



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 10:16 PM UTC

PDB ID : 9V25 / pdb_00009v25
EMDB ID : EMD-64717
Title : Cryo- EM structure of large subunit (LSU) of 75S ribosome with A/P- & P/E-tRNAs from Entamoeba histolytica
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.00 Å(reported)
Based on initial model : .

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

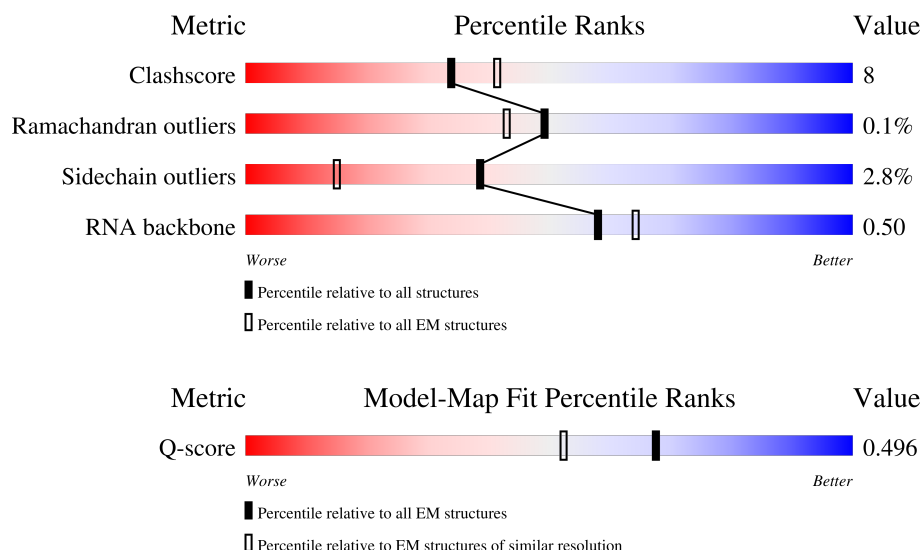
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



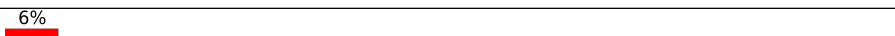
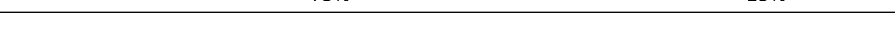
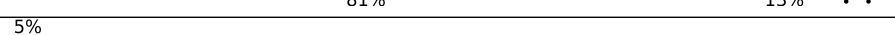
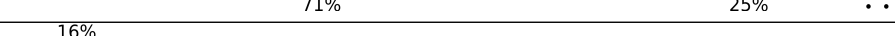
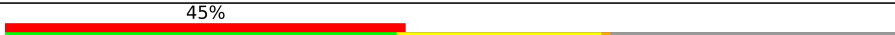
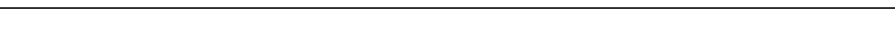
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1A	3503	
2	1B	155	
3	1C	117	

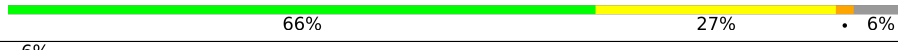
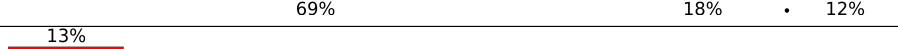
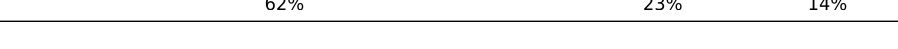
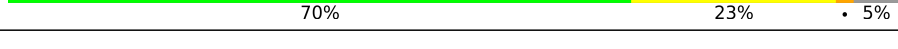
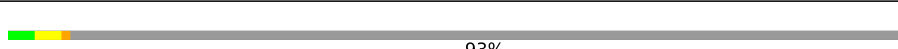
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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	77	
41	lo	51	
42	lp	56	
43	lq	98	
44	sH	6	
45	sI	76	
46	sJ	77	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 123062 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3140	Total	C	N	O	P	0	0
			67107	30085	12178	21704	3140		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	388	Total	C	N	O	S	0	0
			3085	1961	579	530	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	419	Total	C	N	O	S	0	0
			3229	2055	614	546	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	280	Total	C	N	O	S	0	0
			2227	1424	401	394	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	198	Total	C	N	O	S	0	0
			1606	1038	291	272	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	201	Total	C	N	O	S	0	0
			1608	1023	306	265	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	265	Total	C	N	O	S	0	0
			2104	1341	407	348	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1020	654	188	174	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	158	Total	C	N	O	S	0	0
			1232	779	238	210	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1316	832	257	218	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	96	Total	C	N	O	S	0	0
			716	454	121	139	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	124	Total	C	N	O	S	0	0
			1015	655	187	167	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	129	Total	C	N	O	S	0	0
			1058	672	209	172	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38 putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	sH	2	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 45 is a RNA chain called A/P- tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sI	5	Total	C	N	O	P	0	0
			104	47	19	33	5		

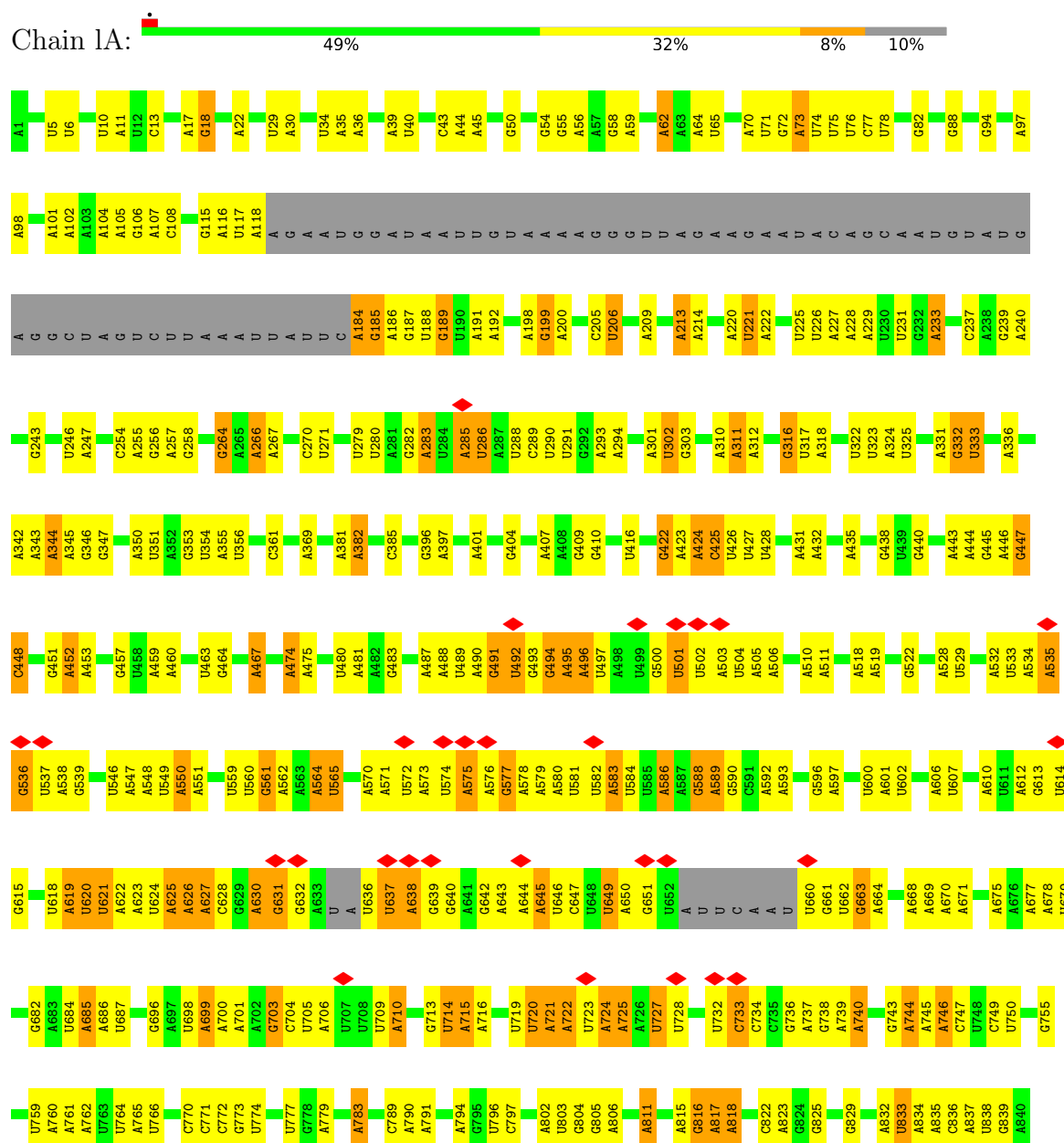
- Molecule 46 is a RNA chain called P/E- tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sJ	16	Total	C	N	O	P	0	0
			339	152	61	110	16		

3 Residue-property plots

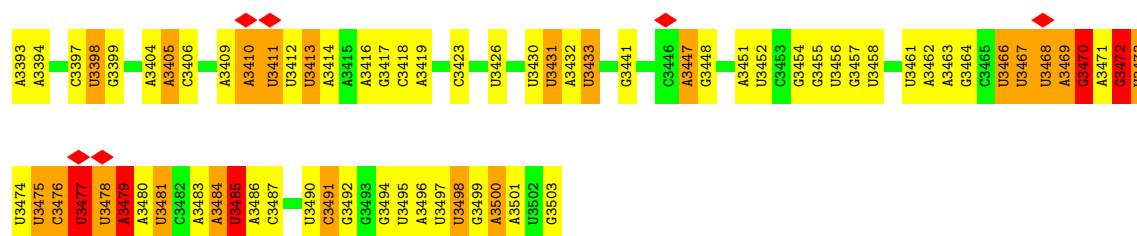
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S rRNA

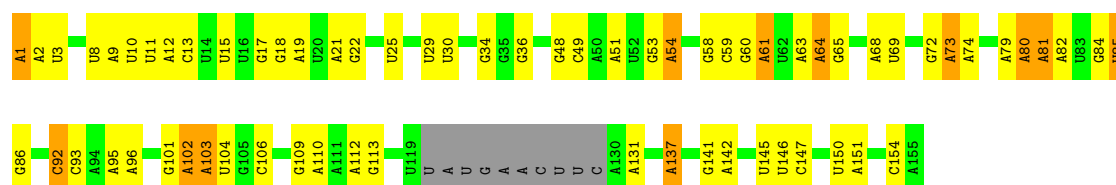




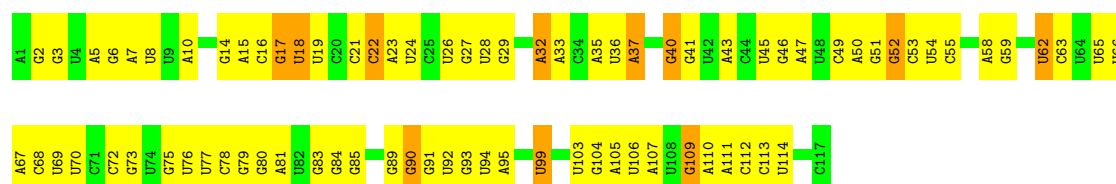
U3313	G3207	C2995	U2905	C2835	G2740	A	C	U2511	A2432	G2325	A2220	A2128
U3314	A3208	U3004	U2906	A2839	A2744	A	U	G2512	A2433	G2329	A2224	G2129
U3315	U3209	U3005	C2907	U2908	A2747	C	G	A2513	A2434	U2330	A2225	C2130
A3322	A3211	U3008	A2909	U2843	G2747	U	A	A2514	C2439	A2331	U2230	A2131
C3323	U3212	C3009	U2911	U2845	A2749	C	A	A2515	A2440	A2332	U2231	A2132
U3326	U3213	C3013	U2912	U2846	A2750		A	U2516	U2441	C2333	G2232	G2142
U3327	U3218	G3014	C2915	A2847	C2753		U	C	U2442	U2334	U2233	G2143
A3328	A3219	A3015	U2916	A2848	G2754		A	A	A2443	A2335	U2234	C2144
U3329	U3220	U3023	U2920	U2849	U2755		C	U	A2444	U2336	U2235	G2150
C3331	G3223	C3024	A2921	A2851	U2756		U	U	G2445	U2337	A2236	
A3332	A3227	U3025	A2925	G2852	G2757		A	U	G2446	C2338	A2237	U2153
U3333	A3228	U3026	U2926	U2856	U2758		U	U	A2449	U2340	A2238	U
U3335	G3229	C3027	U2927	U2857	A2761		G	U	C2450	C2341	U2239	C
G3336	G3232	C3028	U2931	A2858	A2764		C	U	U2451	U2342	U2241	U
A3337	U3239	U3030	C2937	U2860	U2765		A	A	G2452	U2343	U2242	U
A3338	A3240	C3032	U2938	A2861	A2766		U	A	G2453	U2344	A2245	G
U3344	C3243	C3033	U2940	A2863	G2768		U	U	U2456	A2347	G2246	U
A3345	A3245	A3034	C2941	A2864	A2774		C	A	U2457	A2348	A2251	A
U3349	C3247	C3038	A2942	A2865	A2775		U	A	G2466	A2349	U2252	A
U3350	A3248	A3039	U2943	C2866	A2776		A	U	G2467	G2352	A2253	A
G3351	G3147	A3040	A2944	A2867	A2767		G	G	U2469	A2357	U2254	G
U3352	U3254	G3041	A2945	U2868	U2768		U	U	A2473	C2360	A2255	A
U3353	A3149	C3044	A2946	A2869	A2781		U	G	U2478	U2374	U2257	A
A3354	A3260	U3047	A2951	U2870	G2784		A	G	G2479	G2381	G2259	A2173
U3355	A3261	U3048	C2952	G2873	U2791		U	U	A2480	G2382	U2260	U2174
U3356	C3265	U3066	C2953	U2876	G2790		G	A	C2481	G2383	G2261	C2175
A3358	U3266	U3067	U2954	U2877	A2797		C	U	U2482	C2384	U2262	A2178
U3359	G3267	C3068	A2955	A2878	G2798		U	U	C2483	A2385	U2263	U2179
A3360	A3268	A3069	C2957	U2879	U2799		U	U	U2486	U2386	U2264	A2183
U3361	U3276	C3070	G2958	C2880	C2805		C	G	G2487	G2387	U2265	A2184
U3364	C3277	U3073	U2959	U2884	A2815		A	U	U2488	A2388	U2266	A2190
U3365	A3278	U3074	A2960	U2885	A2816		C	C	G2489	A2389	U2267	A2193
G3366	G3284	U3078	C2976	G2887	A2817		U	U	G2494	C2391	A2268	G2197
U3367	A3285	A3083	C2977	U2888	A2818		A	A	A2495	C2395	A2269	G2198
U3368	A3286	A3084	C2978	G2889	U2819		C	C	C2496	A2396	A2270	A2207
U3369	U3287	C3085	A2980	A2890	G2820		U	U	U2499	G2397	A2271	G2210
U3371	U3288	U3085	C2981	U2891	A2821		U	U	U2500	G2410	A2272	U2213
U3372	G3299	G3090	C2982	A2892	U2822		A	A	U2503	G2411	A2273	A2214
A3373	U3302	C3091	C2983	C2893	G2823		C	C	A2504	C2412	A2274	A2215
C3374	A3303	U3096	C2984	C2894	C2824		U	U	U2505	C2413	A2275	A2216
U3375	C3376	U3097	C2985	G	C2825		A	A	A2506	C2414	A2276	U2217
G3376	U3380	U3098	A2988	U	A2828		C	C	C2507	C2415	A2277	A2218
A3381	A3381	U3099	G2991	A	C2829		A	A	A2508	A2417	U2278	A2219
U3382	G3382	U3103	C2992	G2899	G2830		C	C	U2509	U2418		
A3383	A3383	G3104	C2993	U2901	G2831		C	C	G2510			
A3384	G3385	U3105	A2994	A2902	U2903		A	A				
U3385	G3392											



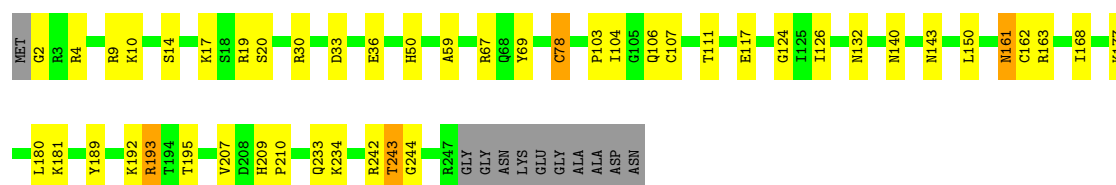
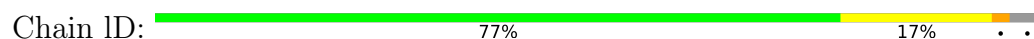
• Molecule 2: 5.8S rRNA



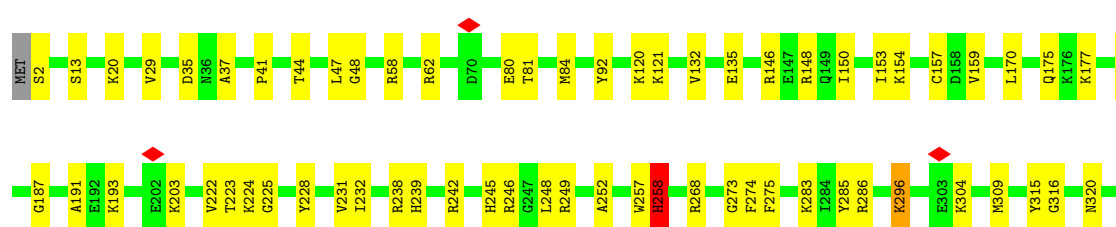
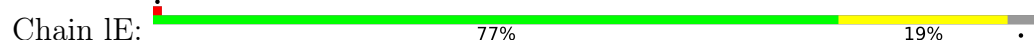
• Molecule 3: 5S rRNA

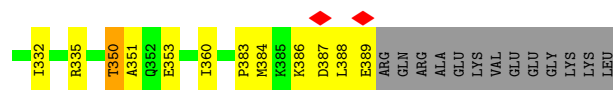


• Molecule 4: Large ribosomal subunit protein uL2

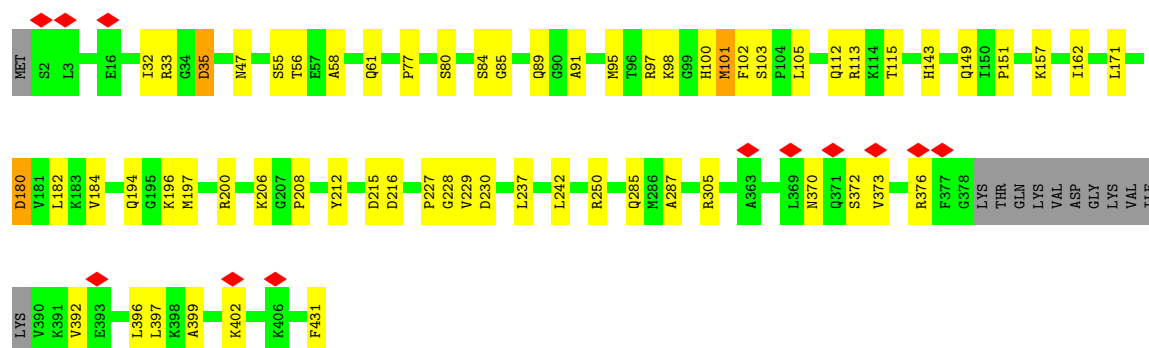
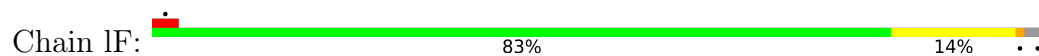


• Molecule 5: 60S ribosomal protein L3, putative

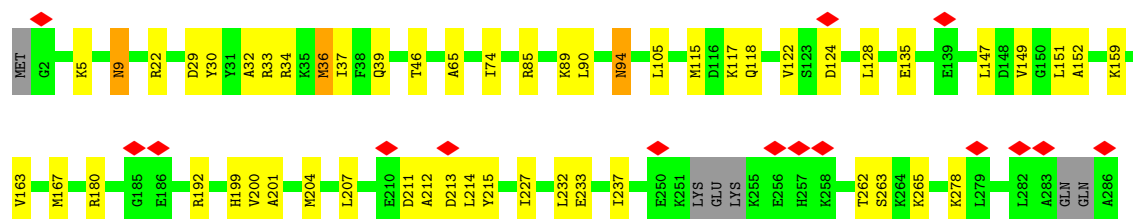
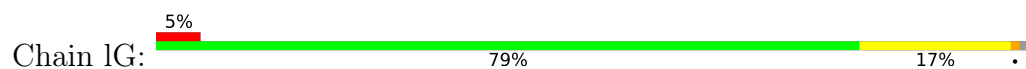




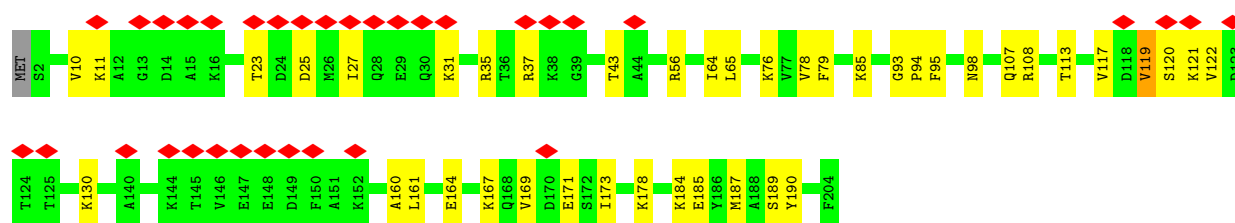
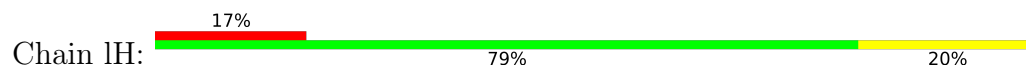
- Molecule 6: 60S ribosomal protein L4, putative



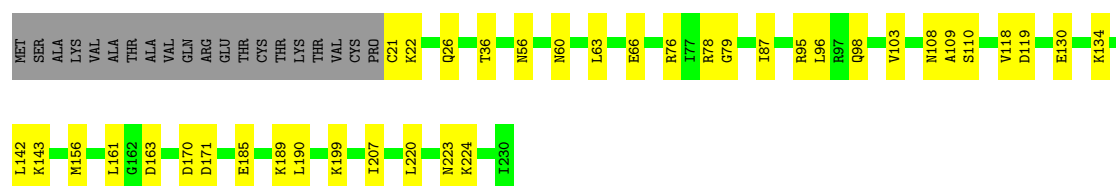
- Molecule 7: 60S ribosomal protein L5, putative



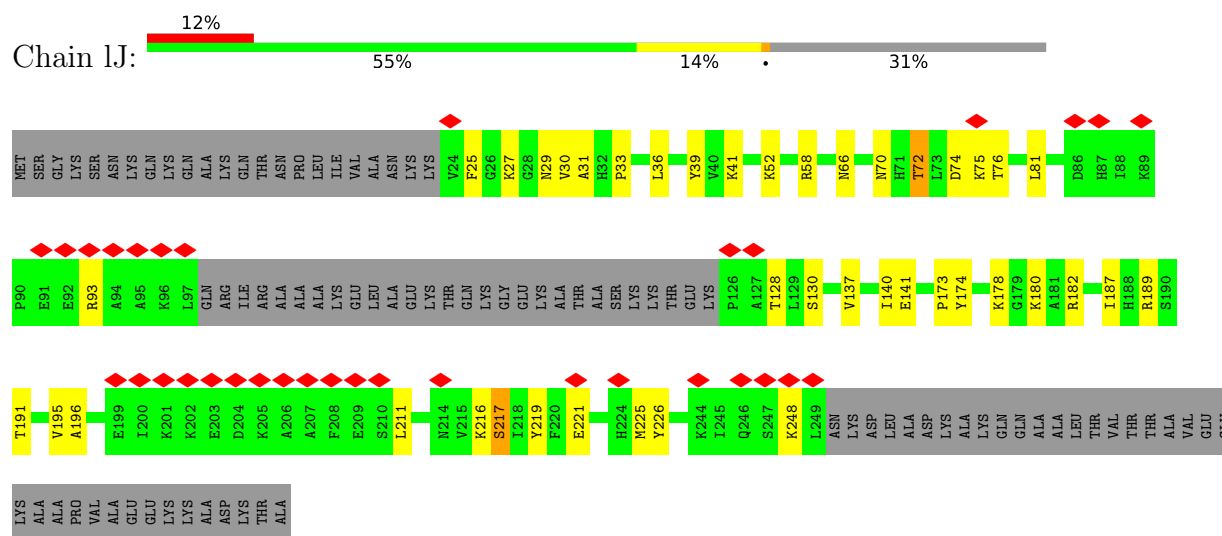
- Molecule 8: Large ribosomal subunit protein eL6



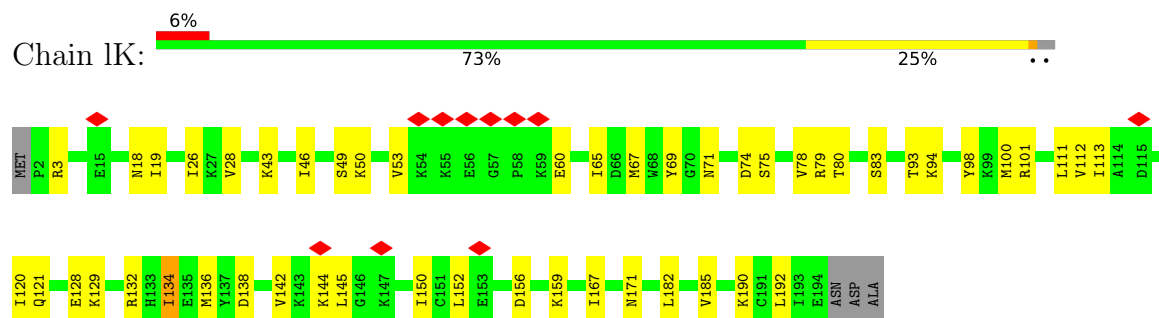
- Molecule 9: 60S ribosomal protein L7, putative



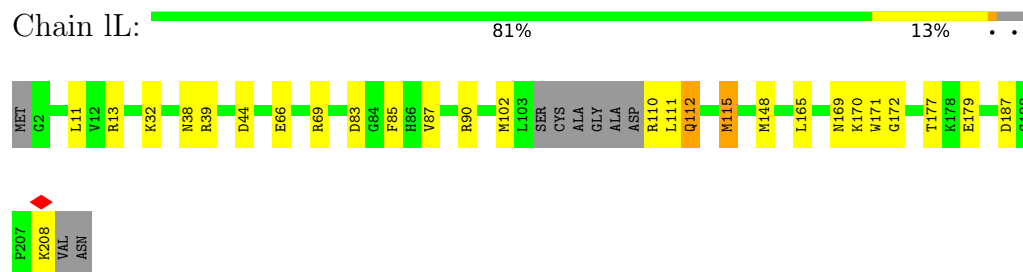
Chain 1J:



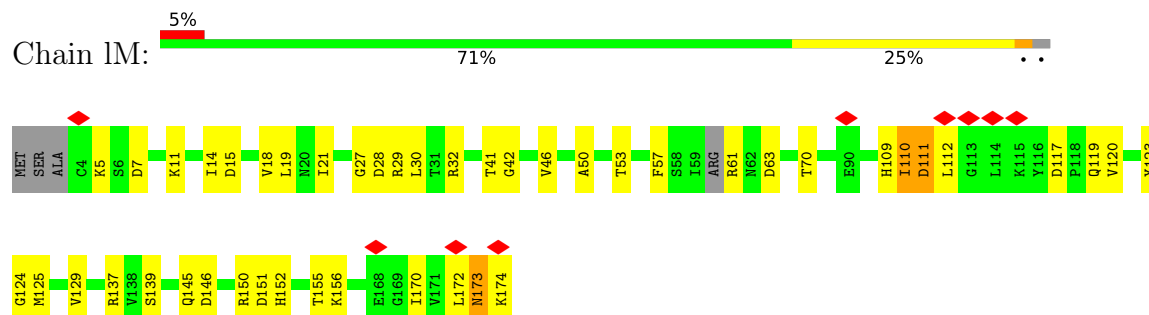
Chain 1K:

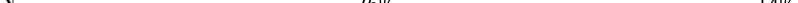


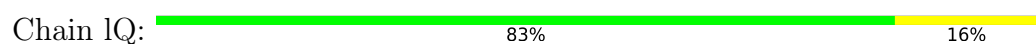
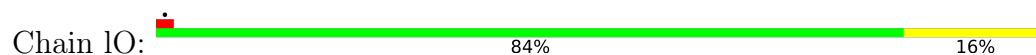
Chain 1L:

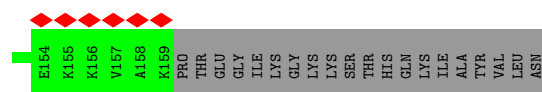


Chain 1M:



- Chain IN: 





- Molecule 19: 60S ribosomal protein L18, putative

Chain IS: 87% 12%



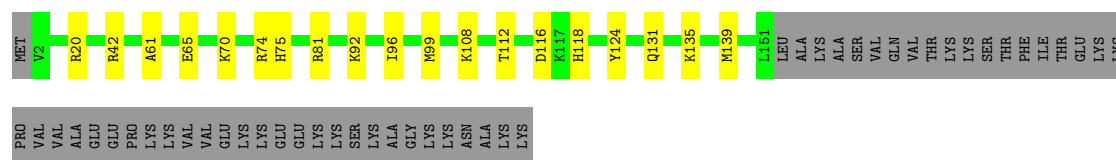
- Molecule 20: 60S ribosomal protein L18a

Chain IT: 87% 12%



- Molecule 21: Ribosomal protein L19

Chain IU: 66% 10% 24%



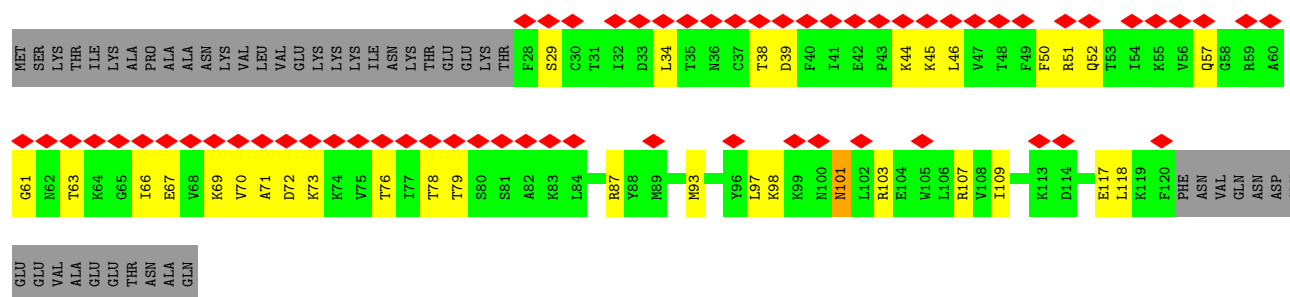
- Molecule 22: 60S ribosomal protein L21, putative

Chain IV: 86% 12%



- Molecule 23: Large ribosomal subunit protein eL22

Chain IW: 45% 44% 23% 32%



- Molecule 24: 60S ribosomal protein L23, putative

Chain IX: 



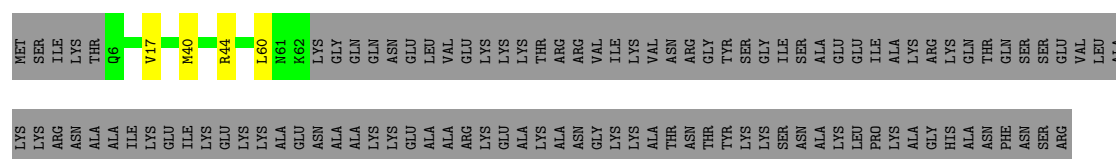
- Molecule 25: Ribosomal protein L23A, putative

