



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 05:05 AM UTC

PDB ID : 7BTB / pdb_00007btb
EMDB ID : EMD-30174
Title : Cryo-EM structure of pre-60S ribosome from *Saccharomyces cerevisiae* rpl4delta63-87 strain at 3.22 Angstroms resolution(state R2)
Authors : Li, Y.; Wilson, D.M.
Deposited on : 2020-04-01
Resolution : 3.22 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

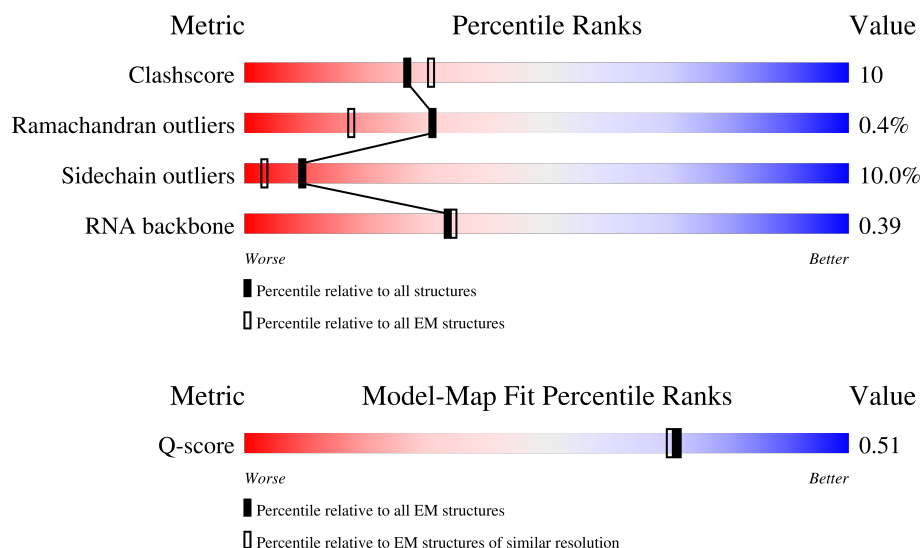
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.22 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	14612 (2.72 - 3.72)

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	L	199	
2	a	149	
3	A	254	

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Mol	Chain	Length	Quality of chain
4	B	387	
5	C	362	
6	D	297	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	J	174	
12	K	376	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	236	
24	X	142	
25	Y	127	
26	Z	136	
27	b	647	
28	c	105	

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Mol	Chain	Length	Quality of chain
29	d	113	
30	e	130	
31	f	107	
32	g	121	
33	h	120	
34	i	100	
35	j	88	
36	k	78	
37	m	486	
38	n	605	
39	o	220	
40	p	92	
41	q	455	
42	r	261	
43	t	322	
44	u	199	
45	v	344	
46	w	203	
47	x	515	
48	y	245	
49	z	106	
50	1	3396	
51	2	158	
52	3	121	
53	6	232	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147931 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	L	185	Total	C	N	O	0	0
			1484	923	305	256		

- Molecule 2 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	193	Total	C	N	O	0	0
			1492	938	294	260		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	336	Total	C	N	O	S	0	0
			2576	1628	483	462	3		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	274	Total	C	N	O	S	0	0
			2197	1388	388	419	2		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	227	Total	C	N	O	S	0	0
			1775	1136	318	318	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 11 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	167	Total	C	N	O	S	0	0
			1336	838	249	245	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	253	Total	C	N	O	S	0	0
			2044	1318	339	384	3		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	183	Total	C	N	O	S	0	0
			1442	896	287	259			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	119	Total	C	N	O	S	0	0
			943	595	180	165	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	104	Total	C	N	O	0	0
			826	534	134	158		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	234	Total	C	N	O	S	0	0
			1885	1194	323	362	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

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

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

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

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

- Molecule 27 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	509	Total	C	N	O	S	0	0
			4137	2624	723	771	19		

- Molecule 28 is a protein called 60S ribosomal protein L30.

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

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	125	Total	C	N	O	S	0	0
			1007	638	203	165	1		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	76	Total	C	N	O	S	0	0
			604	385	114	105			

- Molecule 37 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	469	Total	C	N	O	S	0	0
			3774	2381	685	699	9		

- Molecule 38 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	366	Total	C	N	O	S	0	0
			2988	1936	517	525	10		

- Molecule 39 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	129	Total	C	N	O	S	0	0
			1064	685	192	183	4		

- Molecule 40 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 41 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	158	Total	C	N	O	S	0	0
			1313	827	235	250	1		

- Molecule 42 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	230	Total	C	N	O	S	0	0
			1860	1177	352	324	7		

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

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

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	142	Total	C	N	O	S	0	0
			1196	751	239	197	9		

- Molecule 45 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	287	Total	C	N	O	S	0	0
			2318	1482	408	412	16		

- Molecule 46 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	182	Total	C	N	O	S	0	0
			1448	911	261	271	5		

- Molecule 47 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	488	Total	C	N	O	S	0	0
			3807	2398	677	711	21		

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

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

- Molecule 49 is a protein called UPF0642 protein YBL028C.

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

- Molecule 50 is a RNA chain called RDN25-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	3058	Total	C	N	O	P	0	0
			65427	29223	11807	21339	3058		

- Molecule 51 is a RNA chain called RDN5.8-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

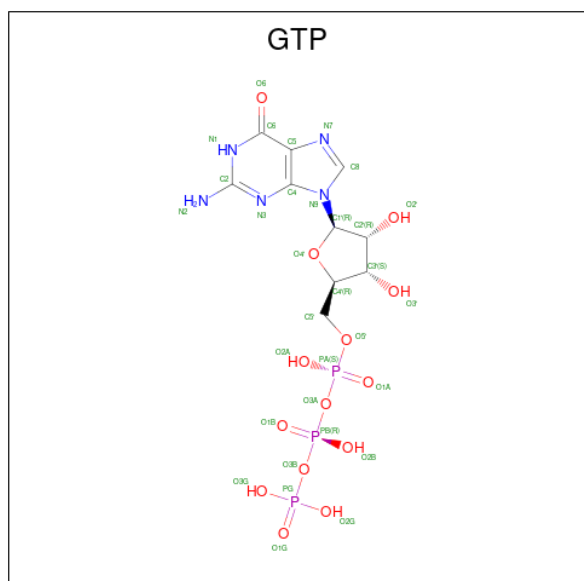
- Molecule 52 is a RNA chain called RDN5-2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 53 is a RNA chain called ITS2-1 miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
54	b	1	Total	C	N	O	P	0
			32	10	5	14	3	
54	m	1	Total	C	N	O	P	0
			32	10	5	14	3	

