



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:02 AM UTC

PDB ID : 7TTU / pdb_00007ttu
EMDB ID : EMD-26124
Title : 50S ribosomal subunit from Staphylococcus aureus (Strain ATCC43300)
Authors : Belousoff, M.J.; Piper, S.; Johnson, R.
Deposited on : 2022-02-01
Resolution : 3.00 Å(reported)

This is a Full wwPDB EM Validation 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:

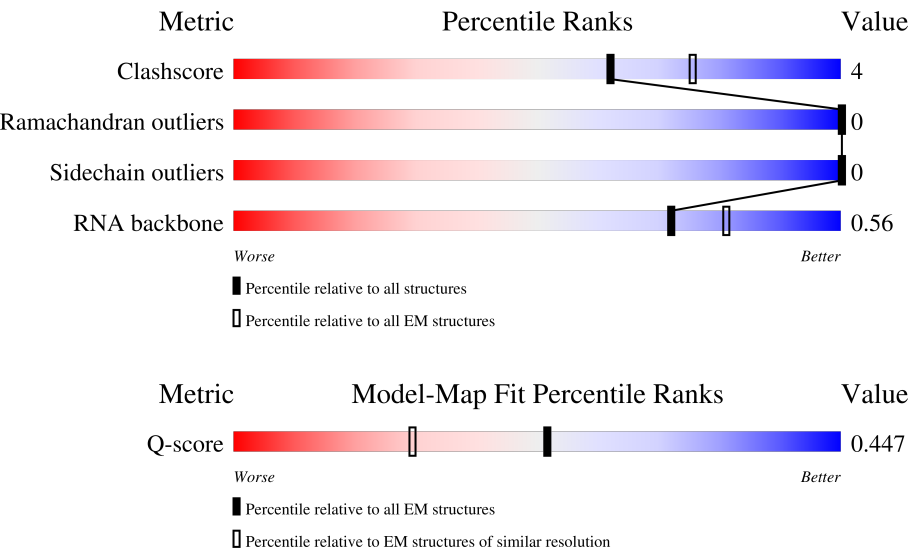
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	116	90% 8%
2	B	277	85% 14%
3	C	118	92% 7%

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Mol	Chain	Length	Quality of chain
4	D	102	
5	E	117	
6	F	87	
7	G	105	
8	H	217	
9	I	94	
10	J	61	
11	K	73	
12	L	220	
13	M	59	
14	N	57	
15	O	49	
16	P	45	
17	Q	65	
18	R	37	
19	S	207	
20	V	145	
21	W	122	
22	X	146	
23	Y	144	
24	Z	122	
25	a	119	
26	1	2923	
27	2	115	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 80724 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 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	113	Total	C	N	O	0	0
			915	576	184	155		

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	273	Total	C	N	O	S	0	0
			2085	1297	413	370	5		

- Molecule 3 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 4 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	100	Total	C	N	O	S	0	0
			785	499	139	146	1		

- Molecule 5 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 6 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	87	Total	C	N	O	S	0	0
			711	447	128	132	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	87	ASP	ILE	conflict	UNP W8TUB4

- Molecule 7 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	90	Total	C	N	O	S	0	0
			698	442	128	127	1		

- Molecule 8 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	S	0	0
			727	465	129	132	1		

- Molecule 9 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	78	Total	C	N	O		0	0
			597	367	116	114			

- Molecule 10 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	59	Total	C	N	O	S	0	0
			463	287	99	76	1		

- Molecule 11 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	61	Total	C	N	O	S	0	0
			503	310	95	97	1		

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	215	Total	C	N	O	S	0	0
			1628	1018	299	306	5		

- Molecule 13 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	56	Total	C	N	O	0	0
			432	269	82	81		

- Molecule 14 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	50	Total	C	N	O	S	0	0
			397	241	83	68	5		

- Molecule 15 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	47	Total	C	N	O	S	0	0
			390	233	79	73	5		

- Molecule 16 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	44	Total	C	N	O	S	0	0
			372	228	90	53	1		

- Molecule 17 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 18 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 19 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	192	Total	C	N	O	S	0	0
			1472	924	271	275	2		

- Molecule 20 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	143	Total	C	N	O	S	0	0
			1138	710	209	217	2		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	121	Total	C	N	O	S	0	0
			911	566	173	168	4		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	144	Total	C	N	O	S	0	0
			1082	669	213	200			

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	136	Total	C	N	O	S	0	0
			1089	698	206	181	4		

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	121	Total	C	N	O	S	0	0
			955	586	183	185	1		

- Molecule 25 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	110	Total	C	N	O	S	0	0
			857	536	165	156			

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	2684	Total	C	N	O	P	0	0
			57543	25704	10562	18603	2674		

- Molecule 27 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	111	Total	C	N	O	P	0	0
			2361	1057	423	771	110		

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.

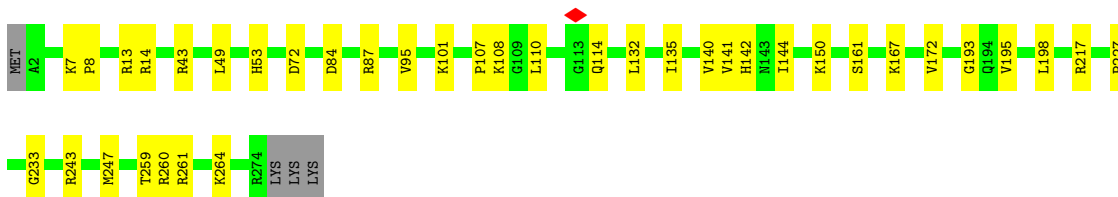
- Molecule 1: 50S ribosomal protein L19

Chain A: 

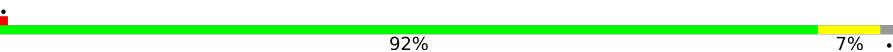


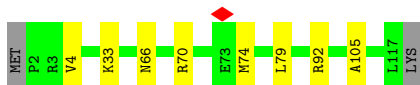
- Molecule 2: 50S ribosomal protein L2

Chain B: 



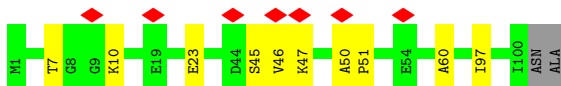
- Molecule 3: 50S ribosomal protein L20

Chain C: 



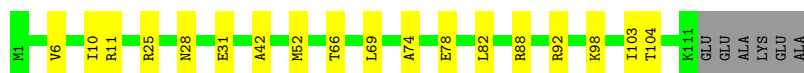
- Molecule 4: 50S ribosomal protein L21

Chain D: 

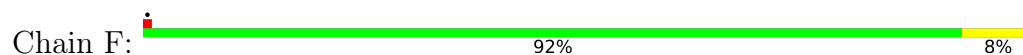


- Molecule 5: 50S ribosomal protein L22

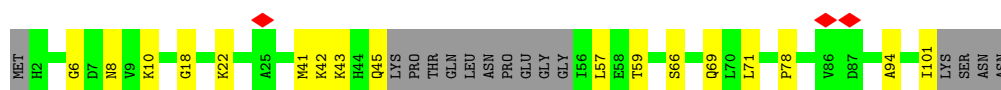
Chain E: 



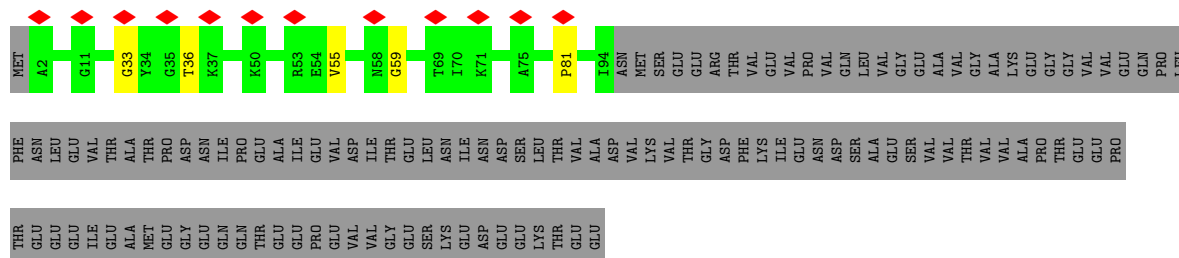
- Molecule 6: 50S ribosomal protein L23



- Molecule 7: 50S ribosomal protein L24



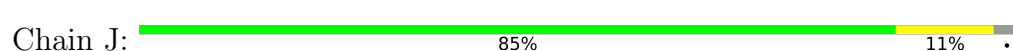
- Molecule 8: 50S ribosomal protein L25



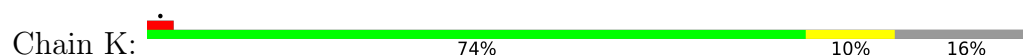
- Molecule 9: 50S ribosomal protein L27

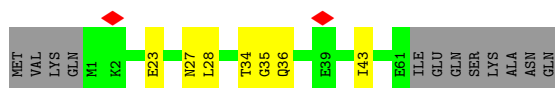


- Molecule 10: 50S ribosomal protein L28

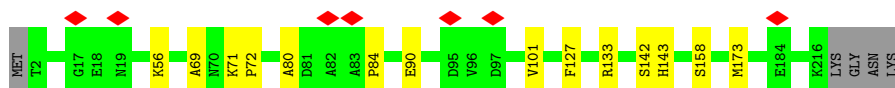


- Molecule 11: 50S ribosomal protein L29

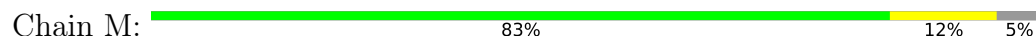




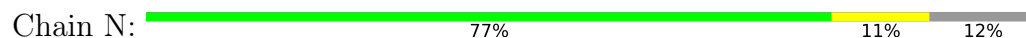
- Molecule 12: 50S ribosomal protein L3



- Molecule 13: 50S ribosomal protein L30



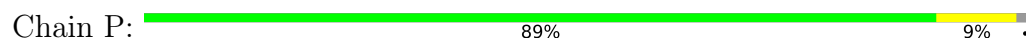
- Molecule 14: 50S ribosomal protein L32



- Molecule 15: 50S ribosomal protein L33



- Molecule 16: 50S ribosomal protein L34

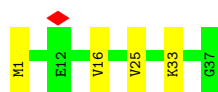


- Molecule 17: 50S ribosomal protein L35

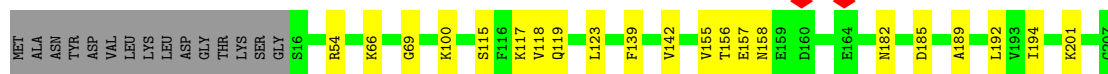
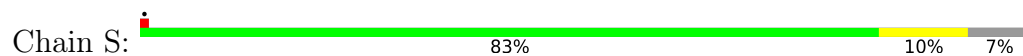


- Molecule 18: 50S ribosomal protein L36

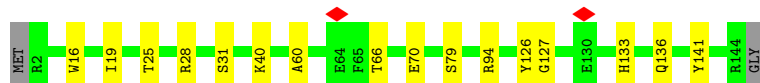
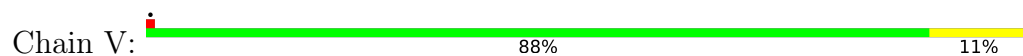




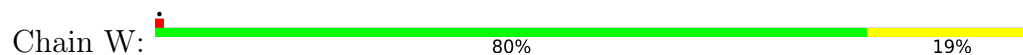
- Molecule 19: 50S ribosomal protein L4



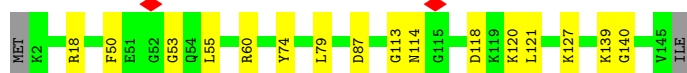
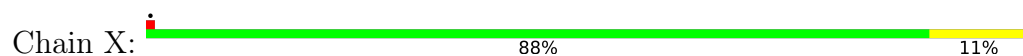
- Molecule 20: 50S ribosomal protein L13



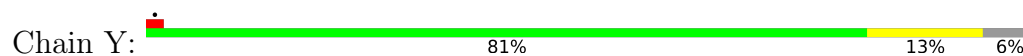
- Molecule 21: 50S ribosomal protein L14



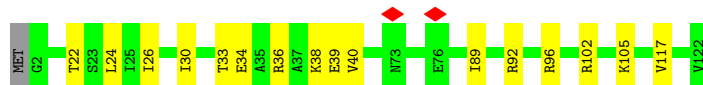
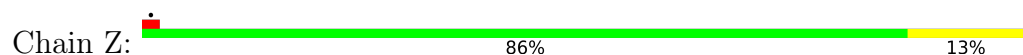
- Molecule 22: 50S ribosomal protein L15



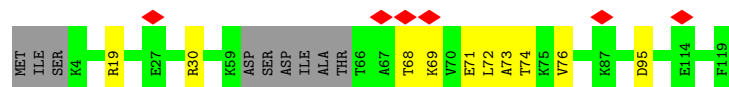
- Molecule 23: 50S ribosomal protein L16



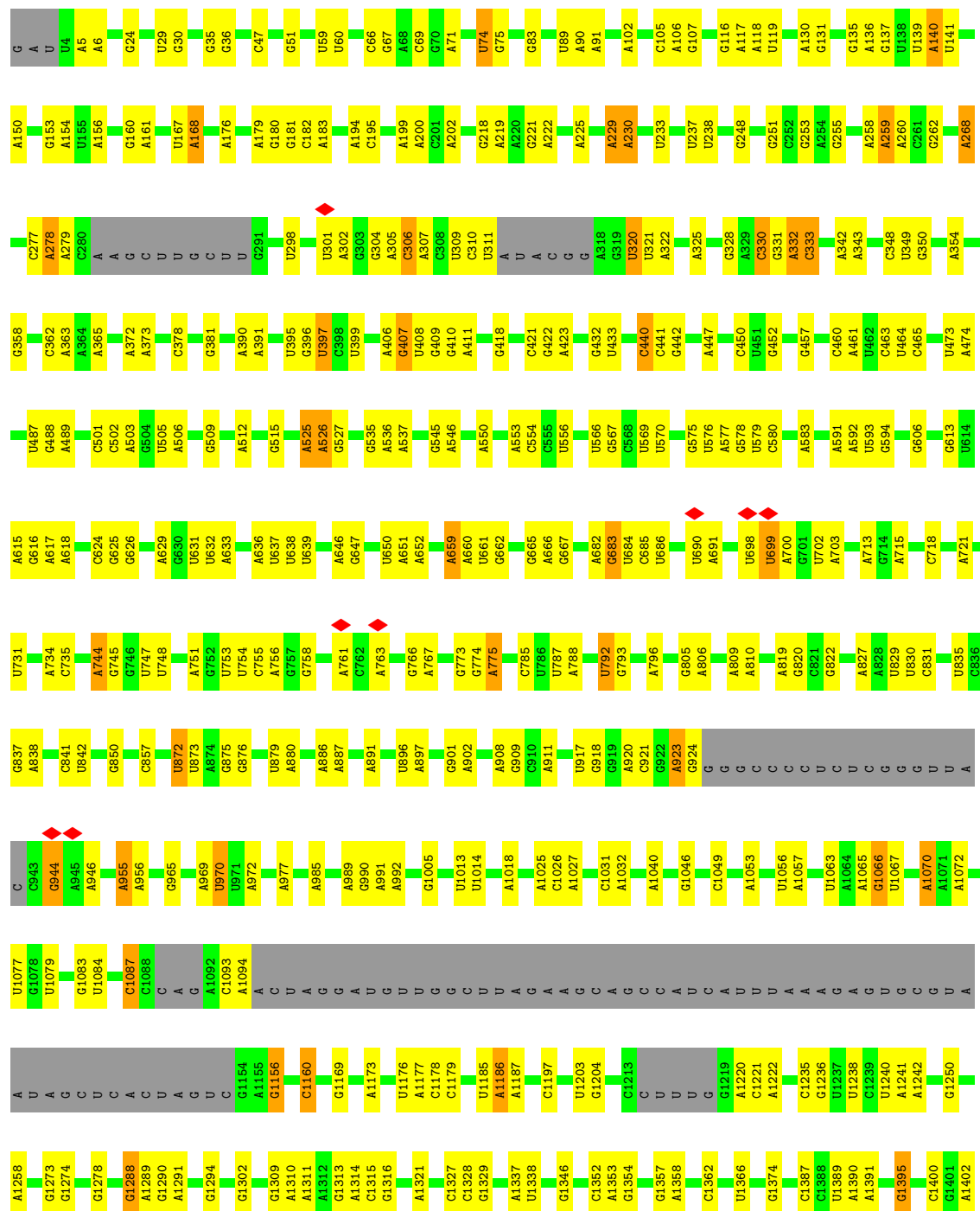
- Molecule 24: 50S ribosomal protein L17



