



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 01:52 AM UTC

PDB ID : 3J9W / pdb_00003j9w
EMDB ID : EMD-6306
Title : Cryo-EM structure of the Bacillus subtilis MifM-stalled ribosome complex
Authors : Sohmen, D.; Chiba, S.; Shimokawa-Chiba, N.; Innis, C.A.; Berninghausen, O.; Beckmann, R.; Ito, K.; Wilson, D.N.
Deposited on : 2015-03-16
Resolution : 3.90 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

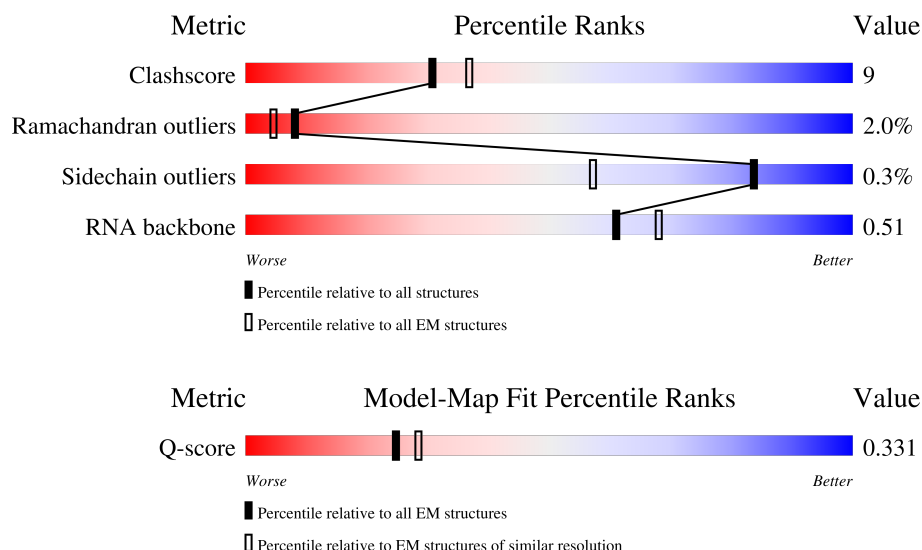
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	AA	1555	
2	AB	246	
3	AC	218	

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Mol	Chain	Length	Quality of chain
4	AD	200	36% 96% .
5	AE	166	41% 95% 5% .
6	AF	95	12% 96% .
7	AG	156	21% 96% ..
8	AH	132	24% 98% ..
9	AI	130	41% 92% 5% .
10	AJ	102	65% 95% 5%
11	AK	131	17% 83% 7% 10%
12	AL	138	14% 93% 7% .
13	AM	121	20% 88% 8% ..
14	AN	61	26% 90% 7% ..
15	AO	89	6% 97% ..
16	AP	90	14% 97% ..
17	AQ	87	15% 97% ..
18	AR	79	25% 84% 5% 10%
19	AS	92	16% 86% 5% 9%
20	AT	88	14% 92% 6% .
21	AX	77	5% 61% 22% 17%
22	AY	19	11% 68% 58% 32%
23	AZ	95	13% 13% 11% .. 75%
24	B0	62	13% 58% 31% 5% 6%
25	B1	66	9% 67% 32% .
26	B2	59	7% 71% 25% ..
27	B3	66	48% 70% 26% ..
28	B4	59	8% 64% 27% 8%

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Mol	Chain	Length	Quality of chain
29	B5	49	
30	B6	44	
31	B7	66	
32	B8	37	
33	BA	2928	
34	BB	119	
35	BD	277	
36	BE	209	
37	BF	207	
38	BG	179	
39	BH	179	
40	BJ	166	
41	BK	141	
42	BM	145	
43	BN	122	
44	BO	146	
45	BP	144	
46	BQ	120	
47	BR	120	
48	BS	115	
49	BT	119	
50	BU	102	
51	BV	113	
52	BW	95	
53	BX	103	

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Mol	Chain	Length	Quality of chain
54	BZ	94	64%23%13%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 135425 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 2 is a protein called 30S ribosomal protein uS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	AB	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 3 is a protein called 30S ribosomal protein uS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	AC	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 4 is a protein called 30S ribosomal protein uS4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AD	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 5 is a protein called 30S ribosomal protein uS5.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	AE	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 6 is a protein called 30S ribosomal protein bS6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	AF	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 7 is a protein called 30S ribosomal protein uS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	AG	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 8 is a protein called 30S ribosomal protein uS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AH	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 9 is a protein called 30S ribosomal protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AI	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 10 is a protein called 30S ribosomal protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AJ	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 11 is a protein called 30S ribosomal protein uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AK	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 12 is a protein called 30S ribosomal protein uS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AL	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 13 is a protein called 30S ribosomal protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AM	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 14 is a protein called 30S ribosomal protein uS14.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AN	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 15 is a protein called 30S ribosomal protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AO	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 16 is a protein called 30S ribosomal protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AP	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 17 is a protein called 30S ribosomal protein uS17.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AQ	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 18 is a protein called 30S ribosomal protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 19 is a protein called 30S ribosomal protein uS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	AS	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 20 is a protein called 30S ribosomal protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AT	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 21 is a RNA chain called tRNA-Asp.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AX	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	19	Total	C	N	O	P	0	0
			415	185	82	129	19		

- Molecule 23 is a protein called MifM.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AZ	24	Total	C	N	O	S	0	0
			107	64	28	14	1		

- Molecule 24 is a protein called 50S ribosomal protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B0	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B1	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B2	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 27 is a protein called 50S ribosomal protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B3	64	Total	C	N	O	S	0	0
			503	314	92	92	5		

- Molecule 28 is a protein called 50S ribosomal protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B4	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 29 is a protein called 50S ribosomal protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B5	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 30 is a protein called 50S ribosomal protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B6	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 31 is a protein called 50S ribosomal protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B7	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 32 is a protein called 50S ribosomal protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B8	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 33 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BA	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

- Molecule 34 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BB	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 35 is a protein called 50S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BD	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 36 is a protein called 50S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BE	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 37 is a protein called 50S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BF	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 38 is a protein called 50S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BG	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 39 is a protein called 50S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BH	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 40 is a protein called 50S ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BJ	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 41 is a protein called 50S ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BK	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 42 is a protein called 50S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BM	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 43 is a protein called 50S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BN	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 44 is a protein called 50S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 45 is a protein called 50S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BP	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 46 is a protein called 50S ribosomal protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BQ	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 47 is a protein called 50S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BR	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 48 is a protein called 50S ribosomal protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	BS	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 49 is a protein called 50S ribosomal protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BT	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 50 is a protein called 50S ribosomal protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BU	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 51 is a protein called 50S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BV	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 52 is a protein called 50S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BW	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 53 is a protein called 50S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BX	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

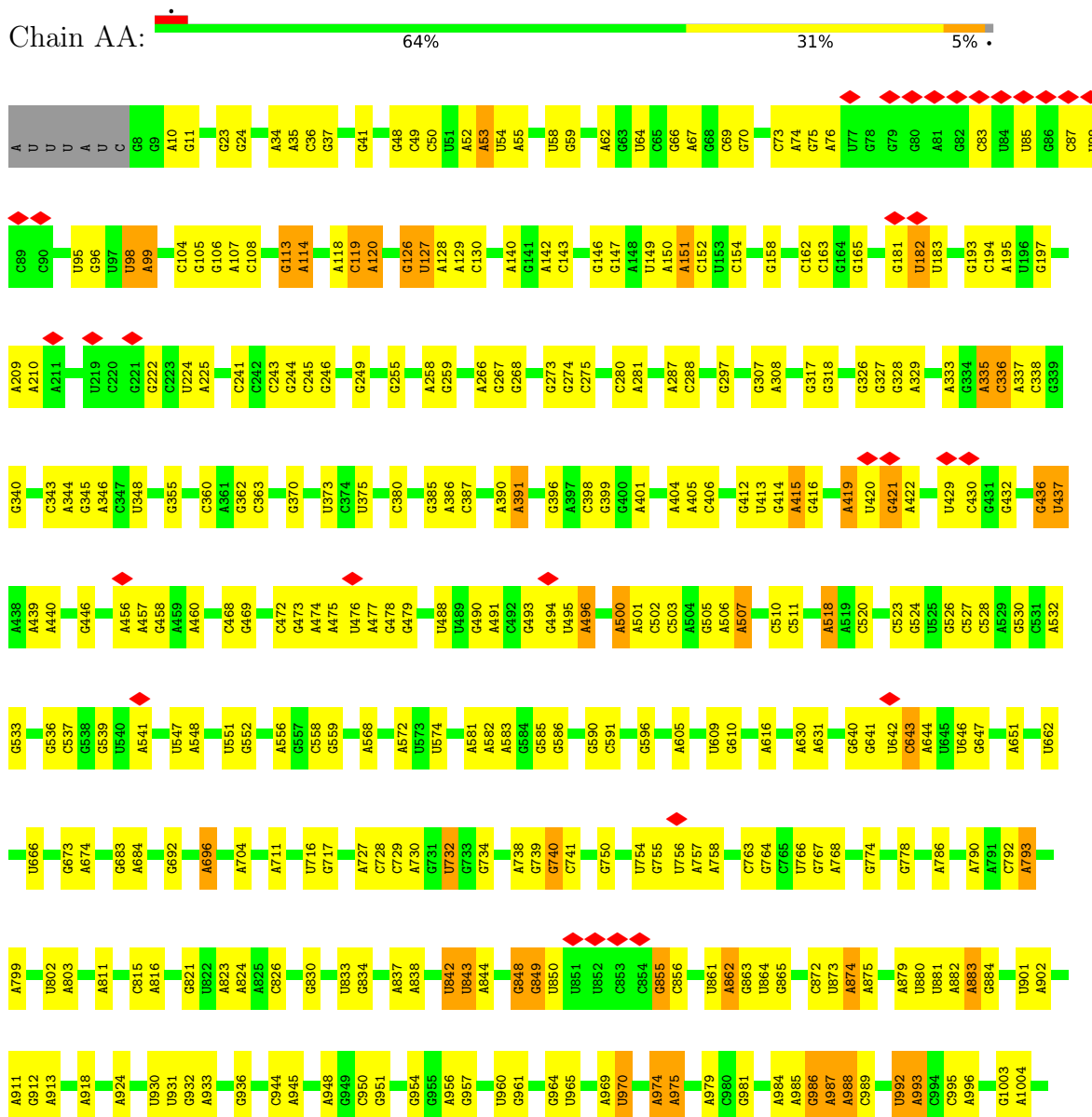
- Molecule 54 is a protein called 50S ribosomal protein bL27.

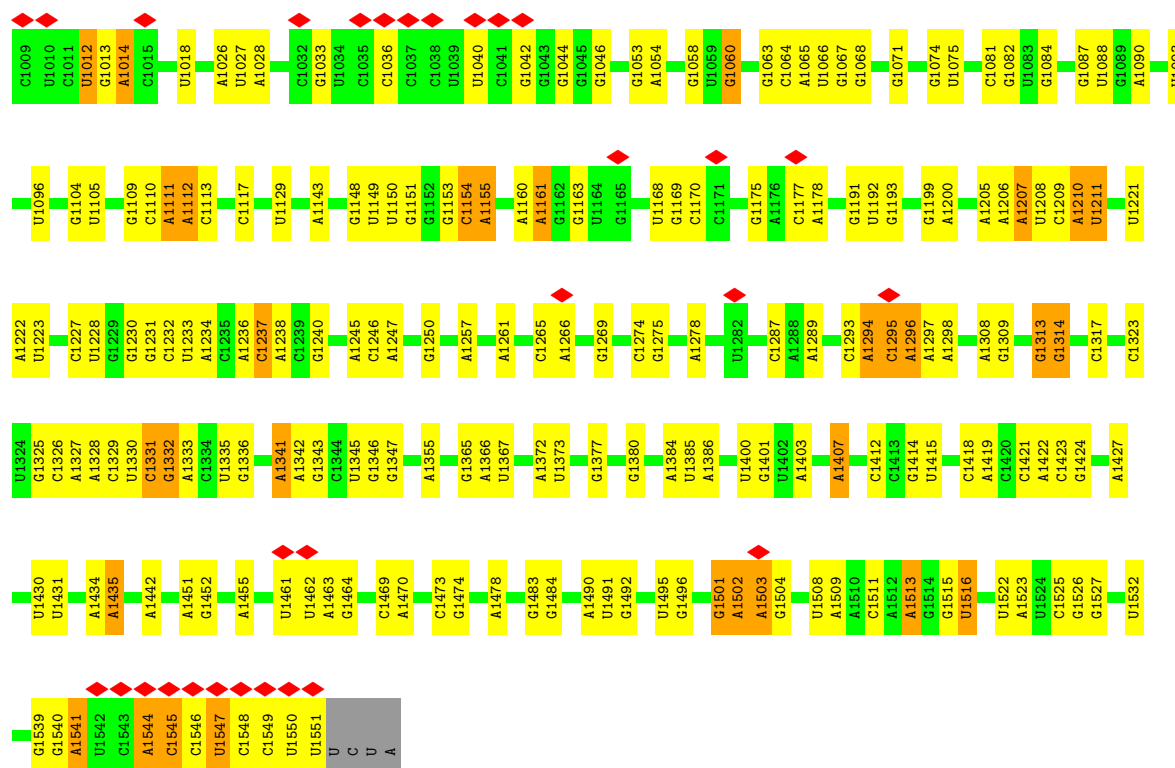
Mol	Chain	Residues	Atoms					AltConf	Trace
54	BZ	82	Total	C	N	O		0	0
			630	390	123	117			

3 Residue-property plots

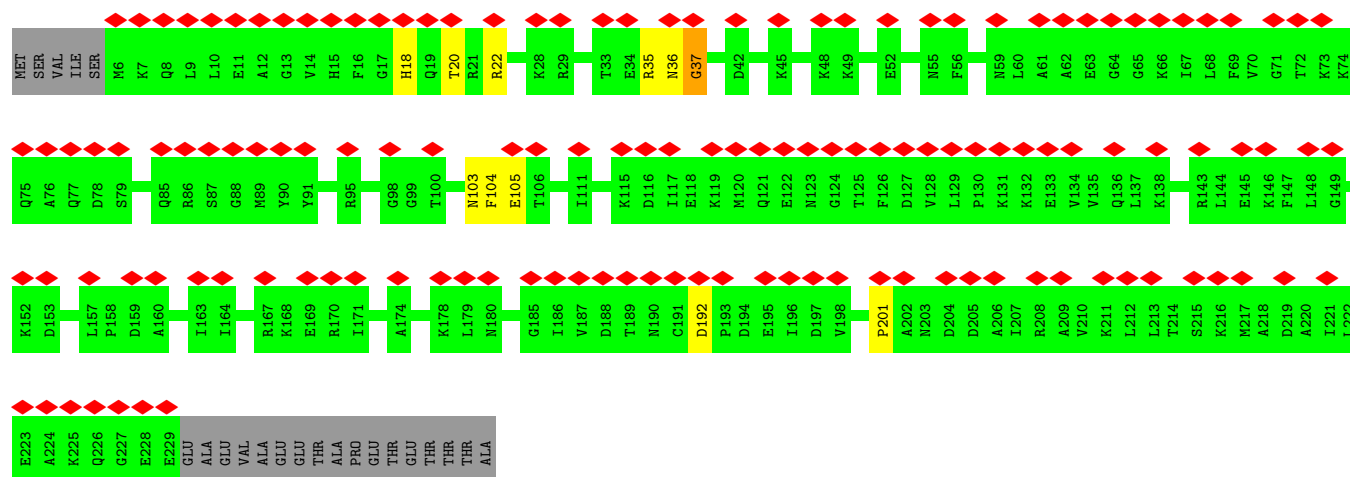
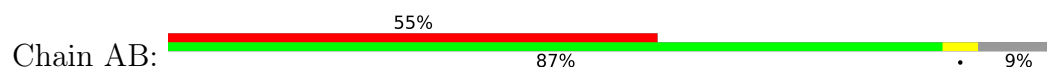
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

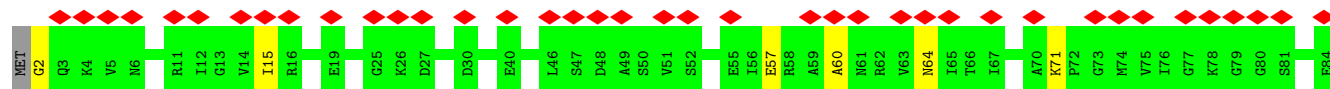
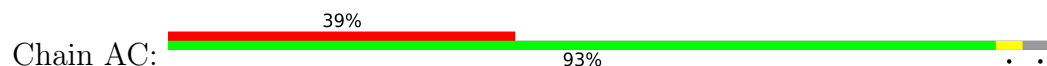


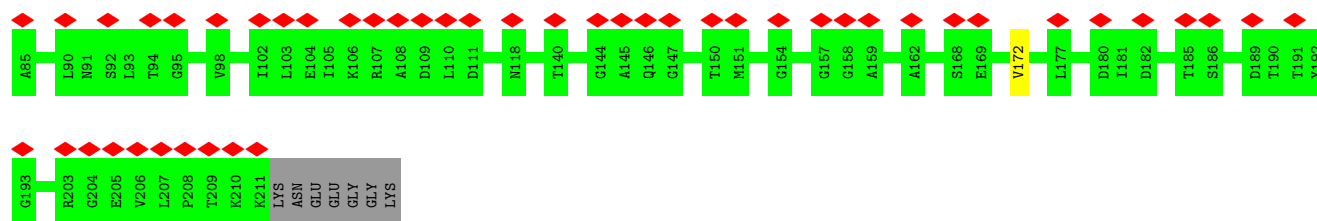


• Molecule 2: 30S ribosomal protein uS2

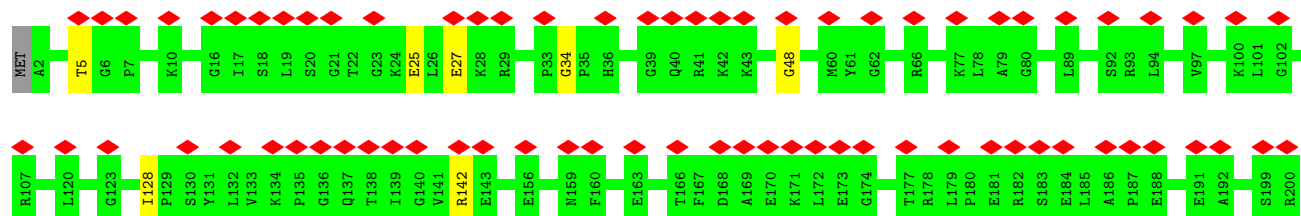


• Molecule 3: 30S ribosomal protein uS3

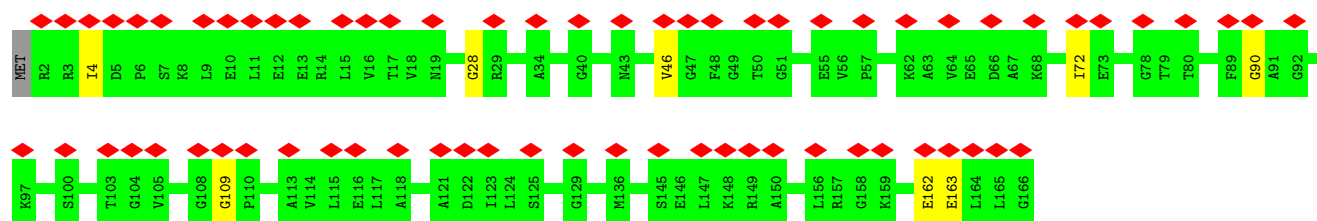
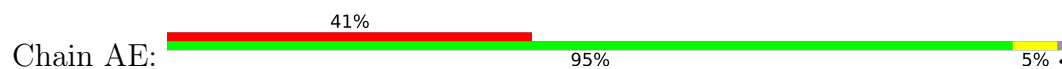




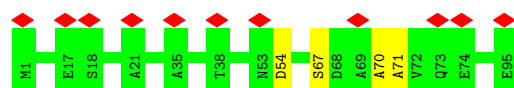
• Molecule 4: 30S ribosomal protein uS4



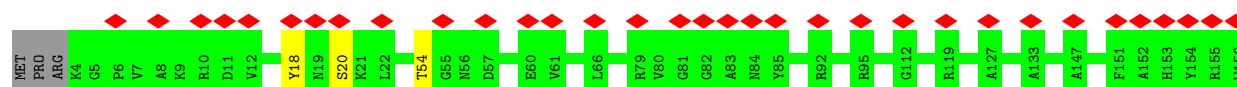
• Molecule 5: 30S ribosomal protein uS5



• Molecule 6: 30S ribosomal protein bS6

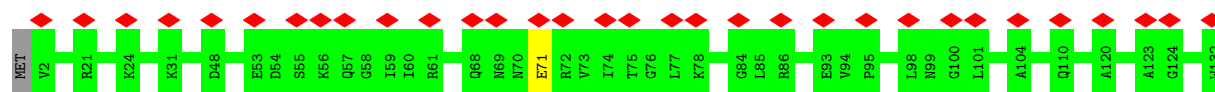


• Molecule 7: 30S ribosomal protein uS7

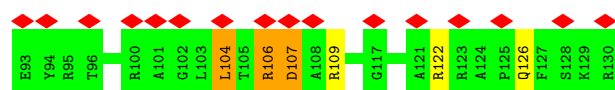
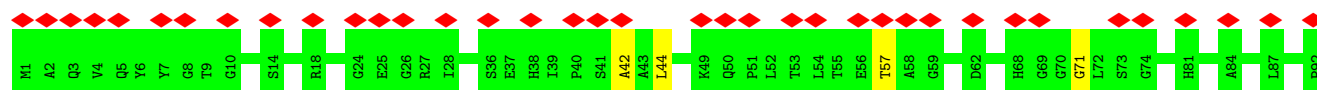
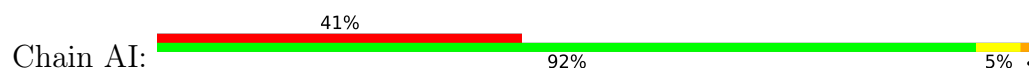


• Molecule 8: 30S ribosomal protein uS8

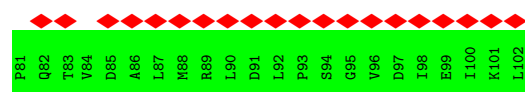
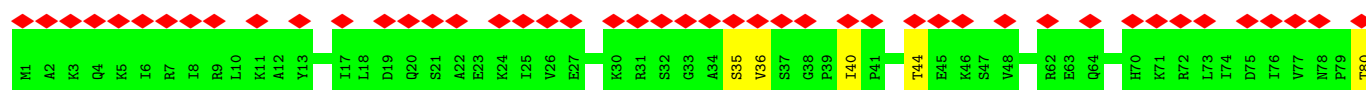




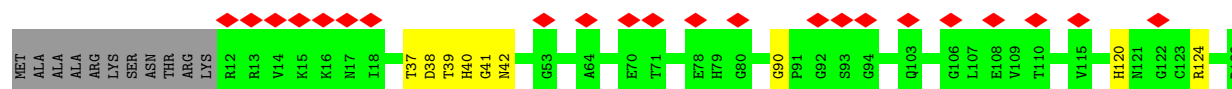
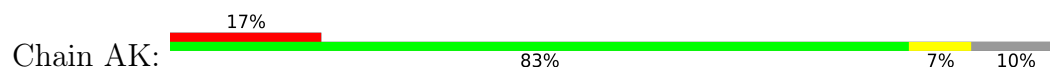
- Molecule 9: 30S ribosomal protein uS9



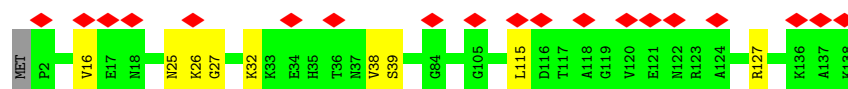
- Molecule 10: 30S ribosomal protein uS10



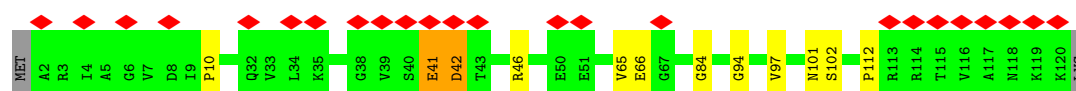
- Molecule 11: 30S ribosomal protein uS11



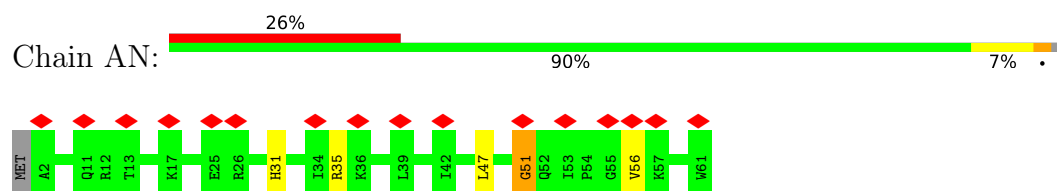
- Molecule 12: 30S ribosomal protein uS12



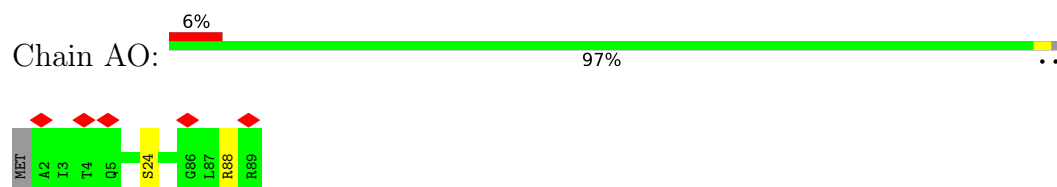
- Molecule 13: 30S ribosomal protein uS13



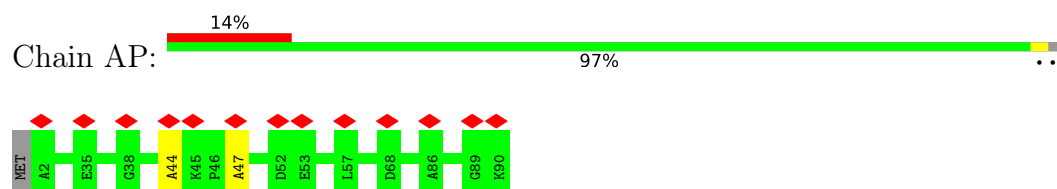
- Molecule 14: 30S ribosomal protein uS14



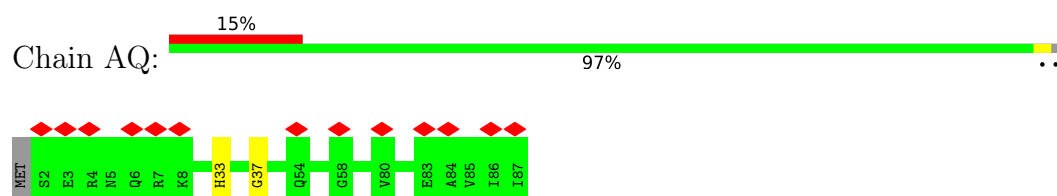
- Molecule 15: 30S ribosomal protein uS15



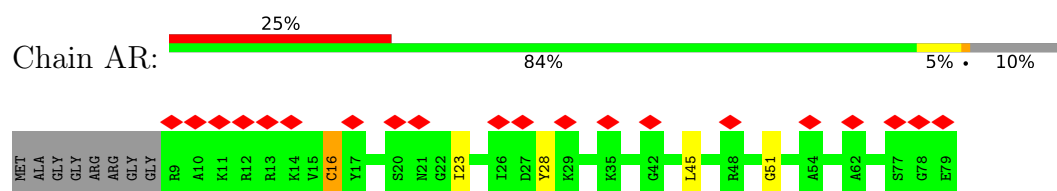
- Molecule 16: 30S ribosomal protein bS16



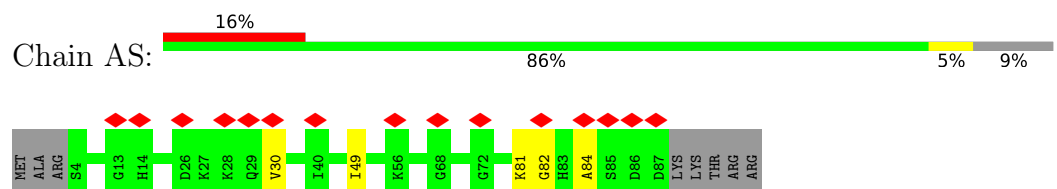
- Molecule 17: 30S ribosomal protein uS17



- Molecule 18: 30S ribosomal protein bS18

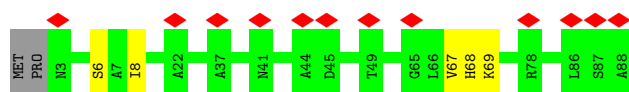


- Molecule 19: 30S ribosomal protein uS19

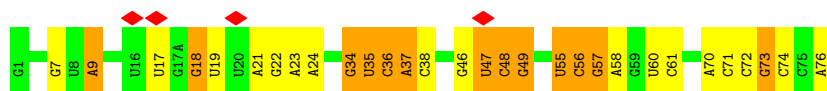


- Molecule 20: 30S ribosomal protein bS20

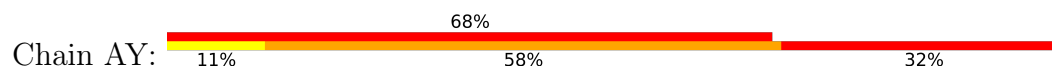




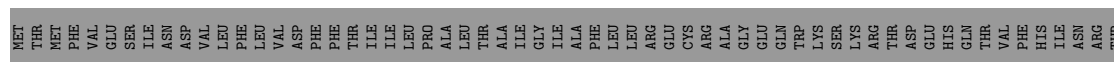
- Molecule 21: tRNA-Asp



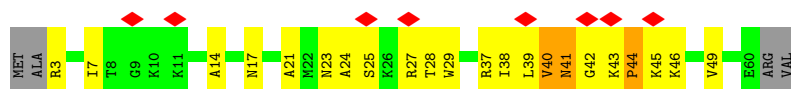
- Molecule 22: mRNA



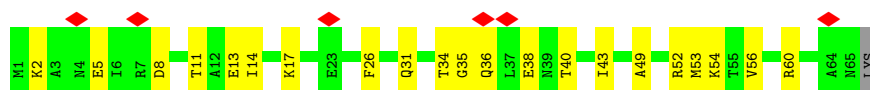
- Molecule 23: MifM



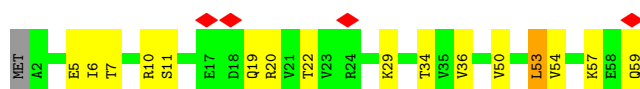
- Molecule 24: 50S ribosomal protein bL28



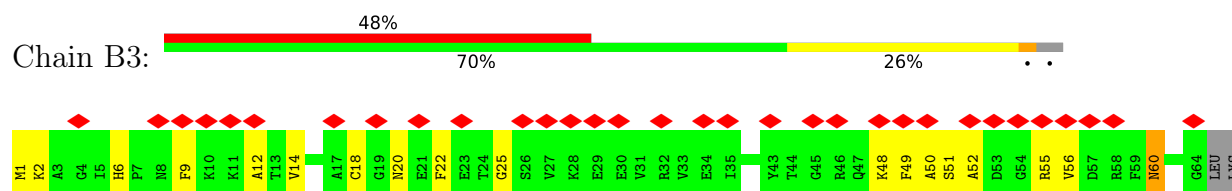
- Molecule 25: 50S ribosomal protein uL29



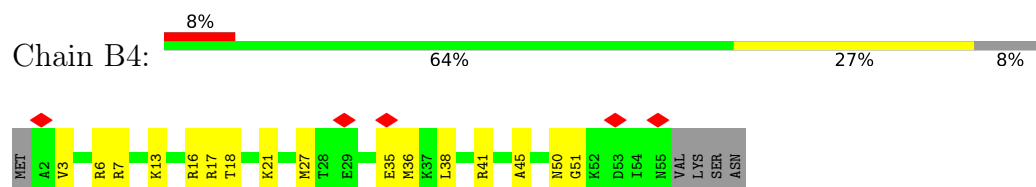
- Molecule 26: 50S ribosomal protein uL30



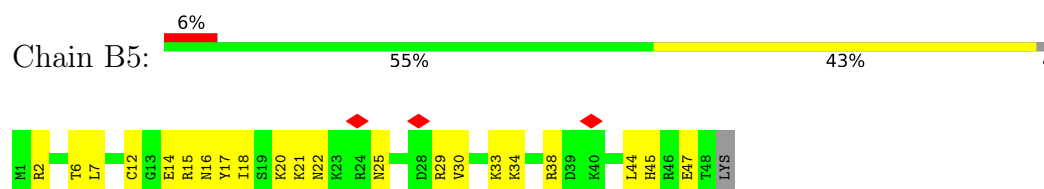
- Molecule 27: 50S ribosomal protein bL31



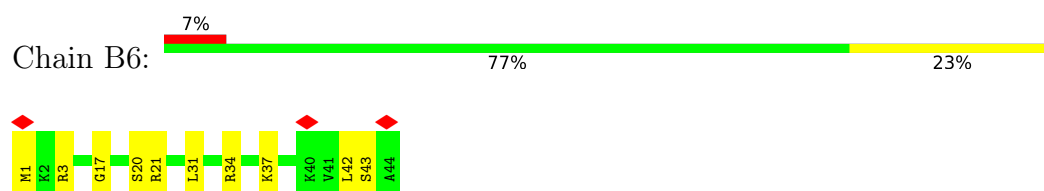
- Molecule 28: 50S ribosomal protein bL32



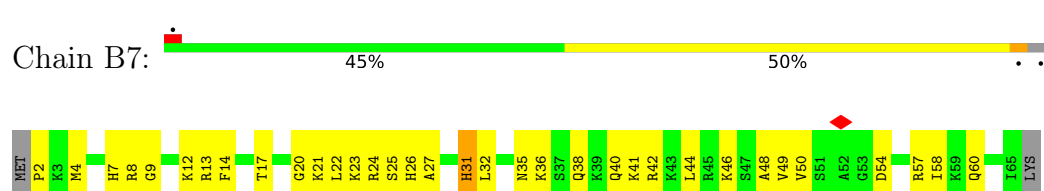
- Molecule 29: 50S ribosomal protein bL33



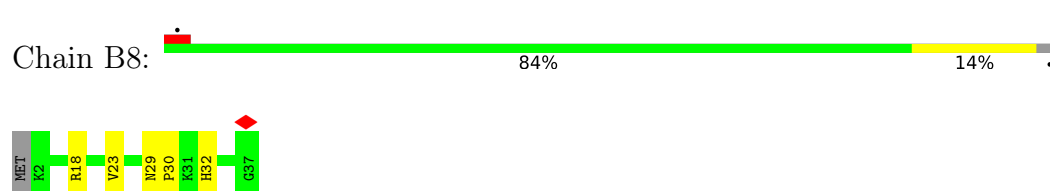
- Molecule 30: 50S ribosomal protein bL34



