



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:02 AM UTC

PDB ID : 6R87 / pdb_00006r87
EMDB ID : EMD-4753
Title : Yeast Vms1 (Q295L)-60S ribosomal subunit complex (pre-state without Arb1)
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;
Neupert, W.; Beckmann, R.
Deposited on : 2019-03-31
Resolution : 3.40 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

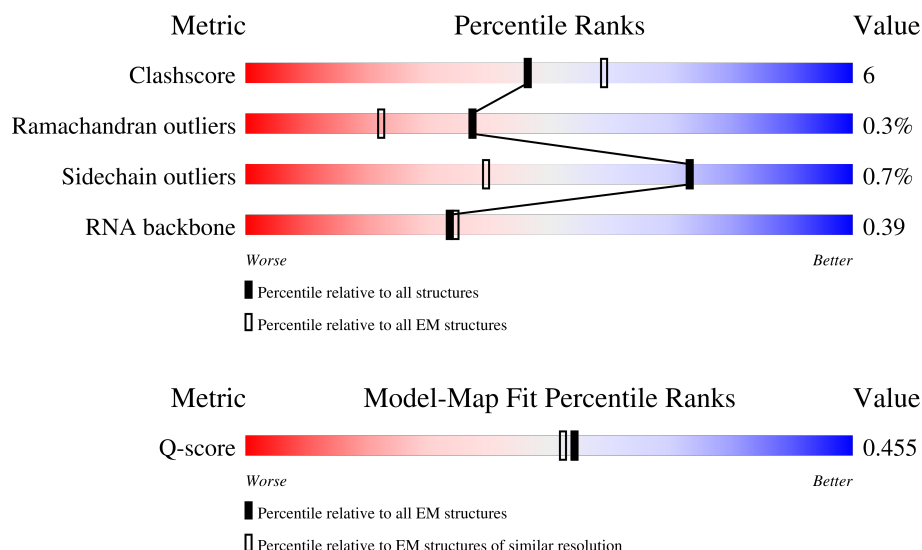
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	R	475	
2	X	224	
3	i	112	

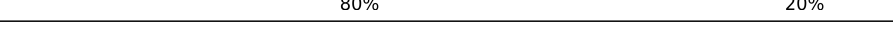
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Mol	Chain	Length	Quality of chain
4	J	222	
5	j	119	
6	K	233	
7	k	99	
8	7	191	
9	l	87	
10	M	169	
11	m	77	
12	N	193	
13	n	50	
14	O	136	
15	o	52	
16	p	203	
17	Q	197	
18	5	183	
19	S	185	
20	s	220	
21	T	152	
22	U	172	
23	V	159	
24	W	100	
25	P	155	
26	r	197	
27	x	136	
28	3	121	

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Mol	Chain	Length	Quality of chain
29	Y	62	 87% 13%
30	4	158	 58% 34% 9%
31	Z	121	 88% 12%
32	a	126	 87% 13%
33	B	76	 41% 43% 14%
34	b	135	 75% 24%
35	C	105	 81% 19%
36	c	148	 76% 24%
37	D	91	 89% 11%
38	d	58	 90% 10%
39	E	252	 75% 25%
40	e	97	 82% 18%
41	F	386	 79% 21%
42	f	109	 80% 20%
43	G	361	 83% 16%
44	g	127	 86% 13%
45	H	296	 84% 16%
46	h	106	 79% 21%
47	I	175	 75% 14% 11%
48	L	204	 54% 82% 18%
49	1	3316	 54% 36% 9%

2 Entry composition [i](#)

There are 50 unique types of molecules in this entry. The entry contains 135255 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein VMS1,Vms1,Protein VMS1,Vms1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	355	Total	C	N	O	S	Se	0	0
			2777	1772	494	498	12	1		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 3 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 7 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L38.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 13 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	P	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 26 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 29 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 30 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 33 is a RNA chain called tRNA-Ala.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

- Molecule 34 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 35 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 36 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 37 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 40 is a protein called 60S ribosomal protein L30.

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

- Molecule 41 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 42 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 43 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 46 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L1-A.

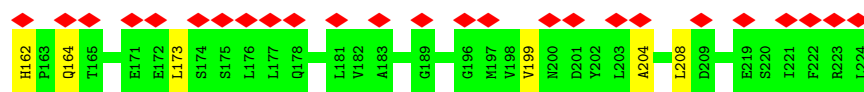
Mol	Chain	Residues	Atoms					AltConf	Trace
48	L	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 49 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	3316	Total	C	N	O	P	0	0
			70924	31675	12770	23163	3316		

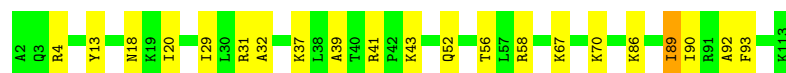
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	R	1	Total	Zn	0
			1	1	



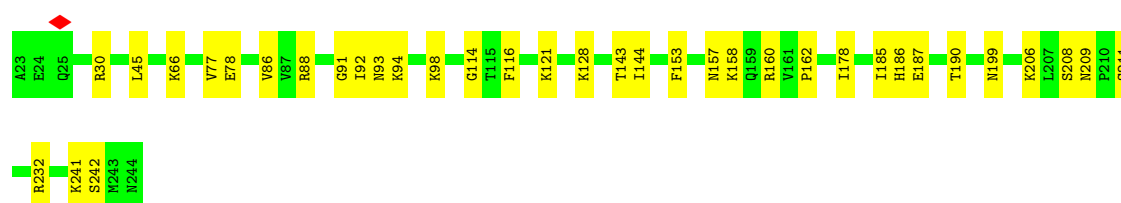
• Molecule 3: 60S ribosomal protein L34-A

Chain i: 81% 18%



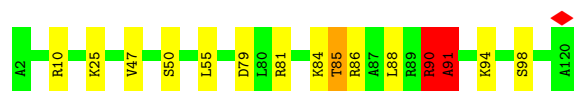
• Molecule 4: 60S ribosomal protein L7-A

Chain J: 84% 16%



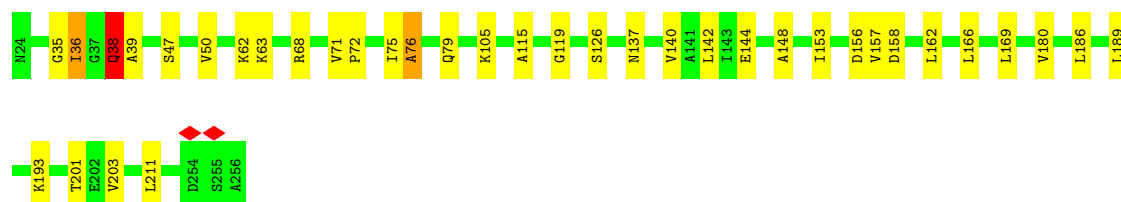
• Molecule 5: 60S ribosomal protein L35-A

Chain j: 87% 10% ..



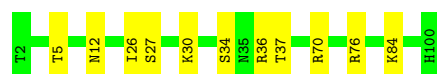
• Molecule 6: 60S ribosomal protein L8-A

Chain K: 84% 15%



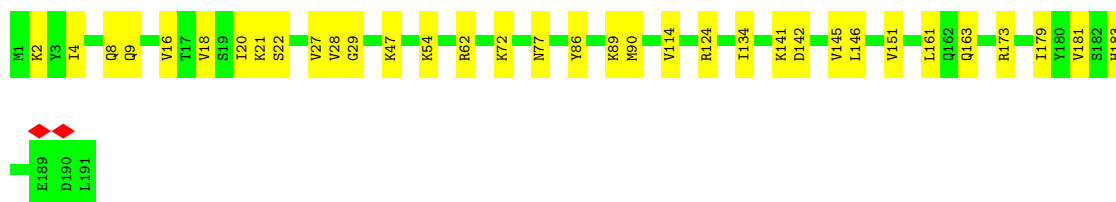
• Molecule 7: 60S ribosomal protein L36-A

Chain k: 89% 11%

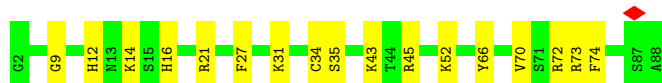
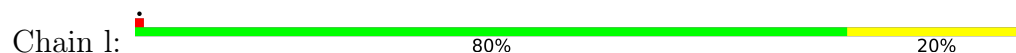


• Molecule 8: 60S ribosomal protein L9-A

Chain 7: 82% 18%



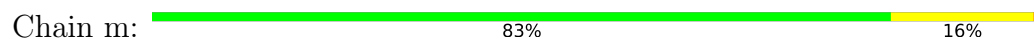
- Molecule 9: 60S ribosomal protein L37-A



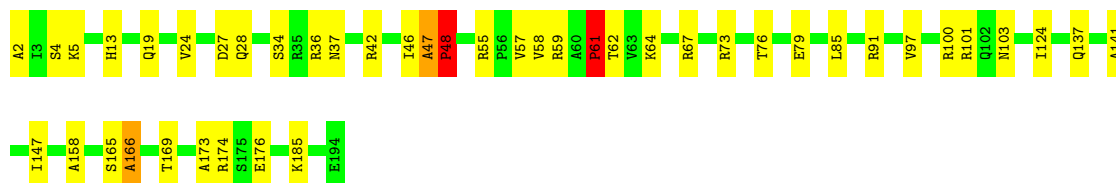
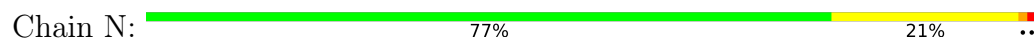
- Molecule 10: 60S ribosomal protein L11-B



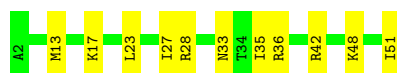
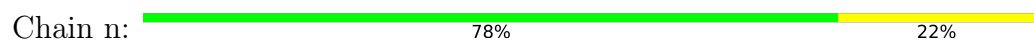
- Molecule 11: 60S ribosomal protein L38



- Molecule 12: 60S ribosomal protein L13-A



- Molecule 13: 60S ribosomal protein L39



- Molecule 14: 60S ribosomal protein L14-A

Chain O:  85% 15%



- Molecule 15: Ubiquitin-60S ribosomal protein L40

Chain o:  85% 15%



- Molecule 16: 60S ribosomal protein L15-A

Chain p:  79% 21%



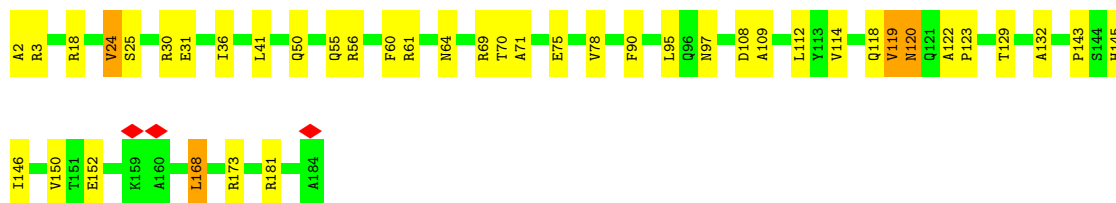
- Molecule 17: 60S ribosomal protein L16-A

Chain Q:  87% 13%



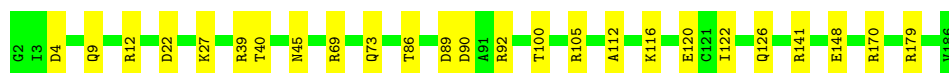
- Molecule 18: 60S ribosomal protein L17-A

Chain 5:  77% 21%



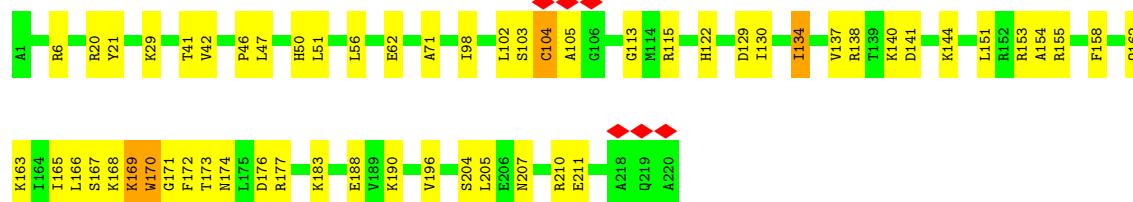
- Molecule 19: 60S ribosomal protein L18-A

Chain S:  86% 14%



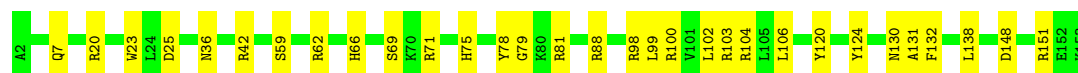
- Molecule 20: 60S ribosomal protein L10

Chain S:  74% 24%



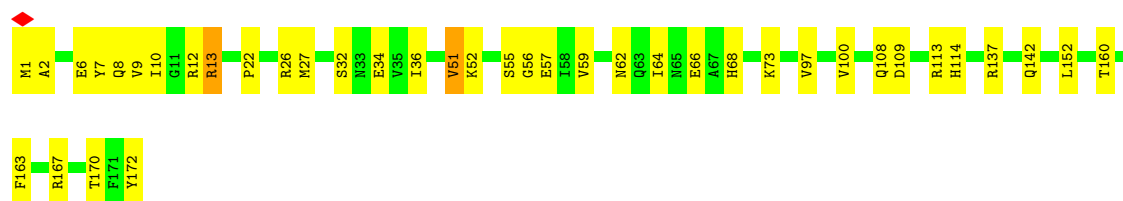
- Molecule 21: 60S ribosomal protein L19-A

Chain T:  80% 20%



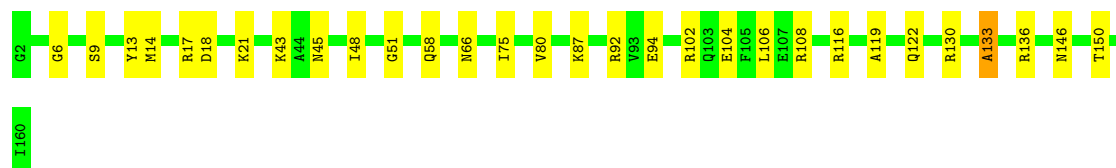
- Molecule 22: 60S ribosomal protein L20-A

Chain U:  77% 22%



- Molecule 23: 60S ribosomal protein L21-A

Chain V:  81% 18%

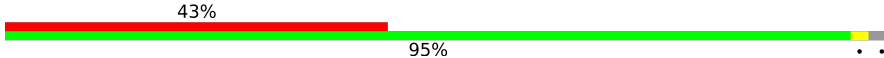


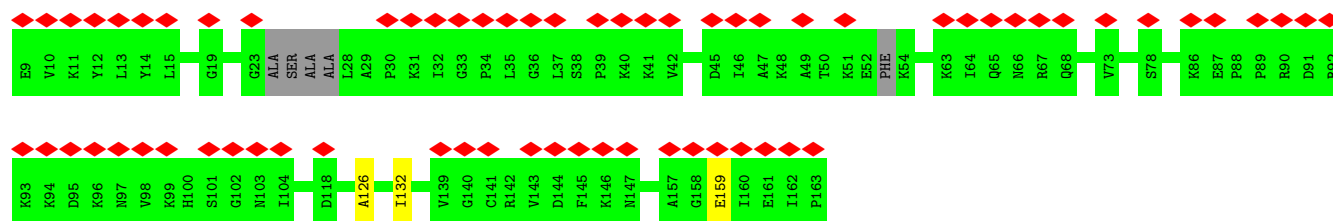
- Molecule 24: 60S ribosomal protein L22-A

Chain W:  88% 12%

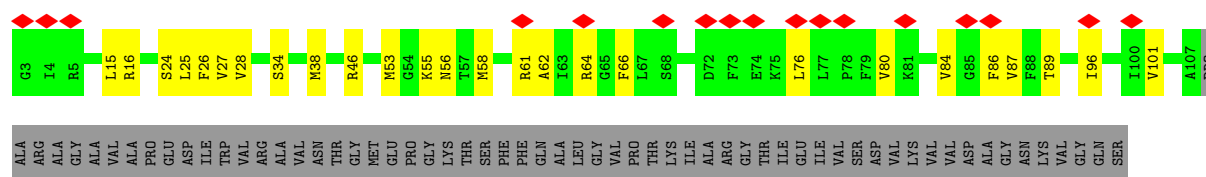


- Molecule 25: 60S ribosomal protein L12-A

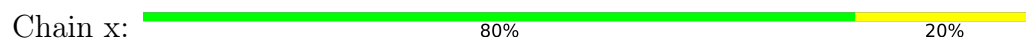
Chain P:  43% 95%



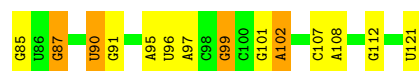
• Molecule 26: 60S acidic ribosomal protein P0



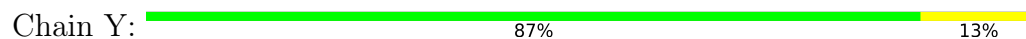
• Molecule 27: 60S ribosomal protein L23-A



• Molecule 28: 5S rRNA

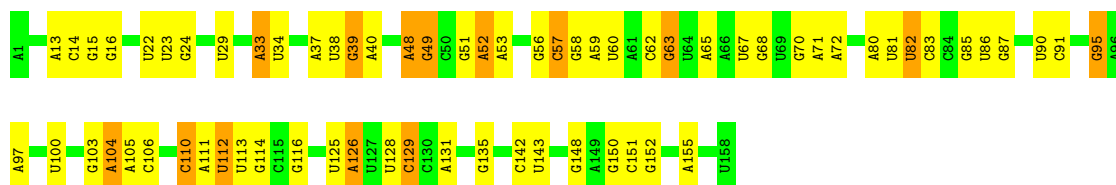


• Molecule 29: 60S ribosomal protein L24-A



• Molecule 30: 5.8S rRNA





- Molecule 31: 60S ribosomal protein L25

Chain Z: 88% 12%



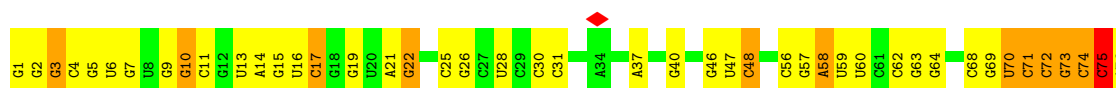
- Molecule 32: 60S ribosomal protein L26-A

Chain a: 87% 13%



- Molecule 33: tRNA-Ala

Chain B: 41% 43% 14%



- Molecule 34: 60S ribosomal protein L27-A

Chain b: 75% 24%



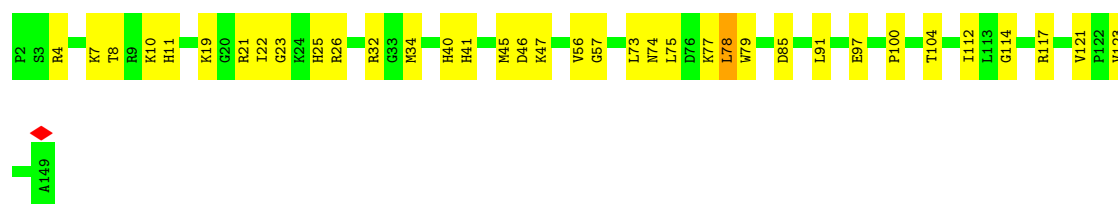
- Molecule 35: 60S ribosomal protein L42-A

Chain C: 81% 19%

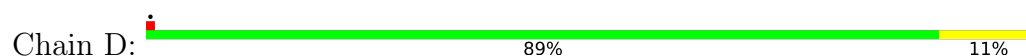


- Molecule 36: 60S ribosomal protein L28

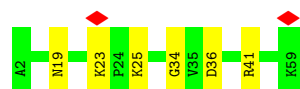
Chain c: 76% 24%



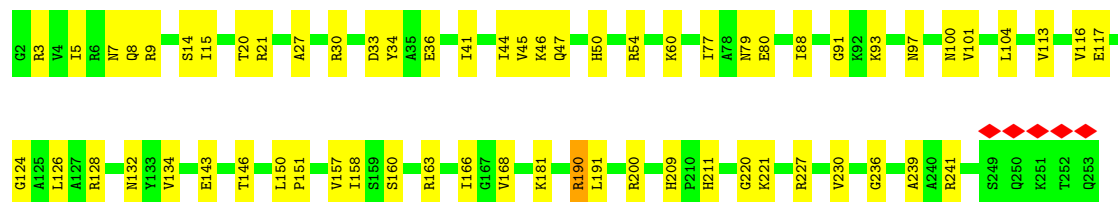
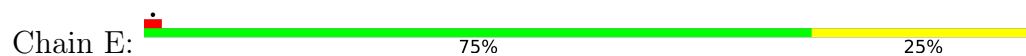
- Molecule 37: 60S ribosomal protein L43-A



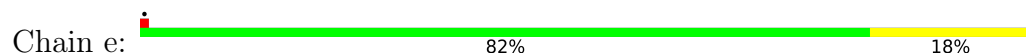
- Molecule 38: 60S ribosomal protein L29



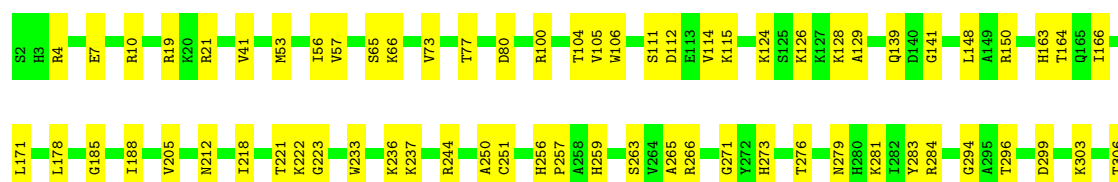
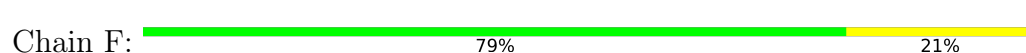
- Molecule 39: 60S ribosomal protein L2-A



- Molecule 40: 60S ribosomal protein L30

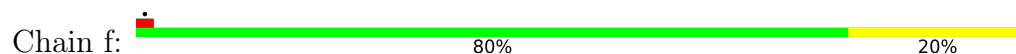


- Molecule 41: 60S ribosomal protein L3

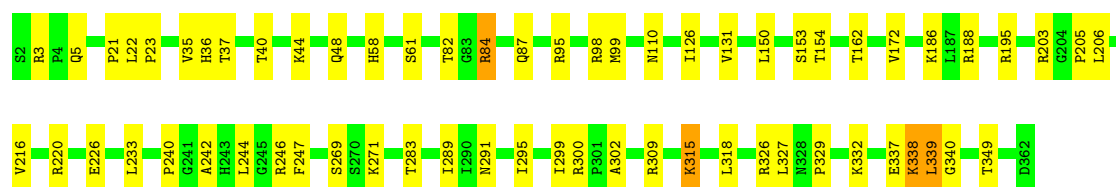
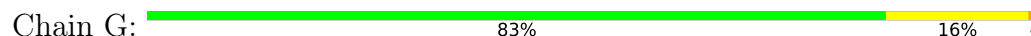




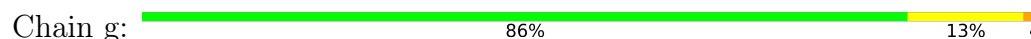
- Molecule 42: 60S ribosomal protein L31-A



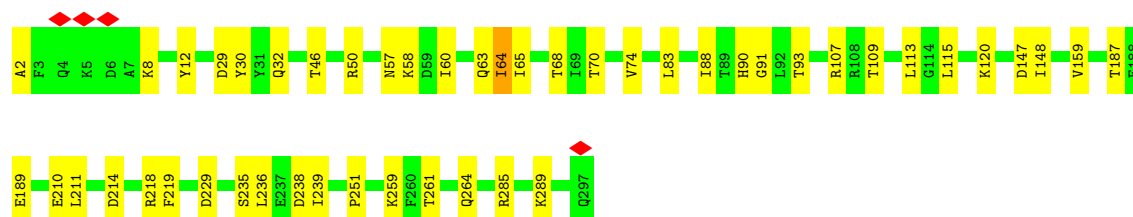
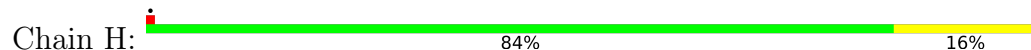
- Molecule 43: 60S ribosomal protein L4-A



- Molecule 44: 60S ribosomal protein L32



- Molecule 45: 60S ribosomal protein L5

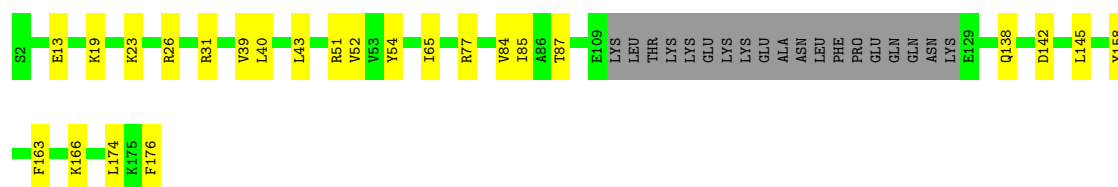


- Molecule 46: 60S ribosomal protein L33-A

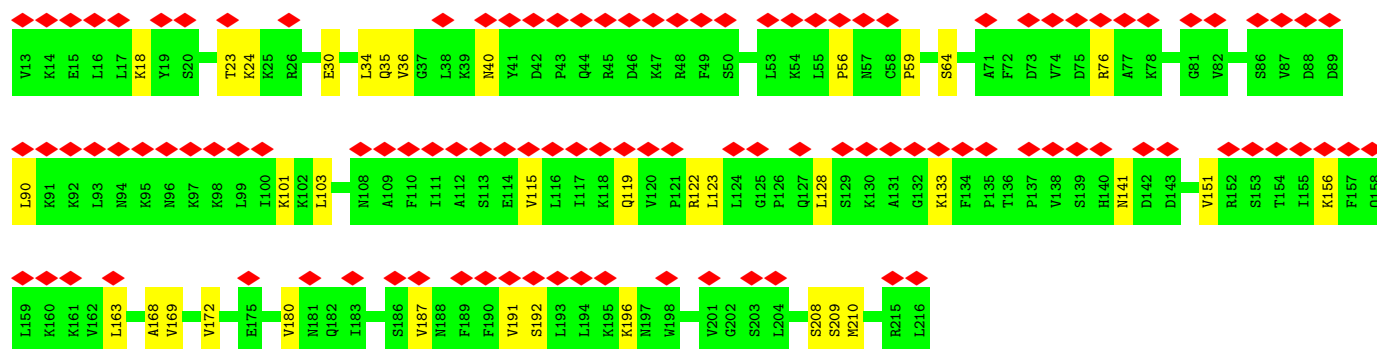
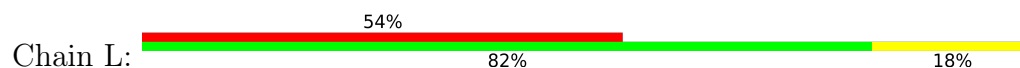