- Molecule 25: 50S ribosomal protein L18



Chain 1: 64% 25% 8%



A2912	G2913	U2920	C	A	A	G2793	A2805	U2806	G2807	C2814	G2815	C2816	U2820	U2821	G2822	G2823	G2824	U2825	U2826	A2827	U2828	A2839	A2840	A2841	G2842	A2843	U2844	G2845	U2853	U2856	A2857	G2858	G2859	U2860	U2861	G2876	G2877	A2880	C2881	A2882	U2883	G2884	U2885	G2886	G2887	G2892	A2893	C2900	U2901	A2902	G2906	A2907	A2911																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
U2640	A2641	U2649	U2657	U2662	U2663	A2668	C2673	U2676	C2677	G2690	A2698	U2699	U2705	A2706	C2710	U2711	G2712	U2716	A2717	A2732	G2741	U2747	A2748	G2749	U2753	G2758	G2759	U2760	A2767	A2768	G2771	A2775	G2778	U2783	A2784	A2791	A2792	G2876	G2877	A2880	C2881	A2882	U2883	G2884	U2885	G2886	G2887	G2892	A2893	C2900	U2901	A2902	G2906	A2907	A2911																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
A2496	G2497	A2503	G2504	A2505	G2521	C2525	G2529	A2530	G2535	C2539	A2540	A2545	U2546	C2547	G2556	C2561	U2574	G2575	G2580	A2593	G2594	A2599	C2600	C2606	U2607	G2608	G2609	U2612	C2613	C2618	G2619	G2624	A2625	A2629	U2631	U2636	C2637	G2638	C2639	C2640	A2641	U2642	A2643	U2644	A2645	A2646	A2647	A2648	A2649	A2650	A2651	A2652	A2653	A2654	A2655	A2656	A2657	A2658	A2659	A2660	A2661	A2662	A2663	A2664	A2665	A2666	A2667	A2668	A2669	A2670	A2671	A2672	A2673	A2674	A2675	A2676	A2677	A2678	A2679	A2680	A2681	A2682	A2683	A2684	A2685	A2686	A2687	A2688	A2689	A2690	A2691	A2692	A2693	A2694	A2695	A2696	A2697	A2698	A2699	A2700	A2701	A2702	A2703	A2704	A2705	A2706	A2707	A2708	A2709	A2710	A2711	A2712	A2713	A2714	A2715	A2716	A2717	A2718	A2719	A2720	A2721	A2722	A2723	A2724	A2725	A2726	A2727	A2728	A2729	A2730	A2731	A2732	A2733	A2734	A2735	A2736	A2737	A2738	A2739	A2740	A2741	A2742	A2743	A2744	A2745	A2746	A2747	A2748	A2749	A2750	A2751	A2752	A2753	A2754	A2755	A2756	A2757	A2758	A2759	A2760	A2761	A2762	A2763	A2764	A2765	A2766	A2767	A2768	A2769	A2770	A2771	A2772	A2773	A2774	A2775	A2776	A2777	A2778	A2779	A2780	A2781	A2782	A2783	A2784	A2785	A2786	A2787	A2788	A2789	A2790	A2791	A2792	A2793	A2794	A2795	A2796	A2797	A2798	A2799	A2800	A2801	A2802	A2803	A2804	A2805	A2806	A2807	A2808	A2809	A2810	A2811	A2812	A2813	A2814	A2815	A2816	A2817	A2818	A2819	A2820	A2821	A2822	A2823	A2824	A2825	A2826	A2827	A2828	A2829	A2830	A2831	A2832	A2833	A2834	A2835	A2836	A2837	A2838	A2839	A2840	A2841	A2842	A2843	A2844	A2845	A2846	A2847	A2848	A2849	A2850	A2851	A2852	A2853	A2854	A2855	A2856	A2857	A2858	A2859	A2860	A2861	A2862	A2863	A2864	A2865	A2866	A2867	A2868	A2869	A2870	A2871	A2872	A2873	A2874	A2875	A2876	A2877	A2878	A2879	A2880	A2881	A2882	A2883	A2884	A2885	A2886	A2887	A2888	A2889	A2890	A2891	A2892	A2893	A2894	A2895	A2896	A2897	A2898	A2899	A2900	A2901	A2902	A2903	A2904	A2905	A2906	A2907	A2908	A2909	A2910	A2911	A2912	A2913	A2914	A2915	A2916	A2917	A2918	A2919	A2920	A2921	A2922	A2923	A2924	A2925	A2926	A2927	A2928	A2929	A2930	A2931	A2932	A2933	A2934	A2935	A2936	A2937	A2938	A2939	A2940	A2941	A2942	A2943	A2944	A2945	A2946	A2947	A2948	A2949	A2950	A2951	A2952	A2953	A2954	A2955	A2956	A2957	A2958	A2959	A2960	A2961	A2962	A2963	A2964	A2965	A2966	A2967	A2968	A2969	A2970	A2971	A2972	A2973	A2974	A2975	A2976	A2977	A2978	A2979	A2980	A2981	A2982	A2983	A2984	A2985	A2986	A2987	A2988	A2989	A2990	A2991	A2992	A2993	A2994	A2995	A2996	A2997	A2998	A2999	A3000	A3001	A3002	A3003	A3004	A3005	A3006	A3007	A3008	A3009	A3010	A3011	A3012	A3013	A3014	A3015	A3016	A3017	A3018	A3019	A3020	A3021	A3022	A3023	A3024	A3025	A3026	A3027	A3028	A3029	A3030	A3031	A3032	A3033	A3034	A3035	A3036	A3037	A3038	A3039	A3040	A3041	A3042	A3043	A3044	A3045	A3046	A3047	A3048	A3049	A3050	A3051	A3052	A3053	A3054	A3055	A3056	A3057	A3058	A3059	A3060	A3061	A3062	A3063	A3064	A3065	A3066	A3067	A3068	A3069	A3070	A3071	A3072	A3073	A3074	A3075	A3076	A3077	A3078	A3079	A3080	A3081	A3082	A3083	A3084	A3085	A3086	A3087	A3088	A3089	A3090	A3091	A3092	A3093	A3094	A3095	A3096	A3097	A3098	A3099	A3100	A3101	A3102	A3103	A3104	A3105	A3106	A3107	A3108	A3109	A3110	A3111	A3112	A3113	A3114	A3115	A3116	A3117	A3118	A3119	A3120	A3121	A3122	A3123	A3124	A3125	A3126	A3127	A3128	A3129	A3130	A3131	A3132	A3133	A3134	A3135	A3136	A3137	A3138	A3139	A3140	A3141	A3142	A3143	A3144	A3145	A3146	A3147	A3148	A3149	A3150	A3151	A3152	A3153	A3154	A3155	A3156	A3157	A3158	A3159	A3160	A3161	A3162	A3163	A3164	A3165	A3166	A3167	A3168	A3169	A3170	A3171	A3172	A3173	A3174	A3175	A3176	A3177	A3178	A3179	A3180	A3181	A3182	A3183	A3184	A3185	A3186	A3187	A3188	A3189	A3190	A3191	A3192	A3193	A3194	A3195	A3196	A3197	A3198	A3199	A3200	A3201	A3202	A3203	A3204	A3205	A3206	A3207	A3208	A3209	A3210	A3211	A3212	A3213	A3214	A3215	A3216	A3217	A3218	A3219	A3220	A3221	A3222	A3223	A3224	A3225	A3226	A3227	A3228	A3229	A3230	A3231	A3232	A3233	A3234	A3235	A3236	A3237	A3238	A3239	A3240	A3241	A3242	A3243	A3244	A3245	A3246	A3247	A3248	A3249	A3250	A3251	A3252	A3253	A3254	A3255	A3256	A3257	A3258	A3259	A3260	A3261	A3262	A3263	A3264	A3265	A3266	A3267	A3268	A3269	A3270	A3271	A3272	A3273	A3274	A3275	A3276	A3277	A3278	A3279	A3280	A3281	A3282	A3283	A3284	A3285	A3286	A3287	A3288	A3289	A3290	A3291	A3292	A3293	A3294	A3295	A3296	A3297	A3298	A3299	A3300	A3301	A3302	A3303	A3304	A3305	A3306	A3307	A3308	A3309	A3310	A3311	A3312	A3313	A3314	A3315	A3316	A3317	A3318	A3319	A3320	A3321	A3322	A3323	A3324	A3325	A3326	A3327	A3328	A3329	A3330	A3331	A3332	A3333	A3334	A3335	A3336	A3337	A3338	A3339	A3340	A3341	A3342	A3343	A3344	A3345	A3346	A3347	A3348	A3349	A3350	A3351	A3352	A3353	A3354	A3355	A3356	A3357	A3358	A3359	A3360	A3361	A3362	A3363	A3364	A3365	A3366	A3367	A3368	A3369	A3370	A3371	A3372	A3373	A3374	A3375	A3376	A3377	A3378	A3379	A3380	A3381	A3382	A3383	A3384	A3385	A3386	A3387	A3388	A3389	A3390	A3391	A3392	A3393	A3394	A3395	A3396	A3397	A3398	A3399	A3400	A3401	A3402	A3403	A3404	A3405	A3406	A3407	A3408	A3409	A3410	A3411	A3412	A3413	A3414	A3415	A3416	A3417	A3418	A3419	A3420	A3421	A3422	A3423	A3424	A3425	A3426	A3427	A3428	A3429	A3430	A3431	A3432	A3433	A3434	A3435	A3436	A3437	A3438	A3439	A3440	A3441	A3442	A3443	A3444	A3445	A3446	A3447	A3448	A3449	A3450	A3451	A3452	A3453	A3454	A3455	A3456	A3457	A3458	A3459	A3460	A3461	A3462	A3463	A3464	A3465	A3466	A3467	A3468	A3469	A3470	A3471	A3472	A3473	A3474	A3475	A3476	A3477	A3478	A3479	A3480	A3481	A3482	A3483	A3484	A3485	A3486	A3487	A3488	A3489	A3490	A3491	A3492	A3493	A3494	A3495	A3496	A3497	A3498	A3499	A3500	A3501	A3502	A3503	A3504	A3505	A3506	A3507	A3508	A3509	A3510	A3511	A3512	A3513	A3514	A3515	A3516	A3517	A3518	A3519	A3520	A3521	A3522	A3523	A3524	A3525	A3526	A3527	A3528	A3529	A3530	A3531	A3532	A3533	A3534	A3535	A3536	A3537	A3538	A3539	A3540	A3541	A3542	A3543	A3544	A3545	A3546	A3547	A3548	A3549	A3550	A3551	A3552	A3553	A3554	A3555	A3556	A3557	A3558	A3559	A3560	A3561	A3562	A3563	A3564	A3565	A3566	A3567	A3568	A3569	A3570	A3571	A3572	A3573	A3574	A3575	A3576	A3577	A3578	A3579	A3580	A3581	A3582	A3583	A3584	A3585	A3586	A3587	A3588	A3589	A3590	A3591	A3592	A3593	A3594	A3595	A3596	A3597	A3598	A3599	A3600	A3601	A3602	A3603	A3604	A3605	A3606	A3607	A3608	A3609	A3610	A3611	A3612	A3613	A3614	A3615	A3616	A3617	A3618	A3619	A3620	A3621	A3622	A3623	A3624	A3625	A3626	A3627	A3628	A3629	A3630	A3631	A3632	A3633	A3634	A3635	A3636	A3637	A3638	A3639	A3640	A3641	A3642	A3643	A3644	A3645	A3646	A3647	A3648	A3649	A3650	A3651	A3652	A3653	A3654	A3655	A3656	A3657	A3658	A3659	A3660	A3661	A3662	A3663	A3664	A3665	A3666	A3667	A3668	A3669	A3670	A3671	A3672	A3673	A3674	A3675	A3676	A3677	A3678	A3679	A3680	A3681	A3682	A3683	A3684	A3685	A3686	A3687	A3688	A3689	A3690	A3691	A3692	A3693	A3694	A3695	A3696	A3697	A3698	A3699	A3700	A3701	A3702	A3703	A3704	A3705	A3706	A3707	A3708	A3709	A3710	A3711	A3712	A3713	A3714	A3715	A3716	A3717	A3718	A3719	A3720	A3721	A3722	A3723	A3724	A3725	A3726	A3727	A3728	A3729	A3730	A3731	A3732	A3733	A3734	A3735	A3736	A3737	A3738	A3739	A3740	A3741	A3742	A3743	A3744	A3745	A3746	A3747	A3748	A3749	A3750	A3751	A3752	A3753	A3754	A3755	A3756	A3757	A3758	A3759	A3760	A3761	A3762	A3763	A3764	A3765	A3766	A3767	A3768	A3769	A3770	A3771	A3772	A3773	A3774	A3775	A3776	A3777	A3778	A3779	A3780	A3781	A3782	A3783	A3784	A3785	A3786	A3787	A3788	A3789	A3790	A3791	A3792	A3793	A3794	A3795	A3796	A3797	A3798	A3799	A3800	A3801	A3802	A3803	A3804	A3805	A3806	A3807	A3808	A3809	A3810	A3811	A3812	A3813	A3814	A3815	A3816	A3817	A3818	A3819	A3820	A3821	A3822	A3823	A3824	A3825	A3826	A3827	A3828	A3829	A3830	A3831	A3832	A3833	A3834	A3835	A3836	A3837	A3838	A3839	A3840	A3841	A3842	A3843	A3844	A384

● Molecule 27: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	157000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.5	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.353	Depositor
Minimum map value	-0.211	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	400.96, 400.96, 400.96	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.895, 0.895, 0.895	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.09	0/927	0.22	0/1239
2	B	0.09	0/2120	0.26	0/2847
3	C	0.09	0/955	0.22	0/1265
4	D	0.09	0/795	0.31	0/1062
5	E	0.09	0/861	0.26	0/1159
6	F	0.11	0/719	0.23	0/959
7	G	0.08	0/704	0.25	0/938
8	H	0.08	0/735	0.21	0/986
9	I	0.09	0/603	0.25	0/801
10	J	0.08	0/469	0.24	0/625
11	K	0.09	0/504	0.28	0/670
12	L	0.10	0/1652	0.26	0/2216
13	M	0.08	0/434	0.25	0/585
14	N	0.10	0/404	0.25	0/537
15	O	0.09	0/393	0.32	0/523
16	P	0.23	0/376	0.32	0/491
17	Q	0.09	0/526	0.22	0/690
18	R	0.09	0/299	0.24	0/393
19	S	0.20	0/1494	0.35	0/2018
20	V	0.09	0/1160	0.24	0/1563
21	W	0.10	0/918	0.30	0/1232
22	X	0.08	0/1096	0.24	0/1461
23	Y	0.10	0/1113	0.25	0/1493
24	Z	0.09	0/959	0.24	0/1282
25	a	0.09	0/865	0.26	0/1154
26	1	0.11	0/64448	0.24	0/100506
27	2	0.08	0/2640	0.21	0/4112
All	All	0.11	0/88169	0.25	0/132807

