



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 09:47 PM UTC

PDB ID : 7U0H / pdb_00007u0h
EMDB ID : EMD-26259
Title : State NE1 nucleolar 60S ribosome biogenesis intermediate - Overall model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2022-02-18
Resolution : 2.76 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:

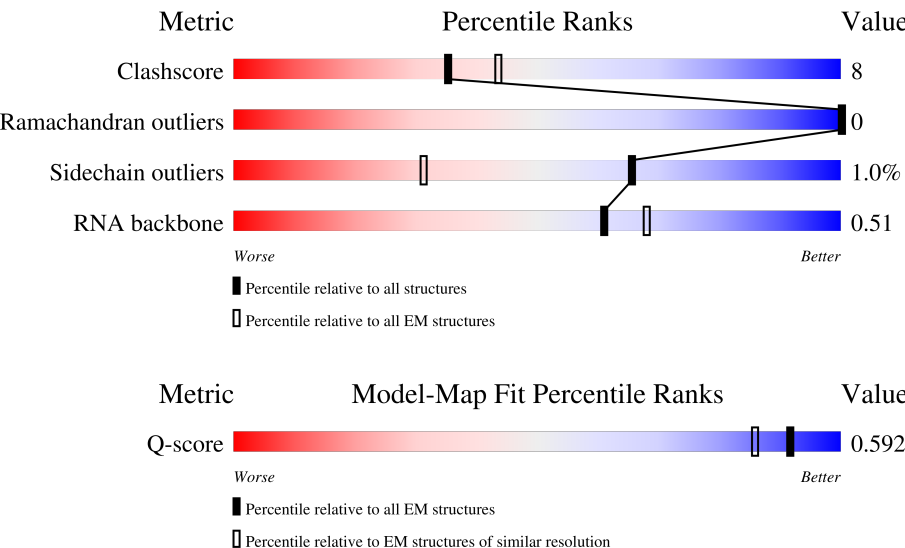
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.76 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	10642 (2.26 - 3.26)

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	1	3396	18% 48% 28% • 20%
2	2	158	11% 58% 42% •
3	6	87	32% 28% 30% 10% 32%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	254	
5	B	387	
6	C	362	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	K	376	
12	L	199	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	236	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	647	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	
34	h	120	
35	i	100	
36	j	88	
37	k	78	
38	m	9	
39	n	605	
40	o	220	
41	p	92	
42	q	455	
43	r	261	
44	s	520	
45	t	322	
46	u	199	
47	w	841	
48	y	245	
49	z	106	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 124932 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 RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2722	Total	C	N	O	P	0	0
			58236	26005	10495	19014	2722		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called ITS2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	59	Total	C	N	O	P	0	0
			1247	559	211	418	59		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	A	176	Total	C	N	O	0	0
			1356	856	263	237		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	340	Total	C	N	O	S	0	0
			2700	1713	502	479	6		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	185	Total	C	N	O	S	0	0
			1470	948	258	262	2		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 11 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	182	Total	C	N	O	0	0
			1459	907	300	252		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	187	Total	C	N	O	S	0	0
			1604	1006	340	257	1		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	170	Total	C	N	O	0	0
			1341	833	265	243		

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	146	Total	C	N	O	S	0	0
			1132	716	218	197	1		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	57	Total	C	N	O	S	0	0
			433	265	87	80	1		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	106	Total	C	N	O	0	0
			844	545	138	161		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 23 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	232	Total	C	N	O	S	0	0
			1870	1184	321	360	5		

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	138	Total	C	N	O	S	0	0
			1082	694	193	193	2		

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	134	Total	C	N	O	0	0
			1087	707	201	179		

- Molecule 27 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	92	Total	C	N	O	S	0	0
			731	477	129	124	1		

- Molecule 28 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	546	Total	C	N	O	S	0	0
			4430	2802	779	826	23		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	126	Total	C	N	O	S	0	0
			1012	641	204	166	1		

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 38 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	9	Total	C	N	O		0	0
			69	43	11	15			

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	368	Total	C	N	O	S	0	0
			3001	1944	519	528	10		

- Molecule 40 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	189	Total	C	N	O	S	0	0
			1588	998	296	293	1		

- Molecule 43 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	164	Total	C	N	O	S	0	0
			1341	846	260	231	4		

- Molecule 44 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 45 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 46 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	141	Total	C	N	O	S	0	0
			1191	748	238	196	9		

- Molecule 47 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	321	Total	C	N	O	S	0	0
			2610	1629	480	485	16		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

- Molecule 49 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 50 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
50	b	1	Total	Mg	0
			1	1	

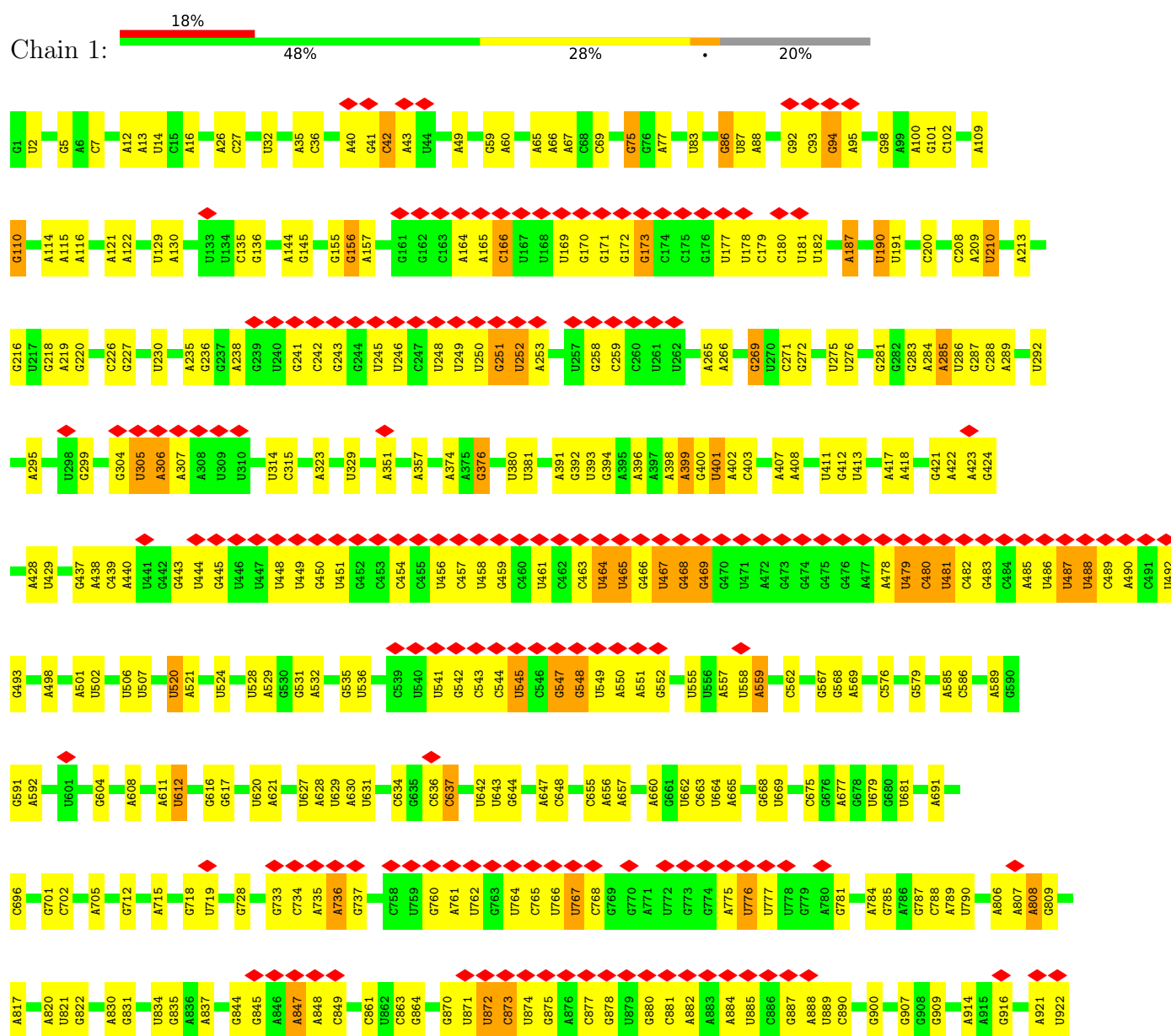
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

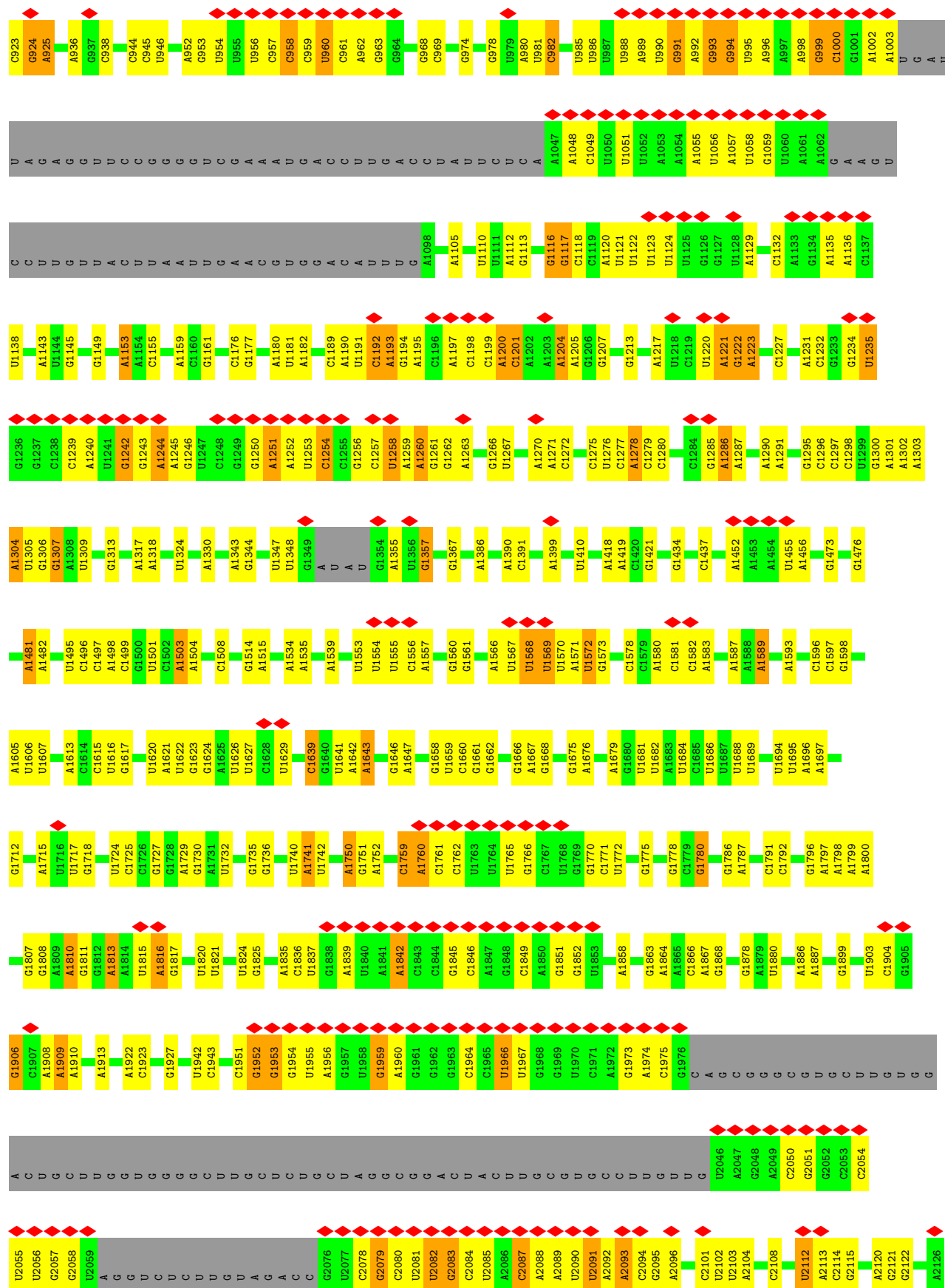
Mol	Chain	Residues	Atoms		AltConf
51	g	1	Total	Zn	0
			1	1	
51	j	1	Total	Zn	0
			1	1	
51	p	1	Total	Zn	0
			1	1	
51	u	1	Total	Zn	0
			1	1	

3 Residue-property plots

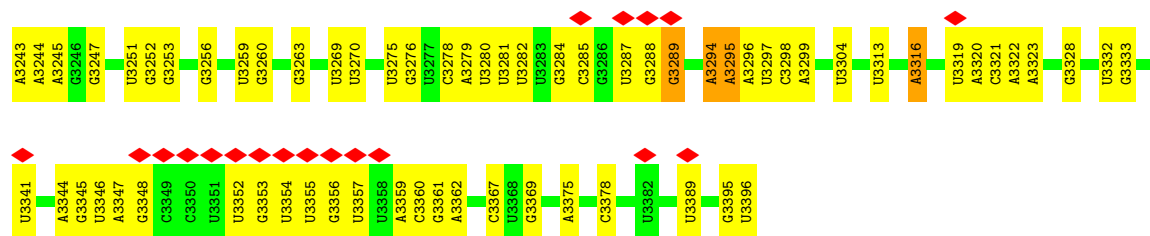
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S rRNA

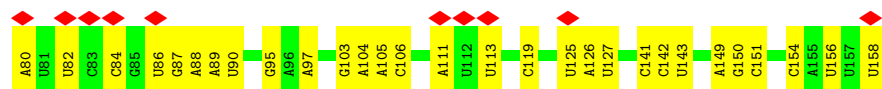
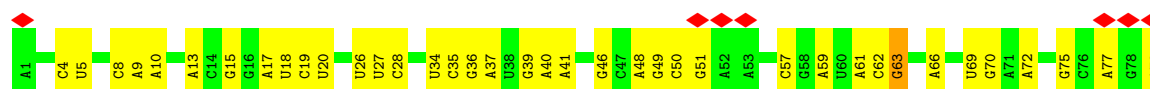




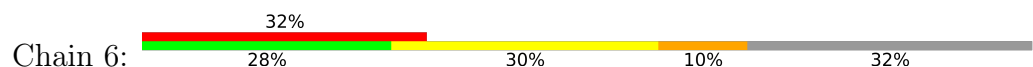
U2127	C2128	U2129	G2130	A2131	C2136	U2137	A2138	U2139	U2140	U2141	A2142	A2143	A2144	U2148	A2149	A2152	U2153	U2154	G2155	C2156	G2157	A2158	U2159	C2160	G2161	U2162	C2163	A2164	G2165	A2166	A2167	A2168	G2169	U2170	U2173	G2174	U2175	U2176	G2177	A2182	A2183	U2184	G2187	A2188	U2189	U2190	U2191	C2192	U	G	C	C	C					
A	G	U	G	C	C	U	G	A	U	U	C	A	A	G	A	A	A	A	U	U	C	A	C	C	U	A	U	U	A	C	C	G	G	U	A	C	C	G	G	A	A	U	A	A	G	A	C											
U	A	U	G	C	U	C	C	U	A	G	G	U	A	C	A	A	U	U	C	C	U	G	C	C	U	A	U	U	A	A	U	U	A	G	G	A	C	C	U	G	A	A	U	G	A2316	A2317												
U2318	U2319	C2322	G2323	A2324	G2325	A2326	U2327	U2328	C2329	A2332	C2333	U2334	G2335	U2336	U2342	C2343	U2344	A2345	C2346	U2347	A2352	A2356	A2357	A2358	C2359	A2363	G2364	A2367	A2368	G2371	A2372	A2373	C2374	G2375	G2376	G2377	C2378	G2385	U2388	G2391	C2392	G2393	G2394	G2395	G2396	A	A	A										
G	A	A	G	A	C2405	C2406	C2407	U2408	G2409	U2410	U2411	G2412	A2413	C2414	C2415	U2416	U2417	G	A	U	C	U	U	U	U	A	C	U	U	U	U	A	A	A	A	A	A	A	G	G	G	U	U	U	U	A	A	A										
U	A	A	U	G	C	C	G	G	C	G	C	G	A	A	C	C	C	U	U	C	A	U	U	U	U	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C									
A	U	A	C	A	A	C	A	G	C	U	A	U	U	U	C	C	C	U	U	C	A	U	U	U	U	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C								
A	U	C	A	C	G	C	G	A	C	U	A	U	U	U	C	C	G	U	C	A	U	U	A	A	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C							
A	U	A	A	A	C	A	G	A	C	U	A	U	U	U	C	C	G	U	C	A	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U					
C	G	A	U	C	U	U2767	U2768	A2769	G2770	U2771	C2772	C2773	U2774	U2775	C2776	G2777	U2781	U2782	U2783	G2784	A2785	G2786	G2787	C2788	U2789	A2790	G2791	A	G	U	U	C	A	A2803	A2804	G2805	U2806	U2807	A2808	C2809	C2810	A2811	C2812	A2813	G2814	G2815	G2816	A2817	U2818	A2819	A2820	C2821						
U2822	G2823	G2824	G2825	U2826	U2829	G2830	G2831	C2832	A2833	G2834	U2835	C2836	A2837	A2838	G2839	C2840	G2841	U2842	U2843	C2844	A2845	U2846	A2847	C2848	C2849	G2850	A2851	C2852	A2853	U2854	U2855	G2856	C2857	U2858	U2859	U2860	U2861	U2862	G2863	A2864	U2865	U2866	C	U	U	C	G2871	A2872	U2873	G2874	U2875	C2876	G2877	G2878	C2879	U2880	C2881	U2882
U2883	C2884	A2887	U2888	A2889	U2891	C2894	G2898	C2899	A2900	G2901	U2909	A2910	A2911	C2912	U2916	G2917	G2918	A2919	U2920	U2921	G2922	U2923	U2924	C2925	A2926	C2927	C2928	C2929	A2930	U2935	A2936	G2937	G2938	A2941	C	G	U	G	A	G2947	C2948	U2949	G2950	G	G	U	U	U	A	G2957	A2958							
C2959	C2960	G2961	U2962	C2963	G2964	U2965	G2966	A2967	G2968	A2969	C2970	A2971	G2972	G2973	U2974	U2975	A2976	G2977	U2978	U2979	U2980	U	A2982	C2983	C2984	C2985	G2990	U2996	G2997	A3000	C3001	A3006	U3007	A3012	U3013	U3014	G3015	A3016	A3017	C3018	A3021	G3022	U3023	A3024	A3027	G3028	A3032	A3033	U3041	U3042								
C3043	U3047	A3048	U3055	U3056	U3057	U3058	G3059	C3063	U3064	C3067	C3072	A3073	G3074	U3078	U3079	G3080	C3084	G3085	A3086	C3089	U3090	A3091	C3092	C3093	C3096	C3097	G3098	C3099	U3100	G3101	G3102	G3109	G3112	C3120	U3121	A3122	A3129	G3216	C3217	A3218	U3219	A3224	U3231	G3232	C3233	A3234	C3235											
U3152	U3153	C3154	U3155	U3156	U3157	U3160	C3161	C3162	A3163	C3164	A3165	C3166	U3171	A3172	G3173	A3174	U3175	G3176	U3179	A3180	C3181	U3185	A3186	A3187	G3188	U3191	U3192	C3193	C3194	U3195	U3196	G3197	U3198	G3205	C3206	U3207	A3213	U3214	A3215	G3216	C3217	A3218	G3219	G3224	U3231	G3232	C3233	A3234	C3235									



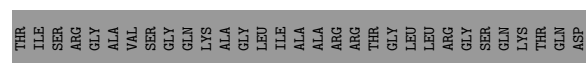
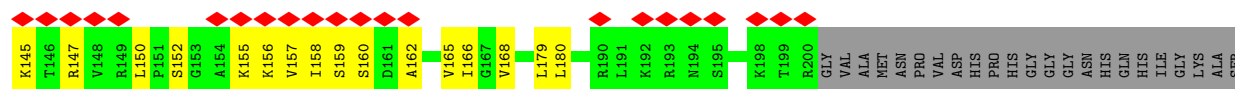
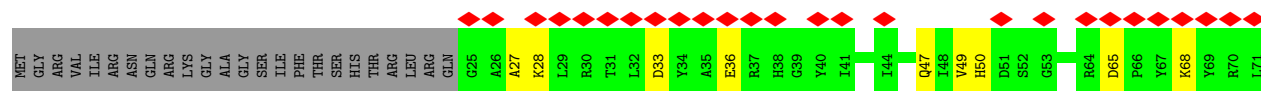
• Molecule 2: 5.8S rRNA



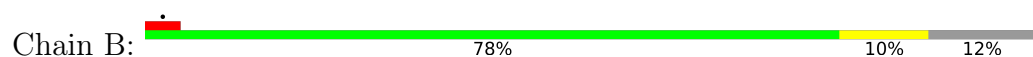
• Molecule 3: ITS2 rRNA

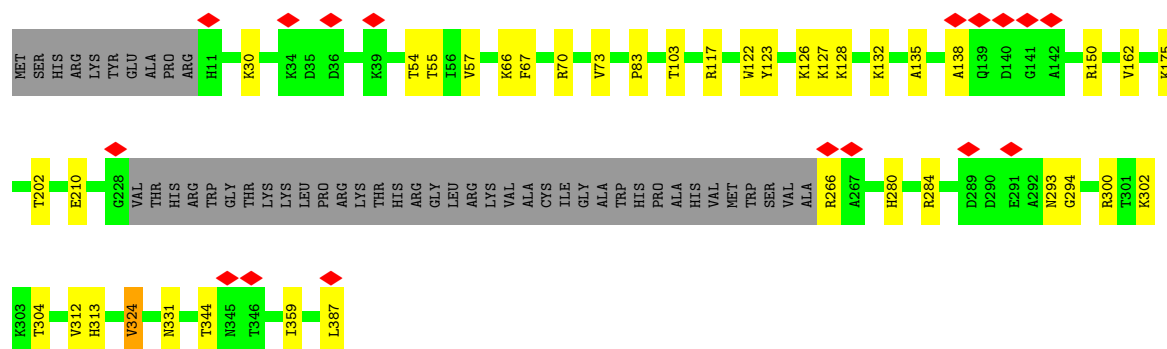


• Molecule 4: 60S ribosomal protein L2-A

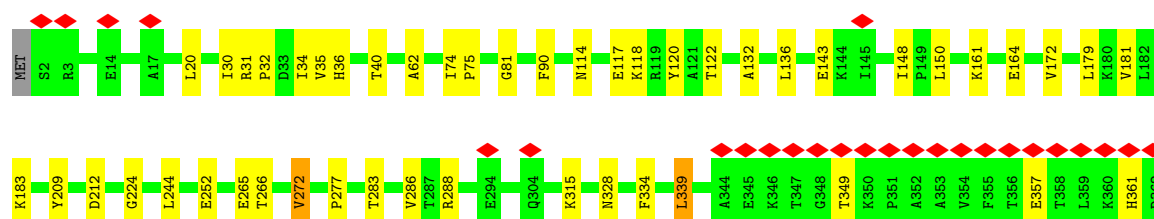
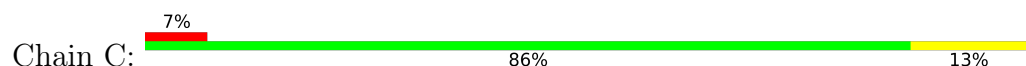


• Molecule 5: 60S ribosomal protein L3

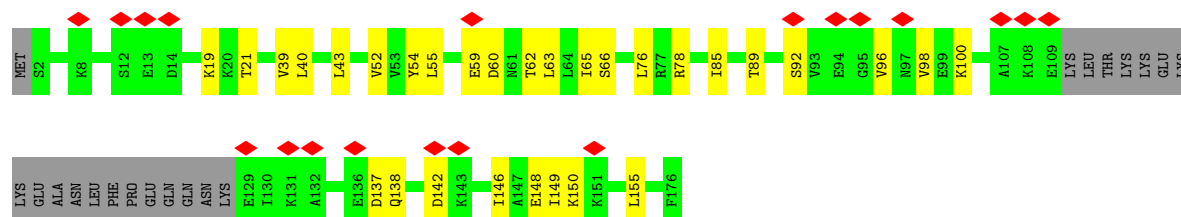




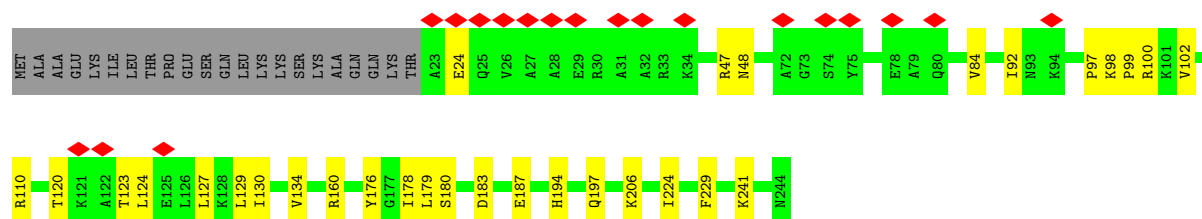
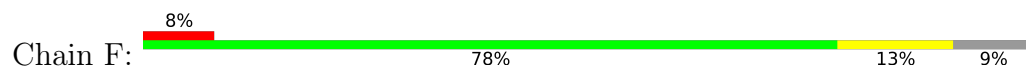
• Molecule 6: 60S ribosomal protein L4-A



• Molecule 7: 60S ribosomal protein L6-A

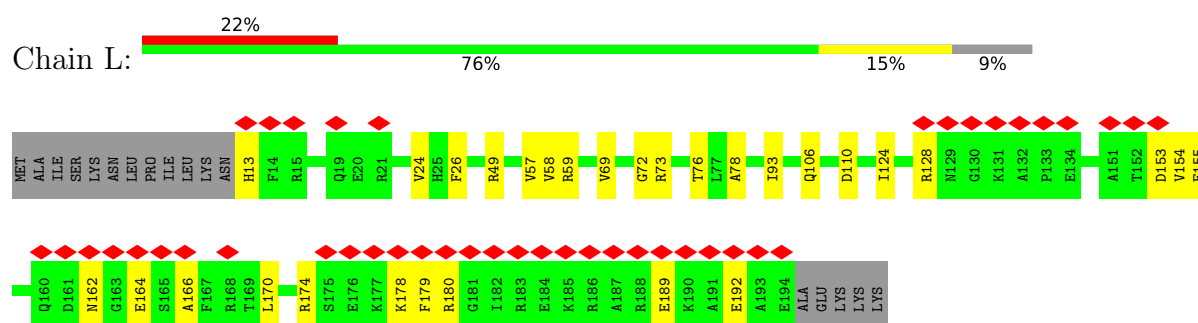


• Molecule 8: 60S ribosomal protein L7-A

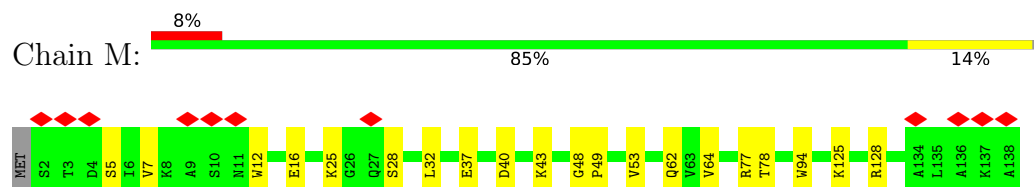


• Molecule 9: 60S ribosomal protein L8-A

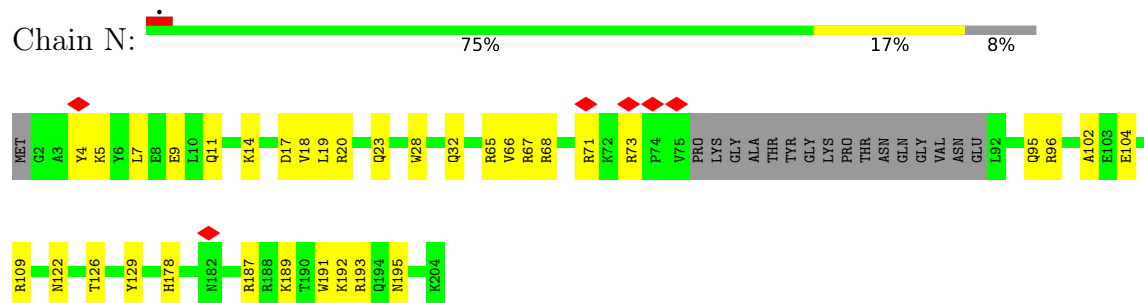




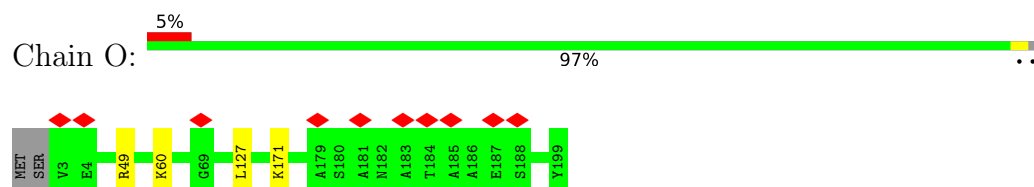
- Molecule 13: 60S ribosomal protein L14-A



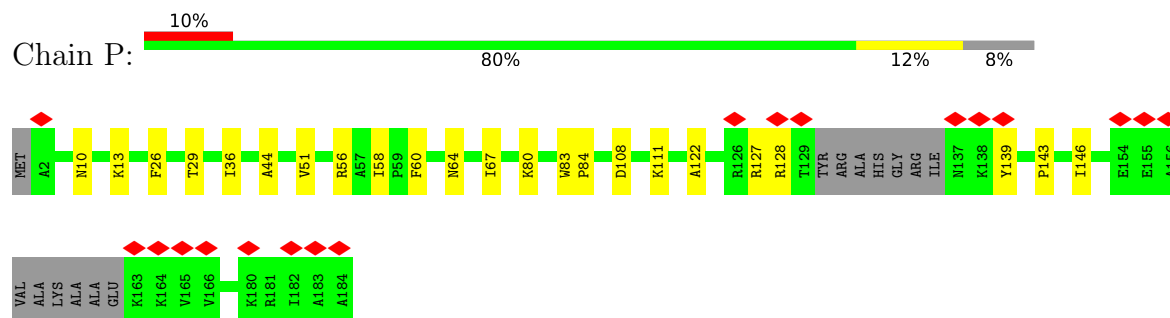
- Molecule 14: 60S ribosomal protein L15-A



- Molecule 15: 60S ribosomal protein L16-A

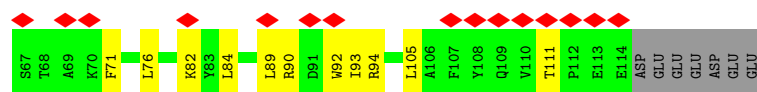


- Molecule 16: 60S ribosomal protein L17-A

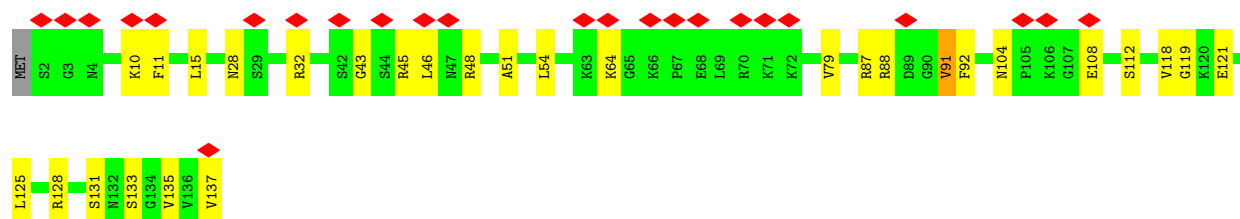
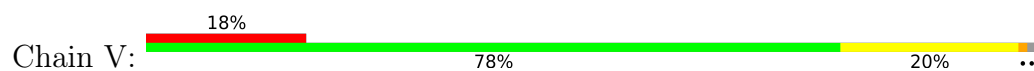


- Molecule 17: 60S ribosomal protein L18-A

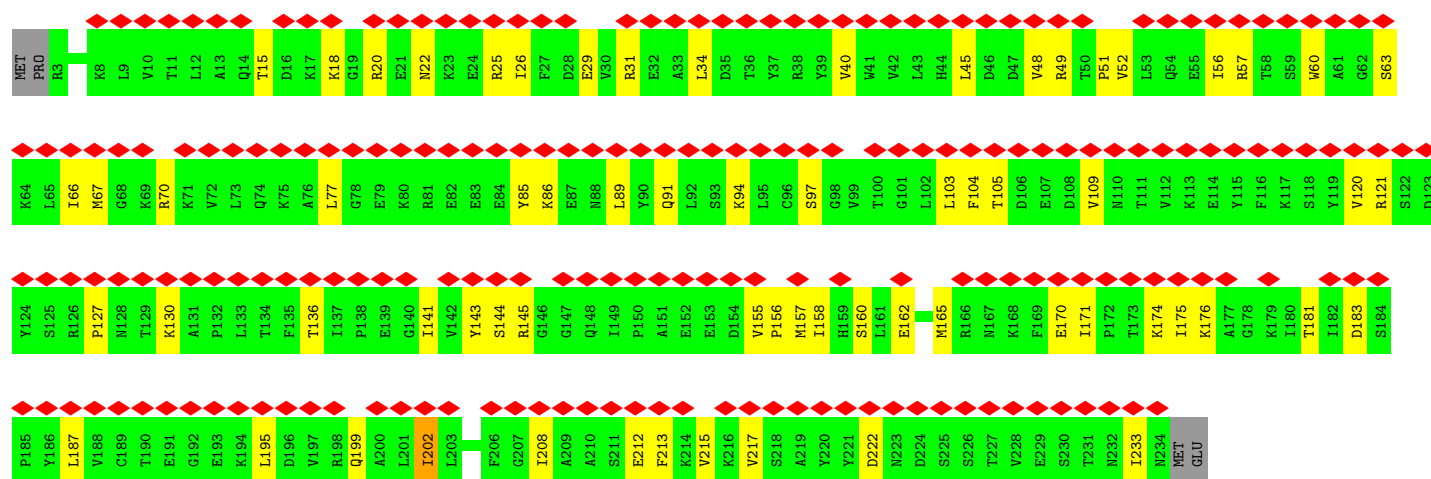
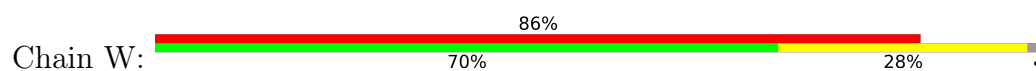