- Molecule 31: 50S ribosomal protein bL35

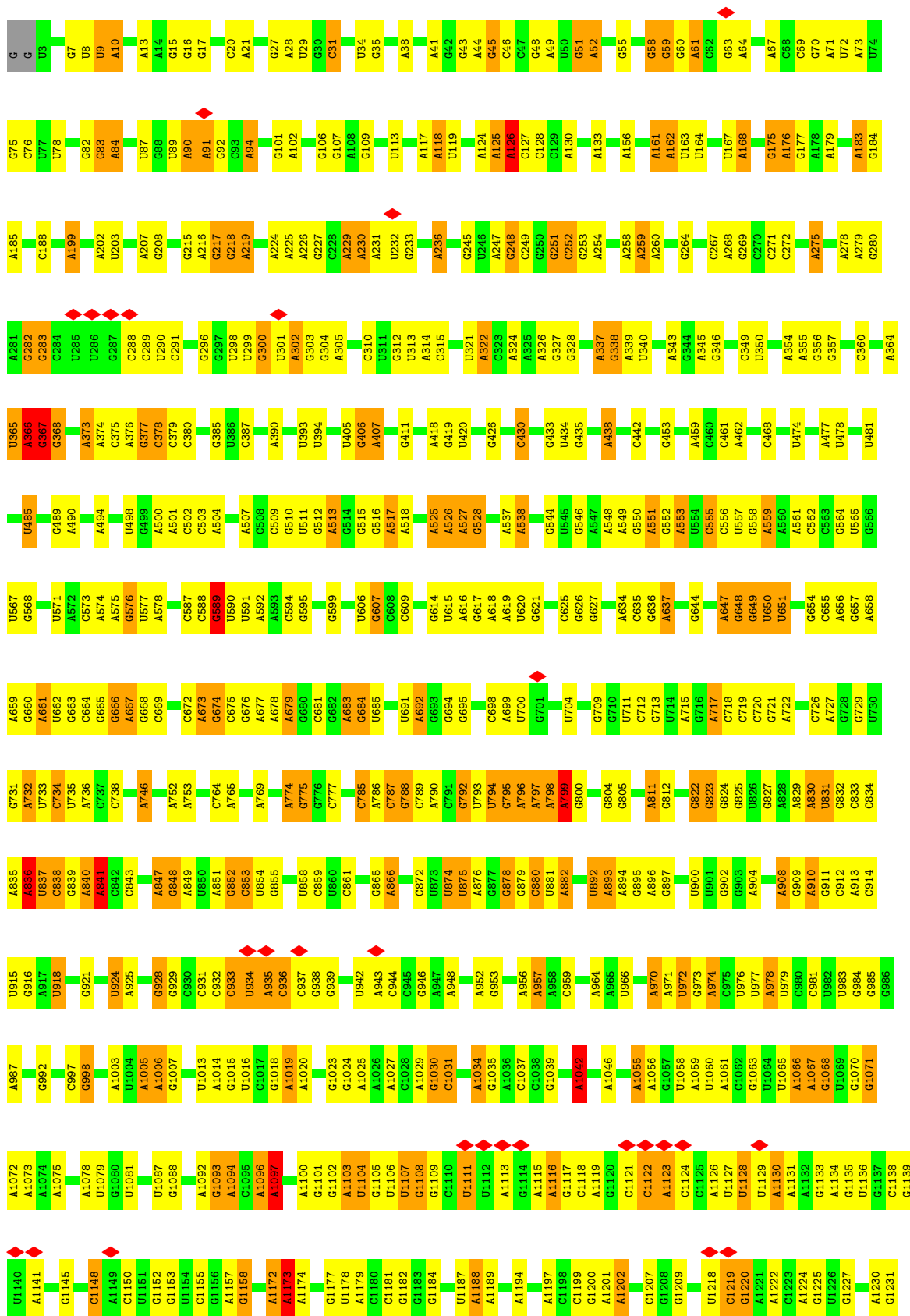


- Molecule 32: 50S ribosomal protein bL36

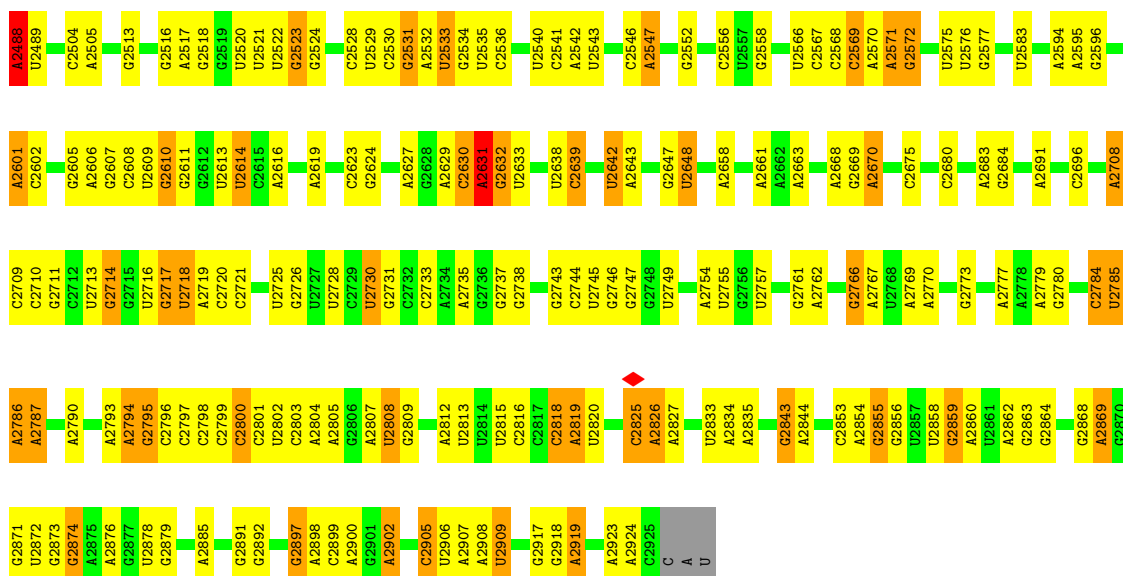


- Molecule 33: 23S ribosomal RNA



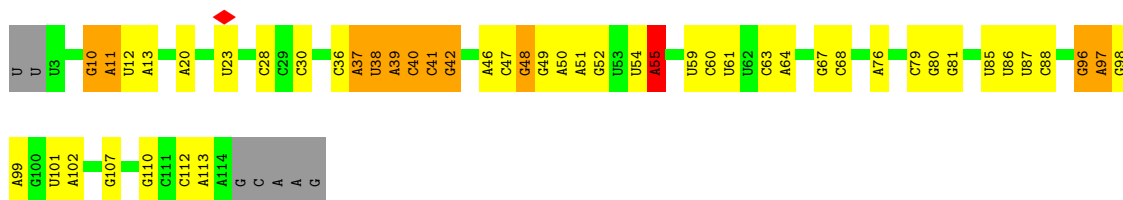


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U2330	G2331	G2332	G2333	U2334	U2335	G2336	G2337	A2338	G2339	A2340	U2341	G2342	A2343	A2344	U2345	A2346	G2347	G2348	A2349	G2350	A2351	G2352	U2355	A2356	A2357	A2358	G2359	A2362	G2363	A2364	A2369	G2370	G2371	U2372	U2373	G2374	A2375	G2376	U2377	G2378	G2379	G2382	A2383	U2386	A2387	G2388	A2389	A2390	G2393	G2394	A2395	G2400																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
U2209	G2210	G2214	A2220	C2221	G2222	U2223	U2224	A2227	G2232	C2233	C2237	U2238	U2239	U2240	A2241	U2242	C2243	G2246	G2252	A2253	A2254	G2255	A2262	G2263	G2267	G2268	C2269	U2278	G2279	A2295	A2296	A2297	A2302	G2308	C2312	G2313	G2314	A2315	A2316	C2324	A2327	G2328	A2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465	G2466	G2467	G2468	G2469	G2470	G2471	G2472	G2473	G2474	G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2482	G2483	G2484	G2485	G2486	G2487	G2488	G2489	G2490	G2491	G2492	G2493	G2494	G2495	G2496	G2497	G2498	G2499	G2500	G2501	G2502	G2503	G2504	G2505	G2506	G2507	G2508	G2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2535	G2536	G2537	G2538	G2539	G2540	G2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565	G2566	G2567	G2568	G2569	G2570	G2571	G2572	G2573	G2574	G2575	G2576	G2577	G2578	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2591	G2592	G2593	G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640	G2641	G2642	G2643	G2644	G2645	G2646	G2647	G2648	G2649	G2650	G2651	G2652	G2653	G2654	G2655	G2656	G2657	G2658	G2659	G2660	G2661	G2662	G2663	G2664	G2665	G2666	G2667	G2668	G2669	G2670	G2671	G2672	G2673	G2674	G2675	G2676	G2677	G2678	G2679	G2680	G2681	G2682	G2683	G2684	G2685	G2686	G2687	G2688	G2689	G2690	G2691	G2692	G2693	G2694	G2695	G2696	G2697	G2698	G2699	G2700	G2701	G2702	G2703	G2704	G2705	G2706	G2707	G2708	G2709	G2710	G2711	G2712	G2713	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2721	G2722	G2723	G2724	G2725	G2726	G2727	G2728	G2729	G2730	G2731	G2732	G2733	G2734	G2735	G2736	G2737	G2738	G2739	G2740	G2741	G2742	G2743	G2744	G2745	G2746	G2747	G2748	G2749	G2750	G2751	G2752	G2753	G2754	G2755	G2756	G2757	G2758	G2759	G2760	G2761	G2762	G2763	G2764	G2765	G2766	G2767	G2768	G2769	G2770	G2771	G2772	G2773	G2774	G2775	G2776	G2777	G2778	G2779	G2780	G2781	G2782	G2783	G2784	G2785	G2786	G2787	G2788	G2789	G2790	G2791	G2792	G2793	G2794	G2795	G2796	G2797	G2798	G2799	G2800	G2801	G2802	G2803	G2804	G2805	G2806	G2807	G2808	G2809	G2810	G2811	G2812	G2813	G2814	G2815	G2816	G2817	G2818	G2819	G2820	G2821	G2822	G2823	G2824	G2825	G2826	G2827	G2828	G2829	G2830	G2831	G2832	G2833	G2834	G2835	G2836	G2837	G2838	G2839	G2840	G2841	G2842	G2843	G2844	G2845	G2846	G2847	G2848	G2849	G2850	G2851	G2852	G2853	G2854	G2855	G2856	G2857	G2858	G2859	G2860	G2861	G2862	G2863	G2864	G2865	G2866	G2867	G2868	G2869	G2870	G2871	G2872	G2873	G2874	G2875	G2876	G2877	G2878	G2879	G2880	G2881	G2882	G2883	G2884	G2885	G2886	G2887	G2888	G2889	G2890	G2891	G2892	G2893	G2894	G2895	G2896	G2897	G2898	G2899	G2900	G2901	G2902	G2903	G2904	G2905	G2906	G2907	G2908	G2909	G2910	G2911	G2912	G2913	G2914	G2915	G2916	G2917	G2918	G2919	G2920	G2921	G2922	G2923	G2924	G2925	G2926	G2927	G2928	G2929	G2930	G2931	G2932	G2933	G2934	G2935	G2936	G2937	G2938	G2939	G2940	G2941	G2942	G2943	G2944	G2945	G2946	G2947	G2948	G2949	G2950	G2951	G2952	G2953	G2954	G2955	G2956	G2957	G2958	G2959	G2960	G2961	G2962	G2963	G2964	G2965	G2966	G2967	G2968	G2969	G2970	G2971	G2972	G2973	G2974	G2975	G2976	G2977	G2978	G2979	G2980	G2981	G2982	G2983	G2984	G2985	G2986	G2987	G2988	G2989	G2990	G2991	G2992	G2993	G2994	G2995	G2996	G2997	G2998	G2999	G3000	G3001	G3002	G3003	G3004	G3005	G3006	G3007	G3008	G3009	G3010	G3011	G3012	G3013	G3014	G3015	G3016	G3017	G3018	G3019	G3020	G3021	G3022	G3023	G3024	G3025	G3026	G3027	G3028	G3029	G3030	G3031	G3032	G3033	G3034	G3035	G3036	G3037	G3038	G3039	G3040	G3041	G3042	G3043	G3044	G3045	G3046	G3047	G3048	G3049	G3050	G3051	G3052	G3053	G3054	G3055	G3056	G3057	G3058	G3059	G3060	G3061	G3062	G3063	G3064	G3065	G3066	G3067	G3068	G3069	G3070	G3071	G3072	G3073	G3074	G3075	G3076	G3077	G3078	G3079	G3080	G3081	G3082	G3083	G3084	G3085	G3086	G3087	G3088	G3089	G3090	G3091	G3092	G3093	G3094	G3095	G3096	G3097	G3098	G3099	G3100	G3101	G3102	G3103	G3104	G3105	G3106	G3107	G3108	G3109	G3110	G3111	G3112	G3113	G3114	G3115	G3116	G3117	G3118	G3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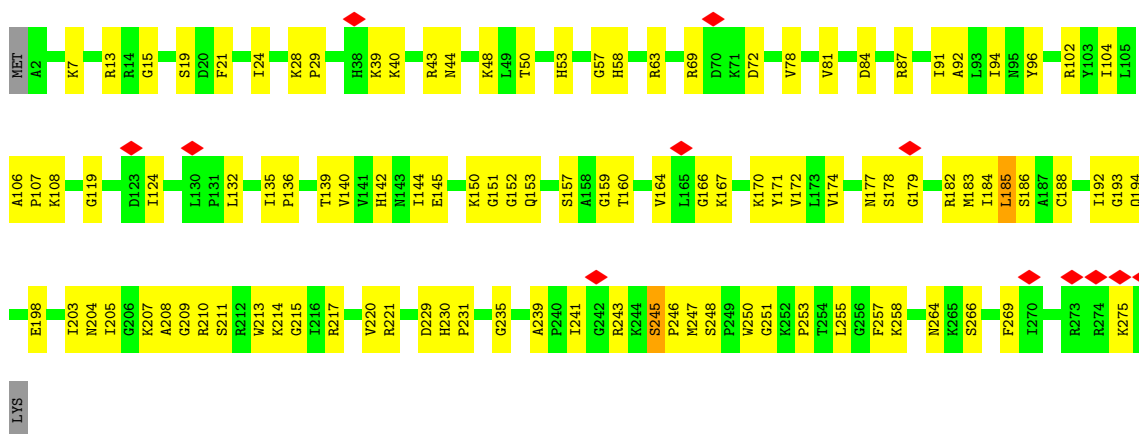
• Molecule 34: 5S ribosomal RNA

Chain BB: 53% 31% 9% 6%



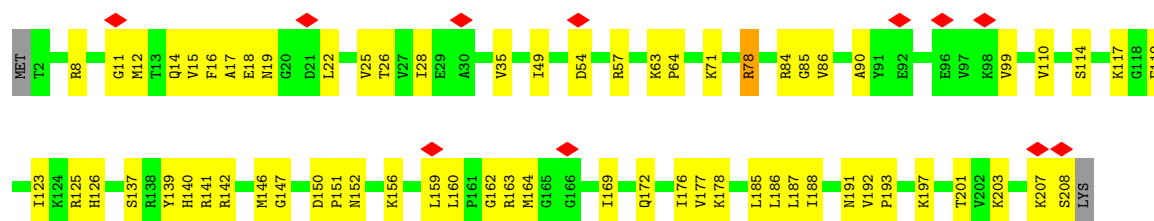
• Molecule 35: 50S ribosomal protein uL2

Chain BD: 61% 37%

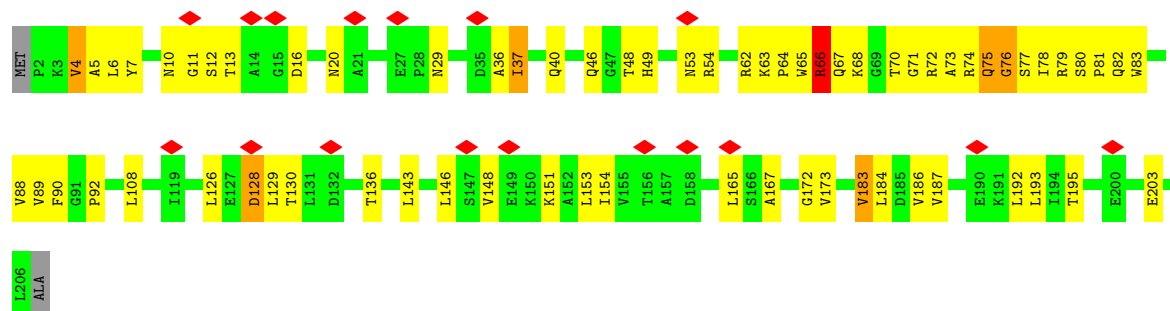


• Molecule 36: 50S ribosomal protein uL3

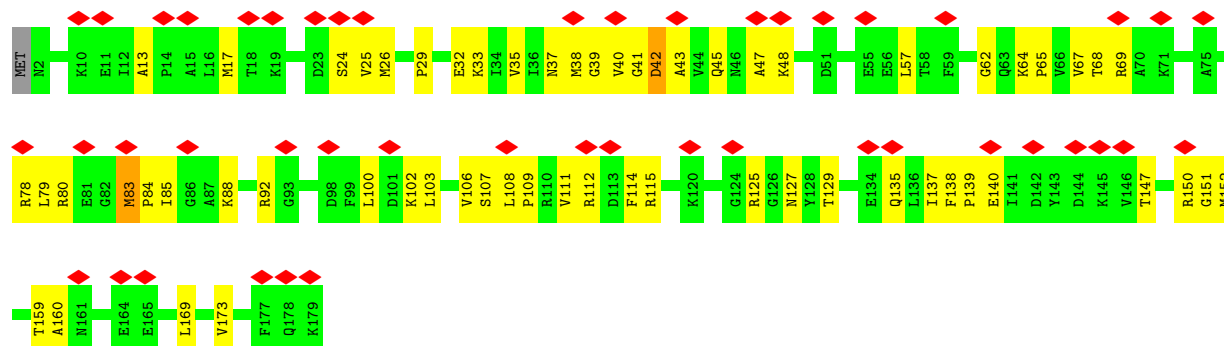
Chain BE: 5% 67% 31%



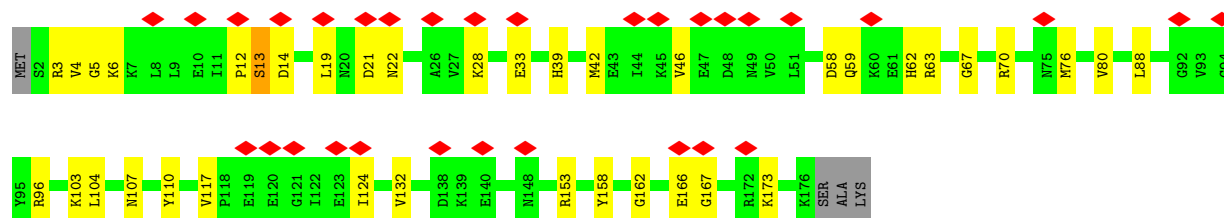
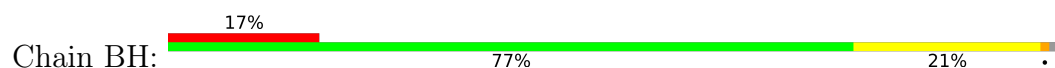
• Molecule 37: 50S ribosomal protein uL4



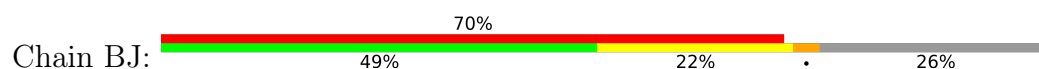
• Molecule 38: 50S ribosomal protein uL5

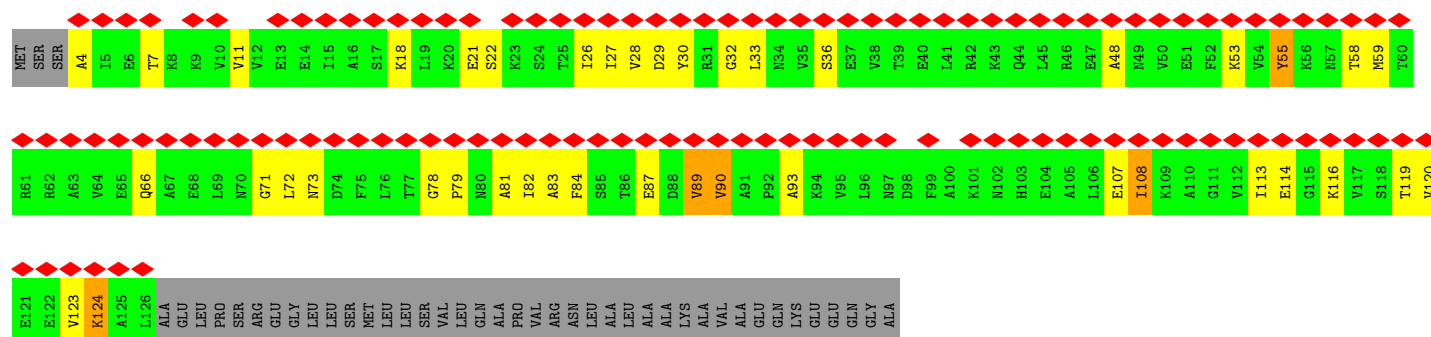


• Molecule 39: 50S ribosomal protein uL6

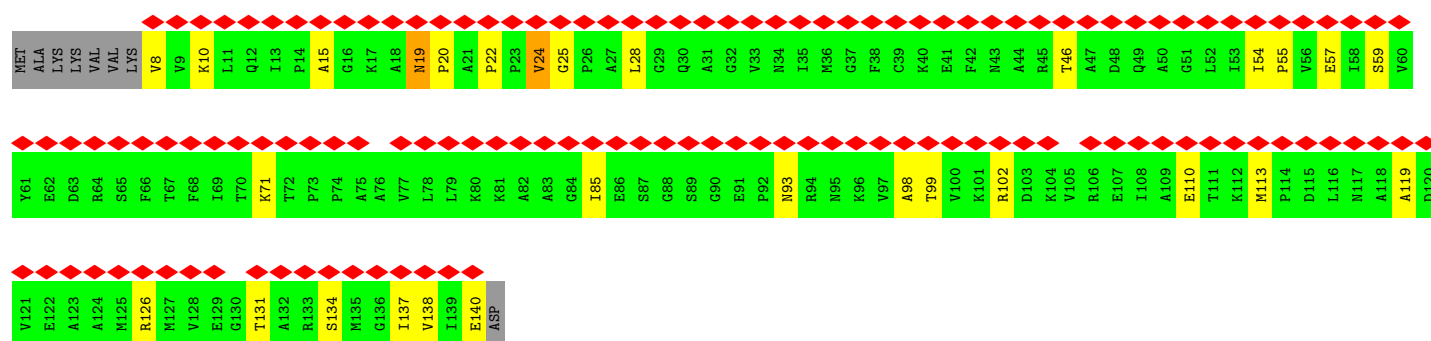
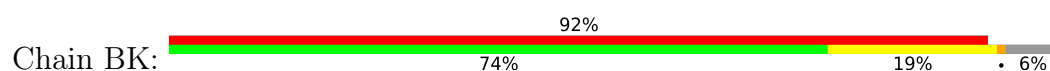


• Molecule 40: 50S ribosomal protein uL10

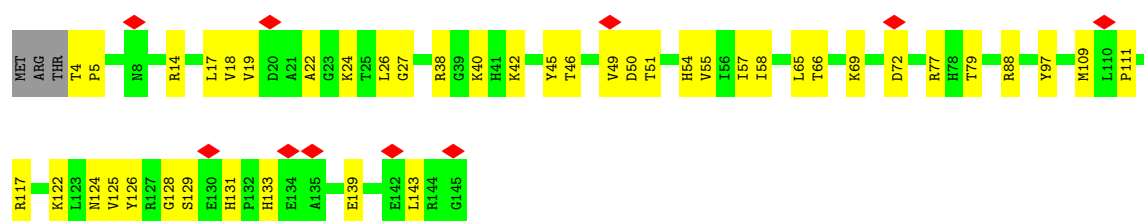




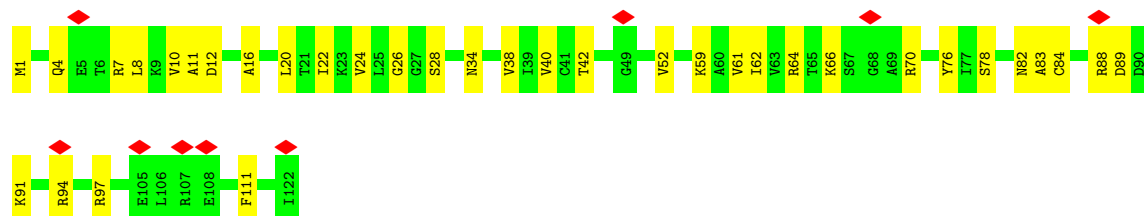
• Molecule 41: 50S ribosomal protein uL11



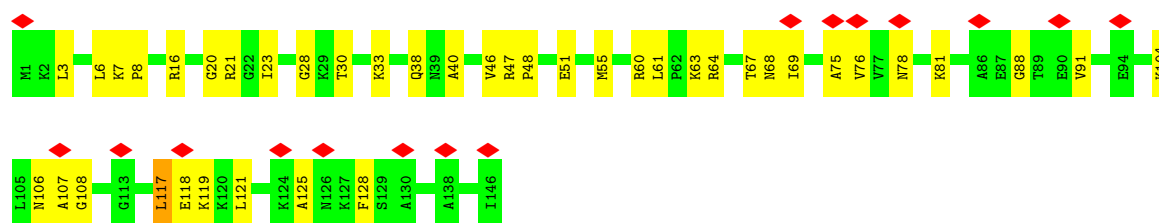
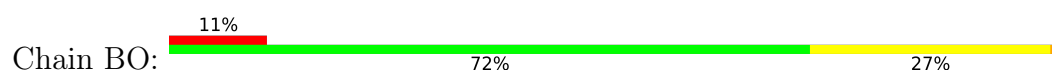
• Molecule 42: 50S ribosomal protein uL13



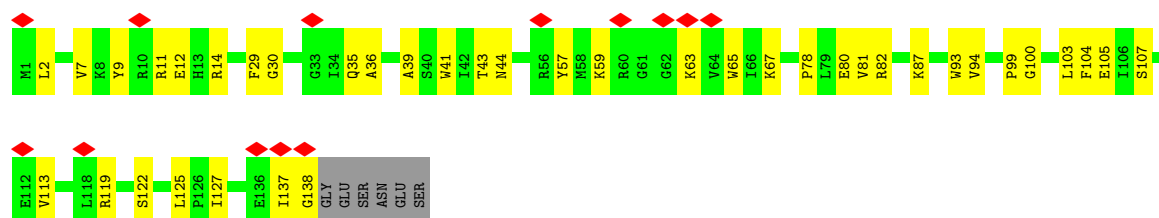
• Molecule 43: 50S ribosomal protein uL14



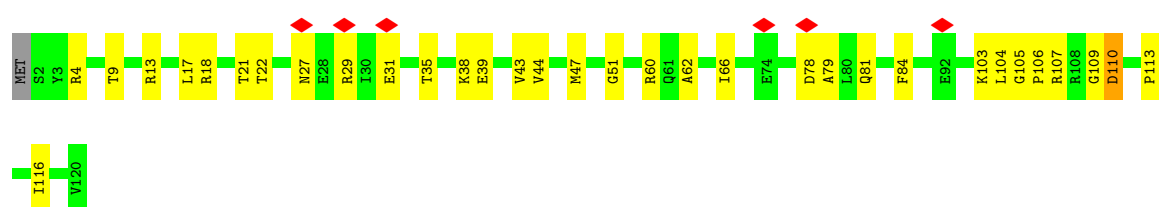
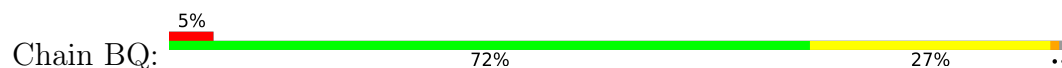
• Molecule 44: 50S ribosomal protein uL15



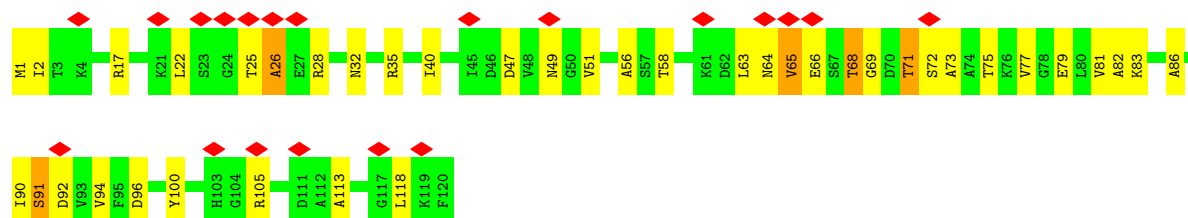
- Molecule 45: 50S ribosomal protein uL16



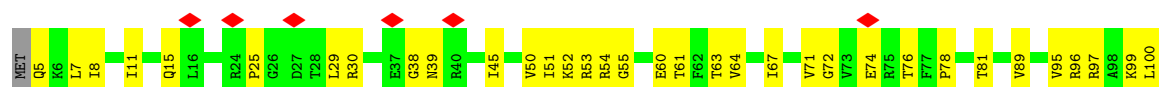
- Molecule 46: 50S ribosomal protein bL17

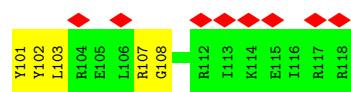


- Molecule 47: 50S ribosomal protein uL18

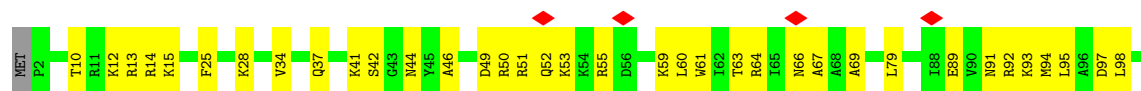


- Molecule 48: 50S ribosomal protein bL19

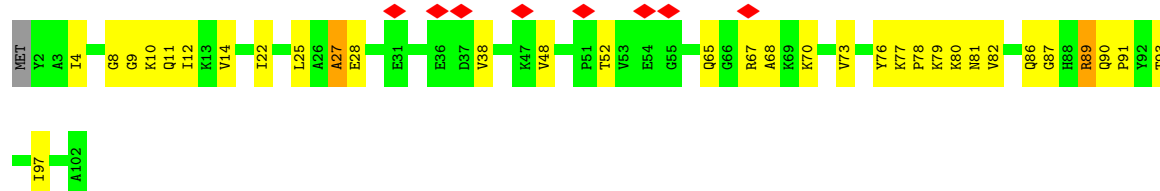




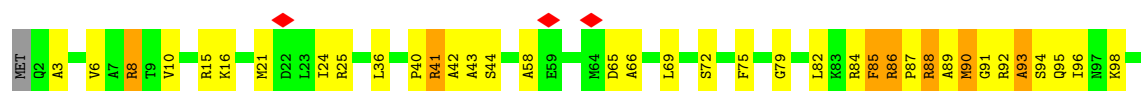
- Molecule 49: 50S ribosomal protein bL20



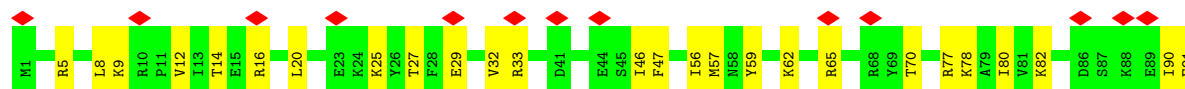
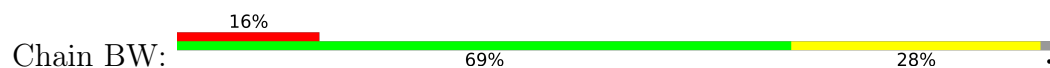
- Molecule 50: 50S ribosomal protein bL21



- Molecule 51: 50S ribosomal protein uL22

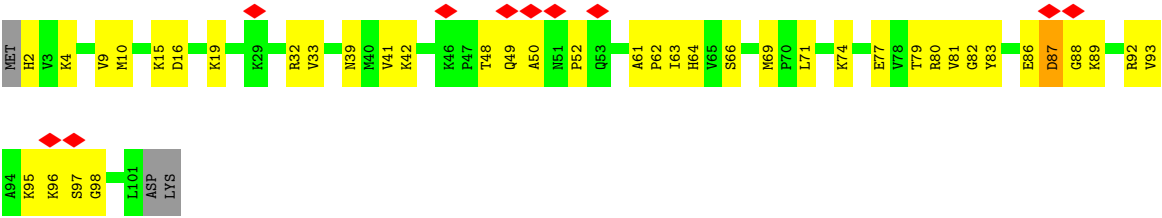


- Molecule 52: 50S ribosomal protein uL23



- Molecule 53: 50S ribosomal protein uL24





• Molecule 54: 50S ribosomal protein bL27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	305045	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	defocus groups	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	125085	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00155	Depositor
Map size ($\text{\AA}$)	407.74402, 407.74402, 407.74402	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.108, 1.108, 1.108	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.52	0/37074	0.53	0/57834
2	AB	0.52	0/895	0.94	2/1117 (0.2%)
3	AC	0.47	0/839	0.92	3/1047 (0.3%)
4	AD	0.44	0/796	1.03	4/992 (0.4%)
5	AE	0.45	0/660	1.05	1/822 (0.1%)
6	AF	0.51	0/380	1.00	2/472 (0.4%)
7	AG	0.43	0/612	0.82	0/762
8	AH	0.41	0/524	0.95	0/652
9	AI	0.44	0/520	0.97	1/647 (0.2%)
10	AJ	0.49	0/408	1.01	2/507 (0.4%)
11	AK	0.43	0/471	1.15	4/587 (0.7%)
12	AL	0.42	0/548	1.12	0/682
13	AM	0.48	0/475	0.99	1/592 (0.2%)
14	AN	0.38	0/240	1.02	0/297
15	AO	0.42	0/352	0.83	0/437
16	AP	0.45	0/356	0.95	0/442
17	AQ	0.44	0/344	0.90	0/427
18	AR	0.48	0/284	0.96	2/352 (0.6%)
19	AS	0.53	0/335	0.99	1/417 (0.2%)
20	AT	0.43	0/344	0.74	0/427
21	AX	0.41	0/1834	0.47	0/2858
22	AY	0.48	0/466	0.87	3/726 (0.4%)
23	AZ	0.78	0/106	1.66	3/122 (2.5%)
24	B0	0.38	0/448	0.89	2/596 (0.3%)
25	B1	0.29	0/531	0.65	0/707
26	B2	0.32	0/457	0.69	0/613
27	B3	0.35	0/513	0.75	0/683
28	B4	0.30	0/433	0.76	0/574
29	B5	0.34	0/406	0.69	0/540
30	B6	0.26	0/370	0.76	1/483 (0.2%)
31	B7	0.28	0/519	0.64	0/680
32	B8	0.26	0/291	0.75	0/383
33	BA	0.54	0/70307	0.57	22/109687 (0.0%)
34	BB	0.49	0/2678	0.52	0/4174

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BD	0.37	0/2148	0.85	2/2881 (0.1%)
36	BE	0.39	0/1597	0.76	2/2140 (0.1%)
37	BF	0.37	0/1580	0.80	3/2132 (0.1%)
38	BG	0.40	0/1423	0.81	5/1910 (0.3%)
39	BH	0.33	0/1360	0.76	0/1832
40	BJ	0.38	0/963	0.73	0/1298
41	BK	0.41	0/995	0.90	5/1346 (0.4%)
42	BM	0.36	0/1146	0.77	2/1542 (0.1%)
43	BN	0.40	0/927	0.80	1/1245 (0.1%)
44	BO	0.30	0/1093	0.78	2/1457 (0.1%)
45	BP	0.29	0/1120	0.72	1/1496 (0.1%)
46	BQ	0.35	0/960	0.69	0/1284
47	BR	0.44	0/921	0.84	1/1236 (0.1%)
48	BS	0.33	0/949	0.73	0/1269
49	BT	0.34	0/952	0.66	0/1266
50	BU	0.38	0/797	0.81	2/1070 (0.2%)
51	BV	0.53	1/851 (0.1%)	0.88	2/1146 (0.2%)
52	BW	0.40	0/759	0.74	0/1011
53	BX	0.37	0/764	0.88	0/1022
54	BZ	0.39	0/638	0.77	0/847
All	All	0.50	1/147759 (0.0%)	0.63	82/221768 (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
1	AA	0	36
21	AX	0	2
22	AY	0	7
33	BA	0	84
34	BB	0	2
37	BF	0	1
51	BV	0	2
All	All	0	134

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	BV	95	GLN	CA-C	-6.25	1.45	1.52

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	BA	589	G	C4'-C3'-O3'	20.99	140.88	109.40
33	BA	83	G	C4'-C3'-O3'	-17.76	82.76	109.40
33	BA	82	G	C4'-C3'-O3'	-15.30	90.05	113.00
33	BA	2487	U	C4'-C3'-O3'	14.71	131.47	109.40
33	BA	366	A	C4'-C3'-O3'	12.42	128.03	109.40
33	BA	589	G	C2'-C3'-O3'	-8.91	96.14	109.50
33	BA	365	U	P-O3'-C3'	-8.58	107.33	120.20
33	BA	2487	U	C2'-C3'-O3'	-8.35	96.97	109.50
23	AZ	81	ASN	N-CA-C	7.91	121.95	111.28
33	BA	1294	A	C4'-C3'-O3'	-7.36	98.37	109.40
11	AK	124	ARG	CA-C-N	7.31	125.00	119.66
11	AK	124	ARG	C-N-CA	7.31	125.00	119.66
33	BA	1294	A	C2'-C3'-O3'	7.26	120.39	109.50
35	BD	28	LYS	CA-C-N	6.99	126.91	119.85
35	BD	28	LYS	C-N-CA	6.99	126.91	119.85
22	AY	2	G	C4'-C3'-O3'	6.96	123.45	113.00
33	BA	83	G	C2'-C3'-O3'	6.92	119.88	109.50
33	BA	590	U	P-O5'-C5'	6.78	131.06	120.90
3	AC	15	ILE	N-CA-C	6.63	120.17	113.47
23	AZ	76	LYS	N-CA-C	6.61	118.48	111.28
33	BA	2488	A	C5'-C4'-C3'	-6.49	106.27	116.00
5	AE	28	GLY	N-CA-C	6.41	118.78	110.45
6	AF	67	SER	N-CA-C	6.39	116.90	107.88
47	BR	65	VAL	N-CA-C	6.20	116.95	110.62
33	BA	1173	A	C5'-C4'-O4'	6.17	118.36	109.10
33	BA	792	G	C2'-C3'-O3'	-6.13	104.50	113.70
37	BF	76	GLY	N-CA-C	6.08	119.55	112.50
42	BM	97	TYR	CA-C-N	6.04	125.92	119.28
42	BM	97	TYR	C-N-CA	6.04	125.92	119.28
2	AB	192	ASP	CA-C-N	6.01	125.90	119.28
2	AB	192	ASP	C-N-CA	6.01	125.90	119.28
33	BA	1173	A	C2'-C3'-O3'	-5.96	100.56	109.50
37	BF	75	GLN	N-CA-C	5.95	119.39	111.30
37	BF	183	VAL	N-CA-C	5.94	116.12	110.42
44	BO	117	LEU	CA-C-N	5.94	132.40	121.70
44	BO	117	LEU	C-N-CA	5.94	132.40	121.70
9	AI	126	GLN	N-CA-C	5.90	117.81	108.79
41	BK	25	GLY	CA-C-N	5.87	125.73	119.28
41	BK	25	GLY	C-N-CA	5.87	125.73	119.28
11	AK	90	GLY	CA-C-N	5.75	125.70	119.78
11	AK	90	GLY	C-N-CA	5.75	125.70	119.78
4	AD	34	GLY	CA-C-N	5.72	125.58	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AD	34	GLY	C-N-CA	5.72	125.58	119.28
33	BA	1172	A	O3'-P-O5'	5.70	112.56	104.00
23	AZ	82	SER	N-CA-C	5.60	121.29	113.57
41	BK	22	PRO	N-CA-C	5.57	117.49	110.70
51	BV	85	PHE	N-CA-C	-5.53	100.97	109.76
3	AC	71	LYS	CA-C-N	5.52	125.35	119.28
3	AC	71	LYS	C-N-CA	5.52	125.35	119.28
4	AD	128	ILE	CA-C-N	5.52	125.35	119.28
4	AD	128	ILE	C-N-CA	5.52	125.35	119.28
41	BK	22	PRO	CA-C-N	-5.51	112.95	119.84
41	BK	22	PRO	C-N-CA	-5.51	112.95	119.84
33	BA	1293	A	C4'-C3'-O3'	5.51	117.66	109.40
24	B0	21	ALA	N-CA-C	-5.47	103.86	111.52
36	BE	147	GLY	CA-C-N	5.44	125.39	119.78
36	BE	147	GLY	C-N-CA	5.44	125.39	119.78
51	BV	93	ALA	N-CA-C	5.41	119.09	111.52
13	AM	94	GLY	N-CA-C	-5.40	107.87	115.32
38	BG	115	ARG	N-CA-C	-5.38	108.49	114.62
10	AJ	40	ILE	CA-C-N	5.30	125.24	119.78
10	AJ	40	ILE	C-N-CA	5.30	125.24	119.78
38	BG	83	MET	CA-C-N	5.30	125.24	119.78
38	BG	83	MET	C-N-CA	5.30	125.24	119.78
22	AY	2	G	C4'-C3'-C2'	-5.29	97.31	102.60
22	AY	2	G	C5'-C4'-C3'	5.25	123.87	116.00
33	BA	82	G	C2'-C3'-O3'	5.24	121.56	113.70
50	BU	27	ALA	CB-CA-C	-5.22	110.12	117.23
19	AS	49	ILE	N-CA-C	5.22	115.48	108.17
45	BP	59	LYS	CB-CA-C	-5.20	110.56	116.54
38	BG	138	PHE	CA-C-N	5.19	124.99	119.28
38	BG	138	PHE	C-N-CA	5.19	124.99	119.28
6	AF	71	ALA	N-CA-C	5.17	116.92	111.28
30	B6	43	SER	CB-CA-C	-5.08	109.74	115.79
43	BN	28	SER	N-CA-C	5.08	116.81	111.28
24	B0	41	ASN	N-CA-C	-5.05	102.90	110.23
33	BA	1173	A	O4'-C1'-C2'	5.04	110.84	105.80
18	AR	45	LEU	CA-C-N	5.04	124.97	119.78
18	AR	45	LEU	C-N-CA	5.04	124.97	119.78
50	BU	89	ARG	N-CA-C	-5.04	101.03	109.24
33	BA	367	G	C4'-C3'-O3'	-5.03	105.45	113.00
33	BA	1173	A	N9-C1'-C2'	5.01	121.52	114.00

There are no chirality outliers.