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	915	0	987	7	0
2	B	2085	0	2192	26	0
3	C	943	0	1014	7	0
4	D	785	0	825	6	0
5	E	853	0	914	12	0
6	F	711	0	743	4	0
7	G	698	0	756	11	0
8	H	727	0	777	3	0
9	I	597	0	607	6	0
10	J	463	0	501	4	0
11	K	503	0	536	4	0
12	L	1628	0	1667	11	0
13	M	432	0	472	5	0
14	N	397	0	407	4	0
15	O	390	0	396	7	0
16	P	372	0	420	3	0
17	Q	521	0	586	2	0
18	R	296	0	340	2	0
19	S	1472	0	1520	12	0
20	V	1138	0	1130	10	0
21	W	911	0	970	16	0
22	X	1082	0	1119	10	0
23	Y	1089	0	1155	13	0
24	Z	955	0	1002	10	0
25	a	857	0	903	6	0
26	1	57543	0	28959	370	0
27	2	2361	0	1197	20	0
All	All	80724	0	52095	539	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (539) 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)
9:I:85:LYS:NZ	26:1:902:A:OP1	2.17	0.76
27:2:5:G:H1	27:2:108:U:H3	1.30	0.76
26:1:1862:G:H1	26:1:1932:C:H5	1.33	0.74
2:B:107:PRO:HD2	2:B:110:LEU:HD22	1.70	0.73
27:2:4:G:H22	27:2:109:G:H1	1.35	0.72
2:B:95:VAL:HG22	2:B:101:LYS:HG2	1.72	0.72
21:W:1:MET:HG2	21:W:2:ILE:HG12	1.72	0.72
26:1:2314:A:H62	26:1:2371:U:H3	1.39	0.71
1:A:53:ARG:NH2	26:1:2710:C:OP1	2.23	0.71
14:N:42:VAL:HG12	14:N:49:TYR:HB2	1.73	0.71
26:1:793:G:N2	26:1:796:A:OP2	2.25	0.70
26:1:1806:U:OP2	26:1:1811:A:N6	2.25	0.70
5:E:25:ARG:NH1	5:E:74:ALA:O	2.26	0.69
26:1:330:C:N3	26:1:397:U:O4	2.26	0.69
23:Y:56:ARG:NH1	26:1:2496:A:O2'	2.25	0.69
26:1:2608:G:OP2	26:1:2608:G:N2	2.21	0.68
16:P:41:LYS:HD3	26:1:505:U:H5''	1.75	0.67
26:1:1487:G:H22	26:1:1596:G:H22	1.43	0.67
2:B:150:LYS:NZ	26:1:2231:C:OP2	2.29	0.66
26:1:1514:A:H61	26:1:1566:G:H1	1.44	0.66
26:1:1941:C:O2'	26:1:1943:A:N1	2.29	0.66
26:1:277:C:N3	26:1:278:A:N6	2.44	0.66
26:1:2126:C:H42	26:1:2218:G:H1	1.44	0.66
26:1:1725:G:HO2'	26:1:1789:A:HO2'	1.41	0.65
26:1:944:G:N2	26:1:944:G:OP1	2.29	0.65
26:1:2822:C:H4'	26:1:2823:G:H2'	1.79	0.65
9:I:27:LYS:NZ	26:1:2288:C:OP1	2.29	0.65
21:W:88:ARG:HG2	21:W:89:ASP:H	1.61	0.65
26:1:1515:G:H22	26:1:1565:U:H3	1.43	0.65
24:Z:102:ARG:NH1	26:1:2902:A:OP1	2.29	0.65
23:Y:16:LYS:HG2	23:Y:18:THR:HG22	1.77	0.64
2:B:142:HIS:ND1	2:B:193:GLY:O	2.27	0.64
15:O:34:LYS:NZ	26:1:2374:C:OP1	2.31	0.64
14:N:6:ARG:NH2	26:1:2046:U:OP2	2.28	0.64
27:2:9:C:H42	27:2:104:A:H61	1.45	0.64
26:1:1462:G:OP2	26:1:1462:G:N2	2.25	0.64
6:F:48:VAL:HG11	6:F:82:LEU:HD13	1.80	0.64
19:S:117:LYS:NZ	19:S:189:ALA:O	2.31	0.64
1:A:85:LYS:HZ1	1:A:87:GLU:HG2	1.63	0.64
17:Q:39:LYS:NZ	26:1:2392:G:N7	2.46	0.63
26:1:506:A:C2	26:1:515:G:N2	2.67	0.63
26:1:632:U:H2'	26:1:633:A:H8	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:721:A:H8	26:1:2096:G:H21	1.45	0.63
26:1:1708:A:H61	26:1:2023:C:H42	1.45	0.63
26:1:2877:G:N2	26:1:2880:A:OP2	2.30	0.63
26:1:591:A:H4'	26:1:592:A:H5'	1.80	0.62
22:X:114:ASN:ND2	26:1:699:U:O4	2.33	0.62
25:a:69:LYS:O	25:a:73:ALA:N	2.32	0.62
20:V:126:TYR:OH	20:V:133:HIS:NE2	2.29	0.62
26:1:1780:G:N2	26:1:1783:G:OP2	2.30	0.62
20:V:31:SER:HG	26:1:1049:C:HO2'	1.48	0.62
26:1:153:G:H2'	26:1:154:A:H8	1.64	0.61
7:G:41:MET:HE1	7:G:43:LYS:HB2	1.82	0.61
10:J:5:CYS:HB3	10:J:10:ARG:H	1.65	0.61
7:G:94:ALA:HB2	7:G:101:ILE:HD11	1.83	0.61
15:O:13:GLY:HA3	15:O:38:ARG:HD2	1.82	0.61
2:B:259:THR:HG1	26:1:1824:C:HO2'	1.49	0.60
12:L:71:LYS:HG3	26:1:2814:C:H4'	1.83	0.60
3:C:92:ARG:NH2	26:1:1197:C:OP1	2.33	0.60
14:N:16:ARG:NH2	26:1:1302:G:OP1	2.30	0.60
26:1:2580:G:H8	26:1:2609:G:H21	1.50	0.60
24:Z:105:LYS:HA	24:Z:117:VAL:HG12	1.83	0.60
26:1:200:A:N6	26:1:2457:A:O2'	2.34	0.60
2:B:107:PRO:HA	2:B:195:VAL:HA	1.84	0.60
26:1:221:G:H22	26:1:238:U:H4'	1.67	0.60
2:B:132:LEU:HD23	2:B:135:ILE:HD12	1.83	0.60
26:1:665:G:H4'	26:1:666:A:H5''	1.84	0.59
26:1:304:G:H2'	26:1:305:A:H8	1.65	0.59
26:1:409:G:OP2	26:1:409:G:N2	2.35	0.59
26:1:2355:A:H2'	26:1:2356:A:C8	2.38	0.59
26:1:342:A:N3	26:1:362:C:O2'	2.31	0.59
12:L:90:GLU:OE1	26:1:2662:U:O2'	2.18	0.59
26:1:2885:U:OP2	26:1:2886:G:O2'	2.18	0.59
19:S:182:ASN:ND2	19:S:185:ASP:OD2	2.32	0.59
21:W:64:ARG:NH1	21:W:101:PRO:O	2.33	0.59
26:1:920:A:N6	26:1:944:G:OP2	2.35	0.59
4:D:60:ALA:HB2	4:D:97:ILE:HD13	1.85	0.59
26:1:262:G:H21	26:1:666:A:H8	1.50	0.59
26:1:1512:U:H2'	26:1:1513:A:C8	2.37	0.58
26:1:1881:A:H62	26:1:1915:G:H8	1.49	0.58
9:I:82:ARG:NH2	27:2:10:U:O2'	2.36	0.58
19:S:54:ARG:NH1	26:1:718:C:OP1	2.33	0.58
22:X:55:LEU:HD23	22:X:60:ARG:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1886:A:H62	26:1:1910:G:H8	1.50	0.58
7:G:69:GLN:HE21	26:1:378:C:H4'	1.69	0.58
26:1:320:U:OP1	26:1:325:A:N6	2.34	0.58
26:1:2816:C:H5	26:1:2913:G:H1	1.52	0.58
26:1:1708:A:H61	26:1:2023:C:N4	2.02	0.58
20:V:60:ALA:HB3	20:V:127:GLY:HA2	1.85	0.58
26:1:1522:G:HO2'	26:1:1607:A:HO2'	1.50	0.58
26:1:1482:U:H2'	26:1:1483:A:H8	1.69	0.57
26:1:1915:G:OP2	26:1:1915:G:N2	2.30	0.57
26:1:2824:G:H2'	26:1:2825:U:O2	2.04	0.57
26:1:1357:G:OP2	26:1:1357:G:N2	2.24	0.57
26:1:1422:A:O2'	26:1:1433:U:O2	2.21	0.57
26:1:1479:G:O6	26:1:1605:A:N6	2.37	0.57
7:G:42:LYS:O	26:1:526:A:O2'	2.19	0.57
1:A:85:LYS:NZ	1:A:87:GLU:HG2	2.17	0.57
26:1:331:G:H1	26:1:395:U:H3	1.52	0.57
21:W:3:GLN:NE2	26:1:2022:U:O2	2.38	0.57
26:1:1346:G:H21	26:1:1655:C:H5'	1.70	0.57
7:G:41:MET:SD	7:G:59:THR:OG1	2.63	0.56
26:1:787:U:H2'	26:1:788:A:C8	2.39	0.56
1:A:29:ARG:HG2	1:A:46:GLU:HG2	1.87	0.56
2:B:167:LYS:HG3	2:B:172:VAL:HG12	1.86	0.56
26:1:106:A:H2'	26:1:107:G:H8	1.70	0.56
26:1:1506:C:H2'	26:1:1507:A:C8	2.40	0.56
26:1:629:A:H62	26:1:1289:A:H2	1.53	0.56
26:1:2618:C:H2'	26:1:2619:G:H8	1.70	0.56
26:1:744:A:H8	26:1:1677:G:HO2'	1.52	0.56
19:S:100:LYS:NZ	26:1:651:A:OP1	2.31	0.56
21:W:7:ARG:HE	21:W:20:LEU:HD12	1.69	0.56
21:W:1:MET:HB2	21:W:8:LEU:HD21	1.88	0.55
26:1:2624:G:H2'	26:1:2625:A:C8	2.41	0.55
26:1:1352:C:H2'	26:1:1353:A:H8	1.71	0.55
2:B:261:ARG:O	2:B:264:LYS:NZ	2.39	0.55
6:F:53:VAL:HG22	6:F:80:VAL:HG12	1.88	0.55
21:W:115:VAL:HG13	21:W:121:VAL:HG21	1.87	0.55
5:E:78:GLU:OE2	26:1:24:G:N2	2.37	0.55
5:E:42:ALA:HB2	26:1:2037:G:H5''	1.88	0.54
26:1:222:A:N3	26:1:237:U:O2'	2.39	0.54
26:1:153:G:H2'	26:1:154:A:C8	2.43	0.54
26:1:328:G:H1	26:1:399:U:H3	1.55	0.54
26:1:1522:G:N1	26:1:1523:G:O6	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1893:A:N6	26:1:1902:G:O2'	2.41	0.54
26:1:350:G:OP2	26:1:350:G:N2	2.40	0.54
26:1:2881:C:H2'	26:1:2882:A:H8	1.71	0.54
23:Y:56:ARG:HH12	26:1:2496:A:HO2'	1.51	0.54
26:1:2418:G:O2'	26:1:2451:C:N4	2.37	0.54
11:K:23:GLU:O	11:K:27:ASN:ND2	2.41	0.53
2:B:110:LEU:HD12	2:B:114:GLN:HG3	1.90	0.53
10:J:56:SER:HB3	26:1:418:G:C8	2.43	0.53
26:1:421:C:H2'	26:1:422:G:H8	1.74	0.53
26:1:2876:G:O6	26:1:2882:A:N6	2.41	0.53
24:Z:89:ILE:HG13	24:Z:92:ARG:HH21	1.74	0.52
26:1:1518:G:H1	26:1:1562:C:H42	1.56	0.52
26:1:1943:A:H5''	26:1:1944:U:H5	1.74	0.52
18:R:1:MET:HG2	18:R:33:LYS:HE3	1.90	0.52
2:B:7:LYS:NZ	26:1:751:A:OP1	2.32	0.52
3:C:105:ALA:HB2	4:D:47:LYS:HE2	1.89	0.52
26:1:1063:U:OP1	26:1:1079:U:O2'	2.21	0.52
26:1:1500:G:N7	26:1:1501:G:N2	2.58	0.52
16:P:25:THR:HG23	16:P:28:GLY:H	1.74	0.52
26:1:2058:A:N3	26:1:2482:G:O2'	2.41	0.52
25:a:19:ARG:NH1	27:2:7:G:OP1	2.43	0.52
27:2:11:A:O2'	27:2:13:A:OP2	2.27	0.52
26:1:509:G:N2	26:1:512:A:OP2	2.38	0.52
26:1:917:U:H2'	26:1:918:G:C8	2.45	0.52
26:1:1487:G:N2	26:1:1596:G:H22	2.07	0.52
26:1:1423:C:O2'	26:1:1512:U:O2	2.24	0.52
26:1:917:U:H2'	26:1:918:G:H8	1.74	0.51
26:1:632:U:H2'	26:1:633:A:C8	2.44	0.51
26:1:787:U:H2'	26:1:788:A:H8	1.75	0.51
26:1:1891:U:OP1	26:1:2437:G:O2'	2.28	0.51
18:R:16:VAL:HG12	18:R:25:VAL:HG22	1.93	0.51
27:2:92:C:H2'	27:2:93:G:O4'	2.11	0.51
8:H:33:GLY:O	8:H:36:THR:HG22	2.10	0.51
26:1:1065:A:H61	26:1:1186:A:H61	1.57	0.51
26:1:116:G:OP2	26:1:118:A:O2'	2.29	0.51
26:1:683:G:H2'	26:1:684:U:C6	2.45	0.51
26:1:556:U:H4'	26:1:1273:G:H4'	1.93	0.51
27:2:12:U:OP2	27:2:68:U:O2'	2.29	0.51
7:G:6:GLY:HA2	7:G:22:LYS:HE2	1.92	0.51
19:S:139:PHE:HA	19:S:142:VAL:HG22	1.92	0.51
20:V:19:ILE:HG12	20:V:141:TYR:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:83:G:H21	26:1:102:A:H2	1.58	0.51
26:1:1516:C:H2'	26:1:1517:A:C8	2.46	0.51
26:1:460:C:H2'	26:1:461:A:H8	1.75	0.51
26:1:1423:C:H2'	26:1:1424:A:H8	1.76	0.51
26:1:2060:A:O2'	26:1:2062:G:OP2	2.26	0.51
26:1:66:C:H2'	26:1:67:G:H8	1.75	0.51
26:1:615:A:H61	26:1:2056:G:H8	1.57	0.51
26:1:896:U:H2'	26:1:897:A:H8	1.77	0.50
26:1:2056:G:OP2	26:1:2056:G:N2	2.29	0.50
2:B:13:ARG:HD2	26:1:773:G:H4'	1.93	0.50
5:E:11:ARG:NH2	5:E:98:LYS:HD2	2.26	0.50
7:G:10:LYS:HE2	7:G:18:GLY:HA2	1.93	0.50
2:B:227:PRO:HA	2:B:233:GLY:HA2	1.94	0.50
6:F:39:LYS:HG3	6:F:50:VAL:HG21	1.93	0.50
24:Z:96:ARG:NH1	26:1:2900:C:O2'	2.44	0.50
26:1:2839:A:O2'	26:1:2841:A:N7	2.42	0.50
26:1:268:A:N6	26:1:474:A:N7	2.59	0.50
26:1:310:C:N4	26:1:407:G:H1	2.09	0.50
26:1:637:U:H2'	26:1:638:U:C6	2.47	0.50
26:1:2402:G:N2	26:1:2405:A:OP2	2.34	0.50
26:1:2618:C:H2'	26:1:2619:G:C8	2.46	0.50
23:Y:44:SER:HB3	23:Y:70:PRO:HG2	1.93	0.50
26:1:2574:U:H2'	26:1:2575:G:H8	1.76	0.50
23:Y:51:ARG:HD3	23:Y:66:ILE:HD11	1.94	0.50
26:1:2098:A:H2'	26:1:2099:G:C8	2.46	0.50
26:1:2052:C:H2'	26:1:2053:U:C6	2.47	0.50
21:W:1:MET:HE2	21:W:6:THR:HG21	1.94	0.49
26:1:1083:G:H1	26:1:1160:C:H42	1.59	0.49
26:1:1185:U:H4'	26:1:1186:A:O4'	2.12	0.49
26:1:2574:U:H2'	26:1:2575:G:C8	2.47	0.49
26:1:872:U:O2'	26:1:2095:U:N3	2.45	0.49
26:1:1390:A:H3'	26:1:1391:A:H8	1.77	0.49
15:O:22:ASN:HB3	15:O:25:ASN:HB2	1.93	0.49
26:1:702:U:H2'	26:1:703:A:C8	2.48	0.49
26:1:1460:U:H3	26:1:1628:A:H61	1.60	0.49
26:1:460:C:H2'	26:1:461:A:C8	2.47	0.49
26:1:755:C:H2'	26:1:756:A:H8	1.78	0.49
2:B:140:VAL:HG13	2:B:161:SER:HB2	1.95	0.49
26:1:59:U:O2'	26:1:74:U:OP2	2.26	0.49
22:X:18:ARG:NH2	26:1:1288:G:N7	2.60	0.49
26:1:901:G:H2'	26:1:902:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1943:A:H5''	26:1:1944:U:C5	2.47	0.49
26:1:2359:C:O2'	26:1:2362:A:O2'	2.27	0.49
26:1:150:A:H61	26:1:179:A:H2	1.60	0.49
26:1:1487:G:H1	26:1:1596:G:H1	1.59	0.49
26:1:1836:A:H2'	26:1:1837:A:C8	2.47	0.49
26:1:2051:C:H2'	26:1:2052:C:C6	2.48	0.49
2:B:135:ILE:O	2:B:167:LYS:NZ	2.46	0.49
19:S:157:GLU:OE2	19:S:201:LYS:NZ	2.41	0.49
22:X:50:PHE:HE2	22:X:53:GLY:HA3	1.78	0.49
26:1:140:A:H2'	26:1:141:U:C6	2.48	0.49
26:1:1521:A:N6	26:1:1559:G:H22	2.11	0.49
2:B:43:ARG:HH11	2:B:49:LEU:HD13	1.78	0.48
19:S:123:LEU:HD12	19:S:192:LEU:HD23	1.95	0.48
26:1:1442:C:H2'	26:1:1443:A:C8	2.48	0.48
26:1:1487:G:H22	26:1:1596:G:H1	1.61	0.48
26:1:2431:C:H2'	26:1:2432:G:O4'	2.13	0.48
26:1:955:A:N3	26:1:2291:C:O2'	2.42	0.48
1:A:64:ARG:HB2	1:A:73:GLU:HG2	1.95	0.48
26:1:1442:C:H2'	26:1:1443:A:H8	1.77	0.48
26:1:1672:G:H2'	26:1:1673:A:H8	1.78	0.48
5:E:82:LEU:HB2	5:E:98:LYS:HB2	1.96	0.48
22:X:74:TYR:CZ	22:X:127:LYS:HD2	2.49	0.48
26:1:1025:A:OP2	26:1:1026:C:N4	2.41	0.48
26:1:1449:A:N1	26:1:1632:A:N6	2.61	0.48
10:J:3:LYS:HE2	10:J:33:LEU:HD12	1.96	0.48
26:1:2705:U:H2'	26:1:2706:A:H8	1.78	0.48
19:S:66:LYS:HE3	19:S:69:GLY:HA3	1.96	0.48
4:D:45:SER:OG	4:D:46:VAL:N	2.46	0.48
26:1:2881:C:H2'	26:1:2882:A:C8	2.49	0.47
3:C:33:LYS:HG2	26:1:1290:G:C2	2.49	0.47
26:1:1563:U:H2'	26:1:1564:G:H8	1.78	0.47
23:Y:28:THR:HG23	23:Y:29:PHE:CD1	2.49	0.47
26:1:194:A:H2'	26:1:195:C:H6	1.79	0.47
26:1:229:A:O2'	26:1:230:A:OP1	2.28	0.47
2:B:141:VAL:HG23	2:B:144:ILE:HD11	1.97	0.47
23:Y:78:PRO:HG2	23:Y:81:VAL:HG11	1.97	0.47
26:1:2041:A:H2'	26:1:2042:A:C8	2.49	0.47
26:1:422:G:H2'	26:1:423:A:C8	2.50	0.47
26:1:1506:C:H2'	26:1:1507:A:H8	1.77	0.47
3:C:33:LYS:HG2	26:1:1290:G:N3	2.30	0.47
26:1:348:C:H2'	26:1:349:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1521:A:H61	26:1:1559:G:H22	1.62	0.47
26:1:1981:G:O2'	26:1:1983:U:O4	2.19	0.47
5:E:66:THR:HA	5:E:69:LEU:HG	1.97	0.47
5:E:92:ARG:NH2	26:1:792:U:O2'	2.48	0.47
19:S:115:SER:HA	19:S:118:VAL:HG12	1.97	0.47
19:S:155:VAL:HG22	19:S:194:ILE:HG22	1.97	0.47
26:1:908:A:O2'	27:2:95:U:O2	2.26	0.47
26:1:1756:U:H3	26:1:1773:A:N6	2.13	0.47
26:1:1514:A:N6	26:1:1566:G:H1	2.11	0.47
5:E:28:ASN:HB3	5:E:31:GLU:HB2	1.97	0.47
20:V:70:GLU:OE1	20:V:94:ARG:NH2	2.47	0.47
26:1:1486:C:H2'	26:1:1487:G:C8	2.50	0.47
26:1:2360:A:H5''	26:1:2362:A:H1'	1.97	0.47
2:B:72:ASP:OD1	2:B:72:ASP:N	2.48	0.46
26:1:1353:A:H2'	26:1:1354:G:H8	1.80	0.46
1:A:29:ARG:HB2	1:A:87:GLU:HB2	1.98	0.46
4:D:50:ALA:HB1	4:D:51:PRO:HA	1.97	0.46
12:L:133:ARG:HG3	12:L:173:MET:HB3	1.98	0.46
27:2:52:G:H2'	27:2:53:U:C6	2.50	0.46
4:D:10:LYS:NZ	4:D:23:GLU:OE2	2.48	0.46
12:L:142:SER:OG	12:L:143:HIS:N	2.48	0.46
19:S:115:SER:O	19:S:119:GLN:HG3	2.15	0.46
23:Y:35:GLN:HE21	23:Y:100:GLY:HA2	1.80	0.46
26:1:106:A:H2'	26:1:107:G:C8	2.49	0.46
27:2:75:U:H3	27:2:94:C:H5	1.61	0.46
9:I:19:LYS:O	9:I:22:ARG:NH2	2.49	0.46
26:1:1567:A:OP2	26:1:1568:U:O2'	2.31	0.46
26:1:1873:G:H2'	26:1:1874:A:C8	2.50	0.46
26:1:1951:C:H2'	26:1:1952:C:C6	2.49	0.46
7:G:69:GLN:OE1	7:G:78:PRO:HB2	2.16	0.46
8:H:55:VAL:HG12	8:H:59:GLY:HA3	1.97	0.46
12:L:80:ALA:HB2	12:L:101:VAL:HG12	1.98	0.46
21:W:111:PHE:HB3	21:W:114:ILE:HD12	1.97	0.46
26:1:1501:G:H3'	26:1:1502:A:C8	2.51	0.46
13:M:29:LYS:HB3	13:M:29:LYS:HE3	1.70	0.46
24:Z:33:THR:HB	24:Z:36:ARG:HG3	1.96	0.46
26:1:2098:A:H2'	26:1:2099:G:H8	1.81	0.46
26:1:2342:U:H2'	26:1:2343:U:C6	2.51	0.46
15:O:31:GLU:OE2	15:O:46:ARG:NH1	2.49	0.46
26:1:135:G:H2'	26:1:136:A:H8	1.81	0.46
26:1:766:G:H2'	26:1:767:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1818:A:C2	26:1:1856:A:H4'	2.50	0.46
26:1:579:U:H2'	26:1:580:C:C6	2.51	0.46
26:1:873:U:H4'	26:1:876:G:N1	2.31	0.46
26:1:1708:A:N6	26:1:2023:C:H42	2.13	0.46
2:B:108:LYS:HD2	2:B:198:LEU:HD11	1.97	0.46
26:1:1315:C:H2'	26:1:1316:G:H8	1.81	0.46
3:C:74:MET:HE2	3:C:79:LEU:HB2	1.98	0.46
12:L:127:PHE:CE2	26:1:1699:A:H1'	2.51	0.46
13:M:2:ALA:O	13:M:3:LYS:NZ	2.35	0.46
24:Z:39:GLU:OE1	26:1:2717:A:N6	2.41	0.46
25:a:71:GLU:O	25:a:74:THR:OG1	2.31	0.46
26:1:886:A:H2'	26:1:887:A:H8	1.82	0.46
26:1:1508:C:H2'	26:1:1593:G:H22	1.80	0.46
21:W:9:LYS:HD2	21:W:81:GLU:OE2	2.16	0.45
21:W:52:VAL:HG22	21:W:94:ARG:HH11	1.81	0.45
26:1:105:C:H2'	26:1:106:A:H8	1.82	0.45
26:1:1453:G:H4'	26:1:1453:G:OP1	2.16	0.45
26:1:2606:C:H2'	26:1:2607:U:O2	2.16	0.45
26:1:754:U:H2'	26:1:755:C:C6	2.51	0.45
26:1:793:G:N3	26:1:793:G:H2'	2.31	0.45
26:1:1629:U:H3	26:1:1630:A:H62	1.62	0.45
26:1:1942:U:H5''	26:1:1943:A:H2	1.82	0.45
26:1:2649:U:O3'	26:1:2845:G:N2	2.49	0.45
12:L:127:PHE:HE2	26:1:1699:A:H1'	1.81	0.45
26:1:830:U:H4'	26:1:1806:U:H4'	1.98	0.45
27:2:4:G:N2	27:2:109:G:H1	2.10	0.45
26:1:2758:G:H2'	26:1:2759:G:C8	2.51	0.45
26:1:631:U:H2'	26:1:632:U:C6	2.52	0.45
26:1:1087:C:H42	26:1:1156:G:H1	1.64	0.45
26:1:1240:U:H2'	26:1:1241:A:H8	1.81	0.45
26:1:1509:G:O4'	26:1:1593:G:N2	2.49	0.45
2:B:43:ARG:NH1	2:B:49:LEU:HD13	2.31	0.45
7:G:66:SER:OG	26:1:378:C:O2	2.35	0.45
26:1:1423:C:H2'	26:1:1424:A:C8	2.52	0.45
26:1:2235:A:H2'	26:1:2236:C:C6	2.51	0.45
26:1:2457:A:N3	26:1:2457:A:H2'	2.32	0.45
21:W:88:ARG:N	21:W:92:GLY:O	2.39	0.45
26:1:268:A:N6	26:1:473:U:O2'	2.49	0.45
26:1:440:C:H2'	26:1:441:C:C6	2.51	0.45
24:Z:34:GLU:O	24:Z:38:LYS:HG2	2.16	0.45
26:1:390:A:H2'	26:1:391:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:120:LYS:HE2	22:X:140:GLY:HA3	1.98	0.45
26:1:363:A:H4'	26:1:365:A:N7	2.32	0.45
26:1:422:G:H2'	26:1:423:A:H8	1.81	0.45
26:1:969:A:OP1	26:1:970:U:N3	2.50	0.45
26:1:1755:U:H2'	26:1:1756:U:C6	2.52	0.45
26:1:2318:U:H2'	26:1:2319:U:C6	2.52	0.45
3:C:66:ASN:O	3:C:70:ARG:HG2	2.17	0.45
26:1:909:G:H21	26:1:911:A:H61	1.62	0.45
26:1:1353:A:H2'	26:1:1354:G:C8	2.52	0.45
26:1:2318:U:OP1	26:1:2407:A:O2'	2.34	0.45
26:1:342:A:H2'	26:1:343:A:C8	2.52	0.44
26:1:1696:C:H2'	26:1:1697:G:O4'	2.18	0.44
1:A:105:LEU:HD12	1:A:109:ALA:HB1	2.00	0.44
26:1:2844:U:H2'	26:1:2845:G:O4'	2.18	0.44
26:1:659:A:H2'	26:1:659:A:N3	2.33	0.44
27:2:28:C:O2	27:2:52:G:N2	2.50	0.44
26:1:625:G:H2'	26:1:626:G:H8	1.81	0.44
26:1:702:U:H2'	26:1:703:A:H8	1.83	0.44
26:1:793:G:H22	26:1:796:A:H5'	1.82	0.44
26:1:1482:U:H2'	26:1:1483:A:C8	2.50	0.44
26:1:1821:U:H2'	26:1:1822:C:C6	2.53	0.44
22:X:121:LEU:HD23	22:X:121:LEU:H	1.83	0.44
25:a:30:ARG:NH1	25:a:95:ASP:OD2	2.50	0.44
26:1:5:A:H2'	26:1:6:A:C8	2.53	0.44
26:1:625:G:H2'	26:1:626:G:C8	2.52	0.44
26:1:955:A:H2'	26:1:956:A:C8	2.53	0.44
26:1:1636:U:H2'	26:1:1637:A:C8	2.51	0.44
26:1:2343:U:H2'	26:1:2344:C:C6	2.52	0.44
26:1:2359:C:HO2'	26:1:2362:A:HO2'	1.57	0.44
26:1:2857:A:H2'	26:1:2858:G:H8	1.83	0.44
26:1:2821:U:O2'	26:1:2823:G:N2	2.48	0.44
26:1:747:U:H2'	26:1:748:U:C6	2.53	0.44
26:1:2336:A:H4'	26:1:2337:A:O5'	2.18	0.44
26:1:2340:C:H2'	26:1:2341:A:C8	2.52	0.44
5:E:10:ILE:HD13	5:E:103:ILE:HD12	2.00	0.44
26:1:685:C:H2'	26:1:686:U:C6	2.53	0.44
26:1:2343:U:H2'	26:1:2344:C:H6	1.83	0.44
22:X:79:LEU:HG	22:X:113:GLY:HA2	2.00	0.43
26:1:130:A:H2'	26:1:131:G:H8	1.83	0.43
26:1:745:G:O2'	26:1:1676:A:H8	2.01	0.43
26:1:991:A:H2'	26:1:992:A:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1966:U:OP1	26:1:2631:U:O2'	2.36	0.43
26:1:2883:U:H2'	26:1:2884:G:C8	2.53	0.43
7:G:8:ASN:HB3	7:G:71:LEU:HD12	1.99	0.43
11:K:35:GLY:O	11:K:36:GLN:NE2	2.51	0.43
13:M:18:THR:OG1	13:M:49:LYS:NZ	2.51	0.43
26:1:259:A:H2'	26:1:260:A:C8	2.53	0.43
26:1:1395:G:N1	26:1:1408:G:N7	2.66	0.43
26:1:2856:U:H2'	26:1:2857:A:C8	2.53	0.43
2:B:243:ARG:NH2	2:B:247:MET:SD	2.90	0.43
9:I:26:SER:OG	26:1:2298:G:OP1	2.36	0.43
26:1:1314:A:H2'	26:1:1315:C:C6	2.53	0.43
26:1:1806:U:O2	26:1:1810:A:N6	2.52	0.43
26:1:2051:C:H2'	26:1:2052:C:H6	1.81	0.43
26:1:306:C:H2'	26:1:307:A:C8	2.53	0.43
26:1:805:G:H2'	26:1:806:A:O4'	2.18	0.43
26:1:1235:C:C2	26:1:1236:G:C8	3.07	0.43
26:1:2747:U:C2	26:1:2748:A:C8	3.07	0.43
26:1:2901:U:H2'	26:1:2902:A:C8	2.54	0.43
21:W:7:ARG:NE	21:W:20:LEU:HD12	2.34	0.43
26:1:506:A:N1	26:1:515:G:C2	2.87	0.43
26:1:734:A:H2'	26:1:735:C:C6	2.54	0.43
20:V:66:THR:HG21	26:1:1185:U:H2'	2.00	0.43
26:1:487:U:H2'	26:1:488:G:C8	2.53	0.43
26:1:2260:A:H2'	26:1:2261:G:H8	1.84	0.43
26:1:2649:U:O2'	26:1:2845:G:N2	2.52	0.43
26:1:1221:C:H2'	26:1:1222:A:H8	1.84	0.43
26:1:1352:C:H2'	26:1:1353:A:C8	2.50	0.43
26:1:505:U:C5	26:1:515:G:N2	2.86	0.43
26:1:902:A:H61	26:1:965:G:H1	1.67	0.43
26:1:1424:A:H5'	26:1:1512:U:H1'	2.00	0.43
26:1:1636:U:H2'	26:1:1637:A:H8	1.82	0.43
26:1:1753:U:H2'	26:1:1754:C:C6	2.53	0.43
26:1:2377:C:H2'	26:1:2378:G:O4'	2.19	0.43
15:O:39:GLU:HB3	15:O:41:LYS:HG2	2.00	0.43
26:1:1481:A:O2'	26:1:1562:C:H4'	2.19	0.43
26:1:1806:U:H5	26:1:1811:A:N7	2.17	0.43
26:1:1865:C:H5	26:1:1928:A:H62	1.67	0.43
26:1:2050:A:H2'	26:1:2051:C:C6	2.54	0.43
26:1:2260:A:H2'	26:1:2261:G:C8	2.54	0.43
26:1:841:C:H2'	26:1:842:U:C6	2.54	0.43
26:1:2539:C:H2'	26:1:2540:A:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:135:ILE:HD13	2:B:141:VAL:HG11	2.00	0.42
19:S:156:THR:OG1	19:S:158:ASN:O	2.29	0.42
26:1:47:C:C2	26:1:181:G:N2	2.87	0.42
26:1:684:U:H2'	26:1:685:C:C6	2.54	0.42
27:2:58:C:C2	27:2:59:U:C5	3.07	0.42
4:D:7:THR:O	4:D:7:THR:HG22	2.19	0.42
12:L:56:LYS:N	12:L:84:PRO:O	2.33	0.42
26:1:1070:A:N1	26:1:1178:C:N4	2.63	0.42
26:1:1856:A:H3'	26:1:1857:C:H6	1.85	0.42
26:1:1901:C:H3'	26:1:1902:G:H8	1.84	0.42
26:1:2270:U:H2'	26:1:2271:U:C6	2.55	0.42
5:E:6:VAL:HG22	5:E:104:THR:HG23	2.01	0.42
26:1:624:C:H2'	26:1:625:G:H8	1.84	0.42
27:2:76:A:H62	27:2:93:G:H21	1.67	0.42
26:1:753:U:H2'	26:1:754:U:C6	2.53	0.42
26:1:2050:A:H2'	26:1:2051:C:H6	1.84	0.42
13:M:20:ARG:HE	13:M:20:ARG:HB3	1.71	0.42
26:1:879:U:H2'	26:1:880:A:H8	1.84	0.42
26:1:1053:A:N3	26:1:1197:C:O2'	2.49	0.42
26:1:2313:A:H4'	26:1:2314:A:O4'	2.20	0.42
26:1:2856:U:H2'	26:1:2857:A:H8	1.84	0.42
27:2:15:C:N4	27:2:103:A:H2	2.16	0.42
2:B:84:ASP:OD2	2:B:87:ARG:HD3	2.19	0.42
20:V:25:THR:HB	20:V:28:ARG:HG3	2.02	0.42
24:Z:36:ARG:O	24:Z:40:VAL:HG23	2.20	0.42
26:1:167:U:H2'	26:1:168:A:H5''	2.01	0.42
26:1:181:G:H2'	26:1:182:C:O4'	2.19	0.42
26:1:1453:G:N2	26:1:1631:G:O4'	2.50	0.42
20:V:79:SER:HB2	26:1:2668:A:H5''	2.02	0.42
26:1:2064:A:H2'	26:1:2065:G:C8	2.55	0.42
3:C:4:VAL:HG22	26:1:1238:U:H1'	2.01	0.42
26:1:636:A:H2'	26:1:637:U:C6	2.55	0.42
26:1:1241:A:H2'	26:1:1242:A:C8	2.55	0.42
26:1:1311:A:N7	26:1:1690:A:O2'	2.44	0.42
26:1:2535:G:H1	26:1:2607:U:H5	1.65	0.42
2:B:53:HIS:HA	2:B:217:ARG:HB2	2.01	0.42
21:W:88:ARG:HG2	21:W:89:ASP:N	2.32	0.42
23:Y:77:LYS:NZ	23:Y:86:GLY:O	2.46	0.42
26:1:1083:G:H2'	26:1:1084:U:C6	2.55	0.42
26:1:2293:A:H4'	26:1:2294:A:N3	2.34	0.42
27:2:30:U:H2'	27:2:31:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:52:MET:HE3	5:E:52:MET:HB3	1.83	0.42
26:1:1476:G:H2'	26:1:1477:U:C6	2.55	0.42
26:1:1573:A:N6	26:1:1592:A:N1	2.68	0.42
23:Y:48:GLU:OE2	23:Y:51:ARG:NH2	2.45	0.41
24:Z:22:THR:O	24:Z:26:ILE:HG12	2.20	0.41
26:1:2113:U:H2'	26:1:2114:G:C8	2.55	0.41
2:B:8:PRO:HB3	2:B:14:ARG:HA	2.01	0.41
20:V:16:TRP:CE2	20:V:136:GLN:HG2	2.55	0.41
22:X:118:ASP:HA	22:X:139:LYS:HE2	2.03	0.41
26:1:1087:C:N4	26:1:1156:G:H1	2.19	0.41
26:1:2406:G:H2'	26:1:2407:A:C8	2.55	0.41
27:2:17:A:H2'	27:2:18:G:H8	1.84	0.41
21:W:1:MET:SD	21:W:65:THR:HG22	2.61	0.41
26:1:638:U:H2'	26:1:639:U:C6	2.55	0.41
26:1:1013:U:H2'	26:1:1014:U:C6	2.55	0.41
26:1:1711:G:O2'	26:1:2018:U:O4	2.30	0.41
26:1:2842:G:O2'	26:1:2844:U:OP2	2.39	0.41
12:L:158:SER:OG	26:1:2599:A:N7	2.44	0.41
20:V:40:LYS:HE2	20:V:40:LYS:HB3	1.91	0.41
26:1:838:A:OP2	26:1:2098:A:O2'	2.38	0.41
26:1:2372:G:N3	26:1:2408:C:H2'	2.34	0.41
8:H:81:PRO:O	23:Y:35:GLN:NE2	2.39	0.41
22:X:87:ASP:N	22:X:87:ASP:OD1	2.53	0.41
26:1:29:U:C2	26:1:30:G:C8	3.09	0.41
26:1:441:C:H2'	26:1:442:G:H8	1.86	0.41
26:1:713:A:H2'	26:1:715:A:H62	1.86	0.41
26:1:744:A:H8	26:1:1677:G:O2'	2.03	0.41
26:1:1880:A:H2'	26:1:1881:A:C8	2.55	0.41
26:1:2860:U:H2'	26:1:2861:U:C6	2.55	0.41
26:1:2906:G:H2'	26:1:2907:A:H8	1.85	0.41
15:O:2:ARG:HG3	26:1:2311:U:OP2	2.21	0.41
15:O:5:VAL:HG11	15:O:21:LYS:HE3	2.02	0.41
26:1:332:A:H2'	26:1:333:C:C6	2.55	0.41
26:1:2767:A:H2'	26:1:2768:A:C8	2.56	0.41
26:1:613:G:H2'	26:1:2057:A:N7	2.36	0.41
26:1:1066:G:N2	26:1:1067:U:O4	2.47	0.41
14:N:50:ASN:OD1	14:N:51:GLY:N	2.53	0.41
21:W:10:VAL:HG11	21:W:86:ILE:HD11	2.03	0.41
26:1:566:U:H2'	26:1:567:G:C8	2.56	0.41
26:1:788:A:O2'	26:1:1703:U:OP1	2.39	0.41
26:1:886:A:H2'	26:1:887:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1598:U:H2'	26:1:1599:G:C8	2.56	0.41
26:1:1680:U:H2'	26:1:1681:U:C6	2.55	0.41
26:1:2083:G:H1	26:1:2639:C:H5	1.66	0.41
26:1:2268:A:H2'	26:1:2269:G:C8	2.56	0.41
2:B:260:ARG:NH1	26:1:1826:G:OP1	2.41	0.41
13:M:15:ARG:HD3	13:M:15:ARG:HA	1.87	0.41
23:Y:59:LYS:HG3	23:Y:61:GLY:H	1.86	0.41
24:Z:24:LEU:HD13	24:Z:30:ILE:HG12	2.02	0.41
25:a:72:LEU:O	25:a:76:VAL:HG23	2.21	0.41
26:1:464:U:H2'	26:1:465:C:C6	2.56	0.41
26:1:1674:U:H2'	26:1:1675:G:O4'	2.21	0.41
26:1:1939:A:O2'	26:1:1941:C:OP2	2.39	0.41
26:1:2676:U:H2'	26:1:2677:C:C6	2.55	0.41
9:I:80:LYS:O	9:I:84:LYS:HB2	2.21	0.41
12:L:71:LYS:HB3	12:L:72:PRO:HD3	2.03	0.41
17:Q:45:ARG:HD3	26:1:2445:A:OP1	2.20	0.41
26:1:569:U:H2'	26:1:570:U:C6	2.56	0.41
26:1:2348:G:H5'	26:1:2349:A:OP2	2.21	0.41
26:1:2705:U:H2'	26:1:2706:A:C8	2.55	0.41
27:2:11:A:H4'	27:2:13:A:H2'	2.03	0.41
7:G:45:GLN:CD	7:G:57:LEU:HD22	2.47	0.40
26:1:1328:C:H2'	26:1:1329:G:H8	1.86	0.40
26:1:2404:A:H2'	26:1:2405:A:C8	2.55	0.40
26:1:2858:G:H1	26:1:2900:C:H41	1.69	0.40
10:J:39:LEU:HB3	10:J:59:VAL:HG21	2.03	0.40
26:1:1203:U:H2'	26:1:1204:G:H8	1.87	0.40
26:1:1400:C:O2'	26:1:1836:A:N3	2.51	0.40
6:F:83:LYS:HE2	6:F:83:LYS:HB3	1.90	0.40
11:K:34:THR:OG1	11:K:36:GLN:OE1	2.36	0.40
12:L:56:LYS:HE3	12:L:69:ALA:HB2	2.04	0.40
25:a:68:THR:OG1	27:2:48:A:OP2	2.28	0.40
26:1:774:G:H5'	26:1:775:A:H5''	2.04	0.40
26:1:830:U:H2'	26:1:831:C:C6	2.57	0.40
26:1:1031:C:H2'	26:1:1032:A:O4'	2.22	0.40
26:1:1823:U:H2'	26:1:1824:C:C6	2.56	0.40
16:P:4:ARG:HA	16:P:4:ARG:HD3	1.90	0.40
26:1:525:A:H1'	26:1:526:A:H5''	2.02	0.40
26:1:923:A:H2	26:1:946:A:C5	2.40	0.40
26:1:1725:G:O2'	26:1:1789:A:O2'	2.18	0.40
5:E:88:ARG:NH2	26:1:793:G:OP1	2.39	0.40
11:K:28:LEU:HD13	11:K:43:ILE:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:69:PHE:HA	23:Y:70:PRO:HD3	1.85	0.40
26:1:651:A:H2'	26:1:652:A:C8	2.56	0.40
26:1:1072:A:N6	26:1:1169:G:H2'	2.36	0.40
26:1:2395:C:H2'	26:1:2396:A:H8	1.87	0.40
26:1:2698:A:H2'	26:1:2699:U:O4'	2.22	0.40

