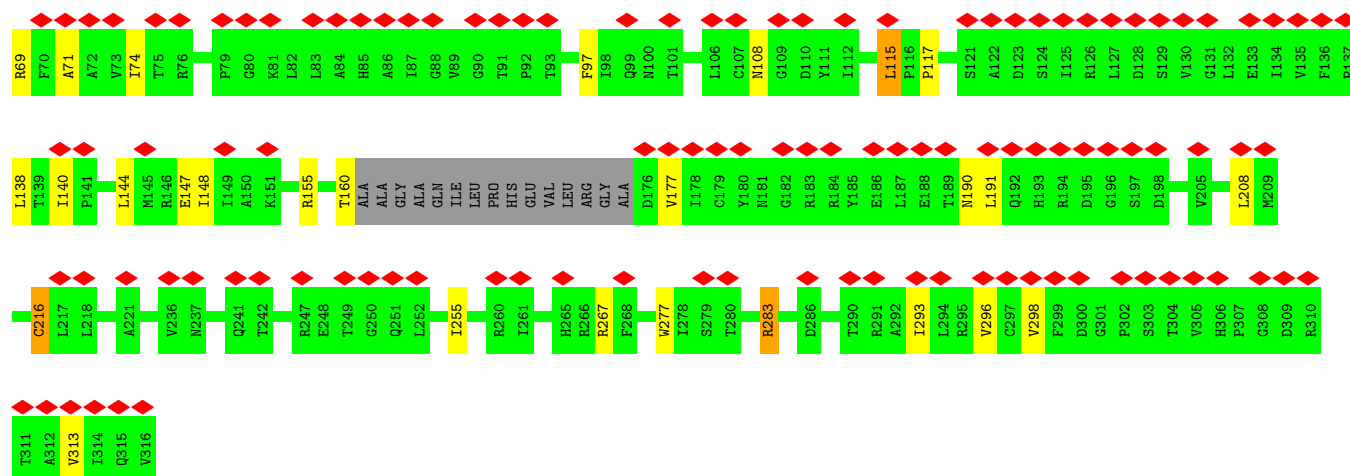


- Molecule 4: ORF41

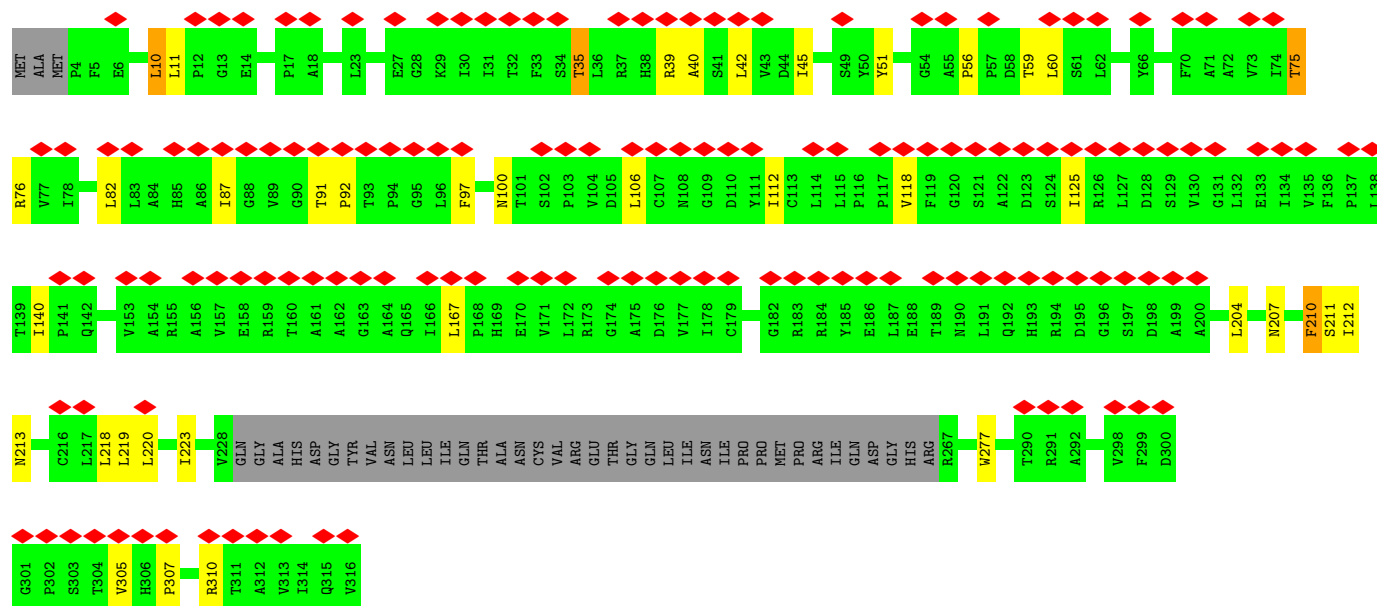
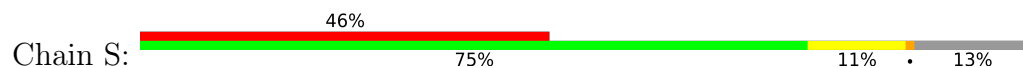