All (134) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1026	A	Sidechain
1	AA	1065	A	Sidechain
1	AA	1207	A	Sidechain
1	AA	1261	A	Sidechain
1	AA	1278	A	Sidechain
1	AA	1294	A	Sidechain
1	AA	1297	A	Sidechain
1	AA	1384	A	Sidechain
1	AA	1407	A	Sidechain
1	AA	1427	A	Sidechain
1	AA	1442	A	Sidechain
1	AA	1478	A	Sidechain
1	AA	209	A	Sidechain
1	AA	308	A	Sidechain
1	AA	335	A	Sidechain
1	AA	391	A	Sidechain
1	AA	401	A	Sidechain
1	AA	415	A	Sidechain
1	AA	419	A	Sidechain
1	AA	496	A	Sidechain
1	AA	500	A	Sidechain
1	AA	53	A	Sidechain
1	AA	532	A	Sidechain
1	AA	583	A	Sidechain
1	AA	696	A	Sidechain
1	AA	76	A	Sidechain
1	AA	790	A	Sidechain
1	AA	811	A	Sidechain
1	AA	862	A	Sidechain
1	AA	879	A	Sidechain
1	AA	883	A	Sidechain
1	AA	911	A	Sidechain
1	AA	918	A	Sidechain
1	AA	969	A	Sidechain
1	AA	975	A	Sidechain
1	AA	988	A	Sidechain
21	AX	37	A	Sidechain
21	AX	9	A	Sidechain
22	AY	12	A	Sidechain
22	AY	15	A	Sidechain
22	AY	16	A	Sidechain
22	AY	18	A	Sidechain

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Mol	Chain	Res	Type	Group
22	AY	5	A	Sidechain
22	AY	6	A	Sidechain
22	AY	9	A	Sidechain
33	BA	1006	A	Sidechain
33	BA	1042	A	Sidechain
33	BA	1075	A	Sidechain
33	BA	1078	A	Sidechain
33	BA	1094	A	Sidechain
33	BA	1097	A	Sidechain
33	BA	1172	A	Sidechain
33	BA	1173	A	Sidechain
33	BA	1253	A	Sidechain
33	BA	126	A	Sidechain
33	BA	1293	A	Sidechain
33	BA	1294	A	Sidechain
33	BA	1302	A	Sidechain
33	BA	1393	A	Sidechain
33	BA	1555	A	Sidechain
33	BA	1618	A	Sidechain
33	BA	1619	A	Sidechain
33	BA	1659	A	Sidechain
33	BA	1661	A	Sidechain
33	BA	168	A	Sidechain
33	BA	1686	A	Sidechain
33	BA	1724	A	Sidechain
33	BA	183	A	Sidechain
33	BA	1831	A	Sidechain
33	BA	1839	A	Sidechain
33	BA	1883	A	Sidechain
33	BA	1888	A	Sidechain
33	BA	1957	A	Sidechain
33	BA	1998	A	Sidechain
33	BA	2006	A	Sidechain
33	BA	2010	A	Sidechain
33	BA	2043	A	Sidechain
33	BA	2062	A	Sidechain
33	BA	2111	A	Sidechain
33	BA	2164	A	Sidechain
33	BA	2176	A	Sidechain
33	BA	2241	A	Sidechain
33	BA	2262	A	Sidechain
33	BA	2316	A	Sidechain

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Mol	Chain	Res	Type	Group
33	BA	2364	A	Sidechain
33	BA	2383	A	Sidechain
33	BA	2395	A	Sidechain
33	BA	2407	A	Sidechain
33	BA	2488	A	Sidechain
33	BA	259	A	Sidechain
33	BA	2601	A	Sidechain
33	BA	2606	A	Sidechain
33	BA	2616	A	Sidechain
33	BA	2627	A	Sidechain
33	BA	2631	A	Sidechain
33	BA	2670	A	Sidechain
33	BA	2691	A	Sidechain
33	BA	2708	A	Sidechain
33	BA	2805	A	Sidechain
33	BA	2819	A	Sidechain
33	BA	2827	A	Sidechain
33	BA	2885	A	Sidechain
33	BA	366	A	Sidechain
33	BA	477	A	Sidechain
33	BA	501	A	Sidechain
33	BA	513	A	Sidechain
33	BA	517	A	Sidechain
33	BA	518	A	Sidechain
33	BA	52	A	Sidechain
33	BA	538	A	Sidechain
33	BA	551	A	Sidechain
33	BA	559	A	Sidechain
33	BA	64	A	Sidechain
33	BA	661	A	Sidechain
33	BA	67	A	Sidechain
33	BA	679	A	Sidechain
33	BA	692	A	Sidechain
33	BA	699	A	Sidechain
33	BA	722	A	Sidechain
33	BA	752	A	Sidechain
33	BA	765	A	Sidechain
33	BA	796	A	Sidechain
33	BA	797	A	Sidechain
33	BA	798	A	Sidechain
33	BA	799	A	Sidechain
33	BA	836	A	Sidechain

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Mol	Chain	Res	Type	Group
33	BA	841	A	Sidechain
33	BA	866	A	Sidechain
33	BA	904	A	Sidechain
34	BB	55	A	Sidechain
34	BB	97	A	Sidechain
37	BF	66	ARG	Sidechain
51	BV	86	ARG	Sidechain
51	BV	88	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	33115	0	16676	248	0
2	AB	896	0	244	3	0
3	AC	840	0	241	3	0
4	AD	797	0	224	3	0
5	AE	661	0	197	2	0
6	AF	381	0	104	0	0
7	AG	613	0	164	1	0
8	AH	525	0	146	0	0
9	AI	521	0	155	4	0
10	AJ	409	0	104	0	0
11	AK	472	0	135	7	0
12	AL	549	0	157	1	0
13	AM	476	0	137	2	0
14	AN	241	0	62	2	0
15	AO	353	0	94	0	0
16	AP	357	0	95	0	0
17	AQ	345	0	90	1	0
18	AR	285	0	76	1	0
19	AS	336	0	93	2	0
20	AT	345	0	89	2	0
21	AX	1643	0	830	30	0
22	AY	415	0	207	79	0
23	AZ	107	0	58	9	0
24	B0	444	0	486	60	0
25	B1	530	0	568	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	B2	455	0	491	12	0
27	B3	503	0	494	12	0
28	B4	426	0	445	16	0
29	B5	401	0	413	18	0
30	B6	367	0	410	20	0
31	B7	512	0	564	32	0
32	B8	288	0	330	3	0
33	BA	62767	0	31584	785	0
34	BB	2395	0	1212	21	0
35	BD	2111	0	2200	87	0
36	BE	1575	0	1642	51	0
37	BF	1561	0	1647	93	0
38	BG	1404	0	1467	47	0
39	BH	1342	0	1388	26	0
40	BJ	955	0	990	28	0
41	BK	981	0	1020	28	0
42	BM	1123	0	1162	32	0
43	BN	920	0	977	21	0
44	BO	1081	0	1132	40	0
45	BP	1097	0	1165	25	0
46	BQ	953	0	983	29	0
47	BR	912	0	947	36	0
48	BS	936	0	1008	31	0
49	BT	940	0	1005	41	0
50	BU	786	0	826	40	0
51	BV	842	0	899	50	0
52	BW	752	0	802	22	0
53	BX	754	0	809	31	0
54	BZ	630	0	644	16	0
All	All	135425	0	80088	1887	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 9.