Chain IY: 



- Molecule 26: 60S ribosomal protein L24, putative

Chain IZ: 



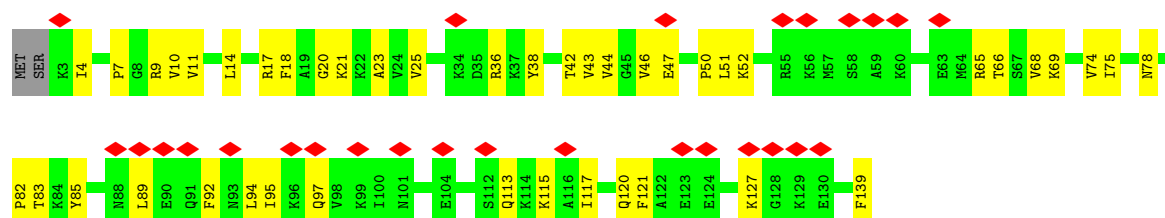
- Molecule 27: 60S ribosomal protein L26, putative

Chain Ia: 



- Molecule 28: 60S ribosomal protein L27, putative

Chain Ib: 



- Molecule 29: Large ribosomal subunit protein uL15A

Chain Ic: 



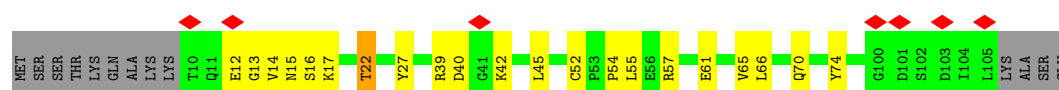
- Molecule 30: 60S ribosomal protein L29

Chain Id: 66% 27% • 6%



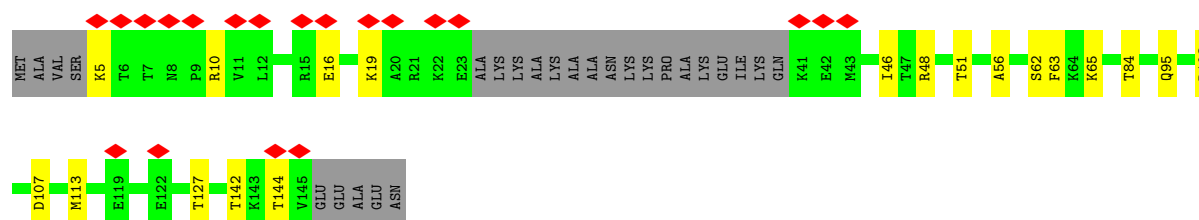
- Molecule 31: 60S ribosomal protein L30, putative

Chain le: 6% 69% 18% • 12%



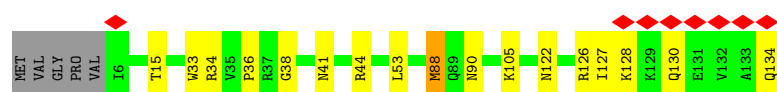
- Molecule 32: 60S ribosomal protein L31, putative

Chain lf: 13% 70% 13% 17%



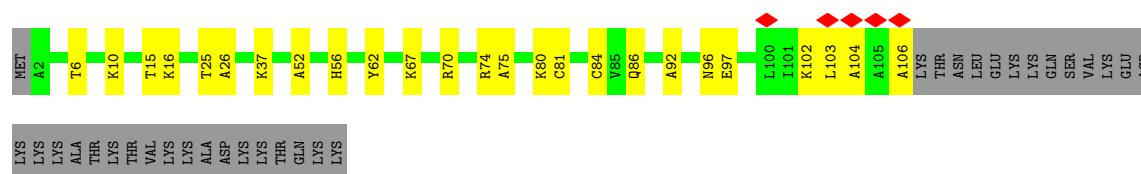
- Molecule 33: 60S ribosomal protein L32, putative

Chain lg: 6% 84% 12% • •



- Molecule 34: 60S ribosomal protein L34, putative

Chain lh: 58% 18% 23%

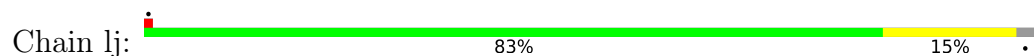


- Molecule 35: uL29

Chain li: 7% 77% 23%



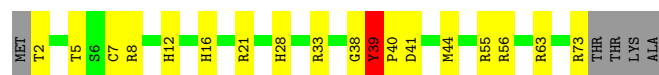
- Molecule 36: 60S ribosomal protein L35a, putative



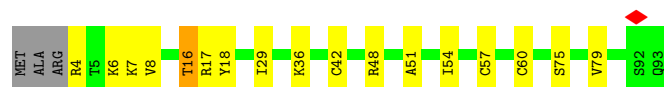
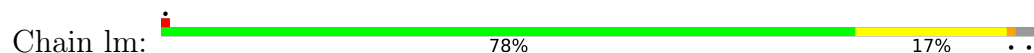
- Molecule 37: 60S ribosomal protein L36, putative



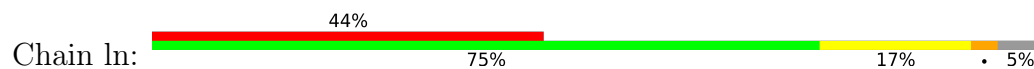
- Molecule 38: 60S ribosomal protein L37-A, putative



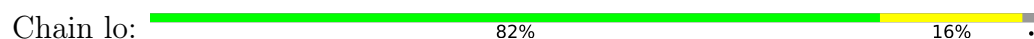
- Molecule 39: 60S ribosomal protein L37a, putative



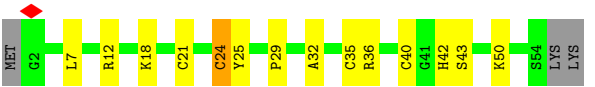
- Molecule 40: 60S ribosomal protein L38 putative



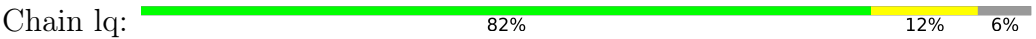
- Molecule 41: Ribosomal protein L39, putative



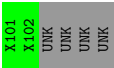
- Molecule 42: 60S ribosomal protein L40, putative



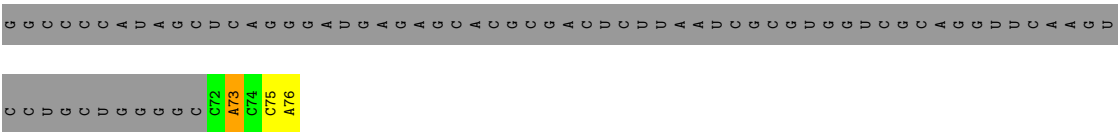
• Molecule 43: 60S ribosomal protein L44, putative



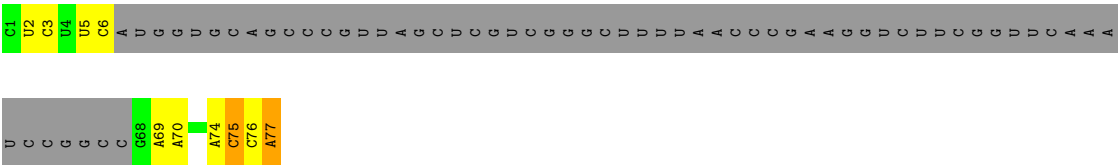
• Molecule 44: Unknown peptide



• Molecule 45: A/P- tRNA



• Molecule 46: P/E- tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39958	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	16.259	Depositor
Minimum map value	-5.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	1A	0.26	7/75197 (0.0%)	0.35	23/117139 (0.0%)
2	1B	0.24	1/3470 (0.0%)	0.30	0/5401
3	1C	0.23	0/2765	0.39	2/4303 (0.0%)
4	1D	0.21	0/1920	0.30	0/2582
5	1E	0.19	0/3149	0.28	0/4228
6	1F	0.19	0/3287	0.27	0/4413
7	1G	0.17	0/2265	0.29	0/3032
8	1H	0.15	0/1640	0.28	0/2204
9	1I	0.18	0/1680	0.26	0/2252
10	1J	0.15	0/1636	0.27	0/2199
11	1K	0.16	0/1562	0.24	0/2103
12	1L	0.18	0/1644	0.28	0/2198
13	1M	0.15	0/1369	0.27	0/1834
14	1N	0.17	0/2132	0.25	0/2844
15	1O	0.20	0/1646	0.28	0/2209
16	1P	0.18	0/1032	0.23	0/1388
17	1Q	0.22	0/1707	0.24	0/2276
18	1R	0.20	0/1251	0.26	0/1675
19	1S	0.20	0/1337	0.29	0/1789
20	1T	0.19	0/1445	0.27	0/1946
21	1U	0.17	0/1253	0.22	0/1666
22	1V	0.19	0/1351	0.26	0/1819
23	1W	0.11	0/774	0.31	0/1031
24	1X	0.20	0/1030	0.29	0/1384
25	1Y	0.17	0/941	0.26	0/1262
26	1Z	0.19	0/492	0.23	0/656
27	1a	0.16	0/1673	0.22	0/2236
28	1b	0.17	0/1112	0.28	0/1489
29	1c	0.23	0/1223	0.27	0/1636
30	1d	0.19	0/485	0.24	0/639
31	1e	0.16	0/724	0.26	0/977
32	1f	0.17	0/1034	0.22	0/1382
33	1g	0.20	0/1075	0.25	0/1434
34	1h	0.18	0/833	0.25	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.15	0/984	0.22	0/1310
36	lj	0.22	0/862	0.29	0/1163
37	lk	0.15	0/721	0.22	0/955
38	ll	0.23	0/602	0.31	0/797
39	lm	0.21	0/696	0.35	0/928
40	ln	0.15	0/592	0.25	0/789
41	lo	0.21	0/444	0.23	0/587
42	lp	0.19	0/425	0.48	1/563 (0.2%)
43	lq	0.19	0/770	0.25	0/1019
45	sI	0.16	0/115	0.46	0/176
46	sJ	0.20	0/377	0.32	0/580
All	All	0.23	8/132722 (0.0%)	0.33	26/195608 (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
5	lE	0	1
20	lT	0	1
38	ll	0	1
All	All	0	3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	lA	3485	U	O3'-P	-6.57	1.51	1.61
1	lA	2511	U	O3'-P	-6.17	1.51	1.61
1	lA	2905	U	O3'-P	-5.71	1.52	1.61
1	lA	2903	A	O3'-P	-5.57	1.52	1.61
1	lA	2347	A	O3'-P	-5.30	1.53	1.61
1	lA	184	A	C1'-N9	-5.22	1.40	1.48
1	lA	2906	U	O3'-P	-5.06	1.53	1.61
2	lB	1	A	C1'-N9	-5.05	1.40	1.48