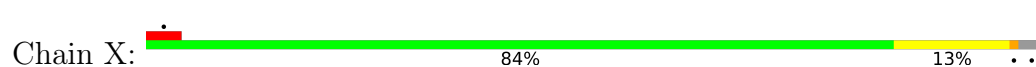
- Molecule 22: 60S ribosomal protein L23-A



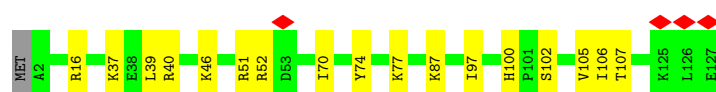
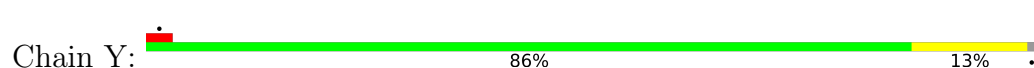
- Molecule 23: Ribosome assembly factor MRT4



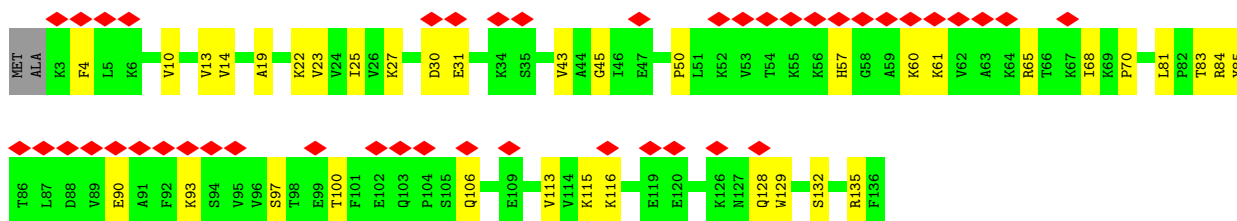
- Molecule 24: 60S ribosomal protein L25



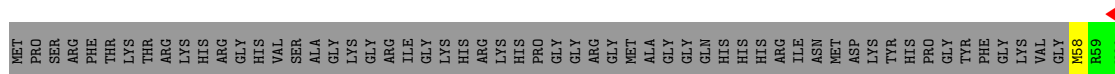
- Molecule 25: 60S ribosomal protein L26-A



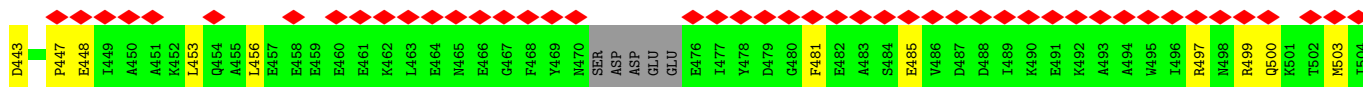
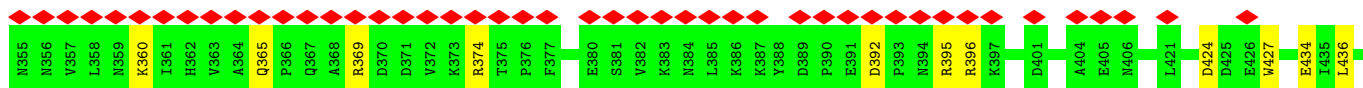
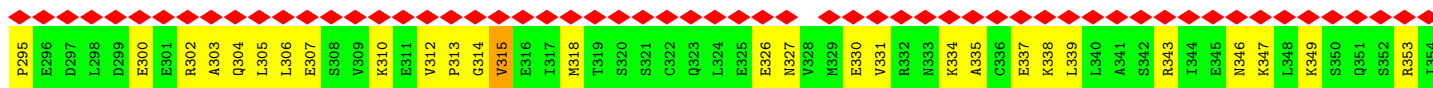
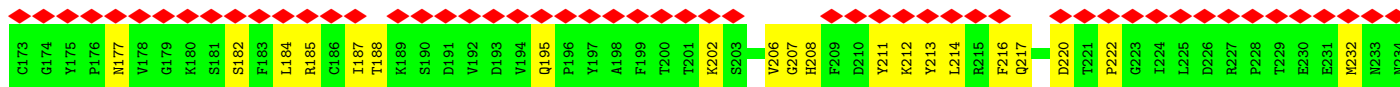
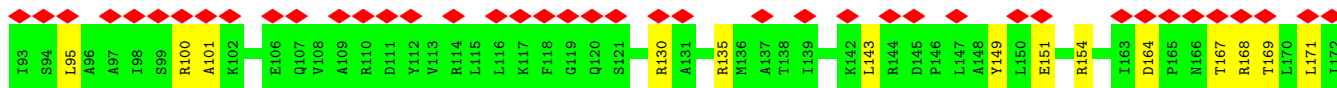
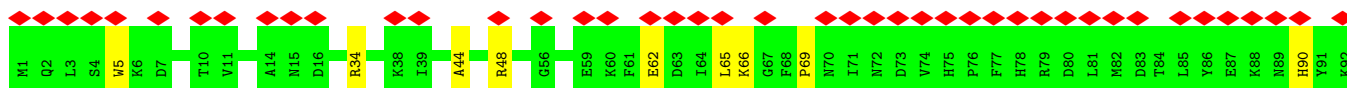
- Molecule 26: 60S ribosomal protein L27-A



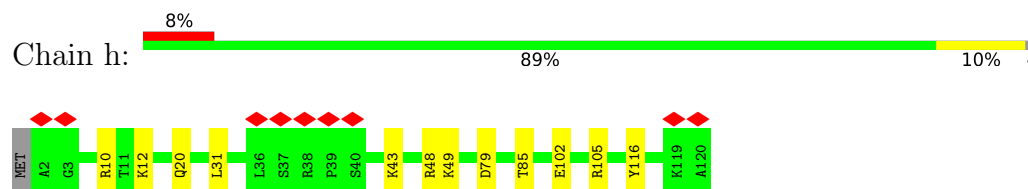
• Molecule 27: 60S ribosomal protein L28



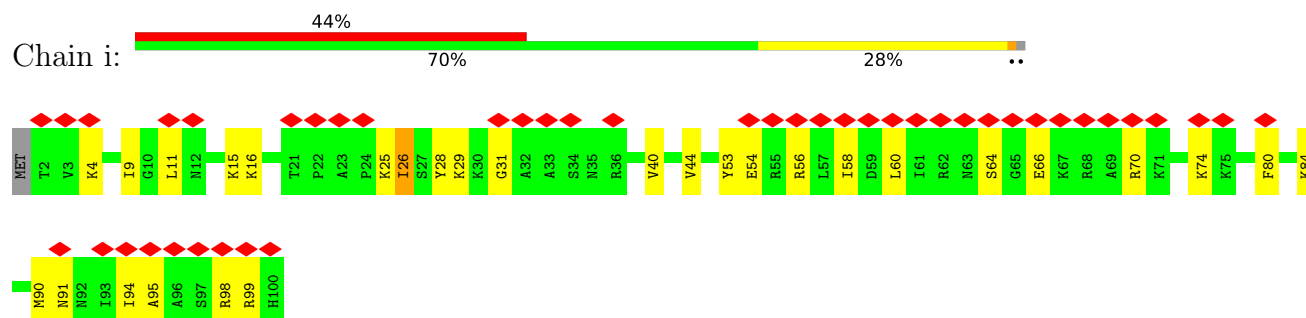
• Molecule 28: Nucleolar GTP-binding protein 1



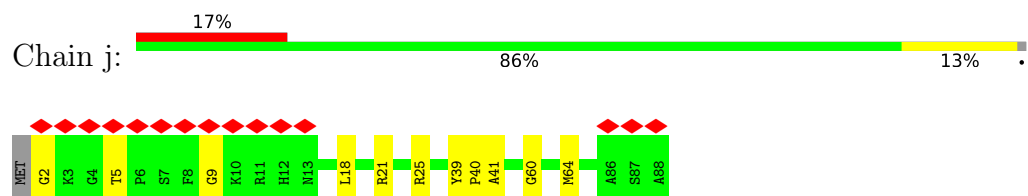
- Molecule 34: 60S ribosomal protein L35-A



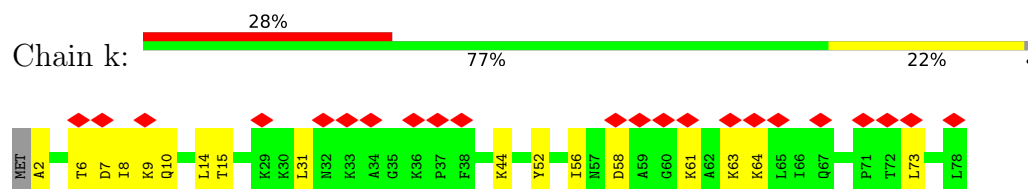
- Molecule 35: 60S ribosomal protein L36-A



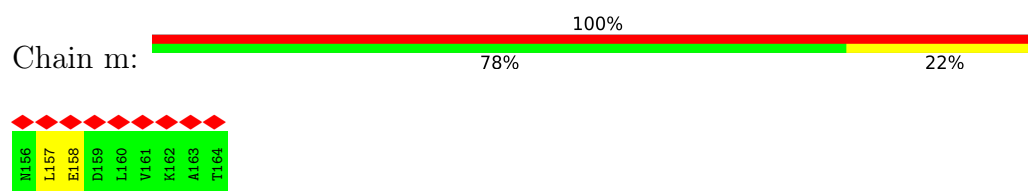
- Molecule 36: 60S ribosomal protein L37-A



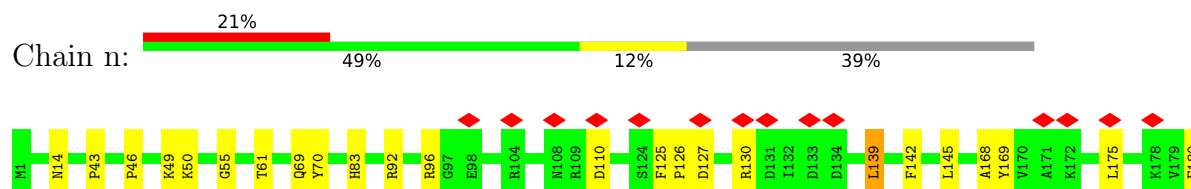
- Molecule 37: 60S ribosomal protein L38

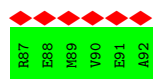


- Molecule 38: Nucleolar GTP-binding protein 2

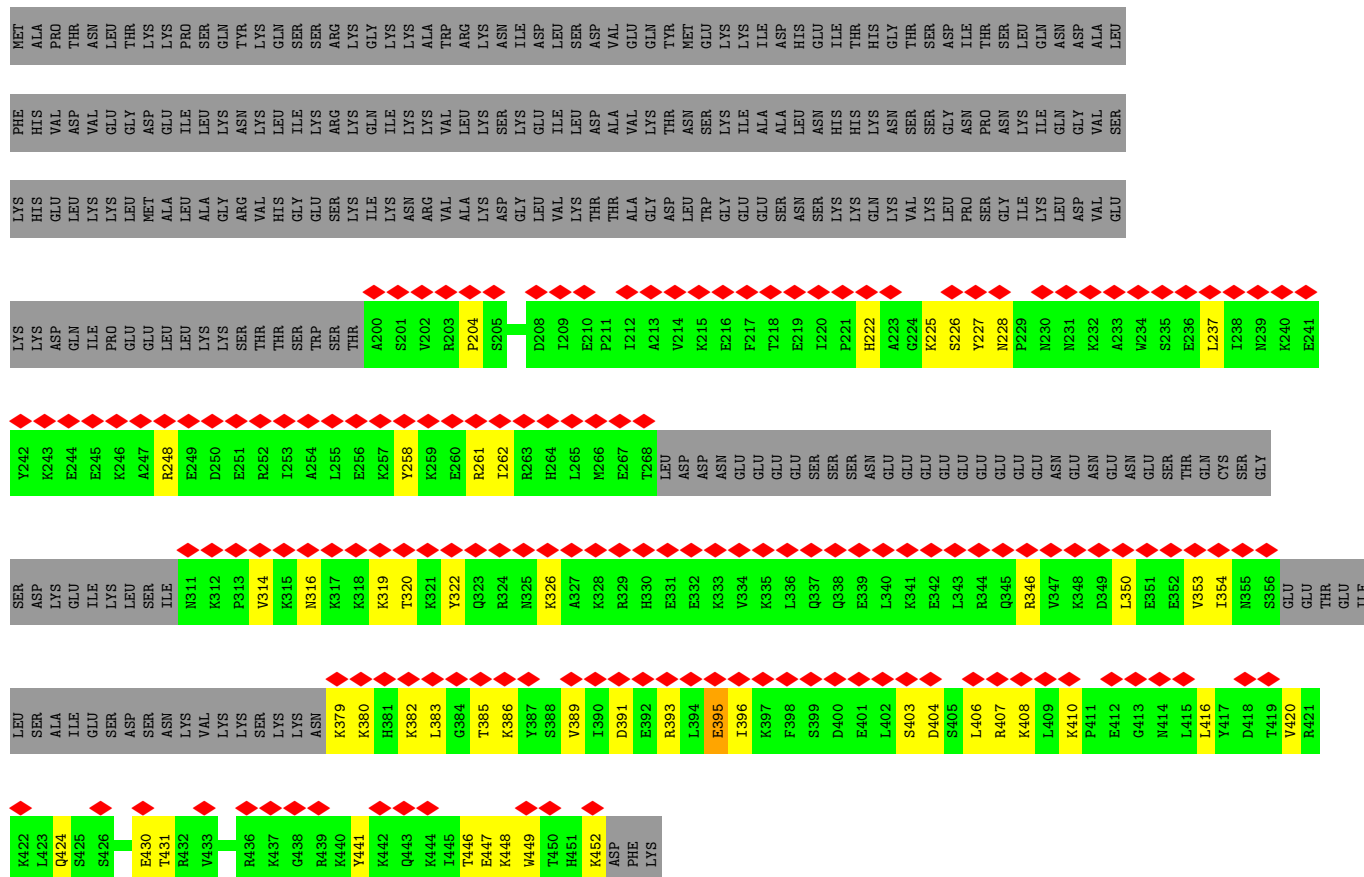
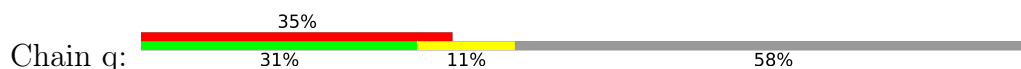


- Molecule 39: Pescadillo homolog

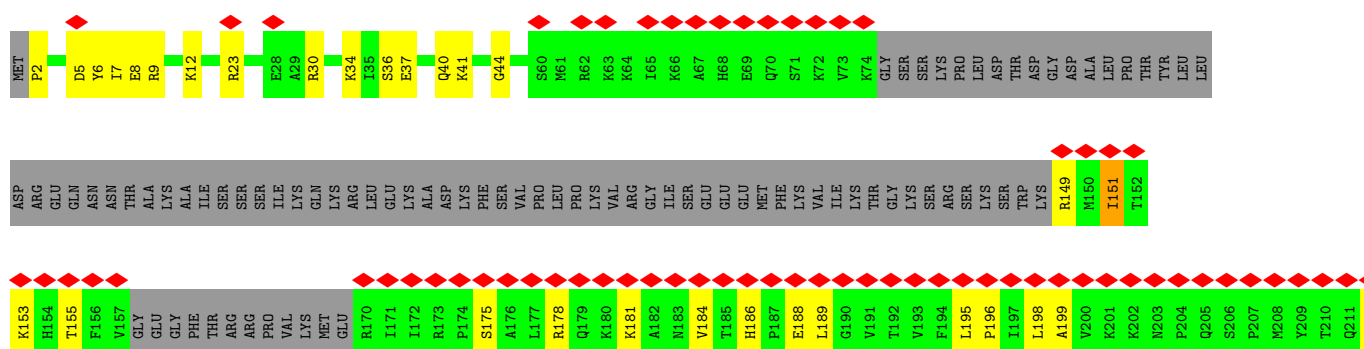
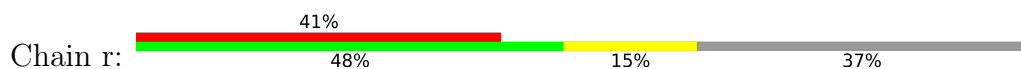


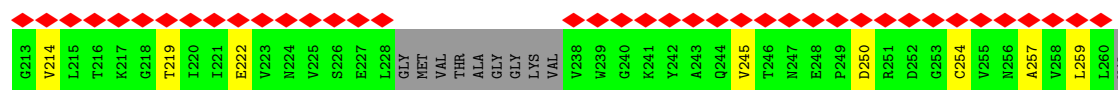


• Molecule 42: Ribosome biogenesis protein NOP53



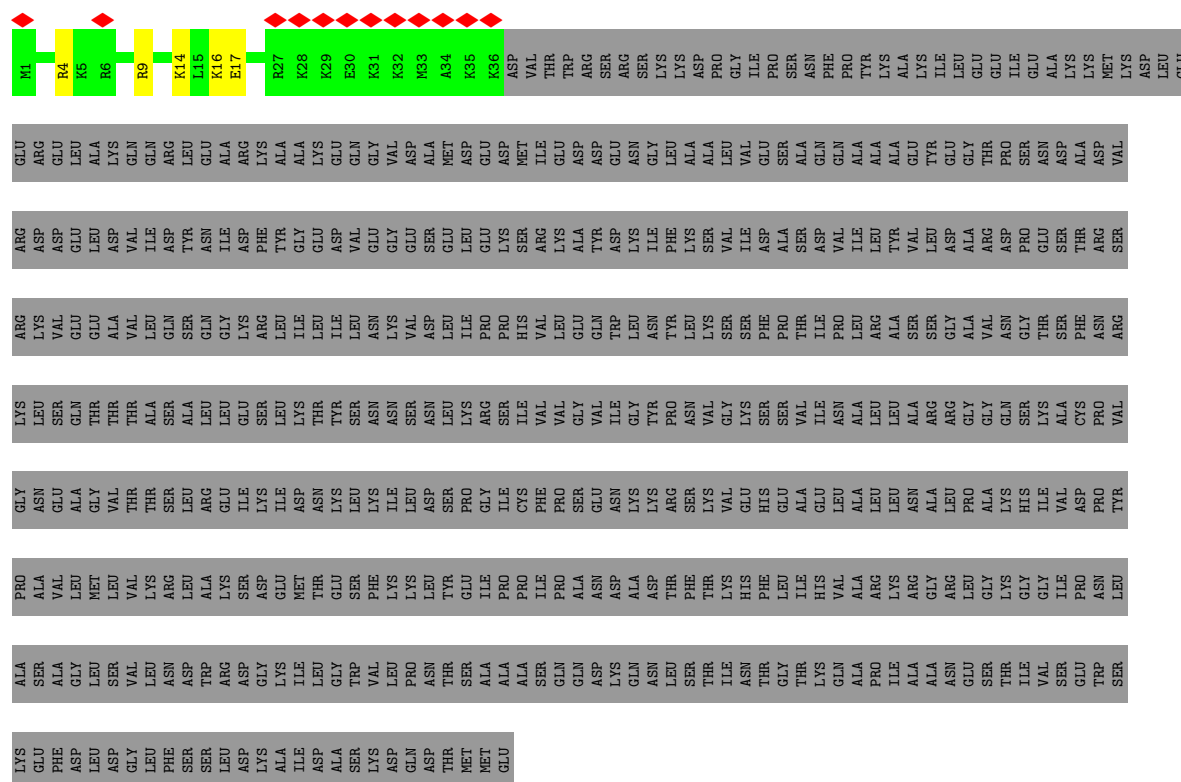
• Molecule 43: Ribosome biogenesis protein NSA2





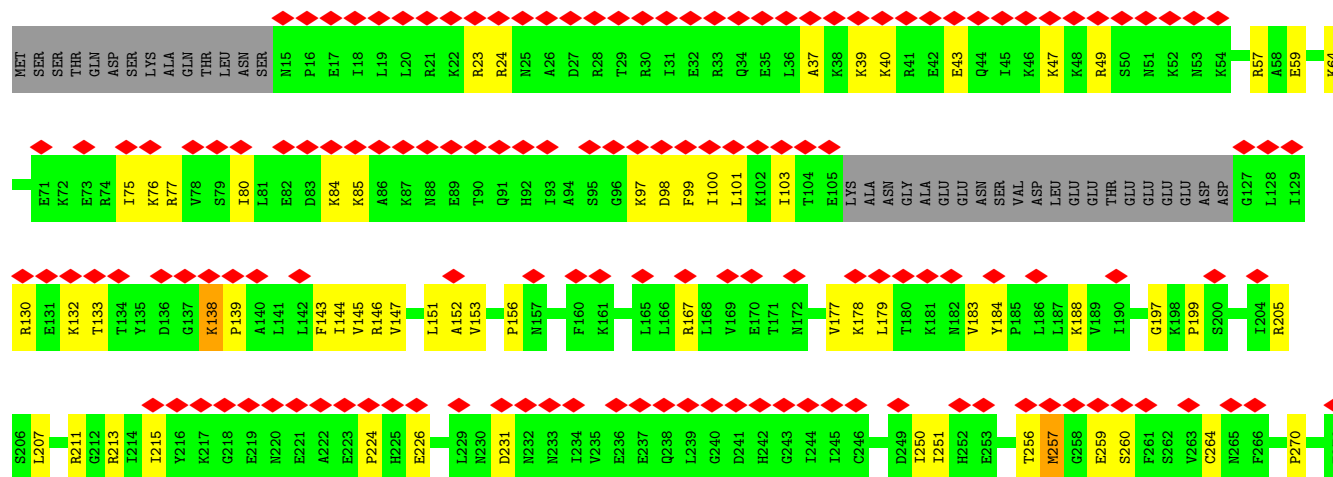
• Molecule 44: Nuclear GTP-binding protein NUG1

Chain s: 6% 93%



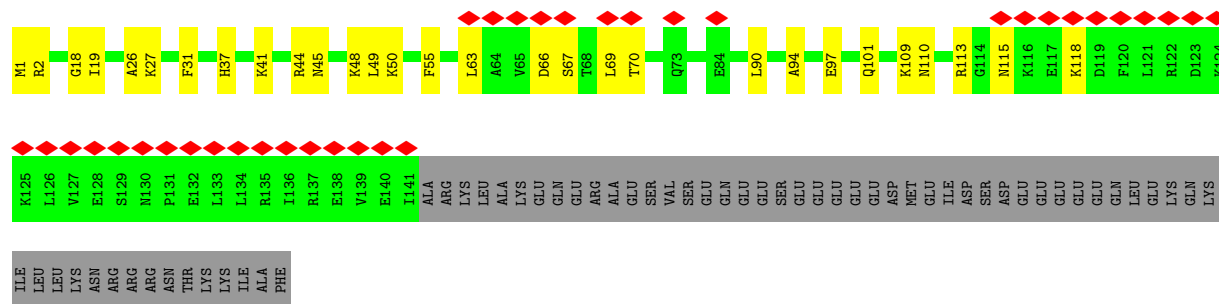
• Molecule 45: Ribosome biogenesis protein RLP7

Chain t: 50% 68% 21% 11%

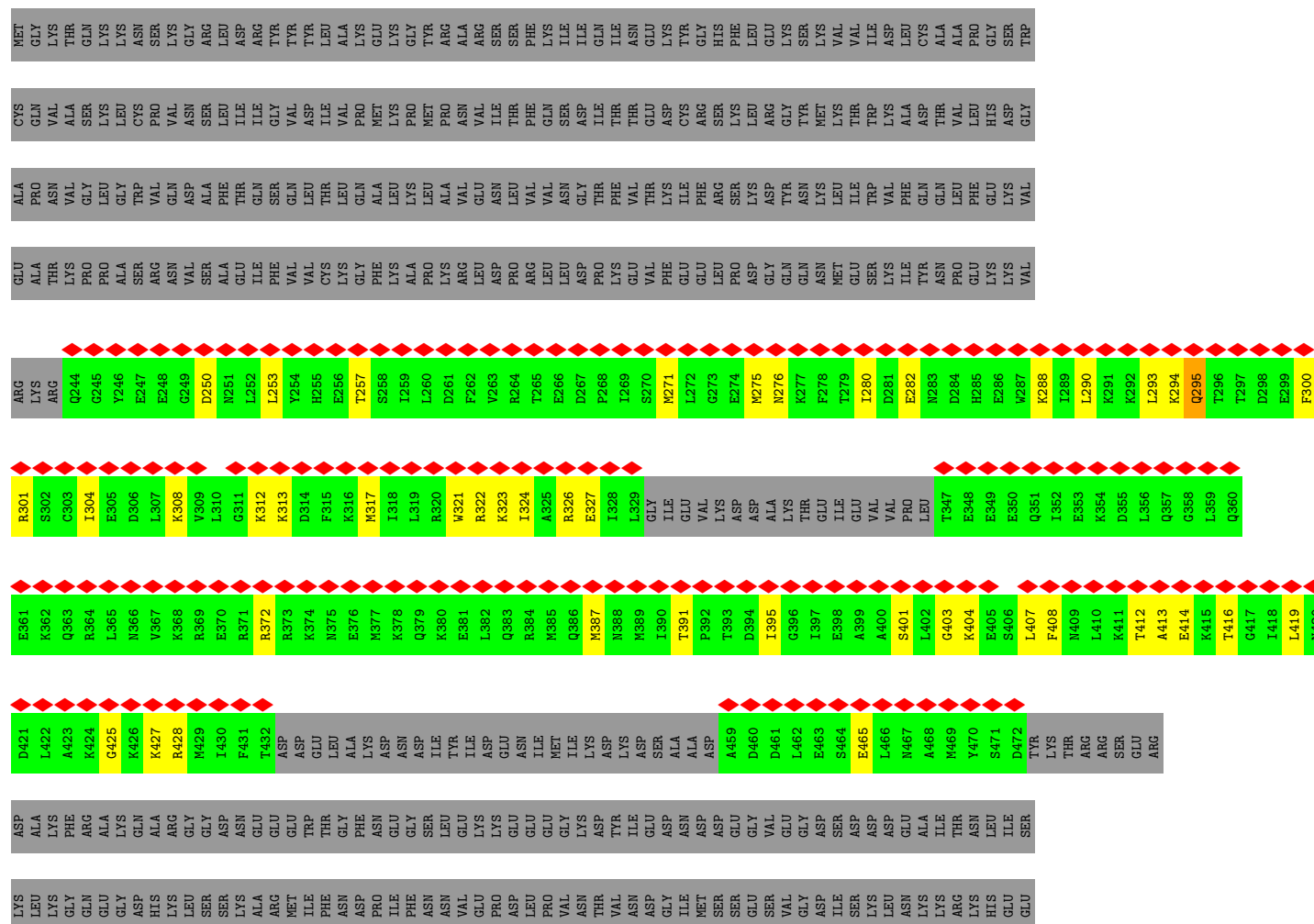




• Molecule 46: Ribosome biogenesis protein RLP24



• Molecule 47: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	83000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.319	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0284	Depositor
Map size ($\text{\AA}$)	411.53998, 411.53998, 411.53998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.02885, 1.02885, 1.02885	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.22	0/65173	0.33	0/101591
2	2	0.26	0/3746	0.35	0/5832
3	6	0.15	0/1390	0.28	0/2156
4	A	0.15	0/1382	0.33	0/1860
5	B	0.19	0/2755	0.35	0/3700
6	C	0.20	0/2801	0.35	0/3792
7	E	0.17	0/1260	0.31	0/1694
8	F	0.20	0/1821	0.35	0/2451
9	G	0.18	0/1496	0.35	0/2023
10	H	0.18	0/1539	0.32	0/2073
11	K	0.13	0/2098	0.30	0/2830
12	L	0.18	0/1483	0.36	0/1991
13	M	0.19	0/1074	0.34	0/1446
14	N	0.22	0/1637	0.39	0/2189
15	O	0.22	0/1585	0.35	0/2128
16	P	0.19	0/1360	0.35	0/1824
17	Q	0.18	0/1149	0.30	0/1550
18	R	0.17	0/1275	0.29	0/1702
19	S	0.18	0/1473	0.33	0/1980
20	T	0.12	0/434	0.26	0/575
21	U	0.15	0/861	0.35	0/1167
22	V	0.18	0/1018	0.35	0/1369
23	W	0.14	0/1902	0.30	0/2564
24	X	0.19	0/1097	0.34	0/1476
25	Y	0.20	0/1004	0.33	0/1341
26	Z	0.16	0/1113	0.29	0/1490
27	a	0.17	0/747	0.28	0/1008
28	b	0.15	0/4508	0.32	0/6068
29	c	0.15	0/751	0.31	0/1008
30	d	0.19	0/887	0.33	0/1191
31	e	0.20	0/1033	0.33	0/1383
32	f	0.22	0/868	0.35	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.20	0/891	0.39	0/1191
34	h	0.18	0/978	0.30	0/1301
35	i	0.16	0/778	0.31	0/1034
36	j	0.22	0/696	0.41	0/923
37	k	0.16	0/618	0.31	0/826
38	m	0.11	0/68	0.31	0/91
39	n	0.17	0/3071	0.30	0/4147
40	o	0.14	0/1129	0.33	0/1502
41	p	0.19	0/701	0.38	0/934
42	q	0.14	0/1610	0.32	0/2143
43	r	0.14	0/1362	0.31	0/1818
44	s	0.15	0/301	0.30	0/386
45	t	0.16	0/2333	0.33	0/3128
46	u	0.18	0/1213	0.35	0/1614
47	w	0.15	0/2633	0.30	0/3493
48	y	0.15	0/1872	0.34	0/2548
49	z	0.16	0/445	0.31	0/585
All	All	0.20	0/133419	0.33	0/194284

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	1	58236	0	29271	611	0
2	2	3353	0	1695	37	0
3	6	1247	0	630	25	0
4	A	1356	0	1407	44	0
5	B	2700	0	2772	26	0
6	C	2749	0	2863	33	0
7	E	1239	0	1326	20	0
8	F	1784	0	1862	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	G	1470	0	1549	29	0
10	H	1518	0	1587	32	0
11	K	2064	0	2156	104	0
12	L	1459	0	1509	33	0
13	M	1059	0	1154	16	0
14	N	1604	0	1666	27	0
15	O	1555	0	1659	6	0
16	P	1341	0	1379	14	0
17	Q	1132	0	1211	15	0
18	R	1258	0	1342	10	0
19	S	1437	0	1475	33	0
20	T	433	0	449	17	0
21	U	844	0	855	26	0
22	V	1003	0	1048	28	0
23	W	1870	0	1902	61	0
24	X	1082	0	1170	11	0
25	Y	993	0	1081	11	0
26	Z	1087	0	1150	27	0
27	a	731	0	773	11	0
28	b	4430	0	4498	115	0
29	c	743	0	797	22	0
30	d	873	0	914	9	0
31	e	1012	0	1079	9	0
32	f	850	0	880	7	0
33	g	881	0	945	31	0
34	h	969	0	1078	10	0
35	i	771	0	849	23	0
36	j	681	0	683	7	0
37	k	612	0	682	14	0
38	m	69	0	71	2	0
39	n	3001	0	3081	73	0
40	o	1107	0	1159	31	0
41	p	694	0	734	27	0
42	q	1588	0	1668	67	0
43	r	1341	0	1416	33	0
44	s	301	0	359	6	0
45	t	2306	0	2454	66	0
46	u	1191	0	1237	27	0
47	w	2610	0	2735	69	0
48	y	1849	0	1836	56	0
49	z	444	0	478	6	0
50	b	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	g	1	0	0	0	0
51	j	1	0	0	0	0
51	p	1	0	0	0	0
51	u	1	0	0	0	0
All	All	124932	0	96574	1734	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.