- Molecule 47: 60S ribosomal protein L6-A

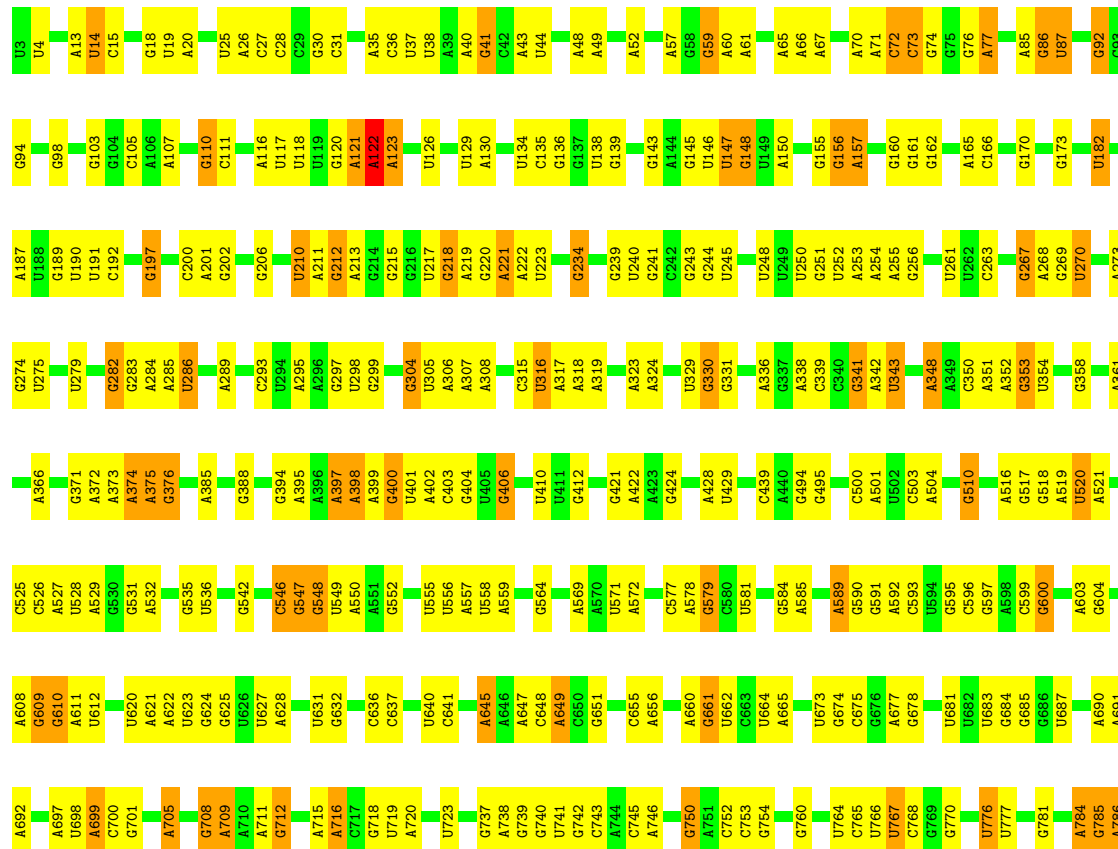


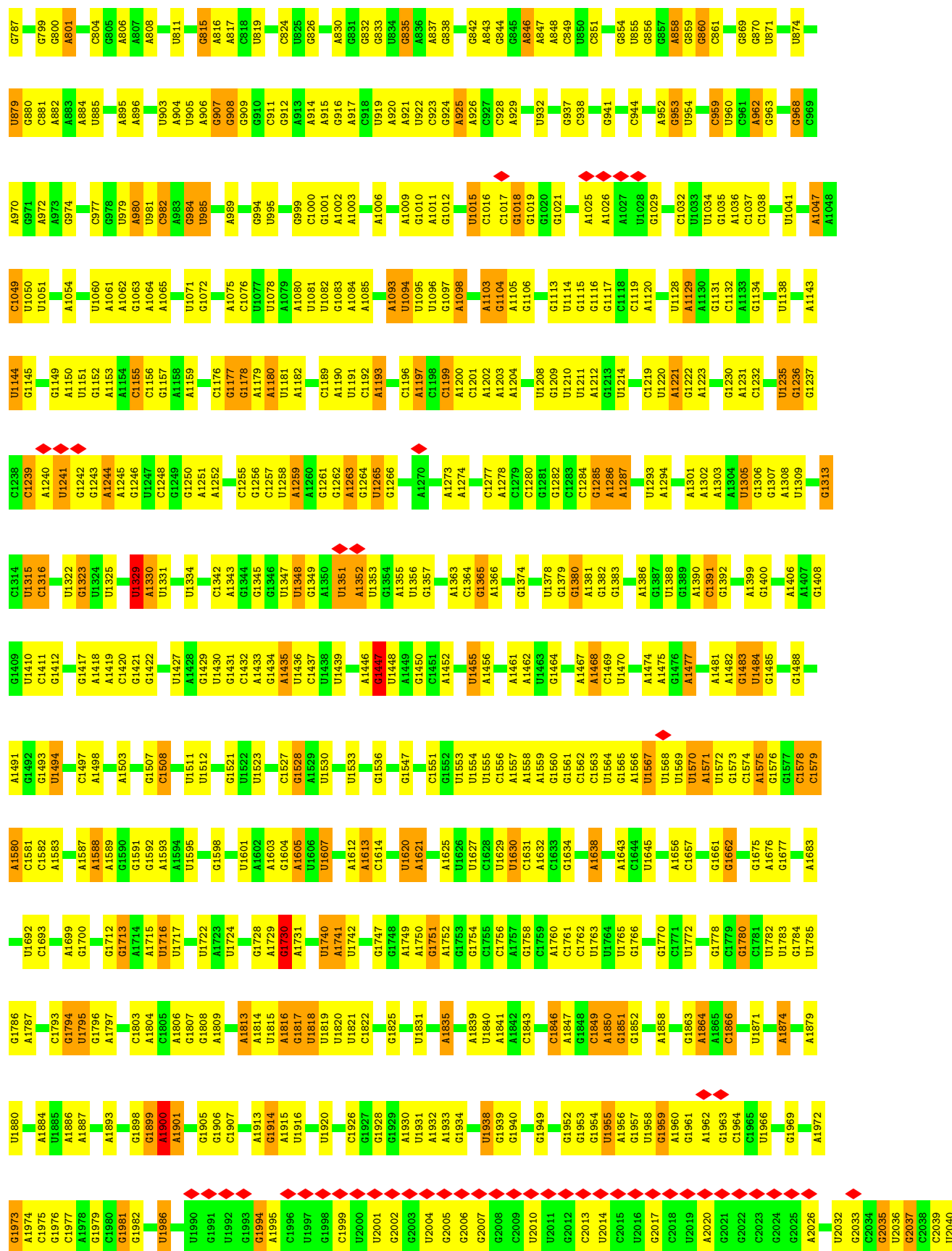


• Molecule 48: 60S ribosomal protein L1-A



• Molecule 49: 25S rRNA





U3304	A2142	G2953	A2449	C9531	U2633	G2742	A2936	G3028	A3218	U3304	G3333
A3305	A2143	U2284	G2450	U2632	U2634	G2834	A2941	A3029	G3219	A3139	U3334
G3309	A2144	A2255	G2451	G2633	A2635	A2837	A2942	G3030	G3220	G3140	G3335
U3313	A2145	A2256	U2453	G2634	A2636	U2842	G2943	A3040	U3221	A3141	G3336
A3314	G2155	U2257	U2454	A2535	A2642	U2843	G2944	U3041	U3222	A3142	A3337
G3315	C2156	U2258	U2455	U2537	U2643	U2844	G2945	U3042	G3223	A3143	G3338
U3316	G2157	A2262	U2456	U2538	U2644	C2844	A2946	U3043	G3224	G3144	A3339
A3317	A2158	C2263	A2456	U2539	G2645	C2845	G2947	G3044	U3231	G3145	U3237
G3318	G2048	C2267	G2457	A2540	U2652	U2846	G2948	G3045	G3232	A3147	G3242
U3319	U2159	U2268	A2458	U2541	U2653	U2847	G2949	A3046	G3233	G3148	C3243
G3320	C2050	U2269	U2459	U2542	U2654	U2848	G2950	U3047	A3234	G3149	U3237
U3321	G2051	C2270	U2460	U2543	U2655	G2849	G2951	A3048	U3235	A3150	U3237
G3322	C2054	A2271	A2462	A2547	A2656	C2857	G2952	A3049	G3236	U3151	U3237
A3323	G2169	G2272	G2466	C2548	A2657	U2860	U2953	U3050	G3237	U3152	U3237
U3324	U2170	G2273	G2467	G2549	G2662	U2861	U2954	U3051	G3238	U3153	G3242
G3325	G2174	U2274	A2468	C2552	G2663	U2862	U2955	U3052	G3239	C3154	A3243
A3326	U2175	U2275	U2469	U2553	C2664	A2674	U2956	U3053	G3240	U3155	A3244
U3327	U2176	A2276	C2470	A2554	U2675	U2866	C2957	U3054	G3241	U3156	A3245
G3328	A2176	G2277	U2471	G2555	A2676	U2867	A2958	U3055	G3242	G3157	G3246
A3329	C2179	C2278	A2389	C2556	U2677	U2868	G2959	U3056	G3243	U3158	G3247
U3330	A2183	U2279	A2390	C2557	U2678	G2870	U2960	G3057	G3244	G3159	C3248
G3331	U2186	A2280	G2391	C2558	U2679	U2871	U2961	U3058	G3245	U3160	A3249
A3332	G2187	U2281	C2392	C2559	U2680	U2872	U2962	U3059	G3246	U3161	G3249
U3333	A2193	G2282	G2393	C2560	U2681	U2873	U2963	G3060	G3247	U3162	U3253
G3334	G2194	U2283	A2401	C2561	U2682	U2874	U2964	U3061	G3248	A3163	G3254
A3335	U2197	C2284	A2402	C2562	U2683	U2875	U2965	U3062	G3249	A3167	U3255
U3336	A2198	G2285	G2403	C2563	U2684	U2876	U2966	G3063	G3250	U3168	U3256
G3337	U2205	U2286	A2404	C2564	U2685	U2877	U2967	U3064	G3251	A3170	U3257
A3338	A2208	C2287	C2405	C2565	U2686	U2878	U2968	U3065	G3252	A3171	G3258
U3339	U2209	U2288	C2406	C2566	U2687	U2879	U2969	U3066	G3253	U3172	U3259
G3340	G2210	G2305	C2407	C2567	U2688	U2880	U2970	U3067	G3254	A3173	G3260
A3341	A2107	C2306	U2408	C2568	U2689	U2881	U2971	U3068	G3255	A3174	U3261
U3342	G2111	G2307	U2411	C2569	U2690	U2882	U2972	U3069	G3256	U3175	G3262
G3343	U2112	C2308	G2412	C2570	U2691	U2883	U2973	G3070	G3257	G3176	U3263
A3344	A2113	U2310	G2418	C2571	U2692	U2884	U2974	U3071	G3258	A3177	U3264
U3345	C2114	A2219	A2419	C2572	U2693	U2885	U2975	U3072	G3259	U3178	U3265
G3346	G2115	A2220	C2422	C2573	U2694	U2886	U2976	U3073	G3260	A3179	U3266
A3347	U2116	U2225	U2423	C2574	U2695	U2887	U2977	U3074	G3261	A3180	U3267
U3348	G2117	A2226	A2424	C2575	U2696	U2888	U2978	A2703	G3262	G3186	G3268
G3349	A2121	A2227	G2425	C2576	U2697	U2889	U2979	A2704	G3263	A3187	G3269
A3350	G2122	A2228	U2434	C2577	U2698	U2890	U2980	A2705	G3264	U3188	U3270
U3351	A2126	A2232	G2435	C2578	U2699	U2891	U2981	A2706	G3265	A3189	G3271
G3352	U2129	G2233	G2440	C2579	U2700	U2892	U2982	A2707	G3266	G3195	U3272
A3353	G2130	A2234	A2441	C2580	U2701	U2893	U2983	A2708	G3267	U3196	A3274
U3354	A2131	A2235	G2442	C2581	U2702	U2894	U2984	A2709	G3268	G3197	U3275
G3355	C2132	A2236	U2443	C2582	U2703	U2895	U2985	A2710	G3269	U3198	G3276
A3356	U2137	G2237	A2444	C2583	U2704	U2896	U2986	A2711	G3270	G3199	U3277
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G3358	G2139	G2239	A2446	C2585	U2706	U2898	U2988	A2713	G3272	C3206	G3279
A3359	U2140	G2240	A2447	C2586	U2707	U2899	U2989	A2714	G3273	G3207	U3280
U3360	G2141	A2241	G2448	C2587	U2708	U2900	U2990	A2715	G3274	A3011	G3281
G3361	A2142	A2242	A2449	C2588	U2709	U2901	U2991	A2716	G3275	A3012	G3282
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U3363	G2144	A2244	U2451	C2590	U2711	U2903	U2993	U2718	G3277	A3014	G3284
G3364	A2145	A2245	A2452	C2591	U2712	U2904	U2994	U2719	G3278	U2905	G3285
A3365	U2146	A2246	G2453	C2592	U2713	U2905	U2995	U2720	G3279	G3206	U3286
U3366	G2147	A2247	U2454	C2593	U2714	U2906	U2996	U2721	G3280	A3017	G3287
G3367	A2148	A2248	A2455	C2594	U2715	U2907	U2997	U2722	G3281	U3018	G3288
A3368	U2149	A2249	G2456	C2595	U2716	U2908	U2998	U2723	G3282	A3019	U3289
U3369	G2150	A2250	U2457	C2596	U2717	U2909	U2999	U2724	G3283	A3020	G3290
G3370	A2151	A2251	A2458	C2597	U2718	U2910	U3000	U2725	G3284	A3021	U3291
A3371	U2152	A2252	U2459	C2598	U2719	U2911	A3001	U2726	G3285	G3022	U3292
U3372	G2153	A2253	U2460	C2599	U2720	U2912	C3002	U2727	G3286	U3023	A3293
G3373	A2154	A2254	A2461	C2600	U2721	U2913	G3003	U2728	G3287	A3024	U3294
A3374	U2155	A2255	U2462	C2601	U2722	U2914	A3011	U2729	G3288	U3025	U3295
U3375	G2156	A2256	U2463	C2602	U2723	U2915	A3012	U2730	G3289	G3026	U3296
G3376	A2157	A2257	A2464	C2603	U2724	U2916	A3013	U2731	G3290	A3027	G3303
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G3379	A2160	A2260	A2467	C2606	U2727	U2919	A3016	U2734	G3293	A3210	U3306
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G3382	A2163	A2263	A2470	C2609	U2730	U2922	A3019	U2737	G3296	U3213	U3309
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G3385	A2166	A2266	U2473	C2612	U2733	U2925	A3022	U2740	G3299	G3216	U3312
A3386	U2167	A2267	U2474	C2613	U2734	U2926	A3023	U2741	G3300	U3217	U3313
U3387	G2168	A2268	U2475	C2614	U2735	U2927	A3024	U2742	G3301	U3218	U3314
G3388	A2169	A2269	U2476	C2615	U2736	U2928	A3025	U2743	G3302	U3219	U3315
A3389	U2170	A2270	U2477	C2616	U2737	U2929	A3026	U2744	G3303	U3220	U3316
U3390	G2171	A2271	U2478	C2617	U2738	U2930	A3027	U2745	G3304	U3221	U3317
G3391	A2172	A2272	U2479	C2618	U2739	U2931	A3028	U2746	G3305	U3222	U3318
A3392	U2173	A2273	U2480	C2619	U2740	U2932	A3029	U2747	G3306	U3223	U3319
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A3395	U2176	A2276	U2483	C2622	U2743	U2935	A3032	U2750	G3309	U3226	U3322
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G3397	A2178	A2278	U2485	C2624	U2745	U2937	A3034	U2752	G3311	U3228	U3324
A3398	U2179	A2279	U2486	C2625	U2746	U2938	A3035	U2753	G3312	U3229	U3325
U3399	G2180	A2280	U2487	C2626	U2747	U2939	A3036	U2754	G3313	U3230	U3326
G3400	A2181	A2281	U2488	C2627	U2748	U2940	A3037	U2755	G3314	U3231	U3327
A3401	U2182	A2282	U2489	C2628	U2749	U2941	A3038	U2756	G3315	U3232	U3328
U3402	G2183	A2283	U2490	C2629	U2750	U2942	A3039	U2757	G3316	U3233	U3329
G3403	A2184	A2284	U2491	C2630	U2751	U2943	A3040	U2758	G3317	U3234	U3330
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A3407	U2188	A2288	U2495	C2634	U2755	U2947	A3044	U2762	G3321	U3238	U3334
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G3409	A2189	A2290	U2497	C2636	U2757	U2949	A3046	U2764	G3323	U3240	U3336
A3410	U2190	A2291	U2498	C2637	U2758	U2950	A3047	U2765	G3324	U3241	U3337
U3411	G2191	A2292	U2499	C2638	U2759	U2951	A3048	U2766	G3325	U3242	U3338
G3412	A2192	A2293	U2500	C2639	U2760	U2952	A3049	U2767	G3326	U3243	U3339
A3413	U2193	A2294	U2501	C2640	U2761	U2953	A3050	U2768	G3327	U3244	U3340
U3414	G2194										

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52740	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 ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.477	Depositor
Minimum map value	-0.263	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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

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	R	0.29	0/2624	0.60	2/3522 (0.1%)
2	X	0.22	0/1653	0.61	2/2255 (0.1%)
3	i	0.74	0/890	0.89	1/1189 (0.1%)
4	J	0.59	0/1821	0.76	0/2451
5	j	0.51	0/978	0.90	6/1301 (0.5%)
6	K	0.52	0/1836	0.82	4/2481 (0.2%)
7	k	0.49	0/778	0.83	0/1034
8	7	0.57	0/1539	0.75	0/2073
9	l	0.80	0/696	0.92	0/923
10	M	0.39	0/1374	0.81	3/1842 (0.2%)
11	m	0.50	0/618	0.72	0/826
12	N	0.58	0/1568	0.92	5/2106 (0.2%)
13	n	0.83	0/443	0.86	1/588 (0.2%)
14	O	0.55	0/1068	0.76	0/1438
15	o	0.60	0/423	0.88	1/562 (0.2%)
16	p	0.73	0/1757	0.93	3/2354 (0.1%)
17	Q	0.71	0/1585	0.84	0/2128
18	5	0.69	0/1443	0.85	0/1944
19	S	0.55	0/1465	0.81	0/1965
20	s	0.57	0/1807	0.90	7/2425 (0.3%)
21	T	0.69	0/1245	0.87	0/1661
22	U	0.64	0/1481	0.84	1/1990 (0.1%)
23	V	0.61	1/1300 (0.1%)	0.79	2/1743 (0.1%)
24	W	0.47	0/812	0.73	1/1099 (0.1%)
25	P	0.25	0/734	0.84	0/1015
26	r	0.24	0/982	0.66	0/1320
27	x	0.65	0/1018	0.78	0/1369
28	3	0.54	0/2883	0.54	1/4491 (0.0%)
29	Y	0.58	0/525	0.78	0/696
30	4	0.67	0/3746	0.60	0/5832
31	Z	0.63	0/979	0.79	1/1321 (0.1%)
32	a	0.54	1/1004 (0.1%)	0.80	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B	0.61	1/1810 (0.1%)	0.64	4/2821 (0.1%)
34	b	0.58	0/1118	0.80	0/1497
35	C	0.54	0/860	0.82	0/1136
36	c	0.62	0/1204	0.86	2/1612 (0.1%)
37	D	0.71	0/701	0.90	0/934
38	d	0.50	0/473	0.73	0/629
39	E	0.75	0/1948	0.85	2/2617 (0.1%)
40	e	0.54	0/751	0.77	0/1008
41	F	0.74	1/3146 (0.0%)	0.85	0/4228
42	f	0.70	0/890	0.79	0/1196
43	G	0.59	0/2800	0.86	3/3790 (0.1%)
44	g	0.60	0/1041	0.81	2/1394 (0.1%)
45	H	0.43	0/2425	0.70	0/3271
46	h	0.69	0/868	0.77	0/1168
47	I	0.48	0/1260	0.69	0/1694
48	L	0.25	0/1634	0.75	1/2195 (0.0%)
49	1	0.66	0/79382	0.63	25/123763 (0.0%)
All	All	0.63	4/145386 (0.0%)	0.70	80/214238 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	J	0	2
5	j	0	2
6	K	0	5
7	k	0	1
8	7	0	1
10	M	0	1
11	m	0	1
12	N	0	4
16	p	0	1
20	s	0	5
34	b	0	2
36	c	0	2
41	F	0	1
43	G	0	4
45	H	0	1
All	All	0	33

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	B	3	G	O3'-P	23.01	1.95	1.61
41	F	237	LYS	C-N	-7.88	1.09	1.33
23	V	133	ALA	C-N	-6.68	1.23	1.33
32	a	47	ALA	C-N	-5.07	1.26	1.32

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	B	3	G	P-O3'-C3'	-12.76	101.06	120.20
12	N	48	PRO	CA-C-N	11.01	140.31	122.48
12	N	48	PRO	C-N-CA	11.01	140.31	122.48
20	s	172	PHE	N-CA-C	-8.30	102.93	113.72
48	L	191	VAL	N-CA-C	-8.19	104.59	112.29
20	s	104	CYS	N-CA-C	-7.78	102.83	113.18
20	s	137	VAL	N-CA-C	7.73	118.61	112.12
33	B	75	C	C1'-C2'-O2'	-7.04	97.84	108.40
12	N	61	PRO	CA-C-N	6.97	134.85	121.54
12	N	61	PRO	C-N-CA	6.97	134.85	121.54
16	p	120	TRP	CA-C-N	-6.81	115.62	122.77
16	p	120	TRP	C-N-CA	-6.81	115.62	122.77
20	s	169	LYS	CA-CB-CG	6.72	127.54	114.10
5	j	90	ARG	CA-C-N	6.52	134.00	121.54
5	j	90	ARG	C-N-CA	6.52	134.00	121.54
15	o	78	ILE	N-CA-C	-6.51	106.79	113.10
43	G	315	LYS	CA-C-N	6.41	129.99	120.83
43	G	315	LYS	C-N-CA	6.41	129.99	120.83
16	p	75	VAL	CA-CB-CG2	6.33	121.17	110.40
28	3	77	G	C2'-C3'-O3'	6.30	118.94	109.50
6	K	38	GLN	CA-C-N	6.17	130.51	121.31
6	K	38	GLN	C-N-CA	6.17	130.51	121.31
33	B	3	G	OP2-P-O3'	6.14	126.41	108.00
49	1	1900	A	C2'-C3'-O3'	6.07	118.60	109.50
5	j	91	ALA	CA-C-N	5.95	129.57	120.82
5	j	91	ALA	C-N-CA	5.95	129.57	120.82
49	1	2541	U	P-O3'-C3'	5.90	129.05	120.20
49	1	282	G	C2'-C3'-O3'	5.84	122.46	113.70
3	i	89	ILE	N-CA-C	-5.74	106.11	111.45
5	j	84	LYS	CA-C-N	5.72	132.47	121.54
5	j	84	LYS	C-N-CA	5.72	132.47	121.54
2	X	161	VAL	CA-C-N	5.72	128.81	120.51
2	X	161	VAL	C-N-CA	5.72	128.81	120.51
49	1	2513	U	P-O3'-C3'	5.71	128.77	120.20
49	1	2403	G	C4'-C3'-O3'	5.70	117.95	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	1	1716	U	C2'-C3'-O3'	5.63	117.94	109.50
49	1	122	A	C4'-C3'-O3'	5.58	117.78	109.40
10	M	95	ASN	N-CA-C	-5.55	106.46	113.23
1	R	284	ARG	N-CA-C	-5.54	100.14	109.07
12	N	141	ALA	N-CA-C	-5.49	107.59	114.56
49	1	2513	U	C4'-C3'-O3'	5.46	117.59	109.40
24	W	59	ASP	N-CA-C	-5.46	107.87	114.75
49	1	2313	A	C4'-C3'-O3'	5.45	117.57	109.40
49	1	1329	U	C2'-C3'-O3'	5.45	117.67	109.50
49	1	156	G	C2'-C3'-O3'	5.43	117.65	109.50
49	1	156	G	P-O3'-C3'	5.43	128.35	120.20
1	R	285	TYR	N-CA-C	5.42	117.54	109.25
20	s	138	ARG	N-CA-C	5.42	117.25	110.91
33	B	3	G	OP1-P-O3'	-5.39	91.83	108.00
49	1	2509	U	P-O3'-C3'	5.38	128.27	120.20
49	1	2468	A	P-O3'-C3'	5.38	128.27	120.20
49	1	2177	G	P-O3'-C3'	5.36	128.25	120.20
36	c	23	GLY	CA-C-N	5.34	128.67	120.82
36	c	23	GLY	C-N-CA	5.34	128.67	120.82
20	s	134	ILE	CA-C-N	5.32	131.69	121.54
20	s	134	ILE	C-N-CA	5.32	131.69	121.54
23	V	133	ALA	CA-C-N	5.29	129.50	121.03
23	V	133	ALA	C-N-CA	5.29	129.50	121.03
44	g	58	GLY	N-CA-C	5.26	117.51	111.36
10	M	26	SER	CA-C-N	5.25	131.71	121.41
10	M	26	SER	C-N-CA	5.25	131.71	121.41
13	n	13	MET	CG-SD-CE	-5.23	89.40	100.90
43	G	84	ARG	N-CA-C	-5.21	105.66	112.23
49	1	1447	G	O4'-C1'-N9	5.21	116.32	108.50
49	1	1391	C	C2'-C3'-O3'	5.21	117.31	109.50
49	1	2513	U	OP1-P-O3'	5.20	123.59	108.00
39	E	143	GLU	CA-C-N	5.17	131.42	121.54
39	E	143	GLU	C-N-CA	5.17	131.42	121.54
49	1	3152	U	P-O3'-C3'	5.15	127.93	120.20
49	1	767	U	P-O3'-C3'	5.15	127.92	120.20
49	1	2273	G	P-O3'-C3'	5.10	127.85	120.20
22	U	12	ARG	N-CA-C	5.09	116.97	110.61
44	g	42	VAL	N-CA-C	-5.09	107.44	111.81
49	1	304	G	P-O3'-C3'	5.08	127.82	120.20
6	K	39	ALA	CA-C-N	5.07	128.10	120.69
6	K	39	ALA	C-N-CA	5.07	128.10	120.69
49	1	2447	A	P-O3'-C3'	5.07	127.81	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	Z	115	ARG	CB-CG-CD	-5.07	99.64	111.30
49	1	2046	U	N1-C1'-C2'	5.04	121.56	114.00
49	1	1730	G	P-O3'-C3'	5.04	127.76	120.20

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	7	21	LYS	Peptide
41	F	385	LYS	Peptide
43	G	131	VAL	Peptide
43	G	291	ASN	Peptide
43	G	318	LEU	Peptide
43	G	338	LYS	Peptide
45	H	259	LYS	Peptide
4	J	157	ASN	Peptide
4	J	232	ARG	Peptide
6	K	156	ASP	Peptide
6	K	36	ILE	Peptide
6	K	38	GLN	Peptide
6	K	76	ALA	Peptide
6	K	79	GLN	Peptide
10	M	172	LEU	Peptide
12	N	165	SER	Peptide
12	N	4	SER	Peptide
12	N	47	ALA	Peptide
12	N	61	PRO	Peptide
34	b	101	PHE	Peptide
34	b	102	GLU	Peptide
36	c	45	MET	Peptide
36	c	46	ASP	Peptide
5	j	90	ARG	Peptide
5	j	91	ALA	Peptide
7	k	27	SER	Peptide
11	m	32	ASN	Peptide
16	p	92	LEU	Peptide
20	s	103	SER	Peptide
20	s	134	ILE	Peptide
20	s	168	LYS	Peptide
20	s	170	TRP	Peptide
20	s	171	GLY	Peptide

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	R	2777	0	2675	54	0
2	X	1633	0	1596	21	0
3	i	880	0	945	17	0
4	J	1784	0	1862	24	0
5	j	969	0	1078	9	0
6	K	1804	0	1877	25	0
7	k	771	0	849	8	0
8	7	1518	0	1587	21	0
9	l	681	0	687	13	0
10	M	1353	0	1383	24	0
11	m	612	0	682	11	0
12	N	1543	0	1608	29	0
13	n	436	0	475	8	0
14	O	1053	0	1149	16	0
15	o	417	0	459	6	0
16	p	1720	0	1779	29	0
17	Q	1555	0	1659	16	0
18	5	1420	0	1437	28	0
19	S	1441	0	1543	22	0
20	s	1770	0	1808	47	0
21	T	1228	0	1314	25	0
22	U	1445	0	1487	31	0
23	V	1276	0	1323	20	0
24	W	796	0	812	6	0
25	P	737	0	341	2	0
26	r	967	0	991	22	0
27	x	1003	0	1048	17	0
28	3	2579	0	1304	36	0
29	Y	513	0	540	5	0
30	4	3353	0	1695	29	0
31	Z	964	0	1025	12	0
32	a	993	0	1081	11	0
33	B	1622	0	818	65	0
34	b	1092	0	1155	24	0
35	C	847	0	918	14	0
36	c	1173	0	1215	22	0
37	D	694	0	738	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	d	462	0	491	6	0
39	E	1914	0	1981	49	0
40	e	743	0	797	10	0
41	F	3075	0	3141	52	0
42	f	876	0	912	14	0
43	G	2748	0	2859	42	0
44	g	1020	0	1090	12	0
45	H	2375	0	2325	32	0
46	h	850	0	880	15	0
47	I	1239	0	1326	17	0
48	L	1609	0	1701	25	0
49	1	70924	0	35641	640	0
50	R	1	0	0	0	0
All	All	135255	0	98087	1343	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 6.