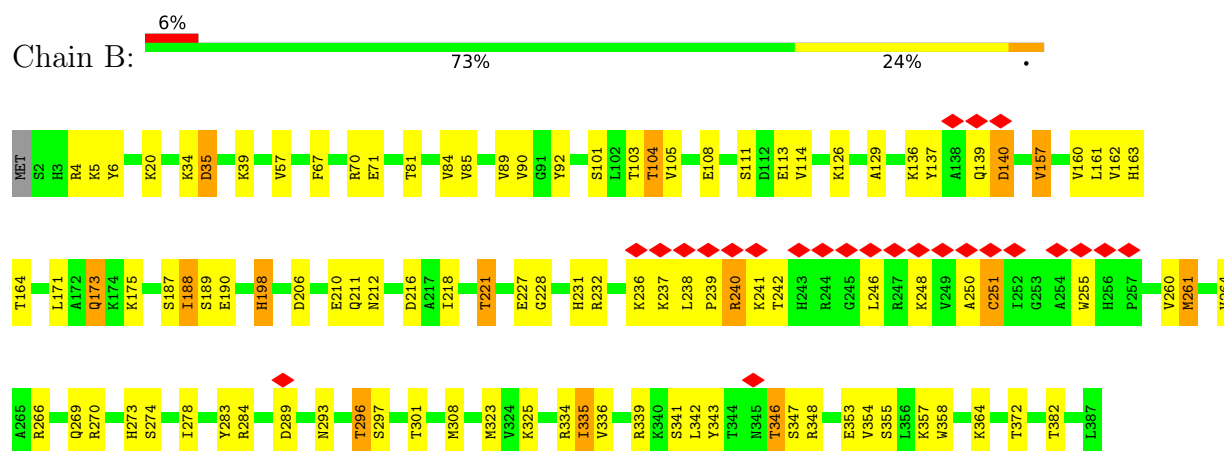
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	b	1	Total	Mg	0
			1	1	
55	m	1	Total	Mg	0
			1	1	

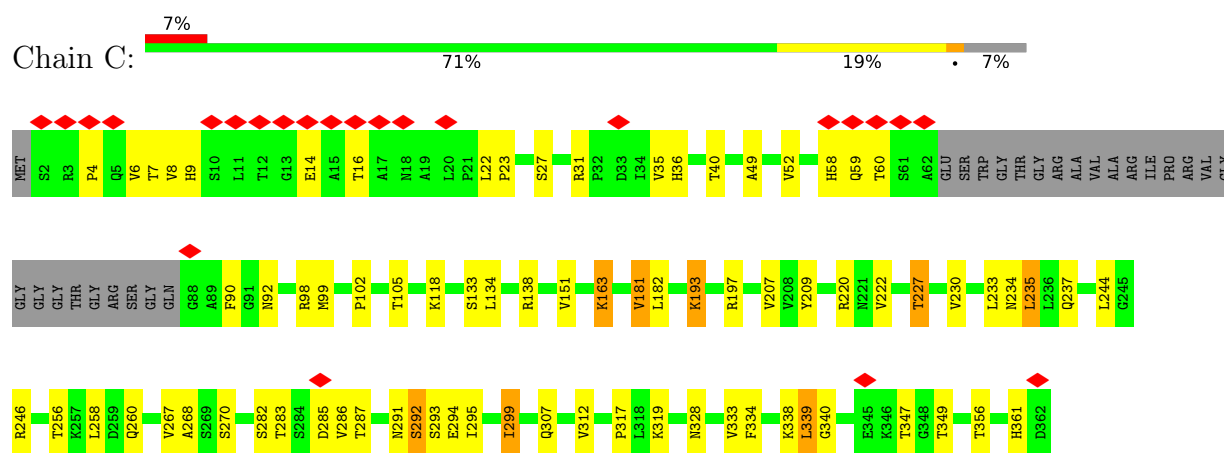
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