All (1734) 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)
41:p:5:THR:CG2	41:p:8:VAL:HG12	1.60	1.31
48:y:59:ILE:O	48:y:63:THR:HG22	1.31	1.28
41:p:5:THR:HG21	41:p:8:VAL:CG1	1.62	1.28
33:g:51:LEU:CD1	33:g:54:ILE:HG13	1.62	1.27
33:g:95:ILE:CD1	47:w:407:LEU:HD23	1.69	1.23
45:t:178:LYS:CG	45:t:257:MET:HE3	1.73	1.17
21:U:14:THR:HG22	21:U:66:VAL:HG22	1.29	1.15
9:G:82:LEU:HD12	9:G:180:VAL:HG12	1.21	1.14
20:T:40:VAL:HG13	20:T:97:LYS:O	1.48	1.13
33:g:51:LEU:CD1	33:g:54:ILE:CG1	2.24	1.13
29:c:24:THR:CG2	29:c:29:SER:HB3	1.78	1.13
11:K:106:PHE:CE1	11:K:234:LEU:HD13	1.87	1.09
45:t:100:ILE:HG13	45:t:133:THR:CG2	1.84	1.08
11:K:106:PHE:CE1	11:K:234:LEU:CD1	2.37	1.07
23:W:63:SER:OG	23:W:105:THR:HG22	1.54	1.07
39:n:372:PRO:CD	42:q:406:LEU:HD21	1.86	1.06
47:w:413:ALA:O	47:w:416:THR:HG22	1.55	1.05
33:g:51:LEU:HD11	33:g:54:ILE:CG1	1.84	1.04
33:g:95:ILE:HD13	47:w:407:LEU:HD23	1.40	1.04
45:t:178:LYS:HG3	45:t:257:MET:HE3	1.05	1.04
23:W:136:THR:HG22	23:W:187:LEU:CB	1.89	1.03
45:t:100:ILE:HG13	45:t:133:THR:HG22	1.39	1.02
4:A:104:LEU:CD1	4:A:158:ILE:HD11	1.87	1.02
41:p:5:THR:HG21	41:p:8:VAL:HG13	1.40	1.02
11:K:234:LEU:HD12	11:K:235:PRO:HD2	1.41	1.01
33:g:51:LEU:HD11	33:g:54:ILE:HG13	1.02	1.00
29:c:24:THR:HG21	29:c:29:SER:HB3	1.01	1.00
39:n:372:PRO:CG	42:q:406:LEU:HD21	1.90	1.00
39:n:372:PRO:HG2	42:q:406:LEU:HD21	1.42	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:101:VAL:HG12	4:A:165:VAL:HG22	1.44	0.98
40:o:93:ILE:HD12	40:o:139:PHE:CE1	1.97	0.98
1:1:1200:A:C2	1:1:2824:G:N1	2.30	0.98
29:c:24:THR:HG21	29:c:29:SER:CB	1.92	0.98
28:b:237:MET:HE3	28:b:241:TYR:CE2	1.99	0.98
11:K:85:ASN:ND2	11:K:297:VAL:HG12	1.79	0.98
45:t:178:LYS:HG3	45:t:257:MET:CE	1.93	0.97
9:G:82:LEU:HD12	9:G:180:VAL:CG1	1.95	0.97
39:n:372:PRO:HD2	42:q:406:LEU:CD2	1.94	0.96
33:g:95:ILE:HD11	47:w:407:LEU:HD23	1.45	0.96
11:K:104:HIS:CD2	11:K:258:GLU:CD	2.44	0.96
41:p:5:THR:CG2	41:p:8:VAL:CG1	2.32	0.95
11:K:104:HIS:NE2	11:K:258:GLU:HG2	1.82	0.95
39:n:372:PRO:CD	42:q:406:LEU:CD2	2.45	0.94
11:K:202:VAL:CG2	11:K:237:LYS:NZ	2.31	0.94
11:K:202:VAL:CG2	11:K:237:LYS:HZ2	1.79	0.94
1:1:1200:A:H2	1:1:2824:G:N1	1.65	0.94
47:w:301:ARG:O	47:w:304:ILE:HG13	1.67	0.93
48:y:232:ILE:O	48:y:232:ILE:HG22	1.69	0.92
11:K:202:VAL:HG23	11:K:237:LYS:HZ2	1.34	0.92
23:W:136:THR:HG22	23:W:187:LEU:HB2	1.49	0.92
3:6:231:A:HO2'	3:6:232:A:H8	1.01	0.92
1:1:3043:C:OP1	22:V:45:ARG:HD3	1.71	0.91
39:n:126:PRO:HB2	39:n:130:ARG:HH12	1.35	0.91
39:n:126:PRO:HB2	39:n:130:ARG:NH1	1.85	0.91
45:t:178:LYS:CG	45:t:257:MET:CE	2.48	0.91
45:t:139:PRO:HB2	45:t:257:MET:HE2	1.52	0.90
1:1:75:G:H5'	12:L:58:VAL:CG1	2.00	0.90
45:t:139:PRO:HA	45:t:179:LEU:O	1.70	0.90
48:y:228:GLN:HB2	48:y:232:ILE:CD1	2.02	0.90
33:g:95:ILE:CD1	47:w:407:LEU:CD2	2.49	0.89
28:b:212:LYS:O	48:y:239:THR:HG22	1.72	0.89
1:1:728:G:H5'	17:Q:43:PRO:HB2	1.53	0.89
11:K:106:PHE:HE1	11:K:234:LEU:CD1	1.86	0.88
39:n:372:PRO:HD2	42:q:406:LEU:HD21	1.52	0.88
45:t:100:ILE:CG1	45:t:133:THR:CG2	2.51	0.88
28:b:237:MET:O	28:b:241:TYR:HD2	1.57	0.88
12:L:180:ARG:HD3	35:i:11:LEU:HD11	1.56	0.88
29:c:24:THR:CG2	29:c:29:SER:CB	2.50	0.88
23:W:63:SER:CB	23:W:105:THR:HG22	2.03	0.87
45:t:100:ILE:CG1	45:t:133:THR:HG23	2.04	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:75:G:C5'	12:L:58:VAL:CG1	2.53	0.87
11:K:104:HIS:CD2	11:K:258:GLU:HG2	2.09	0.86
11:K:72:GLU:O	11:K:76:LYS:HG3	1.75	0.86
28:b:212:LYS:O	48:y:239:THR:CG2	2.22	0.86
48:y:228:GLN:HB2	48:y:232:ILE:HD12	1.57	0.86
1:1:173:G:H1	1:1:245:U:H3	1.24	0.85
28:b:169:THR:HG22	28:b:217:GLN:CG	2.07	0.85
28:b:237:MET:HE3	28:b:241:TYR:HE2	1.41	0.85
11:K:104:HIS:CD2	11:K:258:GLU:CG	2.60	0.85
1:1:870:G:H22	1:1:889:U:H3	1.26	0.84
1:1:445:G:H1	1:1:489:C:H42	1.22	0.84
22:V:87:ARG:HH22	22:V:137:VAL:HG21	1.41	0.84
23:W:85:TYR:CD2	23:W:86:LYS:HE3	2.14	0.83
28:b:90:HIS:CD2	28:b:149:TYR:CE1	2.67	0.83
43:r:37:GLU:HG3	43:r:41:LYS:HD2	1.61	0.83
33:g:95:ILE:HD11	47:w:407:LEU:CD2	2.09	0.82
20:T:40:VAL:CG1	20:T:97:LYS:O	2.27	0.82
40:o:93:ILE:HD12	40:o:139:PHE:HE1	1.41	0.82
13:M:25:LYS:HD2	13:M:62:GLN:OE1	1.80	0.82
39:n:213:VAL:HG21	42:q:420:VAL:HG11	1.61	0.82
4:A:126:LEU:HD11	4:A:156:LYS:NZ	1.95	0.82
6:C:120:TYR:CE2	6:C:277:PRO:HB3	2.15	0.81
47:w:301:ARG:HA	47:w:304:ILE:HG12	1.61	0.81
4:A:137:ILE:HB	4:A:147:ARG:HG3	1.62	0.81
28:b:90:HIS:HD2	28:b:149:TYR:CZ	1.98	0.80
48:y:232:ILE:HG22	48:y:236:LEU:HG	1.62	0.80
20:T:40:VAL:HG12	20:T:41:ASP:N	1.97	0.80
39:n:126:PRO:O	39:n:130:ARG:HG3	1.81	0.80
33:g:51:LEU:CD1	33:g:54:ILE:HG12	2.10	0.80
42:q:237:LEU:CD2	42:q:396:ILE:HD13	2.12	0.79
1:1:1200:A:H2	1:1:2824:G:H1	0.86	0.79
39:n:126:PRO:C	39:n:130:ARG:NH1	2.41	0.79
48:y:4:ARG:HH21	48:y:215:LEU:HD13	1.47	0.79
1:1:2891:U:HO2'	49:z:2:ALA:N	1.81	0.78
11:K:85:ASN:ND2	11:K:297:VAL:CG1	2.47	0.78
1:1:647:A:H2	1:1:2373:A:N1	1.81	0.77
41:p:5:THR:HG23	41:p:8:VAL:HG12	1.63	0.77
28:b:506:GLU:HG2	30:d:97:LEU:HD13	1.65	0.77
1:1:1553:U:H4'	1:1:1554:U:H5'	1.67	0.77
48:y:232:ILE:O	48:y:232:ILE:CG2	2.31	0.77
10:H:171:ASP:OD2	10:H:173:ARG:HB2	1.84	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:90:HIS:HD2	28:b:149:TYR:CE1	2.02	0.77
21:U:27:VAL:O	21:U:27:VAL:HG12	1.83	0.77
47:w:300:PHE:O	47:w:304:ILE:HG23	1.85	0.76
11:K:202:VAL:HG21	11:K:237:LYS:NZ	2.01	0.76
28:b:90:HIS:CD2	28:b:149:TYR:CZ	2.72	0.76
1:1:1223:A:N6	1:1:1285:G:H21	1.82	0.76
11:K:202:VAL:HG21	11:K:237:LYS:HZ3	1.51	0.76
1:1:808:A:H2'	1:1:809:G:C8	2.20	0.76
25:Y:40:ARG:HD2	25:Y:46:LYS:HG2	1.67	0.76
4:A:101:VAL:CG1	4:A:165:VAL:HG22	2.15	0.76
28:b:167:THR:HG22	28:b:168:ARG:N	2.01	0.75
42:q:248:ARG:NH1	45:t:23:ARG:HH21	1.84	0.75
1:1:990:U:H3	1:1:1059:G:H1	1.35	0.75
1:1:3367:C:H4'	46:u:115:ASN:HD21	1.52	0.75
1:1:2393:G:N2	1:1:2394:G:O6	2.18	0.75
25:Y:39:LEU:HD11	25:Y:107:THR:C	2.12	0.75
1:1:75:G:H5''	12:L:58:VAL:HG11	1.69	0.74
1:1:3021:A:H5'	1:1:3023:U:H1'	1.67	0.74
11:K:85:ASN:CG	11:K:297:VAL:HG12	2.13	0.74
28:b:169:THR:HG22	28:b:217:GLN:HG3	1.68	0.74
39:n:372:PRO:HD2	42:q:406:LEU:HD23	1.69	0.74
1:1:305:U:H4'	1:1:306:A:H5'	1.68	0.74
49:z:7:ALA:O	49:z:11:LEU:HG	1.86	0.74
1:1:1197:A:H1'	44:s:16:LYS:HG3	1.68	0.74
1:1:1200:A:N1	1:1:2824:G:O6	2.20	0.74
1:1:2858:U:H5''	1:1:2859:U:H5''	1.69	0.74
1:1:1261:G:H4'	1:1:1278:A:H2	1.52	0.74
5:B:387:LEU:HD21	46:u:109:LYS:HG2	1.70	0.73
41:p:11:THR:O	41:p:11:THR:HG22	1.88	0.73
42:q:314:VAL:HG12	42:q:316:ASN:H	1.53	0.73
1:1:100:A:OP1	14:N:193:ARG:NH1	2.22	0.73
11:K:199:TYR:HA	11:K:205:THR:OG1	1.88	0.73
23:W:60:TRP:CZ2	23:W:103:LEU:CD1	2.72	0.73
41:p:11:THR:HG21	41:p:23:ARG:HB3	1.70	0.73
45:t:178:LYS:HG2	45:t:257:MET:CE	2.19	0.73
28:b:177:ASN:ND2	28:b:195:GLN:O	2.22	0.72
9:G:82:LEU:CD1	9:G:180:VAL:HG12	2.11	0.72
7:E:39:VAL:HB	7:E:89:THR:HG23	1.72	0.72
1:1:1197:A:H8	44:s:16:LYS:HA	1.54	0.72
43:r:181:LYS:HA	43:r:196:PRO:HA	1.70	0.72
1:1:3180:A:OP1	15:O:171:LYS:NZ	2.21	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:46:PRO:HG2	39:n:49:LYS:HG2	1.70	0.72
3:6:8:A:OP1	45:t:132:LYS:NZ	2.23	0.71
23:W:60:TRP:CZ2	23:W:103:LEU:HD11	2.26	0.71
47:w:257:THR:HG23	47:w:275:MET:SD	2.30	0.71
1:1:733:G:N2	1:1:736:A:OP2	2.24	0.71
11:K:199:TYR:CD2	11:K:205:THR:HG23	2.26	0.71
6:C:334:PHE:HA	6:C:339:LEU:HD23	1.72	0.71
1:1:3252:G:H2'	1:1:3253:G:C8	2.26	0.71
1:1:3139:A:OP2	5:B:30:LYS:NZ	2.24	0.71
11:K:271:ILE:HG22	11:K:276:ILE:HB	1.73	0.71
1:1:1481:A:O2'	1:1:1858:A:H1'	1.90	0.70
23:W:70:ARG:NH1	23:W:97:SER:O	2.23	0.70
27:a:76:ASP:HB3	27:a:116:GLY:HA3	1.73	0.70
42:q:237:LEU:HD23	42:q:396:ILE:CD1	2.21	0.70
1:1:1661:G:H2'	1:1:1662:G:C8	2.26	0.70
11:K:106:PHE:HE1	11:K:234:LEU:HD13	1.43	0.70
25:Y:39:LEU:HD12	25:Y:106:ILE:O	1.90	0.70
26:Z:85:TYR:OH	47:w:428:ARG:NH1	2.23	0.70
39:n:61:THR:HG23	42:q:430:GLU:OE2	1.91	0.70
27:a:104:THR:HG21	27:a:112:ILE:HD11	1.72	0.70
28:b:275:LYS:HE2	28:b:312:VAL:HG13	1.73	0.70
2:2:8:C:H2'	2:2:9:A:H8	1.57	0.70
11:K:106:PHE:CE1	11:K:234:LEU:HD12	2.27	0.70
37:k:14:LEU:HD21	37:k:52:TYR:CG	2.27	0.70
42:q:389:VAL:HA	42:q:431:THR:HG21	1.72	0.70
19:S:115:ARG:O	19:S:117:ARG:NH1	2.25	0.69
1:1:1200:A:O2'	1:1:1201:C:O2	2.08	0.69
1:1:115:A:H4'	14:N:4:TYR:CG	2.28	0.69
1:1:3233:C:H2'	1:1:3234:A:C8	2.27	0.69
1:1:75:G:H5'	12:L:58:VAL:HG12	1.75	0.69
2:2:154:C:H5''	9:G:181:LYS:HD2	1.75	0.69
4:A:104:LEU:HD12	4:A:158:ILE:HD11	1.74	0.69
1:1:75:G:H5''	12:L:58:VAL:CG1	2.21	0.69
9:G:203:VAL:HG21	9:G:211:LEU:HD22	1.75	0.69
6:C:265:GLU:HG3	6:C:266:THR:HG23	1.75	0.69
1:1:1253:U:H5'	1:1:1254:C:H5'	1.73	0.69
4:A:104:LEU:HD11	4:A:158:ILE:HD11	1.73	0.69
28:b:252:TYR:OH	28:b:270:LEU:HD23	1.93	0.69
1:1:281:G:H21	1:1:284:A:H2	1.38	0.69
11:K:194:MET:HE2	11:K:206:PRO:HG3	1.75	0.69
42:q:424:GLN:CD	42:q:431:THR:HG22	2.18	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3233:C:H2'	1:1:3234:A:H8	1.58	0.68
5:B:284:ARG:NH1	5:B:293:ASN:O	2.26	0.68
4:A:126:LEU:HD11	4:A:156:LYS:HZ3	1.58	0.68
48:y:163:PRO:HA	48:y:183:ALA:HB1	1.73	0.68
20:T:40:VAL:HG12	20:T:41:ASP:H	1.59	0.68
12:L:24:VAL:HG21	12:L:26:PHE:CE2	2.29	0.68
42:q:237:LEU:HD21	42:q:396:ILE:HD13	1.74	0.68
22:V:87:ARG:HH12	22:V:137:VAL:HG11	1.58	0.68
39:n:127:ASP:N	39:n:130:ARG:HH11	1.92	0.68
48:y:71:LEU:HD21	48:y:132:VAL:HG21	1.76	0.68
18:R:108:LYS:NZ	42:q:322:TYR:OH	2.27	0.68
6:C:20:LEU:HD11	6:C:252:GLU:HG3	1.74	0.68
39:n:430:GLN:NE2	39:n:454:PRO:O	2.24	0.68
21:U:14:THR:CG2	21:U:66:VAL:HG22	2.17	0.68
47:w:280:ILE:HD11	47:w:304:ILE:HD11	1.75	0.68
1:1:1257:C:H42	1:1:1261:G:H22	1.42	0.67
28:b:237:MET:O	28:b:241:TYR:CD2	2.43	0.67
1:1:991:G:H1	1:1:1058:U:H3	0.75	0.67
28:b:294:ARG:HG2	28:b:295:PRO:HD2	1.75	0.67
39:n:126:PRO:C	39:n:130:ARG:HH11	2.02	0.67
9:G:48:ARG:HG3	47:w:465:GLU:HG2	1.74	0.67
19:S:8:GLN:HB3	19:S:64:ILE:HD11	1.76	0.67
39:n:126:PRO:CB	39:n:130:ARG:HH12	2.07	0.67
39:n:242:LEU:HD13	39:n:264:LEU:HD13	1.76	0.67
47:w:768:THR:HG22	47:w:769:GLU:N	2.08	0.67
1:1:787:G:OP2	17:Q:147:ARG:HD3	1.94	0.67
1:1:1191:U:OP2	15:O:49:ARG:NH1	2.27	0.67
1:1:1646:G:O2'	1:1:1808:G:N2	2.27	0.67
46:u:63:LEU:O	46:u:63:LEU:HD12	1.95	0.67
4:A:104:LEU:HG	4:A:162:ALA:O	1.95	0.67
23:W:63:SER:HG	23:W:105:THR:HG22	1.60	0.67
9:G:59:GLN:HA	9:G:62:LYS:HE2	1.75	0.67
14:N:71:ARG:NH1	47:w:710:ASN:OD1	2.28	0.67
45:t:85:LYS:O	45:t:85:LYS:NZ	2.27	0.67
47:w:301:ARG:HA	47:w:304:ILE:CG1	2.24	0.67
1:1:3367:C:H1'	46:u:118:LYS:HE2	1.77	0.66
28:b:169:THR:HG22	28:b:217:GLN:CD	2.20	0.66
1:1:1149:G:OP2	32:f:21:ARG:NH2	2.25	0.66
1:1:3043:C:OP1	22:V:45:ARG:CD	2.42	0.66
1:1:1204:A:H2'	1:1:1205:A:O4'	1.95	0.66
13:M:37:GLU:OE1	19:S:72:VAL:CG2	2.43	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:k:15:THR:HG23	37:k:73:LEU:HD22	1.77	0.66
45:t:100:ILE:CD1	45:t:133:THR:CG2	2.74	0.66
2:2:119:C:OP1	39:n:69:GLN:NE2	2.28	0.66
46:u:63:LEU:HD13	46:u:66:ASP:HB2	1.77	0.66
33:g:98:GLN:HB2	47:w:408:PHE:HA	1.77	0.66
39:n:242:LEU:CD1	39:n:264:LEU:HD13	2.25	0.66
20:T:40:VAL:CG1	20:T:41:ASP:N	2.59	0.66
31:e:42:VAL:O	31:e:52:GLN:NE2	2.29	0.66
2:2:8:C:H2'	2:2:9:A:C8	2.31	0.66
1:1:1903:U:N3	1:1:1906:G:OP2	2.24	0.65
28:b:232:MET:SD	28:b:237:MET:SD	2.94	0.65
1:1:1959:G:H2'	1:1:1960:A:C8	2.32	0.65
1:1:2768:U:H2'	1:1:2769:A:H8	1.61	0.65
11:K:283:THR:HG22	11:K:284:ASN:N	2.10	0.65
23:W:63:SER:OG	23:W:105:THR:CG2	2.39	0.65
1:1:2391:G:H21	5:B:266:ARG:HD2	1.61	0.65
32:f:14:LEU:HD11	32:f:31:LYS:HB2	1.79	0.65
1:1:1954:G:H21	1:1:2087:C:H41	1.44	0.65
3:6:51:U:O2'	3:6:54:A:N7	2.28	0.65
1:1:1568:U:O2'	1:1:1569:U:OP2	2.15	0.65
1:1:1243:G:N2	1:1:1270:A:O2'	2.28	0.65
1:1:1679:A:OP1	21:U:94:ARG:NH1	2.29	0.65
2:2:66:A:OP1	34:h:10:ARG:NH2	2.29	0.65
20:T:40:VAL:CG1	20:T:41:ASP:H	2.09	0.65
1:1:990:U:H1'	20:T:101:CYS:HA	1.78	0.65
5:B:67:PHE:CZ	22:V:88:ARG:HG3	2.31	0.65
11:K:85:ASN:CB	11:K:297:VAL:HG11	2.27	0.65
1:1:2810:C:H2'	1:1:2811:A:H8	1.61	0.65
45:t:250:ILE:HD13	45:t:264:CYS:SG	2.37	0.65
1:1:2894:C:H5'	10:H:166:ARG:HH12	1.61	0.64
23:W:136:THR:HG22	23:W:187:LEU:CA	2.27	0.64
43:r:149:ARG:HH21	43:r:151:ILE:HG12	1.60	0.64
48:y:228:GLN:HB2	48:y:232:ILE:HD11	1.77	0.64
39:n:243:ILE:HD12	39:n:265:GLU:HG3	1.78	0.64
1:1:1863:G:N1	1:1:1866:C:OP2	2.24	0.64
1:1:1813:A:O2'	1:1:1816:A:N3	2.28	0.64
1:1:2149:A:C2	1:1:2188:A:H4'	2.33	0.64
20:T:42:ILE:HB	20:T:60:LYS:HB2	1.78	0.64
40:o:93:ILE:CG2	40:o:164:VAL:HG13	2.28	0.64
1:1:870:G:N2	1:1:871:U:O4	2.21	0.64
6:C:120:TYR:HE2	6:C:277:PRO:HB3	1.61	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:212:LYS:O	48:y:239:THR:HG21	1.97	0.64
33:g:51:LEU:HD13	33:g:54:ILE:HG13	1.73	0.64
19:S:24:LEU:HB3	20:T:148:PRO:HA	1.79	0.64
28:b:167:THR:HG22	28:b:168:ARG:H	1.61	0.64
1:1:75:G:C5'	12:L:58:VAL:HG11	2.25	0.64
1:1:3151:U:OP2	5:B:132:LYS:NZ	2.30	0.63
7:E:39:VAL:HB	7:E:89:THR:CG2	2.28	0.63
11:K:106:PHE:HE1	11:K:234:LEU:HD12	1.63	0.63
42:q:237:LEU:HD23	42:q:396:ILE:HD13	1.77	0.63
39:n:127:ASP:N	39:n:130:ARG:NH1	2.46	0.63
2:2:49:G:OP2	34:h:48:ARG:NH2	2.31	0.63
11:K:234:LEU:HD12	11:K:235:PRO:CD	2.23	0.63
29:c:17:VAL:HG23	29:c:98:SER:HB3	1.81	0.63
39:n:372:PRO:CD	42:q:406:LEU:HD23	2.27	0.63
45:t:197:GLY:HA3	45:t:314:ILE:HB	1.80	0.63
40:o:194:LYS:NZ	40:o:198:ASP:OD2	2.25	0.63
1:1:251:G:H4'	1:1:252:U:H5'	1.81	0.63
35:i:58:ILE:HG23	35:i:94:ILE:HD11	1.79	0.63
26:Z:84:ARG:NH2	47:w:427:LYS:O	2.30	0.63
1:1:1717:U:H2'	1:1:1718:G:C8	2.34	0.63
1:1:2874:G:O2'	1:1:2875:U:O4'	2.14	0.63
28:b:499:ARG:HG3	28:b:503:MET:HE3	1.80	0.63
23:W:63:SER:HB3	23:W:105:THR:HG22	1.81	0.63
37:k:8:ILE:HG13	42:q:350:LEU:HD11	1.81	0.63
1:1:3073:A:O2'	28:b:508:ARG:NH1	2.32	0.62
11:K:81:ILE:HD13	11:K:245:ASN:HB3	1.81	0.62
17:Q:57:ILE:HG13	17:Q:147:ARG:HG2	1.81	0.62
22:V:45:ARG:NH1	22:V:46:LEU:HB3	2.14	0.62
48:y:11:ASN:ND2	48:y:209:ASP:OD2	2.32	0.62
29:c:16:LEU:HD23	29:c:98:SER:HA	1.81	0.62
1:1:627:U:H2'	1:1:628:A:C8	2.34	0.62
8:F:224:ILE:HD11	19:S:35:VAL:HG12	1.80	0.62
11:K:104:HIS:HD2	11:K:258:GLU:OE2	1.83	0.62
37:k:15:THR:CG2	37:k:73:LEU:HD22	2.30	0.62
40:o:157:LEU:HD12	45:t:59:GLU:HG3	1.81	0.62
1:1:1639:C:OP2	33:g:74:ARG:NH1	2.33	0.62
1:1:2871:G:H2'	1:1:2872:A:C8	2.34	0.62
9:G:134:TYR:HB3	9:G:190:VAL:HG11	1.81	0.62
33:g:51:LEU:HD13	33:g:54:ILE:CG1	2.24	0.62
1:1:1200:A:N1	1:1:2824:G:C6	2.67	0.62
1:1:2149:A:N1	1:1:2188:A:H4'	2.14	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:228:LYS:O	11:K:232:ASN:HB2	1.99	0.62
9:G:81:THR:HG22	9:G:179:ILE:HG22	1.81	0.62
47:w:764:ASP:OD1	47:w:765:SER:N	2.32	0.62
1:1:567:G:H2'	1:1:568:G:C8	2.35	0.62
4:A:140:ASN:OD1	4:A:145:LYS:HB2	2.00	0.62
10:H:29:GLY:N	10:H:82:VAL:HG21	2.15	0.62
23:W:60:TRP:CG	23:W:63:SER:HB2	2.35	0.62
6:C:114:ASN:HB2	6:C:117:GLU:HG3	1.82	0.61
42:q:396:ILE:O	45:t:24:ARG:NH2	2.33	0.61
3:6:231:A:O2'	3:6:232:A:H8	1.76	0.61
10:H:132:VAL:HG21	10:H:157:ASN:ND2	2.16	0.61
12:L:180:ARG:HD3	35:i:11:LEU:CD1	2.29	0.61
28:b:360:LYS:HE3	48:y:244:TYR:CD1	2.34	0.61
1:1:806:A:H2'	1:1:807:A:C2	2.35	0.61
47:w:414:GLU:HA	47:w:419:LEU:HD21	1.82	0.61
1:1:1221:A:N7	23:W:20:ARG:NH2	2.48	0.61
45:t:100:ILE:HD11	45:t:133:THR:CG2	2.31	0.61
1:1:1572:U:O2'	39:n:83:HIS:NE2	2.31	0.61
1:1:1682:U:O4	21:U:90:ARG:NH1	2.34	0.61
1:1:541:U:H2'	1:1:542:G:C8	2.35	0.61
1:1:952:A:H2'	1:1:953:G:O4'	2.01	0.61
1:1:2138:A:HO2'	36:j:2:GLY:N	1.99	0.61
1:1:2835:U:H2'	1:1:2836:C:C6	2.35	0.61
11:K:234:LEU:CD1	11:K:235:PRO:HD2	2.26	0.61
1:1:2356:A:H61	1:1:2983:C:H5	1.47	0.61
1:1:2411:U:H2'	1:1:2412:G:C8	2.36	0.61
1:1:718:G:OP1	27:a:117:ARG:NH2	2.33	0.60
23:W:60:TRP:CE2	23:W:103:LEU:HD11	2.36	0.60
23:W:91:GLN:HA	23:W:94:LYS:HE3	1.83	0.60
6:C:120:TYR:CE2	6:C:277:PRO:CB	2.84	0.60
23:W:60:TRP:CH2	23:W:103:LEU:HD21	2.36	0.60
1:1:2788:C:H1'	1:1:2789:U:C5	2.36	0.60
2:2:26:U:H2'	2:2:27:U:C6	2.35	0.60
11:K:211:THR:HG22	11:K:222:LEU:HD13	1.81	0.60
1:1:1667:A:H2'	1:1:1668:G:C8	2.37	0.60
1:1:3295:A:H2'	1:1:3296:A:C8	2.36	0.60
28:b:511:LYS:HG2	28:b:518:ILE:HD11	1.83	0.60
23:W:60:TRP:CZ2	23:W:103:LEU:HD13	2.37	0.60
28:b:365:GLN:NE2	48:y:230:GLU:OE2	2.35	0.60
1:1:1596:C:H2'	1:1:1597:C:C6	2.36	0.60
1:1:3153:U:H4'	1:1:3154:C:H5'	1.84	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:36:G:OP2	34:h:85:THR:HG23	2.01	0.60
10:H:29:GLY:HA3	10:H:82:VAL:HG22	1.84	0.60
1:1:3164:C:O2'	1:1:3165:A:H8	1.84	0.60
1:1:3322:A:H2'	1:1:3323:A:C8	2.36	0.60
11:K:39:LYS:HZ1	40:o:219:LYS:HE3	1.66	0.60
11:K:82:VAL:HG13	11:K:279:ILE:HG12	1.84	0.60
11:K:170:ARG:HG2	11:K:174:ILE:HD12	1.84	0.60
1:1:1852:G:H1'	36:j:9:GLY:HA3	1.84	0.60
1:1:2372:A:OP1	44:s:14:LYS:NZ	2.31	0.60
11:K:104:HIS:CD2	11:K:258:GLU:OE2	2.55	0.60
24:X:22:LYS:HD3	42:q:448:LYS:HG2	1.84	0.60
42:q:424:GLN:CG	42:q:431:THR:HG22	2.32	0.60
1:1:890:C:O2'	1:1:2324:A:N3	2.32	0.59
1:1:962:A:H3'	1:1:963:G:H8	1.67	0.59
4:A:83:HIS:HB3	41:p:64:VAL:HG23	1.84	0.59
10:H:92:TYR:HB3	10:H:179:ILE:HG12	1.84	0.59
43:r:2:PRO:HB2	43:r:6:TYR:CG	2.37	0.59
28:b:288:ASN:OD1	28:b:289:LYS:N	2.35	0.59
12:L:162:ASN:ND2	12:L:164:GLU:OE2	2.36	0.59
23:W:136:THR:HG22	23:W:187:LEU:HA	1.85	0.59
43:r:184:VAL:HG22	43:r:257:ALA:HB3	1.84	0.59
24:X:49:LYS:NZ	24:X:51:VAL:O	2.26	0.59
35:i:66:GLU:OE2	35:i:91:ASN:ND2	2.35	0.59
1:1:1223:A:N6	1:1:1285:G:N2	2.48	0.59
28:b:184:LEU:HD22	28:b:220:ASP:HB2	1.83	0.59
5:B:122:TRP:CE2	5:B:127:LYS:HE3	2.37	0.59
7:E:55:LEU:HD13	7:E:98:VAL:HG11	1.85	0.59
12:L:174:ARG:HG3	35:i:9:ILE:HD12	1.84	0.59
23:W:49:ARG:HG2	23:W:51:PRO:HD2	1.84	0.59
28:b:167:THR:CG2	28:b:168:ARG:N	2.66	0.59
18:R:111:ASP:HB3	42:q:320:THR:HG22	1.84	0.59
45:t:100:ILE:CD1	45:t:133:THR:HG23	2.32	0.59
1:1:662:U:H2'	1:1:663:C:C6	2.38	0.59
1:1:1495:U:H5	1:1:1835:A:N1	2.01	0.59
1:1:1622:U:H2'	1:1:1623:G:H8	1.67	0.59
28:b:369:ARG:NH2	48:y:136:GLU:OE2	2.34	0.59
45:t:77:ARG:NH1	45:t:303:ASN:O	2.36	0.58
1:1:808:A:H2'	1:1:809:G:H8	1.66	0.58
1:1:3275:U:O2'	32:f:99:ARG:NH1	2.36	0.58
11:K:85:ASN:HD22	11:K:297:VAL:CG1	2.15	0.58
1:1:1355:A:H5'	1:1:1357:G:H1'	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1696:A:H2'	1:1:1697:A:C8	2.38	0.58
22:V:45:ARG:HH12	22:V:46:LEU:HB3	1.68	0.58
1:1:115:A:H4'	14:N:4:TYR:CD1	2.37	0.58
29:c:17:VAL:HG11	29:c:92:ILE:HD12	1.86	0.58
1:1:1498:A:H2'	1:1:1499:C:C6	2.39	0.58
46:u:97:GLU:O	46:u:101:GLN:HG2	2.02	0.58
33:g:74:ARG:CZ	33:g:82:ALA:HB2	2.34	0.58
37:k:14:LEU:HD21	37:k:52:TYR:CD1	2.39	0.58
47:w:715:LYS:HE3	47:w:719:MET:HE2	1.86	0.58
1:1:877:C:O2'	1:1:880:G:N3	2.35	0.58
1:1:2377:G:OP1	1:1:2378:C:N4	2.28	0.58
33:g:51:LEU:HD12	33:g:51:LEU:O	2.04	0.58
47:w:312:LYS:HG3	47:w:313:LYS:HD3	1.86	0.58
1:1:2177:G:H2'	4:A:128:ARG:HG3	1.86	0.58
1:1:2364:G:N2	1:1:2396:G:O2'	2.37	0.58
1:1:3252:G:H2'	1:1:3253:G:H8	1.69	0.58
11:K:104:HIS:HD2	11:K:258:GLU:CD	2.09	0.58
26:Z:113:VAL:HG22	26:Z:116:LYS:HZ3	1.69	0.58
34:h:102:GLU:OE2	34:h:105:ARG:NH2	2.37	0.58
45:t:100:ILE:HD11	45:t:133:THR:HG23	1.86	0.58
1:1:531:G:H2'	1:1:532:A:C8	2.39	0.57
2:2:63:G:H22	2:2:97:A:H2	1.52	0.57
22:V:28:ASN:HD21	22:V:112:SER:HB3	1.69	0.57
28:b:396:ARG:NH2	48:y:40:ALA:O	2.37	0.57
43:r:155:THR:HG22	43:r:214:VAL:HA	1.86	0.57
47:w:282:GLU:O	47:w:288:LYS:NZ	2.37	0.57
3:6:32:A:O2'	11:K:285:ARG:NH1	2.37	0.57
6:C:34:ILE:HD12	6:C:120:TYR:CE1	2.39	0.57
1:1:1223:A:H62	1:1:1285:G:N2	2.02	0.57
28:b:541:ASP:OD1	28:b:542:MET:N	2.37	0.57
1:1:1712:G:H1'	42:q:314:VAL:HG23	1.86	0.57
2:2:9:A:H2'	2:2:10:A:C8	2.38	0.57
4:A:112:ILE:HD12	41:p:79:VAL:HG22	1.87	0.57
28:b:167:THR:CG2	28:b:168:ARG:H	2.18	0.57
33:g:51:LEU:HD12	33:g:54:ILE:CG1	2.31	0.57
41:p:46:THR:OG1	41:p:57:CYS:SG	2.61	0.57
1:1:2084:C:H2'	1:1:2085:U:C5	2.39	0.57
19:S:132:THR:HG23	19:S:144:LEU:HD13	1.86	0.57
25:Y:74:TYR:CD1	25:Y:77:LYS:HG2	2.39	0.57
48:y:157:GLN:OE1	48:y:223:ARG:NH1	2.38	0.57
1:1:787:G:OP2	17:Q:147:ARG:CD	2.52	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1279:C:O2'	23:W:18:LYS:NZ	2.37	0.57
47:w:728:MET:HA	47:w:731:ARG:HE	1.70	0.57
48:y:228:GLN:CB	48:y:232:ILE:HD11	2.34	0.57
1:1:585:A:H2'	1:1:586:C:C6	2.40	0.57
23:W:60:TRP:CH2	23:W:103:LEU:CD2	2.88	0.57
41:p:38:ASP:HA	41:p:45:LYS:HA	1.87	0.57
46:u:50:LYS:HG3	46:u:55:PHE:CE1	2.40	0.57
1:1:173:G:O6	1:1:245:U:O4	2.23	0.57
1:1:424:G:H21	31:e:24:ARG:HH21	1.53	0.57
1:1:2812:C:H2'	1:1:2813:A:H8	1.70	0.57
3:6:44:G:O2'	11:K:240:ARG:O	2.22	0.57
6:C:36:HIS:O	6:C:40:THR:HG23	2.04	0.57
1:1:647:A:C2	1:1:2373:A:N1	2.68	0.57
8:F:130:ILE:HD12	8:F:134:VAL:HG11	1.86	0.56
1:1:1307:G:N3	15:O:60:LYS:NZ	2.39	0.56
1:1:1686:U:O4	21:U:82:LYS:NZ	2.38	0.56
1:1:100:A:H2'	1:1:101:G:N3	2.21	0.56
1:1:733:G:O2'	1:1:736:A:N6	2.37	0.56
1:1:3067:C:H3'	18:R:62:ARG:HH22	1.71	0.56
1:1:3288:G:O2'	1:1:3289:G:H5'	2.05	0.56
13:M:48:GLY:HA3	13:M:53:VAL:HB	1.87	0.56
14:N:67:ARG:NH2	14:N:73:ARG:HE	2.02	0.56
16:P:10:ASN:HD22	16:P:13:LYS:HE2	1.70	0.56
40:o:92:ILE:HG23	40:o:167:LEU:HB2	1.88	0.56
47:w:280:ILE:HD11	47:w:304:ILE:CD1	2.33	0.56
1:1:1621:A:H2'	1:1:1622:U:C6	2.40	0.56
6:C:161:LYS:HB2	6:C:164:GLU:HG2	1.85	0.56
31:e:9:ILE:HG12	31:e:63:THR:HB	1.88	0.56
1:1:1899:G:O2'	1:1:2334:U:O4	2.20	0.56
1:1:2392:C:H2'	1:1:2393:G:C8	2.41	0.56
6:C:132:ALA:HB2	6:C:148:ILE:HG21	1.87	0.56
29:c:16:LEU:HD23	29:c:98:SER:CB	2.36	0.56
30:d:111:GLU:O	30:d:112:ASP:OD1	2.23	0.56
1:1:75:G:OP1	12:L:58:VAL:HG13	2.06	0.56
1:1:498:A:OP1	32:f:86:ARG:NH1	2.39	0.56
1:1:787:G:H2'	1:1:788:C:C6	2.40	0.56
48:y:225:GLN:HB2	48:y:228:GLN:HG2	1.86	0.56
1:1:1786:G:H2'	1:1:1787:A:C8	2.40	0.56
1:1:3251:U:H2'	1:1:3252:G:C8	2.41	0.56
18:R:15:VAL:HG11	18:R:52:LYS:HB2	1.86	0.56
23:W:136:THR:HG22	23:W:187:LEU:HB3	1.84	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:t:75:ILE:HD12	45:t:156:PRO:HG2	1.87	0.56
1:1:428:A:H2'	1:1:429:U:C6	2.41	0.56
1:1:458:U:H2'	1:1:459:G:C8	2.41	0.56
1:1:991:G:O6	1:1:1058:U:O4	2.24	0.56
1:1:2788:C:H1'	1:1:2789:U:H5	1.71	0.56
10:H:42:ASP:HB3	10:H:64:HIS:HE2	1.71	0.56
11:K:224:ASN:O	11:K:228:LYS:HG2	2.05	0.56
16:P:122:ALA:HB3	16:P:143:PRO:HB2	1.88	0.56
42:q:248:ARG:HH12	45:t:23:ARG:HH21	1.54	0.56
1:1:1501:U:H3	1:1:1515:A:H61	1.52	0.56
1:1:1620:U:H2'	1:1:1621:A:C8	2.41	0.56
1:1:1622:U:H2'	1:1:1623:G:C8	2.40	0.56
1:1:1975:C:O2'	37:k:63:LYS:NZ	2.39	0.56
1:1:3057:U:O2'	1:1:3059:G:OP1	2.22	0.56
2:2:88:A:O2'	2:2:89:A:O4'	2.24	0.56
9:G:82:LEU:CD1	9:G:180:VAL:CG1	2.80	0.56
1:1:281:G:N2	1:1:284:A:OP2	2.24	0.55
1:1:953:G:H2'	1:1:1116:G:C5	2.41	0.55
1:1:1627:U:O2'	1:1:1813:A:N7	2.35	0.55
9:G:89:GLU:OE2	9:G:92:LYS:NZ	2.39	0.55
11:K:85:ASN:HB2	11:K:297:VAL:HG11	1.87	0.55
24:X:67:ILE:HD12	24:X:121:LYS:HG3	1.87	0.55
40:o:124:ARG:HD2	40:o:178:LYS:HA	1.88	0.55
1:1:94:G:H4'	1:1:95:A:H5''	1.88	0.55
1:1:1261:G:H4'	1:1:1278:A:C2	2.38	0.55
1:1:1295:G:H2'	1:1:1296:C:C6	2.40	0.55
10:H:29:GLY:H	10:H:82:VAL:HG21	1.70	0.55
19:S:79:VAL:HG11	19:S:106:LEU:HD21	1.89	0.55
1:1:637:C:H5''	1:1:2377:G:N2	2.21	0.55
11:K:199:TYR:CE2	11:K:205:THR:HG23	2.41	0.55
1:1:991:G:N2	1:1:1058:U:O2	2.25	0.55
11:K:77:ASP:OD1	11:K:249:GLY:O	2.24	0.55
1:1:1799:A:H2'	1:1:1800:A:C8	2.41	0.55
11:K:81:ILE:N	11:K:280:PHE:O	2.39	0.55
40:o:207:ARG:O	40:o:211:LEU:HG	2.05	0.55
1:1:216:G:OP1	25:Y:16:ARG:NH1	2.37	0.55
1:1:1727:G:OP1	41:p:44:LYS:NZ	2.34	0.55
1:1:3280:U:O2'	1:1:3281:U:H5''	2.07	0.55
28:b:271:PHE:HZ	28:b:315:VAL:HG11	1.70	0.55
45:t:103:ILE:HG12	45:t:130:ARG:HG2	1.88	0.55
47:w:301:ARG:C	47:w:304:ILE:HG13	2.30	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:443:G:H2'	1:1:444:U:C6	2.41	0.55
1:1:2078:C:H2'	1:1:2079:G:H5'	1.88	0.55
3:6:227:C:N4	45:t:153:VAL:O	2.34	0.55
4:A:80:GLU:HG3	41:p:66:GLY:HA2	1.88	0.55
19:S:12:ARG:HB3	19:S:24:LEU:HD12	1.88	0.55
28:b:369:ARG:HH21	28:b:374:ARG:NH2	2.05	0.55
39:n:359:LEU:CD1	39:n:441:LEU:HD11	2.37	0.55
42:q:383:LEU:O	42:q:430:GLU:HG2	2.07	0.55
43:r:37:GLU:CG	43:r:41:LYS:HD2	2.34	0.55
1:1:1234:G:H3'	1:1:1235:U:H2'	1.89	0.55
1:1:2830:G:OP1	28:b:130:ARG:NH2	2.39	0.55
2:2:127:U:O2	39:n:14:ASN:ND2	2.37	0.55
11:K:270:LEU:O	11:K:274:TYR:HB2	2.07	0.55
47:w:294:LYS:HG3	47:w:295:GLN:HG3	1.88	0.55
1:1:32:U:OP2	14:N:95:GLN:NE2	2.40	0.55
11:K:84:ASN:OD1	11:K:85:ASN:N	2.40	0.55
21:U:27:VAL:O	21:U:27:VAL:CG1	2.55	0.55
21:U:93:ILE:HG21	21:U:105:LEU:HD23	1.89	0.55
1:1:1688:U:H2'	1:1:1689:U:C6	2.42	0.54
1:1:1953:G:OP2	42:q:326:LYS:NZ	2.38	0.54
1:1:2082:U:H2'	1:1:2083:G:H5'	1.89	0.54
6:C:283:THR:HG21	6:C:288:ARG:HH11	1.71	0.54
28:b:187:ILE:HG13	28:b:188:THR:HG23	1.89	0.54
48:y:59:ILE:O	48:y:63:THR:CG2	2.27	0.54
1:1:520:U:O4	6:C:349:THR:OG1	2.20	0.54
4:A:180:LEU:HD22	41:p:18:TYR:HB3	1.89	0.54
10:H:16:VAL:HG12	10:H:29:GLY:HA3	1.89	0.54
1:1:1681:U:H5''	28:b:511:LYS:HD2	1.89	0.54
3:6:54:A:OP2	3:6:55:A:N6	2.40	0.54
7:E:149:ILE:HG23	7:E:155:LEU:HD22	1.89	0.54
11:K:283:THR:HG22	11:K:284:ASN:H	1.73	0.54
23:W:143:TYR:HA	23:W:156:PRO:HA	1.88	0.54
1:1:2357:A:H2'	1:1:2358:A:C8	2.43	0.54
10:H:29:GLY:H	10:H:82:VAL:CG2	2.21	0.54
34:h:79:ASP:OD1	34:h:79:ASP:N	2.34	0.54
34:h:102:GLU:CD	34:h:105:ARG:HH21	2.15	0.54
19:S:80:ARG:HH22	20:T:153:PRO:HB3	1.73	0.54
28:b:274:ILE:HA	28:b:277:LEU:HD12	1.90	0.54
47:w:768:THR:HG22	47:w:769:GLU:H	1.72	0.54
1:1:845:G:C2	1:1:847:A:H5''	2.42	0.54
1:1:1122:U:H2'	1:1:1123:U:C6	2.42	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1534:A:H2'	1:1:1535:A:C8	2.42	0.54
4:A:28:LYS:HB3	4:A:123:ARG:HE	1.71	0.54
4:A:126:LEU:HD11	4:A:156:LYS:HZ1	1.71	0.54
1:1:3205:G:C2	19:S:171:PHE:CE2	2.96	0.54
1:1:3348:G:H1	1:1:3357:U:H3	1.55	0.54
42:q:424:GLN:OE1	42:q:431:THR:HG22	2.07	0.54
1:1:656:A:H2'	1:1:657:A:C8	2.43	0.54
28:b:392:ASP:H	28:b:395:ARG:NH1	2.06	0.54
2:2:103:G:OP2	2:2:105:A:O2'	2.25	0.54
12:L:106:GLN:NE2	12:L:110:ASP:OD1	2.40	0.54
12:L:189:GLU:HA	12:L:192:GLU:HG2	1.89	0.54
23:W:144:SER:HA	23:W:157:MET:HG2	1.89	0.54
47:w:295:GLN:HB2	47:w:321:TRP:HD1	1.72	0.54
4:A:28:LYS:HB2	4:A:123:ARG:HH21	1.73	0.54
10:H:57:VAL:HG23	10:H:68:LEU:HD13	1.88	0.54
11:K:183:ASP:O	11:K:187:VAL:HG23	2.08	0.54
30:d:55:LEU:HB2	30:d:95:PRO:HD3	1.90	0.54
1:1:952:A:H4'	1:1:968:G:N2	2.23	0.53
11:K:305:LYS:HE2	40:o:189:ILE:H	1.73	0.53
12:L:76:THR:HG22	12:L:78:ALA:H	1.73	0.53
14:N:65:ARG:HG3	14:N:129:TYR:CE2	2.42	0.53
21:U:21:SER:HB3	21:U:22:PRO:HD3	1.89	0.53
1:1:12:A:H2'	1:1:13:A:C8	2.44	0.53
1:1:445:G:H1	1:1:489:C:N4	2.00	0.53
2:2:141:C:OP1	14:N:109:ARG:NH1	2.41	0.53
10:H:16:VAL:HG12	10:H:29:GLY:CA	2.39	0.53
1:1:547:G:O2'	1:1:548:G:N7	2.42	0.53
1:1:1280:C:H5'	23:W:18:LYS:HZ1	1.73	0.53
1:1:2414:G:O6	1:1:2806:U:O2	2.26	0.53
12:L:155:GLU:OE2	27:a:90:TYR:OH	2.24	0.53
42:q:222:HIS:H	42:q:225:LYS:HD2	1.72	0.53
47:w:295:GLN:HE22	47:w:324:ILE:HG13	1.72	0.53
47:w:768:THR:CG2	47:w:769:GLU:N	2.71	0.53
1:1:992:A:N3	1:1:993:G:N2	2.55	0.53
10:H:9:GLN:HB3	10:H:52:LEU:HD11	1.89	0.53
11:K:106:PHE:CD1	11:K:234:LEU:HD13	2.41	0.53
11:K:216:GLU:OE1	11:K:216:GLU:N	2.42	0.53
28:b:255:ASP:OD1	28:b:256:LEU:N	2.41	0.53
31:e:3:SER:HB3	31:e:71:HIS:CE1	2.44	0.53
47:w:391:THR:HG23	47:w:391:THR:O	2.09	0.53
1:1:286:U:H2'	1:1:287:G:H8	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1176:C:H2'	1:1:1177:G:N2	2.23	0.53
9:G:80:TYR:OH	9:G:229:VAL:HG11	2.08	0.53
1:1:845:G:N2	1:1:848:A:OP2	2.27	0.53
1:1:3006:A:H2'	1:1:3007:U:O4'	2.07	0.53
4:A:113:VAL:HG23	4:A:116:VAL:CG2	2.39	0.53
23:W:136:THR:CG2	23:W:187:LEU:CB	2.76	0.53
24:X:15:VAL:HG13	24:X:16:LYS:HG3	1.91	0.53
28:b:151:GLU:OE2	28:b:154:ARG:NH2	2.42	0.53
28:b:392:ASP:O	28:b:395:ARG:NH1	2.42	0.53
1:1:3084:C:H2'	1:1:3085:G:O4'	2.09	0.53
21:U:89:LEU:HA	21:U:92:TRP:HE1	1.73	0.53
29:c:16:LEU:CD2	29:c:98:SER:HA	2.38	0.53
1:1:285:A:O2'	1:1:304:G:H8	1.92	0.53
1:1:1750:A:OP1	37:k:44:LYS:NZ	2.36	0.53
1:1:1616:U:H2'	1:1:1617:G:C8	2.44	0.53
40:o:211:LEU:HD22	40:o:216:ILE:HD11	1.91	0.53
1:1:2860:U:H2'	1:1:2861:U:H4'	1.90	0.52
2:2:48:A:O2'	2:2:51:G:N2	2.41	0.52
28:b:171:LEU:HD21	28:b:243:ILE:HG12	1.91	0.52
35:i:60:LEU:HD13	35:i:64:SER:HB2	1.91	0.52
37:k:9:LYS:HE2	42:q:353:VAL:HG22	1.91	0.52
1:1:1597:C:H2'	1:1:1598:G:C8	2.44	0.52
1:1:3193:C:H2'	1:1:3194:C:C6	2.44	0.52
9:G:128:LYS:NZ	9:G:202:GLU:OE1	2.30	0.52
14:N:191:TRP:CZ2	14:N:195:ASN:ND2	2.76	0.52
26:Z:57:HIS:CD2	26:Z:61:LYS:HG2	2.45	0.52
40:o:90:SER:OG	40:o:167:LEU:O	2.22	0.52
1:1:187:A:N3	1:1:208:C:O2'	2.40	0.52
1:1:2191:U:H2'	1:1:2192:C:H6	1.75	0.52
1:1:2830:G:H2'	1:1:2831:G:C8	2.44	0.52
2:2:57:C:H4'	2:2:63:G:N7	2.24	0.52
16:P:67:ILE:HD11	16:P:80:LYS:HB3	1.90	0.52
28:b:222:PRO:HD2	28:b:239:SER:HB3	1.92	0.52
48:y:153:SER:HB2	48:y:194:GLY:HA2	1.91	0.52
39:n:359:LEU:HD11	39:n:441:LEU:CD1	2.39	0.52
43:r:186:HIS:ND1	43:r:188:GLU:HB2	2.25	0.52
1:1:489:C:H2'	1:1:490:A:H8	1.73	0.52
1:1:916:G:H8	47:w:739:ALA:HB1	1.75	0.52
11:K:114:SER:OG	11:K:121:PHE:N	2.42	0.52
16:P:127:ARG:O	16:P:128:ARG:NH1	2.39	0.52
28:b:214:LEU:HD13	48:y:242:GLU:HG2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:100:LYS:NZ	7:E:137:ASP:OD2	2.41	0.52
14:N:96:ARG:NH2	14:N:104:GLU:OE1	2.42	0.52
23:W:136:THR:CG2	23:W:187:LEU:HB2	2.30	0.52
26:Z:90:GLU:N	26:Z:90:GLU:OE1	2.41	0.52
39:n:374:ASP:N	39:n:374:ASP:OD1	2.39	0.52
48:y:101:LEU:HD13	48:y:121:ILE:HG22	1.91	0.52
1:1:179:C:H2'	1:1:180:C:C6	2.45	0.52
1:1:400:G:H4'	1:1:401:U:H5''	1.92	0.52
11:K:170:ARG:HG2	11:K:174:ILE:CD1	2.39	0.52
28:b:347:LYS:HA	28:b:353:ARG:HH11	1.75	0.52
47:w:290:LEU:HA	47:w:293:LEU:HD13	1.92	0.52
1:1:1295:G:H2'	1:1:1296:C:H6	1.74	0.52
1:1:1304:A:N1	1:1:2938:G:O2'	2.41	0.52
1:1:1778:G:O2'	1:1:1780:G:OP2	2.27	0.52
1:1:2344:U:H2'	1:1:2345:A:C8	2.45	0.52
11:K:83:VAL:HB	11:K:278:SER:HB3	1.92	0.52
40:o:98:LEU:HD22	40:o:102:PHE:HD2	1.74	0.52
41:p:11:THR:O	41:p:11:THR:CG2	2.58	0.52
42:q:237:LEU:HD23	42:q:396:ILE:HD11	1.92	0.52
7:E:52:VAL:HG21	7:E:65:ILE:HD13	1.91	0.52
12:L:24:VAL:HG21	12:L:26:PHE:HE2	1.72	0.52
28:b:304:GLN:O	28:b:307:GLU:HG3	2.10	0.52
28:b:347:LYS:HA	28:b:353:ARG:NH1	2.25	0.52
48:y:228:GLN:CB	48:y:232:ILE:CD1	2.83	0.52
1:1:3322:A:H2'	1:1:3323:A:H8	1.75	0.51
3:6:8:A:H2'	3:6:9:A:H8	1.75	0.51
5:B:202:THR:O	49:z:44:GLN:NE2	2.39	0.51
10:H:29:GLY:N	10:H:82:VAL:CG2	2.73	0.51
11:K:85:ASN:CB	11:K:297:VAL:CG1	2.87	0.51
16:P:127:ARG:HG3	16:P:139:TYR:HD2	1.75	0.51
17:Q:57:ILE:CG1	17:Q:147:ARG:HG2	2.40	0.51
22:V:133:SER:O	48:y:106:ASN:ND2	2.43	0.51
36:j:21:ARG:NH2	36:j:41:ALA:O	2.33	0.51
1:1:1290:A:H2'	1:1:1291:A:C8	2.45	0.51
1:1:3013:U:H2'	1:1:3014:U:C6	2.45	0.51
9:G:218:ILE:O	9:G:222:PHE:HB3	2.10	0.51
28:b:443:ASP:OD1	46:u:2:ARG:NH1	2.42	0.51
33:g:74:ARG:NH2	33:g:82:ALA:HB2	2.25	0.51
39:n:189:GLN:HE21	39:n:196:GLU:HB3	1.75	0.51
1:1:959:C:N4	1:1:960:U:O4	2.43	0.51
1:1:2776:C:H5''	27:a:65:GLN:HE21	1.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:58:ILE:HD12	16:P:84:PRO:HD2	1.91	0.51
43:r:184:VAL:HB	43:r:195:LEU:HD12	1.92	0.51
43:r:219:THR:O	43:r:245:VAL:HG22	2.10	0.51
46:u:45:ASN:HD22	46:u:48:LYS:HG2	1.75	0.51
1:1:1260:A:H5''	23:W:18:LYS:HE3	1.92	0.51
28:b:65:LEU:HD23	28:b:95:LEU:HD12	1.92	0.51
33:g:41:ARG:O	33:g:43:LYS:NZ	2.36	0.51
47:w:257:THR:HG23	47:w:275:MET:CE	2.40	0.51
49:z:42:LEU:O	49:z:46:LEU:HG	2.10	0.51
1:1:75:G:C5'	12:L:58:VAL:HG13	2.39	0.51
1:1:101:G:OP2	1:1:101:G:N2	2.32	0.51
1:1:900:G:H1'	1:1:1589:A:N6	2.25	0.51
5:B:293:ASN:HB2	5:B:304:THR:HA	1.93	0.51
9:G:80:TYR:OH	9:G:229:VAL:CG1	2.58	0.51
28:b:513:LEU:HD11	28:b:518:ILE:HG13	1.91	0.51
33:g:3:GLN:HB3	33:g:30:LEU:HD12	1.92	0.51
42:q:410:LYS:HD2	45:t:231:ASP:HB2	1.93	0.51
1:1:916:G:H5'	47:w:742:ARG:HH22	1.75	0.51
1:1:2190:U:H2'	1:1:2191:U:C6	2.46	0.51
4:A:47:GLN:HG3	4:A:49:VAL:CG2	2.41	0.51
12:L:24:VAL:CG2	12:L:26:PHE:CE2	2.94	0.51
46:u:67:SER:O	46:u:70:THR:HG22	2.11	0.51
1:1:1250:G:H2'	1:1:1251:A:C8	2.45	0.51
3:6:47:A:OP1	11:K:237:LYS:NZ	2.38	0.51
4:A:140:ASN:OD1	4:A:145:LYS:CB	2.58	0.51
19:S:8:GLN:HG2	19:S:62:ASN:HB2	1.92	0.51
30:d:74:ARG:HB3	30:d:94:GLU:HG2	1.93	0.51
35:i:74:LYS:HD3	35:i:80:PHE:HD1	1.76	0.51
45:t:57:ARG:HB3	45:t:59:GLU:OE1	2.10	0.51
11:K:40:ALA:O	11:K:44:LEU:HG	2.11	0.51
16:P:108:ASP:HB3	16:P:111:LYS:HG3	1.92	0.51
1:1:2901:G:O2'	1:1:3024:A:N1	2.43	0.51
1:1:3023:U:H5	1:1:3032:A:N7	2.09	0.51
7:E:43:LEU:HD11	7:E:85:ILE:HG13	1.92	0.51
12:L:153:ASP:OD1	12:L:154:VAL:N	2.43	0.51
14:N:9:GLU:HB3	35:i:44:VAL:HG11	1.93	0.51
24:X:12:LYS:HG3	24:X:16:LYS:HD2	1.93	0.51
28:b:481:PHE:HB3	28:b:485:GLU:HB2	1.93	0.51
1:1:155:G:H5''	1:1:156:G:H2'	1.93	0.51
1:1:1324:U:H5'	19:S:2:ALA:HA	1.93	0.51
1:1:2182:A:H2'	1:1:2183:A:C8	2.46	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3160:U:H2'	1:1:3161:C:C6	2.46	0.51
11:K:280:PHE:CD2	11:K:288:VAL:HG21	2.46	0.51
22:V:45:ARG:HH11	22:V:46:LEU:H	1.58	0.51
22:V:79:VAL:HB	22:V:118:VAL:HG23	1.93	0.51
23:W:52:VAL:HG11	23:W:213:PHE:HE2	1.76	0.51
28:b:259:GLN:HB3	28:b:289:LYS:HZ3	1.75	0.50
1:1:1410:U:H4'	31:e:75:LEU:HD11	1.94	0.50
22:V:131:SER:O	48:y:106:ASN:ND2	2.45	0.50
26:Z:50:PRO:HD3	26:Z:68:ILE:HG12	1.94	0.50
28:b:169:THR:HG22	28:b:217:GLN:OE1	2.10	0.50
39:n:127:ASP:CA	39:n:130:ARG:HH11	2.24	0.50
39:n:211:SER:HA	39:n:215:PHE:HE2	1.76	0.50
1:1:241:G:H2'	1:1:242:C:C6	2.47	0.50
1:1:1886:A:H2'	1:1:1887:A:C8	2.46	0.50
4:A:147:ARG:HB3	4:A:157:VAL:HG22	1.93	0.50
23:W:77:LEU:HD12	23:W:89:LEU:HD13	1.93	0.50
28:b:283:VAL:HB	28:b:315:VAL:HG12	1.91	0.50
1:1:882:A:O2'	1:1:884:A:H5''	2.10	0.50
11:K:81:ILE:HB	11:K:280:PHE:HB2	1.92	0.50
11:K:256:PRO:HA	11:K:259:PHE:HB2	1.93	0.50
1:1:208:C:H2'	1:1:209:A:O4'	2.12	0.50
1:1:424:G:O2'	31:e:23:ASP:OD2	2.23	0.50
1:1:464:U:O2'	1:1:465:U:O4'	2.30	0.50
1:1:2836:C:H2'	1:1:2837:A:O4'	2.11	0.50
1:1:3188:G:OP1	10:H:22:SER:OG	2.26	0.50
39:n:367:VAL:HG13	39:n:371:VAL:HB	1.93	0.50
43:r:175:SER:HA	43:r:178:ARG:HD2	1.92	0.50
48:y:118:HIS:HB3	48:y:121:ILE:HG23	1.94	0.50
1:1:627:U:H2'	1:1:628:A:H8	1.75	0.50
1:1:1347:U:H2'	1:1:1355:A:H61	1.75	0.50
11:K:85:ASN:CG	11:K:297:VAL:CG1	2.83	0.50
39:n:43:PRO:HG2	42:q:430:GLU:HG3	1.94	0.50
39:n:126:PRO:CB	39:n:130:ARG:NH1	2.67	0.50
46:u:63:LEU:CD1	46:u:69:LEU:CD1	2.90	0.50
48:y:15:VAL:HA	48:y:61:ARG:HG2	1.92	0.50
1:1:190:U:OP1	25:Y:37:LYS:NZ	2.44	0.50
1:1:981:U:H2'	1:1:982:C:O4'	2.11	0.50
1:1:1390:A:N6	1:1:1418:A:O2'	2.44	0.50
1:1:3165:A:H2'	1:1:3166:C:C6	2.46	0.50
5:B:344:THR:HB	49:z:18:ARG:HD3	1.94	0.50
18:R:72:GLU:OE1	18:R:74:ARG:NH1	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:27:VAL:CG1	21:U:92:TRP:HH2	2.25	0.50
45:t:101:LEU:HD11	45:t:130:ARG:HD2	1.94	0.50
46:u:63:LEU:CD1	46:u:69:LEU:HD11	2.41	0.50
47:w:794:THR:H	47:w:813:LYS:HD3	1.76	0.50
1:1:1615:C:H2'	1:1:1616:U:C6	2.47	0.50
1:1:2154:U:H2'	1:1:2155:G:H8	1.77	0.50
1:1:2191:U:H2'	1:1:2192:C:C6	2.46	0.50
1:1:2812:C:H2'	1:1:2813:A:C8	2.47	0.50
21:U:14:THR:HG22	21:U:66:VAL:CG2	2.21	0.50
22:V:32:ARG:HG3	22:V:64:LYS:HE2	1.94	0.50
39:n:127:ASP:HA	39:n:130:ARG:HD2	1.93	0.50
39:n:369:ARG:NH1	39:n:390:GLU:OE2	2.44	0.50
43:r:186:HIS:CD2	43:r:259:LEU:HD23	2.47	0.50
45:t:143:PHE:HB2	45:t:199:PRO:HG3	1.94	0.50
46:u:94:ALA:O	46:u:97:GLU:HG2	2.11	0.50
1:1:407:A:C2	2:2:17:A:H1'	2.46	0.49
1:1:1798:A:H2'	1:1:1799:A:C8	2.47	0.49
1:1:2101:C:O2'	1:1:2102:U:H5''	2.12	0.49
11:K:283:THR:CG2	11:K:284:ASN:N	2.75	0.49
33:g:105:VAL:HG21	47:w:412:THR:HG22	1.93	0.49
1:1:655:C:H2'	1:1:656:A:H8	1.77	0.49
1:1:2841:G:H1'	1:1:2848:G:N2	2.26	0.49
24:X:105:VAL:HG11	24:X:135:ILE:HG12	1.93	0.49
42:q:228:ASN:ND2	42:q:404:ASP:HB2	2.28	0.49
46:u:63:LEU:HD12	46:u:69:LEU:HD11	1.95	0.49
1:1:417:A:H2'	1:1:418:A:C8	2.46	0.49
1:1:647:A:H2'	1:1:648:C:O4'	2.12	0.49
10:H:27:VAL:HG12	10:H:82:VAL:HG11	1.94	0.49
28:b:169:THR:CG2	28:b:217:GLN:OE1	2.60	0.49
39:n:359:LEU:CD1	39:n:441:LEU:CD1	2.90	0.49
1:1:945:C:H2'	1:1:946:U:C6	2.47	0.49
1:1:1578:C:OP1	42:q:441:TYR:OH	2.30	0.49
1:1:1927:G:C8	41:p:16:VAL:HG12	2.47	0.49
1:1:87:U:H2'	1:1:88:A:H8	1.77	0.49
1:1:286:U:H2'	1:1:287:G:C8	2.47	0.49
1:1:314:U:H2'	1:1:315:C:C6	2.47	0.49
1:1:938:C:H4'	47:w:833:ILE:HD13	1.94	0.49
1:1:1456:A:C8	30:d:26:LYS:HD2	2.47	0.49
1:1:2112:U:OP1	46:u:44:ARG:NE	2.44	0.49
1:1:2890:A:H2'	1:1:2891:U:C6	2.47	0.49
3:6:16:U:H2'	3:6:17:G:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:100:LEU:O	11:K:233:GLN:HA	2.12	0.49
17:Q:89:ASP:OD1	17:Q:90:ASP:N	2.43	0.49
19:S:137:ARG:HB3	19:S:139:TYR:CE2	2.48	0.49
23:W:45:LEU:HB3	23:W:48:VAL:HG11	1.94	0.49
29:c:16:LEU:HD23	29:c:98:SER:CA	2.41	0.49
1:1:266:A:N6	35:i:29:LYS:O	2.46	0.49
23:W:45:LEU:HD21	23:W:215:VAL:HG13	1.93	0.49
33:g:51:LEU:HD12	33:g:54:ILE:HG12	1.89	0.49
39:n:180:PHE:CE1	42:q:226:SER:HB2	2.48	0.49
1:1:114:A:N1	1:1:266:A:O2'	2.39	0.49
1:1:1343:A:H2'	1:1:1344:G:C8	2.48	0.49
1:1:2367:A:H2'	1:1:2368:A:C8	2.47	0.49
6:C:120:TYR:CD2	6:C:277:PRO:HG3	2.48	0.49
10:H:183:HIS:NE2	23:W:170:GLU:OE2	2.46	0.49
13:M:28:SER:HB3	13:M:53:VAL:HG22	1.95	0.49
45:t:64:LYS:HA	45:t:152:ALA:HB1	1.93	0.49
48:y:97:VAL:HG12	48:y:128:LEU:HD13	1.93	0.49
48:y:232:ILE:HG23	48:y:235:ASN:HB2	1.94	0.49
1:1:501:A:H2'	1:1:502:U:C6	2.47	0.49
1:1:988:U:H2'	1:1:989:A:C8	2.48	0.49
1:1:2108:C:H1'	1:1:3344:A:C8	2.48	0.49
10:H:132:VAL:HG12	10:H:154:VAL:HG22	1.95	0.49
1:1:41:G:N2	1:1:42:C:O4'	2.41	0.49
1:1:1566:A:H8	1:1:1568:U:H5	1.59	0.49
41:p:11:THR:HG23	41:p:14:TYR:HD2	1.76	0.49
45:t:146:ARG:NH1	45:t:147:VAL:O	2.46	0.49
1:1:1391:C:C2	31:e:103:LYS:HD3	2.48	0.49
1:1:1641:U:O2'	1:1:1642:A:H3'	2.13	0.49
1:1:3016:A:H2'	1:1:3017:A:H8	1.78	0.49
7:E:138:GLN:NE2	7:E:142:ASP:OD1	2.46	0.49
13:M:16:GLU:OE1	19:S:149:LYS:NZ	2.32	0.49
23:W:120:VAL:O	23:W:121:ARG:NE	2.46	0.49
1:1:283:G:H2'	1:1:284:A:N3	2.27	0.48
1:1:2926:A:H5''	1:1:2927:C:H5	1.78	0.48
6:C:181:VAL:HG11	6:C:224:GLY:HA3	1.95	0.48
11:K:305:LYS:NZ	40:o:187:LYS:O	2.31	0.48
24:X:77:GLU:HG2	24:X:133:LEU:HD13	1.95	0.48
48:y:61:ARG:HD3	48:y:106:ASN:OD1	2.12	0.48
1:1:664:U:H2'	1:1:665:A:C8	2.48	0.48
1:1:2982:A:H1'	1:1:2984:C:H41	1.78	0.48
3:6:9:A:OP1	45:t:97:LYS:NZ	2.31	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:42:TRP:CG	19:S:53:LYS:HG2	2.48	0.48
1:1:524:U:OP1	13:M:77:ARG:NH2	2.45	0.48
1:1:887:G:H2'	1:1:888:A:O4'	2.13	0.48
1:1:1740:U:H1'	1:1:1741:A:H2	1.78	0.48
1:1:3121:U:H1'	1:1:3122:A:H5''	1.96	0.48
1:1:3205:G:N3	19:S:171:PHE:CE2	2.81	0.48
3:6:18:U:H2'	3:6:19:U:C6	2.48	0.48
3:6:28:A:OP1	40:o:132:ARG:NE	2.39	0.48
11:K:84:ASN:ND2	11:K:274:TYR:O	2.46	0.48
22:V:54:LEU:HD21	22:V:119:GLY:HA3	1.96	0.48
22:V:104:ASN:OD1	22:V:108:GLU:N	2.40	0.48
23:W:136:THR:HA	23:W:187:LEU:HA	1.95	0.48
26:Z:70:PRO:HG3	26:Z:115:LYS:HB2	1.94	0.48
47:w:764:ASP:O	47:w:772:LYS:NZ	2.36	0.48
48:y:4:ARG:HA	48:y:206:THR:O	2.13	0.48
1:1:492:U:H2'	1:1:493:G:C8	2.49	0.48
1:1:608:A:OP1	6:C:315:LYS:NZ	2.42	0.48
1:1:1732:U:O2	42:q:316:ASN:ND2	2.46	0.48
1:1:3192:U:H2'	1:1:3193:C:C6	2.49	0.48
26:Z:100:THR:HG23	26:Z:106:GLN:HG2	1.96	0.48
29:c:50:VAL:HG21	47:w:403:GLY:HA3	1.95	0.48
45:t:256:THR:O	45:t:256:THR:HG22	2.12	0.48
1:1:180:C:H2'	1:1:181:U:C6	2.48	0.48
1:1:528:U:H2'	1:1:529:A:C8	2.48	0.48
1:1:1807:G:H5''	26:Z:135:ARG:NH1	2.29	0.48
1:1:3021:A:H2	1:1:3033:A:H62	1.58	0.48
2:2:88:A:O2'	2:2:89:A:O5'	2.31	0.48
4:A:101:VAL:HG12	4:A:165:VAL:CG2	2.31	0.48
11:K:78:LEU:HD11	11:K:281:ILE:HG23	1.95	0.48
21:U:111:THR:HG23	28:b:525:THR:HG21	1.96	0.48
40:o:119:GLU:OE2	40:o:121:ARG:NE	2.46	0.48
47:w:768:THR:CG2	47:w:769:GLU:H	2.26	0.48
1:1:69:C:OP1	14:N:178:HIS:ND1	2.28	0.48
4:A:49:VAL:HG12	4:A:50:HIS:N	2.28	0.48
23:W:217:VAL:HG22	23:W:233:ILE:HB	1.96	0.48
30:d:10:ARG:NH1	30:d:12:TYR:OH	2.43	0.48
35:i:15:LYS:HD2	35:i:16:LYS:H	1.79	0.48
41:p:5:THR:HG22	41:p:8:VAL:HG12	1.80	0.48
1:1:844:G:N7	47:w:372:ARG:NH1	2.62	0.48
1:1:1913:A:N3	1:1:2120:A:H2'	2.28	0.48
1:1:2091:U:O2	1:1:2093:A:O2'	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:92:ILE:HG21	17:Q:3:ILE:HG23	1.95	0.48
28:b:481:PHE:HB3	28:b:485:GLU:CB	2.43	0.48
1:1:357:A:O4'	6:C:81:GLY:HA3	2.13	0.48
1:1:489:C:H2'	1:1:490:A:C8	2.49	0.48
5:B:117:ARG:HA	5:B:175:LYS:HD3	1.95	0.48
10:H:12:VAL:HG13	10:H:16:VAL:HG23	1.96	0.48
33:g:51:LEU:HD12	33:g:51:LEU:C	2.38	0.48
42:q:382:LYS:HZ3	42:q:386:LYS:HA	1.79	0.48
45:t:138:LYS:N	45:t:138:LYS:HD2	2.28	0.48
1:1:548:G:H2'	1:1:549:U:C6	2.49	0.48
1:1:2095:G:H2'	1:1:2096:A:C8	2.49	0.48
1:1:2374:C:H2'	1:1:2375:G:N3	2.29	0.48
1:1:2776:C:H5''	27:a:65:GLN:NE2	2.28	0.48
4:A:36:GLU:HG3	4:A:91:GLY:HA2	1.96	0.48
8:F:110:ARG:HB3	17:Q:3:ILE:HG22	1.96	0.48
14:N:66:VAL:HG21	14:N:102:ALA:HB2	1.96	0.48
39:n:415:PRO:HD3	42:q:407:ARG:HH12	1.79	0.48
1:1:591:G:H1'	7:E:19:LYS:HG3	1.94	0.48
1:1:2825:C:C5	28:b:34:ARG:HD2	2.49	0.48
23:W:52:VAL:O	23:W:56:ILE:HG12	2.14	0.48
23:W:165:MET:HE2	23:W:171:ILE:HD12	1.96	0.48
23:W:176:LYS:HD2	23:W:181:THR:HG21	1.95	0.48
43:r:189:LEU:H	43:r:189:LEU:HD23	1.79	0.48
