



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 07:53 AM UTC

PDB ID : 6HHT / pdb_00006hht
EMDB ID : EMD-0217
Title : Echovirus 18 Open particle without two pentamers
Authors : Buchta, D.; Fuzik, T.; Hrebik, D.; Levdansky, Y.; Moravcova, J.; Plevka, P.
Deposited on : 2018-08-29
Resolution : 4.05 Å (reported)
Based on initial model : 6HBH

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:

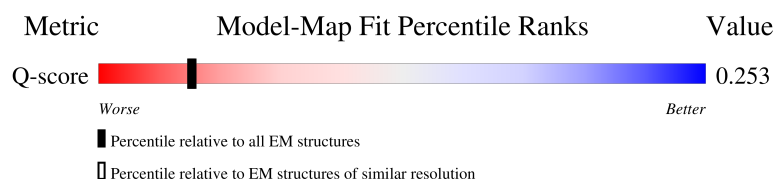
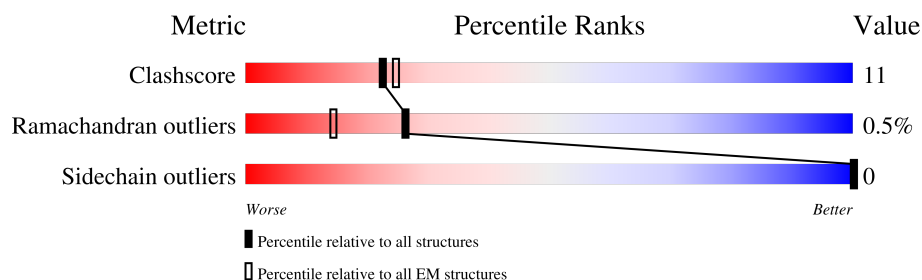
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.05 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.



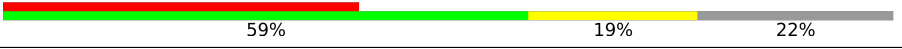
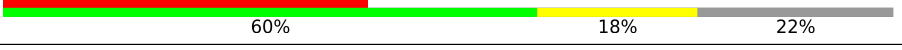
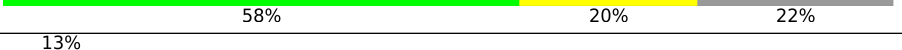
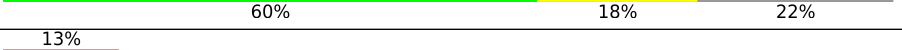
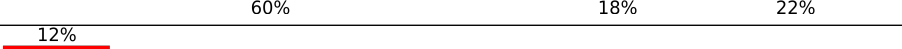
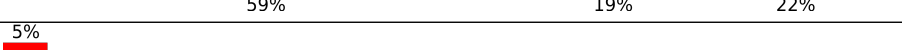
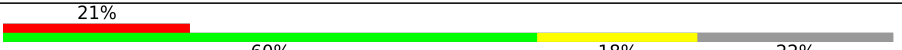
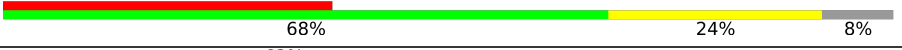
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6569 (3.55 - 4.55)

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	287	21% 59% 19% 22%
1	A2	287	60% 59% 19% 22%
1	D1	287	59% 19% 22%
1	D2	287	66% 59% 19% 22%

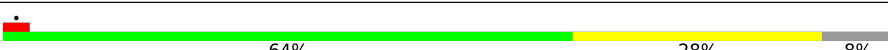
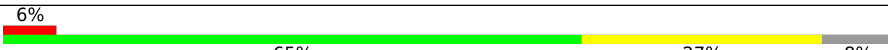
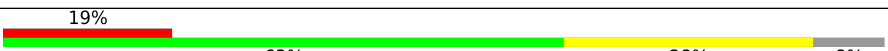
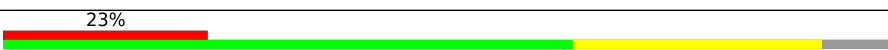
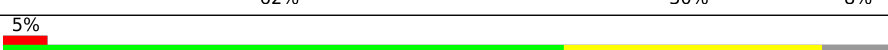
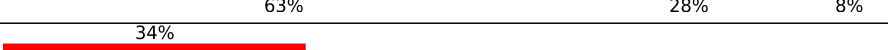
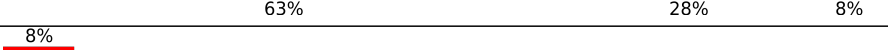
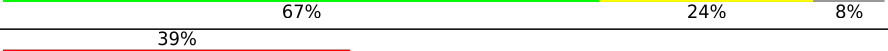
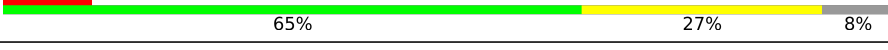
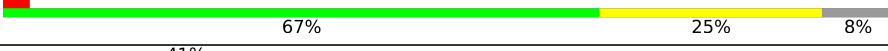
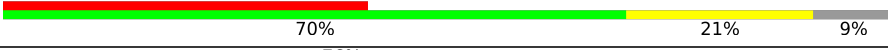
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Mol	Chain	Length	Quality of chain
1	G1	287	
1	G2	287	
1	J1	287	
1	J2	287	
1	M1	287	
1	M2	287	
1	P1	287	
1	P2	287	
1	S1	287	
1	S2	287	
1	V1	287	
1	V2	287	
1	Y2	287	
1	b2	287	
1	e2	287	
1	h2	287	
1	k2	287	
1	n2	287	
1	q2	287	
1	t2	287	
1	w2	287	
2	B1	260	
2	B2	260	
2	E1	260	
2	E2	260	

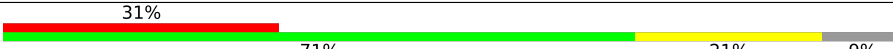
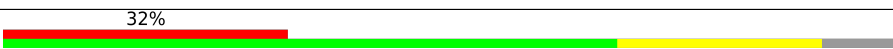
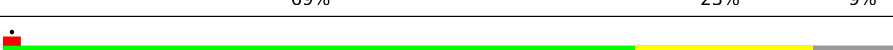
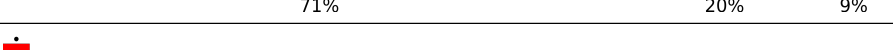
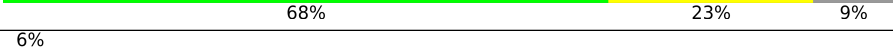
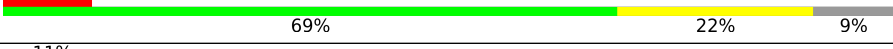
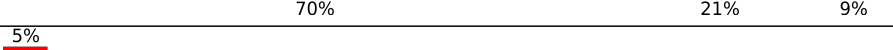
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Mol	Chain	Length	Quality of chain
2	H1	260	
2	H2	260	
2	K1	260	
2	K2	260	
2	N1	260	
2	N2	260	
2	Q1	260	
2	Q2	260	
2	T1	260	
2	T2	260	
2	W1	260	
2	W2	260	
2	Z2	260	
2	c2	260	
2	f2	260	
2	i2	260	
2	l2	260	
2	o2	260	
2	r2	260	
2	u2	260	
2	x2	260	
3	C1	239	
3	C2	239	
3	F1	239	
3	F2	239	

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Mol	Chain	Length	Quality of chain
3	I1	239	
3	I2	239	
3	L1	239	
3	L2	239	
3	O1	239	
3	O2	239	
3	R1	239	
3	R2	239	
3	U1	239	
3	U2	239	
3	X1	239	
3	X2	239	
3	a2	239	
3	d2	239	
3	g2	239	
3	j2	239	
3	m2	239	
3	p2	239	
3	s2	239	
3	v2	239	
3	y2	239	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 129900 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 Echovirus 18 capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	V1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	S1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	P1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	M1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	J1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	G1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	D1	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	A2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	w2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	t2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	q2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	n2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	k2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	h2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	e2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	b2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	V2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	S2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	P2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	M2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	J2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	G2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		
1	D2	224	Total	C	N	O	S	0	0
			1741	1117	305	305	14		

- Molecule 2 is a protein called Echovirus 18 capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	W1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	T1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	Q1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	N1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	K1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	H1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	E1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	B1	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	x2	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	u2	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		
2	r2	238	Total	C	N	O	S	0	0
			1821	1172	302	332	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	o2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	l2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	i2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	f2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	c2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	Z2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	W2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	T2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	Q2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	N2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	K2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	H2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	E2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0
2	B2	238	Total 1821	C 1172	N 302	O 332	S 15	0	0

- Molecule 3 is a protein called Echovirus 18 capsid protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	X1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	U1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	R1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	O1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	L1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0

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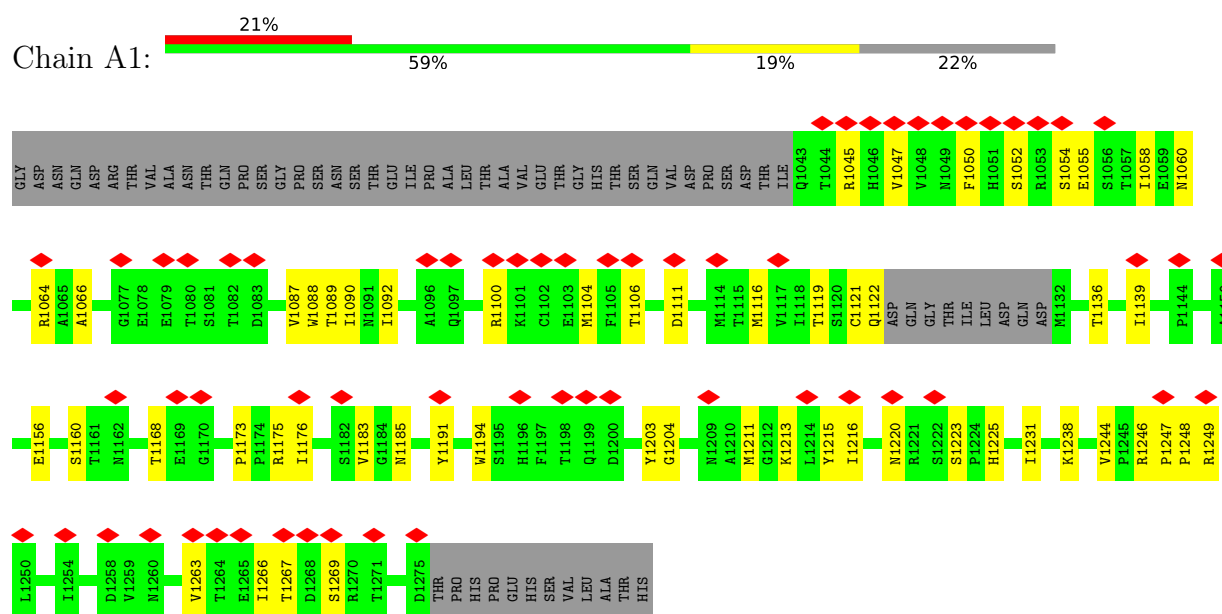
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	I1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	F1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	C1	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	y2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	v2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	s2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	p2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	m2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	j2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	g2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	d2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	a2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	X2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	U2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	R2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	O2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	L2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	I2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	F2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0
3	C2	218	Total 1634	C 1045	N 265	O 308	S 16	0	0

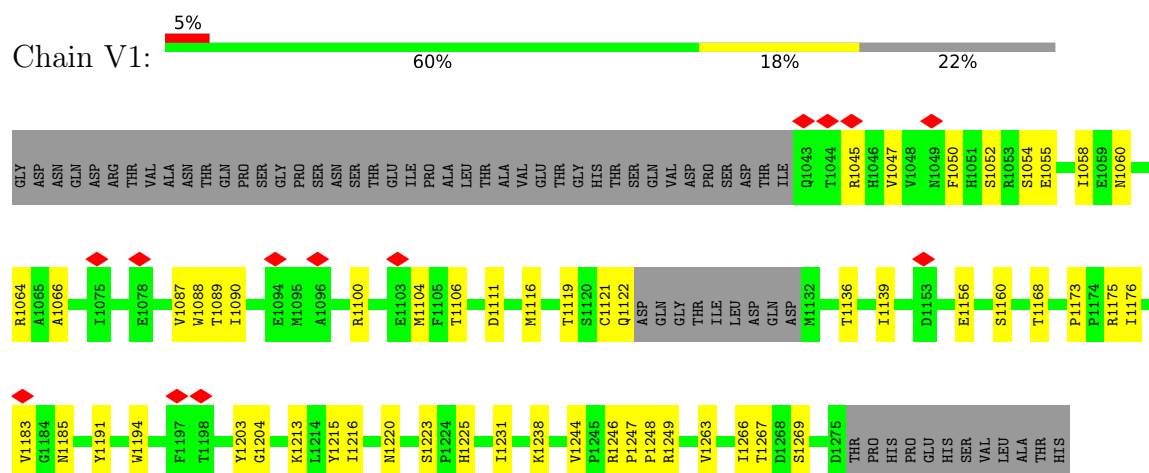
3 Residue-property plots

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

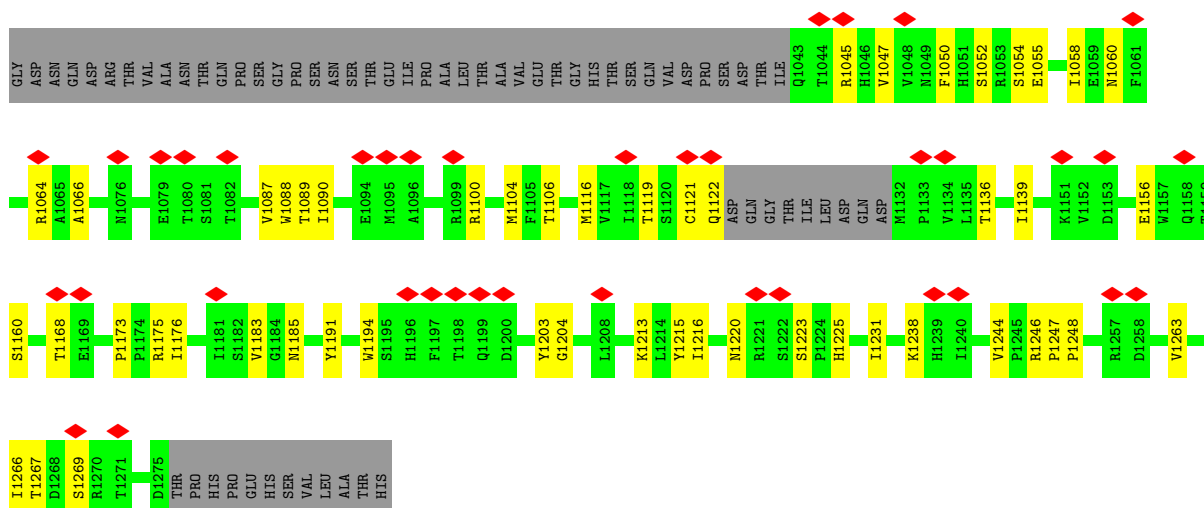
• Molecule 1: Echovirus 18 capsid protein 1



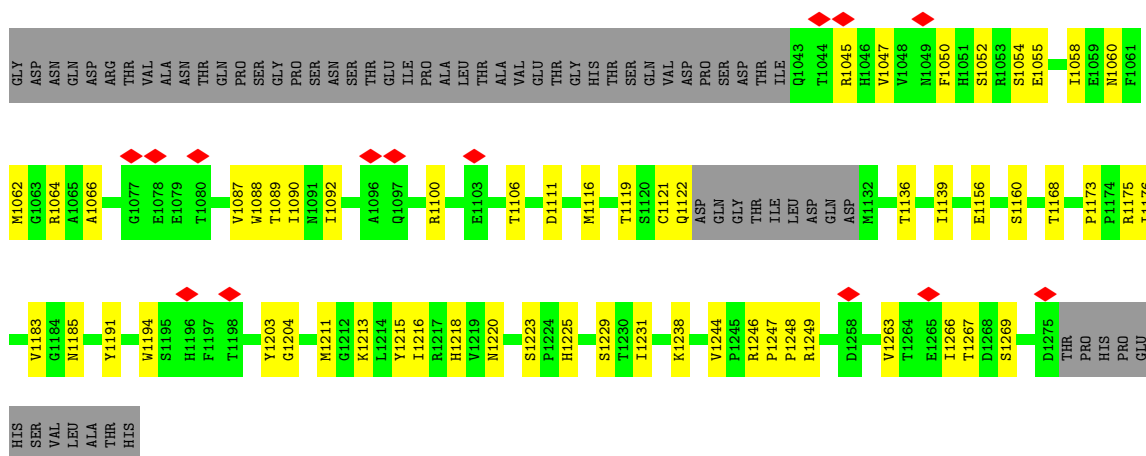
• Molecule 1: Echovirus 18 capsid protein 1



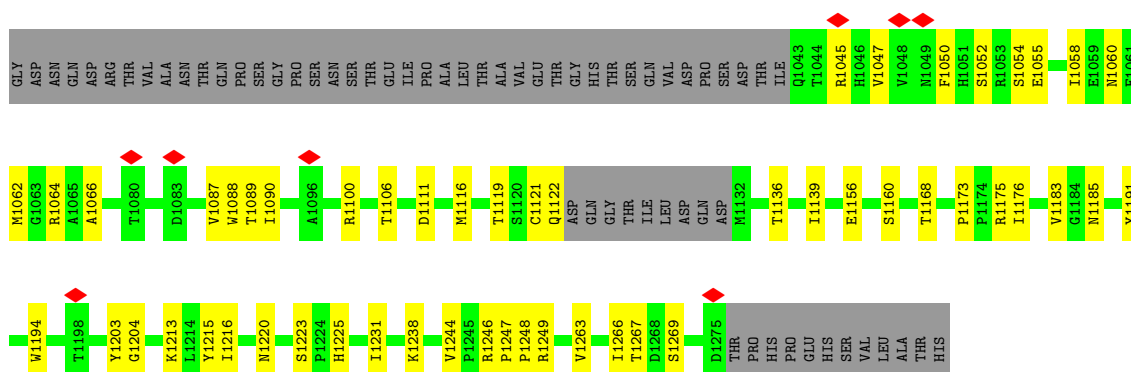
• Molecule 1: Echovirus 18 capsid protein 1



• Molecule 1: Echovirus 18 capsid protein 1

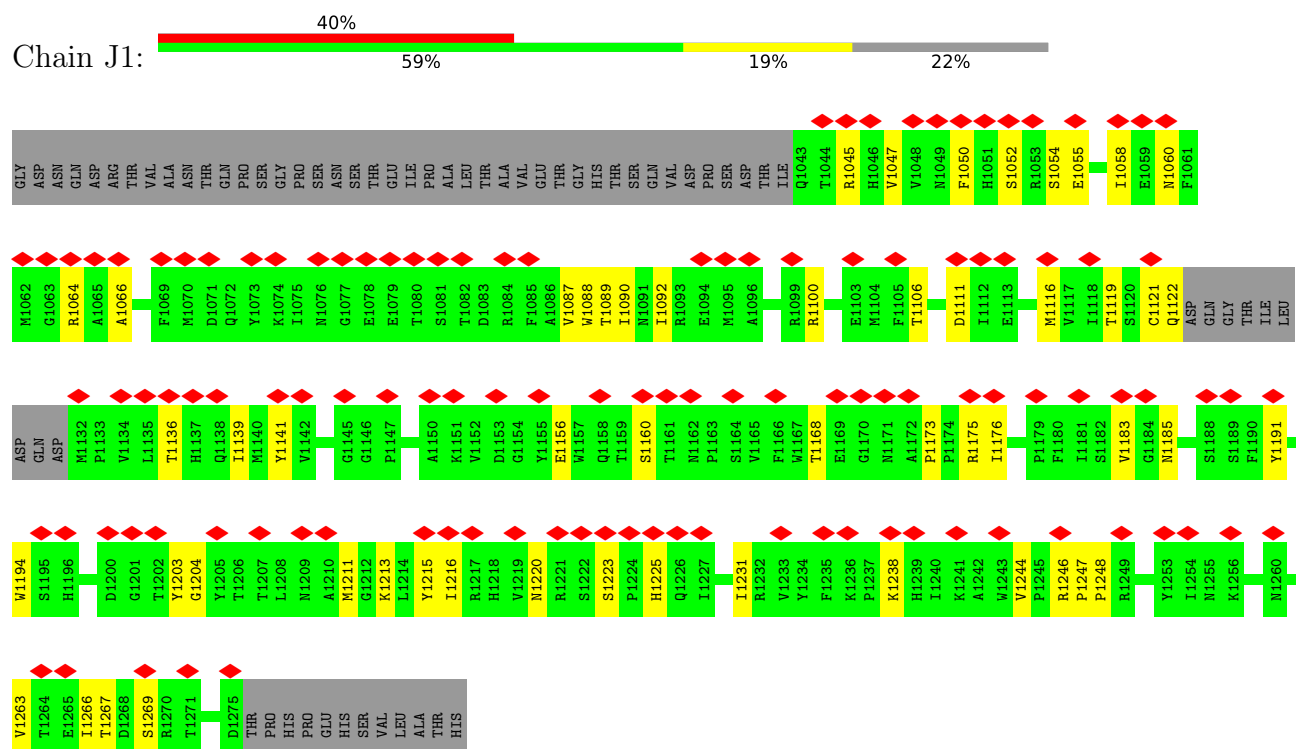


• Molecule 1: Echovirus 18 capsid protein 1



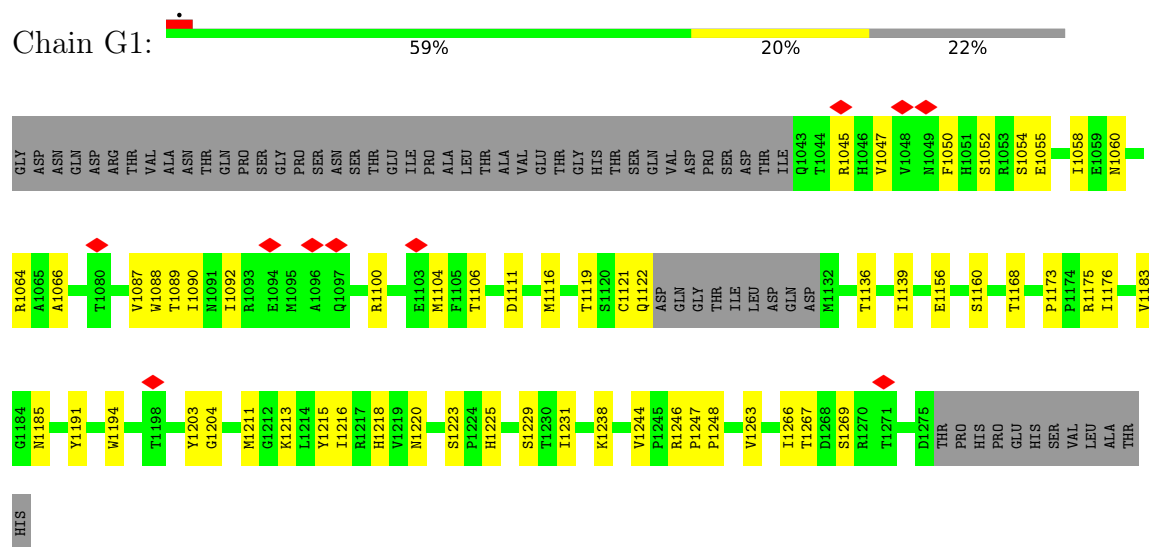
- Molecule 1: Echovirus 18 capsid protein 1

Chain J1:



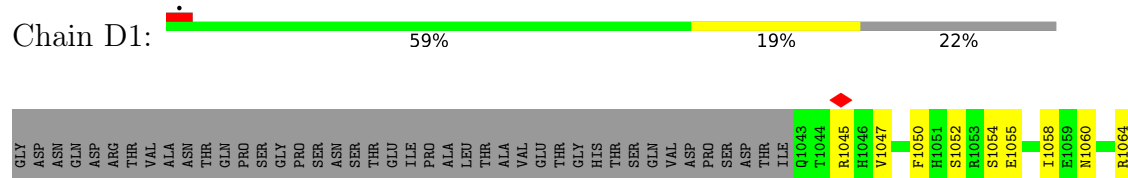
- Molecule 1: Echovirus 18 capsid protein 1

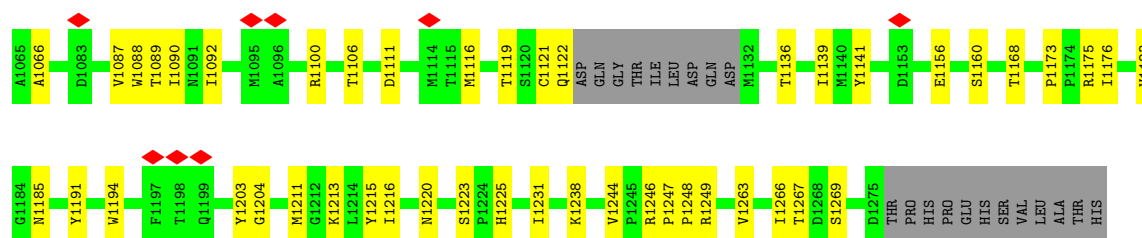
Chain G1:



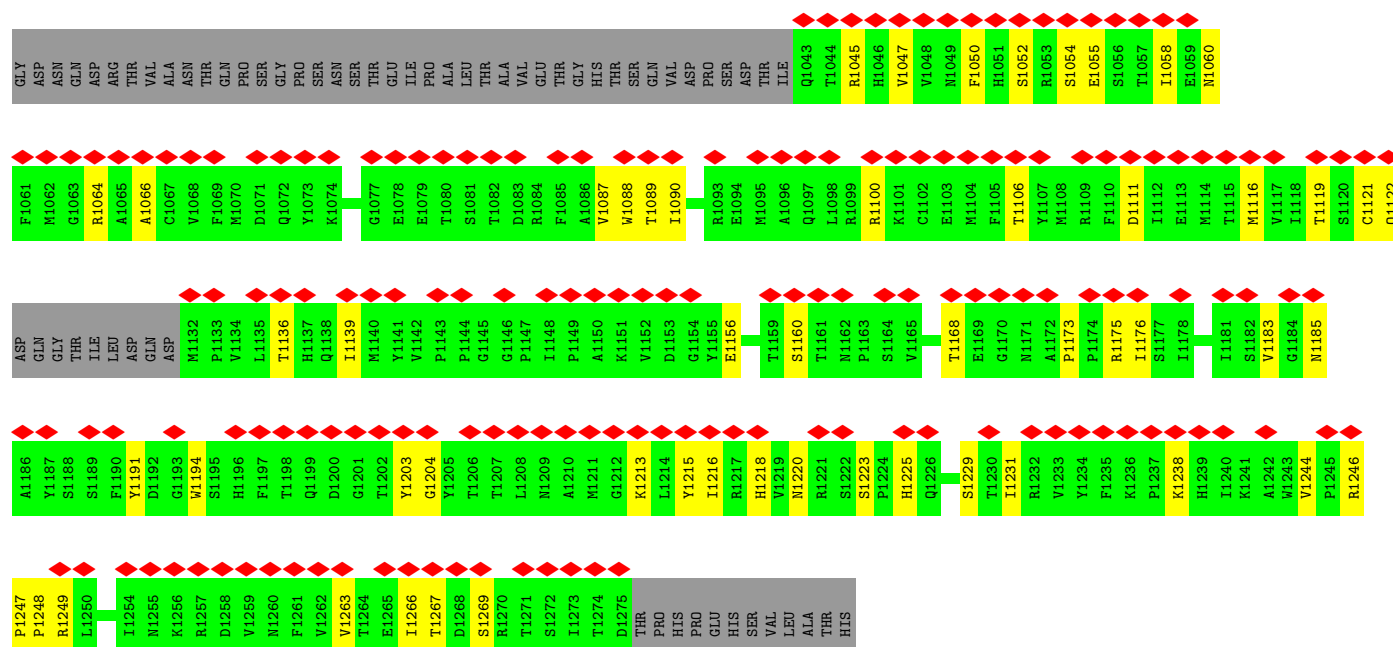
- Molecule 1: Echovirus 18 capsid protein 1

Chain D1:

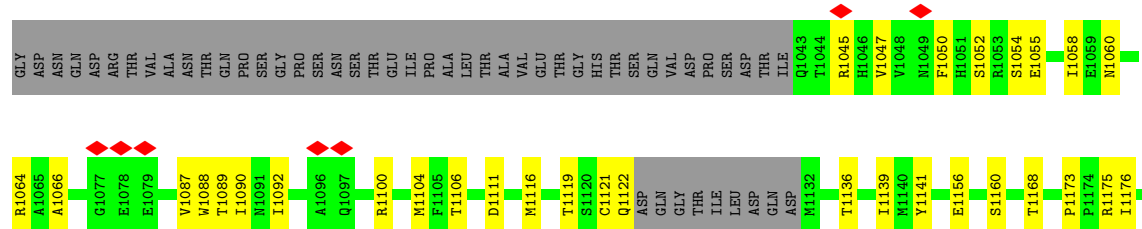




• Molecule 1: Echovirus 18 capsid protein 1

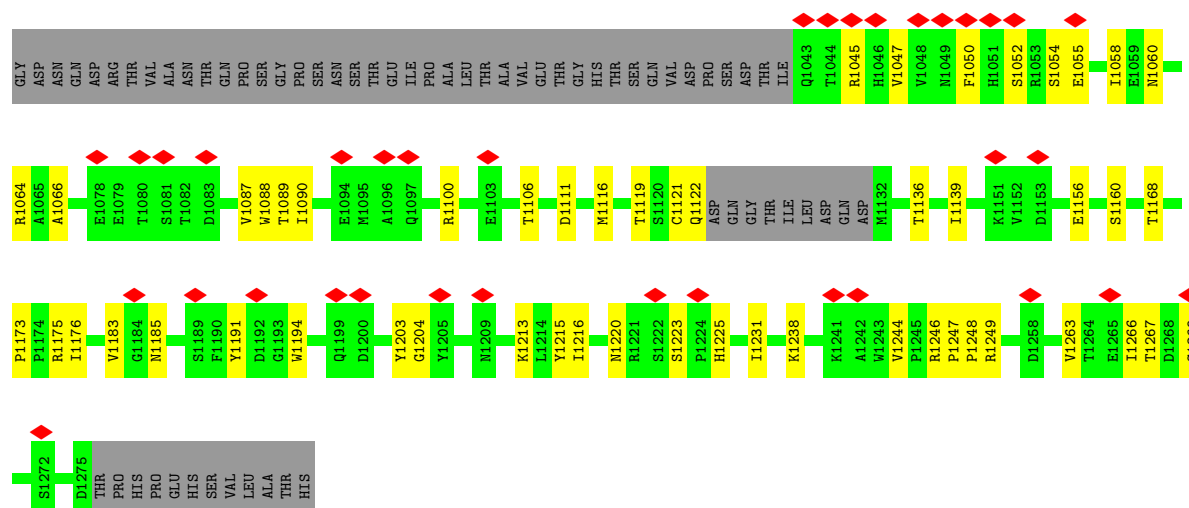


• Molecule 1: Echovirus 18 capsid protein 1

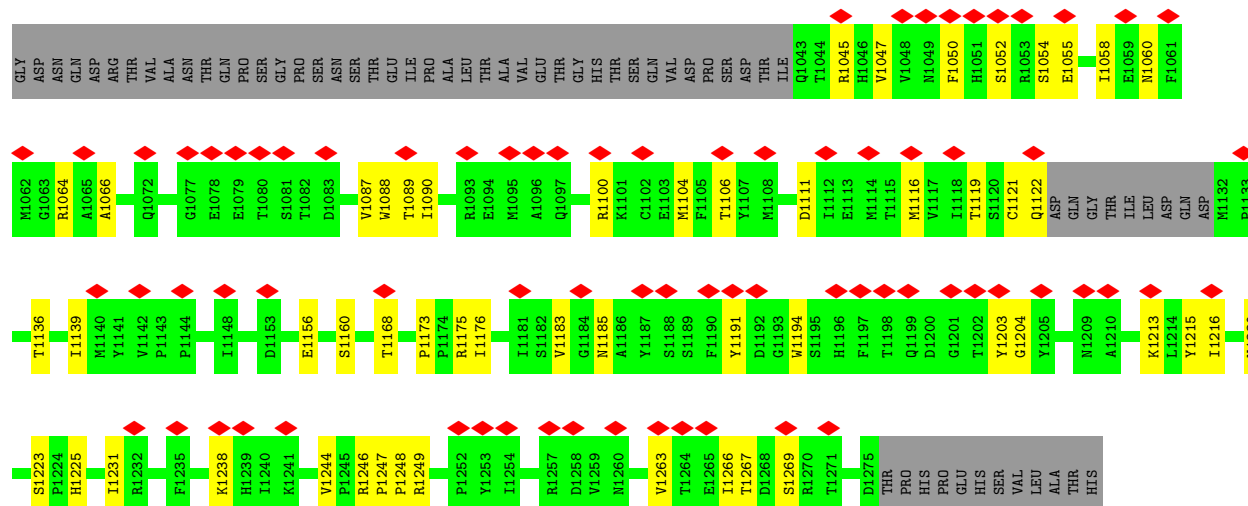


• Molecule 1: Echovirus 18 capsid protein 1

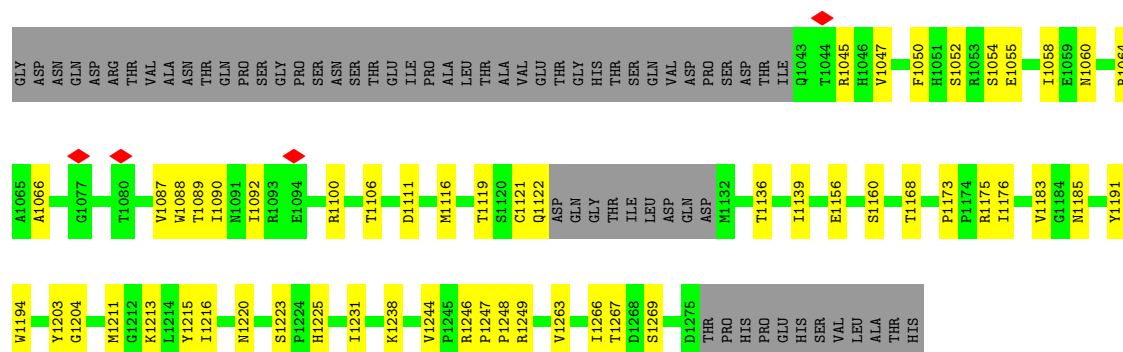




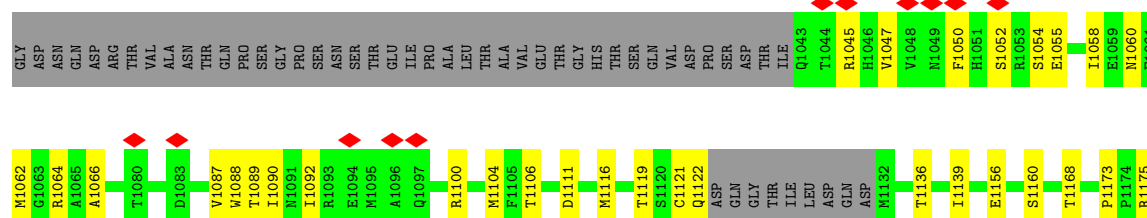
- Molecule 1: Echovirus 18 capsid protein 1



- Molecule 1: Echovirus 18 capsid protein 1

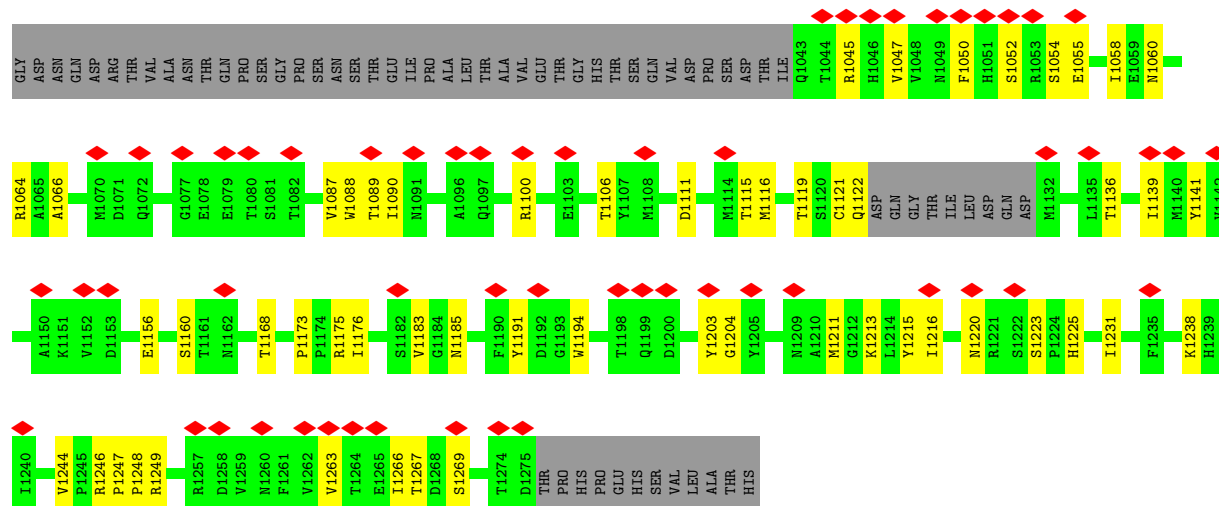


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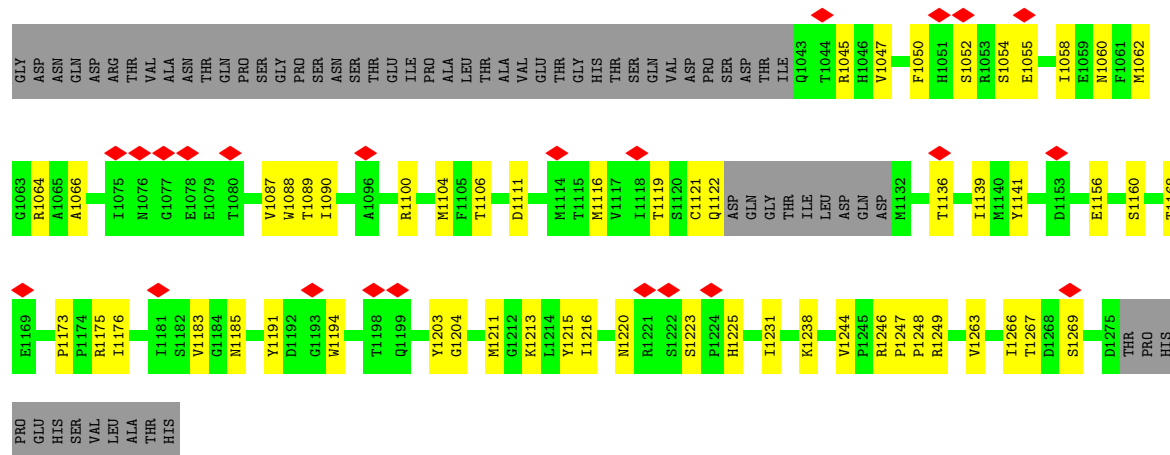




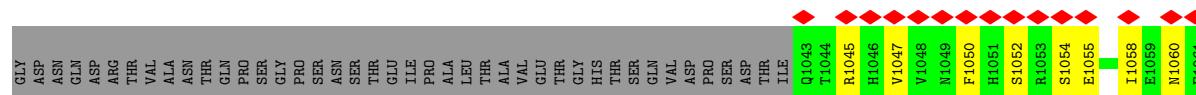
• Molecule 1: Echovirus 18 capsid protein 1

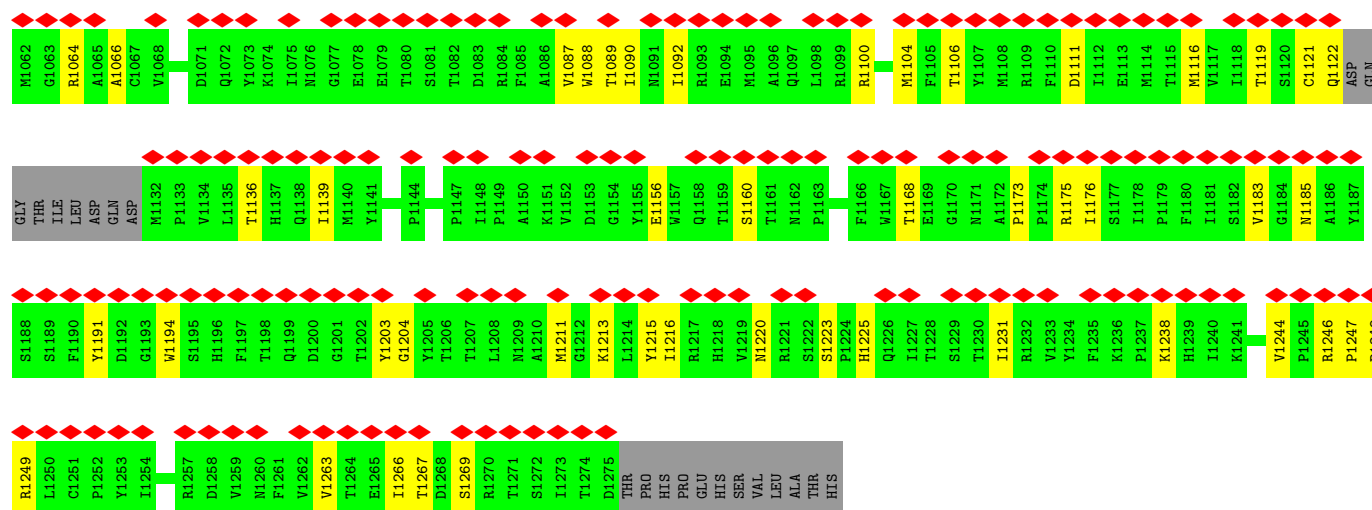


• Molecule 1: Echovirus 18 capsid protein 1

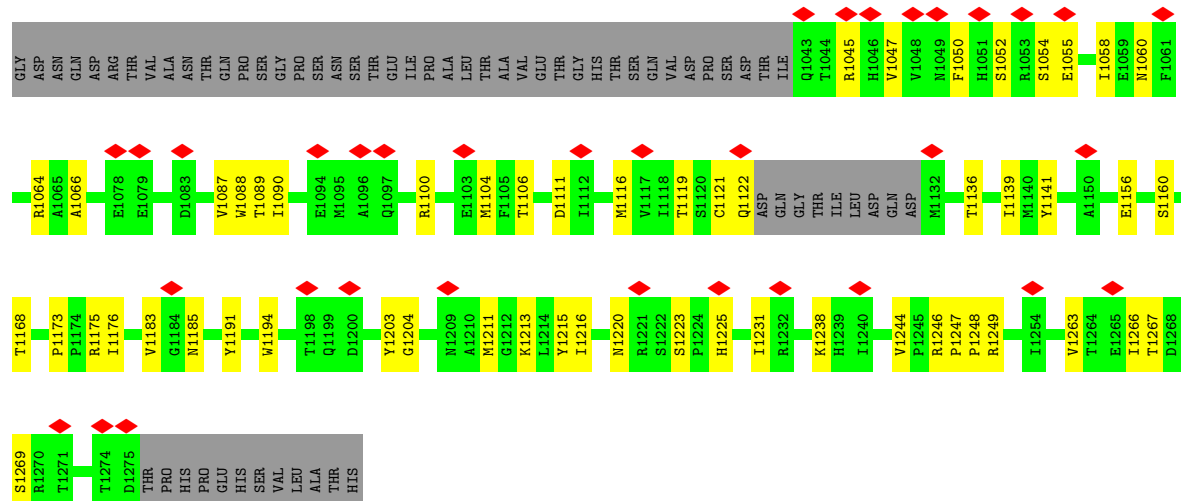


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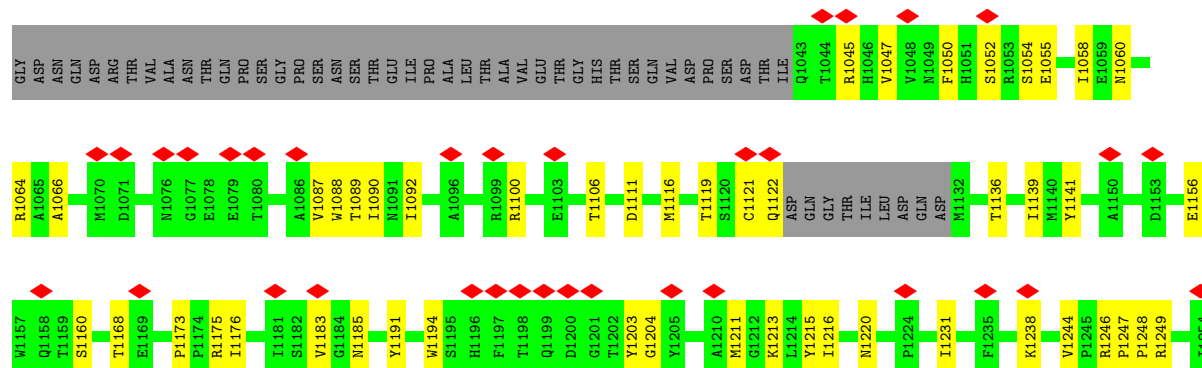


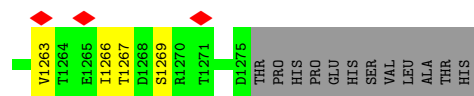


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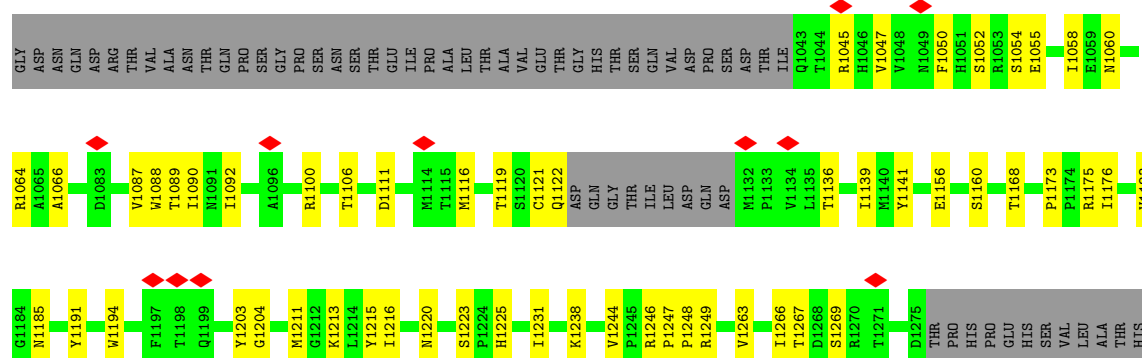
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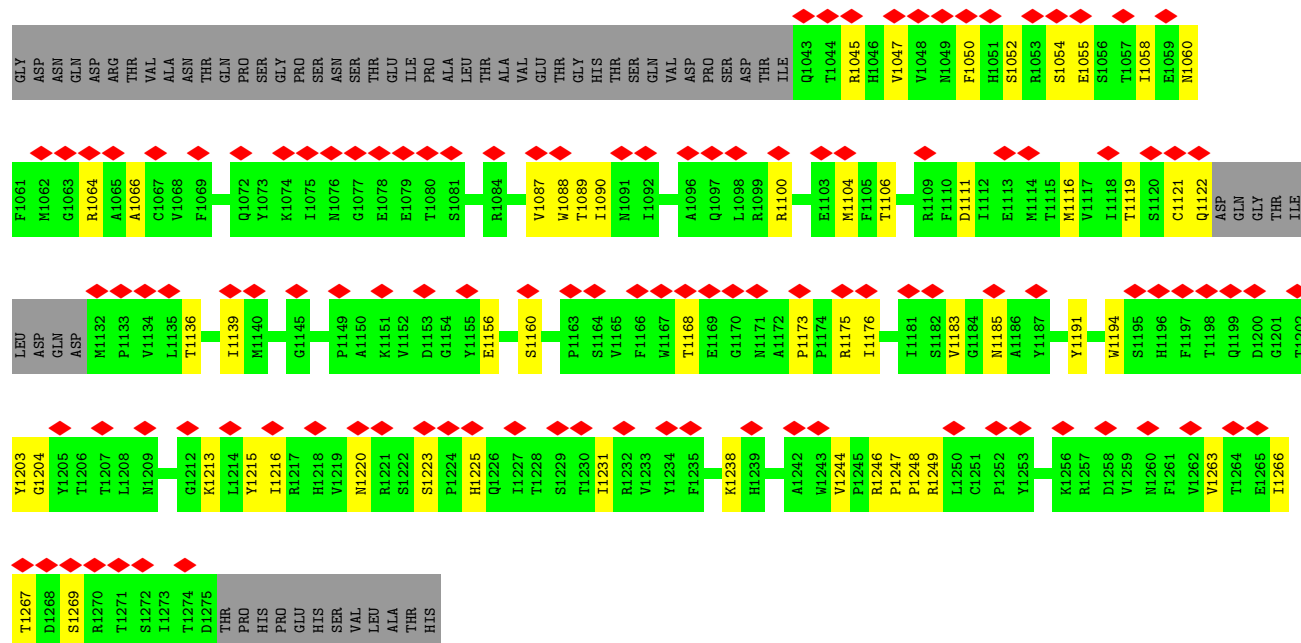
• Molecule 1: Echovirus 18 capsid protein 1

Chain M2: 59% 19% 22%



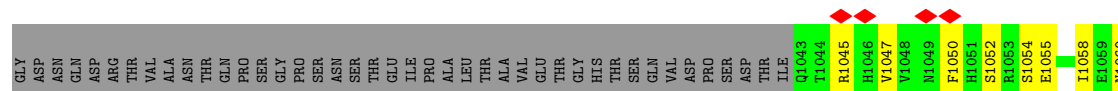
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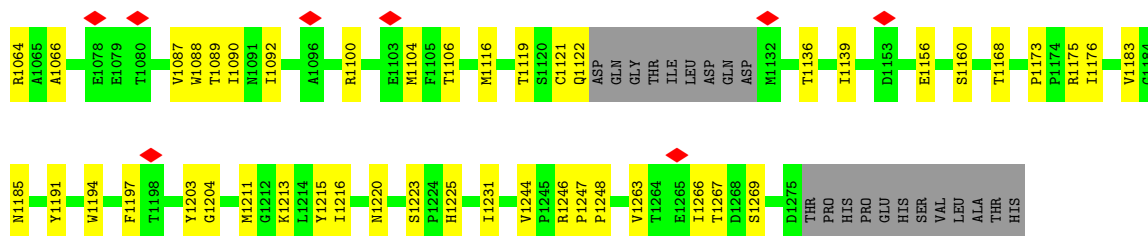
Chain J2: 41% 60% 18% 22%