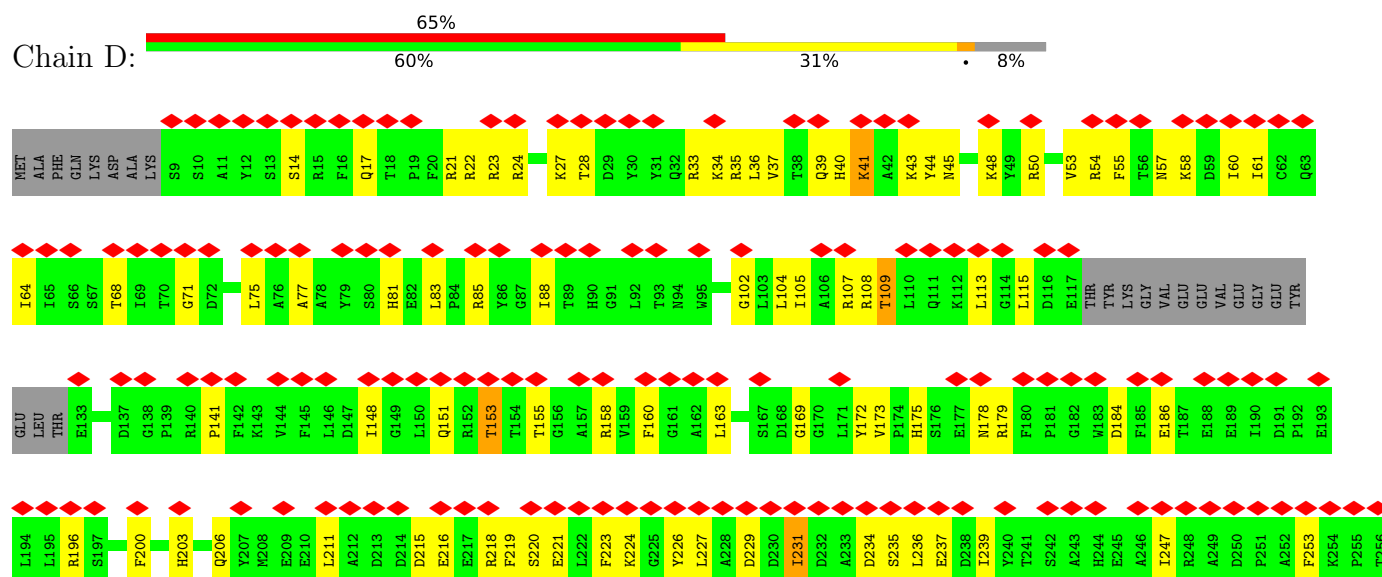
- Molecule 4: 60S ribosomal protein L3



- Molecule 5: 60S ribosomal protein L4-A

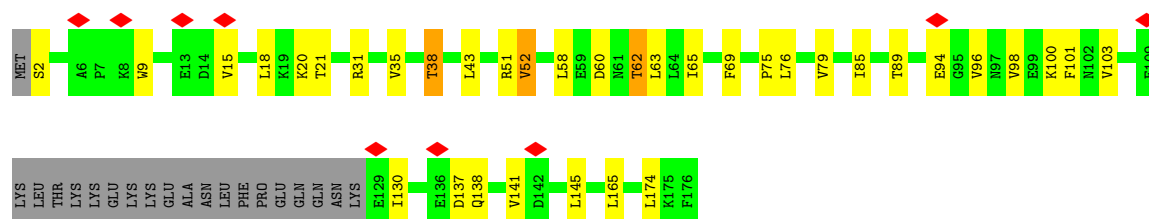


- Molecule 6: 60S ribosomal protein L5

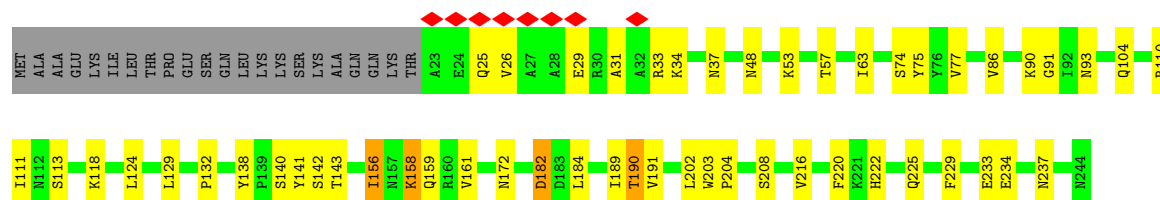




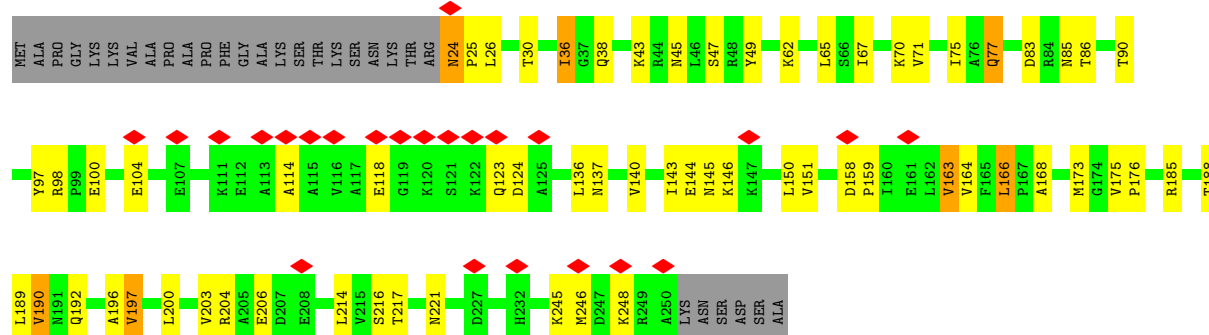
• Molecule 7: 60S ribosomal protein L6-A



• Molecule 8: 60S ribosomal protein L7-A

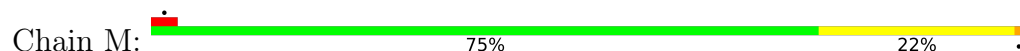


• Molecule 9: 60S ribosomal protein L8-A



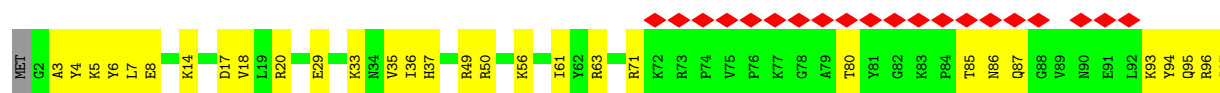
• Molecule 10: 60S ribosomal protein L9-A







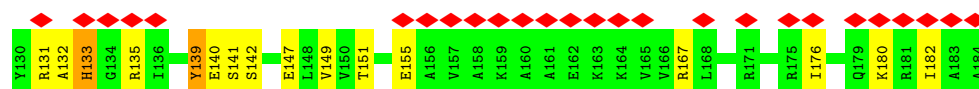
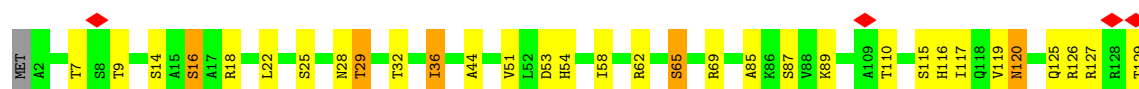
- Molecule 14: 60S ribosomal protein L15-A



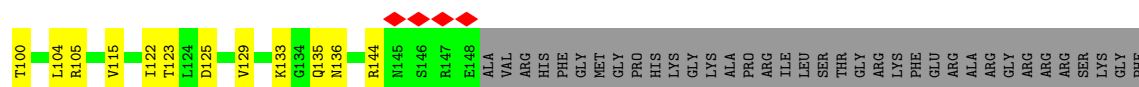
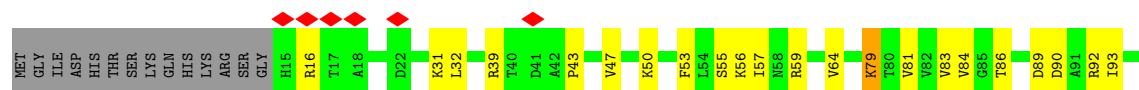
- Molecule 15: 60S ribosomal protein L16-A