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	lA	3473	U	C1'-C2'-O2'	-10.53	92.61	108.40
1	lA	2346	A	C3'-C2'-O2'	-9.46	96.52	110.70
3	lC	62	U	OP2-P-O3'	-8.96	81.13	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	lA	2902	G	C1'-C2'-O2'	-8.87	95.09	108.40
3	lC	62	U	OP1-P-O3'	-8.68	81.97	108.00
1	lA	2345	U	C4'-C3'-O3'	7.27	123.91	113.00
1	lA	2901	U	C4'-C3'-O3'	-7.09	102.37	113.00
1	lA	3471	A	C1'-C2'-O2'	-6.99	97.92	108.40
1	lA	3472	G	C4'-C3'-O3'	-6.98	102.53	113.00
1	lA	3484	A	O4'-C4'-C3'	-6.94	97.06	104.00
42	lp	24	CYS	CA-CB-SG	6.91	130.30	114.40
1	lA	2343	C	C3'-C2'-O2'	6.86	124.89	114.60
1	lA	2345	U	O4'-C4'-C3'	-6.79	97.21	104.00
1	lA	3471	A	C4'-C3'-O3'	-6.66	103.01	113.00
1	lA	3477	U	C4'-C3'-O3'	6.47	119.11	109.40
1	lA	2343	C	C4'-C3'-O3'	6.11	118.56	109.40
1	lA	2343	C	C4'-C3'-C2'	-5.93	96.67	102.60
1	lA	2347	A	C4'-C3'-O3'	-5.89	104.16	113.00
1	lA	3470	G	C4'-C3'-O3'	-5.75	104.37	113.00
1	lA	2344	U	O5'-P-OP1	-5.68	90.96	108.00
1	lA	3479	A	C2'-C3'-O3'	-5.56	105.36	113.70
1	lA	2348	G	O4'-C1'-C2'	-5.38	100.42	105.80
1	lA	2343	C	O3'-P-O5'	5.33	111.99	104.00
1	lA	2346	A	C1'-C2'-O2'	-5.17	100.64	108.40
1	lA	2343	C	N1-C1'-C2'	-5.14	106.29	114.00
1	lA	2345	U	C4'-C3'-C2'	-5.05	97.55	102.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
20	lT	172	LEU	Peptide
38	ll	39	TYR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	lA	67107	0	33663	1017	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	lB	3097	0	1552	49	0
3	lC	2477	0	1252	88	0
4	lD	1881	0	1928	36	0
5	lE	3085	0	3215	61	0
6	lF	3229	0	3433	41	0
7	lG	2227	0	2308	34	0
8	lH	1608	0	1728	29	0
9	lI	1658	0	1802	25	0
10	lJ	1606	0	1708	24	0
11	lK	1538	0	1598	33	0
12	lL	1608	0	1667	22	0
13	lM	1350	0	1390	35	0
14	lN	2104	0	2297	38	0
15	lO	1616	0	1700	22	0
16	lP	1020	0	1104	23	0
17	lQ	1676	0	1777	21	0
18	lR	1232	0	1307	24	0
19	lS	1316	0	1420	15	0
20	lT	1413	0	1479	17	0
21	lU	1235	0	1369	13	0
22	lV	1320	0	1406	20	0
23	lW	763	0	818	22	0
24	lX	1015	0	1054	13	0
25	lY	926	0	997	15	0
26	lZ	481	0	518	1	0
27	la	1651	0	1822	24	0
28	lb	1094	0	1174	31	0
29	lc	1192	0	1205	16	0
30	ld	478	0	507	13	0
31	le	716	0	750	13	0
32	lf	1015	0	1086	10	0
33	lg	1058	0	1140	13	0
34	lh	820	0	864	18	0
35	li	974	0	1093	18	0
36	lj	841	0	878	11	0
37	lk	712	0	755	18	0
38	ll	591	0	617	16	0
39	lm	688	0	726	15	0
40	ln	584	0	643	7	0
41	lo	432	0	444	7	0
42	lp	420	0	450	12	0
43	lq	756	0	821	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	sH	9	0	4	0	0
45	sI	104	0	56	4	0
46	sJ	339	0	175	4	0
All	All	123062	0	89700	1701	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (1701) 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)
1:1A:3139:G:H1'	2:1B:1:A:H2	1.11	1.14
5:1E:383:PRO:CB	5:1E:388:LEU:HD11	1.81	1.09
5:1E:383:PRO:HB2	5:1E:388:LEU:HD11	1.31	1.08
1:1A:3139:G:H1'	2:1B:1:A:C2	1.92	1.05
1:1A:869:G:H21	1:1A:872:A:N6	1.53	1.04
1:1A:3469:A:N6	1:1A:3485:U:H3	1.57	1.01
1:1A:3469:A:H62	1:1A:3485:U:H3	1.06	0.99
1:1A:2345:U:H3'	1:1A:2345:U:H6	1.27	0.97
1:1A:869:G:N2	1:1A:872:A:N6	2.14	0.94
1:1A:869:G:N2	1:1A:872:A:H62	1.67	0.92
1:1A:3467:U:H3	1:1A:3486:A:H2	1.17	0.92
28:1b:92:PHE:HB3	28:1b:95:ILE:HD12	1.49	0.92
3:1C:27:G:H1	3:1C:50:A:H61	1.08	0.91
1:1A:1841:G:H22	1:1A:1975:G:H1	1.15	0.90
3:1C:59:G:H5'	7:1G:265:LYS:HG2	1.52	0.90
1:1A:3474:U:H3	1:1A:3480:A:H62	1.21	0.88
1:1A:2345:U:H3'	1:1A:2345:U:C6	2.09	0.88
1:1A:2583:U:H1'	1:1A:2584:U:H5'	1.54	0.87
1:1A:2856:G:H8	1:1A:2903:A:H62	0.91	0.87
1:1A:3466:U:H3	1:1A:3487:C:H42	1.18	0.86
1:1A:3454:G:H1	1:1A:3501:A:H2	1.24	0.85
5:1E:386:LYS:O	5:1E:387:ASP:HB2	1.77	0.85
3:1C:69:U:H3	3:1C:104:G:H1	1.23	0.85
3:1C:52:G:N2	3:1C:54:U:O4	2.11	0.84
3:1C:80:G:H22	3:1C:94:U:H3	1.24	0.82
3:1C:27:G:H1	3:1C:50:A:N6	1.76	0.81
1:1A:2269:U:H5'	1:1A:2270:G:H5'	1.63	0.81
1:1A:1818:C:OP2	34:1h:74:ARG:NH2	2.14	0.81
33:1g:41:ASN:HB3	33:1g:44:ARG:HG2	1.61	0.81
1:1A:3452:U:H3	1:1A:3503:G:H22	1.26	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:737:A:H3'	1:1A:738:G:H21	1.45	0.81
37:1k:1:MET:HE3	37:1k:2:ALA:H	1.43	0.81
13:1M:109:HIS:HE1	13:1M:123:TYR:H	1.28	0.80
4:1D:107:CYS:HB3	4:1D:111:THR:HG21	1.64	0.80
3:1C:6:G:H1	3:1C:111:A:H2	1.28	0.79
5:1E:383:PRO:HB3	5:1E:388:LEU:HD11	1.62	0.79
1:1A:774:U:OP1	29:1c:21:ARG:NH2	2.15	0.79
1:1A:1345:U:H4'	1:1A:1346:G:H5'	1.64	0.79
1:1A:225:U:H3	1:1A:282:G:H1	1.30	0.79
3:1C:27:G:N2	3:1C:50:A:N1	2.27	0.79
1:1A:3458:U:H3	1:1A:3494:G:H1	1.30	0.79
1:1A:3473:U:H2'	1:1A:3474:U:O4'	1.82	0.79
1:1A:184:A:N1	1:1A:185:G:C8	2.51	0.79
1:1A:2857:A:N1	1:1A:2901:U:H5	1.82	0.78
17:1Q:116:LEU:O	17:1Q:117:ASN:ND2	2.16	0.78
1:1A:3456:U:H3	1:1A:3496:A:H2	1.32	0.78
1:1A:409:G:OP2	38:1l:56:ARG:NH2	2.16	0.78
1:1A:869:G:N2	1:1A:872:A:C6	2.53	0.77
1:1A:3476:C:H5	1:1A:3479:A:OP1	1.68	0.76
19:1S:73:HIS:HB3	19:1S:76:GLU:HG3	1.66	0.76
1:1A:1605:A:H2	1:1A:3430:U:H3	1.31	0.76
1:1A:703:G:N1	1:1A:744:A:N6	2.34	0.76
1:1A:2213:U:OP2	1:1A:2218:A:N6	2.18	0.75
7:1G:204:MET:HB3	7:1G:215:TYR:HE1	1.52	0.75
11:1K:43:LYS:HE3	15:1O:132:PRO:HG2	1.67	0.75
1:1A:1093:G:OP1	19:1S:19:ARG:NH2	2.20	0.75
1:1A:3454:G:N1	1:1A:3501:A:C2	2.50	0.75
3:1C:79:G:H1	3:1C:95:A:H2	1.35	0.74
3:1C:26:U:H3	3:1C:51:G:H22	1.35	0.74
34:1h:25:THR:HG22	34:1h:26:ALA:H	1.53	0.74
1:1A:869:G:N2	1:1A:872:A:C5	2.56	0.73
1:1A:1822:U:HO2'	34:1h:67:LYS:HZ2	1.37	0.73
1:1A:2333:C:H1'	1:1A:2334:U:H5''	1.70	0.72
1:1A:3476:C:H5''	1:1A:3477:U:C5	2.24	0.72
4:1D:19:ARG:NH1	4:1D:189:TYR:O	2.23	0.72
1:1A:1944:C:OP1	23:1W:107:ARG:NH2	2.22	0.72
1:1A:3468:U:H3'	1:1A:3469:A:C5'	2.19	0.72
1:1A:3463:A:H3'	1:1A:3464:G:H21	1.53	0.71
11:1K:136:MET:HE1	11:1K:152:LEU:HD23	1.70	0.71
1:1A:213:A:H5'	14:1N:133:LYS:H	1.54	0.71
28:1b:52:LYS:O	28:1b:65:ARG:NH1	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2856:G:H8	1:1A:2903:A:N6	1.77	0.71
1:1A:816:G:N2	1:1A:829:G:OP2	2.24	0.71
10:1J:174:TYR:HH	10:1J:226:TYR:HH	1.34	0.71
1:1A:663:G:OP2	16:1P:72:THR:OG1	2.08	0.71
1:1A:2979:C:H5	1:1A:2995:C:H42	1.39	0.71
1:1A:3475:U:H2'	1:1A:3476:C:O2	1.90	0.70
10:1J:219:TYR:HD1	10:1J:225:MET:HE1	1.56	0.70
29:1c:111:LYS:HG3	29:1c:129:TYR:HB2	1.72	0.70
1:1A:1813:G:N7	28:1b:17:ARG:NH2	2.38	0.70
1:1A:3468:U:H3'	1:1A:3469:A:H5'	1.73	0.70
1:1A:457:G:N2	18:1R:5:CYS:SG	2.65	0.70
1:1A:685:A:O4'	1:1A:1450:A:N6	2.25	0.70
1:1A:40:U:H5''	17:1Q:85:ALA:HB2	1.72	0.70
4:1D:126:ILE:HG21	4:1D:150:LEU:HD22	1.73	0.70
1:1A:1186:G:H21	1:1A:1220:A:H61	1.40	0.70
1:1A:3329:U:H4'	1:1A:3411:U:H4'	1.74	0.70
1:1A:534:A:N7	14:1N:145:LYS:NZ	2.40	0.70
1:1A:2261:G:O2'	1:1A:2390:U:OP2	2.10	0.70
18:1R:18:ARG:NH1	18:1R:20:ASP:OD1	2.24	0.70
1:1A:1269:U:OP2	33:1g:44:ARG:NH2	2.25	0.69
1:1A:3367:U:H2'	1:1A:3368:G:C8	2.27	0.69
1:1A:1661:G:O2'	1:1A:1751:A:N6	2.25	0.69
1:1A:1763:C:H2'	1:1A:1764:A:H8	1.55	0.69
1:1A:920:A:OP1	29:1c:27:LYS:NZ	2.24	0.69
1:1A:3457:G:H1	1:1A:3495:U:H3	1.40	0.69
32:1f:48:ARG:NH1	32:1f:144:THR:OG1	2.25	0.69
24:1X:22:ASN:ND2	24:1X:40:ILE:O	2.26	0.69
34:1h:81:CYS:SG	34:1h:84:CYS:N	2.63	0.69
1:1A:184:A:C6	1:1A:185:G:N7	2.61	0.69
1:1A:1502:A:N6	19:1S:15:SER:OG	2.23	0.69
1:1A:3483:A:H2'	1:1A:3484:A:H2	1.58	0.68
1:1A:2345:U:C6	1:1A:2345:U:C3'	2.72	0.68
1:1A:2848:A:N1	1:1A:2911:U:H5	1.92	0.68
1:1A:3476:C:H5''	1:1A:3477:U:H5	1.59	0.68
22:1V:88:ARG:NH2	30:1d:28:ALA:O	2.24	0.68
1:1A:3477:U:H1'	1:1A:3478:U:OP1	1.94	0.68
6:1F:101:MET:HE1	6:1F:105:LEU:HG	1.75	0.68
4:1D:117:GLU:HG2	4:1D:124:GLY:H	1.58	0.68
35:1i:-7:LEU:HD22	35:1i:42:ASP:HB3	1.75	0.68
1:1A:1314:A:OP2	15:1O:134:ARG:NH2	2.26	0.68
1:1A:873:U:H2'	1:1A:874:A:H8	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:1528:A:OP1	33:lg:126:ARG:NH2	2.25	0.67
10:lJ:81:LEU:HD12	10:lJ:211:LEU:HD21	1.76	0.67
3:lC:17:G:H1	3:lC:59:G:H22	1.41	0.67
1:lA:310:A:N1	1:lA:2873:G:O2'	2.25	0.67
9:II:21:CYS:SG	9:II:22:LYS:N	2.67	0.67
1:lA:2991:G:OP1	42:lp:25:TYR:OH	2.13	0.67
1:lA:3497:U:H4'	1:lA:3498:U:H5'	1.75	0.67
27:la:21:ALA:O	27:la:26:ARG:NH1	2.27	0.67
3:lC:84:G:H1	3:lC:91:G:H22	1.43	0.67
6:lF:143:HIS:N	6:lF:180:ASP:OD1	2.28	0.67
1:lA:493:G:O2'	1:lA:578:A:N6	2.27	0.67
1:lA:3486:A:H8	1:lA:3486:A:O5'	1.78	0.67
12:lL:66:GLU:OE1	12:lL:69:ARG:NH2	2.28	0.67
1:lA:331:A:OP2	43:lq:39:ARG:NH1	2.27	0.66
36:lj:5:ARG:NH1	36:lj:7:HIS:O	2.28	0.66
10:lJ:74:ASP:OD1	10:lJ:75:LYS:N	2.28	0.66
18:lR:34:ASP:OD1	18:lR:37:ARG:NH1	2.26	0.66
1:lA:3038:C:O2'	42:lp:25:TYR:O	2.13	0.66
2:IB:60:G:O6	38:ll:63:ARG:NH2	2.28	0.66
1:lA:2582:U:C6	1:lA:2583:U:C5	2.84	0.66
1:lA:639:G:H22	1:lA:650:A:H2	1.44	0.66
3:lC:2:G:O2'	3:lC:24:U:O2	2.14	0.66
1:lA:2381:G:OP2	1:lA:2381:G:N2	2.28	0.66
13:lM:109:HIS:CE1	13:lM:123:TYR:H	2.12	0.66
23:IW:51:ARG:O	23:IW:63:THR:OG1	2.14	0.66
11:lK:112:VAL:HB	11:lK:121:GLN:HB2	1.76	0.65
1:lA:2064:G:N1	1:lA:2067:A:OP2	2.29	0.65
25:IY:75:LYS:NZ	25:IY:86:VAL:O	2.25	0.65
1:lA:836:C:H2'	1:lA:837:A:H8	1.60	0.65
1:lA:2688:G:O2'	1:lA:3008:U:OP1	2.14	0.65
37:lk:2:ALA:O	37:lk:4:GLY:N	2.29	0.65
38:ll:33:ARG:NH2	38:ll:41:ASP:OD2	2.29	0.65
1:lA:493:G:H21	1:lA:580:A:H62	1.44	0.65
1:lA:500:G:H1	1:lA:572:U:H3	1.43	0.65
1:lA:625:A:O2'	1:lA:664:A:N6	2.29	0.65
1:lA:1744:A:H2'	1:lA:1745:A:C8	2.31	0.65
1:lA:2233:G:H4'	1:lA:2234:A:H5'	1.79	0.65
1:lA:3476:C:N4	1:lA:3479:A:C6	2.64	0.65
1:lA:896:A:O2'	1:lA:2790:U:OP1	2.14	0.65
1:lA:3107:G:N2	1:lA:3110:A:OP2	2.26	0.65
2:IB:154:C:OP1	10:lJ:75:LYS:NZ	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IH:56:ARG:NH2	8:IH:107:GLN:O	2.29	0.65
12:IL:112:GLN:HB2	45:sI:73:A:H8	1.60	0.65
1:lA:2432:A:H61	1:lA:3126:C:H5	1.45	0.65
1:lA:3469:A:N6	1:lA:3485:U:N3	2.39	0.65
1:lA:1086:G:H1	1:lA:1240:C:H5	1.45	0.65
23:IW:93:MET:HE3	23:IW:118:LEU:HD11	1.79	0.65
1:lA:3455:G:N1	1:lA:3500:A:C2	2.63	0.64
13:IM:125:MET:N	13:IM:125:MET:SD	2.70	0.64
12:IL:206:LEU:O	12:IL:208:LYS:NZ	2.30	0.64
16:IP:39:ASP:OD2	16:IP:49:ARG:NH2	2.30	0.64
28:lb:42:THR:HG22	28:lb:74:VAL:HG22	1.78	0.64
1:lA:221:U:H2'	1:lA:222:A:H8	1.62	0.64
3:lC:3:G:H22	3:lC:114:U:H3	1.45	0.64
34:lh:92:ALA:O	34:lh:96:ASN:ND2	2.31	0.64
1:lA:3211:A:H2	1:lA:3239:G:H21	1.46	0.64
1:lA:576:A:H62	1:lA:577:G:H21	1.44	0.64
11:lK:93:THR:HG22	11:lK:94:LYS:HG3	1.79	0.64
1:lA:184:A:C6	1:lA:185:G:C8	2.86	0.64
5:lE:383:PRO:HB2	5:lE:388:LEU:CD1	2.21	0.64
13:IM:50:ALA:HB3	13:IM:61:ARG:HA	1.79	0.64
38:ll:7:CYS:SG	38:ll:8:ARG:NH1	2.70	0.64
1:lA:1511:G:OP1	6:lF:200:ARG:NH1	2.31	0.64
1:lA:3474:U:H3	1:lA:3480:A:N6	1.95	0.64
2:lB:11:U:H2'	2:lB:12:A:H8	1.62	0.64
1:lA:1555:U:H2'	1:lA:1556:G:H8	1.63	0.64
1:lA:2645:G:H3'	1:lA:2646:G:H5''	1.80	0.64
1:lA:2911:U:H2'	1:lA:2912:U:C6	2.33	0.64
1:lA:1992:A:H2'	1:lA:1993:G:H8	1.63	0.63
1:lA:2857:A:H2	1:lA:2901:U:O4	1.81	0.63
3:lC:22:C:H2'	3:lC:23:A:H8	1.63	0.63
11:lK:100:MET:HE2	11:lK:152:LEU:HD11	1.79	0.63
1:lA:3463:A:H3'	1:lA:3464:G:N2	2.13	0.63
9:II:26:GLN:OE1	9:II:26:GLN:N	2.23	0.63
1:lA:705:U:H2'	1:lA:706:A:H8	1.62	0.63
1:lA:1648:U:OP2	1:lA:2081:A:O2'	2.16	0.63
1:lA:2416:U:O2'	1:lA:3246:A:N1	2.25	0.63
1:lA:3476:C:C4	1:lA:3479:A:C5	2.87	0.63
8:IH:56:ARG:NH1	36:lj:108:ILE:O	2.31	0.63
1:lA:43:C:OP2	1:lA:44:A:O2'	2.13	0.63
1:lA:312:A:OP2	37:lk:28:THR:OG1	2.12	0.63
30:ld:36:ASN:HB3	30:ld:39:VAL:HB	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:lp:29:PRO:HG2	42:lp:32:ALA:HB2	1.79	0.63
1:lA:1184:A:OP2	30:ld:26:LYS:NZ	2.27	0.63
1:lA:1763:C:H2'	1:lA:1764:A:C8	2.34	0.63
3:lC:22:C:H2'	3:lC:23:A:C8	2.33	0.63
9:II:220:LEU:O	9:II:223:ASN:ND2	2.31	0.63
24:IX:83:ARG:NH2	24:IX:118:THR:O	2.31	0.63
40:ln:38:ASN:N	40:ln:38:ASN:OD1	2.32	0.63
1:lA:1209:U:OP1	1:lA:1211:A:O2'	2.17	0.63
1:lA:1892:C:H2'	1:lA:1893:A:H8	1.61	0.63
1:lA:3248:A:OP2	24:IX:15:ARG:NH2	2.31	0.63
1:lA:3476:C:N3	1:lA:3477:U:C2	2.67	0.63
6:lF:61:GLN:OE1	38:II:55:ARG:NH2	2.29	0.63
1:lA:1561:U:OP2	29:lc:4:ARG:NH1	2.29	0.63
3:lC:81:A:H2	3:lC:93:G:H1	1.47	0.63
16:lP:25:ALA:HA	16:lP:40:GLY:HA3	1.79	0.63
1:lA:589:A:OP1	8:lH:35:ARG:NH1	2.30	0.63
25:IY:56:GLU:N	25:IY:56:GLU:OE2	2.32	0.63
5:lE:92:TYR:HB2	5:lE:159:VAL:HB	1.80	0.62
1:lA:1476:G:O2'	1:lA:1477:A:H5'	1.99	0.62
1:lA:1846:A:H2'	1:lA:1847:A:C8	2.34	0.62
8:lH:23:THR:OG1	8:lH:25:ASP:OD1	2.17	0.62
9:II:87:ILE:HG23	9:II:118:VAL:HG12	1.81	0.62
1:lA:1760:A:OP1	40:ln:31:ARG:NH2	2.32	0.62
1:lA:732:U:O2'	1:lA:733:C:O5'	2.15	0.62
1:lA:1157:A:H5'	7:lG:5:LYS:HE2	1.82	0.62
4:lD:242:ARG:NH1	4:lD:243:THR:O	2.32	0.62
16:lP:12:VAL:O	16:lP:60:THR:OG1	2.15	0.62
12:IL:187:ASP:O	12:IL:189:LYS:NZ	2.32	0.62
13:lM:21:ILE:HD11	13:lM:125:MET:HG3	1.81	0.62
1:lA:1728:A:N7	1:lA:1729:G:N2	2.47	0.62
23:IW:70:VAL:HG22	23:IW:72:ASP:H	1.63	0.62
13:lM:32:ARG:HH21	13:lM:120:VAL:HG22	1.65	0.62
1:lA:873:U:H2'	1:lA:874:A:C8	2.34	0.61
1:lA:2101:G:O2'	1:lA:2410:U:O4	2.14	0.61
1:lA:789:C:H2'	1:lA:790:A:H8	1.65	0.61
1:lA:3470:G:C6	1:lA:3483:A:C6	2.88	0.61
1:lA:1312:A:H62	1:lA:1441:U:H3	1.48	0.61
1:lA:2114:U:N3	1:lA:2198:G:OP2	2.32	0.61
1:lA:2815:G:N2	1:lA:2818:A:OP2	2.30	0.61
1:lA:3426:U:O4	5:lE:121:LYS:NZ	2.32	0.61
1:lA:960:G:O2'	21:lU:131:GLN:OE1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3476:C:N4	1:1A:3479:A:C5	2.69	0.61
1:1A:3469:A:P	1:1A:3469:A:C2	2.94	0.61
4:1D:36:GLU:OE1	4:1D:163:ARG:NH1	2.33	0.61
20:1T:69:LYS:NZ	20:1T:93:VAL:O	2.32	0.61
16:1P:54:LEU:HD23	16:1P:57:ILE:HD11	1.80	0.61
1:1A:2865:A:O2'	1:1A:2866:C:O4'	2.16	0.61
5:1E:58:ARG:NH1	5:1E:353:GLU:OE2	2.34	0.61
1:1A:1841:G:N2	1:1A:1975:G:H22	1.99	0.60
1:1A:3276:U:OP2	42:lp:36:ARG:NH1	2.31	0.60
5:1E:386:LYS:O	5:1E:387:ASP:CB	2.49	0.60
6:1F:372:SER:HB3	6:1F:396:LEU:HD12	1.83	0.60
1:1A:1406:A:H2'	1:1A:1407:U:C6	2.35	0.60
1:1A:1538:G:N2	1:1A:1541:A:OP2	2.33	0.60
1:1A:2257:G:OP1	4:1D:193:ARG:NH2	2.34	0.60
38:ll:39:TYR:O	38:ll:41:ASP:N	2.35	0.60
1:1A:1523:U:OP1	33:lg:105:LYS:NZ	2.33	0.60
1:1A:3091:C:OP1	5:1E:246:ARG:NH1	2.32	0.60
6:1F:230:ASP:OD2	6:1F:250:ARG:NH2	2.34	0.60
1:1A:1965:U:H3	1:1A:2150:G:H21	1.47	0.60
1:1A:2857:A:C2	1:1A:2901:U:C5	2.89	0.60
2:1B:49:C:O2'	2:1B:63:A:O2'	2.14	0.60
1:1A:869:G:C5	1:1A:870:A:H1'	2.36	0.60
1:1A:1198:U:H3	1:1A:1204:A:H62	1.50	0.60
1:1A:1863:U:O4	23:1W:103:ARG:NH1	2.34	0.60
3:1C:29:G:O6	3:1C:46:G:O6	2.20	0.60
34:lh:62:TYR:O	34:lh:70:ARG:NH1	2.35	0.60
1:1A:447:G:N2	2:1B:17:G:OP2	2.35	0.60
19:1S:35:LEU:O	19:1S:39:THR:OG1	2.15	0.60
1:1A:511:A:H62	1:1A:561:G:H21	1.50	0.60
1:1A:1864:C:OP1	23:1W:98:LYS:NZ	2.33	0.60
6:1F:287:ALA:N	19:1S:121:ASP:OD2	2.31	0.60
12:1L:171:TRP:CD1	12:1L:172:GLY:H	2.19	0.60
1:1A:2857:A:C2	1:1A:2901:U:H5	2.20	0.60
1:1A:3476:C:C5'	1:1A:3477:U:H5	2.14	0.60
1:1A:2468:C:O2'	5:1E:268:ARG:NH1	2.23	0.60
1:1A:2343:C:H1'	1:1A:2344:U:OP2	2.03	0.59
3:1C:85:G:H22	3:1C:90:G:H1	1.49	0.59
1:1A:537:U:O2	1:1A:2861:U:N3	2.35	0.59
1:1A:720:U:H2'	1:1A:721:A:H8	1.65	0.59
1:1A:1639:U:H2'	1:1A:1640:A:H8	1.67	0.59
1:1A:1823:C:H2'	1:1A:1824:A:C4	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:ll:21:ARG:NH2	38:ll:38:GLY:O	2.35	0.59
1:lA:2079:A:H2'	1:lA:2080:A:O4'	2.01	0.59
1:lA:574:U:H2'	1:lA:575:A:C8	2.38	0.59
1:lA:2289:A:H2'	1:lA:2290:A:C8	2.37	0.59
2:lB:11:U:H2'	2:lB:12:A:C8	2.36	0.59
1:lA:344:A:N7	37:lk:32:HIS:NE2	2.51	0.59
1:lA:871:A:H2'	1:lA:872:A:C8	2.37	0.59
1:lA:1186:G:H21	1:lA:1220:A:N6	1.99	0.59
5:lE:223:THR:OG1	5:lE:273:GLY:O	2.20	0.59
13:lM:151:ASP:N	13:lM:151:ASP:OD1	2.36	0.59
19:lS:152:VAL:HA	19:lS:159:ALA:H	1.66	0.59
1:lA:573:A:H2'	1:lA:574:U:C6	2.38	0.59
2:lB:61:A:OP2	2:lB:96:A:O2'	2.16	0.59
3:lC:6:G:OP1	7:lG:33:ARG:NH1	2.36	0.59
1:lA:206:U:H3	1:lA:303:G:H1	1.49	0.59
1:lA:662:U:H2'	1:lA:663:G:O4'	2.03	0.59
1:lA:2583:U:C1'	1:lA:2584:U:H5'	2.31	0.59
3:lC:79:G:N1	3:lC:95:A:C2	2.57	0.59
4:lD:140:ASN:ND2	4:lD:143:ASN:OD1	2.36	0.59
6:lF:77:PRO:HB2	6:lF:91:ALA:HB3	1.83	0.59
1:lA:404:G:N2	1:lA:407:A:OP2	2.30	0.59
1:lA:698:U:O2'	1:lA:699:A:N3	2.36	0.59
1:lA:1115:A:O2'	3:lC:76:U:O2	2.20	0.59
1:lA:626:A:N6	1:lA:663:G:O2'	2.35	0.59
1:lA:645:A:H61	16:lP:82:GLN:HA	1.66	0.59
1:lA:1308:A:OP1	16:lP:55:ASN:ND2	2.35	0.59
1:lA:1639:U:H2'	1:lA:1640:A:C8	2.38	0.59
25:lY:6:ARG:NH2	25:lY:10:ALA:O	2.35	0.59
1:lA:424:A:O2'	1:lA:425:C:OP2	2.22	0.58
1:lA:467:A:N1	1:lA:2438:C:O2'	2.27	0.58
1:lA:3472:G:H2'	1:lA:3473:U:O2	2.03	0.58
6:lF:194:GLN:HG3	6:lF:197:MET:HE3	1.83	0.58
28:lb:10:VAL:O	28:lb:83:THR:OG1	2.15	0.58
1:lA:979:G:C5	4:lD:181:LYS:HB3	2.38	0.58
3:lC:84:G:H22	3:lC:91:G:N2	2.00	0.58
4:lD:103:PRO:HG2	4:lD:106:GLN:HG2	1.85	0.58
37:lk:73:THR:HB	37:lk:76:ARG:HB2	1.85	0.58
1:lA:682:G:H5'	20:lT:2:LYS:HD3	1.85	0.58
1:lA:699:A:H2'	1:lA:700:A:C8	2.38	0.58
1:lA:1555:U:H2'	1:lA:1556:G:C8	2.38	0.58
1:lA:3477:U:H1'	1:lA:3478:U:P	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:853:A:N6	1:1A:889:A:O2'	2.36	0.58
1:1A:817:A:H2'	1:1A:818:A:C8	2.39	0.58
1:1A:1292:A:H61	1:1A:1457:A:H61	1.50	0.58
1:1A:2062:A:O2'	1:1A:3220:U:OP1	2.20	0.58
1:1A:2100:G:HO2'	24:1X:24:SER:HG	1.50	0.58
1:1A:1019:G:H1'	1:1A:1737:A:N6	2.19	0.58
1:1A:1118:A:H2	1:1A:1165:A:H62	1.51	0.58
1:1A:1335:U:O2	20:1T:109:GLN:NE2	2.33	0.58
3:1C:18:U:H3	3:1C:58:A:H61	1.52	0.58
1:1A:440:G:N1	1:1A:443:A:OP2	2.32	0.58
1:1A:1883:A:H62	1:1A:1931:U:H3	1.50	0.58
1:1A:3405:A:N6	8:1H:164:GLU:OE1	2.37	0.58
5:1E:304:LYS:NZ	5:1E:360:ILE:O	2.34	0.58
3:1C:40:G:N2	3:1C:43:A:C2	2.70	0.58
6:1F:212:TYR:HB2	6:1F:216:ASP:HB2	1.86	0.58
20:1T:158:ARG:O	36:1j:35:ASN:ND2	2.32	0.58
1:1A:637:U:O2'	1:1A:638:A:N7	2.30	0.58
1:1A:765:A:C2	36:1j:92:PRO:HG2	2.38	0.58
1:1A:1912:A:H61	39:1m:42:CYS:HA	1.69	0.58
8:1H:122:VAL:HG12	8:1H:169:VAL:HG13	1.86	0.58
23:1W:52:GLN:HA	23:1W:61:GLY:HA2	1.85	0.58
32:1f:84:THR:OG1	32:1f:127:THR:OG1	2.22	0.58
4:1D:10:LYS:HE2	4:1D:195:THR:HG22	1.86	0.57
9:1I:76:ARG:NH2	9:1I:79:GLY:O	2.34	0.57
1:1A:500:G:N2	1:1A:572:U:O2	2.34	0.57
1:1A:1057:C:OP2	29:1c:26:ARG:NH1	2.37	0.57
1:1A:1177:A:H2'	1:1A:1178:A:C8	2.39	0.57
1:1A:1220:A:H2'	1:1A:1220:A:N3	2.17	0.57
2:1B:141:G:H2'	2:1B:142:A:H8	1.69	0.57
19:1S:17:THR:OG1	19:1S:26:LYS:NZ	2.37	0.57
42:1p:21:CYS:HB3	42:1p:24:CYS:HB2	1.86	0.57
20:1T:5:TYR:HB2	20:1T:60:ILE:HD11	1.85	0.57
21:1U:99:MET:HE2	21:1U:99:MET:HA	1.86	0.57
1:1A:640:G:H1	1:1A:649:U:H3	1.50	0.57
1:1A:703:G:C6	1:1A:744:A:N6	2.73	0.57
1:1A:1841:G:N2	1:1A:1975:G:H1	1.96	0.57
9:1I:56:ASN:O	9:1I:60:ASN:ND2	2.31	0.57
12:1L:170:LYS:HA	12:1L:177:THR:HA	1.87	0.57
1:1A:1121:A:N1	1:1A:1168:C:O2'	2.36	0.57
1:1A:2214:A:HO2'	38:1l:2:THR:N	2.02	0.57
1:1A:3146:U:H4'	1:1A:3147:U:H5''	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:ln:56:ASP:HB3	40:ln:59:LYS:HG3	1.84	0.57
1:lA:1897:A:C2	1:lA:1913:G:N2	2.69	0.57
1:lA:2865:A:H4'	37:lk:21:ALA:HA	1.86	0.57
5:lE:175:GLN:NE2	5:lE:177:LYS:O	2.36	0.57
11:lK:101:ARG:HE	42:lp:7:LEU:HD21	1.68	0.57
24:IX:43:LYS:HG3	24:IX:60:MET:HG2	1.85	0.57
37:lk:53:ASP:OD2	37:lk:57:ARG:NH1	2.37	0.57
1:lA:564:A:H1'	1:lA:565:U:OP2	2.04	0.57
1:lA:709:U:O2'	1:lA:710:A:OP1	2.23	0.57
1:lA:220:A:H2'	1:lA:221:U:C6	2.40	0.57
1:lA:1405:U:H2'	1:lA:1406:A:C8	2.40	0.57
8:lH:76:LYS:O	8:lH:98:ASN:ND2	2.38	0.57
1:lA:191:A:H2'	1:lA:192:A:C8	2.40	0.56
1:lA:996:C:O2'	1:lA:999:G:O2'	2.20	0.56
1:lA:1458:C:OP1	9:lI:98:GLN:NE2	2.38	0.56
1:lA:1764:A:H2'	1:lA:1765:A:H8	1.70	0.56
1:lA:3397:C:OP2	1:lA:3398:U:O2'	2.23	0.56
1:lA:908:A:H2'	1:lA:909:A:C8	2.40	0.56
1:lA:1313:U:O2'	1:lA:1315:A:N7	2.36	0.56
1:lA:2131:A:H4'	1:lA:2397:C:H5'	1.86	0.56
1:lA:3476:C:H3'	1:lA:3477:U:C6	2.39	0.56
3:lC:55:C:O2'	13:lM:146:ASP:OD2	2.22	0.56
5:lE:222:VAL:O	5:lE:335:ARG:NH1	2.37	0.56
6:lF:184:VAL:HG11	6:lF:228:GLY:HA3	1.86	0.56
1:lA:199:G:N1	1:lA:311:A:OP2	2.37	0.56
1:lA:501:U:H2'	1:lA:502:U:H6	1.69	0.56
1:lA:2183:A:H2'	1:lA:2184:A:H8	1.70	0.56
1:lA:3149:A:H2'	1:lA:3150:A:C8	2.40	0.56
1:lA:3306:U:HO2'	1:lA:3322:A:HO2'	1.39	0.56
2:lB:48:G:OP2	41:lo:15:LYS:NZ	2.29	0.56
23:lW:67:GLU:O	23:lW:69:LYS:NZ	2.38	0.56
2:lB:93:C:OP1	38:ll:73:ARG:NH1	2.37	0.56
20:lT:70:ASN:OD1	20:lT:91:ARG:NH1	2.36	0.56
1:lA:535:A:N1	14:lN:218:ASN:ND2	2.46	0.56
1:lA:760:A:H2'	1:lA:761:A:H8	1.71	0.56
1:lA:919:G:H22	6:lF:103:SER:HB2	1.71	0.56
1:lA:926:A:H62	1:lA:1053:G:H1	1.52	0.56
1:lA:2900:G:H2'	1:lA:2901:U:O2	2.06	0.56
11:lK:49:SER:OG	11:lK:50:LYS:N	2.39	0.56
22:IV:75:MET:SD	22:IV:88:ARG:NH1	2.79	0.56
31:le:52:CYS:O	31:le:57:ARG:NH2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1519:A:H5'	1:1A:1521:A:H61	1.71	0.56
1:1A:2677:G:OP1	4:1D:233:GLN:NE2	2.37	0.56
1:1A:2767:A:H2'	1:1A:2768:G:C8	2.40	0.56
1:1A:2829:A:H5''	1:1A:2830:C:H5'	1.88	0.56
3:1C:10:A:N1	3:1C:65:U:O2'	2.38	0.56
18:1R:50:ASN:ND2	18:1R:56:GLU:OE1	2.38	0.56
27:1a:48:PRO:O	27:1a:113:ARG:NH2	2.39	0.56
1:1A:3469:A:C2	1:1A:3469:A:OP1	2.59	0.56
3:1C:109:G:H2'	3:1C:110:A:C8	2.41	0.56
13:1M:29:ARG:NE	13:1M:123:TYR:OH	2.34	0.56
1:1A:2334:U:H2'	1:1A:2335:A:C8	2.40	0.56
1:1A:3454:G:N1	1:1A:3501:A:H2	1.95	0.56
2:1B:92:C:H1'	38:1l:73:ARG:HG3	1.88	0.56
5:1E:224:LYS:HB2	5:1E:332:ILE:HG23	1.88	0.56
1:1A:1554:C:OP2	6:1F:196:LYS:NZ	2.35	0.56
1:1A:2649:G:OP2	1:1A:2650:A:O2'	2.22	0.56
1:1A:3372:U:O2'	1:1A:3374:C:OP2	2.22	0.56
2:1B:141:G:H2'	2:1B:142:A:C8	2.41	0.56
7:1G:65:ALA:HB2	7:1G:74:ILE:HD13	1.88	0.56
1:1A:233:A:N3	1:1A:254:C:O2'	2.39	0.55
1:1A:453:A:N3	1:1A:789:C:O2'	2.38	0.55
1:1A:897:A:H8	1:1A:898:U:O2'	1.90	0.55
1:1A:1744:A:H2'	1:1A:1745:A:H8	1.70	0.55
1:1A:2343:C:O2'	1:1A:2344:U:P	2.64	0.55
1:1A:2433:A:H2'	1:1A:2434:A:C8	2.40	0.55
3:1C:17:G:H22	3:1C:59:G:N2	2.03	0.55
4:1D:117:GLU:OE2	4:1D:163:ARG:NH2	2.36	0.55
8:1H:76:LYS:NZ	8:1H:189:SER:O	2.35	0.55
10:1J:27:LYS:HE2	10:1J:33:PRO:HD2	1.88	0.55
17:1Q:80:VAL:HB	17:1Q:82:ARG:HD2	1.88	0.55
27:1a:87:LYS:O	27:1a:89:ASN:N	2.39	0.55
1:1A:789:C:H2'	1:1A:790:A:C8	2.41	0.55
1:1A:2230:U:H2'	1:1A:2231:C:C6	2.41	0.55
3:1C:78:C:H2'	3:1C:79:G:H8	1.71	0.55
14:1N:9:ASN:HB2	19:1S:165:LYS:HB2	1.88	0.55
1:1A:191:A:H2'	1:1A:192:A:H8	1.71	0.55
1:1A:660:U:H2'	1:1A:661:G:H8	1.71	0.55
1:1A:3044:G:O2'	1:1A:3178:A:N1	2.37	0.55
8:1H:64:ILE:O	8:1H:113:THR:OG1	2.25	0.55
1:1A:184:A:C2	1:1A:185:G:C8	2.94	0.55
1:1A:2236:A:H2'	1:1A:2237:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IC:85:G:N2	3:IC:90:G:H22	2.04	0.55
1:IA:1342:U:H2'	1:IA:1343:A:H4'	1.88	0.55
1:IA:3470:G:N2	1:IA:3484:A:C2	2.75	0.55
11:IK:94:LYS:HB2	11:IK:192:LEU:HD23	1.89	0.55
22:IV:151:ASP:OD1	22:IV:151:ASP:N	2.40	0.55
1:IA:586:A:N6	8:IH:43:THR:O	2.39	0.55
1:IA:700:A:OP2	1:IA:745:A:N6	2.40	0.55
1:IA:1405:U:H2'	1:IA:1406:A:H8	1.72	0.55
1:IA:3103:C:H2'	1:IA:3104:G:H8	1.71	0.55
1:IA:3149:A:H2'	1:IA:3150:A:H8	1.72	0.55
3:IC:2:G:H2'	3:IC:3:G:H8	1.72	0.55
3:IC:103:U:H2'	3:IC:104:G:C8	2.42	0.55
7:IG:9:ASN:N	7:IG:9:ASN:OD1	2.39	0.55
35:li:9:ALA:HB1	35:li:45:ARG:HH12	1.70	0.55
1:IA:643:A:OP1	16:IP:91:LYS:NZ	2.36	0.55
4:ID:168:ILE:HD11	39:lm:79:VAL:HG21	1.89	0.55
7:IG:149:VAL:HG12	7:IG:152:ALA:HB3	1.88	0.55
1:IA:1876:U:H2'	1:IA:1936:A:H61	1.71	0.55
25:IY:116:THR:HG22	25:IY:121:PHE:HB2	1.89	0.55
1:IA:487:A:H2'	1:IA:488:A:H8	1.71	0.55
1:IA:1071:A:H4'	1:IA:1087:G:N2	2.22	0.55
1:IA:1327:A:H2'	1:IA:1328:A:C8	2.42	0.55
1:IA:2297:G:N7	37:lk:61:LYS:NZ	2.55	0.55
1:IA:777:U:O2'	1:IA:1278:A:N1	2.34	0.54
1:IA:2318:U:H5''	4:ID:244:GLY:HA3	1.88	0.54
1:IA:3467:U:N3	1:IA:3486:A:H2	1.96	0.54
4:ID:161:ASN:OD1	4:ID:161:ASN:N	2.40	0.54
1:IA:596:G:OP1	8:IH:108:ARG:NH2	2.40	0.54
1:IA:1846:A:H2'	1:IA:1847:A:H8	1.72	0.54
2:IB:101:G:OP2	2:IB:103:A:O2'	2.25	0.54
33:lg:33:TRP:O	33:lg:34:ARG:NH1	2.40	0.54
1:IA:760:A:H2'	1:IA:761:A:C8	2.42	0.54
1:IA:118:A:N6	1:IA:189:G:O2'	2.36	0.54
1:IA:686:A:H5'	9:II:134:LYS:HE3	1.90	0.54
1:IA:2173:A:H2'	1:IA:2174:U:C6	2.43	0.54
3:IC:17:G:H1	3:IC:59:G:H1	1.55	0.54
14:IN:82:LYS:NZ	14:IN:215:LYS:O	2.37	0.54
17:IQ:31:ARG:NH1	17:IQ:124:ASP:OD2	2.38	0.54
23:IW:73:LYS:O	23:IW:73:LYS:NZ	2.33	0.54
32:If:63:PHE:HB3	32:If:103:ARG:HG2	1.88	0.54
1:IA:2341:C:C2'	1:IA:2342:U:H5'	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2730:U:H2'	1:1A:2731:G:H8	1.71	0.54
2:1B:25:U:OP2	27:1a:15:ARG:NH1	2.40	0.54
7:1G:204:MET:HB3	7:1G:215:TYR:CE1	2.39	0.54
33:1g:130:GLN:HG3	33:1g:134:GLN:HG2	1.89	0.54
1:1A:494:G:H4'	1:1A:495:A:OP1	2.07	0.54
1:1A:2343:C:O2'	1:1A:2344:U:OP1	2.23	0.54
1:1A:2721:G:H1	1:1A:2941:C:H5	1.54	0.54
1:1A:2846:U:H2'	1:1A:2847:A:C8	2.42	0.54
1:1A:3476:C:C4	1:1A:3479:A:N7	2.76	0.54
3:1C:17:G:H1	3:1C:59:G:N2	2.04	0.54
3:1C:29:G:N7	3:1C:46:G:N1	2.48	0.54
3:1C:89:G:H4'	12:1L:11:LEU:HD22	1.89	0.54
25:1Y:38:GLU:OE2	25:1Y:38:GLU:N	2.32	0.54
1:1A:425:C:H2'	1:1A:426:U:H6	1.73	0.54
1:1A:3454:G:H22	1:1A:3501:A:H2	1.54	0.54
1:1A:3483:A:H2'	1:1A:3484:A:C2	2.41	0.54
1:1A:98:A:H4'	14:1N:59:MET:HE2	1.88	0.54
1:1A:502:U:H2'	1:1A:503:A:H8	1.72	0.54
1:1A:816:G:H22	1:1A:829:G:P	2.29	0.54
1:1A:1940:A:H2'	1:1A:1941:A:H8	1.73	0.54
24:1X:8:GLY:O	24:1X:10:GLN:NE2	2.41	0.54
32:1f:107:ASP:N	32:1f:107:ASP:OD1	2.40	0.54
43:1q:54:PRO:O	46:sJ:76:C:O2'	2.20	0.54
1:1A:336:A:H5''	17:1Q:97:SER:HB3	1.89	0.54
1:1A:1520:A:H4'	1:1A:1521:A:O5'	2.08	0.54
3:1C:2:G:H2'	3:1C:3:G:C8	2.42	0.54
12:1L:169:ASN:OD1	12:1L:170:LYS:NZ	2.41	0.54
13:1M:63:ASP:OD1	13:1M:63:ASP:N	2.33	0.54
13:1M:110:ILE:HD12	13:1M:111:ASP:H	1.72	0.54
30:1d:7:ARG:NH2	30:1d:9:SER:OG	2.40	0.54
1:1A:3469:A:C5'	1:1A:3469:A:N3	2.71	0.54
29:1c:43:THR:O	29:1c:47:THR:OG1	2.19	0.54
18:1R:61:ARG:O	18:1R:64:ASN:ND2	2.41	0.53
20:1T:106:LEU:HD13	20:1T:110:TYR:HD2	1.72	0.53
28:1b:20:GLY:HA3	28:1b:139:PHE:CZ	2.43	0.53
1:1A:422:G:O5'	27:1a:87:LYS:NZ	2.42	0.53
1:1A:590:G:OP1	8:1H:37:ARG:NH1	2.35	0.53
1:1A:1090:A:H2'	1:1A:1091:A:C8	2.43	0.53
1:1A:3176:G:O2'	1:1A:3185:G:O6	2.24	0.53
1:1A:452:A:C2	2:1B:19:A:H1'	2.43	0.53
1:1A:487:A:H2'	1:1A:488:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:732:U:O2'	1:1A:733:C:H6	1.90	0.53
1:1A:1112:G:O2'	1:1A:1172:G:O6	2.25	0.53
1:1A:1327:A:H2'	1:1A:1328:A:H8	1.73	0.53
3:1C:103:U:H2'	3:1C:104:G:H8	1.72	0.53
18:1R:57:ILE:HB	18:1R:72:GLN:HB2	1.91	0.53
24:1X:123:LYS:HG2	24:1X:139:ILE:HG22	1.90	0.53
29:1c:6:ARG:HB3	29:1c:8:THR:HG22	1.89	0.53
1:1A:1814:G:N2	1:1A:1817:A:OP2	2.40	0.53
1:1A:2128:A:H2'	39:1m:7:LYS:HE3	1.88	0.53
1:1A:2981:A:N6	1:1A:2993:G:O2'	2.40	0.53
2:1B:141:G:H5''	17:1Q:60:VAL:HG11	1.88	0.53
10:1J:72:THR:HG21	10:1J:178:LYS:HG3	1.89	0.53
1:1A:703:G:H1	1:1A:744:A:N6	2.04	0.53
1:1A:1095:A:H2	1:1A:1099:A:H2	1.56	0.53
1:1A:1764:A:H2'	1:1A:1765:A:C8	2.44	0.53
1:1A:1844:U:H2'	1:1A:1845:G:H8	1.73	0.53
2:1B:10:U:H2'	2:1B:11:U:C6	2.44	0.53
1:1A:17:A:H2	2:1B:137:A:H61	1.56	0.53
1:1A:1252:G:N2	1:1A:1255:A:OP2	2.35	0.53
1:1A:2236:A:H2'	1:1A:2237:A:H8	1.73	0.53
1:1A:2489:A:H2'	1:1A:2490:G:H8	1.73	0.53
1:1A:2911:U:H2'	1:1A:2912:U:H6	1.72	0.53
1:1A:3083:A:OP2	5:1E:2:SER:N	2.41	0.53
3:1C:3:G:H1	3:1C:114:U:H3	1.57	0.53
27:1a:194:HIS:O	27:1a:198:ASN:ND2	2.42	0.53
1:1A:221:U:H2'	1:1A:222:A:C8	2.43	0.53
1:1A:779:A:O2'	1:1A:783:A:N6	2.42	0.53
1:1A:3103:C:H2'	1:1A:3104:G:C8	2.43	0.53
1:1A:3352:G:H4'	1:1A:3353:U:H5''	1.90	0.53
3:1C:6:G:N1	3:1C:111:A:H2	2.03	0.53
1:1A:1440:A:OP2	15:1O:134:ARG:HD3	2.09	0.53
1:1A:3368:G:H2'	1:1A:3369:U:C6	2.44	0.53
1:1A:3476:C:C2	1:1A:3477:U:C6	2.96	0.53
1:1A:3478:U:O3'	1:1A:3478:U:OP2	2.27	0.53
29:1c:148:THR:HG23	37:1k:2:ALA:HB3	1.91	0.53
1:1A:822:C:H2'	1:1A:823:A:C8	2.43	0.53
1:1A:889:A:H5'	30:1d:44:LYS:HE3	1.90	0.53
1:1A:2499:U:H2'	1:1A:2500:A:H8	1.74	0.53
10:1J:66:ASN:OD1	10:1J:70:ASN:ND2	2.35	0.53
1:1A:765:A:H2	36:1j:92:PRO:HG2	1.73	0.52
1:1A:1749:U:OP2	21:1U:42:ARG:NH2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2582:U:H2'	1:1A:2583:U:C6	2.44	0.52
1:1A:2857:A:H5''	1:1A:2902:G:H22	1.73	0.52
1:1A:3024:C:H2'	1:1A:3025:U:C6	2.44	0.52
1:1A:836:C:H2'	1:1A:837:A:C8	2.41	0.52
1:1A:1912:A:N6	39:1m:42:CYS:HA	2.25	0.52
1:1A:2632:A:O2'	28:1b:139:PHE:O	2.26	0.52
1:1A:3150:A:H2'	1:1A:3151:A:H8	1.74	0.52
5:1E:80:GLU:OE1	5:1E:315:TYR:OH	2.24	0.52
5:1E:232:ILE:HG13	5:1E:249:ARG:HB3	1.90	0.52
11:1K:111:LEU:O	11:1K:144:LYS:NZ	2.34	0.52
11:1K:182:LEU:HD11	42:1p:12:ARG:HE	1.74	0.52
1:1A:1206:A:H2'	1:1A:1207:C:C6	2.45	0.52
1:1A:2944:A:O2'	1:1A:2945:A:H2'	2.09	0.52
2:1B:10:U:H2'	2:1B:11:U:H6	1.74	0.52
22:1V:80:VAL:CG1	22:1V:81:ASN:H	2.23	0.52
1:1A:1640:A:H2'	1:1A:1641:A:H8	1.74	0.52
13:1M:53:THR:HB	13:1M:61:ARG:HG3	1.91	0.52
1:1A:184:A:N6	1:1A:185:G:N7	2.57	0.52
1:1A:1206:A:OP1	22:1V:35:LYS:NZ	2.39	0.52
1:1A:1892:C:H2'	1:1A:1893:A:C8	2.44	0.52
3:1C:75:G:H1	3:1C:99:U:H5	1.55	0.52
13:1M:5:LYS:HG3	13:1M:7:ASP:H	1.74	0.52
1:1A:3376:C:O3'	32:1f:10:ARG:NH2	2.41	0.52
9:1I:95:ARG:NH2	9:1I:190:LEU:O	2.43	0.52
11:1K:71:ASN:OD1	11:1K:71:ASN:N	2.42	0.52
23:1W:34:LEU:O	23:1W:38:THR:OG1	2.21	0.52
37:1k:2:ALA:HB1	37:1k:13:TYR:HE1	1.75	0.52
1:1A:316:G:OP1	17:1Q:47:ARG:NE	2.43	0.52
1:1A:3431:U:H3	1:1A:3441:G:H1	1.57	0.52
3:1C:5:A:OP2	7:1G:22:ARG:NH2	2.43	0.52
14:1N:105:GLU:OE1	14:1N:105:GLU:N	2.43	0.52
16:1P:11:ARG:NH1	16:1P:60:THR:O	2.42	0.52
20:1T:11:THR:HG22	20:1T:17:PRO:HB3	1.92	0.52
1:1A:2732:A:H2'	1:1A:2733:A:H8	1.75	0.52
3:1C:21:C:N4	3:1C:52:G:O2'	2.41	0.52
28:1b:21:LYS:NZ	28:1b:47:GLU:O	2.40	0.52
1:1A:227:A:H2'	1:1A:228:A:C8	2.44	0.52
1:1A:1533:U:O2'	1:1A:1534:U:OP1	2.25	0.52
1:1A:1688:A:H2'	1:1A:1689:A:C8	2.45	0.52
1:1A:2937:G:H5'	46:sJ:77:A:H62	1.75	0.52
1:1A:3008:U:O2'	1:1A:3009:C:OP1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IC:17:G:H22	3:IC:59:G:H22	1.58	0.52
35:li:34:SER:HA	35:li:37:ARG:HD3	1.92	0.52
1:IA:213:A:H2'	14:IN:127:VAL:HG21	1.92	0.51
1:IA:493:G:N2	1:IA:580:A:H62	2.08	0.51
1:IA:1562:A:H2'	29:lc:3:THR:HG21	1.91	0.51
1:IA:3478:U:H4'	1:IA:3479:A:C2	2.45	0.51
8:IH:43:THR:OG1	8:IH:85:LYS:NZ	2.43	0.51
23:IW:71:ALA:HB2	23:IW:76:THR:HG22	1.92	0.51
28:lb:11:VAL:HG12	28:lb:82:PRO:HA	1.92	0.51
1:IA:58:G:H22	1:IA:75:U:H4'	1.75	0.51
1:IA:258:G:C8	6:IF:227:PRO:HG3	2.45	0.51
1:IA:355:A:H2'	1:IA:356:U:C6	2.45	0.51
1:IA:1535:A:H2'	1:IA:1536:A:H8	1.75	0.51
1:IA:2345:U:H6	1:IA:2346:A:OP2	1.93	0.51
1:IA:2415:C:OP2	24:IX:51:ARG:NH1	2.44	0.51
1:IA:2486:U:H5	1:IA:2944:A:N1	2.08	0.51
1:IA:2767:A:H2'	1:IA:2768:G:H8	1.75	0.51
1:IA:2939:G:N7	43:lq:61:LYS:NZ	2.58	0.51
1:IA:1513:A:H5'	6:IF:206:LYS:HG2	1.92	0.51
1:IA:2634:A:OP1	4:ID:69:TYR:OH	2.23	0.51
1:IA:2869:A:H61	1:IA:2884:U:H3	1.58	0.51
1:IA:3476:C:H3'	1:IA:3477:U:H6	1.75	0.51
13:IM:29:ARG:NH2	13:IM:119:GLN:O	2.41	0.51
16:IP:124:ALA:O	16:IP:128:ILE:HG12	2.11	0.51
1:IA:619:A:O2'	1:IA:620:U:O5'	2.27	0.51
1:IA:868:A:H2'	1:IA:869:G:C8	2.46	0.51
1:IA:1640:A:H2'	1:IA:1641:A:C8	2.45	0.51
1:IA:3170:A:H2'	1:IA:3171:A:H8	1.74	0.51
1:IA:3368:G:H2'	1:IA:3369:U:H6	1.76	0.51
2:IB:21:A:H2'	2:IB:22:G:C8	2.45	0.51
28:lb:44:VAL:HG11	28:lb:117:ILE:HG21	1.91	0.51
1:IA:628:C:O2'	20:IT:141:HIS:NE2	2.42	0.51
1:IA:759:U:H2'	1:IA:760:A:H8	1.75	0.51
1:IA:1086:G:H2'	1:IA:1087:G:C8	2.46	0.51
1:IA:2075:A:OP2	21:IU:20:ARG:NH1	2.41	0.51
2:IB:25:U:H4'	27:la:16:LYS:HB2	1.92	0.51
7:IG:30:TYR:O	7:IG:34:ARG:HG3	2.10	0.51
1:IA:493:G:H1'	1:IA:579:A:H61	1.76	0.51
1:IA:501:U:H2'	1:IA:502:U:C6	2.45	0.51
1:IA:1476:G:H2'	1:IA:1476:G:N3	2.24	0.51
1:IA:1864:C:H1'	1:IA:1865:U:H5''	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3456:U:H5''	5:1E:309:MET:HE2	1.92	0.51
9:1I:142:LEU:HD12	9:1I:156:MET:HE2	1.93	0.51
17:1Q:121:ILE:HG13	17:1Q:131:GLU:HG3	1.93	0.51
30:1d:2:SER:O	30:1d:2:SER:OG	2.26	0.51
1:1A:431:A:H2'	1:1A:432:A:C8	2.45	0.51
1:1A:445:G:H5''	1:1A:448:C:H1'	1.92	0.51
1:1A:765:A:H2'	1:1A:766:U:C6	2.45	0.51
1:1A:2915:U:OP2	1:1A:2915:U:H6	1.93	0.51
1:1A:3476:C:N4	1:1A:3478:U:OP1	2.44	0.51
9:1I:185:GLU:OE1	9:1I:185:GLU:N	2.40	0.51
33:1g:36:PRO:HG2	33:1g:44:ARG:HB3	1.93	0.51
1:1A:536:G:H5'	14:1N:155:PHE:CZ	2.46	0.51
1:1A:1086:G:H2'	1:1A:1087:G:H8	1.76	0.51
1:1A:1974:A:H2'	1:1A:1975:G:C8	2.46	0.51
1:1A:2780:A:H2'	1:1A:2781:U:C6	2.45	0.51
1:1A:3469:A:H5''	1:1A:3469:A:C4	2.46	0.51
7:1G:128:LEU:HB2	7:1G:192:ARG:HG3	1.93	0.51
31:1e:14:VAL:HA	31:1e:17:LYS:HB2	1.92	0.51
1:1A:511:A:H62	1:1A:561:G:N2	2.09	0.51
1:1A:3468:U:O2	1:1A:3468:U:P	2.69	0.51
2:1B:21:A:H2'	2:1B:22:G:H8	1.76	0.51
3:1C:104:G:H2'	3:1C:105:A:H8	1.76	0.51
4:1D:2:GLY:HA2	4:1D:207:VAL:HG23	1.92	0.51
7:1G:124:ASP:OD1	7:1G:124:ASP:N	2.41	0.51
1:1A:671:A:H5''	6:1F:399:ALA:HB2	1.92	0.51
13:1M:14:ILE:HD12	13:1M:129:VAL:HG13	1.92	0.51
1:1A:1636:U:H5	1:1A:2036:A:N1	2.09	0.50
1:1A:1904:U:OP2	21:1U:124:TYR:OH	2.28	0.50
1:1A:3025:U:H2'	1:1A:3026:U:C6	2.46	0.50
1:1A:3168:A:H2'	1:1A:3169:C:C6	2.46	0.50
1:1A:3333:A:N1	1:1A:3392:G:O2'	2.43	0.50
1:1A:3432:A:O2'	1:1A:3433:U:OP1	2.29	0.50
1:1A:409:G:O2'	6:1F:80:SER:O	2.29	0.50
1:1A:534:A:H4'	1:1A:535:A:H2	1.76	0.50
1:1A:2857:A:H2	1:1A:2901:U:C4	2.28	0.50
1:1A:2857:A:H2'	1:1A:2893:C:H41	1.75	0.50
1:1A:2863:A:C8	14:1N:104:LYS:HD2	2.46	0.50
1:1A:3498:U:H5''	32:1f:56:ALA:HB1	1.93	0.50
3:1C:28:U:H3'	3:1C:29:G:H21	1.75	0.50
17:1Q:17:ASP:OD1	17:1Q:20:ARG:NH2	2.45	0.50
1:1A:2699:U:O2'	1:1A:2828:A:O2'	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3480:A:H2'	1:1A:3481:U:O4'	2.11	0.50
25:1Y:26:PRO:HD2	35:1i:69:PRO:HG3	1.94	0.50
1:1A:1479:A:H4'	1:1A:1480:U:O5'	2.10	0.50
1:1A:3500:A:H2'	1:1A:3501:A:H8	1.77	0.50
31:1e:22:THR:HG22	31:1e:27:TYR:HE2	1.76	0.50
1:1A:626:A:OP1	1:1A:664:A:N6	2.37	0.50
1:1A:934:G:OP1	38:1l:16:HIS:NE2	2.32	0.50
1:1A:3198:A:H4'	5:1E:13:SER:HB2	1.93	0.50
3:1C:26:U:H3	3:1C:51:G:N2	2.05	0.50
1:1A:1940:A:H2'	1:1A:1941:A:C8	2.46	0.50
1:1A:2349:G:O2'	1:1A:2387:G:O6	2.15	0.50
1:1A:2383:G:O2'	1:1A:2386:U:OP2	2.30	0.50
1:1A:2466:G:N2	5:1E:228:TYR:OH	2.32	0.50
1:1A:2839:A:H5''	43:1q:78:LYS:HD2	1.94	0.50
3:1C:17:G:N2	3:1C:59:G:H22	2.09	0.50
3:1C:35:A:H2	3:1C:40:G:H22	1.59	0.50
1:1A:2334:U:O2'	1:1A:2335:A:OP1	2.29	0.50
1:1A:2433:A:H2'	1:1A:2434:A:H8	1.76	0.50
36:1j:34:VAL:HG13	36:1j:39:ASP:HB2	1.94	0.50
1:1A:560:U:O2'	1:1A:561:G:H5'	2.11	0.50
1:1A:1883:A:N6	1:1A:1931:U:H3	2.10	0.50
1:1A:2418:U:OP1	1:1A:3243:C:O2'	2.24	0.50
1:1A:3409:A:O2'	1:1A:3410:A:OP2	2.24	0.50
1:1A:3468:U:OP1	1:1A:3469:A:H4'	2.11	0.50
1:1A:3476:C:C5'	1:1A:3477:U:C5	2.92	0.50
2:1B:145:U:H2'	2:1B:146:U:C6	2.47	0.50
10:1J:137:VAL:HA	10:1J:140:ILE:HD12	1.93	0.50
11:1K:19:ILE:HG12	11:1K:28:VAL:HG22	1.93	0.50
1:1A:333:U:O2'	17:1Q:180:ARG:O	2.30	0.50
1:1A:547:A:H2'	1:1A:548:A:H8	1.77	0.50
1:1A:851:A:OP2	29:1c:113:LEU:HB3	2.12	0.50
1:1A:1247:G:H1	3:1C:92:U:H5	1.59	0.50
1:1A:2123:A:H2'	1:1A:2124:A:C8	2.46	0.50
1:1A:2482:C:H2'	1:1A:2483:C:C6	2.47	0.50
1:1A:3243:C:OP1	5:1E:224:LYS:NZ	2.38	0.50
1:1A:3469:A:C2	1:1A:3486:A:C2	3.00	0.50
25:1Y:57:ASP:OD1	25:1Y:57:ASP:N	2.45	0.50
1:1A:401:A:N1	6:1F:84:SER:HB3	2.26	0.49
1:1A:3314:U:O2'	1:1A:3417:G:OP2	2.24	0.49
14:1N:53:LYS:HB2	14:1N:69:LEU:HD22	1.94	0.49
18:1R:127:ARG:HB2	18:1R:139:PHE:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:713:G:H3'	1:1A:714:U:C5'	2.42	0.49
1:1A:1847:A:H2'	1:1A:1848:A:C8	2.47	0.49
3:1C:84:G:H1	3:1C:91:G:N2	2.10	0.49
9:1I:108:ASN:HB2	22:1V:138:PRO:HB2	1.94	0.49
1:1A:642:G:H4'	16:1P:88:ARG:NH1	2.27	0.49
1:1A:2109:C:O2	5:1E:242:ARG:NH2	2.43	0.49
28:1b:50:PRO:HD3	28:1b:68:VAL:HG22	1.94	0.49
1:1A:630:A:H2'	1:1A:631:G:O4'	2.13	0.49
1:1A:721:A:H2'	1:1A:722:A:C8	2.46	0.49
1:1A:1312:A:HO2'	1:1A:1420:U:HO2'	1.57	0.49
1:1A:2732:A:H2'	1:1A:2733:A:C8	2.47	0.49
1:1A:3074:U:H5''	24:1X:43:LYS:HD3	1.95	0.49
17:1Q:68:ARG:HD3	17:1Q:128:ARG:HB2	1.94	0.49
23:1W:29:SER:HA	23:1W:78:THR:HA	1.95	0.49
1:1A:104:A:N6	14:1N:53:LYS:HE2	2.27	0.49
1:1A:1593:A:H2'	1:1A:1594:A:C8	2.47	0.49
5:1E:384:MET:O	5:1E:388:LEU:HD12	2.12	0.49
13:1M:139:SER:O	13:1M:145:GLN:NE2	2.40	0.49
28:1b:4:ILE:O	28:1b:9:ARG:NH1	2.46	0.49
1:1A:94:G:N7	14:1N:11:HIS:NE2	2.58	0.49
1:1A:502:U:H2'	1:1A:503:A:C8	2.48	0.49
1:1A:601:A:H2'	1:1A:602:U:C6	2.48	0.49
1:1A:934:G:OP1	38:1I:28:HIS:HD2	1.95	0.49
5:1E:41:PRO:HA	5:1E:187:GLY:HA3	1.93	0.49
14:1N:45:PHE:CE1	14:1N:229:GLN:HB3	2.46	0.49
27:1a:22:ASN:OD1	27:1a:25:GLN:NE2	2.33	0.49
36:1j:48:VAL:HG22	36:1j:101:VAL:HG22	1.92	0.49
1:1A:353:G:H2'	1:1A:354:U:C6	2.48	0.49
1:1A:361:C:OP1	14:1N:100:LYS:NZ	2.42	0.49
1:1A:1103:U:H2'	1:1A:1104:A:H8	1.77	0.49
1:1A:2955:C:H2'	1:1A:2956:A:H8	1.77	0.49
4:1D:209:HIS:CD2	4:1D:210:PRO:HD2	2.47	0.49
7:1G:199:HIS:CE1	7:1G:200:VAL:HG23	2.47	0.49
8:1H:120:SER:O	8:1H:121:LYS:HG2	2.13	0.49
24:1X:87:THR:HA	24:1X:97:TYR:HB3	1.95	0.49
1:1A:34:U:H2'	1:1A:35:A:O4'	2.13	0.49
1:1A:1293:U:H5'	9:1I:199:LYS:HD3	1.94	0.49
1:1A:2128:A:H5''	39:1m:8:VAL:HG21	1.95	0.49
8:1H:98:ASN:HD21	8:1H:187:MET:HE3	1.77	0.49
18:1R:18:ARG:NH2	18:1R:147:GLU:HG2	2.27	0.49
43:1q:72:CYS:HB3	43:1q:77:TYR:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1877:A:H2'	1:1A:1878:A:C8	2.47	0.49
1:1A:1904:U:O2'	1:1A:1906:A:N7	2.43	0.49
1:1A:2958:G:O2'	1:1A:2959:G:OP1	2.27	0.49
1:1A:397:A:N6	41:1o:35:ILE:HG23	2.28	0.49
1:1A:425:C:H2'	1:1A:426:U:C6	2.48	0.49
1:1A:467:A:C2	1:1A:2439:A:H4'	2.48	0.49
1:1A:489:U:H2'	1:1A:490:A:C8	2.48	0.49
1:1A:2345:U:O4	1:1A:2347:A:N7	2.46	0.49
6:1F:180:ASP:HB3	6:1F:208:PRO:HD3	1.93	0.49
25:1Y:17:LYS:HD3	25:1Y:17:LYS:HA	1.62	0.49
1:1A:596:G:C2	1:1A:597:A:C8	3.01	0.48
1:1A:804:G:H2'	1:1A:805:G:C8	2.48	0.48
1:1A:3454:G:O6	1:1A:3501:A:N1	2.46	0.48
1:1A:3470:G:C6	1:1A:3483:A:N6	2.81	0.48
18:1R:124:SER:HB2	18:1R:126:ARG:HH12	1.77	0.48
22:1V:4:SER:O	22:1V:9:ARG:HD3	2.13	0.48
24:1X:13:LYS:HB2	24:1X:128:LEU:HD11	1.96	0.48
29:1c:3:THR:HA	29:1c:6:ARG:HD3	1.95	0.48
1:1A:50:G:HO2'	1:1A:1688:A:HO2'	1.61	0.48
1:1A:1675:A:H2'	1:1A:1676:A:C8	2.47	0.48
1:1A:2287:U:OP1	46:sJ:3:C:O2'	2.28	0.48
1:1A:3302:U:H2'	1:1A:3303:A:H8	1.78	0.48
12:1L:87:VAL:HG22	12:1L:148:MET:HE1	1.95	0.48
1:1A:97:A:H2'	1:1A:98:A:O4'	2.14	0.48
1:1A:3285:A:C6	1:1A:3287:U:H1'	2.48	0.48
3:1C:76:U:H2'	3:1C:77:U:O4'	2.13	0.48
10:1J:141:GLU:OE2	17:1Q:6:TYR:OH	2.24	0.48
1:1A:451:G:OP1	1:1A:1549:U:O2'	2.27	0.48
1:1A:505:A:H2'	1:1A:506:A:C8	2.48	0.48
1:1A:838:U:O2'	1:1A:907:U:OP1	2.31	0.48
1:1A:1282:G:OP1	9:1I:78:ARG:NH1	2.47	0.48
1:1A:1300:C:O2'	15:1O:88:MET:O	2.30	0.48
1:1A:2325:G:C8	1:1A:2348:G:C8	3.00	0.48
18:1R:16:GLN:HG2	18:1R:149:ILE:HG12	1.95	0.48
1:1A:487:A:OP2	1:1A:588:G:N2	2.36	0.48
1:1A:948:C:O2'	1:1A:949:G:N7	2.45	0.48
1:1A:2482:C:H2'	1:1A:2483:C:H6	1.78	0.48
1:1A:2499:U:H2'	1:1A:2500:A:C8	2.48	0.48
1:1A:3332:A:H2'	1:1A:3333:A:C8	2.48	0.48
5:1E:153:ILE:O	5:1E:157:CYS:HB2	2.13	0.48
12:1L:112:GLN:HG3	45:sI:73:A:H1'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:lb:20:GLY:HA3	28:lb:139:PHE:HZ	1.78	0.48
1:1A:3454:G:C6	1:1A:3501:A:N1	2.81	0.48
21:1U:92:LYS:O	21:1U:96:ILE:HG13	2.14	0.48
1:1A:76:U:H2'	1:1A:77:C:H6	1.78	0.48
1:1A:764:U:H2'	1:1A:765:A:H8	1.78	0.48
1:1A:1346:G:O2'	1:1A:1409:G:N1	2.46	0.48
1:1A:2511:U:C2'	1:1A:2512:G:H5'	2.43	0.48
1:1A:3447:A:H2'	1:1A:3448:G:O4'	2.14	0.48
6:1F:33:ARG:NH2	6:1F:35:ASP:OD2	2.33	0.48
1:1A:435:A:OP1	18:1R:4:TYR:OH	2.19	0.48
1:1A:547:A:H2'	1:1A:548:A:C8	2.49	0.48
1:1A:2416:U:OP2	5:1E:239:HIS:ND1	2.47	0.48
7:1G:39:GLN:NE2	7:1G:46:THR:O	2.40	0.48
22:1V:80:VAL:HG12	22:1V:81:ASN:H	1.78	0.48
39:1m:51:ALA:HB3	39:1m:54:ILE:HD12	1.95	0.48
1:1A:10:U:H2'	1:1A:11:A:H8	1.79	0.48
1:1A:493:G:H2'	1:1A:494:G:N3	2.28	0.48
1:1A:846:A:H2'	1:1A:847:A:C8	2.48	0.48
1:1A:886:A:H4'	30:1d:27:SER:HB2	1.95	0.48
1:1A:2890:A:H2'	1:1A:2891:G:C8	2.49	0.48
15:1O:127:ILE:HD12	20:1T:170:THR:HG23	1.96	0.48
39:1m:16:THR:O	39:1m:16:THR:OG1	2.29	0.48
1:1A:550:A:H2'	1:1A:551:A:C8	2.49	0.48
1:1A:724:A:O2'	1:1A:725:A:H5''	2.13	0.48
1:1A:790:A:H2'	1:1A:791:A:C8	2.48	0.48
1:1A:1508:U:H2'	1:1A:1509:A:C8	2.49	0.48
1:1A:1752:U:H2'	1:1A:1753:A:O4'	2.14	0.48
1:1A:2129:G:C8	39:1m:16:THR:HB	2.48	0.48
1:1A:2443:A:H2'	1:1A:2444:A:C8	2.49	0.48
1:1A:2912:U:H6	1:1A:2912:U:O5'	1.97	0.48
2:1B:112:A:OP1	41:1o:8:SER:OG	2.29	0.48
5:1E:146:ARG:O	5:1E:150:ILE:HG12	2.13	0.48
5:1E:283:LYS:NZ	5:1E:351:ALA:O	2.39	0.48
15:1O:62:ARG:HD2	15:1O:67:PRO:HB3	1.95	0.48
35:1i:79:LYS:O	35:1i:83:GLN:HG2	2.14	0.48
1:1A:424:A:OP2	1:1A:438:G:H1'	2.13	0.47
1:1A:493:G:H1'	1:1A:579:A:N6	2.29	0.47
1:1A:668:A:H2'	1:1A:669:A:C8	2.49	0.47
1:1A:719:U:H2'	1:1A:720:U:C6	2.48	0.47