All (1887) 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)
23:AZ:74:ILE:CA	51:BV:85:PHE:HE2	1.11	1.60
23:AZ:74:ILE:CA	51:BV:85:PHE:CE2	1.99	1.44
24:B0:37:ARG:NH1	24:B0:44:PRO:HG3	1.37	1.40
37:BF:80:SER:OG	37:BF:81:PRO:HD2	1.30	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BK:15:ALA:HB1	41:BK:46:THR:CG2	1.62	1.28
24:B0:37:ARG:HD2	24:B0:44:PRO:CB	1.65	1.24
22:AY:4:G:H2'	22:AY:5:A:H5'	1.21	1.18
47:BR:64:ASN:HB3	47:BR:66:GLU:HG2	1.23	1.14
41:BK:15:ALA:CB	41:BK:46:THR:CG2	2.26	1.14
41:BK:15:ALA:CB	41:BK:46:THR:HG21	1.79	1.12
53:BX:87:ASP:HB3	53:BX:88:GLY:HA3	1.31	1.12
24:B0:38:ILE:HD11	24:B0:49:VAL:HB	1.30	1.11
33:BA:374:A:C2	33:BA:1250:G:H2'	1.84	1.11
41:BK:46:THR:HG23	41:BK:54:ILE:HD12	1.31	1.11
41:BK:15:ALA:HB1	41:BK:46:THR:HG22	1.14	1.10
24:B0:37:ARG:HD3	24:B0:45:LYS:CG	1.83	1.09
22:AY:4:G:C2'	22:AY:5:A:H5'	1.83	1.08
47:BR:22:LEU:HD22	47:BR:94:VAL:HG11	1.34	1.08
24:B0:37:ARG:HD2	24:B0:44:PRO:HB2	1.08	1.07
30:B6:34:ARG:HG2	30:B6:42:LEU:HD12	1.28	1.06
39:BH:21:ASP:HB3	39:BH:22:ASN:HB2	1.36	1.05
24:B0:37:ARG:CD	24:B0:44:PRO:HB2	1.86	1.05
24:B0:45:LYS:HB3	24:B0:46:LYS:HB2	1.37	1.03
37:BF:77:SER:HB2	37:BF:80:SER:HB2	1.40	1.02
37:BF:80:SER:HB3	37:BF:83:TRP:HD1	1.23	1.02
33:BA:377:G:H2'	33:BA:378:C:C6	1.94	1.02
30:B6:34:ARG:HG2	30:B6:42:LEU:CD1	1.91	1.00
33:BA:377:G:H2'	33:BA:378:C:H6	1.22	1.00
33:BA:924:U:H3	33:BA:946:G:H1	1.10	1.00
37:BF:66:ARG:HH11	37:BF:70:THR:CG2	1.76	0.98
33:BA:1264:G:H4'	50:BU:87:GLY:O	1.63	0.98
33:BA:1024:G:H1	33:BA:1031:C:N4	1.61	0.98
24:B0:37:ARG:HG3	24:B0:45:LYS:HG2	1.46	0.98
24:B0:37:ARG:CG	24:B0:45:LYS:HG2	1.95	0.96
37:BF:65:TRP:CZ2	37:BF:75:GLN:HB2	2.00	0.96
24:B0:37:ARG:HH11	24:B0:44:PRO:CG	1.78	0.96
24:B0:37:ARG:CD	24:B0:45:LYS:HG2	1.94	0.96
33:BA:1353:C:H42	33:BA:1377:G:H1	0.97	0.95
24:B0:45:LYS:HB3	24:B0:46:LYS:CB	1.95	0.95
24:B0:37:ARG:CD	24:B0:45:LYS:CG	2.44	0.95
33:BA:528:G:H1	33:BA:555:C:N4	1.63	0.95
33:BA:2009:G:C6	33:BA:2011:U:C4	2.55	0.95
1:AA:774:G:H1	1:AA:821:G:HO2'	1.15	0.94
22:AY:2:G:H2'	22:AY:2:G:N3	1.84	0.93
1:AA:1551:U:H3	22:AY:2:G:H22	1.07	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BF:73:ALA:HB3	37:BF:75:GLN:HG2	1.49	0.92
33:BA:2799:C:C5	33:BA:2800:C:C5	2.58	0.91
24:B0:37:ARG:HB2	24:B0:45:LYS:HD3	1.51	0.91
33:BA:1295:U:C4	37:BF:72:ARG:O	2.23	0.91
37:BF:65:TRP:CZ2	37:BF:75:GLN:CB	2.54	0.90
33:BA:796:A:H61	33:BA:800:G:H21	1.19	0.90
37:BF:66:ARG:HH11	37:BF:70:THR:HG22	1.33	0.90
37:BF:75:GLN:HE22	37:BF:82:GLN:NE2	1.68	0.90
33:BA:797:A:C2	33:BA:799:A:H5'	2.07	0.90
33:BA:1024:G:H1	33:BA:1031:C:H42	1.04	0.90
35:BD:243:ARG:HH22	35:BD:247:MET:CB	1.85	0.90
11:AK:38:ASP:O	11:AK:41:GLY:CA	2.19	0.89
33:BA:1364:C:C2	51:BV:86:ARG:CZ	2.56	0.89
24:B0:37:ARG:HD2	24:B0:44:PRO:CG	2.02	0.89
50:BU:67:ARG:HH11	50:BU:89:ARG:NH1	1.69	0.89
37:BF:75:GLN:NE2	37:BF:82:GLN:NE2	2.21	0.88
33:BA:609:C:OP2	50:BU:79:LYS:HD3	1.73	0.88
22:AY:3:U:H2'	22:AY:4:G:C8	2.09	0.88
11:AK:40:HIS:N	11:AK:41:GLY:HA2	1.87	0.88
24:B0:40:VAL:HG12	24:B0:41:ASN:H	1.36	0.88
33:BA:2089:A:H3'	37:BF:68:LYS:HE2	1.56	0.88
33:BA:528:G:H1	33:BA:555:C:H42	0.87	0.87
53:BX:87:ASP:CB	53:BX:88:GLY:HA3	2.04	0.87
37:BF:66:ARG:NH1	37:BF:70:THR:HG22	1.88	0.87
30:B6:34:ARG:CG	30:B6:42:LEU:CD1	2.53	0.87
47:BR:64:ASN:CB	47:BR:66:GLU:HG2	2.04	0.86
33:BA:1353:C:N4	33:BA:1377:G:H1	1.71	0.86
49:BT:103:LEU:HD12	49:BT:104:THR:HA	1.55	0.86
22:AY:5:A:H2'	22:AY:6:A:H5''	1.56	0.86
47:BR:65:VAL:CG1	47:BR:73:ALA:HB1	2.06	0.85
33:BA:2355:U:H3	33:BA:2418:G:H1	1.24	0.85
37:BF:80:SER:OG	37:BF:81:PRO:CD	2.21	0.85
1:AA:732:U:C4	22:AY:7:C:O2'	2.30	0.85
11:AK:38:ASP:O	11:AK:41:GLY:HA3	1.76	0.84
22:AY:1:U:H2'	22:AY:2:G:H1'	1.58	0.84
33:BA:1294:A:H3'	33:BA:1295:U:H5''	1.60	0.84
47:BR:22:LEU:CD2	47:BR:94:VAL:HG11	2.08	0.83
37:BF:62:ARG:O	37:BF:78:ILE:HG13	1.78	0.83
21:AX:74:C:H5'	33:BA:2631:A:H5''	1.58	0.82
47:BR:22:LEU:HD22	47:BR:94:VAL:CG1	2.09	0.82
22:AY:5:A:C2	22:AY:6:A:H1'	2.15	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2089:A:H3'	37:BF:68:LYS:CE	2.10	0.82
44:BO:117:LEU:HA	44:BO:118:GLU:HB3	1.60	0.82
33:BA:1711:G:H1	33:BA:2023:C:H42	1.24	0.82
22:AY:10:U:O2'	22:AY:11:G:C4	2.32	0.81
24:B0:45:LYS:HB3	24:B0:46:LYS:CA	2.09	0.81
21:AX:72:C:H6	21:AX:72:C:H5''	1.43	0.81
51:BV:88:ARG:HD2	51:BV:94:SER:OG	1.79	0.81
1:AA:268:G:N2	1:AA:273:G:N7	2.29	0.81
33:BA:1656:C:O2'	33:BA:1657:C:H5'	1.80	0.80
1:AA:964:G:H21	1:AA:1236:A:H62	1.30	0.80
26:B2:11:SER:HB2	33:BA:1034:A:H5''	1.63	0.80
30:B6:34:ARG:CG	30:B6:42:LEU:HD13	2.11	0.80
33:BA:1297:C:H5'	37:BF:75:GLN:OE1	1.81	0.80
24:B0:37:ARG:HH11	24:B0:44:PRO:HG3	0.98	0.80
33:BA:2009:G:C5	33:BA:2011:U:C5	2.69	0.80
41:BK:46:THR:CG2	41:BK:54:ILE:HD12	2.10	0.80
51:BV:82:LEU:HB2	51:BV:98:LYS:HB2	1.62	0.80
24:B0:37:ARG:HD3	24:B0:45:LYS:HG3	1.64	0.79
33:BA:2799:C:H5	33:BA:2800:C:C5	1.98	0.79
33:BA:1834:C:H42	33:BA:1841:G:H1	1.30	0.79
33:BA:15:G:H1	33:BA:571:U:H3	1.29	0.79
24:B0:45:LYS:CB	24:B0:46:LYS:HB2	2.11	0.79
37:BF:62:ARG:O	37:BF:78:ILE:CG1	2.30	0.79
47:BR:65:VAL:CG1	47:BR:73:ALA:CB	2.60	0.79
22:AY:5:A:C4	22:AY:6:A:C8	2.69	0.79
33:BA:2799:C:H5	33:BA:2800:C:H5	1.29	0.78
41:BK:46:THR:HG23	41:BK:54:ILE:CD1	2.11	0.78
24:B0:37:ARG:HD3	24:B0:45:LYS:CD	2.14	0.78
37:BF:80:SER:HB3	37:BF:83:TRP:CD1	2.14	0.78
33:BA:364:A:H4'	33:BA:366:A:C8	2.18	0.77
33:BA:1103:A:N6	33:BA:1133:G:OP2	2.17	0.77
33:BA:1263:G:C5	50:BU:70:LYS:NZ	2.52	0.77
51:BV:89:ALA:O	51:BV:90:MET:HB2	1.84	0.77
33:BA:2799:C:C5	33:BA:2800:C:H5	1.99	0.77
1:AA:1546:C:H2'	1:AA:1547:U:C6	2.19	0.77
37:BF:65:TRP:HZ2	37:BF:75:GLN:CB	1.98	0.77
1:AA:1323:C:H42	1:AA:1332:G:H1	1.29	0.77
24:B0:37:ARG:CD	24:B0:44:PRO:CB	2.54	0.77
33:BA:2799:C:H5'	33:BA:2800:C:OP2	1.85	0.76
24:B0:37:ARG:HB2	24:B0:45:LYS:CD	2.14	0.76
28:B4:50:ASN:ND2	33:BA:2909:U:O2	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BK:15:ALA:HB2	41:BK:46:THR:HG21	1.67	0.76
33:BA:528:G:N2	33:BA:555:C:N3	2.33	0.76
24:B0:37:ARG:NH1	24:B0:44:PRO:CG	2.33	0.76
33:BA:1294:A:H3'	33:BA:1295:U:C5'	2.16	0.75
29:B5:21:LYS:HD3	33:BA:2315:A:H62	1.51	0.75
33:BA:426:G:H1	33:BA:442:C:H42	1.35	0.75
33:BA:797:A:H2	33:BA:799:A:H5'	1.48	0.75
37:BF:80:SER:HG	37:BF:81:PRO:HD2	1.51	0.75
30:B6:31:LEU:CD2	30:B6:42:LEU:HD11	2.17	0.74
33:BA:374:A:N1	33:BA:1250:G:H2'	2.01	0.74
33:BA:775:G:H5'	35:BD:13:ARG:HH21	1.52	0.74
47:BR:65:VAL:HG11	47:BR:73:ALA:CB	2.17	0.74
33:BA:1659:A:H2	51:BV:93:ALA:HB2	1.52	0.74
35:BD:243:ARG:NH2	35:BD:247:MET:HB3	2.01	0.74
29:B5:33:LYS:NZ	33:BA:2373:U:OP1	2.19	0.74
35:BD:247:MET:HG2	35:BD:248:SER:O	1.86	0.74
50:BU:67:ARG:HD3	50:BU:89:ARG:CZ	2.17	0.74
33:BA:1829:C:H42	33:BA:1846:G:H22	1.33	0.74
33:BA:1364:C:C2	51:BV:86:ARG:NH2	2.55	0.74
52:BW:32:VAL:O	52:BW:77:ARG:NH1	2.21	0.74
34:BB:76:A:H62	34:BB:96:G:H21	1.35	0.74
35:BD:243:ARG:HH22	35:BD:247:MET:HB3	1.51	0.74
37:BF:67:GLN:HE22	37:BF:74:ARG:CB	2.01	0.74
47:BR:65:VAL:HG13	47:BR:73:ALA:HB1	1.70	0.73
50:BU:68:ALA:N	50:BU:90:GLN:O	2.20	0.73
43:BN:24:VAL:HG12	43:BN:26:GLY:H	1.53	0.73
33:BA:1353:C:N3	33:BA:1377:G:N2	2.35	0.73
33:BA:2039:G:H5''	51:BV:42:ALA:HB2	1.71	0.73
33:BA:2295:A:H62	33:BA:2302:A:H62	1.35	0.73
37:BF:66:ARG:NH1	37:BF:70:THR:CG2	2.47	0.73
22:AY:8:G:C6	22:AY:9:A:C6	2.77	0.73
22:AY:10:U:O2'	22:AY:11:G:OP1	2.07	0.73
1:AA:850:U:H3	1:AA:855:G:H22	1.34	0.72
33:BA:785:C:N4	33:BA:805:G:H1	1.86	0.72
43:BN:88:ARG:HD3	43:BN:94:ARG:HH21	1.53	0.72
24:B0:44:PRO:HB2	24:B0:45:LYS:HG2	1.70	0.72
33:BA:1799:G:H1	33:BA:2011:U:H3	1.37	0.72
50:BU:25:LEU:HD12	50:BU:27:ALA:H	1.52	0.72
22:AY:8:G:H3'	22:AY:9:A:H8	1.55	0.72
33:BA:1474:C:H42	33:BA:1618:A:H62	1.37	0.72
50:BU:8:GLY:HA3	50:BU:10:LYS:H	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2552:G:H1	33:BA:2569:C:H42	1.37	0.72
50:BU:67:ARG:HD3	50:BU:89:ARG:NH1	2.04	0.72
53:BX:86:GLU:O	53:BX:87:ASP:CB	2.38	0.72
33:BA:2031:G:OP1	46:BQ:13:ARG:NH2	2.23	0.71
1:AA:861:U:O4	1:AA:862:A:N6	2.23	0.71
44:BO:23:ILE:CG2	50:BU:81:ASN:O	2.37	0.71
36:BE:123:ILE:HD13	36:BE:141:ARG:HE	1.55	0.71
27:B3:51:SER:HA	27:B3:52:ALA:HB3	1.72	0.71
35:BD:243:ARG:HH22	35:BD:247:MET:HB2	1.56	0.71
1:AA:965:U:N3	1:AA:1234:A:C2	2.58	0.71
33:BA:2123:A:H61	33:BA:2224:U:H3	1.35	0.71
21:AX:71:C:H6	21:AX:71:C:H5''	1.56	0.71
22:AY:5:A:C5	22:AY:6:A:C8	2.79	0.71
33:BA:875:U:H3	33:BA:876:A:H62	1.36	0.71
33:BA:1654:A:N6	33:BA:1692:U:O4	2.17	0.71
33:BA:365:U:H3	33:BA:385:G:HO2'	1.38	0.70
50:BU:79:LYS:C	50:BU:80:LYS:HG2	2.16	0.70
48:BS:63:THR:HG22	48:BS:76:THR:HG22	1.73	0.70
21:AX:72:C:H5''	21:AX:72:C:C6	2.25	0.70
33:BA:607:G:H21	49:BT:37:GLN:HE22	1.37	0.70
33:BA:1317:G:O2'	46:BQ:27:ASN:ND2	2.24	0.70
33:BA:957:A:H62	45:BP:12:GLU:HA	1.57	0.70
33:BA:1894:U:O2	33:BA:1905:A:N7	2.25	0.70
33:BA:831:U:H5	33:BA:840:A:C2	2.09	0.70
33:BA:1250:G:C5'	33:BA:1251:U:H5''	2.21	0.70
33:BA:1659:A:C2	51:BV:93:ALA:HB2	2.27	0.70
1:AA:970:U:H2'	1:AA:1234:A:H62	1.57	0.70
11:AK:38:ASP:O	11:AK:41:GLY:HA2	1.91	0.70
29:B5:2:ARG:HD2	29:B5:20:LYS:HB3	1.74	0.70
37:BF:154:ILE:HG12	37:BF:193:LEU:HD12	1.73	0.70
33:BA:831:U:C5	33:BA:840:A:C2	2.80	0.69
47:BR:65:VAL:HG13	47:BR:73:ALA:CB	2.21	0.69
1:AA:437:U:H3	1:AA:439:A:H62	1.37	0.69
33:BA:1347:A:H62	33:BA:1651:G:H8	1.38	0.69
33:BA:785:C:N3	33:BA:805:G:N2	2.38	0.69
42:BM:19:VAL:HG13	42:BM:143:LEU:HD11	1.72	0.69
24:B0:40:VAL:HG12	24:B0:41:ASN:N	2.07	0.69
33:BA:374:A:H2	33:BA:1250:G:H2'	1.53	0.69
29:B5:33:LYS:HB3	29:B5:44:LEU:HD23	1.75	0.69
50:BU:8:GLY:HA3	50:BU:10:LYS:N	2.08	0.69
22:AY:8:G:H3'	22:AY:9:A:C8	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:B6:31:LEU:HD23	30:B6:42:LEU:HD11	1.73	0.69
33:BA:1815:A:H5''	33:BA:2009:G:N2	2.08	0.69
51:BV:88:ARG:HB2	51:BV:92:ARG:HB2	1.73	0.69
21:AX:22:G:N7	21:AX:46:G:N2	2.32	0.69
22:AY:5:A:H2'	22:AY:6:A:C5'	2.22	0.69
33:BA:715:A:H2'	33:BA:717:A:H62	1.57	0.69
51:BV:72:SER:OG	51:BV:106:VAL:CG1	2.41	0.69
1:AA:732:U:N3	22:AY:7:C:O2'	2.26	0.68
33:BA:2009:G:C4	33:BA:2011:U:C5	2.80	0.68
38:BG:57:LEU:HD23	38:BG:65:PRO:HB3	1.75	0.68
33:BA:1364:C:N3	51:BV:86:ARG:NH2	2.41	0.68
31:B7:41:LYS:NZ	33:BA:2448:U:OP1	2.26	0.68
33:BA:2009:G:C5	33:BA:2011:U:C4	2.82	0.68
33:BA:2766:G:H1	33:BA:2796:C:H42	1.41	0.68
39:BH:103:LYS:HG2	39:BH:117:VAL:HG22	1.73	0.68
47:BR:65:VAL:HG11	47:BR:73:ALA:HB1	1.74	0.68
53:BX:39:ASN:HB3	53:BX:61:ALA:HB3	1.74	0.68
1:AA:128:A:N6	1:AA:193:G:O2'	2.26	0.68
33:BA:2374:G:H5'	33:BA:2376:C:H5'	1.74	0.68
22:AY:3:U:H2'	22:AY:4:G:H8	1.57	0.68
38:BG:135:GLN:HE22	38:BG:150:ARG:H	1.41	0.68
33:BA:2613:U:C3'	33:BA:2614:U:H5'	2.24	0.68
23:AZ:88:GLU:O	33:BA:2090:G:N2	2.27	0.68
35:BD:142:HIS:ND1	35:BD:193:GLY:O	2.27	0.68
54:BZ:46:TYR:HB3	54:BZ:67:LEU:HD12	1.76	0.68
22:AY:11:G:O2'	22:AY:12:A:OP2	2.11	0.68
33:BA:738:C:OP1	35:BD:217:ARG:NH2	2.23	0.68
33:BA:2669:G:H1	33:BA:2803:C:H42	1.42	0.68
28:B4:38:LEU:HD11	28:B4:41:ARG:HD2	1.74	0.67
33:BA:2709:C:H5'	36:BE:193:PRO:HA	1.76	0.67
1:AA:965:U:O4	1:AA:1234:A:N1	2.27	0.67
52:BW:5:ARG:HA	52:BW:46:ILE:HD11	1.75	0.67
30:B6:37:LYS:NZ	33:BA:515:G:OP2	2.27	0.67
1:AA:1245:A:H4'	1:AA:1313:G:H4'	1.76	0.67
24:B0:37:ARG:HD3	24:B0:45:LYS:HD3	1.75	0.67
37:BF:73:ALA:HB3	37:BF:75:GLN:CG	2.24	0.67
32:B8:30:PRO:HB2	33:BA:2556:C:H5'	1.75	0.67
33:BA:651:U:O2	33:BA:667:A:N7	2.26	0.67
33:BA:795:G:H5'	33:BA:796:A:OP2	1.94	0.67
33:BA:1257:C:OP1	49:BT:15:LYS:NZ	2.27	0.67
35:BD:171:TYR:HB2	35:BD:183:MET:HB3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BX:86:GLU:O	53:BX:87:ASP:HB3	1.94	0.67
22:AY:1:U:C2'	22:AY:2:G:H1'	2.24	0.67
33:BA:797:A:H2'	33:BA:797:A:N3	2.10	0.67
33:BA:1111:U:O2	33:BA:1119:A:N7	2.28	0.67
1:AA:1367:U:O2	1:AA:1372:A:N7	2.27	0.67
33:BA:1518:G:H3'	33:BA:1519:C:H5''	1.77	0.67
50:BU:67:ARG:HA	50:BU:90:GLN:O	1.95	0.67
33:BA:2090:G:OP1	37:BF:68:LYS:NZ	2.25	0.67
35:BD:29:PRO:HB3	35:BD:63:ARG:HE	1.58	0.67
39:BH:21:ASP:HB3	39:BH:22:ASN:CB	2.21	0.67
33:BA:1042:A:H5'	49:BT:92:ARG:HE	1.59	0.66
26:B2:5:GLU:HB2	26:B2:57:LYS:HB3	1.77	0.66
33:BA:1371:G:N7	33:BA:1654:A:O2'	2.26	0.66
1:AA:666:U:H3	1:AA:758:A:H61	1.43	0.66
33:BA:918:U:H3	33:BA:953:G:H1	1.42	0.66
48:BS:67:ILE:HA	48:BS:72:GLY:HA2	1.76	0.66
31:B7:24:ARG:HD3	31:B7:50:VAL:HG22	1.78	0.66
32:B8:29:ASN:HB2	32:B8:32:HIS:HD2	1.61	0.66
38:BG:78:ARG:HB3	38:BG:79:LEU:HB2	1.78	0.66
39:BH:13:SER:HB3	39:BH:14:ASP:HA	1.78	0.66
24:B0:45:LYS:CE	24:B0:46:LYS:HE2	2.26	0.66
37:BF:4:VAL:HG12	37:BF:5:ALA:H	1.59	0.66
36:BE:178:LYS:HB2	36:BE:187:LEU:HD12	1.77	0.66
33:BA:1711:G:H1	33:BA:2023:C:N4	1.93	0.66
36:BE:28:ILE:HB	36:BE:186:LEU:HB2	1.77	0.65
43:BN:11:ALA:HB2	43:BN:83:ALA:HB1	1.77	0.65
43:BN:22:ILE:HD12	43:BN:40:VAL:HG12	1.75	0.65
31:B7:8:ARG:NH1	33:BA:247:A:OP2	2.29	0.65
33:BA:2571:A:H4'	33:BA:2572:G:H5'	1.78	0.65
33:BA:1522:U:O2	33:BA:1563:G:N2	2.30	0.65
1:AA:1313:G:H21	1:AA:1342:A:H62	1.44	0.65
21:AX:35:U:H5'	21:AX:35:U:H6	1.61	0.65
33:BA:507:A:H62	33:BA:516:G:H21	1.43	0.65
33:BA:1268:G:OP2	49:BT:12:LYS:NZ	2.30	0.65
33:BA:1379:U:H5''	52:BW:57:MET:HE1	1.76	0.65
33:BA:1931:C:H5''	35:BD:241:ILE:HG21	1.77	0.65
33:BA:2818:C:O2'	33:BA:2917:G:N2	2.29	0.65
38:BG:64:LYS:HD2	38:BG:65:PRO:HD2	1.78	0.65
33:BA:1783:C:N3	33:BA:2745:U:O2'	2.29	0.65
51:BV:72:SER:OG	51:BV:106:VAL:HG12	1.96	0.65
22:AY:12:A:H1'	22:AY:13:G:P	2.37	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2105:U:OP2	33:BA:2267:G:N2	2.28	0.65
36:BE:201:THR:CG2	36:BE:203:LYS:HG3	2.27	0.65
37:BF:36:ALA:HB1	37:BF:183:VAL:HG21	1.79	0.65
47:BR:56:ALA:HB3	47:BR:81:VAL:HG22	1.78	0.65
1:AA:268:G:N2	1:AA:273:G:C5	2.65	0.65
28:B4:16:ARG:NH2	33:BA:1304:G:OP1	2.30	0.65
1:AA:992:U:H4'	1:AA:993:A:H5'	1.79	0.65
33:BA:729:G:O6	33:BA:841:A:N6	2.30	0.64
33:BA:1250:G:H4'	33:BA:1251:U:OP2	1.96	0.64
22:AY:5:A:C6	22:AY:6:A:C5	2.86	0.64
36:BE:125:ARG:NH1	36:BE:163:ARG:O	2.29	0.64
24:B0:44:PRO:HB2	24:B0:45:LYS:CG	2.27	0.64
33:BA:1808:U:OP2	33:BA:1813:A:N6	2.29	0.64
37:BF:37:ILE:HG23	37:BF:184:LEU:HD21	1.79	0.64
24:B0:39:LEU:N	24:B0:39:LEU:HD12	2.11	0.64
31:B7:57:ARG:NH2	33:BA:880:C:O2'	2.30	0.64
37:BF:66:ARG:HH11	37:BF:70:THR:HG23	1.60	0.64
29:B5:22:ASN:ND2	33:BA:2315:A:OP2	2.31	0.64
35:BD:39:LYS:NZ	35:BD:57:GLY:O	2.30	0.64
37:BF:67:GLN:NE2	37:BF:74:ARG:HG2	2.12	0.64
33:BA:831:U:C5	33:BA:840:A:N1	2.66	0.64
33:BA:1019:A:O2'	33:BA:1227:G:N2	2.31	0.64
24:B0:45:LYS:HB3	24:B0:46:LYS:HA	1.80	0.64
31:B7:13:ARG:NH1	44:BO:61:LEU:O	2.31	0.64
33:BA:377:G:H4'	33:BA:378:C:OP1	1.96	0.64
33:BA:1096:A:H3'	33:BA:1097:A:H8	1.62	0.64
35:BD:164:VAL:HG12	35:BD:166:GLY:H	1.63	0.64
22:AY:1:U:H2'	22:AY:2:G:O2'	1.98	0.63
29:B5:29:ARG:HG3	29:B5:47:GLU:HB3	1.80	0.63
33:BA:1847:U:H5''	35:BD:157:SER:HB3	1.79	0.63
33:BA:831:U:O4	33:BA:840:A:N1	2.30	0.63
33:BA:1056:A:OP1	49:BT:66:ASN:ND2	2.31	0.63
33:BA:837:U:H4'	33:BA:838:C:OP1	1.96	0.63
33:BA:2009:G:C6	33:BA:2011:U:O4	2.50	0.63
1:AA:446:G:N2	1:AA:505:G:N7	2.45	0.63
38:BG:100:LEU:HD23	38:BG:103:LEU:HD12	1.80	0.63
42:BM:54:HIS:HB3	42:BM:122:LYS:HB3	1.80	0.63
33:BA:2777:A:H5''	39:BH:4:VAL:HG21	1.81	0.63
22:AY:12:A:H1'	22:AY:13:G:OP1	1.98	0.63
50:BU:67:ARG:HD3	50:BU:89:ARG:NE	2.13	0.63
31:B7:31:HIS:ND1	33:BA:2421:A:OP1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1263:G:C6	50:BU:70:LYS:NZ	2.66	0.63
47:BR:65:VAL:N	47:BR:66:GLU:HA	2.13	0.63
22:AY:11:G:O2'	22:AY:12:A:P	2.57	0.63
33:BA:1123:A:O2'	41:BK:93:ASN:ND2	2.32	0.63
40:BJ:26:ILE:HG13	40:BJ:114:GLU:HB2	1.81	0.63
41:BK:15:ALA:HB2	41:BK:46:THR:CG2	2.21	0.63
1:AA:591:C:OP2	1:AA:767:G:N1	2.26	0.62
33:BA:528:G:O2'	33:BA:552:G:N2	2.31	0.62
40:BJ:11:VAL:HA	40:BJ:66:GLN:HE21	1.64	0.62
1:AA:458:G:O6	1:AA:493:G:O6	2.18	0.62
1:AA:1412:C:N4	22:AY:19:C:OP1	2.31	0.62
1:AA:1544:A:H8	1:AA:1544:A:O5'	1.81	0.62
1:AA:1546:C:H2'	1:AA:1547:U:H6	1.64	0.62
51:BV:6:VAL:HG22	51:BV:104:THR:HG22	1.80	0.62
51:BV:89:ALA:O	51:BV:92:ARG:HG2	1.99	0.62
1:AA:965:U:H3	1:AA:1234:A:H2	1.42	0.62
33:BA:798:A:H5''	33:BA:799:A:OP1	1.98	0.62
51:BV:92:ARG:HA	51:BV:92:ARG:HE	1.64	0.62
43:BN:16:ALA:HB2	43:BN:52:VAL:HG11	1.82	0.62
54:BZ:78:GLU:O	54:BZ:86:LYS:N	2.32	0.62
33:BA:839:G:H4'	33:BA:840:A:H5'	1.81	0.62
35:BD:132:LEU:HD23	35:BD:135:ILE:HD12	1.81	0.62
33:BA:793:U:H5'	33:BA:795:G:H1'	1.80	0.62
33:BA:1250:G:H4'	33:BA:1251:U:H5''	1.81	0.62
33:BA:2010:A:H3'	33:BA:2011:U:H5'	1.82	0.62
22:AY:10:U:H1'	22:AY:11:G:OP1	1.99	0.62
33:BA:1024:G:N2	33:BA:1031:C:N3	2.41	0.62
33:BA:1250:G:H5''	33:BA:1251:U:H5''	1.82	0.62
33:BA:1846:G:OP1	35:BD:87:ARG:NH2	2.33	0.62
47:BR:113:ALA:HB1	47:BR:118:LEU:HD12	1.81	0.62
33:BA:1897:C:H42	33:BA:1902:G:H1	1.45	0.62
33:BA:835:A:H5''	33:BA:837:U:H5	1.65	0.62
33:BA:2128:U:H2'	33:BA:2129:G:H8	1.65	0.62
24:B0:43:LYS:O	24:B0:44:PRO:O	2.18	0.61
37:BF:65:TRP:HZ2	37:BF:75:GLN:HB2	1.51	0.61
45:BP:78:PRO:HG2	45:BP:81:VAL:HG21	1.82	0.61
33:BA:41:A:H2	33:BA:485:U:H3	1.47	0.61
33:BA:2434:G:H4'	44:BO:69:ILE:HD12	1.82	0.61
42:BM:18:VAL:HG13	42:BM:58:ILE:HD13	1.82	0.61
21:AX:34:G:C2	21:AX:35:U:C6	2.88	0.61
30:B6:1:MET:HG3	33:BA:800:G:OP1	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B7:14:PHE:HB3	31:B7:22:LEU:HD23	1.82	0.61
33:BA:2730:U:O4	33:BA:2735:A:N1	2.33	0.61
33:BA:678:A:H2'	33:BA:679:A:H8	1.65	0.61
33:BA:1291:A:OP1	49:BT:13:ARG:NH2	2.32	0.61
33:BA:2479:A:N6	33:BA:2530:C:O2	2.33	0.61
38:BG:38:MET:HE1	38:BG:152:MET:HG2	1.81	0.61
22:AY:5:A:C2	22:AY:6:A:C1'	2.84	0.61
22:AY:10:U:H1'	22:AY:11:G:P	2.40	0.61
1:AA:1096:U:H3	1:AA:1109:G:H22	1.48	0.61
40:BJ:29:ASP:HB2	40:BJ:81:ALA:HB1	1.82	0.61
41:BK:15:ALA:CA	41:BK:46:THR:HG21	2.30	0.61
33:BA:811:A:H5''	35:BD:209:GLY:HA2	1.83	0.61
33:BA:1706:G:N2	33:BA:2717:G:OP1	2.34	0.61
33:BA:2518:G:N2	33:BA:2520:U:O4	2.33	0.61
33:BA:350:U:O2'	33:BA:1251:U:C5	2.52	0.61
33:BA:839:G:C4'	33:BA:840:A:H5'	2.31	0.61
39:BH:59:GLN:HB2	39:BH:62:HIS:HD2	1.66	0.61
40:BJ:28:VAL:HG12	40:BJ:30:TYR:H	1.65	0.61
31:B7:4:MET:HE2	33:BA:713:G:H1'	1.83	0.61
31:B7:32:LEU:O	31:B7:36:LYS:NZ	2.33	0.61
33:BA:1065:U:N3	33:BA:1188:A:N6	2.48	0.61
45:BP:2:LEU:O	45:BP:44:ASN:ND2	2.33	0.60
22:AY:5:A:C6	22:AY:6:A:C4	2.89	0.60
33:BA:1829:C:N4	33:BA:1846:G:H22	1.98	0.60
33:BA:1928:A:H4'	33:BA:1930:A:H5''	1.82	0.60
33:BA:2900:A:HO2'	48:BS:5:GLN:N	1.98	0.60
33:BA:498:U:O2	33:BA:500:A:N6	2.34	0.60
33:BA:797:A:N3	33:BA:799:A:H5'	2.16	0.60
33:BA:2613:U:H2'	33:BA:2614:U:H5'	1.84	0.60
37:BF:126:LEU:HD13	37:BF:193:LEU:HD22	1.82	0.60
1:AA:69:C:H2'	1:AA:70:G:C8	2.36	0.60
1:AA:965:U:N3	1:AA:1234:A:H2	1.98	0.60
32:B8:18:ARG:HA	32:B8:23:VAL:HA	1.82	0.60
33:BA:609:C:H5	50:BU:79:LYS:HE2	1.67	0.60
33:BA:644:G:H1	33:BA:704:U:H3	1.50	0.60
51:BV:6:VAL:HG12	51:BV:8:ARG:HG3	1.82	0.60
30:B6:34:ARG:CG	30:B6:42:LEU:HD12	2.14	0.60
48:BS:30:ARG:HD3	48:BS:45:ILE:HD11	1.83	0.60
22:AY:7:C:O2	22:AY:7:C:H2'	2.00	0.60
33:BA:1815:A:H5''	33:BA:2009:G:H22	1.66	0.60
44:BO:75:ALA:HB1	44:BO:76:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:385:G:O6	1:AA:386:A:N6	2.35	0.60
33:BA:636:G:H1	33:BA:712:C:H42	1.48	0.60
1:AA:673:G:H22	1:AA:750:G:H1	1.50	0.60
33:BA:787:C:H42	33:BA:804:G:H1	1.49	0.60
33:BA:1537:G:H2'	33:BA:1538:G:H8	1.67	0.60
33:BA:1835:C:O2	35:BD:44:ASN:ND2	2.35	0.60
24:B0:29:TRP:HZ3	33:BA:426:G:H21	1.50	0.59
24:B0:43:LYS:HB3	24:B0:44:PRO:HD2	1.83	0.59
33:BA:41:A:N1	33:BA:485:U:O4	2.35	0.59
33:BA:1250:G:H4'	33:BA:1251:U:C5'	2.32	0.59
33:BA:1501:U:O4	33:BA:2733:C:N3	2.35	0.59
37:BF:66:ARG:HD3	37:BF:70:THR:HG23	1.83	0.59
42:BM:57:ILE:HD12	42:BM:125:VAL:HG22	1.82	0.59
33:BA:830:A:H2'	33:BA:831:U:H4'	1.84	0.59
33:BA:2123:A:N6	33:BA:2224:U:H3	2.00	0.59
31:B7:27:ALA:HB3	33:BA:2390:A:H5'	1.82	0.59
1:AA:1549:C:C2	1:AA:1550:U:C6	2.91	0.59
33:BA:576:G:N2	33:BA:2052:A:OP2	2.34	0.59
33:BA:822:G:H4'	33:BA:823:G:H5'	1.84	0.59
33:BA:902:G:O2'	54:BZ:35:ASP:OD2	2.20	0.59
33:BA:106:G:H2'	33:BA:107:G:H8	1.68	0.59
33:BA:2833:U:H2'	33:BA:2834:A:H8	1.66	0.59
33:BA:2855:G:OP1	36:BE:78:ARG:NH2	2.35	0.59
35:BD:241:ILE:HG23	35:BD:241:ILE:O	2.01	0.59
37:BF:73:ALA:CB	37:BF:75:GLN:HG2	2.27	0.59
42:BM:65:LEU:HD13	42:BM:69:LYS:HB2	1.85	0.59
33:BA:515:G:O2'	37:BF:62:ARG:NH2	2.36	0.59
33:BA:721:G:H5''	37:BF:76:GLY:H	1.67	0.59
33:BA:1834:C:N4	33:BA:1841:G:H1	1.98	0.59
1:AA:412:G:N2	1:AA:507:A:O2'	2.36	0.59
1:AA:1551:U:H3	22:AY:2:G:N2	1.91	0.59
33:BA:1173:A:O2'	33:BA:1174:A:H5''	2.01	0.59
33:BA:2487:U:O2	33:BA:2487:U:H2'	2.02	0.59
35:BD:15:GLY:O	35:BD:204:ASN:ND2	2.35	0.59
44:BO:117:LEU:HB2	44:BO:119:LYS:N	2.17	0.59
46:BQ:17:LEU:HD21	46:BQ:39:GLU:CD	2.28	0.59
53:BX:16:ASP:HB3	53:BX:19:LYS:HD2	1.85	0.59
21:AX:36:C:H6	21:AX:36:C:H5''	1.68	0.59
33:BA:217:G:N1	33:BA:218:G:C6	2.71	0.59
33:BA:1394:G:OP1	35:BD:43:ARG:NH2	2.35	0.59
22:AY:12:A:O2'	22:AY:13:G:OP1	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:BV:92:ARG:HA	51:BV:92:ARG:NE	2.18	0.58
50:BU:10:LYS:HG3	50:BU:12:ILE:HD11	1.85	0.58
53:BX:86:GLU:HG3	53:BX:87:ASP:H	1.68	0.58
33:BA:1245:G:OP2	33:BA:1245:G:N2	2.34	0.58
33:BA:264:G:O2'	33:BA:654:G:O2'	2.20	0.58
33:BA:673:A:O2'	33:BA:674:G:O4'	2.21	0.58
33:BA:1207:C:H1'	50:BU:9:GLY:H	1.68	0.58
33:BA:1578:G:N2	33:BA:1587:U:OP2	2.36	0.58
39:BH:88:LEU:HB2	39:BH:132:VAL:HB	1.84	0.58
33:BA:588:C:N4	33:BA:589:G:O6	2.36	0.58
33:BA:861:C:O2'	33:BA:1264:G:N2	2.36	0.58
1:AA:1295:C:H2'	1:AA:1296:A:H4'	1.84	0.58
33:BA:350:U:H4'	33:BA:1251:U:H5	1.67	0.58
33:BA:1101:G:H4'	40:BJ:33:LEU:HA	1.85	0.58
33:BA:2613:U:C2'	33:BA:2614:U:H5'	2.33	0.58
26:B2:7:THR:HG22	26:B2:34:THR:HG22	1.86	0.58
33:BA:1365:U:HO2'	33:BA:2039:G:HO2'	1.51	0.58
37:BF:67:GLN:HE22	37:BF:74:ARG:CG	2.16	0.58
52:BW:20:LEU:HD22	52:BW:25:LYS:HD2	1.85	0.58
1:AA:1323:C:N4	1:AA:1332:G:H1	1.99	0.58
33:BA:377:G:C4	33:BA:378:C:C5	2.92	0.58
24:B0:45:LYS:NZ	24:B0:46:LYS:HE2	2.19	0.58
26:B2:5:GLU:HG2	26:B2:36:VAL:HG22	1.86	0.58
33:BA:673:A:H62	44:BO:78:ASN:ND2	2.02	0.58
33:BA:792:G:H5'	33:BA:793:U:OP2	2.04	0.58
33:BA:934:U:H4'	33:BA:935:A:H8	1.69	0.58
33:BA:2717:G:N1	33:BA:2749:U:OP2	2.36	0.58
35:BD:150:LYS:HG2	35:BD:153:GLN:HE22	1.68	0.58
1:AA:1508:U:O2'	22:AY:18:A:OP1	2.17	0.57
24:B0:3:ARG:NH1	33:BA:1403:G:OP1	2.36	0.57
33:BA:683:A:O2'	33:BA:684:G:OP2	2.22	0.57
33:BA:835:A:H5''	33:BA:837:U:C5	2.39	0.57
33:BA:1261:C:N3	33:BA:1268:G:O6	2.36	0.57
33:BA:2714:G:OP2	48:BS:52:LYS:NZ	2.37	0.57
34:BB:112:C:H2'	34:BB:113:A:H8	1.69	0.57
31:B7:38:GLN:HA	31:B7:41:LYS:HD3	1.86	0.57
36:BE:177:VAL:HG12	36:BE:178:LYS:HG3	1.86	0.57
38:BG:47:ALA:N	38:BG:48:LYS:HA	2.19	0.57
33:BA:831:U:C4	33:BA:840:A:N1	2.72	0.57
33:BA:2799:C:C5	33:BA:2800:C:C6	2.93	0.57
35:BD:214:LYS:N	35:BD:215:GLY:HA2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1154:C:H4'	1:AA:1155:A:O5'	2.04	0.57
30:B6:21:ARG:NH2	33:BA:513:A:OP1	2.34	0.57
33:BA:2472:C:H2'	33:BA:2473:G:H8	1.69	0.57
37:BF:136:THR:HG22	37:BF:167:ALA:H	1.69	0.57
39:BH:39:HIS:CE1	39:BH:42:MET:HG2	2.40	0.57
53:BX:48:THR:HB	53:BX:49:GLN:C	2.30	0.57
33:BA:1897:C:N4	33:BA:1902:G:H1	2.03	0.57
38:BG:40:VAL:HG12	38:BG:42:ASP:H	1.68	0.57
33:BA:881:U:O4	33:BA:882:A:N6	2.38	0.57
40:BJ:27:ILE:HB	40:BJ:83:ALA:HB3	1.86	0.57
45:BP:137:ILE:N	45:BP:138:GLY:HA3	2.19	0.57
52:BW:47:PHE:HD1	52:BW:90:ILE:HD13	1.70	0.57
33:BA:794:U:C4	33:BA:2642:U:C5	2.93	0.57
33:BA:910:A:O2'	34:BB:98:G:O2'	2.21	0.57
33:BA:2071:A:N6	42:BM:117:ARG:HH12	2.03	0.57
36:BE:185:LEU:HD21	48:BS:7:LEU:HD21	1.86	0.57
44:BO:55:MET:O	44:BO:60:ARG:NH1	2.38	0.57
21:AX:36:C:N4	21:AX:37:A:N6	2.52	0.57
24:B0:37:ARG:CG	24:B0:45:LYS:CG	2.76	0.57
33:BA:837:U:H3'	33:BA:837:U:H6	1.70	0.57
33:BA:1829:C:N3	33:BA:1846:G:N1	2.43	0.57
1:AA:106:G:H5'	1:AA:107:A:H5''	1.87	0.57
7:AG:18:TYR:O	7:AG:20:SER:N	2.34	0.57
27:B3:48:LYS:O	27:B3:50:ALA:N	2.37	0.57
41:BK:46:THR:HG22	41:BK:46:THR:O	2.05	0.57
44:BO:117:LEU:HB2	44:BO:119:LYS:H	1.69	0.57
1:AA:1293:C:H3'	1:AA:1294:A:H8	1.69	0.56
33:BA:1600:G:O2'	33:BA:1601:A:O4'	2.22	0.56
33:BA:1828:G:O2'	35:BD:182:ARG:NH2	2.38	0.56
33:BA:2423:C:H5''	44:BO:63:LYS:HE3	1.87	0.56
49:BT:95:LEU:HD12	49:BT:98:LEU:HD11	1.85	0.56
26:B2:6:ILE:HG23	26:B2:54:VAL:HG13	1.88	0.56
33:BA:1108:G:H2'	33:BA:1109:G:H8	1.70	0.56
33:BA:2154:G:H21	33:BA:2202:A:H62	1.53	0.56
43:BN:70:ARG:HG3	43:BN:76:TYR:HE1	1.70	0.56
48:BS:95:VAL:HG12	48:BS:97:ARG:H	1.69	0.56
1:AA:1087:G:N2	1:AA:1090:A:OP2	2.38	0.56
1:AA:1110:C:N4	1:AA:1113:C:OP1	2.39	0.56
38:BG:24:SER:O	38:BG:26:MET:N	2.33	0.56
41:BK:85:ILE:HD12	41:BK:98:ALA:HB2	1.88	0.56
42:BM:17:LEU:HB2	42:BM:55:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BM:42:LYS:NZ	42:BM:51:THR:O	2.34	0.56
44:BO:78:ASN:HB2	44:BO:81:LYS:HG2	1.85	0.56
33:BA:1855:C:O2'	33:BA:2000:A:OP2	2.22	0.56
33:BA:2489:U:H5	33:BA:2521:U:H3	1.53	0.56
51:BV:21:MET:HA	51:BV:24:ILE:HD12	1.87	0.56
22:AY:12:A:C1'	22:AY:13:G:P	2.94	0.56
31:B7:32:LEU:HD11	31:B7:35:ASN:HD22	1.71	0.56
33:BA:787:C:H2'	33:BA:788:G:H5''	1.88	0.56
33:BA:839:G:H4'	33:BA:840:A:N3	2.20	0.56
33:BA:1528:U:H4'	33:BA:1529:G:H5'	1.88	0.56
33:BA:2267:G:H1'	33:BA:2269:C:H5	1.69	0.56
24:B0:45:LYS:HE3	24:B0:46:LYS:CE	2.35	0.56
33:BA:854:U:H2'	33:BA:855:G:C8	2.40	0.56
40:BJ:53:LYS:HB3	40:BJ:55:TYR:HD2	1.70	0.56
47:BR:65:VAL:CG1	47:BR:73:ALA:HB2	2.35	0.56
51:BV:75:PHE:O	51:BV:104:THR:OG1	2.24	0.56
1:AA:1544:A:C5'	1:AA:1544:A:C8	2.89	0.56
39:BH:12:PRO:O	39:BH:13:SER:HB2	2.06	0.56
33:BA:2784:C:O2'	33:BA:2785:U:O5'	2.24	0.56
50:BU:14:VAL:HG11	50:BU:97:ILE:HD12	1.87	0.56
37:BF:65:TRP:HZ2	37:BF:75:GLN:CG	2.19	0.55
1:AA:64:U:O2'	1:AA:387:C:O2	2.23	0.55
24:B0:17:ASN:HD21	24:B0:27:ARG:HD2	1.71	0.55
33:BA:426:G:H1	33:BA:442:C:N4	2.02	0.55
33:BA:805:G:HO2'	33:BA:2010:A:H8	1.55	0.55
35:BD:44:ASN:HB2	35:BD:50:THR:HG23	1.88	0.55
36:BE:119:PHE:HA	36:BE:163:ARG:HA	1.87	0.55
37:BF:63:LYS:HA	37:BF:76:GLY:O	2.06	0.55
1:AA:1071:G:OP2	3:AC:2:GLY:N	2.39	0.55
21:AX:34:G:H2'	21:AX:35:U:H5''	1.88	0.55
33:BA:921:G:OP1	45:BP:63:LYS:NZ	2.40	0.55
33:BA:2535:U:O2	33:BA:2535:U:H2'	2.07	0.55
47:BR:25:THR:HG21	47:BR:47:ASP:HB2	1.87	0.55
1:AA:113:G:H4'	1:AA:114:A:O5'	2.03	0.55
30:B6:31:LEU:HD22	30:B6:42:LEU:HD11	1.87	0.55
33:BA:1314:A:N6	33:BA:1335:A:H4'	2.21	0.55
41:BK:55:PRO:HG2	41:BK:71:LYS:HB2	1.88	0.55
33:BA:827:G:N1	35:BD:229:ASP:OD2	2.35	0.55
33:BA:934:U:O2'	33:BA:936:C:OP2	2.23	0.55
33:BA:1067:A:H2'	33:BA:1068:G:H4'	1.88	0.55
33:BA:2696:C:H1'	39:BH:110:TYR:HD1	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BM:38:ARG:HH12	42:BM:111:PRO:HG3	1.71	0.55
47:BR:22:LEU:CD2	47:BR:94:VAL:CG1	2.78	0.55
51:BV:84:ARG:HB2	51:BV:96:ILE:HB	1.87	0.55
53:BX:33:VAL:N	53:BX:63:ILE:O	2.32	0.55
11:AK:38:ASP:C	11:AK:41:GLY:HA2	2.31	0.55
24:B0:43:LYS:C	24:B0:44:PRO:O	2.49	0.55
34:BB:10:G:N1	54:BZ:79:ARG:O	2.40	0.55
54:BZ:80:PHE:N	54:BZ:84:ARG:O	2.39	0.55
33:BA:2147:U:N3	33:BA:2176:A:O2'	2.37	0.55
47:BR:91:SER:OG	47:BR:92:ASP:N	2.36	0.55
33:BA:673:A:H62	44:BO:78:ASN:HD22	1.54	0.55
45:BP:30:GLY:HA2	45:BP:107:SER:HB3	1.87	0.55
31:B7:24:ARG:NH2	33:BA:2389:A:OP1	2.40	0.55
33:BA:1931:C:H5''	35:BD:241:ILE:CG2	2.36	0.55
35:BD:140:VAL:HG11	35:BD:194:GLN:HB3	1.89	0.55
38:BG:78:ARG:HD2	38:BG:79:LEU:HD13	1.88	0.55
1:AA:799:A:OP1	21:AX:38:C:O2'	2.23	0.55
22:AY:3:U:H5	22:AY:3:U:OP2	1.90	0.55
33:BA:1103:A:O2'	33:BA:1104:U:OP1	2.23	0.55
42:BM:131:HIS:HD2	42:BM:133:HIS:HB2	1.72	0.55
22:AY:1:U:H2'	22:AY:2:G:C1'	2.33	0.54
29:B5:21:LYS:HE2	29:B5:30:VAL:HB	1.88	0.54
33:BA:565:U:O3'	51:BV:25:ARG:NH1	2.40	0.54
33:BA:1111:U:O2	33:BA:1119:A:C5	2.60	0.54
43:BN:38:VAL:HG22	43:BN:61:VAL:HG22	1.89	0.54
49:BT:103:LEU:HG	49:BT:104:THR:HG22	1.89	0.54
1:AA:986:G:O5'	1:AA:1367:U:O2'	2.24	0.54
1:AA:1549:C:C4	22:AY:5:A:N6	2.75	0.54
22:AY:8:G:C5	22:AY:9:A:C5	2.95	0.54
24:B0:42:GLY:CA	24:B0:43:LYS:HD3	2.38	0.54
27:B3:9:PHE:HZ	38:BG:62:GLY:HA3	1.71	0.54
50:BU:67:ARG:NH1	50:BU:89:ARG:NH1	2.49	0.54
1:AA:970:U:H2'	1:AA:1234:A:N6	2.21	0.54
26:B2:10:ARG:HB3	26:B2:53:LEU:HD13	1.88	0.54
33:BA:796:A:H61	33:BA:800:G:N2	1.99	0.54
33:BA:1094:A:H1'	33:BA:1158:G:H21	1.73	0.54
33:BA:1710:A:O2'	43:BN:1:MET:O	2.25	0.54
33:BA:2344:U:OP1	38:BG:33:LYS:NZ	2.39	0.54
1:AA:1549:C:C4	1:AA:1550:U:C5	2.95	0.54
25:B1:54:LYS:NZ	33:BA:72:U:OP2	2.40	0.54
31:B7:25:SER:OG	44:BO:64:ARG:NH1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BS:95:VAL:HG13	48:BS:100:LEU:HD21	1.88	0.54
21:AX:7:G:O2'	21:AX:49:G:O5'	2.24	0.54
22:AY:3:U:O5'	22:AY:3:U:H6	1.91	0.54
24:B0:37:ARG:CZ	24:B0:44:PRO:HG3	2.26	0.54
24:B0:37:ARG:CB	24:B0:45:LYS:HD3	2.31	0.54
35:BD:21:PHE:HB3	35:BD:24:ILE:HD12	1.90	0.54
1:AA:348:U:OP2	43:BN:97:ARG:NH2	2.39	0.54
33:BA:1500:U:OP1	46:BQ:81:GLN:NE2	2.40	0.54
35:BD:230:HIS:ND1	35:BD:231:PRO:HD2	2.23	0.54
42:BM:26:LEU:N	42:BM:27:GLY:HA3	2.23	0.54
46:BQ:4:ARG:HH12	46:BQ:38:LYS:HD2	1.73	0.54
46:BQ:22:THR:HG22	46:BQ:66:ILE:HG23	1.89	0.54
33:BA:794:U:O5'	33:BA:794:U:H6	1.89	0.54
33:BA:1024:G:N1	33:BA:1031:C:N4	2.42	0.54
33:BA:1581:A:C6	33:BA:1584:U:O2	2.60	0.54
36:BE:35:VAL:HG13	36:BE:49:ILE:HG23	1.88	0.54
37:BF:29:ASN:HD22	37:BF:108:LEU:HD21	1.73	0.54
37:BF:54:ARG:NH2	37:BF:77:SER:OG	2.40	0.54
1:AA:526:G:N2	1:AA:539:G:OP1	2.39	0.54
22:AY:5:A:C2'	22:AY:6:A:C5'	2.85	0.54
26:B2:5:GLU:OE2	26:B2:59:GLN:NE2	2.41	0.54
1:AA:66:G:N2	1:AA:70:G:O6	2.30	0.54
1:AA:1325:G:N1	1:AA:1328:A:OP2	2.40	0.54
17:AQ:33:HIS:O	17:AQ:37:GLY:N	2.40	0.54
21:AX:56:C:O2'	21:AX:57:G:O4'	2.23	0.54
35:BD:248:SER:OG	35:BD:250:TRP:O	2.25	0.54
26:B2:20:ARG:NH2	33:BA:1016:U:OP1	2.41	0.54
33:BA:2529:U:O2'	33:BA:2533:U:OP1	2.25	0.54
33:BA:2747:G:O2'	33:BA:2872:U:OP1	2.26	0.54
33:BA:510:G:N2	33:BA:513:A:OP2	2.40	0.53
33:BA:517:A:OP1	37:BF:79:ARG:NH1	2.41	0.53
33:BA:848:G:O4'	37:BF:54:ARG:NH1	2.41	0.53
33:BA:1322:G:N2	33:BA:1325:A:OP2	2.41	0.53
33:BA:2552:G:H1	33:BA:2569:C:N4	2.06	0.53
35:BD:230:HIS:CG	35:BD:231:PRO:HD2	2.43	0.53
54:BZ:18:THR:O	54:BZ:20:ASN:N	2.39	0.53
54:BZ:64:ASP:HB3	54:BZ:66:THR:HG23	1.90	0.53
33:BA:2900:A:O2'	48:BS:5:GLN:N	2.41	0.53
40:BJ:22:SER:OG	40:BJ:87:GLU:OE1	2.26	0.53
33:BA:51:G:H21	33:BA:117:A:H62	1.55	0.53
33:BA:367:G:O2'	33:BA:368:G:OP2	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:683:A:H4'	33:BA:684:G:O5'	2.07	0.53
1:AA:48:G:O2'	1:AA:373:U:O2	2.24	0.53
1:AA:105:G:OP1	1:AA:333:A:N6	2.38	0.53
33:BA:377:G:N3	33:BA:378:C:C5	2.77	0.53
33:BA:557:U:O2'	33:BA:1255:G:N2	2.39	0.53
33:BA:797:A:H2	33:BA:799:A:C5'	2.19	0.53
33:BA:1055:A:OP1	42:BM:40:LYS:NZ	2.41	0.53
33:BA:1066:A:O2'	33:BA:1067:A:O5'	2.22	0.53
33:BA:1070:G:H3'	33:BA:1071:G:H5''	1.90	0.53
33:BA:2345:U:O2'	38:BG:125:ARG:NH1	2.32	0.53
49:BT:28:LYS:HA	49:BT:34:VAL:HG23	1.91	0.53
22:AY:8:G:C6	22:AY:9:A:C5	2.97	0.53
24:B0:45:LYS:HB2	33:BA:2246:G:OP1	2.09	0.53
33:BA:1127:U:OP1	41:BK:126:ARG:NH1	2.41	0.53
33:BA:1568:G:OP2	33:BA:1568:G:N2	2.34	0.53
33:BA:1829:C:H42	33:BA:1846:G:N2	2.02	0.53
33:BA:2800:C:O2'	36:BE:172:GLN:NE2	2.38	0.53
40:BJ:58:THR:HG22	40:BJ:84:PHE:CD2	2.44	0.53
29:B5:34:LYS:HB2	29:B5:45:HIS:CE1	2.43	0.53
33:BA:1968:U:OP1	33:BA:2633:U:O2'	2.26	0.53
51:BV:89:ALA:O	51:BV:90:MET:CB	2.55	0.53
1:AA:518:A:H5'	4:AD:48:GLY:HA3	1.89	0.53
11:AK:37:THR:CA	11:AK:42:ASN:O	2.57	0.53
21:AX:55:U:H3'	21:AX:56:C:H5''	1.91	0.53
33:BA:1474:C:N4	33:BA:1618:A:H62	2.07	0.53
33:BA:1755:C:O2'	33:BA:1756:U:OP1	2.24	0.53
33:BA:2524:G:OP1	45:BP:82:ARG:NE	2.35	0.53
48:BS:78:PRO:HG2	48:BS:81:THR:HB	1.89	0.53
1:AA:1074:G:O2'	1:AA:1199:G:N2	2.42	0.53
27:B3:6:HIS:HE1	38:BG:64:LYS:H	1.55	0.53
33:BA:2479:A:N6	33:BA:2530:C:C2	2.77	0.53
33:BA:2785:U:O2'	33:BA:2786:A:OP2	2.20	0.53
39:BH:4:VAL:O	39:BH:70:ARG:NE	2.42	0.53
54:BZ:73:GLY:HA2	54:BZ:92:VAL:HG23	1.90	0.53
1:AA:1365:G:H2'	1:AA:1366:A:C8	2.44	0.53
25:B1:8:ASP:HB3	25:B1:13:GLU:HG3	1.91	0.53
34:BB:11:A:H8	34:BB:67:G:H21	1.54	0.53
49:BT:92:ARG:N	50:BU:11:GLN:OE1	2.42	0.53
22:AY:2:G:N3	22:AY:2:G:C2'	2.64	0.53
22:AY:14:G:O2'	22:AY:15:A:C2	2.58	0.53
33:BA:2871:G:OP1	48:BS:55:GLY:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BK:19:ASN:H	41:BK:20:PRO:HD2	1.72	0.53
1:AA:692:G:H1	1:AA:716:U:H3	1.56	0.52
24:B0:25:SER:HG	33:BA:2109:G:HO2'	1.54	0.52
33:BA:2351:A:O2'	33:BA:2352:G:OP1	2.25	0.52
35:BD:182:ARG:HG3	35:BD:269:PHE:HB3	1.91	0.52
2:AB:35:ARG:O	2:AB:37:GLY:N	2.42	0.52
33:BA:1524:A:H2'	33:BA:1525:G:C8	2.44	0.52
35:BD:145:GLU:HB2	35:BD:188:CYS:SG	2.49	0.52
37:BF:186:VAL:HG13	37:BF:192:LEU:HD21	1.91	0.52
50:BU:90:GLN:OE1	50:BU:91:PRO:HD2	2.09	0.52
22:AY:10:U:OP2	22:AY:10:U:H6	1.93	0.52
24:B0:43:LYS:O	24:B0:44:PRO:C	2.50	0.52
33:BA:1455:C:O2'	33:BA:1456:A:OP1	2.27	0.52
41:BK:10:LYS:HE2	41:BK:57:GLU:HG2	1.91	0.52
46:BQ:17:LEU:HD21	46:BQ:39:GLU:OE2	2.10	0.52
11:AK:39:THR:C	11:AK:41:GLY:HA2	2.35	0.52
22:AY:8:G:C3'	22:AY:9:A:H8	2.21	0.52
30:B6:34:ARG:HG3	30:B6:42:LEU:HD13	1.91	0.52
33:BA:2324:C:H41	47:BR:17:ARG:HH12	1.58	0.52
36:BE:201:THR:HG22	36:BE:203:LYS:HG3	1.91	0.52
37:BF:62:ARG:O	37:BF:78:ILE:CD1	2.58	0.52
37:BF:67:GLN:NE2	37:BF:74:ARG:CG	2.71	0.52
37:BF:153:LEU:HB2	37:BF:192:LEU:HB2	1.92	0.52
41:BK:99:THR:HG22	41:BK:138:VAL:HB	1.90	0.52
1:AA:495:U:H2'	1:AA:496:A:H8	1.74	0.52
21:AX:17:U:OP1	21:AX:60:U:O2'	2.22	0.52
37:BF:80:SER:CB	37:BF:83:TRP:HD1	2.10	0.52
51:BV:88:ARG:CB	51:BV:92:ARG:HB2	2.39	0.52
1:AA:343:C:H2'	1:AA:344:A:C8	2.45	0.52
33:BA:1093:G:H21	33:BA:1157:A:H62	1.57	0.52
33:BA:1130:A:H4'	40:BJ:55:TYR:HA	1.91	0.52
33:BA:2160:U:H5'	33:BA:2161:G:H5''	1.92	0.52
33:BA:2187:A:O2'	33:BA:2188:G:O4'	2.28	0.52
1:AA:960:U:H3	1:AA:1240:G:H1	1.57	0.52
1:AA:1335:U:H2'	1:AA:1336:G:H8	1.74	0.52
27:B3:12:ALA:H	27:B3:25:GLY:HA2	1.75	0.52
33:BA:1039:G:OP1	49:BT:50:ARG:NH2	2.42	0.52
34:BB:38:U:O2'	34:BB:39:A:OP1	2.27	0.52
37:BF:151:LYS:HG2	37:BF:172:GLY:HA2	1.89	0.52
1:AA:842:U:O2'	1:AA:843:U:OP1	2.26	0.52
22:AY:5:A:C5	22:AY:6:A:N7	2.78	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AY:5:A:N3	22:AY:6:A:C1'	2.72	0.52
33:BA:78:U:H3	33:BA:107:G:H1	1.56	0.52
33:BA:2008:C:H2'	33:BA:2009:G:H5''	1.92	0.52
36:BE:114:SER:HB3	36:BE:169:ILE:HD12	1.92	0.52
1:AA:1545:C:H2'	1:AA:1545:C:O2	2.09	0.52
18:AR:16:CYS:H	18:AR:51:GLY:HA3	1.75	0.52
33:BA:617:G:N1	33:BA:2060:A:OP1	2.35	0.52
1:AA:778:G:H4'	1:AA:1523:A:H4'	1.92	0.52
33:BA:732:A:H1'	33:BA:735:U:H3	1.74	0.52
33:BA:1133:G:H1	33:BA:1148:C:H42	1.58	0.52
33:BA:2816:C:H1'	36:BE:64:PRO:HB3	1.91	0.52
34:BB:101:U:H2'	34:BB:102:A:H8	1.75	0.52
36:BE:8:ARG:NH1	36:BE:197:LYS:O	2.42	0.52
38:BG:29:PRO:HA	38:BG:159:THR:HB	1.92	0.52
49:BT:91:ASN:HD22	49:BT:109:LEU:HD21	1.75	0.52
22:AY:10:U:C1'	22:AY:11:G:P	2.98	0.51
33:BA:573:C:OP2	33:BA:2808:U:N3	2.37	0.51
33:BA:644:G:N2	33:BA:650:U:OP1	2.43	0.51
33:BA:1013:U:O4	33:BA:1014:A:N6	2.43	0.51
36:BE:11:GLY:HA3	48:BS:8:ILE:HD11	1.92	0.51
1:AA:1549:C:N3	1:AA:1550:U:C5	2.78	0.51
27:B3:14:VAL:HB	27:B3:22:PHE:HB2	1.92	0.51
33:BA:831:U:C5	33:BA:840:A:H2	2.27	0.51
33:BA:1202:A:O4'	49:BT:51:ARG:NH1	2.43	0.51
33:BA:1873:U:H5''	35:BD:258:LYS:HG2	1.93	0.51
33:BA:1887:G:N2	33:BA:1912:G:O2'	2.40	0.51
43:BN:91:LYS:HE2	43:BN:111:PHE:CE1	2.45	0.51
45:BP:39:ALA:HB2	45:BP:99:PRO:HD3	1.91	0.51
53:BX:82:GLY:N	53:BX:93:VAL:O	2.37	0.51
21:AX:35:U:H5'	21:AX:35:U:C6	2.45	0.51
22:AY:11:G:HO2'	22:AY:12:A:P	2.33	0.51
33:BA:89:U:H3'	33:BA:90:A:H8	1.75	0.51
33:BA:430:C:O2	33:BA:438:A:N6	2.43	0.51
33:BA:854:U:H5'	33:BA:2474:G:H4'	1.91	0.51
33:BA:998:G:H21	33:BA:2296:A:H2	1.57	0.51
38:BG:41:GLY:O	38:BG:43:ALA:N	2.43	0.51
41:BK:24:VAL:HG13	41:BK:28:LEU:HD12	1.93	0.51
1:AA:901:U:H2'	1:AA:902:A:H8	1.74	0.51
1:AA:1274:C:H2'	1:AA:1275:G:H8	1.74	0.51
46:BQ:21:THR:HG22	46:BQ:44:VAL:HG22	1.91	0.51
1:AA:988:A:O2'	1:AA:1330:U:O4	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:343:A:C2	33:BA:377:G:O2'	2.61	0.51
33:BA:527:A:O2'	53:BX:42:LYS:O	2.29	0.51
33:BA:2071:A:H62	42:BM:117:ARG:HH12	1.59	0.51
33:BA:2140:U:OP2	33:BA:2174:C:N4	2.43	0.51
33:BA:2713:U:OP2	48:BS:54:ARG:NH1	2.42	0.51
35:BD:78:VAL:HG22	35:BD:94:ILE:HG12	1.93	0.51
35:BD:124:ILE:HG23	35:BD:192:ILE:HD13	1.91	0.51
49:BT:92:ARG:HG3	49:BT:94:MET:HG2	1.91	0.51
33:BA:199:A:H62	33:BA:878:G:H21	1.56	0.51
33:BA:275:A:H62	33:BA:296:G:H21	1.59	0.51
33:BA:1434:A:H4'	33:BA:1435:U:OP1	2.10	0.51
33:BA:2334:U:H3	38:BG:151:GLY:HA3	1.75	0.51
33:BA:2786:A:H3'	33:BA:2787:A:H5''	1.93	0.51
22:AY:5:A:C2'	22:AY:6:A:H5''	2.36	0.51
31:B7:24:ARG:HB2	44:BO:61:LEU:HD13	1.93	0.51
33:BA:106:G:H2'	33:BA:107:G:C8	2.46	0.51
33:BA:365:U:C6	37:BF:165:LEU:HD13	2.46	0.51
33:BA:1527:C:O2'	33:BA:1528:U:OP1	2.27	0.51
33:BA:1901:A:O2'	33:BA:1902:G:O5'	2.28	0.51
33:BA:2766:G:H1	33:BA:2796:C:N4	2.08	0.51
51:BV:86:ARG:HG2	51:BV:87:PRO:HD2	1.93	0.51
52:BW:59:TYR:HE2	52:BW:78:LYS:HE3	1.75	0.51
1:AA:1550:U:C2	22:AY:4:G:C2	2.98	0.51
33:BA:792:G:N2	33:BA:800:G:C6	2.79	0.51
53:BX:2:HIS:HD2	53:BX:81:VAL:HG21	1.76	0.51
33:BA:934:U:H4'	33:BA:935:A:C8	2.44	0.51
33:BA:1581:A:C5	33:BA:1584:U:O2	2.63	0.51
43:BN:40:VAL:HG22	43:BN:59:LYS:HG2	1.91	0.51
51:BV:40:PRO:O	51:BV:44:SER:OG	2.27	0.51
1:AA:154:C:H42	1:AA:165:G:H1	1.58	0.51
21:AX:72:C:H6	21:AX:72:C:C5'	2.17	0.51
33:BA:793:U:H5'	33:BA:795:G:C1'	2.41	0.51
35:BD:145:GLU:HA	35:BD:152:GLY:HA2	1.93	0.51
1:AA:370:G:N2	1:AA:373:U:OP2	2.32	0.50
33:BA:2719:A:C2	46:BQ:17:LEU:CD1	2.93	0.50
35:BD:53:HIS:HA	35:BD:217:ARG:HD2	1.93	0.50
41:BK:8:VAL:HG22	41:BK:59:SER:HA	1.92	0.50
42:BM:77:ARG:HH12	42:BM:88:ARG:HE	1.56	0.50
47:BR:79:GLU:HG2	47:BR:83:LYS:HE3	1.93	0.50
50:BU:89:ARG:O	50:BU:89:ARG:HG3	2.10	0.50
1:AA:683:G:H2'	1:AA:684:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1153:G:H21	1:AA:1155:A:H62	1.57	0.50
33:BA:526:A:H1'	33:BA:527:A:H5''	1.93	0.50
33:BA:1629:C:N4	33:BA:1630:G:O6	2.45	0.50
33:BA:2785:U:C4	33:BA:2787:A:N7	2.79	0.50
33:BA:2794:A:OP2	33:BA:2795:G:N2	2.42	0.50
33:BA:2799:C:C5'	33:BA:2800:C:OP2	2.59	0.50
37:BF:62:ARG:O	37:BF:78:ILE:HD11	2.11	0.50
39:BH:104:LEU:HD22	39:BH:124:ILE:HG21	1.92	0.50
1:AA:1314:G:H21	1:AA:1341:A:H2	1.59	0.50
1:AA:1367:U:OP1	14:AN:35:ARG:N	2.43	0.50
33:BA:1377:G:H5''	52:BW:14:THR:HG22	1.91	0.50
33:BA:2876:A:O3'	46:BQ:60:ARG:NH1	2.45	0.50
36:BE:146:MET:HE1	36:BE:160:LEU:HD21	1.93	0.50
51:BV:41:ARG:HG3	51:BV:43:ALA:H	1.77	0.50
1:AA:317:G:H2'	1:AA:318:G:H8	1.76	0.50
1:AA:596:G:N2	1:AA:763:C:OP2	2.37	0.50
26:B2:50:VAL:HG12	26:B2:53:LEU:HB3	1.92	0.50
33:BA:248:G:OP2	44:BO:67:THR:OG1	2.24	0.50
33:BA:338:G:H2'	33:BA:339:A:H8	1.76	0.50
33:BA:1631:A:H4'	33:BA:1632:G:H4'	1.93	0.50
33:BA:2738:G:H5''	46:BQ:18:ARG:HH22	1.76	0.50
33:BA:2785:U:O4	33:BA:2787:A:N7	2.45	0.50
33:BA:2815:U:OP1	36:BE:71:LYS:NZ	2.44	0.50
39:BH:13:SER:CB	39:BH:14:ASP:HA	2.35	0.50
1:AA:1237:C:H2'	1:AA:1238:A:H8	1.76	0.50
33:BA:350:U:H4'	33:BA:1251:U:C5	2.45	0.50
33:BA:785:C:N4	33:BA:805:G:N1	2.49	0.50
33:BA:1365:U:O4	33:BA:1692:U:O2'	2.22	0.50
36:BE:126:HIS:CE1	36:BE:159:LEU:HD22	2.46	0.50
38:BG:29:PRO:HB2	38:BG:169:LEU:HD22	1.93	0.50
45:BP:36:ALA:HB2	45:BP:103:LEU:HD11	1.94	0.50
46:BQ:17:LEU:HD13	46:BQ:43:VAL:HG21	1.94	0.50
1:AA:1058:G:H2'	1:AA:1060:G:H8	1.77	0.50
33:BA:1174:A:N6	33:BA:2547:A:N6	2.60	0.50
47:BR:32:ASN:HA	47:BR:96:ASP:HB2	1.92	0.50
29:B5:30:VAL:HG12	29:B5:47:GLU:HB2	1.94	0.50
33:BA:1432:A:O2'	33:BA:1433:U:H5'	2.12	0.50
35:BD:205:ILE:HG23	35:BD:210:ARG:HB2	1.94	0.50
39:BH:58:ASP:O	39:BH:63:ARG:NE	2.44	0.50
53:BX:77:GLU:OE1	53:BX:96:LYS:NZ	2.39	0.50
1:AA:62:A:N6	1:AA:108:C:N3	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1265:C:O2'	1:AA:1287:C:N4	2.45	0.50
25:B1:40:THR:HA	25:B1:43:ILE:HD12	1.93	0.50
33:BA:1339:A:H4'	33:BA:1340:A:O5'	2.11	0.50
33:BA:1658:G:C2	33:BA:1664:G:C6	3.00	0.50
33:BA:2488:A:OP2	33:BA:2489:U:OP2	2.30	0.50
33:BA:2629:A:O2'	33:BA:2630:C:H5'	2.12	0.50
40:BJ:27:ILE:O	40:BJ:83:ALA:N	2.45	0.50
45:BP:103:LEU:HD13	45:BP:125:LEU:HD13	1.94	0.50
29:B5:7:LEU:HB2	29:B5:17:TYR:HB2	1.93	0.50
36:BE:16:PHE:O	48:BS:15:GLN:NE2	2.45	0.50
37:BF:53:ASN:OD1	37:BF:54:ARG:N	2.45	0.50
1:AA:630:A:N6	1:AA:631:A:N6	2.60	0.49
33:BA:2357:A:H2'	33:BA:2358:A:C8	2.47	0.49
33:BA:2382:G:N2	54:BZ:42:GLY:O	2.43	0.49
35:BD:145:GLU:HG2	35:BD:151:GLY:C	2.37	0.49
53:BX:49:GLN:N	53:BX:50:ALA:HA	2.27	0.49
31:B7:9:GLY:O	31:B7:13:ARG:HG2	2.12	0.49
33:BA:721:G:H1'	37:BF:74:ARG:HD2	1.94	0.49
33:BA:997:C:H2'	33:BA:998:G:H8	1.77	0.49
36:BE:110:VAL:HG11	36:BE:192:VAL:HG13	1.92	0.49
37:BF:65:TRP:HZ2	37:BF:75:GLN:HG3	1.77	0.49
1:AA:439:A:H2'	1:AA:440:A:H8	1.76	0.49
27:B3:56:VAL:HG11	27:B3:60:ASN:HD22	1.77	0.49
31:B7:21:LYS:HD2	31:B7:49:VAL:HG11	1.94	0.49
33:BA:69:C:O2	33:BA:73:A:O2'	2.30	0.49
33:BA:2009:G:H3'	33:BA:2010:A:H5''	1.93	0.49
34:BB:52:G:H21	38:BG:26:MET:HE1	1.76	0.49
39:BH:153:ARG:HG2	39:BH:162:GLY:HA3	1.93	0.49
48:BS:55:GLY:HA2	48:BS:60:GLU:HG2	1.93	0.49
50:BU:79:LYS:C	50:BU:80:LYS:CG	2.84	0.49
53:BX:10:MET:HG2	53:BX:71:LEU:HD11	1.93	0.49
12:AL:26:LYS:N	12:AL:27:GLY:HA2	2.28	0.49
22:AY:1:U:C3'	22:AY:2:G:H1'	2.42	0.49
22:AY:1:U:O3'	22:AY:2:G:H4'	2.13	0.49
24:B0:45:LYS:HE3	24:B0:46:LYS:HE2	1.92	0.49
33:BA:364:A:O2'	33:BA:366:A:H2'	2.12	0.49
33:BA:648:G:O2'	33:BA:649:G:O5'	2.27	0.49
1:AA:95:U:H2'	1:AA:96:G:C8	2.48	0.49
22:AY:6:A:H2'	22:AY:7:C:C6	2.47	0.49
24:B0:39:LEU:N	24:B0:39:LEU:CD1	2.76	0.49
28:B4:18:THR:HG22	33:BA:15:G:H4'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:568:G:O2'	33:BA:587:C:O2'	2.28	0.49
33:BA:1659:A:N6	51:BV:88:ARG:O	2.44	0.49
1:AA:1328:A:O2'	1:AA:1332:G:N7	2.42	0.49
14:AN:47:LEU:O	14:AN:51:GLY:N	2.46	0.49
28:B4:27:MET:HE2	28:B4:36:MET:HE3	1.95	0.49
33:BA:461:C:H2'	33:BA:462:A:C8	2.47	0.49
33:BA:910:A:N6	33:BA:911:G:O6	2.46	0.49
33:BA:970:A:H2'	33:BA:971:A:C8	2.48	0.49
35:BD:159:GLY:HA2	35:BD:198:GLU:HG2	1.94	0.49
40:BJ:18:LYS:HA	40:BJ:21:GLU:HB2	1.95	0.49
46:BQ:31:GLU:HG2	46:BQ:116:ILE:HG12	1.94	0.49
46:BQ:106:PRO:HA	46:BQ:113:PRO:HA	1.95	0.49
50:BU:79:LYS:O	50:BU:80:LYS:HG2	2.13	0.49
52:BW:29:GLU:HA	52:BW:78:LYS:HA	1.94	0.49
1:AA:616:A:OP1	1:AA:640:G:N2	2.37	0.49
19:AS:81:LYS:H	19:AS:82:GLY:HA2	1.77	0.49
33:BA:1929:A:H1'	33:BA:1999:A:H2'	1.94	0.49
35:BD:243:ARG:HH12	35:BD:247:MET:HE3	1.77	0.49
38:BG:39:GLY:O	38:BG:41:GLY:N	2.40	0.49
44:BO:117:LEU:HA	44:BO:118:GLU:CB	2.37	0.49
47:BR:58:THR:HG22	47:BR:77:VAL:HG21	1.95	0.49
53:BX:48:THR:HA	53:BX:49:GLN:HB2	1.95	0.49
54:BZ:79:ARG:HG2	54:BZ:81:GLY:H	1.77	0.49
1:AA:437:U:O2	1:AA:439:A:N7	2.45	0.49
33:BA:1295:U:C5	37:BF:72:ARG:O	2.64	0.49
37:BF:65:TRP:CZ2	37:BF:75:GLN:HB3	2.43	0.49
39:BH:96:ARG:HG3	39:BH:107:ASN:HD22	1.78	0.49
40:BJ:26:ILE:HD13	40:BJ:116:LYS:HE3	1.94	0.49
42:BM:69:LYS:HA	42:BM:72:ASP:HB3	1.94	0.49
50:BU:73:VAL:N	50:BU:86:GLN:O	2.46	0.49
1:AA:1385:U:H2'	1:AA:1386:A:H8	1.76	0.49
30:B6:34:ARG:NH2	33:BA:513:A:OP1	2.33	0.49
33:BA:565:U:H4'	51:BV:25:ARG:HH22	1.77	0.49
33:BA:934:U:O2'	33:BA:935:A:O5'	2.23	0.49
33:BA:1452:C:H2'	33:BA:1453:A:H8	1.78	0.49
33:BA:2609:U:H5'	36:BE:137:SER:HA	1.94	0.49
33:BA:2728:U:H3	33:BA:2737:G:H1	1.59	0.49
33:BA:2761:G:H5''	33:BA:2762:A:C8	2.47	0.49
33:BA:2793:A:N6	33:BA:2795:G:N7	2.61	0.49
35:BD:167:LYS:HB2	35:BD:172:VAL:HG22	1.95	0.49
50:BU:73:VAL:HB	50:BU:86:GLN:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:666:U:H3	1:AA:758:A:N6	2.10	0.49
33:BA:852:G:O4'	44:BO:38:GLN:NE2	2.46	0.49
33:BA:1250:G:C4'	33:BA:1251:U:H5''	2.42	0.49
33:BA:2342:C:H1'	38:BG:37:ASN:HD21	1.78	0.49
44:BO:91:VAL:HG21	44:BO:121:LEU:HD22	1.94	0.49
33:BA:1398:A:N7	33:BA:1411:U:O4	2.46	0.48
33:BA:2100:A:H2'	33:BA:2101:G:C8	2.48	0.48
33:BA:2670:A:H5''	42:BM:79:THR:HG22	1.95	0.48
35:BD:264:ASN:ND2	35:BD:266:SER:OG	2.46	0.48
42:BM:45:TYR:O	49:BT:64:ARG:NE	2.38	0.48
46:BQ:27:ASN:C	46:BQ:29:ARG:H	2.20	0.48
48:BS:29:LEU:HB3	48:BS:89:VAL:HG22	1.95	0.48
22:AY:13:G:H4'	22:AY:14:G:OP1	2.13	0.48
31:B7:60:GLN:NE2	33:BA:637:A:O2'	2.44	0.48
33:BA:588:C:N4	33:BA:589:G:C6	2.82	0.48
33:BA:2253:G:H4'	33:BA:2255:C:C2	2.48	0.48
33:BA:2540:U:O2'	36:BE:139:TYR:OH	2.25	0.48
35:BD:108:LYS:HE3	35:BD:194:GLN:HE21	1.77	0.48
33:BA:636:G:H1	33:BA:712:C:N4	2.10	0.48
33:BA:2605:G:O2'	33:BA:2608:C:OP2	2.30	0.48
49:BT:44:ASN:HB2	50:BU:76:TYR:CE2	2.47	0.48
22:AY:5:A:O2'	22:AY:6:A:O5'	2.23	0.48