- Molecule 4: ORF41

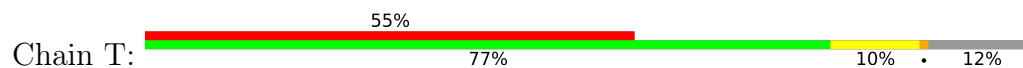


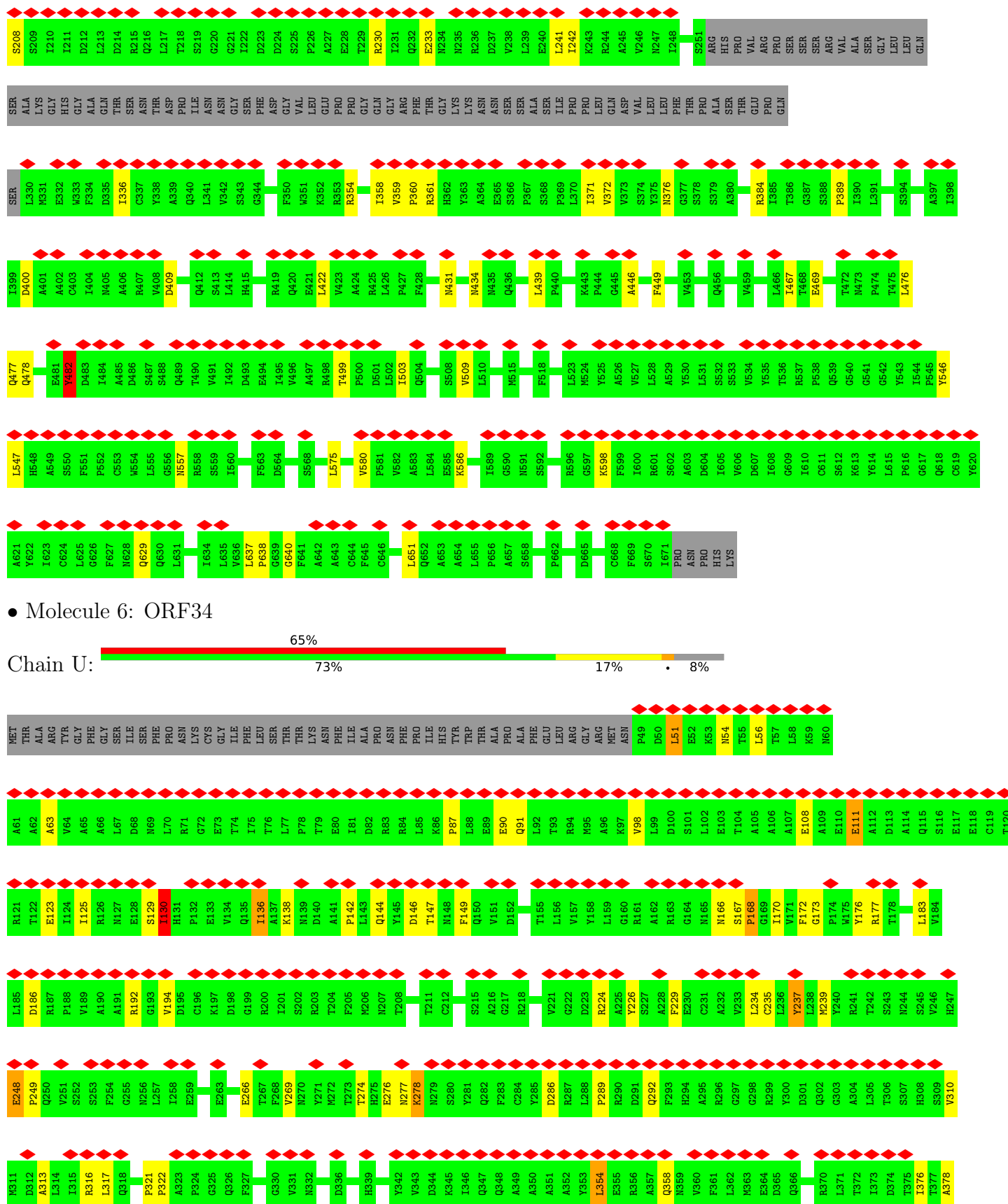


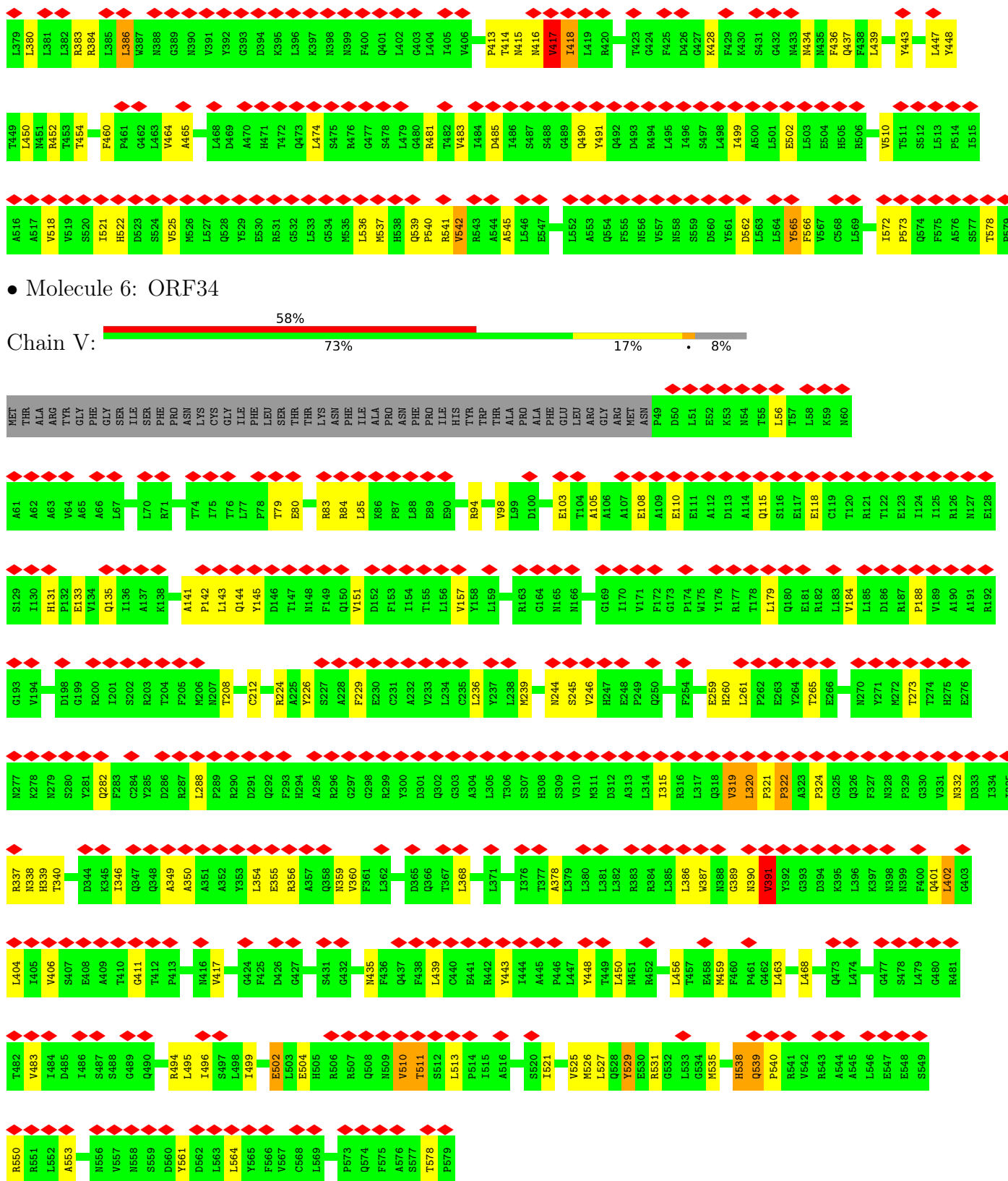
• Molecule 4: ORF41



• Molecule 5: ORF43





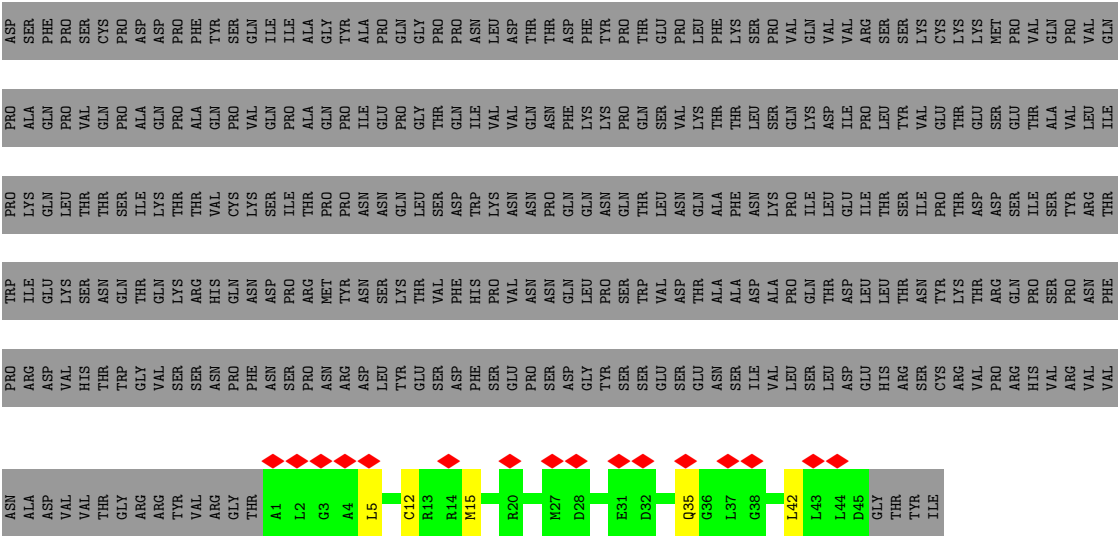


• Molecule 7: Large tegument protein deneddylase

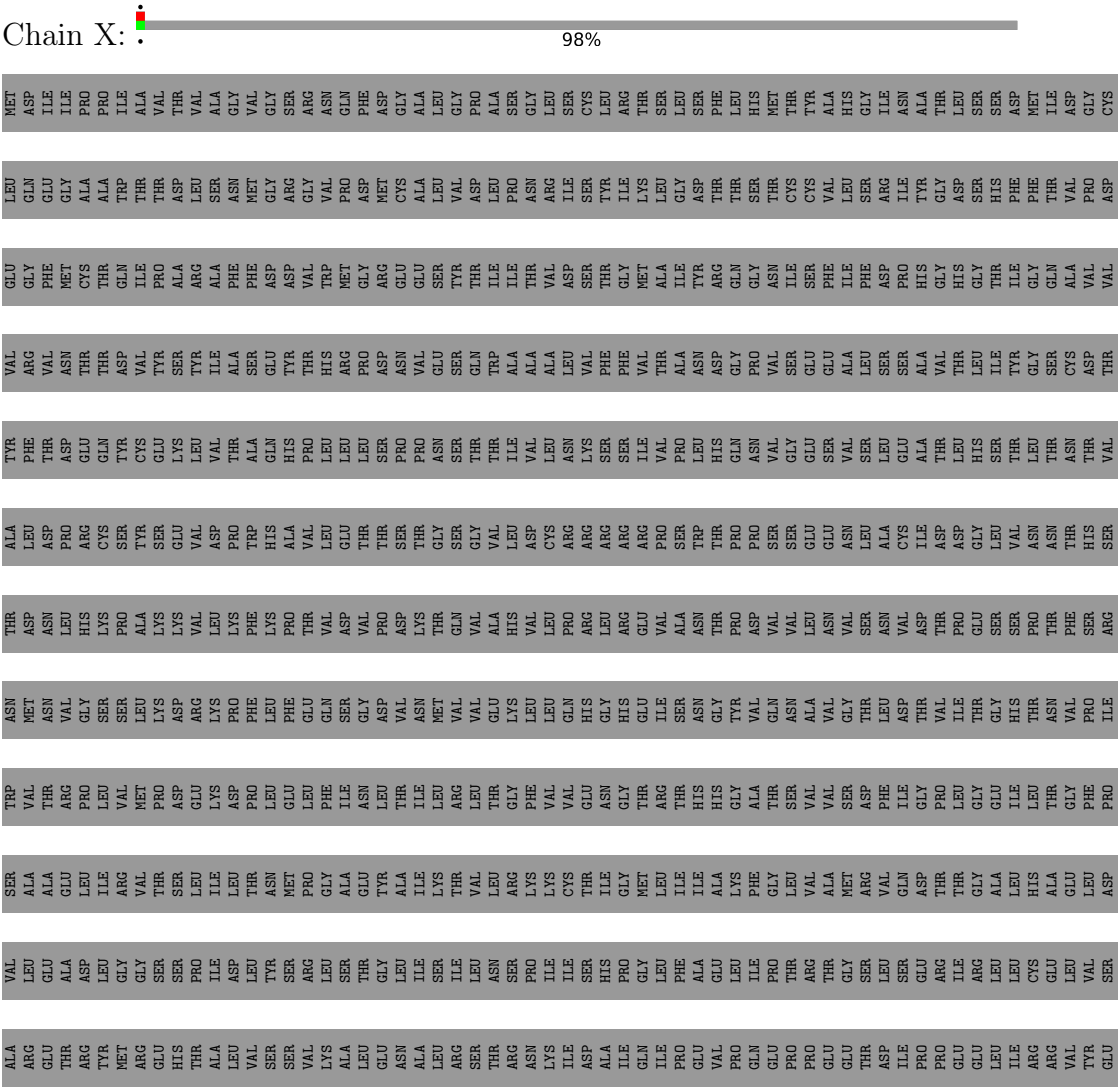








● Molecule 7: Large tegument protein deneddylase







4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of subtomograms used	3804	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 ($e^-/\text{\AA}^2$)	82.3	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	14.690	Depositor
Minimum map value	-7.382	Depositor
Average map value	0.033	Depositor
Map value standard deviation	0.423	Depositor
Recommended contour level	1.05	Depositor
Map size ($\text{\AA}$)	660.48, 660.48, 660.48	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.4399998, 3.4399998, 3.4399998	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	A	0.09	0/9259	0.23	0/12619
1	B	0.08	0/10530	0.22	0/14358
1	D	0.15	0/10493	0.25	0/14326
1	F	0.08	0/10575	0.21	0/14419
1	H	0.08	0/10059	0.21	0/13730
1	J	0.09	0/10085	0.24	0/13758
1	L	0.13	0/10430	0.26	2/14225 (0.0%)
2	C	0.09	0/741	0.23	0/1022
2	E	0.10	0/727	0.25	0/997
2	G	0.09	0/753	0.22	0/1036
2	I	0.09	0/759	0.23	0/1043
2	K	0.09	0/759	0.20	0/1043
2	M	0.10	0/738	0.25	0/1019
3	N	0.07	0/2829	0.20	0/3850
3	Q	0.08	0/2832	0.21	0/3854
4	O	0.08	0/2331	0.23	0/3178
4	P	0.09	0/2119	0.21	0/2892
4	R	0.08	0/2331	0.22	0/3178
4	S	0.08	0/2122	0.22	0/2896
5	T	0.08	0/4700	0.23	0/6406
6	U	0.11	0/4277	0.30	0/5806
6	V	0.15	0/4277	0.32	0/5806
7	W	0.06	0/361	0.12	0/484
7	X	0.07	0/361	0.15	0/484
All	All	0.10	0/104448	0.24	2/142429 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	1377	LEU	CA-C-N	-5.41	115.13	123.14
1	L	1377	LEU	C-N-CA	-5.41	115.13	123.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9043	0	8818	81	0
1	B	10283	0	10047	73	0
1	D	10245	0	9938	83	0
1	F	10328	0	10090	71	0
1	H	9821	0	9535	71	0
1	J	9850	0	9593	101	0
1	L	10181	0	9923	103	0
2	C	724	0	696	2	0
2	E	712	0	706	7	0
2	G	736	0	718	5	0
2	I	742	0	729	4	0
2	K	742	0	729	10	0
2	M	721	0	687	4	0
3	N	2767	0	2675	22	0
3	Q	2770	0	2679	21	0
4	O	2288	0	2352	25	0
4	P	2080	0	2136	16	0
4	R	2288	0	2352	21	0
4	S	2083	0	2138	18	0
5	T	4593	0	4609	39	0
6	U	4200	0	4166	64	0
6	V	4200	0	4166	61	0
7	W	358	0	379	3	0
7	X	358	0	379	9	0
All	All	102113	0	100240	834	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 4.

The worst 5 of 834 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:898:PHE:O	1:J:902:HIS:HB3	1.66	0.96
1:J:737:GLU:O	1:J:741:ASN:HB2	1.69	0.93
1:B:25:ILE:HG13	1:B:26:PRO:HD3	1.59	0.85
1:D:602:LEU:HG	1:D:605:ILE:HD12	1.64	0.80
6:U:248:GLU:H	6:U:249:PRO:HD2	1.50	0.77

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1148/1396 (82%)	1081 (94%)	63 (6%)	4 (0%)	36	72