1:1:1193:A:OP1	15:O:49:ARG:NH1	2.38	0.47
10:H:129:ARG:NH1	10:H:160:ASP:OD2	2.38	0.47
48:y:4:ARG:NH2	48:y:215:LEU:HD13	2.24	0.47
1:1:114:A:H2'	1:1:115:A:O4'	2.14	0.47
1:1:1257:C:H42	1:1:1261:G:N2	2.10	0.47
1:1:2163:C:H2'	1:1:2164:A:H8	1.79	0.47
1:1:3316:A:OP2	5:B:123:TYR:HB2	2.14	0.47
8:F:24:GLU:OE1	8:F:24:GLU:N	2.46	0.47
28:b:182:SER:HA	28:b:185:ARG:HG2	1.95	0.47
30:d:6:ASP:O	30:d:77:ARG:HD2	2.14	0.47
35:i:58:ILE:HD11	35:i:90:MET:HE3	1.96	0.47
38:m:158:GLU:OE1	38:m:158:GLU:N	2.43	0.47
39:n:183:ILE:HD11	42:q:395:GLU:HB2	1.95	0.47
39:n:359:LEU:HD11	39:n:441:LEU:HD11	1.95	0.47
40:o:98:LEU:HD22	40:o:102:PHE:CD2	2.49	0.47
1:1:536:U:H1'	1:1:559:A:C8	2.49	0.47
1:1:545:U:H5''	1:1:547:G:N2	2.29	0.47
1:1:2849:C:H3'	1:1:2850:G:H8	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:9:A:H2'	2:2:10:A:H8	1.78	0.47
11:K:211:THR:HG22	11:K:222:LEU:CD1	2.44	0.47
17:Q:83:VAL:O	17:Q:103:ALA:HA	2.14	0.47
19:S:2:ALA:HB3	19:S:32:SER:HB3	1.95	0.47
28:b:249:CYS:SG	28:b:335:ALA:HB1	2.54	0.47
28:b:268:VAL:HG21	28:b:305:LEU:HB3	1.96	0.47
45:t:101:LEU:HD21	45:t:130:ARG:HD2	1.95	0.47
45:t:207:LEU:HD11	45:t:318:LEU:HD13	1.95	0.47
1:1:3018:C:H4'	48:y:8:GLU:HG3	1.95	0.47
21:U:19:VAL:HG23	21:U:105:LEU:HD22	1.95	0.47
1:1:110:G:OP2	12:L:73:ARG:NH2	2.35	0.47
1:1:585:A:H4'	32:f:72:THR:HG23	1.97	0.47
1:1:2344:U:H2'	1:1:2345:A:H8	1.79	0.47
5:B:280:HIS:HB3	5:B:324:VAL:HG13	1.96	0.47
7:E:76:LEU:N	7:E:138:GLN:OE1	2.47	0.47
10:H:47:LYS:NZ	13:M:5:SER:O	2.45	0.47
16:P:29:THR:HG21	16:P:146:ILE:HD11	1.97	0.47
19:S:152:LEU:HD12	19:S:172:TYR:HE2	1.79	0.47
21:U:43:VAL:HG12	21:U:44:GLU:HG3	1.96	0.47
28:b:509:ASN:O	30:d:57:GLN:NE2	2.48	0.47
39:n:435:CYS:SG	39:n:442:VAL:HG22	2.54	0.47
1:1:999:G:H1'	1:1:1000:C:H2'	1.95	0.47
1:1:3164:C:O2'	1:1:3165:A:O5'	2.24	0.47
3:6:16:U:H2'	3:6:17:G:C8	2.49	0.47
10:H:28:VAL:HG22	10:H:33:THR:HG23	1.96	0.47
21:U:19:VAL:HG21	21:U:28:PHE:CE1	2.50	0.47
25:Y:87:LYS:HB2	25:Y:97:ILE:HD11	1.97	0.47
27:a:71:PRO:HG2	27:a:109:TYR:HA	1.96	0.47
36:j:18:LEU:HA	36:j:25:ARG:HA	1.96	0.47
42:q:258:TYR:O	42:q:262:ILE:HG23	2.14	0.47
1:1:87:U:H2'	1:1:88:A:C8	2.49	0.47
1:1:179:C:H2'	1:1:180:C:H6	1.78	0.47
1:1:461:U:H3	1:1:469:G:H22	1.63	0.47
1:1:655:C:H2'	1:1:656:A:C8	2.49	0.47
1:1:701:G:H2'	1:1:702:C:C6	2.49	0.47
1:1:820:A:H2'	1:1:821:U:C6	2.49	0.47
1:1:1192:C:N4	44:s:4:ARG:O	2.33	0.47
1:1:1257:C:N4	1:1:1261:G:H22	2.11	0.47
1:1:1570:U:H1'	45:t:279:GLY:HA2	1.97	0.47
1:1:1666:G:H2'	1:1:1667:A:H8	1.80	0.47
1:1:1824:U:C2	1:1:1825:G:C8	3.03	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3109:G:OP1	43:r:23:ARG:NH1	2.47	0.47
2:2:69:U:H2'	2:2:70:G:O4'	2.14	0.47
9:G:144:GLU:HA	9:G:173:MET:HE3	1.97	0.47
25:Y:100:HIS:ND1	25:Y:102:SER:OG	2.42	0.47
28:b:164:ASP:OD2	28:b:167:THR:OG1	2.32	0.47
31:e:79:VAL:HG13	31:e:111:ARG:HG2	1.96	0.47
39:n:139:LEU:HD13	39:n:222:LEU:HD11	1.97	0.47
45:t:143:PHE:CE2	45:t:145:VAL:CG2	2.98	0.47
47:w:714:THR:HG23	47:w:717:ALA:H	1.78	0.47
48:y:188:ARG:HG3	48:y:209:ASP:O	2.14	0.47
49:z:16:VAL:HG12	49:z:19:ARG:HH22	1.80	0.47
1:1:1231:A:H5''	1:1:1232:C:H5'	1.96	0.47
1:1:1473:G:H5'	18:R:24:LEU:O	2.15	0.47
11:K:37:VAL:HG11	11:K:260:VAL:HA	1.97	0.47
21:U:56:VAL:HG22	21:U:65:VAL:HG22	1.97	0.47
23:W:158:ILE:HG12	23:W:160:SER:H	1.80	0.47
30:d:12:TYR:O	30:d:72:ARG:HD2	2.15	0.47
39:n:168:ALA:HA	39:n:259:LEU:HD11	1.97	0.47
45:t:188:LYS:HE3	45:t:307:ALA:HB3	1.96	0.47
1:1:481:U:H1'	1:1:483:G:OP2	2.15	0.47
1:1:1259:A:N3	1:1:1280:C:O2'	2.41	0.47
1:1:1659:U:H2'	1:1:1660:C:C6	2.50	0.47
11:K:42:ASN:O	11:K:45:ILE:HG22	2.15	0.47
11:K:82:VAL:HG21	11:K:270:LEU:HD12	1.97	0.47
14:N:189:LYS:HA	14:N:189:LYS:HD3	1.72	0.47
39:n:70:TYR:CD1	42:q:204:PRO:HD3	2.50	0.47
39:n:255:ILE:HG22	39:n:256:ILE:HG12	1.96	0.47
39:n:420:LYS:HG2	39:n:426:TYR:HE2	1.79	0.47
48:y:143:SER:HB2	48:y:165:THR:HA	1.97	0.47
1:1:67:A:O2'	1:1:315:C:O2	2.33	0.47
1:1:1845:G:H21	36:j:5:THR:HG21	1.80	0.47
6:C:62:ALA:HB3	6:C:90:PHE:CE2	2.50	0.47
11:K:281:ILE:HB	11:K:289:LEU:HD22	1.97	0.47
28:b:249:CYS:SG	28:b:339:LEU:HD11	2.55	0.47
33:g:82:ALA:HA	33:g:85:VAL:HB	1.97	0.47
1:1:129:U:H2'	1:1:130:A:C8	2.50	0.46
1:1:424:G:H22	1:1:637:C:P	2.38	0.46
1:1:924:G:H4'	1:1:925:A:C2	2.50	0.46
1:1:1942:U:H2'	1:1:1943:C:O4'	2.15	0.46
1:1:2155:G:H2'	1:1:2156:C:C6	2.50	0.46
1:1:2864:A:N1	28:b:100:ARG:NH2	2.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:1:C:C5	45:t:59:GLU:HG2	2.50	0.46
5:B:67:PHE:HA	5:B:70:ARG:HD2	1.97	0.46
11:K:280:PHE:HB3	11:K:288:VAL:HG23	1.96	0.46
23:W:199:GLN:HA	23:W:202:ILE:HG22	1.97	0.46
26:Z:128:GLN:O	26:Z:132:SER:HB2	2.15	0.46
35:i:95:ALA:HA	35:i:99:ARG:HD3	1.98	0.46
39:n:145:LEU:HD22	39:n:209:ILE:HD11	1.95	0.46
47:w:401:SER:HA	47:w:404:LYS:HD2	1.97	0.46
1:1:1112:A:H2'	1:1:1113:G:C8	2.50	0.46
1:1:1200:A:H2	1:1:2824:G:C2	2.31	0.46
1:1:2084:C:H2'	1:1:2085:U:C6	2.50	0.46
4:A:144:ASN:HB2	4:A:160:SER:HB3	1.97	0.46
23:W:77:LEU:HD11	23:W:89:LEU:HD22	1.97	0.46
45:t:39:LYS:O	45:t:43:GLU:HG2	2.15	0.46
48:y:126:GLU:HG2	48:y:137:VAL:HG11	1.98	0.46
1:1:92:G:N2	1:1:94:G:O4'	2.49	0.46
1:1:315:C:OP2	35:i:28:TYR:OH	2.28	0.46
1:1:2815:G:H2'	1:1:2816:G:C8	2.50	0.46
1:1:3096:C:H2'	1:1:3097:C:C6	2.50	0.46
3:6:230:A:H5''	3:6:231:A:H5'	1.95	0.46
4:A:120:PRO:HD3	4:A:159:SER:HB3	1.96	0.46
11:K:184:ASP:N	11:K:184:ASP:OD1	2.46	0.46
12:L:178:LYS:HE3	12:L:179:PHE:CE2	2.50	0.46
45:t:37:ALA:HA	45:t:40:LYS:HG2	1.97	0.46
1:1:1231:A:H4'	1:1:1261:G:H8	1.80	0.46
1:1:2153:U:H2'	1:1:2154:U:C6	2.51	0.46
1:1:3298:C:C2	1:1:3299:A:C8	3.04	0.46
2:2:27:U:H2'	2:2:28:C:C6	2.50	0.46
2:2:72:A:N3	2:2:89:A:H5'	2.30	0.46
8:F:160:ARG:NH2	8:F:206:LYS:HD3	2.30	0.46
9:G:148:ALA:HA	9:G:201:THR:HG22	1.97	0.46
14:N:17:ASP:OD1	14:N:20:ARG:NH2	2.48	0.46
21:U:27:VAL:CG1	28:b:540:HIS:CD2	2.98	0.46
22:V:121:GLU:OE1	22:V:121:GLU:N	2.43	0.46
28:b:5:TRP:CG	28:b:69:PRO:HG3	2.50	0.46
28:b:286:VAL:HA	28:b:318:MET:O	2.16	0.46
1:1:411:U:H2'	1:1:412:G:H8	1.79	0.46
1:1:1300:G:H5''	1:1:1301:A:H5'	1.97	0.46
1:1:1613:A:OP1	37:k:2:ALA:N	2.49	0.46
1:1:1813:A:OP2	42:q:380:LYS:NZ	2.45	0.46
1:1:1922:A:H2'	1:1:1923:C:O4'	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:8:LYS:HD3	17:Q:11:LYS:HD3	1.97	0.46
17:Q:64:VAL:HG23	17:Q:93:ILE:HD11	1.97	0.46
22:V:135:VAL:HG11	46:u:26:ALA:CB	2.45	0.46
26:Z:84:ARG:HH11	47:w:425:GLY:HA2	1.80	0.46
28:b:101:ALA:HB2	28:b:143:LEU:HD13	1.97	0.46
1:1:26:A:H2'	1:1:27:C:H6	1.80	0.46
1:1:3164:C:HO2'	1:1:3165:A:P	2.38	0.46
1:1:3296:A:H2'	1:1:3297:U:H6	1.80	0.46
3:6:8:A:H2'	3:6:9:A:C8	2.50	0.46
6:C:328:ASN:OD1	8:F:48:ASN:ND2	2.47	0.46
9:G:203:VAL:HG12	9:G:204:ARG:N	2.30	0.46
14:N:23:GLN:NE2	14:N:122:ASN:OD1	2.47	0.46
39:n:61:THR:OG1	42:q:430:GLU:OE1	2.31	0.46
43:r:2:PRO:HB2	43:r:6:TYR:CD2	2.51	0.46
1:1:1194:G:OP2	44:s:9:ARG:NH1	2.49	0.46
1:1:1231:A:H4'	1:1:1261:G:C8	2.50	0.46
1:1:1307:G:C4	15:O:60:LYS:HD3	2.51	0.46
2:2:156:U:O4	42:q:448:LYS:NZ	2.48	0.46
13:M:37:GLU:OE1	19:S:72:VAL:HG21	2.15	0.46
23:W:212:GLU:OE1	23:W:212:GLU:N	2.49	0.46
24:X:100:LYS:NZ	24:X:106:ASP:OD1	2.49	0.46
35:i:70:ARG:HH11	35:i:84:LYS:HA	1.79	0.46
1:1:551:A:O2'	1:1:552:G:H8	1.99	0.46
1:1:1257:C:H2'	1:1:1258:U:O4'	2.16	0.46
1:1:2154:U:H2'	1:1:2155:G:C8	2.50	0.46
1:1:3295:A:H2'	1:1:3296:A:H8	1.80	0.46
4:A:108:PRO:HG2	41:p:86:LEU:HD13	1.98	0.46
4:A:156:LYS:HE3	4:A:156:LYS:HB3	1.69	0.46
8:F:97:PRO:HA	8:F:100:ARG:HG2	1.97	0.46
26:Z:61:LYS:HE2	26:Z:65:ARG:HD2	1.98	0.46
47:w:257:THR:OG1	47:w:271:MET:HE2	2.16	0.46
48:y:121:ILE:HD12	48:y:125:THR:HG23	1.97	0.46
48:y:199:VAL:HG23	48:y:204:ALA:HB2	1.97	0.46
1:1:269:G:H5''	14:N:14:LYS:HE2	1.97	0.46
1:1:449:U:H2'	1:1:450:G:C5	2.51	0.46
1:1:985:U:H2'	1:1:986:U:H6	1.80	0.46
4:A:147:ARG:HH21	4:A:155:LYS:HE2	1.81	0.46
33:g:95:ILE:CG1	47:w:407:LEU:CD2	2.94	0.46
42:q:382:LYS:NZ	42:q:386:LYS:HA	2.30	0.46
1:1:2316:G:H2'	1:1:2317:A:C8	2.50	0.46
1:1:3089:C:H2'	1:1:3090:U:O4'	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3278:C:H2'	1:1:3278:C:O2	2.15	0.46
1:1:3294:A:H2'	1:1:3295:A:O4'	2.16	0.46
4:A:33:ASP:N	4:A:33:ASP:OD1	2.49	0.46
5:B:300:ARG:HB2	28:b:436:LEU:HD13	1.96	0.46
10:H:86:TYR:CE2	10:H:151:VAL:HB	2.51	0.46
11:K:144:LEU:HB3	11:K:149:ILE:HB	1.98	0.46
18:R:102:LEU:HD22	18:R:138:LEU:HD22	1.98	0.46
23:W:121:ARG:O	23:W:213:PHE:N	2.38	0.46
25:Y:51:ARG:HG2	25:Y:52:ARG:H	1.80	0.46
35:i:26:ILE:H	35:i:26:ILE:HG13	1.57	0.46
40:o:110:TYR:O	40:o:113:GLN:HG2	2.16	0.46
46:u:45:ASN:ND2	46:u:48:LYS:HG2	2.31	0.46
1:1:2190:U:H2'	1:1:2191:U:H6	1.81	0.45
2:2:142:C:H2'	2:2:143:U:C6	2.51	0.45
9:G:46:LEU:O	9:G:50:VAL:HG23	2.16	0.45
22:V:43:GLY:O	22:V:48:ARG:NH2	2.48	0.45
28:b:44:ALA:O	28:b:48:ARG:HG3	2.14	0.45
43:r:153:LYS:NZ	43:r:250:ASP:OD2	2.49	0.45
45:t:98:ASP:HB3	45:t:184:TYR:CE2	2.50	0.45
45:t:259:GLU:O	45:t:260:SER:OG	2.31	0.45
1:1:299:G:C4	35:i:31:GLY:HA3	2.51	0.45
1:1:958:C:N4	1:1:961:C:OP2	2.49	0.45
1:1:1667:A:H2'	1:1:1668:G:H8	1.79	0.45
1:1:3055:U:O2'	1:1:3057:U:OP1	2.33	0.45
8:F:176:TYR:HB3	8:F:194:HIS:ND1	2.32	0.45
10:H:137:SER:HB2	10:H:143:GLU:HB3	1.98	0.45
17:Q:36:LEU:O	17:Q:40:THR:HB	2.17	0.45
45:t:143:PHE:HE2	45:t:145:VAL:CG2	2.29	0.45
46:u:37:HIS:CE1	46:u:41:LYS:HD2	2.50	0.45
46:u:63:LEU:HD12	46:u:63:LEU:C	2.41	0.45
48:y:85:ARG:NH2	48:y:89:PRO:O	2.49	0.45
48:y:101:LEU:HB3	48:y:107:VAL:HG11	1.97	0.45
1:1:258:G:H2'	1:1:259:C:H6	1.80	0.45
1:1:882:A:H1'	1:1:885:U:H1'	1.97	0.45
1:1:1597:C:H2'	1:1:1598:G:H8	1.80	0.45
1:1:2367:A:H2'	1:1:2368:A:H8	1.82	0.45
1:1:2861:U:O2	1:1:2862:U:H5''	2.16	0.45
1:1:3185:U:HO2'	19:S:170:THR:HG1	1.65	0.45
1:1:3295:A:OP2	5:B:126:LYS:N	2.40	0.45
1:1:3296:A:H2'	1:1:3297:U:C6	2.52	0.45
2:2:19:C:H2'	2:2:20:U:C6	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:120:TYR:CD2	6:C:277:PRO:CG	2.99	0.45
11:K:250:ASN:HB3	11:K:253:TRP:CG	2.51	0.45
28:b:5:TRP:CD1	28:b:69:PRO:HG3	2.51	0.45
39:n:184:LYS:HD3	42:q:395:GLU:CD	2.41	0.45
47:w:323:LYS:O	47:w:327:GLU:HG2	2.16	0.45
1:1:75:G:H5'	12:L:58:VAL:HG13	1.92	0.45
1:1:144:A:H2'	1:1:145:G:O4'	2.16	0.45
1:1:787:G:OP2	17:Q:147:ARG:NH1	2.50	0.45
1:1:1194:G:H2'	1:1:1195:A:C8	2.52	0.45
2:2:158:U:C4	45:t:151:LEU:HD12	2.51	0.45
8:F:127:LEU:HD23	8:F:130:ILE:HD11	1.99	0.45
22:V:87:ARG:HB2	22:V:91:VAL:HG13	1.97	0.45
39:n:431:TRP:HD1	39:n:447:TYR:CD1	2.34	0.45
47:w:821:GLY:O	47:w:824:LYS:HG2	2.16	0.45
1:1:630:A:H2'	1:1:631:U:C6	2.52	0.45
1:1:2363:A:H2'	1:1:2364:G:O4'	2.16	0.45
2:2:40:A:H2'	2:2:41:A:C8	2.52	0.45
28:b:302:ARG:O	28:b:306:LEU:HG	2.15	0.45
41:p:29:LEU:HD23	41:p:69:TYR:CD2	2.52	0.45
1:1:226:C:H2'	1:1:227:G:O4'	2.16	0.45
1:1:3231:U:H2'	1:1:3232:G:H8	1.82	0.45
1:1:3281:U:H2'	1:1:3282:U:O4'	2.16	0.45
1:1:3332:U:H2'	1:1:3333:G:O4'	2.17	0.45
3:6:232:A:OP1	45:t:49:ARG:NE	2.50	0.45
23:W:162:GLU:HG3	23:W:175:ILE:HG13	1.99	0.45
25:Y:77:LYS:HB3	25:Y:77:LYS:HE2	1.71	0.45
26:Z:90:GLU:HA	26:Z:93:LYS:HG3	1.99	0.45
28:b:202:LYS:HG2	28:b:235:ILE:HD13	1.99	0.45
1:1:95:A:N1	12:L:13:HIS:N	2.64	0.45
1:1:1266:G:H2'	1:1:1267:U:C6	2.52	0.45
1:1:1278:A:O2'	23:W:15:THR:O	2.28	0.45
1:1:1910:A:N3	1:1:2333:C:O2'	2.36	0.45
1:1:2095:G:H2'	1:1:2096:A:H8	1.82	0.45
1:1:2883:U:H2'	1:1:2884:C:C6	2.52	0.45
1:1:2968:G:H2'	1:1:2969:A:O4'	2.17	0.45
10:H:132:VAL:HG21	10:H:157:ASN:HD22	1.81	0.45
11:K:211:THR:CG2	11:K:222:LEU:HD13	2.45	0.45
23:W:34:LEU:HD13	23:W:40:VAL:HG21	1.99	0.45
37:k:6:THR:HB	42:q:346:ARG:CZ	2.47	0.45
45:t:64:LYS:HG2	45:t:152:ALA:HA	1.98	0.45
1:1:32:U:P	14:N:95:GLN:HE21	2.39	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:169:U:H5'	12:L:128:ARG:HD2	1.98	0.45
3:6:5:C:OP2	45:t:303:ASN:HB2	2.17	0.45
8:F:178:ILE:HD11	8:F:187:GLU:HG3	1.97	0.45
11:K:33:PRO:HG2	11:K:36:ARG:HG3	1.99	0.45
11:K:201:LYS:HE2	11:K:203:GLU:HB3	1.99	0.45
20:T:42:ILE:HG23	20:T:95:HIS:ND1	2.31	0.45
23:W:22:ASN:O	23:W:26:ILE:HG12	2.17	0.45
23:W:130:LYS:H	23:W:130:LYS:HD2	1.81	0.45
27:a:75:LEU:HD11	27:a:134:ALA:HA	1.98	0.45
28:b:213:TYR:HE2	48:y:236:LEU:HD22	1.81	0.45
28:b:271:PHE:HA	28:b:274:ILE:HG12	1.99	0.45
29:c:13:LYS:HD3	29:c:100:ILE:HG13	1.97	0.45
33:g:95:ILE:HG12	47:w:407:LEU:CD2	2.46	0.45
42:q:393:ARG:HD3	42:q:393:ARG:HA	1.74	0.45
43:r:181:LYS:HG2	43:r:196:PRO:HB3	1.99	0.45
1:1:210:U:C2	1:1:230:U:H4'	2.51	0.45
1:1:1259:A:N7	23:W:67:MET:SD	2.89	0.45
1:1:1836:C:H2'	1:1:1837:U:C6	2.51	0.45
22:V:10:LYS:NZ	22:V:121:GLU:HB3	2.32	0.45
23:W:127:PRO:HA	23:W:195:LEU:HB3	1.99	0.45
27:a:88:ASP:O	27:a:92:LYS:HG2	2.17	0.45
45:t:167:ARG:HG3	45:t:270:PRO:HG3	1.98	0.45
1:1:235:A:H2'	1:1:236:G:C8	2.52	0.45
1:1:562:C:H5''	19:S:71:LYS:HD2	1.99	0.45
1:1:634:C:H5'	32:f:21:ARG:O	2.17	0.45
1:1:821:U:H2'	1:1:822:G:H8	1.82	0.45
1:1:1966:U:H2'	1:1:1967:U:O4'	2.17	0.45
2:2:4:C:H2'	2:2:5:U:C6	2.52	0.45
8:F:176:TYR:CZ	8:F:197:GLN:HG2	2.52	0.45
11:K:155:ILE:HD12	11:K:173:PHE:CE1	2.52	0.45
23:W:222:ASP:OD1	23:W:222:ASP:N	2.49	0.45
37:k:7:ASP:OD2	37:k:10:GLN:HG2	2.15	0.45
43:r:199:ALA:HB3	43:r:222:GLU:HB3	1.99	0.45
47:w:775:GLU:O	47:w:779:LEU:HG	2.16	0.45
1:1:164:A:H2'	1:1:165:A:O4'	2.17	0.44
1:1:380:U:H2'	1:1:381:U:C6	2.52	0.44
1:1:1213:G:H5'	19:S:137:ARG:HH21	1.81	0.44
1:1:1735:G:OP1	42:q:319:LYS:NZ	2.34	0.44
2:2:46:G:O2'	2:2:61:A:N1	2.47	0.44
4:A:100:ASN:O	4:A:166:ILE:HG12	2.17	0.44
48:y:62:MET:HE3	48:y:73:PRO:HG3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:487:U:H3'	1:1:488:U:H5''	1.99	0.44
1:1:890:C:O2	1:1:2324:A:H2	2.00	0.44
1:1:2148:U:H2'	1:1:2149:A:C8	2.52	0.44
1:1:2911:A:H4'	1:1:2912:G:C8	2.52	0.44
2:2:154:C:H4'	9:G:181:LYS:HB3	1.99	0.44
3:6:1:C:C4	45:t:59:GLU:HG2	2.51	0.44
7:E:40:LEU:CD2	7:E:54:TYR:HB2	2.46	0.44
11:K:209:ILE:HG12	11:K:225:ASN:HB3	1.99	0.44
20:T:102:ARG:O	20:T:106:LEU:HG	2.17	0.44
26:Z:10:VAL:O	26:Z:83:THR:OG1	2.30	0.44
29:c:9:SER:HB3	29:c:12:GLN:HG2	1.99	0.44
35:i:98:ARG:HB3	35:i:99:ARG:HH11	1.82	0.44
42:q:424:GLN:HB3	42:q:431:THR:CG2	2.47	0.44
45:t:84:LYS:HE3	45:t:84:LYS:HB2	1.84	0.44
1:1:1886:A:H2'	1:1:1887:A:H8	1.80	0.44
1:1:2787:G:O3'	27:a:58:MET:N	2.50	0.44
1:1:3320:A:H2'	1:1:3321:C:C6	2.52	0.44
11:K:202:VAL:CG2	11:K:237:LYS:HZ3	2.09	0.44
1:1:165:A:H2'	1:1:166:C:C6	2.52	0.44
1:1:170:G:H1	1:1:248:U:H3	1.64	0.44
1:1:437:G:H2'	1:1:438:A:H2'	2.00	0.44
1:1:1153:A:H2	1:1:2371:G:N3	2.14	0.44
1:1:2103:U:H2'	1:1:2104:A:C8	2.52	0.44
1:1:3196:U:O2'	1:1:3197:G:OP2	2.34	0.44
2:2:27:U:H2'	2:2:28:C:H6	1.82	0.44
40:o:118:LYS:HA	40:o:118:LYS:HD2	1.86	0.44
1:1:1367:G:OP1	31:e:45:ARG:NH2	2.48	0.44
6:C:179:LEU:HD11	6:C:183:LYS:HE3	1.99	0.44
10:H:29:GLY:CA	10:H:82:VAL:HG22	2.46	0.44
34:h:31:LEU:HD11	34:h:43:LYS:HD3	1.99	0.44
1:1:412:G:H2'	1:1:413:U:C6	2.52	0.44
1:1:412:G:H2'	1:1:413:U:H6	1.82	0.44
1:1:834:U:H2'	1:1:835:G:O4'	2.17	0.44
1:1:1123:U:H2'	1:1:1124:U:O4'	2.18	0.44
1:1:1791:C:H2'	1:1:1792:C:C6	2.53	0.44
1:1:2921:U:H4'	1:1:2922:G:H5''	1.99	0.44
5:B:331:ASN:OD1	5:B:331:ASN:N	2.50	0.44
11:K:108:LYS:HG3	11:K:230:TYR:HE1	1.82	0.44
11:K:283:THR:CG2	11:K:284:ASN:H	2.30	0.44
14:N:189:LYS:O	14:N:193:ARG:HG3	2.18	0.44
20:T:100:LYS:HB3	20:T:103:GLN:CD	2.43	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:k:56:ILE:HG22	37:k:58:ASP:H	1.83	0.44
39:n:360:PHE:HA	39:n:363:PHE:HD2	1.83	0.44
1:1:629:U:H2'	1:1:630:A:C8	2.52	0.44
1:1:872:U:H2'	1:1:873:C:C6	2.53	0.44
1:1:994:G:H4'	1:1:995:U:O4'	2.17	0.44
1:1:3205:G:C4	19:S:171:PHE:CZ	3.05	0.44
21:U:38:ILE:HD11	21:U:56:VAL:HB	2.00	0.44
39:n:110:ASP:OD1	39:n:110:ASP:N	2.49	0.44
40:o:93:ILE:HG23	40:o:164:VAL:HG13	1.98	0.44
47:w:317:MET:HE3	47:w:317:MET:HB3	1.76	0.44
1:1:292:U:H5'	47:w:710:ASN:O	2.18	0.44
1:1:989:A:H2'	1:1:990:U:C6	2.52	0.44
1:1:1694:U:O2'	1:1:1695:U:H5'	2.18	0.44
1:1:2829:U:OP2	28:b:130:ARG:NH1	2.51	0.44
6:C:118:LYS:O	6:C:122:THR:HG22	2.18	0.44
11:K:84:ASN:HB2	11:K:88:PHE:CZ	2.52	0.44
14:N:11:GLN:HA	14:N:19:LEU:HD21	2.00	0.44
26:Z:4:PHE:HE2	29:c:63:SER:HB3	1.83	0.44
28:b:327:ASN:O	28:b:331:VAL:HG23	2.18	0.44
39:n:266:SER:O	39:n:267:ARG:HG2	2.18	0.44
48:y:197:MET:HE2	48:y:197:MET:HB3	1.76	0.44
1:1:177:U:H2'	1:1:178:U:H6	1.83	0.44
1:1:767:U:H1'	1:1:768:C:C5	2.53	0.44
1:1:789:A:H2'	1:1:790:U:C6	2.53	0.44
1:1:1256:G:H2'	1:1:1257:C:C6	2.53	0.44
1:1:1666:G:H2'	1:1:1667:A:C8	2.53	0.44
1:1:1908:A:H2'	1:1:1909:A:C8	2.53	0.44
1:1:2152:A:H2'	1:1:2153:U:H6	1.83	0.44
1:1:2773:C:H2'	1:1:2774:C:H6	1.83	0.44
1:1:3057:U:O2	1:1:3057:U:H2'	2.17	0.44
8:F:180:SER:OG	8:F:183:ASP:OD1	2.35	0.44
13:M:32:LEU:HD11	13:M:94:TRP:CG	2.52	0.44
14:N:195:ASN:OD1	14:N:195:ASN:O	2.36	0.44
22:V:87:ARG:HH22	22:V:137:VAL:CG2	2.20	0.44
23:W:145:ARG:HH12	23:W:208:ILE:HB	1.82	0.44
34:h:12:LYS:NZ	34:h:20:GLN:OE1	2.42	0.44
1:1:3346:U:H2'	1:1:3347:A:C8	2.53	0.43
8:F:120:THR:O	8:F:124:LEU:HB2	2.17	0.43
9:G:190:VAL:HG23	9:G:192:GLN:HG2	1.99	0.43
11:K:72:GLU:CD	11:K:72:GLU:H	2.26	0.43
12:L:124:ILE:O	12:L:124:ILE:HG23	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:28:THR:HG21	42:q:441:TYR:CZ	2.53	0.43
26:Z:27:LYS:HZ1	26:Z:97:SER:HB3	1.82	0.43
28:b:62:GLU:O	28:b:66:LYS:HG2	2.18	0.43
28:b:151:GLU:CD	28:b:154:ARG:HH21	2.25	0.43
28:b:237:MET:HB3	28:b:241:TYR:HE2	1.83	0.43
28:b:282:SER:HB3	28:b:338:LYS:HD3	2.00	0.43
28:b:346:ASN:O	28:b:349:LYS:HB2	2.17	0.43
1:1:1343:A:H2'	1:1:1344:G:H8	1.83	0.43
1:1:2094:C:H2'	1:1:2095:G:H8	1.83	0.43
1:1:2177:G:C6	4:A:125:ALA:HB1	2.53	0.43
1:1:2768:U:H2'	1:1:2769:A:C8	2.48	0.43
1:1:3047:U:O2'	1:1:3048:A:H5'	2.18	0.43
1:1:3191:G:H2'	1:1:3192:U:C6	2.52	0.43
6:C:31:ARG:HG3	6:C:120:TYR:CE1	2.53	0.43
6:C:74:ILE:HD12	6:C:75:PRO:HD2	2.01	0.43
11:K:72:GLU:HB3	11:K:76:LYS:HE3	2.00	0.43
14:N:5:LYS:HB3	35:i:40:VAL:HG11	2.00	0.43
19:S:112:ALA:O	19:S:115:ARG:NH1	2.52	0.43
39:n:126:PRO:HB2	39:n:130:ARG:CZ	2.45	0.43
40:o:102:PHE:HD1	40:o:102:PHE:HA	1.69	0.43
41:p:20:SER:O	41:p:24:ARG:HG3	2.18	0.43
47:w:743:LYS:HE3	47:w:743:LYS:HB3	1.78	0.43
1:1:41:G:H5''	1:1:42:C:H5	1.83	0.43
1:1:41:G:H5'	1:1:42:C:OP2	2.18	0.43
1:1:1242:G:H2'	1:1:1243:G:C8	2.52	0.43
1:1:2115:G:H22	1:1:2120:A:H1'	1.84	0.43
9:G:112:GLU:O	9:G:116:VAL:N	2.50	0.43
11:K:182:ALA:HB3	11:K:187:VAL:HG22	1.99	0.43
13:M:37:GLU:OE1	19:S:72:VAL:HG23	2.19	0.43
16:P:36:ILE:HD12	16:P:44:ALA:HB1	2.00	0.43
22:V:10:LYS:HE2	22:V:125:LEU:HD22	2.00	0.43
33:g:99:LYS:HE2	33:g:99:LYS:HB2	1.83	0.43
46:u:110:ASN:O	46:u:113:ARG:HG2	2.19	0.43
1:1:86:G:N2	1:1:98:G:H2'	2.33	0.43
1:1:989:A:H2'	1:1:990:U:H6	1.83	0.43
1:1:2342:U:H2'	1:1:2343:C:H6	1.83	0.43
1:1:2881:C:H2'	1:1:2882:U:C6	2.52	0.43
7:E:66:SER:HB2	7:E:76:LEU:HD23	2.00	0.43
11:K:265:LEU:HA	11:K:268:GLU:HG2	2.00	0.43
13:M:12:TRP:CZ2	19:S:153:PRO:HB3	2.53	0.43
21:U:84:LEU:HD22	21:U:89:LEU:HB2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:30:ASP:OD1	26:Z:31:GLU:N	2.52	0.43
28:b:343:ARG:HB3	28:b:347:LYS:NZ	2.33	0.43
35:i:54:GLU:HB3	35:i:90:MET:HE2	2.01	0.43
37:k:61:LYS:HB3	42:q:350:LEU:HD23	2.00	0.43
43:r:30:ARG:O	43:r:34:LYS:HG2	2.19	0.43
1:1:1498:A:H2'	1:1:1499:C:H6	1.80	0.43
3:6:18:U:H2'	3:6:19:U:H6	1.82	0.43
7:E:96:VAL:HG12	7:E:98:VAL:HG13	1.99	0.43
21:U:92:TRP:CD1	28:b:535:MET:HE1	2.54	0.43
22:V:87:ARG:NH2	22:V:137:VAL:HG21	2.21	0.43
28:b:531:MET:O	28:b:535:MET:HG2	2.18	0.43
39:n:175:LEU:HD13	39:n:191:ASN:O	2.18	0.43
43:r:198:LEU:HB2	43:r:222:GLU:HG3	2.00	0.43
45:t:144:ILE:HD12	45:t:177:VAL:HG21	1.99	0.43
1:1:101:G:H2'	1:1:102:C:O4'	2.18	0.43
1:1:412:G:H5'	16:P:26:PHE:HZ	1.84	0.43
1:1:664:U:H2'	1:1:665:A:H8	1.82	0.43
1:1:2909:U:H2'	1:1:2910:A:O4'	2.19	0.43
4:A:126:LEU:HD13	4:A:150:LEU:HD22	2.01	0.43
6:C:35:VAL:HG21	6:C:244:LEU:HD21	2.00	0.43
11:K:75:LYS:HA	11:K:284:ASN:HB2	2.00	0.43
18:R:77:GLY:O	18:R:81:ARG:HG3	2.19	0.43
21:U:27:VAL:HG11	21:U:92:TRP:HH2	1.83	0.43
36:j:39:TYR:CD1	36:j:40:PRO:HA	2.53	0.43
40:o:158:MET:HE2	40:o:158:MET:HB3	1.77	0.43
45:t:213:ARG:NE	45:t:226:GLU:OE2	2.51	0.43
46:u:27:LYS:HE2	46:u:27:LYS:HB2	1.67	0.43
1:1:668:G:H2'	1:1:669:U:H6	1.84	0.43
1:1:2332:A:H2'	1:1:2333:C:O4'	2.18	0.43
1:1:3041:U:H2'	1:1:3042:U:C6	2.52	0.43
1:1:3112:G:O6	1:1:3120:C:H5''	2.18	0.43
1:1:3163:A:N6	1:1:3288:G:O6	2.50	0.43
6:C:357:GLU:O	6:C:361:HIS:HB2	2.17	0.43
13:M:49:PRO:HG3	13:M:78:THR:HG23	2.01	0.43
29:c:16:LEU:HG	29:c:98:SER:HB2	2.01	0.43
48:y:22:THR:O	48:y:47:PRO:HD2	2.19	0.43
1:1:1626:U:H2'	1:1:1627:U:C6	2.53	0.43
1:1:1867:A:H2'	1:1:1868:G:C8	2.53	0.43
1:1:1952:G:OP1	42:q:326:LYS:HE2	2.18	0.43
1:1:3063:C:H2'	1:1:3064:U:H6	1.84	0.43
5:B:66:LYS:HE2	48:y:57:ARG:CZ	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:14:LEU:O	29:c:18:ILE:HG12	2.19	0.43
29:c:24:THR:HG22	29:c:29:SER:CB	2.45	0.43
36:j:60:GLY:HA2	36:j:64:MET:HE2	2.01	0.43
39:n:366:TYR:HB2	39:n:407:VAL:HG11	2.00	0.43
43:r:184:VAL:HG11	43:r:259:LEU:HD13	1.99	0.43
45:t:43:GLU:HB3	45:t:47:LYS:NZ	2.33	0.43
48:y:182:VAL:HG12	48:y:221:ILE:HG12	2.01	0.43
1:1:173:G:N1	1:1:245:U:N3	2.42	0.43
1:1:258:G:H2'	1:1:259:C:C6	2.54	0.43
4:A:119:LYS:HB2	4:A:119:LYS:HE2	1.66	0.43
5:B:83:PRO:HB2	5:B:202:THR:HB	2.01	0.43
7:E:92:SER:HB3	7:E:148:GLU:CD	2.44	0.43
11:K:219:LEU:HD23	11:K:219:LEU:H	1.84	0.43
13:M:125:LYS:HG2	13:M:128:ARG:HH21	1.84	0.43
28:b:369:ARG:HB2	48:y:178:GLN:NE2	2.34	0.43
42:q:385:THR:HG23	42:q:430:GLU:OE1	2.18	0.43
1:1:3099:C:HO2'	1:1:3100:U:H6	1.64	0.43
5:B:54:THR:OG1	5:B:55:THR:N	2.51	0.43
11:K:174:ILE:HG21	11:K:198:ALA:HB2	2.01	0.43
28:b:284:MET:HE1	28:b:334:LYS:HB3	2.01	0.43
42:q:389:VAL:HG12	42:q:424:GLN:HB3	2.01	0.43
1:1:171:G:N1	1:1:248:U:O4	2.52	0.42
1:1:768:C:H5'	12:L:179:PHE:CZ	2.54	0.42
11:K:202:VAL:O	11:K:202:VAL:HG12	2.19	0.42
12:L:49:ARG:HD2	34:h:116:TYR:CE1	2.54	0.42
21:U:27:VAL:HG11	28:b:540:HIS:CD2	2.54	0.42
21:U:57:THR:HG22	21:U:58:GLU:O	2.19	0.42
47:w:764:ASP:HB3	47:w:772:LYS:HE2	2.00	0.42
1:1:962:A:H3'	1:1:963:G:C8	2.51	0.42
1:1:2898:G:O6	43:r:8:GLU:HG2	2.19	0.42
1:1:3027:A:H2'	1:1:3028:G:O4'	2.19	0.42
12:L:166:ALA:N	27:a:135:GLU:OE2	2.52	0.42
21:U:89:LEU:HA	21:U:92:TRP:NE1	2.34	0.42
26:Z:23:VAL:HG12	26:Z:45:GLY:HA3	2.01	0.42
40:o:104:GLU:OE2	40:o:124:ARG:NE	2.39	0.42
42:q:379:LYS:HA	42:q:379:LYS:HD2	1.75	0.42
1:1:1317:A:O2'	1:1:1318:A:H3'	2.19	0.42
1:1:2050:C:H3'	1:1:2051:G:C8	2.54	0.42
1:1:2054:C:H2'	1:1:2055:U:C6	2.55	0.42
1:1:2158:A:C8	1:1:2160:G:C4	3.07	0.42
4:A:180:LEU:HD11	41:p:26:VAL:HG21	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:113:VAL:HA	26:Z:116:LYS:NZ	2.34	0.42
29:c:74:ASN:OD1	29:c:74:ASN:N	2.52	0.42
39:n:169:TYR:HB2	39:n:237:TYR:CE1	2.53	0.42
43:r:5:ASP:O	43:r:9:ARG:HG3	2.20	0.42
1:1:1904:C:C4	1:1:2950:G:H5'	2.54	0.42
1:1:2176:U:OP1	4:A:128:ARG:NH2	2.53	0.42
2:2:63:G:O2'	34:h:49:LYS:HE3	2.18	0.42
4:A:27:ALA:O	4:A:128:ARG:NH1	2.37	0.42
6:C:31:ARG:HG3	6:C:120:TYR:HE1	1.83	0.42
10:H:129:ARG:O	10:H:132:VAL:HG22	2.20	0.42
19:S:49:HIS:ND1	19:S:51:VAL:HG23	2.34	0.42
26:Z:85:TYR:CE1	47:w:428:ARG:HD2	2.54	0.42
46:u:44:ARG:CZ	46:u:49:LEU:HD21	2.49	0.42
48:y:236:LEU:O	48:y:240:LEU:HG	2.19	0.42
1:1:374:A:N3	1:1:376:G:H5''	2.35	0.42
1:1:992:A:H5''	20:T:43:LYS:HG3	2.01	0.42
1:1:2881:C:H2'	1:1:2882:U:H6	1.84	0.42
11:K:212:HIS:HA	11:K:217:PHE:HA	2.01	0.42
22:V:10:LYS:HD3	22:V:11:PHE:N	2.34	0.42
26:Z:81:LEU:HD22	33:g:90:ILE:HG12	2.01	0.42
28:b:511:LYS:HE3	28:b:513:LEU:HD23	2.01	0.42
39:n:417:LEU:H	39:n:417:LEU:HD23	1.83	0.42
42:q:258:TYR:HA	42:q:261:ARG:HG2	2.02	0.42
48:y:232:ILE:CG2	48:y:236:LEU:HG	2.43	0.42
1:1:2:U:H5'	24:X:21:LYS:HB2	2.01	0.42
1:1:696:C:OP1	6:C:272:VAL:HG12	2.18	0.42
1:1:1298:C:O2'	43:r:40:GLN:O	2.33	0.42
12:L:57:VAL:C	12:L:58:VAL:HG23	2.45	0.42
12:L:59:ARG:HD2	12:L:69:VAL:HG12	2.01	0.42
22:V:92:PHE:O	46:u:19:ILE:HG13	2.20	0.42
23:W:31:ARG:HD3	23:W:31:ARG:HA	1.87	0.42
28:b:239:SER:O	28:b:243:ILE:HG13	2.20	0.42
28:b:277:LEU:HG	38:m:157:LEU:HB3	2.02	0.42
1:1:1117:G:H2'	1:1:1118:C:C6	2.54	0.42
1:1:2149:A:H4'	4:A:179:LEU:HB2	2.00	0.42
1:1:3234:A:H61	1:1:3253:G:H1	1.67	0.42
7:E:150:LYS:HA	7:E:150:LYS:HD2	1.80	0.42
11:K:80:LEU:HB2	11:K:248:LEU:HD21	2.01	0.42
14:N:192:LYS:HB3	14:N:192:LYS:HE2	1.66	0.42
22:V:118:VAL:HG12	22:V:135:VAL:O	2.19	0.42
39:n:127:ASP:HA	39:n:130:ARG:HH11	1.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:145:LEU:HD21	42:q:416:LEU:HD11	2.01	0.42
41:p:82:THR:O	41:p:86:LEU:HG	2.20	0.42
1:1:1222:G:H1'	1:1:1286:A:N6	2.35	0.42
3:6:20:U:H2'	3:6:21:G:C8	2.55	0.42
7:E:63:LEU:O	7:E:78:ARG:HA	2.20	0.42
11:K:49:SER:O	11:K:49:SER:OG	2.37	0.42
11:K:231:MET:HE3	11:K:231:MET:HB2	1.83	0.42
47:w:695:LEU:HD13	47:w:699:PHE:CE2	2.54	0.42
47:w:764:ASP:OD2	47:w:767:LYS:HE3	2.20	0.42
48:y:104:LEU:HA	48:y:107:VAL:HG22	2.01	0.42
1:1:7:C:OP1	39:n:92:ARG:NH2	2.52	0.42
1:1:391:A:H2'	1:1:392:G:O4'	2.20	0.42
1:1:2094:C:H2'	1:1:2095:G:C8	2.55	0.42
1:1:2161:G:H2'	1:1:2162:U:C6	2.54	0.42
4:A:49:VAL:CG1	4:A:50:HIS:N	2.83	0.42
6:C:30:ILE:O	6:C:32:PRO:HD3	2.19	0.42
7:E:40:LEU:HD21	7:E:54:TYR:HB2	2.01	0.42
25:Y:52:ARG:O	25:Y:70:ILE:HB	2.20	0.42
28:b:313:PRO:HA	28:b:314:GLY:HA2	1.71	0.42
39:n:183:ILE:HG13	39:n:184:LYS:HG3	2.01	0.42
40:o:204:HIS:O	40:o:208:ILE:HG13	2.20	0.42
42:q:403:SER:HB3	42:q:408:LYS:HD3	2.02	0.42
43:r:151:ILE:HD12	43:r:212:LEU:HD13	2.01	0.42
45:t:64:LYS:HA	45:t:152:ALA:O	2.20	0.42
46:u:63:LEU:HD12	46:u:69:LEU:CD1	2.50	0.42
47:w:276:ASN:HD22	47:w:308:LYS:HE3	1.84	0.42
48:y:219:GLU:HG3	48:y:224:LEU:HB2	2.01	0.42
1:1:288:C:H2'	1:1:289:A:C8	2.55	0.42
1:1:288:C:H2'	1:1:289:A:H8	1.85	0.42
1:1:1514:G:N7	1:1:1842:A:C8	2.88	0.42
1:1:2352:A:H5''	16:P:83:TRP:O	2.20	0.42
1:1:2882:U:H2'	1:1:2883:U:C6	2.55	0.42
1:1:3359:A:H2'	1:1:3360:C:C6	2.55	0.42
4:A:47:GLN:HG3	4:A:49:VAL:HG23	2.02	0.42
9:G:80:TYR:CZ	9:G:229:VAL:CG1	3.02	0.42
9:G:203:VAL:CG1	9:G:207:ASP:HB2	2.50	0.42
28:b:300:GLU:HA	28:b:303:ALA:HB3	2.00	0.42
39:n:50:LYS:HB3	39:n:55:GLY:HA2	2.01	0.42
39:n:411:ILE:HG12	39:n:427:ILE:HG13	2.02	0.42
40:o:90:SER:OG	40:o:92:ILE:HG22	2.20	0.42
42:q:449:TRP:CZ3	42:q:452:LYS:HE3	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:322:ARG:NH1	47:w:326:ARG:HD2	2.35	0.42
47:w:793:VAL:N	47:w:813:LYS:HZ1	2.18	0.42
1:1:396:A:O2'	1:1:399:A:OP1	2.26	0.41
1:1:628:A:H2'	1:1:629:U:O4'	2.20	0.41
1:1:775:A:H2'	1:1:776:U:C6	2.54	0.41
1:1:1347:U:H2'	1:1:1355:A:N6	2.35	0.41
14:N:68:ARG:HG3	14:N:126:THR:O	2.20	0.41
16:P:51:VAL:HA	16:P:56:ARG:O	2.20	0.41
26:Z:25:ILE:HA	26:Z:43:VAL:HG12	2.02	0.41
28:b:90:HIS:NE2	28:b:149:TYR:CD1	2.87	0.41
28:b:295:PRO:HB3	28:b:306:LEU:HD13	2.01	0.41
28:b:453:LEU:HD12	28:b:456:LEU:HD23	2.02	0.41
39:n:188:TYR:O	39:n:198:ARG:HA	2.20	0.41
40:o:200:MET:HE3	40:o:200:MET:HB3	1.94	0.41
1:1:479:U:H1'	1:1:480:C:H2'	2.01	0.41
1:1:506:U:H2'	1:1:507:U:O4'	2.20	0.41
1:1:1207:G:O2'	43:r:36:SER:OG	2.39	0.41
1:1:1279:C:H2'	1:1:1280:C:C6	2.55	0.41
1:1:2082:U:N3	1:1:2083:G:N7	2.68	0.41
1:1:2894:C:H5'	10:H:166:ARG:NH1	2.32	0.41
6:C:286:VAL:HG21	17:Q:32:LEU:HB2	2.02	0.41
15:O:127:LEU:HD22	19:S:156:VAL:HG13	2.02	0.41
26:Z:13:VAL:HG12	26:Z:19:ALA:HA	2.01	0.41
26:Z:84:ARG:NH2	33:g:100:ILE:HG21	2.35	0.41
28:b:258:GLU:OE1	28:b:263:THR:HA	2.20	0.41
28:b:310:LYS:HE3	28:b:310:LYS:HB2	1.85	0.41
28:b:360:LYS:HE3	48:y:244:TYR:CE1	2.55	0.41
47:w:308:LYS:HE2	47:w:308:LYS:HB2	1.66	0.41
1:1:863:C:H2'	1:1:864:G:O4'	2.21	0.41
1:1:1605:A:H4'	1:1:1607:U:C5	2.55	0.41
1:1:1771:C:H2'	1:1:1772:U:O4'	2.20	0.41
1:1:2057:G:H2'	1:1:2058:G:O4'	2.19	0.41
1:1:2851:A:H2'	1:1:2852:C:O4'	2.20	0.41
1:1:3361:G:H2'	1:1:3362:A:C2	2.55	0.41
3:6:33:U:H5'	11:K:285:ARG:HA	2.01	0.41
6:C:136:LEU:HD21	6:C:143:GLU:HG3	2.03	0.41
8:F:47:ARG:CZ	8:F:179:LEU:HD23	2.51	0.41
10:H:42:ASP:HB3	10:H:64:HIS:NE2	2.34	0.41
19:S:26:ARG:HG2	20:T:150:THR:HA	2.02	0.41
21:U:71:PHE:HE2	21:U:76:LEU:HD12	1.85	0.41
28:b:268:VAL:HG21	28:b:305:LEU:HD13	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:t:98:ASP:HB3	45:t:184:TYR:CZ	2.56	0.41
1:1:408:A:N6	2:2:15:G:H1'	2.36	0.41
1:1:576:C:OP1	8:F:241:LYS:NZ	2.53	0.41
1:1:1243:G:H2'	1:1:1244:A:H5'	2.02	0.41
1:1:2157:G:N7	4:A:152:SER:OG	2.52	0.41
1:1:2316:G:H2'	1:1:2317:A:H8	1.84	0.41
1:1:3027:A:H1'	28:b:207:GLY:HA2	2.02	0.41
6:C:150:LEU:HD21	6:C:172:VAL:HG12	2.01	0.41
8:F:229:PHE:CD1	8:F:229:PHE:C	2.99	0.41
12:L:170:LEU:HB3	35:i:9:ILE:HD11	2.01	0.41
16:P:60:PHE:HB3	16:P:64:ASN:HB3	2.01	0.41
22:V:15:LEU:HD13	22:V:51:ALA:HB3	2.02	0.41
23:W:104:PHE:C	23:W:105:THR:HG23	2.45	0.41
28:b:447:PRO:O	28:b:448:GLU:HG2	2.20	0.41
28:b:497:ARG:HA	28:b:500:GLN:HE21	1.84	0.41
29:c:18:ILE:HG13	29:c:81:VAL:HG13	2.01	0.41
47:w:815:LYS:HB3	47:w:815:LYS:HE3	1.83	0.41
1:1:612:U:OP1	7:E:21:THR:OG1	2.27	0.41
1:1:1297:C:C2	1:1:1298:C:C5	3.09	0.41
1:1:1606:U:O4	33:g:9:ARG:NE	2.42	0.41
1:1:1621:A:H2'	1:1:1622:U:H6	1.85	0.41
1:1:3000:A:H2'	1:1:3001:C:C6	2.55	0.41
1:1:3072:C:H2'	1:1:3073:A:O4'	2.21	0.41
2:2:18:U:H2'	2:2:19:C:C6	2.55	0.41
6:C:209:TYR:CE1	6:C:212:ASP:HB2	2.56	0.41
8:F:98:LYS:HB3	8:F:99:PRO:HD3	2.02	0.41
9:G:80:TYR:CZ	9:G:229:VAL:HG11	2.55	0.41
11:K:98:LYS:HB3	11:K:236:VAL:HG23	2.02	0.41
19:S:124:LEU:HD22	20:T:153:PRO:O	2.20	0.41
19:S:152:LEU:HB2	19:S:172:TYR:HD2	1.86	0.41
28:b:326:GLU:O	28:b:330:GLU:HG2	2.21	0.41
39:n:438:LYS:HE2	39:n:442:VAL:HG12	2.01	0.41
45:t:76:LYS:O	45:t:80:ILE:HG12	2.21	0.41
1:1:1799:A:H2'	1:1:1800:A:H8	1.85	0.41
1:1:2323:G:O2'	1:1:2325:G:OP2	2.31	0.41
1:1:2872:A:H2'	1:1:2873:U:C6	2.55	0.41
1:1:3297:U:H2'	1:1:3298:C:H6	1.84	0.41
7:E:59:GLU:N	7:E:59:GLU:OE1	2.54	0.41
8:F:120:THR:H	8:F:123:THR:HG1	1.67	0.41
9:G:162:LEU:HD23	14:N:7:LEU:HD11	2.03	0.41
10:H:4:ILE:HD11	19:S:143:PHE:CE2	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:187:VAL:HG21	11:K:208:SER:HA	2.02	0.41
13:M:25:LYS:HD2	13:M:62:GLN:CD	2.43	0.41
14:N:187:ARG:HA	14:N:187:ARG:HD2	1.77	0.41
20:T:143:THR:O	20:T:143:THR:OG1	2.39	0.41
23:W:183:ASP:N	23:W:183:ASP:OD1	2.48	0.41
1:1:1301:A:O4'	43:r:44:GLY:HA2	2.20	0.41
1:1:1497:C:H2'	1:1:1498:A:C8	2.55	0.41
1:1:2322:C:O2'	1:1:2323:G:H5'	2.21	0.41
2:2:37:A:H5''	2:2:39:G:O4'	2.20	0.41
2:2:48:A:O2'	2:2:50:C:OP2	2.35	0.41
8:F:98:LYS:O	8:F:102:VAL:HG23	2.20	0.41
11:K:107:TYR:HB3	11:K:230:TYR:CZ	2.56	0.41
14:N:28:TRP:O	14:N:32:GLN:HG2	2.20	0.41
16:P:67:ILE:HG12	16:P:80:LYS:HD2	2.02	0.41
28:b:534:HIS:O	28:b:538:LEU:HG	2.20	0.41
29:c:24:THR:CG2	29:c:29:SER:HB2	2.46	0.41
29:c:50:VAL:HG21	47:w:403:GLY:C	2.46	0.41
39:n:366:TYR:CB	39:n:407:VAL:HG11	2.50	0.41
40:o:97:ARG:HD2	40:o:161:LEU:O	2.20	0.41
40:o:161:LEU:HD12	40:o:161:LEU:HA	1.95	0.41
42:q:407:ARG:HH21	42:q:408:LYS:HD2	1.86	0.41
42:q:446:THR:OG1	42:q:447:GLU:N	2.53	0.41
43:r:212:LEU:HB2	43:r:214:VAL:HG23	2.02	0.41
45:t:211:ARG:NE	45:t:322:ASN:OD1	2.49	0.41
45:t:215:ILE:HD11	45:t:224:PRO:HB2	2.01	0.41
48:y:229:PRO:HD2	48:y:232:ILE:HG13	2.03	0.41
1:1:837:A:OP2	41:p:4:ARG:NE	2.46	0.41
1:1:1306:G:O2'	1:1:1307:G:H5''	2.20	0.41
1:1:1927:G:P	41:p:5:THR:HG23	2.61	0.41
1:1:2113:A:O2'	1:1:2114:C:H5'	2.20	0.41
2:2:149:A:H2'	2:2:150:G:C8	2.55	0.41
5:B:135:ALA:O	5:B:138:ALA:HB2	2.21	0.41
11:K:205:THR:HA	11:K:206:PRO:HD3	1.95	0.41
11:K:268:GLU:HA	11:K:271:ILE:HG12	2.03	0.41
12:L:58:VAL:HG21	12:L:72:GLY:HA3	2.02	0.41
26:Z:60:LYS:HA	26:Z:60:LYS:HD2	1.78	0.41
32:f:15:SER:HA	32:f:94:PHE:CE1	2.56	0.41
39:n:142:PHE:HE2	39:n:218:MET:HG2	1.86	0.41
40:o:93:ILE:HD11	40:o:145:ALA:HA	2.02	0.41
43:r:7:ILE:HD13	43:r:7:ILE:HA	1.91	0.41
46:u:18:GLY:HA3	46:u:31:PHE:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:156:G:OP2	35:i:25:LYS:HB3	2.20	0.41
1:1:393:U:H2'	1:1:394:G:O4'	2.21	0.41
1:1:448:U:H3	1:1:487:U:H1'	1.86	0.41
1:1:968:G:H2'	1:1:969:C:H6	1.85	0.41
1:1:1135:A:H2'	1:1:1136:A:C8	2.56	0.41
1:1:1503:A:H2'	1:1:1504:A:H8	1.85	0.41
1:1:1759:C:H5'	1:1:1760:A:OP2	2.21	0.41
1:1:1927:G:O5'	41:p:5:THR:HG23	2.21	0.41
1:1:2161:G:H2'	1:1:2162:U:H6	1.86	0.41
1:1:2412:G:C4	1:1:2413:A:C8	3.09	0.41
1:1:2769:A:H2'	1:1:2770:G:H4'	2.03	0.41
1:1:2929:C:H2'	1:1:2930:A:O4'	2.20	0.41
5:B:103:THR:OG1	5:B:150:ARG:HD2	2.20	0.41
7:E:60:ASP:OD1	7:E:62:THR:OG1	2.38	0.41
9:G:192:GLN:O	39:n:96:ARG:NH2	2.48	0.41
11:K:256:PRO:O	11:K:260:VAL:HG12	2.20	0.41
28:b:135:ARG:NH2	43:r:254:CYS:HB3	2.35	0.41
28:b:211:TYR:HB3	28:b:216:PHE:CE1	2.56	0.41
33:g:24:LYS:HE3	33:g:24:LYS:HB2	1.93	0.41
37:k:64:LYS:HE3	42:q:354:ILE:HG21	2.02	0.41
39:n:415:PRO:HD3	42:q:407:ARG:NH1	2.36	0.41
45:t:97:LYS:HE3	45:t:99:PHE:CE1	2.56	0.41
46:u:1:MET:HE3	46:u:1:MET:HB2	1.88	0.41
47:w:250:ASP:OD2	47:w:253:LEU:HD23	2.21	0.41
47:w:778:ARG:O	47:w:782:LYS:HG3	2.21	0.41
1:1:1951:C:H2'	1:1:1952:G:O4'	2.20	0.41
1:1:2880:U:H2'	1:1:2881:C:O4'	2.21	0.41
1:1:3027:A:H8	28:b:208:HIS:CD2	2.39	0.41
1:1:3395:G:N2	1:1:3396:U:O4	2.46	0.41
4:A:65:ASP:HB3	4:A:68:LYS:O	2.21	0.41
5:B:294:GLY:HA2	5:B:359:ILE:HD12	2.03	0.41
5:B:312:VAL:HG12	5:B:313:HIS:ND1	2.35	0.41
9:G:208:GLU:H	9:G:208:GLU:HG2	1.66	0.41
10:H:47:LYS:HG2	13:M:7:VAL:HB	2.03	0.41
22:V:108:GLU:HA	22:V:128:ARG:HG3	2.03	0.41
23:W:174:LYS:HE2	23:W:174:LYS:HB2	1.90	0.41
45:t:100:ILE:HD11	45:t:133:THR:HG21	2.03	0.41
1:1:180:C:H2'	1:1:181:U:H6	1.86	0.40
1:1:423:A:H2'	1:1:424:G:O4'	2.21	0.40
1:1:675:C:O2'	1:1:679:U:OP1	2.37	0.40
1:1:2371:G:N3	1:1:2371:G:H2'	2.36	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:126:LYS:HB2	5:B:128:LYS:HG2	2.03	0.40
26:Z:22:LYS:NZ	26:Z:129:TRP:O	2.46	0.40
35:i:53:TYR:HA	35:i:56:ARG:HG2	2.03	0.40
41:p:80:ARG:NH2	47:w:395:ILE:HA	2.36	0.40
42:q:391:ASP:OD1	42:q:391:ASP:N	2.54	0.40
46:u:49:LEU:HD23	46:u:49:LEU:HA	1.86	0.40
1:1:173:G:O6	1:1:245:U:C4	2.74	0.40
1:1:275:U:H2'	1:1:276:U:C6	2.56	0.40
1:1:449:U:H2'	1:1:450:G:C4	2.56	0.40
1:1:831:G:O2'	1:1:1864:A:N3	2.50	0.40
1:1:848:A:C5	1:1:849:C:H1'	2.57	0.40
1:1:1120:A:H2'	1:1:1121:U:H6	1.85	0.40
1:1:1270:A:OP2	43:r:12:LYS:HE3	2.20	0.40
1:1:1275:C:H2'	1:1:1276:U:O4'	2.21	0.40
1:1:2394:G:H2'	1:1:2395:G:C8	2.57	0.40
1:1:2411:U:H2'	1:1:2412:G:H8	1.83	0.40
1:1:2781:U:H2'	1:1:2782:U:C6	2.56	0.40
23:W:155:VAL:HG13	23:W:156:PRO:HD2	2.02	0.40
45:t:205:ARG:HG2	45:t:251:ILE:HG21	2.03	0.40
1:1:115:A:H2'	1:1:265:A:N3	2.37	0.40
1:1:467:U:O2'	1:1:468:G:O5'	2.37	0.40
1:1:616:G:H2'	1:1:617:G:C8	2.56	0.40
1:1:885:U:O3'	1:1:1851:G:H4'	2.22	0.40
1:1:1122:U:H2'	1:1:1123:U:H6	1.87	0.40
1:1:1258:U:O5'	23:W:57:ARG:NH1	2.55	0.40
1:1:1456:A:N1	1:1:1476:G:O2'	2.46	0.40
1:1:2162:U:H2'	1:1:2163:C:O4'	2.21	0.40
9:G:223:ALA:O	9:G:227:ASP:HB2	2.21	0.40
18:R:11:ALA:CB	18:R:22:VAL:HG11	2.51	0.40
23:W:25:ARG:O	23:W:29:GLU:HG2	2.21	0.40
39:n:125:PHE:N	39:n:126:PRO:HD2	2.37	0.40
1:1:35:A:H2'	1:1:36:C:H6	1.86	0.40
1:1:245:U:H2'	1:1:246:U:C6	2.56	0.40
1:1:271:C:H2'	1:1:272:G:O4'	2.21	0.40
1:1:784:A:C6	17:Q:93:ILE:HG22	2.56	0.40
1:1:1190:A:O2'	1:1:1193:A:OP2	2.39	0.40
1:1:1624:G:O2'	1:1:1643:A:N1	2.51	0.40
1:1:1729:A:C6	29:c:49:PRO:HD3	2.55	0.40
1:1:2371:G:N7	44:s:17:GLU:HG3	2.36	0.40
1:1:2947:G:H2'	1:1:2948:C:C6	2.57	0.40
1:1:3284:G:H2'	1:1:3285:C:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:115:ASN:OD1	4:A:128:ARG:HD2	2.21	0.40
5:B:57:VAL:HG22	5:B:73:VAL:HG12	2.03	0.40
13:M:40:ASP:OD1	13:M:43:LYS:N	2.52	0.40
18:R:151:ARG:HG2	18:R:155:LEU:HD13	2.03	0.40
26:Z:27:LYS:HZ1	26:Z:97:SER:CB	2.35	0.40
28:b:392:ASP:H	28:b:395:ARG:HH11	1.69	0.40
28:b:424:ASP:HB3	28:b:427:TRP:CD2	2.56	0.40
35:i:4:LYS:O	35:i:16:LYS:NZ	2.35	0.40
43:r:186:HIS:HD2	43:r:259:LEU:HD23	1.86	0.40
43:r:245:VAL:HA	43:r:257:ALA:HA	2.04	0.40
1:1:916:G:N3	1:1:916:G:H2'	2.37	0.40
1:1:1675:G:H2'	1:1:1676:A:H8	1.86	0.40
1:1:1810:A:H2'	1:1:1811:G:C8	2.57	0.40
1:1:2152:A:H2'	1:1:2153:U:C6	2.56	0.40
1:1:2359:C:OP1	47:w:803:LYS:HE2	2.21	0.40
1:1:3016:A:H2'	1:1:3017:A:C8	2.56	0.40
1:1:3188:G:P	10:H:22:SER:OG	2.79	0.40
3:6:9:A:H2'	3:6:10:A:C8	2.57	0.40
19:S:77:VAL:HG13	19:S:126:VAL:HG22	2.03	0.40
24:X:24:LEU:HD13	24:X:24:LEU:HA	1.95	0.40
28:b:284:MET:HE3	28:b:284:MET:HB2	1.99	0.40
40:o:95:VAL:HG22	40:o:164:VAL:HG22	2.03	0.40
40:o:193:VAL:HG23	40:o:194:LYS:N	2.36	0.40
45:t:314:ILE:HD12	45:t:314:ILE:HA	1.93	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
4	A	174/254 (68%)	164 (94%)	10 (6%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	B	336/387 (87%)	328 (98%)	8 (2%)	0	100	100
6	C	359/362 (99%)	351 (98%)	8 (2%)	0	100	100
7	E	152/176 (86%)	149 (98%)	3 (2%)	0	100	100
8	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
9	G	181/256 (71%)	179 (99%)	2 (1%)	0	100	100
10	H	189/191 (99%)	185 (98%)	4 (2%)	0	100	100
11	K	252/376 (67%)	244 (97%)	8 (3%)	0	100	100
12	L	180/199 (90%)	176 (98%)	4 (2%)	0	100	100
13	M	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
14	N	183/204 (90%)	176 (96%)	7 (4%)	0	100	100
15	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
16	P	164/184 (89%)	157 (96%)	7 (4%)	0	100	100
17	Q	144/186 (77%)	140 (97%)	4 (3%)	0	100	100
18	R	154/189 (82%)	152 (99%)	2 (1%)	0	100	100
19	S	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
20	T	49/160 (31%)	48 (98%)	1 (2%)	0	100	100
21	U	104/121 (86%)	96 (92%)	8 (8%)	0	100	100
22	V	134/137 (98%)	128 (96%)	6 (4%)	0	100	100
23	W	230/236 (98%)	223 (97%)	7 (3%)	0	100	100
24	X	136/142 (96%)	133 (98%)	3 (2%)	0	100	100
25	Y	124/127 (98%)	124 (100%)	0	0	100	100
26	Z	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
27	a	90/149 (60%)	83 (92%)	7 (8%)	0	100	100
28	b	542/647 (84%)	517 (95%)	25 (5%)	0	100	100
29	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
30	d	105/113 (93%)	104 (99%)	1 (1%)	0	100	100
31	e	124/130 (95%)	121 (98%)	3 (2%)	0	100	100
32	f	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
33	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
34	h	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
35	i	97/100 (97%)	95 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	j	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
37	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
38	m	7/9 (78%)	7 (100%)	0	0	100	100
39	n	362/605 (60%)	349 (96%)	13 (4%)	0	100	100
40	o	131/220 (60%)	119 (91%)	12 (9%)	0	100	100
41	p	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
42	q	183/455 (40%)	174 (95%)	9 (5%)	0	100	100
43	r	156/261 (60%)	150 (96%)	6 (4%)	0	100	100
44	s	34/520 (6%)	34 (100%)	0	0	100	100
45	t	283/322 (88%)	274 (97%)	9 (3%)	0	100	100
46	u	139/199 (70%)	137 (99%)	2 (1%)	0	100	100
47	w	311/841 (37%)	300 (96%)	11 (4%)	0	100	100
48	y	242/245 (99%)	232 (96%)	10 (4%)	0	100	100
49	z	53/106 (50%)	53 (100%)	0	0	100	100
All	All	7630/10409 (73%)	7395 (97%)	235 (3%)	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	
4	A	138/196 (70%)	136 (99%)	2 (1%)	59	75
5	B	284/323 (88%)	280 (99%)	4 (1%)	59	75
6	C	288/289 (100%)	286 (99%)	2 (1%)	76	86
7	E	134/153 (88%)	133 (99%)	1 (1%)	76	86
8	F	186/205 (91%)	184 (99%)	2 (1%)	65	79
9	G	155/208 (74%)	152 (98%)	3 (2%)	50	70
10	H	171/171 (100%)	169 (99%)	2 (1%)	63	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	236/346 (68%)	229 (97%)	7 (3%)	36	60
12	L	144/159 (91%)	143 (99%)	1 (1%)	76	86
13	M	108/109 (99%)	107 (99%)	1 (1%)	70	82
14	N	163/176 (93%)	162 (99%)	1 (1%)	78	88
15	O	160/162 (99%)	160 (100%)	0	100	100
16	P	137/146 (94%)	137 (100%)	0	100	100
17	Q	121/151 (80%)	120 (99%)	1 (1%)	73	84
18	R	129/154 (84%)	129 (100%)	0	100	100
19	S	155/156 (99%)	155 (100%)	0	100	100
20	T	45/137 (33%)	44 (98%)	1 (2%)	45	67
21	U	93/107 (87%)	93 (100%)	0	100	100
22	V	104/105 (99%)	103 (99%)	1 (1%)	68	81
23	W	209/213 (98%)	205 (98%)	4 (2%)	50	70
24	X	115/118 (98%)	112 (97%)	3 (3%)	40	63
25	Y	109/110 (99%)	108 (99%)	1 (1%)	70	82
26	Z	115/116 (99%)	114 (99%)	1 (1%)	70	82
27	a	76/119 (64%)	76 (100%)	0	100	100
28	b	490/573 (86%)	484 (99%)	6 (1%)	63	78
29	c	81/88 (92%)	78 (96%)	3 (4%)	30	54
30	d	94/97 (97%)	94 (100%)	0	100	100
31	e	108/111 (97%)	108 (100%)	0	100	100
32	f	90/91 (99%)	90 (100%)	0	100	100
33	g	95/103 (92%)	95 (100%)	0	100	100
34	h	104/105 (99%)	104 (100%)	0	100	100
35	i	81/82 (99%)	80 (99%)	1 (1%)	63	78
36	j	70/71 (99%)	70 (100%)	0	100	100
37	k	68/69 (99%)	67 (98%)	1 (2%)	57	74
38	m	8/8 (100%)	8 (100%)	0	100	100
39	n	331/548 (60%)	330 (100%)	1 (0%)	86	93
40	o	118/199 (59%)	115 (98%)	3 (2%)	42	64
41	p	71/72 (99%)	70 (99%)	1 (1%)	59	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	q	177/420 (42%)	175 (99%)	2 (1%)	65	79
43	r	146/229 (64%)	145 (99%)	1 (1%)	76	86
44	s	32/445 (7%)	32 (100%)	0	100	100
45	t	256/287 (89%)	252 (98%)	4 (2%)	55	73
46	u	126/180 (70%)	125 (99%)	1 (1%)	73	84
47	w	282/745 (38%)	280 (99%)	2 (1%)	76	86
48	y	210/211 (100%)	210 (100%)	0	100	100
49	z	48/95 (50%)	48 (100%)	0	100	100
All	All	6661/8958 (74%)	6597 (99%)	64 (1%)	65	81