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	111/116 (96%)	106 (96%)	5 (4%)	0	100	100
2	B	271/277 (98%)	264 (97%)	7 (3%)	0	100	100
3	C	114/118 (97%)	114 (100%)	0	0	100	100
4	D	98/102 (96%)	93 (95%)	5 (5%)	0	100	100
5	E	109/117 (93%)	107 (98%)	2 (2%)	0	100	100
6	F	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
7	G	86/105 (82%)	79 (92%)	7 (8%)	0	100	100
8	H	91/217 (42%)	87 (96%)	4 (4%)	0	100	100
9	I	76/94 (81%)	71 (93%)	5 (7%)	0	100	100
10	J	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
11	K	59/73 (81%)	56 (95%)	3 (5%)	0	100	100
12	L	213/220 (97%)	205 (96%)	8 (4%)	0	100	100
13	M	54/59 (92%)	52 (96%)	2 (4%)	0	100	100
14	N	48/57 (84%)	44 (92%)	4 (8%)	0	100	100
15	O	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
16	P	42/45 (93%)	42 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
18	R	35/37 (95%)	35 (100%)	0	0	100	100
19	S	190/207 (92%)	180 (95%)	10 (5%)	0	100	100
20	V	141/145 (97%)	138 (98%)	3 (2%)	0	100	100
21	W	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
22	X	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
23	Y	134/144 (93%)	132 (98%)	2 (2%)	0	100	100
24	Z	119/122 (98%)	115 (97%)	4 (3%)	0	100	100
25	a	106/119 (89%)	102 (96%)	4 (4%)	0	100	100
All	All	2607/2904 (90%)	2513 (96%)	94 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	99/102 (97%)	99 (100%)	0	100	100
2	B	220/224 (98%)	220 (100%)	0	100	100
3	C	96/98 (98%)	96 (100%)	0	100	100
4	D	85/86 (99%)	85 (100%)	0	100	100
5	E	90/94 (96%)	90 (100%)	0	100	100
6	F	79/79 (100%)	79 (100%)	0	100	100
7	G	77/90 (86%)	77 (100%)	0	100	100
8	H	81/190 (43%)	81 (100%)	0	100	100
9	I	61/75 (81%)	61 (100%)	0	100	100
10	J	49/51 (96%)	49 (100%)	0	100	100
11	K	55/66 (83%)	55 (100%)	0	100	100
12	L	173/177 (98%)	173 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	50/53 (94%)	50 (100%)	0	100	100
14	N	45/50 (90%)	45 (100%)	0	100	100
15	O	45/47 (96%)	45 (100%)	0	100	100
16	P	39/40 (98%)	39 (100%)	0	100	100
17	Q	55/56 (98%)	55 (100%)	0	100	100
18	R	35/35 (100%)	35 (100%)	0	100	100
19	S	158/170 (93%)	158 (100%)	0	100	100
20	V	122/123 (99%)	122 (100%)	0	100	100
21	W	99/100 (99%)	99 (100%)	0	100	100
22	X	110/112 (98%)	110 (100%)	0	100	100
23	Y	113/119 (95%)	113 (100%)	0	100	100
24	Z	101/102 (99%)	101 (100%)	0	100	100
25	a	87/95 (92%)	87 (100%)	0	100	100
All	All	2224/2434 (91%)	2224 (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. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	75	ASN
2	B	86	ASN
2	B	163	GLN
2	B	204	ASN
2	B	226	ASN
3	C	44	GLN
4	D	11	GLN
4	D	18	GLN
14	N	19	HIS
14	N	32	ASN
15	O	22	ASN
15	O	45	HIS
17	Q	40	GLN
19	S	29	ASN
20	V	48	HIS
20	V	97	ASN
22	X	38	GLN