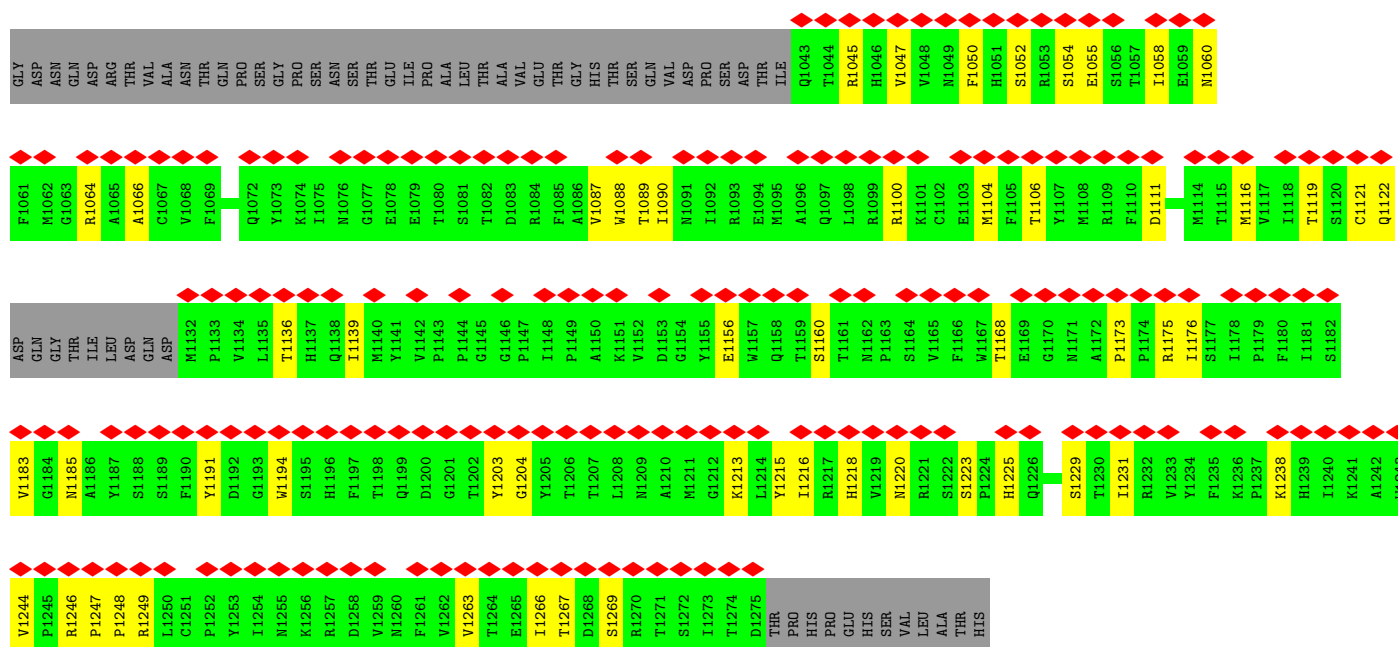
• Molecule 1: Echovirus 18 capsid protein 1

Chain G2: 60% 18% 22%

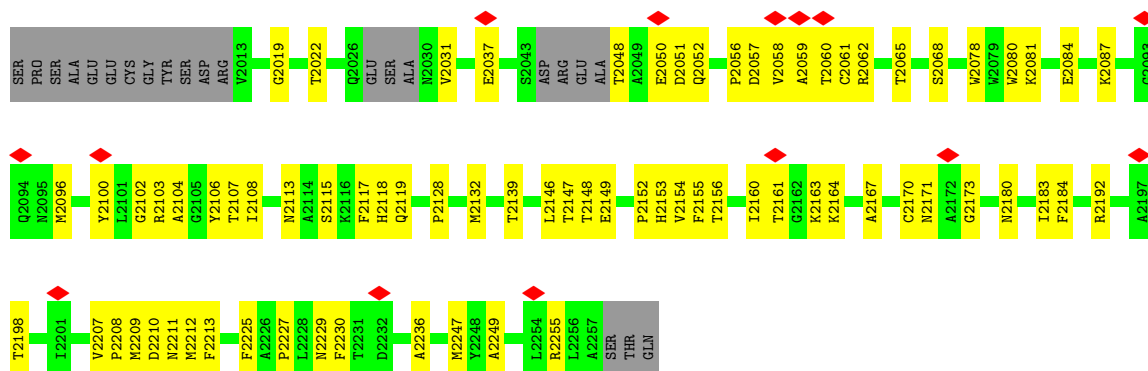




• Molecule 1: Echovirus 18 capsid protein 1

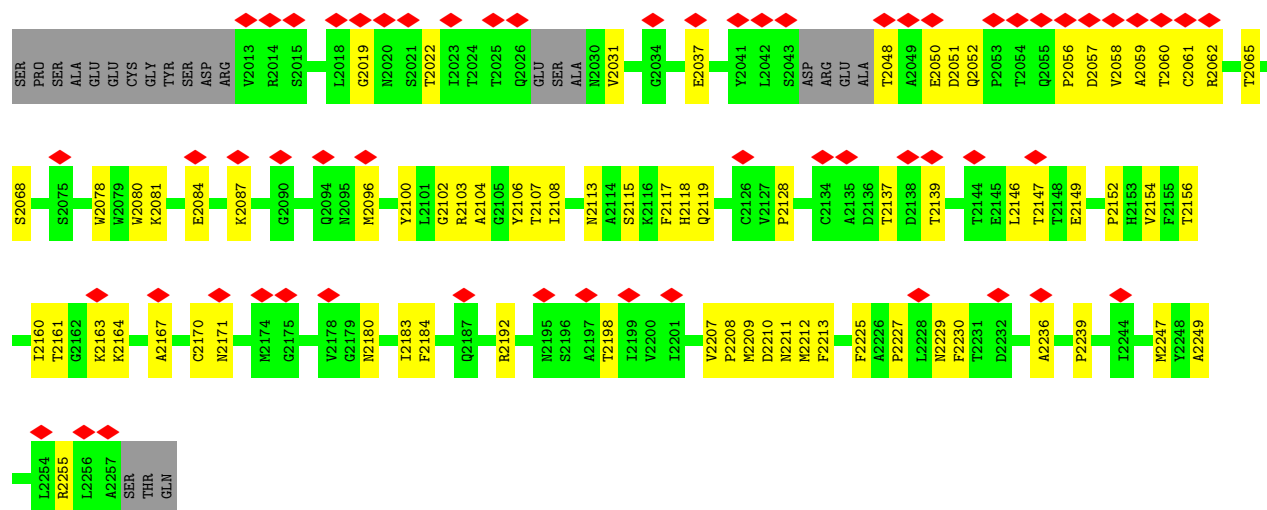


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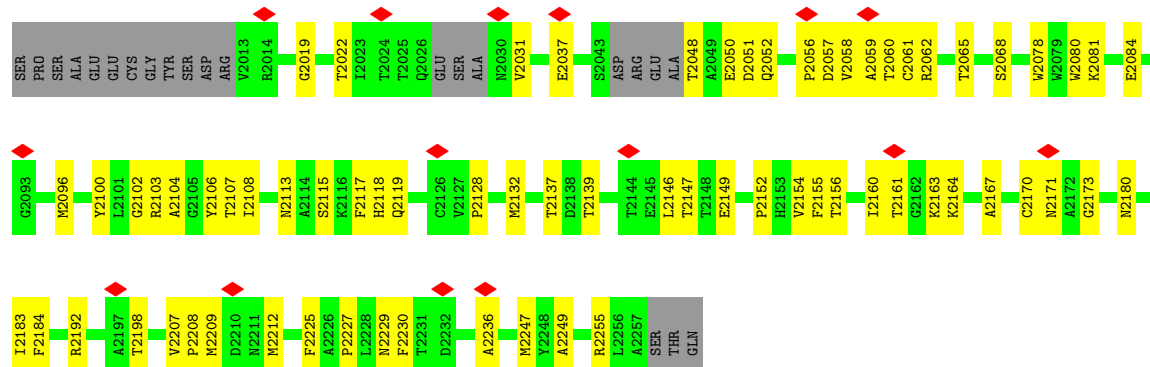


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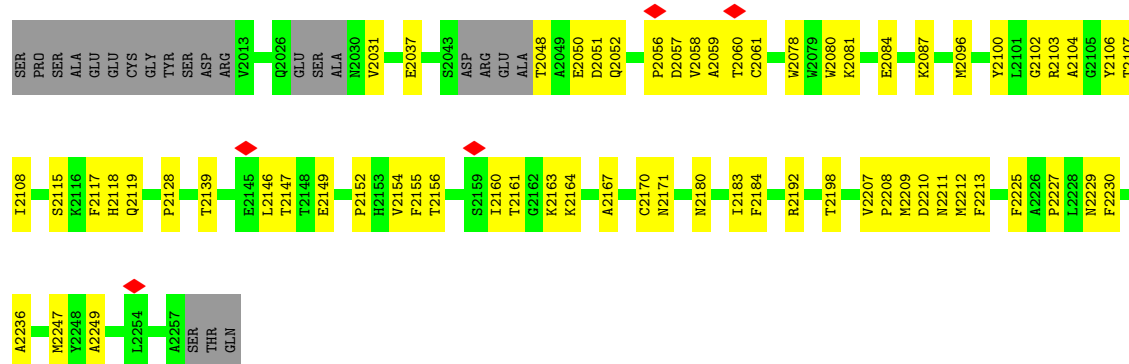




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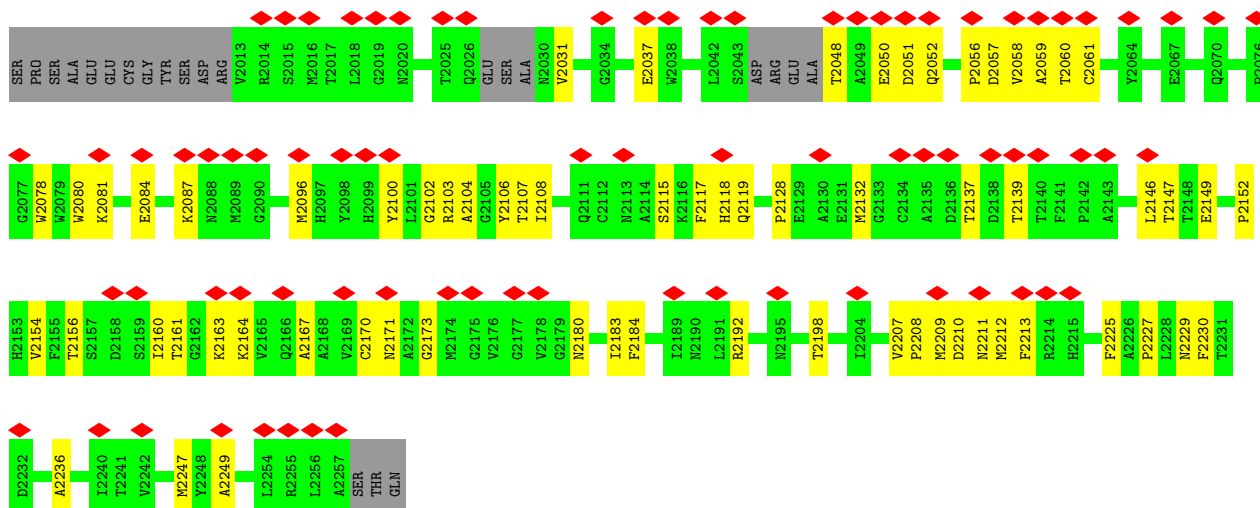


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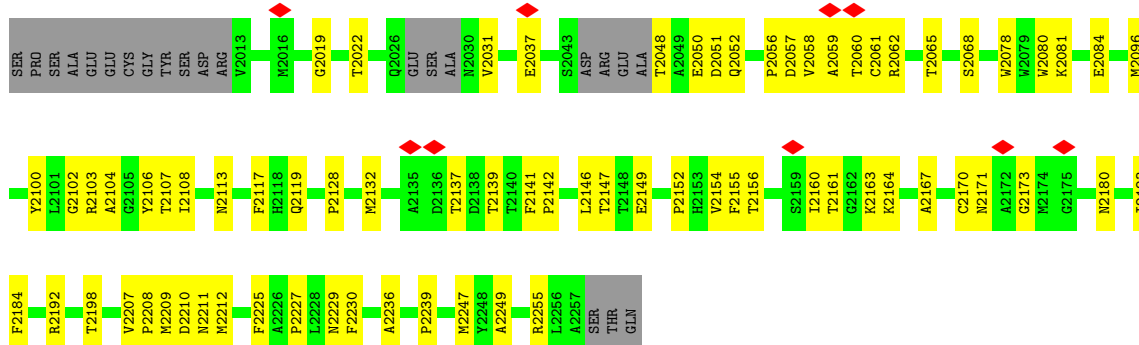


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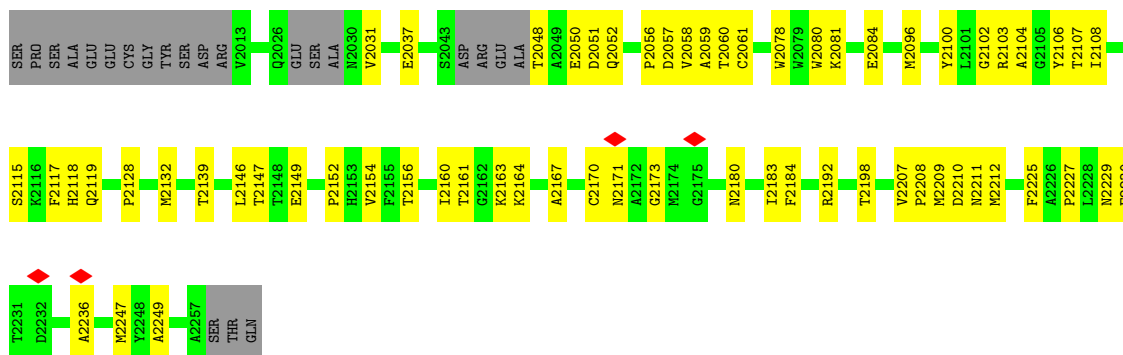




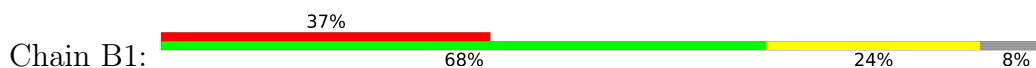
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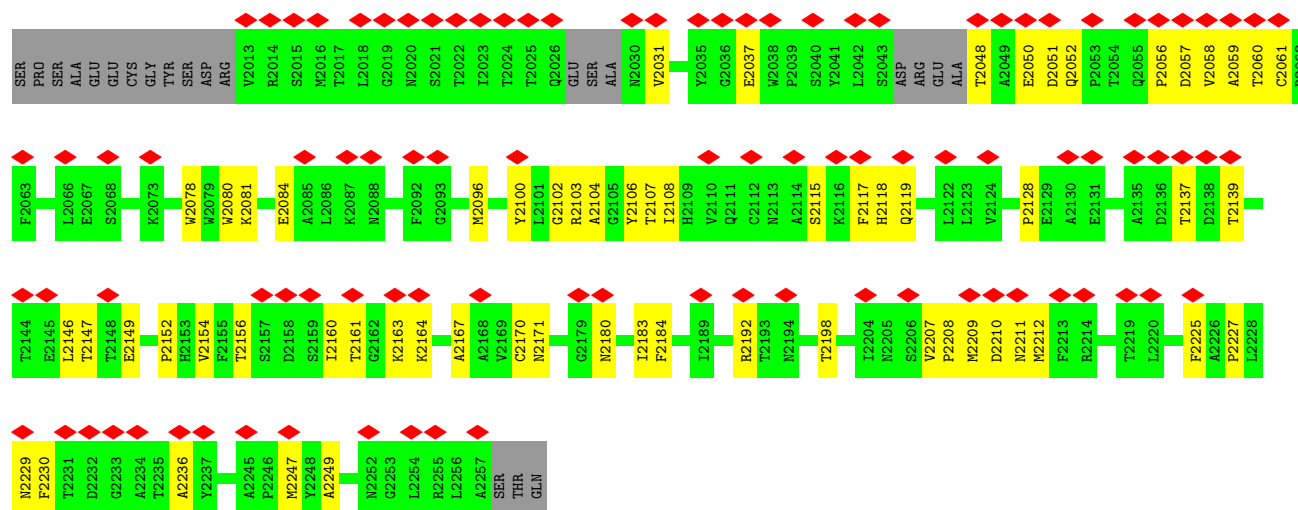


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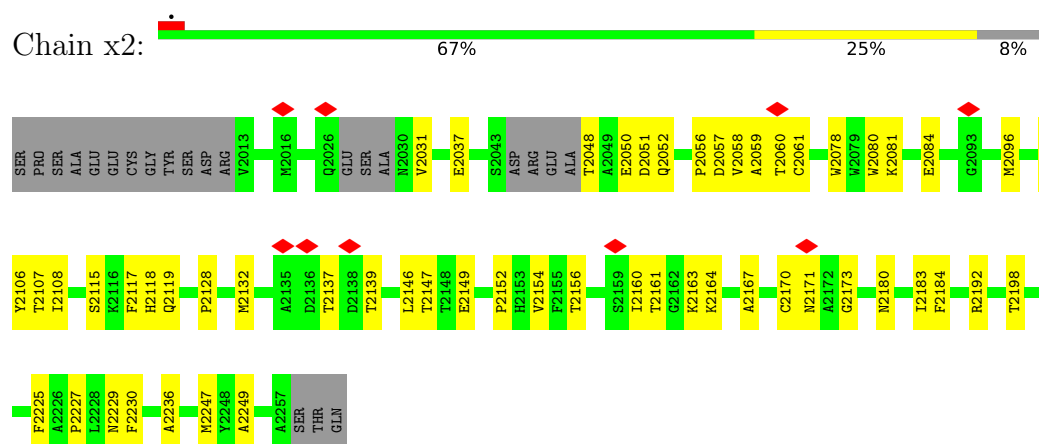


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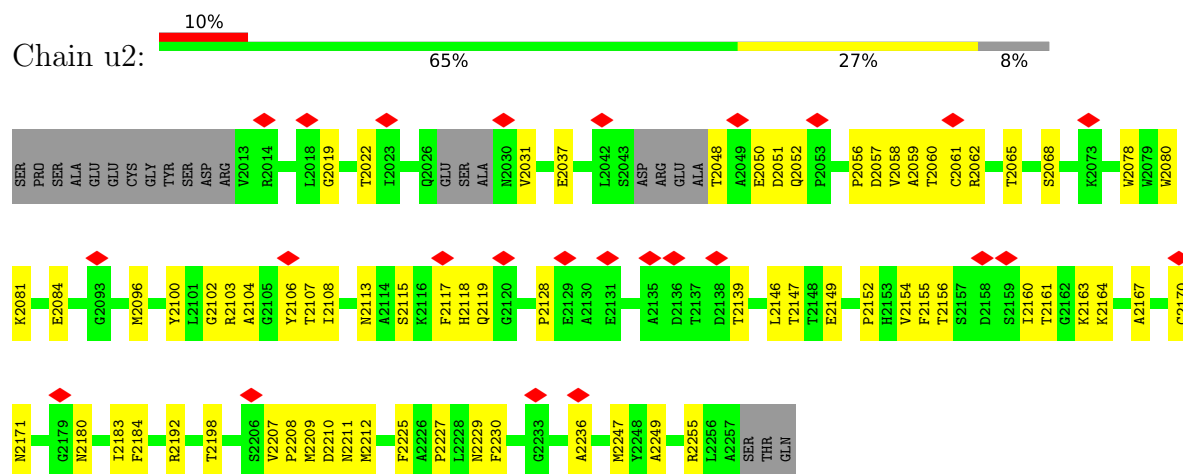




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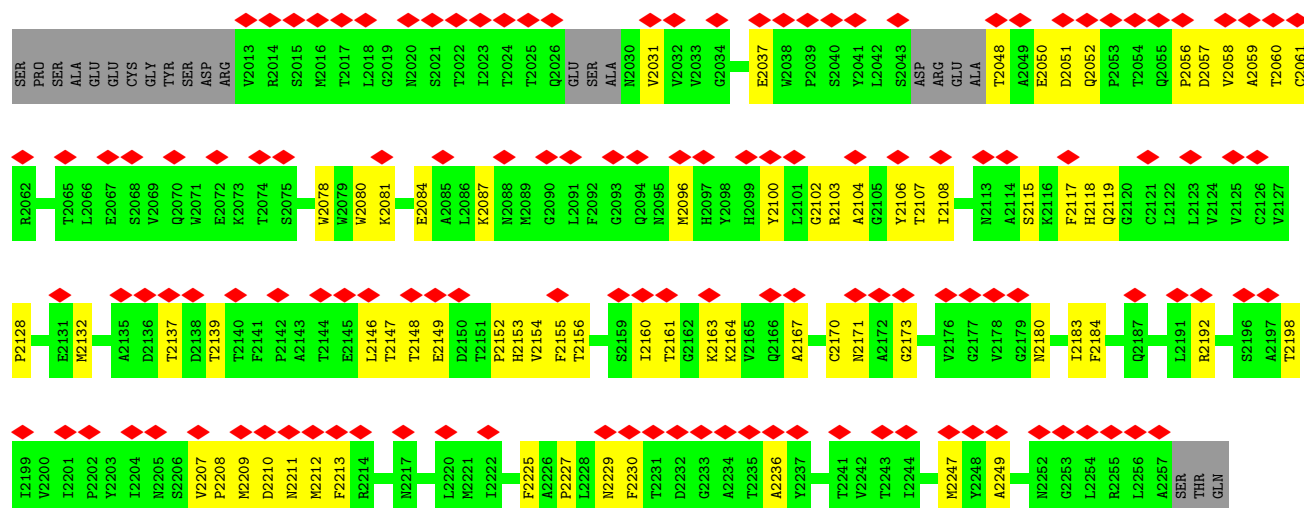


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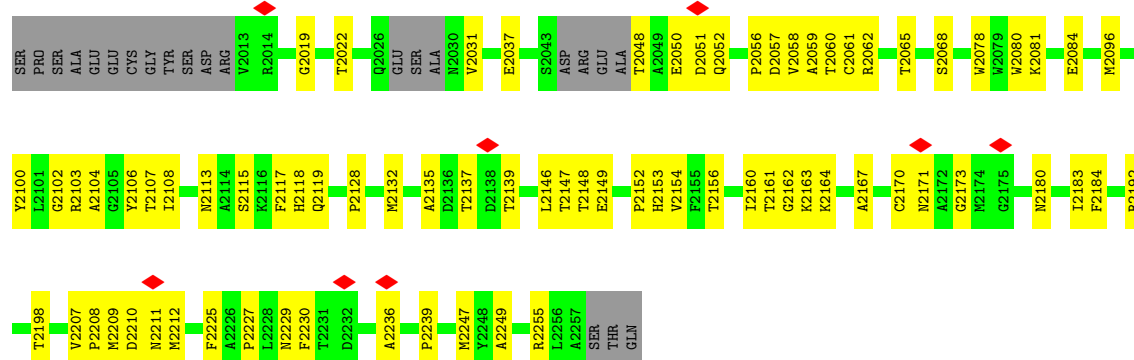


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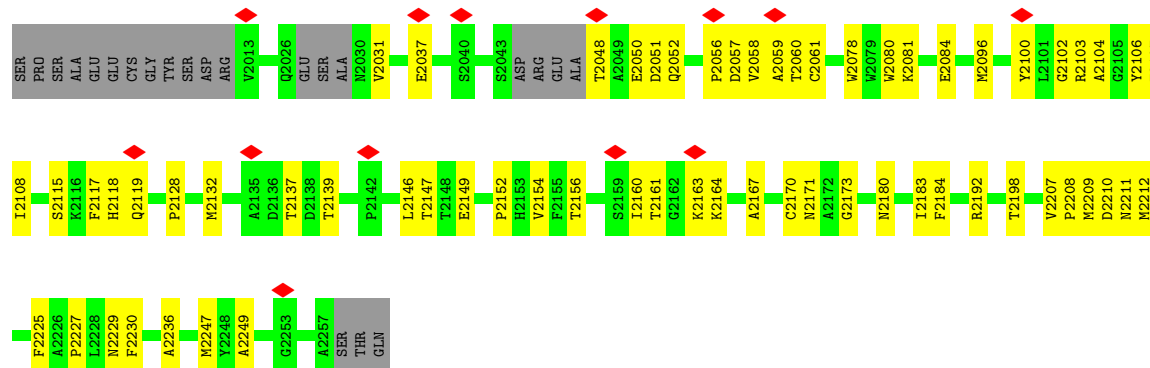