29:B5:22:ASN:HD21	33:BA:2314:C:P	2.37	0.48
33:BA:795:G:C5	33:BA:797:A:C5	3.01	0.48
33:BA:1291:A:H5''	49:BT:13:ARG:NH2	2.29	0.48
33:BA:2856:G:OP1	36:BE:57:ARG:NH2	2.46	0.48
54:BZ:53:ILE:HG21	54:BZ:87:VAL:HG23	1.95	0.48
22:AY:8:G:C6	22:AY:9:A:N6	2.81	0.48
23:AZ:81:ASN:N	23:AZ:81:ASN:ND2	2.60	0.48
25:B1:11:THR:HA	25:B1:14:ILE:HD12	1.95	0.48
33:BA:113:U:O2'	52:BW:33:ARG:NH1	2.46	0.48
33:BA:1524:A:H2'	33:BA:1525:G:H8	1.78	0.48
35:BD:243:ARG:HH12	35:BD:247:MET:CE	2.26	0.48
36:BE:139:TYR:HA	36:BE:142:ARG:HH21	1.79	0.48
37:BF:64:PRO:HB2	37:BF:65:TRP:CE3	2.48	0.48
1:AA:126:G:O2'	1:AA:127:U:OP1	2.23	0.48
24:B0:42:GLY:HA3	24:B0:43:LYS:HD3	1.95	0.48
33:BA:52:A:H62	33:BA:118:A:H62	1.61	0.48
33:BA:364:A:H4'	33:BA:366:A:H8	1.73	0.48
33:BA:1128:U:OP1	41:BK:119:ALA:N	2.43	0.48
33:BA:1292:G:H1	49:BT:37:GLN:HE21	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2082:G:H4'	36:BE:152:ASN:HD22	1.79	0.48
1:AA:766:U:H2'	1:AA:767:G:O4'	2.14	0.48
1:AA:1227:C:H2'	1:AA:1228:U:C6	2.47	0.48
27:B3:9:PHE:CZ	38:BG:62:GLY:HA3	2.49	0.48
33:BA:84:A:H3'	53:BX:4:LYS:HB2	1.95	0.48
33:BA:1537:G:H2'	33:BA:1538:G:C8	2.49	0.48
33:BA:1894:U:O2'	33:BA:1904:G:N2	2.45	0.48
33:BA:2572:G:H21	33:BA:2675:C:H5''	1.79	0.48
1:AA:23:G:H2'	1:AA:24:G:C8	2.48	0.48
1:AA:843:U:H2'	1:AA:844:A:C8	2.48	0.48
29:B5:15:ARG:NH2	33:BA:2427:U:O2'	2.35	0.48
31:B7:20:GLY:HA2	31:B7:21:LYS:O	2.13	0.48
33:BA:83:G:H4'	33:BA:84:A:OP1	2.10	0.48
33:BA:1364:C:C2	51:BV:86:ARG:NH1	2.82	0.48
33:BA:1815:A:OP1	33:BA:2009:G:N2	2.45	0.48
49:BT:52:GLN:HA	49:BT:55:ARG:HG2	1.96	0.48
28:B4:13:LYS:O	28:B4:17:ARG:HG2	2.14	0.48
33:BA:681:C:O2'	33:BA:685:U:OP1	2.32	0.48
33:BA:1184:G:N3	42:BM:109:MET:HE1	2.29	0.48
33:BA:1353:C:N4	33:BA:1377:G:N1	2.43	0.48
36:BE:12:MET:SD	36:BE:26:THR:HG22	2.54	0.48
41:BK:15:ALA:CB	41:BK:46:THR:HG22	2.05	0.48
46:BQ:78:ASP:HB3	46:BQ:81:GLN:HG3	1.96	0.48
1:AA:547:U:H2'	1:AA:548:A:C8	2.49	0.48
1:AA:732:U:C2	22:AY:7:C:O2'	2.67	0.48
1:AA:1117:C:OP1	3:AC:172:VAL:N	2.47	0.48
1:AA:1469:C:H2'	1:AA:1470:A:H8	1.79	0.48
21:AX:23:A:H2'	21:AX:24:A:C8	2.48	0.48
21:AX:34:G:C6	21:AX:35:U:C5	3.01	0.48
22:AY:5:A:N1	22:AY:6:A:C4	2.82	0.48
33:BA:7:G:O6	33:BA:2919:A:N6	2.47	0.48
33:BA:1438:C:O2'	33:BA:1439:U:OP1	2.30	0.48
33:BA:2039:G:OP2	51:BV:41:ARG:NH1	2.47	0.48
33:BA:2540:U:HO2'	36:BE:139:TYR:HH	1.57	0.48
47:BR:69:GLY:O	47:BR:105:ARG:NH2	2.47	0.48
53:BX:48:THR:O	53:BX:52:PRO:HA	2.14	0.48
1:AA:956:A:H2'	1:AA:957:G:C8	2.49	0.47
1:AA:965:U:C4	1:AA:1234:A:N1	2.81	0.47
33:BA:1335:A:OP1	33:BA:2738:G:O2'	2.26	0.47
1:AA:404:A:O2'	1:AA:406:C:OP1	2.24	0.47
1:AA:421:G:N2	1:AA:436:G:H1'	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:528:G:H2'	33:BA:553:A:H62	1.78	0.47
33:BA:852:G:H5'	33:BA:853:C:H5	1.79	0.47
33:BA:1155:C:H41	40:BJ:59:MET:HE1	1.80	0.47
37:BF:65:TRP:CH2	37:BF:72:ARG:NH2	2.83	0.47
44:BO:20:GLY:HA2	44:BO:28:GLY:HA2	1.96	0.47
48:BS:100:LEU:HB3	48:BS:103:LEU:HD23	1.96	0.47
33:BA:128:C:H5'	33:BA:1644:C:O2'	2.15	0.47
33:BA:377:G:N3	33:BA:378:C:C6	2.82	0.47
33:BA:2522:U:O2'	45:BP:80:GLU:OE2	2.23	0.47
35:BD:53:HIS:HB2	35:BD:217:ARG:HB3	1.96	0.47
52:BW:9:LYS:HB2	52:BW:29:GLU:HB2	1.96	0.47
33:BA:1347:A:N6	33:BA:1651:G:H8	2.09	0.47
33:BA:2766:G:H2'	33:BA:2767:A:C8	2.50	0.47
1:AA:987:A:N6	1:AA:1233:U:O5'	2.48	0.47
21:AX:37:A:C2	22:AY:17:G:C6	3.03	0.47
31:B7:57:ARG:NH2	44:BO:51:GLU:OE1	2.40	0.47
33:BA:839:G:C4'	33:BA:840:A:C2	2.97	0.47
33:BA:1290:G:OP2	44:BO:21:ARG:NH1	2.47	0.47
37:BF:20:ASN:ND2	37:BF:203:GLU:OE1	2.46	0.47
21:AX:74:C:H5'	33:BA:2631:A:C5'	2.38	0.47
33:BA:875:U:H3	33:BA:876:A:N6	2.08	0.47
33:BA:1658:G:C6	33:BA:1664:G:O6	2.68	0.47
33:BA:2386:U:OP1	54:BZ:28:ARG:NH1	2.48	0.47
33:BA:2719:A:N1	46:BQ:39:GLU:OE2	2.47	0.47
33:BA:2853:C:H2'	33:BA:2854:A:H8	1.79	0.47
36:BE:176:ILE:HA	36:BE:188:ILE:HA	1.96	0.47
1:AA:643:C:H2'	1:AA:644:A:H8	1.80	0.47
1:AA:842:U:HO2'	1:AA:843:U:P	2.36	0.47
1:AA:1313:G:N2	1:AA:1342:A:H62	2.10	0.47
23:AZ:74:ILE:CA	51:BV:85:PHE:CD2	2.83	0.47
33:BA:874:U:H4'	33:BA:875:U:C6	2.50	0.47
33:BA:1969:U:OP1	33:BA:2632:G:N2	2.42	0.47
33:BA:2815:U:O2'	36:BE:64:PRO:O	2.27	0.47
36:BE:207:LYS:HA	36:BE:208:SER:HA	1.61	0.47
39:BH:3:ARG:HB2	39:BH:6:LYS:HE2	1.95	0.47
40:BJ:33:LEU:O	40:BJ:36:SER:OG	2.27	0.47
45:BP:41:TRP:HB3	45:BP:94:VAL:HG11	1.97	0.47
51:BV:92:ARG:HE	51:BV:92:ARG:CA	2.27	0.47
1:AA:413:U:H1'	1:AA:507:A:H2'	1.97	0.47
1:AA:1501:G:O2'	1:AA:1502:A:OP1	2.29	0.47
3:AC:57:GLU:O	3:AC:64:ASN:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:B6:34:ARG:CB	30:B6:42:LEU:HD13	2.45	0.47
33:BA:694:G:H2'	33:BA:695:G:H8	1.79	0.47
35:BD:132:LEU:HA	35:BD:135:ILE:HD12	1.96	0.47
39:BH:158:TYR:HA	39:BH:173:LYS:HB2	1.97	0.47
1:AA:848:G:H2'	1:AA:849:G:C8	2.50	0.47
1:AA:954:G:N1	1:AA:1347:G:OP2	2.32	0.47
1:AA:1066:U:H2'	1:AA:1067:G:H8	1.79	0.47
1:AA:1525:C:H2'	1:AA:1526:G:C8	2.50	0.47
22:AY:14:G:H2'	22:AY:15:A:C6	2.50	0.47
24:B0:40:VAL:CG1	24:B0:41:ASN:H	2.13	0.47
33:BA:1433:U:O2	33:BA:1433:U:H2'	2.14	0.47
33:BA:2669:G:H1	33:BA:2803:C:N4	2.08	0.47
33:BA:2834:A:N6	33:BA:2835:A:N6	2.63	0.47
37:BF:71:GLY:O	37:BF:72:ARG:HD2	2.15	0.47
51:BV:3:ALA:HB2	51:BV:58:ALA:HB2	1.96	0.47
1:AA:754:U:OP1	1:AA:861:U:O2'	2.29	0.47
1:AA:872:C:H1'	1:AA:884:G:H5''	1.96	0.47
24:B0:14:ALA:HA	24:B0:28:THR:HA	1.97	0.47
33:BA:304:G:H2'	33:BA:305:A:H8	1.80	0.47
35:BD:170:LYS:HA	35:BD:171:TYR:HA	1.74	0.47
42:BM:46:THR:O	42:BM:49:VAL:HG12	2.15	0.47
53:BX:97:SER:HA	53:BX:98:GLY:HA2	1.64	0.47
30:B6:34:ARG:HB3	30:B6:42:LEU:HD13	1.98	0.46
33:BA:269:G:H1'	33:BA:322:A:H2	1.79	0.46
33:BA:567:U:H2'	33:BA:568:G:H8	1.80	0.46
33:BA:678:A:H2'	33:BA:679:A:C8	2.49	0.46
33:BA:822:G:H4'	33:BA:823:G:C5'	2.45	0.46
33:BA:1656:C:O2'	33:BA:1657:C:C5'	2.58	0.46
37:BF:6:LEU:HD13	37:BF:7:TYR:N	2.30	0.46
1:AA:345:G:H2'	1:AA:346:A:C8	2.51	0.46
1:AA:1237:C:H2'	1:AA:1238:A:C8	2.50	0.46
31:B7:13:ARG:HD3	44:BO:63:LYS:HA	1.97	0.46
31:B7:57:ARG:HG3	31:B7:58:ILE:HG23	1.96	0.46
33:BA:1309:G:O2'	33:BA:1364:C:N4	2.47	0.46
35:BD:106:ALA:HA	35:BD:107:PRO:HD2	1.82	0.46
37:BF:67:GLN:HE22	37:BF:74:ARG:HB3	1.78	0.46
38:BG:68:THR:OG1	38:BG:85:ILE:O	2.32	0.46
42:BM:14:ARG:NH2	42:BM:50:ASP:OD2	2.45	0.46
42:BM:24:LYS:HE2	42:BM:143:LEU:HD22	1.97	0.46
48:BS:99:LYS:HB3	48:BS:101:TYR:CE2	2.50	0.46
52:BW:20:LEU:HB3	52:BW:25:LYS:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1068:G:H1	1:AA:1208:U:H3	1.61	0.46
22:AY:8:G:O6	22:AY:9:A:N6	2.49	0.46
29:B5:22:ASN:HD22	29:B5:25:ASN:HD22	1.64	0.46
30:B6:34:ARG:CB	30:B6:42:LEU:CD1	2.93	0.46
33:BA:106:G:H4'	33:BA:337:A:H5''	1.97	0.46
33:BA:337:A:O2'	33:BA:338:G:O4'	2.34	0.46
33:BA:675:C:N4	33:BA:676:G:O6	2.48	0.46
52:BW:12:VAL:HG21	52:BW:78:LYS:HE2	1.97	0.46
53:BX:87:ASP:CB	53:BX:88:GLY:CA	2.84	0.46
1:AA:343:C:H2'	1:AA:344:A:H8	1.81	0.46
28:B4:18:THR:O	28:B4:21:LYS:NZ	2.48	0.46
31:B7:54:ASP:OD2	33:BA:2388:C:O2'	2.25	0.46
33:BA:282:G:H1'	33:BA:283:G:C8	2.51	0.46
33:BA:1294:A:C3'	33:BA:1295:U:C5'	2.90	0.46
34:BB:98:G:H3'	34:BB:99:A:C8	2.51	0.46
35:BD:241:ILE:HD11	35:BD:246:PRO:HA	1.97	0.46
48:BS:50:VAL:HG22	48:BS:64:VAL:HG22	1.98	0.46
49:BT:60:LEU:O	49:BT:63:THR:OG1	2.30	0.46
21:AX:56:C:C5	38:BG:80:ARG:HD3	2.50	0.46
33:BA:275:A:H62	33:BA:296:G:N2	2.13	0.46
33:BA:734:C:H42	33:BA:834:C:H4'	1.81	0.46
33:BA:1251:U:O2	33:BA:1251:U:O2'	2.26	0.46
33:BA:1715:C:O2	33:BA:2022:U:O2'	2.23	0.46
33:BA:2335:U:H3'	33:BA:2336:G:H5''	1.97	0.46
38:BG:35:VAL:HG13	38:BG:88:LYS:HG3	1.97	0.46
46:BQ:47:MET:HE1	46:BQ:62:ALA:HA	1.96	0.46
1:AA:54:U:H2'	1:AA:55:A:C8	2.51	0.46
1:AA:243:C:H2'	1:AA:244:G:H8	1.80	0.46
33:BA:837:U:C3'	33:BA:837:U:C6	2.99	0.46
33:BA:2629:A:C2'	33:BA:2630:C:H5'	2.45	0.46
25:B1:40:THR:HG21	33:BA:61:A:H1'	1.97	0.46
33:BA:647:A:H4'	33:BA:648:G:O5'	2.15	0.46
33:BA:1015:G:N2	33:BA:1031:C:OP1	2.44	0.46
43:BN:52:VAL:HG22	43:BN:94:ARG:HH11	1.81	0.46
50:BU:77:LYS:HB2	50:BU:82:VAL:HB	1.97	0.46
53:BX:79:THR:HB	53:BX:95:LYS:H	1.80	0.46
1:AA:415:A:H2'	1:AA:416:G:C8	2.51	0.46
1:AA:848:G:O2'	1:AA:849:G:OP1	2.31	0.46
4:AD:25:GLU:C	4:AD:27:GLU:H	2.23	0.46
24:B0:37:ARG:CD	24:B0:45:LYS:HG3	2.33	0.46
33:BA:615:U:O5'	33:BA:2059:A:N6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BF:4:VAL:HG12	37:BF:5:ALA:N	2.30	0.46
37:BF:12:SER:HB2	37:BF:13:THR:HB	1.97	0.46
53:BX:48:THR:HB	53:BX:50:ALA:N	2.31	0.46
1:AA:510:C:O2	1:AA:558:C:O2'	2.33	0.46
1:AA:833:U:H2'	1:AA:834:G:H8	1.81	0.46
22:AY:8:G:H8	22:AY:8:G:O5'	1.99	0.46
22:AY:15:A:H2'	22:AY:16:A:H5''	1.98	0.46
33:BA:753:A:OP1	35:BD:7:LYS:NZ	2.45	0.46
33:BA:837:U:H3'	33:BA:837:U:C6	2.49	0.46
33:BA:1893:U:OP1	33:BA:2439:G:O2'	2.31	0.46
35:BD:253:PRO:HG2	35:BD:257:PHE:CG	2.50	0.46
45:BP:29:PHE:HB2	45:BP:105:GLU:OE1	2.16	0.46
1:AA:66:G:H4'	1:AA:67:A:H5''	1.98	0.46
1:AA:98:U:O2'	1:AA:99:A:OP1	2.24	0.46
1:AA:1210:A:H4'	1:AA:1211:U:O5'	2.16	0.46
24:B0:38:ILE:C	24:B0:39:LEU:HD12	2.41	0.46
25:B1:31:GLN:O	25:B1:35:GLY:N	2.44	0.46
33:BA:9:U:H2'	33:BA:10:A:H8	1.81	0.46
33:BA:229:A:O2'	33:BA:230:A:OP1	2.33	0.46
35:BD:243:ARG:NH2	35:BD:247:MET:CB	2.59	0.46
47:BR:35:ARG:HA	47:BR:40:ILE:HG13	1.98	0.46
48:BS:38:GLY:HA2	48:BS:39:ASN:HA	1.56	0.46
49:BT:89:GLU:HG2	50:BU:48:VAL:HG13	1.98	0.46
54:BZ:75:VAL:HG22	54:BZ:89:VAL:HG22	1.98	0.46
23:AZ:89:ASP:HB2	33:BA:2614:U:C2	2.51	0.45
33:BA:1788:A:H5''	33:BA:2744:C:H1'	1.97	0.45
33:BA:2009:G:O6	33:BA:2011:U:O4	2.33	0.45
33:BA:2777:A:H4'	39:BH:67:GLY:HA3	1.97	0.45
47:BR:71:THR:OG1	47:BR:72:SER:N	2.45	0.45
49:BT:69:ALA:HB2	49:BT:79:LEU:HD22	1.98	0.45
9:AI:107:ASP:O	9:AI:109:ARG:N	2.47	0.45
21:AX:72:C:N4	21:AX:73:G:O6	2.49	0.45
33:BA:626:G:H2'	33:BA:627:G:C8	2.51	0.45
33:BA:721:G:C1'	37:BF:74:ARG:HD2	2.46	0.45
33:BA:789:C:H2'	33:BA:790:A:C8	2.51	0.45
33:BA:928:G:H2'	33:BA:929:G:C8	2.52	0.45
33:BA:1104:U:H2'	33:BA:1105:G:C8	2.51	0.45
33:BA:1983:G:O2'	33:BA:1985:U:O4	2.29	0.45
33:BA:2144:G:O2'	33:BA:2194:G:O6	2.33	0.45
33:BA:2648:U:H4'	36:BE:156:LYS:HA	1.97	0.45
35:BD:58:HIS:HB2	35:BD:213:TRP:HE3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BD:94:ILE:HD12	35:BD:104:ILE:HD12	1.98	0.45
36:BE:15:VAL:HB	36:BE:25:VAL:HG21	1.97	0.45
36:BE:140:HIS:O	36:BE:142:ARG:N	2.46	0.45
36:BE:185:LEU:HD13	48:BS:11:ILE:HD11	1.99	0.45
47:BR:90:ILE:HA	47:BR:91:SER:HB3	1.98	0.45
25:B1:26:PHE:HE1	52:BW:8:LEU:HB2	1.81	0.45
33:BA:338:G:H2'	33:BA:339:A:C8	2.51	0.45
33:BA:1829:C:P	35:BD:182:ARG:HH22	2.40	0.45
34:BB:11:A:H62	34:BB:68:C:H5'	1.81	0.45
37:BF:67:GLN:HE22	37:BF:74:ARG:CA	2.28	0.45
39:BH:5:GLY:HA2	39:BH:70:ARG:HD3	1.98	0.45
44:BO:106:ASN:O	44:BO:108:GLY:N	2.47	0.45
21:AX:34:G:H2'	21:AX:34:G:N3	2.32	0.45
25:B1:17:LYS:HB3	25:B1:53:MET:HE1	1.99	0.45
33:BA:2859:G:H21	33:BA:2908:A:H62	1.64	0.45
42:BM:77:ARG:NH2	42:BM:88:ARG:HH21	2.14	0.45
43:BN:64:ARG:HH12	48:BS:71:VAL:HG21	1.81	0.45
46:BQ:104:LEU:HD13	46:BQ:105:GLY:N	2.32	0.45
47:BR:91:SER:HG	47:BR:92:ASP:H	1.61	0.45
1:AA:224:U:H2'	1:AA:225:A:C8	2.52	0.45
1:AA:960:U:H2'	1:AA:961:G:H8	1.81	0.45
1:AA:1491:U:H2'	1:AA:1492:G:C8	2.52	0.45
22:AY:1:U:H3'	22:AY:2:G:H1'	1.97	0.45
22:AY:8:G:O5'	22:AY:8:G:C8	2.70	0.45
25:B1:38:GLU:OE2	33:BA:94:A:O2'	2.28	0.45
30:B6:3:ARG:NH1	33:BA:836:A:N1	2.65	0.45
33:BA:377:G:C2	33:BA:378:C:C4	3.05	0.45
33:BA:1242:U:H2'	33:BA:1243:A:C8	2.51	0.45
33:BA:1501:U:O2'	33:BA:2878:U:OP1	2.32	0.45
33:BA:2472:C:H2'	33:BA:2473:G:C8	2.50	0.45
35:BD:177:ASN:OD1	35:BD:178:SER:N	2.48	0.45
35:BD:247:MET:HE2	35:BD:251:GLY:O	2.16	0.45
40:BJ:89:VAL:HG12	40:BJ:90:VAL:H	1.81	0.45
43:BN:78:SER:OG	48:BS:74:GLU:OE1	2.34	0.45
45:BP:119:ARG:O	45:BP:122:SER:OG	2.22	0.45
52:BW:27:THR:HG22	52:BW:80:ILE:HG13	1.98	0.45
29:B5:14:GLU:O	29:B5:16:ASN:ND2	2.49	0.45
33:BA:224:A:H1'	33:BA:236:A:H1'	1.99	0.45
33:BA:677:A:OP1	44:BO:64:ARG:NH2	2.49	0.45
33:BA:938:G:H2'	33:BA:939:G:H8	1.81	0.45
33:BA:1478:G:H2'	33:BA:1479:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1754:U:H2'	33:BA:1755:C:C6	2.52	0.45
33:BA:2516:G:H2'	33:BA:2517:A:C8	2.52	0.45
33:BA:2784:C:H4'	33:BA:2785:U:OP1	2.17	0.45
34:BB:39:A:H3'	34:BB:40:C:H5'	1.98	0.45
36:BE:123:ILE:HD11	36:BE:141:ARG:HA	1.98	0.45
39:BH:166:GLU:HA	39:BH:167:GLY:HA2	1.50	0.45
1:AA:956:A:H2'	1:AA:957:G:H8	1.82	0.45
1:AA:960:U:H2'	1:AA:961:G:C8	2.51	0.45
1:AA:1074:G:H21	1:AA:1199:G:H1'	1.80	0.45
1:AA:1175:G:O2'	1:AA:1178:A:N6	2.47	0.45
33:BA:1108:G:H21	33:BA:1123:A:H62	1.64	0.45
33:BA:1613:C:H2'	33:BA:1614:A:H2'	1.97	0.45
33:BA:2009:G:C4	33:BA:2011:U:C6	3.04	0.45
33:BA:2835:A:H5''	36:BE:63:LYS:HD2	1.97	0.45
34:BB:76:A:H62	34:BB:96:G:N2	2.07	0.45
35:BD:40:LYS:O	35:BD:43:ARG:HG2	2.16	0.45
1:AA:104:C:H2'	1:AA:105:G:C8	2.52	0.45
1:AA:1246:C:O2'	1:AA:1309:G:N2	2.40	0.45
1:AA:1400:U:H2'	1:AA:1401:G:C8	2.52	0.45
1:AA:1421:C:H2'	1:AA:1422:A:C8	2.51	0.45
33:BA:839:G:O4'	33:BA:840:A:C2	2.70	0.45
33:BA:1599:U:H2'	33:BA:1600:G:H5'	1.98	0.45
33:BA:2330:A:H61	33:BA:2344:U:H3	1.64	0.45
33:BA:2332:G:O2'	38:BG:129:THR:OG1	2.24	0.45
42:BM:40:LYS:O	49:BT:67:ALA:HB2	2.17	0.45
49:BT:49:ASP:O	49:BT:53:LYS:N	2.47	0.45
1:AA:1013:G:H2'	1:AA:1014:A:H4'	1.99	0.45
31:B7:40:GLN:O	31:B7:44:LEU:HG	2.17	0.45
33:BA:719:C:H5'	33:BA:848:G:H22	1.82	0.45
33:BA:1298:C:H2'	33:BA:1299:G:C8	2.52	0.45
33:BA:2100:A:H2'	33:BA:2101:G:H8	1.81	0.45
33:BA:2267:G:O2'	33:BA:2269:C:OP2	2.27	0.45
33:BA:2923:A:H2'	33:BA:2924:A:C8	2.52	0.45
37:BF:46:GLN:HG2	37:BF:48:THR:HG23	1.99	0.45
38:BG:67:VAL:HB	38:BG:84:PRO:HB2	1.99	0.45
44:BO:117:LEU:HD13	44:BO:119:LYS:O	2.17	0.45
1:AA:73:C:H2'	1:AA:74:A:C8	2.52	0.45
1:AA:307:G:N2	1:AA:574:U:O2	2.50	0.45
1:AA:974:A:H5''	1:AA:1207:A:O3'	2.17	0.45
1:AA:1544:A:H8	1:AA:1544:A:C5'	2.29	0.45
33:BA:356:G:H2'	33:BA:357:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1187:U:OP2	42:BM:66:THR:OG1	2.35	0.45
33:BA:1219:C:H3'	33:BA:1220:G:H4'	1.98	0.45
33:BA:1755:C:H2'	33:BA:1756:U:C6	2.52	0.45
33:BA:2349:A:O2'	33:BA:2362:A:N6	2.50	0.45
33:BA:2757:U:O2	36:BE:191:ASN:ND2	2.49	0.45
34:BB:30:C:H42	34:BB:48:G:H1	1.63	0.45
35:BD:81:VAL:HA	35:BD:92:ALA:HA	1.99	0.45
49:BT:37:GLN:O	49:BT:41:LYS:HG2	2.17	0.45
49:BT:42:SER:O	49:BT:46:ALA:N	2.50	0.45
49:BT:92:ARG:NH1	49:BT:93:LYS:HB2	2.32	0.45
50:BU:4:ILE:O	50:BU:38:VAL:HG13	2.17	0.45
1:AA:1111:A:H4'	1:AA:1112:A:O5'	2.18	0.44
1:AA:1257:A:H2	1:AA:1298:A:H62	1.65	0.44
1:AA:1317:C:OP1	13:AM:97:VAL:N	2.48	0.44
1:AA:1495:U:H2'	1:AA:1496:G:H8	1.81	0.44
33:BA:17:G:H4'	49:BT:25:PHE:HE1	1.83	0.44
33:BA:217:G:O2'	33:BA:219:A:O2'	2.32	0.44
33:BA:825:G:O6	33:BA:833:C:N3	2.50	0.44
33:BA:1848:A:H5''	35:BD:160:THR:HG21	1.99	0.44
33:BA:2718:U:H5'	33:BA:2897:G:H22	1.82	0.44
37:BF:71:GLY:O	37:BF:72:ARG:HG2	2.16	0.44
40:BJ:4:ALA:O	40:BJ:7:THR:OG1	2.25	0.44
45:BP:67:LYS:HD2	45:BP:105:GLU:OE2	2.17	0.44
53:BX:86:GLU:HG3	53:BX:87:ASP:N	2.31	0.44
1:AA:523:C:H2'	1:AA:524:G:H8	1.83	0.44
22:AY:13:G:C8	22:AY:13:G:OP2	2.70	0.44
27:B3:55:ARG:HA	27:B3:56:VAL:HA	1.55	0.44
33:BA:609:C:C5	50:BU:79:LYS:HE2	2.51	0.44
34:BB:98:G:H3'	34:BB:99:A:H8	1.82	0.44
37:BF:71:GLY:C	37:BF:72:ARG:HG2	2.41	0.44
42:BM:5:PRO:HB3	49:BT:61:TRP:HE1	1.82	0.44
42:BM:14:ARG:NH2	42:BM:50:ASP:O	2.50	0.44
1:AA:328:G:H2'	1:AA:329:A:C8	2.52	0.44
22:AY:13:G:O2'	22:AY:14:G:C6	2.70	0.44
33:BA:377:G:C2'	33:BA:378:C:H6	2.11	0.44
33:BA:1003:A:N1	33:BA:2487:U:H4'	2.32	0.44
33:BA:1364:C:N3	51:BV:86:ARG:CZ	2.79	0.44
33:BA:1438:C:OP1	52:BW:82:LYS:NZ	2.40	0.44
40:BJ:58:THR:HG21	40:BJ:82:ILE:O	2.18	0.44
45:BP:57:TYR:CE2	45:BP:113:VAL:HG13	2.53	0.44
47:BR:26:ALA:C	47:BR:28:ARG:H	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BX:32:ARG:HB3	53:BX:62:PRO:HB2	1.99	0.44
1:AA:58:U:H2'	1:AA:59:G:C8	2.53	0.44
1:AA:716:U:H2'	1:AA:717:G:H8	1.81	0.44
1:AA:1385:U:H2'	1:AA:1386:A:C8	2.52	0.44
21:AX:18:G:O2'	21:AX:57:G:N2	2.51	0.44
22:AY:3:U:OP2	22:AY:3:U:C5	2.70	0.44
33:BA:1619:A:H2'	33:BA:1620:A:C8	2.52	0.44
33:BA:2078:A:N6	33:BA:2647:G:O6	2.51	0.44
38:BG:79:LEU:HD23	38:BG:83:MET:HB2	1.99	0.44
40:BJ:32:GLY:HA2	40:BJ:108:ILE:HD11	1.99	0.44
41:BK:131:THR:O	41:BK:134:SER:OG	2.24	0.44
1:AA:1469:C:H2'	1:AA:1470:A:C8	2.53	0.44
33:BA:29:U:O2	33:BA:1255:G:O2'	2.36	0.44
33:BA:406:G:H2'	33:BA:407:A:C8	2.53	0.44
33:BA:823:G:H2'	33:BA:824:G:OP1	2.18	0.44
40:BJ:84:PHE:HA	40:BJ:116:LYS:NZ	2.32	0.44
51:BV:3:ALA:HB3	51:BV:107:VAL:HB	1.99	0.44
9:AI:104:LEU:O	9:AI:106:ARG:N	2.38	0.44
33:BA:675:C:O2	33:BA:685:U:O2'	2.34	0.44
33:BA:897:G:O6	33:BA:974:A:N6	2.50	0.44
33:BA:938:G:H2'	33:BA:939:G:C8	2.53	0.44
33:BA:1817:C:OP1	35:BD:221:ARG:NH1	2.50	0.44
33:BA:1886:G:H21	33:BA:1914:A:H62	1.65	0.44
34:BB:36:C:H2'	34:BB:37:A:O4'	2.17	0.44
35:BD:84:ASP:HB2	35:BD:91:ILE:HG13	2.00	0.44
36:BE:84:ARG:HA	36:BE:85:GLY:HA2	1.61	0.44
39:BH:19:LEU:HD21	39:BH:46:VAL:HG23	2.00	0.44
42:BM:124:ASN:HB3	42:BM:126:TYR:HE2	1.83	0.44
1:AA:505:G:N2	1:AA:507:A:OP2	2.51	0.44
1:AA:1335:U:H2'	1:AA:1336:G:C8	2.51	0.44
1:AA:1502:A:H5'	1:AA:1503:A:OP2	2.18	0.44
20:AT:6:SER:O	20:AT:8:ILE:N	2.44	0.44
21:AX:36:C:N4	21:AX:37:A:H62	2.16	0.44
26:B2:19:GLN:O	26:B2:22:THR:OG1	2.22	0.44
28:B4:7:ARG:HB3	33:BA:2046:U:O2	2.17	0.44
31:B7:7:HIS:HE2	33:BA:254:A:P	2.40	0.44
33:BA:302:A:H2'	33:BA:303:G:C8	2.52	0.44
33:BA:2010:A:H3'	33:BA:2011:U:C5'	2.47	0.44
33:BA:2041:G:OP2	51:BV:16:LYS:NZ	2.51	0.44
49:BT:10:THR:O	49:BT:14:ARG:HG2	2.18	0.44
49:BT:46:ALA:O	49:BT:50:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1074:G:N2	1:AA:1199:G:H1'	2.32	0.44
22:AY:13:G:O2'	22:AY:14:G:C5	2.71	0.44
33:BA:794:U:H2'	33:BA:795:G:OP1	2.17	0.44
33:BA:1029:A:N6	33:BA:1030:G:C6	2.86	0.44
33:BA:2164:A:H62	33:BA:2185:G:H21	1.66	0.44
33:BA:2221:C:H2'	33:BA:2222:C:H5'	2.00	0.44
36:BE:150:ASP:N	36:BE:151:PRO:HD2	2.33	0.44
40:BJ:71:GLY:O	40:BJ:73:ASN:N	2.45	0.44
53:BX:9:VAL:HG13	53:BX:69:MET:H	1.82	0.44
13:AM:41:GLU:CA	13:AM:42:ASP:O	2.66	0.44
33:BA:279:A:H2'	33:BA:280:G:C8	2.52	0.44
33:BA:1046:A:H62	33:BA:1200:G:H2'	1.83	0.44
33:BA:1305:A:HO2'	51:BV:15:ARG:HH22	1.64	0.44
33:BA:1364:C:C4	51:BV:86:ARG:NH1	2.86	0.44
33:BA:1659:A:N7	33:BA:1660:C:H5	2.15	0.44
33:BA:1696:G:O5'	46:BQ:35:THR:OG1	2.30	0.44
1:AA:126:G:H1	1:AA:241:C:N4	2.16	0.43
20:AT:67:VAL:H	20:AT:68:HIS:CA	2.30	0.43
23:AZ:89:ASP:HB2	33:BA:2614:U:O2	2.18	0.43
33:BA:1348:G:H21	33:BA:1656:C:H5'	1.83	0.43
33:BA:2070:U:H2'	33:BA:2071:A:H8	1.82	0.43
34:BB:79:C:N4	34:BB:80:G:O6	2.51	0.43
38:BG:107:SER:HB2	38:BG:137:ILE:HG22	1.99	0.43
38:BG:108:LEU:N	38:BG:109:PRO:HD2	2.32	0.43
47:BR:65:VAL:HB	47:BR:68:THR:H	1.82	0.43
49:BT:103:LEU:HA	49:BT:104:THR:HA	1.76	0.43
22:AY:6:A:H2'	22:AY:7:C:H6	1.83	0.43
23:AZ:86:ASP:O	23:AZ:87:GLU:HB2	2.18	0.43
31:B7:26:HIS:CE1	31:B7:48:ALA:HB2	2.54	0.43
33:BA:1023:G:H5'	49:BT:55:ARG:NH1	2.33	0.43
33:BA:1377:G:O6	52:BW:62:LYS:NZ	2.40	0.43
37:BF:10:ASN:H	37:BF:12:SER:HB3	1.83	0.43
42:BM:77:ARG:NH1	42:BM:88:ARG:HE	2.15	0.43
48:BS:5:GLN:HB2	48:BS:8:ILE:HB	1.99	0.43
1:AA:500:A:H2'	1:AA:501:A:H8	1.83	0.43
1:AA:646:U:H2'	1:AA:647:G:H8	1.83	0.43
24:B0:23:ASN:HB2	24:B0:24:ALA:HA	2.00	0.43
33:BA:199:A:H62	33:BA:878:G:N2	2.16	0.43
33:BA:377:G:C2	33:BA:378:C:C5	3.06	0.43
33:BA:1023:G:H5'	49:BT:55:ARG:HH12	1.83	0.43
33:BA:1374:C:OP1	52:BW:65:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2152:A:H2'	33:BA:2153:G:H8	1.82	0.43
33:BA:2476:G:N2	33:BA:2479:A:OP2	2.51	0.43
33:BA:2862:A:H2'	33:BA:2863:G:C8	2.53	0.43
35:BD:207:LYS:HE2	35:BD:209:GLY:HA3	2.01	0.43
37:BF:37:ILE:HD13	44:BO:6:LEU:HD21	2.01	0.43
43:BN:8:LEU:HD22	43:BN:82:ASN:HB3	2.00	0.43
44:BO:125:ALA:HB3	44:BO:128:PHE:CZ	2.53	0.43
47:BR:65:VAL:HG21	47:BR:68:THR:HA	2.00	0.43
51:BV:88:ARG:HD2	51:BV:94:SER:HG	1.80	0.43
52:BW:12:VAL:HG11	52:BW:78:LYS:NZ	2.34	0.43
1:AA:1516:U:N3	1:AA:1532:U:OP1	2.44	0.43
9:AI:42:ALA:O	9:AI:44:LEU:N	2.45	0.43
25:B1:2:LYS:HE2	33:BA:78:U:H5''	2.00	0.43
33:BA:507:A:H62	33:BA:516:G:N2	2.12	0.43
33:BA:879:G:H2'	33:BA:880:C:C6	2.53	0.43
33:BA:1248:C:H2'	33:BA:1248:C:O2	2.17	0.43
33:BA:2906:U:O4	33:BA:2907:A:N6	2.52	0.43
35:BD:179:GLY:HA3	35:BD:275:LYS:HD3	1.99	0.43
41:BK:15:ALA:HA	41:BK:46:THR:HG21	2.00	0.43
47:BR:35:ARG:HB3	47:BR:100:TYR:CE2	2.54	0.43
49:BT:114:LYS:HA	49:BT:117:LEU:HD12	1.99	0.43
1:AA:930:U:H2'	1:AA:931:U:C6	2.54	0.43
1:AA:1063:G:N7	1:AA:1209:C:H5''	2.34	0.43
1:AA:1066:U:H2'	1:AA:1067:G:C8	2.52	0.43
33:BA:666:G:H4'	33:BA:667:A:C5'	2.48	0.43
33:BA:966:U:H4'	34:BB:79:C:H4'	1.99	0.43
33:BA:1242:U:H2'	33:BA:1243:A:H8	1.83	0.43
33:BA:1438:C:H2'	33:BA:1439:U:C6	2.53	0.43
33:BA:1932:G:H2'	33:BA:1933:G:H8	1.83	0.43
33:BA:2327:A:H62	33:BA:2347:G:H8	1.67	0.43
33:BA:2346:C:N4	33:BA:2347:G:N7	2.67	0.43
35:BD:245:SER:HA	35:BD:246:PRO:HD2	1.78	0.43
38:BG:69:ARG:HA	38:BG:84:PRO:HA	2.00	0.43
38:BG:111:VAL:HG22	38:BG:137:ILE:HG12	1.99	0.43
45:BP:36:ALA:HB1	45:BP:127:ILE:HG21	2.00	0.43
47:BR:72:SER:O	47:BR:75:THR:OG1	2.22	0.43
1:AA:609:U:H2'	1:AA:610:G:C8	2.53	0.43
1:AA:643:C:H2'	1:AA:644:A:C8	2.54	0.43
1:AA:734:G:OP1	1:AA:863:G:N2	2.41	0.43
25:B1:52:ARG:O	25:B1:56:VAL:HG23	2.19	0.43
26:B2:10:ARG:HD3	33:BA:1034:A:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:300:G:N7	33:BA:468:C:H2'	2.33	0.43
33:BA:1105:G:H2'	33:BA:1106:U:C5	2.54	0.43
33:BA:1108:G:H1	33:BA:1122:C:H42	1.66	0.43
33:BA:1783:C:H5'	48:BS:102:TYR:CZ	2.54	0.43
33:BA:2029:G:H2'	33:BA:2030:A:H8	1.84	0.43
37:BF:129:LEU:HD12	37:BF:195:THR:HG22	2.00	0.43
38:BG:64:LYS:HA	38:BG:65:PRO:HD2	1.91	0.43
51:BV:8:ARG:C	51:BV:10:VAL:H	2.27	0.43
1:AA:398:C:H2'	1:AA:399:G:C8	2.54	0.43
1:AA:950:C:H2'	1:AA:951:G:C8	2.54	0.43
1:AA:1403:A:N6	1:AA:1511:C:H5'	2.34	0.43
33:BA:365:U:H4'	37:BF:165:LEU:O	2.19	0.43
33:BA:683:A:O2'	33:BA:684:G:O4'	2.24	0.43
33:BA:720:C:N4	33:BA:721:G:O6	2.51	0.43
33:BA:746:A:H4'	33:BA:1679:A:C6	2.54	0.43
33:BA:1482:G:O2'	33:BA:1523:U:O2	2.31	0.43
33:BA:1818:A:H5''	35:BD:220:VAL:HA	2.01	0.43
33:BA:2468:A:H5'	33:BA:2468:A:H8	1.83	0.43
33:BA:2577:G:O2'	43:BN:4:GLN:OE1	2.36	0.43
38:BG:135:GLN:HE22	38:BG:150:ARG:N	2.11	0.43
1:AA:398:C:H2'	1:AA:399:G:H8	1.83	0.43
1:AA:551:U:H2'	1:AA:552:G:C8	2.53	0.43
1:AA:609:U:H2'	1:AA:610:G:H8	1.83	0.43
19:AS:81:LYS:N	19:AS:82:GLY:HA2	2.33	0.43
25:B1:34:THR:HG22	25:B1:36:GLN:HG3	2.01	0.43
33:BA:373:A:N6	53:BX:15:LYS:H	2.17	0.43
33:BA:661:A:O2'	37:BF:40:GLN:OE1	2.23	0.43
33:BA:719:C:H5'	33:BA:848:G:N2	2.33	0.43
33:BA:2038:G:H1'	46:BQ:110:ASP:O	2.19	0.43
33:BA:2405:A:N6	33:BA:2406:A:C6	2.87	0.43
38:BG:32:GLU:HG3	47:BR:2:ILE:HD12	2.01	0.43
41:BK:98:ALA:HB3	41:BK:137:ILE:HG12	2.00	0.43
44:BO:23:ILE:HG21	50:BU:81:ASN:O	2.16	0.43
1:AA:473:G:N2	1:AA:478:G:O6	2.52	0.43
1:AA:995:C:H2'	1:AA:996:A:C8	2.54	0.43
33:BA:774:A:OP1	33:BA:1477:A:O2'	2.28	0.43
33:BA:1018:G:H3'	33:BA:1019:A:H5''	2.00	0.43
33:BA:1759:U:O4	33:BA:1774:A:N7	2.52	0.43
35:BD:171:TYR:HB3	35:BD:184:ILE:O	2.18	0.43
46:BQ:17:LEU:CD2	46:BQ:39:GLU:OE2	2.67	0.43
50:BU:65:GLN:HG2	50:BU:93:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BZ:80:PHE:HB2	54:BZ:84:ARG:HB3	2.01	0.43
1:AA:95:U:H2'	1:AA:96:G:H8	1.83	0.43
27:B3:1:MET:N	34:BB:38:U:O4	2.43	0.43
33:BA:970:A:H4'	54:BZ:37:GLN:HE22	1.83	0.43
33:BA:1340:A:N6	33:BA:1686:A:C2	2.86	0.43
33:BA:2610:G:H22	33:BA:2639:C:H2'	1.84	0.43
35:BD:29:PRO:HB3	35:BD:63:ARG:NE	2.31	0.43
49:BT:64:ARG:HD2	49:BT:97:ASP:OD2	2.18	0.43
1:AA:266:A:H2'	1:AA:267:G:C8	2.54	0.42
1:AA:989:C:OP1	1:AA:1232:C:N4	2.52	0.42
31:B7:8:ARG:HG2	33:BA:249:C:H41	1.84	0.42
33:BA:125:A:N6	33:BA:126:A:N1	2.67	0.42
33:BA:625:C:H2'	33:BA:626:G:C8	2.54	0.42
33:BA:647:A:C2	33:BA:672:C:H4'	2.54	0.42
33:BA:709:G:H5''	44:BO:16:ARG:HA	2.01	0.42
33:BA:1355:U:H5'	33:BA:1431:G:H1'	2.01	0.42
33:BA:1813:A:H4'	33:BA:1814:A:O5'	2.18	0.42
33:BA:2648:U:H5'	36:BE:156:LYS:HG3	2.01	0.42
40:BJ:119:THR:OG1	40:BJ:120:VAL:N	2.52	0.42
42:BM:17:LEU:HD23	42:BM:139:GLU:HB2	2.01	0.42
43:BN:7:ARG:HA	43:BN:20:LEU:HA	2.01	0.42
45:BP:43:THR:HA	45:BP:94:VAL:HG22	2.01	0.42
49:BT:103:LEU:CD1	49:BT:104:THR:HA	2.38	0.42
1:AA:1231:G:OP2	1:AA:1331:C:N4	2.48	0.42
1:AA:1547:U:H6	1:AA:1547:U:O5'	2.01	0.42
33:BA:175:G:O2'	33:BA:176:A:OP1	2.37	0.42
33:BA:527:A:H1'	53:BX:41:VAL:HG11	2.01	0.42
33:BA:673:A:N7	44:BO:76:VAL:HG11	2.34	0.42
33:BA:839:G:H4'	33:BA:840:A:C2	2.54	0.42
33:BA:2336:G:OP1	33:BA:2336:G:N2	2.49	0.42
33:BA:2721:C:O2	33:BA:2872:U:O2'	2.31	0.42
33:BA:2801:C:C2	33:BA:2802:U:C5	3.07	0.42
33:BA:2864:G:O6	33:BA:2902:A:N6	2.50	0.42
35:BD:235:GLY:HA3	35:BD:239:ALA:HB2	2.00	0.42
36:BE:49:ILE:HD12	36:BE:86:VAL:HG21	2.00	0.42
37:BF:67:GLN:HE22	37:BF:74:ARG:HA	1.84	0.42
38:BG:38:MET:HE3	38:BG:57:LEU:HD13	2.01	0.42
38:BG:106:VAL:HG11	38:BG:139:PRO:HG3	2.01	0.42
38:BG:169:LEU:O	38:BG:173:VAL:HG23	2.19	0.42
42:BM:45:TYR:H	49:BT:64:ARG:NE	2.17	0.42
46:BQ:107:ARG:HG2	46:BQ:109:GLY:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BT:92:ARG:CG	49:BT:94:MET:HG2	2.49	0.42
1:AA:149:U:H2'	1:AA:150:A:H8	1.84	0.42
1:AA:326:G:H2'	1:AA:327:G:H8	1.84	0.42
1:AA:739:G:C5	1:AA:740:G:H1'	2.53	0.42
1:AA:1160:A:HO2'	1:AA:1161:A:H8	1.66	0.42
21:AX:34:G:C2'	21:AX:35:U:H5''	2.50	0.42
24:B0:42:GLY:HA2	24:B0:43:LYS:HA	1.64	0.42
28:B4:35:GLU:HA	28:B4:36:MET:HA	1.72	0.42
29:B5:6:THR:HG22	29:B5:18:ILE:HG12	2.00	0.42
33:BA:275:A:N6	33:BA:296:G:H21	2.17	0.42
33:BA:278:A:H2'	33:BA:279:A:C8	2.54	0.42
33:BA:678:A:O3'	44:BO:68:ASN:ND2	2.32	0.42
33:BA:1003:A:C2	33:BA:2487:U:H4'	2.54	0.42
33:BA:1133:G:H1	33:BA:1148:C:N4	2.17	0.42
33:BA:1231:G:OP1	44:BO:30:THR:OG1	2.36	0.42
33:BA:1250:G:H5''	33:BA:1252:G:O4'	2.18	0.42
33:BA:1694:G:H2'	33:BA:1695:A:C8	2.54	0.42
33:BA:2262:A:H2'	33:BA:2263:G:C8	2.54	0.42
35:BD:136:PRO:HG2	35:BD:139:THR:HG21	2.01	0.42
35:BD:185:LEU:HD12	35:BD:186:SER:N	2.34	0.42
37:BF:11:GLY:N	37:BF:12:SER:HB3	2.34	0.42
45:BP:14:ARG:HD3	45:BP:41:TRP:HH2	1.85	0.42
52:BW:65:ARG:HB3	52:BW:70:THR:HG22	2.00	0.42
1:AA:119:C:H4'	1:AA:120:A:O5'	2.17	0.42
1:AA:1525:C:H2'	1:AA:1526:G:H8	1.83	0.42
27:B3:18:CYS:SG	27:B3:20:ASN:ND2	2.93	0.42
31:B7:26:HIS:ND1	31:B7:46:LYS:O	2.50	0.42
33:BA:970:A:O2'	54:BZ:37:GLN:NE2	2.52	0.42
33:BA:1065:U:C2	33:BA:1188:A:N6	2.88	0.42
33:BA:1345:U:O2'	33:BA:1346:A:H5''	2.20	0.42
36:BE:140:HIS:C	36:BE:142:ARG:H	2.28	0.42
39:BH:21:ASP:HA	39:BH:22:ASN:HA	1.85	0.42
45:BP:104:PHE:HE2	45:BP:125:LEU:HD11	1.83	0.42
46:BQ:51:GLY:HA2	46:BQ:84:PHE:CE1	2.54	0.42
1:AA:104:C:H2'	1:AA:105:G:H8	1.85	0.42
1:AA:1081:C:H2'	1:AA:1082:G:H8	1.85	0.42
22:AY:3:U:O5'	22:AY:3:U:C6	2.70	0.42
24:B0:38:ILE:HG22	24:B0:39:LEU:N	2.34	0.42
33:BA:20:C:H2'	33:BA:21:A:C8	2.55	0.42
33:BA:513:A:H8	33:BA:513:A:O5'	2.01	0.42
33:BA:972:U:HO2'	33:BA:973:G:H5''	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1065:U:OP1	33:BA:1081:U:O2'	2.37	0.42
33:BA:1305:A:O2'	33:BA:1306:G:O5'	2.29	0.42
33:BA:1808:U:O2	33:BA:1812:A:N6	2.53	0.42
33:BA:2769:A:N6	33:BA:2770:A:N6	2.67	0.42
40:BJ:78:GLY:N	40:BJ:79:PRO:HD2	2.34	0.42
44:BO:75:ALA:HA	44:BO:76:VAL:HA	1.76	0.42
45:BP:35:GLN:HE21	45:BP:100:GLY:HA2	1.85	0.42
50:BU:22:ILE:O	50:BU:93:THR:N	2.40	0.42
1:AA:73:C:H2'	1:AA:74:A:H8	1.85	0.42
1:AA:181:G:HO2'	1:AA:182:U:H6	1.65	0.42
1:AA:974:A:N6	1:AA:975:A:N6	2.67	0.42
27:B3:2:LYS:NZ	34:BB:40:C:OP1	2.52	0.42
29:B5:22:ASN:HD22	29:B5:25:ASN:ND2	2.18	0.42
33:BA:1224:A:H2'	33:BA:1225:G:H8	1.85	0.42
33:BA:1362:G:H3'	33:BA:1363:G:H5''	2.01	0.42
33:BA:2011:U:O2'	33:BA:2012:C:H5'	2.20	0.42
33:BA:2488:A:N6	33:BA:2523:G:C2	2.88	0.42
33:BA:2746:G:O2'	48:BS:97:ARG:NH1	2.52	0.42
33:BA:2868:G:H2'	33:BA:2869:A:H8	1.85	0.42
40:BJ:123:VAL:O	40:BJ:124:LYS:HB2	2.19	0.42
49:BT:59:LYS:O	49:BT:63:THR:HG23	2.20	0.42
1:AA:1012:U:H2'	1:AA:1013:G:O4'	2.20	0.42
1:AA:1473:C:H2'	1:AA:1474:G:H8	1.84	0.42
1:AA:1508:U:OP2	22:AY:17:G:O2'	2.37	0.42
22:AY:8:G:O6	22:AY:9:A:C6	2.72	0.42
22:AY:10:U:OP2	22:AY:10:U:C6	2.73	0.42
30:B6:34:ARG:HB3	30:B6:42:LEU:CD1	2.50	0.42
33:BA:787:C:N4	33:BA:804:G:H1	2.15	0.42
33:BA:1398:A:H62	33:BA:1411:U:H3	1.67	0.42
33:BA:1407:G:H2'	33:BA:1408:G:H8	1.84	0.42
33:BA:1694:G:H2'	33:BA:1695:A:H8	1.85	0.42
33:BA:1848:A:OP1	35:BD:157:SER:OG	2.28	0.42
33:BA:2134:A:H2'	33:BA:2135:G:C8	2.55	0.42
33:BA:2358:A:N6	33:BA:2359:G:C6	2.88	0.42
33:BA:2825:C:H3'	33:BA:2826:A:H8	1.85	0.42
35:BD:72:ASP:HB2	35:BD:119:GLY:HA2	2.02	0.42
43:BN:10:VAL:HG12	43:BN:12:ASP:H	1.85	0.42
1:AA:280:C:H2'	1:AA:281:A:H8	1.84	0.42
1:AA:754:U:H2'	1:AA:755:G:C8	2.54	0.42
1:AA:875:A:H5'	1:AA:1088:U:C5	2.55	0.42
1:AA:1434:A:O2'	1:AA:1435:A:H5''	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B7:17:THR:HG21	31:B7:23:LYS:HG3	2.01	0.42
33:BA:259:A:H2'	33:BA:260:A:C8	2.54	0.42
33:BA:509:C:N4	33:BA:510:G:O6	2.53	0.42
33:BA:1108:G:H2'	33:BA:1109:G:C8	2.53	0.42
34:BB:41:C:O2'	34:BB:42:G:H5'	2.19	0.42
35:BD:174:VAL:HG21	35:BD:184:ILE:HD12	2.02	0.42
42:BM:4:THR:N	42:BM:5:PRO:HD2	2.35	0.42
42:BM:128:GLY:HA2	42:BM:129:SER:HA	1.68	0.42
44:BO:33:LYS:HB3	44:BO:40:ALA:HA	2.01	0.42
53:BX:4:LYS:N	53:BX:92:ARG:HH22	2.17	0.42
24:B0:45:LYS:HE3	24:B0:46:LYS:HE3	2.02	0.42
29:B5:12:CYS:SG	29:B5:38:ARG:HD3	2.60	0.42
29:B5:14:GLU:HG2	29:B5:16:ASN:H	1.84	0.42
33:BA:377:G:O2'	33:BA:378:C:OP1	2.38	0.42
33:BA:694:G:H2'	33:BA:695:G:C8	2.55	0.42
33:BA:1298:C:H2'	33:BA:1299:G:H8	1.85	0.42
33:BA:1433:U:H4'	33:BA:1648:A:H4'	2.01	0.42
33:BA:1659:A:N6	51:BV:91:GLY:HA2	2.35	0.42
33:BA:2181:C:H2'	33:BA:2182:G:C8	2.55	0.42
33:BA:2295:A:N6	33:BA:2302:A:H62	2.10	0.42
35:BD:19:SER:HB3	35:BD:203:ILE:HD11	2.02	0.42
37:BF:66:ARG:CD	37:BF:70:THR:HG23	2.49	0.42
38:BG:42:ASP:HB3	38:BG:45:GLN:H	1.84	0.42
44:BO:7:LYS:HA	44:BO:8:PRO:HD3	1.92	0.42
45:BP:7:VAL:HG12	45:BP:9:TYR:H	1.84	0.42
47:BR:49:ASN:HB3	47:BR:51:VAL:HG23	2.02	0.42
1:AA:74:A:H2'	1:AA:75:G:O4'	2.20	0.42
1:AA:126:G:H1	1:AA:241:C:H42	1.68	0.42
1:AA:833:U:H2'	1:AA:834:G:C8	2.55	0.42
33:BA:511:U:H2'	33:BA:512:G:O4'	2.20	0.42
33:BA:731:G:N2	33:BA:835:A:OP2	2.47	0.42
33:BA:933:C:H2'	33:BA:934:U:H5'	2.02	0.42
33:BA:1005:A:H2'	33:BA:1006:A:C8	2.55	0.42
33:BA:1093:G:N2	33:BA:1157:A:H62	2.17	0.42
33:BA:2042:A:O2'	51:BV:94:SER:HB3	2.20	0.42
33:BA:2089:A:H1'	33:BA:2531:G:H1'	2.01	0.42
33:BA:2607:G:OP1	33:BA:2643:A:N6	2.53	0.42
33:BA:2874:G:N2	33:BA:2891:G:H1'	2.35	0.42
35:BD:144:ILE:HG21	35:BD:184:ILE:HD13	2.01	0.42
36:BE:201:THR:HG21	36:BE:203:LYS:HG3	1.99	0.42
40:BJ:53:LYS:HB3	40:BJ:55:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BQ:9:THR:O	46:BQ:13:ARG:HG3	2.20	0.42
48:BS:107:ARG:HA	48:BS:108:GLY:HA2	1.59	0.42
51:BV:36:LEU:HB3	51:BV:44:SER:HB2	2.02	0.42
51:BV:79:GLY:H	51:BV:101:SER:HA	1.84	0.42
1:AA:146:G:H2'	1:AA:147:G:C8	2.55	0.41
1:AA:345:G:H2'	1:AA:346:A:H8	1.84	0.41
1:AA:510:C:H2'	1:AA:511:C:C6	2.55	0.41
1:AA:874:A:H5'	5:AE:90:GLY:C	2.45	0.41
4:AD:25:GLU:O	4:AD:27:GLU:N	2.45	0.41
24:B0:7:ILE:HD12	24:B0:49:VAL:HG23	2.00	0.41
33:BA:614:G:H2'	33:BA:2059:A:N7	2.35	0.41
33:BA:908:A:H2'	33:BA:909:G:O4'	2.20	0.41
33:BA:1835:C:O3'	35:BD:48:LYS:NZ	2.44	0.41
33:BA:2157:C:H2'	33:BA:2158:C:C6	2.55	0.41
33:BA:2186:G:O2'	33:BA:2187:A:O4'	2.30	0.41
33:BA:2296:A:H5''	33:BA:2297:A:H5'	2.01	0.41
33:BA:2342:C:H2'	33:BA:2343:A:C8	2.55	0.41
33:BA:2468:A:H4'	33:BA:2469:C:O5'	2.19	0.41
35:BD:69:ARG:NH1	35:BD:104:ILE:HD13	2.35	0.41
36:BE:117:LYS:HG3	36:BE:164:MET:HE3	2.01	0.41
37:BF:75:GLN:NE2	37:BF:82:GLN:HE22	2.14	0.41
40:BJ:84:PHE:HA	40:BJ:116:LYS:HZ3	1.85	0.41
1:AA:35:A:N6	1:AA:559:G:O6	2.53	0.41
1:AA:478:G:H2'	1:AA:479:G:C8	2.55	0.41
1:AA:502:C:H2'	1:AA:503:C:C6	2.55	0.41
1:AA:815:C:N4	1:AA:816:A:H62	2.19	0.41
28:B4:27:MET:HE2	28:B4:36:MET:HB2	2.02	0.41
33:BA:58:G:H2'	33:BA:59:G:C8	2.55	0.41
33:BA:430:C:C2	33:BA:438:A:N6	2.87	0.41
33:BA:978:A:O3'	33:BA:979:U:O4'	2.39	0.41
33:BA:1626:U:H2'	33:BA:1627:A:H8	1.84	0.41
33:BA:1938:C:H2'	33:BA:1939:G:C8	2.55	0.41
35:BD:96:TYR:HE2	35:BD:102:ARG:HB2	1.85	0.41
36:BE:119:PHE:CE1	36:BE:162:GLY:HA2	2.55	0.41
37:BF:128:ASP:OD1	37:BF:130:THR:HG23	2.20	0.41
41:BK:110:GLU:HA	41:BK:113:MET:HG2	2.03	0.41
43:BN:66:LYS:N	43:BN:82:ASN:OD1	2.48	0.41
1:AA:1483:G:H2'	1:AA:1484:G:C8	2.55	0.41
2:AB:103:ASN:O	2:AB:105:GLU:N	2.53	0.41
21:AX:58:A:N6	21:AX:61:C:O2	2.53	0.41
22:AY:4:G:C3'	22:AY:5:A:H5'	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B4:3:VAL:H	33:BA:2085:G:H21	1.67	0.41
28:B4:16:ARG:HH12	33:BA:1304:G:H5''	1.85	0.41
33:BA:574:A:H62	33:BA:2072:C:C5'	2.34	0.41
33:BA:1056:A:H1'	33:BA:1199:C:H1'	2.02	0.41
33:BA:1107:U:C6	33:BA:1116:A:H4'	2.55	0.41
33:BA:2708:A:H2	36:BE:191:ASN:HD22	1.67	0.41
36:BE:139:TYR:OH	36:BE:142:ARG:O	2.37	0.41
37:BF:187:VAL:HG12	44:BO:3:LEU:HB2	2.01	0.41
41:BK:54:ILE:HG23	41:BK:71:LYS:O	2.21	0.41
45:BP:11:ARG:HE	45:BP:87:LYS:HD3	1.85	0.41
50:BU:90:GLN:HA	50:BU:91:PRO:HD2	1.94	0.41
1:AA:530:G:H1	1:AA:537:C:H42	1.69	0.41
1:AA:912:G:H2'	1:AA:913:A:C8	2.56	0.41
1:AA:1430:U:H2'	1:AA:1431:U:C6	2.56	0.41
21:AX:71:C:H5''	21:AX:71:C:C6	2.44	0.41
33:BA:91:A:H5''	33:BA:92:G:H8	1.86	0.41
33:BA:377:G:O2'	33:BA:378:C:P	2.78	0.41
33:BA:825:G:H5''	35:BD:48:LYS:HE3	2.02	0.41
33:BA:1782:G:H4'	48:BS:96:ARG:HG2	2.03	0.41
33:BA:2123:A:N1	33:BA:2224:U:O2	2.54	0.41
33:BA:2843:G:H2'	33:BA:2844:A:C8	2.56	0.41
37:BF:11:GLY:HA3	37:BF:12:SER:HA	1.93	0.41
37:BF:143:LEU:O	37:BF:148:VAL:HG22	2.21	0.41
38:BG:127:ASN:N	47:BR:1:MET:SD	2.86	0.41
48:BS:51:ILE:HG23	48:BS:100:LEU:N	2.36	0.41
1:AA:861:U:C4	1:AA:862:A:N6	2.87	0.41
28:B4:13:LYS:HA	28:B4:16:ARG:HE	1.85	0.41
33:BA:251:G:O5'	33:BA:252:C:H5''	2.20	0.41
33:BA:1103:A:HO2'	33:BA:1104:U:P	2.42	0.41
33:BA:1199:C:H2'	33:BA:1200:G:O4'	2.19	0.41
33:BA:1525:G:H2'	33:BA:1526:G:C8	2.56	0.41
33:BA:1905:A:N6	33:BA:1906:A:C6	2.88	0.41
33:BA:2440:A:H2'	33:BA:2441:A:C8	2.55	0.41
34:BB:55:A:H5'	38:BG:24:SER:HB3	2.03	0.41
37:BF:88:VAL:O	37:BF:90:PHE:N	2.54	0.41
39:BH:28:LYS:HA	39:BH:33:GLU:HG2	2.02	0.41
25:B1:5:GLU:O	25:B1:60:ARG:NH2	2.53	0.41
33:BA:161:A:H2'	33:BA:162:A:C8	2.55	0.41
33:BA:1262:C:H2'	33:BA:1263:G:H8	1.86	0.41
33:BA:1512:G:O2'	33:BA:1594:G:O2'	2.37	0.41
33:BA:1813:A:O2'	33:BA:1814:A:OP2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:2329:A:N6	33:BA:2330:A:N6	2.68	0.41
37:BF:6:LEU:H	37:BF:16:ASP:HA	1.85	0.41
37:BF:167:ALA:HB1	37:BF:173:VAL:HG11	2.01	0.41
38:BG:29:PRO:HB3	38:BG:160:ALA:HB2	2.03	0.41
43:BN:62:ILE:HA	43:BN:84:CYS:SG	2.61	0.41
45:BP:7:VAL:HG21	45:BP:93:TRP:CH2	2.56	0.41
1:AA:1414:G:H2'	1:AA:1415:U:C6	2.55	0.41
5:AE:46:VAL:O	5:AE:72:ILE:N	2.49	0.41
28:B4:50:ASN:N	28:B4:51:GLY:HA2	2.36	0.41
31:B7:12:LYS:NZ	33:BA:252:C:O2	2.53	0.41
33:BA:16:G:H2'	33:BA:17:G:H8	1.85	0.41
33:BA:525:A:N6	33:BA:546:G:O2'	2.52	0.41
33:BA:1441:U:O2'	33:BA:1568:G:O2'	2.38	0.41
33:BA:2066:A:H2'	33:BA:2067:G:C8	2.56	0.41
33:BA:2371:C:O2'	33:BA:2403:C:H5''	2.21	0.41
36:BE:17:ALA:O	36:BE:19:ASN:N	2.54	0.41
1:AA:36:C:H2'	1:AA:37:G:C8	2.56	0.41
1:AA:266:A:H2'	1:AA:267:G:H8	1.86	0.41
1:AA:1084:G:H1	1:AA:1093:U:H3	1.68	0.41
1:AA:1380:G:O3'	9:AI:71:GLY:HA3	2.21	0.41
1:AA:1423:C:H2'	1:AA:1424:G:H8	1.85	0.41
31:B7:42:ARG:NH2	33:BA:2378:G:OP2	2.54	0.41
33:BA:45:G:N7	33:BA:218:G:O2'	2.43	0.41
33:BA:659:A:N1	37:BF:46:GLN:HG3	2.36	0.41
33:BA:661:A:H2'	33:BA:662:U:O4'	2.20	0.41
33:BA:726:C:H2'	33:BA:727:A:C8	2.56	0.41
33:BA:970:A:H2'	33:BA:971:A:H8	1.84	0.41
33:BA:983:U:H2'	33:BA:984:G:C8	2.56	0.41
33:BA:984:G:H2'	33:BA:985:G:H8	1.85	0.41
33:BA:1847:U:H4'	33:BA:1850:A:H1'	2.02	0.41
33:BA:2144:G:O6	33:BA:2146:A:H3'	2.21	0.41
33:BA:2488:A:N6	33:BA:2523:G:N3	2.68	0.41
33:BA:2623:C:N4	33:BA:2624:G:O6	2.54	0.41
33:BA:2719:A:C2	46:BQ:17:LEU:HD11	2.55	0.41
35:BD:246:PRO:HG3	35:BD:255:LEU:HD12	2.03	0.41
1:AA:151:A:H3'	1:AA:152:C:H6	1.86	0.41
1:AA:245:C:H2'	1:AA:246:G:C8	2.55	0.41
1:AA:390:A:H2'	1:AA:391:A:H8	1.85	0.41
1:AA:590:G:N1	1:AA:768:A:OP2	2.38	0.41
1:AA:738:A:N6	1:AA:739:G:C6	2.89	0.41
1:AA:792:C:H2'	1:AA:793:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:792:C:H2'	1:AA:793:A:C8	2.56	0.41
1:AA:988:A:N6	1:AA:1327:A:H62	2.19	0.41
1:AA:1495:U:H2'	1:AA:1496:G:C8	2.55	0.41
1:AA:1513:A:H5'	1:AA:1541:A:O4'	2.20	0.41
1:AA:1522:U:H2'	1:AA:1523:A:C8	2.56	0.41
22:AY:8:G:C3'	22:AY:9:A:C8	3.00	0.41
28:B4:6:ARG:NH2	33:BA:2048:U:H3'	2.35	0.41
30:B6:17:GLY:O	30:B6:20:SER:OG	2.29	0.41
33:BA:167:U:H2'	33:BA:168:A:C8	2.55	0.41
33:BA:340:U:H5''	53:BX:83:TYR:HB2	2.02	0.41
33:BA:343:A:OP2	53:BX:80:ARG:NH2	2.45	0.41
33:BA:620:U:O2'	33:BA:2531:G:O6	2.37	0.41
33:BA:621:G:H5'	33:BA:2531:G:C6	2.56	0.41
33:BA:669:C:OP2	44:BO:104:LYS:NZ	2.40	0.41
33:BA:837:U:O2'	33:BA:838:C:P	2.78	0.41
33:BA:1013:U:H2'	33:BA:1014:A:C8	2.56	0.41
33:BA:1029:A:N6	33:BA:1030:G:O6	2.51	0.41
33:BA:1586:G:O2'	33:BA:1587:U:O4'	2.29	0.41
33:BA:1600:G:OP2	33:BA:1600:G:N2	2.30	0.41
33:BA:2237:C:H2'	33:BA:2238:C:C6	2.56	0.41
33:BA:2393:C:H2'	33:BA:2394:G:O4'	2.21	0.41
33:BA:2613:U:H3'	33:BA:2614:U:H5'	2.01	0.41
33:BA:2725:U:H2'	33:BA:2726:G:C8	2.56	0.41
38:BG:111:VAL:HB	38:BG:114:PHE:HB3	2.02	0.41
40:BJ:71:GLY:C	40:BJ:73:ASN:H	2.26	0.41
44:BO:46:VAL:HG22	44:BO:47:ARG:H	1.86	0.41
47:BR:82:ALA:O	47:BR:86:ALA:N	2.54	0.41
50:BU:67:ARG:HD2	50:BU:89:ARG:HB2	2.02	0.41
50:BU:67:ARG:CA	50:BU:90:GLN:O	2.67	0.41
52:BW:56:ILE:CG2	52:BW:77:ARG:HE	2.33	0.41
52:BW:91:GLU:HG3	52:BW:92:ILE:HG13	2.03	0.41
53:BX:64:HIS:HD2	53:BX:66:SER:OG	2.03	0.41
1:AA:335:A:O2'	1:AA:336:C:O4'	2.37	0.41
1:AA:363:C:H1'	1:AA:396:G:H1'	2.02	0.41
2:AB:20:THR:C	2:AB:22:ARG:H	2.29	0.41
23:AZ:80:MET:HG3	23:AZ:81:ASN:N	2.35	0.41
24:B0:37:ARG:CD	24:B0:45:LYS:HD3	2.47	0.41
24:B0:37:ARG:HH11	24:B0:44:PRO:CB	2.29	0.41
33:BA:726:C:H2'	33:BA:727:A:H8	1.86	0.41
33:BA:847:A:H1'	33:BA:849:A:OP2	2.21	0.41
33:BA:892:U:O2'	33:BA:893:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BA:1060:U:H2'	33:BA:1061:A:H8	1.85	0.41
33:BA:1378:G:H5'	52:BW:16:ARG:HG3	2.02	0.41
33:BA:1820:A:H4'	35:BD:205:ILE:HB	2.03	0.41
33:BA:1823:U:H2'	33:BA:1824:C:C6	2.55	0.41
33:BA:2188:G:H2'	33:BA:2189:G:C8	2.56	0.41
33:BA:2878:U:H2'	33:BA:2879:G:C8	2.56	0.41
37:BF:126:LEU:O	37:BF:195:THR:HA	2.22	0.41
38:BG:102:LYS:NZ	38:BG:140:GLU:OE2	2.41	0.41
39:BH:4:VAL:HG13	39:BH:70:ARG:HH21	1.86	0.41
41:BK:102:ARG:HG3	41:BK:140:GLU:C	2.46	0.41
51:BV:66:ALA:HA	51:BV:69:LEU:HD12	2.03	0.41
30:B6:1:MET:CG	33:BA:800:G:OP1	2.69	0.40
33:BA:1006:A:H8	33:BA:1006:A:O5'	2.04	0.40
33:BA:1596:U:H2'	33:BA:1597:C:C6	2.56	0.40
33:BA:1657:C:C5'	33:BA:1657:C:H6	2.34	0.40
33:BA:2334:U:N3	38:BG:151:GLY:HA3	2.35	0.40
33:BA:2863:G:H1	33:BA:2905:C:H42	1.67	0.40
35:BD:208:ALA:O	35:BD:211:SER:OG	2.30	0.40
36:BE:14:GLN:HB3	36:BE:22:LEU:HD11	2.03	0.40
37:BF:65:TRP:CZ2	37:BF:75:GLN:HG3	2.56	0.40
43:BN:22:ILE:HD11	43:BN:42:THR:HG23	2.03	0.40
44:BO:47:ARG:HA	44:BO:48:PRO:HD3	1.95	0.40
46:BQ:78:ASP:OD1	46:BQ:79:ALA:N	2.53	0.40
48:BS:61:THR:HG22	48:BS:78:PRO:HA	2.02	0.40
51:BV:8:ARG:HA	51:BV:102:HIS:CD2	2.56	0.40
1:AA:468:C:H2'	1:AA:469:G:H8	1.87	0.40
1:AA:495:U:H2'	1:AA:496:A:C8	2.56	0.40
1:AA:1129:U:H3	1:AA:1163:G:H1	1.68	0.40
33:BA:365:U:O2	33:BA:365:U:O2'	2.26	0.40
33:BA:790:A:O2'	33:BA:1704:U:OP1	2.35	0.40
33:BA:852:G:H5'	33:BA:853:C:C5	2.56	0.40
33:BA:865:G:H21	33:BA:1230:A:H62	1.68	0.40
33:BA:1247:G:O2'	33:BA:1248:C:H6	2.05	0.40
33:BA:1304:G:H2'	33:BA:2043:A:N6	2.36	0.40
33:BA:1396:C:H2'	33:BA:1397:G:O4'	2.22	0.40
33:BA:1474:C:H42	33:BA:1618:A:N6	2.11	0.40
33:BA:1825:U:H2'	33:BA:1826:C:C6	2.55	0.40
33:BA:2070:U:H2'	33:BA:2071:A:C8	2.56	0.40
33:BA:2468:A:H5'	33:BA:2468:A:C8	2.56	0.40
33:BA:2568:C:H2'	33:BA:2569:C:H5''	2.03	0.40
33:BA:2868:G:H2'	33:BA:2869:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BG:33:LYS:HD3	38:BG:92:ARG:NH1	2.36	0.40
44:BO:23:ILE:HG23	50:BU:81:ASN:O	2.20	0.40
46:BQ:17:LEU:HD21	46:BQ:39:GLU:OE1	2.21	0.40
48:BS:25:PRO:HG3	48:BS:53:ARG:HG3	2.03	0.40
50:BU:78:PRO:O	50:BU:79:LYS:HB2	2.21	0.40
1:AA:268:G:N2	1:AA:273:G:C6	2.89	0.40
1:AA:848:G:H2'	1:AA:849:G:H8	1.86	0.40
1:AA:1332:G:H2'	1:AA:1333:A:C8	2.56	0.40
1:AA:1418:C:N4	1:AA:1419:A:H62	2.19	0.40
33:BA:31:C:O2'	33:BA:1278:G:OP1	2.35	0.40
33:BA:275:A:N6	33:BA:296:G:N2	2.69	0.40
33:BA:1153:G:OP1	40:BJ:59:MET:HG2	2.21	0.40
33:BA:1251:U:O2	33:BA:1251:U:C2'	2.69	0.40
33:BA:1660:C:O2'	33:BA:1661:A:H3'	2.22	0.40
33:BA:1756:U:H2'	33:BA:1757:G:C2	2.57	0.40
35:BD:231:PRO:HB2	35:BD:243:ARG:NH2	2.36	0.40
38:BG:13:ALA:O	38:BG:17:MET:HG2	2.22	0.40
39:BH:76:MET:O	39:BH:80:VAL:HG23	2.21	0.40
51:BV:72:SER:HG	51:BV:106:VAL:HG12	1.83	0.40
1:AA:932:G:H2'	1:AA:933:A:C8	2.56	0.40
1:AA:988:A:C6	1:AA:1327:A:N6	2.89	0.40
21:AX:47:U:H4'	21:AX:48:C:H5'	2.04	0.40
26:B2:22:THR:HG22	33:BA:897:G:O2'	2.20	0.40
28:B4:41:ARG:HG2	46:BQ:103:LYS:HB3	2.03	0.40
33:BA:721:G:H1'	37:BF:74:ARG:CD	2.51	0.40
33:BA:1087:U:H2'	33:BA:1088:G:H8	1.86	0.40
33:BA:1562:A:H3'	33:BA:1563:G:C8	2.55	0.40
33:BA:1867:C:H4'	33:BA:1868:G:C8	2.56	0.40
33:BA:2010:A:N3	33:BA:2010:A:C2'	2.84	0.40
33:BA:2405:A:H2'	33:BA:2406:A:O4'	2.21	0.40
33:BA:2566:U:H2'	33:BA:2567:C:C6	2.56	0.40
37:BF:126:LEU:HD21	37:BF:146:LEU:HD11	2.03	0.40
51:BV:8:ARG:O	51:BV:10:VAL:N	2.50	0.40
25:B1:49:ALA:HA	25:B1:52:ARG:HG2	2.04	0.40
31:B7:2:PRO:N	33:BA:635:C:H1'	2.37	0.40
33:BA:2468:A:O2'	33:BA:2469:C:OP2	2.33	0.40
37:BF:49:HIS:CD2	37:BF:92:PRO:HB2	2.56	0.40
45:BP:65:TRP:HB2	45:BP:105:GLU:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
2	AB	222/246 (90%)	204 (92%)	13 (6%)	5 (2%)	5	30
3	AC	208/218 (95%)	193 (93%)	14 (7%)	1 (0%)	24	59
4	AD	197/200 (98%)	191 (97%)	4 (2%)	2 (1%)	12	45
5	AE	163/166 (98%)	150 (92%)	9 (6%)	4 (2%)	4	29
6	AF	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	31
7	AG	151/156 (97%)	144 (95%)	6 (4%)	1 (1%)	18	53
8	AH	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	50
9	AI	128/130 (98%)	113 (88%)	10 (8%)	5 (4%)	2	21
10	AJ	100/102 (98%)	88 (88%)	8 (8%)	4 (4%)	2	21
11	AK	116/131 (88%)	106 (91%)	9 (8%)	1 (1%)	14	47
12	AL	135/138 (98%)	119 (88%)	9 (7%)	7 (5%)	1	17
13	AM	117/121 (97%)	94 (80%)	13 (11%)	10 (8%)	0	10
14	AN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	1	17
15	AO	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	30
16	AP	87/90 (97%)	82 (94%)	3 (3%)	2 (2%)	5	30
17	AQ	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
18	AR	69/79 (87%)	64 (93%)	2 (3%)	3 (4%)	2	20
19	AS	82/92 (89%)	75 (92%)	5 (6%)	2 (2%)	4	29
20	AT	84/88 (96%)	77 (92%)	6 (7%)	1 (1%)	10	41
23	AZ	22/95 (23%)	17 (77%)	2 (9%)	3 (14%)	0	3
24	B0	56/62 (90%)	53 (95%)	1 (2%)	2 (4%)	2	23
25	B1	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
26	B2	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	34
27	B3	62/66 (94%)	56 (90%)	4 (6%)	2 (3%)	3	25
28	B4	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	B5	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
30	B6	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
31	B7	62/66 (94%)	56 (90%)	5 (8%)	1 (2%)	7	36
32	B8	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
35	BD	273/277 (99%)	264 (97%)	8 (3%)	1 (0%)	30	64
36	BE	205/209 (98%)	189 (92%)	11 (5%)	5 (2%)	4	29
37	BF	203/207 (98%)	184 (91%)	16 (8%)	3 (2%)	8	37
38	BG	176/179 (98%)	154 (88%)	18 (10%)	4 (2%)	5	30
39	BH	173/179 (97%)	165 (95%)	7 (4%)	1 (1%)	21	55
40	BJ	121/166 (73%)	97 (80%)	14 (12%)	10 (8%)	0	10
41	BK	131/141 (93%)	122 (93%)	7 (5%)	2 (2%)	8	37
42	BM	140/145 (97%)	130 (93%)	9 (6%)	1 (1%)	18	53
43	BN	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7	35
44	BO	144/146 (99%)	132 (92%)	10 (7%)	2 (1%)	9	38
45	BP	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
46	BQ	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	47
47	BR	118/120 (98%)	106 (90%)	7 (6%)	5 (4%)	2	20
48	BS	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
49	BT	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
50	BU	99/102 (97%)	82 (83%)	15 (15%)	2 (2%)	6	32
51	BV	107/113 (95%)	96 (90%)	8 (8%)	3 (3%)	4	27
52	BW	91/95 (96%)	86 (94%)	5 (6%)	0	100	100
53	BX	98/103 (95%)	87 (89%)	8 (8%)	3 (3%)	3	25
54	BZ	80/94 (85%)	77 (96%)	3 (4%)	0	100	100
All	All	5563/5920 (94%)	5116 (92%)	336 (6%)	111 (2%)	8	32

