



wwPDB EM Validation Summary Report ⓘ

May 2, 2026 – 02:14 PM EDT

PDB ID : 9DGR / pdb_00009dgr
EMDB ID : EMD-46845
Title : Composite structure of dynein-dynactin on microtubules
Authors : Rao, Q.; Chai, P.; Zhang, K.
Deposited on : 2024-09-03
Resolution : 15.00 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

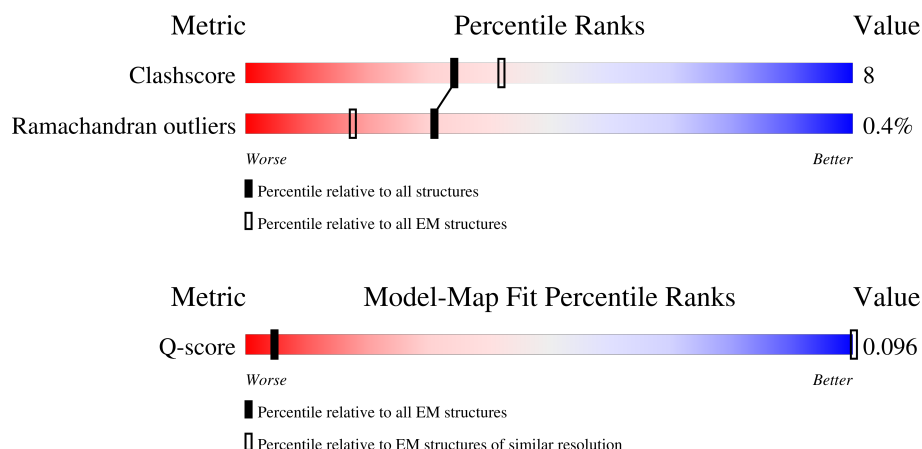
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.00 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.



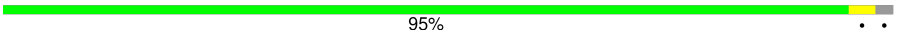
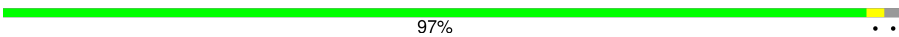
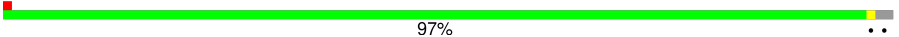
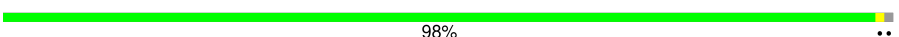


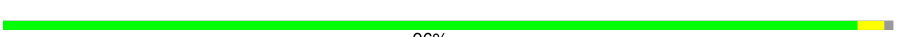



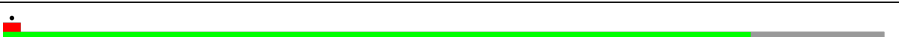


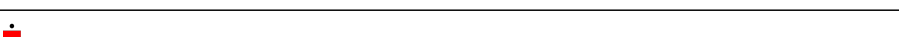
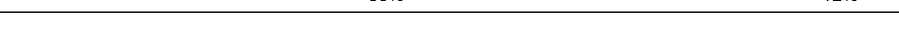
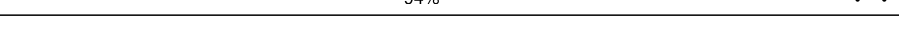



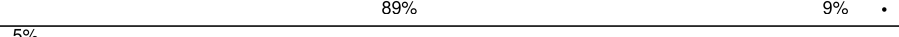

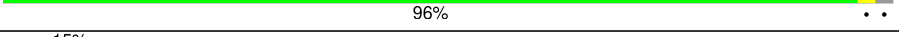
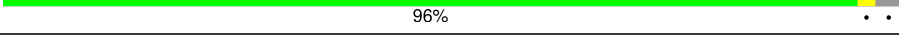


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	37 (14.50 - 15.50)

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	376	 95% ..
1	B	376	 96% ..
1	C	376	 98% .
1	D	376	 95% ..
1	E	376	 96% ..


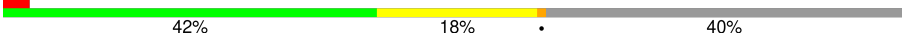
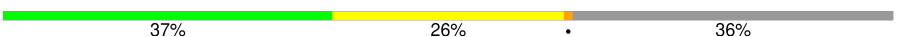






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Mol	Chain	Length	Quality of chain
1	F	376	
1	G	376	
1	I	376	
2	H	375	
3	J	417	
4	K	286	
5	L	272	
6	M	405	
6	N	405	
6	P	405	
6	Q	405	
7	O	186	
7	R	186	
8	U	190	
9	V	182	
10	W	1281	
10	Z	1281	
11	Y	467	
12	e	4646	
12	f	4646	
12	m	4646	
12	n	4646	
13	g	612	
13	h	612	
13	o	612	

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Mol	Chain	Length	Quality of chain
13	p	612	
14	i	492	
14	j	492	
14	q	492	
14	r	492	
15	k	96	
15	l	96	
15	s	96	
15	t	96	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 131638 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 Alpha-centractin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	B	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	C	375	Total	C	N	O	0	0
			1847	1097	375	375		
1	D	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	E	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	F	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	G	370	Total	C	N	O	0	0
			1822	1082	370	370		
1	I	370	Total	C	N	O	0	0
			1822	1082	370	370		

- Molecule 2 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	H	370	Total	C	N	O	0	0
			1822	1082	370	370		

- Molecule 3 is a protein called Actin-related protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	379	Total	C	N	O	0	0
			1868	1110	379	379		

- Molecule 4 is a protein called F-actin-capping protein subunit alpha-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	K	278	Total	C	N	O	0	0
			1378	822	278	278		

- Molecule 5 is a protein called F-actin-capping protein subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L	269	Total	C	N	O	0	0
			1327	789	269	269		

- Molecule 6 is a protein called Dynactin subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	340	Total	C	N	O	0	0
			1689	1009	340	340		
6	N	280	Total	C	N	O	0	0
			1394	834	280	280		
6	P	325	Total	C	N	O	0	0
			1612	962	325	325		
6	Q	343	Total	C	N	O	0	0
			1707	1021	343	343		

- Molecule 7 is a protein called Dynactin subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	179	Total	C	N	O	0	0
			888	530	179	179		
7	R	170	Total	C	N	O	0	0
			844	504	170	170		

- Molecule 8 is a protein called Dynactin subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	U	167	Total	C	N	O	0	0
			822	488	167	167		

- Molecule 9 is a protein called Dynactin subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	V	179	Total	C	N	O	0	0
			881	523	179	179		

- Molecule 10 is a protein called Dynactin subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	W	152	Total	C	N	O	0	0
			754	450	152	152		
10	Z	192	Total	C	N	O	0	0
			952	568	192	192		

- Molecule 11 is a protein called Dynactin subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Y	410	Total	C	N	O	0	0
			2038	1218	410	410		

- Molecule 12 is a protein called Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	e	4569	Total	C	N	O	0	0
			22644	13506	4569	4569		
12	f	4565	Total	C	N	O	0	0
			22625	13495	4565	4565		
12	m	4562	Total	C	N	O	0	0
			18883	9759	4562	4562		
12	n	4526	Total	C	N	O	0	0
			18703	9651	4526	4526		

- Molecule 13 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	g	358	Total	C	N	O	0	0
			1767	1051	358	358		
13	h	358	Total	C	N	O	0	0
			1767	1051	358	358		
13	o	358	Total	C	N	O	0	0
			1767	1051	358	358		
13	p	358	Total	C	N	O	0	0
			1767	1051	358	358		

- Molecule 14 is a protein called Dynein light intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	i	297	Total	C	N	O	0	0
			1472	878	297	297		
14	j	314	Total	C	N	O	0	0
			1555	927	314	314		

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Mol	Chain	Residues	Atoms				AltConf	Trace
14	q	309	Total	C	N	O	0	0
			1241	623	309	309		
14	r	297	Total	C	N	O	0	0
			1193	599	297	297		

- Molecule 15 is a protein called Dynein light chain roadblock.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	k	93	Total	C	N	O	0	0
			462	276	93	93		
15	l	93	Total	C	N	O	0	0
			462	276	93	93		
15	s	93	Total	C	N	O	0	0
			374	188	93	93		
15	t	93	Total	C	N	O	0	0
			374	188	93	93		

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
16	Y	3	Total	Zn	0
			3	3	

- Molecule 17 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
17	m	1	Total	Mg	0
			1	1	
17	n	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Alpha-centractin

Chain A:  95%



- Molecule 1: Alpha-centractin

Chain B:  96%



- Molecule 1: Alpha-centractin

Chain C:  98%



- Molecule 1: Alpha-centractin

Chain D:  95%



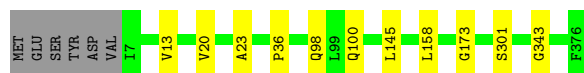
- Molecule 1: Alpha-centractin

Chain E:  96%



- Molecule 1: Alpha-centractin

Chain F:  95%



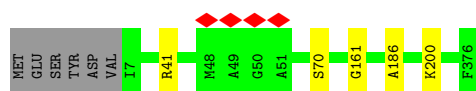
- Molecule 1: Alpha-centractin

Chain G:  97%



- Molecule 1: Alpha-centractin

Chain I:  97%



- Molecule 2: Actin, cytoplasmic 1

Chain H:  98%



- Molecule 3: Actin-related protein 10

Chain J:  89%



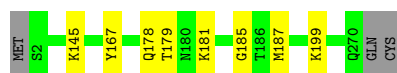
- Molecule 4: F-actin-capping protein subunit alpha-1

Chain K:  92%




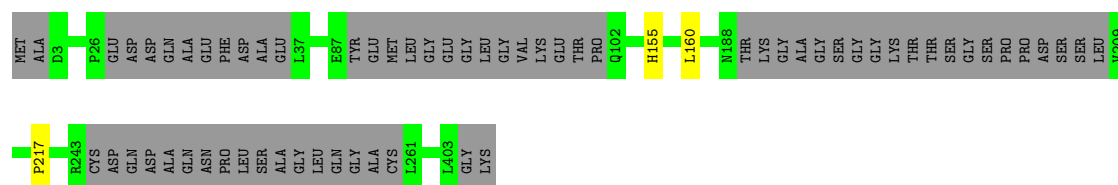
- Molecule 5: F-actin-capping protein subunit beta

Chain L:  96%



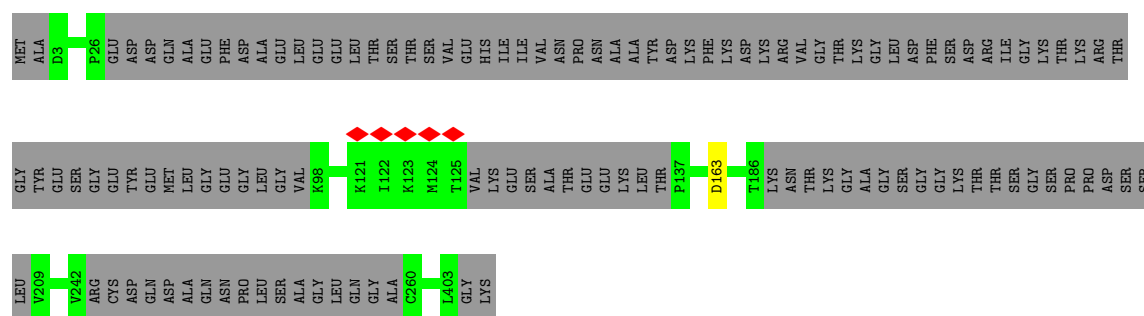
- Molecule 6: Dynactin subunit 2

Chain M: 