All (1343) 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)
20:s:104:CYS:SG	33:B:1:G:H4'	1.35	1.64
20:s:104:CYS:SG	33:B:1:G:C4'	2.10	1.40
33:B:2:G:N2	33:B:71:C:O2	1.67	1.27
33:B:2:G:N1	33:B:71:C:N3	1.92	1.15
20:s:104:CYS:HB2	33:B:1:G:C1'	1.77	1.13
1:R:247:ALA:HA	1:R:281:THR:HG22	1.34	1.09
20:s:104:CYS:HB2	33:B:1:G:O4'	1.52	1.08
20:s:104:CYS:HG	33:B:1:G:C4'	1.62	1.03
49:1:1958:U:C2	49:1:2083:G:O6	2.14	1.00
33:B:3:G:N2	33:B:70:U:O2	1.98	0.95
20:s:104:CYS:HB2	33:B:1:G:H1'	1.47	0.95
1:R:247:ALA:CA	1:R:281:THR:HG22	1.97	0.94
49:1:3348:G:H1	49:1:3357:U:H3	1.01	0.94
49:1:1564:U:H3	49:1:1576:G:H1	1.12	0.92
49:1:1958:U:O2	49:1:2083:G:C6	2.23	0.92
33:B:3:G:H1	33:B:70:U:H3	0.96	0.92
1:R:284:ARG:NH2	33:B:1:G:OP2	2.04	0.90
1:R:285:TYR:CE1	33:B:72:C:O2'	2.22	0.90
49:1:542:G:H1	49:1:549:U:H3	1.21	0.89
20:s:104:CYS:CB	33:B:1:G:O4'	2.20	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B:2:G:O6	33:B:71:C:N4	2.08	0.86
49:1:1257:C:H42	49:1:1261:G:N2	1.75	0.85
49:1:1257:C:H42	49:1:1261:G:H22	1.24	0.84
1:R:247:ALA:CB	1:R:281:THR:HG22	2.09	0.82
33:B:15:G:H22	33:B:48:C:H42	1.26	0.82
49:1:1257:C:N4	49:1:1261:G:H22	1.79	0.80
49:1:3234:A:H2	49:1:3253:G:H1	1.29	0.79
1:R:247:ALA:HA	1:R:281:THR:CG2	2.11	0.78
1:R:284:ARG:NH2	33:B:1:G:P	2.58	0.76
49:1:3232:G:H1	49:1:3255:U:H3	1.33	0.76
20:s:104:CYS:SG	33:B:1:G:C5'	2.74	0.75
33:B:2:G:N2	33:B:71:C:C2	2.37	0.73
49:1:3047:U:O4	49:1:3094:A:N1	2.21	0.73
49:1:1966:U:H3	49:1:2057:G:H1	1.35	0.72
49:1:182:U:H3	49:1:234:G:H1	1.37	0.72
30:4:81:U:H5''	30:4:82:U:H5'	1.72	0.72
49:1:1562:C:H42	49:1:1578:C:H42	1.36	0.72
16:p:53:TYR:HB2	16:p:133:ILE:HD11	1.70	0.71
22:U:6:GLU:O	22:U:64:ILE:HB	1.90	0.70
49:1:1018:G:H1	49:1:1034:U:H3	1.38	0.70
21:T:103:ARG:NH1	21:T:124:TYR:OH	2.26	0.69
6:K:68:ARG:HG3	49:1:2514:U:H5'	1.74	0.69
41:F:139:GLN:HG3	41:F:141:GLY:H	1.57	0.69
3:i:39:ALA:HB2	3:i:58:ARG:HD2	1.74	0.69
12:N:91:ARG:HE	12:N:97:VAL:HB	1.56	0.68
49:1:160:G:H1	49:1:261:U:H3	1.40	0.68
49:1:589:A:N6	49:1:610:G:O2'	2.27	0.68
31:Z:71:THR:HG21	49:1:1603:A:H61	1.59	0.68
34:b:54:THR:HG23	34:b:56:LYS:H	1.60	0.67
30:4:150:G:OP1	31:Z:27:ARG:NH2	2.28	0.66
33:B:15:G:N2	33:B:48:C:H42	1.92	0.66
49:1:510:G:H1	49:1:581:U:H3	1.43	0.66
1:R:284:ARG:NH2	33:B:1:G:O5'	2.28	0.66
44:g:42:VAL:HG12	44:g:52:GLN:HE21	1.60	0.66
49:1:1958:U:C2	49:1:2083:G:C6	2.82	0.66
49:1:1078:U:O2	49:1:1082:U:N3	2.27	0.66
26:r:25:LEU:HB3	26:r:191:TYR:HB3	1.77	0.66
33:B:2:G:C2	33:B:71:C:N3	2.63	0.66
36:c:8:THR:HG21	49:1:661:G:H3'	1.77	0.65
3:i:29:ILE:HD11	3:i:31:ARG:HH21	1.60	0.65
20:s:104:CYS:SG	33:B:1:G:O4'	2.55	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:H:64:ILE:HD13	45:H:109:THR:HG21	1.77	0.65
33:B:15:G:H22	33:B:48:C:N4	1.94	0.65
33:B:75:C:OP1	49:1:2971:A:H3'	1.96	0.65
49:1:1949:G:H1	49:1:2097:U:H3	1.44	0.65
21:T:100:ARG:NH1	49:1:1722:U:OP1	2.30	0.65
1:R:502:ASN:HD21	1:R:506:ARG:HE	1.44	0.65
12:N:59:ARG:NH1	49:1:73:C:N3	2.45	0.65
39:E:21:ARG:HD3	49:1:824:C:H5''	1.79	0.65
18:5:31:GLU:HG2	18:5:60:PHE:HA	1.78	0.65
19:S:112:ALA:O	19:S:116:LYS:HB2	1.96	0.65
18:5:36:ILE:HD11	18:5:95:LEU:HD11	1.78	0.64
49:1:2137:U:OP2	49:1:2142:A:N6	2.30	0.64
12:N:76:THR:HG22	12:N:101:ARG:HG3	1.79	0.64
49:1:2281:A:O2'	49:1:2973:G:N2	2.30	0.64
49:1:1959:G:C6	49:1:2082:U:O2	2.50	0.64
49:1:2193:U:H5'	49:1:2194:G:H5'	1.78	0.64
49:1:2971:A:H4'	49:1:2972:G:OP2	1.98	0.64
22:U:109:ASP:OD1	22:U:113:ARG:NH1	2.31	0.64
20:s:29:LYS:HG3	20:s:62:GLU:HG3	1.79	0.63
45:H:50:ARG:NH1	45:H:147:ASP:OD2	2.31	0.63
26:r:46:ARG:HH22	49:1:1257:C:H4'	1.62	0.63
16:p:155:VAL:O	16:p:162:ARG:NH2	2.32	0.63
12:N:166:ALA:O	12:N:169:THR:HB	1.98	0.63
1:R:452:LYS:HG3	1:R:494:ILE:HG12	1.78	0.63
26:r:89:THR:HG21	26:r:96:ILE:HG13	1.80	0.63
33:B:25:C:H2'	33:B:26:G:H8	1.64	0.63
18:5:109:ALA:HA	18:5:112:LEU:HD13	1.81	0.63
1:R:193:PHE:O	1:R:203:VAL:HA	1.99	0.62
28:3:17:A:OP1	45:H:2:ALA:N	2.31	0.62
4:J:92:ILE:HD11	19:S:4:ASP:HB2	1.81	0.62
8:7:16:VAL:HG12	8:7:29:GLY:HA3	1.81	0.62
16:p:201:ARG:HB3	43:G:110:ASN:HD22	1.62	0.62
27:x:10:LYS:NZ	27:x:54:LEU:O	2.32	0.62
10:M:15:GLU:HB3	10:M:130:VAL:HG13	1.81	0.62
32:a:12:ARG:NH1	49:1:215:G:OP1	2.32	0.62
14:O:128:ARG:NH1	49:1:3214:U:OP2	2.33	0.62
26:r:27:VAL:HB	26:r:189:GLN:HB2	1.80	0.62
17:Q:49:ARG:NH1	49:1:1193:A:OP1	2.31	0.62
34:b:69:LYS:NZ	49:1:1632:A:OP1	2.32	0.62
37:D:62:LYS:NZ	49:1:2554:A:N7	2.46	0.62
2:X:106:ASN:ND2	2:X:150:SER:OG	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:173:ALA:O	12:N:176:GLU:HB3	2.00	0.62
19:S:92:ARG:NH1	49:1:784:A:O2'	2.33	0.62
35:C:63:LYS:NZ	49:1:2761:G:N7	2.44	0.61
49:1:1966:U:O2	49:1:2057:G:N2	2.32	0.61
39:E:80:GLU:HB3	39:E:168:VAL:HG23	1.82	0.61
33:B:69:G:N1	33:B:70:U:C4	2.68	0.61
45:H:46:THR:HG21	49:1:1078:U:H4'	1.83	0.61
27:x:14:SER:O	27:x:81:GLN:NE2	2.31	0.61
33:B:70:U:H2'	33:B:71:C:H6	1.64	0.61
14:O:23:ILE:O	14:O:30:GLY:N	2.33	0.61
27:x:81:GLN:O	27:x:98:ASN:ND2	2.34	0.61
35:C:45:ARG:NH2	49:1:279:U:O4	2.33	0.61
42:f:55:LEU:HB2	42:f:95:PRO:HD3	1.81	0.61
49:1:2816:G:N2	49:1:2819:A:OP2	2.33	0.61
49:1:2970:C:H5'	49:1:2971:A:OP1	1.99	0.61
8:7:173:ARG:NH1	49:1:2899:C:N3	2.49	0.61
10:M:137:ARG:NH1	28:3:28:C:OP1	2.33	0.61
20:s:207:ASN:HA	20:s:210:ARG:HG2	1.82	0.61
48:L:209:SER:HB2	49:1:2466:G:H21	1.65	0.61
9:l:52:LYS:NZ	49:1:353:G:O6	2.33	0.61
38:d:25:LYS:NZ	49:1:1106:G:O3'	2.34	0.61
6:K:148:ALA:HA	6:K:201:THR:HG22	1.83	0.61
39:E:9:ARG:NH1	49:1:912:G:OP2	2.33	0.61
41:F:244:ARG:NH2	49:1:2948:C:OP1	2.34	0.61
2:X:151:TYR:OH	27:x:132:ASN:ND2	2.34	0.60
48:L:192:SER:HB2	48:L:196:LYS:HD2	1.82	0.60
49:1:1940:G:H21	49:1:3362:A:H8	1.47	0.60
49:1:2618:G:N2	49:1:2645:G:OP1	2.34	0.60
49:1:2305:G:OP2	49:1:2305:G:N2	2.29	0.60
31:Z:108:LEU:HG	31:Z:127:THR:HG22	1.83	0.60
41:F:4:ARG:HD2	41:F:7:GLU:HA	1.82	0.60
26:r:56:ASN:HD22	49:1:1282:G:H5'	1.66	0.60
40:e:28:LYS:NZ	49:1:1712:G:O6	2.33	0.60
49:1:1231:A:HO2'	49:1:1261:G:HO2'	1.50	0.60
1:R:247:ALA:CB	1:R:281:THR:CG2	2.78	0.60
3:i:41:ARG:HG2	3:i:56:THR:HG21	1.82	0.60
6:K:126:SER:O	49:1:120:G:N2	2.35	0.60
16:p:37:HIS:HE1	16:p:63:ARG:HH11	1.48	0.60
20:s:155:ARG:HH12	20:s:163:LYS:HA	1.66	0.60
21:T:20:ARG:NH1	49:1:1874:A:N7	2.49	0.60
1:R:245:HIS:HB3	1:R:283:HIS:CE1	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:13:TYR:OH	49:1:1050:U:OP2	2.19	0.60
46:h:86:ARG:NH2	49:1:623:U:O2'	2.35	0.60
16:p:56:LYS:NZ	16:p:145:ASP:OD2	2.35	0.59
22:U:108:GLN:NE2	49:1:1322:U:O2	2.34	0.59
49:1:170:G:H1	49:1:248:U:H3	1.49	0.59
49:1:984:G:N2	49:1:1138:U:OP1	2.35	0.59
49:1:1003:A:N1	49:1:1049:C:O2'	2.34	0.59
28:3:96:U:H2'	28:3:97:A:H8	1.66	0.59
49:1:122:A:N6	49:1:148:G:O2'	2.36	0.59
49:1:2483:G:N2	49:1:2486:A:OP2	2.35	0.59
49:1:3234:A:N1	49:1:3253:G:O6	2.35	0.59
12:N:73:ARG:NH1	49:1:110:G:OP2	2.34	0.59
28:3:28:C:OP2	45:H:57:ASN:ND2	2.34	0.59
36:c:4:ARG:NH2	49:1:1427:U:OP2	2.33	0.59
49:1:1564:U:O2	49:1:1576:G:N2	2.35	0.59
16:p:108:ARG:NH2	49:1:1547:G:OP1	2.34	0.59
20:s:205:LEU:HD23	45:H:289:LYS:HD2	1.84	0.59
22:U:66:GLU:HG3	22:U:68:HIS:H	1.68	0.59
26:r:26:PHE:HB2	26:r:87:VAL:HB	1.83	0.59
30:4:39:G:O2'	30:4:104:A:N6	2.35	0.59
49:1:908:G:N3	49:1:925:A:N6	2.49	0.59
49:1:1551:C:HO2'	49:1:2170:U:HO2'	1.44	0.59
2:X:107:VAL:HG13	2:X:118:HIS:H	1.66	0.59
18:5:181:ARG:NH1	49:1:3268:A:OP1	2.35	0.59
30:4:33:A:H2'	49:1:59:G:H2'	1.84	0.59
39:E:93:LYS:NZ	49:1:2548:C:OP2	2.36	0.59
34:b:107:ARG:NH1	49:1:1634:G:OP1	2.35	0.59
1:R:74:CYS:SG	1:R:77:CYS:HB2	2.43	0.59
22:U:137:ARG:NH2	49:1:1214:U:OP2	2.36	0.59
23:V:51:GLY:HA3	23:V:92:ARG:HG3	1.84	0.59
49:1:3047:U:C4	49:1:3094:A:N1	2.70	0.59
8:7:8:GLN:HB3	8:7:72:LYS:HD2	1.83	0.59
20:s:104:CYS:CB	33:B:1:G:C4'	2.78	0.59
9:l:21:ARG:NH1	9:l:43:LYS:O	2.34	0.59
16:p:4:TYR:OH	49:1:148:G:OP2	2.21	0.59
19:S:39:ARG:NH1	49:1:1348:U:OP2	2.36	0.59
35:C:23:HIS:HA	35:C:73:GLU:O	2.03	0.59
33:B:17:C:O2'	33:B:57:G:N2	2.36	0.58
49:1:907:G:N2	49:1:925:A:O2'	2.36	0.58
33:B:74:C:O2'	33:B:75:C:H5'	2.02	0.58
19:S:86:THR:HG22	19:S:105:ARG:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:130:ARG:NH2	49:1:1062:A:N3	2.48	0.58
49:1:306:A:N6	49:1:2784:G:C2	2.70	0.58
37:D:46:THR:OG1	37:D:57:CYS:SG	2.61	0.58
49:1:1899:G:O2'	49:1:1901:A:N6	2.36	0.58
23:V:119:ALA:HA	23:V:122:GLN:HB3	1.86	0.58
1:R:246:PHE:HD2	1:R:282:PHE:HE1	1.52	0.58
19:S:89:ASP:O	49:1:785:G:N2	2.28	0.58
30:4:16:G:H22	49:1:406:G:H2'	1.68	0.58
38:d:41:ARG:NH1	49:1:776:U:OP1	2.36	0.58
39:E:27:ALA:HB3	39:E:128:ARG:HH21	1.69	0.58
48:L:30:GLU:HB2	48:L:34:LEU:HD11	1.85	0.58
49:1:2631:U:OP1	49:1:2757:U:O2'	2.21	0.58
16:p:45:PRO:O	16:p:49:ARG:HB2	2.03	0.58
22:U:52:LYS:NZ	28:3:101:G:N7	2.51	0.58
48:L:18:LYS:HG3	48:L:24:LYS:H	1.67	0.58
1:R:246:PHE:HD2	1:R:282:PHE:CE1	2.22	0.58
12:N:100:ARG:NH1	49:1:76:G:O2'	2.31	0.58
12:N:169:THR:O	12:N:173:ALA:N	2.37	0.58
6:K:105:LYS:NZ	49:1:123:A:OP1	2.32	0.58
12:N:100:ARG:HH11	49:1:76:G:HO2'	1.52	0.58
39:E:104:LEU:HD22	39:E:158:ILE:HD11	1.86	0.58
41:F:126:LYS:HG3	49:1:3294:A:H5'	1.85	0.58
49:1:542:G:N2	49:1:549:U:O2	2.37	0.58
5:j:79:ASP:OD1	5:j:79:ASP:N	2.31	0.58
7:k:5:THR:HG23	7:k:12:ASN:HB2	1.84	0.57
10:M:47:GLN:HG2	10:M:67:VAL:HG12	1.85	0.57
10:M:133:ARG:NH2	10:M:158:ASP:OD2	2.37	0.57
12:N:2:ALA:HB3	36:c:41:HIS:HE1	1.69	0.57
17:Q:82:LYS:NZ	49:1:1313:G:OP1	2.36	0.57
19:S:12:ARG:NH2	49:1:972:A:OP1	2.37	0.57
6:K:137:ASN:ND2	49:1:148:G:N7	2.51	0.57
12:N:19:GLN:HE22	49:1:801:A:H61	1.51	0.57
12:N:34:SER:O	12:N:37:ASN:HB2	2.05	0.57
23:V:116:ARG:NH1	49:1:1093:A:OP1	2.38	0.57
31:Z:42:ARG:NE	49:1:14:U:O2'	2.37	0.57
39:E:54:ARG:NH2	49:1:2176:U:OP1	2.34	0.57
46:h:13:HIS:ND1	46:h:93:THR:O	2.35	0.57
49:1:173:G:H1	49:1:245:U:H3	1.52	0.57
18:5:56:ARG:NH1	18:5:75:GLU:OE2	2.37	0.57
9:l:14:LYS:NZ	49:1:1491:A:OP1	2.37	0.57
1:R:74:CYS:SG	1:R:77:CYS:SG	3.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:952:A:N3	49:1:1114:U:O2'	2.37	0.57
4:J:160:ARG:NH1	49:1:1363:A:OP1	2.37	0.57
21:T:148:ASP:OD1	21:T:151:ARG:NH2	2.37	0.57
22:U:1:MET:HE1	22:U:36:ILE:HG21	1.86	0.57
30:4:63:G:H1	30:4:97:A:H2	1.51	0.57
10:M:21:ILE:HD11	10:M:125:MET:HE2	1.87	0.57
10:M:92:ARG:HA	10:M:172:LEU:HB2	1.87	0.57
30:4:103:G:OP2	30:4:105:A:O2'	2.23	0.57
41:F:236:LYS:NZ	49:1:2338:C:OP1	2.29	0.57
42:f:13:THR:HG23	42:f:72:ARG:HH11	1.70	0.57
4:J:94:LYS:NZ	49:1:1156:C:OP2	2.37	0.57
6:K:162:LEU:HA	16:p:7:LEU:HD11	1.87	0.57
33:B:14:A:N1	33:B:21:A:O2'	2.36	0.57
37:D:17:ARG:NH2	49:1:860:G:OP1	2.38	0.57
41:F:115:LYS:NZ	41:F:129:ALA:O	2.38	0.57
41:F:126:LYS:NZ	49:1:3294:A:OP2	2.37	0.57
41:F:266:ARG:NH2	49:1:2392:C:O2'	2.37	0.57
15:o:97:ARG:HE	15:o:122:ARG:HB3	1.70	0.56
33:B:21:A:N6	33:B:48:C:OP2	2.37	0.56
47:I:54:TYR:HA	47:I:65:ILE:HG22	1.86	0.56
30:4:71:A:O2'	32:a:52:ARG:NH2	2.38	0.56
35:C:41:ARG:NH1	49:1:284:A:OP2	2.38	0.56
39:E:209:HIS:CD2	39:E:211:HIS:H	2.23	0.56
49:1:221:A:O2'	49:1:223:U:OP2	2.21	0.56
16:p:38:ARG:NH1	30:4:142:C:OP1	2.39	0.56
28:3:77:G:O2'	28:3:101:G:N1	2.37	0.56
30:4:110:C:O2'	30:4:112:U:OP2	2.23	0.56
37:D:66:GLY:HA2	39:E:80:GLU:HG3	1.87	0.56
49:1:1959:G:O6	49:1:2082:U:O2	2.23	0.56
49:1:2534:G:H2'	49:1:2535:A:H8	1.70	0.56
1:R:282:PHE:CD1	1:R:282:PHE:N	2.73	0.56
18:5:3:ARG:O	18:5:18:ARG:NH2	2.39	0.56
18:5:30:ARG:NH1	18:5:31:GLU:OE1	2.39	0.56
20:s:190:LYS:NZ	20:s:211:GLU:OE1	2.37	0.56
37:D:51:ALA:HB1	39:E:50:HIS:HB2	1.87	0.56
39:E:117:GLU:HG2	39:E:124:GLY:H	1.69	0.56
41:F:19:ARG:NH2	49:1:3045:G:OP1	2.39	0.56
2:X:140:GLN:HG2	2:X:173:LEU:HD21	1.87	0.56
9:l:35:SER:O	9:l:45:ARG:NH1	2.38	0.56
41:F:332:ARG:HH21	49:1:3377:G:H21	1.52	0.56
43:G:98:ARG:NH2	49:1:804:C:OP1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:141:ARG:NH1	49:1:743:C:N3	2.54	0.56
45:H:107:ARG:HG3	45:H:251:PRO:HG3	1.88	0.56
49:1:1778:G:O2'	49:1:1780:G:OP2	2.24	0.56
10:M:109:HIS:HD2	10:M:123:PHE:H	1.54	0.56
21:T:98:ARG:NH2	21:T:132:PHE:O	2.37	0.56
29:Y:16:GLY:O	49:1:3050:U:O2'	2.21	0.56
44:g:63:THR:HA	44:g:66:LEU:HD12	1.87	0.56
49:1:1713:G:H1	49:1:1730:G:H2'	1.70	0.56
3:i:52:GLN:NE2	49:1:1638:A:O2'	2.39	0.56
47:I:43:LEU:HD11	47:I:85:ILE:HG13	1.86	0.56
49:1:1627:U:O2	49:1:1817:G:N2	2.29	0.56
13:n:42:ARG:NH2	49:1:1494:U:OP1	2.29	0.56
16:p:35:VAL:HA	16:p:65:ARG:HD3	1.88	0.56
49:1:1813:A:O2'	49:1:1817:G:N3	2.38	0.56
49:1:2842:U:OP1	49:1:2844:C:N4	2.39	0.56
17:Q:34:VAL:HA	17:Q:103:LYS:O	2.05	0.56
1:R:313:ARG:HG2	33:B:73:G:N2	2.22	0.55
34:b:65:ARG:NH2	49:1:1809:A:OP1	2.39	0.55
42:f:57:GLN:NE2	49:1:1474:A:O2'	2.37	0.55
49:1:3150:A:HO2'	49:1:3294:A:HO2'	1.51	0.55
9:l:72:ARG:NH1	30:4:95:G:OP2	2.39	0.55
32:a:55:GLU:HB2	32:a:108:LYS:HB2	1.87	0.55
49:1:2693:C:H5'	49:1:2694:A:H5''	1.87	0.55
49:1:2768:U:H2'	49:1:2769:A:H8	1.71	0.55
1:R:245:HIS:CE1	1:R:283:HIS:HB3	2.41	0.55
10:M:32:ARG:NH1	10:M:120:ILE:O	2.35	0.55
12:N:174:ARG:NH1	49:1:712:G:OP1	2.40	0.55
19:S:148:GLU:N	49:1:787:G:OP1	2.40	0.55
25:P:126:ALA:HB3	25:P:159:GLU:HA	1.87	0.55
26:r:28:VAL:O	26:r:84:VAL:HA	2.06	0.55
49:1:1959:G:O6	49:1:2082:U:C2	2.58	0.55
49:1:3162:C:H2'	49:1:3163:A:H8	1.72	0.55
43:G:195:ARG:NH2	49:1:341:G:N7	2.53	0.55
49:1:815:G:O2'	49:1:920:A:N7	2.38	0.55
8:7:163:GLN:NE2	49:1:3109:G:O2'	2.39	0.55
33:B:68:C:H2'	33:B:69:G:C8	2.42	0.55
44:g:90:LYS:N	47:I:13:GLU:OE2	2.37	0.55
6:K:72:PRO:HG3	16:p:18:VAL:HA	1.87	0.55
13:n:48:LYS:NZ	49:1:1843:C:OP1	2.38	0.55
21:T:7:GLN:HE21	21:T:36:ASN:HA	1.72	0.55
1:R:352:LYS:HG2	1:R:356:ASP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:17:ARG:NH1	23:V:45:ASN:OD1	2.40	0.55
32:a:103:LYS:NZ	49:1:217:U:O2	2.38	0.55
49:1:718:G:H1	49:1:750:G:H21	1.55	0.55
49:1:1564:U:O4	49:1:1576:G:O6	2.25	0.55
49:1:86:G:O2'	49:1:98:G:O6	2.25	0.55
49:1:510:G:O6	49:1:581:U:O4	2.25	0.55
4:J:121:LYS:HB2	23:V:133:ALA:HB3	1.89	0.54
40:e:57:GLU:OE2	40:e:69:TYR:OH	2.25	0.54
45:H:210:GLU:O	45:H:214:ASP:HB2	2.07	0.54
22:U:26:ARG:NH1	23:V:150:THR:OG1	2.38	0.54
33:B:1:G:H2'	33:B:2:G:H8	1.72	0.54
44:g:19:ARG:HH21	44:g:33:ARG:HD2	1.73	0.54
47:I:19:LYS:NZ	49:1:593:C:OP2	2.37	0.54
48:L:122:ARG:NH1	49:1:2483:G:OP2	2.40	0.54
21:T:79:GLY:N	49:1:1938:U:O2'	2.40	0.54
48:L:40:ASN:HB2	48:L:163:LEU:HB3	1.90	0.54
49:1:664:U:H2'	49:1:665:A:C8	2.42	0.54
49:1:1018:G:H2'	49:1:1019:G:H8	1.72	0.54
49:1:2815:G:N2	49:1:2818:U:O2	2.39	0.54
1:R:344:ARG:HH11	1:R:346:ARG:HG3	1.71	0.54
20:s:104:CYS:SG	33:B:1:G:H5'	2.46	0.54
49:1:218:G:H1'	49:1:372:A:H1'	1.88	0.54
49:1:684:G:N2	49:1:697:A:N1	2.55	0.54
49:1:2234:G:O2'	49:1:2603:G:O2'	2.24	0.54
49:1:3055:U:O2'	49:1:3057:U:OP2	2.24	0.54
18:5:2:ALA:N	49:1:398:A:OP2	2.41	0.54
29:Y:17:ARG:NH1	41:F:368:GLY:O	2.41	0.54
33:B:15:G:N1	33:B:48:C:N3	2.51	0.54
39:E:146:THR:OG1	39:E:160:SER:OG	2.26	0.54
41:F:251:CYS:SG	49:1:2943:G:N2	2.81	0.54
49:1:2794:G:O2'	49:1:2795:U:O4'	2.22	0.54
30:4:63:G:O6	30:4:97:A:N1	2.40	0.54
49:1:2457:G:O2'	49:1:2481:G:N2	2.40	0.54
31:Z:90:ALA:O	31:Z:120:LYS:NZ	2.41	0.54
43:G:216:VAL:O	43:G:220:ARG:HB3	2.08	0.54
46:h:86:ARG:NH1	46:h:87:ASN:OD1	2.40	0.54
49:1:2351:U:H2'	49:1:2352:A:H8	1.73	0.54
9:l:27:PHE:HA	9:l:34:CYS:HA	1.90	0.54
17:Q:159:LYS:NZ	49:1:3243:A:OP1	2.41	0.54
39:E:241:ARG:NH1	49:1:2155:G:OP1	2.41	0.54
28:3:77:G:N2	28:3:102:A:OP2	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:1149:G:H21	49:1:1199:C:H42	1.54	0.53
49:1:1468:A:N6	49:1:1508:C:O2	2.41	0.53
49:1:3057:U:OP1	49:1:3085:G:N2	2.39	0.53
17:Q:164:SER:O	17:Q:167:TYR:HB3	2.08	0.53
22:U:22:PRO:O	23:V:146:ASN:ND2	2.41	0.53
26:r:34:SER:HA	49:1:1230:G:H4'	1.89	0.53
49:1:2085:U:H2'	49:1:2086:A:H8	1.73	0.53
49:1:3234:A:N1	49:1:3253:G:C6	2.77	0.53
19:S:69:ARG:HH21	49:1:784:A:H5'	1.72	0.53
23:V:66:ASN:ND2	38:d:34:GLY:O	2.41	0.53
43:G:206:LEU:HB2	43:G:246:ARG:HH21	1.74	0.53
45:H:58:LYS:HA	45:H:93:THR:HG21	1.90	0.53
48:L:18:LYS:HB2	48:L:23:THR:HB	1.90	0.53
49:1:1411:C:H2'	49:1:1412:G:H8	1.72	0.53
49:1:3216:G:H22	49:1:3258:U:H5''	1.73	0.53
6:K:144:GLU:OE1	7:k:36:ARG:NH1	2.40	0.53
36:c:10:LYS:NZ	49:1:1374:G:O6	2.40	0.53
49:1:348:A:N3	49:1:352:A:O2'	2.42	0.53
16:p:97:SER:HB3	49:1:289:A:H5''	1.90	0.53
36:c:7:LYS:O	36:c:11:HIS:ND1	2.41	0.53
47:I:77:ARG:NH2	49:1:3273:A:OP2	2.40	0.53
23:V:75:ILE:HA	23:V:87:LYS:O	2.09	0.53
41:F:41:VAL:HG22	41:F:185:GLY:HA3	1.90	0.53
48:L:76:ARG:O	48:L:141:ASN:ND2	2.42	0.53
10:M:22:SER:HB2	49:1:2675:C:H42	1.73	0.53
10:M:107:ASP:HA	10:M:124:GLY:HA2	1.91	0.53
13:n:17:LYS:NZ	49:1:1521:G:O6	2.42	0.53
27:x:87:ARG:HH22	27:x:137:VAL:HG13	1.74	0.53
11:m:2:ALA:HA	49:1:1747:G:H21	1.74	0.53
21:T:78:TYR:O	49:1:1914:G:N2	2.42	0.53
10:M:23:VAL:HG12	10:M:25:GLU:H	1.74	0.53
18:5:50:GLN:HB3	18:5:55:GLN:HB3	1.90	0.53
35:C:10:THR:O	35:C:20:HIS:HA	2.09	0.53
41:F:244:ARG:NH1	49:1:2946:A:O2'	2.41	0.53
46:h:107:ILE:O	47:I:31:ARG:NE	2.42	0.53
49:1:577:C:O2'	49:1:579:G:OP1	2.27	0.53
49:1:835:G:O2'	49:1:858:A:N6	2.42	0.53
49:1:920:A:OP1	49:1:923:C:N4	2.42	0.52
49:1:1015:U:H3	49:1:1035:G:H22	1.57	0.52
49:1:1464:G:H22	49:1:1467:A:H5'	1.74	0.52
49:1:953:G:N2	49:1:1115:G:OP1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:k:26:ILE:HD13	49:1:157:A:C8	2.44	0.52
49:1:197:G:N2	49:1:218:G:O2'	2.41	0.52
49:1:394:G:N1	49:1:397:A:OP2	2.36	0.52
49:1:2829:U:H2'	49:1:2830:G:H8	1.75	0.52
36:c:104:THR:HG21	36:c:112:ILE:HD11	1.92	0.52
45:H:90:HIS:NE2	45:H:229:ASP:OD2	2.35	0.52
18:5:120:ASN:OD1	18:5:120:ASN:N	2.40	0.52
20:s:173:THR:OG1	20:s:174:ASN:N	2.42	0.52
45:H:8:LYS:NZ	49:1:2687:G:OP1	2.43	0.52
48:L:169:VAL:HB	48:L:172:VAL:HG23	1.91	0.52
49:1:3042:U:OP2	49:1:3092:C:N4	2.42	0.52
2:X:15:VAL:HA	2:X:61:ARG:HG2	1.91	0.52
18:5:70:THR:OG1	18:5:71:ALA:N	2.37	0.52
22:U:57:GLU:HG3	23:V:136:ARG:HH21	1.73	0.52
22:U:160:THR:N	49:1:3207:U:O4	2.41	0.52
27:x:112:SER:O	27:x:132:ASN:ND2	2.42	0.52
49:1:651:G:O2'	49:1:1435:A:OP1	2.27	0.52
49:1:3092:C:O2'	49:1:3094:A:OP2	2.27	0.52
1:R:315:TYR:HE2	20:s:104:CYS:HB3	1.75	0.52
21:T:71:ARG:HH12	49:1:2100:A:H5'	1.73	0.52
46:h:54:ARG:HG2	46:h:64:ILE:HG12	1.91	0.52
49:1:591:G:N2	49:1:612:U:OP1	2.38	0.52
49:1:1477:A:OP1	49:1:3075:G:O2'	2.28	0.52
49:1:2043:U:O4	49:1:2045:G:N2	2.42	0.52
15:o:99:CYS:HB3	15:o:115:CYS:HB3	1.91	0.52
17:Q:72:HIS:O	17:Q:74:ARG:NH1	2.42	0.52
21:T:102:LEU:HD22	21:T:138:LEU:HD13	1.90	0.52
41:F:57:VAL:HG22	41:F:73:VAL:HG12	1.92	0.52
49:1:753:C:H2'	49:1:754:G:H8	1.74	0.52
49:1:1277:C:H2'	49:1:1278:A:H8	1.75	0.52
49:1:2901:G:O2'	49:1:3024:A:N1	2.43	0.52
24:W:21:SER:O	24:W:25:ASN:ND2	2.42	0.52
41:F:218:ILE:HG12	41:F:276:THR:HG23	1.92	0.52
42:f:26:LYS:HD3	42:f:64:VAL:HG21	1.91	0.52
43:G:82:THR:HG23	43:G:84:ARG:H	1.74	0.52
48:L:56:PRO:HG3	48:L:187:VAL:HG21	1.92	0.52
49:1:938:C:OP1	49:1:962:A:O2'	2.28	0.52
49:1:1093:A:O2'	49:1:1094:U:O4'	2.28	0.52
2:X:102:SER:OG	2:X:103:ALA:N	2.43	0.51
10:M:142:LYS:NZ	49:1:2664:C:OP2	2.37	0.51
14:O:46:ILE:O	14:O:55:ARG:HA	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:99:LEU:HD11	21:T:103:ARG:HH21	1.75	0.51
23:V:43:LYS:HG3	23:V:58:GLN:HE22	1.76	0.51
33:B:15:G:O6	33:B:48:C:O2	2.28	0.51
41:F:53:MET:HG2	41:F:77:THR:HG22	1.91	0.51
8:7:114:VAL:HB	8:7:124:ARG:HB2	1.91	0.51
14:O:23:ILE:O	14:O:30:GLY:CA	2.58	0.51
23:V:18:ASP:HB2	23:V:21:LYS:HB2	1.91	0.51
28:3:5:G:O2'	45:H:63:GLN:NE2	2.44	0.51
28:3:13:A:H5''	28:3:14:U:H5	1.75	0.51
40:e:17:VAL:HG11	40:e:92:ILE:HD12	1.92	0.51
47:I:51:ARG:HH21	47:I:163:PHE:HD1	1.57	0.51
49:1:1243:G:O6	49:1:1248:C:N4	2.43	0.51
3:i:20:ILE:HD12	3:i:32:ALA:HB1	1.92	0.51
4:J:143:THR:HG22	4:J:241:LYS:HE3	1.93	0.51
6:K:140:VAL:HG22	6:K:166:LEU:HD21	1.92	0.51
18:5:168:LEU:O	18:5:173:ARG:NH2	2.43	0.51
34:b:33:SER:OG	34:b:34:LYS:N	2.44	0.51
39:E:181:LYS:NZ	49:1:860:G:OP2	2.39	0.51
43:G:35:VAL:HG21	43:G:244:LEU:HD21	1.92	0.51
43:G:203:ARG:NH2	43:G:226:GLU:OE1	2.43	0.51
49:1:397:A:O2'	49:1:400:G:OP2	2.28	0.51
2:X:18:LYS:HB3	2:X:25:LEU:HB2	1.91	0.51
2:X:27:ALA:O	2:X:35:TYR:OH	2.26	0.51
41:F:10:ARG:NH2	41:F:263:SER:O	2.43	0.51
41:F:303:LYS:HD2	41:F:361:THR:HG21	1.91	0.51
46:h:19:SER:OG	49:1:1330:A:OP1	2.28	0.51
49:1:371:G:N1	49:1:374:A:OP2	2.44	0.51
49:1:1149:G:H21	49:1:1199:C:N4	2.07	0.51
4:J:45:LEU:HD12	43:G:329:PRO:HB2	1.92	0.51
16:p:38:ARG:NH2	30:4:143:U:OP1	2.42	0.51
22:U:2:ALA:HB3	22:U:32:SER:HB2	1.92	0.51
28:3:19:C:H2'	28:3:20:A:H8	1.75	0.51
49:1:655:C:H2'	49:1:656:A:H8	1.75	0.51
49:1:1235:U:H4'	49:1:1236:G:H5'	1.93	0.51
1:R:101:LYS:NZ	2:X:120:ASP:OD1	2.43	0.51
15:o:114:LYS:NZ	49:1:2908:G:O2'	2.44	0.51
18:5:61:ARG:HE	18:5:78:VAL:HG21	1.76	0.51
34:b:54:THR:HG22	34:b:57:HIS:CD2	2.46	0.51
49:1:120:G:O2'	49:1:121:A:N7	2.42	0.51
8:7:134:ILE:HG13	8:7:146:LEU:HG	1.93	0.51
20:s:113:GLY:HA2	49:1:2864:A:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:F:364:LYS:HD2	49:1:3049:A:H4'	1.93	0.51
49:1:3016:A:H2'	49:1:3017:A:H8	1.75	0.51
1:R:285:TYR:O	1:R:316:ASN:ND2	2.44	0.51
27:x:12:ARG:NH1	49:1:3041:U:OP1	2.41	0.51
12:N:158:ALA:HA	36:c:97:GLU:HA	1.93	0.51
44:g:75:LEU:HD11	49:1:1410:U:H4'	1.92	0.51
49:1:1252:A:N6	49:1:1263:A:O2'	2.41	0.51
6:K:50:VAL:HG12	31:Z:30:ALA:HA	1.92	0.51
28:3:6:C:O3'	45:H:50:ARG:NH2	2.43	0.51
28:3:62:U:O3'	45:H:285:ARG:NH1	2.44	0.51
34:b:88:ASP:O	34:b:121:ARG:NH2	2.44	0.51
49:1:19:U:H2'	49:1:20:A:C8	2.46	0.51
49:1:624:G:H2'	49:1:625:G:H8	1.76	0.51
49:1:1975:C:H3'	49:1:1976:G:H8	1.76	0.51
1:R:462:LEU:HD11	1:R:500:ILE:HD13	1.93	0.50
2:X:66:ASN:OD1	2:X:69:GLY:N	2.44	0.50
11:m:43:PHE:O	11:m:53:THR:HA	2.11	0.50
12:N:28:GLN:NE2	49:1:683:U:OP2	2.40	0.50
49:1:1134:G:O2'	49:1:2642:A:N3	2.36	0.50
1:R:439:LEU:HD22	1:R:448:ILE:HD12	1.93	0.50
4:J:116:PHE:O	4:J:199:ASN:ND2	2.38	0.50
17:Q:173:ALA:O	17:Q:176:LYS:HB3	2.10	0.50
22:U:7:TYR:HE2	22:U:34:GLU:HA	1.74	0.50
39:E:221:LYS:NZ	49:1:2965:U:O2	2.44	0.50
43:G:61:SER:O	43:G:61:SER:OG	2.26	0.50
21:T:62:ARG:HH12	49:1:3067:C:H3'	1.77	0.50
9:l:16:HIS:NE2	49:1:815:G:OP1	2.40	0.50
34:b:95:VAL:HG21	34:b:113:VAL:HG11	1.93	0.50
41:F:166:ILE:HD11	41:F:171:LEU:HD12	1.94	0.50
49:1:542:G:O6	49:1:549:U:O4	2.28	0.50
3:i:41:ARG:O	3:i:43:LYS:NZ	2.44	0.50
13:n:27:ILE:O	13:n:33:ASN:ND2	2.45	0.50
20:s:104:CYS:HG	33:B:1:G:H4'	0.68	0.50
42:f:75:ILE:HG12	42:f:93:VAL:HG22	1.93	0.50
5:j:10:ARG:NH2	30:4:65:A:O2'	2.44	0.50
28:3:79:A:H62	28:3:101:G:H21	1.59	0.50
29:Y:6:ASP:OD1	29:Y:32:GLN:N	2.43	0.50
43:G:58:HIS:NE2	43:G:98:ARG:HD3	2.27	0.50
18:5:122:ALA:HB3	18:5:143:PRO:HG2	1.92	0.50
20:s:183:LYS:NZ	20:s:188:GLU:OE1	2.38	0.50
49:1:28:C:O2'	49:1:61:A:N3	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:2227:C:H2'	49:1:2228:A:H8	1.76	0.50
8:7:90:MET:HE2	8:7:179:ILE:HG22	1.92	0.50
19:S:179:ARG:NH1	49:1:709:A:OP1	2.37	0.50
31:Z:86:VAL:HG21	31:Z:95:ILE:HG12	1.93	0.50
36:c:26:ARG:HH12	49:1:938:C:H3'	1.76	0.50
43:G:326:ARG:NH1	49:1:608:A:O3'	2.45	0.50
43:G:332:LYS:NZ	49:1:599:C:OP1	2.42	0.50
49:1:103:G:HO2'	49:1:699:A:HO2'	1.57	0.50
49:1:856:G:OP1	49:1:1722:U:O2'	2.29	0.50
20:s:104:CYS:CB	33:B:1:G:C1'	2.71	0.50
20:s:169:LYS:HB3	20:s:176:ASP:HA	1.92	0.50
32:a:114:ASP:O	32:a:118:LEU:HB2	2.12	0.50
43:G:98:ARG:NH1	43:G:99:MET:O	2.45	0.50
47:I:40:LEU:HD13	47:I:84:VAL:HG11	1.92	0.50
49:1:2285:C:H3'	49:1:2286:U:H2'	1.94	0.50
3:i:13:TYR:O	3:i:18:ASN:ND2	2.45	0.49
5:j:47:VAL:O	5:j:50:SER:HB2	2.12	0.49
12:N:13:HIS:NE2	49:1:98:G:N7	2.60	0.49
12:N:79:GLU:OE2	12:N:103:ASN:ND2	2.44	0.49
20:s:46:PRO:HD2	20:s:140:LYS:HA	1.93	0.49
41:F:223:GLY:HA2	41:F:271:GLY:HA3	1.94	0.49
49:1:627:U:H2'	49:1:628:A:C8	2.47	0.49
49:1:2307:G:O2'	49:1:2310:U:OP2	2.30	0.49
49:1:2810:C:OP2	49:1:2955:U:O2'	2.30	0.49
3:i:37:LYS:NZ	49:1:1591:G:OP1	2.42	0.49
13:n:28:ARG:NH1	13:n:36:ARG:O	2.42	0.49
20:s:105:ALA:H	33:B:1:G:H1'	1.77	0.49
23:V:108:ARG:NH1	49:1:1098:A:OP2	2.43	0.49
32:a:2:ALA:N	49:1:212:G:OP2	2.44	0.49
40:e:16:LEU:O	40:e:20:SER:OG	2.24	0.49
41:F:163:HIS:ND1	41:F:164:THR:O	2.42	0.49
49:1:371:G:H22	49:1:374:A:H5''	1.76	0.49
49:1:584:G:H2'	49:1:585:A:H8	1.77	0.49
49:1:2568:C:OP1	49:1:2569:A:N6	2.46	0.49
4:J:86:VAL:O	4:J:114:GLY:HA2	2.12	0.49
10:M:17:LEU:HD13	10:M:129:VAL:HG22	1.95	0.49
12:N:42:ARG:HG2	12:N:46:ILE:HG12	1.95	0.49
49:1:3348:G:O6	49:1:3357:U:O4	2.30	0.49
4:J:88:ARG:NH2	4:J:91:GLY:O	2.46	0.49
27:x:45:ARG:HB3	27:x:48:ARG:HE	1.76	0.49
33:B:70:U:H2'	33:B:71:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:G:309:ARG:NH1	49:1:590:G:O2'	2.44	0.49
44:g:73:THR:OG1	44:g:95:GLU:OE1	2.28	0.49
47:I:26:ARG:NH1	49:1:503:C:O5'	2.44	0.49
49:1:1015:U:O4	49:1:1035:G:N1	2.36	0.49
49:1:3258:U:O2'	49:1:3260:G:OP1	2.22	0.49
30:4:126:A:O2'	30:4:129:C:N4	2.45	0.49
39:E:14:SER:OG	39:E:15:ILE:N	2.45	0.49
39:E:30:ARG:HH12	39:E:41:ILE:HD13	1.76	0.49
41:F:221:THR:HB	41:F:273:HIS:H	1.77	0.49
49:1:129:U:H2'	49:1:130:A:C8	2.47	0.49
13:n:27:ILE:HD13	30:4:52:A:H62	1.78	0.49
20:s:144:LYS:HD2	20:s:166:LEU:HD11	1.94	0.49
29:Y:46:PRO:HB2	29:Y:54:LEU:HD22	1.94	0.49
45:H:148:ILE:HG12	45:H:159:VAL:HG11	1.94	0.49
49:1:339:C:OP1	49:1:1380:G:O2'	2.30	0.49
49:1:2085:U:H2'	49:1:2086:A:C8	2.47	0.49
1:R:247:ALA:HB2	1:R:281:THR:HG22	1.92	0.49
10:M:105:GLY:HA3	49:1:2674:A:H5''	1.95	0.49
11:m:46:ARG:HH11	11:m:51:LEU:HB2	1.76	0.49
16:p:68:ARG:HA	16:p:98:LEU:HD21	1.95	0.49
16:p:179:LYS:O	49:1:286:U:O2'	2.31	0.49
28:3:11:A:N1	28:3:67:G:O2'	2.42	0.49
28:3:72:A:C5	28:3:74:C:N4	2.81	0.49
30:4:114:G:OP1	49:1:1831:U:O2'	2.27	0.49
43:G:269:SER:OG	43:G:271:LYS:O	2.26	0.49
46:h:56:SER:O	46:h:63:LYS:NZ	2.46	0.49
49:1:1250:G:H2'	49:1:1251:A:C8	2.48	0.49
49:1:1261:G:N2	49:1:1261:G:OP2	2.46	0.49
1:R:246:PHE:O	1:R:281:THR:HA	2.12	0.49
4:J:178:ILE:HD11	4:J:187:GLU:HG3	1.95	0.49
19:S:170:ARG:HD2	36:c:57:GLY:HA3	1.95	0.49
20:s:42:VAL:HG21	20:s:196:VAL:HG23	1.95	0.49
28:3:72:A:C6	28:3:74:C:C4	3.01	0.49
49:1:2892:A:N3	49:1:3129:A:O2'	2.38	0.49
8:7:62:ARG:NH2	49:1:3115:C:OP1	2.42	0.49
19:S:40:THR:OG1	19:S:45:ASN:ND2	2.46	0.49
26:r:64:ARG:NH1	49:1:1221:A:OP2	2.46	0.49
33:B:75:C:OP2	49:1:2971:A:H8	1.96	0.49
34:b:90:GLU:HA	34:b:93:LYS:HB2	1.94	0.49
49:1:52:A:N3	49:1:811:U:O2'	2.46	0.49
49:1:649:A:OP2	49:1:2868:U:O2'	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:1155:C:O2'	49:1:1197:A:N1	2.46	0.49
8:7:9:GLN:HG2	8:7:54:LYS:HG2	1.94	0.49
23:V:102:ARG:HH21	23:V:106:LEU:HD11	1.78	0.49
41:F:306:THR:HG21	41:F:316:GLU:HG2	1.95	0.49
49:1:716:A:OP1	49:1:752:C:O2'	2.31	0.49
49:1:2904:U:H2'	49:1:2905:U:H6	1.78	0.49
49:1:3011:A:N1	49:1:3043:C:O2'	2.41	0.49
34:b:24:VAL:HG11	34:b:87:LEU:HD23	1.95	0.48
43:G:315:LYS:NZ	49:1:609:G:OP2	2.38	0.48
49:1:1863:G:N1	49:1:1866:C:OP2	2.42	0.48
16:p:176:LYS:NZ	49:1:77:A:O2'	2.37	0.48
21:T:88:ARG:NH1	49:1:1864:A:OP1	2.46	0.48
34:b:74:VAL:HG23	34:b:101:PHE:HE2	1.78	0.48
48:L:59:PRO:HG2	48:L:180:VAL:HG22	1.93	0.48
49:1:2129:U:H2'	49:1:2130:G:C8	2.49	0.48
49:1:2946:A:H5''	49:1:2947:G:H5'	1.94	0.48
1:R:191:ILE:HG13	1:R:208:LYS:HG2	1.94	0.48
2:X:23:TYR:OH	2:X:69:GLY:O	2.30	0.48
27:x:23:MET:HE1	27:x:78:VAL:HG22	1.94	0.48
39:E:209:HIS:HD2	39:E:211:HIS:H	1.61	0.48
43:G:150:LEU:HD21	43:G:172:VAL:HG11	1.95	0.48
48:L:103:LEU:HG	48:L:128:LEU:HD22	1.96	0.48
49:1:373:A:C6	49:1:375:A:C6	3.00	0.48
49:1:1259:A:N3	49:1:1280:C:O2'	2.46	0.48
12:N:27:ASP:HB3	30:4:29:U:H5''	1.95	0.48
34:b:10:VAL:HG22	34:b:24:VAL:HG12	1.95	0.48
39:E:113:VAL:HG12	39:E:166:ILE:HD13	1.95	0.48
49:1:1378:U:H2'	49:1:1379:G:H8	1.78	0.48
2:X:108:ILE:HG12	2:X:117:VAL:HG12	1.95	0.48
7:k:76:ARG:O	49:1:293:C:O2'	2.27	0.48
9:l:66:TYR:OH	9:l:73:ARG:NH2	2.39	0.48
27:x:28:ASN:HD21	27:x:112:SER:HG	1.61	0.48
43:G:240:PRO:HB2	49:1:1383:G:H4'	1.95	0.48
43:G:326:ARG:HG3	43:G:327:LEU:HD12	1.94	0.48
45:H:68:THR:HG22	45:H:70:THR:H	1.78	0.48
49:1:1381:A:H2'	49:1:1382:G:H8	1.79	0.48
18:5:132:ALA:HB3	49:1:879:U:H4'	1.96	0.48
39:E:33:ASP:OD1	39:E:33:ASP:N	2.47	0.48
49:1:1693:C:HO2'	49:1:1772:U:HO2'	1.58	0.48
49:1:2761:G:O2'	49:1:2800:G:N2	2.47	0.48
5:j:25:LYS:NZ	31:Z:58:ASP:OD2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:j:86:ARG:NH1	30:4:37:A:OP2	2.43	0.48
7:k:34:SER:O	7:k:37:THR:OG1	2.31	0.48
18:5:24:VAL:HG22	18:5:90:PHE:HD2	1.78	0.48
18:5:129:THR:HG22	49:1:1507:G:H8	1.77	0.48
27:x:22:ILE:HG12	27:x:35:TYR:HD1	1.79	0.48
28:3:36:C:H2'	28:3:37:G:C8	2.49	0.48
46:h:52:VAL:HG22	46:h:66:VAL:HG22	1.96	0.48
49:1:903:U:H2'	49:1:904:A:H8	1.78	0.48
49:1:1018:G:O6	49:1:1034:U:O4	2.31	0.48
49:1:1255:C:H2'	49:1:1256:G:H8	1.79	0.48
49:1:1273:A:H3'	49:1:1274:A:H8	1.79	0.48
49:1:2449:A:H61	49:1:2497:U:H3	1.62	0.48
49:1:2821:C:N4	49:1:2869:U:H3	2.11	0.48
5:j:85:THR:HG23	5:j:88:LEU:H	1.79	0.48
39:E:116:VAL:HG13	39:E:126:LEU:HB2	1.94	0.48
39:E:134:VAL:HG12	39:E:151:PRO:HD3	1.96	0.48
49:1:516:A:H2'	49:1:517:G:H8	1.78	0.48
49:1:2112:U:H4'	49:1:2113:A:H5'	1.95	0.48
6:K:115:ALA:O	6:K:119:GLY:N	2.47	0.48
33:B:9:G:O2'	33:B:10:G:N7	2.45	0.48
48:L:210:MET:SD	49:1:2489:C:O2'	2.71	0.48
49:1:500:C:H2'	49:1:501:A:H8	1.79	0.48
49:1:980:A:H2	49:1:1104:G:H21	1.60	0.48
49:1:1018:G:H2'	49:1:1019:G:C8	2.48	0.48
49:1:1129:A:N6	49:1:2864:A:O2'	2.46	0.48
49:1:1231:A:H4'	49:1:1261:G:H8	1.78	0.48
49:1:1566:A:H2'	49:1:1567:U:H4'	1.96	0.48
49:1:1604:G:H4'	49:1:1835:A:H4'	1.96	0.48
49:1:1900:A:O2'	49:1:1901:A:OP2	2.31	0.48
49:1:1977:C:N3	49:1:2046:U:O2'	2.44	0.48
5:j:94:LYS:O	5:j:98:SER:HB3	2.14	0.48
12:N:55:ARG:NH1	12:N:73:ARG:O	2.41	0.48
26:r:55:LYS:HD3	26:r:58:MET:HB2	1.96	0.48
28:3:8:G:OP2	45:H:30:TYR:OH	2.24	0.48
35:C:3:ASN:HB3	49:1:2655:U:H5'	1.96	0.48
40:e:22:LYS:HB2	40:e:94:GLU:HB2	1.96	0.48
49:1:270:U:HO2'	49:1:318:A:HO2'	1.55	0.48
49:1:275:U:OP2	49:1:285:A:N6	2.46	0.48
49:1:2662:G:H2'	49:1:2663:G:C8	2.49	0.48
8:7:141:LYS:NZ	8:7:142:ASP:OD2	2.42	0.47
18:5:118:GLN:OE1	49:1:412:G:N2	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:E:132:ASN:ND2	49:1:2178:A:OP1	2.47	0.47
43:G:37:THR:O	43:G:40:THR:OG1	2.32	0.47
1:R:28:LEU:HD13	1:R:227:ASN:HD22	1.79	0.47
9:l:21:ARG:HG3	30:4:103:G:H4'	1.96	0.47
10:M:51:ARG:O	10:M:61:ARG:NH2	2.47	0.47
14:O:57:ALA:HB2	22:U:97:VAL:HG21	1.96	0.47
16:p:188:ARG:NH2	49:1:31:C:OP2	2.47	0.47
26:r:55:LYS:HG2	26:r:58:MET:H	1.79	0.47
26:r:101:VAL:HG22	26:r:186:THR:HA	1.96	0.47
27:x:97:ASP:N	27:x:97:ASP:OD1	2.46	0.47
34:b:11:ALA:HA	34:b:81:LEU:O	2.14	0.47
43:G:5:GLN:HE22	43:G:21:PRO:HG3	1.78	0.47
49:1:2361:A:N6	49:1:2376:G:O6	2.47	0.47
49:1:2560:C:N4	49:1:2575:G:OP2	2.47	0.47
49:1:3153:U:O2'	49:1:3155:U:OP1	2.29	0.47
49:1:3232:G:O6	49:1:3255:U:O4	2.31	0.47
11:m:44:LYS:NZ	49:1:1751:G:O6	2.39	0.47
12:N:185:LYS:HD3	49:1:2781:U:H4'	1.96	0.47
43:G:338:LYS:O	43:G:340:GLY:N	2.47	0.47
49:1:1240:A:N1	49:1:1248:C:N4	2.62	0.47
17:Q:133:ARG:NE	49:1:1316:C:OP2	2.47	0.47
26:r:27:VAL:HG21	26:r:76:LEU:HD21	1.96	0.47
42:f:16:LEU:N	42:f:69:TYR:O	2.47	0.47
43:G:300:ARG:NH2	49:1:1347:U:OP2	2.47	0.47
49:1:2007:G:N2	49:1:2014:U:O2	2.40	0.47