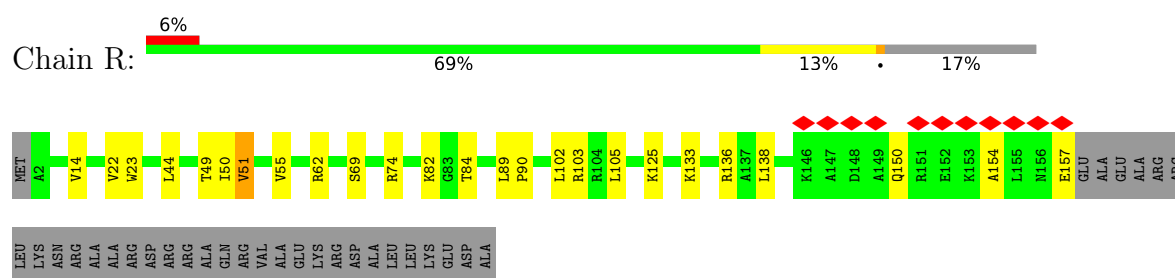
- Molecule 16: 60S ribosomal protein L17-A



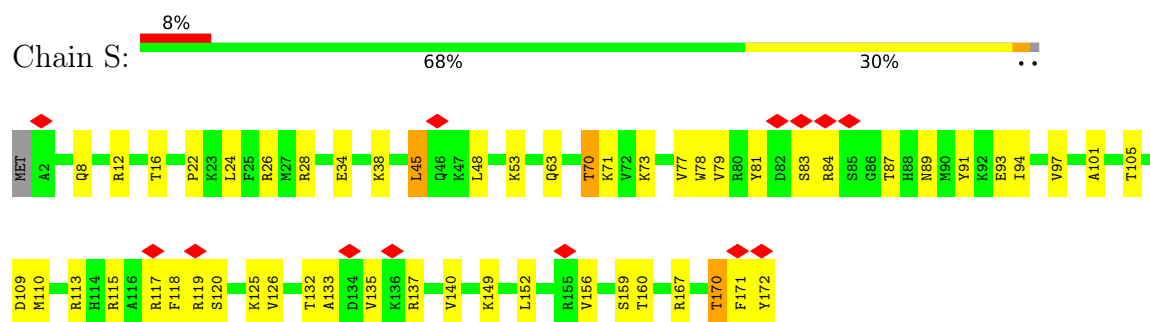
- Molecule 17: 60S ribosomal protein L18-A



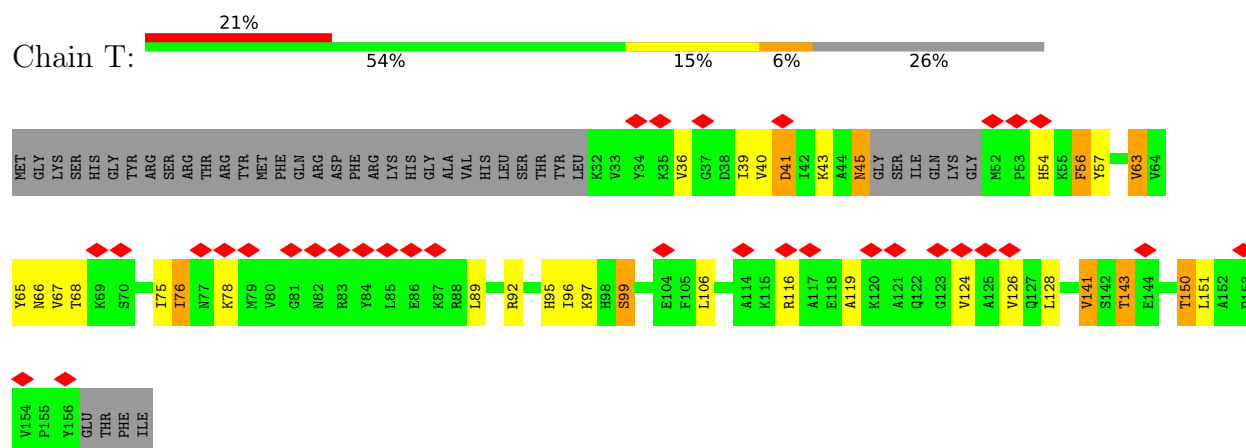
- Molecule 18: 60S ribosomal protein L19-A



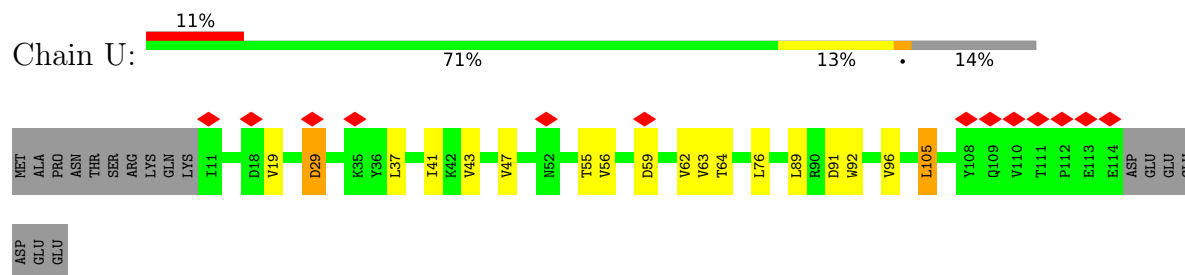
- Molecule 19: 60S ribosomal protein L20-A



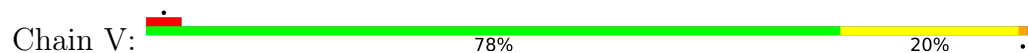
- Molecule 20: 60S ribosomal protein L21-A