1:1A:739:A:H2'	1:1A:740:A:H8	1.79	0.47
1:1A:796:U:H2'	1:1A:797:C:C6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1314:A:H2	15:1O:135:LYS:H	1.62	0.47
1:1A:835:A:H2'	1:1A:836:C:O4'	2.14	0.47
1:1A:1207:C:H2'	1:1A:1208:U:O4'	2.13	0.47
1:1A:1208:U:H4'	30:1d:43:THR:HG23	1.96	0.47
1:1A:2304:A:H2'	1:1A:2305:C:C6	2.49	0.47
1:1A:2504:U:H2'	1:1A:2505:A:C8	2.48	0.47
1:1A:2866:C:H4'	1:1A:2867:A:OP1	2.14	0.47
1:1A:3470:G:N2	1:1A:3484:A:H2	2.12	0.47
1:1A:3476:C:N4	1:1A:3478:U:P	2.87	0.47
3:1C:6:G:O3'	7:1G:33:ARG:NH2	2.47	0.47
12:1L:115:MET:H	12:1L:115:MET:HG2	1.47	0.47
28:1b:36:ARG:HG3	28:1b:38:TYR:CZ	2.49	0.47
31:1e:45:LEU:HD12	31:1e:70:GLN:HB2	1.95	0.47
1:1A:1985:A:H2'	1:1A:1986:A:C8	2.50	0.47
1:1A:2731:G:H2'	1:1A:2732:A:H8	1.79	0.47
27:1a:83:LEU:HD22	27:1a:97:ILE:HD11	1.95	0.47
1:1A:576:A:H62	1:1A:577:G:N2	2.12	0.47
1:1A:1030:C:OP2	4:1D:9:ARG:NH1	2.44	0.47
1:1A:2505:A:H2'	1:1A:2506:U:C6	2.50	0.47
1:1A:2701:U:H2'	1:1A:2702:G:H8	1.78	0.47
1:1A:2848:A:H2'	1:1A:2849:U:C6	2.50	0.47
1:1A:3470:G:O6	1:1A:3483:A:N6	2.47	0.47
1:1A:3490:U:OP2	5:1E:389:GLU:OE2	2.32	0.47
5:1E:35:ASP:OD2	5:1E:193:LYS:NZ	2.48	0.47
18:1R:70:LYS:HD3	18:1R:70:LYS:HA	1.61	0.47
20:1T:6:ILE:HD11	20:1T:33:ALA:HB1	1.95	0.47
21:1U:135:LYS:O	21:1U:139:MET:HG3	2.14	0.47
1:1A:428:U:O2'	18:1R:100:ASP:OD2	2.27	0.47
1:1A:518:A:H2'	1:1A:519:A:O4'	2.14	0.47
1:1A:534:A:H4'	1:1A:535:A:C2	2.50	0.47
1:1A:1430:G:O6	1:1A:2442:C:O2'	2.31	0.47
1:1A:1887:A:H2'	1:1A:1888:A:C8	2.49	0.47
1:1A:2633:C:H2'	1:1A:2634:A:O4'	2.14	0.47
1:1A:3265:C:H2'	1:1A:3266:U:C6	2.49	0.47
7:1G:201:ALA:HB2	7:1G:232:LEU:HD12	1.96	0.47
11:1K:43:LYS:HD2	15:1O:133:THR:HG23	1.96	0.47
21:1U:70:LYS:HE3	21:1U:75:HIS:HB2	1.96	0.47
28:1b:51:LEU:HB2	28:1b:65:ARG:HG2	1.95	0.47
1:1A:381:A:H2'	1:1A:382:A:H8	1.79	0.47
1:1A:576:A:N6	1:1A:577:G:H21	2.12	0.47
1:1A:705:U:N3	1:1A:743:G:N7	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:1634:G:OP2	1:lA:1634:G:N2	2.42	0.47
1:lA:2041:U:H4'	1:lA:2042:A:H5''	1.96	0.47
1:lA:2091:G:OP1	5:lE:248:LEU:N	2.46	0.47
1:lA:2415:C:OP1	24:lX:54:ARG:NH2	2.47	0.47
1:lA:3040:A:H5''	42:lp:50:LYS:HG3	1.97	0.47
3:lC:79:G:H22	3:lC:95:A:H2	1.61	0.47
16:lP:12:VAL:HG22	16:lP:26:VAL:HG22	1.97	0.47
28:lb:23:ALA:HB1	28:lb:43:VAL:HB	1.96	0.47
39:lm:36:LYS:HG2	39:lm:48:ARG:HE	1.79	0.47
1:lA:220:A:H2'	1:lA:221:U:H6	1.79	0.47
1:lA:699:A:H3'	1:lA:746:A:H62	1.79	0.47
1:lA:897:A:O2'	1:lA:899:A:N1	2.40	0.47
1:lA:1003:A:OP1	38:ll:5:THR:OG1	2.17	0.47
1:lA:1030:C:OP1	4:lD:14:SER:OG	2.33	0.47
1:lA:1130:U:H2'	1:lA:1131:G:H8	1.80	0.47
1:lA:1163:U:OP1	12:lL:90:ARG:NH2	2.37	0.47
1:lA:1485:A:H2'	1:lA:1486:C:O4'	2.14	0.47
1:lA:1569:A:H5''	1:lA:1570:U:O5'	2.15	0.47
1:lA:2744:A:N6	13:lM:124:GLY:O	2.48	0.47
1:lA:2753:U:H2'	1:lA:2754:C:C6	2.49	0.47
2:lB:15:U:H5'	18:lR:2:VAL:HG13	1.96	0.47
2:lB:73:A:H5'	27:la:73:ARG:HH22	1.79	0.47
11:lK:98:TYR:CE1	11:lK:190:LYS:HB3	2.50	0.47
16:lP:102:ILE:HA	16:lP:105:GLU:HG2	1.97	0.47
32:lf:62:SER:HB2	32:lf:65:LYS:HD3	1.96	0.47
33:lg:128:LYS:HD3	33:lg:128:LYS:HA	1.69	0.47
1:lA:745:A:H2'	1:lA:746:A:C4	2.49	0.47
1:lA:1437:A:O2'	1:lA:1442:A:N1	2.46	0.47
1:lA:1502:A:H3'	1:lA:1502:A:N3	2.30	0.47
1:lA:2660:U:H2'	1:lA:2661:U:C6	2.49	0.47
2:lB:2:A:H2'	2:lB:3:U:H6	1.79	0.47
9:ll:63:LEU:HB2	22:lV:147:ILE:HB	1.97	0.47
15:lO:107:GLU:HG2	15:lO:148:TRP:CZ2	2.50	0.47
22:lV:80:VAL:HG12	22:lV:81:ASN:N	2.30	0.47
28:lb:7:PRO:HA	28:lb:25:VAL:HG12	1.97	0.47
1:lA:1107:G:H2'	1:lA:1108:A:C8	2.50	0.47
1:lA:2508:A:H5''	1:lA:2509:U:OP2	2.15	0.47
1:lA:2835:C:O3'	43:lq:37:GLY:HA3	2.14	0.47
7:lG:89:LYS:HG3	7:lG:90:LEU:HG	1.97	0.47
28:lb:94:LEU:HB2	28:lb:120:GLN:OE1	2.15	0.47
31:le:40:ASP:N	31:le:40:ASP:OD1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:lp:40:CYS:O	42:lp:43:SER:OG	2.32	0.47
1:lA:205:C:H3'	1:lA:206:U:H5''	1.97	0.47
1:lA:209:A:O3'	14:lN:215:LYS:NZ	2.48	0.47
1:lA:228:A:H2'	1:lA:229:A:C8	2.50	0.47
1:lA:897:A:H4'	1:lA:898:U:OP1	2.14	0.47
5:lE:273:GLY:O	5:lE:275:PHE:N	2.47	0.47
21:lU:61:ALA:O	21:lU:65:GLU:HG2	2.15	0.47
43:lq:72:CYS:SG	43:lq:75:CYS:N	2.87	0.47
1:lA:761:A:H2'	1:lA:762:A:C8	2.51	0.46
1:lA:993:U:OP2	1:lA:2109:C:O2'	2.29	0.46
1:lA:1888:A:H2'	1:lA:1889:U:C6	2.50	0.46
1:lA:2589:C:H5'	10:lJ:58:ARG:HG2	1.96	0.46
1:lA:3287:U:H2'	1:lA:3288:U:C6	2.50	0.46
27:la:26:ARG:O	27:la:30:MET:HG3	2.15	0.46
1:lA:64:A:OP2	1:lA:347:G:N2	2.39	0.46
1:lA:290:U:H2'	1:lA:291:U:C6	2.50	0.46
1:lA:1006:A:H2'	1:lA:1007:C:C6	2.50	0.46
4:lD:192:LYS:HD3	4:lD:193:ARG:NH2	2.30	0.46
5:lE:285:TYR:CZ	5:lE:326:LYS:HB2	2.50	0.46
8:lH:65:LEU:HD11	8:lH:79:PHE:HB2	1.97	0.46
15:lO:193:LYS:HE2	15:lO:193:LYS:HA	1.97	0.46
23:lW:46:LEU:HD22	23:lW:50:PHE:HE2	1.80	0.46
29:lc:138:ILE:O	29:lc:141:VAL:HG12	2.15	0.46
34:lh:15:THR:HG22	34:lh:16:LYS:H	1.80	0.46
1:lA:893:U:H3	1:lA:897:A:H2	1.63	0.46
1:lA:2251:A:N7	4:lD:20:SER:OG	2.42	0.46
1:lA:2514:A:C2	1:lA:2584:U:N3	2.84	0.46
1:lA:2816:A:OP1	7:lG:180:ARG:NE	2.42	0.46
1:lA:2978:C:H2'	1:lA:2979:C:O2	2.14	0.46
1:lA:3393:A:H2'	1:lA:3394:A:C8	2.51	0.46
10:lJ:217:SER:O	10:lJ:221:GLU:HB3	2.15	0.46
18:lR:29:THR:HG21	18:lR:146:ILE:HD11	1.95	0.46
1:lA:1604:A:O2'	1:lA:1606:A:OP2	2.34	0.46
1:lA:1605:A:H2	1:lA:3430:U:N3	2.07	0.46
1:lA:1633:G:H1'	1:lA:2044:C:H5''	1.96	0.46
1:lA:1757:C:H2'	1:lA:1758:U:C6	2.50	0.46
1:lA:2357:A:H8	1:lA:3117:U:H1'	1.79	0.46
2:lB:2:A:H2'	2:lB:3:U:C6	2.50	0.46
9:lI:143:LYS:HB2	9:lI:143:LYS:HE3	1.72	0.46
10:lJ:187:ILE:HG13	10:lJ:189:ARG:HG3	1.98	0.46
14:lN:124:LEU:HD21	35:li:109:PHE:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:lb:47:GLU:OE1	28:lb:69:LYS:HE3	2.16	0.46
28:lb:127:LYS:HD3	28:lb:127:LYS:N	2.30	0.46
37:lk:51:MET:CE	37:lk:67:ALA:HB2	2.45	0.46
42:lp:24:CYS:HA	42:lp:40:CYS:HB3	1.98	0.46
1:lA:832:A:O2'	1:lA:833:U:OP1	2.28	0.46
1:lA:1465:G:H2'	1:lA:1466:U:C6	2.51	0.46
1:lA:1593:A:H2'	1:lA:1594:A:H8	1.81	0.46
1:lA:1921:A:H2'	1:lA:1922:U:O2	2.15	0.46
1:lA:1982:U:H2'	4:lD:50:HIS:CD2	2.51	0.46
21:lU:108:LYS:O	21:lU:112:THR:OG1	2.23	0.46
1:lA:965:A:H2'	1:lA:966:A:O4'	2.15	0.46
1:lA:1105:U:H2'	1:lA:1106:U:C6	2.50	0.46
1:lA:1886:A:H2'	1:lA:1887:A:C8	2.51	0.46
1:lA:2677:G:H5'	4:lD:233:GLN:HB3	1.96	0.46
1:lA:3315:U:O2'	1:lA:3418:C:OP2	2.28	0.46
1:lA:3383:A:OP2	5:lE:148:ARG:NH2	2.35	0.46
3:lC:14:G:H2'	3:lC:15:A:H8	1.80	0.46
11:lK:134:ILE:HG21	11:lK:167:ILE:HG12	1.97	0.46
11:lK:144:LYS:HA	11:lK:150:ILE:HG22	1.98	0.46
13:lM:11:LYS:HD3	13:lM:11:LYS:HA	1.72	0.46
14:lN:49:ILE:O	14:lN:232:ASP:HA	2.16	0.46
15:lO:158:GLU:O	15:lO:162:LYS:HG2	2.15	0.46
1:lA:243:G:O2'	1:lA:264:G:N2	2.49	0.46
1:lA:2514:A:C2	1:lA:2584:U:C2	3.04	0.46
1:lA:2848:A:N1	1:lA:2911:U:C5	2.80	0.46
6:lF:162:ILE:HD11	6:lF:171:LEU:HD13	1.97	0.46
27:la:108:PHE:O	27:la:113:ARG:HD2	2.14	0.46
30:ld:23:LYS:HE3	30:ld:23:LYS:HB2	1.64	0.46
33:lg:88:MET:SD	33:lg:88:MET:N	2.81	0.46
1:lA:2239:U:OP2	4:lD:234:LYS:NZ	2.43	0.46
1:lA:2598:A:H2'	10:lJ:39:TYR:O	2.16	0.46
3:lC:68:C:H42	3:lC:105:A:H61	1.64	0.46
6:lF:113:ARG:HA	6:lF:113:ARG:HD3	1.76	0.46
17:lQ:152:CYS:HB2	35:li:84:LEU:HD11	1.98	0.46
31:le:15:ASN:OD1	31:le:74:TYR:OH	2.28	0.46
1:lA:71:U:OP2	14:lN:102:SER:OG	2.26	0.46
1:lA:548:A:H2'	1:lA:549:U:C6	2.50	0.46
1:lA:732:U:O2'	1:lA:733:C:O4'	2.34	0.46
1:lA:1090:A:H2'	1:lA:1091:A:H8	1.79	0.46
1:lA:2721:G:H5''	1:lA:2722:U:O4'	2.15	0.46
3:lC:78:C:H2'	3:lC:79:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:ID:59:ALA:HB2	4:ID:78:CYS:SG	2.56	0.46
15:IO:77:PRO:O	15:IO:81:VAL:HG23	2.16	0.46
1:IA:332:G:C6	43:lq:43:ARG:HD3	2.51	0.46
1:IA:1346:G:O2'	1:IA:1347:A:OP2	2.33	0.46
1:IA:2344:U:P	1:IA:2344:U:O4'	2.74	0.46
1:IA:3412:U:H3'	1:IA:3413:U:C5'	2.46	0.46
4:ID:30:ARG:NH2	4:ID:33:ASP:OD2	2.50	0.46
9:II:161:LEU:HD21	9:II:189:LYS:HG3	1.98	0.46
30:ld:32:THR:OG1	30:ld:35:MET:SD	2.65	0.46
30:ld:54:LYS:HB2	30:ld:54:LYS:HE3	1.78	0.46
1:IA:2857:A:N1	1:IA:2901:U:C5	2.72	0.45
1:IA:2857:A:H4'	1:IA:2858:A:OP1	2.16	0.45
1:IA:3008:U:P	12:IL:115:MET:HB2	2.56	0.45
4:ID:17:LYS:HE3	4:ID:17:LYS:HB2	1.77	0.45
39:lm:57:CYS:SG	39:lm:60:CYS:HB3	2.56	0.45
43:lq:8:ARG:O	43:lq:21:HIS:N	2.47	0.45
1:IA:660:U:H2'	1:IA:661:G:C8	2.49	0.45
1:IA:668:A:H2'	1:IA:669:A:H8	1.80	0.45
1:IA:804:G:H22	1:IA:911:U:H3	1.63	0.45
1:IA:907:U:H2'	1:IA:908:A:C8	2.50	0.45
1:IA:1177:A:H4'	1:IA:2708:A:C4	2.51	0.45
1:IA:2330:U:H2'	1:IA:2337:G:N2	2.31	0.45
1:IA:2594:C:H2'	1:IA:2595:G:H5'	1.98	0.45
1:IA:2843:U:H3'	1:IA:2844:U:C6	2.51	0.45
1:IA:3154:A:H5''	5:IE:120:LYS:HE3	1.97	0.45
1:IA:3207:G:H2'	1:IA:3208:A:C8	2.50	0.45
1:IA:3478:U:OP2	1:IA:3479:A:P	2.74	0.45
3:IC:69:U:H2'	3:IC:70:U:C6	2.51	0.45
11:IK:136:MET:HE3	11:IK:136:MET:HB3	1.73	0.45
13:IM:111:ASP:HB3	13:IM:112:LEU:H	1.42	0.45
1:IA:410:G:N7	38:IL:56:ARG:NH1	2.65	0.45
1:IA:721:A:H2'	1:IA:722:A:H8	1.80	0.45
1:IA:749:C:H2'	1:IA:750:U:H6	1.81	0.45
1:IA:858:A:O2'	1:IA:1185:A:N7	2.49	0.45
1:IA:1469:A:H2'	1:IA:1470:A:H8	1.82	0.45
1:IA:2230:U:H2'	1:IA:2231:C:H6	1.80	0.45
1:IA:2876:U:O2'	1:IA:2877:U:O4'	2.27	0.45
1:IA:3467:U:C4	1:IA:3469:A:C2	3.05	0.45
1:IA:3486:A:C8	1:IA:3486:A:H3'	2.51	0.45
5:IE:20:LYS:HE3	5:IE:20:LYS:HB3	1.61	0.45
28:lb:115:LYS:HA	28:lb:115:LYS:HD3	1.77	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:871:A:O2'	1:1A:872:A:O5'	2.30	0.45
1:1A:1582:U:OP1	18:1R:82:ARG:NH2	2.47	0.45
1:1A:2730:U:H2'	1:1A:2731:G:C8	2.50	0.45
1:1A:3309:U:O4	1:1A:3330:A:N6	2.49	0.45
2:1B:12:A:H2'	2:1B:13:C:C6	2.51	0.45
6:1F:85:GLY:O	6:1F:89:GLN:NE2	2.49	0.45
6:1F:237:LEU:HD22	6:1F:242:LEU:HD21	1.97	0.45
7:1G:90:LEU:HD12	7:1G:227:ILE:HD12	1.98	0.45
10:1J:173:PRO:HG3	10:1J:216:LYS:HE3	1.98	0.45
11:1K:100:MET:HE1	11:1K:167:ILE:HD12	1.98	0.45
11:1K:145:LEU:HD23	11:1K:145:LEU:HA	1.82	0.45
13:1M:15:ASP:C	13:1M:15:ASP:OD1	2.60	0.45
34:1h:25:THR:HG22	34:1h:26:ALA:N	2.27	0.45
1:1A:606:A:H2'	1:1A:607:U:C6	2.52	0.45
1:1A:1314:A:H5'	1:1A:1315:A:O4'	2.16	0.45
1:1A:1664:G:OP2	1:1A:1752:U:O2'	2.29	0.45
1:1A:2183:A:H2'	1:1A:2184:A:C8	2.51	0.45
1:1A:3311:U:H2'	1:1A:3312:U:C6	2.52	0.45
1:1A:3500:A:H2'	1:1A:3501:A:C8	2.51	0.45
3:1C:8:U:OP1	22:1V:28:SER:OG	2.30	0.45
5:1E:132:VAL:HA	5:1E:135:GLU:HG2	1.98	0.45
7:1G:211:ASP:OD1	7:1G:212:ALA:N	2.50	0.45
7:1G:278:LYS:HE3	7:1G:278:LYS:HB2	1.77	0.45
10:1J:219:TYR:CD1	10:1J:225:MET:HE1	2.45	0.45
27:1a:2:LYS:HE3	27:1a:2:LYS:HB3	1.68	0.45
1:1A:426:U:H2'	1:1A:427:U:C6	2.51	0.45
1:1A:811:A:N1	1:1A:839:G:O2'	2.46	0.45
1:1A:884:A:H2'	1:1A:885:U:C6	2.52	0.45
1:1A:3033:C:H2'	1:1A:3034:A:C8	2.51	0.45
16:1P:69:ARG:HE	20:1T:141:HIS:CE1	2.35	0.45
23:1W:97:LEU:HB3	23:1W:103:ARG:HB2	1.97	0.45
35:1i:-2:ILE:HA	35:1i:1:MET:HE2	1.99	0.45
1:1A:494:G:C6	1:1A:577:G:H2'	2.52	0.45
1:1A:1490:U:H2'	1:1A:1491:A:H8	1.82	0.45
1:1A:1534:U:H2'	1:1A:1535:A:C8	2.52	0.45
1:1A:2308:A:H2'	1:1A:2309:A:C8	2.51	0.45
1:1A:3148:C:H2'	1:1A:3149:A:H8	1.81	0.45
1:1A:3323:C:O2'	1:1A:3419:A:N1	2.47	0.45
1:1A:3454:G:N2	1:1A:3501:A:H2	2.15	0.45
1:1A:3469:A:N3	1:1A:3469:A:O5'	2.50	0.45
9:1I:163:ASP:OD1	9:1I:163:ASP:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:la:56:LYS:NZ	27:la:63:LYS:O	2.39	0.45
28:lb:4:ILE:HD12	31:le:66:LEU:HB3	1.98	0.45
1:la:227:A:H2'	1:la:228:A:H8	1.81	0.45
1:la:1765:A:H2'	1:la:1766:G:O4'	2.17	0.45
1:la:1922:U:H2'	1:la:1923:U:C6	2.51	0.45
1:la:2112:C:C2	1:la:2113:A:C8	3.05	0.45
1:la:2766:A:H2'	1:la:2767:A:C8	2.51	0.45
1:la:3156:U:O2'	5:le:182:GLU:OE2	2.23	0.45
3:lc:104:G:H2'	3:lc:105:A:C8	2.52	0.45
6:lf:97:ARG:HG2	6:lf:98:LYS:HG2	1.99	0.45
6:lf:98:LYS:HB3	6:lf:98:LYS:HE2	1.73	0.45
9:li:109:ALA:HB2	22:iv:139:LYS:HB3	1.99	0.45
31:le:57:ARG:O	31:le:61:GLU:HG3	2.16	0.45
1:la:279:U:H2'	1:la:280:U:C6	2.52	0.45
1:la:618:U:H4'	16:lp:42:GLN:HB3	1.98	0.45
1:la:860:G:O2'	1:la:1097:U:OP1	2.32	0.45
1:la:2297:G:N2	1:la:2300:A:OP2	2.36	0.45
1:la:2513:A:C2'	1:la:2514:A:H5'	2.46	0.45
1:la:2585:C:H2'	1:la:2586:A:C8	2.51	0.45
1:la:3456:U:N3	1:la:3496:A:H2	2.08	0.45
12:il:32:LYS:HE3	12:il:32:LYS:HB3	1.79	0.45
16:lp:108:THR:H	16:lp:111:ASP:HB2	1.81	0.45
32:lf:5:LYS:HA	32:lf:5:LYS:HD2	1.79	0.45
35:li:59:ARG:HG2	35:li:72:LEU:HD22	1.99	0.45
1:la:270:C:H2'	1:la:271:U:C6	2.52	0.45
1:la:592:A:H2'	1:la:593:A:C8	2.52	0.45
1:la:723:U:O2'	1:la:724:A:H5'	2.17	0.45
1:la:1495:A:H2'	1:la:1496:A:H8	1.82	0.45
1:la:1508:U:H2'	1:la:1509:A:H8	1.81	0.45
1:la:3150:A:H2'	1:la:3151:A:C8	2.52	0.45
1:la:3464:G:N2	1:la:3464:G:OP2	2.49	0.45
1:la:3476:C:O2	1:la:3477:U:C5	2.69	0.45
1:la:3486:A:C8	1:la:3486:A:C3'	3.00	0.45
7:lg:94:ASN:N	7:lg:94:ASN:OD1	2.49	0.45
8:lh:187:MET:HE3	8:lh:187:MET:HB3	1.75	0.45
17:lq:121:ILE:CG1	17:lq:131:GLU:HG3	2.47	0.45
1:la:491:G:C5	1:la:492:U:C4	3.04	0.44
1:la:677:A:H2'	1:la:678:A:H8	1.82	0.44
1:la:764:U:H2'	1:la:765:A:C8	2.52	0.44
1:la:1858:A:H2'	1:la:1859:G:H8	1.82	0.44
1:la:2033:C:OP1	25:iy:67:GLN:NE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3461:U:H4'	1:1A:3462:A:H5'	1.97	0.44
1:1A:3476:C:O2	1:1A:3476:C:O4'	2.33	0.44
25:IY:69:ALA:O	25:IY:99:LYS:NZ	2.46	0.44
1:1A:10:U:H2'	1:1A:11:A:C8	2.52	0.44
1:1A:13:C:OP2	25:IY:27:ARG:NH2	2.51	0.44
1:1A:78:U:H1'	1:1A:817:A:H8	1.81	0.44
1:1A:619:A:H2'	1:1A:619:A:N3	2.32	0.44
1:1A:953:U:H2'	1:1A:954:G:O4'	2.16	0.44
1:1A:1027:G:H4'	1:1A:1028:G:O5'	2.17	0.44
1:1A:1094:U:OP2	19:IS:19:ARG:NH1	2.44	0.44
1:1A:1553:A:OP1	2:IB:22:G:O2'	2.34	0.44
1:1A:1752:U:H4'	1:1A:2036:A:H4'	1.98	0.44
1:1A:1811:A:C8	1:1A:1824:A:H2'	2.53	0.44
1:1A:2343:C:HO2'	1:1A:2344:U:P	2.40	0.44
1:1A:2670:U:H2'	1:1A:2671:A:H8	1.82	0.44
1:1A:3196:U:H2'	1:1A:3197:C:C6	2.51	0.44
1:1A:3356:U:OP2	1:1A:3357:U:O2'	2.33	0.44
1:1A:3483:A:C2'	1:1A:3484:A:C2	3.00	0.44
3:IC:14:G:H2'	3:IC:15:A:C8	2.52	0.44
33:lg:90:ASN:OD1	33:lg:90:ASN:N	2.48	0.44
40:ln:14:GLU:HG2	40:ln:17:GLN:HG3	2.00	0.44
1:1A:678:A:H2'	1:1A:679:U:C6	2.51	0.44
1:1A:815:A:H4'	1:1A:817:A:OP1	2.17	0.44
1:1A:1431:G:OP2	15:IO:60:ARG:NH1	2.50	0.44
1:1A:1545:A:H4'	33:lg:122:ASN:HD21	1.82	0.44
1:1A:1847:A:H2'	1:1A:1848:A:H8	1.82	0.44
1:1A:3466:U:H3	1:1A:3487:C:N4	1.99	0.44
1:1A:3473:U:O2	1:1A:3473:U:O4'	2.35	0.44
5:IE:62:ARG:HD3	5:IE:350:THR:HA	1.99	0.44
8:IH:160:ALA:O	8:IH:164:GLU:HG2	2.17	0.44
33:lg:38:GLY:O	33:lg:44:ARG:HD3	2.18	0.44
1:1A:624:U:H2'	1:1A:625:A:O4'	2.16	0.44
1:1A:1859:G:N7	23:IW:87:ARG:NH2	2.65	0.44
1:1A:3090:G:N3	5:IE:252:ALA:HB1	2.32	0.44
1:1A:3455:G:O6	1:1A:3500:A:N1	2.51	0.44
1:1A:3476:C:C5	1:1A:3479:A:OP1	2.58	0.44
7:IG:117:LYS:HA	7:IG:117:LYS:HD3	1.78	0.44
27:la:75:LYS:HB2	27:la:77:VAL:HG22	1.99	0.44
1:1A:59:A:N3	1:1A:74:U:O2'	2.34	0.44
1:1A:187:G:H4'	1:1A:188:U:H5''	1.99	0.44
1:1A:1305:A:HO2'	1:1A:1306:A:H8	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2329:G:H1	1:1A:2339:C:H41	1.64	0.44
1:1A:3218:U:H2'	1:1A:3219:A:H8	1.81	0.44
1:1A:3227:A:H2'	1:1A:3228:A:O4'	2.17	0.44
6:1F:47:ASN:HA	6:1F:112:GLN:HG3	2.00	0.44
14:1N:82:LYS:NZ	14:1N:214:THR:OG1	2.34	0.44
28:1b:46:VAL:HG13	28:1b:68:VAL:HG13	1.99	0.44
1:1A:474:A:H2'	1:1A:475:A:C8	2.53	0.44
1:1A:493:G:N7	1:1A:494:G:C6	2.85	0.44
1:1A:721:A:O2'	1:1A:722:A:OP1	2.33	0.44
1:1A:2299:A:H2'	1:1A:2300:A:C8	2.53	0.44
1:1A:2340:U:H2'	1:1A:2341:C:O4'	2.18	0.44
3:1C:80:G:N2	3:1C:94:U:H3	2.03	0.44
7:1G:262:THR:OG1	7:1G:263:SER:N	2.51	0.44
10:1J:30:VAL:HG12	10:1J:31:ALA:H	1.81	0.44
13:1M:41:THR:OG1	13:1M:42:GLY:N	2.51	0.44
14:1N:45:PHE:CD1	14:1N:229:GLN:HB3	2.53	0.44
23:1W:57:GLN:OE1	23:1W:57:GLN:HA	2.17	0.44
23:1W:66:ILE:HD12	23:1W:79:THR:HG21	1.98	0.44
1:1A:998:U:H2'	18:1R:131:ARG:HH21	1.82	0.44
1:1A:1337:A:H2'	1:1A:1338:U:H6	1.82	0.44
1:1A:2937:G:O2'	1:1A:2938:U:OP2	2.30	0.44
1:1A:3452:U:H3	1:1A:3503:G:N2	2.04	0.44
1:1A:3469:A:N3	1:1A:3469:A:H5''	2.32	0.44
1:1A:3475:U:H3	1:1A:3479:A:H62	1.66	0.44
3:1C:7:A:H5''	22:1V:27:THR:HB	1.99	0.44
6:1F:208:PRO:HG2	6:1F:229:VAL:HG22	2.00	0.44
22:1V:52:LEU:HD12	22:1V:53:PRO:HD2	1.99	0.44
1:1A:570:A:H2'	1:1A:571:A:C8	2.53	0.44
1:1A:1467:U:H2'	1:1A:1468:A:C8	2.53	0.44
1:1A:1745:A:H2'	1:1A:1746:G:C8	2.52	0.44
1:1A:1856:G:H2'	1:1A:1857:A:H8	1.83	0.44
1:1A:2241:U:OP1	4:1D:4:ARG:NH2	2.42	0.44
1:1A:2504:U:H2'	1:1A:2505:A:H8	1.83	0.44
1:1A:2730:U:OP1	1:1A:2820:G:O2'	2.36	0.44
1:1A:2756:U:H2'	1:1A:2757:G:O4'	2.18	0.44
1:1A:3476:C:C4	1:1A:3477:U:C1'	3.01	0.44
1:1A:3477:U:C1'	1:1A:3478:U:P	3.06	0.44
2:1B:68:A:H2'	2:1B:69:U:C6	2.53	0.44
8:1H:178:LYS:HD3	8:1H:184:LYS:HG3	2.00	0.44
11:1K:129:LYS:HA	11:1K:129:LYS:HD2	1.83	0.44
14:1N:164:LYS:O	14:1N:168:ILE:HG13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:IT:9:ARG:NH1	20:IT:17:PRO:O	2.51	0.44
37:lk:39:ARG:HA	37:lk:39:ARG:HD3	1.80	0.44
1:lA:638:A:H2'	1:lA:639:G:H8	1.82	0.44
1:lA:737:A:O5'	1:lA:738:G:N2	2.51	0.44
1:lA:1651:C:H2'	1:lA:1653:U:C5	2.53	0.44
1:lA:2262:U:H2'	1:lA:2263:G:O4'	2.18	0.44
1:lA:2452:G:H2'	1:lA:2453:G:C8	2.53	0.44
1:lA:2629:A:H8	31:le:54:PRO:HB3	1.83	0.44
1:lA:2959:G:N7	1:lA:3013:C:H5'	2.32	0.44
2:lB:84:G:OP1	2:lB:85:U:O2'	2.24	0.44
8:lH:119:VAL:HG12	8:lH:122:VAL:HG22	2.00	0.44
15:lO:36:LEU:HB2	15:lO:39:CYS:SG	2.58	0.44
16:lP:100:LYS:HD3	16:lP:104:ARG:NH2	2.33	0.44
18:lR:53:ILE:HG13	18:lR:55:LYS:HG2	2.00	0.44
35:li:-5:ILE:HA	35:li:-5:ILE:HD13	1.79	0.44
1:lA:73:A:N7	14:lN:71:ARG:NH2	2.65	0.43
1:lA:642:G:H4'	16:lP:88:ARG:HH11	1.83	0.43
1:lA:1035:G:H5'	1:lA:1036:A:OP1	2.18	0.43
1:lA:1219:A:H4'	1:lA:1220:A:H5'	2.00	0.43
1:lA:2445:G:H2'	1:lA:2446:G:C8	2.53	0.43
1:lA:2981:A:H2'	1:lA:2982:G:O4'	2.18	0.43
1:lA:3312:U:H2'	1:lA:3313:U:C6	2.53	0.43
1:lA:3361:A:OP1	8:lH:190:TYR:N	2.39	0.43
5:lE:170:LEU:O	5:lE:320:ASN:ND2	2.50	0.43
36:lj:40:THR:HG22	36:lj:44:ILE:HD11	1.99	0.43
1:lA:699:A:H3'	1:lA:746:A:N6	2.33	0.43
1:lA:992:U:H3'	1:lA:993:U:H4'	2.00	0.43
1:lA:1242:G:H2'	1:lA:1243:C:C6	2.53	0.43
1:lA:1320:U:O2'	3:lC:83:G:N2	2.50	0.43
1:lA:2908:U:O2'	1:lA:2909:A:H5'	2.19	0.43
1:lA:3380:C:H2'	1:lA:3381:A:O4'	2.18	0.43
2:lB:54:A:H5'	41:lo:21:ARG:HD3	1.99	0.43
3:lC:36:U:H2'	3:lC:37:A:C8	2.53	0.43
8:lH:78:VAL:HG11	8:lH:173:ILE:HD13	1.99	0.43
11:lK:113:ILE:HG12	11:lK:120:ILE:HG13	2.00	0.43
14:lN:106:CYS:SG	14:lN:109:ARG:NH2	2.91	0.43
1:lA:62:A:N6	1:lA:72:G:H1'	2.34	0.43
1:lA:511:A:N6	1:lA:561:G:H21	2.15	0.43
1:lA:804:G:H2'	1:lA:805:G:H8	1.84	0.43
1:lA:941:A:H2'	1:lA:942:C:C6	2.53	0.43
1:lA:1310:A:N3	20:IT:108:SER:OG	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2513:A:O2'	1:1A:2514:A:H5'	2.18	0.43
1:1A:3165:A:N1	1:1A:3197:C:O2'	2.47	0.43
1:1A:3200:G:H5'	5:1E:223:THR:HG21	1.99	0.43
8:1H:167:LYS:HA	8:1H:167:LYS:HD2	1.69	0.43
11:1K:3:ARG:HD3	11:1K:69:TYR:CE2	2.54	0.43
14:1N:246:GLU:HG2	29:1c:101:VAL:HB	2.00	0.43
15:1O:63:VAL:HG23	15:1O:70:GLY:HA2	2.00	0.43
1:1A:2032:U:O2	2:1B:112:A:O2'	2.36	0.43
1:1A:2955:C:H2'	1:1A:2956:A:C8	2.53	0.43
1:1A:2958:G:N2	1:1A:2961:U:O2	2.48	0.43
3:1C:54:U:H4'	13:1M:152:HIS:HB2	1.99	0.43
27:1a:81:ASP:OD1	27:1a:82:LYS:HG2	2.19	0.43
36:1j:76:HIS:N	36:1j:81:VAL:O	2.51	0.43
42:1p:35:CYS:O	42:1p:42:HIS:HA	2.18	0.43
1:1A:189:G:H5'	17:1Q:55:PRO:HG3	1.99	0.43
1:1A:583:A:C6	1:1A:584:U:O4	2.72	0.43
1:1A:1615:A:O2'	32:1f:95:GLN:OE1	2.36	0.43
1:1A:1634:G:O6	41:1o:2:THR:N	2.52	0.43
1:1A:2599:A:C4	10:1J:36:LEU:HD22	2.53	0.43
1:1A:2739:U:H2'	1:1A:2740:G:H8	1.84	0.43
1:1A:3473:U:O2	1:1A:3473:U:O5'	2.36	0.43
10:1J:225:MET:HE2	10:1J:226:TYR:CZ	2.54	0.43
27:1a:86:THR:HA	27:1a:92:THR:HA	2.00	0.43
35:1i:2:SER:OG	35:1i:3:LYS:N	2.51	0.43
35:1i:46:LEU:O	35:1i:50:MET:HG3	2.18	0.43
37:1k:62:LYS:HA	37:1k:62:LYS:HD3	1.77	0.43
1:1A:301:A:H2'	1:1A:302:U:C6	2.54	0.43
1:1A:882:C:O2	19:1S:137:ARG:NE	2.43	0.43
1:1A:926:A:N1	1:1A:2487:U:O2'	2.42	0.43
1:1A:1225:A:H5''	9:1I:95:ARG:HD2	2.00	0.43
1:1A:2341:C:O2'	1:1A:2342:U:H5'	2.19	0.43
1:1A:2514:A:H2'	1:1A:2515:A:C8	2.54	0.43
1:1A:2594:C:C2'	1:1A:2595:G:H5'	2.48	0.43
1:1A:2731:G:H2'	1:1A:2732:A:C8	2.53	0.43
1:1A:2865:A:O2'	1:1A:2866:C:OP1	2.36	0.43
1:1A:3370:A:H2'	1:1A:3371:U:C6	2.54	0.43
1:1A:3476:C:N3	1:1A:3477:U:N1	2.67	0.43
5:1E:238:ARG:HE	5:1E:238:ARG:HB2	1.66	0.43
11:1K:128:GLU:OE1	11:1K:132:ARG:NH2	2.48	0.43
14:1N:49:ILE:HA	14:1N:231:LEU:O	2.18	0.43
18:1R:41:VAL:HG21	18:1R:150:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:IV:80:VAL:CG1	22:IV:81:ASN:N	2.82	0.43
1:IA:1598:G:N2	1:IA:1601:G:OP1	2.51	0.43
1:IA:1992:A:H2'	1:IA:1993:G:C8	2.49	0.43
1:IA:2860:U:OP1	1:IA:2891:G:O2'	2.30	0.43
1:IA:3091:C:H5''	5:IE:245:HIS:HB3	2.01	0.43
2:IB:80:A:N3	35:II:34:SER:OG	2.50	0.43
2:IB:154:C:H5'	10:IJ:182:ARG:HH12	1.83	0.43
3:IC:16:C:OP1	13:IM:150:ARG:HG3	2.18	0.43
3:IC:79:G:N1	3:IC:95:A:H2	2.05	0.43
5:IE:48:GLY:HA3	5:IE:81:THR:HG22	2.01	0.43
17:IQ:14:LYS:O	17:IQ:23:ARG:NH2	2.50	0.43
17:IQ:145:ASP:OD1	17:IQ:148:MET:N	2.52	0.43
27:IA:70:ALA:HB3	27:IA:79:ASN:HB2	1.99	0.43
34:Ih:74:ARG:HG2	34:Ih:75:ALA:N	2.33	0.43
1:IA:1641:A:H2'	1:IA:1642:A:O4'	2.19	0.43
1:IA:2028:U:H2'	1:IA:2029:U:C6	2.54	0.43
1:IA:3268:A:OP1	11:IK:83:SER:OG	2.33	0.43
27:IA:81:ASP:OD1	27:IA:82:LYS:N	2.51	0.43
35:II:13:LEU:HD12	35:II:46:LEU:HD22	2.00	0.43
1:IA:941:A:H2'	1:IA:942:C:H6	1.84	0.43
1:IA:1627:G:H21	34:Ih:6:THR:HG22	1.84	0.43
5:IE:286:ARG:NH2	5:IE:296:LYS:O	2.51	0.43
9:II:224:LYS:H	9:II:224:LYS:HG3	1.65	0.43
11:IK:26:ILE:HD11	11:IK:46:ILE:HG21	2.01	0.43
26:IZ:40:MET:O	26:IZ:44:ARG:HG3	2.19	0.43
29:IC:36:GLY:HA3	29:IC:40:HIS:CE1	2.54	0.43
1:IA:82:G:O2'	1:IA:94:G:O6	2.35	0.43
1:IA:1596:A:H2'	1:IA:1597:A:C8	2.54	0.43
1:IA:2220:A:H1'	1:IA:2357:A:H61	1.84	0.43
1:IA:2645:G:H2'	1:IA:2646:G:C8	2.53	0.43
1:IA:2747:G:H2'	1:IA:2747:G:N3	2.34	0.43
1:IA:3305:U:H2'	1:IA:3306:U:O4'	2.19	0.43
3:IC:32:A:H2'	3:IC:33:A:C8	2.53	0.43
6:IF:32:ILE:HG21	27:IA:178:LEU:HD13	2.00	0.43
14:IN:154:LYS:HG3	14:IN:155:PHE:N	2.34	0.43
28:IB:94:LEU:O	28:IB:97:GLN:NE2	2.51	0.43
38:II:44:MET:HE3	38:II:44:MET:HB3	1.82	0.43
45:SI:75:C:H6	45:SI:75:C:H2'	1.54	0.43
1:IA:1830:U:H2'	1:IA:1831:U:C6	2.54	0.42
1:IA:2857:A:H1'	1:IA:2858:A:H5''	2.00	0.42
1:IA:3023:U:O2	5:IE:252:ALA:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3194:U:H2'	1:1A:3195:G:H8	1.84	0.42
1:1A:3260:A:H2'	1:1A:3261:A:C8	2.54	0.42
3:1C:85:G:N2	3:1C:90:G:H1	2.16	0.42
6:1F:102:PHE:O	6:1F:103:SER:C	2.62	0.42
7:1G:233:GLU:O	7:1G:237:ILE:HG12	2.19	0.42
14:1N:46:PRO:HB3	14:1N:49:ILE:HD12	2.01	0.42
1:1A:35:A:H5''	29:1c:35:ALA:HB2	2.01	0.42
1:1A:239:G:H2'	1:1A:240:A:C8	2.54	0.42
1:1A:1117:G:N3	1:1A:1120:A:N6	2.68	0.42
1:1A:1407:U:H2'	1:1A:1408:C:O4'	2.19	0.42
1:1A:1434:G:O2'	1:1A:2456:U:O2'	2.20	0.42
1:1A:2701:U:H2'	1:1A:2702:G:C8	2.54	0.42
6:1F:100:HIS:ND1	6:1F:101:MET:O	2.41	0.42
6:1F:431:PHE:HE1	20:1T:5:TYR:HE1	1.66	0.42
14:1N:153:LYS:HE2	14:1N:153:LYS:HB3	1.83	0.42
14:1N:175:LYS:HB2	14:1N:175:LYS:HE2	1.93	0.42
21:1U:116:ASP:OD2	21:1U:118:HIS:ND1	2.41	0.42
28:1b:78:ASN:OD1	31:1e:39:ARG:NH2	2.52	0.42
1:1A:13:C:P	25:1Y:27:ARG:HH22	2.41	0.42
1:1A:381:A:H2'	1:1A:382:A:C8	2.54	0.42
1:1A:670:A:H2	6:1F:397:LEU:HD23	1.84	0.42
1:1A:759:U:H2'	1:1A:760:A:C8	2.54	0.42
1:1A:841:A:H4'	1:1A:842:G:H5'	2.01	0.42
1:1A:877:U:H2'	1:1A:878:U:C6	2.54	0.42
1:1A:1194:A:O2'	1:1A:1195:G:H5'	2.19	0.42
1:1A:1631:A:O2'	38:1l:12:HIS:O	2.32	0.42
1:1A:1743:U:C2	1:1A:1761:A:C2	3.07	0.42
1:1A:1968:U:H2'	1:1A:1969:U:C6	2.54	0.42
1:1A:2438:C:H2'	1:1A:2439:A:O4'	2.19	0.42
1:1A:2846:U:H2'	1:1A:2847:A:H8	1.84	0.42
1:1A:3309:U:C4	1:1A:3330:A:C6	3.07	0.42
5:1E:257:TRP:CD1	5:1E:257:TRP:C	2.97	0.42
6:1F:402:LYS:HD2	6:1F:402:LYS:HA	1.86	0.42
11:1K:171:ASN:HD22	11:1K:185:VAL:HG23	1.84	0.42
12:1L:102:MET:HE1	12:1L:115:MET:O	2.19	0.42
14:1N:44:VAL:HG23	14:1N:47:ALA:HB2	2.00	0.42
15:1O:33:LYS:HA	15:1O:102:ASN:HB3	2.00	0.42
16:1P:92:THR:O	16:1P:96:LYS:HG3	2.19	0.42
1:1A:231:U:H4'	27:1a:123:SER:HB3	2.02	0.42
1:1A:459:A:H2'	1:1A:460:A:H8	1.85	0.42
1:1A:474:A:H2'	1:1A:475:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:622:A:H2'	1:1A:623:A:H8	1.84	0.42
1:1A:1266:C:O2'	1:1A:1278:A:N3	2.49	0.42
1:1A:1858:A:H2'	1:1A:1859:G:C8	2.54	0.42
1:1A:2503:U:H2'	1:1A:2504:U:C6	2.55	0.42
1:1A:2514:A:N1	1:1A:2515:A:C2	2.87	0.42
1:1A:3084:A:H8	1:1A:3084:A:OP2	2.03	0.42
1:1A:3168:A:H2'	1:1A:3169:C:H6	1.85	0.42
1:1A:3404:A:H2'	8:1H:95:PHE:CZ	2.54	0.42
2:1B:9:A:H2'	2:1B:10:U:C6	2.55	0.42
3:1C:16:C:H2'	3:1C:17:G:O4'	2.20	0.42
11:1K:67:MET:HE1	11:1K:74:ASP:HB3	2.02	0.42
13:1M:150:ARG:HD2	13:1M:150:ARG:HA	1.81	0.42
14:1N:15:ASP:OD2	14:1N:18:SER:OG	2.28	0.42
22:1V:26:ASN:HB2	22:1V:29:THR:HG23	2.00	0.42
25:1Y:66:GLU:OE1	25:1Y:68:LYS:NZ	2.52	0.42
28:1b:18:PHE:HE1	28:1b:47:GLU:OE2	2.02	0.42
36:1j:55:ASN:OD1	36:1j:55:ASN:N	2.40	0.42
1:1A:322:U:H2'	1:1A:323:U:C6	2.53	0.42
1:1A:887:G:H2'	1:1A:888:U:O4'	2.19	0.42
1:1A:1111:G:N3	1:1A:2707:A:H2'	2.35	0.42
1:1A:1533:U:HO2'	1:1A:1534:U:P	2.40	0.42
1:1A:1624:G:C8	1:1A:1626:G:C8	3.08	0.42
2:1B:29:U:H2'	2:1B:30:U:C6	2.53	0.42
3:1C:45:U:OP1	7:1G:159:LYS:N	2.51	0.42
4:1D:180:LEU:HD22	39:1m:18:TYR:HB3	2.02	0.42
14:1N:197:LYS:O	14:1N:201:VAL:HG23	2.19	0.42
15:1O:196:VAL:O	15:1O:200:LYS:HG2	2.19	0.42
16:1P:39:ASP:CG	16:1P:49:ARG:HE	2.27	0.42
25:1Y:95:LEU:HD22	41:1o:10:LYS:HE3	2.01	0.42
27:1a:181:LYS:HA	27:1a:181:LYS:HD3	1.82	0.42
30:1d:38:GLN:NE2	30:1d:42:ASN:OD1	2.51	0.42
31:1e:42:LYS:H	31:1e:42:LYS:HG2	1.62	0.42
35:1i:41:LYS:HA	35:1i:41:LYS:HD3	1.81	0.42
36:1j:92:PRO:O	36:1j:95:MET:HG3	2.20	0.42
1:1A:623:A:H2'	1:1A:624:U:C6	2.54	0.42
1:1A:957:G:N7	39:1m:4:ARG:NH2	2.67	0.42
1:1A:1818:C:OP1	34:1h:52:ALA:HB3	2.20	0.42
1:1A:2100:G:O2'	24:1X:24:SER:OG	2.27	0.42
1:1A:2395:C:O2'	1:1A:2396:A:H8	2.03	0.42
1:1A:2858:A:N6	1:1A:2902:G:O2'	2.42	0.42
2:1B:8:U:H2'	2:1B:9:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IB:48:G:N3	2:IB:63:A:H2	2.18	0.42
3:IC:43:A:OP2	13:IM:137:ARG:NH1	2.41	0.42
4:ID:104:ILE:HD12	4:ID:104:ILE:HA	1.93	0.42
12:IL:165:LEU:HA	12:IL:165:LEU:HD12	1.78	0.42
12:IL:179:GLU:OE2	12:IL:179:GLU:N	2.43	0.42
14:IN:198:LYS:HD3	14:IN:198:LYS:HA	1.80	0.42
17:IQ:71:ARG:HD3	17:IQ:71:ARG:HA	1.88	0.42
1:IA:720:U:H2'	1:IA:721:A:C8	2.51	0.42
1:IA:1071:A:H4'	1:IA:1087:G:H21	1.85	0.42
1:IA:1186:G:N2	1:IA:1220:A:H61	2.13	0.42
1:IA:1876:U:H2'	1:IA:1936:A:N6	2.34	0.42
1:IA:2079:A:H3'	1:IA:2079:A:N3	2.35	0.42
1:IA:2254:A:H5''	4:ID:132:ASN:OD1	2.18	0.42
1:IA:2750:A:C2	13:IM:57:PHE:HB3	2.55	0.42
1:IA:3008:U:HO2'	1:IA:3009:C:P	2.41	0.42
1:IA:3364:U:H2'	1:IA:3365:C:C6	2.55	0.42
10:IJ:248:LYS:HA	10:IJ:248:LYS:HD3	1.76	0.42
11:IK:98:TYR:CZ	11:IK:190:LYS:HB3	2.55	0.42
11:IK:156:ASP:HB3	11:IK:159:LYS:HG3	2.01	0.42
15:IO:40:GLU:H	15:IO:40:GLU:HG3	1.73	0.42
21:IU:74:ARG:HA	21:IU:74:ARG:HD3	1.80	0.42
1:IA:1105:U:H2'	1:IA:1106:U:H6	1.83	0.42
1:IA:1491:A:H4'	29:lc:21:ARG:HG3	2.02	0.42
1:IA:2174:U:H2'	1:IA:2175:C:C6	2.54	0.42
1:IA:2334:U:H2'	1:IA:2335:A:H8	1.85	0.42
1:IA:2343:C:H4'	1:IA:2343:C:OP1	2.18	0.42
1:IA:2818:A:N3	7:IG:36:MET:HG2	2.34	0.42
1:IA:3084:A:OP1	5:IE:257:TRP:HB3	2.19	0.42
3:IC:66:U:H2'	3:IC:67:A:H8	1.85	0.42
3:IC:106:U:H2'	3:IC:107:A:H8	1.84	0.42
5:IE:81:THR:O	5:IE:81:THR:OG1	2.38	0.42
8:IH:11:LYS:NZ	8:IH:27:ILE:O	2.52	0.42
12:IL:110:ARG:HB3	12:IL:111:LEU:H	1.64	0.42
13:IM:27:GLY:O	13:IM:29:ARG:N	2.52	0.42
14:IN:46:PRO:HA	14:IN:49:ILE:HB	2.02	0.42
15:IO:63:VAL:HG12	15:IO:66:ASN:H	1.84	0.42
1:IA:285:A:H4'	1:IA:286:U:C5'	2.49	0.42
1:IA:909:A:H2'	1:IA:910:A:H8	1.84	0.42
1:IA:1465:G:H2'	1:IA:1466:U:H6	1.84	0.42
1:IA:1739:G:H5''	34:lh:37:LYS:NZ	2.35	0.42
1:IA:1934:G:O3'	40:ln:51:THR:HG21	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:ID:20:SER:OG	4:ID:20:SER:O	2.37	0.42
8:IH:31:LYS:HE2	8:IH:31:LYS:HB2	1.86	0.42
9:II:66:GLU:O	22:IV:142:ARG:NH1	2.52	0.42
13:IM:30:LEU:HA	13:IM:30:LEU:HD23	1.77	0.42
13:IM:173:ASN:OD1	13:IM:173:ASN:N	2.53	0.42
14:IN:104:LYS:HB2	37:Ik:16:HIS:HB2	2.01	0.42
19:IS:156:LYS:HD2	19:IS:156:LYS:HA	1.84	0.42
1:IA:1581:G:N7	18:IR:27:LYS:HB2	2.35	0.42
1:IA:2867:A:N6	1:IA:2887:G:C2	2.88	0.42
1:IA:2902:G:H2'	1:IA:2903:A:C8	2.55	0.42
1:IA:3311:U:H2'	1:IA:3312:U:H6	1.84	0.42
1:IA:3335:U:H3'	1:IA:3336:G:H5''	2.02	0.42
1:IA:3369:U:H2'	1:IA:3370:A:C8	2.55	0.42
3:IC:79:G:O6	3:IC:95:A:N1	2.53	0.42
5:IE:37:ALA:HA	5:IE:187:GLY:O	2.19	0.42
6:IF:372:SER:HB2	6:IF:392:VAL:HG11	2.02	0.42
7:IG:207:LEU:HD23	7:IG:207:LEU:HA	1.88	0.42
11:IK:144:LYS:HE3	11:IK:144:LYS:HB2	1.86	0.42
28:lb:14:LEU:HB3	34:lh:86:GLN:HG2	2.02	0.42
28:lb:89:LEU:HD23	28:lb:89:LEU:HA	1.85	0.42
1:IA:18:G:H1'	2:IB:102:A:N3	2.35	0.41
1:IA:1303:A:N3	1:IA:1453:U:O2'	2.53	0.41
1:IA:2863:A:N7	1:IA:2890:A:H2	2.18	0.41
1:IA:3028:C:O2'	1:IA:3029:U:H5'	2.20	0.41
1:IA:3268:A:H4'	11:IK:79:ARG:HG2	2.01	0.41
3:IC:8:U:OP1	22:IV:26:ASN:HB3	2.19	0.41
3:IC:84:G:H2'	3:IC:84:G:N3	2.35	0.41
16:IP:29:GLU:OE2	16:IP:69:ARG:HD2	2.19	0.41
19:IS:132:LYS:HA	19:IS:132:LYS:HD2	1.91	0.41
28:lb:85:TYR:OH	34:lh:97:GLU:OE2	2.25	0.41
42:lp:18:LYS:HE3	42:lp:18:LYS:HB3	1.92	0.41
1:IA:226:U:H2'	1:IA:227:A:C8	2.55	0.41
1:IA:559:U:H2'	1:IA:560:U:H6	1.85	0.41
1:IA:564:A:H4'	1:IA:565:U:O5'	2.20	0.41
1:IA:2850:U:O2	1:IA:2910:G:N2	2.53	0.41
1:IA:3491:C:O2'	5:IE:384:MET:SD	2.78	0.41
1:IA:3501:A:H4'	5:IE:316:GLY:HA2	2.01	0.41
5:IE:47:LEU:HB3	5:IE:84:MET:HE3	2.01	0.41
7:IG:163:VAL:O	7:IG:167:MET:HG3	2.20	0.41
13:IM:117:ASP:HB3	13:IM:119:GLN:HG2	2.02	0.41
27:la:180:SER:OG	27:la:183:THR:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:li:20:LEU:HD13	35:li:36:LEU:HA	2.02	0.41
1:1A:343:A:H62	17:lQ:12:ARG:HH12	1.68	0.41
1:1A:592:A:H2'	1:1A:593:A:H8	1.85	0.41
1:1A:761:A:H2'	1:1A:762:A:H8	1.85	0.41
1:1A:918:G:O2'	14:lN:16:TRP:NE1	2.53	0.41
1:1A:2495:A:H2'	1:1A:2496:C:C6	2.56	0.41
1:1A:2681:U:H2'	1:1A:2682:U:C6	2.55	0.41
2:1B:58:G:H2'	2:1B:59:C:O4'	2.20	0.41
3:1C:79:G:C6	3:1C:95:A:N1	2.88	0.41
3:1C:112:C:H2'	3:1C:113:C:C6	2.54	0.41
31:le:13:GLY:O	31:le:16:SER:N	2.52	0.41
1:1A:247:A:H5'	1:1A:266:A:O2'	2.21	0.41
1:1A:279:U:H2'	1:1A:280:U:H6	1.84	0.41
1:1A:285:A:H4'	1:1A:286:U:O5'	2.19	0.41
1:1A:606:A:H2'	1:1A:607:U:H6	1.86	0.41
1:1A:645:A:H62	6:lF:376:ARG:HD3	1.85	0.41
1:1A:739:A:H2'	1:1A:740:A:C8	2.55	0.41
1:1A:745:A:H3'	1:1A:745:A:OP1	2.20	0.41
1:1A:1293:U:O4	1:1A:1454:G:O2'	2.24	0.41
1:1A:1606:A:H5''	18:lR:53:ILE:HB	2.02	0.41
1:1A:2224:U:H2'	1:1A:2225:A:C8	2.56	0.41
1:1A:3207:G:H2'	1:1A:3208:A:H8	1.86	0.41
1:1A:3303:A:H2'	1:1A:3304:C:C6	2.56	0.41
5:lE:154:LYS:HD3	5:lE:191:ALA:HA	2.03	0.41
19:lS:72:LYS:H	19:lS:72:LYS:HG2	1.60	0.41
23:lW:44:LYS:HG3	23:lW:45:LYS:N	2.35	0.41
1:1A:586:A:H5''	8:lH:130:LYS:HE2	2.02	0.41
1:1A:979:G:H3'	1:1A:979:G:N3	2.35	0.41
1:1A:2207:A:C8	1:1A:2264:A:C8	3.08	0.41
1:1A:2207:A:N6	39:lm:17:ARG:O	2.42	0.41
1:1A:2894:C:O2	1:1A:2899:G:N1	2.52	0.41
1:1A:3169:C:H2'	1:1A:3170:A:H8	1.86	0.41
2:1B:64:A:H2'	2:1B:64:A:N3	2.36	0.41
3:1C:27:G:N2	3:1C:50:A:C2	2.80	0.41
5:lE:225:GLY:HA2	5:lE:273:GLY:HA3	2.02	0.41
28:lb:75:ILE:HD12	28:lb:75:ILE:HA	1.85	0.41
34:lh:102:LYS:O	34:lh:106:ALA:HB2	2.20	0.41
1:1A:324:A:H2'	1:1A:325:U:C6	2.55	0.41
1:1A:480:U:H2'	1:1A:481:A:O4'	2.19	0.41
1:1A:626:A:O2'	1:1A:627:A:H8	2.04	0.41
1:1A:1841:G:H22	1:1A:1975:G:H22	1.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1889:U:H2'	1:1A:1890:U:C6	2.55	0.41
1:1A:2343:C:OP1	1:1A:2343:C:C4'	2.68	0.41
1:1A:2630:A:H8	31:1e:55:LEU:HD13	1.86	0.41
1:1A:2901:U:O2	1:1A:2901:U:O4'	2.37	0.41
2:1B:8:U:C2	2:1B:9:A:C8	3.08	0.41
7:1G:29:ASP:HB2	7:1G:151:LEU:HD21	2.02	0.41
9:1I:96:LEU:HD21	9:1I:103:VAL:HG22	2.02	0.41
12:1L:85:PHE:HD2	12:1L:87:VAL:HG23	1.85	0.41
34:1h:103:LEU:HD12	34:1h:104:ALA:N	2.35	0.41
1:1A:76:U:H2'	1:1A:77:C:C6	2.55	0.41
1:1A:317:U:C2	1:1A:318:A:C8	3.09	0.41
1:1A:496:A:H2'	1:1A:497:U:O4'	2.20	0.41
1:1A:528:A:H2'	1:1A:529:U:C6	2.55	0.41
1:1A:3142:G:N3	1:1A:3143:A:N6	2.69	0.41
1:1A:3371:U:H2'	1:1A:3372:U:C6	2.55	0.41
3:1C:6:G:H2'	3:1C:7:A:C8	2.56	0.41
9:1I:36:THR:HG23	9:1I:170:ASP:OD2	2.21	0.41
13:1M:110:ILE:HD12	13:1M:111:ASP:N	2.34	0.41
18:1R:124:SER:HB2	18:1R:126:ARG:NH1	2.35	0.41
1:1A:1441:U:O2'	1:1A:1442:A:H3'	2.21	0.41
1:1A:1469:A:H2'	1:1A:1470:A:C8	2.56	0.41
1:1A:3026:U:H2'	1:1A:3027:C:H6	1.84	0.41
1:1A:3139:G:O2'	2:1B:1:A:N3	2.38	0.41
1:1A:3369:U:H2'	1:1A:3370:A:H8	1.85	0.41
3:1C:84:G:N2	3:1C:91:G:N2	2.68	0.41
32:1f:16:GLU:HA	32:1f:19:LYS:HB3	2.03	0.41
37:1k:73:THR:HG22	37:1k:75:LYS:H	1.85	0.41
37:1k:88:LEU:HD12	37:1k:88:LEU:HA	1.83	0.41
40:1n:19:LEU:O	40:1n:23:LYS:HG2	2.20	0.41
1:1A:101:A:H2'	1:1A:102:A:H8	1.85	0.41
1:1A:198:A:C6	37:1k:23:ARG:HD3	2.56	0.41
1:1A:463:U:O2'	1:1A:464:G:H5'	2.21	0.41
1:1A:500:G:O6	1:1A:573:A:N6	2.53	0.41
1:1A:862:G:C6	1:1A:880:A:C2	3.09	0.41
1:1A:1095:A:H2	1:1A:1099:A:C2	2.37	0.41
1:1A:1222:U:O2'	22:1V:136:ARG:O	2.30	0.41
1:1A:1285:C:P	19:1S:2:ALA:HB2	2.61	0.41
1:1A:1337:A:H2'	1:1A:1338:U:C6	2.56	0.41
1:1A:1471:A:OP1	6:1F:305:ARG:NH2	2.53	0.41
1:1A:1635:U:H4'	1:1A:1636:U:O5'	2.21	0.41
1:1A:2116:G:N2	21:1U:81:ARG:O	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2598:A:C5	10:1J:41:LYS:HG3	2.55	0.41
1:1A:2844:U:O5'	1:1A:2844:U:H6	2.03	0.41
1:1A:3004:U:H2'	1:1A:3005:U:O4'	2.21	0.41
1:1A:3084:A:OP2	5:1E:258:HIS:HB2	2.21	0.41
1:1A:3326:U:H2'	1:1A:3327:A:O4'	2.21	0.41
1:1A:3356:U:H5'	15:1O:6:LYS:HG3	2.03	0.41
2:1B:17:G:H2'	2:1B:18:G:O4'	2.21	0.41
7:1G:135:GLU:OE1	7:1G:135:GLU:N	2.54	0.41
12:1L:13:ARG:HE	12:1L:13:ARG:HB3	1.58	0.41
13:1M:110:ILE:H	13:1M:110:ILE:HG13	1.43	0.41
14:1N:108:ASN:O	14:1N:112:GLN:HG3	2.21	0.41
33:1g:127:ILE:HG23	33:1g:128:LYS:O	2.21	0.41
40:1n:27:ILE:HD11	40:1n:30:VAL:HG22	2.02	0.41
41:1o:51:MET:HB2	41:1o:51:MET:HE3	1.78	0.41
46:sJ:74:A:O2'	46:sJ:75:C:H5'	2.21	0.41
1:1A:255:A:H4'	1:1A:257:A:N7	2.36	0.41
1:1A:282:G:H2'	1:1A:283:A:C8	2.56	0.41
1:1A:621:U:H4'	6:1F:392:VAL:HB	2.02	0.41
1:1A:686:A:OP1	9:1I:134:LYS:NZ	2.46	0.41
1:1A:1107:G:H2'	1:1A:1108:A:H8	1.86	0.41
1:1A:1482:U:H2'	1:1A:1483:U:C6	2.56	0.41
1:1A:2512:G:H3'	1:1A:2512:G:C8	2.56	0.41
1:1A:2816:A:C2	7:1G:147:LEU:HD23	2.55	0.41
1:1A:3098:U:OP2	1:1A:3120:G:N1	2.43	0.41
1:1A:3128:C:H2'	1:1A:3129:U:O4'	2.21	0.41
3:1C:80:G:H2'	3:1C:81:A:C8	2.56	0.41
4:1D:104:ILE:N	4:1D:162:CYS:O	2.44	0.41
5:1E:203:LYS:HA	5:1E:203:LYS:HD3	1.85	0.41
7:1G:32:ALA:O	7:1G:36:MET:HG3	2.20	0.41
10:1J:130:SER:HB2	10:1J:196:ALA:HB3	2.03	0.41
13:1M:155:THR:HG22	13:1M:156:LYS:N	2.36	0.41
15:1O:39:CYS:HB3	15:1O:81:VAL:HG21	2.03	0.41
16:1P:100:LYS:O	16:1P:104:ARG:HG2	2.21	0.41
1:1A:491:G:O6	1:1A:582:U:N3	2.54	0.40
1:1A:715:A:C8	1:1A:727:U:H5''	2.56	0.40
1:1A:1188:A:H2'	1:1A:1189:U:C6	2.55	0.40
1:1A:1738:G:H5''	34:1h:15:THR:HG21	2.02	0.40
1:1A:1840:A:H2'	1:1A:1841:G:C8	2.56	0.40
1:1A:2583:U:O2'	1:1A:2584:U:H6	2.04	0.40
1:1A:2851:A:H2'	1:1A:2852:G:H8	1.86	0.40
1:1A:3066:U:H2'	1:1A:3067:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3148:C:H2'	1:1A:3149:A:C8	2.55	0.40
1:1A:3469:A:N3	1:1A:3469:A:O4'	2.54	0.40
1:1A:3476:C:N4	1:1A:3478:U:OP2	2.53	0.40
2:1B:80:A:O2'	2:1B:81:A:OP1	2.37	0.40
3:1C:85:G:N2	3:1C:90:G:N2	2.70	0.40
3:1C:112:C:H2'	3:1C:113:C:H6	1.87	0.40
6:1F:157:LYS:HE3	27:1a:145:VAL:HG12	2.02	0.40
11:1K:67:MET:HE1	11:1K:74:ASP:CB	2.51	0.40
20:1T:22:ARG:HH21	22:1V:156:THR:HG1	1.66	0.40
23:1W:39:ASP:OD1	23:1W:39:ASP:N	2.49	0.40
23:1W:109:ILE:HD13	23:1W:109:ILE:HA	1.90	0.40
25:1Y:44:PHE:CD1	35:1i:25:VAL:HG21	2.57	0.40
34:1h:10:LYS:HD3	34:1h:10:LYS:HA	1.80	0.40
1:1A:806:A:OP1	19:1S:19:ARG:HD3	2.21	0.40
1:1A:1636:U:C5	1:1A:2036:A:N1	2.89	0.40
1:1A:2142:G:H2'	1:1A:2143:C:C6	2.56	0.40
1:1A:3096:U:H2'	1:1A:3097:U:H2'	2.02	0.40
1:1A:3170:A:H2'	1:1A:3171:A:C8	2.55	0.40
1:1A:3349:G:OP2	16:1P:5:ARG:NH2	2.45	0.40
1:1A:3373:A:H1'	1:1A:3385:G:C4	2.56	0.40
3:1C:84:G:N2	3:1C:91:G:H22	2.19	0.40
6:1F:55:SER:HB3	6:1F:58:ALA:HB2	2.03	0.40
15:1O:36:LEU:HD11	15:1O:103:LEU:HD11	2.02	0.40
23:1W:101:ASN:N	23:1W:101:ASN:OD1	2.52	0.40
37:1k:36:ASP:O	37:1k:40:GLU:HG2	2.21	0.40
1:1A:426:U:H2'	1:1A:427:U:H6	1.85	0.40
1:1A:503:A:H2'	1:1A:504:U:C6	2.56	0.40
1:1A:532:A:H2'	1:1A:533:U:C6	2.56	0.40
1:1A:837:A:H2'	1:1A:838:U:C6	2.56	0.40
1:1A:1201:A:H2'	1:1A:1202:A:O4'	2.21	0.40
1:1A:2304:A:H2'	1:1A:2305:C:H6	1.86	0.40
1:1A:2902:G:H4'	1:1A:2903:A:OP1	2.21	0.40
1:1A:3104:G:H2'	1:1A:3105:U:C6	2.56	0.40
8:1H:93:GLY:O	8:1H:94:PRO:C	2.65	0.40
12:1L:112:GLN:HB2	45:1i:73:A:C8	2.49	0.40
17:1Q:191:ASN:ND2	17:1Q:194:ARG:HH21	2.19	0.40
18:1R:60:PHE:O	18:1R:64:ASN:HB3	2.21	0.40
20:1T:172:LEU:HA	20:1T:172:LEU:HD12	1.74	0.40
23:1W:51:ARG:HH12	23:1W:69:LYS:H	1.69	0.40
39:1m:6:LYS:HA	39:1m:6:LYS:HD3	1.85	0.40
1:1A:5:U:H2'	1:1A:6:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:575:A:OP2	1:1A:575:A:H8	2.03	0.40
1:1A:772:C:N4	1:1A:773:G:O6	2.54	0.40
1:1A:790:A:H2'	1:1A:791:A:H8	1.84	0.40
1:1A:1126:U:H2'	1:1A:1127:A:O4'	2.22	0.40
1:1A:1131:G:H2'	1:1A:1132:U:C6	2.56	0.40
1:1A:2414:C:OP1	5:1E:238:ARG:NH1	2.51	0.40
1:1A:2583:U:C2	1:1A:2584:U:C6	3.09	0.40
1:1A:2645:G:H2'	1:1A:2646:G:C4	2.57	0.40
1:1A:2976:A:C2	1:1A:2977:G:C8	3.10	0.40
1:1A:2983:C:H2'	1:1A:2984:G:O4'	2.21	0.40
1:1A:3360:U:H3	8:1H:185:GLU:HG2	1.85	0.40
1:1A:3476:C:C5	1:1A:3477:U:O4'	2.74	0.40
4:1D:177:LYS:HA	39:1m:29:ILE:HD13	2.03	0.40
11:1K:65:ILE:HG22	11:1K:78:VAL:HG13	2.03	0.40
12:1L:38:ASN:HB2	12:1L:83:ASP:HA	2.03	0.40
13:1M:18:VAL:HG22	13:1M:70:THR:HG22	2.02	0.40
17:1Q:143:ARG:NH2	35:1i:82:ARG:O	2.51	0.40
30:1d:7:ARG:HG2	30:1d:8:SER:N	2.37	0.40
1:1A:546:U:H2'	1:1A:547:A:C8	2.57	0.40
1:1A:709:U:HO2'	1:1A:710:A:P	2.43	0.40
1:1A:802:A:H2'	1:1A:803:U:C6	2.57	0.40
1:1A:2582:U:C6	1:1A:2583:U:C4	3.10	0.40
1:1A:2856:G:C8	1:1A:2903:A:N6	2.66	0.40
1:1A:3312:U:H2'	1:1A:3313:U:H6	1.86	0.40
1:1A:3430:U:O5'	1:1A:3431:U:H5''	2.21	0.40
6:1F:149:GLN:HB3	6:1F:151:PRO:HD2	2.02	0.40
7:1G:211:ASP:HB3	7:1G:214:LEU:HB2	2.04	0.40
10:1J:180:LYS:HE3	10:1J:191:THR:HG21	2.03	0.40
13:1M:172:LEU:HB3	13:1M:174:LYS:HG2	2.02	0.40
18:1R:13:LYS:HA	18:1R:13:LYS:HD2	1.92	0.40
28:1b:113:GLN:O	28:1b:117:ILE:HG13	2.22	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	
4	ID	244/257 (95%)	233 (96%)	11 (4%)	0	100	100
5	IE	386/402 (96%)	372 (96%)	14 (4%)	0	100	100
6	IF	415/431 (96%)	395 (95%)	20 (5%)	0	100	100
7	IG	275/286 (96%)	256 (93%)	19 (7%)	0	100	100
8	IH	201/204 (98%)	185 (92%)	15 (8%)	1 (0%)	24	60
9	II	208/230 (90%)	200 (96%)	8 (4%)	0	100	100
10	IJ	194/286 (68%)	186 (96%)	8 (4%)	0	100	100
11	IK	191/197 (97%)	183 (96%)	7 (4%)	1 (0%)	24	60
12	IL	197/210 (94%)	188 (95%)	9 (5%)	0	100	100
13	IM	166/174 (95%)	157 (95%)	8 (5%)	1 (1%)	21	56
14	IN	259/291 (89%)	248 (96%)	11 (4%)	0	100	100
15	IO	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	IP	128/135 (95%)	125 (98%)	3 (2%)	0	100	100
17	IQ	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
18	IR	156/179 (87%)	154 (99%)	2 (1%)	0	100	100
19	IS	165/168 (98%)	154 (93%)	11 (7%)	0	100	100
20	IT	171/173 (99%)	160 (94%)	11 (6%)	0	100	100
21	IU	148/198 (75%)	147 (99%)	1 (1%)	0	100	100
22	IV	163/166 (98%)	158 (97%)	5 (3%)	0	100	100
23	IW	91/137 (66%)	85 (93%)	6 (7%)	0	100	100
24	IX	131/140 (94%)	125 (95%)	6 (5%)	0	100	100
25	IY	114/121 (94%)	111 (97%)	3 (3%)	0	100	100
26	IZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	201 (97%)	7 (3%)	0	100	100
28	lb	135/139 (97%)	132 (98%)	3 (2%)	0	100	100
29	lc	146/149 (98%)	138 (94%)	8 (6%)	0	100	100
30	ld	58/64 (91%)	55 (95%)	3 (5%)	0	100	100
31	le	94/109 (86%)	88 (94%)	6 (6%)	0	100	100
32	lf	120/150 (80%)	115 (96%)	5 (4%)	0	100	100
33	lg	127/134 (95%)	122 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	lh	103/137 (75%)	97 (94%)	6 (6%)	0	100	100
35	li	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	50
36	lj	104/108 (96%)	99 (95%)	5 (5%)	0	100	100
37	lk	83/104 (80%)	82 (99%)	1 (1%)	0	100	100
38	ll	70/77 (91%)	65 (93%)	3 (4%)	2 (3%)	3	20
39	lm	88/93 (95%)	82 (93%)	6 (7%)	0	100	100
40	ln	71/77 (92%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/51 (94%)	48 (100%)	0	0	100	100
42	lp	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
43	lq	90/98 (92%)	86 (96%)	4 (4%)	0	100	100
All	All	6178/6839 (90%)	5913 (96%)	259 (4%)	6 (0%)	49	80