49:1:2385:G:O2'	49:1:2386:A:O5'	2.28	0.47
49:1:2441:A:H2'	49:1:2442:G:C8	2.49	0.47
49:1:3152:U:H1'	49:1:3294:A:C5	2.49	0.47
8:7:20:ILE:HD13	14:O:7:VAL:HG22	1.96	0.47
22:U:73:LYS:NZ	22:U:97:VAL:O	2.35	0.47
43:G:162:THR:N	49:1:210:U:OP2	2.43	0.47
45:H:261:THR:OG1	45:H:264:GLN:OE1	2.21	0.47
48:L:30:GLU:HG2	49:1:2470:C:H4'	1.96	0.47
49:1:129:U:H2'	49:1:130:A:H8	1.79	0.47
4:J:77:VAL:HG12	22:U:59:VAL:HA	1.96	0.47
22:U:170:THR:OG1	49:1:3186:A:OP2	2.33	0.47
38:d:19:ASN:ND2	49:1:970:A:OP2	2.47	0.47
49:1:1255:C:H2'	49:1:1256:G:C8	2.49	0.47
1:R:512:ASN:HB3	1:R:521:PHE:HB2	1.96	0.47
3:i:58:ARG:NH2	49:1:1592:G:OP1	2.41	0.47
8:7:2:LYS:O	22:U:142:GLN:NE2	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:99:THR:O	10:M:154:THR:OG1	2.33	0.47
12:N:57:VAL:HG22	12:N:147:ILE:HG23	1.97	0.47
20:s:115:ARG:NH2	49:1:2617:U:O2'	2.48	0.47
28:3:107:C:H2'	28:3:108:A:H8	1.79	0.47
33:B:62:C:H2'	33:B:63:G:H8	1.79	0.47
41:F:65:SER:OG	41:F:66:LYS:N	2.47	0.47
42:f:10:ARG:HH11	42:f:44:MET:HE1	1.79	0.47
49:1:838:G:O6	49:1:855:U:O2	2.33	0.47
49:1:843:A:H2'	49:1:844:G:H8	1.79	0.47
49:1:1497:C:H2'	49:1:1498:A:C8	2.49	0.47
49:1:1955:U:O4	49:1:1956:A:N6	2.48	0.47
49:1:2007:G:H1	49:1:2014:U:H3	1.61	0.47
49:1:3016:A:H2'	49:1:3017:A:C8	2.49	0.47
18:5:119:VAL:HG12	18:5:146:ILE:HG23	1.97	0.47
22:U:52:LYS:H	22:U:55:SER:HG	1.60	0.47
33:B:3:G:C6	33:B:4:C:C4	3.03	0.47
49:1:87:U:OP2	49:1:98:G:N1	2.47	0.47
49:1:1047:A:N3	49:1:2633:U:O2'	2.48	0.47
49:1:3233:C:H2'	49:1:3234:A:C8	2.50	0.47
2:X:112:ASP:OD2	2:X:156:ASN:ND2	2.48	0.47
27:x:18:PRO:HA	27:x:51:ALA:HA	1.96	0.47
49:1:708:G:N2	49:1:711:A:OP2	2.48	0.47
6:K:62:LYS:NZ	6:K:158:ASP:OD2	2.47	0.47
11:m:2:ALA:N	49:1:1613:A:OP1	2.48	0.47
32:a:114:ASP:O	32:a:118:LEU:CB	2.63	0.47
33:B:13:U:O2	33:B:22:G:O6	2.33	0.47
49:1:664:U:H2'	49:1:665:A:H8	1.80	0.47
49:1:684:G:H2'	49:1:685:G:H8	1.80	0.47
49:1:1203:A:H2'	49:1:1204:A:H8	1.80	0.47
49:1:1605:A:O2'	49:1:1607:U:OP2	2.27	0.47
49:1:2568:C:O2'	49:1:2569:A:O4'	2.32	0.47
14:O:40:ASP:N	14:O:40:ASP:OD1	2.46	0.46
41:F:128:LYS:HE2	49:1:3293:U:H5'	1.97	0.46
49:1:531:G:H2'	49:1:532:A:C8	2.50	0.46
17:Q:9:ILE:HD11	22:U:163:PHE:HE1	1.80	0.46
21:T:23:TRP:CH2	21:T:25:ASP:HB3	2.50	0.46
40:e:9:SER:OG	40:e:10:ILE:N	2.49	0.46
41:F:327:CYS:HB2	49:1:3047:U:O2'	2.15	0.46
49:1:2049:A:H8	49:1:2050:C:H4'	1.80	0.46
49:1:2999:U:H2'	49:1:3000:A:C8	2.50	0.46
14:O:23:ILE:O	14:O:30:GLY:HA2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:130:ASN:OD1	49:1:854:G:O2'	2.33	0.46
48:L:18:LYS:HZ2	48:L:24:LYS:HB3	1.79	0.46
4:J:94:LYS:NZ	49:1:1155:C:OP2	2.34	0.46
14:O:50:LYS:HD3	14:O:85:TRP:CD1	2.51	0.46
21:T:106:LEU:HB3	21:T:120:TYR:HE1	1.80	0.46
37:D:56:THR:HG22	37:D:63:THR:HG23	1.96	0.46
48:L:64:SER:HB3	48:L:151:VAL:HG21	1.97	0.46
49:1:737:G:H2'	49:1:738:A:H8	1.80	0.46
4:J:208:SER:OG	4:J:209:ASN:N	2.47	0.46
8:7:18:VAL:HG12	8:7:27:VAL:HG22	1.97	0.46
17:Q:119:VAL:HG11	22:U:167:ARG:HD2	1.98	0.46
31:Z:86:VAL:O	31:Z:120:LYS:HB3	2.16	0.46
41:F:100:ARG:NE	49:1:3244:A:OP1	2.41	0.46
49:1:526:C:H2'	49:1:527:A:H8	1.80	0.46
49:1:1150:A:N6	49:1:2369:G:O2'	2.49	0.46
49:1:1816:A:O2'	49:1:1817:G:O5'	2.31	0.46
49:1:2213:A:H2'	49:1:2214:A:C8	2.50	0.46
4:J:206:LYS:HB3	49:1:1334:U:H5''	1.96	0.46
18:5:123:PRO:HD3	30:4:14:C:H5''	1.98	0.46
36:c:21:ARG:NH1	49:1:640:U:OP1	2.46	0.46
49:1:1574:C:H2'	49:1:1575:A:C8	2.50	0.46
49:1:1981:G:N2	49:1:2042:G:H22	2.14	0.46
49:1:2156:C:H2'	49:1:2178:A:H61	1.80	0.46
12:N:27:ASP:OD1	12:N:27:ASP:N	2.40	0.46
44:g:33:ARG:NH2	49:1:1408:G:OP1	2.39	0.46
49:1:816:A:O2'	49:1:819:U:O4	2.31	0.46
49:1:1675:G:H2'	49:1:1676:A:H8	1.81	0.46
15:o:125:LYS:NZ	49:1:2898:G:O6	2.49	0.46
20:s:98:ILE:HG12	20:s:122:HIS:HB2	1.98	0.46
32:a:27:ARG:NH1	32:a:75:ARG:O	2.41	0.46
48:L:133:LYS:HD2	48:L:156:LYS:HZ2	1.80	0.46
49:1:270:U:O2'	49:1:318:A:O2'	2.27	0.46
49:1:1850:A:O2'	49:1:1851:G:OP1	2.33	0.46
49:1:3343:G:H21	49:1:3362:A:H2	1.62	0.46
2:X:6:GLN:HE21	2:X:208:LEU:HB2	1.81	0.46
41:F:106:TRP:HH2	41:F:178:LEU:HD21	1.81	0.46
45:H:60:ILE:HD11	45:H:93:THR:HA	1.97	0.46
48:L:36:VAL:HA	48:L:208:SER:HA	1.98	0.46
49:1:595:G:H1	49:1:609:G:H5''	1.81	0.46
49:1:1421:G:H2'	49:1:1422:G:H8	1.79	0.46
3:i:90:ILE:HD11	34:b:14:VAL:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:l:12:HIS:O	9:l:12:HIS:ND1	2.49	0.46
16:p:116:LEU:HB3	16:p:133:ILE:HG23	1.98	0.46
34:b:46:ILE:HA	34:b:70:PRO:HA	1.98	0.46
39:E:97:ASN:H	39:E:100:ASN:HD22	1.62	0.46
43:G:349:THR:N	49:1:520:U:O4	2.48	0.46
49:1:1846:C:OP1	49:1:1849:C:N4	2.46	0.46
49:1:2769:A:H2'	49:1:2770:G:C8	2.51	0.46
2:X:28:VAL:HG12	2:X:50:HIS:HB3	1.98	0.45
4:J:66:LYS:NZ	4:J:78:GLU:OE2	2.41	0.45
19:S:100:THR:HG23	19:S:120:GLU:HB3	1.97	0.45
26:r:61:ARG:HA	26:r:64:ARG:HD2	1.97	0.45
30:4:48:A:O2'	30:4:49:G:OP1	2.34	0.45
36:c:77:LYS:O	36:c:79:TRP:N	2.49	0.45
39:E:191:LEU:HD13	49:1:1794:G:H4'	1.98	0.45
43:G:188:ARG:NH1	49:1:1382:G:OP2	2.40	0.45
49:1:655:C:H2'	49:1:656:A:C8	2.50	0.45
49:1:1284:C:H2'	49:1:1285:G:C4	2.51	0.45
49:1:2657:A:H5'	49:1:2657:A:H8	1.80	0.45
49:1:2941:A:H5''	49:1:2943:G:H4'	1.98	0.45
49:1:3234:A:H2	49:1:3253:G:N1	2.08	0.45
33:B:75:C:OP2	49:1:2971:A:C8	2.69	0.45
34:b:23:VAL:HG12	34:b:45:GLY:HA3	1.97	0.45
49:1:1302:A:N7	49:1:2857:C:O2'	2.43	0.45
49:1:2186:U:O2'	49:1:2313:A:N3	2.40	0.45
1:R:316:ASN:HD21	20:s:105:ALA:HB2	1.80	0.45
1:R:350:ASP:HA	1:R:353:ILE:HD12	1.98	0.45
11:m:44:LYS:HA	11:m:52:TYR:O	2.16	0.45
16:p:46:ASP:OD1	16:p:46:ASP:N	2.49	0.45
41:F:233:TRP:CD1	41:F:265:ALA:HB1	2.51	0.45
49:1:1189:C:N4	49:1:1315:U:O2'	2.46	0.45
49:1:2584:G:H2'	49:1:2585:G:H4'	1.98	0.45
9:l:70:VAL:O	9:l:74:PHE:N	2.48	0.45
26:r:38:MET:HE2	49:1:1259:A:H62	1.82	0.45
34:b:54:THR:H	34:b:57:HIS:HD2	1.62	0.45
39:E:44:ILE:HD12	39:E:46:LYS:HD3	1.97	0.45
39:E:126:LEU:HD13	39:E:150:LEU:HD21	1.97	0.45
49:1:107:A:O2'	49:1:324:A:N3	2.40	0.45
49:1:1740:U:H1'	49:1:1741:A:H2	1.81	0.45
1:R:502:ASN:HD21	1:R:506:ARG:HB2	1.82	0.45
4:J:30:ARG:NH2	49:1:595:G:OP1	2.50	0.45
8:7:77:ASN:HB3	8:7:151:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:s:153:ARG:NH1	49:1:2837:A:O3'	2.50	0.45
35:C:30:ALA:O	49:1:2767:U:O2'	2.26	0.45
43:G:84:ARG:NH1	43:G:87:GLN:OE1	2.47	0.45
44:g:23:ASP:OD2	49:1:424:G:O2'	2.26	0.45
47:I:52:VAL:HG21	47:I:65:ILE:HD13	1.98	0.45
1:R:74:CYS:SG	1:R:77:CYS:CB	3.05	0.45
3:i:67:LYS:HD2	49:1:1821:U:C4	2.51	0.45
7:k:70:ARG:HH12	7:k:84:LYS:HG2	1.82	0.45
22:U:9:VAL:O	22:U:26:ARG:HA	2.16	0.45
48:L:35:GLN:HA	48:L:169:VAL:HA	1.98	0.45
49:1:1203:A:H2'	49:1:1204:A:C8	2.51	0.45
49:1:1236:G:N2	49:1:1241:U:O4	2.49	0.45
49:1:1528:G:HO2'	49:1:1588:A:HO2'	1.44	0.45
49:1:1915:A:H2'	49:1:1916:U:C6	2.52	0.45
49:1:3162:C:H2'	49:1:3163:A:C8	2.52	0.45
16:p:99:ARG:NH2	16:p:118:SER:O	2.50	0.45
40:e:78:GLY:HA2	40:e:87:VAL:HG12	1.97	0.45
49:1:631:U:H2'	49:1:632:G:C8	2.52	0.45
49:1:842:G:H2'	49:1:843:A:C8	2.52	0.45
49:1:1177:G:O2'	49:1:1178:G:H8	2.00	0.45
49:1:2227:C:H2'	49:1:2228:A:C8	2.52	0.45
49:1:2268:U:H2'	49:1:2269:U:H2'	1.98	0.45
49:1:2403:G:HO2'	49:1:2404:A:C5'	2.30	0.45
49:1:2745:G:N2	49:1:2748:A:OP2	2.29	0.45
5:j:55:LEU:HD23	5:j:55:LEU:HA	1.80	0.45
10:M:49:LYS:HB3	10:M:62:ASN:HA	1.98	0.45
18:5:97:ASN:HD21	49:1:388:G:H1'	1.81	0.45
28:3:49:G:C5	45:H:58:LYS:HG3	2.52	0.45
41:F:257:PRO:HG3	49:1:1305:U:H1'	1.98	0.45
49:1:2538:U:O2'	49:1:2541:U:O4	2.32	0.45
23:V:48:ILE:HG13	23:V:94:GLU:HG2	1.98	0.45
31:Z:53:HIS:ND1	31:Z:54:TYR:O	2.48	0.45
40:e:10:ILE:HD12	40:e:13:LYS:HD2	1.99	0.45
45:H:236:LEU:HA	45:H:239:ILE:HD12	1.98	0.45
49:1:343:U:N3	49:1:1439:U:O2	2.50	0.45
49:1:739:G:H2'	49:1:740:G:H8	1.82	0.45
49:1:1190:A:C8	49:1:1193:A:H1'	2.52	0.45
49:1:1265:U:H2'	49:1:1266:G:C8	2.52	0.45
49:1:2036:U:H2'	49:1:2037:G:H8	1.82	0.45
49:1:2043:U:OP2	49:1:2044:U:N3	2.50	0.45
3:i:70:LYS:NZ	49:1:1803:C:O3'	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:5:168:LEU:H	18:5:168:LEU:HG	1.65	0.45
21:T:42:ARG:NH2	49:1:1601:U:OP1	2.41	0.45
28:3:107:C:H2'	28:3:108:A:C8	2.52	0.45
33:B:1:G:H2'	33:B:2:G:C8	2.51	0.45
49:1:267:G:C6	49:1:319:A:C5	3.05	0.45
49:1:3316:A:O5'	49:1:3318:G:N2	2.48	0.45
1:R:488:LEU:O	1:R:492:SER:OG	2.33	0.44
3:i:31:ARG:HH22	49:1:1598:G:P	2.40	0.44
16:p:18:VAL:HG13	16:p:19:LEU:HD12	1.99	0.44
26:r:24:SER:HB2	26:r:89:THR:O	2.17	0.44
28:3:72:A:C6	28:3:74:C:N4	2.85	0.44
30:4:114:G:O2'	49:1:1530:U:O2'	2.28	0.44
33:B:46:G:O2'	33:B:48:C:OP2	2.35	0.44
39:E:30:ARG:O	39:E:163:ARG:NH1	2.46	0.44
49:1:3255:U:H2'	49:1:3256:G:H8	1.81	0.44
1:R:285:TYR:O	1:R:285:TYR:CD2	2.70	0.44
6:K:36:ILE:HD13	39:E:34:TYR:HE2	1.82	0.44
12:N:34:SER:HA	12:N:37:ASN:HD22	1.82	0.44
14:O:19:ARG:HB3	14:O:35:ILE:HD12	1.99	0.44
14:O:117:ARG:HH12	47:I:174:LEU:HD13	1.82	0.44
20:s:51:LEU:HD12	20:s:151:LEU:HB3	1.99	0.44
21:T:66:HIS:O	21:T:69:SER:OG	2.31	0.44
25:P:132:ILE:HA	49:1:1255:C:H1'	1.99	0.44
40:e:50:VAL:HG11	49:1:2552:C:H2'	1.99	0.44
42:f:31:ARG:O	42:f:35:GLU:HB2	2.17	0.44
43:G:22:LEU:HA	43:G:23:PRO:HD3	1.76	0.44
49:1:138:U:H2'	49:1:139:G:H8	1.81	0.44
49:1:273:A:H2'	49:1:274:G:C8	2.51	0.44
49:1:1625:A:N6	49:1:1818:U:O4	2.47	0.44
18:5:61:ARG:O	18:5:64:ASN:ND2	2.50	0.44
49:1:928:C:H2'	49:1:929:A:C8	2.53	0.44
49:1:1239:C:N4	49:1:1244:A:O2'	2.50	0.44
49:1:1497:C:H2'	49:1:1498:A:H8	1.83	0.44
49:1:1956:A:H2'	49:1:1957:G:C8	2.52	0.44
1:R:312:LEU:HD23	20:s:102:LEU:HD13	1.99	0.44
4:J:93:ASN:OD1	4:J:93:ASN:N	2.51	0.44
21:T:104:ARG:NH1	49:1:1949:G:OP1	2.51	0.44
34:b:51:LEU:HB2	34:b:65:ARG:HD2	2.00	0.44
39:E:47:GLN:HB3	39:E:60:LYS:HZ2	1.82	0.44
41:F:56:ILE:HA	41:F:56:ILE:HD13	1.70	0.44
41:F:284:ARG:HB2	41:F:323:MET:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:F:294:GLY:HA2	41:F:359:ILE:HD12	2.00	0.44
6:K:142:LEU:HD13	6:K:201:THR:HG21	1.99	0.44
8:7:89:LYS:HB2	8:7:183:HIS:HB3	1.98	0.44
18:5:41:LEU:HD12	18:5:150:VAL:HG11	1.99	0.44
20:s:105:ALA:HB3	33:B:1:G:C2	2.52	0.44
22:U:62:ASN:ND2	49:1:519:A:OP1	2.50	0.44
36:c:117:ARG:HD2	49:1:716:A:C6	2.53	0.44
7:k:30:LYS:NZ	49:1:317:A:OP2	2.34	0.44
12:N:100:ARG:NH1	49:1:76:G:HO2'	2.12	0.44
17:Q:26:GLN:HB2	17:Q:33:ILE:HD11	1.98	0.44
23:V:14:MET:HE2	23:V:58:GLN:HB3	2.00	0.44
24:W:56:VAL:HG22	24:W:65:VAL:HG22	1.99	0.44
35:C:25:VAL:HG22	35:C:72:LEU:HD23	1.99	0.44
41:F:124:LYS:NZ	49:1:3297:U:O4	2.50	0.44
48:L:18:LYS:NZ	48:L:24:LYS:O	2.51	0.44
49:1:745:C:H2'	49:1:746:A:H8	1.81	0.44
49:1:2999:U:H2'	49:1:3000:A:H8	1.83	0.44
8:7:86:TYR:CE2	8:7:151:VAL:HG22	2.53	0.44
10:M:48:SER:O	10:M:65:ILE:N	2.50	0.44
12:N:36:ARG:NH2	49:1:687:U:OP2	2.50	0.44
20:s:204:SER:HA	28:3:64:A:H5''	2.00	0.44
28:3:85:G:O2'	28:3:87:G:OP1	2.30	0.44
35:C:36:PHE:HE2	49:1:2225:U:H4'	1.82	0.44
39:E:79:ASN:ND2	39:E:166:ILE:O	2.51	0.44
41:F:212:ASN:O	41:F:281:LYS:NZ	2.51	0.44
41:F:296:THR:H	41:F:299:ASP:HB3	1.83	0.44
44:g:34:LYS:NZ	44:g:52:GLN:OE1	2.50	0.44
49:1:1803:C:H2'	49:1:1804:A:C8	2.53	0.44
1:R:225:PHE:O	1:R:228:SER:OG	2.32	0.44
2:X:162:HIS:HE1	2:X:164:GLN:HB2	1.83	0.44
6:K:47:SER:OG	49:1:2585:G:O6	2.36	0.44
20:s:56:LEU:HB2	20:s:130:ILE:HG13	1.98	0.44
34:b:64:LYS:HE3	49:1:1630:U:H5	1.83	0.44
37:D:46:THR:HB	37:D:58:SER:HB2	2.00	0.44
44:g:79:VAL:HG13	44:g:111:ARG:HG2	2.00	0.44
45:H:65:ILE:HG12	45:H:74:VAL:HG22	2.00	0.44
48:L:119:GLN:HB3	48:L:123:LEU:HD12	2.00	0.44
49:1:299:G:H1	49:1:316:U:H3	1.64	0.44
49:1:1364:C:H2'	49:1:1365:G:C8	2.52	0.44
1:R:77:CYS:SG	1:R:99:ASN:ND2	2.89	0.44
4:J:153:PHE:CD1	4:J:162:PRO:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:141:ARG:NH2	49:1:977:C:OP1	2.51	0.44
20:s:141:ASP:OD1	20:s:141:ASP:N	2.47	0.44
28:3:27:A:H2'	28:3:28:C:C6	2.53	0.44
35:C:74:CYS:SG	35:C:75:VAL:N	2.91	0.44
39:E:7:ASN:HB2	49:1:2183:A:H5''	2.00	0.44
39:E:88:ILE:HD13	39:E:88:ILE:HA	1.86	0.44
40:e:27:TYR:O	40:e:30:THR:OG1	2.30	0.44
46:h:97:SER:OG	49:1:3174:A:OP1	2.33	0.44
49:1:673:U:H2'	49:1:674:G:C8	2.53	0.44
49:1:2357:A:H2'	49:1:2358:A:C8	2.53	0.44
19:S:89:ASP:OD1	19:S:90:ASP:N	2.51	0.43
20:s:20:ARG:NH1	20:s:21:TYR:OH	2.50	0.43
26:r:15:LEU:HD22	26:r:62:ALA:HB1	2.00	0.43
35:C:46:LYS:NZ	49:1:92:G:O5'	2.51	0.43
46:h:75:HIS:HB2	46:h:82:ARG:HG3	1.99	0.43
49:1:376:G:H1'	49:1:400:G:H21	1.82	0.43
49:1:631:U:H2'	49:1:632:G:H8	1.83	0.43
49:1:2450:G:H2'	49:1:2451:G:H8	1.83	0.43
1:R:23:LEU:HD12	1:R:227:ASN:HD21	1.83	0.43
10:M:14:ILE:HD12	10:M:77:GLU:HG2	2.01	0.43
10:M:77:GLU:O	10:M:80:LEU:HB3	2.18	0.43
14:O:77:ARG:NH2	49:1:525:C:OP2	2.46	0.43
42:f:11:GLU:HA	42:f:73:LEU:O	2.18	0.43
49:1:306:A:N6	49:1:2784:G:N2	2.66	0.43
49:1:1119:C:H2'	49:1:1120:A:C8	2.53	0.43
1:R:484:LYS:HD2	1:R:519:HIS:HB3	2.00	0.43
6:K:140:VAL:HG21	16:p:3:ALA:HB2	1.99	0.43
28:3:4:U:H2'	28:3:5:G:H8	1.83	0.43
33:B:62:C:H2'	33:B:63:G:C8	2.53	0.43
36:c:32:ARG:HG3	49:1:38:U:H4'	2.01	0.43
39:E:132:ASN:HD21	49:1:2178:A:H5''	1.83	0.43
45:H:12:TYR:OH	49:1:2688:U:OP1	2.32	0.43
49:1:571:U:H2'	49:1:572:A:H8	1.83	0.43
49:1:596:C:N3	49:1:608:A:O2'	2.49	0.43
49:1:786:A:H4'	49:1:787:G:H5'	2.00	0.43
2:X:101:LEU:HD23	2:X:101:LEU:HA	1.88	0.43
17:Q:22:VAL:HG21	17:Q:120:VAL:HG11	2.01	0.43
17:Q:45:GLY:O	17:Q:136:THR:OG1	2.32	0.43
28:3:90:U:C2	49:1:1203:A:H5'	2.54	0.43
39:E:181:LYS:HB2	49:1:860:G:C6	2.52	0.43
48:L:35:GLN:HG3	48:L:169:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L:101:LYS:NZ	48:L:122:ARG:O	2.51	0.43
49:1:1579:C:H2'	49:1:1580:A:C8	2.54	0.43
49:1:1816:A:O2'	49:1:1817:G:O4'	2.35	0.43
49:1:2768:U:H2'	49:1:2769:A:C8	2.52	0.43
49:1:3242:G:H1'	49:1:3245:A:H1'	1.99	0.43
4:J:98:LYS:HG3	49:1:985:U:H5''	2.01	0.43
6:K:186:LEU:HD23	6:K:189:LEU:HD21	1.99	0.43
18:5:119:VAL:HA	18:5:145:HIS:O	2.17	0.43
27:x:25:CYS:HB2	27:x:34:LEU:HG	1.99	0.43
41:F:259:HIS:HE2	49:1:2366:C:P	2.41	0.43
43:G:44:LYS:HZ1	49:1:1427:U:H5'	1.83	0.43
43:G:205:PRO:HB3	43:G:247:PHE:HD2	1.83	0.43
49:1:600:G:N2	49:1:603:A:OP2	2.39	0.43
49:1:1570:U:H4'	49:1:1571:A:C4	2.53	0.43
49:1:2769:A:H2'	49:1:2770:G:H8	1.83	0.43
1:R:276:PHE:HE2	1:R:379:VAL:HG13	1.84	0.43
18:5:108:ASP:N	18:5:152:GLU:OE2	2.52	0.43
19:S:73:GLN:NE2	49:1:741:U:O2'	2.51	0.43
24:W:19:VAL:N	24:W:61:THR:O	2.51	0.43
38:d:23:LYS:HG3	49:1:982:C:H5'	2.01	0.43
41:F:80:ASP:OD2	41:F:314:TYR:OH	2.32	0.43
41:F:222:LYS:HE3	41:F:331:ASN:HB3	2.01	0.43
45:H:29:ASP:OD2	45:H:32:GLN:N	2.52	0.43
45:H:211:LEU:HB3	45:H:219:PHE:HB2	2.00	0.43
45:H:235:SER:O	45:H:238:ASP:HB2	2.18	0.43
47:I:138:GLN:NE2	47:I:142:ASP:OD2	2.36	0.43
49:1:3000:A:H2'	49:1:3001:C:C6	2.53	0.43
49:1:3338:C:H2'	49:1:3339:A:H8	1.83	0.43
1:R:235:ILE:HG22	1:R:252:SER:HA	2.01	0.43
3:i:4:ARG:HD3	49:1:1858:A:H1'	2.00	0.43
6:K:63:LYS:HD3	6:K:63:LYS:HA	1.86	0.43
28:3:4:U:H2'	28:3:5:G:C8	2.54	0.43
33:B:63:G:H2'	33:B:64:G:C8	2.54	0.43
37:D:4:ARG:NH2	49:1:837:A:OP2	2.50	0.43
39:E:220:GLY:HA2	49:1:2966:G:H5'	2.01	0.43
39:E:227:ARG:NH2	49:1:2155:G:O2'	2.51	0.43
39:E:227:ARG:HB2	39:E:239:ALA:HB2	2.01	0.43
43:G:95:ARG:NH1	49:1:366:A:OP1	2.45	0.43
49:1:147:U:O2'	49:1:148:G:OP1	2.36	0.43
49:1:903:U:H2'	49:1:904:A:C8	2.53	0.43
49:1:2376:G:H2'	49:1:2377:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:2945:G:H5''	49:1:2947:G:C8	2.54	0.43
49:1:3157:U:H4'	49:1:3158:G:H8	1.84	0.43
4:J:92:ILE:HD12	4:J:92:ILE:HA	1.77	0.43
5:j:81:ARG:NH2	49:1:18:G:OP1	2.52	0.43
16:p:55:ALA:HB3	49:1:148:G:H5''	2.01	0.43
17:Q:37:ARG:HA	17:Q:107:GLY:H	1.84	0.43
23:V:104:GLU:OE1	49:1:989:A:O2'	2.27	0.43
27:x:70:ARG:NH2	49:1:2294:U:OP1	2.52	0.43
49:1:255:A:H2'	49:1:256:G:H8	1.83	0.43
49:1:645:A:H1'	49:1:647:A:N7	2.34	0.43
49:1:1974:A:OP1	49:1:2048:G:N2	2.52	0.43
2:X:118:HIS:HD1	2:X:120:ASP:H	1.67	0.43
6:K:193:LYS:NZ	49:1:145:G:OP2	2.37	0.43
32:a:62:SER:N	49:1:218:G:O6	2.44	0.43
43:G:337:GLU:HB2	43:G:339:LEU:HG	1.99	0.43
46:h:48:ARG:HG3	46:h:104:PRO:HD3	1.99	0.43
47:I:87:THR:HA	47:I:176:PHE:HB3	1.99	0.43
49:1:2450:G:H2'	49:1:2451:G:C8	2.54	0.43
1:R:379:VAL:HG21	33:B:68:C:H5''	2.01	0.43
3:i:86:LYS:O	3:i:90:ILE:HG12	2.19	0.43
39:E:5:ILE:HG12	39:E:8:GLN:HG3	2.01	0.43
39:E:200:ARG:HD3	49:1:2186:U:H5	1.84	0.43
42:f:51:LEU:HD22	42:f:55:LEU:HD22	2.01	0.43
49:1:330:G:H2'	49:1:331:G:H8	1.83	0.43
49:1:1692:U:HO2'	49:1:1754:G:HO2'	1.64	0.43
49:1:2423:U:H2'	49:1:2424:A:C8	2.53	0.43
49:1:3334:U:O2'	49:1:3368:U:O2	2.37	0.43
2:X:115:ALA:HB3	2:X:137:VAL:HA	2.00	0.42
17:Q:160:ARG:O	17:Q:164:SER:N	2.52	0.42
22:U:152:LEU:HD12	22:U:172:TYR:HE2	1.83	0.42
24:W:18:ASP:HA	24:W:62:VAL:HG22	2.01	0.42
32:a:63:LYS:HG2	32:a:85:VAL:HG13	2.01	0.42
41:F:111:SER:OG	41:F:112:ASP:N	2.52	0.42
49:1:428:A:H2'	49:1:429:U:C6	2.54	0.42
1:R:237:ALA:HB3	1:R:341:ILE:HG12	2.01	0.42
9:l:9:GLY:HA3	49:1:1852:G:H1'	2.00	0.42
9:l:31:LYS:NZ	49:1:815:G:OP2	2.41	0.42
13:n:23:LEU:HD11	13:n:35:ILE:HG22	2.01	0.42
21:T:75:HIS:ND1	49:1:1940:G:OP1	2.51	0.42
23:V:6:GLY:H	23:V:9:SER:HB2	1.84	0.42
33:B:4:C:H2'	33:B:5:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:f:10:ARG:HH21	49:1:3386:G:H5'	1.84	0.42
49:1:1455:U:N3	49:1:3077:A:OP1	2.51	0.42
49:1:2456:A:N3	49:1:2482:U:O2'	2.50	0.42
49:1:2662:G:H2'	49:1:2663:G:H8	1.83	0.42
27:x:12:ARG:HB2	49:1:3040:A:H5''	2.00	0.42
45:H:83:LEU:HB3	45:H:88:ILE:HB	2.01	0.42
49:1:700:C:H2'	49:1:701:G:H8	1.83	0.42
49:1:1084:A:H2'	49:1:1085:A:C8	2.54	0.42
49:1:1421:G:H2'	49:1:1422:G:C8	2.55	0.42
49:1:2047:A:O2'	49:1:2048:G:O4'	2.26	0.42
49:1:2253:G:H2'	49:1:2254:U:C6	2.54	0.42
19:S:112:ALA:O	19:S:116:LYS:CB	2.67	0.42
30:4:126:A:O2'	30:4:128:U:OP2	2.37	0.42
36:c:85:ASP:OD1	36:c:85:ASP:N	2.51	0.42
39:E:3:ARG:HD3	49:1:911:C:N4	2.34	0.42
39:E:236:GLY:N	49:1:2183:A:O2'	2.38	0.42
43:G:295:ILE:O	43:G:299:ILE:HG12	2.19	0.42
49:1:1699:A:H2'	49:1:1700:G:H8	1.82	0.42
1:R:376:ARG:HA	1:R:377:PRO:HD3	1.84	0.42
19:S:122:ILE:HG23	19:S:126:GLN:HB2	2.00	0.42
20:s:129:ASP:OD1	20:s:130:ILE:N	2.52	0.42
20:s:170:TRP:HD1	20:s:177:ARG:HA	1.84	0.42
22:U:10:ILE:O	22:U:59:VAL:N	2.52	0.42
26:r:25:LEU:HD11	26:r:86:PHE:HD1	1.85	0.42
30:4:56:G:H2'	30:4:57:C:O4'	2.19	0.42
39:E:36:GLU:HG3	39:E:91:GLY:HA2	2.02	0.42
44:g:44:ARG:HD2	44:g:46:PHE:HE2	1.84	0.42
49:1:35:A:H2'	49:1:36:C:H6	1.85	0.42
49:1:70:A:H2	49:1:72:C:H42	1.67	0.42
49:1:1060:U:H2'	49:1:1061:A:H8	1.85	0.42
49:1:1351:U:H2'	49:1:1352:A:H2'	2.01	0.42
49:1:2219:A:H2'	49:1:2220:A:C8	2.54	0.42
49:1:2904:U:H2'	49:1:2905:U:C6	2.55	0.42
1:R:490:LEU:HD23	1:R:494:ILE:HD12	2.01	0.42
4:J:186:HIS:O	4:J:190:THR:OG1	2.33	0.42
16:p:45:PRO:O	16:p:49:ARG:CB	2.68	0.42
41:F:256:HIS:ND1	49:1:2941:A:OP2	2.41	0.42
47:I:39:VAL:HG11	47:I:158:TYR:HE2	1.84	0.42
49:1:500:C:H2'	49:1:501:A:C8	2.55	0.42
49:1:843:A:H2'	49:1:844:G:C8	2.54	0.42
49:1:1461:A:H2'	49:1:1462:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:284:ARG:HH22	33:B:1:G:P	2.34	0.42
19:S:39:ARG:HH22	43:G:302:ALA:HB2	1.85	0.42
28:3:19:C:H2'	28:3:20:A:C8	2.53	0.42
30:4:63:G:N1	30:4:97:A:C2	2.80	0.42
33:B:5:G:C6	33:B:69:G:C6	3.07	0.42
39:E:230:VAL:HG21	49:1:2424:A:N1	2.34	0.42
49:1:842:G:H2'	49:1:843:A:H8	1.85	0.42
49:1:1994:G:H2'	49:1:1995:A:H8	1.84	0.42
49:1:2573:G:H2'	49:1:2574:G:C8	2.55	0.42
49:1:2703:A:H5''	49:1:2704:A:H5'	2.02	0.42
11:m:7:ASP:HB3	11:m:10:GLN:HB3	2.02	0.42
15:o:100:TYR:O	49:1:2895:G:O2'	2.26	0.42
20:s:50:HIS:CD2	20:s:167:SER:HB2	2.55	0.42
42:f:19:ARG:HB3	42:f:35:GLU:HG2	2.01	0.42
12:N:48:PRO:HB2	12:N:137:GLN:HB3	2.02	0.42
14:O:88:ALA:O	14:O:93:LYS:NZ	2.41	0.42
15:o:122:ARG:NH2	49:1:2896:A:O3'	2.48	0.42
16:p:58:GLY:HA3	16:p:142:ILE:HD11	2.01	0.42
16:p:144:ARG:NH1	49:1:126:U:OP1	2.53	0.42
24:W:42:LYS:H	24:W:75:TYR:HH	1.67	0.42
26:r:61:ARG:HA	26:r:64:ARG:HB2	2.02	0.42
28:3:49:G:OP2	45:H:91:GLY:N	2.38	0.42
30:4:135:G:H5''	31:Z:49:LYS:HD3	2.01	0.42
41:F:283:TYR:HB3	41:F:356:LEU:HD21	2.01	0.42
49:1:1060:U:H2'	49:1:1061:A:C8	2.54	0.42
49:1:1782:U:H2'	49:1:1783:U:O4'	2.20	0.42
49:1:1974:A:N6	49:1:2049:A:O4'	2.49	0.42
3:i:92:ALA:HB2	49:1:2555:G:H1'	2.01	0.42
6:K:166:LEU:HA	6:K:166:LEU:HD23	1.82	0.42
12:N:42:ARG:O	12:N:46:ILE:N	2.52	0.42
20:s:71:ALA:HB2	20:s:154:ALA:HB2	2.02	0.42
26:r:56:ASN:HB3	26:r:80:VAL:HG22	2.01	0.42
28:3:16:U:H2'	28:3:17:A:C8	2.54	0.42
36:c:75:LEU:HG	36:c:114:GLY:HA2	2.01	0.42
43:G:126:ILE:HD11	43:G:233:LEU:HD13	2.02	0.42
43:G:283:THR:HB	43:G:289:ILE:HD11	2.02	0.42
47:I:145:LEU:HD23	47:I:145:LEU:HA	1.85	0.42
48:L:90:LEU:HD22	48:L:115:VAL:HG21	2.01	0.42
49:1:307:A:H2'	49:1:308:A:C8	2.55	0.42
49:1:1071:U:H2'	49:1:1072:G:H8	1.85	0.42
49:1:1661:G:H2'	49:1:1662:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:199:VAL:HG23	2:X:204:ALA:HB2	2.01	0.41
11:m:19:ASP:N	11:m:19:ASP:OD1	2.51	0.41
16:p:65:ARG:HG2	16:p:129:TYR:CE1	2.55	0.41
22:U:52:LYS:O	22:U:56:GLY:N	2.52	0.41
24:W:104:ARG:NH2	49:1:1758:G:OP1	2.52	0.41
36:c:91:LEU:HA	36:c:121:VAL:HG21	2.02	0.41
41:F:250:ALA:HB1	49:1:2947:G:C2	2.55	0.41
41:F:259:HIS:NE2	49:1:2366:C:O5'	2.53	0.41
45:H:107:ARG:NH2	45:H:120:LYS:O	2.52	0.41
49:1:1177:G:O2'	49:1:1178:G:O5'	2.37	0.41
8:7:89:LYS:HG2	8:7:145:VAL:HG22	2.01	0.41
11:m:51:LEU:HD22	49:1:1612:A:H5''	2.02	0.41
20:s:41:THR:OG1	20:s:42:VAL:N	2.53	0.41
20:s:47:LEU:HD11	20:s:166:LEU:HD21	2.01	0.41
26:r:53:MET:HB2	49:1:1259:A:C8	2.55	0.41
49:1:546:C:H5'	49:1:547:G:C5	2.55	0.41
49:1:1144:U:H6	49:1:1144:U:H2'	1.56	0.41
49:1:3147:G:H2'	49:1:3148:U:O4'	2.20	0.41
10:M:10:ARG:HG3	10:M:133:ARG:HD3	2.01	0.41
10:M:18:VAL:HG22	10:M:70:THR:HG22	2.01	0.41
11:m:32:ASN:O	11:m:35:GLY:N	2.54	0.41
18:5:25:SER:OG	49:1:1447:G:N7	2.45	0.41
21:T:81:ARG:HH11	21:T:81:ARG:HD3	1.72	0.41
43:G:36:HIS:HA	43:G:242:ALA:HB1	2.02	0.41
49:1:919:U:H3'	49:1:923:C:H41	1.85	0.41
49:1:1620:U:H2'	49:1:1621:A:C8	2.55	0.41
49:1:1786:G:H2'	49:1:1787:A:C8	2.55	0.41
6:K:169:LEU:HD11	16:p:6:TYR:CZ	2.56	0.41
19:S:22:ASP:OD1	19:S:27:LYS:NZ	2.48	0.41
21:T:59:SER:N	49:1:3068:U:OP1	2.41	0.41
28:3:62:U:O4	28:3:63:A:N6	2.54	0.41
35:C:7:THR:HB	35:C:22:GLN:NE2	2.35	0.41
36:c:73:LEU:HD11	36:c:77:LYS:HB2	2.03	0.41
43:G:3:ARG:HB3	43:G:22:LEU:H	1.86	0.41
48:L:36:VAL:HG12	48:L:168:ALA:H	1.85	0.41
1:R:491:LEU:HD22	1:R:528:LEU:HD21	2.03	0.41
3:i:89:ILE:O	3:i:93:PHE:N	2.50	0.41
6:K:75:ILE:HG22	6:K:76:ALA:H	1.86	0.41
12:N:64:LYS:O	12:N:67:ARG:NH1	2.53	0.41
33:B:58:A:O2'	33:B:60:U:OP2	2.31	0.41
34:b:23:VAL:HB	34:b:43:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:19:LYS:HB3	36:c:25:HIS:HB2	2.01	0.41
39:E:50:HIS:NE2	49:1:1795:U:OP2	2.54	0.41
41:F:105:VAL:HG21	41:F:148:LEU:HD12	2.02	0.41
49:1:2491:A:H2'	49:1:2492:C:C6	2.56	0.41
49:1:2821:C:H42	49:1:2869:U:H3	1.68	0.41
36:c:34:MET:HE3	36:c:34:MET:HB3	1.78	0.41
39:E:15:ILE:HD13	49:1:911:C:H5''	2.02	0.41
41:F:279:ASN:ND2	41:F:343:TYR:OH	2.43	0.41
47:I:23:LYS:HD3	47:I:23:LYS:HA	1.90	0.41
49:1:201:A:H2'	49:1:202:G:H8	1.86	0.41
49:1:952:A:H4'	49:1:968:G:H22	1.85	0.41
49:1:1806:A:H2'	49:1:1807:G:O4'	2.20	0.41
49:1:2270:A:H2'	49:1:2271:A:C8	2.56	0.41
49:1:2492:C:H2'	49:1:2493:U:C6	2.55	0.41
49:1:3157:U:H4'	49:1:3158:G:C8	2.55	0.41
6:K:35:GLY:HA3	6:K:38:GLN:HE21	1.85	0.41
6:K:153:ILE:O	6:K:180:VAL:N	2.50	0.41
8:7:4:ILE:HB	22:U:142:GLN:HE21	1.86	0.41
8:7:90:MET:HG2	8:7:181:VAL:HG22	2.02	0.41
34:b:25:ILE:HG23	34:b:41:ALA:HB1	2.02	0.41
36:c:74:ASN:ND2	49:1:705:A:H62	2.19	0.41
39:E:132:ASN:ND2	49:1:2178:A:H5''	2.34	0.41
49:1:584:G:H2'	49:1:585:A:C8	2.56	0.41
49:1:1210:U:H2'	49:1:1211:U:C6	2.54	0.41
49:1:3375:A:O2'	49:1:3376:A:O4'	2.36	0.41
1:R:282:PHE:N	1:R:282:PHE:HD1	2.17	0.41
10:M:10:ARG:HB2	28:3:55:A:H1'	2.02	0.41
17:Q:130:LYS:HA	17:Q:131:PRO:HD3	1.91	0.41
21:T:130:ASN:O	21:T:132:PHE:N	2.54	0.41
30:4:67:U:H2'	30:4:68:G:H8	1.86	0.41
33:B:30:C:H2'	33:B:31:C:H6	1.86	0.41
42:f:10:ARG:HG2	42:f:108:VAL:HG22	2.03	0.41
46:h:6:ARG:NH2	47:I:166:LYS:O	2.53	0.41
49:1:273:A:H2'	49:1:274:G:H8	1.86	0.41
49:1:1178:G:N2	49:1:1329:U:O4'	2.51	0.41
49:1:2094:C:H2'	49:1:2095:G:H8	1.85	0.41
1:R:344:ARG:HB2	1:R:370:PHE:HD2	1.85	0.41
2:X:146:ILE:HG13	2:X:147:LEU:HD12	2.03	0.41
11:m:48:SER:HB2	49:1:1825:G:H5''	2.03	0.41
14:O:20:VAL:O	14:O:66:THR:OG1	2.27	0.41
14:O:36:VAL:HG11	14:O:55:ARG:HH12	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:9:GLN:HE22	49:1:1103:A:N6	2.19	0.41
33:B:6:U:H2'	33:B:7:G:C8	2.56	0.41
33:B:9:G:H2'	33:B:11:C:H41	1.85	0.41
33:B:69:G:C6	33:B:70:U:C4	3.08	0.41
33:B:74:C:H2'	33:B:75:C:C6	2.56	0.41
34:b:34:LYS:HZ2	34:b:34:LYS:HG3	1.61	0.41
34:b:83:THR:HG23	34:b:85:TYR:H	1.85	0.41
35:C:2:VAL:N	35:C:90:HIS:O	2.53	0.41
38:d:36:ASP:OD1	49:1:2737:C:O2'	2.37	0.41
39:E:77:ILE:HD11	39:E:128:ARG:HE	1.86	0.41
39:E:190:ARG:HG3	39:E:191:LEU:HD12	2.03	0.41
41:F:266:ARG:NH1	49:1:2988:C:O2	2.54	0.41
43:G:186:LYS:NZ	49:1:1388:U:O4	2.48	0.41
46:h:99:ARG:NH2	49:1:3175:U:O4	2.52	0.41
49:1:847:A:H2'	49:1:848:A:C8	2.56	0.41
49:1:1342:C:H2'	49:1:1343:A:C8	2.56	0.41
49:1:1483:G:O2'	49:1:1484:U:OP1	2.31	0.41
49:1:1982:G:N2	49:1:2040:U:H3	2.18	0.41
49:1:2039:C:H2'	49:1:2040:U:C2	2.56	0.41
49:1:2219:A:H2'	49:1:2220:A:H8	1.86	0.41
49:1:2232:A:H2'	49:1:2233:A:C8	2.56	0.41
49:1:2953:U:H2'	49:1:2954:U:H2'	2.02	0.41
49:1:3337:G:H2'	49:1:3338:C:C6	2.56	0.41
4:J:144:ILE:HG22	4:J:185:ILE:HG23	2.03	0.41
4:J:211:SER:H	4:J:242:SER:HB2	1.86	0.41
7:k:26:ILE:HG21	49:1:157:A:C8	2.55	0.41
20:s:51:LEU:HD21	20:s:162:GLN:HG3	2.03	0.41
21:T:42:ARG:HH22	49:1:1601:U:P	2.42	0.41
21:T:104:ARG:HH12	49:1:1949:G:H5''	1.86	0.41
28:3:31:U:O2'	45:H:218:ARG:NH2	2.41	0.41
32:a:97:ILE:HD13	32:a:97:ILE:HA	1.94	0.41
41:F:21:ARG:NH1	49:1:2991:A:O3'	2.53	0.41
49:1:1011:A:H2'	49:1:1012:G:H8	1.86	0.41
8:7:16:VAL:HA	8:7:28:VAL:O	2.21	0.40
22:U:1:MET:HA	49:1:1323:G:H5'	2.02	0.40
22:U:114:HIS:NE2	49:1:1212:A:O2'	2.45	0.40
30:4:135:G:OP1	31:Z:49:LYS:NZ	2.48	0.40
42:f:20:LEU:HD11	42:f:32:ALA:HB2	2.02	0.40
49:1:548:G:H2'	49:1:549:U:O4'	2.21	0.40
49:1:846:A:H2'	49:1:847:A:C8	2.56	0.40
49:1:1699:A:H2'	49:1:1700:G:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:1986:U:H3	49:1:2035:G:H1	1.69	0.40
49:1:2899:C:O2'	49:1:2901:G:OP2	2.28	0.40
18:5:69:ARG:HD3	49:1:3309:G:H1'	2.03	0.40
27:x:104:ASN:OD1	27:x:108:GLU:N	2.52	0.40
28:3:27:A:H2'	28:3:28:C:H6	1.85	0.40
29:Y:8:PHE:HB3	29:Y:36:SER:HB2	2.03	0.40
34:b:54:THR:H	34:b:57:HIS:CD2	2.38	0.40
36:c:22:ILE:HB	49:1:1114:U:H5'	2.02	0.40
45:H:113:LEU:HB3	45:H:115:LEU:HD13	2.02	0.40
45:H:187:THR:HG23	45:H:189:GLU:HG3	2.03	0.40
46:h:77:ASN:HB2	49:1:1180:A:H5''	2.03	0.40
49:1:41:G:N2	49:1:2803:A:H62	2.18	0.40
49:1:503:C:H2'	49:1:504:A:H8	1.87	0.40
49:1:881:C:H2'	49:1:882:A:H8	1.86	0.40
1:R:212:ASN:HD22	1:R:212:ASN:HA	1.63	0.40
8:7:47:LYS:HD2	14:O:5:SER:HB2	2.03	0.40
26:r:16:ARG:HH21	26:r:66:PHE:HE1	1.68	0.40
35:C:42:ARG:HH11	35:C:42:ARG:HD2	1.69	0.40
41:F:150:ARG:HH11	41:F:150:ARG:HD2	1.76	0.40
43:G:153:SER:OG	43:G:154:THR:N	2.55	0.40
46:h:67:MET:HE1	46:h:90:PRO:HD3	2.03	0.40
49:1:358:G:N2	49:1:361:A:OP2	2.44	0.40
49:1:528:U:H2'	49:1:529:A:C8	2.56	0.40
49:1:1009:A:H2'	49:1:1010:G:H8	1.86	0.40
49:1:1011:A:H2'	49:1:1012:G:C8	2.56	0.40
49:1:1573:G:H2'	49:1:1574:C:O4'	2.21	0.40
49:1:1784:G:H2'	49:1:1785:U:O4'	2.20	0.40
49:1:2971:A:O2'	49:1:2972:G:P	2.78	0.40
4:J:128:LYS:HE3	28:3:99:G:H4'	2.04	0.40
10:M:71:VAL:HG11	10:M:79:ILE:HD12	2.04	0.40
13:n:51:ILE:HG12	49:1:1493:G:H22	1.87	0.40
20:s:105:ALA:HB3	33:B:1:G:N3	2.37	0.40
20:s:158:PHE:HB2	20:s:162:GLN:NE2	2.37	0.40
22:U:8:GLN:HA	22:U:27:MET:O	2.22	0.40
22:U:13:ARG:HH11	22:U:51:VAL:HG12	1.87	0.40
41:F:114:VAL:H	41:F:114:VAL:HG22	1.66	0.40
43:G:48:GLN:NE2	49:1:336:A:O2'	2.55	0.40
44:g:27:ARG:N	49:1:655:C:OP1	2.54	0.40
49:1:35:A:H2'	49:1:36:C:C6	2.57	0.40
49:1:542:G:N1	49:1:549:U:N3	2.43	0.40
49:1:1973:G:N2	49:1:2049:A:H62	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1:2094:C:H2'	49:1:2095:G:C8	2.55	0.40
49:1:2406:C:H2'	49:1:2407:C:C6	2.56	0.40
49:1:2697:A:H2'	49:1:2698:G:C8	2.56	0.40
49:1:3313:U:O4	49:1:3314:A:N6	2.54	0.40
6:K:203:VAL:HG11	6:K:211:LEU:HD22	2.03	0.40
33:B:2:G:H1	33:B:71:C:N4	2.18	0.40
36:c:100:PRO:HD2	36:c:123:VAL:HG22	2.04	0.40
49:1:397:A:H5'	49:1:398:A:H5'	2.03	0.40
49:1:959:C:O2	49:1:2614:G:O2'	2.29	0.40
49:1:999:G:H2'	49:1:1000:C:C6	2.56	0.40
49:1:1286:A:N3	49:1:1287:A:H1'	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	299/475 (63%)	288 (96%)	11 (4%)	0	100	100
2	X	222/224 (99%)	211 (95%)	11 (5%)	0	100	100
3	i	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
4	J	220/222 (99%)	202 (92%)	17 (8%)	1 (0%)	24	54
5	j	117/119 (98%)	105 (90%)	9 (8%)	3 (3%)	4	21
6	K	231/233 (99%)	212 (92%)	18 (8%)	1 (0%)	30	59
7	k	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
8	7	189/191 (99%)	177 (94%)	11 (6%)	1 (0%)	24	54
9	l	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
10	M	167/169 (99%)	148 (89%)	17 (10%)	2 (1%)	10	35
11	m	75/77 (97%)	69 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	N	191/193 (99%)	174 (91%)	11 (6%)	6 (3%)	3	18
13	n	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
14	O	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
15	o	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
16	p	201/203 (99%)	179 (89%)	21 (10%)	1 (0%)	24	54
17	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
18	5	181/183 (99%)	167 (92%)	14 (8%)	0	100	100
19	S	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
20	s	218/220 (99%)	193 (88%)	25 (12%)	0	100	100
21	T	150/152 (99%)	139 (93%)	10 (7%)	1 (1%)	18	47
22	U	170/172 (99%)	152 (89%)	17 (10%)	1 (1%)	21	50
23	V	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
24	W	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
25	P	144/155 (93%)	121 (84%)	23 (16%)	0	100	100
26	r	117/197 (59%)	109 (93%)	8 (7%)	0	100	100
27	x	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
29	Y	60/62 (97%)	60 (100%)	0	0	100	100
31	Z	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
32	a	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
34	b	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	44
35	C	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
36	c	146/148 (99%)	126 (86%)	17 (12%)	3 (2%)	5	24
37	D	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
38	d	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
39	E	250/252 (99%)	226 (90%)	24 (10%)	0	100	100
40	e	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
41	F	384/386 (100%)	348 (91%)	35 (9%)	1 (0%)	36	65
42	f	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
43	G	359/361 (99%)	314 (88%)	44 (12%)	1 (0%)	36	65
44	g	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
45	H	294/296 (99%)	273 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	h	104/106 (98%)	96 (92%)	8 (8%)	0	100	100
47	I	152/175 (87%)	144 (95%)	8 (5%)	0	100	100
48	L	202/204 (99%)	167 (83%)	35 (17%)	0	100	100
All	All	7085/7457 (95%)	6476 (91%)	586 (8%)	23 (0%)	37	65