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Mol	Chain	Res	Type
22	X	83	ASN
23	Y	13	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	1	2673/2923 (91%)	388 (14%)	5 (0%)
27	2	110/115 (95%)	21 (19%)	1 (0%)
All	All	2783/3038 (91%)	409 (14%)	6 (0%)

All (409) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	1	35	G
26	1	36	G
26	1	51	G
26	1	60	U
26	1	69	C
26	1	71	A
26	1	74	U
26	1	75	G
26	1	89	U
26	1	90	A
26	1	91	A
26	1	117	A
26	1	119	U
26	1	137	G
26	1	139	U
26	1	140	A
26	1	156	A
26	1	160	G
26	1	161	A
26	1	168	A
26	1	176	A
26	1	180	G
26	1	183	A
26	1	199	A
26	1	202	A
26	1	218	G
26	1	219	A
26	1	225	A

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Mol	Chain	Res	Type
26	1	230	A
26	1	233	U
26	1	248	G
26	1	251	G
26	1	253	G
26	1	255	G
26	1	258	A
26	1	259	A
26	1	268	A
26	1	278	A
26	1	279	A
26	1	298	U
26	1	301	U
26	1	302	A
26	1	306	C
26	1	309	U
26	1	311	U
26	1	320	U
26	1	321	U
26	1	322	A
26	1	330	C
26	1	332	A
26	1	333	C
26	1	354	A
26	1	358	G
26	1	372	A
26	1	373	A
26	1	381	G
26	1	396	G
26	1	397	U
26	1	406	A
26	1	407	G
26	1	408	U
26	1	410	G
26	1	411	A
26	1	432	G
26	1	433	U
26	1	440	C
26	1	447	A
26	1	450	C
26	1	452	G
26	1	457	G

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Mol	Chain	Res	Type
26	1	463	C
26	1	489	A
26	1	501	C
26	1	502	C
26	1	503	A
26	1	526	A
26	1	527	G
26	1	535	G
26	1	536	A
26	1	537	A
26	1	545	G
26	1	546	A
26	1	550	A
26	1	553	A
26	1	554	C
26	1	575	G
26	1	576	U
26	1	577	A
26	1	578	G
26	1	583	A
26	1	593	U
26	1	594	G
26	1	606	G
26	1	616	G
26	1	617	A
26	1	618	A
26	1	646	A
26	1	647	G
26	1	650	U
26	1	659	A
26	1	660	A
26	1	661	U
26	1	662	G
26	1	667	G
26	1	682	A
26	1	683	G
26	1	690	U
26	1	691	A
26	1	698	U
26	1	699	U
26	1	700	A
26	1	731	U

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Mol	Chain	Res	Type
26	1	744	A
26	1	758	G
26	1	761	A
26	1	763	A
26	1	775	A
26	1	785	C
26	1	792	U
26	1	809	A
26	1	810	A
26	1	819	A
26	1	820	G
26	1	822	G
26	1	827	A
26	1	829	U
26	1	835	U
26	1	837	G
26	1	850	G
26	1	857	C
26	1	872	U
26	1	875	G
26	1	891	A
26	1	921	C
26	1	923	A
26	1	924	G
26	1	944	G
26	1	955	A
26	1	970	U
26	1	972	A
26	1	977	A
26	1	985	A
26	1	989	A
26	1	990	G
26	1	1005	G
26	1	1018	A
26	1	1027	A
26	1	1040	A
26	1	1046	G
26	1	1056	U
26	1	1057	A
26	1	1066	G
26	1	1070	A
26	1	1077	U