- Molecule 21: 60S ribosomal protein L22-A

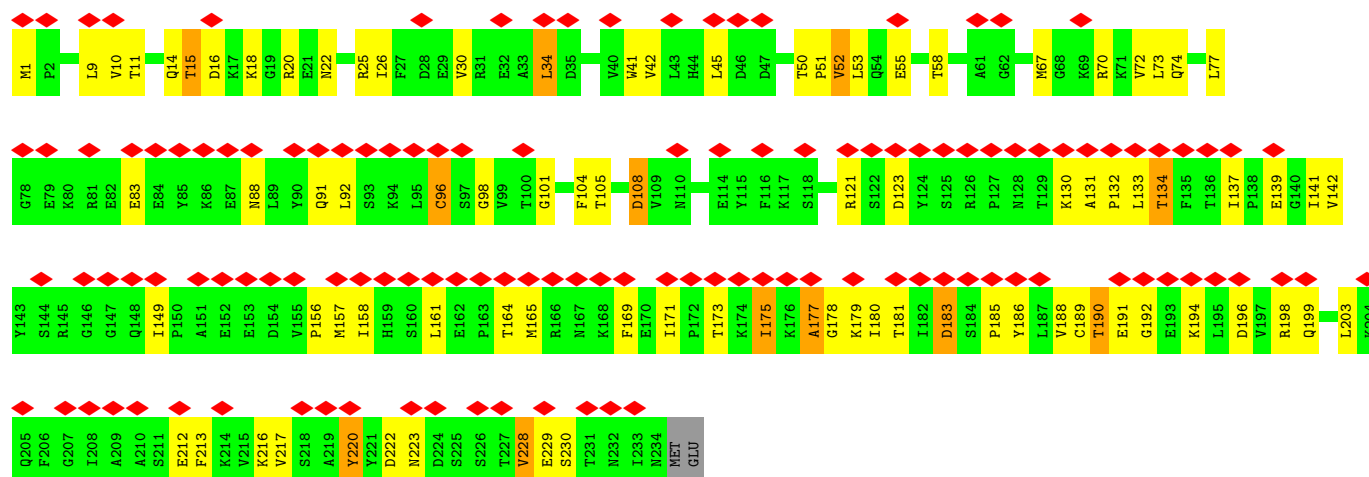


- Molecule 22: 60S ribosomal protein L23-A

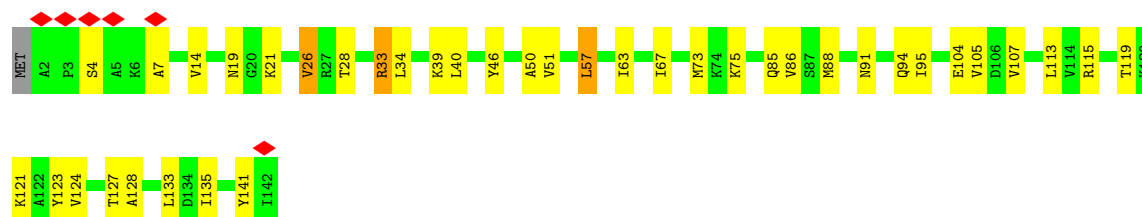




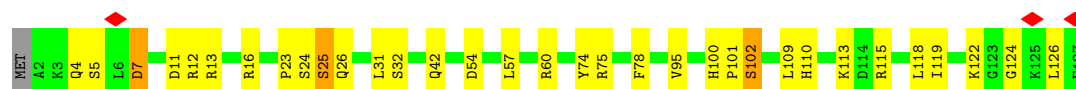
• Molecule 23: Ribosome assembly factor MRT4



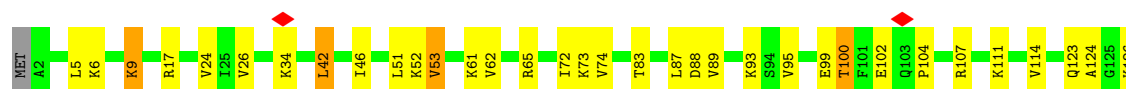
• Molecule 24: 60S ribosomal protein L25



• Molecule 25: 60S ribosomal protein L26-A

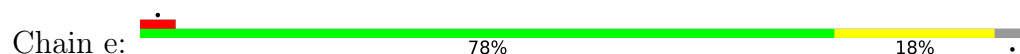


• Molecule 26: 60S ribosomal protein L27-A





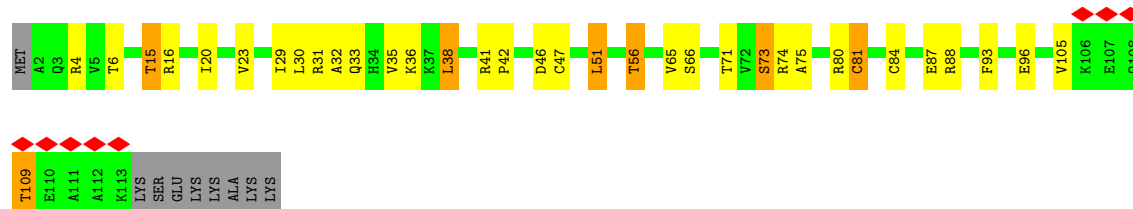
- Molecule 30: 60S ribosomal protein L32



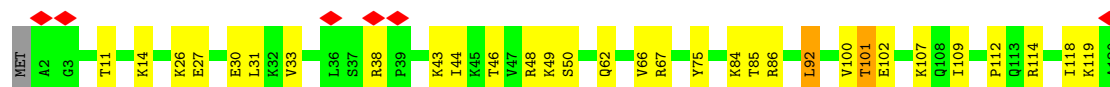
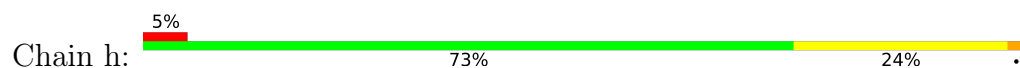
- Molecule 31: 60S ribosomal protein L33-A



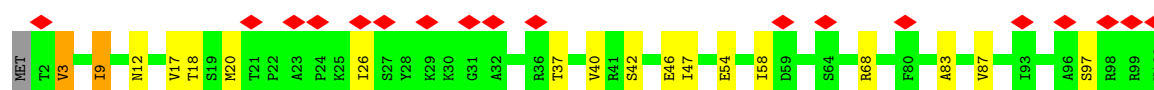
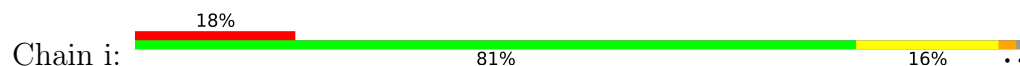
- Molecule 32: 60S ribosomal protein L34-A