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	c	47	LYS
43	G	339	LEU
4	J	158	LYS
5	j	85	THR
5	j	91	ALA
6	K	157	VAL
12	N	62	THR
34	b	102	GLU
36	c	78	LEU
8	7	22	SER
12	N	48	PRO
16	p	74	PRO
21	T	131	ALA
36	c	40	HIS
5	j	90	ARG
10	M	173	ASP
12	N	5	LYS
22	U	13	ARG
12	N	61	PRO
12	N	166	ALA
12	N	47	ALA
41	F	188	ILE
10	M	8	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	287/392 (73%)	284 (99%)	3 (1%)	68	75
2	X	177/192 (92%)	177 (100%)	0	100	100
3	i	95/95 (100%)	95 (100%)	0	100	100
4	J	186/186 (100%)	186 (100%)	0	100	100
5	j	104/104 (100%)	104 (100%)	0	100	100
6	K	187/191 (98%)	186 (100%)	1 (0%)	81	81
7	k	81/81 (100%)	81 (100%)	0	100	100
8	7	171/171 (100%)	170 (99%)	1 (1%)	78	80
9	l	70/70 (100%)	70 (100%)	0	100	100
10	M	147/147 (100%)	146 (99%)	1 (1%)	76	78
11	m	68/68 (100%)	68 (100%)	0	100	100
12	N	154/154 (100%)	150 (97%)	4 (3%)	40	61
13	n	45/45 (100%)	45 (100%)	0	100	100
14	O	107/107 (100%)	106 (99%)	1 (1%)	70	76
15	o	47/47 (100%)	47 (100%)	0	100	100
16	p	175/175 (100%)	173 (99%)	2 (1%)	65	74
17	Q	160/160 (100%)	158 (99%)	2 (1%)	61	71
18	5	140/145 (97%)	135 (96%)	5 (4%)	31	56
19	S	150/150 (100%)	150 (100%)	0	100	100
20	s	184/186 (99%)	182 (99%)	2 (1%)	65	74
21	T	126/126 (100%)	126 (100%)	0	100	100
22	U	156/156 (100%)	154 (99%)	2 (1%)	61	71
23	V	136/136 (100%)	135 (99%)	1 (1%)	76	78
24	W	87/87 (100%)	87 (100%)	0	100	100
26	r	105/166 (63%)	105 (100%)	0	100	100
27	x	104/104 (100%)	102 (98%)	2 (2%)	50	66
29	Y	54/54 (100%)	54 (100%)	0	100	100
31	Z	104/105 (99%)	104 (100%)	0	100	100
32	a	109/109 (100%)	108 (99%)	1 (1%)	70	76
34	b	115/115 (100%)	115 (100%)	0	100	100
35	C	90/90 (100%)	90 (100%)	0	100	100
36	c	118/118 (100%)	116 (98%)	2 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	D	71/71 (100%)	71 (100%)	0	100	100
38	d	46/46 (100%)	46 (100%)	0	100	100
39	E	193/194 (100%)	188 (97%)	5 (3%)	40	61
40	e	81/81 (100%)	81 (100%)	0	100	100
41	F	319/322 (99%)	317 (99%)	2 (1%)	78	80
42	f	92/96 (96%)	92 (100%)	0	100	100
43	G	288/288 (100%)	288 (100%)	0	100	100
44	g	109/109 (100%)	108 (99%)	1 (1%)	70	76
45	H	244/244 (100%)	243 (100%)	1 (0%)	84	83
46	h	90/90 (100%)	90 (100%)	0	100	100
47	I	134/152 (88%)	134 (100%)	0	100	100
48	L	185/185 (100%)	185 (100%)	0	100	100
All	All	5891/6110 (96%)	5852 (99%)	39 (1%)	73	78