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	107	VAL
4	A	168	VAL
5	B	162	VAL
5	B	210	GLU
5	B	302	LYS
5	B	324	VAL
6	C	272	VAL
6	C	339	LEU
7	E	146	ILE
8	F	84	VAL
8	F	129	LEU
9	G	65	LEU
9	G	132	VAL
9	G	188	THR
10	H	35	THR
10	H	55	VAL
11	K	97	LEU
11	K	129	ASP
11	K	135	VAL
11	K	155	ILE
11	K	165	LYS
11	K	232	ASN
11	K	295	GLN
12	L	93	ILE
13	M	64	VAL
14	N	18	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	Q	13	SER
20	T	147	VAL
22	V	91	VAL
23	W	66	ILE
23	W	109	VAL
23	W	141	ILE
23	W	202	ILE
24	X	24	LEU
24	X	74	LYS
24	X	99	VAL
25	Y	105	VAL
26	Z	14	VAL
28	b	206	VAL
28	b	264	ILE
28	b	286	VAL
28	b	315	VAL
28	b	337	GLU
28	b	434	GLU
29	c	17	VAL
29	c	74	ASN
29	c	89	VAL
35	i	26	ILE
37	k	31	LEU
39	n	139	LEU
40	o	102	PHE
40	o	173	ILE
40	o	185	VAL
41	p	60	CYS
42	q	227	TYR
42	q	395	GLU
43	r	151	ILE
45	t	138	LYS
45	t	183	VAL
45	t	257	MET
45	t	306	THR
46	u	90	LEU
47	w	295	GLN
47	w	387	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	47	GLN
5	B	11	HIS
6	C	87	GLN
6	C	116	ASN
6	C	237	GLN
8	F	157	ASN
8	F	172	ASN
8	F	200	ASN
10	H	51	GLN
10	H	96	HIS
10	H	157	ASN
10	H	169	ASN
11	K	85	ASN
11	K	104	HIS
11	K	225	ASN
11	K	284	ASN
13	M	56	GLN
13	M	105	GLN
14	N	138	GLN
15	O	31	GLN
16	P	50	GLN
16	P	54	HIS
18	R	36	ASN
19	S	88	HIS
21	U	101	ASN
23	W	199	GLN
23	W	205	GLN
26	Z	78	ASN
26	Z	122	HIS
27	a	65	GLN
28	b	90	HIS
28	b	500	GLN
30	d	43	HIS
31	e	49	ASN
33	g	69	HIS
34	h	68	GLN
34	h	99	GLN
35	i	92	ASN
36	j	13	ASN
36	j	20	ASN
36	j	69	HIS
39	n	69	GLN
39	n	395	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
40	o	103	HIS
40	o	125	ASN
40	o	199	ASN
41	p	25	GLN
42	q	325	ASN
43	r	10	HIS
43	r	68	HIS
45	t	269	GLN
45	t	291	GLN
46	u	101	GLN
46	u	115	ASN
47	w	295	GLN
48	y	50	HIS
48	y	170	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2708/3396 (79%)	494 (18%)	7 (0%)
2	2	157/158 (99%)	23 (14%)	0
3	6	56/87 (64%)	21 (37%)	0
All	All	2921/3641 (80%)	538 (18%)	7 (0%)