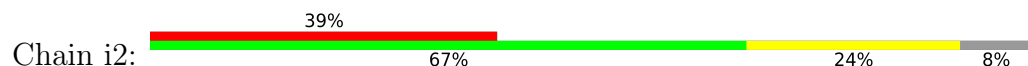
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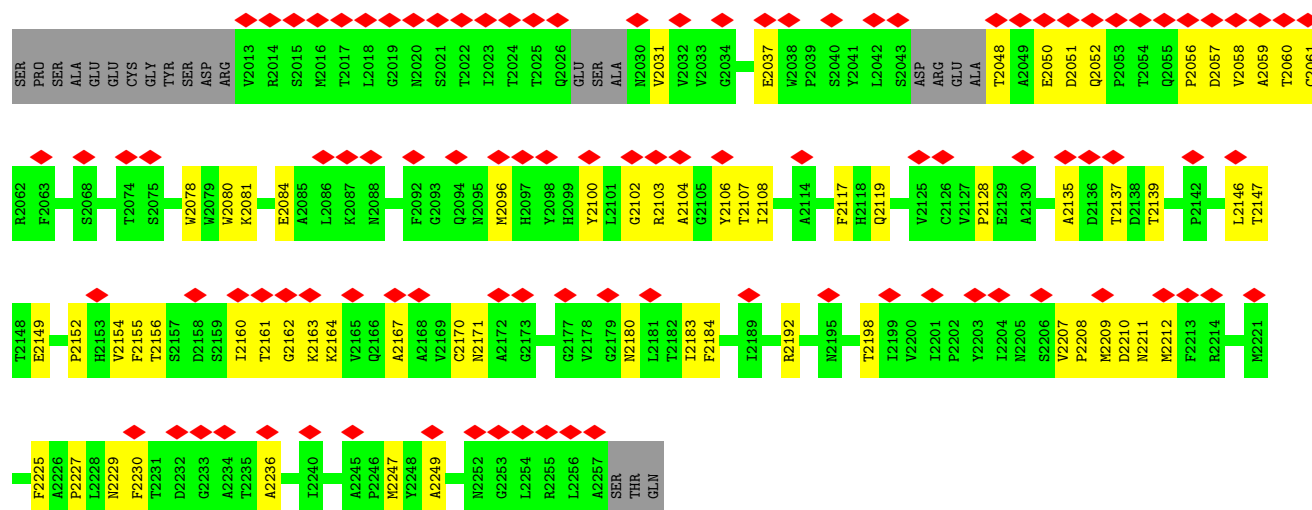


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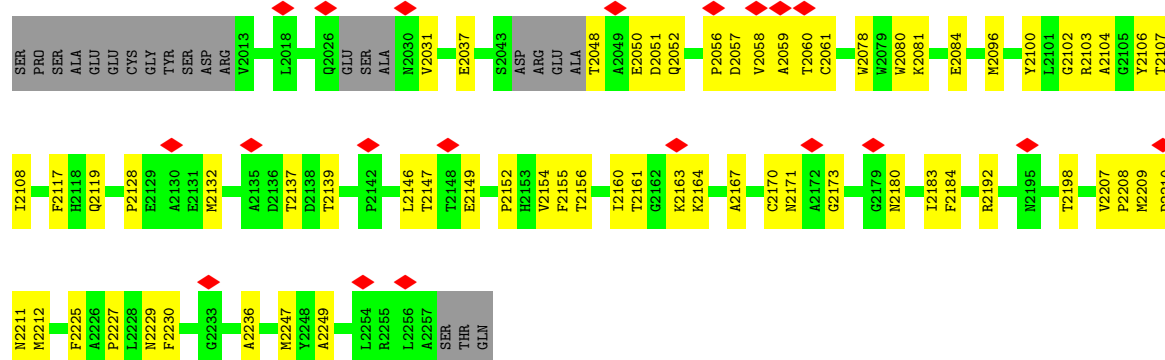


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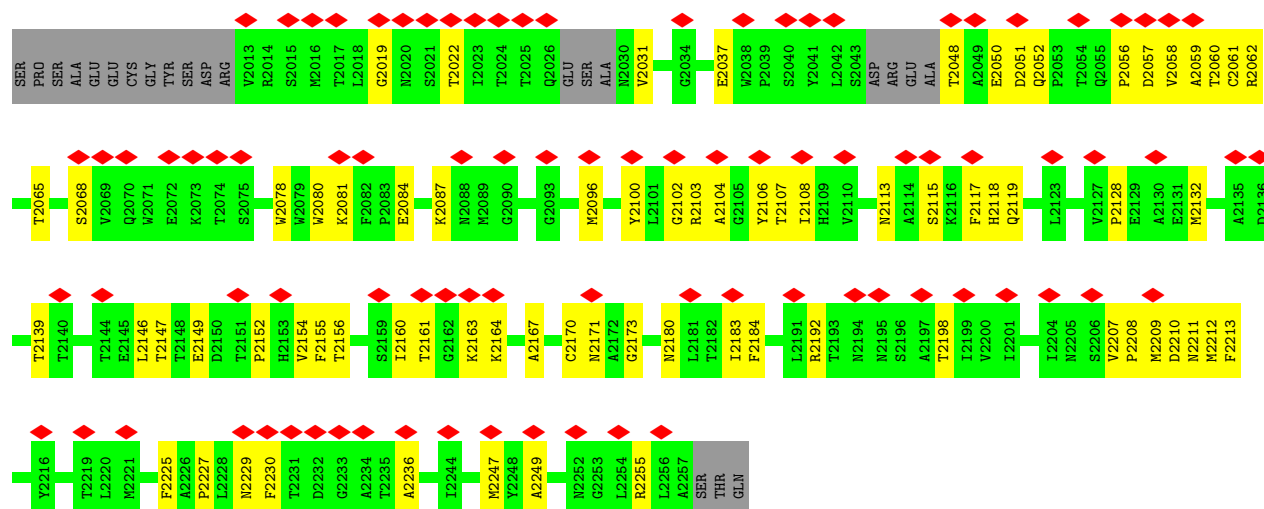




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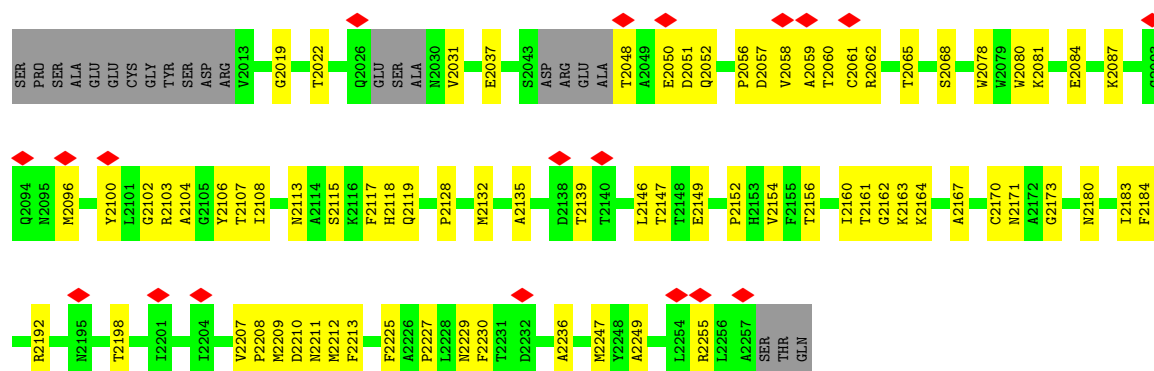


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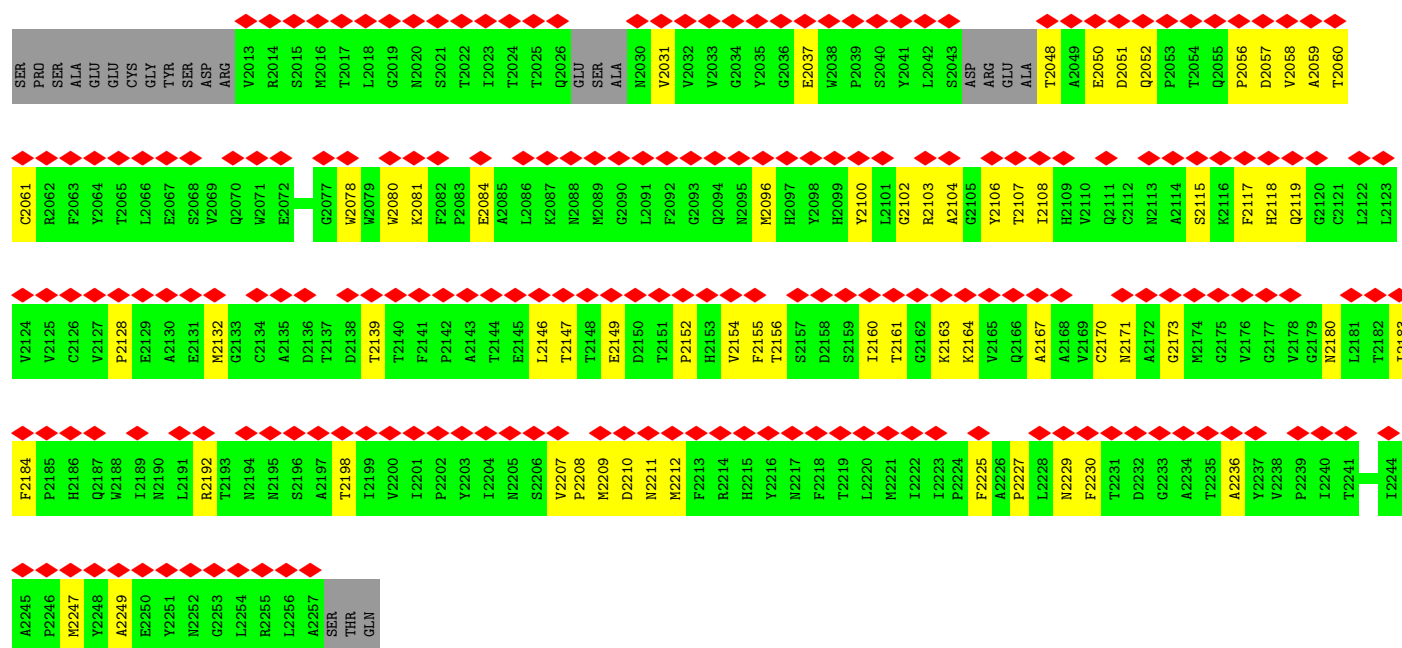
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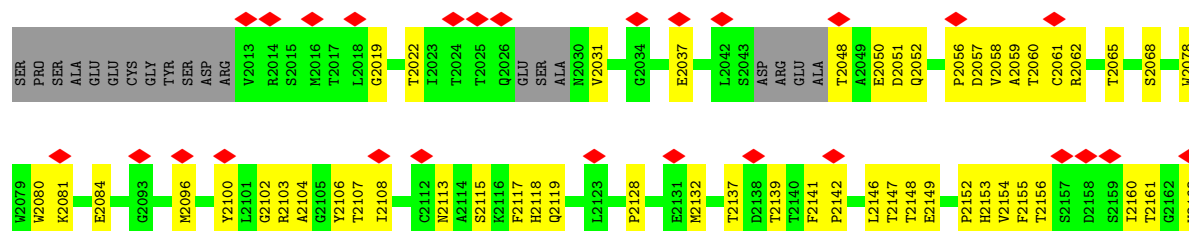
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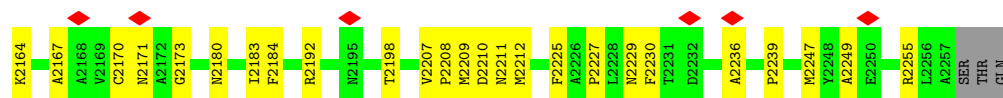
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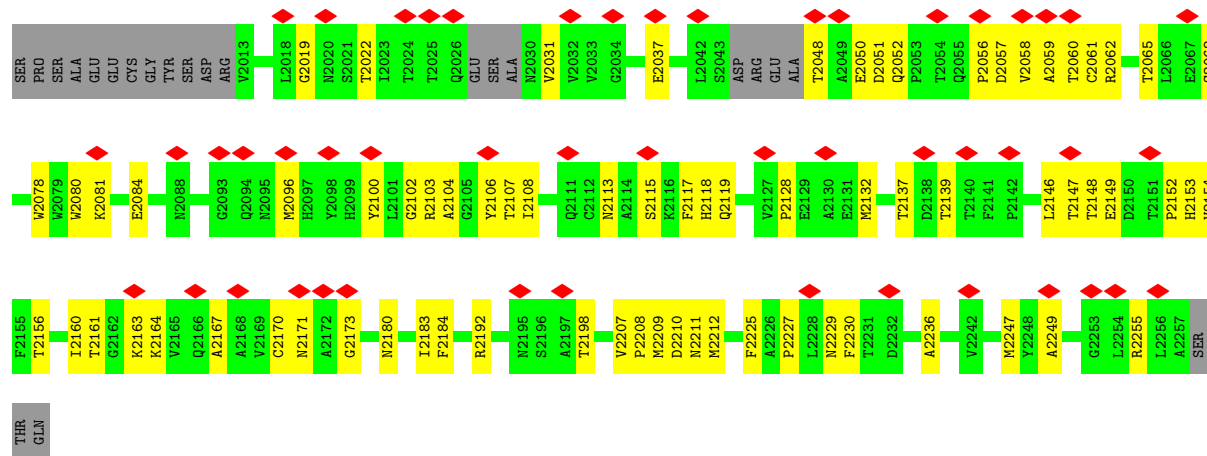
- Molecule 2: Echovirus 18 capsid protein 2

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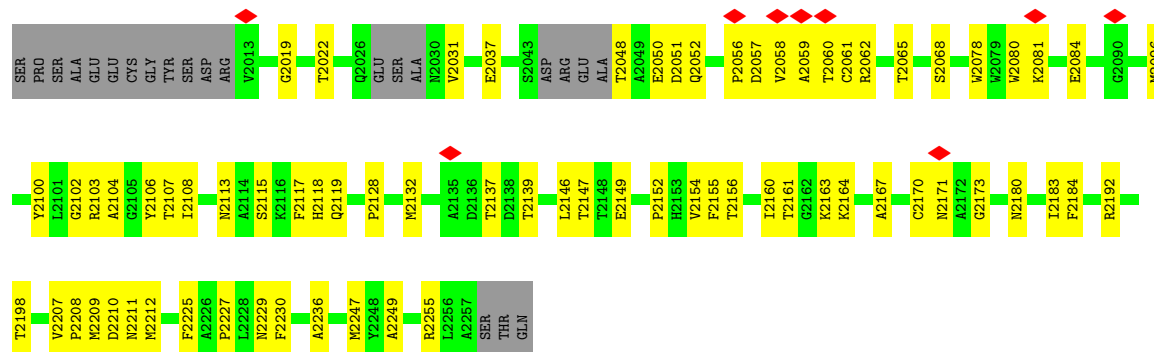




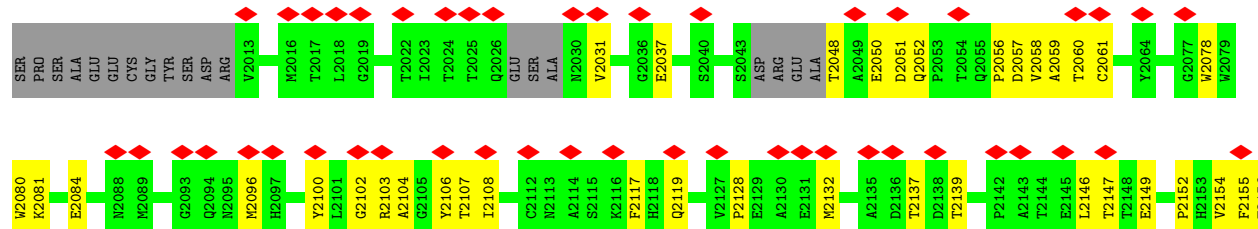
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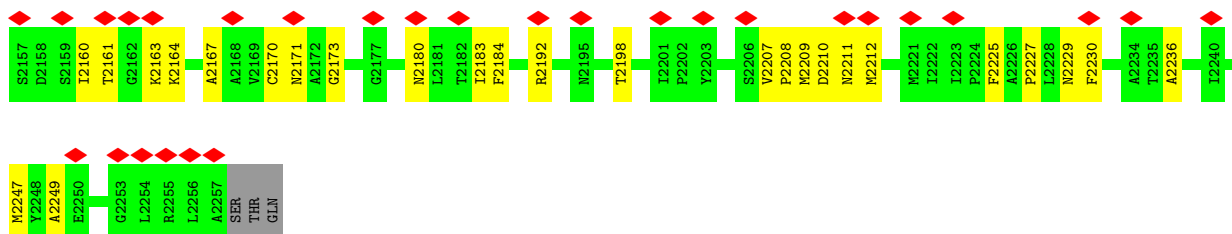


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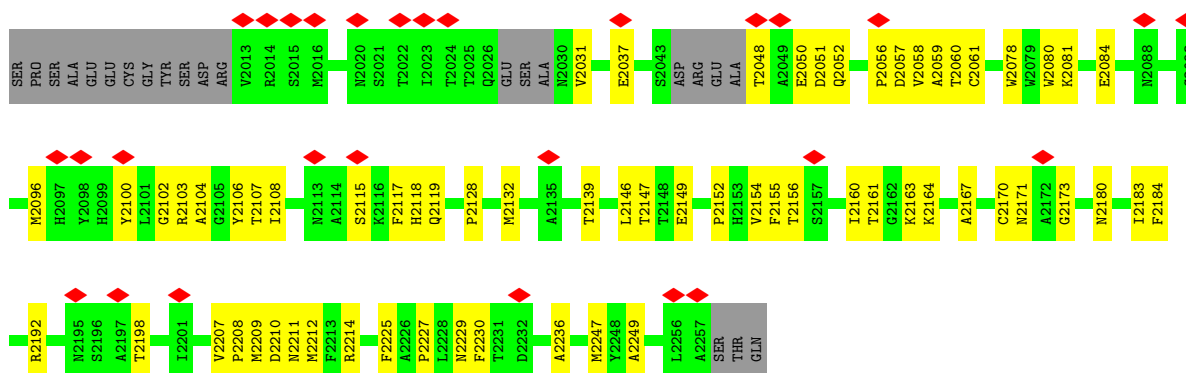


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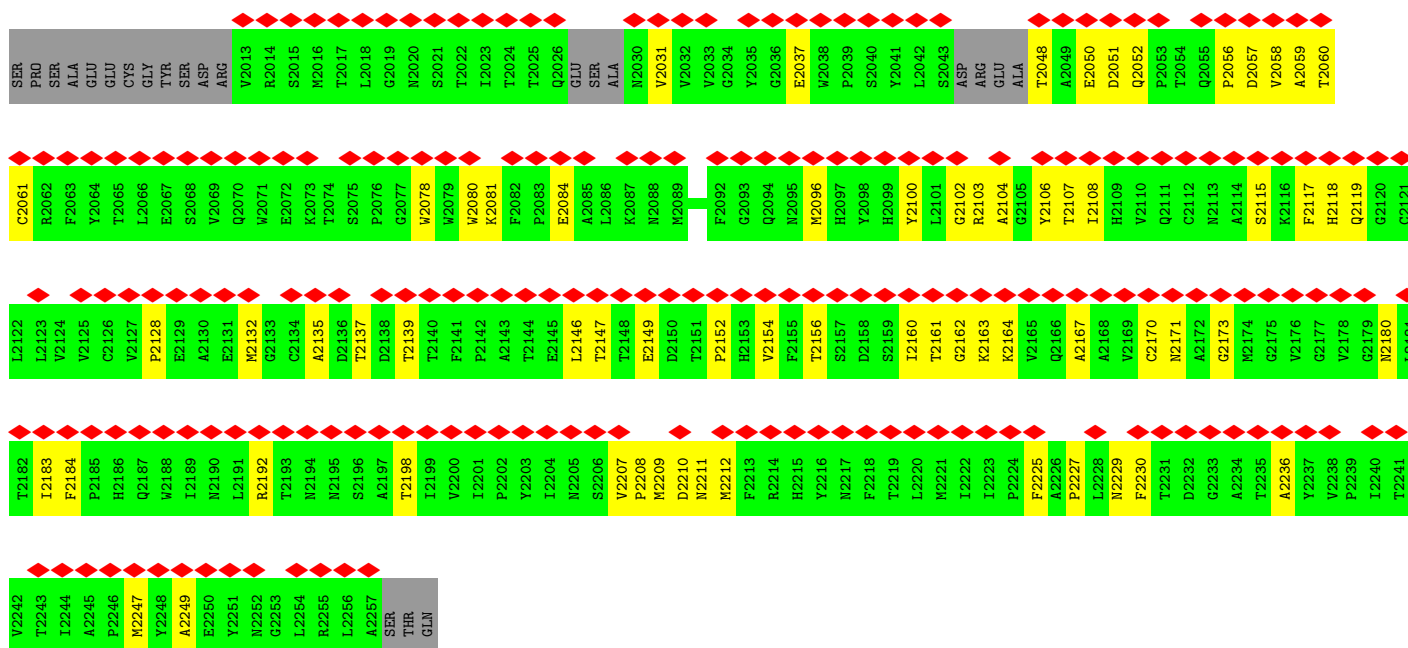
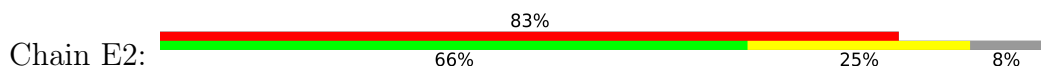




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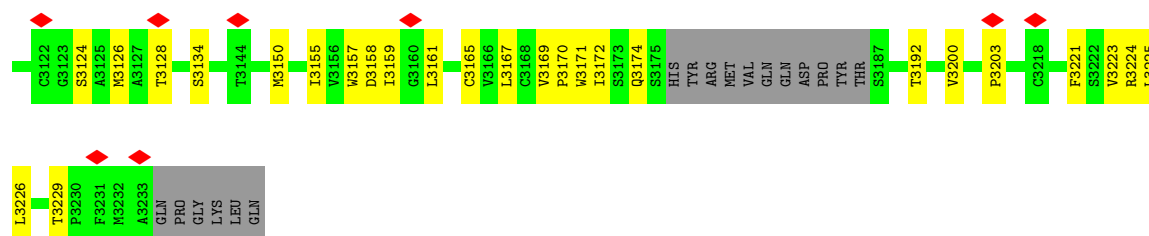


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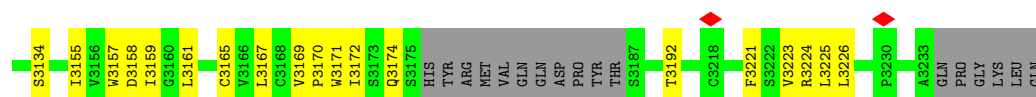


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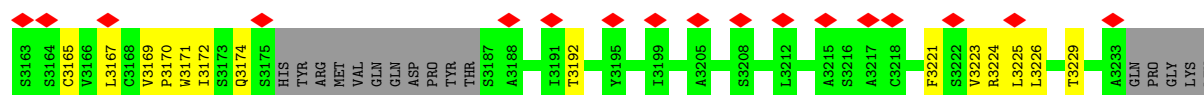
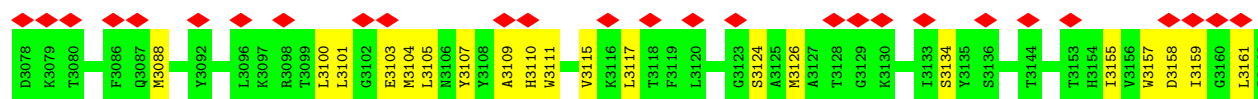
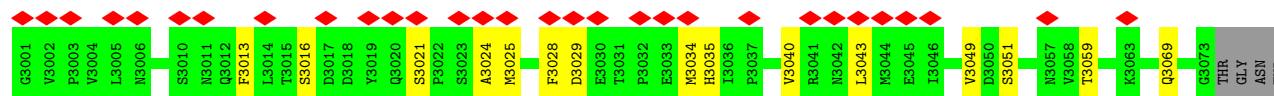




- Molecule 3: Echovirus 18 capsid protein 3

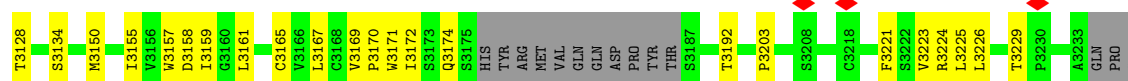


- Molecule 3: Echovirus 18 capsid protein 3



GLN

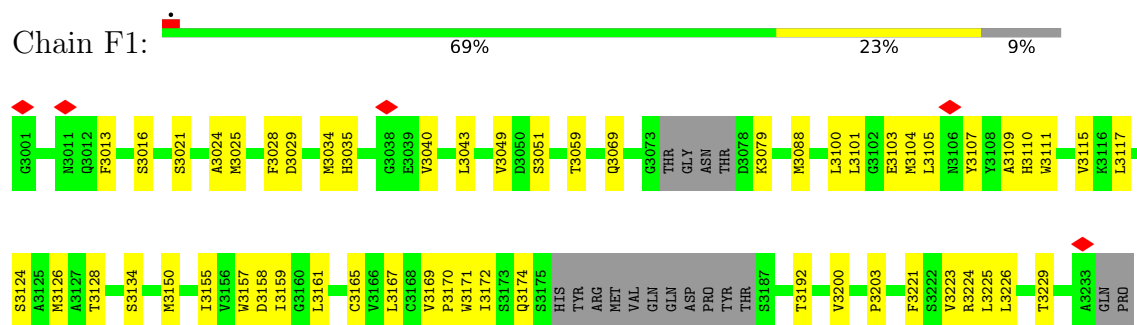
- Molecule 3: Echovirus 18 capsid protein 3