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	ll	40	PRO
35	li	-6	LYS
38	ll	39	TYR
8	lH	119	VAL
11	lK	134	ILE
13	lM	28	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	lD	195/201 (97%)	190 (97%)	5 (3%)	40	72
5	lE	331/343 (96%)	324 (98%)	7 (2%)	47	75
6	lF	332/345 (96%)	321 (97%)	11 (3%)	33	67
7	lG	225/231 (97%)	215 (96%)	10 (4%)	25	60
8	lH	172/173 (99%)	168 (98%)	4 (2%)	44	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	II	178/195 (91%)	173 (97%)	5 (3%)	38	70
10	IJ	174/242 (72%)	165 (95%)	9 (5%)	21	55
11	IK	171/174 (98%)	164 (96%)	7 (4%)	27	61
12	IL	170/176 (97%)	165 (97%)	5 (3%)	37	70
13	IM	144/147 (98%)	138 (96%)	6 (4%)	26	61
14	IN	220/243 (90%)	217 (99%)	3 (1%)	59	80
15	IO	167/168 (99%)	163 (98%)	4 (2%)	43	73
16	IP	113/118 (96%)	112 (99%)	1 (1%)	70	85
17	IQ	171/172 (99%)	165 (96%)	6 (4%)	32	65
18	IR	129/147 (88%)	126 (98%)	3 (2%)	44	74
19	IS	141/143 (99%)	137 (97%)	4 (3%)	38	70
20	IT	156/156 (100%)	155 (99%)	1 (1%)	78	88
21	IU	132/174 (76%)	132 (100%)	0	100	100
22	IV	144/145 (99%)	140 (97%)	4 (3%)	38	70
23	IW	86/125 (69%)	84 (98%)	2 (2%)	44	74
24	IX	109/113 (96%)	104 (95%)	5 (5%)	24	58
25	IY	99/102 (97%)	94 (95%)	5 (5%)	21	55
26	IZ	52/137 (38%)	50 (96%)	2 (4%)	29	63
27	la	177/179 (99%)	173 (98%)	4 (2%)	44	74
28	lb	121/123 (98%)	119 (98%)	2 (2%)	53	78
29	lc	120/121 (99%)	115 (96%)	5 (4%)	26	61
30	ld	50/54 (93%)	48 (96%)	2 (4%)	28	62
31	le	81/92 (88%)	78 (96%)	3 (4%)	30	64
32	lf	109/128 (85%)	105 (96%)	4 (4%)	30	64
33	lg	112/116 (97%)	109 (97%)	3 (3%)	39	71
34	lh	86/116 (74%)	84 (98%)	2 (2%)	44	74
35	li	103/103 (100%)	102 (99%)	1 (1%)	68	84
36	lj	89/91 (98%)	88 (99%)	1 (1%)	65	83
37	lk	71/82 (87%)	69 (97%)	2 (3%)	38	70
38	ll	60/64 (94%)	60 (100%)	0	100	100
39	lm	72/75 (96%)	70 (97%)	2 (3%)	38	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	ln	63/66 (96%)	57 (90%)	6 (10%)	8	31
41	lo	44/45 (98%)	43 (98%)	1 (2%)	44	74
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	63	82
All	All	5299/5764 (92%)	5151 (97%)	148 (3%)	38	70