1	B	1324/1396 (95%)	1252 (95%)	70 (5%)	2 (0%)	43	78
1	D	1331/1396 (95%)	1238 (93%)	87 (6%)	6 (0%)	24	63
1	F	1331/1396 (95%)	1268 (95%)	58 (4%)	5 (0%)	30	67
1	H	1271/1396 (91%)	1213 (95%)	55 (4%)	3 (0%)	43	78
1	J	1269/1396 (91%)	1189 (94%)	76 (6%)	4 (0%)	36	72
1	L	1308/1396 (94%)	1231 (94%)	72 (6%)	5 (0%)	30	67
2	C	99/235 (42%)	93 (94%)	5 (5%)	1 (1%)	12	49
2	E	93/235 (40%)	90 (97%)	3 (3%)	0	100	100
2	G	99/235 (42%)	93 (94%)	6 (6%)	0	100	100
2	I	99/235 (42%)	95 (96%)	4 (4%)	0	100	100
2	K	99/235 (42%)	94 (95%)	5 (5%)	0	100	100
2	M	99/235 (42%)	90 (91%)	9 (9%)	0	100	100
3	N	353/483 (73%)	337 (96%)	16 (4%)	0	100	100
3	Q	353/483 (73%)	341 (97%)	12 (3%)	0	100	100
4	O	294/316 (93%)	283 (96%)	9 (3%)	2 (1%)	18	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	P	271/316 (86%)	261 (96%)	9 (3%)	1 (0%)	30	67
4	R	294/316 (93%)	283 (96%)	9 (3%)	2 (1%)	18	56
4	S	271/316 (86%)	263 (97%)	8 (3%)	0	100	100
5	T	589/676 (87%)	558 (95%)	29 (5%)	2 (0%)	36	72
6	U	529/579 (91%)	466 (88%)	55 (10%)	8 (2%)	8	40
6	V	529/579 (91%)	464 (88%)	60 (11%)	5 (1%)	14	51
7	W	43/2763 (2%)	43 (100%)	0	0	100	100
7	X	43/2763 (2%)	43 (100%)	0	0	100	100
All	All	13139/20772 (63%)	12369 (94%)	720 (6%)	50 (0%)	31	67

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	392	VAL
1	A	425	VAL
1	D	550	PRO
1	D	1241	ILE
1	F	599	PRO

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	A	964/1182 (82%)	918 (95%)	46 (5%)	23	44
1	B	1097/1182 (93%)	1044 (95%)	53 (5%)	23	44
1	D	1087/1182 (92%)	1043 (96%)	44 (4%)	28	49
1	F	1102/1182 (93%)	1066 (97%)	36 (3%)	33	55
1	H	1040/1182 (88%)	1001 (96%)	39 (4%)	29	50
1	J	1050/1182 (89%)	1009 (96%)	41 (4%)	28	49
1	L	1089/1182 (92%)	1048 (96%)	41 (4%)	29	50
2	C	72/189 (38%)	71 (99%)	1 (1%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	72/189 (38%)	67 (93%)	5 (7%)	14	36
2	G	74/189 (39%)	73 (99%)	1 (1%)	59	72
2	I	75/189 (40%)	74 (99%)	1 (1%)	61	74
2	K	75/189 (40%)	71 (95%)	4 (5%)	20	41
2	M	71/189 (38%)	71 (100%)	0	100	100
3	N	288/410 (70%)	282 (98%)	6 (2%)	47	65
3	Q	289/410 (70%)	281 (97%)	8 (3%)	38	60
4	O	256/267 (96%)	247 (96%)	9 (4%)	32	53
4	P	229/267 (86%)	224 (98%)	5 (2%)	45	64
4	R	256/267 (96%)	247 (96%)	9 (4%)	32	53
4	S	230/267 (86%)	217 (94%)	13 (6%)	18	40
5	T	503/573 (88%)	487 (97%)	16 (3%)	34	56
6	U	457/497 (92%)	440 (96%)	17 (4%)	30	51
6	V	457/497 (92%)	431 (94%)	26 (6%)	18	40
7	W	38/2413 (2%)	37 (97%)	1 (3%)	40	62
7	X	38/2413 (2%)	37 (97%)	1 (3%)	40	62
All	All	10909/17689 (62%)	10486 (96%)	423 (4%)	30	49

5 of 423 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	475	MET
1	L	506	VAL
6	V	157	VAL
1	J	673	GLU
1	J	1166	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 219 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	468	GLN
1	L	414	ASN
5	T	434	ASN
1	J	653	ASN
1	J	1074	GLN

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.