LYS
LEU
GLN

• Molecule 3: Echovirus 18 capsid protein 3

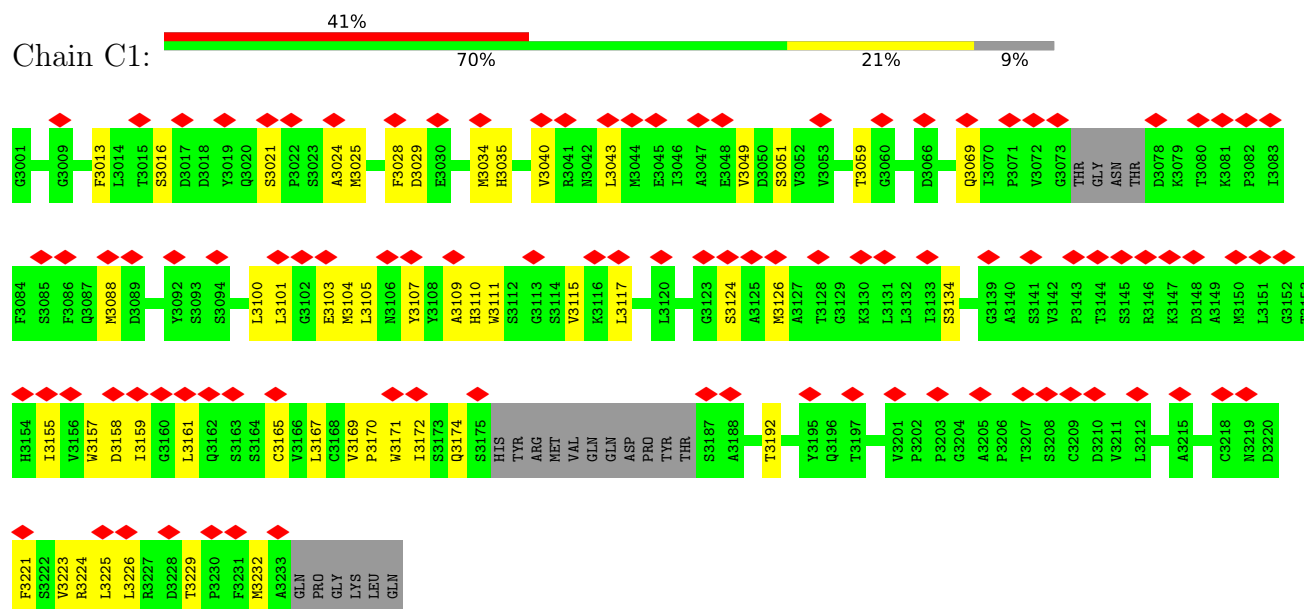
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GLY
LYS
LEU
GLN

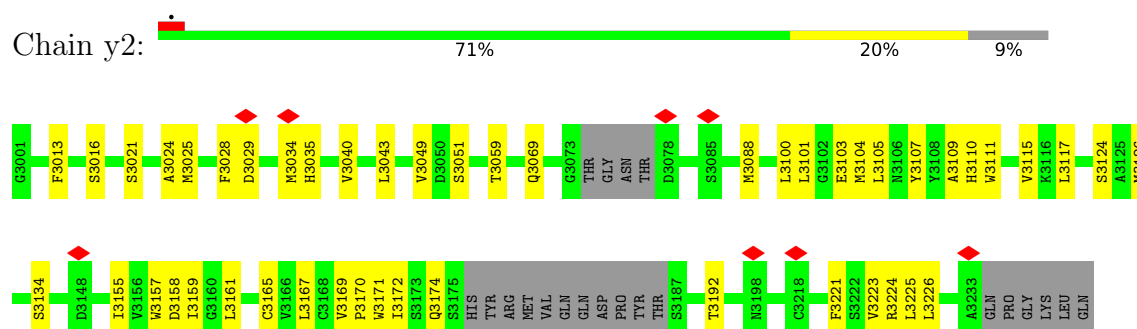
• Molecule 3: Echovirus 18 capsid protein 3

Chain C1:

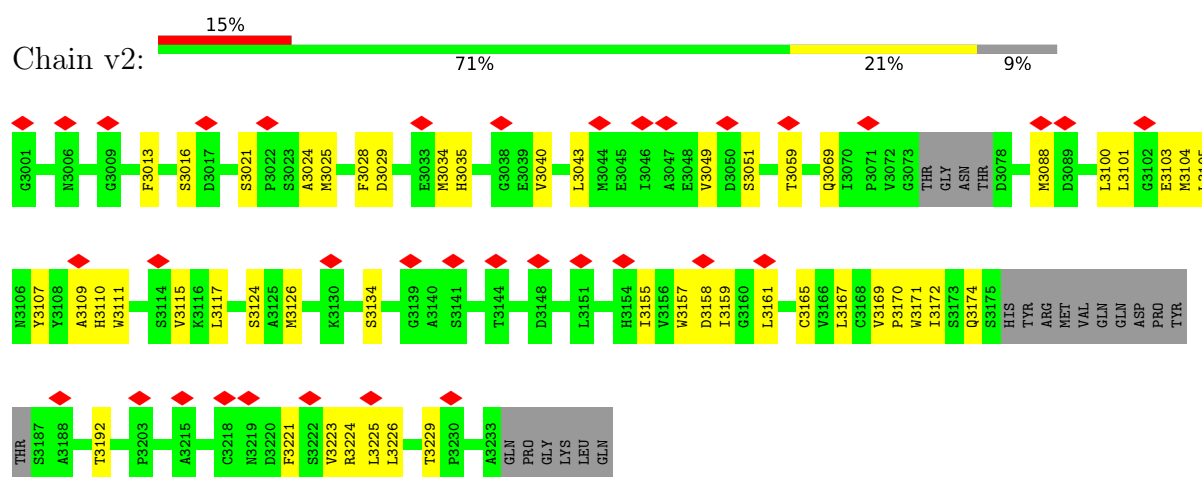


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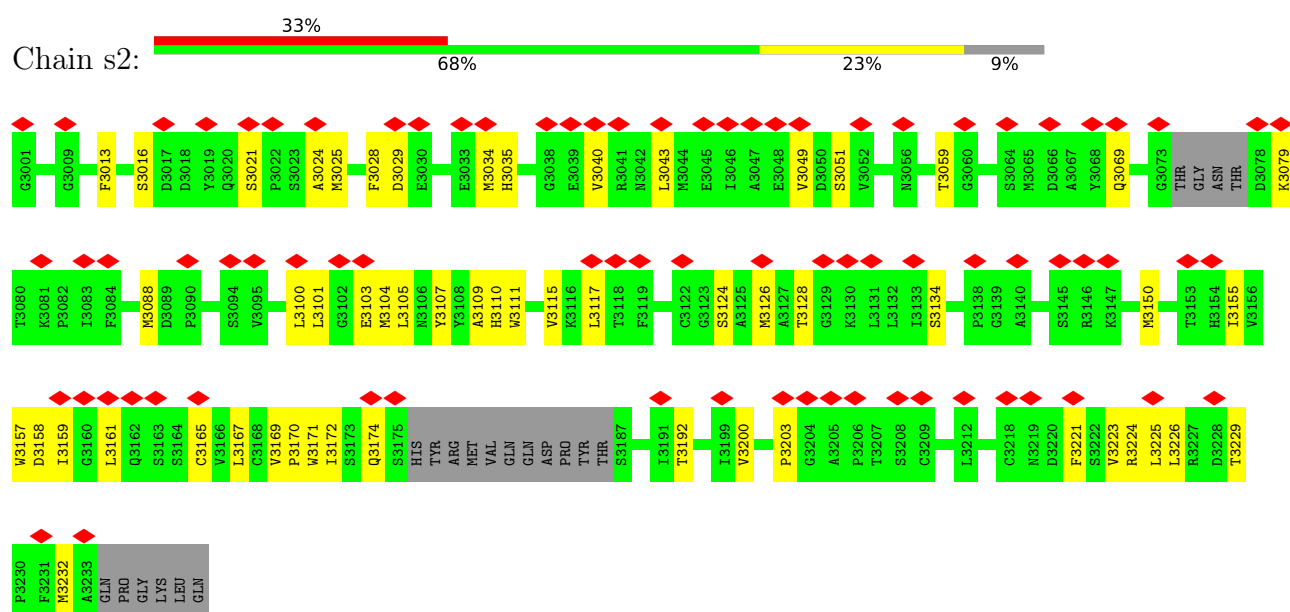
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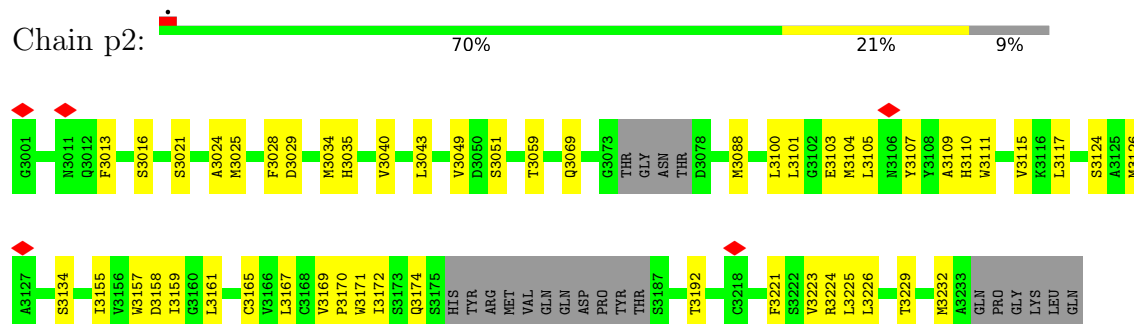
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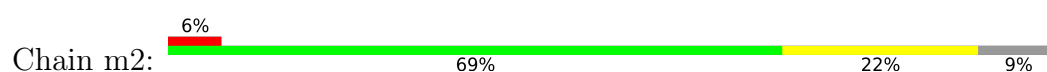
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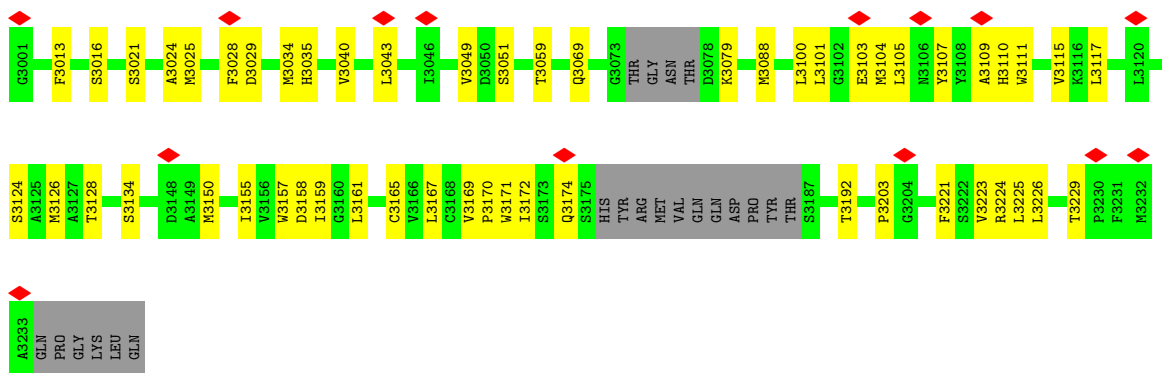


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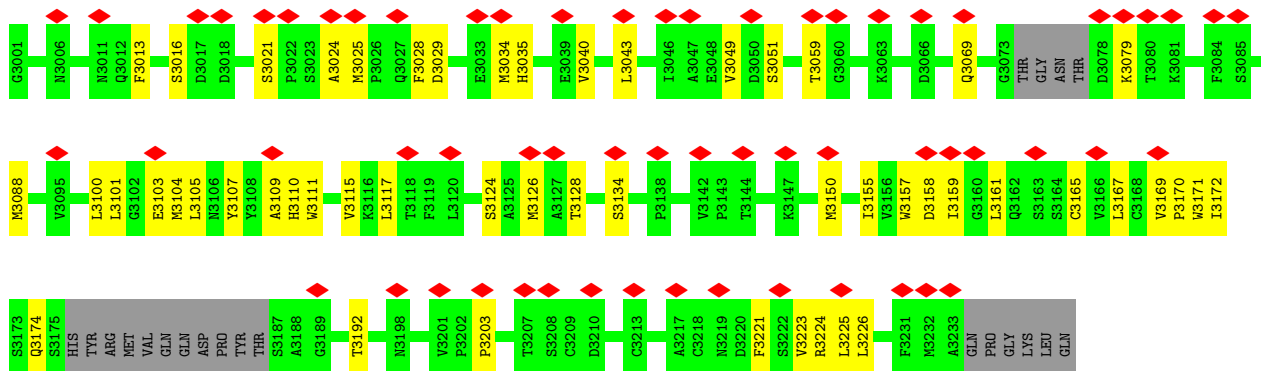


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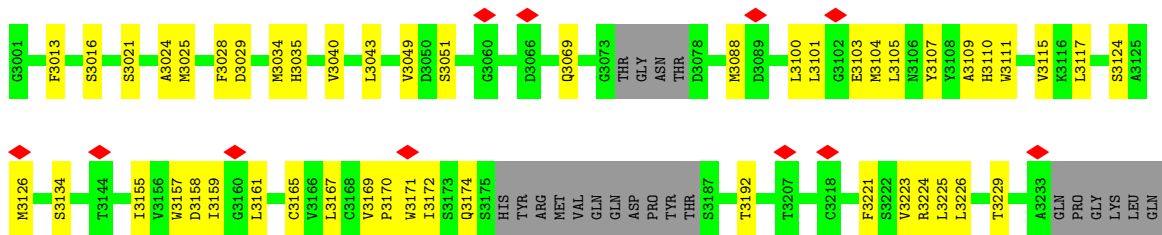
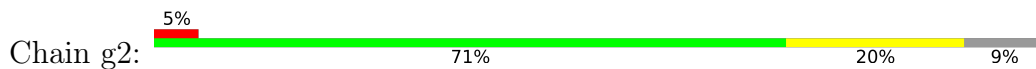




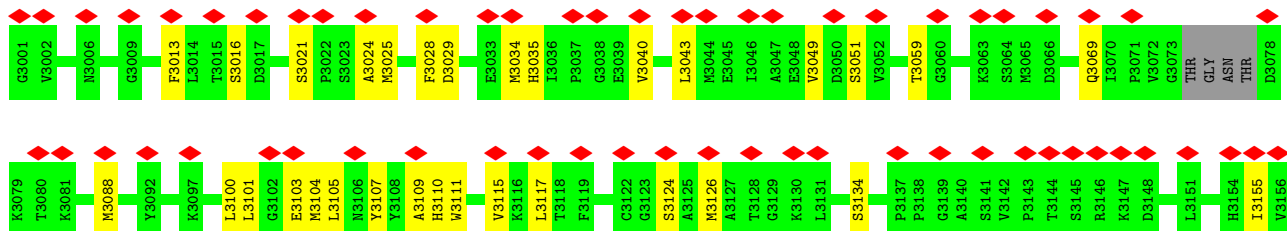
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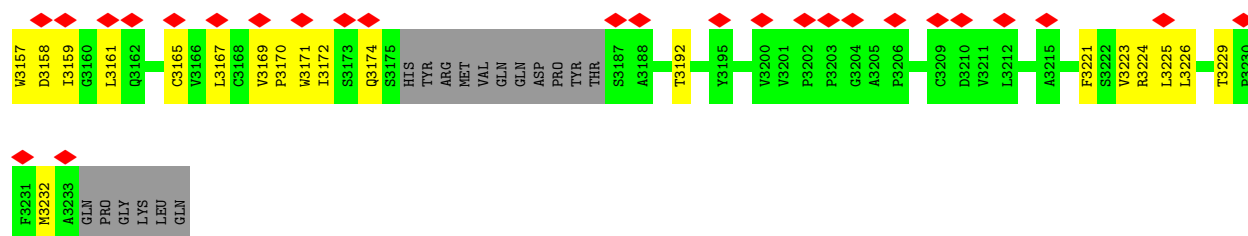


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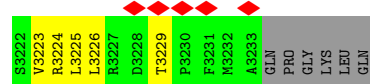
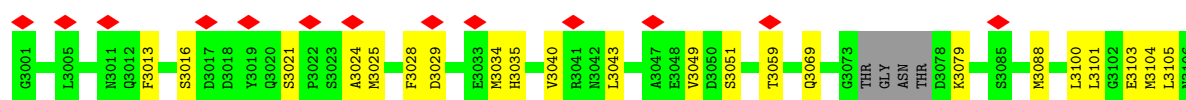


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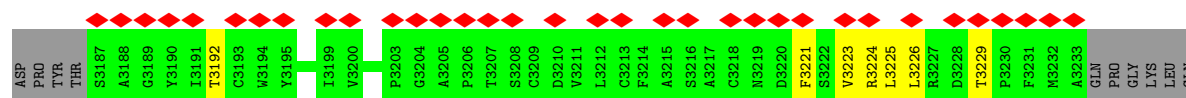
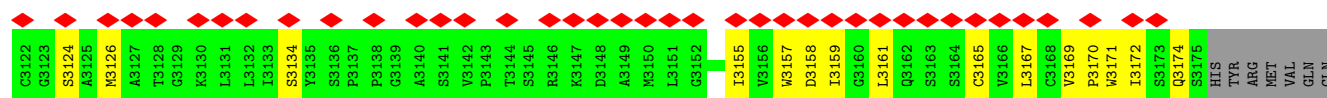
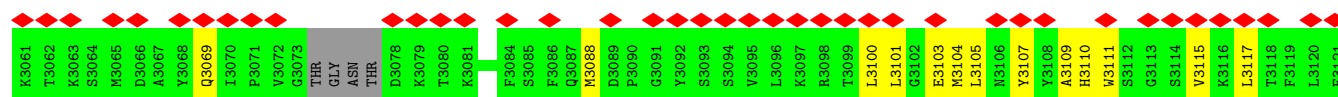
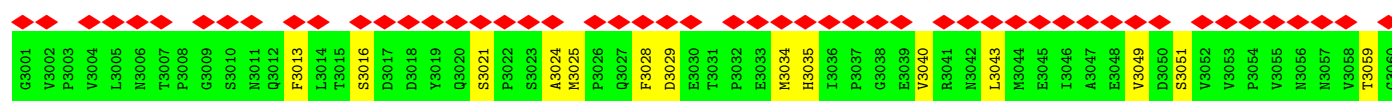
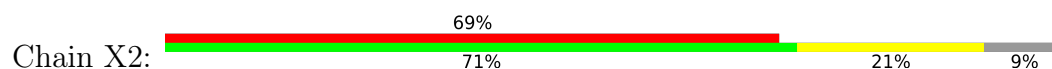




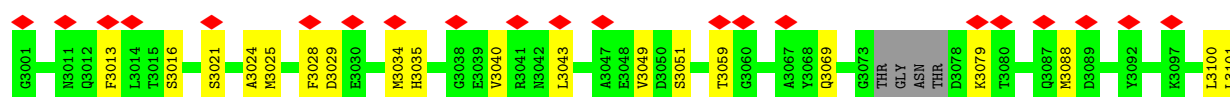
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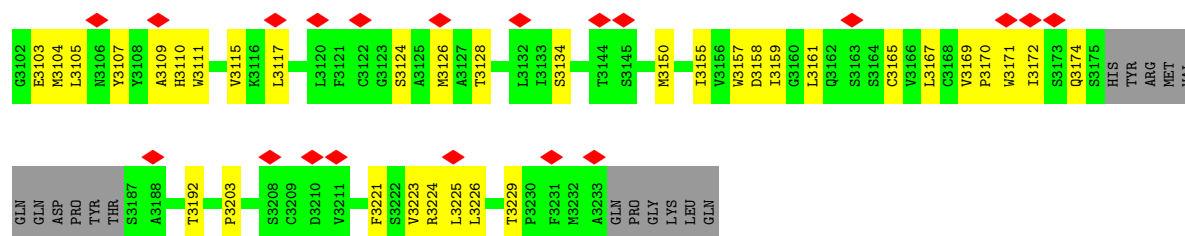


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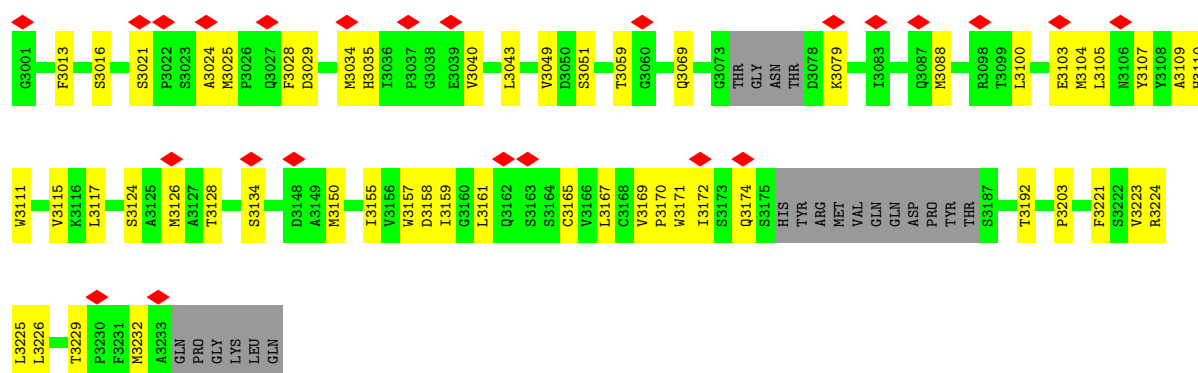


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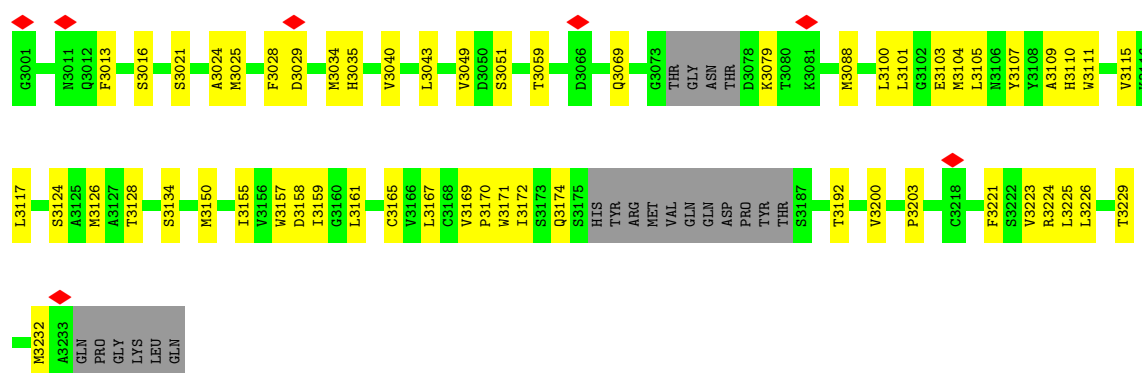




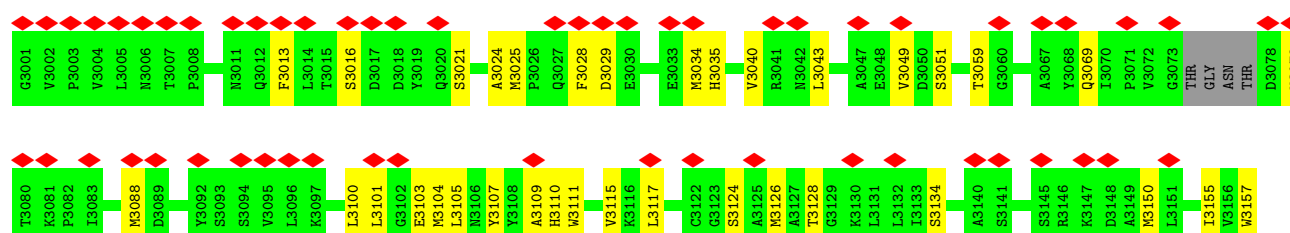
• Molecule 3: Echovirus 18 capsid protein 3