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	212	ASN
1	R	282	PHE
1	R	285	TYR
6	K	71	VAL
8	7	161	LEU
10	M	84	LEU
12	N	24	VAL
12	N	58	VAL
12	N	85	LEU
12	N	124	ILE
14	O	53	VAL
16	p	64	VAL
16	p	183	THR
17	Q	34	VAL
17	Q	118	VAL
18	5	24	VAL
18	5	114	VAL
18	5	119	VAL
18	5	120	ASN
18	5	168	LEU
20	s	6	ARG

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Mol	Chain	Res	Type
20	s	165	ILE
22	U	51	VAL
22	U	100	VAL
23	V	80	VAL
27	x	73	VAL
27	x	102	ILE
32	a	80	VAL
36	c	56	VAL
36	c	78	LEU
39	E	20	THR
39	E	45	VAL
39	E	101	VAL
39	E	157	VAL
39	E	190	ARG
41	F	104	THR
41	F	205	VAL
44	g	27	ARG
45	H	64	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	16	ASN
1	R	103	ASN
1	R	212	ASN
1	R	227	ASN
1	R	316	ASN
2	X	6	GLN
2	X	9	ASN
2	X	106	ASN
2	X	170	GLN
3	i	11	ASN
3	i	34	HIS
3	i	52	GLN
4	J	231	ASN
5	j	99	GLN
6	K	137	ASN
6	K	243	GLN
7	k	100	HIS
8	7	58	HIS
8	7	149	ASN
8	7	163	GLN