All (148) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	lD	67	ARG
4	lD	78	CYS
4	lD	161	ASN
4	lD	193	ARG
4	lD	243	THR
5	lE	29	VAL
5	lE	44	THR
5	lE	231	VAL
5	lE	258	HIS
5	lE	274	PHE
5	lE	296	LYS
5	lE	350	THR
6	lF	35	ASP
6	lF	56	THR
6	lF	95	MET
6	lF	101	MET
6	lF	115	THR
6	lF	180	ASP
6	lF	182	LEU
6	lF	215	ASP
6	lF	285	GLN
6	lF	370	ASN
6	lF	373	VAL
7	lG	9	ASN
7	lG	36	MET
7	lG	37	ILE
7	lG	85	ARG
7	lG	94	ASN
7	lG	105	LEU
7	lG	115	MET
7	lG	118	GLN
7	lG	122	VAL

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Mol	Chain	Res	Type
7	IG	213	ASP
8	IH	10	VAL
8	IH	117	VAL
8	IH	161	LEU
8	IH	171	GLU
9	II	110	SER
9	II	119	ASP
9	II	130	GLU
9	II	171	ASP
9	II	207	ILE
10	IJ	25	PHE
10	IJ	29	ASN
10	IJ	52	LYS
10	IJ	72	THR
10	IJ	76	THR
10	IJ	93	ARG
10	IJ	128	THR
10	IJ	195	VAL
10	IJ	217	SER
11	IK	18	ASN
11	IK	53	VAL
11	IK	60	GLU
11	IK	75	SER
11	IK	80	THR
11	IK	138	ASP
11	IK	142	VAL
12	IL	39	ARG
12	IL	44	ASP
12	IL	112	GLN
12	IL	115	MET
12	IL	202	THR
13	IM	19	LEU
13	IM	46	VAL
13	IM	110	ILE
13	IM	111	ASP
13	IM	170	ILE
13	IM	173	ASN
14	IN	100	LYS
14	IN	155	PHE
14	IN	254	MET
15	IO	7	VAL
15	IO	82	ARG