All (111) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AE	4	ILE
6	AF	70	ALA
12	AL	127	ARG
13	AM	101	ASN
23	AZ	78	PHE

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Mol	Chain	Res	Type
23	AZ	84	VAL
40	BJ	93	ALA
41	BK	19	ASN
47	BR	26	ALA
53	BX	87	ASP
2	AB	18	HIS
2	AB	36	ASN
2	AB	104	PHE
5	AE	163	GLU
6	AF	54	ASP
7	AG	54	THR
8	AH	71	GLU
9	AI	106	ARG
9	AI	122	ARG
12	AL	38	VAL
13	AM	41	GLU
13	AM	46	ARG
13	AM	65	VAL
13	AM	102	SER
13	AM	112	PRO
27	B3	49	PHE
36	BE	18	GLU
36	BE	78	ARG
36	BE	90	ALA
36	BE	99	VAL
38	BG	42	ASP
40	BJ	48	ALA
40	BJ	72	LEU
40	BJ	89	VAL
40	BJ	108	ILE
40	BJ	124	LYS
47	BR	68	THR
47	BR	91	SER
51	BV	8	ARG
3	AC	60	ALA
4	AD	5	THR
9	AI	57	THR
10	AJ	35	SER
12	AL	32	LYS
12	AL	39	SER
12	AL	115	LEU
13	AM	42	ASP