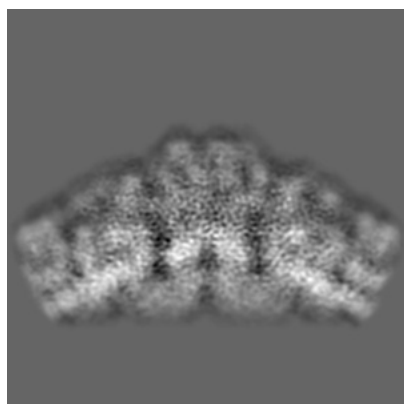
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49591. These allow visual inspection of the internal detail of the map and identification of artifacts.

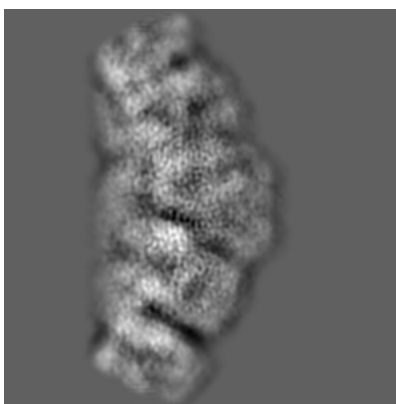
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

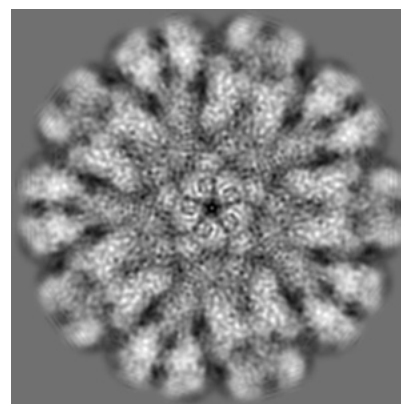
6.1.1 Primary map



X

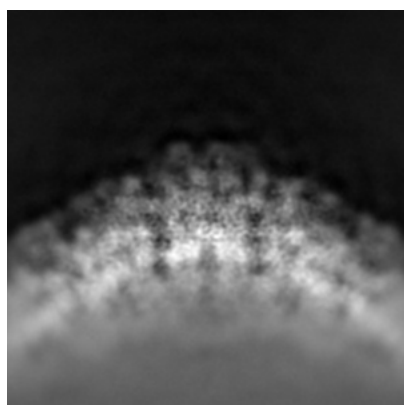


Y

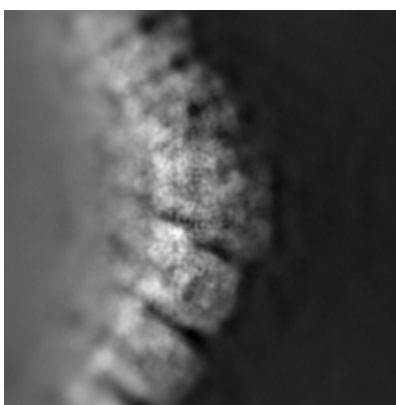


Z

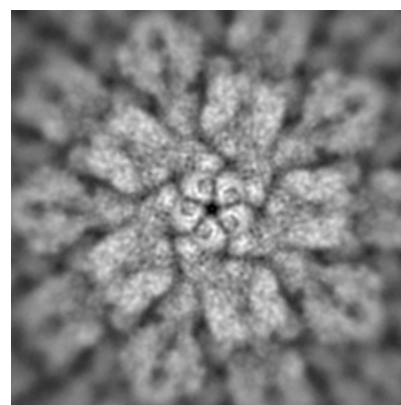
6.1.2 Raw map



X



Y

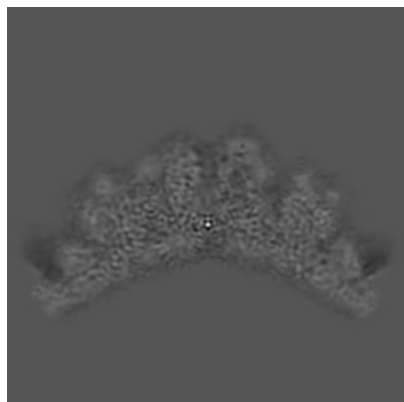


Z

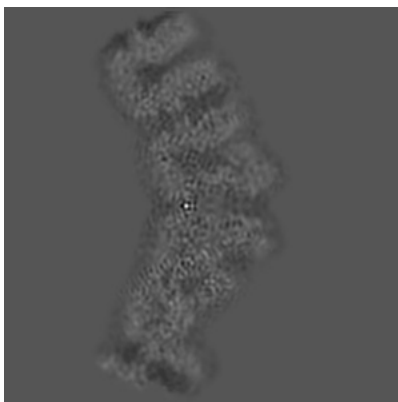
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

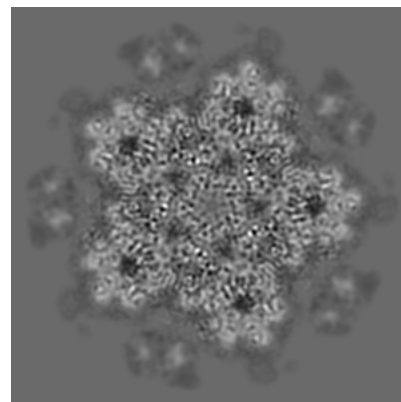
6.2.1 Primary map



X Index: 96

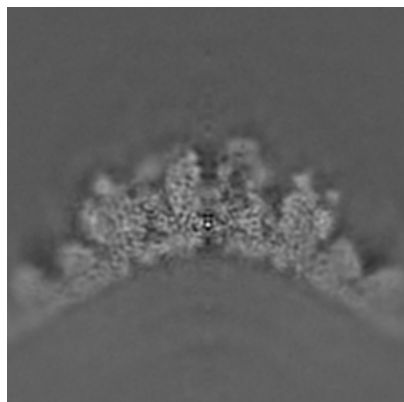


Y Index: 96

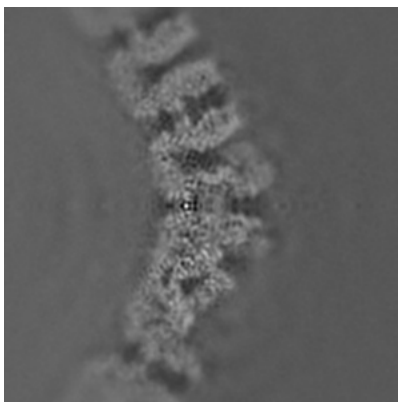


Z Index: 96

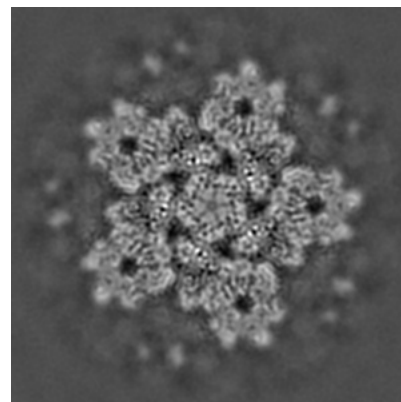
6.2.2 Raw map



X Index: 96



Y Index: 96

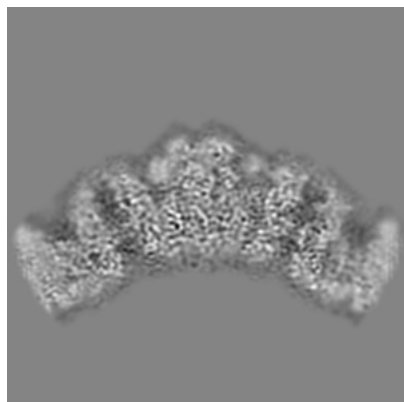


Z Index: 96

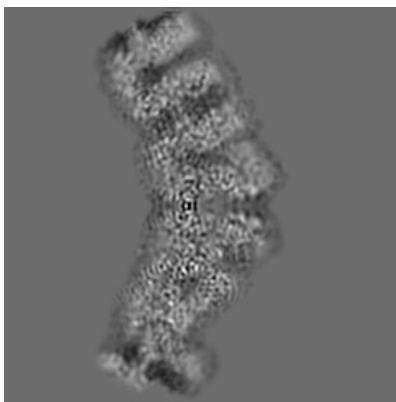
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