All (538) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	14	U
1	1	16	A
1	1	40	A
1	1	42	C
1	1	43	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	75	G
1	1	77	A
1	1	83	U
1	1	86	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	93	C
1	1	94	G
1	1	109	A
1	1	110	G
1	1	116	A
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G
1	1	156	G
1	1	157	A
1	1	166	C
1	1	172	G
1	1	173	G
1	1	182	U
1	1	187	A
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	213	A
1	1	218	G
1	1	219	A
1	1	220	G
1	1	238	A
1	1	243	G
1	1	249	U
1	1	250	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	269	G
1	1	285	A
1	1	295	A
1	1	305	U
1	1	306	A
1	1	307	A
1	1	323	A
1	1	329	U
1	1	351	A
1	1	376	G
1	1	398	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	399	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	421	G
1	1	422	A
1	1	439	C
1	1	440	A
1	1	451	U
1	1	454	C
1	1	457	C
1	1	463	C
1	1	464	U
1	1	465	U
1	1	466	G
1	1	467	U
1	1	468	G
1	1	469	G
1	1	478	A
1	1	479	U
1	1	480	C
1	1	481	U
1	1	482	C
1	1	485	A
1	1	486	U
1	1	487	U
1	1	488	U
1	1	520	U
1	1	521	A
1	1	535	G
1	1	543	C
1	1	544	C
1	1	545	U
1	1	547	G
1	1	548	G
1	1	550	A
1	1	555	U
1	1	557	A
1	1	558	U
1	1	559	A
1	1	569	A
1	1	579	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	589	A
1	1	592	A
1	1	604	G
1	1	611	A
1	1	612	U
1	1	620	U
1	1	621	A
1	1	636	C
1	1	637	C
1	1	642	U
1	1	643	U
1	1	644	G
1	1	660	A
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A
1	1	712	G
1	1	715	A
1	1	719	U
1	1	734	C
1	1	735	A
1	1	736	A
1	1	737	G
1	1	760	G
1	1	761	A
1	1	762	U
1	1	764	U
1	1	765	C
1	1	766	U
1	1	767	U
1	1	776	U
1	1	777	U
1	1	781	G
1	1	785	G
1	1	808	A
1	1	817	A
1	1	830	A
1	1	847	A
1	1	861	C
1	1	872	U
1	1	873	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	874	U
1	1	875	G
1	1	878	G
1	1	881	C
1	1	907	G
1	1	909	G
1	1	914	A
1	1	921	A
1	1	922	U
1	1	923	C
1	1	924	G
1	1	925	A
1	1	936	A
1	1	944	C
1	1	954	U
1	1	957	C
1	1	958	C
1	1	960	U
1	1	974	G
1	1	978	G
1	1	980	A
1	1	982	C
1	1	991	G
1	1	993	G
1	1	994	G
1	1	996	A
1	1	998	A
1	1	999	G
1	1	1000	C
1	1	1002	A
1	1	1003	A
1	1	1048	A
1	1	1049	C
1	1	1051	U
1	1	1055	A
1	1	1056	U
1	1	1057	A
1	1	1105	A
1	1	1110	U
1	1	1116	G
1	1	1117	G
1	1	1129	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1132	C
1	1	1138	U
1	1	1143	A
1	1	1145	G
1	1	1153	A
1	1	1155	C
1	1	1159	A
1	1	1161	G
1	1	1180	A
1	1	1181	U
1	1	1182	A
1	1	1189	C
1	1	1192	C
1	1	1193	A
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1201	C
1	1	1204	A
1	1	1217	A
1	1	1220	U
1	1	1221	A
1	1	1222	G
1	1	1223	A
1	1	1227	C
1	1	1235	U
1	1	1239	C
1	1	1240	A
1	1	1242	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1251	A
1	1	1252	A
1	1	1254	C
1	1	1258	U
1	1	1260	A
1	1	1262	G
1	1	1263	A
1	1	1271	A
1	1	1272	C
1	1	1277	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1278	A
1	1	1286	A
1	1	1287	A
1	1	1302	A
1	1	1303	A
1	1	1304	A
1	1	1305	U
1	1	1307	G
1	1	1309	U
1	1	1313	G
1	1	1330	A
1	1	1348	U
1	1	1357	G
1	1	1386	A
1	1	1399	A
1	1	1419	A
1	1	1421	G
1	1	1434	G
1	1	1437	C
1	1	1452	A
1	1	1455	U
1	1	1481	A
1	1	1482	A
1	1	1496	C
1	1	1503	A
1	1	1508	C
1	1	1539	A
1	1	1555	U
1	1	1556	C
1	1	1557	A
1	1	1560	G
1	1	1561	G
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1572	U
1	1	1573	G
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1583	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1587	A
1	1	1589	A
1	1	1593	A
1	1	1629	U
1	1	1639	C
1	1	1643	A
1	1	1647	A
1	1	1658	G
1	1	1684	U
1	1	1715	A
1	1	1724	U
1	1	1725	C
1	1	1730	G
1	1	1736	G
1	1	1741	A
1	1	1742	U
1	1	1750	A
1	1	1751	G
1	1	1752	A
1	1	1759	C
1	1	1760	A
1	1	1761	C
1	1	1762	C
1	1	1765	U
1	1	1766	G
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1796	G
1	1	1797	A
1	1	1810	A
1	1	1813	A
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1820	U
1	1	1821	U
1	1	1839	A
1	1	1842	A
1	1	1846	C
1	1	1849	C
1	1	1878	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1880	U
1	1	1906	G
1	1	1909	A
1	1	1952	G
1	1	1953	G
1	1	1955	U
1	1	1956	A
1	1	1959	G
1	1	1964	C
1	1	1966	U
1	1	1973	G
1	1	1974	A
1	1	2056	U
1	1	2079	G
1	1	2080	C
1	1	2081	U
1	1	2082	U
1	1	2083	G
1	1	2087	C
1	1	2088	A
1	1	2089	A
1	1	2090	U
1	1	2091	U
1	1	2092	A
1	1	2093	A
1	1	2112	U
1	1	2121	G
1	1	2122	G
1	1	2131	A
1	1	2140	U
1	1	2142	A
1	1	2158	A
1	1	2163	C
1	1	2167	A
1	1	2168	A
1	1	2169	G
1	1	2177	G
1	1	2187	G
1	1	2188	A
1	1	2329	C
1	1	2334	U
1	1	2336	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2347	U
1	1	2364	G
1	1	2373	A
1	1	2374	C
1	1	2375	G
1	1	2385	G
1	1	2388	U
1	1	2394	G
1	1	2412	G
1	1	2770	G
1	1	2771	U
1	1	2772	C
1	1	2777	G
1	1	2781	U
1	1	2785	A
1	1	2786	G
1	1	2788	C
1	1	2808	A
1	1	2816	G
1	1	2818	U
1	1	2819	A
1	1	2820	A
1	1	2821	C
1	1	2822	U
1	1	2824	G
1	1	2825	C
1	1	2826	U
1	1	2833	A
1	1	2834	G
1	1	2838	A
1	1	2842	U
1	1	2847	A
1	1	2848	G
1	1	2854	U
1	1	2855	U
1	1	2856	G
1	1	2858	U
1	1	2861	U
1	1	2863	G
1	1	2864	A
1	1	2865	U
1	1	2866	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2874	G
1	1	2875	U
1	1	2879	C
1	1	2880	U
1	1	2887	A
1	1	2889	C
1	1	2898	G
1	1	2899	C
1	1	2916	U
1	1	2918	G
1	1	2922	G
1	1	2926	A
1	1	2930	A
1	1	2935	U
1	1	2936	A
1	1	2941	A
1	1	2964	G
1	1	2967	A
1	1	2969	A
1	1	2970	C
1	1	2971	A
1	1	2976	A
1	1	2979	U
1	1	2980	U
1	1	2983	C
1	1	2990	G
1	1	2996	U
1	1	2997	G
1	1	3012	A
1	1	3022	G
1	1	3023	U
1	1	3032	A
1	1	3056	U
1	1	3059	G
1	1	3074	G
1	1	3078	U
1	1	3080	G
1	1	3086	A
1	1	3092	C
1	1	3093	C
1	1	3100	U
1	1	3102	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3151	U
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3165	A
1	1	3171	U
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3181	C
1	1	3187	A
1	1	3198	U
1	1	3207	U
1	1	3213	A
1	1	3215	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3224	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3256	G
1	1	3259	U
1	1	3260	G
1	1	3263	G
1	1	3270	U
1	1	3276	G
1	1	3279	A
1	1	3287	U
1	1	3289	G
1	1	3294	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	3295	A
1	1	3304	U
1	1	3313	U
1	1	3316	A
1	1	3319	U
1	1	3328	G
1	1	3341	U
1	1	3345	G
1	1	3352	U
1	1	3353	G
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3369	G
1	1	3375	A
1	1	3378	C
1	1	3389	U
2	2	13	A
2	2	34	U
2	2	35	C
2	2	59	A
2	2	62	C
2	2	63	G
2	2	75	G
2	2	77	A
2	2	79	A
2	2	80	A
2	2	82	U
2	2	84	C
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	104	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	125	U
2	2	126	A
2	2	151	C
3	6	4	U
3	6	5	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	6	6	U
3	6	7	C
3	6	8	A
3	6	13	U
3	6	14	U
3	6	15	C
3	6	16	U
3	6	23	U
3	6	33	U
3	6	34	A
3	6	43	A
3	6	47	A
3	6	52	G
3	6	54	A
3	6	56	U
3	6	58	G
3	6	230	A
3	6	231	A
3	6	232	A