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Mol	Chain	Res	Type
13	AM	66	GLU
15	AO	88	ARG
19	AS	84	ALA
23	AZ	77	VAL
31	B7	31	HIS
37	BF	4	VAL
40	BJ	55	TYR
40	BJ	90	VAL
40	BJ	113	ILE
43	BN	89	ASP
47	BR	63	LEU
50	BU	28	GLU
51	BV	41	ARG
51	BV	65	ASP
53	BX	74	LYS
53	BX	89	LYS
2	AB	37	GLY
4	AD	142	ARG
10	AJ	44	THR
12	AL	25	ASN
13	AM	10	PRO
16	AP	44	ALA
16	AP	47	ALA
18	AR	28	TYR
26	B2	29	LYS
28	B4	45	ALA
35	BD	245	SER
36	BE	54	ASP
37	BF	128	ASP
38	BG	112	ARG
38	BG	147	THR
39	BH	13	SER
43	BN	34	ASN
47	BR	71	THR
10	AJ	36	VAL
12	AL	16	VAL
14	AN	31	HIS
14	AN	56	VAL
18	AR	16	CYS
19	AS	30	VAL
24	B0	44	PRO
27	B3	60	ASN

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Mol	Chain	Res	Type
37	BF	89	VAL
40	BJ	107	GLU
42	BM	22	ALA
44	BO	107	ALA
46	BQ	110	ASP
50	BU	52	THR
5	AE	162	GLU
9	AI	104	LEU
9	AI	107	ASP
11	AK	120	HIS
20	AT	69	LYS
24	B0	40	VAL
5	AE	109	GLY
13	AM	84	GLY
14	AN	51	GLY
44	BO	88	GLY
10	AJ	80	THR
15	AO	24	SER
18	AR	23	ILE
2	AB	201	PRO
38	BG	25	VAL
41	BK	24	VAL

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	
23	AZ	6/87 (7%)	4 (67%)	2 (33%)	0	2
24	B0	47/50 (94%)	47 (100%)	0	100	100
25	B1	56/57 (98%)	56 (100%)	0	100	100
26	B2	52/53 (98%)	51 (98%)	1 (2%)	50	66
27	B3	53/55 (96%)	53 (100%)	0	100	100
28	B4	48/53 (91%)	48 (100%)	0	100	100
29	B5	46/47 (98%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	B6	39/39 (100%)	39 (100%)	0	100	100
31	B7	54/56 (96%)	54 (100%)	0	100	100
32	B8	34/35 (97%)	34 (100%)	0	100	100
35	BD	223/225 (99%)	222 (100%)	1 (0%)	84	83
36	BE	168/170 (99%)	168 (100%)	0	100	100
37	BF	169/170 (99%)	167 (99%)	2 (1%)	63	72
38	BG	153/154 (99%)	153 (100%)	0	100	100
39	BH	148/151 (98%)	148 (100%)	0	100	100
40	BJ	105/138 (76%)	105 (100%)	0	100	100
41	BK	103/110 (94%)	103 (100%)	0	100	100
42	BM	120/123 (98%)	120 (100%)	0	100	100
43	BN	101/101 (100%)	101 (100%)	0	100	100
44	BO	110/110 (100%)	110 (100%)	0	100	100
45	BP	111/116 (96%)	111 (100%)	0	100	100
46	BQ	99/100 (99%)	99 (100%)	0	100	100
47	BR	93/93 (100%)	93 (100%)	0	100	100
48	BS	99/100 (99%)	99 (100%)	0	100	100
49	BT	96/98 (98%)	96 (100%)	0	100	100
50	BU	83/84 (99%)	83 (100%)	0	100	100
51	BV	90/93 (97%)	89 (99%)	1 (1%)	65	74
52	BW	84/85 (99%)	84 (100%)	0	100	100
53	BX	84/87 (97%)	84 (100%)	0	100	100
54	BZ	64/74 (86%)	64 (100%)	0	100	100
All	All	2738/2914 (94%)	2731 (100%)	7 (0%)	84	85

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	AZ	81	ASN
23	AZ	86	ASP
26	B2	53	LEU
35	BD	185	LEU
37	BF	37	ILE
37	BF	66	ARG

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Mol	Chain	Res	Type
51	BV	90	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
26	B2	37	HIS
27	B3	20	ASN
27	B3	60	ASN
29	B5	25	ASN
30	B6	26	ASN
31	B7	35	ASN
31	B7	40	GLN
31	B7	60	GLN
35	BD	38	HIS
35	BD	54	GLN
35	BD	194	GLN
35	BD	199	GLN
35	BD	264	ASN
36	BE	152	ASN
36	BE	172	GLN
36	BE	191	ASN
37	BF	29	ASN
37	BF	67	GLN
37	BF	75	GLN
37	BF	82	GLN
38	BG	37	ASN
38	BG	135	GLN
39	BH	62	HIS
39	BH	107	ASN
41	BK	93	ASN
42	BM	59	ASN
44	BO	38	GLN
44	BO	78	ASN
44	BO	106	ASN
46	BQ	27	ASN
46	BQ	76	ASN
48	BS	80	HIS
49	BT	37	GLN
49	BT	91	ASN
50	BU	45	ASN
51	BV	60	HIS
51	BV	102	HIS

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Mol	Chain	Res	Type
53	BX	2	HIS
53	BX	39	ASN
53	BX	64	HIS
54	BZ	37	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1543/1555 (99%)	235 (15%)	17 (1%)
21	AX	76/77 (98%)	15 (19%)	1 (1%)
22	AY	18/19 (94%)	14 (77%)	3 (16%)
33	BA	2922/2928 (99%)	792 (27%)	80 (2%)
34	BB	111/119 (93%)	32 (28%)	4 (3%)
All	All	4670/4698 (99%)	1088 (23%)	105 (2%)

All (1088) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	10	A
1	AA	11	G
1	AA	34	A
1	AA	41	G
1	AA	49	C
1	AA	50	C
1	AA	52	A
1	AA	53	A
1	AA	83	C
1	AA	85	U
1	AA	87	C
1	AA	88	U
1	AA	99	A
1	AA	114	A
1	AA	118	A
1	AA	119	C
1	AA	120	A
1	AA	127	U
1	AA	129	A
1	AA	130	C
1	AA	140	A
1	AA	142	A
1	AA	143	C

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Mol	Chain	Res	Type
1	AA	151	A
1	AA	158	G
1	AA	162	C
1	AA	163	C
1	AA	182	U
1	AA	183	U
1	AA	194	C
1	AA	195	A
1	AA	197	G
1	AA	210	A
1	AA	222	G
1	AA	249	G
1	AA	255	G
1	AA	258	A
1	AA	259	G
1	AA	274	G
1	AA	275	C
1	AA	287	A
1	AA	288	C
1	AA	297	G
1	AA	336	C
1	AA	337	A
1	AA	338	C
1	AA	340	G
1	AA	355	G
1	AA	360	C
1	AA	362	G
1	AA	375	U
1	AA	380	C
1	AA	405	A
1	AA	414	G
1	AA	419	A
1	AA	420	U
1	AA	421	G
1	AA	422	A
1	AA	429	U
1	AA	430	C
1	AA	432	G
1	AA	437	U
1	AA	456	A
1	AA	457	A
1	AA	460	A

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Mol	Chain	Res	Type
1	AA	472	C
1	AA	474	A
1	AA	475	A
1	AA	476	U
1	AA	477	A
1	AA	488	U
1	AA	490	G
1	AA	491	A
1	AA	494	G
1	AA	506	A
1	AA	507	A
1	AA	518	A
1	AA	520	C
1	AA	527	C
1	AA	528	C
1	AA	533	G
1	AA	536	G
1	AA	541	A
1	AA	556	A
1	AA	568	A
1	AA	572	A
1	AA	581	A
1	AA	582	A
1	AA	585	G
1	AA	586	G
1	AA	605	A
1	AA	642	U
1	AA	643	C
1	AA	651	A
1	AA	662	U
1	AA	674	A
1	AA	696	A
1	AA	704	A
1	AA	711	A
1	AA	727	A
1	AA	728	C
1	AA	729	C
1	AA	730	A
1	AA	732	U
1	AA	740	G
1	AA	741	C
1	AA	756	U

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Mol	Chain	Res	Type
1	AA	757	A
1	AA	764	G
1	AA	786	A
1	AA	793	A
1	AA	802	U
1	AA	803	A
1	AA	823	A
1	AA	824	A
1	AA	826	C
1	AA	830	G
1	AA	837	A
1	AA	838	A
1	AA	843	U
1	AA	849	G
1	AA	856	C
1	AA	865	G
1	AA	874	A
1	AA	880	U
1	AA	881	U
1	AA	882	A
1	AA	883	A
1	AA	924	A
1	AA	936	G
1	AA	944	C
1	AA	945	A
1	AA	948	A
1	AA	970	U
1	AA	974	A
1	AA	979	A
1	AA	981	G
1	AA	984	A
1	AA	985	A
1	AA	986	G
1	AA	987	A
1	AA	992	U
1	AA	993	A
1	AA	1003	G
1	AA	1004	A
1	AA	1012	U
1	AA	1014	A
1	AA	1018	U
1	AA	1027	U

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Mol	Chain	Res	Type
1	AA	1028	A
1	AA	1033	G
1	AA	1036	C
1	AA	1040	U
1	AA	1042	G
1	AA	1044	G
1	AA	1046	G
1	AA	1053	G
1	AA	1054	A
1	AA	1060	G
1	AA	1064	C
1	AA	1075	U
1	AA	1104	G
1	AA	1105	U
1	AA	1111	A
1	AA	1112	A
1	AA	1143	A
1	AA	1148	G
1	AA	1149	U
1	AA	1150	U
1	AA	1151	G
1	AA	1155	A
1	AA	1161	A
1	AA	1168	U
1	AA	1169	G
1	AA	1170	C
1	AA	1177	C
1	AA	1191	G
1	AA	1192	U
1	AA	1193	G
1	AA	1200	A
1	AA	1205	A
1	AA	1206	A
1	AA	1210	A
1	AA	1211	U
1	AA	1221	U
1	AA	1222	A
1	AA	1223	U
1	AA	1230	G
1	AA	1237	C
1	AA	1247	A
1	AA	1250	G

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Mol	Chain	Res	Type
1	AA	1266	A
1	AA	1269	G
1	AA	1289	A
1	AA	1295	C
1	AA	1296	A
1	AA	1308	A
1	AA	1313	G
1	AA	1314	G
1	AA	1326	C
1	AA	1329	C
1	AA	1331	C
1	AA	1332	G
1	AA	1341	A
1	AA	1343	G
1	AA	1345	U
1	AA	1346	G
1	AA	1355	A
1	AA	1373	U
1	AA	1377	G
1	AA	1407	A
1	AA	1435	A
1	AA	1451	A
1	AA	1452	G
1	AA	1455	A
1	AA	1461	U
1	AA	1462	U
1	AA	1463	A
1	AA	1464	G
1	AA	1490	A
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1509	A
1	AA	1513	A
1	AA	1515	G
1	AA	1516	U
1	AA	1527	G
1	AA	1539	G
1	AA	1540	G
1	AA	1541	A
1	AA	1544	A
1	AA	1545	C

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Mol	Chain	Res	Type
1	AA	1547	U
1	AA	1548	C
21	AX	9	A
21	AX	18	G
21	AX	19	U
21	AX	21	A
21	AX	34	G
21	AX	35	U
21	AX	36	C
21	AX	48	C
21	AX	49	G
21	AX	55	U
21	AX	56	C
21	AX	57	G
21	AX	70	A
21	AX	73	G
21	AX	76	A
22	AY	2	G
22	AY	3	U
22	AY	4	G
22	AY	5	A
22	AY	6	A
22	AY	7	C
22	AY	8	G
22	AY	9	A
22	AY	11	G
22	AY	12	A
22	AY	13	G
22	AY	14	G
22	AY	16	A
22	AY	17	G
33	BA	8	U
33	BA	9	U
33	BA	10	A
33	BA	13	A
33	BA	27	G
33	BA	28	A
33	BA	31	C
33	BA	34	U
33	BA	35	G
33	BA	38	A
33	BA	44	A

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Mol	Chain	Res	Type
33	BA	45	G
33	BA	46	C
33	BA	48	G
33	BA	49	A
33	BA	51	G
33	BA	55	G
33	BA	59	G
33	BA	60	G
33	BA	61	A
33	BA	63	G
33	BA	70	G
33	BA	71	A
33	BA	75	G
33	BA	76	C
33	BA	84	A
33	BA	87	U
33	BA	90	A
33	BA	91	A
33	BA	94	A
33	BA	101	G
33	BA	102	A
33	BA	109	G
33	BA	118	A
33	BA	119	U
33	BA	124	A
33	BA	125	A
33	BA	126	A
33	BA	127	C
33	BA	130	A
33	BA	133	A
33	BA	156	A
33	BA	161	A
33	BA	162	A
33	BA	163	U
33	BA	164	U
33	BA	176	A
33	BA	177	G
33	BA	179	A
33	BA	183	A
33	BA	184	G
33	BA	185	A
33	BA	188	C

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Mol	Chain	Res	Type
33	BA	199	A
33	BA	202	A
33	BA	203	U
33	BA	207	A
33	BA	208	G
33	BA	215	G
33	BA	216	A
33	BA	217	G
33	BA	218	G
33	BA	219	A
33	BA	225	A
33	BA	226	A
33	BA	227	G
33	BA	230	A
33	BA	231	A
33	BA	232	U
33	BA	233	G
33	BA	236	A
33	BA	245	G
33	BA	248	G
33	BA	251	G
33	BA	252	C
33	BA	253	G
33	BA	258	A
33	BA	267	C
33	BA	268	A
33	BA	272	C
33	BA	275	A
33	BA	282	G
33	BA	283	G
33	BA	289	C
33	BA	290	U
33	BA	291	C
33	BA	299	U
33	BA	300	G
33	BA	301	U
33	BA	302	A
33	BA	310	C
33	BA	312	G
33	BA	313	U
33	BA	314	A
33	BA	315	C

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Mol	Chain	Res	Type
33	BA	321	U
33	BA	322	A
33	BA	324	A
33	BA	326	A
33	BA	327	G
33	BA	328	G
33	BA	337	A
33	BA	338	G
33	BA	345	A
33	BA	346	G
33	BA	349	C
33	BA	354	A
33	BA	355	A
33	BA	360	C
33	BA	367	G
33	BA	368	G
33	BA	373	A
33	BA	375	C
33	BA	376	A
33	BA	378	C
33	BA	379	C
33	BA	380	C
33	BA	387	C
33	BA	390	A
33	BA	393	U
33	BA	394	U
33	BA	405	U
33	BA	406	G
33	BA	407	A
33	BA	411	G
33	BA	418	A
33	BA	419	G
33	BA	420	U
33	BA	430	C
33	BA	433	G
33	BA	434	U
33	BA	435	G
33	BA	438	A
33	BA	453	G
33	BA	459	A
33	BA	474	U
33	BA	478	U

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Mol	Chain	Res	Type
33	BA	481	U
33	BA	485	U
33	BA	489	G
33	BA	490	A
33	BA	494	A
33	BA	502	C
33	BA	503	C
33	BA	504	A
33	BA	525	A
33	BA	526	A
33	BA	527	A
33	BA	528	G
33	BA	537	A
33	BA	538	A
33	BA	544	G
33	BA	548	A
33	BA	550	G
33	BA	551	A
33	BA	553	A
33	BA	555	C
33	BA	556	C
33	BA	558	G
33	BA	559	A
33	BA	561	A
33	BA	562	C
33	BA	564	G
33	BA	575	A
33	BA	576	G
33	BA	577	U
33	BA	578	A
33	BA	589	G
33	BA	591	U
33	BA	592	A
33	BA	594	C
33	BA	595	G
33	BA	599	G
33	BA	606	U
33	BA	607	G
33	BA	616	A
33	BA	618	A
33	BA	619	A
33	BA	634	A

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Mol	Chain	Res	Type
33	BA	637	A
33	BA	647	A
33	BA	648	G
33	BA	649	G
33	BA	650	U
33	BA	651	U
33	BA	655	C
33	BA	656	A
33	BA	657	G
33	BA	658	A
33	BA	660	G
33	BA	663	G
33	BA	664	C
33	BA	665	G
33	BA	666	G
33	BA	667	A
33	BA	668	G
33	BA	673	A
33	BA	674	G
33	BA	684	G
33	BA	691	U
33	BA	692	A
33	BA	698	C
33	BA	700	U
33	BA	711	U
33	BA	718	C
33	BA	732	A
33	BA	733	U
33	BA	734	C
33	BA	736	A
33	BA	746	A
33	BA	764	C
33	BA	769	A
33	BA	774	A
33	BA	775	G
33	BA	777	C
33	BA	785	C
33	BA	786	A
33	BA	787	C
33	BA	788	G
33	BA	794	U
33	BA	795	G

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Mol	Chain	Res	Type
33	BA	799	A
33	BA	811	A
33	BA	812	G
33	BA	822	G
33	BA	823	G
33	BA	829	A
33	BA	830	A
33	BA	831	U
33	BA	832	G
33	BA	836	A
33	BA	837	U
33	BA	838	C
33	BA	840	A
33	BA	841	A
33	BA	843	C
33	BA	847	A
33	BA	848	G
33	BA	851	A
33	BA	852	G
33	BA	853	C
33	BA	858	U
33	BA	859	C
33	BA	866	A
33	BA	872	C
33	BA	874	U
33	BA	875	U
33	BA	878	G
33	BA	880	C
33	BA	882	A
33	BA	892	U
33	BA	893	A
33	BA	894	A
33	BA	895	G
33	BA	896	A
33	BA	900	U
33	BA	908	A
33	BA	910	A
33	BA	912	C
33	BA	913	A
33	BA	914	C
33	BA	915	U
33	BA	916	G

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Mol	Chain	Res	Type
33	BA	918	U
33	BA	924	U
33	BA	925	A
33	BA	928	G
33	BA	931	C
33	BA	932	C
33	BA	933	C
33	BA	934	U
33	BA	935	A
33	BA	937	C
33	BA	942	U
33	BA	943	A
33	BA	944	C
33	BA	948	A
33	BA	952	A
33	BA	956	A
33	BA	957	A
33	BA	959	C
33	BA	964	A
33	BA	970	A
33	BA	972	U
33	BA	974	A
33	BA	976	U
33	BA	977	U
33	BA	978	A
33	BA	981	C
33	BA	987	A
33	BA	992	G
33	BA	998	G
33	BA	1005	A
33	BA	1007	G
33	BA	1019	A
33	BA	1020	A
33	BA	1025	A
33	BA	1027	A
33	BA	1030	G
33	BA	1031	C
33	BA	1034	A
33	BA	1035	G
33	BA	1037	C
33	BA	1042	A
33	BA	1055	A

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Mol	Chain	Res	Type
33	BA	1058	U
33	BA	1059	A
33	BA	1063	G
33	BA	1067	A
33	BA	1068	G
33	BA	1071	G
33	BA	1072	A
33	BA	1073	A
33	BA	1079	U
33	BA	1093	G
33	BA	1096	A
33	BA	1097	A
33	BA	1100	A
33	BA	1102	G
33	BA	1103	A
33	BA	1104	U
33	BA	1107	U
33	BA	1108	G
33	BA	1111	U
33	BA	1113	A
33	BA	1115	A
33	BA	1116	A
33	BA	1117	G
33	BA	1118	C
33	BA	1121	C
33	BA	1122	C
33	BA	1123	A
33	BA	1124	C
33	BA	1126	A
33	BA	1128	U
33	BA	1129	U
33	BA	1130	A
33	BA	1131	A
33	BA	1134	A
33	BA	1135	G
33	BA	1136	U
33	BA	1138	C
33	BA	1139	G
33	BA	1141	A
33	BA	1145	G
33	BA	1148	C
33	BA	1150	C

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Mol	Chain	Res	Type
33	BA	1152	G
33	BA	1158	G
33	BA	1177	G
33	BA	1178	U
33	BA	1179	A
33	BA	1181	C
33	BA	1182	G
33	BA	1188	A
33	BA	1189	A
33	BA	1194	A
33	BA	1197	A
33	BA	1201	A
33	BA	1202	A
33	BA	1209	G
33	BA	1218	U
33	BA	1219	C
33	BA	1220	G
33	BA	1222	A
33	BA	1236	G
33	BA	1244	A
33	BA	1246	G
33	BA	1247	G
33	BA	1248	C
33	BA	1249	U
33	BA	1250	G
33	BA	1251	U
33	BA	1268	G
33	BA	1269	A
33	BA	1278	G
33	BA	1286	A
33	BA	1289	U
33	BA	1293	A
33	BA	1295	U
33	BA	1296	G
33	BA	1305	A
33	BA	1306	G
33	BA	1312	A
33	BA	1313	A
33	BA	1314	A
33	BA	1315	G
33	BA	1319	G
33	BA	1327	U

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Mol	Chain	Res	Type
33	BA	1339	A
33	BA	1340	A
33	BA	1341	U
33	BA	1344	C
33	BA	1345	U
33	BA	1346	A
33	BA	1352	U
33	BA	1360	A
33	BA	1363	G
33	BA	1364	C
33	BA	1375	A
33	BA	1376	G
33	BA	1380	U
33	BA	1381	A
33	BA	1382	G
33	BA	1384	C
33	BA	1388	A
33	BA	1404	A
33	BA	1417	A
33	BA	1418	U
33	BA	1423	A
33	BA	1424	A
33	BA	1426	A
33	BA	1432	A
33	BA	1433	U
33	BA	1434	A
33	BA	1435	U
33	BA	1436	U
33	BA	1439	U
33	BA	1441	U
33	BA	1442	A
33	BA	1450	C
33	BA	1456	A
33	BA	1459	U
33	BA	1460	G
33	BA	1464	A
33	BA	1473	A
33	BA	1474	C
33	BA	1495	C
33	BA	1496	G
33	BA	1497	G
33	BA	1498	U

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Mol	Chain	Res	Type
33	BA	1499	A
33	BA	1504	A
33	BA	1507	U
33	BA	1513	U
33	BA	1516	A
33	BA	1517	A
33	BA	1519	C
33	BA	1520	A
33	BA	1521	G
33	BA	1523	U
33	BA	1524	A
33	BA	1528	U
33	BA	1529	G
33	BA	1530	G
33	BA	1536	A
33	BA	1539	C
33	BA	1543	U
33	BA	1553	A
33	BA	1555	A
33	BA	1558	C
33	BA	1561	G
33	BA	1562	A
33	BA	1572	G
33	BA	1573	C
33	BA	1578	G
33	BA	1581	A
33	BA	1582	U
33	BA	1583	A
33	BA	1584	U
33	BA	1585	A
33	BA	1596	U
33	BA	1600	G
33	BA	1601	A
33	BA	1607	C
33	BA	1608	A
33	BA	1615	A
33	BA	1617	A
33	BA	1626	U
33	BA	1631	A
33	BA	1632	G
33	BA	1638	A
33	BA	1640	G

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Mol	Chain	Res	Type
33	BA	1647	U
33	BA	1648	A
33	BA	1651	G
33	BA	1652	C
33	BA	1653	A
33	BA	1655	A
33	BA	1657	C
33	BA	1658	G
33	BA	1660	C
33	BA	1667	A
33	BA	1674	G
33	BA	1679	A
33	BA	1680	A
33	BA	1688	G
33	BA	1691	A
33	BA	1693	C
33	BA	1695	A
33	BA	1696	G
33	BA	1697	A
33	BA	1707	U
33	BA	1708	U
33	BA	1712	G
33	BA	1713	A
33	BA	1719	G
33	BA	1727	A
33	BA	1728	C
33	BA	1739	C
33	BA	1744	G
33	BA	1745	A
33	BA	1752	G
33	BA	1756	U
33	BA	1757	G
33	BA	1758	U
33	BA	1759	U
33	BA	1767	A
33	BA	1769	G
33	BA	1771	C
33	BA	1774	A
33	BA	1776	A
33	BA	1777	G
33	BA	1778	A
33	BA	1780	C

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Mol	Chain	Res	Type
33	BA	1781	C
33	BA	1782	G
33	BA	1785	G
33	BA	1787	G
33	BA	1788	A
33	BA	1790	U
33	BA	1791	A
33	BA	1792	G
33	BA	1793	G
33	BA	1796	C
33	BA	1802	A
33	BA	1810	G
33	BA	1811	C
33	BA	1814	A
33	BA	1829	C
33	BA	1830	G
33	BA	1831	A
33	BA	1832	A
33	BA	1834	C
33	BA	1839	A
33	BA	1858	A
33	BA	1862	C
33	BA	1876	A
33	BA	1877	A
33	BA	1882	A
33	BA	1897	C
33	BA	1900	A
33	BA	1901	A
33	BA	1902	G
33	BA	1910	G
33	BA	1912	G
33	BA	1913	A
33	BA	1916	U
33	BA	1918	A
33	BA	1919	A
33	BA	1925	A
33	BA	1930	A
33	BA	1935	G
33	BA	1942	A
33	BA	1943	C
33	BA	1944	U
33	BA	1948	A

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Mol	Chain	Res	Type
33	BA	1954	C
33	BA	1959	G
33	BA	1960	U
33	BA	1966	A
33	BA	1967	A
33	BA	1968	U
33	BA	1969	U
33	BA	1972	U
33	BA	1981	A
33	BA	1984	U
33	BA	1992	C
33	BA	1995	A
33	BA	1996	C
33	BA	1999	A
33	BA	2000	A
33	BA	2001	G
33	BA	2010	A
33	BA	2011	U
33	BA	2012	C
33	BA	2020	U
33	BA	2024	U
33	BA	2026	A
33	BA	2027	A
33	BA	2033	G
33	BA	2042	A
33	BA	2047	A
33	BA	2052	A
33	BA	2059	A
33	BA	2060	A
33	BA	2062	A
33	BA	2072	C
33	BA	2084	C
33	BA	2085	G
33	BA	2088	A
33	BA	2089	A
33	BA	2090	G
33	BA	2091	A
33	BA	2092	C
33	BA	2098	G
33	BA	2111	A
33	BA	2116	G
33	BA	2121	U