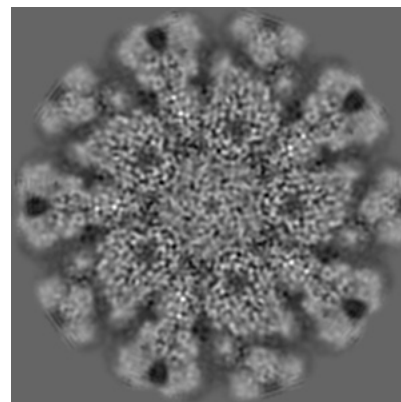
6.3.1 Primary map



X Index: 110

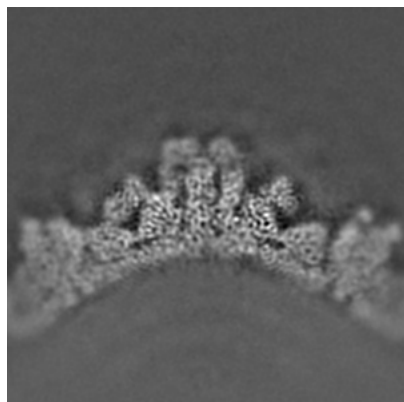


Y Index: 95

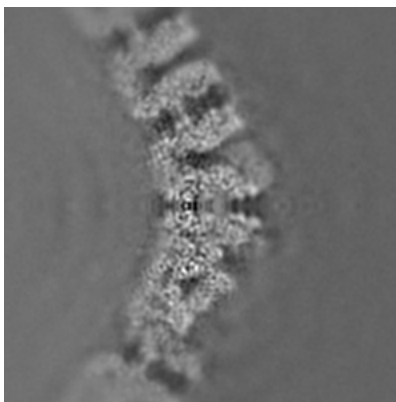


Z Index: 80

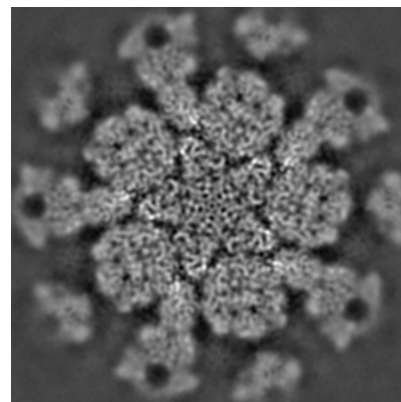
6.3.2 Raw map



X Index: 85



Y Index: 95

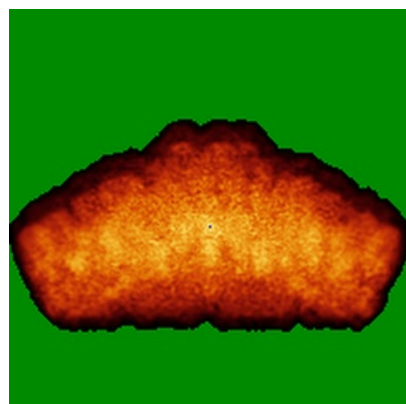


Z Index: 84

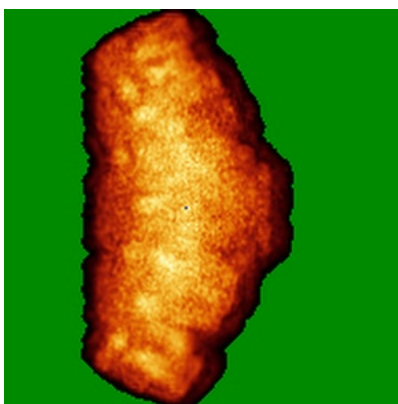
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

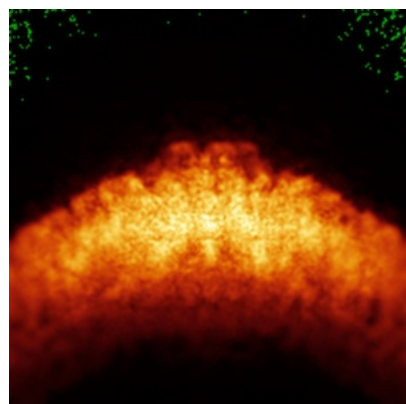


Y

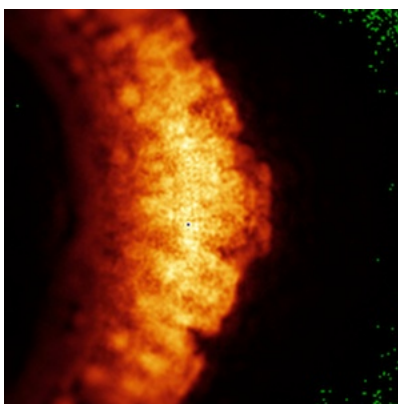


Z

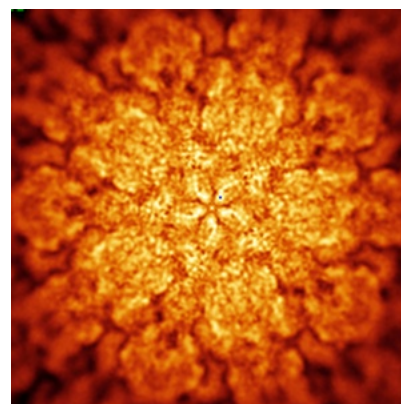
6.4.2 Raw map



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.

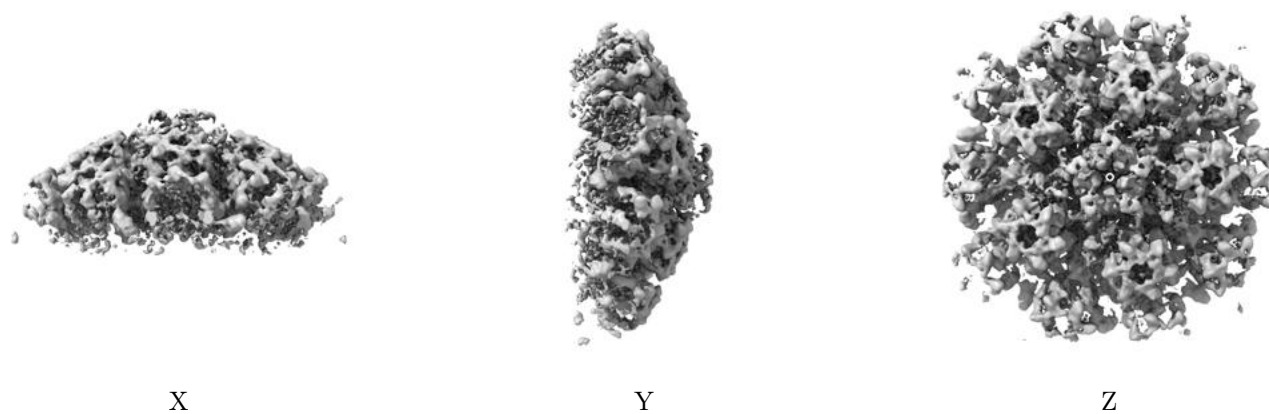
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.05. 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.

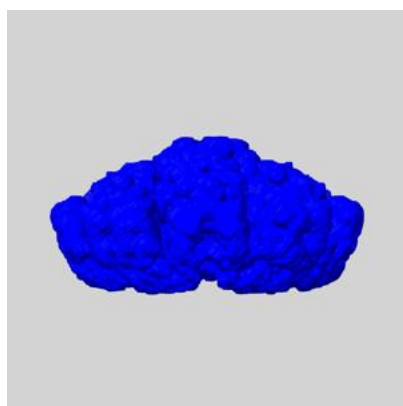
6.6 Mask visualisation [i](#)

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

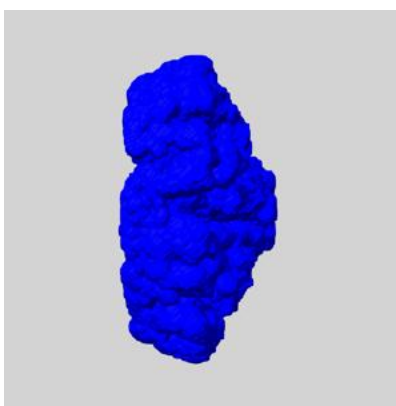
A mask typically either:

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

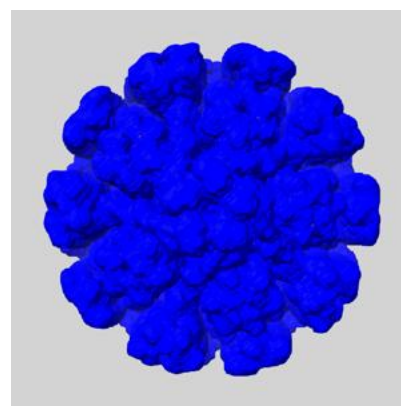
6.6.1 emd_49591_msk_1.map [i](#)