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Mol	Chain	Res	Type
9	l	76	ASN
10	M	68	HIS
11	m	67	GLN
12	N	19	GLN
12	N	37	ASN
14	O	62	GLN
14	O	126	GLN
16	p	37	HIS
17	Q	55	HIS
17	Q	182	ASN
17	Q	193	GLN
18	5	97	ASN
18	5	133	HIS
19	S	5	HIS
19	S	9	GLN
21	T	66	HIS
21	T	144	GLN
22	U	49	HIS
22	U	88	HIS
22	U	122	HIS
23	V	122	GLN
24	W	87	ASN
24	W	88	GLN
26	r	32	ASN
26	r	56	ASN
27	x	98	ASN
27	x	132	ASN
29	Y	32	GLN
29	Y	58	HIS
29	Y	59	HIS
32	a	120	GLN
34	b	57	HIS
35	C	22	GLN
35	C	82	GLN
35	C	99	GLN
36	c	40	HIS
36	c	74	ASN
37	D	25	GLN
38	d	12	GLN
38	d	43	HIS
39	E	115	ASN
39	E	132	ASN

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Mol	Chain	Res	Type
39	E	205	ASN
39	E	209	HIS
41	F	139	GLN
41	F	224	HIS
41	F	231	HIS
42	f	57	GLN
43	G	5	GLN
43	G	9	HIS
43	G	48	GLN
43	G	110	ASN
43	G	114	ASN
43	G	260	GLN
44	g	13	HIS
44	g	21	HIS
44	g	49	ASN
44	g	88	HIS
45	H	17	GLN
45	H	63	GLN
45	H	81	HIS
45	H	244	HIS
47	I	167	ASN
48	L	44	GLN
48	L	57	ASN
48	L	96	ASN
48	L	127	GLN
48	L	158	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	3	120/121 (99%)	29 (24%)	1 (0%)
30	4	157/158 (99%)	45 (28%)	6 (3%)
33	B	75/76 (98%)	20 (26%)	5 (6%)
49	1	3313/3316 (99%)	979 (29%)	181 (5%)
All	All	3665/3671 (99%)	1073 (29%)	193 (5%)

All (1073) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	3	10	C
28	3	11	A

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Mol	Chain	Res	Type
28	3	12	U
28	3	13	A
28	3	14	U
28	3	22	A
28	3	33	U
28	3	38	U
28	3	41	G
28	3	42	A
28	3	48	U
28	3	49	G
28	3	53	U
28	3	55	A
28	3	62	U
28	3	64	A
28	3	65	G
28	3	68	C
28	3	76	A
28	3	77	G
28	3	78	U
28	3	87	G
28	3	90	U
28	3	91	G
28	3	95	A
28	3	99	G
28	3	102	A
28	3	112	G
28	3	121	U
30	4	13	A
30	4	15	G
30	4	22	U
30	4	23	U
30	4	24	G
30	4	33	A
30	4	34	U
30	4	39	G
30	4	40	A
30	4	49	G
30	4	51	G
30	4	52	A
30	4	53	A
30	4	57	C
30	4	59	A

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Mol	Chain	Res	Type
30	4	60	U
30	4	62	C
30	4	63	G
30	4	70	G
30	4	72	A
30	4	80	A
30	4	82	U
30	4	83	C
30	4	85	G
30	4	86	U
30	4	87	G
30	4	90	U
30	4	91	C
30	4	95	G
30	4	100	U
30	4	104	A
30	4	106	C
30	4	110	C
30	4	111	A
30	4	112	U
30	4	113	U
30	4	116	G
30	4	125	U
30	4	126	A
30	4	129	C
30	4	131	A
30	4	148	G
30	4	151	C
30	4	152	G
30	4	155	A
33	B	10	G
33	B	16	U
33	B	17	C
33	B	19	G
33	B	22	G
33	B	28	U
33	B	37	A
33	B	40	G
33	B	47	U
33	B	48	C
33	B	56	C
33	B	58	A

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Mol	Chain	Res	Type
33	B	59	U
33	B	70	U
33	B	71	C
33	B	72	C
33	B	73	G
33	B	74	C
33	B	75	C
33	B	76	A
49	1	4	U
49	1	13	A
49	1	14	U
49	1	15	C
49	1	25	U
49	1	26	A
49	1	27	C
49	1	30	G
49	1	37	U
49	1	40	A
49	1	41	G
49	1	43	A
49	1	44	U
49	1	48	A
49	1	49	A
49	1	57	A
49	1	59	G
49	1	60	A
49	1	65	A
49	1	66	A
49	1	67	A
49	1	71	A
49	1	72	C
49	1	73	C
49	1	74	G
49	1	77	A
49	1	85	A
49	1	86	G
49	1	87	U
49	1	92	G
49	1	94	G
49	1	105	C
49	1	110	G
49	1	111	C

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Mol	Chain	Res	Type
49	1	116	A
49	1	117	U
49	1	118	U
49	1	121	A
49	1	122	A
49	1	123	A
49	1	134	U
49	1	135	C
49	1	136	G
49	1	143	G
49	1	146	U
49	1	147	U
49	1	148	G
49	1	150	A
49	1	155	G
49	1	156	G
49	1	157	A
49	1	161	G
49	1	162	G
49	1	165	A
49	1	166	C
49	1	182	U
49	1	187	A
49	1	189	G
49	1	190	U
49	1	191	U
49	1	192	C
49	1	197	G
49	1	200	C
49	1	206	G
49	1	210	U
49	1	211	A
49	1	212	G
49	1	213	A
49	1	218	G
49	1	219	A
49	1	220	G
49	1	221	A
49	1	222	A
49	1	234	G
49	1	240	U
49	1	241	G

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Mol	Chain	Res	Type
49	1	243	G
49	1	244	G
49	1	250	U
49	1	251	G
49	1	252	U
49	1	253	A
49	1	254	A
49	1	263	C
49	1	267	G
49	1	268	A
49	1	270	U
49	1	283	G
49	1	286	U
49	1	295	A
49	1	297	G
49	1	298	U
49	1	304	G
49	1	305	U
49	1	315	C
49	1	316	U
49	1	323	A
49	1	329	U
49	1	330	G
49	1	338	A
49	1	342	A
49	1	343	U
49	1	348	A
49	1	350	C
49	1	351	A
49	1	354	U
49	1	375	A
49	1	376	G
49	1	385	A
49	1	395	A
49	1	397	A
49	1	398	A
49	1	399	A
49	1	401	U
49	1	402	A
49	1	403	C
49	1	404	G
49	1	406	G

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Mol	Chain	Res	Type
49	1	410	U
49	1	421	G
49	1	422	A
49	1	439	C
49	1	495	G
49	1	510	G
49	1	518	G
49	1	520	U
49	1	521	A
49	1	535	G
49	1	536	U
49	1	546	C
49	1	547	G
49	1	548	G
49	1	550	A
49	1	552	G
49	1	555	U
49	1	556	U
49	1	557	A
49	1	558	U
49	1	559	A
49	1	564	G
49	1	569	A
49	1	578	A
49	1	579	G
49	1	589	A
49	1	592	A
49	1	597	G
49	1	600	G
49	1	604	G
49	1	609	G
49	1	610	G
49	1	611	A
49	1	620	U
49	1	621	A
49	1	622	A
49	1	636	C
49	1	637	C
49	1	641	C
49	1	645	A
49	1	648	C
49	1	649	A

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Mol	Chain	Res	Type
49	1	660	A
49	1	661	G
49	1	662	U
49	1	675	C
49	1	677	A
49	1	678	G
49	1	681	U
49	1	690	A
49	1	691	A
49	1	692	A
49	1	698	U
49	1	699	A
49	1	705	A
49	1	708	G
49	1	709	A
49	1	712	G
49	1	715	A
49	1	716	A
49	1	719	U
49	1	720	A
49	1	723	U
49	1	742	G
49	1	750	G
49	1	760	G
49	1	764	U
49	1	765	C
49	1	766	U
49	1	767	U
49	1	768	C
49	1	770	G
49	1	776	U
49	1	777	U
49	1	781	G
49	1	784	A
49	1	786	A
49	1	799	G
49	1	800	G
49	1	801	A
49	1	806	A
49	1	808	A
49	1	815	G
49	1	817	A

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Mol	Chain	Res	Type
49	1	826	G
49	1	830	A
49	1	832	G
49	1	833	G
49	1	835	G
49	1	846	A
49	1	849	C
49	1	851	C
49	1	858	A
49	1	860	G
49	1	861	C
49	1	869	G
49	1	871	U
49	1	874	U
49	1	879	U
49	1	880	G
49	1	884	A
49	1	885	U
49	1	895	A
49	1	905	U
49	1	906	A
49	1	907	G
49	1	908	G
49	1	909	G
49	1	914	A
49	1	915	A
49	1	916	G
49	1	917	A
49	1	921	A
49	1	922	U
49	1	924	G
49	1	925	A
49	1	926	A
49	1	932	U
49	1	937	G
49	1	941	G
49	1	944	C
49	1	953	G
49	1	954	U
49	1	959	C
49	1	960	U
49	1	962	A

Continued on next page...

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Mol	Chain	Res	Type
49	1	963	G
49	1	968	G
49	1	974	G
49	1	980	A
49	1	981	U
49	1	982	C
49	1	984	G
49	1	985	U
49	1	995	U
49	1	1001	G
49	1	1002	A
49	1	1006	A
49	1	1015	U
49	1	1016	C
49	1	1017	C
49	1	1018	G
49	1	1021	G
49	1	1025	A
49	1	1026	A
49	1	1029	G
49	1	1032	C
49	1	1036	A
49	1	1037	C
49	1	1038	C
49	1	1041	U
49	1	1047	A
49	1	1049	C
49	1	1051	U
49	1	1054	A
49	1	1063	G
49	1	1065	A
49	1	1075	A
49	1	1076	C
49	1	1080	A
49	1	1081	U
49	1	1083	G
49	1	1093	A
49	1	1094	U
49	1	1095	U
49	1	1096	U
49	1	1097	G
49	1	1098	A

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Mol	Chain	Res	Type
49	1	1103	A
49	1	1104	G
49	1	1105	A
49	1	1113	G
49	1	1117	G
49	1	1128	U
49	1	1129	A
49	1	1131	G
49	1	1132	C
49	1	1143	A
49	1	1144	U
49	1	1145	G
49	1	1151	U
49	1	1152	G
49	1	1153	A
49	1	1155	C
49	1	1157	G
49	1	1159	A
49	1	1176	C
49	1	1177	G
49	1	1178	G
49	1	1179	A
49	1	1180	A
49	1	1181	U
49	1	1182	A
49	1	1191	U
49	1	1192	C
49	1	1193	A
49	1	1196	C
49	1	1197	A
49	1	1199	C
49	1	1200	A
49	1	1201	C
49	1	1202	A
49	1	1208	U
49	1	1209	G
49	1	1219	C
49	1	1220	U
49	1	1221	A
49	1	1222	G
49	1	1223	A
49	1	1232	C

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Mol	Chain	Res	Type
49	1	1235	U
49	1	1236	G
49	1	1237	G
49	1	1239	C
49	1	1241	U
49	1	1242	G
49	1	1244	A
49	1	1245	A
49	1	1246	G
49	1	1258	U
49	1	1259	A
49	1	1262	G
49	1	1263	A
49	1	1264	G
49	1	1265	U
49	1	1285	G
49	1	1286	A
49	1	1287	A
49	1	1293	U
49	1	1294	A
49	1	1301	A
49	1	1303	A
49	1	1305	U
49	1	1306	G
49	1	1307	G
49	1	1308	A
49	1	1309	U
49	1	1313	G
49	1	1315	U
49	1	1316	C
49	1	1323	G
49	1	1325	U
49	1	1329	U
49	1	1330	A
49	1	1331	U
49	1	1345	G
49	1	1349	G
49	1	1351	U
49	1	1352	A
49	1	1353	U
49	1	1355	A
49	1	1356	U

Continued on next page...

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Mol	Chain	Res	Type
49	1	1357	G
49	1	1366	A
49	1	1380	G
49	1	1386	A
49	1	1390	A
49	1	1391	C
49	1	1392	G
49	1	1399	A
49	1	1400	G
49	1	1406	A
49	1	1418	A
49	1	1419	A
49	1	1420	C
49	1	1429	G
49	1	1430	U
49	1	1431	G
49	1	1432	C
49	1	1433	A
49	1	1434	G
49	1	1435	A
49	1	1436	U
49	1	1437	C
49	1	1446	A
49	1	1447	G
49	1	1448	U
49	1	1450	G
49	1	1452	A
49	1	1455	U
49	1	1456	A
49	1	1468	A
49	1	1469	C
49	1	1470	U
49	1	1475	A
49	1	1477	A
49	1	1481	A
49	1	1482	A
49	1	1483	G
49	1	1484	U
49	1	1485	G
49	1	1488	G
49	1	1494	U
49	1	1503	A

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Mol	Chain	Res	Type
49	1	1508	C
49	1	1511	U
49	1	1512	U
49	1	1523	U
49	1	1527	C
49	1	1528	G
49	1	1533	U
49	1	1536	G
49	1	1554	U
49	1	1555	U
49	1	1556	C
49	1	1557	A
49	1	1558	A
49	1	1559	A
49	1	1560	G
49	1	1561	G
49	1	1563	C
49	1	1565	G
49	1	1567	U
49	1	1568	U
49	1	1569	U
49	1	1570	U
49	1	1571	A
49	1	1572	U
49	1	1575	A
49	1	1578	C
49	1	1579	C
49	1	1580	A
49	1	1581	C
49	1	1582	C
49	1	1583	A
49	1	1587	A
49	1	1588	A
49	1	1589	A
49	1	1593	A
49	1	1595	U
49	1	1605	A
49	1	1607	U
49	1	1613	A
49	1	1614	C
49	1	1620	U
49	1	1621	A

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Mol	Chain	Res	Type
49	1	1629	U
49	1	1630	U
49	1	1631	C
49	1	1638	A
49	1	1643	A
49	1	1645	U
49	1	1656	A
49	1	1657	C
49	1	1662	G
49	1	1677	G
49	1	1683	A
49	1	1713	G
49	1	1715	A
49	1	1716	U
49	1	1717	U
49	1	1724	U
49	1	1728	G
49	1	1729	A
49	1	1730	G
49	1	1731	A
49	1	1741	A
49	1	1742	U
49	1	1749	A
49	1	1750	A
49	1	1751	G
49	1	1752	A
49	1	1756	C
49	1	1760	A
49	1	1761	C
49	1	1762	C
49	1	1763	U
49	1	1765	U
49	1	1766	G
49	1	1770	G
49	1	1780	G
49	1	1794	G
49	1	1795	U
49	1	1796	G
49	1	1797	A
49	1	1808	G
49	1	1813	A
49	1	1814	A

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Mol	Chain	Res	Type
49	1	1815	U
49	1	1816	A
49	1	1817	G
49	1	1818	U
49	1	1819	U
49	1	1820	U
49	1	1822	C
49	1	1835	A
49	1	1839	A
49	1	1840	U
49	1	1841	A
49	1	1846	C
49	1	1847	A
49	1	1849	C
49	1	1850	A
49	1	1851	G
49	1	1864	A
49	1	1866	C
49	1	1871	U
49	1	1874	A
49	1	1879	A
49	1	1880	U
49	1	1884	A
49	1	1886	A
49	1	1887	A
49	1	1893	A
49	1	1898	G
49	1	1899	G
49	1	1901	A
49	1	1905	G
49	1	1906	G
49	1	1907	C
49	1	1913	A
49	1	1914	G
49	1	1920	U
49	1	1926	C
49	1	1928	G
49	1	1930	A
49	1	1931	U
49	1	1932	A
49	1	1933	A
49	1	1934	G

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Mol	Chain	Res	Type
49	1	1939	G
49	1	1952	G
49	1	1953	G
49	1	1954	G
49	1	1955	U
49	1	1959	G
49	1	1960	A
49	1	1961	G
49	1	1962	A
49	1	1963	G
49	1	1964	C
49	1	1969	G
49	1	1972	A
49	1	1973	G
49	1	1979	G
49	1	1981	G
49	1	1986	U
49	1	1994	G
49	1	1999	C
49	1	2001	U
49	1	2002	G
49	1	2004	U
49	1	2005	G
49	1	2006	G
49	1	2010	U
49	1	2013	C
49	1	2017	G
49	1	2020	A
49	1	2026	A
49	1	2032	U
49	1	2033	G
49	1	2035	G
49	1	2037	G
49	1	2043	U
49	1	2044	U
49	1	2047	A
49	1	2048	G
49	1	2049	A
49	1	2050	C
49	1	2051	G
49	1	2054	C
49	1	2058	G

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Mol	Chain	Res	Type
49	1	2081	U
49	1	2082	U
49	1	2087	C
49	1	2094	C
49	1	2101	C
49	1	2102	U
49	1	2107	A
49	1	2112	U
49	1	2113	A
49	1	2114	C
49	1	2115	G
49	1	2116	G
49	1	2117	A
49	1	2121	G
49	1	2122	G
49	1	2126	A
49	1	2131	A
49	1	2132	C
49	1	2137	U
49	1	2139	A
49	1	2140	U
49	1	2142	A
49	1	2144	A
49	1	2145	A
49	1	2159	U
49	1	2160	G
49	1	2169	G
49	1	2170	U
49	1	2174	G
49	1	2175	U
49	1	2176	U
49	1	2177	G
49	1	2178	A
49	1	2179	C
49	1	2186	U
49	1	2187	G
49	1	2197	C
49	1	2198	A
49	1	2205	U
49	1	2208	A
49	1	2209	U
49	1	2210	G

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Mol	Chain	Res	Type
49	1	2225	U
49	1	2232	A
49	1	2243	A
49	1	2244	A
49	1	2249	G
49	1	2250	G
49	1	2253	G
49	1	2254	U
49	1	2256	A
49	1	2257	C
49	1	2258	U
49	1	2262	A
49	1	2263	C
49	1	2268	U
49	1	2270	A
49	1	2272	G
49	1	2273	G
49	1	2274	U
49	1	2276	G
49	1	2279	A
49	1	2281	A
49	1	2282	U
49	1	2283	G
49	1	2284	C
49	1	2285	C
49	1	2286	U
49	1	2287	C
49	1	2298	U
49	1	2299	A
49	1	2306	C
49	1	2307	G
49	1	2308	C
49	1	2310	U
49	1	2313	A
49	1	2314	U
49	1	2315	G
49	1	2319	U
49	1	2334	U
49	1	2336	U
49	1	2340	U
49	1	2372	A
49	1	2373	A

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Mol	Chain	Res	Type
49	1	2374	C
49	1	2375	G
49	1	2377	G
49	1	2378	C
49	1	2385	G
49	1	2386	A
49	1	2387	A
49	1	2388	U
49	1	2390	A
49	1	2393	G
49	1	2397	A
49	1	2401	A
49	1	2402	A
49	1	2403	G
49	1	2404	A
49	1	2408	U
49	1	2411	U
49	1	2412	G
49	1	2418	G
49	1	2419	A
49	1	2422	C
49	1	2425	G
49	1	2434	U
49	1	2435	G
49	1	2440	G
49	1	2442	G
49	1	2443	A
49	1	2444	C
49	1	2448	G
49	1	2453	U
49	1	2454	G
49	1	2459	A
49	1	2460	U
49	1	2462	A
49	1	2467	G
49	1	2469	G
49	1	2471	U
49	1	2482	U
49	1	2486	A
49	1	2487	U
49	1	2488	A
49	1	2496	C

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Mol	Chain	Res	Type
49	1	2500	A
49	1	2503	G
49	1	2505	U
49	1	2506	U
49	1	2509	U
49	1	2510	U
49	1	2514	U
49	1	2515	A
49	1	2522	G
49	1	2523	A
49	1	2525	G
49	1	2531	C
49	1	2532	U
49	1	2533	G
49	1	2534	G
49	1	2537	U
49	1	2538	U
49	1	2539	C
49	1	2540	A
49	1	2541	U
49	1	2542	U
49	1	2543	U
49	1	2547	A
49	1	2549	G
49	1	2552	C
49	1	2554	A
49	1	2561	A
49	1	2568	C
49	1	2569	A
49	1	2570	U
49	1	2571	U
49	1	2572	C
49	1	2573	G
49	1	2581	U
49	1	2585	G
49	1	2593	A
49	1	2594	C
49	1	2595	A
49	1	2606	G
49	1	2607	G
49	1	2614	G
49	1	2617	U

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Mol	Chain	Res	Type
49	1	2618	G
49	1	2619	G
49	1	2626	A
49	1	2635	A
49	1	2636	A
49	1	2644	C
49	1	2652	U
49	1	2655	U
49	1	2657	A
49	1	2674	A
49	1	2676	A
49	1	2678	A
49	1	2681	U
49	1	2688	U
49	1	2689	A
49	1	2691	A
49	1	2694	A
49	1	2703	A
49	1	2707	C
49	1	2713	U
49	1	2716	U
49	1	2719	U
49	1	2720	G
49	1	2725	U
49	1	2727	A
49	1	2728	G
49	1	2729	U
49	1	2737	C
49	1	2742	C
49	1	2749	G
49	1	2752	U
49	1	2753	G
49	1	2754	G
49	1	2755	C
49	1	2762	A
49	1	2772	C
49	1	2773	C
49	1	2777	G
49	1	2778	G
49	1	2795	U
49	1	2797	C
49	1	2798	C

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Mol	Chain	Res	Type
49	1	2799	A
49	1	2800	G
49	1	2801	A
49	1	2802	A
49	1	2804	A
49	1	2809	C
49	1	2810	C
49	1	2814	G
49	1	2816	G
49	1	2817	A
49	1	2818	U
49	1	2819	A
49	1	2828	G
49	1	2834	G
49	1	2842	U
49	1	2843	U
49	1	2845	A
49	1	2847	A
49	1	2849	C
49	1	2860	U
49	1	2861	U
49	1	2866	U
49	1	2867	C
49	1	2871	G
49	1	2872	A
49	1	2873	U
49	1	2874	G
49	1	2875	U
49	1	2886	U
49	1	2887	A
49	1	2888	U
49	1	2889	C
49	1	2896	A
49	1	2898	G
49	1	2911	A
49	1	2912	G
49	1	2923	U
49	1	2928	C
49	1	2935	U
49	1	2936	A
49	1	2941	A
49	1	2942	C

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Mol	Chain	Res	Type
49	1	2945	G
49	1	2946	A
49	1	2950	G
49	1	2951	G
49	1	2966	G
49	1	2972	G
49	1	2978	U
49	1	2979	U
49	1	2982	A
49	1	2983	C
49	1	2990	G
49	1	2992	U
49	1	2996	U
49	1	2997	G
49	1	3003	G
49	1	3011	A
49	1	3012	A
49	1	3021	A
49	1	3022	G
49	1	3023	U
49	1	3026	G
49	1	3028	G
49	1	3030	G
49	1	3047	U
49	1	3049	A
49	1	3055	U
49	1	3058	U
49	1	3059	G
49	1	3069	G
49	1	3078	U
49	1	3079	U
49	1	3086	A
49	1	3091	A
49	1	3092	C
49	1	3100	U
49	1	3104	U
49	1	3109	G
49	1	3113	A
49	1	3115	C
49	1	3117	C
49	1	3119	U
49	1	3122	A

Continued on next page...

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Mol	Chain	Res	Type
49	1	3129	A
49	1	3130	A
49	1	3131	U
49	1	3139	A
49	1	3141	A
49	1	3142	A
49	1	3143	C
49	1	3144	G
49	1	3145	C
49	1	3151	U
49	1	3153	U
49	1	3155	U
49	1	3156	U
49	1	3157	U
49	1	3158	G
49	1	3167	A
49	1	3170	A
49	1	3172	A
49	1	3173	G
49	1	3174	A
49	1	3175	U
49	1	3176	G
49	1	3179	U
49	1	3180	A
49	1	3181	C
49	1	3186	A
49	1	3187	A
49	1	3194	C
49	1	3196	U
49	1	3197	G
49	1	3199	G
49	1	3205	G
49	1	3206	C
49	1	3207	U
49	1	3208	G
49	1	3209	A
49	1	3210	A
49	1	3215	A
49	1	3216	G
49	1	3217	C
49	1	3218	A
49	1	3219	G

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Mol	Chain	Res	Type
49	1	3220	G
49	1	3222	U
49	1	3224	G
49	1	3231	U
49	1	3237	U
49	1	3242	G
49	1	3243	A
49	1	3244	A
49	1	3245	A
49	1	3246	G
49	1	3247	G
49	1	3249	C
49	1	3253	G
49	1	3259	U
49	1	3260	G
49	1	3263	G
49	1	3268	A
49	1	3269	U
49	1	3270	U
49	1	3271	G
49	1	3272	C
49	1	3275	U
49	1	3276	G
49	1	3278	C
49	1	3279	A
49	1	3287	U
49	1	3288	G
49	1	3289	G
49	1	3290	G
49	1	3293	U
49	1	3295	A
49	1	3304	U
49	1	3305	A
49	1	3309	G
49	1	3313	U
49	1	3316	A
49	1	3317	U
49	1	3318	G
49	1	3319	U
49	1	3333	G
49	1	3335	A
49	1	3341	U

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Mol	Chain	Res	Type
49	1	3345	G
49	1	3347	A
49	1	3351	U
49	1	3352	U
49	1	3353	G
49	1	3354	U
49	1	3355	U
49	1	3356	G
49	1	3357	U
49	1	3358	U
49	1	3363	U
49	1	3368	U
49	1	3369	G
49	1	3375	A
49	1	3378	C
49	1	3383	G
49	1	3386	G
49	1	3389	U
49	1	3390	G
49	1	3395	G
49	1	3396	U

All (193) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	3	77	G
30	4	22	U
30	4	23	U
30	4	38	U
30	4	48	A
30	4	51	G
30	4	58	G
33	B	70	U
33	B	71	C
33	B	72	C
33	B	73	G
33	B	74	C
49	1	14	U
49	1	43	A
49	1	71	A
49	1	73	C
49	1	86	G

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Mol	Chain	Res	Type
49	1	116	A
49	1	122	A
49	1	147	U
49	1	155	G
49	1	156	G
49	1	189	G
49	1	211	A
49	1	218	G
49	1	219	A
49	1	239	G
49	1	269	G
49	1	282	G
49	1	304	G
49	1	341	G
49	1	353	G
49	1	374	A
49	1	400	G
49	1	494	G
49	1	547	G
49	1	556	U
49	1	558	U
49	1	621	A
49	1	648	C
49	1	661	G
49	1	677	A
49	1	690	A
49	1	715	A
49	1	764	U
49	1	767	U
49	1	785	G
49	1	859	G
49	1	870	G
49	1	879	U
49	1	884	A
49	1	896	A
49	1	906	A
49	1	914	A
49	1	916	G
49	1	924	G
49	1	962	A
49	1	979	U
49	1	981	U

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Mol	Chain	Res	Type
49	1	994	G
49	1	1064	A
49	1	1075	A
49	1	1095	U
49	1	1116	G
49	1	1144	U
49	1	1152	G
49	1	1177	G
49	1	1181	U
49	1	1191	U
49	1	1199	C
49	1	1241	U
49	1	1307	G
49	1	1329	U
49	1	1348	U
49	1	1355	A
49	1	1365	G
49	1	1390	A
49	1	1391	C
49	1	1417	G
49	1	1418	A
49	1	1433	A
49	1	1434	G
49	1	1447	G
49	1	1455	U
49	1	1481	A
49	1	1483	G
49	1	1553	U
49	1	1554	U
49	1	1557	A
49	1	1568	U
49	1	1580	A
49	1	1589	A
49	1	1643	A
49	1	1716	U
49	1	1730	G
49	1	1740	U
49	1	1793	C
49	1	1794	G
49	1	1795	U
49	1	1815	U
49	1	1816	A

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Mol	Chain	Res	Type
49	1	1840	U
49	1	1847	A
49	1	1849	C
49	1	1850	A
49	1	1900	A
49	1	1913	A
49	1	1931	U
49	1	1938	U
49	1	1953	G
49	1	1959	G
49	1	2046	U
49	1	2047	A
49	1	2086	A
49	1	2093	A
49	1	2101	C
49	1	2111	G
49	1	2112	U
49	1	2139	A
49	1	2144	A
49	1	2158	A
49	1	2175	U
49	1	2177	G
49	1	2178	A
49	1	2208	A
49	1	2262	A
49	1	2267	C
49	1	2271	A
49	1	2273	G
49	1	2282	U
49	1	2283	G
49	1	2286	U
49	1	2313	A
49	1	2372	A
49	1	2373	A
49	1	2377	G
49	1	2385	G
49	1	2402	A
49	1	2403	G
49	1	2447	A
49	1	2468	A
49	1	2486	A
49	1	2487	U

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Mol	Chain	Res	Type
49	1	2509	U
49	1	2513	U
49	1	2537	U
49	1	2541	U
49	1	2593	A
49	1	2617	U
49	1	2625	C
49	1	2635	A
49	1	2656	A
49	1	2715	A
49	1	2727	A
49	1	2728	G
49	1	2772	C
49	1	2794	G
49	1	2797	C
49	1	2803	A
49	1	2816	G
49	1	2818	U
49	1	2866	U
49	1	2872	A
49	1	2911	A
49	1	2941	A
49	1	2950	G
49	1	2971	A
49	1	2983	C
49	1	3021	A
49	1	3022	G
49	1	3078	U
49	1	3121	U
49	1	3143	C
49	1	3152	U
49	1	3154	C
49	1	3156	U
49	1	3175	U
49	1	3179	U
49	1	3186	A
49	1	3208	G
49	1	3216	G
49	1	3218	A
49	1	3219	G
49	1	3244	A
49	1	3246	G

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Mol	Chain	Res	Type
49	1	3259	U
49	1	3269	U
49	1	3275	U
49	1	3293	U
49	1	3303	G
49	1	3304	U
49	1	3334	U
49	1	3368	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 [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	4
49	1	4
33	B	1
45	H	1
41	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	173:UNK	C	188:SER	N	35.01
1	1	2087:C	O3'	2093:A	P	28.51
1	R	105:ARG	C	113:UNK	N	19.16
1	R	529:GLY	C	535:UNK	N	16.65
1	R	123:UNK	C	156:UNK	N	13.22
1	1	440:A	O3'	494:G	P	12.95
1	1	2059:U	O3'	2080:C	P	11.59
1	1	1984:C	O3'	1985:G	P	6.24
1	B	3:G	O3'	4:C	P	1.95
1	H	139:PRO	C	140:ARG	N	1.20
1	F	237:LYS	C	238:LEU	N	1.09

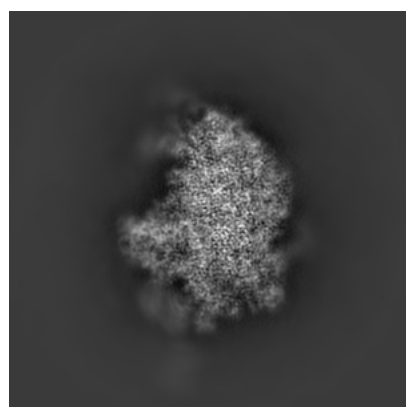
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4753. These allow visual inspection of the internal detail of the map and identification of artifacts.