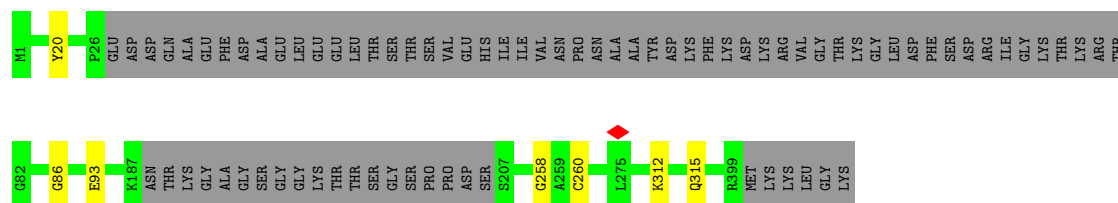
• Molecule 6: Dynactin subunit 2

Chain N: 




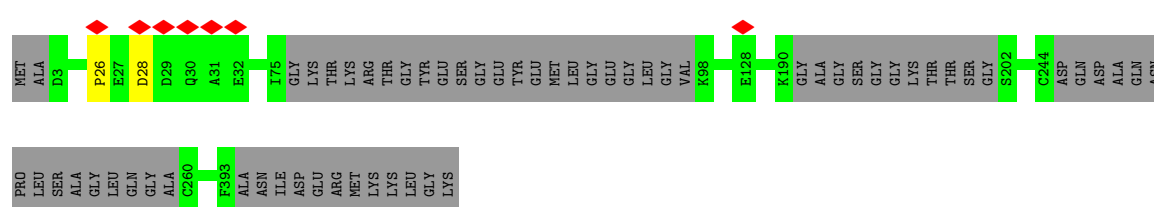
• Molecule 6: Dynactin subunit 2

Chain P: 



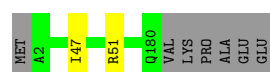
• Molecule 6: Dynactin subunit 2

Chain Q: 

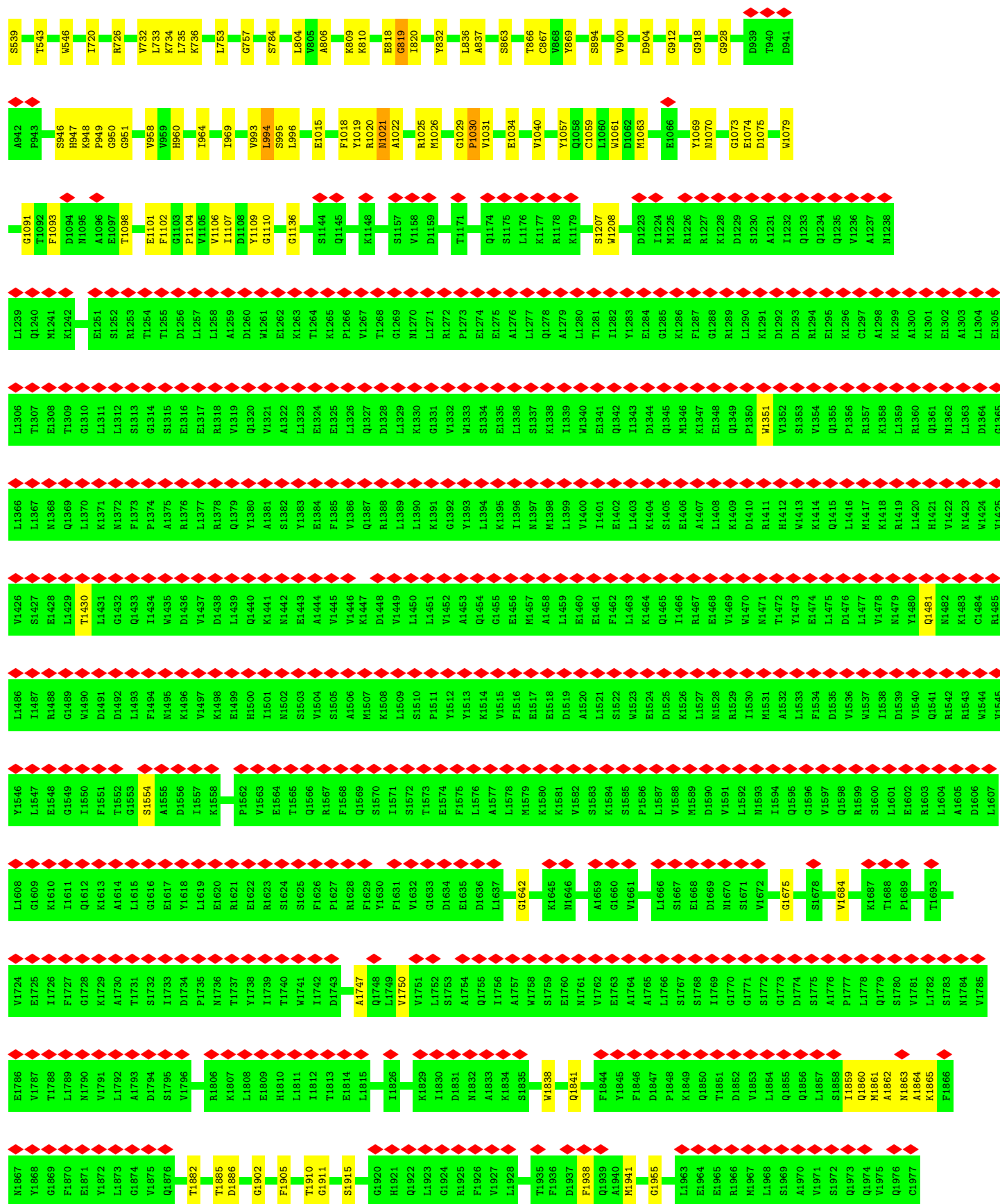


• Molecule 7: Dynactin subunit 3

Chain O: 