X



Y

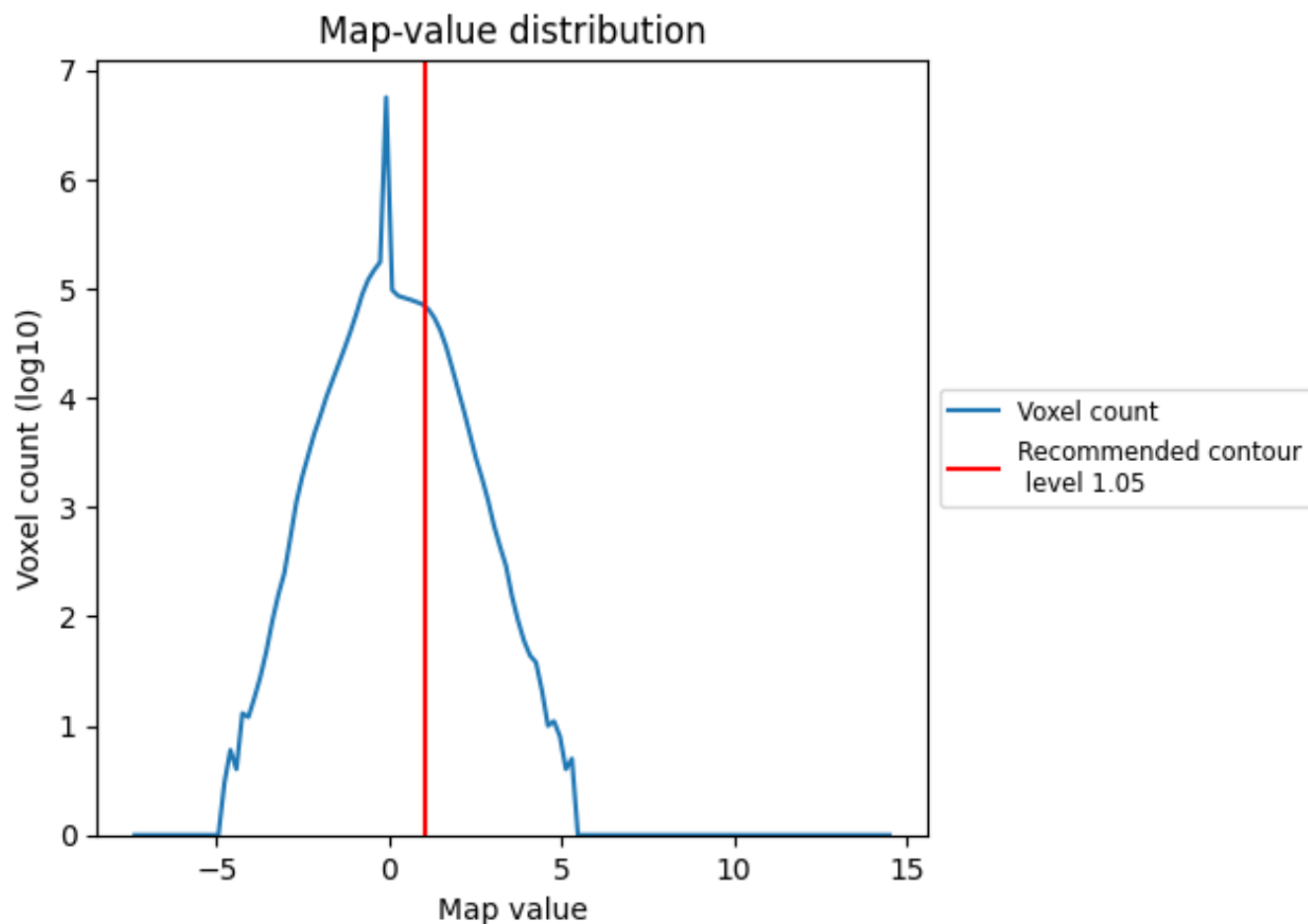


Z

7 Map analysis [i](#)

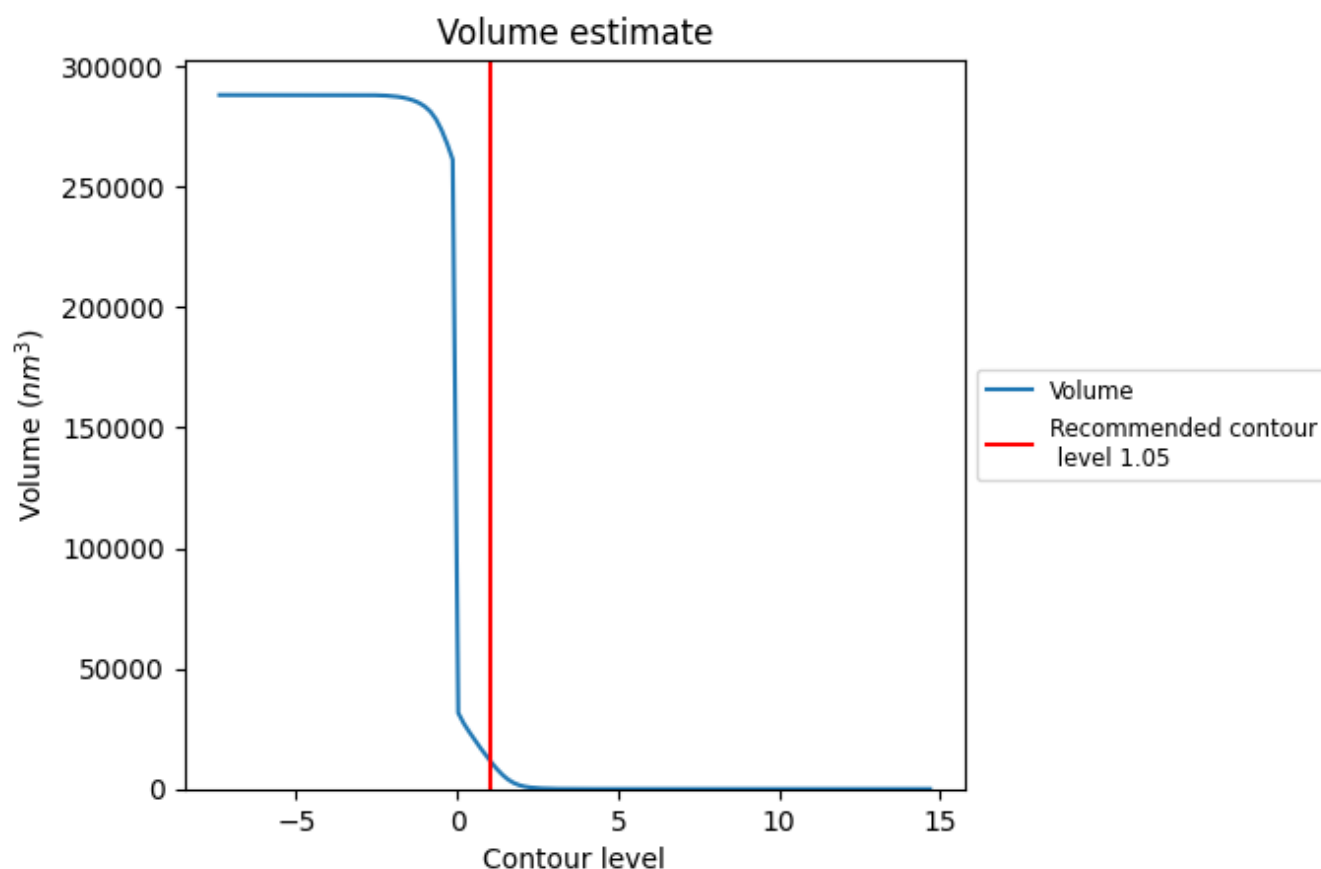
This section contains the results of statistical analysis of the map.

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.