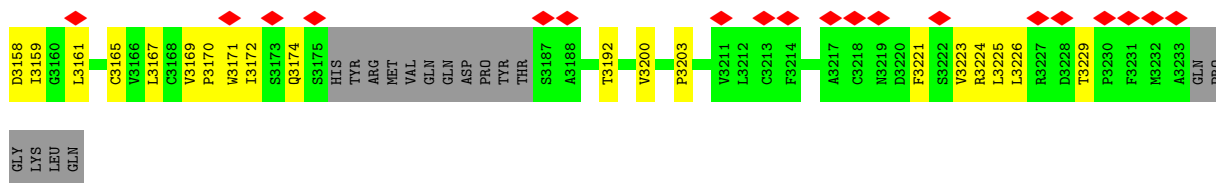


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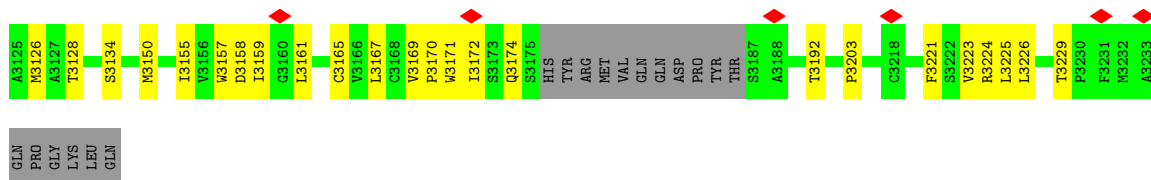
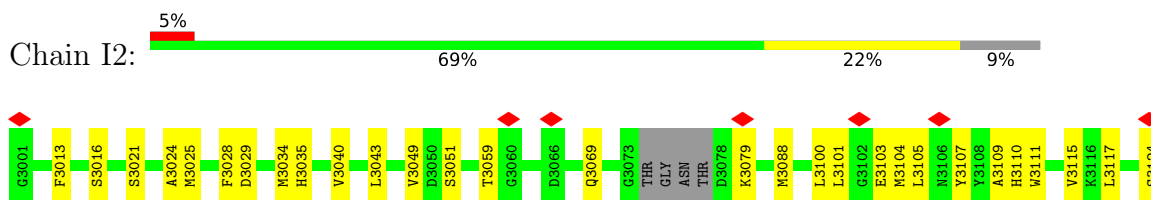


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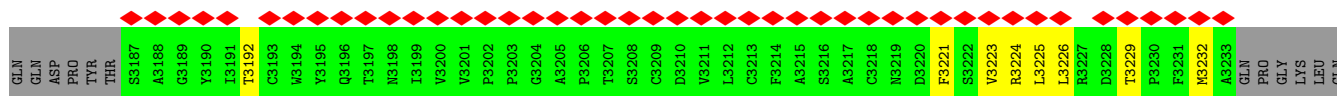
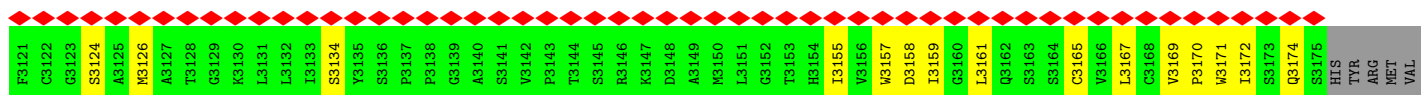
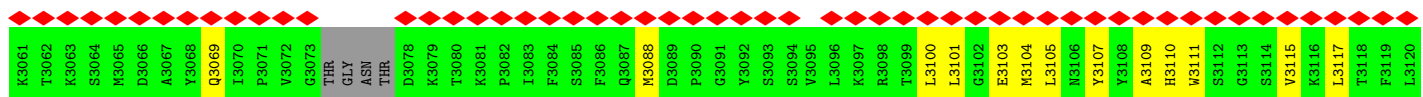
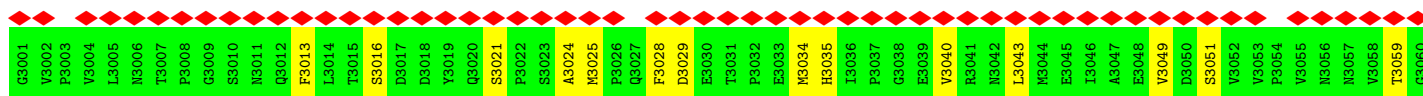
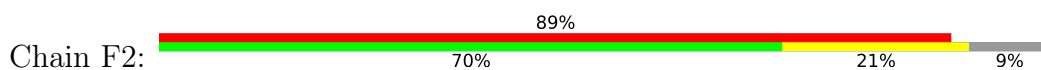




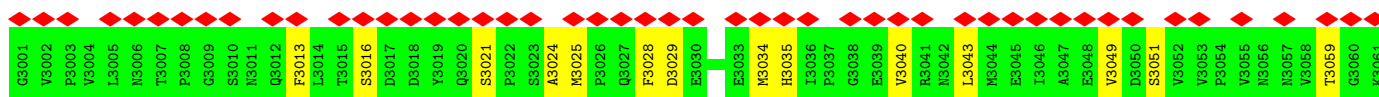
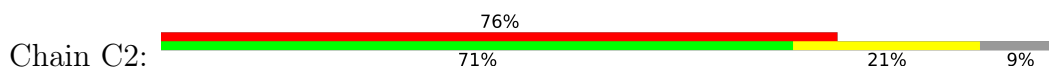
• Molecule 3: Echovirus 18 capsid protein 3



• Molecule 3: Echovirus 18 capsid protein 3



• Molecule 3: Echovirus 18 capsid protein 3



ASP	PRO	TYR	THR		G3123	G3124	G3125	G3126	G3127	G3128	G3129	G3130	G3131	G3132	G3133	G3134	G3135	G3136	G3137	G3138	G3139	G3140	G3141	G3142	G3143	G3144	G3145	G3146	G3147	G3148	G3149	G3150	G3151	G3152	G3153	G3154	G3155	G3156	G3157	G3158	G3159	G3160	G3161	G3162	G3163	G3164	G3165	G3166	G3167	G3168	G3169	G3170	G3171	G3172	G3173	G3174	G3175	G3176	G3177	G3178	G3179	G3180	G3181	G3182	G3183	G3184	G3185	G3186	G3187	G3188	G3189	G3190	G3191	G3192	G3193	G3194	G3195	G3196	G3197	G3198	G3199	G3200	G3201	G3202	G3203	G3204	G3205	G3206	G3207	G3208	G3209	G3210	G3211	G3212	G3213	G3214	G3215	G3216	G3217	G3218	G3219	G3220	G3221	G3222	G3223	G3224	G3225	G3226	G3227	G3228	G3229	G3230	G3231	G3232	G3233	G3234	G3235	G3236	G3237	G3238	G3239	G3240	G3241	G3242	G3243	G3244	G3245	G3246	G3247	G3248	G3249	G3250	G3251	G3252	G3253	G3254	G3255	G3256	G3257	G3258	G3259	G3260	G3261	G3262	G3263	G3264	G3265	G3266	G3267	G3268	G3269	G3270	G3271	G3272	G3273	G3274	G3275	G3276	G3277	G3278	G3279	G3280	G3281	G3282	G3283	G3284	G3285	G3286	G3287	G3288	G3289	G3290	G3291	G3292	G3293	G3294	G3295	G3296	G3297	G3298	G3299	G3300	G3301	G3302	G3303	G3304	G3305	G3306	G3307	G3308	G3309	G3310	G3311	G3312	G3313	G3314	G3315	G3316	G3317	G3318	G3319	G3320	G3321	G3322	G3323	G3324	G3325	G3326	G3327	G3328	G3329	G3330	G3331	G3332	G3333	G3334	G3335	G3336	G3337	G3338	G3339	G3340	G3341	G3342	G3343	G3344	G3345	G3346	G3347	G3348	G3349	G3350	G3351	G3352	G3353	G3354	G3355	G3356	G3357	G3358	G3359	G3360	G3361	G3362	G3363	G3364	G3365	G3366	G3367	G3368	G3369	G3370	G3371	G3372	G3373	G3374	G3375	G3376	G3377	G3378	G3379	G3380	G3381	G3382	G3383	G3384	G3385	G3386	G3387	G3388	G3389	G3390	G3391	G3392	G3393	G3394	G3395	G3396	G3397	G3398	G3399	G3400	G3401	G3402	G3403	G3404	G3405	G3406	G3407	G3408	G3409	G3410	G3411	G3412	G3413	G3414	G3415	G3416	G3417	G3418	G3419	G3420	G3421	G3422	G3423	G3424	G3425	G3426	G3427	G3428	G3429	G3430	G3431	G3432	G3433	G3434	G3435	G3436	G3437	G3438	G3439	G3440	G3441	G3442	G3443	G3444	G3445	G3446	G3447	G3448	G3449	G3450	G3451	G3452	G3453	G3454	G3455	G3456	G3457	G3458	G3459	G3460	G3461	G3462	G3463	G3464	G3465	G3466	G3467	G3468	G3469	G3470	G3471	G3472	G3473	G3474	G3475	G3476	G3477	G3478	G3479	G3480	G3481	G3482	G3483	G3484	G3485	G3486	G3487	G3488	G3489	G3490	G3491	G3492	G3493	G3494	G3495	G3496	G3497	G3498	G3499	G3500	G3501	G3502	G3503	G3504	G3505	G3506	G3507	G3508	G3509	G3510	G3511	G3512	G3513	G3514	G3515	G3516	G3517	G3518	G3519	G3520	G3521	G3522	G3523	G3524	G3525	G3526	G3527	G3528	G3529	G3530	G3531	G3532	G3533	G3534	G3535	G3536	G3537	G3538	G3539	G3540	G3541	G3542	G3543	G3544	G3545	G3546	G3547	G3548	G3549	G3550	G3551	G3552	G3553	G3554	G3555	G3556	G3557	G3558	G3559	G3560	G3561	G3562	G3563	G3564	G3565	G3566	G3567	G3568	G3569	G3570	G3571	G3572	G3573	G3574	G3575	G3576	G3577	G3578	G3579	G3580	G3581	G3582	G3583	G3584	G3585	G3586	G3587	G3588	G3589	G3590	G3591	G3592	G3593	G3594	G3595	G3596	G3597	G3598	G3599	G3600	G3601	G3602	G3603	G3604	G3605	G3606	G3607	G3608	G3609	G3610	G3611	G3612	G3613	G3614	G3615	G3616	G3617	G3618	G3619	G3620	G3621	G3622	G3623	G3624	G3625	G3626	G3627	G3628	G3629	G3630	G3631	G3632	G3633	G3634	G3635	G3636	G3637	G3638	G3639	G3640	G3641	G3642	G3643	G3644	G3645	G3646	G3647	G3648	G3649	G3650	G3651	G3652	G3653	G3654	G3655	G3656	G3657	G3658	G3659	G3660	G3661	G3662	G3663	G3664	G3665	G3666	G3667	G3668	G3669	G3670	G3671	G3672	G3673	G3674	G3675	G3676	G3677	G3678	G3679	G3680	G3681	G3682	G3683	G3684	G3685	G3686	G3687	G3688	G3689	G3690	G3691	G3692	G3693	G3694	G3695	G3696	G3697	G3698	G3699	G3700	G3701	G3702	G3703	G3704	G3705	G3706	G3707	G3708	G3709	G3710	G3711	G3712	G3713	G3714	G3715	G3716	G3717	G3718	G3719	G3720	G3721	G3722	G3723	G3724	G3725	G3726	G3727	G3728	G3729	G3730	G3731	G3732	G3733	G3734	G3735	G3736	G3737	G3738	G3739	G3740	G3741	G3742	G3743	G3744	G3745	G3746	G3747	G3748	G3749	G3750	G3751	G3752	G3753	G3754	G3755	G3756	G3757	G3758	G3759	G3760	G3761	G3762	G3763	G3764	G3765	G3766	G3767	G3768	G3769	G3770	G3771	G3772	G3773	G3774	G3775	G3776	G3777	G3778	G3779	G3780	G3781	G3782	G3783	G3784	G3785	G3786	G3787	G3788	G3789	G3790	G3791	G3792	G3793	G3794	G3795	G3796	G3797	G3798	G3799	G3800	G3801	G3802	G3803	G3804	G3805	G3806	G3807	G3808	G3809	G3810	G3811	G3812	G3813	G3814	G3815	G3816	G3817	G3818	G3819	G3820	G3821	G3822	G3823	G3824	G3825	G3826	G3827	G3828	G3829	G3830	G3831	G3832	G3833	G3834	G3835	G3836	G3837	G3838	G3839	G3840	G3841	G3842	G3843	G3844	G3845	G3846	G3847	G3848	G3849	G3850	G3851	G3852	G3853	G3854	G3855	G3856	G3857	G3858	G3859	G3860	G3861	G3862	G3863	G3864	G3865	G3866	G3867	G3868	G3869	G3870	G3871	G3872	G3873	G3874	G3875	G3876	G3877	G3878	G3879	G3880	G3881	G3882	G3883	G3884	G3885	G3886	G3887	G3888	G3889	G3890	G3891	G3892	G3893	G3894	G3895	G3896	G3897	G3898	G3899	G3900	G3901	G3902	G3903	G3904	G3905	G3906	G3907	G3908	G3909	G3910	G3911	G3912	G3913	G3914	G3915	G3916	G3917	G3918	G3919	G3920	G3921	G3922	G3923	G3924	G3925	G3926	G3927	G3928	G3929	G3930	G3931	G3932	G3933	G3934	G3935	G3936	G3937	G3938	G3939	G3940	G3941	G3942	G3943	G3944	G3945	G3946	G3947	G3948	G3949	G3950	G3951	G3952	G3953	G3954	G3955	G3956	G3957	G3958	G3959	G3960	G3961	G3962	G3963	G3964	G3965	G3966	G3967	G3968	G3969	G3970	G3971	G3972	G3973	G3974	G3975	G3976	G3977	G3978	G3979	G3980	G3981	G3982	G3983	G3984	G3985	G3986	G3987	G3988	G3989	G3990	G3991	G3992	G3993	G3994	G3995	G3996	G3997	G3998	G3999	G4000	G4001	G4002	G4003	G4004	G4005	G4006	G4007	G4008	G4009	G4010	G4011	G4012	G4013	G4014	G4015	G4016	G4017	G4018	G4019	G4020	G4021	G4022	G4023	G4024	G4025	G4026	G4027	G4028	G4029	G4030	G4031	G4032	G4033	G4034	G4035	G4036	G4037	G4038	G4039	G4040	G4041	G4042	G4043	G4044	G4045	G4046	G4047	G4048	G4049	G4050	G4051	G4052	G4053	G4054	G4055	G4056	G4057	G4058	G4059	G4060	G4061	G4062	G4063	G4064	G4065	G4066	G4067	G4068	G4069	G4070	G4071
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	7635	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.2	Depositor
Minimum defocus (nm)	651	Depositor
Maximum defocus (nm)	3282	Depositor
Magnification	79575	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.439	Depositor
Minimum map value	-0.251	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	371.35, 371.35, 371.35	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.061, 1.061, 1.061	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	A1	0.14	0/1791	0.38	0/2442
1	A2	0.14	0/1791	0.38	0/2442
1	D1	0.14	0/1791	0.38	0/2442
1	D2	0.14	0/1791	0.38	0/2442
1	G1	0.14	0/1791	0.38	0/2442
1	G2	0.14	0/1791	0.38	0/2442
1	J1	0.14	0/1791	0.38	0/2442
1	J2	0.14	0/1791	0.38	0/2442
1	M1	0.14	0/1791	0.38	0/2442
1	M2	0.14	0/1791	0.38	0/2442
1	P1	0.14	0/1791	0.38	0/2442
1	P2	0.14	0/1791	0.38	0/2442
1	S1	0.14	0/1791	0.38	0/2442
1	S2	0.14	0/1791	0.38	0/2442
1	V1	0.14	0/1791	0.38	0/2442
1	V2	0.14	0/1791	0.38	0/2442
1	Y2	0.14	0/1791	0.38	0/2442
1	b2	0.14	0/1791	0.38	0/2442
1	e2	0.14	0/1791	0.38	0/2442
1	h2	0.14	0/1791	0.38	0/2442
1	k2	0.14	0/1791	0.38	0/2442
1	n2	0.14	0/1791	0.38	0/2442
1	q2	0.14	0/1791	0.38	0/2442
1	t2	0.14	0/1791	0.38	0/2442
1	w2	0.14	0/1791	0.38	0/2442
2	B1	0.16	0/1874	0.46	2/2567 (0.1%)
2	B2	0.16	0/1874	0.46	0/2567
2	E1	0.16	0/1874	0.46	0/2567
2	E2	0.16	0/1874	0.46	2/2567 (0.1%)
2	H1	0.16	0/1874	0.46	2/2567 (0.1%)
2	H2	0.16	0/1874	0.46	0/2567
2	K1	0.16	0/1874	0.46	2/2567 (0.1%)
2	K2	0.16	0/1874	0.46	2/2567 (0.1%)
2	N1	0.16	0/1874	0.46	0/2567

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	N2	0.16	0/1874	0.46	2/2567 (0.1%)
2	Q1	0.16	0/1874	0.46	2/2567 (0.1%)
2	Q2	0.16	0/1874	0.46	2/2567 (0.1%)
2	T1	0.16	0/1874	0.46	2/2567 (0.1%)
2	T2	0.16	0/1874	0.46	2/2567 (0.1%)
2	W1	0.16	0/1874	0.46	0/2567
2	W2	0.16	0/1874	0.46	0/2567
2	Z2	0.16	0/1874	0.46	0/2567
2	c2	0.16	0/1874	0.46	0/2567
2	f2	0.16	0/1874	0.46	2/2567 (0.1%)
2	i2	0.16	0/1874	0.46	2/2567 (0.1%)
2	l2	0.16	0/1874	0.46	2/2567 (0.1%)
2	o2	0.16	0/1874	0.46	2/2567 (0.1%)
2	r2	0.16	0/1874	0.46	2/2567 (0.1%)
2	u2	0.16	0/1874	0.46	0/2567
2	x2	0.16	0/1874	0.46	2/2567 (0.1%)
3	C1	0.14	0/1676	0.36	0/2287
3	C2	0.14	0/1676	0.36	0/2287
3	F1	0.14	0/1676	0.36	0/2287
3	F2	0.14	0/1676	0.36	0/2287
3	I1	0.14	0/1676	0.36	0/2287
3	I2	0.14	0/1676	0.36	0/2287
3	L1	0.14	0/1676	0.36	0/2287
3	L2	0.14	0/1676	0.36	0/2287
3	O1	0.14	0/1676	0.36	0/2287
3	O2	0.14	0/1676	0.36	0/2287
3	R1	0.14	0/1676	0.36	0/2287
3	R2	0.14	0/1676	0.36	0/2287
3	U1	0.14	0/1676	0.36	0/2287
3	U2	0.14	0/1676	0.36	0/2287
3	X1	0.14	0/1676	0.36	0/2287
3	X2	0.14	0/1676	0.36	0/2287
3	a2	0.14	0/1676	0.36	0/2287
3	d2	0.14	0/1676	0.36	0/2287
3	g2	0.14	0/1676	0.36	0/2287
3	j2	0.14	0/1676	0.36	0/2287
3	m2	0.14	0/1676	0.36	0/2287
3	p2	0.14	0/1676	0.36	0/2287
3	s2	0.14	0/1676	0.36	0/2287
3	v2	0.14	0/1676	0.36	0/2287
3	y2	0.14	0/1676	0.36	0/2287
All	All	0.15	0/133525	0.41	32/182400 (0.0%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	i2	2137	THR	CA-C-N	5.03	131.15	121.54
2	i2	2137	THR	C-N-CA	5.03	131.15	121.54
2	E2	2137	THR	CA-C-N	5.03	131.14	121.54
2	E2	2137	THR	C-N-CA	5.03	131.14	121.54
2	K2	2137	THR	CA-C-N	5.02	131.14	121.54

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	A1	1741	0	1659	49	0
1	A2	1741	0	1659	49	0
1	D1	1741	0	1659	48	0
1	D2	1741	0	1659	50	0
1	G1	1741	0	1659	49	0
1	G2	1741	0	1659	47	0
1	J1	1741	0	1659	47	0
1	J2	1741	0	1659	47	0
1	M1	1741	0	1659	48	0
1	M2	1741	0	1659	49	0
1	P1	1741	0	1659	49	0
1	P2	1741	0	1659	48	0
1	S1	1741	0	1659	47	0
1	S2	1741	0	1659	49	0
1	V1	1741	0	1659	48	0
1	V2	1741	0	1659	49	0
1	Y2	1741	0	1659	50	0
1	b2	1741	0	1659	49	0
1	e2	1741	0	1659	49	0
1	h2	1741	0	1659	48	0
1	k2	1741	0	1659	48	0
1	n2	1741	0	1659	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	q2	1741	0	1659	48	0
1	t2	1741	0	1659	47	0
1	w2	1741	0	1659	51	0
2	B1	1821	0	1739	45	0
2	B2	1821	0	1739	55	0
2	E1	1821	0	1739	47	0
2	E2	1821	0	1739	47	0
2	H1	1821	0	1739	57	0
2	H2	1821	0	1739	49	0
2	K1	1821	0	1739	47	0
2	K2	1821	0	1739	46	0
2	N1	1821	0	1739	48	0
2	N2	1821	0	1739	55	0
2	Q1	1821	0	1739	55	0
2	Q2	1821	0	1739	55	0
2	T1	1821	0	1739	55	0
2	T2	1821	0	1739	58	0
2	W1	1821	0	1739	57	0
2	W2	1821	0	1739	47	0
2	Z2	1821	0	1739	58	0
2	c2	1821	0	1739	58	0
2	f2	1821	0	1739	47	0
2	i2	1821	0	1739	46	0
2	l2	1821	0	1739	46	0
2	o2	1821	0	1739	58	0
2	r2	1821	0	1739	51	0
2	u2	1821	0	1739	54	0
2	x2	1821	0	1739	47	0
3	C1	1634	0	1596	53	0
3	C2	1634	0	1596	52	0
3	F1	1634	0	1596	60	0
3	F2	1634	0	1596	53	0
3	I1	1634	0	1596	58	0
3	I2	1634	0	1596	58	0
3	L1	1634	0	1596	52	0
3	L2	1634	0	1596	59	0
3	O1	1634	0	1596	51	0
3	O2	1634	0	1596	60	0
3	R1	1634	0	1596	58	0
3	R2	1634	0	1596	59	0
3	U1	1634	0	1596	52	0
3	U2	1634	0	1596	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	X1	1634	0	1596	54	0
3	X2	1634	0	1596	52	0
3	a2	1634	0	1596	58	0
3	d2	1634	0	1596	53	0
3	g2	1634	0	1596	51	0
3	j2	1634	0	1596	57	0
3	m2	1634	0	1596	58	0
3	p2	1634	0	1596	53	0
3	s2	1634	0	1596	60	0
3	v2	1634	0	1596	52	0
3	y2	1634	0	1596	51	0
All	All	129900	0	124850	2889	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 11.