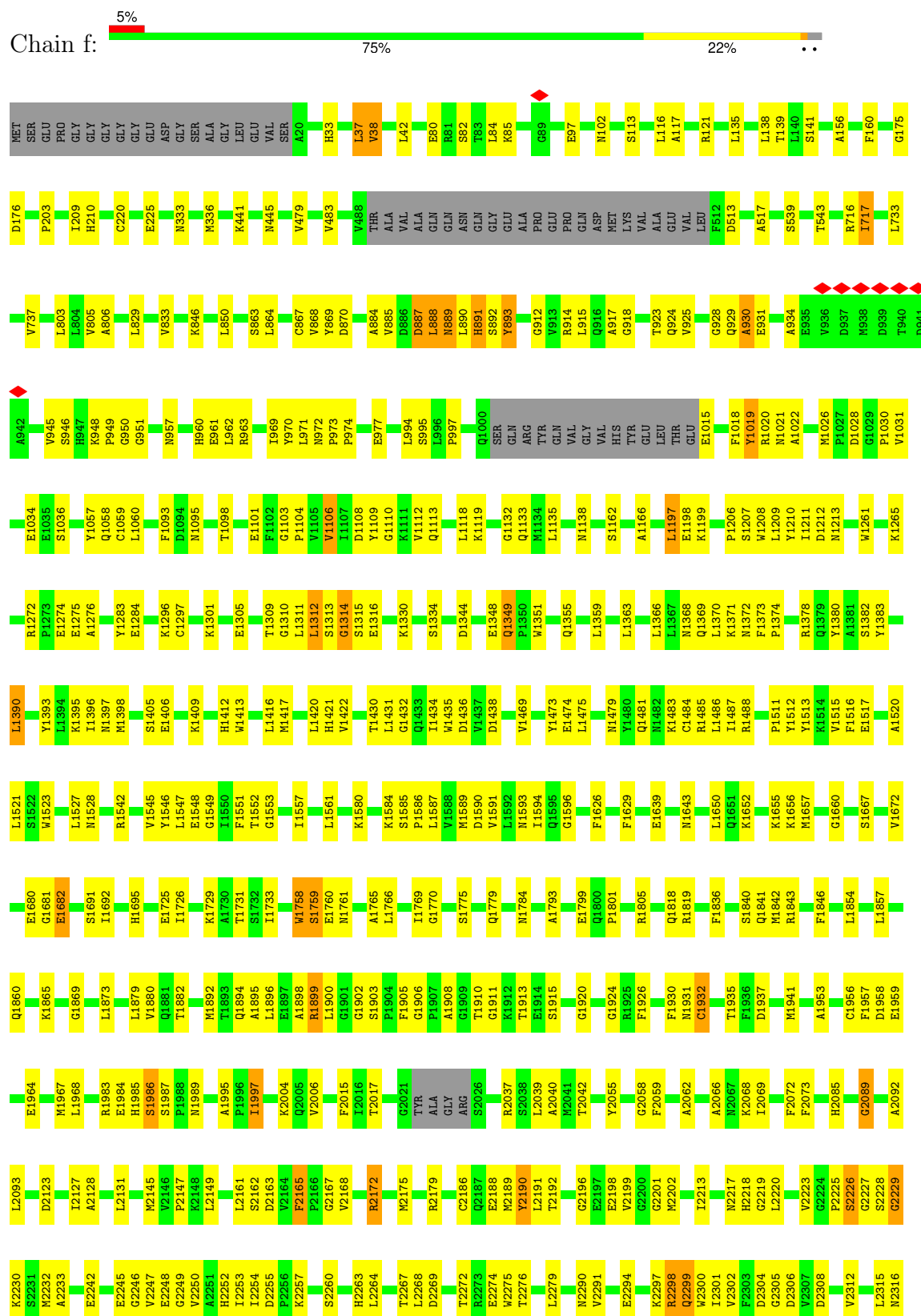






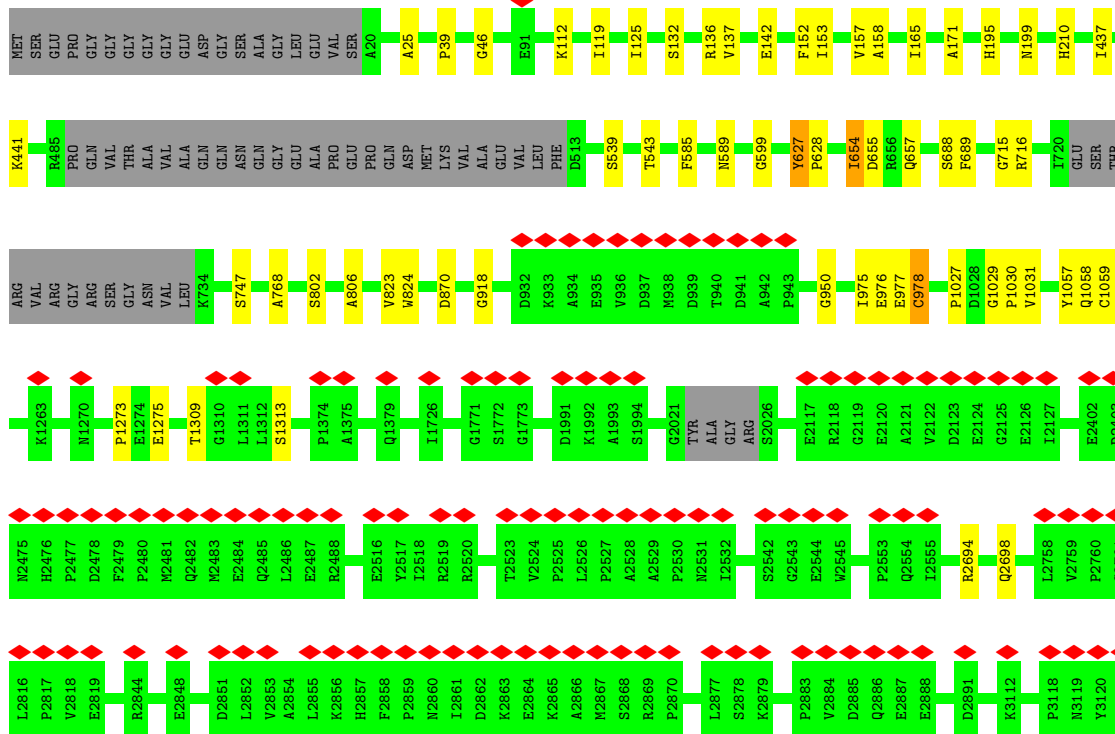
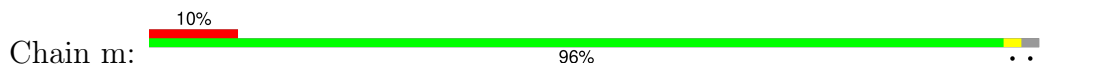
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R4378	T4379	T4401	V4402	D4403	N4404	I4405	E4439	N4446	G4458	I4459	M4473	T4474	A4496	A4497	S4498	G4499	G4500	A4501	K4502	E4503	L4504	K4505	L4511	G4512	G4513	Y4527	V4528	A4529	Q4530	A4531	N4532	S4533	L4534	S4535	L4536	E4537	L4538	I4544	V4545	T4546	T4547	S4548	Q4549	S4550	A4551	T4552	L4553	D4554	A4555									
Q4307	V4308	V4309	E4310	L4311	D4312	P4313	D4314	T4315	Q4316	T4317	P4318	S4319	V4320	L4321	G4322	L4323	P4324	N4325	N4326	A4327	L4331	L4332	T4333	T4334	Q4335	G4336	V4337	D4338	M4339	L4340	N4343	D4353	ASP	LEU	ALA	TYR	GLU	GLU	LYS	THR	THR	THR	ASP	SER	THR	ALA	ASP	GLY	ARG	ARG	PHE	A4375	V4376	N4377				
F4118	H4119	A4120	C4121	F4122	R4123	L4124	F4125	L4126	T4127	M4128	E4129	I4130	N4131	P4132	K4133	V4134	A4141	V4146	F4147	P4150	P4151	G4152	V4166	S4167	K4171	P4172	S4173	F4177	K4178	Y4179	Y4180	F4181	L4182	L4183	A4184	W4185	F4186	H4187	A4188	I4189	I4190	Q4191	E4192	R4193	L4194	R4195	G4208	V4219	D4220	T4221								
W4222	D4225	T4226	A4227	K4228	C4229	R4230	Q4231	N4232	I4233	S4234	P4235	D4236	K4237	I4238	L4246	M4247	A4248	Q4249	S4250	I4251	Y4252	G4253	C4254	D4255	T4274	S4277	F4278	D4279	S4280	E4281	F4282	K4283	L4284	A4285	C4286	K4287	V4288	D4289	Q4290	H4291	D4292	D4293	I4294	Q4295	M4296	P4297	D4298	G4299	R4301	R4302	E4303	F4305	V4306					
Q4307	V4308	V4309	E4310	L4311	D4312	P4313	D4314	T4315	Q4316	T4317	P4318	S4319	V4320	L4321	G4322	L4323	P4324	N4325	N4326	A4327	L4331	L4332	T4333	T4334	Q4335	G4336	V4337	D4338	M4339	L4340	N4343	D4353	ASP	LEU	ALA	TYR	GLU	GLU	LYS	THR	THR	THR	ASP	SER	THR	ALA	ASP	GLY	ARG	ARG	PHE	A4375	V4376	N4377				
R4378	T4379	T4401	V4402	D4403	N4404	I4405	E4439	N4446	G4458	I4459	M4473	T4474	A4496	A4497	S4498	G4499	G4500	A4501	K4502	E4503	L4504	K4505	L4511	G4512	G4513	Y4527	V4528	A4529	Q4530	A4531	N4532	S4533	L4534	S4535	L4536	E4537	L4538	I4544	V4545	T4546	T4547	S4548	Q4549	S4550	A4551	T4552	L4553	D4554	A4555									

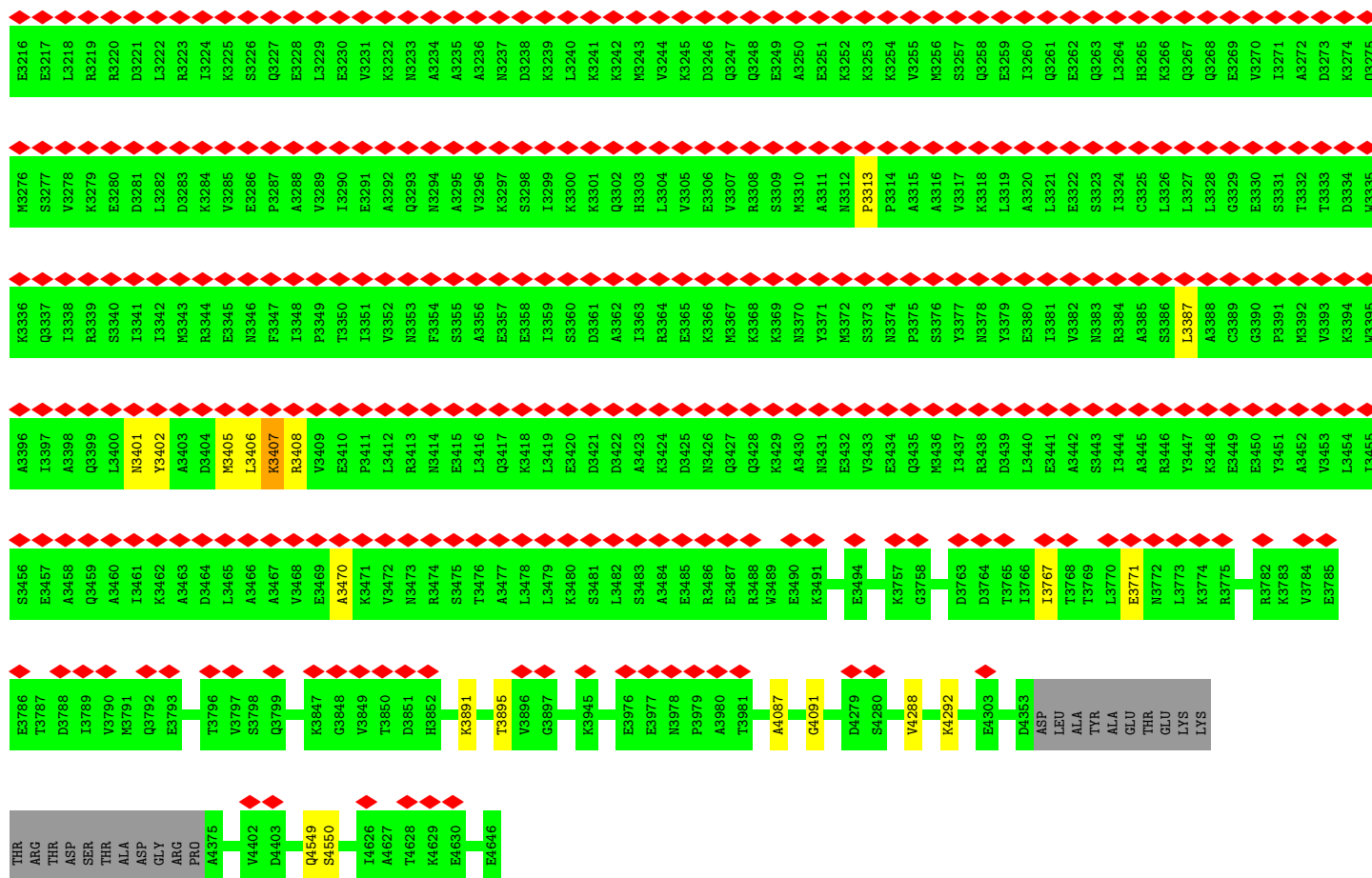
● Molecule 12: Cytoplasmic dynein 1 heavy chain 1