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Mol	Chain	Res	Type
26	1	1087	C
26	1	1093	C
26	1	1094	A
26	1	1156	G
26	1	1160	C
26	1	1173	A
26	1	1176	U
26	1	1177	A
26	1	1179	C
26	1	1186	A
26	1	1187	A
26	1	1220	A
26	1	1250	G
26	1	1258	A
26	1	1274	G
26	1	1278	G
26	1	1288	G
26	1	1291	A
26	1	1294	G
26	1	1309	G
26	1	1310	A
26	1	1313	G
26	1	1321	A
26	1	1327	C
26	1	1337	A
26	1	1338	U
26	1	1358	A
26	1	1362	C
26	1	1366	U
26	1	1374	G
26	1	1387	C
26	1	1389	U
26	1	1395	G
26	1	1402	A
26	1	1416	U
26	1	1421	A
26	1	1429	G
26	1	1432	A
26	1	1433	U
26	1	1451	U
26	1	1452	C
26	1	1453	G

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Mol	Chain	Res	Type
26	1	1454	U
26	1	1463	A
26	1	1471	A
26	1	1472	C
26	1	1489	A
26	1	1490	G
26	1	1491	C
26	1	1497	A
26	1	1503	U
26	1	1504	U
26	1	1516	C
26	1	1519	U
26	1	1557	C
26	1	1561	G
26	1	1566	G
26	1	1570	G
26	1	1578	A
26	1	1588	U
26	1	1593	G
26	1	1605	A
26	1	1606	C
26	1	1616	A
26	1	1628	A
26	1	1629	U
26	1	1634	A
26	1	1639	G
26	1	1651	C
26	1	1652	A
26	1	1654	A
26	1	1663	G
26	1	1683	U
26	1	1690	A
26	1	1691	G
26	1	1692	C
26	1	1711	G
26	1	1718	G
26	1	1740	G
26	1	1744	A
26	1	1758	A
26	1	1759	G
26	1	1773	A
26	1	1790	G

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Mol	Chain	Res	Type
26	1	1791	G
26	1	1800	A
26	1	1811	A
26	1	1827	C
26	1	1828	U
26	1	1829	A
26	1	1836	A
26	1	1843	U
26	1	1854	U
26	1	1856	A
26	1	1860	C
26	1	1897	U
26	1	1898	C
26	1	1901	C
26	1	1910	G
26	1	1933	G
26	1	1940	A
26	1	1941	C
26	1	1942	U
26	1	1943	A
26	1	1944	U
26	1	1946	A
26	1	1957	G
26	1	1965	A
26	1	1982	U
26	1	1994	C
26	1	1997	A
26	1	1998	A
26	1	1999	G
26	1	2004	A
26	1	2009	U
26	1	2018	U
26	1	2020	U
26	1	2021	C
26	1	2050	A
26	1	2058	A
26	1	2059	G
26	1	2060	A
26	1	2070	C
26	1	2082	C
26	1	2083	G
26	1	2087	A

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Mol	Chain	Res	Type
26	1	2088	G
26	1	2089	A
26	1	2090	C
26	1	2096	G
26	1	2120	G
26	1	2124	U
26	1	2126	C
26	1	2226	A
26	1	2231	C
26	1	2232	A
26	1	2238	U
26	1	2252	A
26	1	2265	G
26	1	2266	G
26	1	2295	A
26	1	2302	C
26	1	2306	G
26	1	2307	G
26	1	2310	C
26	1	2333	U
26	1	2335	G
26	1	2336	A
26	1	2337	A
26	1	2338	A
26	1	2339	U
26	1	2346	U
26	1	2348	G
26	1	2349	A
26	1	2350	G
26	1	2352	G
26	1	2361	U
26	1	2362	A
26	1	2363	A
26	1	2372	G
26	1	2374	C
26	1	2377	C
26	1	2398	G
26	1	2399	G
26	1	2410	G
26	1	2412	C
26	1	2429	U
26	1	2430	C

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Mol	Chain	Res	Type
26	1	2450	U
26	1	2452	A
26	1	2456	G
26	1	2457	A
26	1	2468	C
26	1	2475	A
26	1	2497	G
26	1	2503	A
26	1	2505	A
26	1	2521	G
26	1	2525	C
26	1	2529	G
26	1	2530	A
26	1	2545	A
26	1	2547	C
26	1	2556	G
26	1	2561	C
26	1	2593	A
26	1	2594	G
26	1	2599	A
26	1	2600	C
26	1	2609	G
26	1	2612	U
26	1	2613	C
26	1	2629	A
26	1	2636	U
26	1	2637	C
26	1	2640	U
26	1	2641	A
26	1	2657	G
26	1	2663	U
26	1	2673	C
26	1	2677	C
26	1	2690	G
26	1	2712	G
26	1	2716	U
26	1	2717	A
26	1	2732	A
26	1	2741	G
26	1	2749	G
26	1	2753	U
26	1	2760	A

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Mol	Chain	Res	Type
26	1	2771	G
26	1	2775	A
26	1	2778	G
26	1	2784	A
26	1	2791	A
26	1	2792	A
26	1	2793	G
26	1	2805	A
26	1	2807	G
26	1	2820	U
26	1	2821	U
26	1	2822	C
26	1	2823	G
26	1	2824	G
26	1	2827	A
26	1	2828	U
26	1	2840	A
26	1	2853	U
26	1	2887	G
26	1	2892	G
26	1	2893	A
26	1	2900	C
26	1	2911	A
26	1	2913	G
27	2	4	G
27	2	10	U
27	2	12	U
27	2	13	A
27	2	23	U
27	2	39	G
27	2	40	C
27	2	42	G
27	2	43	A
27	2	45	C
27	2	49	G
27	2	50	A
27	2	71	A
27	2	84	U
27	2	86	A
27	2	94	C
27	2	100	U
27	2	104	A

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Mol	Chain	Res	Type
27	2	105	C
27	2	106	G
27	2	109	G

All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	1	229	A
26	1	525	A
26	1	2336	A
26	1	2783	U
26	1	2827	A
27	2	49	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

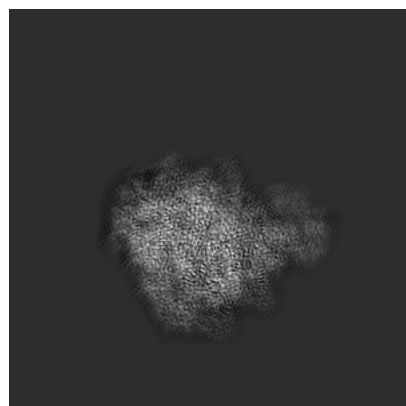
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26124. These allow visual inspection of the internal detail of the map and identification of artifacts.

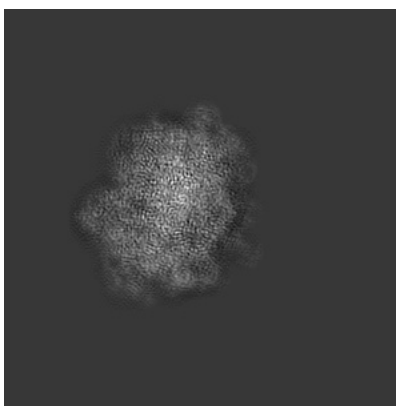
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

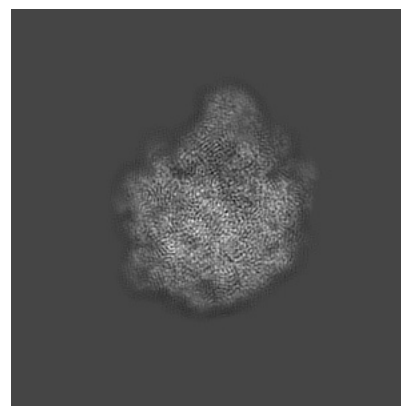
6.1.1 Primary map



X

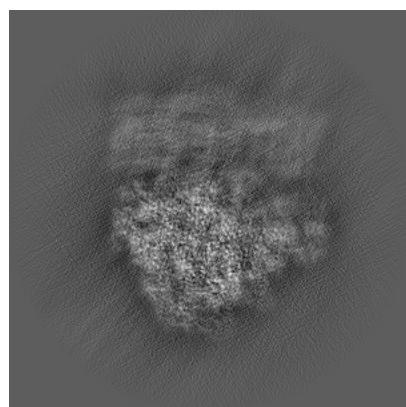


Y

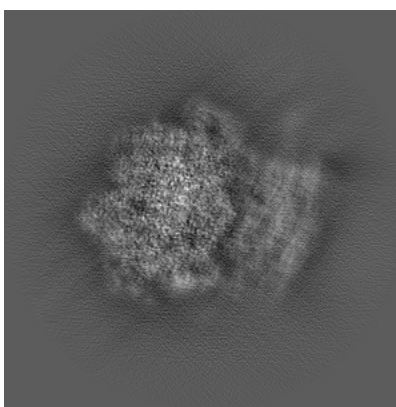


Z

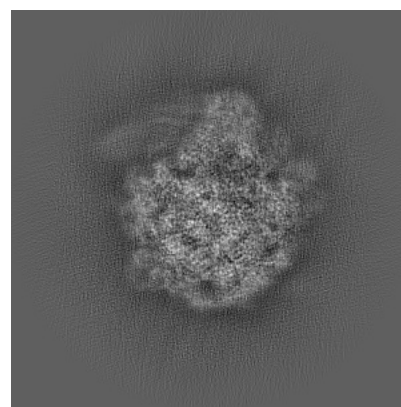
6.1.2 Raw map



X



Y

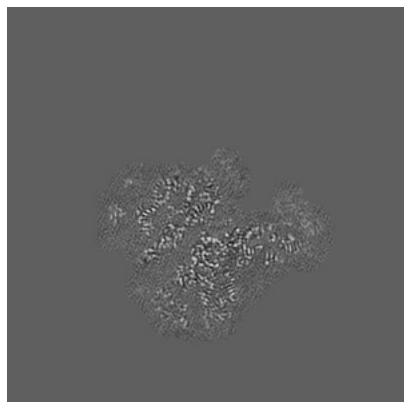


Z

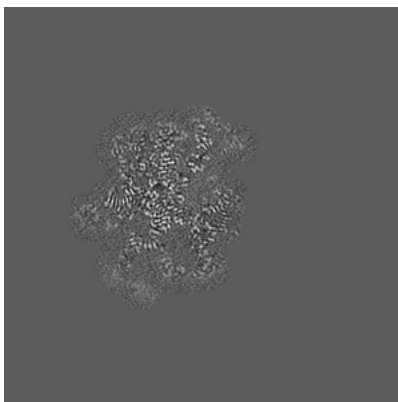
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

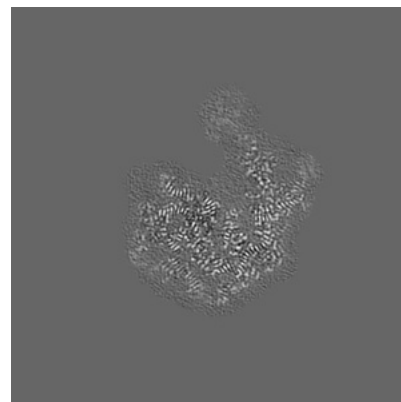
6.2.1 Primary map



X Index: 224

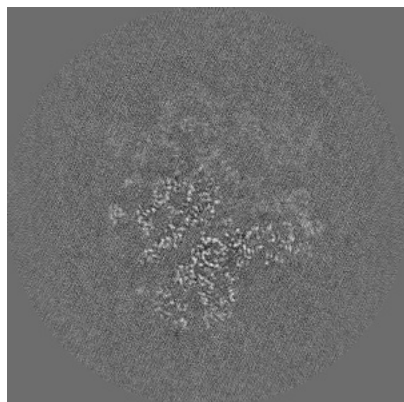


Y Index: 224

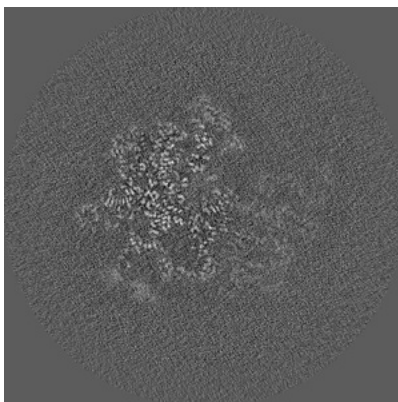


Z Index: 224

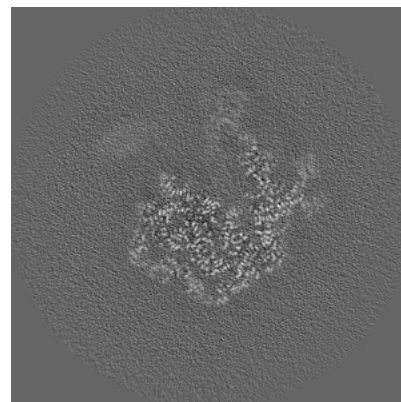
6.2.2 Raw map



X Index: 224



Y Index: 224

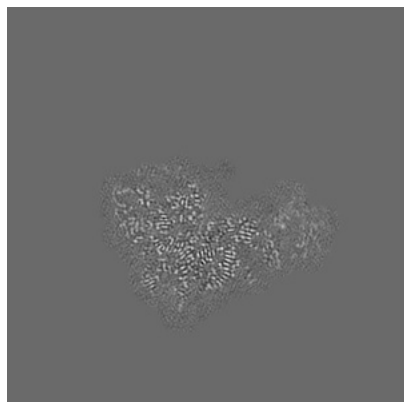


Z Index: 224

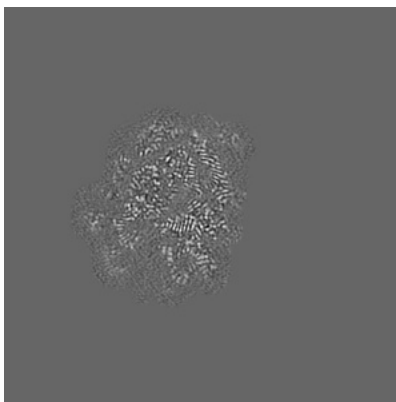
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

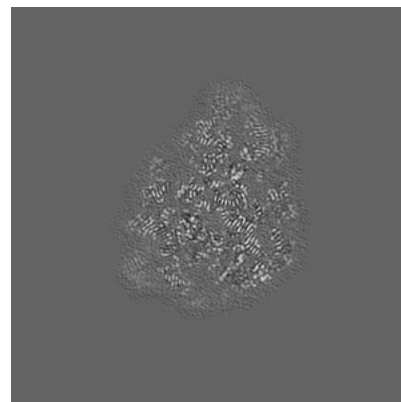
6.3.1 Primary map



X Index: 247

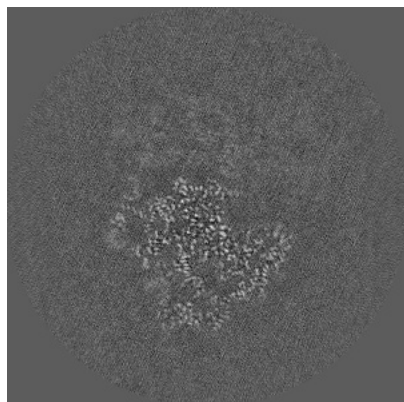


Y Index: 210

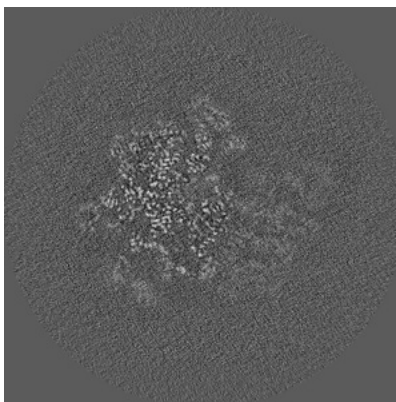


Z Index: 191

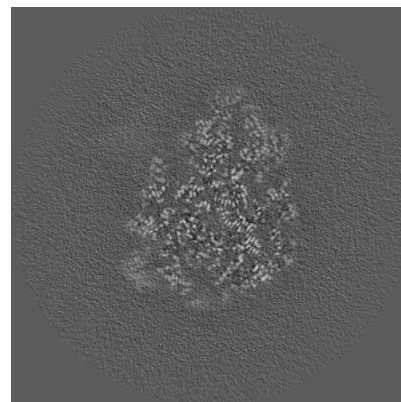
6.3.2 Raw map



X Index: 209



Y Index: 223

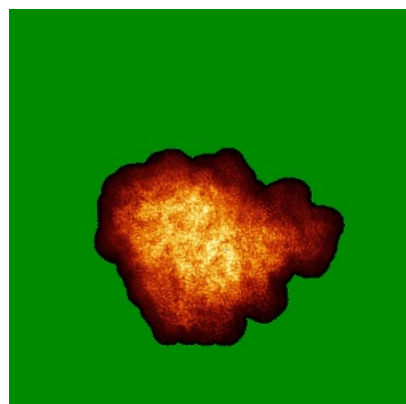


Z Index: 191

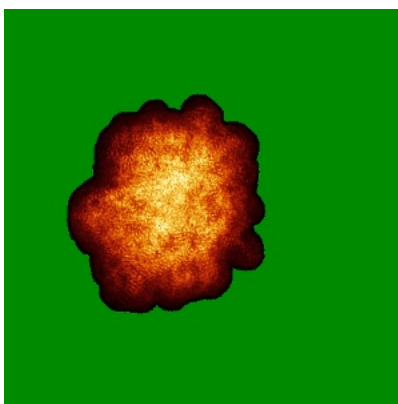
The images above show the largest variance slices of the map in three orthogonal directions.