All (7) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	456	U
1	1	480	C
1	1	761	A
1	1	956	U
1	1	1568	U
1	1	3121	U
1	1	3269	U

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

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

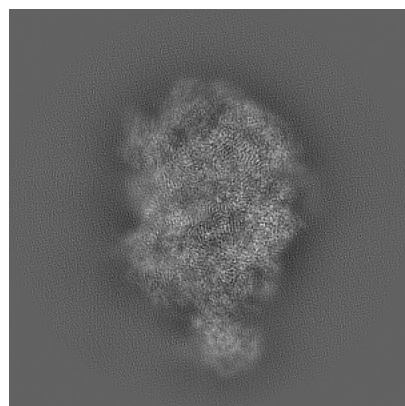
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26259. These allow visual inspection of the internal detail of the map and identification of artifacts.

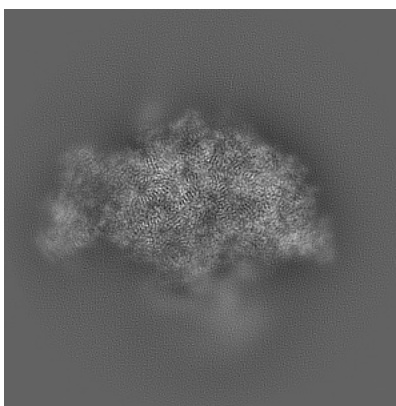
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

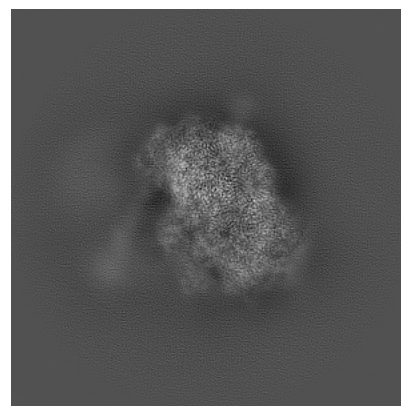
6.1.1 Primary map



X

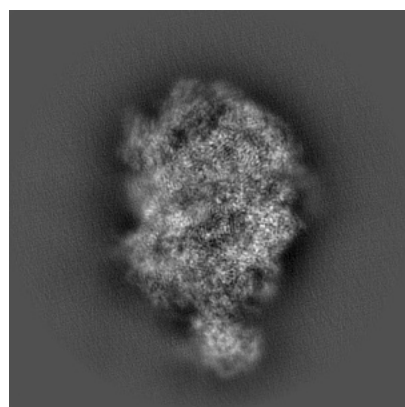


Y

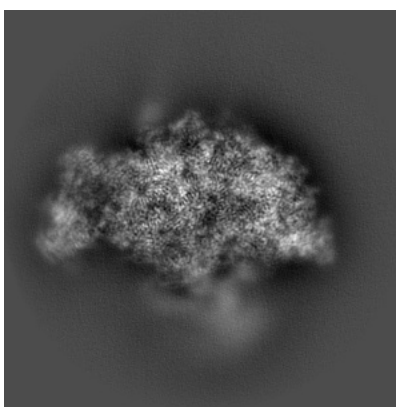


Z

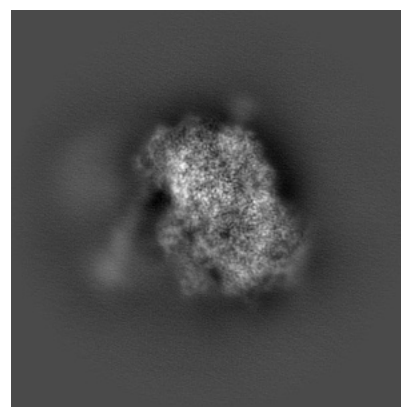
6.1.2 Raw map



X



Y

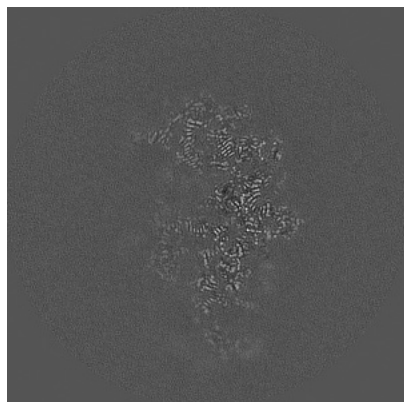


Z

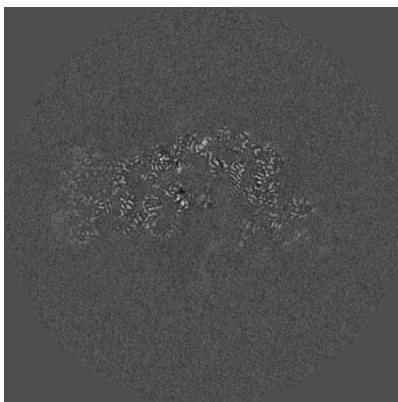
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

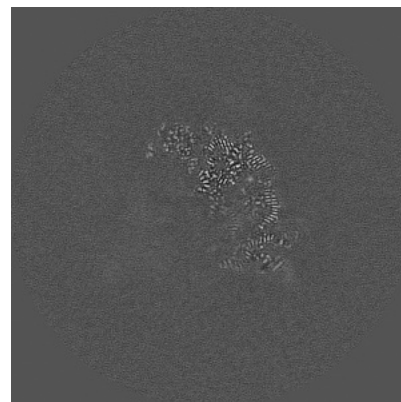
6.2.1 Primary map



X Index: 200

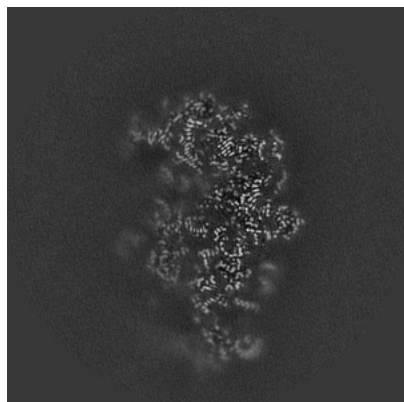


Y Index: 200

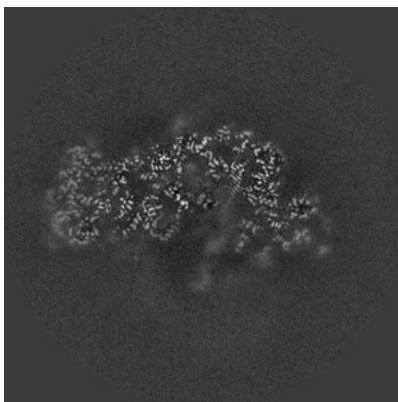


Z Index: 200

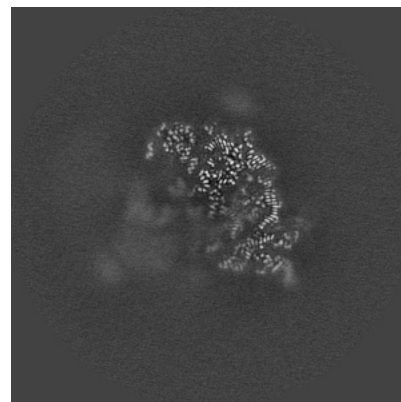
6.2.2 Raw map



X Index: 200



Y Index: 200

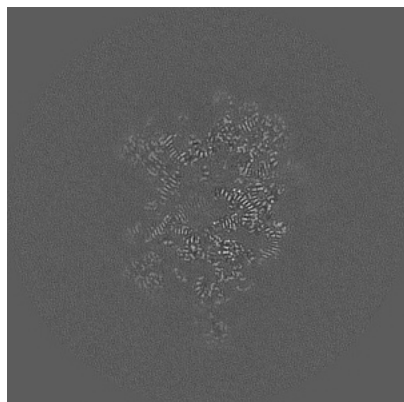


Z Index: 200

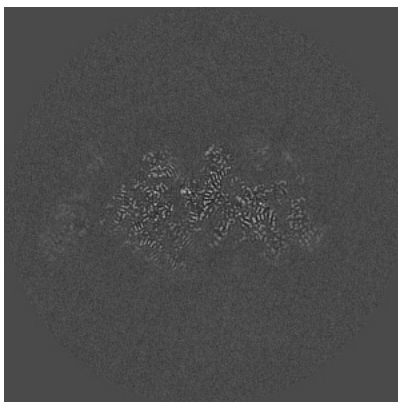
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

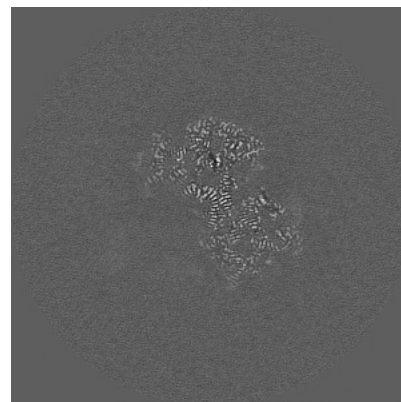
6.3.1 Primary map



X Index: 221

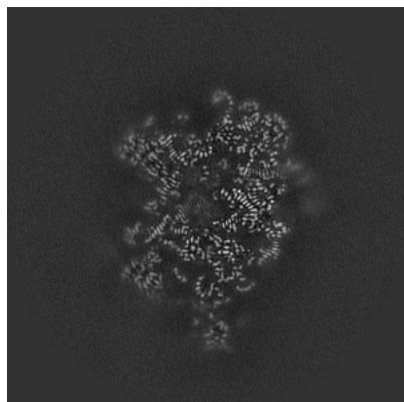


Y Index: 230

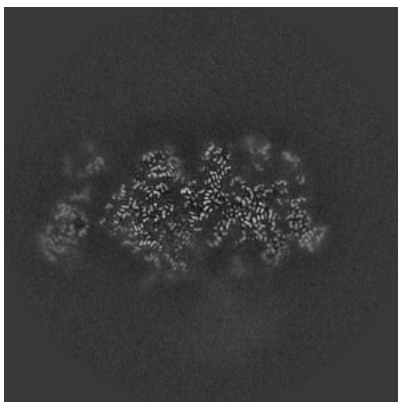


Z Index: 177

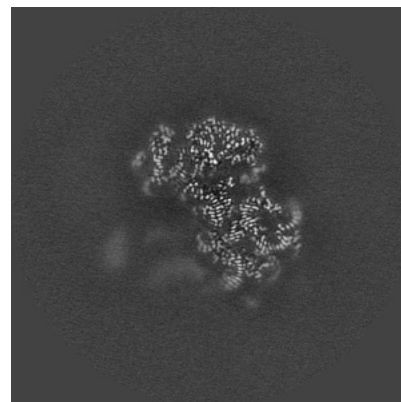
6.3.2 Raw map



X Index: 221



Y Index: 230

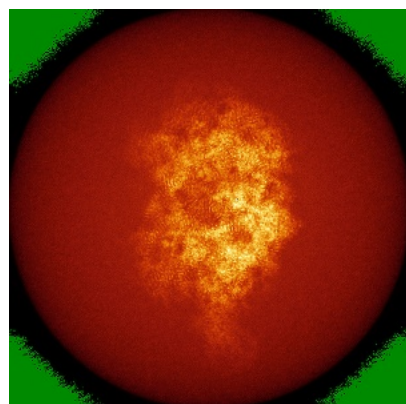


Z Index: 175

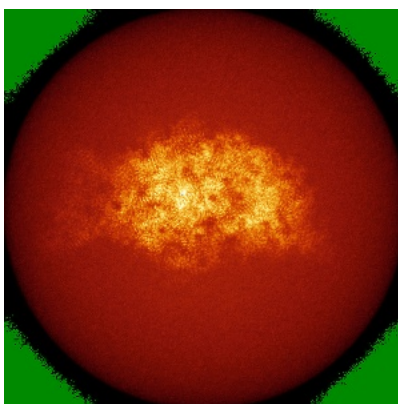
The images above show the largest variance slices of the map in three orthogonal directions.