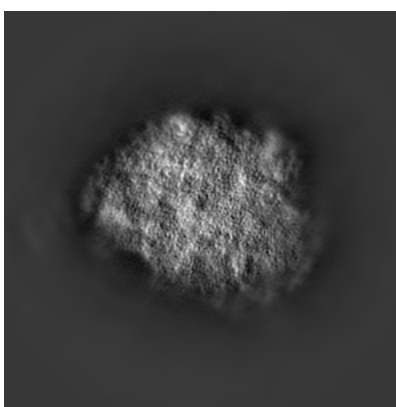
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

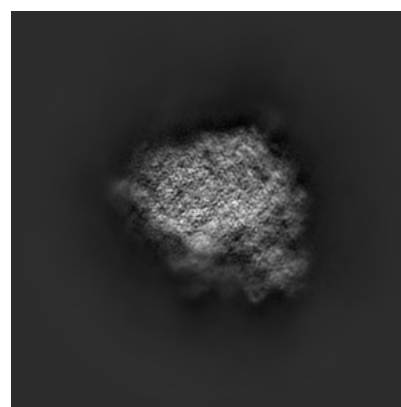
6.1.1 Primary map



X



Y

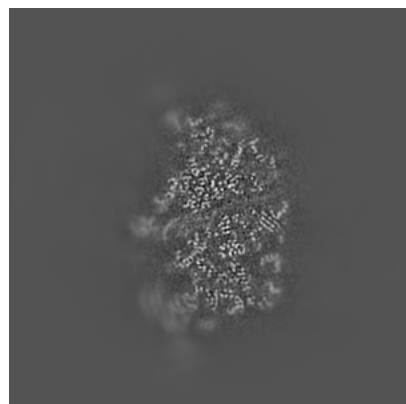


Z

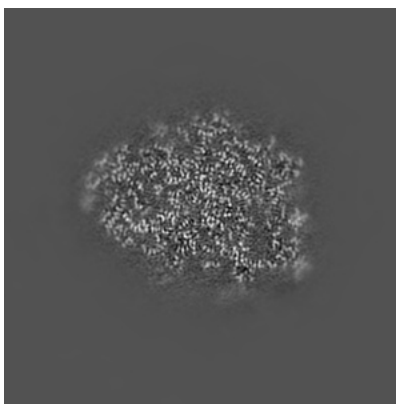
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

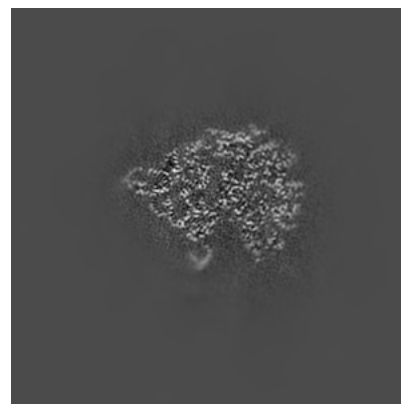
6.2.1 Primary map



X Index: 198



Y Index: 198

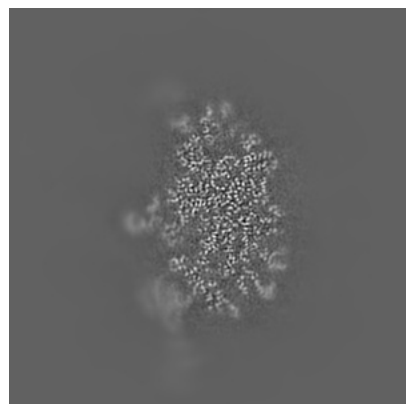


Z Index: 198

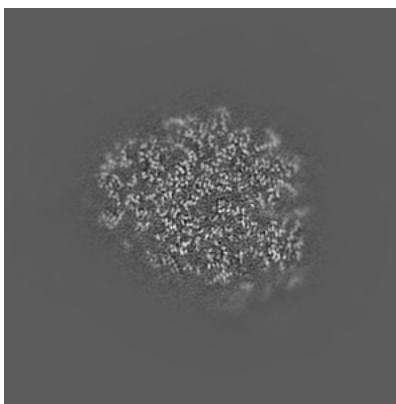
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

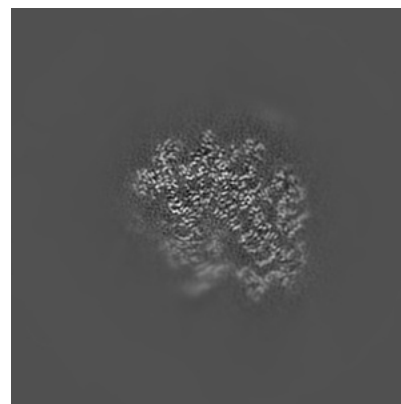
6.3.1 Primary map



X Index: 187



Y Index: 207

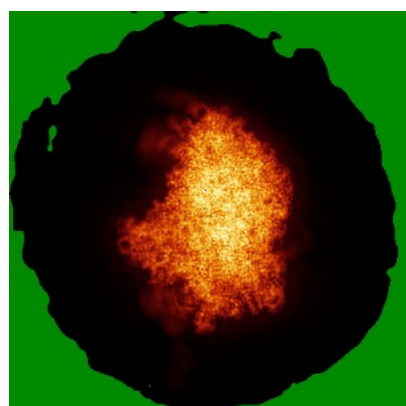


Z Index: 182

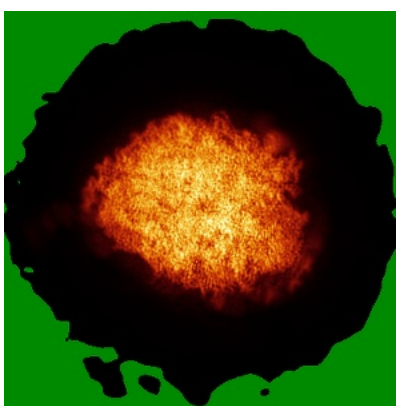
The images above show the largest variance slices of the map in three orthogonal directions.

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

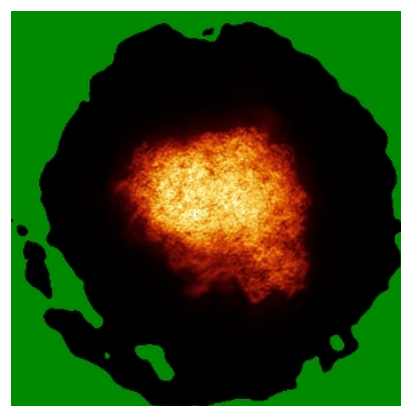
6.4.1 Primary map



X



Y

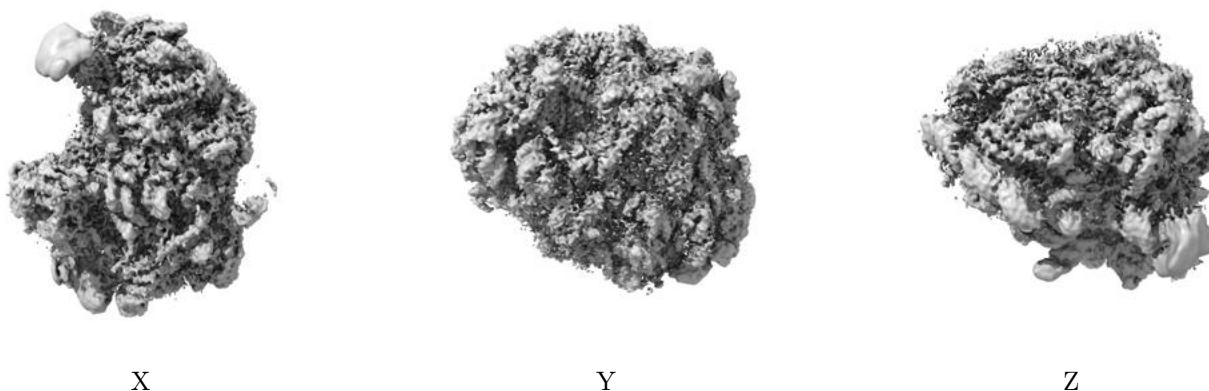


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

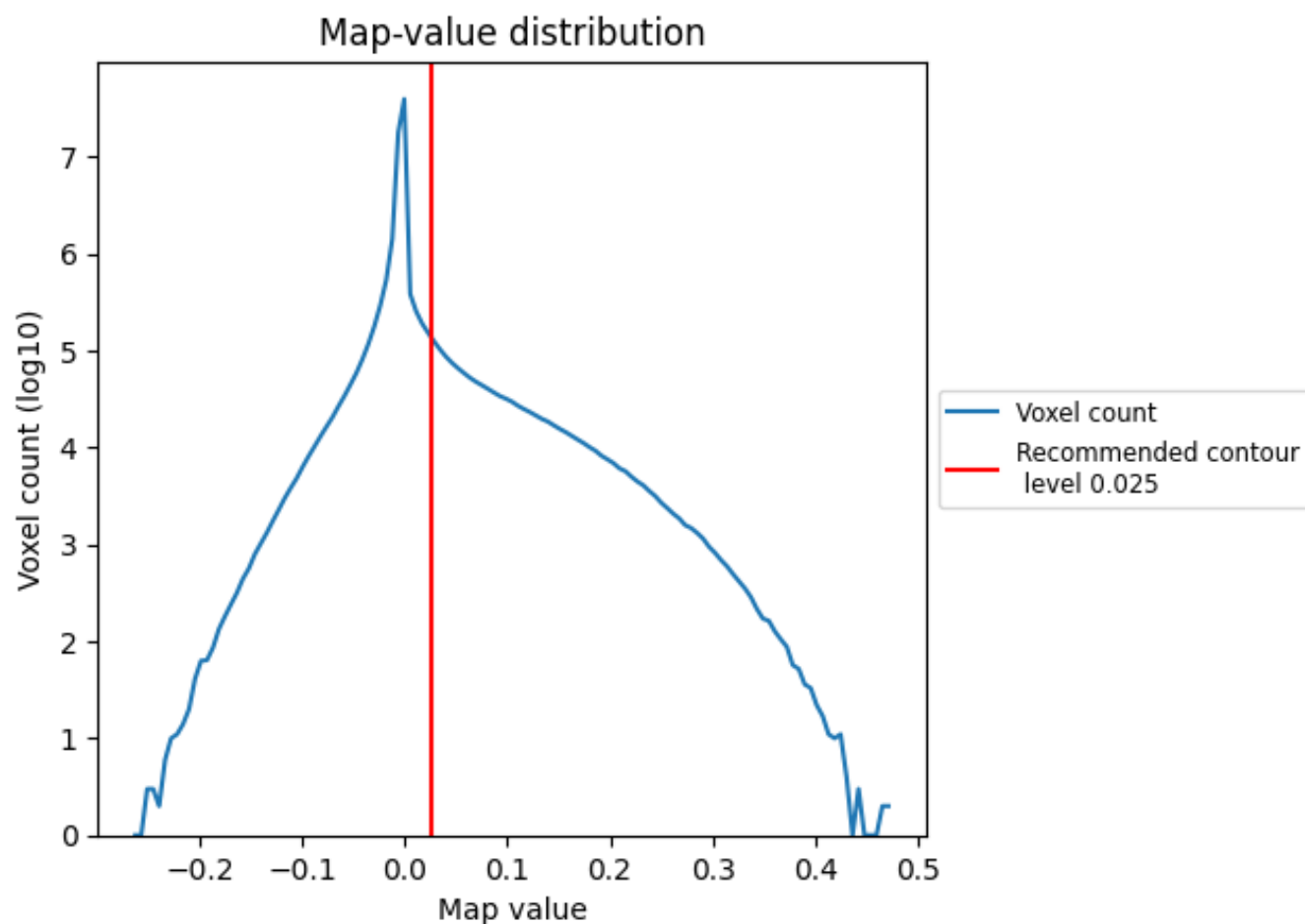
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

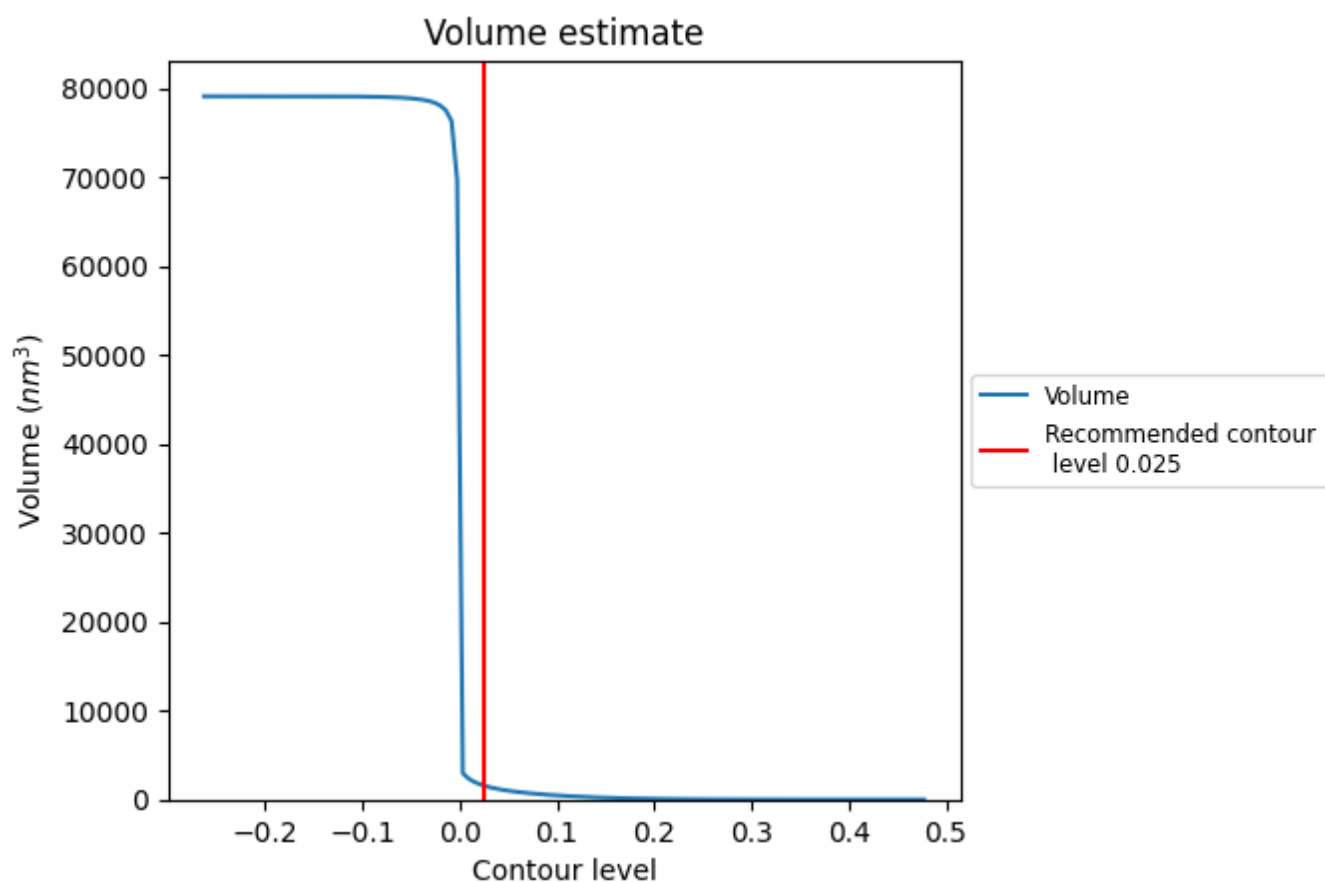
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

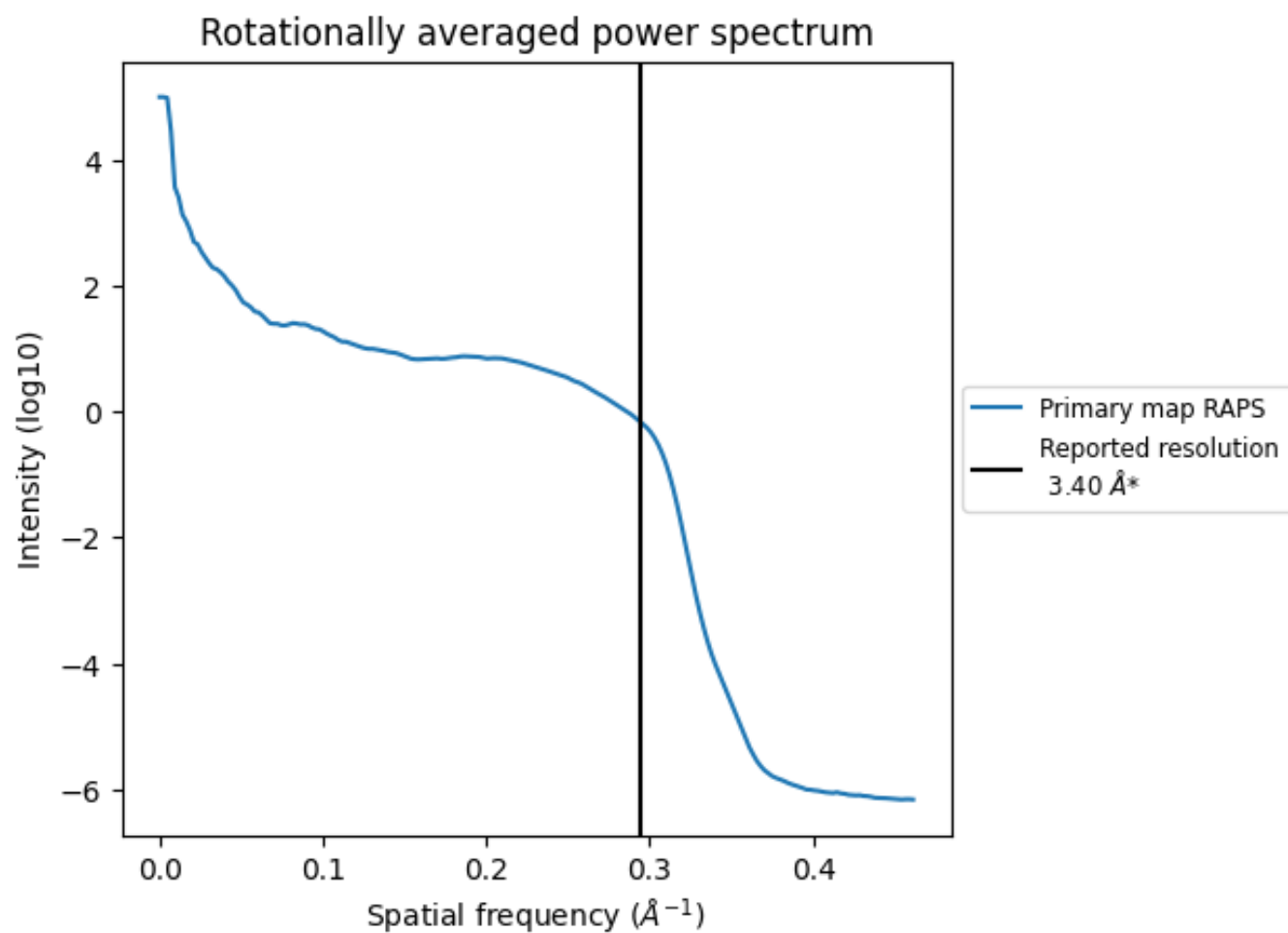
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1576 nm³; this corresponds to an approximate mass of 1423 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 0.294 Å⁻¹

8 Fourier-Shell correlation

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

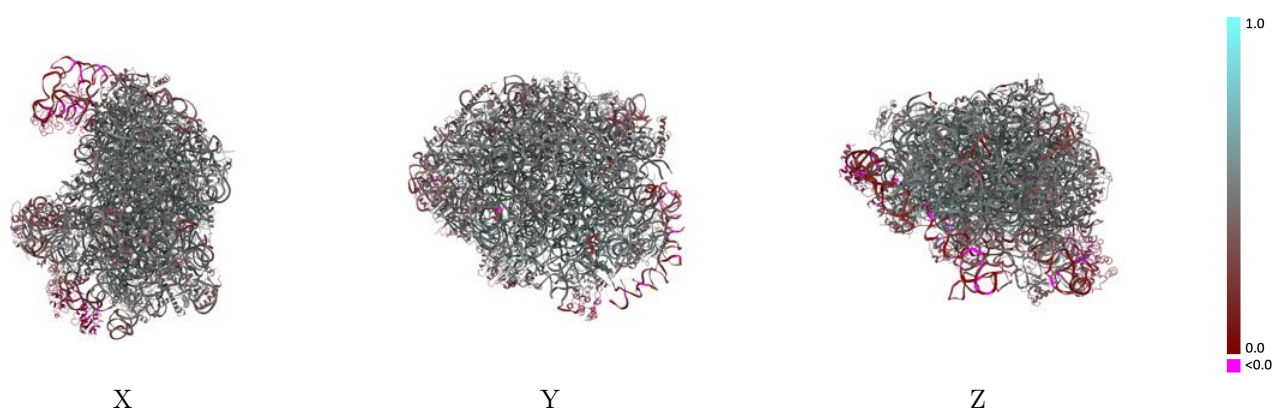
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4753 and PDB model 6R87. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

This section was not generated.

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

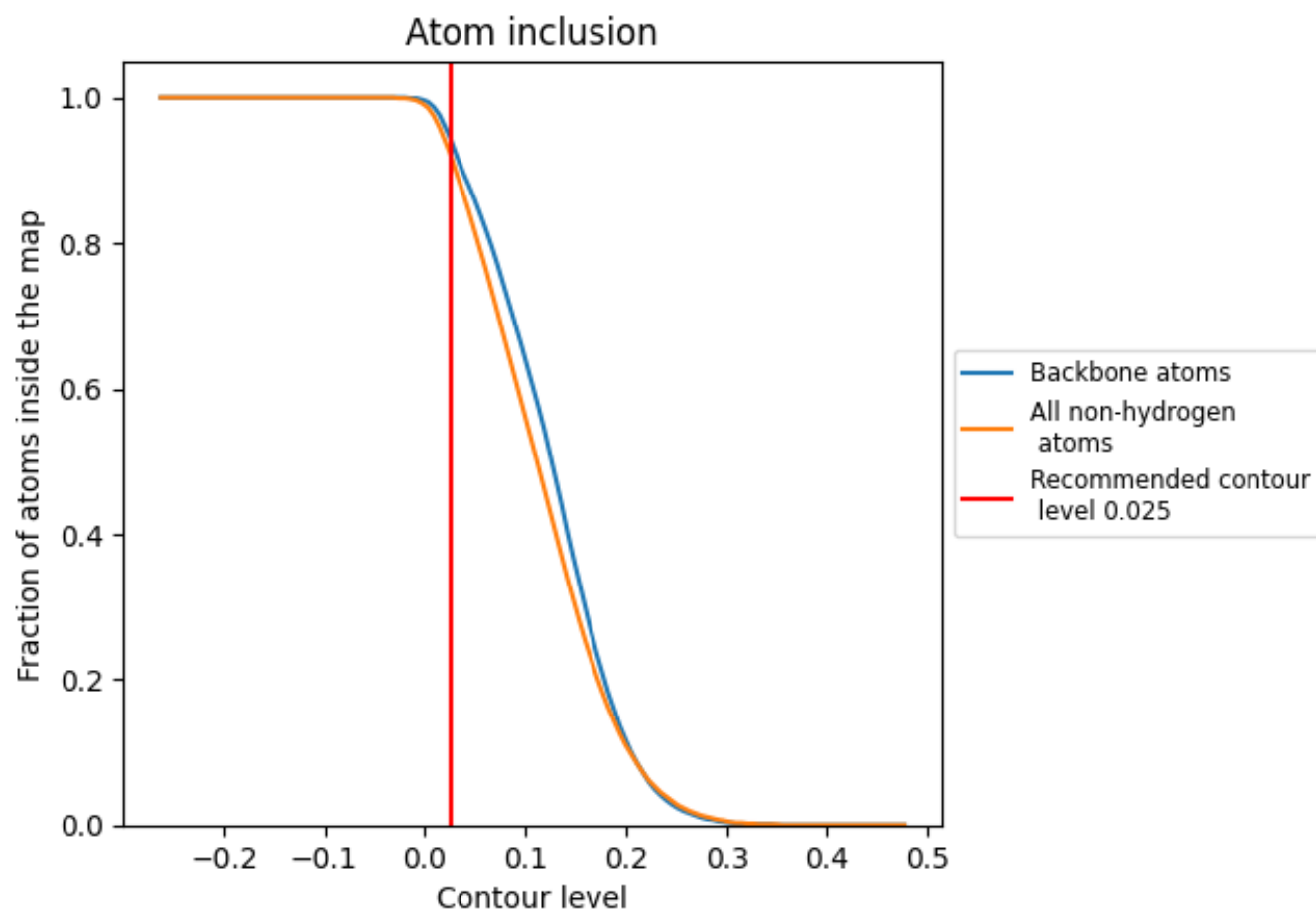


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9240	 0.4550
1	 0.9610	 0.4660
3	 0.9910	 0.4600
4	 0.9860	 0.5000
5	 0.9290	 0.5000
7	 0.9270	 0.4830
B	 0.9330	 0.2550
C	 0.8960	 0.4630
D	 0.9420	 0.5070
E	 0.9360	 0.5290
F	 0.9500	 0.5170
G	 0.9230	 0.4860
H	 0.8850	 0.3900
I	 0.9130	 0.4590
J	 0.9130	 0.4730
K	 0.9160	 0.4480
L	 0.4100	 0.0660
M	 0.8790	 0.3840
N	 0.9220	 0.4730
O	 0.9180	 0.4690
P	 0.5470	 0.1000
Q	 0.9450	 0.5180
R	 0.5930	 0.2820
S	 0.9200	 0.4850
T	 0.9390	 0.5050
U	 0.9210	 0.5010
V	 0.9060	 0.4850
W	 0.9140	 0.4440
X	 0.4590	 0.3440
Y	 0.9340	 0.4980
Z	 0.9490	 0.5090
a	 0.9390	 0.4800
b	 0.9220	 0.4760
c	 0.9260	 0.4890
d	 0.8940	 0.4440



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Chain	Atom inclusion	Q-score
e	 0.9120	 0.4580
f	 0.9140	 0.5080
g	 0.9430	 0.5120
h	 0.9440	 0.5220
i	 0.9510	 0.5190
j	 0.9190	 0.4690
k	 0.8980	 0.4480
l	 0.9500	 0.5380
m	 0.8560	 0.4360
n	 0.9520	 0.5290
o	 0.9450	 0.4990
p	 0.9460	 0.5300
r	 0.7330	 0.0850
s	 0.8890	 0.4550
x	 0.9340	 0.5120