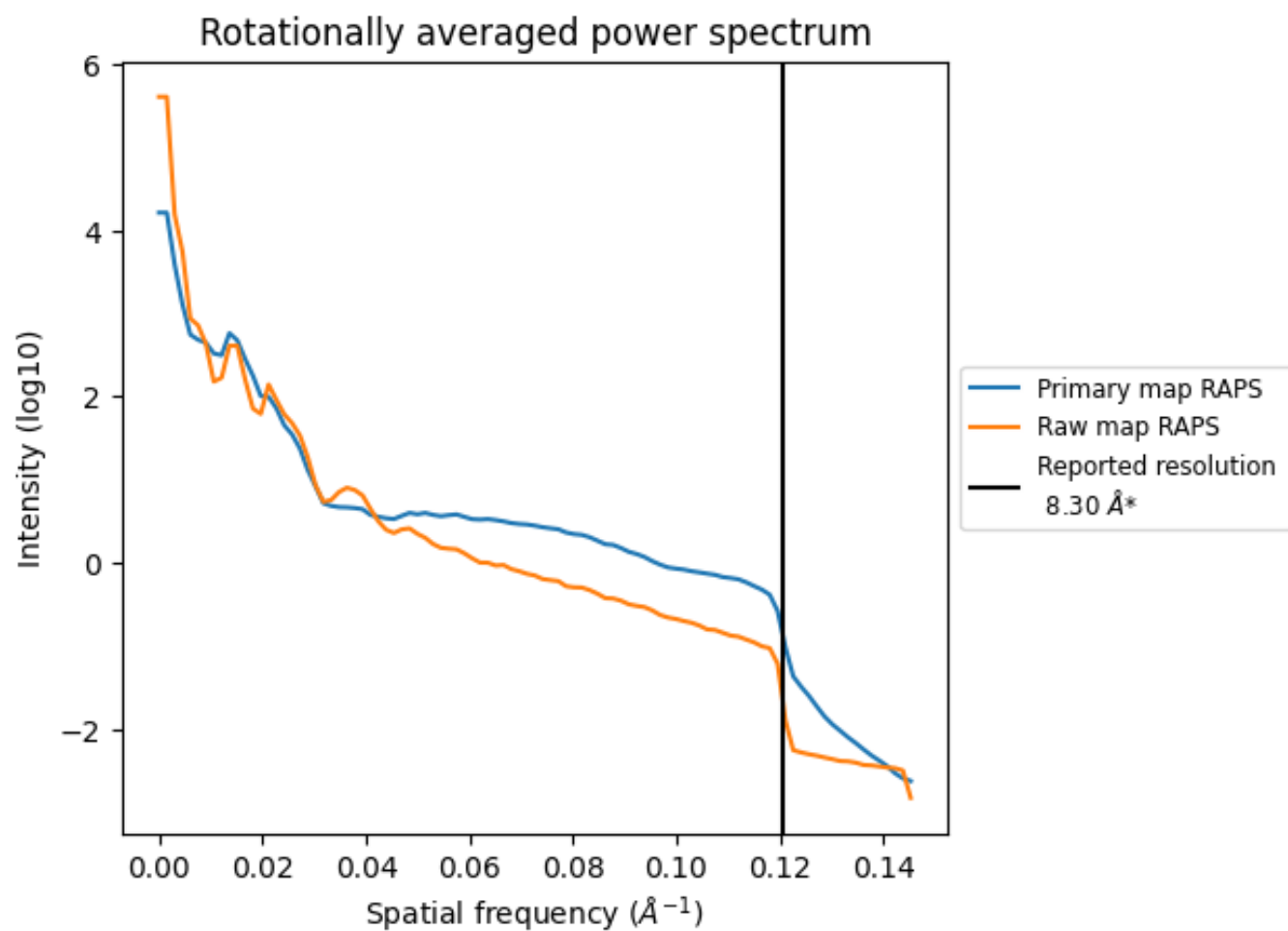
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11235 nm^3 ; this corresponds to an approximate mass of 10149 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 ⓘ

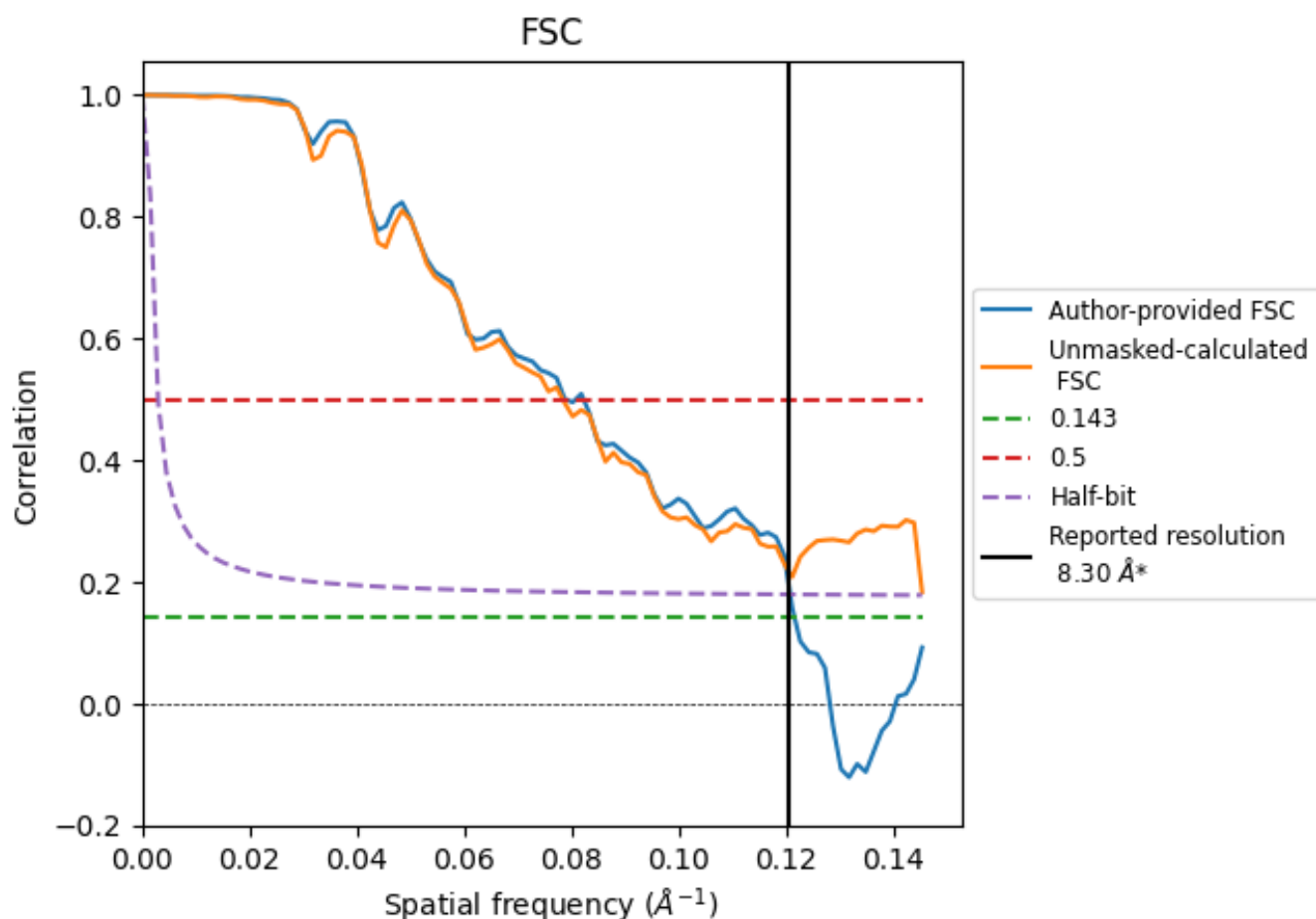


*Reported resolution corresponds to spatial frequency of 0.120 Å⁻¹

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 0.120 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

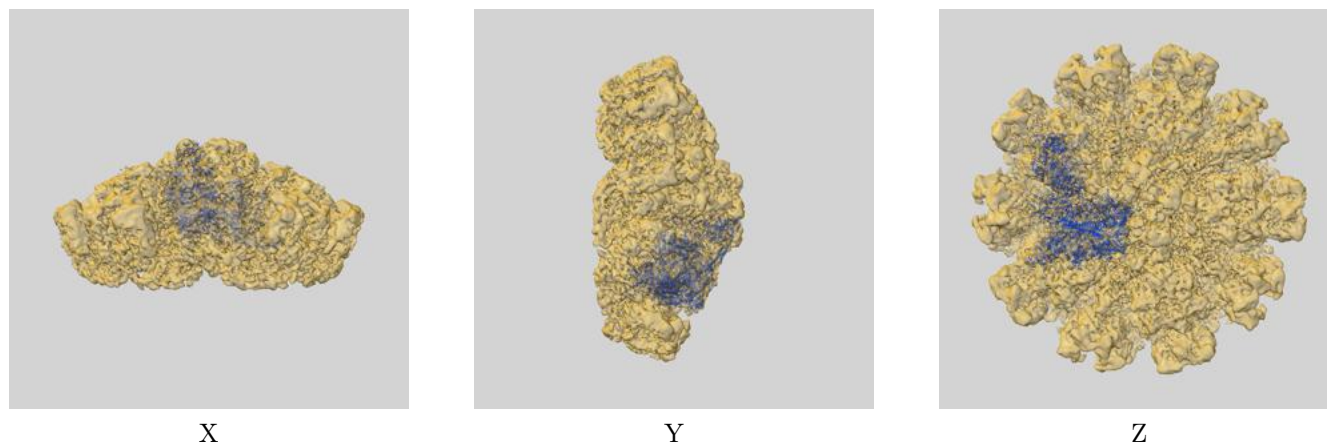
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.30	-	-
Author-provided FSC curve	8.23	12.67	8.29
Unmasked-calculated*	-	12.76	-