- Molecule 33: 60S ribosomal protein L35-A

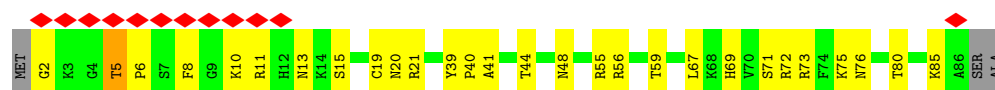


- Molecule 34: 60S ribosomal protein L36-A



- Molecule 35: 60S ribosomal protein L37-A

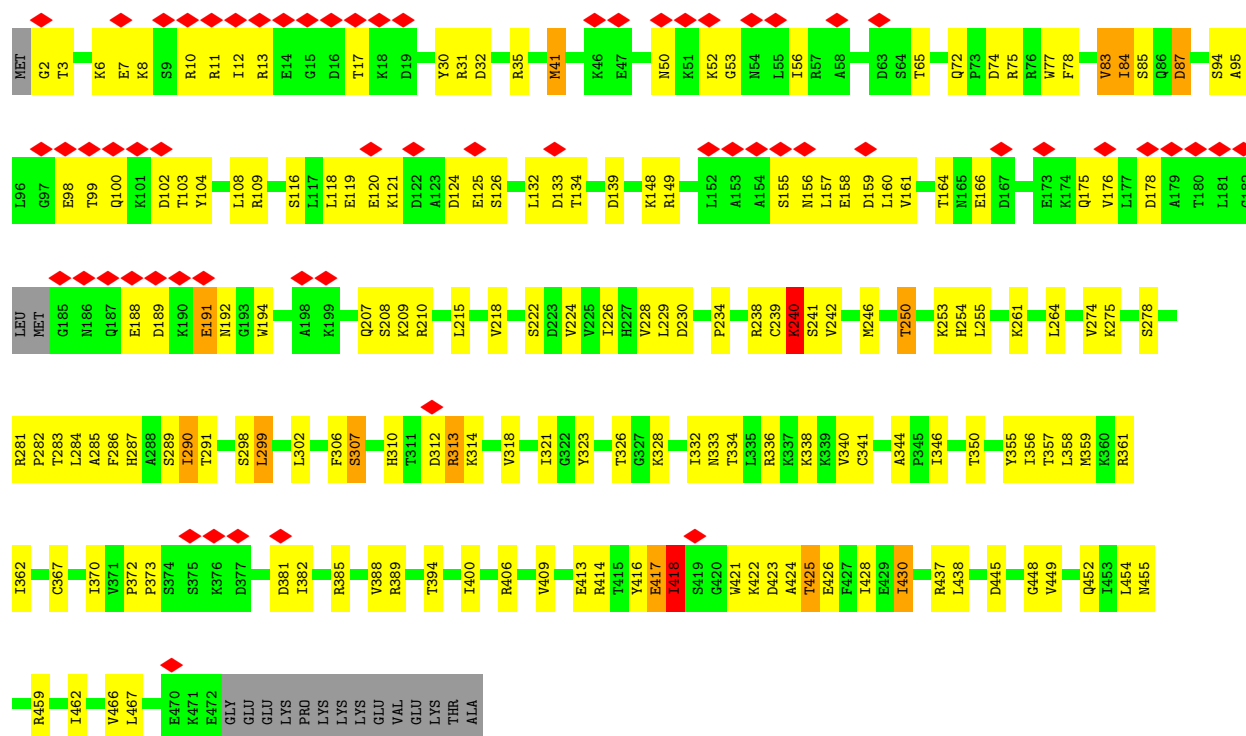




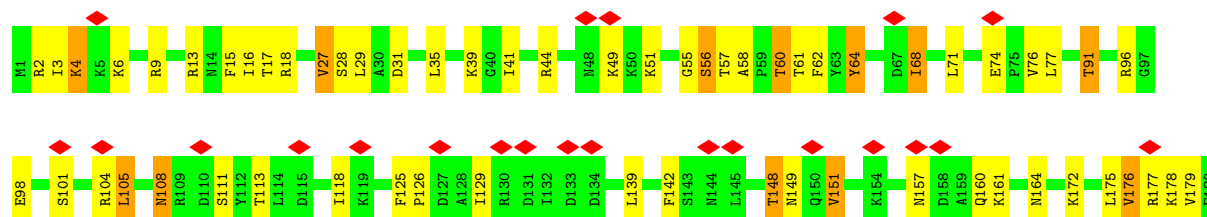
- Molecule 36: 60S ribosomal protein L38



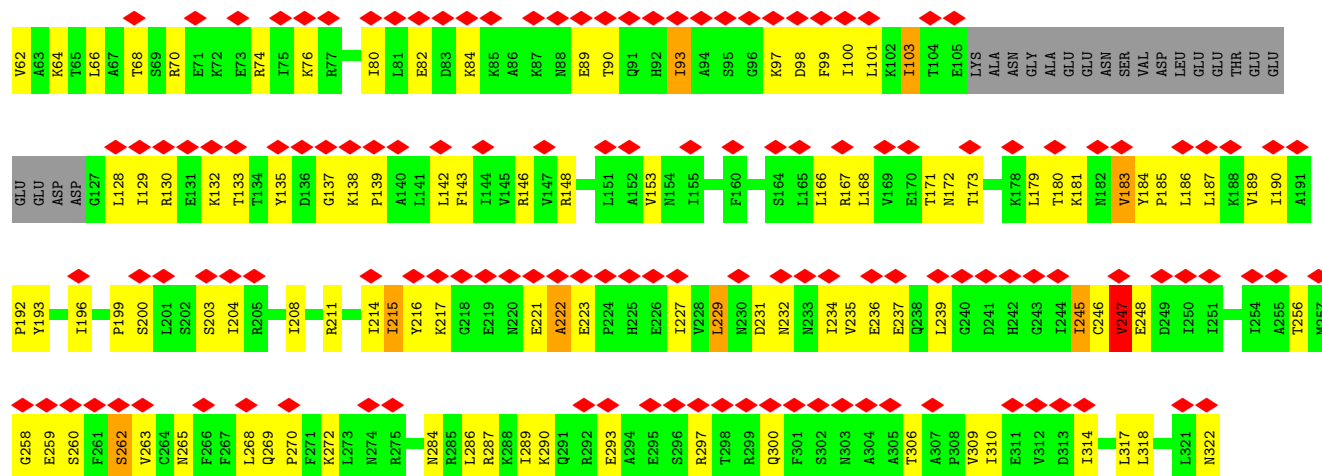
- Molecule 37: Nucleolar GTP-binding protein 2