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

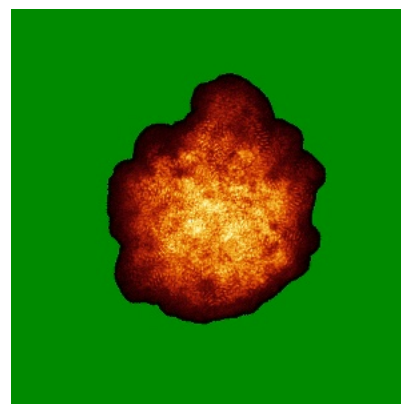
6.4.1 Primary map



X

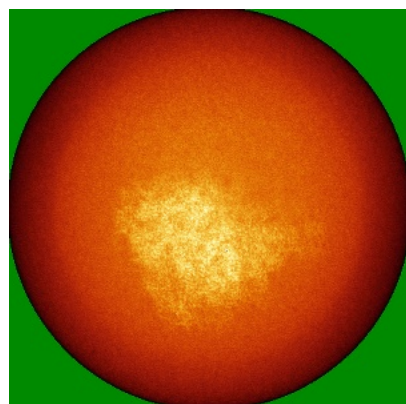


Y

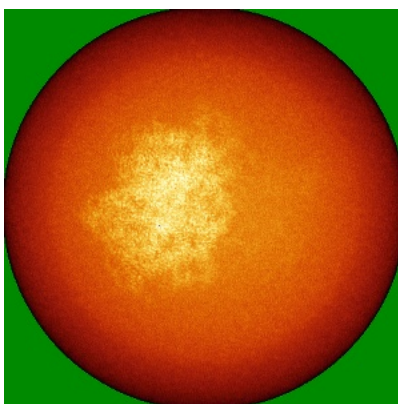


Z

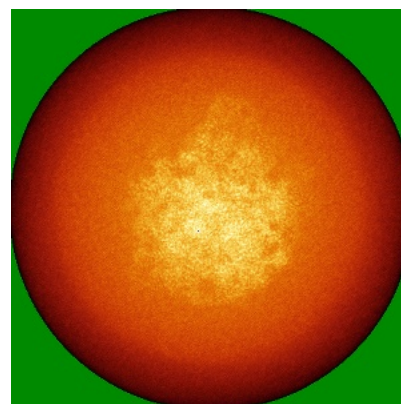
6.4.2 Raw map



X



Y

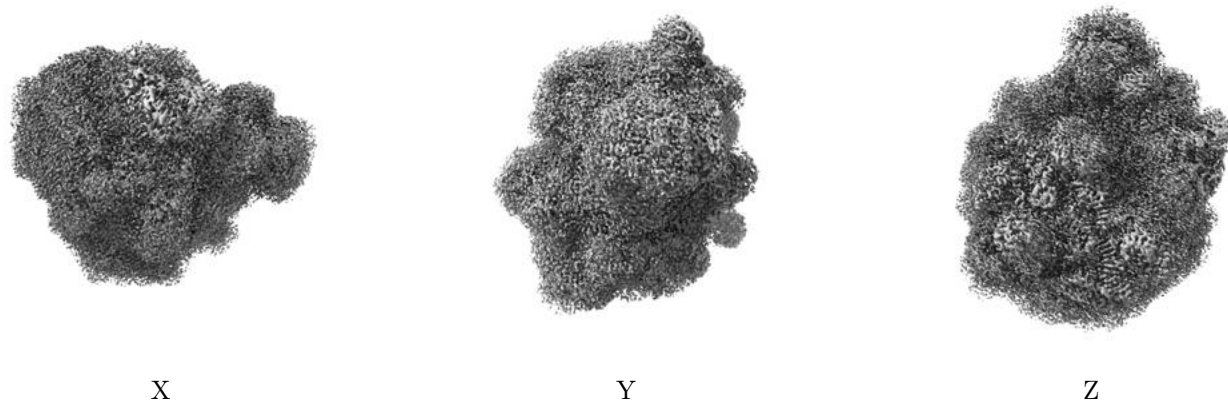


Z

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.

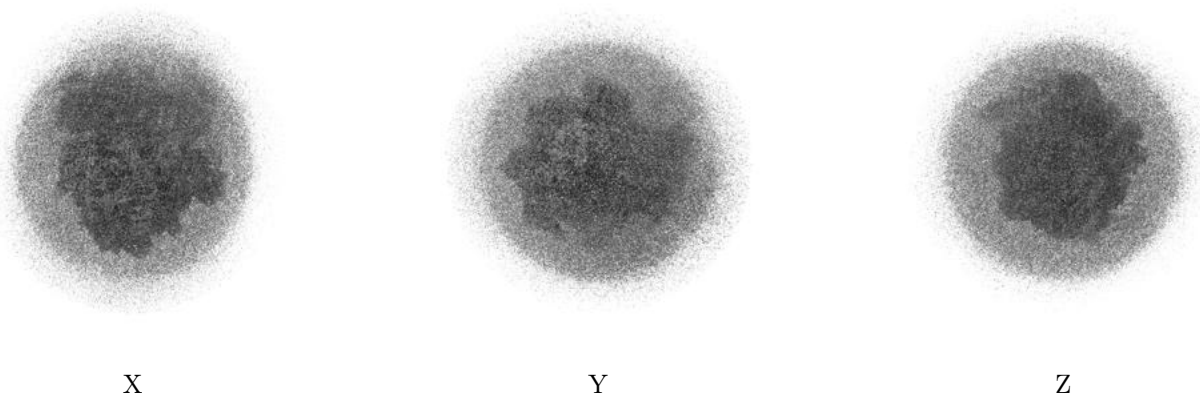
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

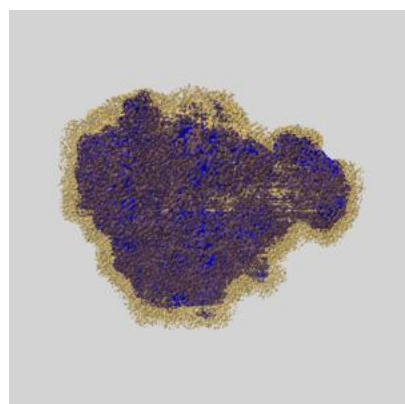
6.6 Mask visualisation [i](#)

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

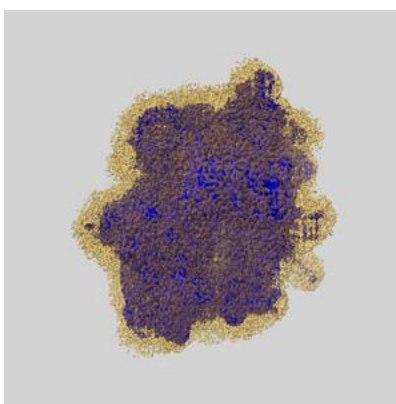
A mask typically either:

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

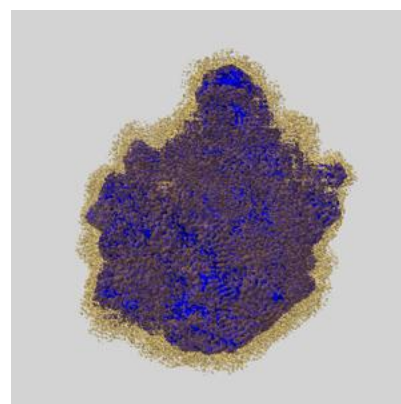
6.6.1 emd_26124_msk_1.map [i](#)



X



Y

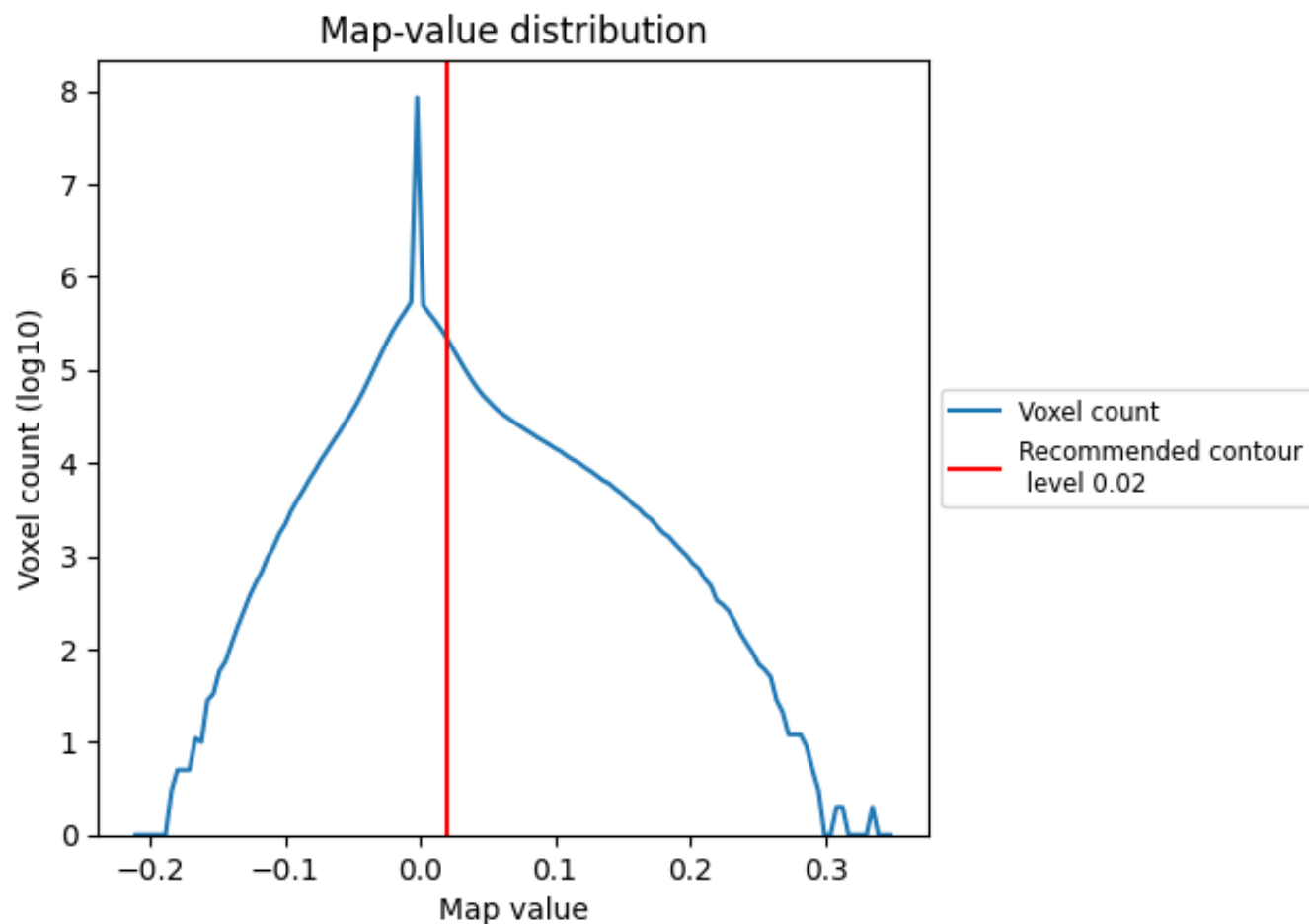


Z

7 Map analysis [i](#)

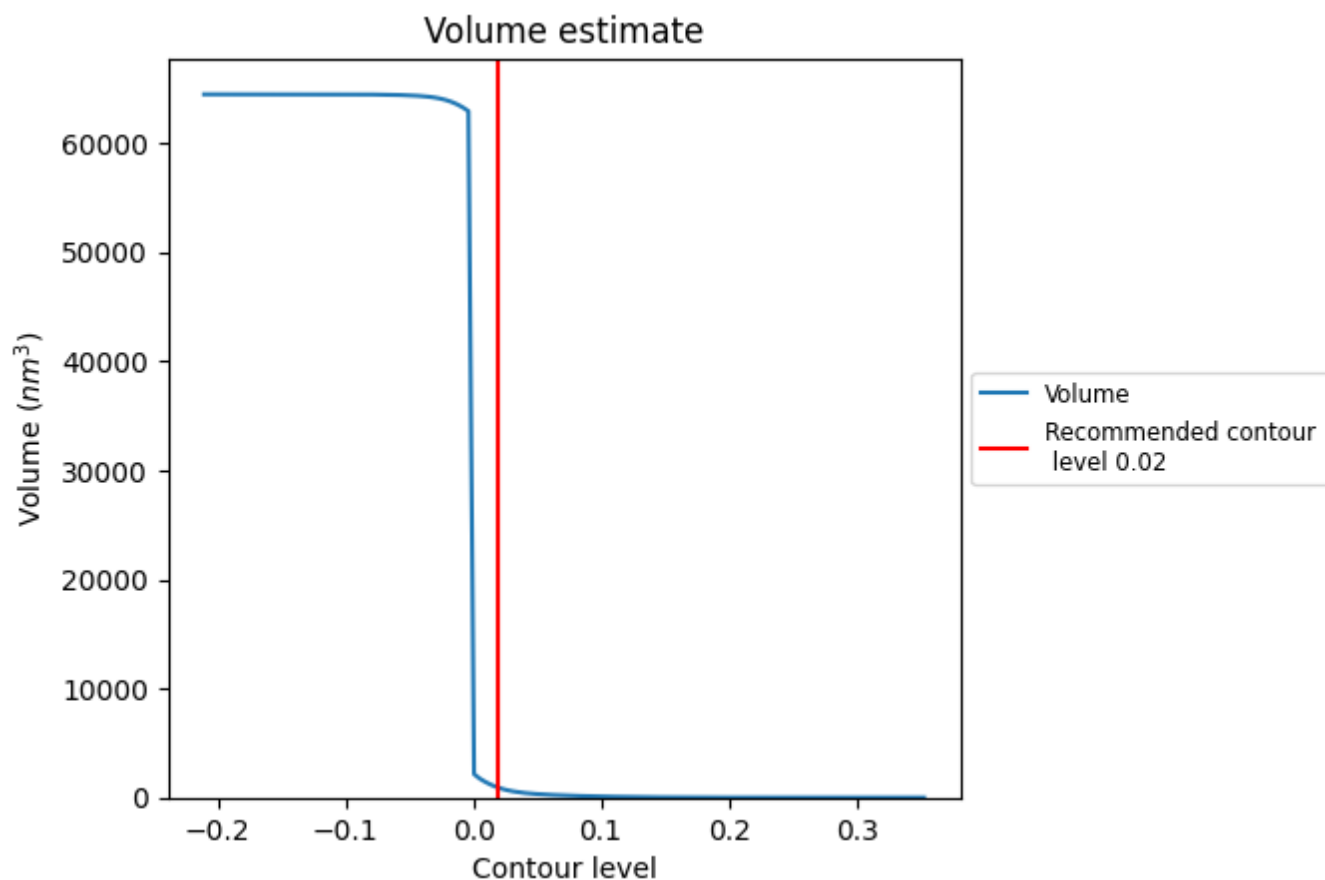
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