R3682	R3683	S3566	L3567	N3576	D3691	L3692	C3693	S3694	R3695	L3688	D3591	N3602	K3605	T3612	S3613	D3617	A3618	F3619	R3620	K3621	N3622	A3626	L3627	G3630	N3631	Q3636	G3758	R3759	I3760	L3761	D3762	L3645	L3649	R3773	K3774	R3775	E3776	G3657	G3658	F3659	V3660	L3661	D3670	L3671	S3672	L3679	S3680	T3681											
I3455	S3456	E3457	A3458	Q3459	A3460	I3461	K3462	A3463	V3472	L3482	S3483	A3484	N3489	S3490	T3491	T3492	S3493	N3498	K3621	N3622	A3626	L3627	G3630	N3631	Q3636	G3758	R3759	I3760	L3761	D3762	L3645	L3649	R3773	K3774	R3775	E3776	G3657	G3658	F3659	V3660	L3661	D3670	L3671	S3672	L3679	S3680	T3681												
W3395	K3396	Q3397	I3398	A3399	L3400	R3401	F3402	A3403	D3404	F3405	L3406	K3407	R3408	F3409	E3410	F3411	L3412	R3413	R3414	E3415	L3416	Q3417	K3418	L3419	E3420	D3421	D3422	A3423	K3424	D3425	H3426	Q3427	Q3428	K3429	A3430	F3431	F3432	F3433	E3434	Q3435	H3436	L3437	R3438	D3439	L3440	E3441	A3442	S3443	T3444	A3445	R3446	F3447	E3448	E3449	E3450	F3451	A3452	F3453	L3454
Q3275	M3276	S3277	V3278	R3279	E3280	D3281	L3282	D3283	K3284	V3285	E3286	F3287	A3288	V3289	T3290	E3291	A3292	Q3293	N3294	S3295	A3296	V3296	K3297	S3298	I3299	K3300	K3301	Q3302	H3303	L3304	V3305	E3306	Q3307	K3308	S3309	M3310	A3311	N3312	F3313	F3314	A3315	A3316	V3317	K3318	L3319	A3320	L3321	E3322	S3323	T3324	C3325	L3326	V3327	L3328	Q3329	E3330	S3331	T3332	D3333
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W3395	A3396	I3397	A3398	Q3399	L3400	R3401	F3402	A3403	D3404	F3405	L3406	K3407	R3408	F3409	E3410	F3411	L3412	R3413	R3414	E3415	L3416	Q3417	K3418	L3419	E3420	D3421	D3422	A3423	K3424	D3425	H3426	Q3427	Q3428	K3429	A3430	F3431	F3432	F3433	E3434	Q3435	H3436	L3437	R3438	D3439	L3440	E3441	A3442	S3443	T3444	A3445	R3446	F3447	E3448	E3449	E3450	F3451	A3452	F3453	L3454
I3455	S3456	E3457	A3458	Q3459	A3460	I3461	K3462	A3463	V3472	L3482	S3483	A3484	N3489	S3490	T3491	T3492	S3493	N3498	K3621	N3622	A3626	L3627	G3630	N3631	Q3636	G3758	R3759	I3760	L3761	D3762	L3645	L3649	R3773	K3774	R3775	E3776	G3657	G3658	F3659	V3660	L3661	D3670	L3671	S3672	L3679	S3680	T3681												
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Q2677	R2678	V2679	S2681	M2686	G2691	P2697	R2705	S2706	L2706	Q2707	K2601	L2602	M2603	T2604	P2613	D2614	E2615	V2617	V2618	G2619	L2620	N2621	F2622	S2623	S2624	A2625	F2635	Y2638	E2640	Y2641	T2644	N2645	N2646	V2649	P2652	V2653	M2755	L2756	L2658	L2659	V2660	L2661	F2662	C2663	L2664	N2665	T2666	A2765	L2769										
T2770	A2771	N2772	S2773	E2774	F2775	T2776	T2777	S2778	R2779	L2925	S2780	Q2781	E2782	R2783	F2784	Q2785	Q2786	Q2787	S2789	F2796	R2797	E2798	A2829	L2830	Q2834	D2835	R2836	E2839	Y2735	T2736	D2737	Y2738	P2739	G2740	P2741	A2742	S2743	L2744	T2750	D2862	A2866	Y2873	S2874	N2875	W2876	L2877	S2878	T2882	P2883	K2898	V2899								
F2900	Y2901	E2902	E2903	F2912	L2916	R2924	L2925	F2926	H2927	Q2928	P2929	Q2930	T2931	H2932	L2933	I2936	G2937	K2943	T2944	T2945	A2951	W2952	G2955	L2956	V2958	I2961	K2962	V2963	T2968	F2972	R2981	K2982	S2983	K2986	N2987	E2988	K2989	L2990	F2992	E3006	T3010	L3011																	
E3016	G3019	D3024	A3027	A3037	G3041	L3042	D3045	V3058	R3059	N3061	L3062	H3063	V3064	S3065	F3066	T3067	K3068	N3069	P3070	F3086	G3089	V3090	L3091	N3092	K3093	F3094	G3095	S3098	L3102	V3103	Q3104	G3106	K3107	E3108	F3109	T3110	S3111	V3129	R3131	K3132	L3133	P3134	T3010	L3011															
E3189	Q3198	M3199	H3200	L3201	V3212	E3217	L3218	R3219	R3220	E3230	V3231	K3232	N3233	A3234	A3235	A3236	N3237	D3238	K3239	L3240	K3241	K3242	M3243	V3244	K3245	D3246	Q3247	Q3248	E3249	A3250	E3251	K3252	K3253	K3254	V3255	M3256	S3257	Q3258	E3259	L3260	K3261	E3262	Q3263	L3264	H3265	K3266	Q3267	Q3268	E3269	V3270	I3271	A3272	D3273	K3274					
Q3275	M3276	S3277	V3278	R3279	E3280	D3281	L3282	D3283	K3284	V3285	E3286	F3287	A3288	V3289	T3290	E3291	A3292	Q3293	N3294	S3295	A3296	V3296	K3297	S3298	I3299	K3300	K3301	Q3302	H3303	L3304	V3305	E3306	Q3307	K3308	S3309	M3310	A3311	N3312	F3313	F3314	A3315	A3316	V3317	K3318	L3319	A3320	L3321	E3322	S3323	T3324	C3325	L3326	V3327	L3328	Q3329	E3330	S3331	T3332	D3333
W3335	K3336	Q3337	I3338	R3339	S3340	I3341	L3342	M3343	R3344	E3345	N3346	F3347	I3348	P3349	T3350	I3351	V3352	N3353	F3354	S3355	A3356	E3357	I3358	I3359	K3360	D3361	A3362	I3363	R3364	E3365	K3366	M3367	K3368	K3369	N3370	F3371	M3372	S3373	N3374	F3375	F3376	L3377	R3378	D3379	E3380	D3381	S3382	R3383	T3384	A3385	S3386	L3387	A3388	C3389	G3390	F3391	M3392	V3393	K3394
W3395	A3396	I3397	A3398	Q3399	L3400	R3401	F3402	A3403	D3404	F3405	L3406	K3407	R3408	F3409	E3410	F3411	L3412	R3413	R3414	E3415	L3416	Q3417	K3418	L3419	E3420	D3421	D3422	A3423	K3424	D3425	H3426	Q3427	Q3428	K3429	A3430	F3431	F3432	F3433	E3434	Q3435	H3436	L3437	R3438	D3439	L3440	E3441	A3442	S3443	T3444	A3445	R3446	F3447	E3448	E3449	E3450	F3451	A3452	F3453	L3454
I3455	S3456	E3457	A3458	Q3459	A3460	I3461	K3462	A3463	V3472	L3482	S3483	A3484	N3489	S3490	T3491	T3492	S3493	N3498	K3621	N3622	A3626	L3627	G3630	N3631	Q3636	G3758	R3759	I3760	L3761	D3762	L3645	L3649	R3773	K3774	R3775	E3776	G3657	G3658	F3659	V3660	L3661	D3670	L3671	S3672	L3679	S3680	T3681												
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P2425	Y2426	P2427	T2428	P2429	M2430	G2431	S2434	L2435	E2438	H2439	K2442	L2443	N2473	P2480	M2481	Q2482	Q2485	L2486	Y2489	L2499	W2500	S2501	L2502	S2503	G2504	D2505	V2505	T2518	T2522	P2533	D2536	Y2537	E2538	Q2543	P2547	W2548	K2551	V2552	T2555	E2556	V2557	E2558	T2559	D2566	V2569														
P2570	L2591	L2592	L2593	G2595	P2596	P2597	G2598	R2705	S2706	L2706	Q2707	K2601	L2602	M2603	T2604	P2613	D2614	E2615	V2617	V2618	G2619	L2620	N2621	F2622	S2623	S2624	A2625	F2635	Y2638	E2640	Y2641	T2644	N2645	N2646	V2649	P2652	V2653	M2755	L2756	L2658	L2659	V2660	L2661	F2662	C2663	L2664	N2665	T2666	A2765	L2769									
Q2677	R2678	V2679	S2681	M2686	G2691	P2697	R2705	S2706	L2706	Q2707	K2601	L2602	M2603	T2604	P2613	D2614	E2615	V2617	V2618	G2619	L2620	N2621	F2622	S2623	S2624	A2625	F2635	Y2638	E2640	Y2641	T2644	N2645	N2646	V2649	P2652	V2653	M2755	L2756	L2658	L2659	V2660	L2661	F2662	C2663	L2664	N2665	T2666	A2765	L2769										
T2770	A2771	N2772	S2773	E2774	F2775	T2776	T2777	S2778	R2779	L2925	S2780	Q2781	E2782	R2783	F2784	Q2785	Q2786	Q2787	S2789	F2796	R2797	E2798	A2829	L2830	Q2834	D2835	R2836	E2839	Y2735	T2736	D2737	Y2738	P2739	G2740	P2741	A2742	S2743	L2744	T2750	D2862	A2866	Y2873	S2874	N2875	W2876	L2877	S2878	T2882	P2883	K2898	V2899								
F2900	Y2901	E2902	E2903	F2912	L2916	R2924	L2925	F2926	H2927	Q2928	P2929	Q2930	T2931	H2932	L2933	I2936	G2937	K2943	T2944	T2945	A2951	W2952	G2955	L2956	V2958	I2961	K2962	V2963	T2968	F2972	R2981	K2982	S2983	K2986	N2987	E2988	K2989	L2990	F2992	E3006	T3010	L3011																	
E3016	G3019	D3024	A3027	A3037	G3041	L3042	D3045	V3058	R3059	N3061	L3062	H3063	V3064	S3065	F3066	T3067	K3068	N3069	P3070	F3086	G3089	V3090	L3091	N3092	K3093	F3094	G3095	S3098	L3102	V3103	Q3104	G3106	K3107	E3108	F3109	T3110	S3111	V3129	R3131	K3132	L3133	P3134	T3010	L3011															
E3189	Q																																																										

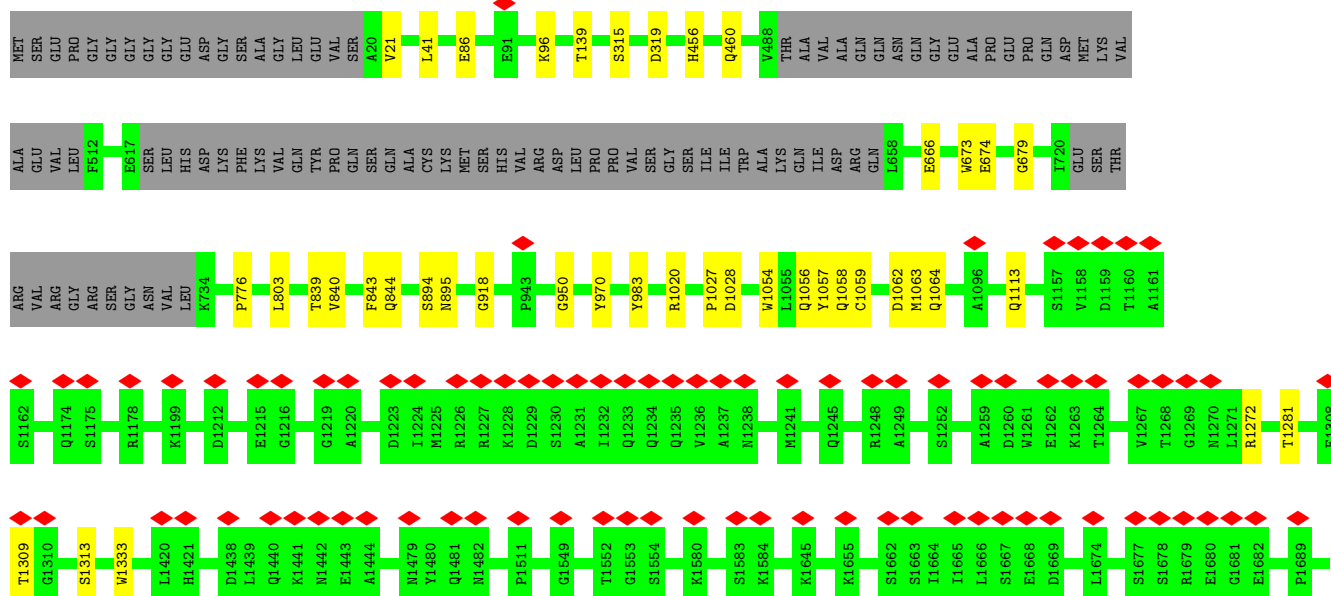
- Molecule 12: Cytoplasmic dynein 1 heavy chain 1