The worst 5 of 2889 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:k2:1216:ILE:HD13	1:k2:1231:ILE:HD13	1.56	0.88
1:J1:1216:ILE:HD13	1:J1:1231:ILE:HD13	1.56	0.88
1:b2:1216:ILE:HD13	1:b2:1231:ILE:HD13	1.56	0.88
1:n2:1216:ILE:HD13	1:n2:1231:ILE:HD13	1.56	0.87
1:S1:1216:ILE:HD13	1:S1:1231:ILE:HD13	1.56	0.87

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	A1	220/287 (77%)	200 (91%)	20 (9%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	D1	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	D2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	G1	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	G2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	J1	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	J2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	M1	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	M2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	P1	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	P2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	S1	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	S2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	V1	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	V2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	Y2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	b2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	e2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	h2	220/287 (77%)	199 (90%)	21 (10%)	0	100	100
1	k2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	n2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	q2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	t2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
1	w2	220/287 (77%)	200 (91%)	20 (9%)	0	100	100
2	B1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	B2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	E1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	E2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	H1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	H2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	K1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	N1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	N2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	Q1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	Q2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	T1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	T2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	W1	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	W2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	Z2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	c2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	f2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	i2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	l2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	o2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	r2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	u2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
2	x2	232/260 (89%)	204 (88%)	25 (11%)	3 (1%)	9	41
3	C1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	C2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	F1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	F2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	I1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	I2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	L1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	L2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	O1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	O2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	R1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	R2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	U1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	U2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	X1	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	X2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	a2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	d2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	g2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	j2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	m2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	p2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	s2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	v2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
3	y2	212/239 (89%)	197 (93%)	15 (7%)	0	100	100
All	All	16600/19650 (84%)	15015 (90%)	1510 (9%)	75 (0%)	26	61

5 of 75 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	W1	2060	THR
2	W1	2149	GLU
2	T1	2060	THR
2	T1	2149	GLU
2	Q1	2060	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	182/259 (70%)	182 (100%)	0	100	100
1	A2	182/259 (70%)	182 (100%)	0	100	100
1	D1	182/259 (70%)	182 (100%)	0	100	100
1	D2	182/259 (70%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G1	182/259 (70%)	182 (100%)	0	100	100
1	G2	182/259 (70%)	182 (100%)	0	100	100
1	J1	182/259 (70%)	182 (100%)	0	100	100
1	J2	182/259 (70%)	182 (100%)	0	100	100
1	M1	182/259 (70%)	182 (100%)	0	100	100
1	M2	182/259 (70%)	182 (100%)	0	100	100
1	P1	182/259 (70%)	182 (100%)	0	100	100
1	P2	182/259 (70%)	182 (100%)	0	100	100
1	S1	182/259 (70%)	182 (100%)	0	100	100
1	S2	182/259 (70%)	182 (100%)	0	100	100
1	V1	182/259 (70%)	182 (100%)	0	100	100
1	V2	182/259 (70%)	182 (100%)	0	100	100
1	Y2	182/259 (70%)	182 (100%)	0	100	100
1	b2	182/259 (70%)	182 (100%)	0	100	100
1	e2	182/259 (70%)	182 (100%)	0	100	100
1	h2	182/259 (70%)	182 (100%)	0	100	100
1	k2	182/259 (70%)	182 (100%)	0	100	100
1	n2	182/259 (70%)	182 (100%)	0	100	100
1	q2	182/259 (70%)	182 (100%)	0	100	100
1	t2	182/259 (70%)	182 (100%)	0	100	100
1	w2	182/259 (70%)	182 (100%)	0	100	100
2	B1	193/221 (87%)	193 (100%)	0	100	100
2	B2	193/221 (87%)	193 (100%)	0	100	100
2	E1	193/221 (87%)	193 (100%)	0	100	100
2	E2	193/221 (87%)	193 (100%)	0	100	100
2	H1	193/221 (87%)	193 (100%)	0	100	100
2	H2	193/221 (87%)	193 (100%)	0	100	100
2	K1	193/221 (87%)	193 (100%)	0	100	100
2	K2	193/221 (87%)	193 (100%)	0	100	100
2	N1	193/221 (87%)	193 (100%)	0	100	100
2	N2	193/221 (87%)	193 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Q1	193/221 (87%)	193 (100%)	0	100	100
2	Q2	193/221 (87%)	193 (100%)	0	100	100
2	T1	193/221 (87%)	193 (100%)	0	100	100
2	T2	193/221 (87%)	193 (100%)	0	100	100
2	W1	193/221 (87%)	193 (100%)	0	100	100
2	W2	193/221 (87%)	193 (100%)	0	100	100
2	Z2	193/221 (87%)	193 (100%)	0	100	100
2	c2	193/221 (87%)	193 (100%)	0	100	100
2	f2	193/221 (87%)	193 (100%)	0	100	100
2	i2	193/221 (87%)	193 (100%)	0	100	100
2	l2	193/221 (87%)	193 (100%)	0	100	100
2	o2	193/221 (87%)	193 (100%)	0	100	100
2	r2	193/221 (87%)	193 (100%)	0	100	100
2	u2	193/221 (87%)	193 (100%)	0	100	100
2	x2	193/221 (87%)	193 (100%)	0	100	100
3	C1	184/209 (88%)	184 (100%)	0	100	100
3	C2	184/209 (88%)	184 (100%)	0	100	100
3	F1	184/209 (88%)	184 (100%)	0	100	100
3	F2	184/209 (88%)	184 (100%)	0	100	100
3	I1	184/209 (88%)	184 (100%)	0	100	100
3	I2	184/209 (88%)	184 (100%)	0	100	100
3	L1	184/209 (88%)	184 (100%)	0	100	100
3	L2	184/209 (88%)	184 (100%)	0	100	100
3	O1	184/209 (88%)	184 (100%)	0	100	100
3	O2	184/209 (88%)	184 (100%)	0	100	100
3	R1	184/209 (88%)	184 (100%)	0	100	100
3	R2	184/209 (88%)	184 (100%)	0	100	100
3	U1	184/209 (88%)	184 (100%)	0	100	100
3	U2	184/209 (88%)	184 (100%)	0	100	100
3	X1	184/209 (88%)	184 (100%)	0	100	100
3	X2	184/209 (88%)	184 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	a2	184/209 (88%)	184 (100%)	0	100	100
3	d2	184/209 (88%)	184 (100%)	0	100	100
3	g2	184/209 (88%)	184 (100%)	0	100	100
3	j2	184/209 (88%)	184 (100%)	0	100	100
3	m2	184/209 (88%)	184 (100%)	0	100	100
3	p2	184/209 (88%)	184 (100%)	0	100	100
3	s2	184/209 (88%)	184 (100%)	0	100	100
3	v2	184/209 (88%)	184 (100%)	0	100	100
3	y2	184/209 (88%)	184 (100%)	0	100	100
All	All	13975/17225 (81%)	13975 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
3	g2	3110	HIS
2	T2	2094	GLN
2	c2	2094	GLN
2	Z2	2187	GLN
2	Q2	2052	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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.

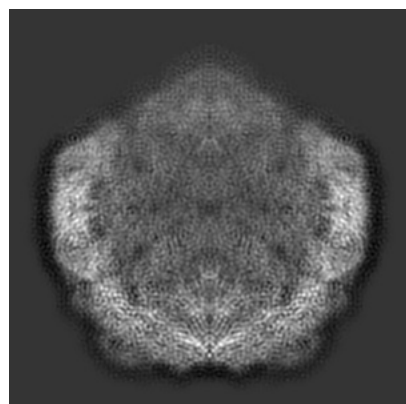
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0217. These allow visual inspection of the internal detail of the map and identification of artifacts.

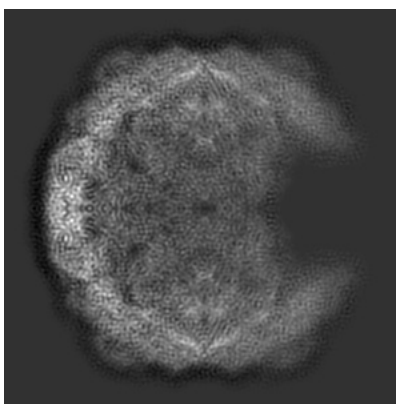
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

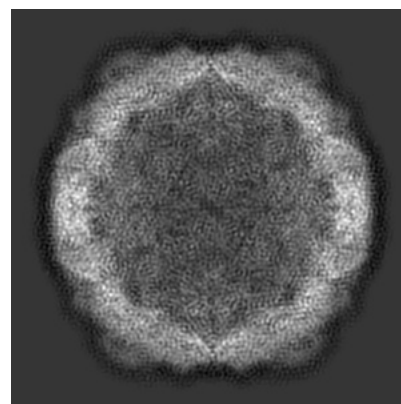
6.1.1 Primary map



X

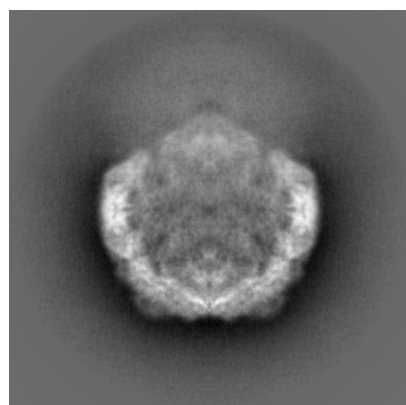


Y

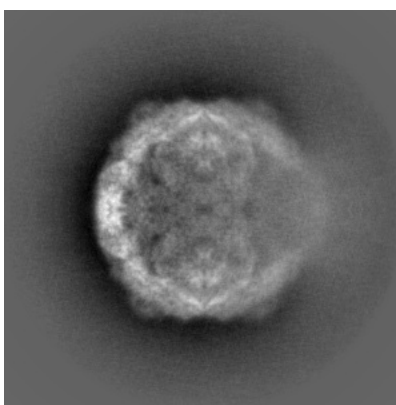


Z

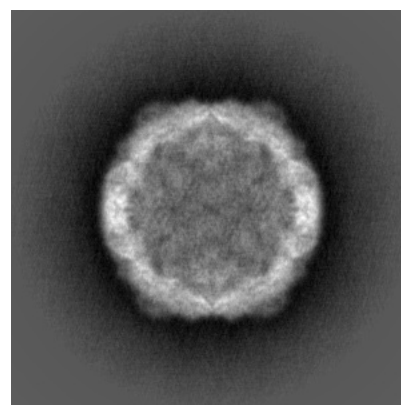
6.1.2 Raw map



X



Y



Z

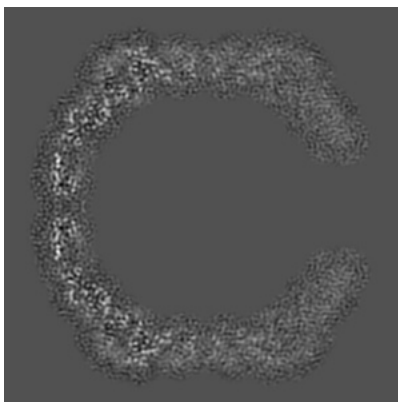
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

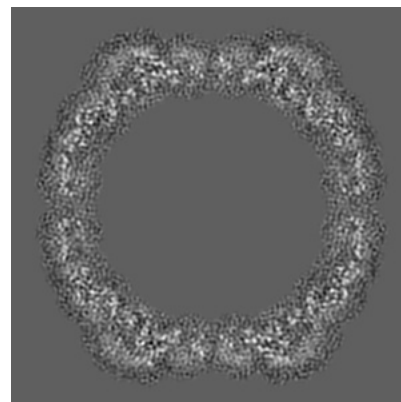
6.2.1 Primary map



X Index: 175

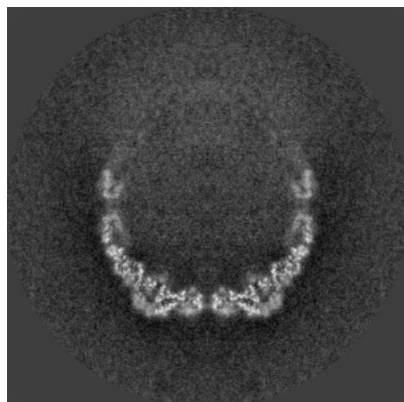


Y Index: 175

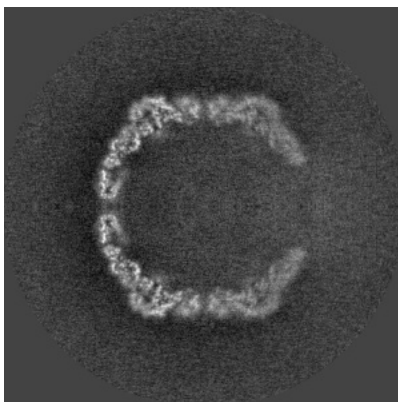


Z Index: 175

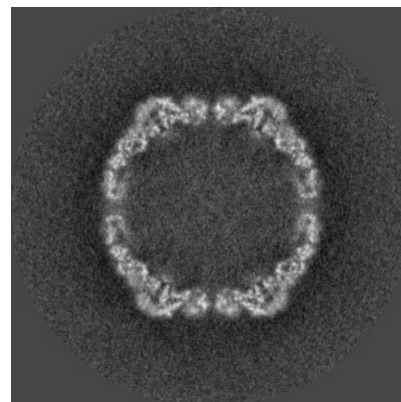
6.2.2 Raw map



X Index: 256



Y Index: 256

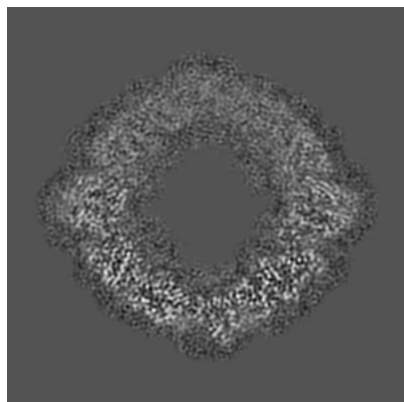


Z Index: 256

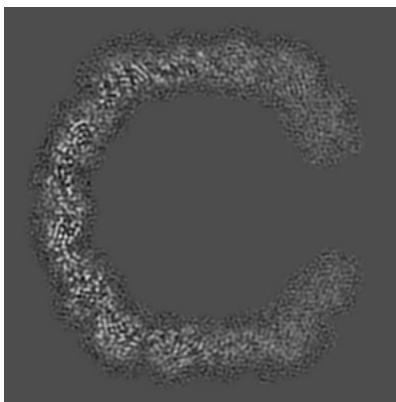
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

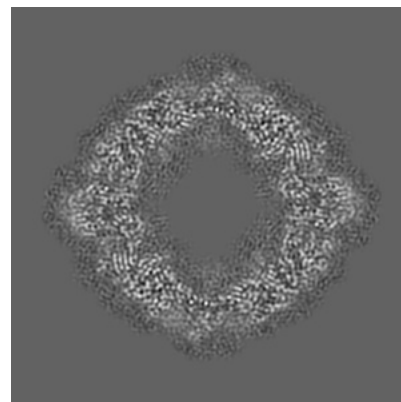
6.3.1 Primary map



X Index: 263

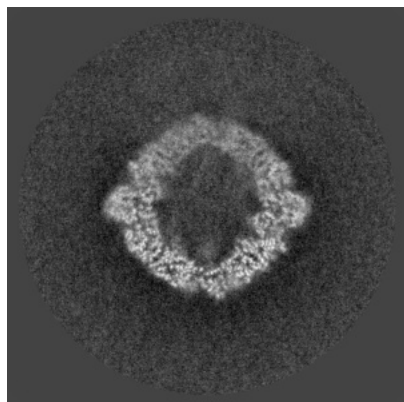


Y Index: 159

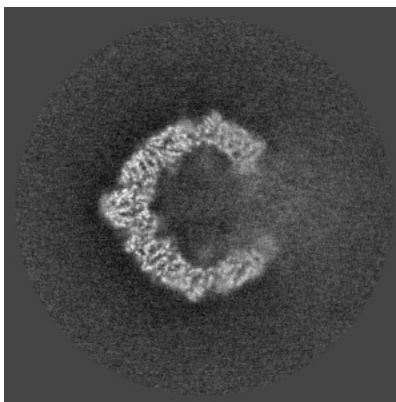


Z Index: 85

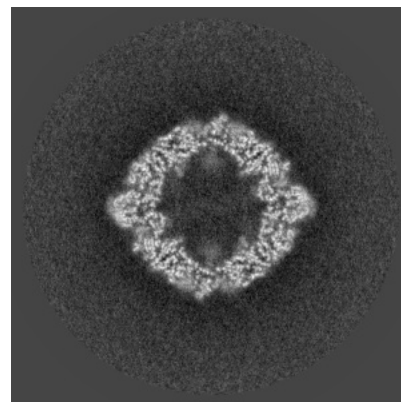
6.3.2 Raw map



X Index: 346



Y Index: 168

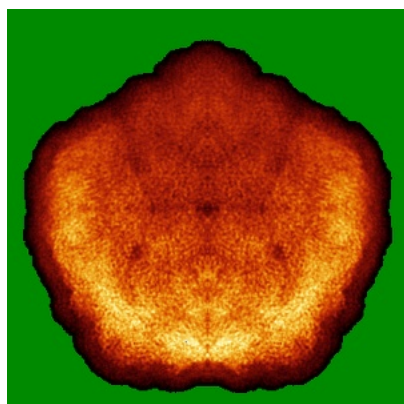


Z Index: 166

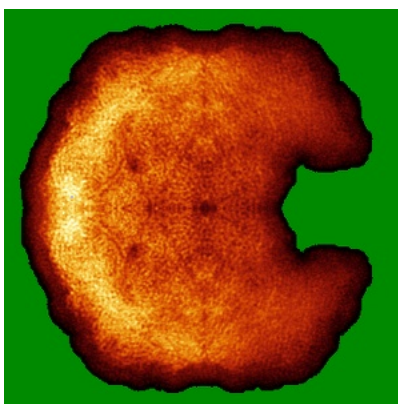
The images above show the largest variance slices of the map in three orthogonal directions.

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

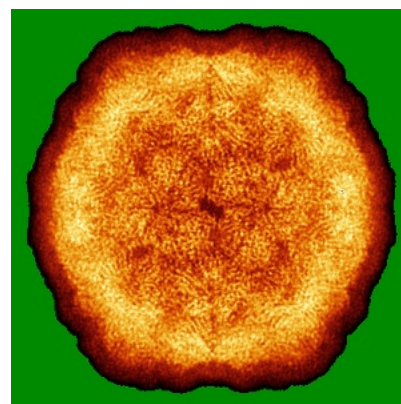
6.4.1 Primary map



X

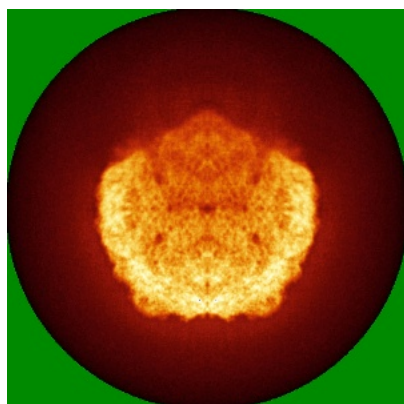


Y

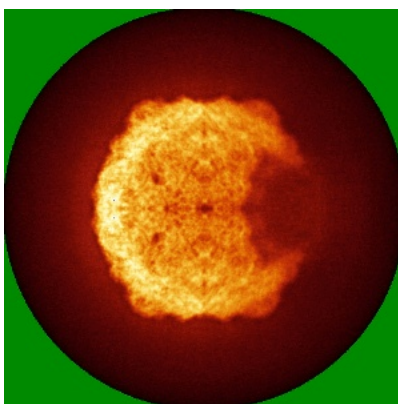


Z

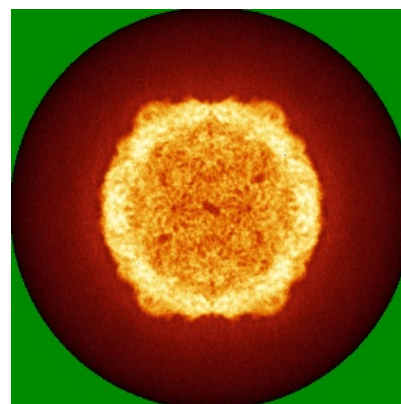
6.4.2 Raw map



X



Y

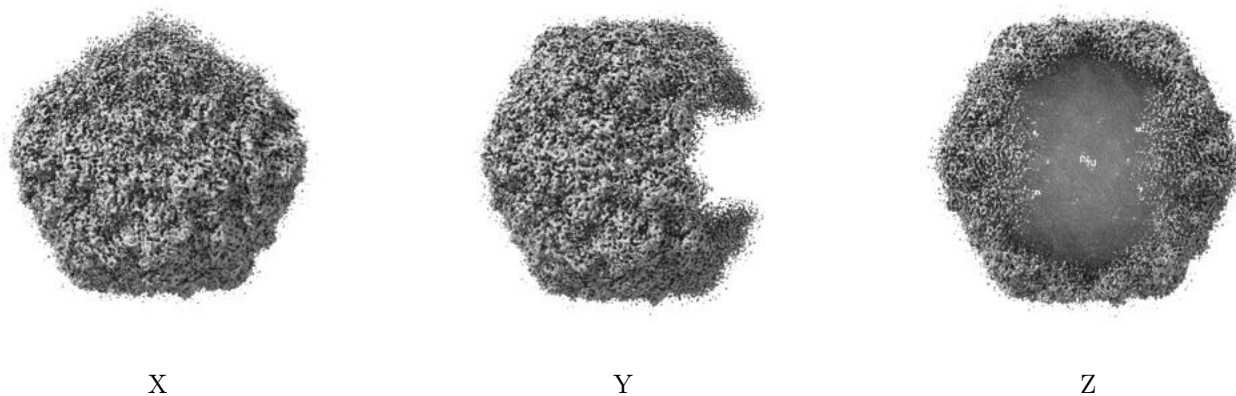


Z

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.

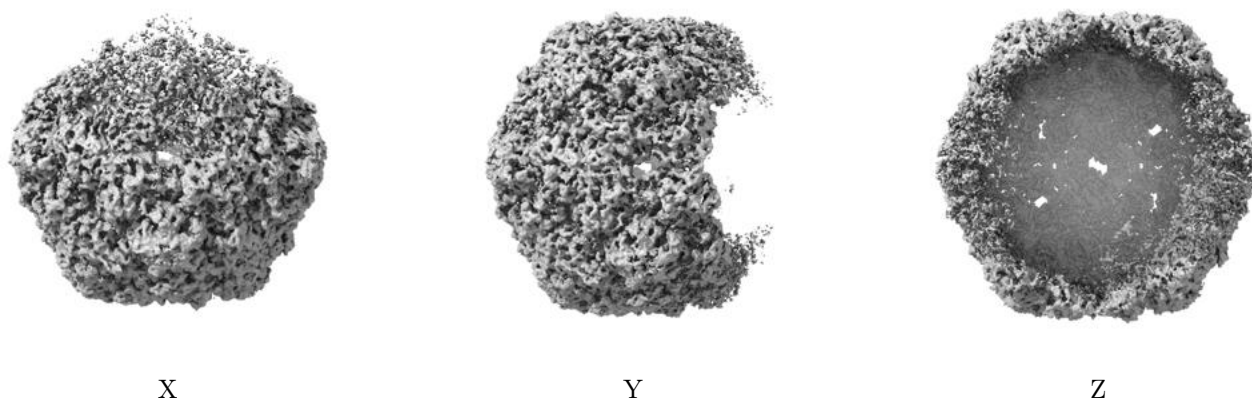
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

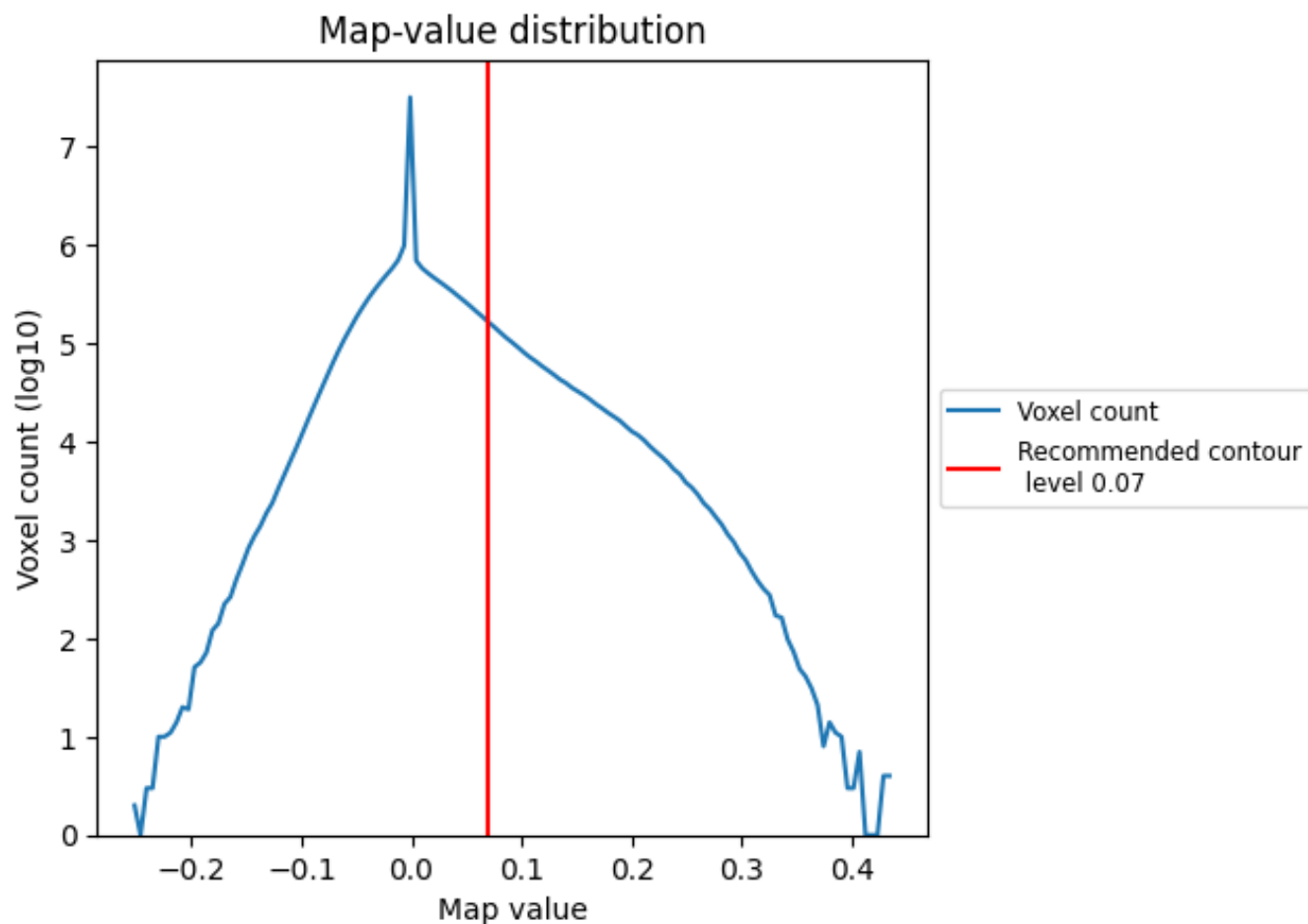
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

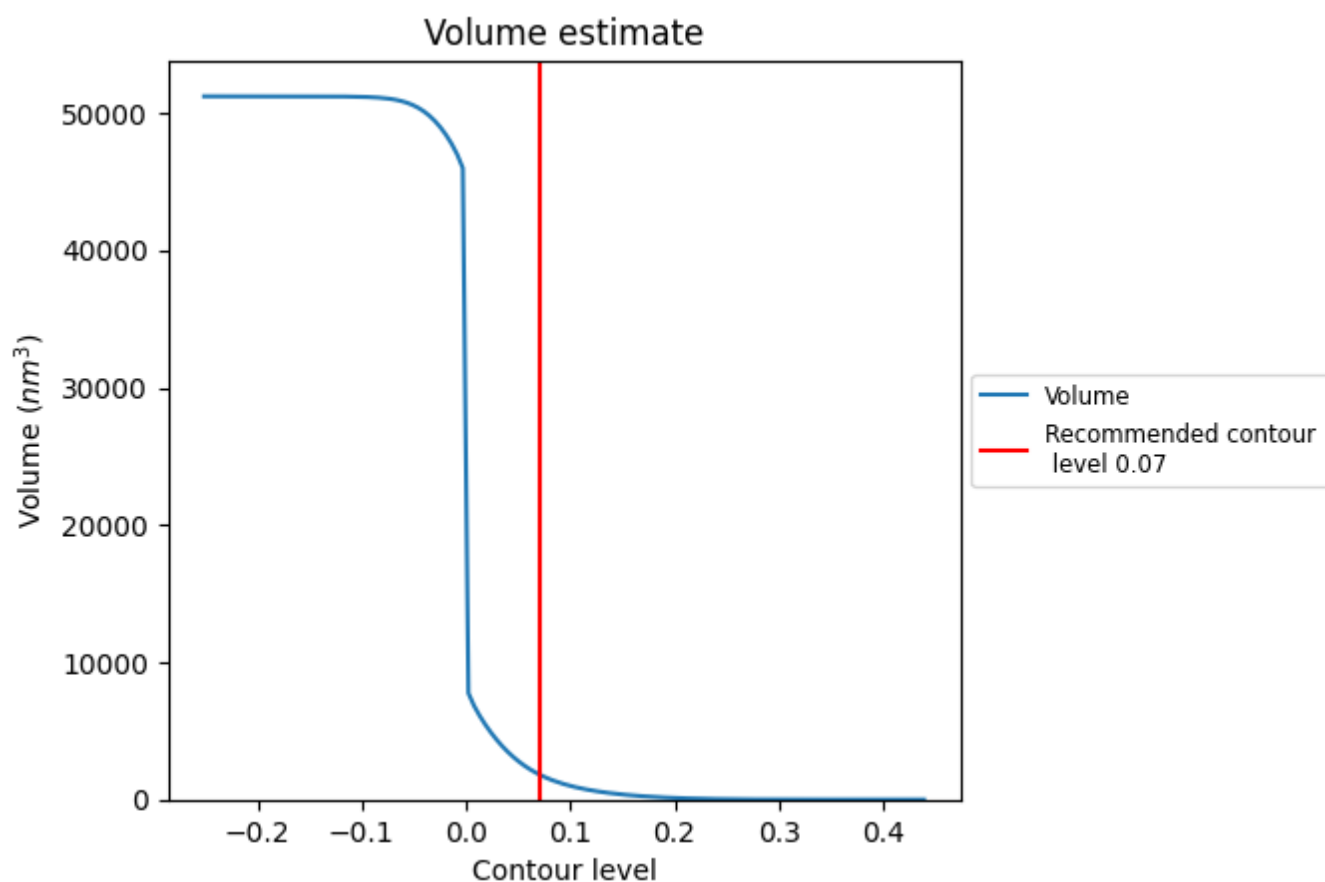
This section contains the results of statistical analysis of the map.