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

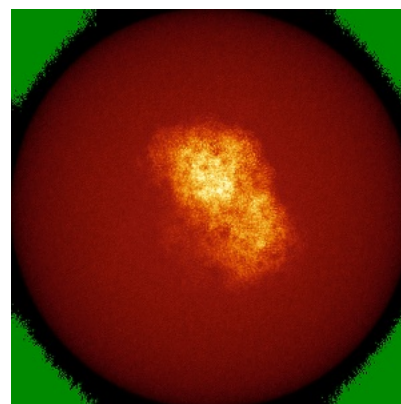
6.4.1 Primary map



X

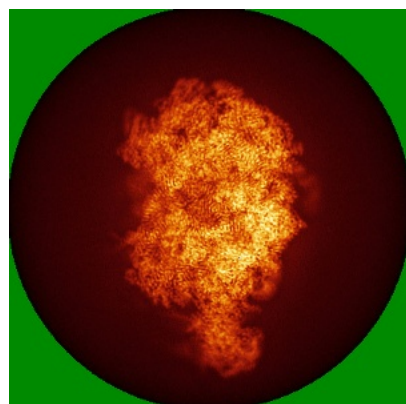


Y

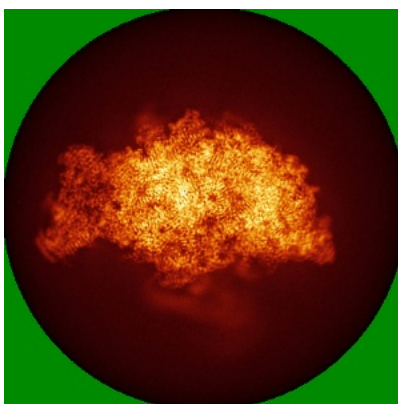


Z

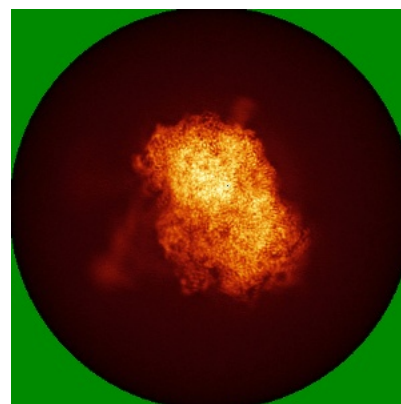
6.4.2 Raw map



X



Y

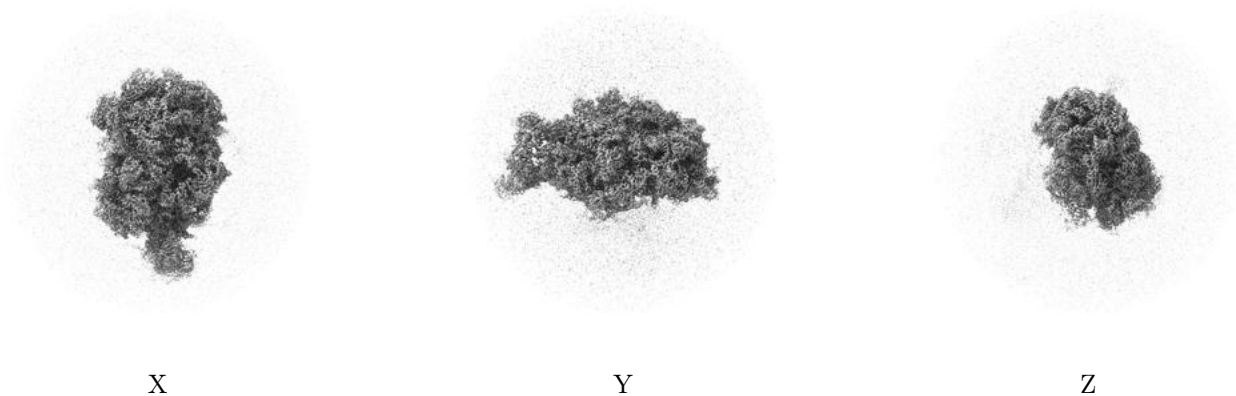


Z

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 0.0284. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

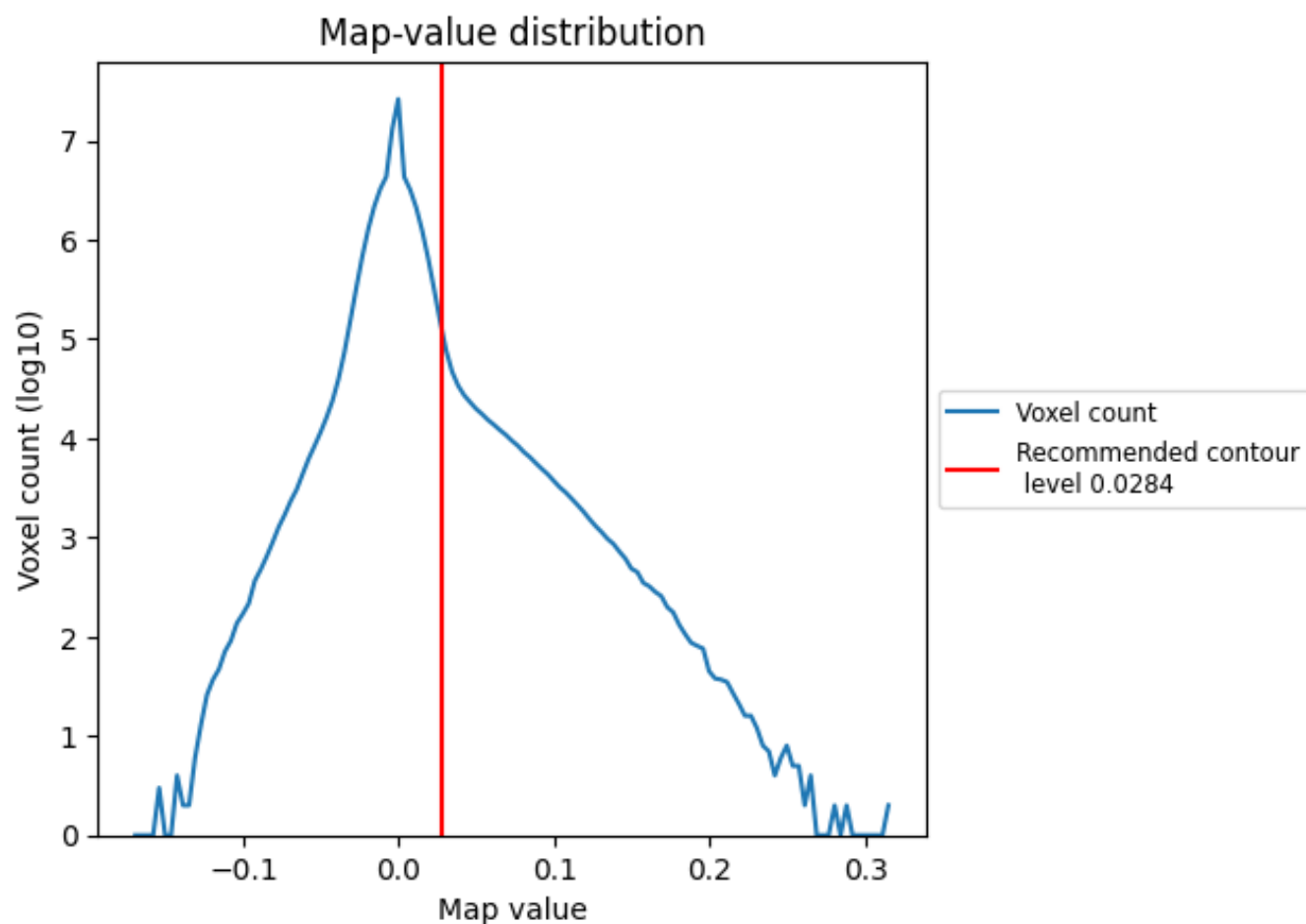
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

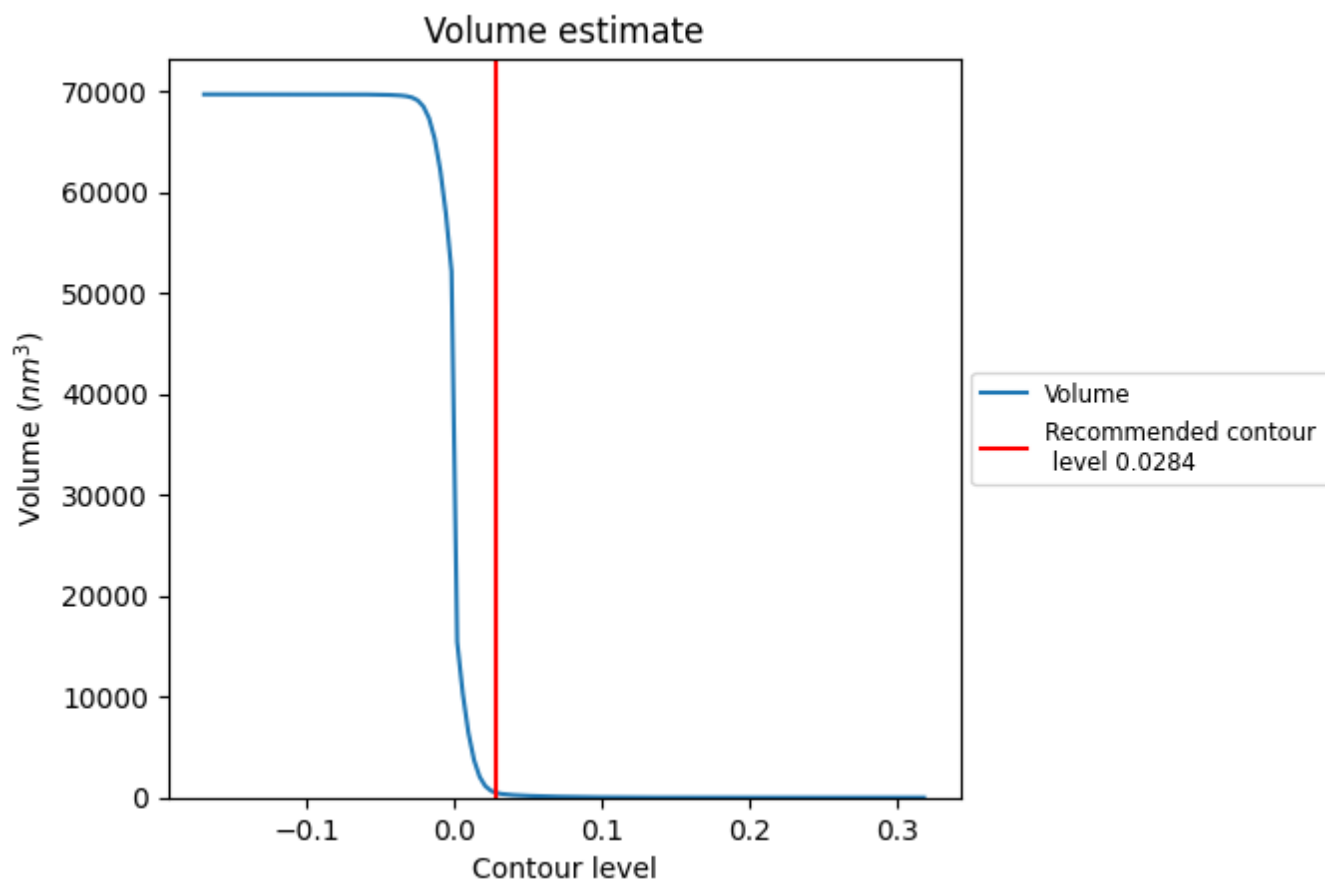
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

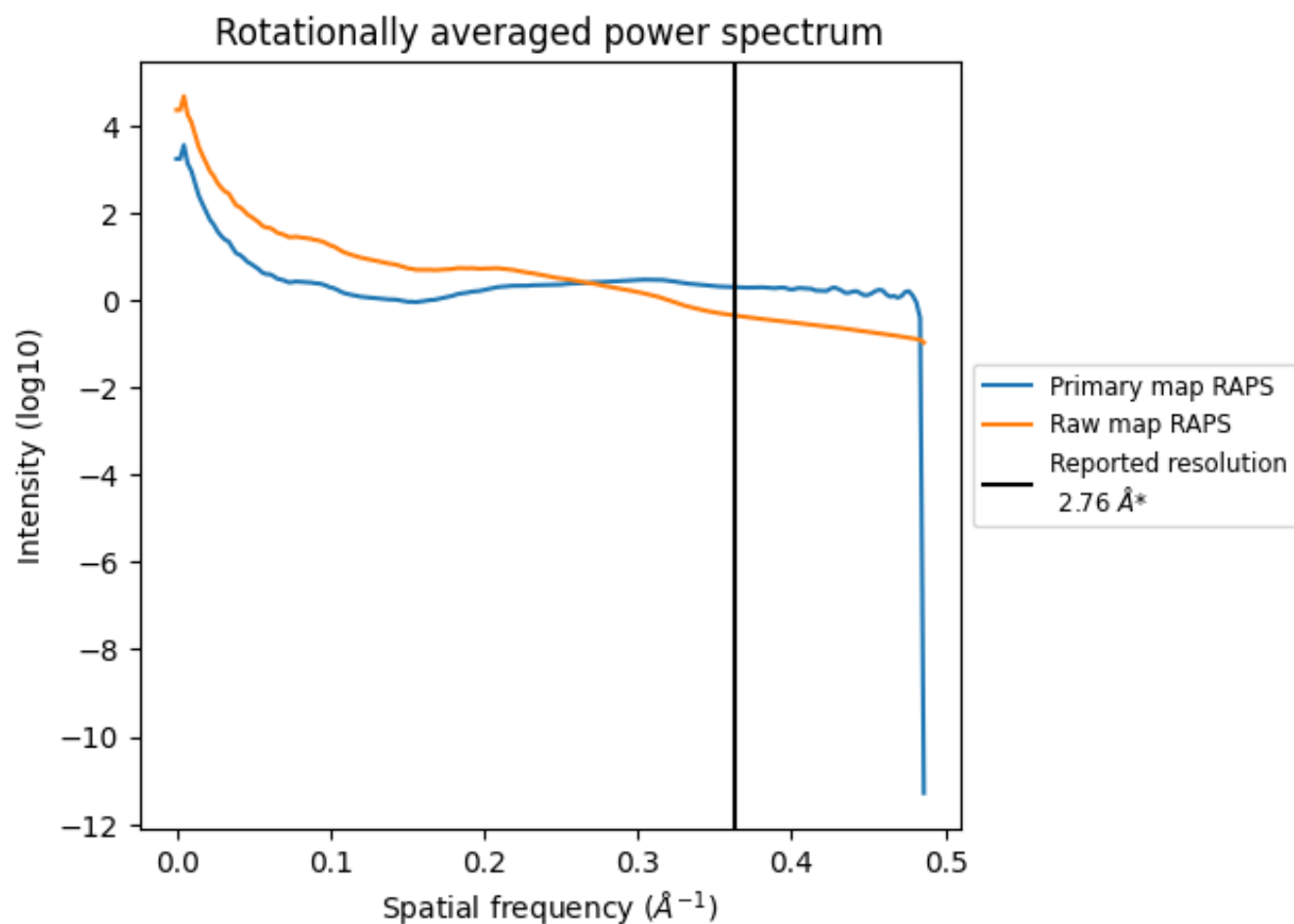
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 490 nm³; this corresponds to an approximate mass of 442 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 ⓘ

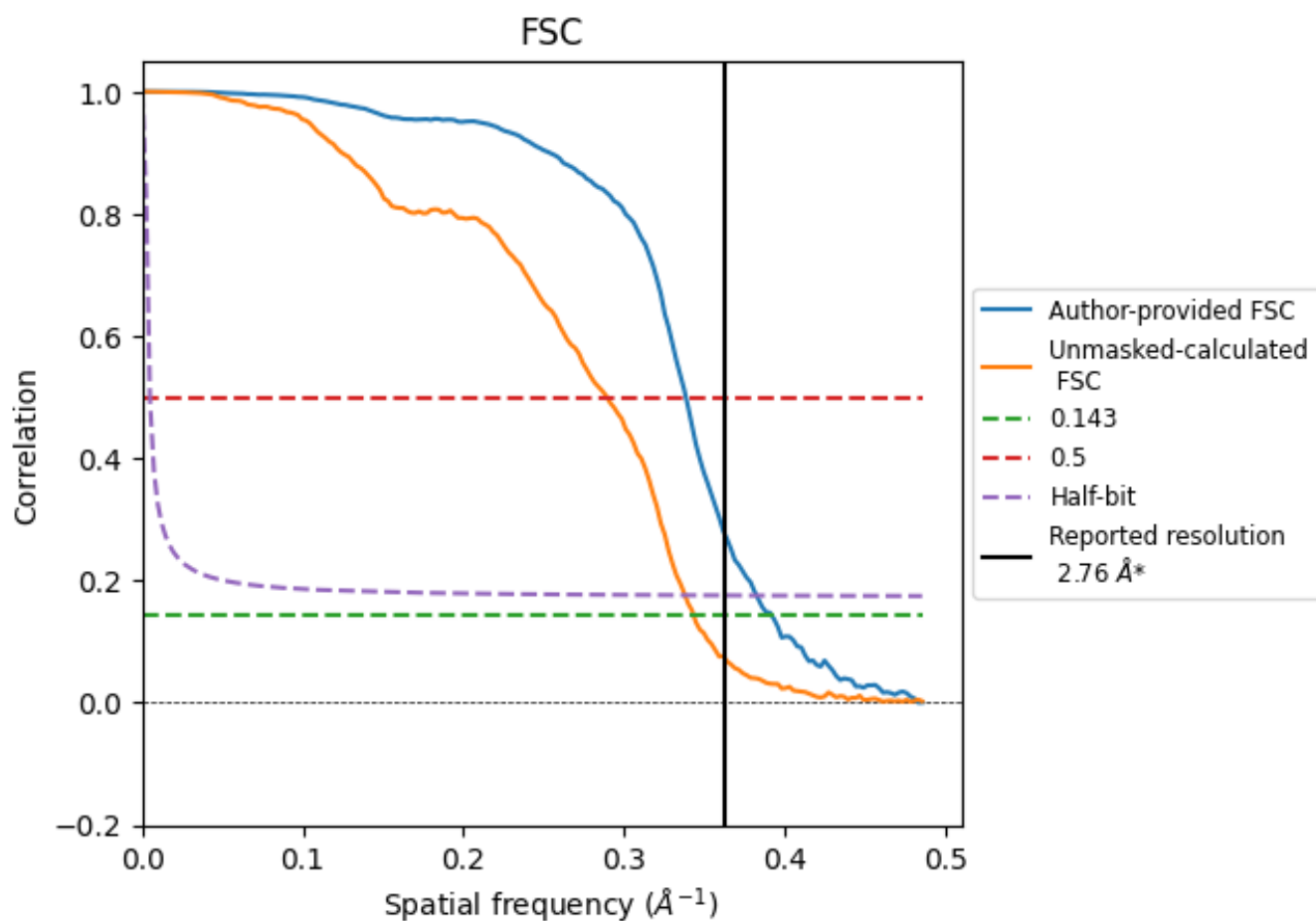


*Reported resolution corresponds to spatial frequency of 0.362 Å⁻¹

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 0.362 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

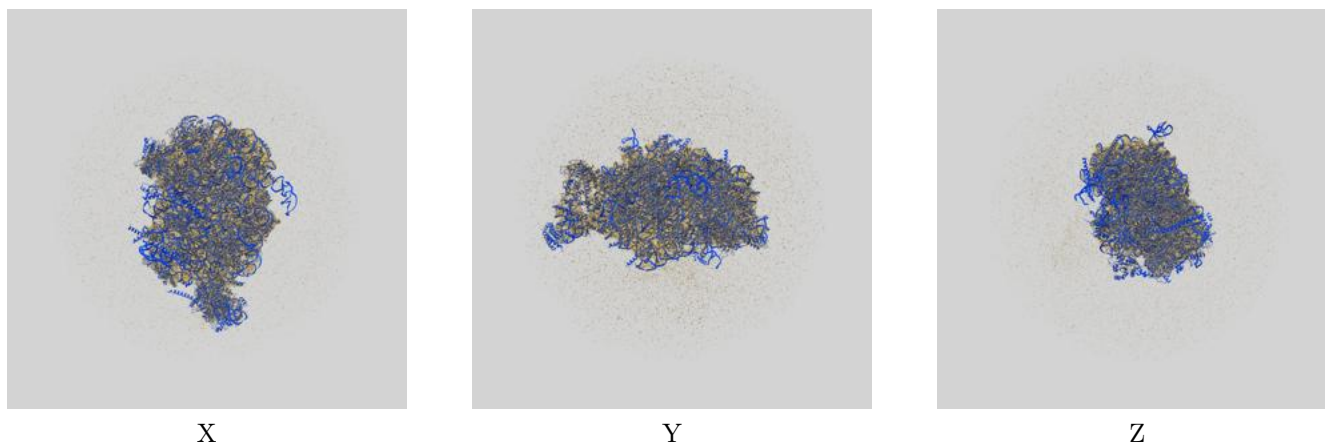
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.55	2.95	2.61
Unmasked-calculated*	2.91	3.45	2.96

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

9 Map-model fit [i](#)

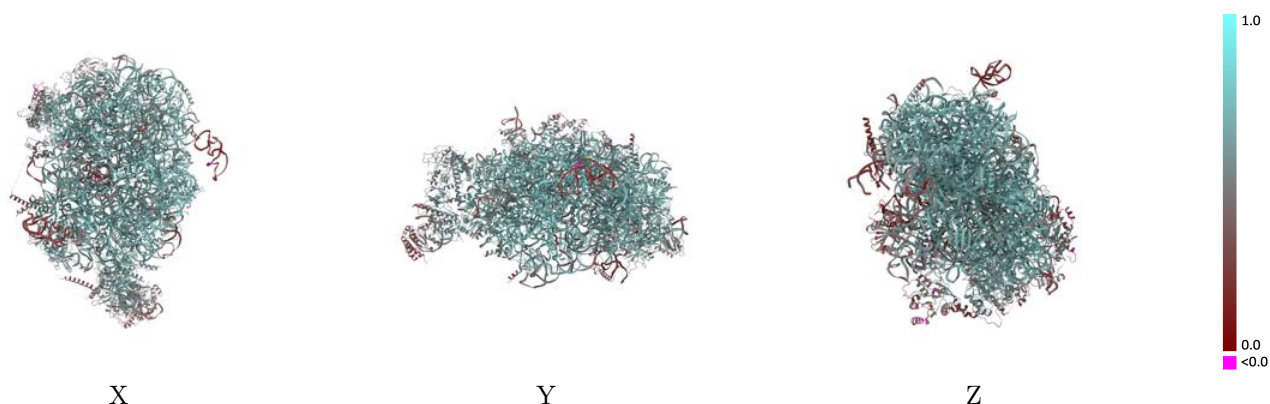
This section contains information regarding the fit between EMDB map EMD-26259 and PDB model 7U0H. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



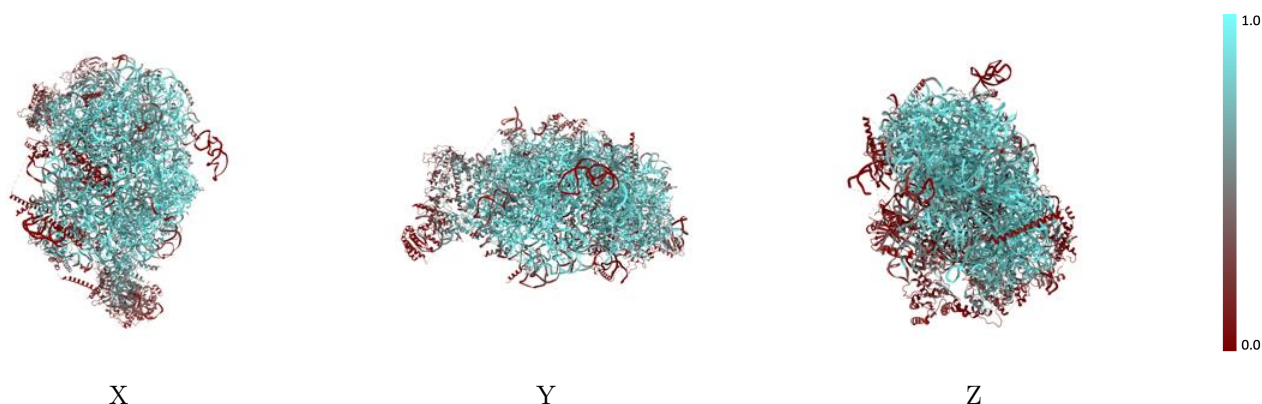
The images above show the 3D surface view of the map at the recommended contour level 0.0284 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



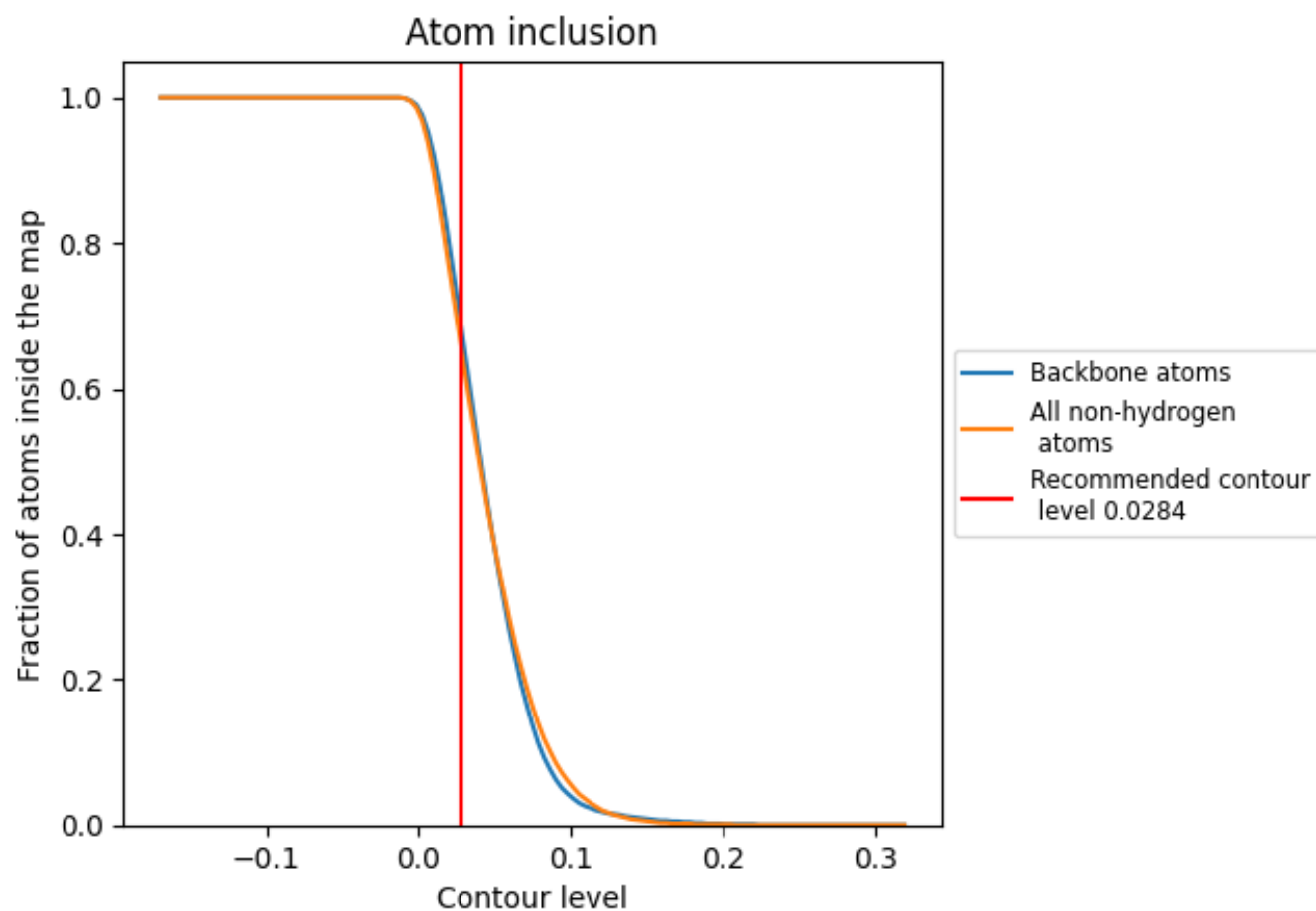
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0284).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 65% 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 (0.0284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6490	 0.5920
1	 0.7110	 0.5930
2	 0.8590	 0.6600
6	 0.4190	 0.4830
A	 0.4290	 0.5860
B	 0.8750	 0.6890
C	 0.8510	 0.6900
E	 0.7400	 0.6420
F	 0.8200	 0.6610
G	 0.7100	 0.6300
H	 0.7010	 0.6300
K	 0.1600	 0.4190
L	 0.6990	 0.6340
M	 0.8000	 0.6560
N	 0.9000	 0.7010
O	 0.8820	 0.6970
P	 0.8120	 0.6690
Q	 0.8110	 0.6560
R	 0.7660	 0.6530
S	 0.6580	 0.6090
T	 0.0070	 0.2750
U	 0.4290	 0.5210
V	 0.6660	 0.6340
W	 0.1950	 0.4470
X	 0.8140	 0.6770
Y	 0.8470	 0.6780
Z	 0.5760	 0.6080
a	 0.7330	 0.6410
b	 0.2800	 0.4730
c	 0.4800	 0.5610
d	 0.7730	 0.6540
e	 0.8790	 0.7000
f	 0.9430	 0.7160
g	 0.7630	 0.6470
h	 0.8020	 0.6690



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.4580	 0.5640
j	 0.7850	 0.6630
k	 0.5830	 0.6040
m	 0.0150	 0.3200
n	 0.5560	 0.5840
o	 0.3550	 0.4660
p	 0.5630	 0.6110
q	 0.1830	 0.4720
r	 0.3120	 0.4980
s	 0.4600	 0.6020
t	 0.3750	 0.5230
u	 0.6380	 0.6200
w	 0.1890	 0.4580
y	 0.5720	 0.5700
z	 0.0810	 0.5060