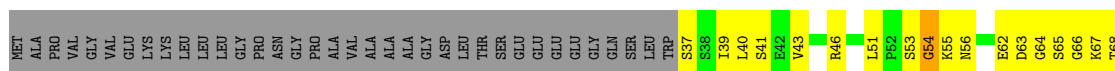


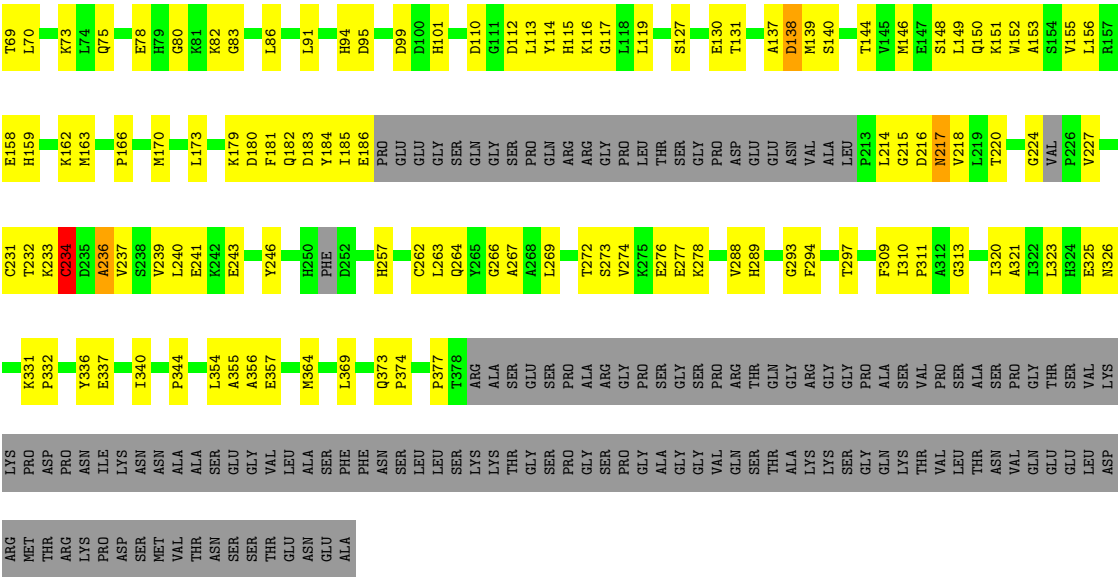
• Molecule 12: Cytoplasmic dynein 1 heavy chain 1

Chain n: 15% 96%

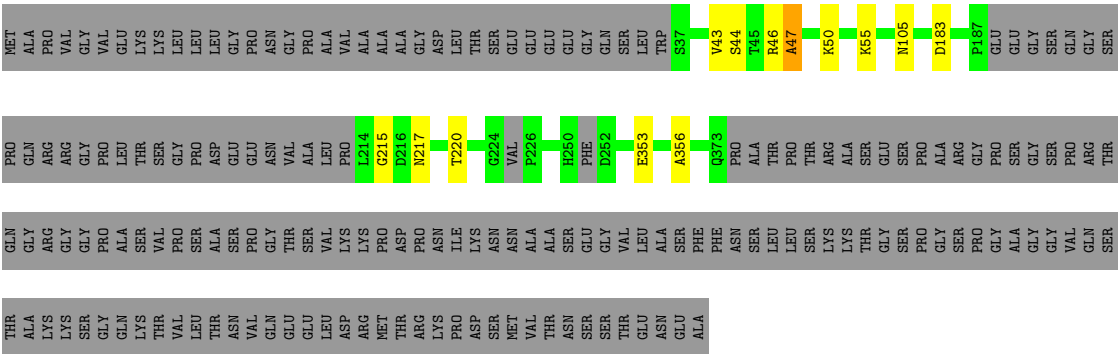




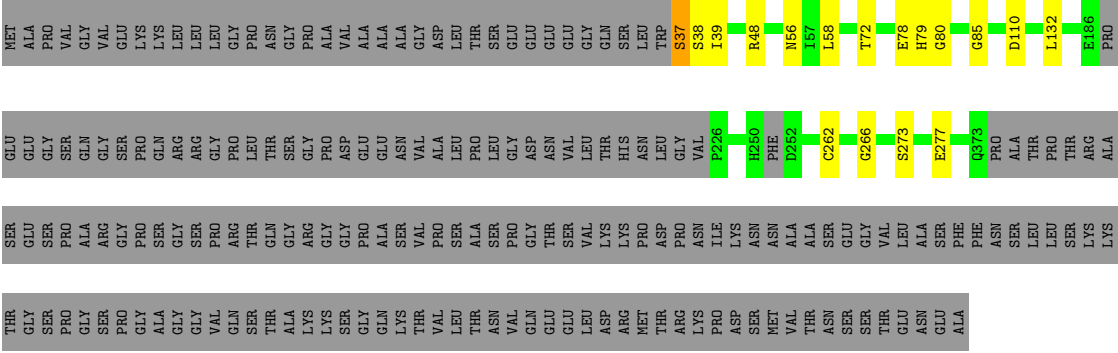




• Molecule 14: Dynein light intermediate chain



• Molecule 14: Dynein light intermediate chain



• Molecule 15: Dynein light chain roadblock

Chain k:  66% 31%



- Molecule 15: Dynein light chain roadblock

Chain l:  67% 30%



- Molecule 15: Dynein light chain roadblock

Chain s:  97%



- Molecule 15: Dynein light chain roadblock

Chain t:  97%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16372	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.404	Depositor
Minimum map value	-0.041	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	990.0, 990.0, 990.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.3, 3.3, 3.3	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.16	0/1821	0.40	0/2531
1	B	0.18	0/1821	0.48	0/2531
1	C	0.18	0/1846	0.46	0/2566
1	D	0.17	0/1821	0.42	0/2531
1	E	0.17	0/1821	0.46	0/2531
1	F	0.18	0/1821	0.46	0/2531
1	G	0.18	0/1821	0.44	0/2531
1	I	0.15	0/1821	0.43	0/2531
2	H	0.17	0/1821	0.40	0/2531
3	J	0.28	0/1867	0.50	0/2596
4	K	0.16	0/1377	0.40	0/1919
5	L	0.16	0/1326	0.37	0/1844
6	M	0.17	0/1684	0.45	0/2343
6	N	0.15	0/1389	0.40	0/1933
6	P	0.17	0/1609	0.42	0/2240
6	Q	0.16	0/1703	0.39	0/2373
7	O	0.15	0/887	0.44	0/1236
7	R	0.17	0/843	0.49	0/1175
8	U	0.21	0/821	0.54	0/1140
9	V	0.15	0/880	0.42	0/1222
10	W	0.16	0/750	0.45	0/1040
10	Z	0.17	0/951	0.48	0/1325
11	Y	0.40	0/2035	0.58	1/2837 (0.0%)
12	e	0.40	1/22639 (0.0%)	0.72	15/31566 (0.0%)
12	f	0.59	3/22620 (0.0%)	0.91	42/31540 (0.1%)
12	m	0.60	1/18878 (0.0%)	0.82	21/24065 (0.1%)
12	n	0.64	6/18697 (0.0%)	0.86	41/23810 (0.2%)
13	g	0.18	0/1766	0.32	0/2457
13	h	0.14	0/1766	0.40	0/2457
13	o	0.13	0/1766	0.37	1/2457 (0.0%)
13	p	0.14	0/1766	0.37	1/2457 (0.0%)
14	i	0.62	1/1469 (0.1%)	1.38	6/2044 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
14	j	0.79	0/1551	1.16	6/2156 (0.3%)
14	q	1.39	2/1237 (0.2%)	1.68	8/1543 (0.5%)
14	r	0.75	2/1190 (0.2%)	1.12	7/1486 (0.5%)
15	k	0.68	1/461 (0.2%)	0.99	1/642 (0.2%)
15	l	0.78	0/461	1.22	2/642 (0.3%)
15	s	1.02	0/373	1.18	0/466
15	t	1.00	0/373	1.16	0/466
All	All	0.50	17/131549 (0.0%)	0.76	152/178291 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	e	0	2
12	f	0	26
14	j	0	2
14	q	0	1
14	r	0	2
15	l	0	1
All	All	0	34

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	i	362	PHE	C-N	-9.03	1.22	1.33
12	n	1063	MET	C-O	8.29	1.33	1.24
12	n	1062	ASP	C-O	-8.15	1.14	1.24
14	r	79	HIS	C-N	7.88	1.38	1.33
12	f	2715	PRO	CA-CB	-7.72	1.42	1.53

The worst 5 of 152 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	i	363	LEU	N-CA-CB	-42.24	48.73	109.98
14	r	79	HIS	CA-C-N	-14.07	108.83	122.20
14	r	79	HIS	C-N-CA	-14.07	108.83	122.20
14	i	362	PHE	CA-C-N	-13.45	102.34	120.63
14	i	362	PHE	C-N-CA	-13.45	102.34	120.63

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	e	3079	ALA	Peptide
12	e	4316	GLN	Peptide
12	f	1106	VAL	Peptide
12	f	1118	LEU	Peptide
12	f	934	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1822	0	820	7	0
1	B	1822	0	820	7	0
1	C	1847	0	830	5	0
1	D	1822	0	820	9	0
1	E	1822	0	820	6	0
1	F	1822	0	820	6	0
1	G	1822	0	820	4	0
1	I	1822	0	820	3	0
2	H	1822	0	835	3	0
3	J	1868	0	823	4	0
4	K	1378	0	611	7	0
5	L	1327	0	585	4	0
6	M	1689	0	765	1	0
6	N	1394	0	632	0	0
6	P	1612	0	747	6	0
6	Q	1707	0	769	1	0
7	O	888	0	413	1	0
7	R	844	0	385	1	0
8	U	822	0	370	2	0
9	V	881	0	379	4	0
10	W	754	0	336	1	0
10	Z	952	0	434	3	0
11	Y	2038	0	886	6	0
12	e	22644	0	10062	295	0
12	f	22625	0	10053	725	0
12	m	18883	0	5554	44	0
12	n	18703	0	5475	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	g	1767	0	796	10	0
13	h	1767	0	796	12	0
13	o	1767	0	796	7	0
13	p	1767	0	796	11	0
14	i	1472	0	645	91	0
14	j	1555	0	681	99	0
14	q	1241	0	329	10	0
14	r	1193	0	315	6	0
15	k	462	0	192	23	0
15	l	462	0	192	24	0
15	s	374	0	95	0	0
15	t	374	0	95	0	0
16	Y	3	0	0	0	0
17	m	1	0	0	0	0
17	n	1	0	0	0	0
All	All	131638	0	52412	1411	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 8.