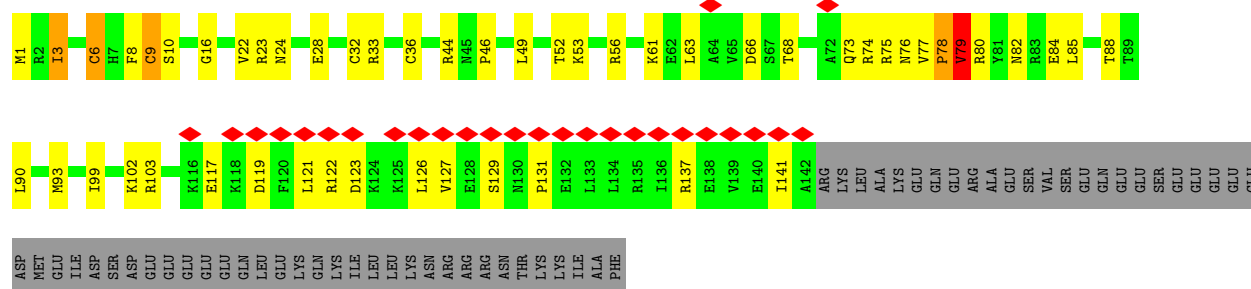
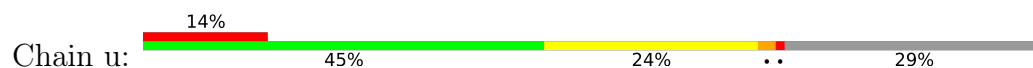
- Molecule 38: Pescadillo homolog



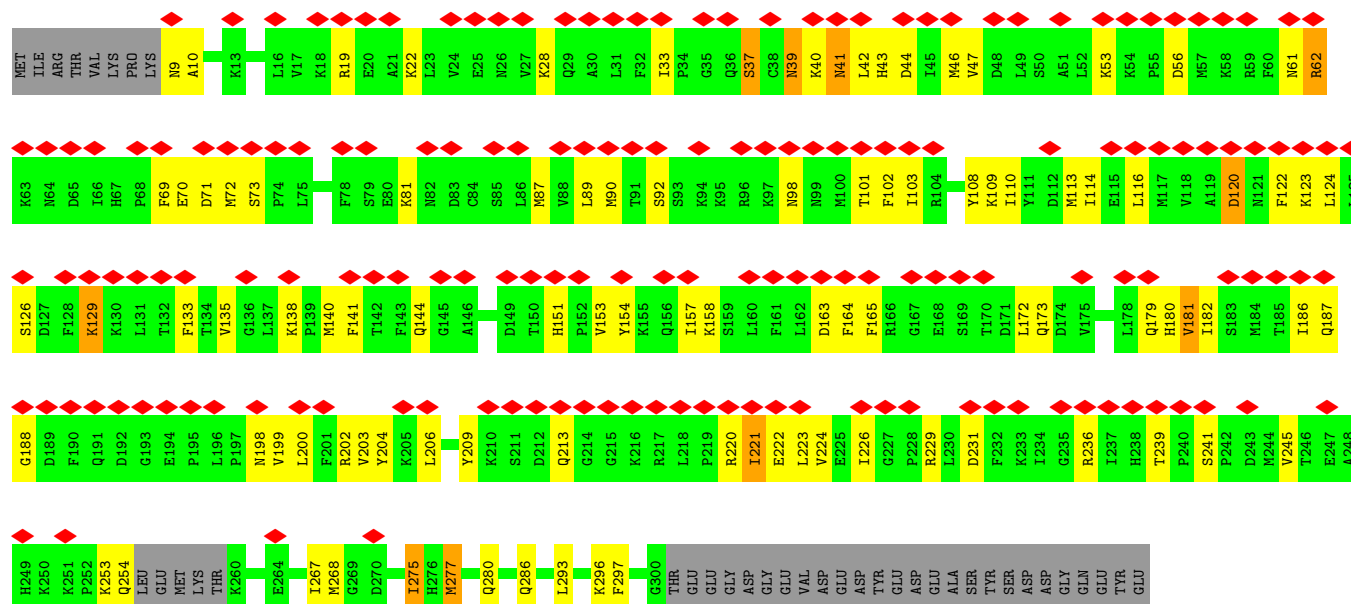




• Molecule 44: Ribosome biogenesis protein RLP24



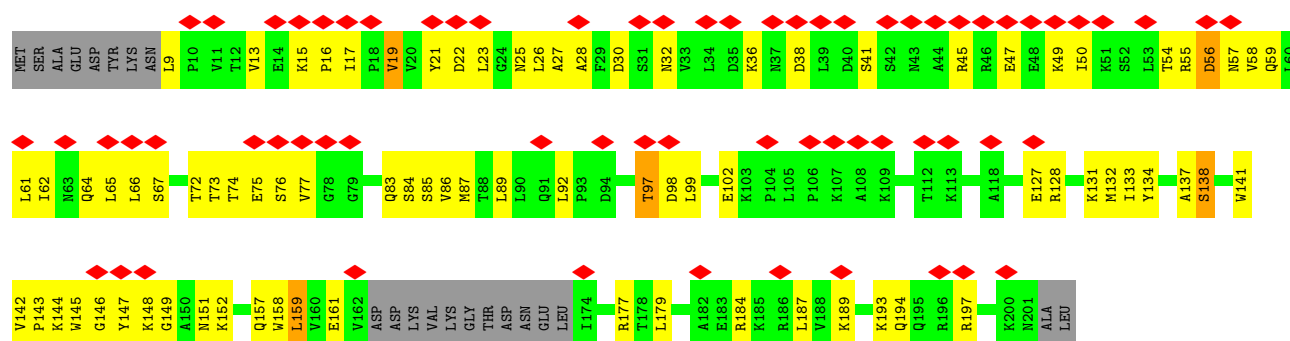
• Molecule 45: Ribosome biogenesis protein RPF2