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Mol	Chain	Res	Type
33	BA	2122	G
33	BA	2123	A
33	BA	2124	A
33	BA	2125	U
33	BA	2133	C
33	BA	2140	U
33	BA	2142	C
33	BA	2143	A
33	BA	2145	G
33	BA	2147	U
33	BA	2149	G
33	BA	2155	A
33	BA	2156	G
33	BA	2157	C
33	BA	2161	G
33	BA	2162	G
33	BA	2165	A
33	BA	2175	C
33	BA	2176	A
33	BA	2177	G
33	BA	2188	G
33	BA	2190	C
33	BA	2195	G
33	BA	2197	G
33	BA	2200	A
33	BA	2202	A
33	BA	2205	A
33	BA	2214	G
33	BA	2220	A
33	BA	2222	C
33	BA	2227	A
33	BA	2232	G
33	BA	2233	C
33	BA	2240	U
33	BA	2241	A
33	BA	2243	C
33	BA	2246	G
33	BA	2252	A
33	BA	2254	A
33	BA	2255	C
33	BA	2267	G
33	BA	2268	G

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Mol	Chain	Res	Type
33	BA	2279	G
33	BA	2295	A
33	BA	2296	A
33	BA	2308	G
33	BA	2312	C
33	BA	2315	A
33	BA	2333	G
33	BA	2334	U
33	BA	2335	U
33	BA	2336	G
33	BA	2337	G
33	BA	2339	A
33	BA	2340	A
33	BA	2343	A
33	BA	2345	U
33	BA	2346	C
33	BA	2347	G
33	BA	2348	C
33	BA	2349	A
33	BA	2350	G
33	BA	2351	A
33	BA	2352	G
33	BA	2356	A
33	BA	2357	A
33	BA	2362	A
33	BA	2363	C
33	BA	2364	A
33	BA	2369	A
33	BA	2376	C
33	BA	2377	U
33	BA	2379	C
33	BA	2387	A
33	BA	2390	A
33	BA	2400	G
33	BA	2411	G
33	BA	2412	G
33	BA	2414	C
33	BA	2420	G
33	BA	2421	A
33	BA	2431	U
33	BA	2435	C
33	BA	2453	C

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Mol	Chain	Res	Type
33	BA	2454	A
33	BA	2455	A
33	BA	2456	C
33	BA	2458	G
33	BA	2459	A
33	BA	2460	U
33	BA	2463	A
33	BA	2464	A
33	BA	2468	A
33	BA	2469	C
33	BA	2470	C
33	BA	2477	A
33	BA	2483	G
33	BA	2505	A
33	BA	2513	G
33	BA	2523	G
33	BA	2528	C
33	BA	2531	G
33	BA	2532	A
33	BA	2533	U
33	BA	2534	G
33	BA	2536	C
33	BA	2541	C
33	BA	2542	A
33	BA	2543	U
33	BA	2546	C
33	BA	2547	A
33	BA	2558	G
33	BA	2569	C
33	BA	2570	A
33	BA	2571	A
33	BA	2572	G
33	BA	2575	U
33	BA	2576	U
33	BA	2583	U
33	BA	2594	A
33	BA	2595	A
33	BA	2596	G
33	BA	2601	A
33	BA	2602	C
33	BA	2610	G
33	BA	2611	G

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Mol	Chain	Res	Type
33	BA	2614	U
33	BA	2619	A
33	BA	2630	C
33	BA	2631	A
33	BA	2632	G
33	BA	2638	U
33	BA	2639	C
33	BA	2642	U
33	BA	2648	U
33	BA	2658	A
33	BA	2661	A
33	BA	2663	A
33	BA	2668	A
33	BA	2680	C
33	BA	2683	A
33	BA	2684	G
33	BA	2711	G
33	BA	2714	G
33	BA	2717	G
33	BA	2718	U
33	BA	2720	C
33	BA	2730	U
33	BA	2731	G
33	BA	2743	G
33	BA	2754	A
33	BA	2755	U
33	BA	2766	G
33	BA	2773	G
33	BA	2779	A
33	BA	2780	G
33	BA	2784	C
33	BA	2785	U
33	BA	2786	A
33	BA	2787	A
33	BA	2790	A
33	BA	2794	A
33	BA	2795	G
33	BA	2797	C
33	BA	2798	C
33	BA	2800	C
33	BA	2804	A
33	BA	2807	A

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Mol	Chain	Res	Type
33	BA	2808	U
33	BA	2809	G
33	BA	2813	U
33	BA	2818	C
33	BA	2819	A
33	BA	2820	U
33	BA	2825	C
33	BA	2826	A
33	BA	2843	G
33	BA	2855	G
33	BA	2858	U
33	BA	2859	G
33	BA	2860	A
33	BA	2869	A
33	BA	2873	G
33	BA	2874	G
33	BA	2892	G
33	BA	2897	G
33	BA	2898	A
33	BA	2899	C
33	BA	2902	A
33	BA	2905	C
33	BA	2909	U
33	BA	2918	G
33	BA	2919	A
34	BB	10	G
34	BB	11	A
34	BB	12	U
34	BB	13	A
34	BB	20	A
34	BB	23	U
34	BB	28	C
34	BB	37	A
34	BB	39	A
34	BB	40	C
34	BB	41	C
34	BB	42	G
34	BB	46	A
34	BB	48	G
34	BB	49	G
34	BB	50	A
34	BB	51	A

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Mol	Chain	Res	Type
34	BB	55	A
34	BB	59	U
34	BB	60	C
34	BB	61	U
34	BB	63	C
34	BB	64	A
34	BB	81	G
34	BB	85	U
34	BB	86	U
34	BB	87	U
34	BB	88	C
34	BB	96	G
34	BB	97	A
34	BB	107	G
34	BB	110	G

All (105) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	98	U
1	AA	113	G
1	AA	119	C
1	AA	126	G
1	AA	436	G
1	AA	641	G
1	AA	842	U
1	AA	848	G
1	AA	855	G
1	AA	864	U
1	AA	873	U
1	AA	1111	A
1	AA	1154	C
1	AA	1210	A
1	AA	1461	U
1	AA	1501	G
1	AA	1544	A
21	AX	47	U
22	AY	10	U
22	AY	12	A
22	AY	13	G
33	BA	43	G
33	BA	58	G

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Mol	Chain	Res	Type
33	BA	90	A
33	BA	118	A
33	BA	124	A
33	BA	163	U
33	BA	175	G
33	BA	183	A
33	BA	207	A
33	BA	229	A
33	BA	252	C
33	BA	271	C
33	BA	288	C
33	BA	298	U
33	BA	366	A
33	BA	377	G
33	BA	405	U
33	BA	419	G
33	BA	526	A
33	BA	549	A
33	BA	647	A
33	BA	649	G
33	BA	666	G
33	BA	683	A
33	BA	717	A
33	BA	785	C
33	BA	837	U
33	BA	847	A
33	BA	934	U
33	BA	936	C
33	BA	1019	A
33	BA	1066	A
33	BA	1092	A
33	BA	1103	A
33	BA	1107	U
33	BA	1117	G
33	BA	1173	A
33	BA	1245	G
33	BA	1250	G
33	BA	1305	A
33	BA	1339	A
33	BA	1351	U
33	BA	1434	A
33	BA	1438	C

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Mol	Chain	Res	Type
33	BA	1455	C
33	BA	1527	C
33	BA	1535	U
33	BA	1581	A
33	BA	1595	U
33	BA	1630	G
33	BA	1652	C
33	BA	1679	A
33	BA	1755	C
33	BA	1779	G
33	BA	1784	A
33	BA	1813	A
33	BA	1876	A
33	BA	1965	A
33	BA	2155	A
33	BA	2187	A
33	BA	2254	A
33	BA	2267	G
33	BA	2278	U
33	BA	2295	A
33	BA	2334	U
33	BA	2348	C
33	BA	2351	A
33	BA	2454	A
33	BA	2468	A
33	BA	2504	C
33	BA	2595	A
33	BA	2631	A
33	BA	2683	A
33	BA	2710	C
33	BA	2716	U
33	BA	2779	A
33	BA	2784	C
33	BA	2785	U
33	BA	2807	A
33	BA	2812	A
34	BB	38	U
34	BB	47	C
34	BB	54	U
34	BB	59	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

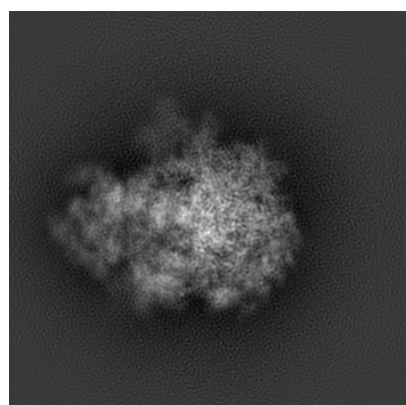
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6306. These allow visual inspection of the internal detail of the map and identification of artifacts.

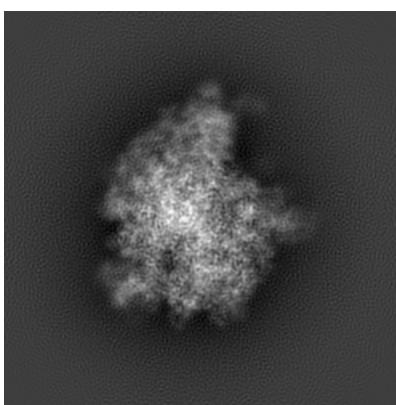
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

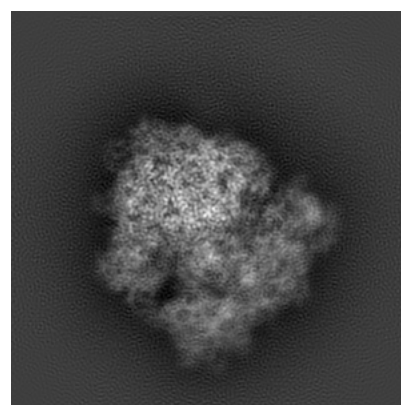
6.1.1 Primary map



X



Y

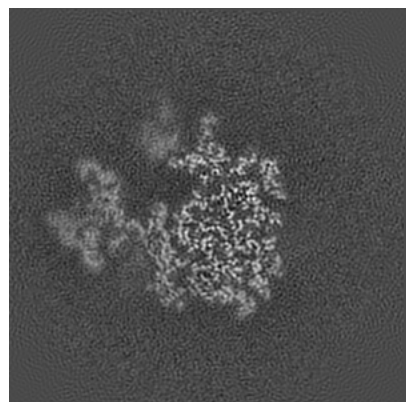


Z

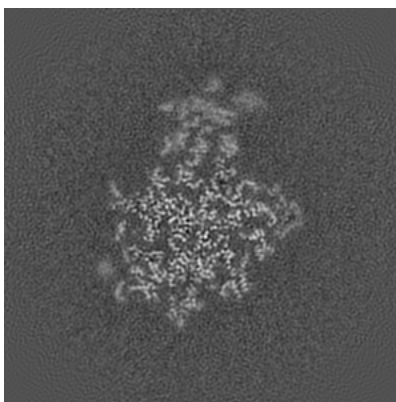
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

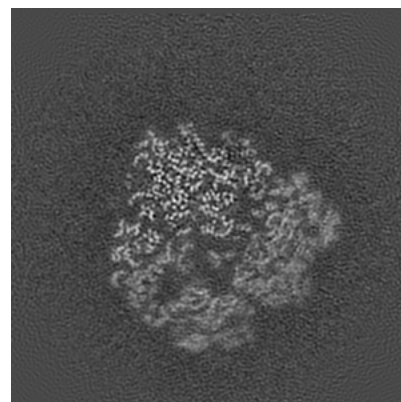
6.2.1 Primary map



X Index: 184



Y Index: 184

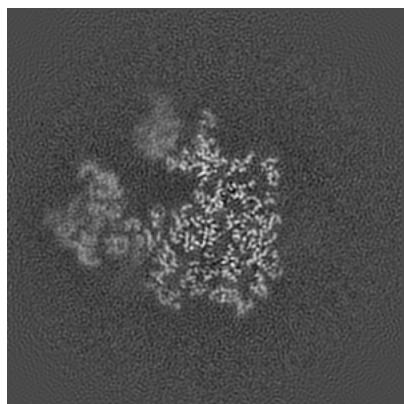


Z Index: 184

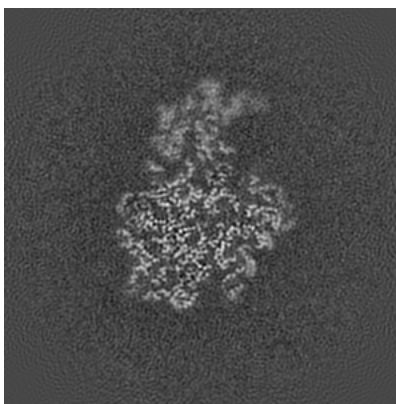
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

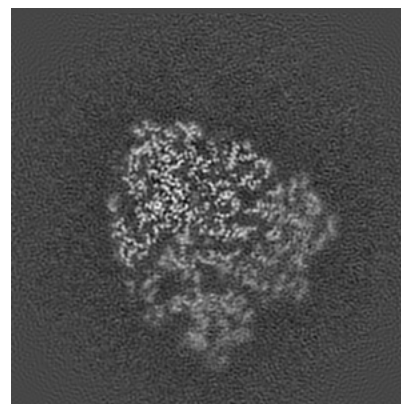
6.3.1 Primary map



X Index: 181



Y Index: 176

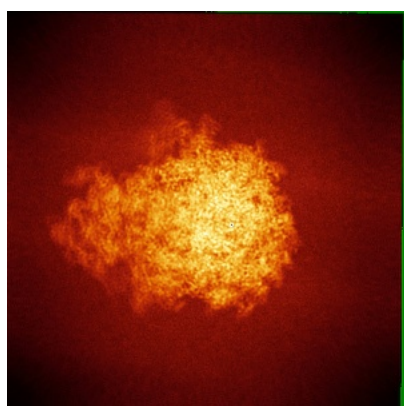


Z Index: 179

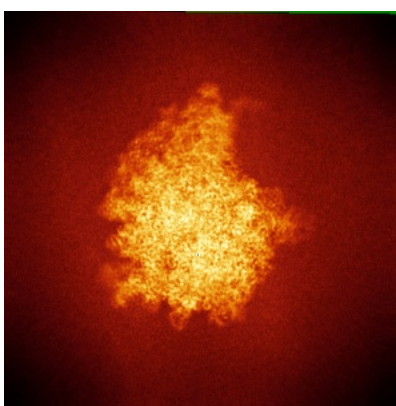
The images above show the largest variance slices of the map in three orthogonal directions.

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

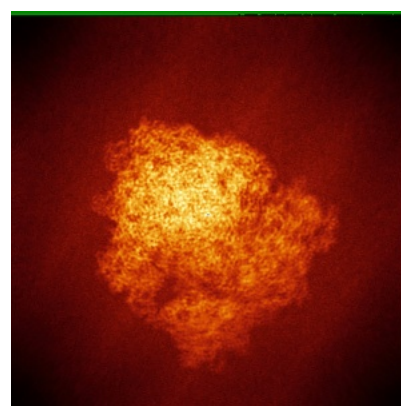
6.4.1 Primary map



X



Y

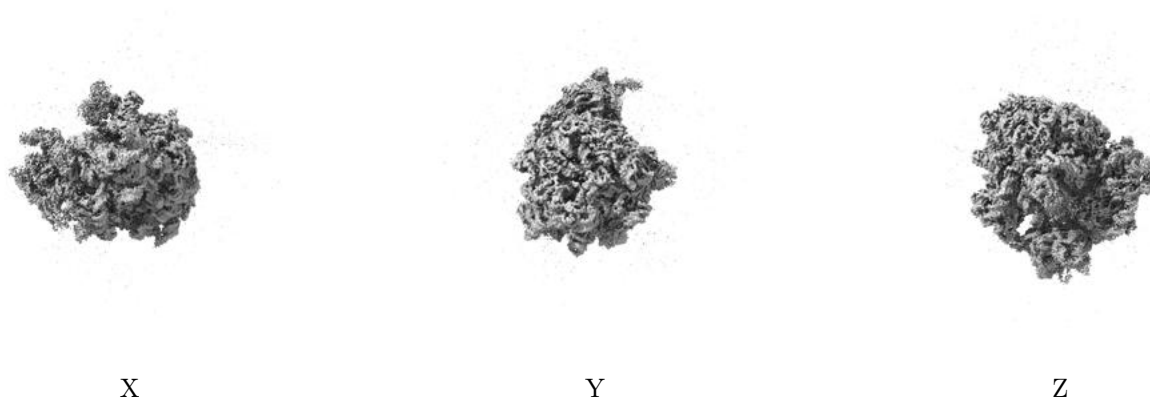


Z

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 0.00155. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

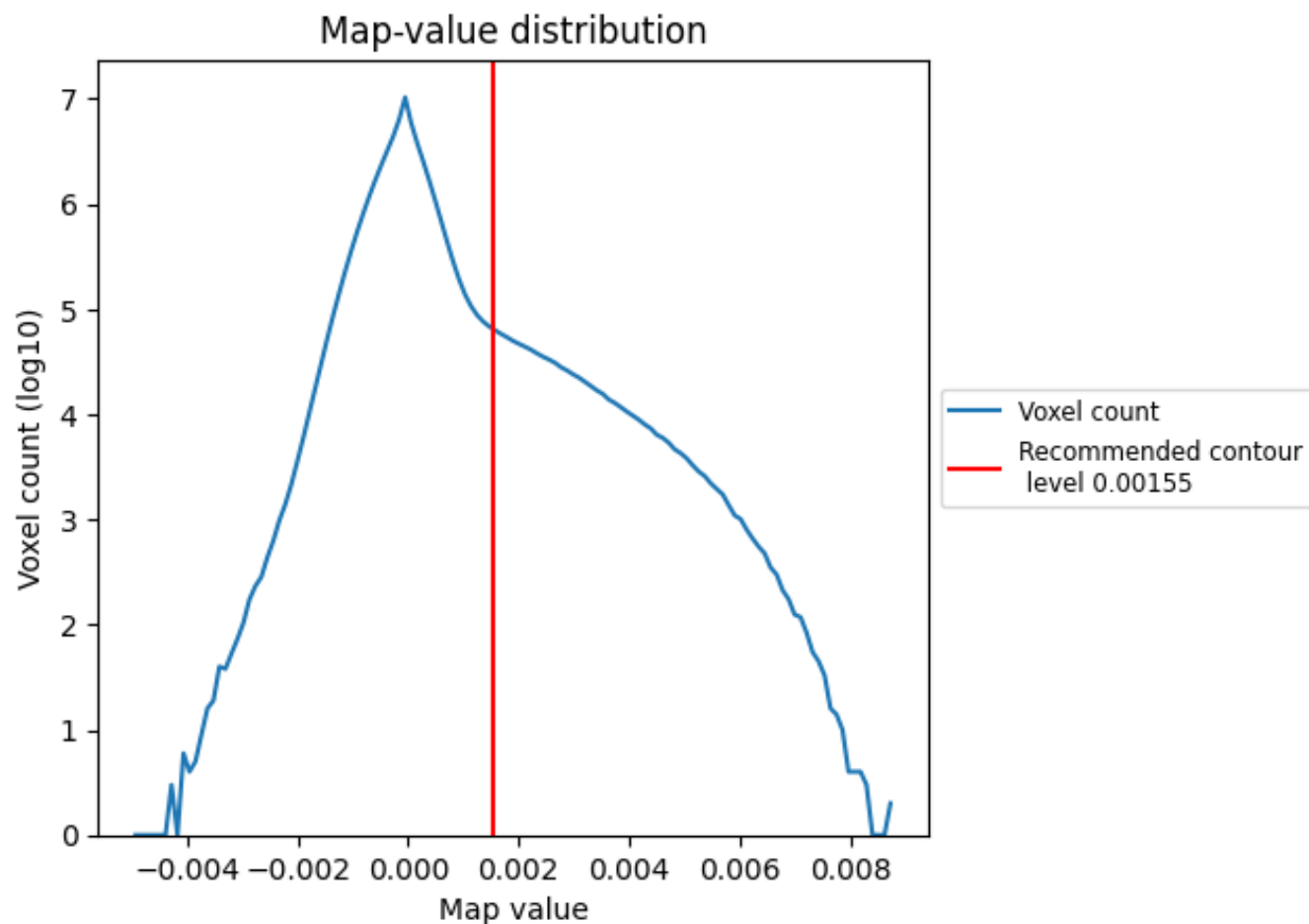
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

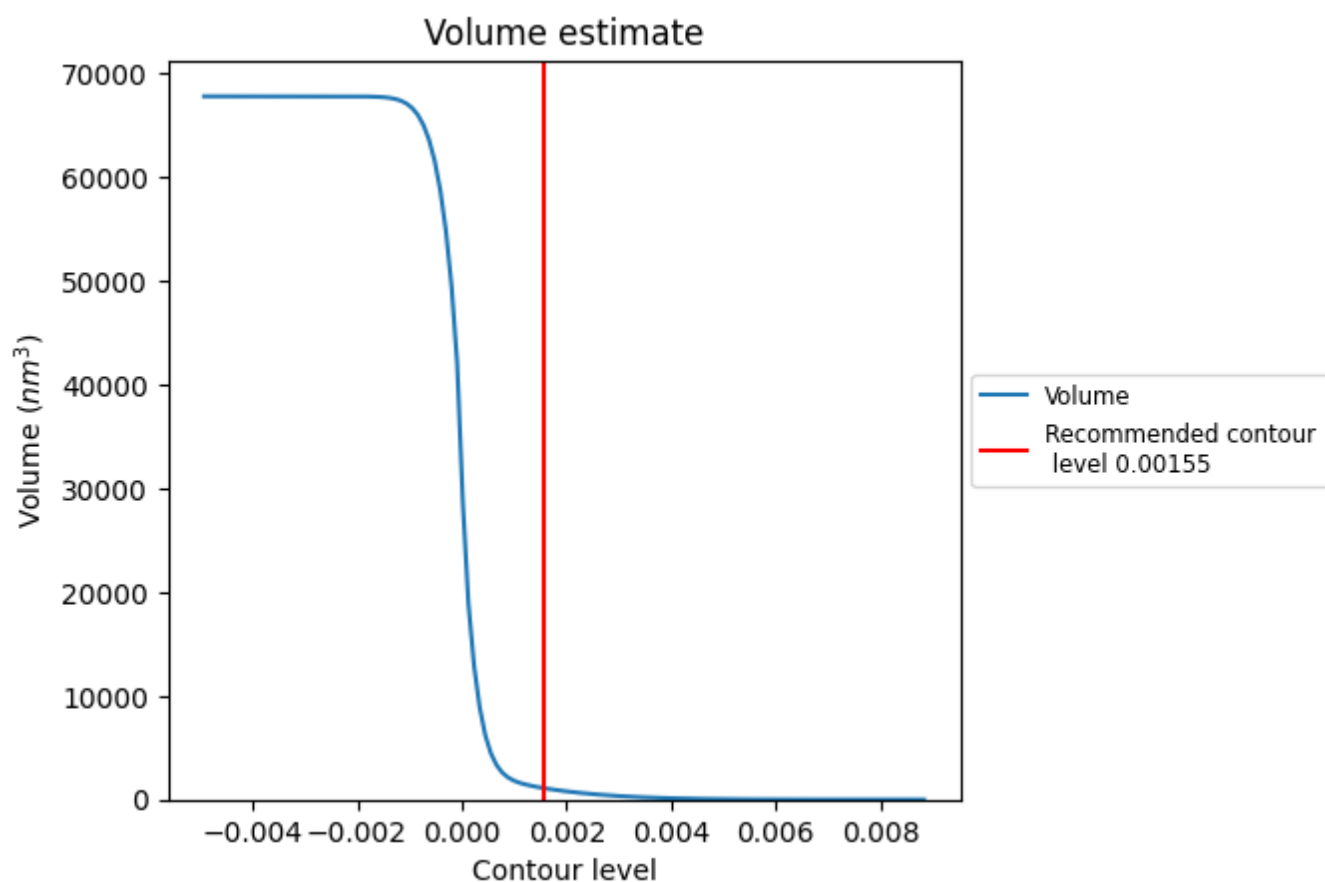
This section contains the results of statistical analysis of the map.

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.

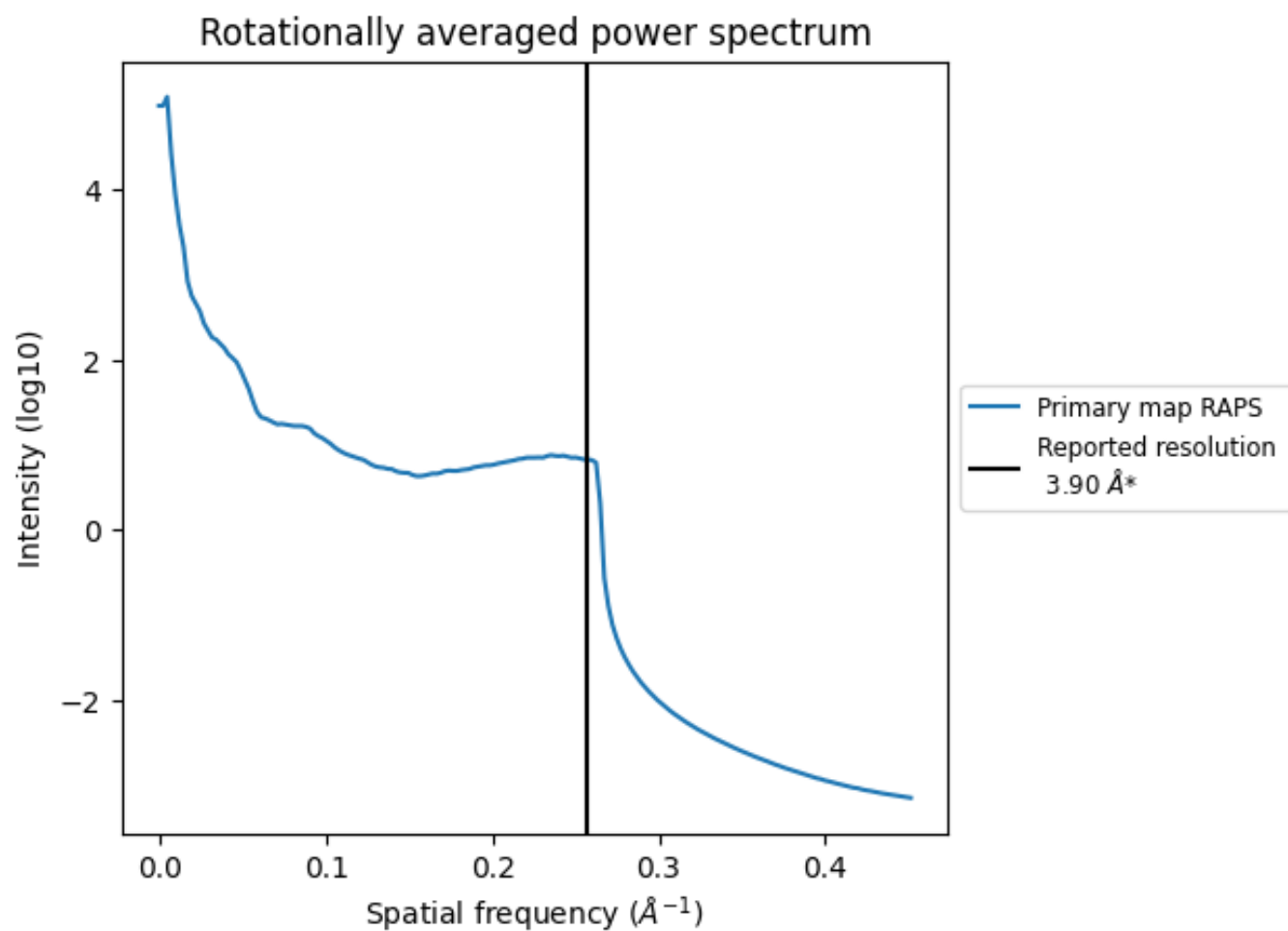
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1114 nm³; this corresponds to an approximate mass of 1007 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 0.256 Å⁻¹

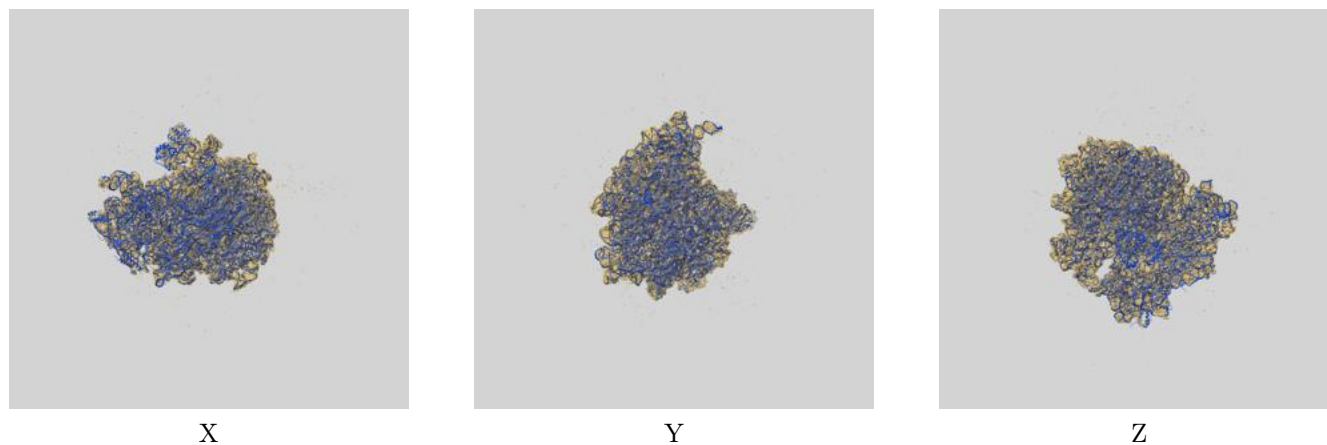
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

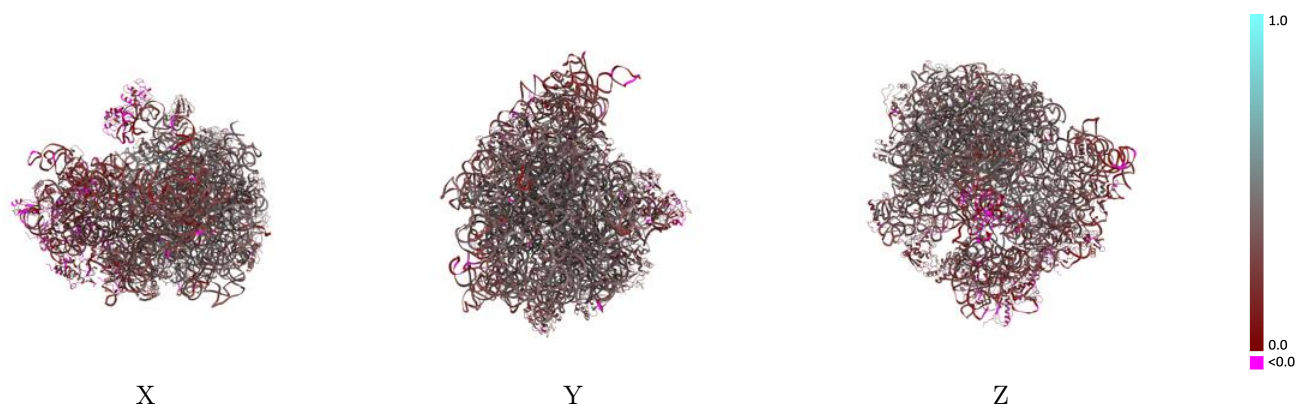
This section contains information regarding the fit between EMDB map EMD-6306 and PDB model 3J9W. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



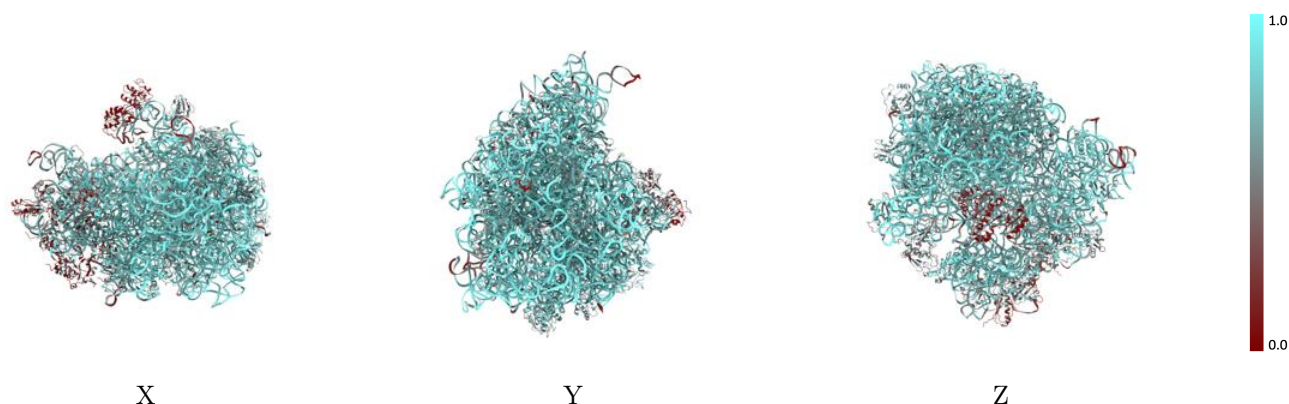
The images above show the 3D surface view of the map at the recommended contour level 0.00155 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



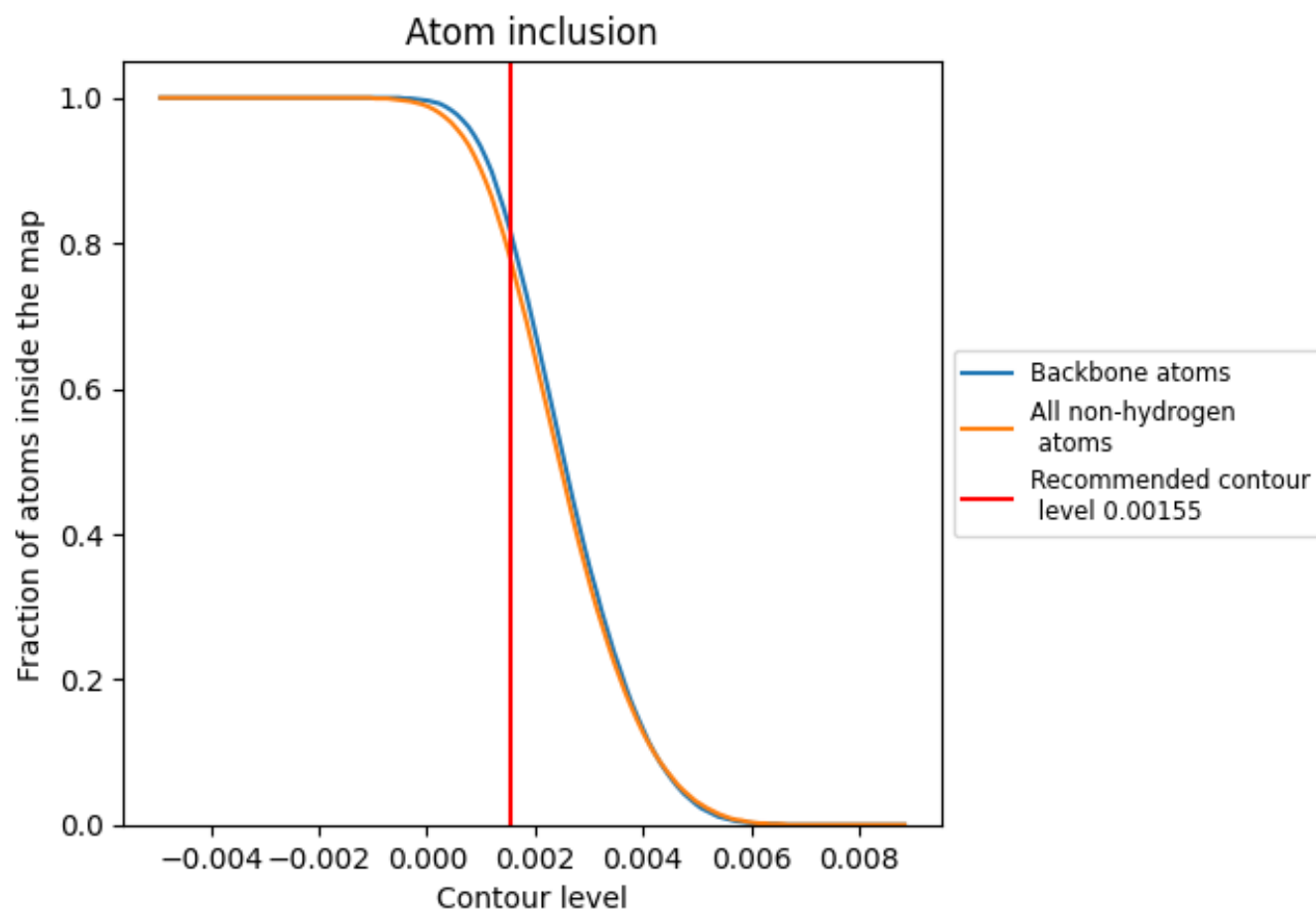
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00155).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.00155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7770	 0.3310
AA	 0.8030	 0.2870
AB	 0.3240	 0.1870
AC	 0.4710	 0.2100
AD	 0.5060	 0.2030
AE	 0.4780	 0.2410
AF	 0.7580	 0.3250
AG	 0.6720	 0.2690
AH	 0.6100	 0.2660
AI	 0.4300	 0.1660
AJ	 0.3010	 0.1370
AK	 0.6610	 0.3210
AL	 0.7050	 0.3380
AM	 0.6930	 0.2840
AN	 0.6100	 0.2250
AO	 0.8440	 0.3280
AP	 0.6920	 0.3000
AQ	 0.7100	 0.3010
AR	 0.6250	 0.2540
AS	 0.6610	 0.2440
AT	 0.7650	 0.2640
AX	 0.8170	 0.3370
AY	 0.3640	 0.1620
AZ	 0.5710	 0.4570
B0	 0.5830	 0.3470
B1	 0.5990	 0.2730
B2	 0.6720	 0.3690
B3	 0.4000	 0.1850
B4	 0.7050	 0.3740
B5	 0.6460	 0.3430
B6	 0.6960	 0.3790
B7	 0.7150	 0.4180
B8	 0.6700	 0.3790
BA	 0.8610	 0.3720
BB	 0.8870	 0.3550



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Chain	Atom inclusion	Q-score
BD	 0.6890	 0.3790
BE	 0.6840	 0.3720
BF	 0.6630	 0.3510
BG	 0.5290	 0.2470
BH	 0.5960	 0.2850
BJ	 0.1040	 0.0480
BK	 0.0360	 0.0280
BM	 0.6790	 0.3530
BN	 0.6510	 0.3710
BO	 0.6420	 0.3440
BP	 0.6770	 0.3780
BQ	 0.6890	 0.3560
BR	 0.5990	 0.2690
BS	 0.6260	 0.3180
BT	 0.7070	 0.3500
BU	 0.6660	 0.3550
BV	 0.6870	 0.3880
BW	 0.6050	 0.3330
BX	 0.6080	 0.3180
BZ	 0.6760	 0.3730