The worst 5 of 1411 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)
12:e:733:LEU:CB	14:i:360:GLN:HA	1.53	1.37
12:e:806:ALA:HA	14:i:356:ALA:N	1.45	1.32
12:n:776:PRO:CB	13:p:375:LEU:O	1.81	1.29
12:f:2645:PRO:O	14:q:220:THR:O	1.60	1.18
12:f:2645:PRO:O	14:q:220:THR:C	1.88	1.15

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	368/376 (98%)	359 (98%)	9 (2%)	0	100	100
1	B	368/376 (98%)	356 (97%)	12 (3%)	0	100	100
1	C	373/376 (99%)	361 (97%)	12 (3%)	0	100	100
1	D	368/376 (98%)	356 (97%)	12 (3%)	0	100	100
1	E	368/376 (98%)	356 (97%)	12 (3%)	0	100	100
1	F	368/376 (98%)	357 (97%)	11 (3%)	0	100	100
1	G	368/376 (98%)	357 (97%)	11 (3%)	0	100	100
1	I	368/376 (98%)	354 (96%)	14 (4%)	0	100	100
2	H	368/375 (98%)	357 (97%)	11 (3%)	0	100	100
3	J	377/417 (90%)	365 (97%)	12 (3%)	0	100	100
4	K	276/286 (96%)	268 (97%)	8 (3%)	0	100	100
5	L	267/272 (98%)	261 (98%)	6 (2%)	0	100	100
6	M	330/405 (82%)	311 (94%)	18 (6%)	1 (0%)	36	72
6	N	270/405 (67%)	262 (97%)	7 (3%)	1 (0%)	30	67
6	P	319/405 (79%)	312 (98%)	7 (2%)	0	100	100
6	Q	335/405 (83%)	318 (95%)	17 (5%)	0	100	100
7	O	177/186 (95%)	165 (93%)	12 (7%)	0	100	100
7	R	168/186 (90%)	160 (95%)	8 (5%)	0	100	100
8	U	165/190 (87%)	157 (95%)	8 (5%)	0	100	100
9	V	177/182 (97%)	172 (97%)	5 (3%)	0	100	100
10	W	144/1281 (11%)	138 (96%)	5 (4%)	1 (1%)	18	56
10	Z	190/1281 (15%)	185 (97%)	5 (3%)	0	100	100
11	Y	404/467 (86%)	377 (93%)	24 (6%)	3 (1%)	18	56
12	e	4559/4646 (98%)	4166 (91%)	378 (8%)	15 (0%)	36	72
12	f	4555/4646 (98%)	3899 (86%)	583 (13%)	73 (2%)	7	38
12	m	4552/4646 (98%)	4431 (97%)	115 (2%)	6 (0%)	48	83
12	n	4514/4646 (97%)	4402 (98%)	110 (2%)	2 (0%)	100	100
13	g	356/612 (58%)	352 (99%)	4 (1%)	0	100	100
13	h	356/612 (58%)	346 (97%)	10 (3%)	0	100	100
13	o	356/612 (58%)	350 (98%)	6 (2%)	0	100	100
13	p	356/612 (58%)	350 (98%)	6 (2%)	0	100	100
14	i	291/492 (59%)	248 (85%)	40 (14%)	3 (1%)	12	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	j	306/492 (62%)	233 (76%)	61 (20%)	12 (4%)	2	19
14	q	301/492 (61%)	293 (97%)	8 (3%)	0	100	100
14	r	291/492 (59%)	277 (95%)	14 (5%)	0	100	100
15	k	91/96 (95%)	69 (76%)	22 (24%)	0	100	100
15	l	91/96 (95%)	69 (76%)	21 (23%)	1 (1%)	11	46
15	s	91/96 (95%)	84 (92%)	7 (8%)	0	100	100
15	t	91/96 (95%)	86 (94%)	5 (6%)	0	100	100
All	All	28073/33135 (85%)	26319 (94%)	1636 (6%)	118 (0%)	31	67

5 of 118 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	217	PRO
10	W	1142	PRO
11	Y	175	PRO
11	Y	441	PRO
12	e	4550	SER

5.3.2 Protein sidechains [i](#)

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

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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

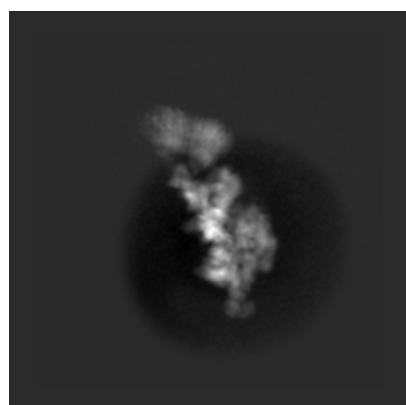
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46845. These allow visual inspection of the internal detail of the map and identification of artifacts.

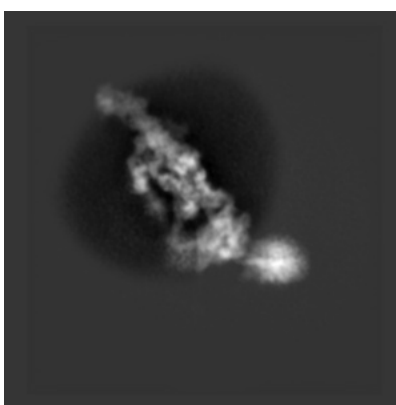
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

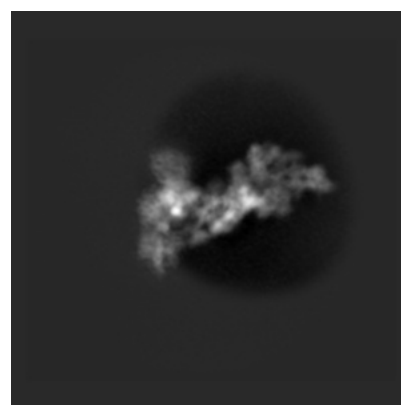
6.1.1 Primary map



X



Y

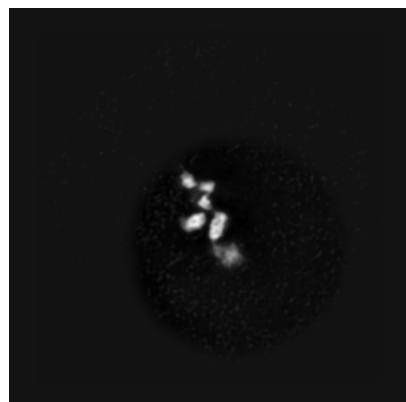


Z

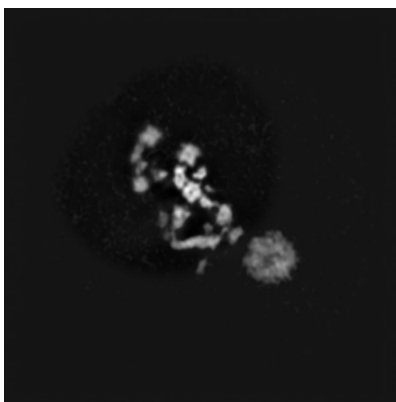
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

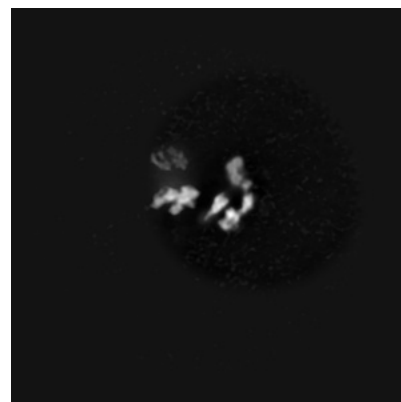
6.2.1 Primary map



X Index: 150



Y Index: 150

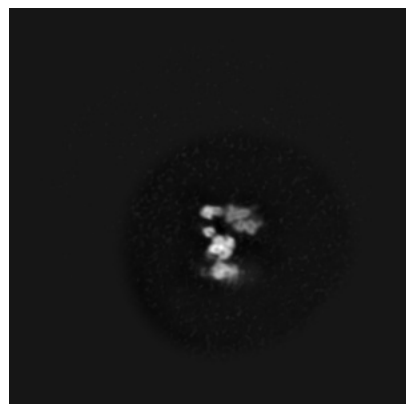


Z Index: 150

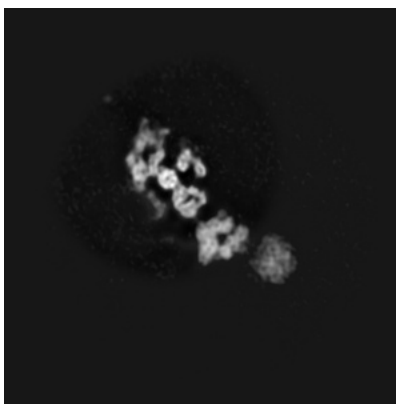
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

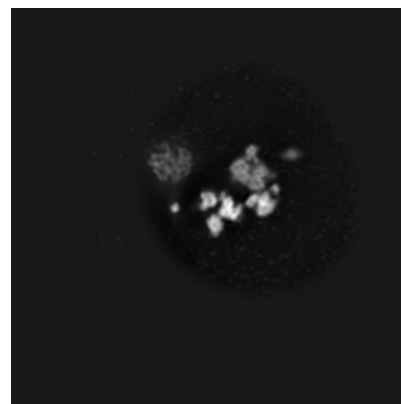
6.3.1 Primary map



X Index: 174



Y Index: 157

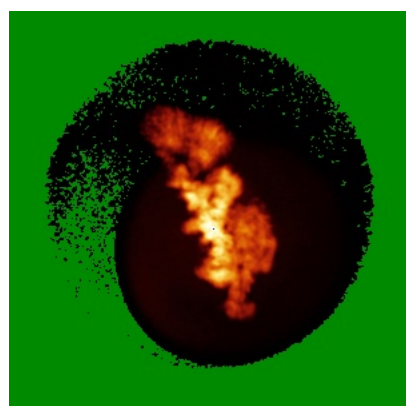


Z Index: 136

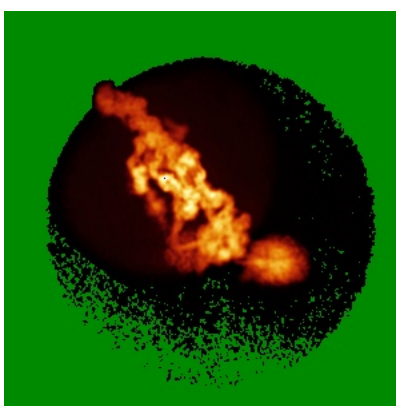
The images above show the largest variance slices of the map in three orthogonal directions.