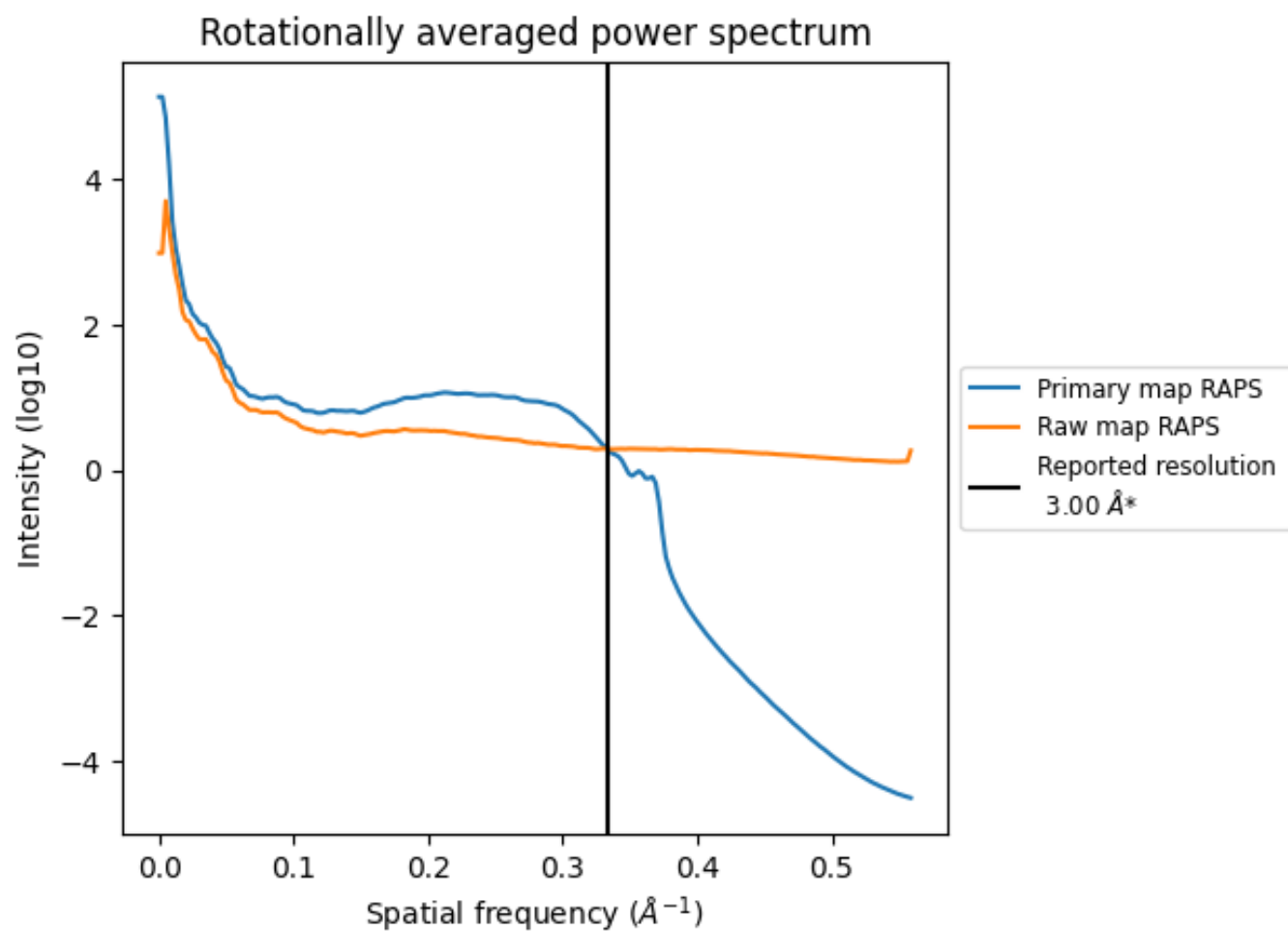
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 903 nm³; this corresponds to an approximate mass of 816 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 ⓘ

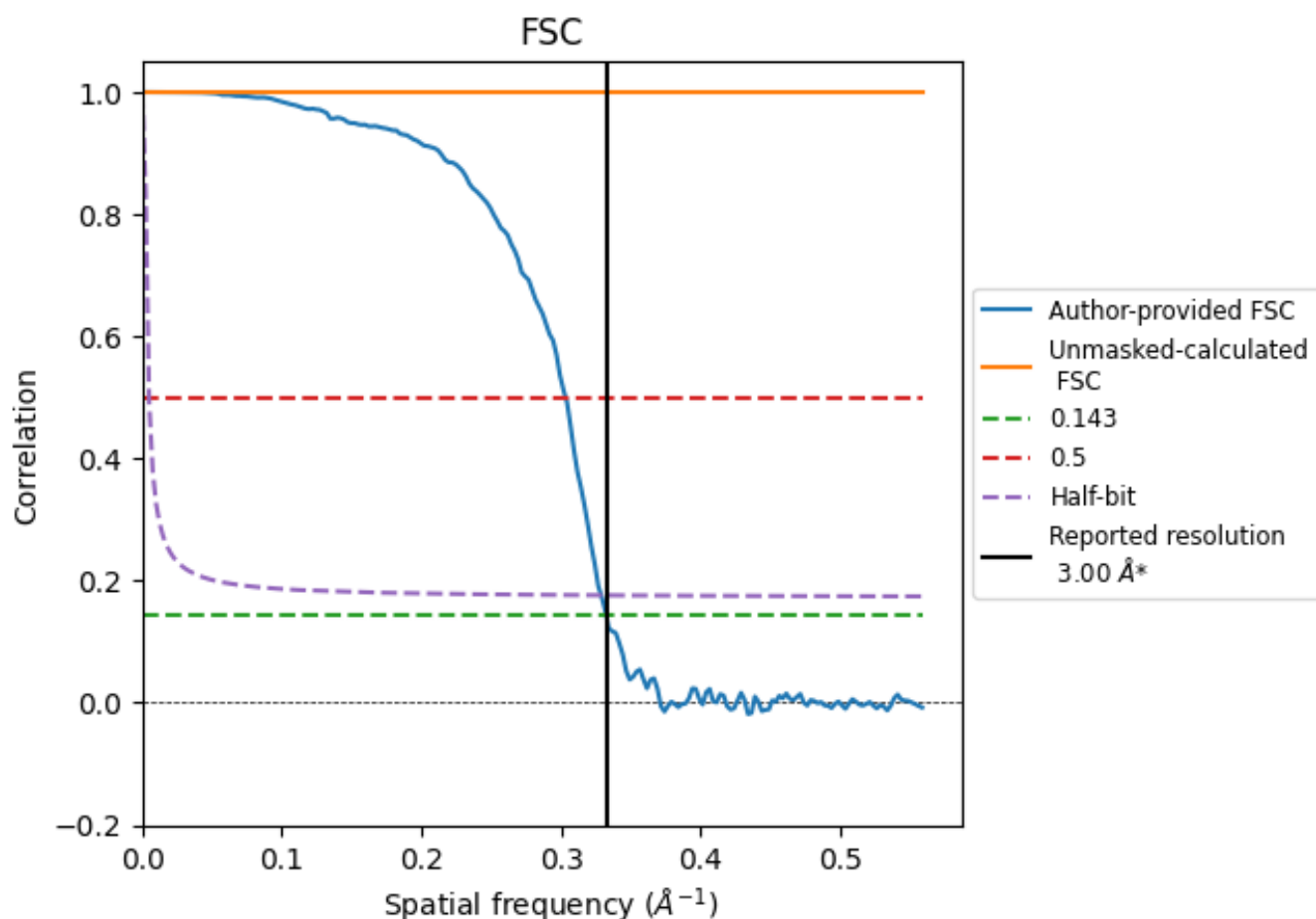


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.333 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

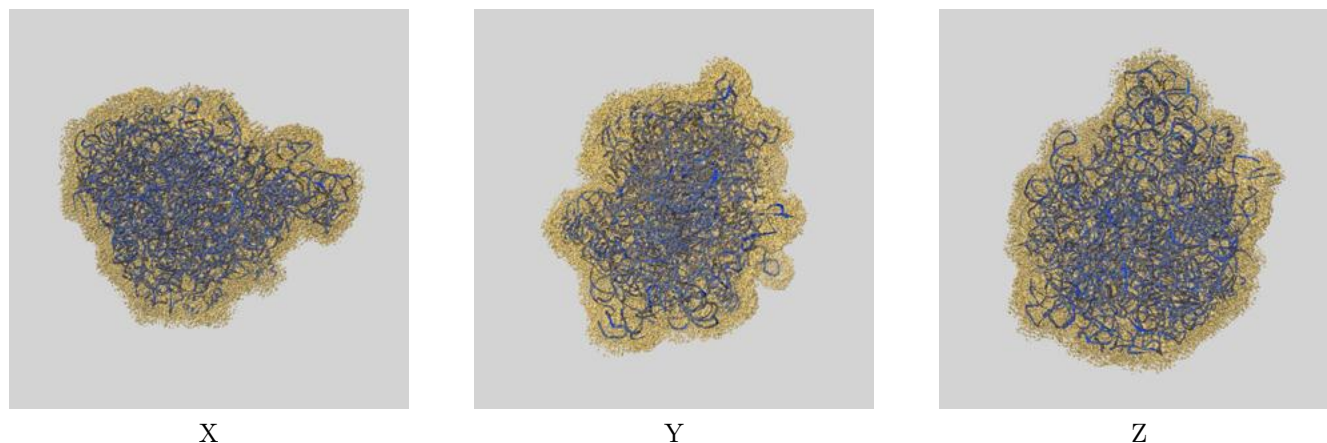
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.01	3.30	3.04
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

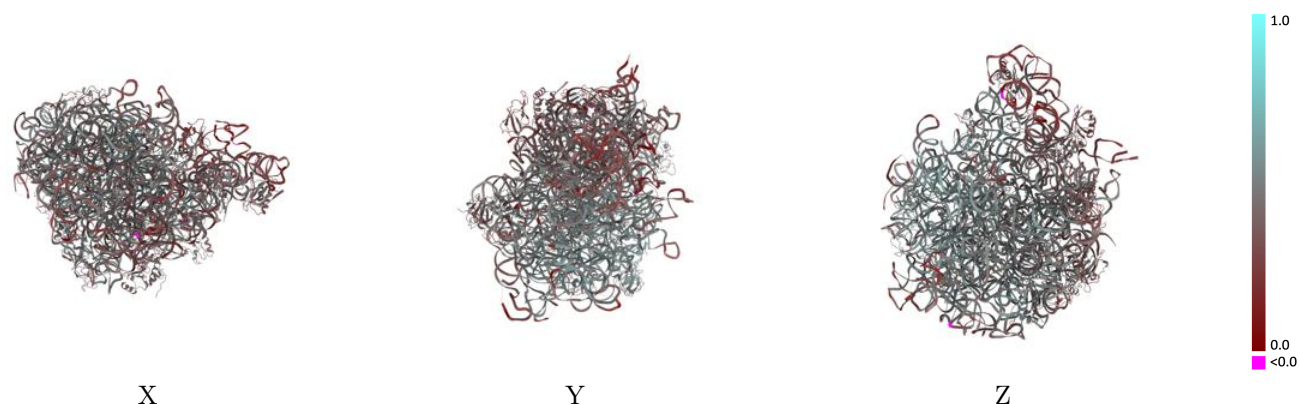
This section contains information regarding the fit between EMDB map EMD-26124 and PDB model 7TTU. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



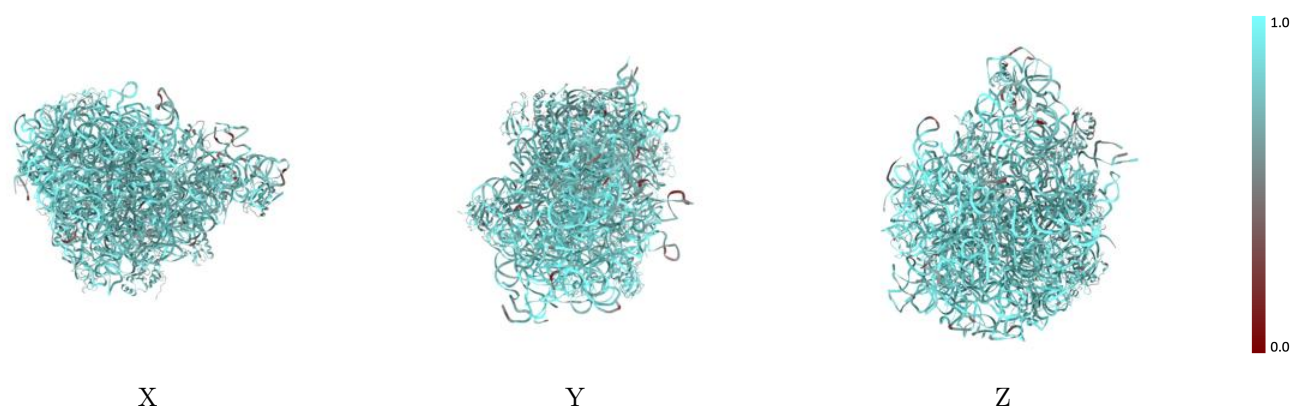
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



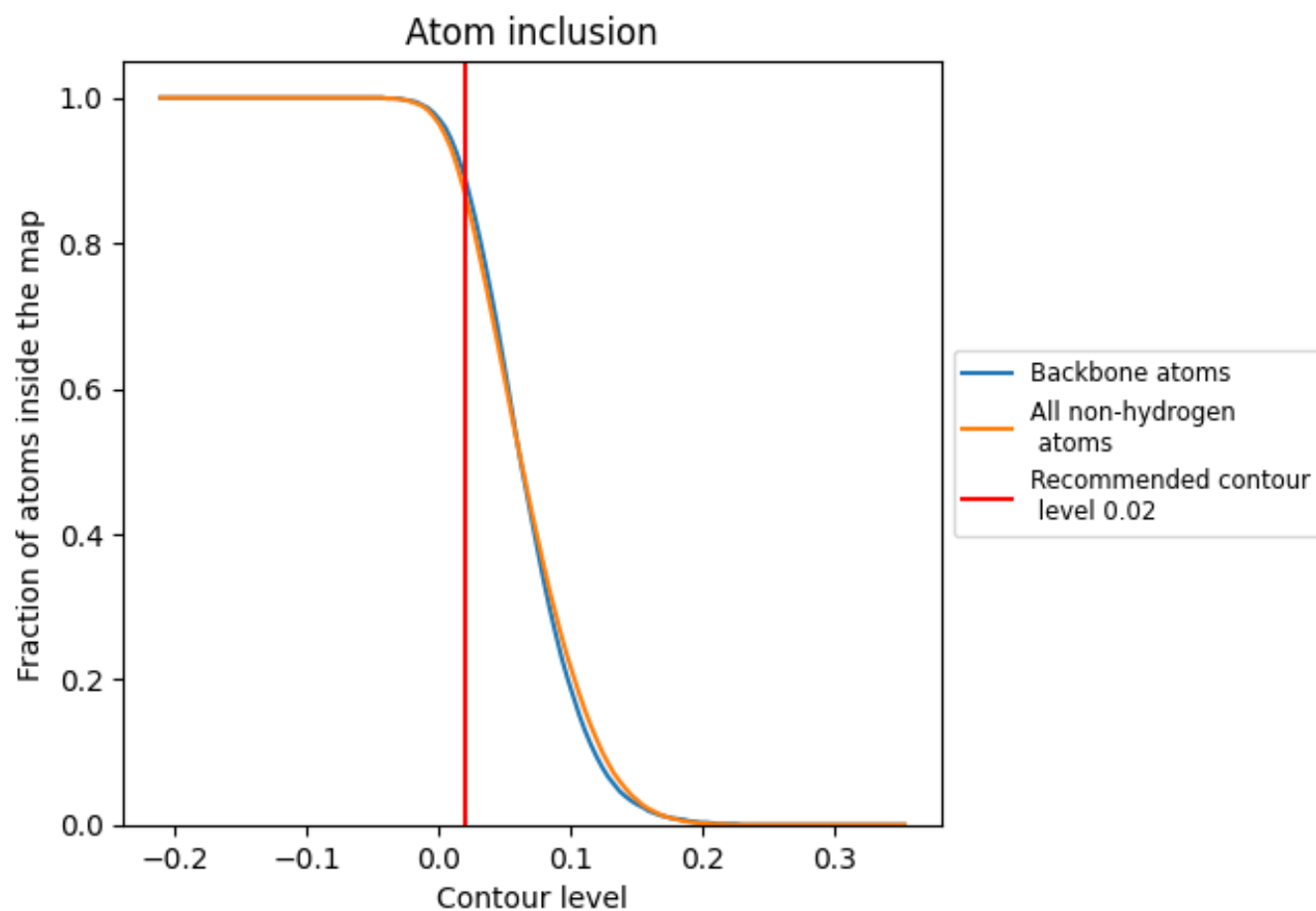
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.4470
1	 0.8870	 0.4580
2	 0.7760	 0.3340
A	 0.8080	 0.4420
B	 0.8940	 0.5270
C	 0.8230	 0.3960
D	 0.7570	 0.3500
E	 0.8650	 0.4600
F	 0.8670	 0.4760
G	 0.7610	 0.3820
H	 0.6440	 0.3270
I	 0.8110	 0.4240
J	 0.8840	 0.4930
K	 0.8500	 0.4090
L	 0.8340	 0.4280
M	 0.7880	 0.3850
N	 0.8960	 0.4520
O	 0.7900	 0.4180
P	 0.9540	 0.5620
Q	 0.8880	 0.5010
R	 0.7650	 0.3730
S	 0.8320	 0.4380
V	 0.8030	 0.3880
W	 0.8040	 0.4160
X	 0.8350	 0.4430
Y	 0.7910	 0.4120
Z	 0.8640	 0.4690
a	 0.7310	 0.3610