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.

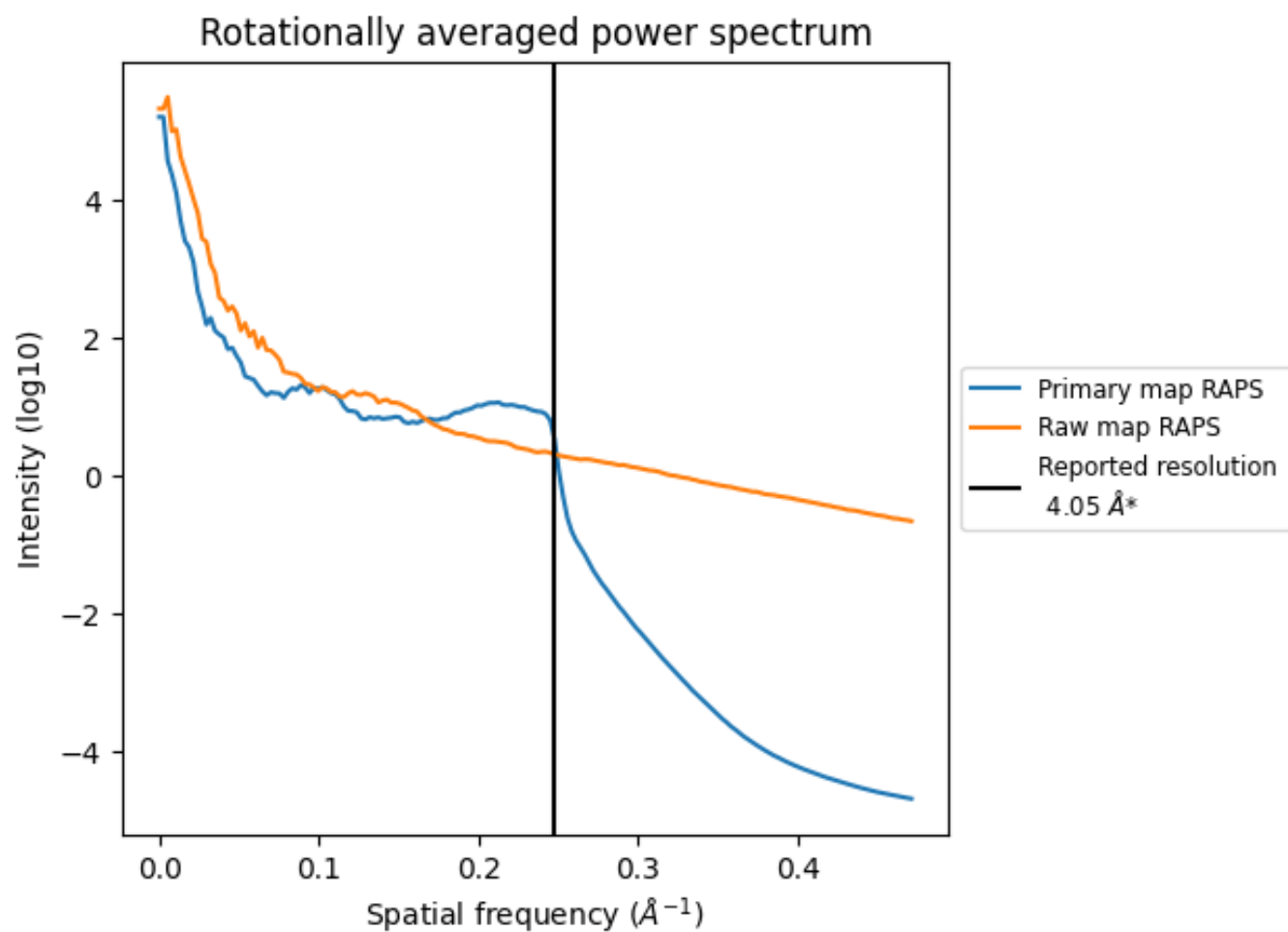
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1838 nm³; this corresponds to an approximate mass of 1661 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 ⓘ

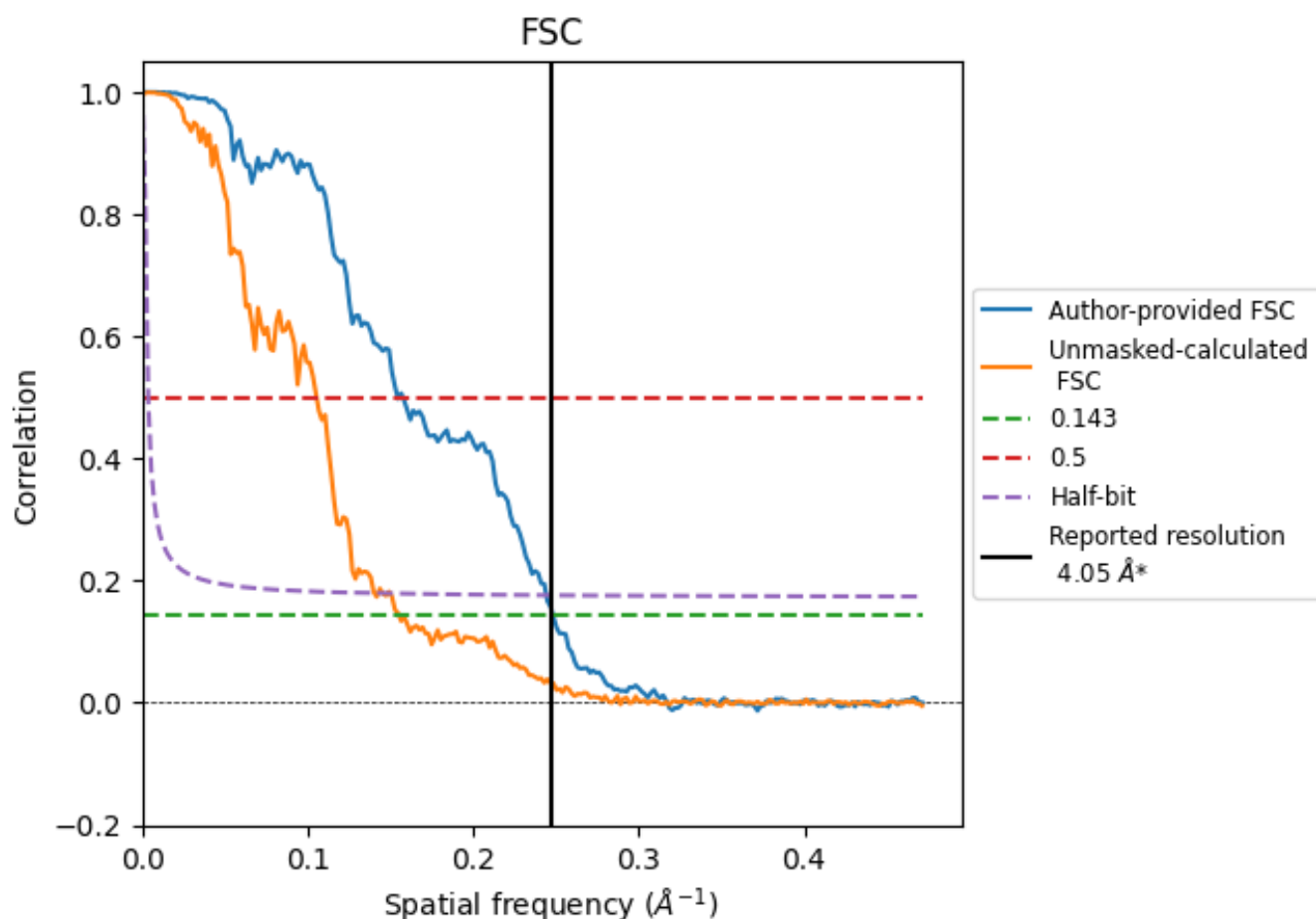


*Reported resolution corresponds to spatial frequency of 0.247 $\text{\AA}^{-1}$

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 $0.247 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.05	-	-
Author-provided FSC curve	4.03	6.48	4.10
Unmasked-calculated*	6.44	9.49	7.13

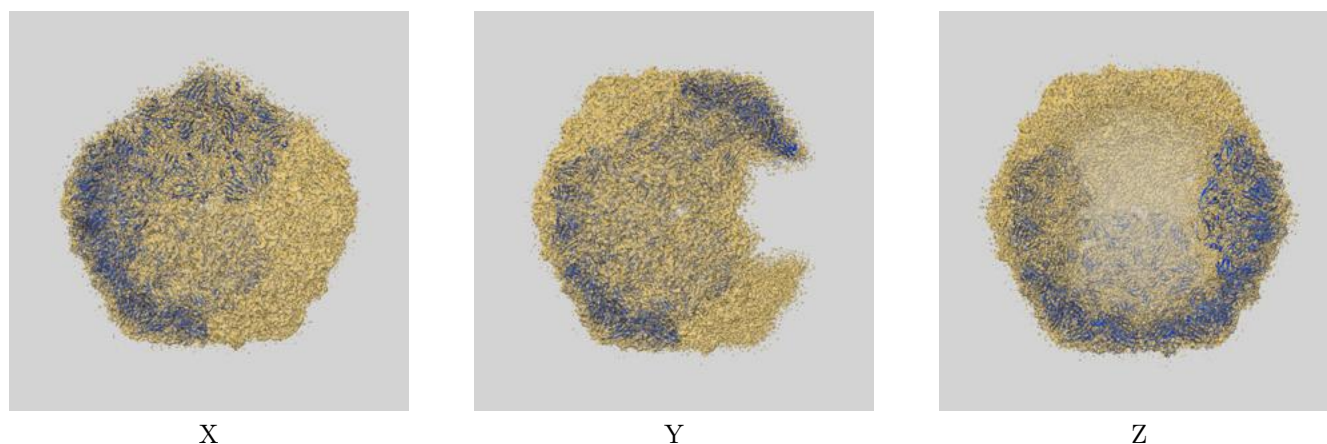
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.44 differs from the reported value 4.05 by more than 10 %

9 Map-model fit ⓘ

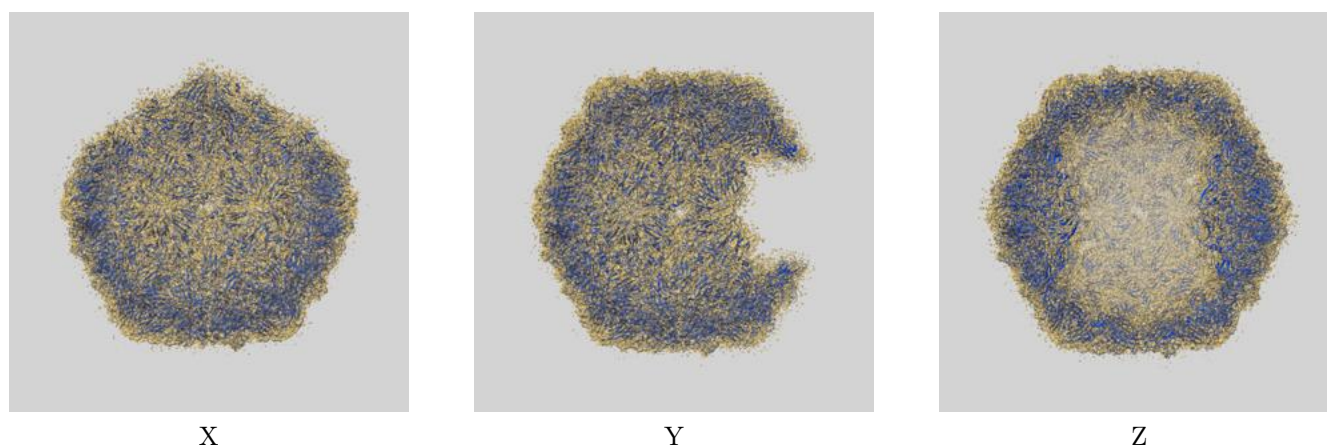
This section contains information regarding the fit between EMDB map EMD-0217 and PDB model 6HHT. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlays

9.1.1 Map-model overlay ⓘ

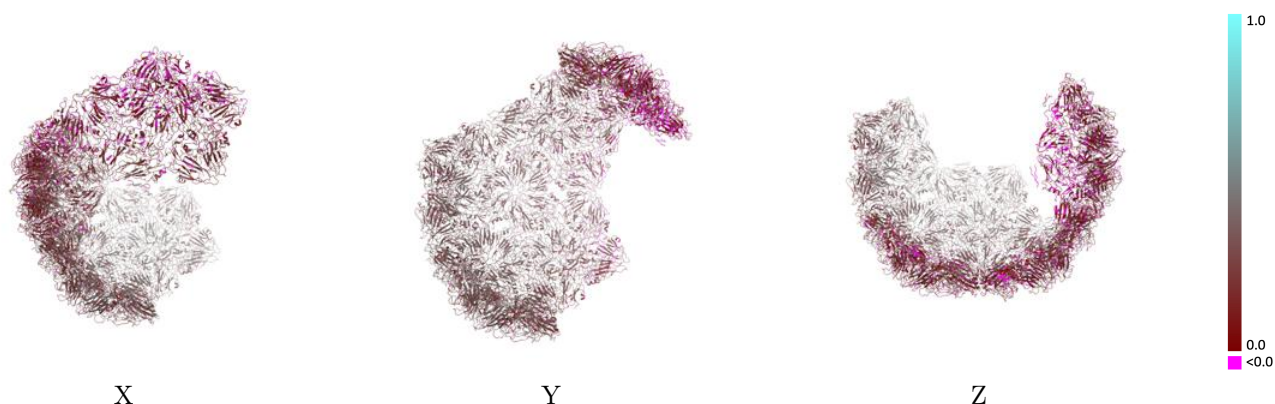


9.1.2 Map-model assembly overlay ⓘ



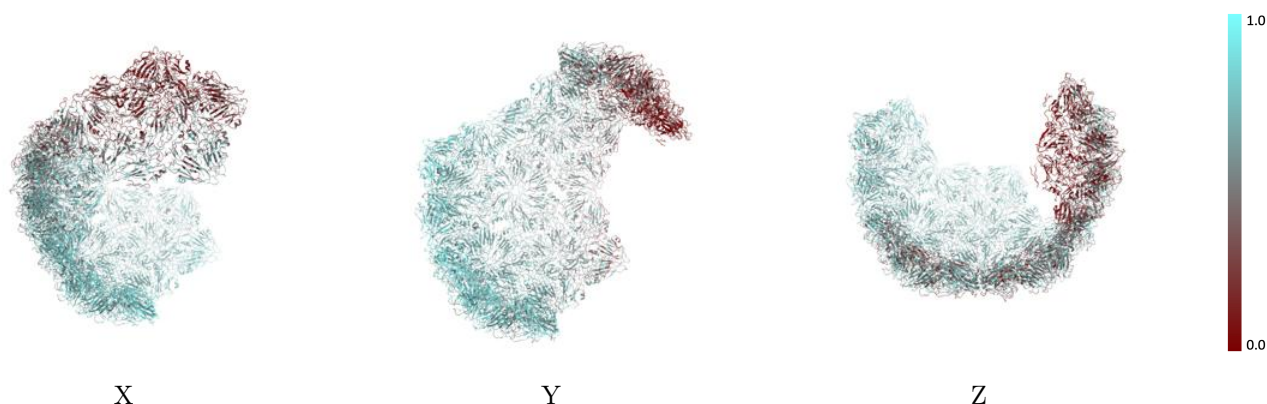
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



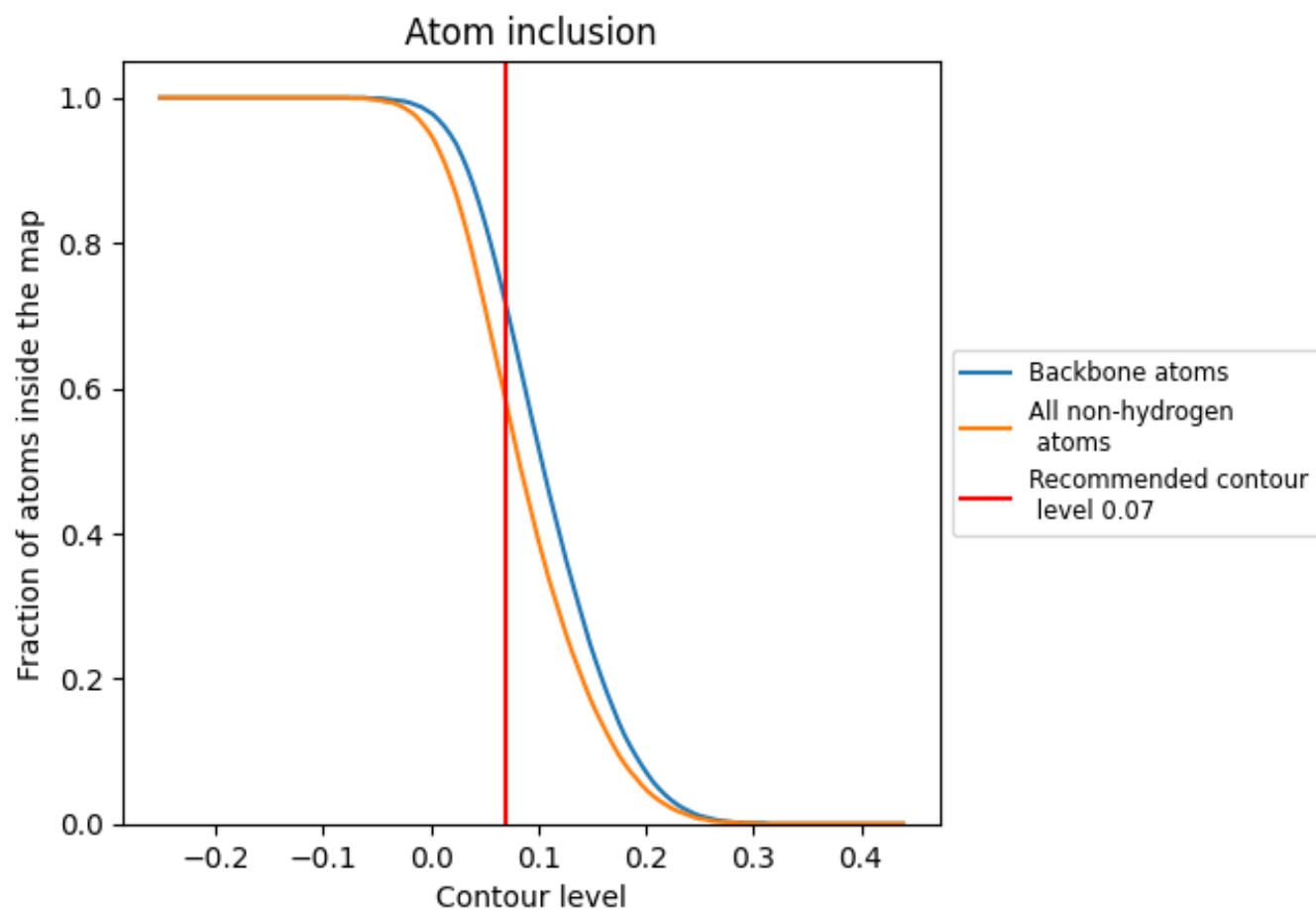
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 72% of all backbone atoms, 58% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5810	 0.2530
A1	 0.5440	 0.2090
A2	 0.2680	 0.1100
B1	 0.4540	 0.1680
B2	 0.3070	 0.1490
C1	 0.4330	 0.1480
C2	 0.2250	 0.1140
D1	 0.7300	 0.3280
D2	 0.2160	 0.0950
E1	 0.7430	 0.3340
E2	 0.1210	 0.0750
F1	 0.7400	 0.3420
F2	 0.1110	 0.0810
G1	 0.7340	 0.3220
G2	 0.7010	 0.3370
H1	 0.7250	 0.3350
H2	 0.6630	 0.3120
I1	 0.7280	 0.3200
I2	 0.6930	 0.3360
J1	 0.3970	 0.1770
J2	 0.4010	 0.1810
K1	 0.4980	 0.2370
K2	 0.5070	 0.2400
L1	 0.4790	 0.2390
L2	 0.4780	 0.2150
M1	 0.7410	 0.3260
M2	 0.7280	 0.3520
N1	 0.7340	 0.3380
N2	 0.7200	 0.3360
O1	 0.7540	 0.3440
O2	 0.7200	 0.3390
P1	 0.7170	 0.3070
P2	 0.5980	 0.2290
Q1	 0.6790	 0.2690
Q2	 0.5950	 0.2260



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Chain	Atom inclusion	Q-score
R1	 0.6890	 0.2900
R2	 0.6350	 0.2440
S1	 0.6190	 0.2430
S2	 0.6230	 0.2380
T1	 0.5830	 0.2580
T2	 0.6240	 0.2460
U1	 0.6400	 0.2730
U2	 0.5800	 0.2150
V1	 0.7100	 0.3080
V2	 0.2580	 0.1220
W1	 0.6990	 0.3020
W2	 0.1780	 0.0930
X1	 0.7100	 0.3290
X2	 0.2720	 0.1550
Y2	 0.6610	 0.2660
Z2	 0.6820	 0.2930
a2	 0.6610	 0.2980
b2	 0.5460	 0.1820
c2	 0.4920	 0.1700
d2	 0.4770	 0.1500
e2	 0.7040	 0.3350
f2	 0.6840	 0.3200
g2	 0.6840	 0.3170
h2	 0.5330	 0.1960
i2	 0.4570	 0.1890
j2	 0.5310	 0.2020
k2	 0.6520	 0.2670
l2	 0.6850	 0.2950
m2	 0.6720	 0.2870
n2	 0.7600	 0.3590
o2	 0.7550	 0.3540
p2	 0.7420	 0.3560
q2	 0.5110	 0.2000
r2	 0.3900	 0.1630
s2	 0.4920	 0.1970
t2	 0.6360	 0.2640
u2	 0.6470	 0.2650
v2	 0.6110	 0.2450
w2	 0.7280	 0.3520
x2	 0.7360	 0.3410
y2	 0.7290	 0.3440