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

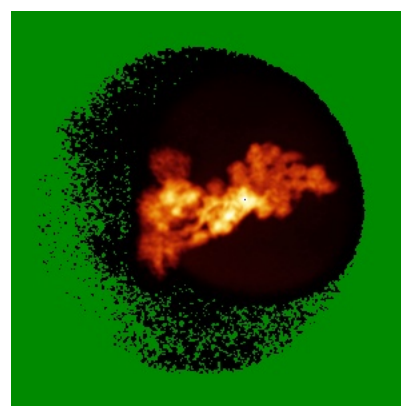
6.4.1 Primary map



X



Y



Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

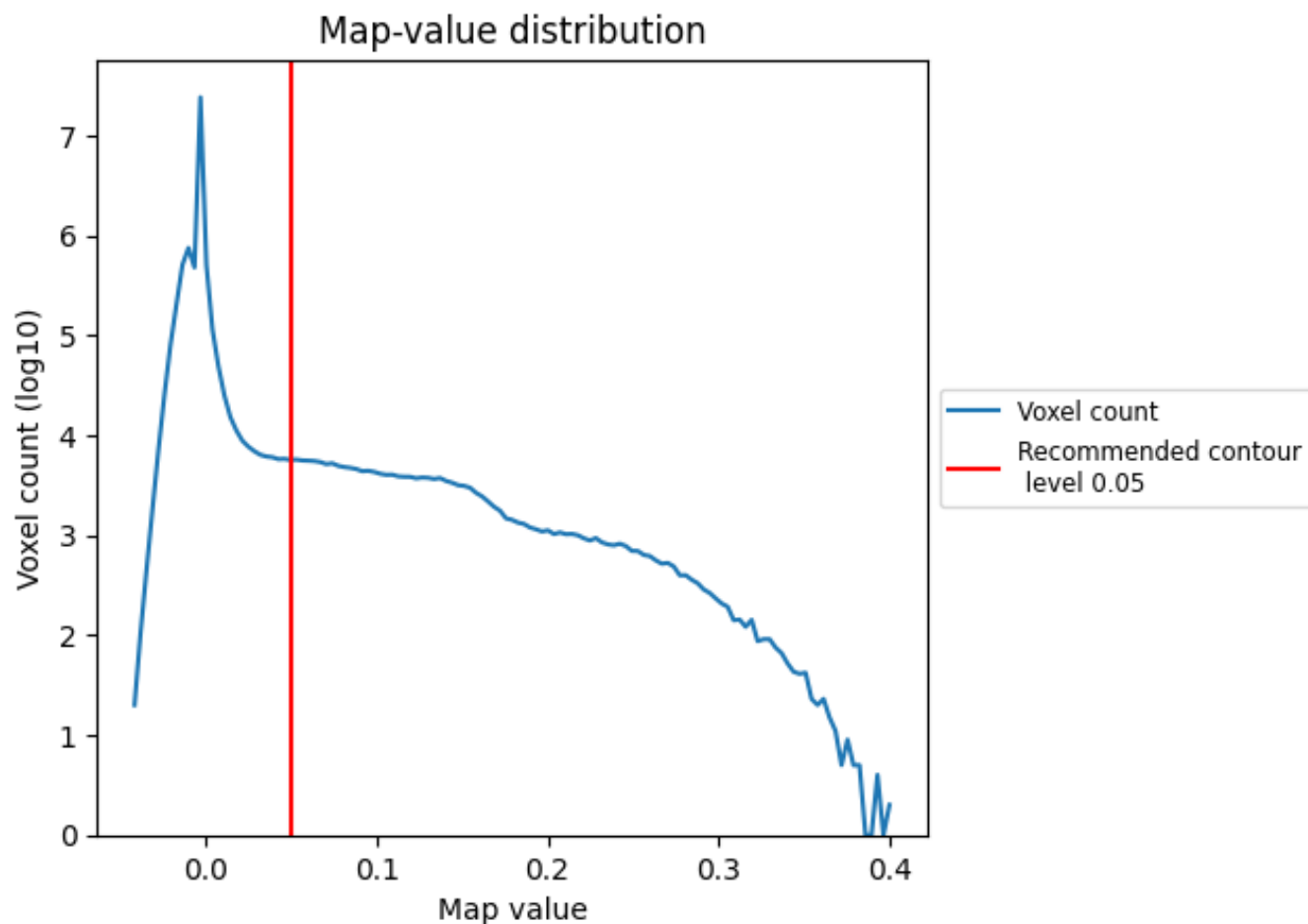
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

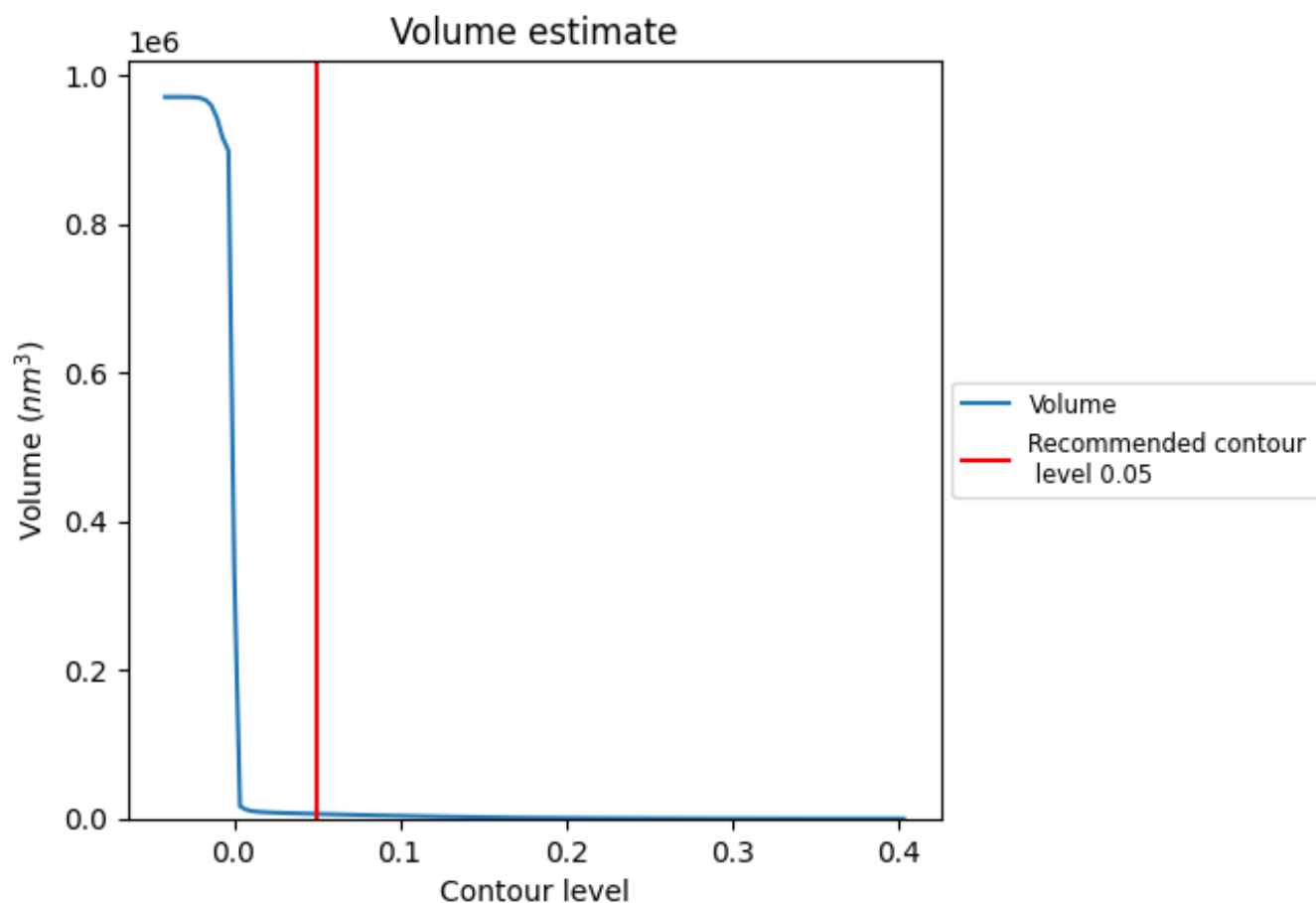
This section contains the results of statistical analysis of the map.

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.

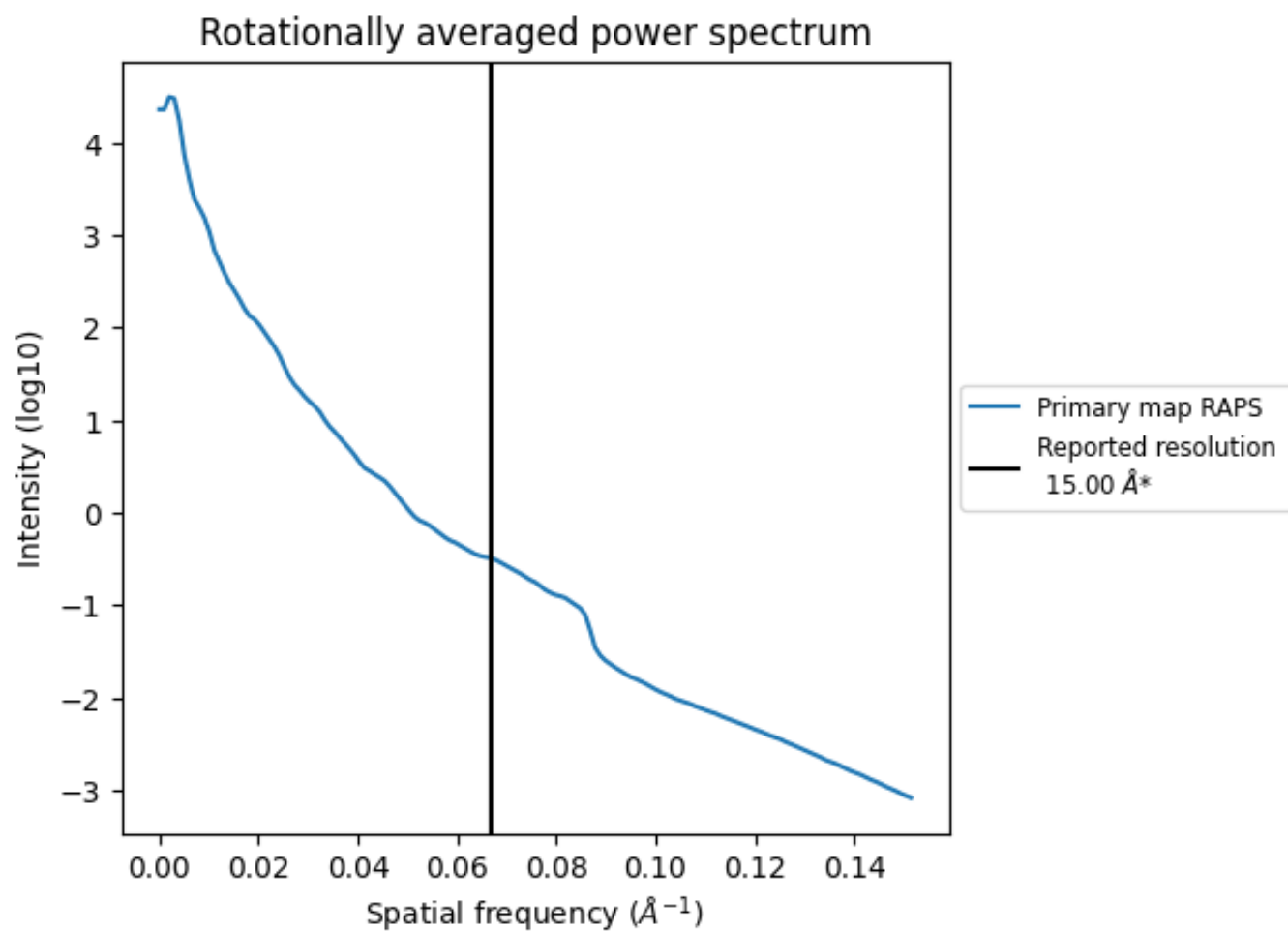
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6296 nm^3 ; this corresponds to an approximate mass of 5688 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 0.067 Å⁻¹