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Mol	Chain	Res	Type
15	lO	185	LYS
15	lO	190	GLU
16	lP	103	LEU
17	lQ	77	LYS
17	lQ	86	CYS
17	lQ	117	ASN
17	lQ	126	THR
17	lQ	135	VAL
17	lQ	139	ASN
18	lR	18	ARG
18	lR	128	ARG
18	lR	139	PHE
19	lS	10	VAL
19	lS	46	THR
19	lS	56	VAL
19	lS	161	GLN
20	lT	1	MET
22	lV	28	SER
22	lV	92	SER
22	lV	129	LEU
22	lV	151	ASP
23	lW	101	ASN
23	lW	117	GLU
24	lX	17	THR
24	lX	30	ASP
24	lX	64	THR
24	lX	101	ASN
24	lX	134	SER
25	lY	9	THR
25	lY	32	ASN
25	lY	57	ASP
25	lY	72	THR
25	lY	120	LEU
26	lZ	17	VAL
26	lZ	60	LEU
27	la	93	VAL
27	la	109	LEU
27	la	130	LEU
27	la	162	THR
28	lb	66	THR
28	lb	121	PHE
29	lc	8	THR

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Mol	Chain	Res	Type
29	lc	29	ARG
29	lc	58	MET
29	lc	141	VAL
29	lc	148	THR
30	ld	39	VAL
30	ld	56	GLU
31	le	12	GLU
31	le	22	THR
31	le	65	VAL
32	lf	46	ILE
32	lf	51	THR
32	lf	113	MET
32	lf	142	THR
33	lg	15	THR
33	lg	53	LEU
33	lg	88	MET
34	lh	56	HIS
34	lh	80	LYS
35	li	76	THR
36	lj	36	THR
37	lk	9	LEU
37	lk	20	THR
39	lm	16	THR
39	lm	75	SER
40	ln	15	PHE
40	ln	19	LEU
40	ln	24	SER
40	ln	38	ASN
40	ln	43	VAL
40	ln	78	LYS
41	lo	29	MET
43	lq	18	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
4	lD	21	HIS
4	lD	38	HIS
4	lD	68	GLN
4	lD	140	ASN
4	lD	233	GLN
5	lE	129	GLN

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Mol	Chain	Res	Type
5	lE	184	GLN
6	lF	50	GLN
6	lF	107	ASN
6	lF	118	GLN
6	lF	167	GLN
6	lF	269	GLN
6	lF	283	HIS
7	lG	234	ASN
8	lH	30	GLN
8	lH	115	GLN
9	lI	81	ASN
10	lJ	144	GLN
11	lK	106	HIS
12	lL	59	ASN
14	lN	21	HIS
14	lN	160	ASN
16	lP	65	ASN
18	lR	21	ASN
18	lR	97	ASN
18	lR	145	HIS
19	lS	57	ASN
20	lT	101	GLN
20	lT	136	HIS
22	lV	22	HIS
25	lY	18	ASN
27	la	194	HIS
31	le	11	GLN
34	lh	40	ASN
34	lh	82	HIS
34	lh	98	HIS
35	li	83	GLN
37	lk	74	HIS
38	ll	46	GLN
41	lo	33	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3126/3503 (89%)	590 (18%)	0
2	lB	143/155 (92%)	31 (21%)	0
3	lC	116/117 (99%)	19 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	sI	4/76 (5%)	2 (50%)	0
46	sJ	14/77 (18%)	7 (50%)	0
All	All	3403/3928 (86%)	649 (19%)	0

All (649) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A
1	lA	39	A
1	lA	45	A
1	lA	54	G
1	lA	55	G
1	lA	56	A
1	lA	62	A
1	lA	65	U
1	lA	70	A
1	lA	73	A
1	lA	88	G
1	lA	105	A
1	lA	106	G
1	lA	107	A
1	lA	108	C
1	lA	115	G
1	lA	116	A
1	lA	117	U
1	lA	185	G
1	lA	186	A
1	lA	189	G
1	lA	199	G
1	lA	200	A
1	lA	206	U
1	lA	213	A
1	lA	214	A
1	lA	221	U
1	lA	233	A
1	lA	237	C
1	lA	246	U
1	lA	256	G

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Mol	Chain	Res	Type
1	lA	264	G
1	lA	266	A
1	lA	267	A
1	lA	283	A
1	lA	285	A
1	lA	286	U
1	lA	288	U
1	lA	289	C
1	lA	293	A
1	lA	294	A
1	lA	302	U
1	lA	311	A
1	lA	316	G
1	lA	332	G
1	lA	333	U
1	lA	342	A
1	lA	344	A
1	lA	345	A
1	lA	346	G
1	lA	350	A
1	lA	351	U
1	lA	369	A
1	lA	382	A
1	lA	385	C
1	lA	396	G
1	lA	416	U
1	lA	422	G
1	lA	423	A
1	lA	424	A
1	lA	425	C
1	lA	444	A
1	lA	446	A
1	lA	447	G
1	lA	448	C
1	lA	452	A
1	lA	467	A
1	lA	474	A
1	lA	483	G
1	lA	491	G
1	lA	492	U
1	lA	494	G
1	lA	495	A

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Mol	Chain	Res	Type
1	lA	496	A
1	lA	501	U
1	lA	510	A
1	lA	522	G
1	lA	535	A
1	lA	536	G
1	lA	538	A
1	lA	539	G
1	lA	550	A
1	lA	561	G
1	lA	562	A
1	lA	564	A
1	lA	565	U
1	lA	575	A
1	lA	577	G
1	lA	581	U
1	lA	583	A
1	lA	586	A
1	lA	588	G
1	lA	589	A
1	lA	600	U
1	lA	610	A
1	lA	612	A
1	lA	613	G
1	lA	614	U
1	lA	615	G
1	lA	619	A
1	lA	620	U
1	lA	621	U
1	lA	625	A
1	lA	626	A
1	lA	627	A
1	lA	630	A
1	lA	631	G
1	lA	632	G
1	lA	636	U
1	lA	637	U
1	lA	638	A
1	lA	644	A
1	lA	645	A
1	lA	646	U
1	lA	647	C

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Mol	Chain	Res	Type
1	lA	649	U
1	lA	651	G
1	lA	663	G
1	lA	675	A
1	lA	684	U
1	lA	685	A
1	lA	687	U
1	lA	696	G
1	lA	699	A
1	lA	701	A
1	lA	703	G
1	lA	704	C
1	lA	710	A
1	lA	714	U
1	lA	715	A
1	lA	716	A
1	lA	720	U
1	lA	721	A
1	lA	722	A
1	lA	724	A
1	lA	725	A
1	lA	727	U
1	lA	728	U
1	lA	733	C
1	lA	734	C
1	lA	736	G
1	lA	740	A
1	lA	744	A
1	lA	746	A
1	lA	747	C
1	lA	755	G
1	lA	770	C
1	lA	771	C
1	lA	783	A
1	lA	794	A
1	lA	811	A
1	lA	816	G
1	lA	817	A
1	lA	818	A
1	lA	825	G
1	lA	833	U
1	lA	834	A

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Mol	Chain	Res	Type
1	lA	841	A
1	lA	851	A
1	lA	853	A
1	lA	855	A
1	lA	864	G
1	lA	872	A
1	lA	873	U
1	lA	874	A
1	lA	875	C
1	lA	881	G
1	lA	888	U
1	lA	889	A
1	lA	898	U
1	lA	903	G
1	lA	904	A
1	lA	905	A
1	lA	911	U
1	lA	918	G
1	lA	925	A
1	lA	934	G
1	lA	935	A
1	lA	936	A
1	lA	968	C
1	lA	980	A
1	lA	993	U
1	lA	998	U
1	lA	1025	A
1	lA	1026	G
1	lA	1027	G
1	lA	1028	G
1	lA	1033	A
1	lA	1035	G
1	lA	1036	A
1	lA	1042	C
1	lA	1043	G
1	lA	1056	G
1	lA	1063	C
1	lA	1078	C
1	lA	1079	U
1	lA	1092	A
1	lA	1096	U
1	lA	1097	U

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Mol	Chain	Res	Type
1	lA	1098	A
1	lA	1099	A
1	lA	1100	U
1	lA	1112	G
1	lA	1119	U
1	lA	1120	A
1	lA	1154	A
1	lA	1156	C
1	lA	1166	A
1	lA	1168	C
1	lA	1183	G
1	lA	1184	A
1	lA	1210	C
1	lA	1211	A
1	lA	1219	A
1	lA	1220	A
1	lA	1221	A
1	lA	1222	U
1	lA	1242	G
1	lA	1256	G
1	lA	1269	U
1	lA	1275	A
1	lA	1278	A
1	lA	1279	A
1	lA	1284	A
1	lA	1291	G
1	lA	1292	A
1	lA	1293	U
1	lA	1306	A
1	lA	1312	A
1	lA	1314	A
1	lA	1315	A
1	lA	1316	C
1	lA	1343	A
1	lA	1345	U
1	lA	1347	A
1	lA	1409	G
1	lA	1410	A
1	lA	1411	A
1	lA	1417	G
1	lA	1431	G
1	lA	1433	U

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Mol	Chain	Res	Type
1	lA	1437	A
1	lA	1440	A
1	lA	1441	U
1	lA	1447	C
1	lA	1450	A
1	lA	1455	A
1	lA	1474	A
1	lA	1475	A
1	lA	1476	G
1	lA	1477	A
1	lA	1478	C
1	lA	1480	U
1	lA	1495	A
1	lA	1499	G
1	lA	1502	A
1	lA	1503	U
1	lA	1505	G
1	lA	1516	A
1	lA	1517	C
1	lA	1518	A
1	lA	1521	A
1	lA	1527	A
1	lA	1534	U
1	lA	1553	A
1	lA	1568	G
1	lA	1570	U
1	lA	1571	C
1	lA	1580	A
1	lA	1584	G
1	lA	1602	A
1	lA	1603	A
1	lA	1606	A
1	lA	1607	A
1	lA	1622	A
1	lA	1624	G
1	lA	1644	A
1	lA	1649	U
1	lA	1664	G
1	lA	1674	U
1	lA	1690	A
1	lA	1698	G
1	lA	1729	G

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Mol	Chain	Res	Type
1	lA	1735	A
1	lA	1737	A
1	lA	1738	G
1	lA	1752	U
1	lA	1753	A
1	lA	1754	G
1	lA	1818	C
1	lA	1821	A
1	lA	1822	U
1	lA	1823	C
1	lA	1864	C
1	lA	1865	U
1	lA	1883	A
1	lA	1897	A
1	lA	1898	A
1	lA	1907	A
1	lA	1913	G
1	lA	1925	A
1	lA	1926	U
1	lA	1927	U
1	lA	1928	G
1	lA	1936	A
1	lA	1937	A
1	lA	1938	G
1	lA	1958	A
1	lA	1959	U
1	lA	1961	G
1	lA	1965	U
1	lA	1972	G
1	lA	1975	G
1	lA	1984	A
1	lA	1995	G
1	lA	2040	A
1	lA	2043	A
1	lA	2044	C
1	lA	2050	C
1	lA	2051	A
1	lA	2067	A
1	lA	2079	A
1	lA	2080	A
1	lA	2081	A
1	lA	2082	U

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Mol	Chain	Res	Type
1	lA	2083	A
1	lA	2095	G
1	lA	2108	G
1	lA	2109	C
1	lA	2132	A
1	lA	2178	A
1	lA	2179	U
1	lA	2190	A
1	lA	2193	G
1	lA	2197	G
1	lA	2198	G
1	lA	2207	A
1	lA	2210	G
1	lA	2216	U
1	lA	2218	A
1	lA	2233	G
1	lA	2234	A
1	lA	2245	A
1	lA	2246	G
1	lA	2252	U
1	lA	2263	G
1	lA	2274	A
1	lA	2281	U
1	lA	2285	U
1	lA	2286	G
1	lA	2299	A
1	lA	2308	A
1	lA	2331	A
1	lA	2332	A
1	lA	2333	C
1	lA	2334	U
1	lA	2335	A
1	lA	2339	C
1	lA	2340	U
1	lA	2342	U
1	lA	2343	C
1	lA	2344	U
1	lA	2345	U
1	lA	2346	A
1	lA	2348	G
1	lA	2349	G
1	lA	2352	G

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Mol	Chain	Res	Type
1	lA	2355	A
1	lA	2356	A
1	lA	2357	A
1	lA	2360	C
1	lA	2374	U
1	lA	2383	G
1	lA	2384	C
1	lA	2386	U
1	lA	2389	A
1	lA	2390	U
1	lA	2391	G
1	lA	2395	C
1	lA	2396	A
1	lA	2410	U
1	lA	2411	G
1	lA	2412	U
1	lA	2439	A
1	lA	2441	U
1	lA	2449	A
1	lA	2450	C
1	lA	2451	G
1	lA	2461	G
1	lA	2462	G
1	lA	2469	G
1	lA	2473	A
1	lA	2478	A
1	lA	2479	G
1	lA	2480	A
1	lA	2487	U
1	lA	2494	G
1	lA	2509	U
1	lA	2512	G
1	lA	2515	A
1	lA	2583	U
1	lA	2584	U
1	lA	2586	A
1	lA	2589	C
1	lA	2590	A
1	lA	2594	C
1	lA	2595	G
1	lA	2597	U
1	lA	2598	A

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Mol	Chain	Res	Type
1	lA	2629	A
1	lA	2635	U
1	lA	2637	A
1	lA	2638	A
1	lA	2646	G
1	lA	2647	U
1	lA	2651	A
1	lA	2655	G
1	lA	2656	G
1	lA	2663	A
1	lA	2676	G
1	lA	2677	G
1	lA	2684	G
1	lA	2689	G
1	lA	2696	A
1	lA	2715	G
1	lA	2722	U
1	lA	2726	A
1	lA	2727	A
1	lA	2744	A
1	lA	2747	G
1	lA	2748	A
1	lA	2759	A
1	lA	2761	A
1	lA	2764	A
1	lA	2766	A
1	lA	2774	A
1	lA	2775	A
1	lA	2784	G
1	lA	2791	G
1	lA	2797	A
1	lA	2798	G
1	lA	2799	U
1	lA	2805	C
1	lA	2822	U
1	lA	2823	G
1	lA	2825	C
1	lA	2832	A
1	lA	2842	U
1	lA	2843	U
1	lA	2858	A
1	lA	2859	U

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Mol	Chain	Res	Type
1	lA	2860	U
1	lA	2861	U
1	lA	2862	A
1	lA	2864	A
1	lA	2865	A
1	lA	2866	C
1	lA	2867	A
1	lA	2878	A
1	lA	2880	C
1	lA	2889	G
1	lA	2890	A
1	lA	2900	G
1	lA	2901	U
1	lA	2902	G
1	lA	2903	A
1	lA	2904	U
1	lA	2909	A
1	lA	2910	G
1	lA	2911	U
1	lA	2912	U
1	lA	2915	U
1	lA	2916	C
1	lA	2920	U
1	lA	2921	A
1	lA	2925	A
1	lA	2926	U
1	lA	2931	C
1	lA	2939	G
1	lA	2943	G
1	lA	2944	A
1	lA	2945	A
1	lA	2946	A
1	lA	2951	A
1	lA	2953	C
1	lA	2959	G
1	lA	2960	A
1	lA	2977	G
1	lA	2985	C
1	lA	2988	A
1	lA	3009	C
1	lA	3015	A
1	lA	3030	A

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Mol	Chain	Res	Type
1	lA	3032	C
1	lA	3041	G
1	lA	3047	U
1	lA	3066	U
1	lA	3068	C
1	lA	3070	C
1	lA	3073	U
1	lA	3078	U
1	lA	3079	A
1	lA	3085	C
1	lA	3090	G
1	lA	3114	A
1	lA	3126	C
1	lA	3133	G
1	lA	3141	A
1	lA	3142	G
1	lA	3143	A
1	lA	3144	U
1	lA	3146	U
1	lA	3147	U
1	lA	3148	C
1	lA	3151	A
1	lA	3159	G
1	lA	3166	G
1	lA	3200	G
1	lA	3210	U
1	lA	3212	U
1	lA	3213	U
1	lA	3223	G
1	lA	3232	G
1	lA	3240	A
1	lA	3246	A
1	lA	3247	C
1	lA	3254	U
1	lA	3277	C
1	lA	3278	A
1	lA	3284	G
1	lA	3285	A
1	lA	3286	A
1	lA	3287	U
1	lA	3299	G
1	lA	3327	A

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Mol	Chain	Res	Type
1	lA	3332	A
1	lA	3334	U
1	lA	3335	U
1	lA	3336	G
1	lA	3337	A
1	lA	3338	A
1	lA	3344	U
1	lA	3345	A
1	lA	3351	U
1	lA	3353	U
1	lA	3354	A
1	lA	3357	U
1	lA	3359	U
1	lA	3360	U
1	lA	3361	A
1	lA	3366	G
1	lA	3383	A
1	lA	3384	A
1	lA	3385	G
1	lA	3398	U
1	lA	3399	G
1	lA	3405	A
1	lA	3406	C
1	lA	3410	A
1	lA	3411	U
1	lA	3413	U
1	lA	3414	A
1	lA	3416	A
1	lA	3423	C
1	lA	3431	U
1	lA	3433	U
1	lA	3447	A
1	lA	3451	A
1	lA	3466	U
1	lA	3467	U
1	lA	3468	U
1	lA	3469	A
1	lA	3470	G
1	lA	3472	G
1	lA	3475	U
1	lA	3476	C
1	lA	3477	U

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Mol	Chain	Res	Type
1	lA	3478	U
1	lA	3479	A
1	lA	3481	U
1	lA	3485	U
1	lA	3491	C
1	lA	3492	G
1	lA	3498	U
1	lA	3499	G
1	lA	3500	A
2	lB	34	G
2	lB	36	G
2	lB	51	A
2	lB	53	G
2	lB	54	A
2	lB	61	A
2	lB	64	A
2	lB	65	G
2	lB	72	G
2	lB	73	A
2	lB	74	A
2	lB	79	A
2	lB	80	A
2	lB	81	A
2	lB	82	A
2	lB	85	U
2	lB	86	G
2	lB	92	C
2	lB	95	A
2	lB	102	A
2	lB	103	A
2	lB	104	U
2	lB	106	C
2	lB	109	G
2	lB	110	A
2	lB	113	G
2	lB	131	A
2	lB	137	A
2	lB	147	C
2	lB	150	U
2	lB	151	A
3	lC	17	G
3	lC	18	U

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Mol	Chain	Res	Type
3	lC	19	U
3	lC	22	C
3	lC	32	A
3	lC	37	A
3	lC	40	G
3	lC	41	G
3	lC	47	A
3	lC	49	C
3	lC	52	G
3	lC	53	C
3	lC	62	U
3	lC	63	C
3	lC	72	C
3	lC	73	G
3	lC	90	G
3	lC	99	U
3	lC	109	G
45	sI	73	A
45	sI	76	A
46	sJ	2	U
46	sJ	5	U
46	sJ	6	C
46	sJ	69	A
46	sJ	70	A
46	sJ	75	C
46	sJ	77	A

There are no RNA pucker outliers to report.

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.

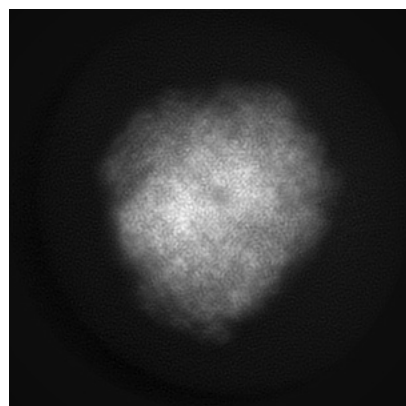
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64717. These allow visual inspection of the internal detail of the map and identification of artifacts.

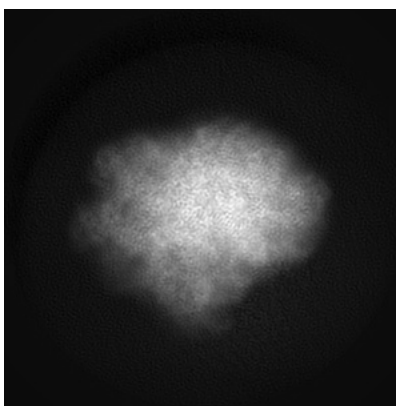
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

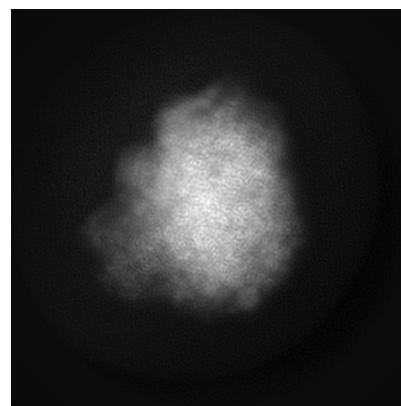
6.1.1 Primary map



X

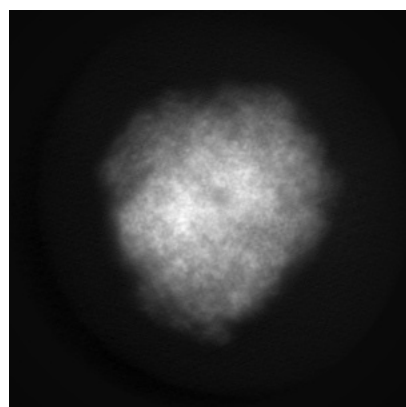


Y

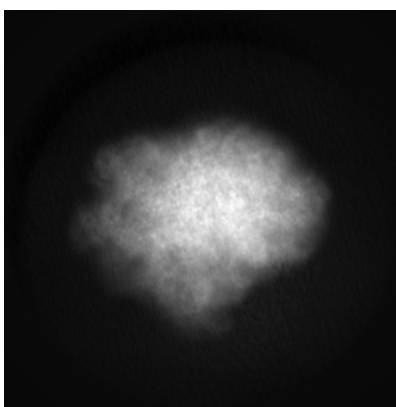


Z

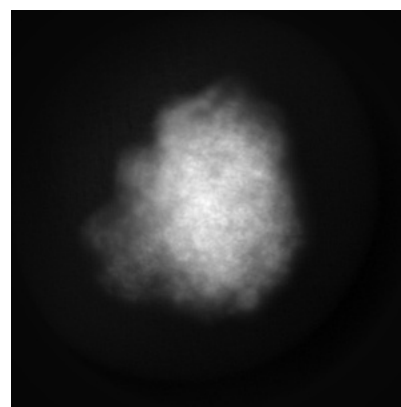
6.1.2 Raw map



X



Y

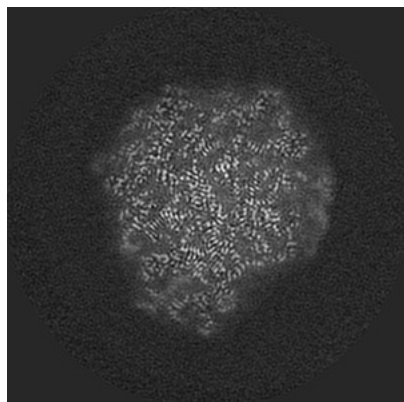


Z

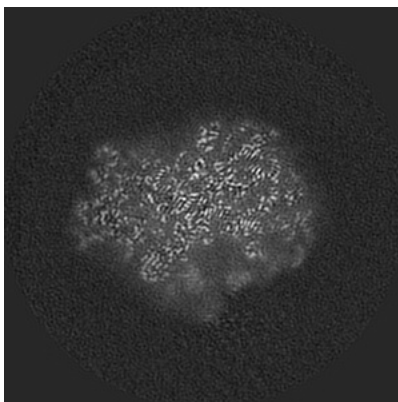
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

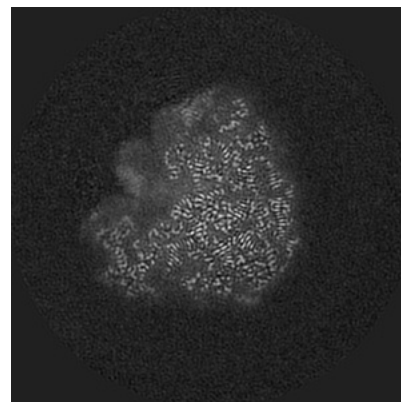
6.2.1 Primary map



X Index: 175

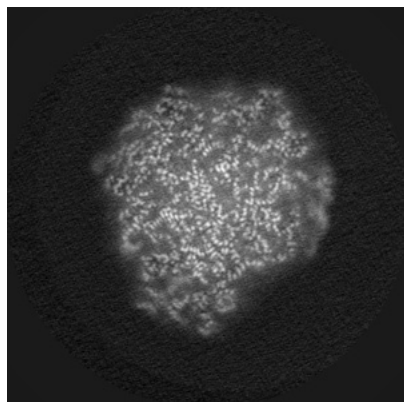


Y Index: 175

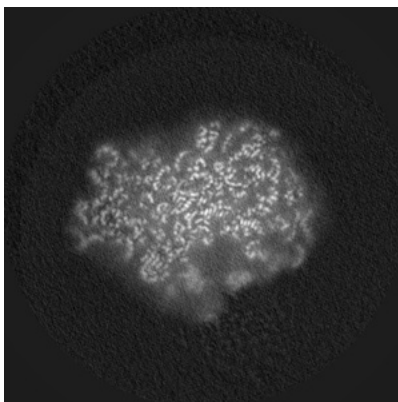


Z Index: 175

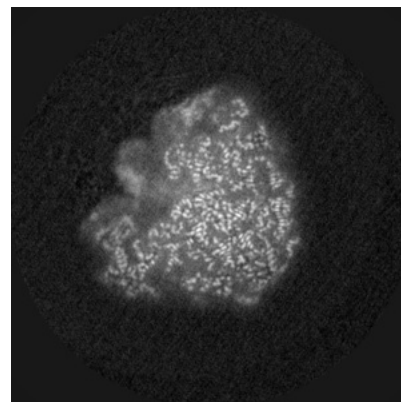
6.2.2 Raw map



X Index: 175



Y Index: 175

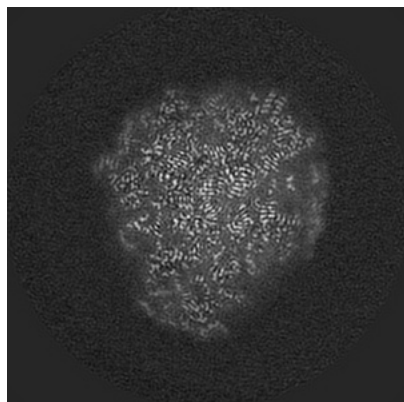


Z Index: 175

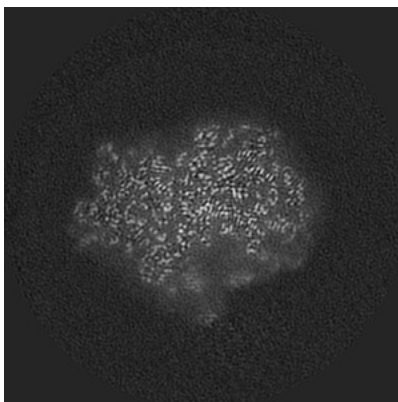
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

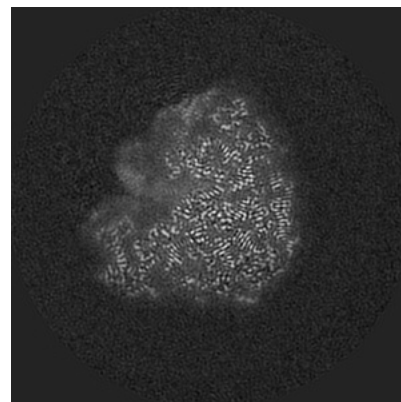
6.3.1 Primary map



X Index: 169

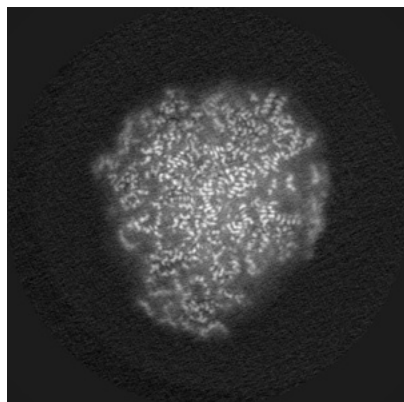


Y Index: 173

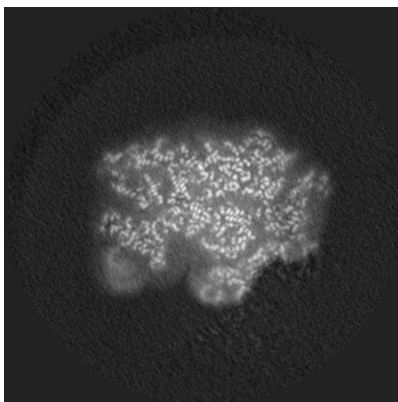


Z Index: 174

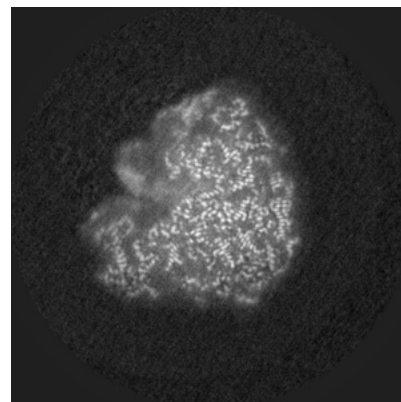
6.3.2 Raw map



X Index: 169



Y Index: 206

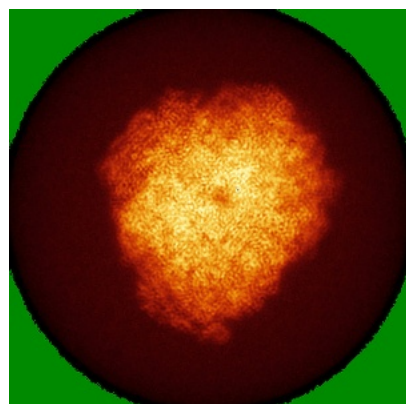


Z Index: 174

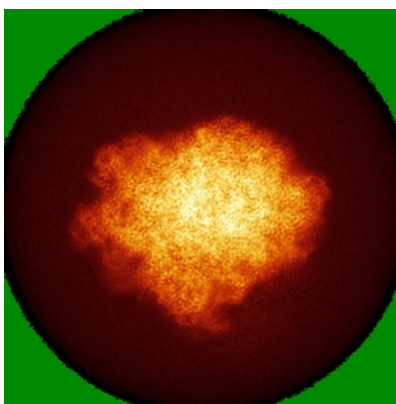
The images above show the largest variance slices of the map in three orthogonal directions.