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

9 Map-model fit [i](#)

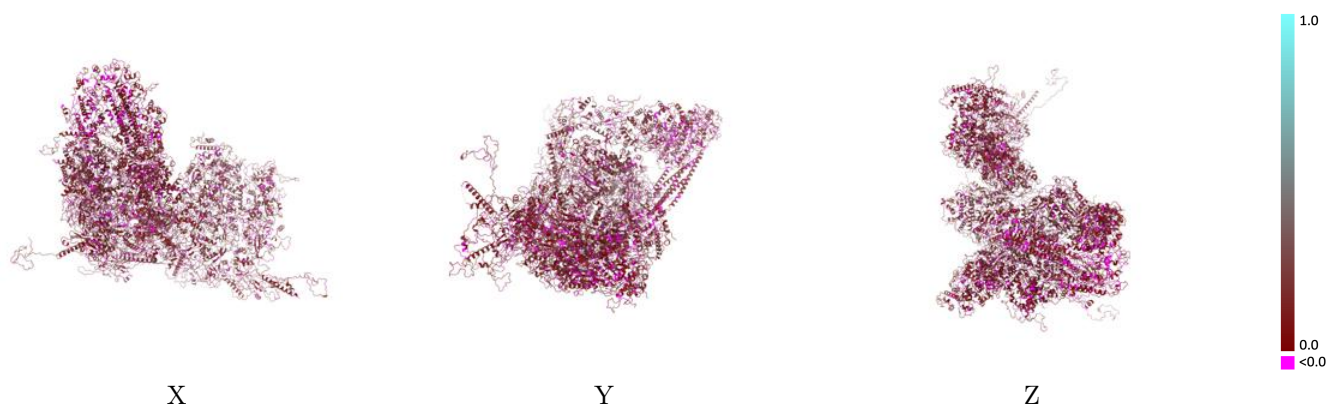
This section contains information regarding the fit between EMDB map EMD-49591 and PDB model 9NO1. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



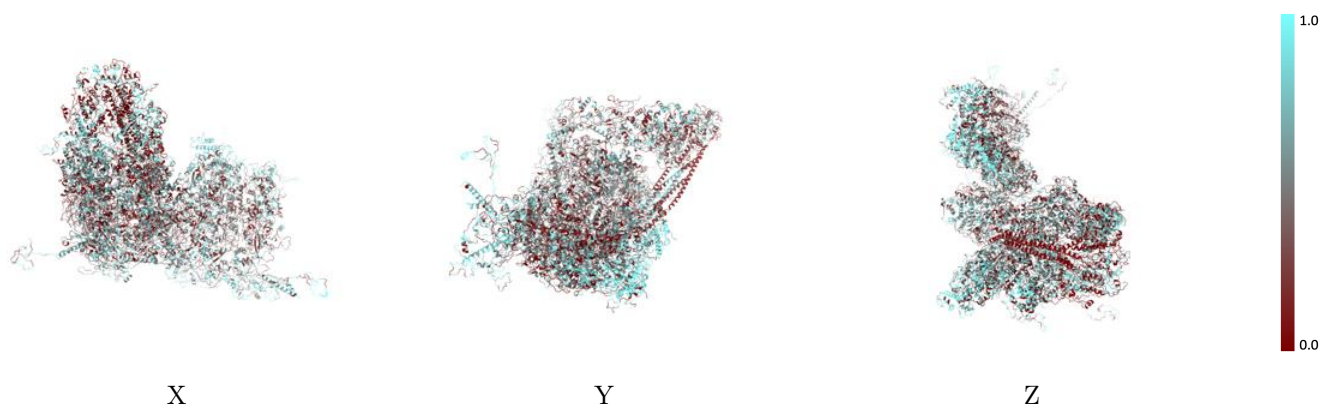
The images above show the 3D surface view of the map at the recommended contour level 1.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



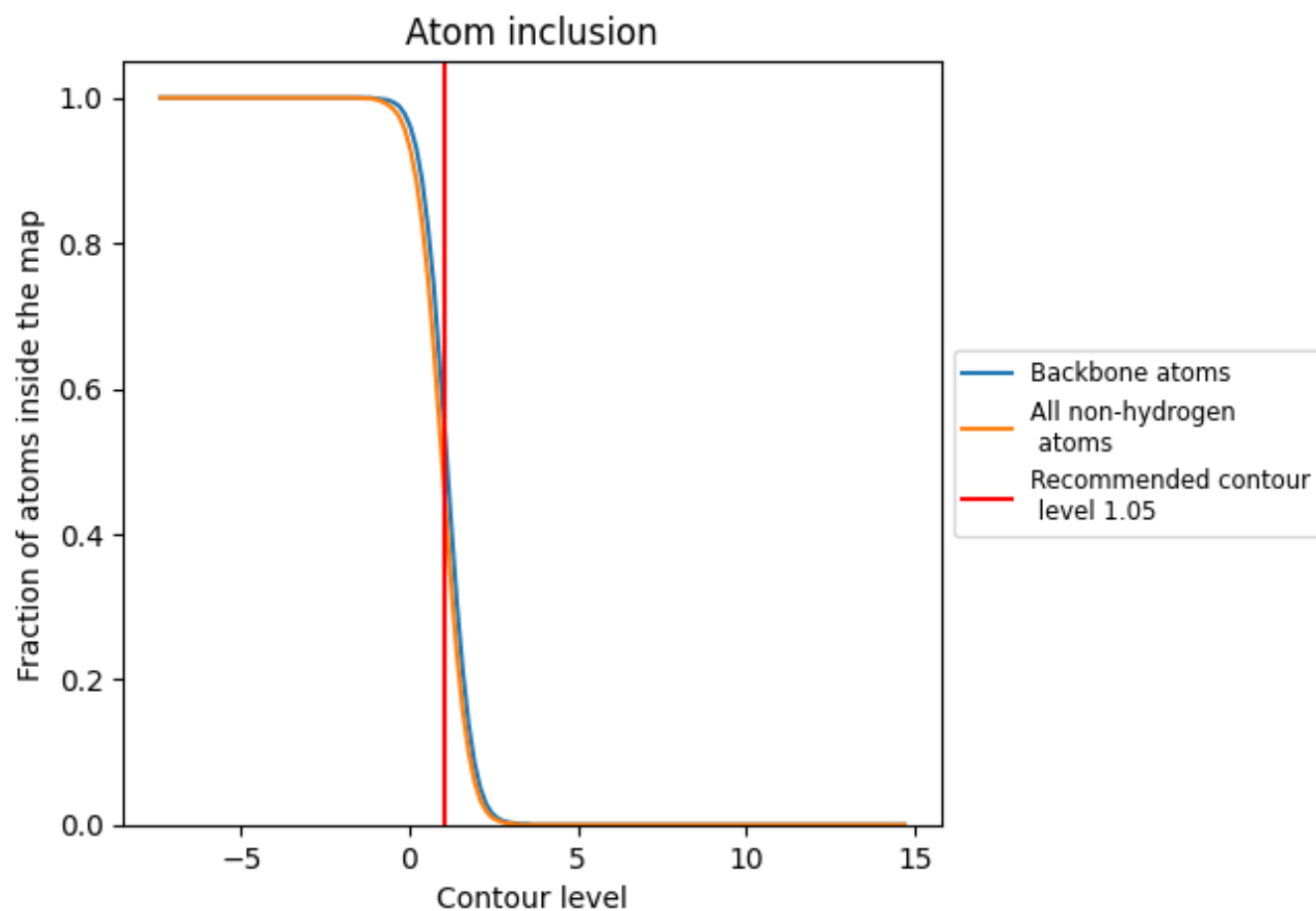
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 45% 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 (1.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4500	 0.1170
A	 0.4480	 0.1270
B	 0.4660	 0.1120
C	 0.6990	 0.1060
D	 0.4970	 0.1200
E	 0.7370	 0.1210
F	 0.4660	 0.1290
G	 0.7680	 0.1510
H	 0.5030	 0.1200
I	 0.7670	 0.1270
J	 0.4240	 0.1150
K	 0.6740	 0.1120
L	 0.4480	 0.1240
M	 0.7050	 0.1240
N	 0.4170	 0.1370
O	 0.4160	 0.1400
P	 0.4080	 0.1430
Q	 0.4900	 0.1210
R	 0.4150	 0.1290
S	 0.4190	 0.1410
T	 0.3260	 0.1100
U	 0.2520	 0.0660
V	 0.3440	 0.0490
W	 0.5400	 0.1040
X	 0.0920	 0.0440