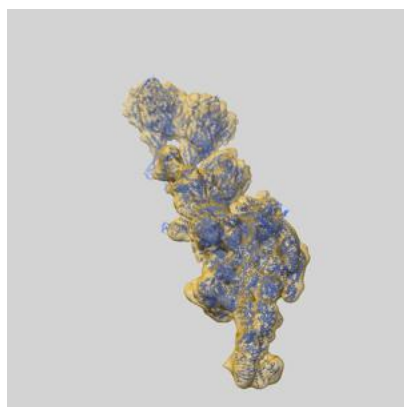
8 Fourier-Shell correlation ⓘ

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

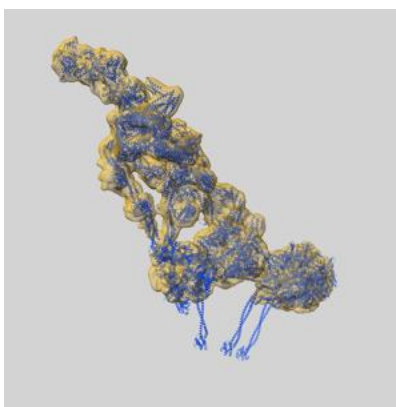
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46845 and PDB model 9DGR. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

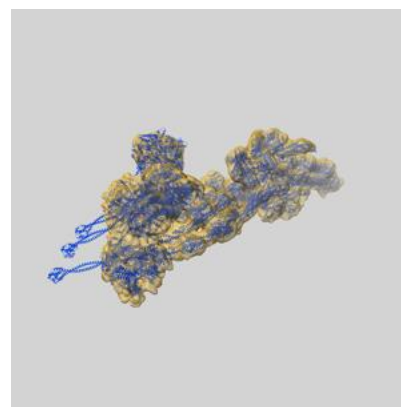
9.1 Map-model overlay [i](#)



X



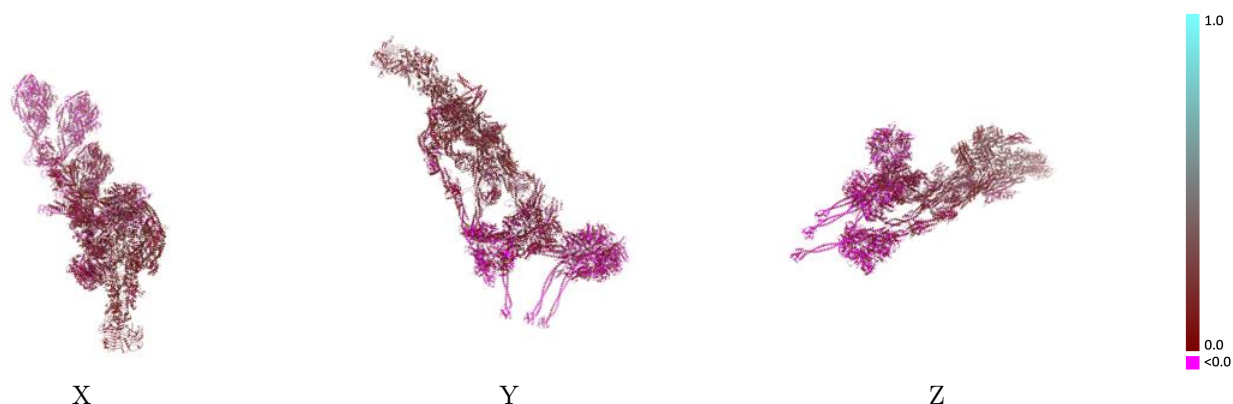
Y



Z

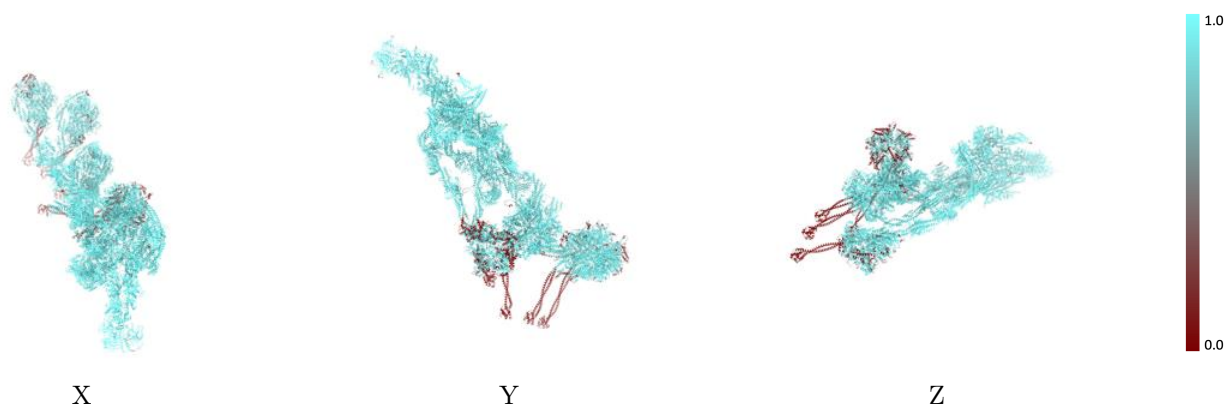
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



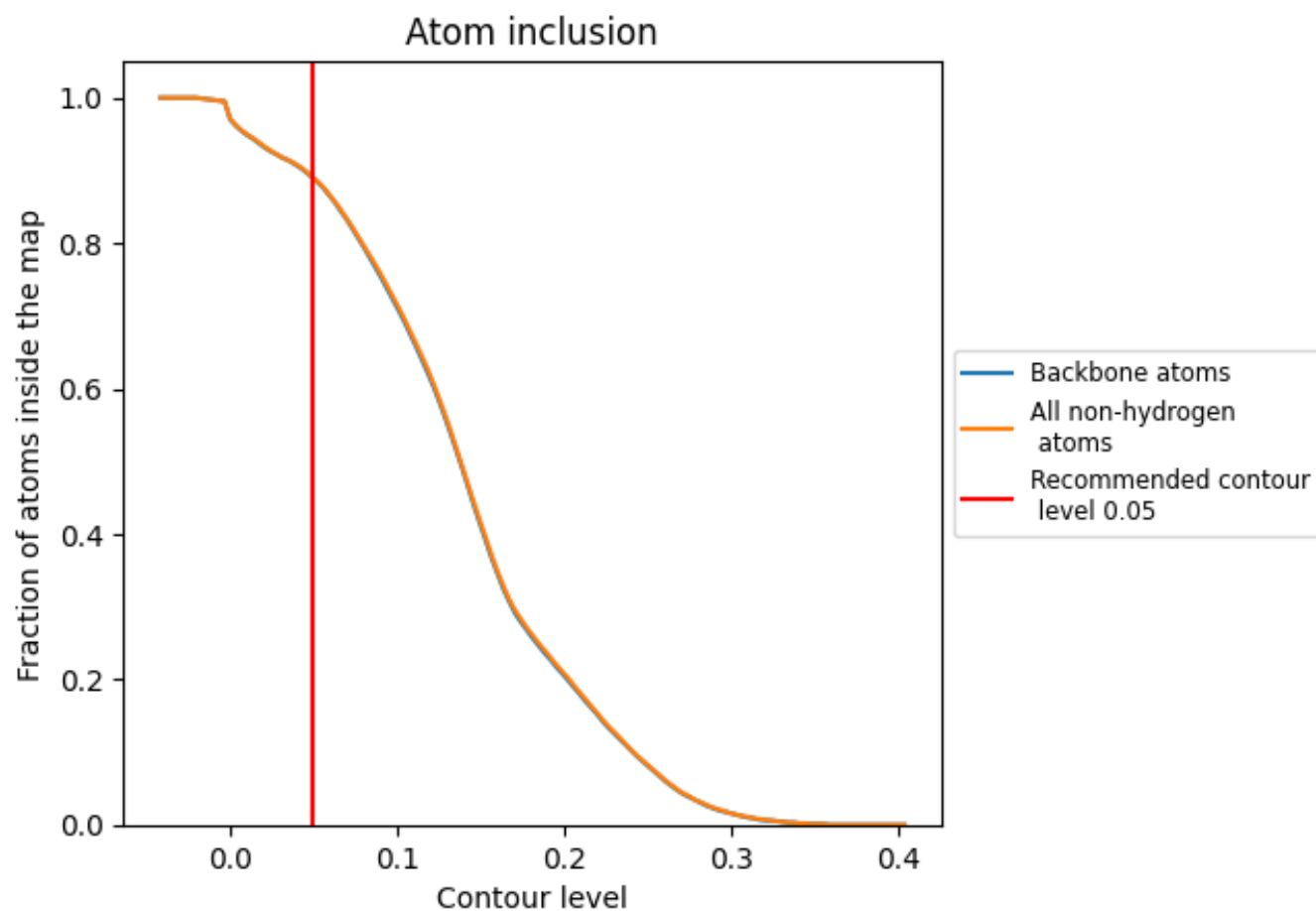
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.0960
A	 1.0000	 0.1630
B	 1.0000	 0.1730
C	 1.0000	 0.1720
D	 1.0000	 0.1690
E	 1.0000	 0.1690
F	 1.0000	 0.1710
G	 1.0000	 0.1720
H	 1.0000	 0.1580
I	 0.9900	 0.1630
J	 0.9970	 0.1600
K	 1.0000	 0.1540
L	 0.9990	 0.1650
M	 0.9950	 0.1500
N	 0.9800	 0.1540
O	 1.0000	 0.1550
P	 0.9960	 0.1750
Q	 0.9780	 0.1660
R	 1.0000	 0.1550
U	 0.9780	 0.1210
V	 1.0000	 0.1350
W	 1.0000	 0.1400
Y	 0.9580	 0.1330
Z	 0.9990	 0.1740
e	 0.6470	 0.0500
f	 0.9470	 0.1060
g	 1.0000	 0.0740
h	 1.0000	 0.0950
i	 0.9600	 0.0840
j	 1.0000	 0.1310
k	 1.0000	 0.1220
l	 1.0000	 0.0990
m	 0.8960	 0.0640
n	 0.8400	 0.0540
o	 1.0000	 0.0970



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Chain	Atom inclusion	Q-score
p	 0.9990	 0.0840
q	 1.0000	 0.1170
r	 0.9970	 0.0810
s	 0.9950	 0.0960
t	 1.0000	 0.1000