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

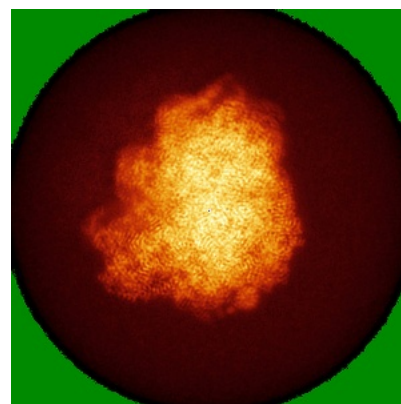
6.4.1 Primary map



X

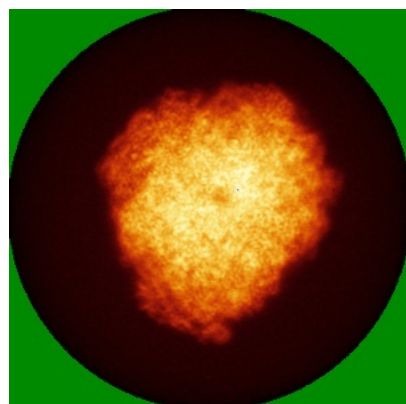


Y

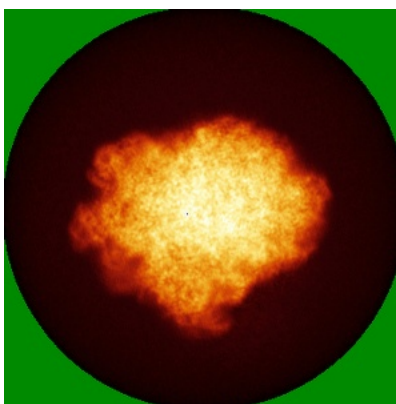


Z

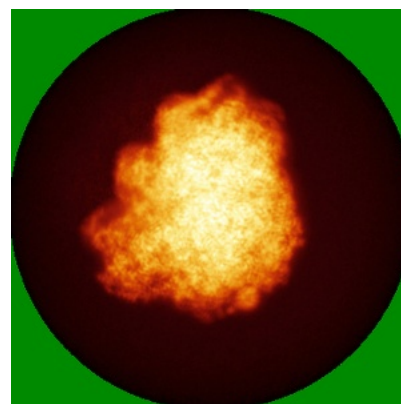
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

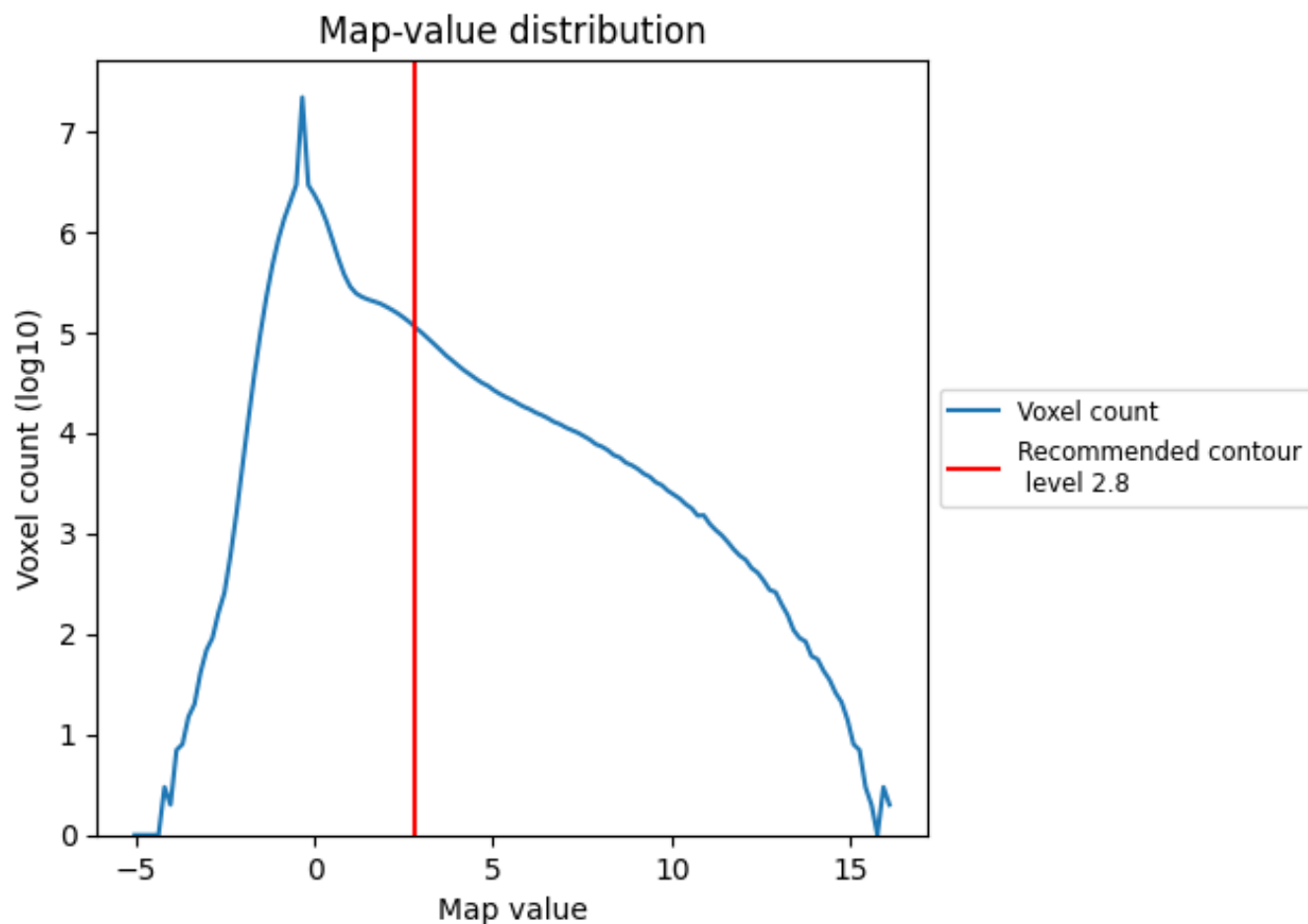
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

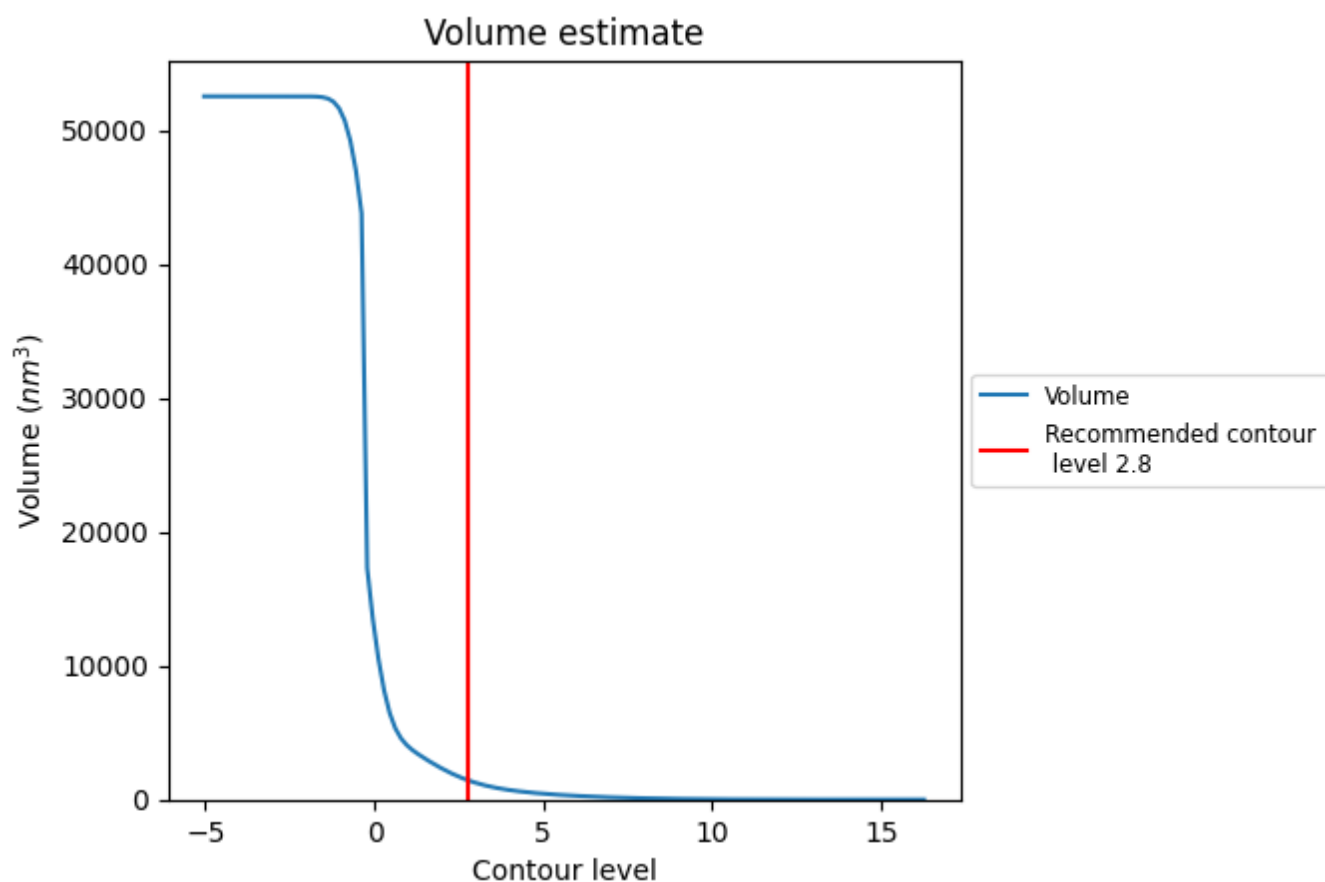
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

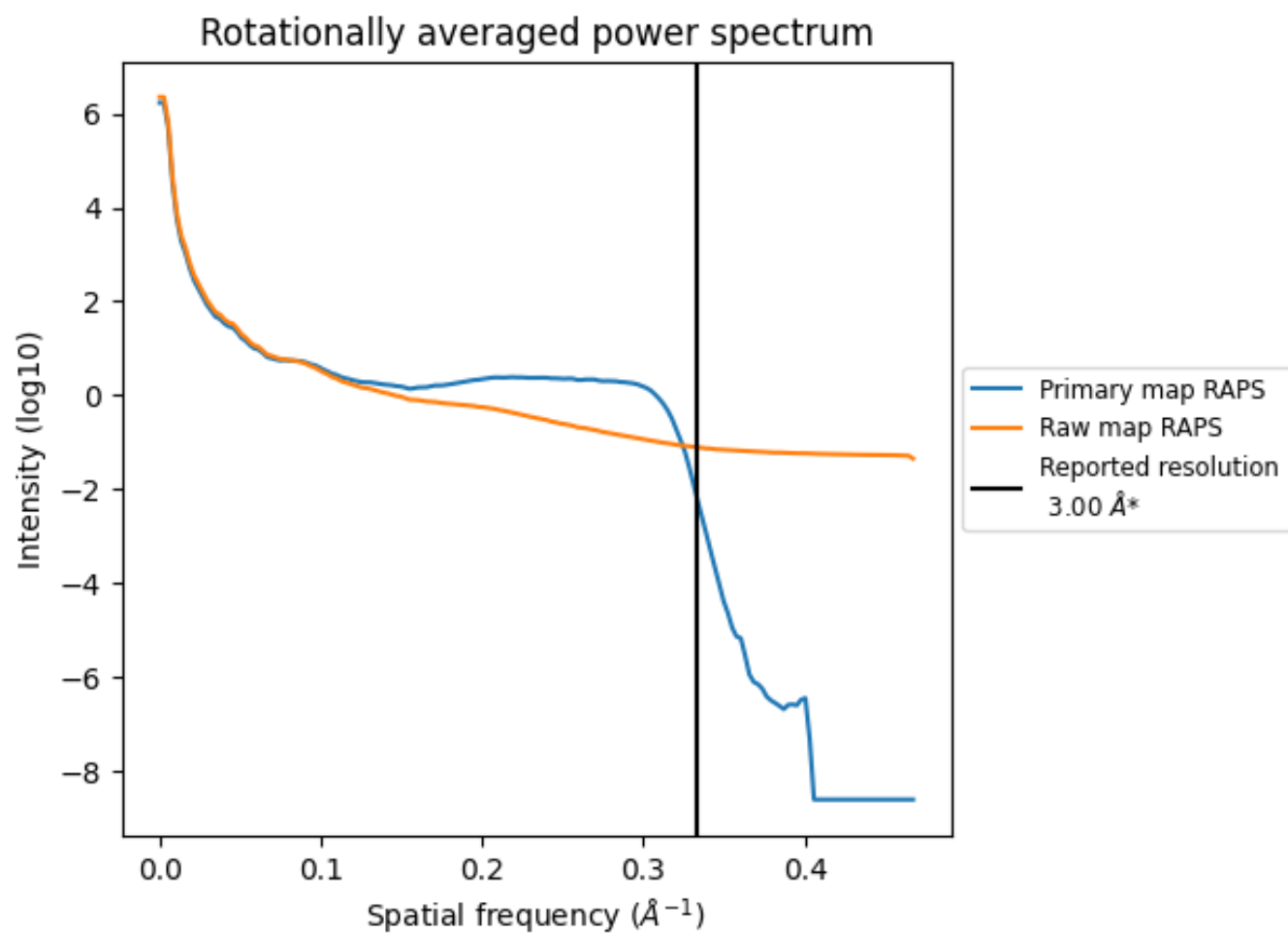
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1417 nm³; this corresponds to an approximate mass of 1280 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

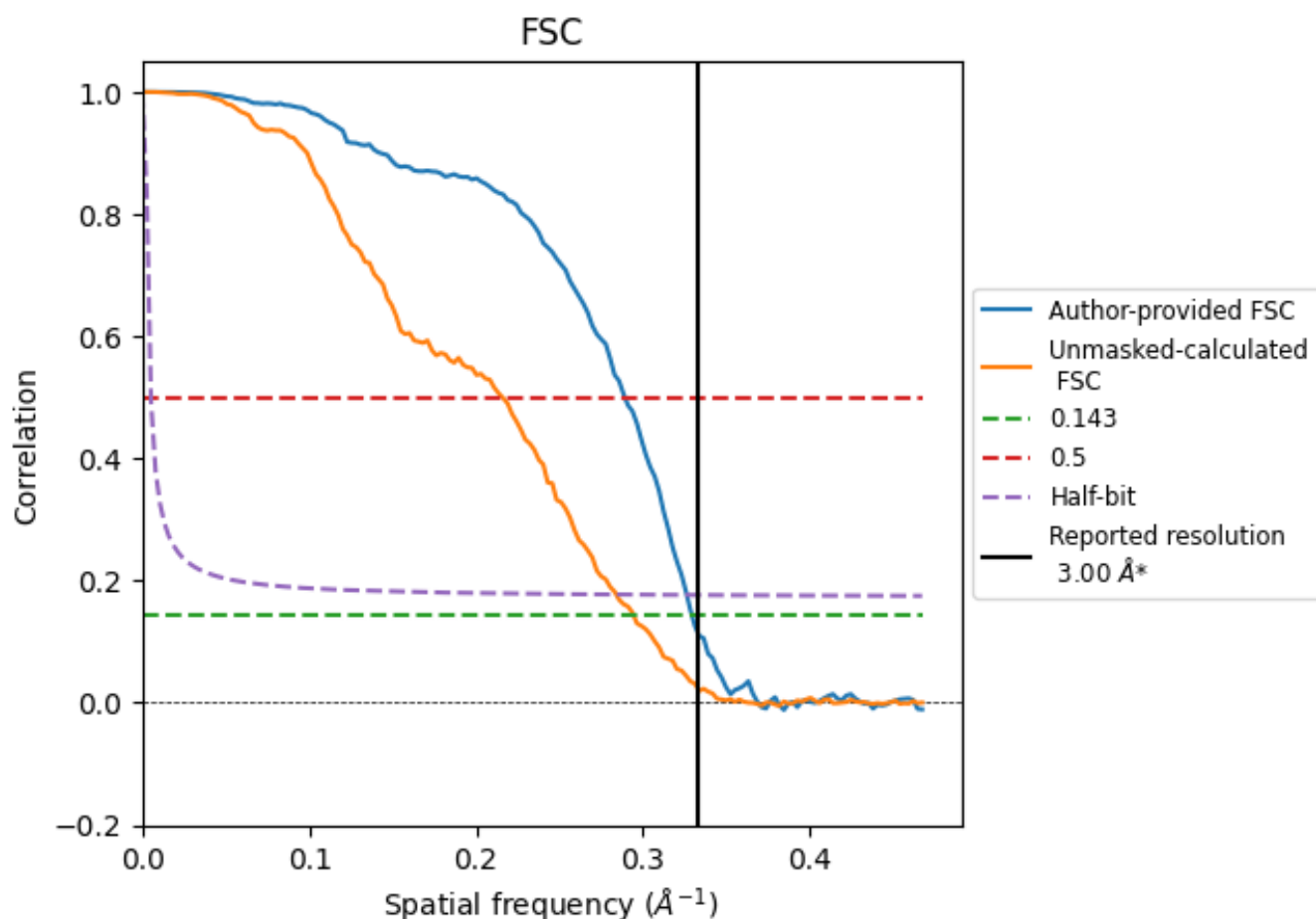


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

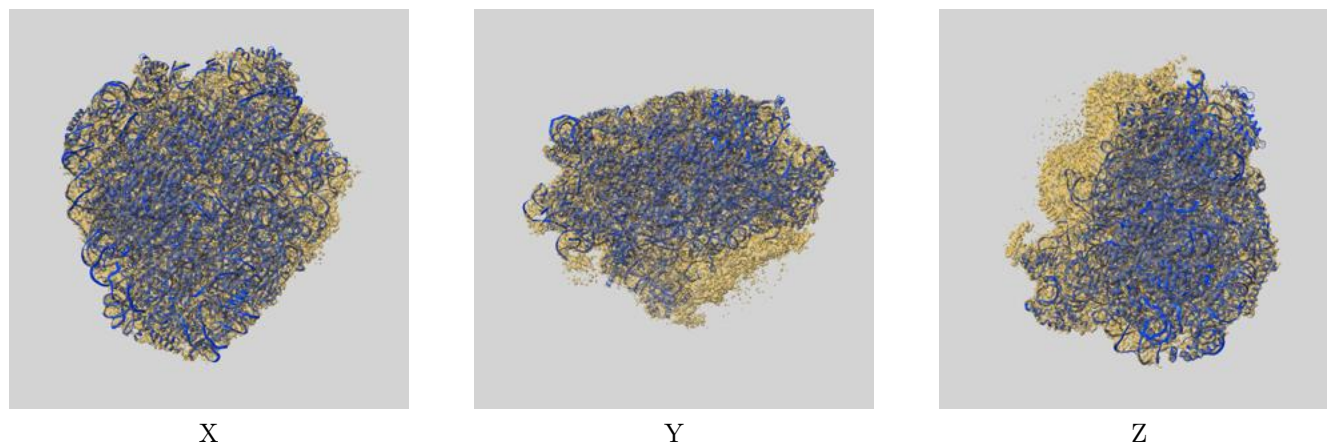
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.46	3.06
Unmasked-calculated*	3.40	4.63	3.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.40 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

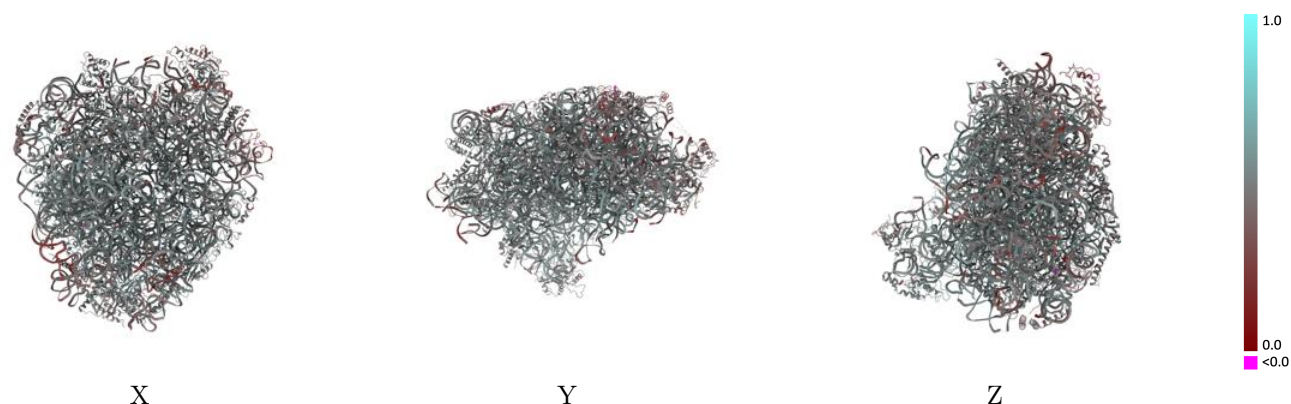
This section contains information regarding the fit between EMDB map EMD-64717 and PDB model 9V25. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



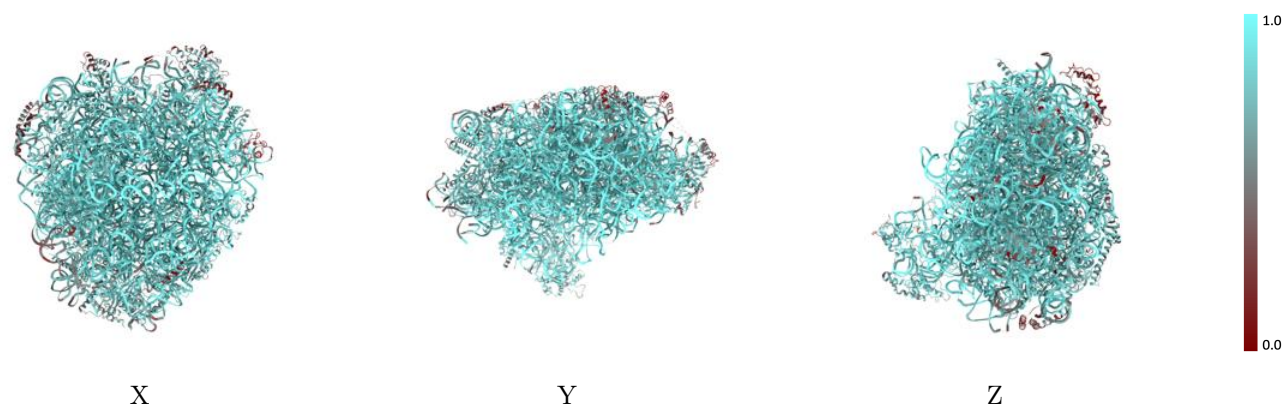
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



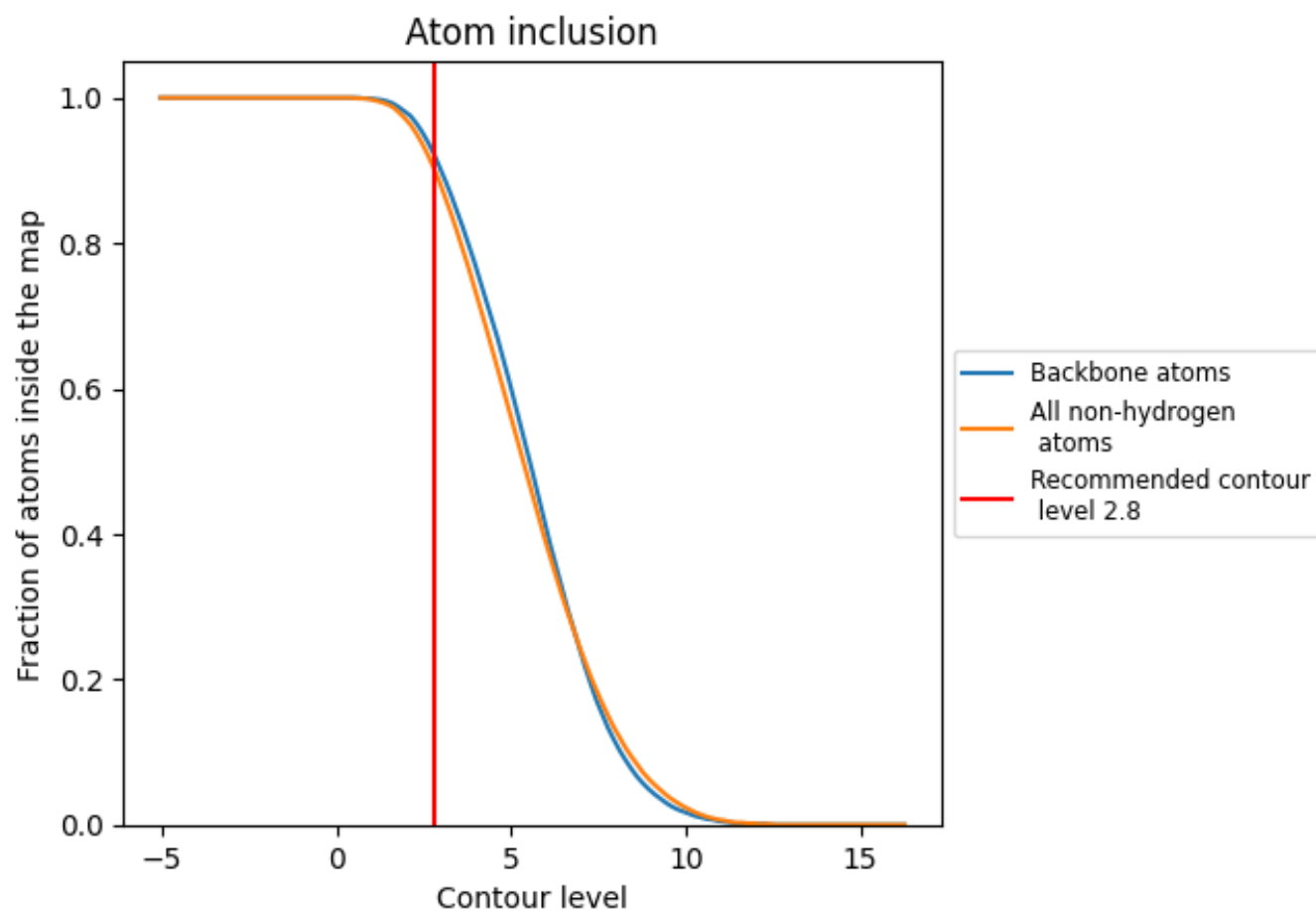
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9020	 0.4960
1A	 0.9380	 0.4960
1B	 0.9500	 0.5010
1C	 0.9670	 0.5030
1D	 0.9610	 0.5030
1E	 0.8990	 0.5040
1F	 0.8630	 0.5150
1G	 0.8100	 0.5180
1H	 0.6650	 0.4770
1I	 0.9070	 0.5290
1J	 0.6940	 0.4650
1K	 0.8040	 0.5000
1L	 0.9390	 0.5120
1M	 0.8160	 0.4700
1N	 0.7190	 0.4840
1O	 0.8940	 0.5160
1P	 0.8430	 0.5210
1Q	 0.9620	 0.5180
1R	 0.8920	 0.4980
1S	 0.9490	 0.5300
1T	 0.9290	 0.5380
1U	 0.8720	 0.4700
1V	 0.9180	 0.5340
1W	 0.3320	 0.3140
1X	 0.9600	 0.5010
1Y	 0.7960	 0.4720
1Z	 0.9400	 0.4920
1a	 0.7960	 0.4880
1b	 0.6100	 0.4200
1c	 0.9370	 0.5360
1d	 0.9550	 0.5380
1e	 0.7700	 0.4550
1f	 0.7570	 0.4370
1g	 0.8950	 0.5100
1h	 0.8840	 0.4760



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Chain	Atom inclusion	Q-score
li	 0.7910	 0.4740
lj	 0.9250	 0.5290
lk	 0.8550	 0.4950
ll	 0.9840	 0.5120
lm	 0.9410	 0.4850
ln	 0.4710	 0.4010
lo	 0.9760	 0.5080
lp	 0.8760	 0.4980
lq	 0.9530	 0.5270
sH	 1.0000	 0.4900
sI	 0.9900	 0.3750
sJ	 0.9850	 0.4850