GLU
GLU
PHE
VAL
SER
SER
ALA
THR
ASP
ILE
GLU
PRO
SER
ALA
LYS
ARG
GLN
LYS
LYS

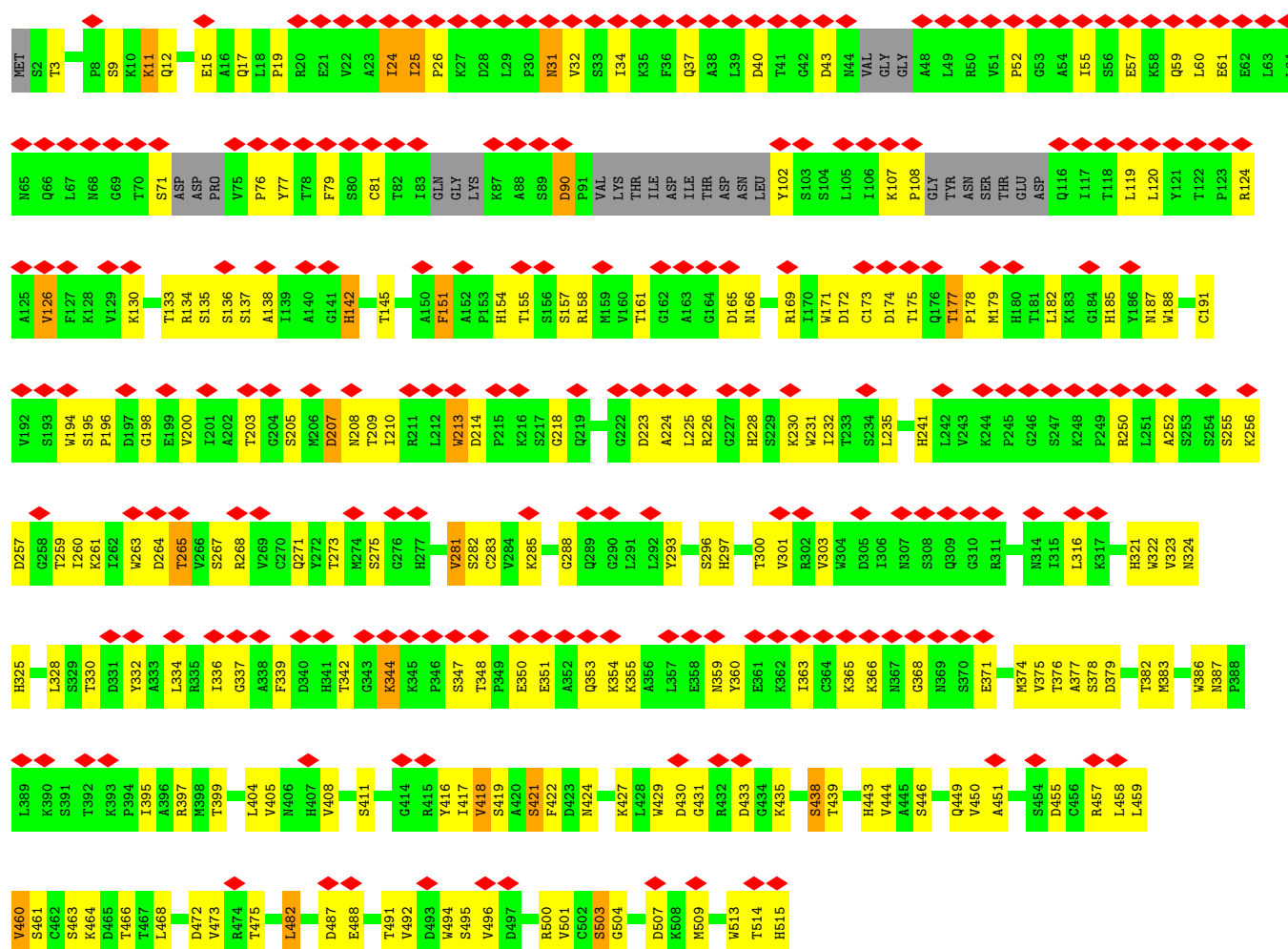
• Molecule 46: Regulator of ribosome biosynthesis

Chain w: 

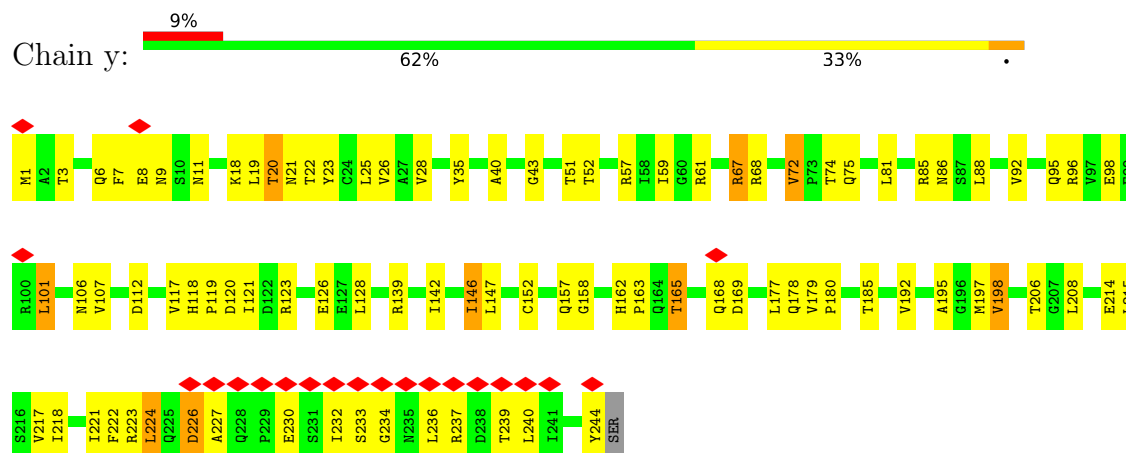


• Molecule 47: Ribosome assembly protein 4

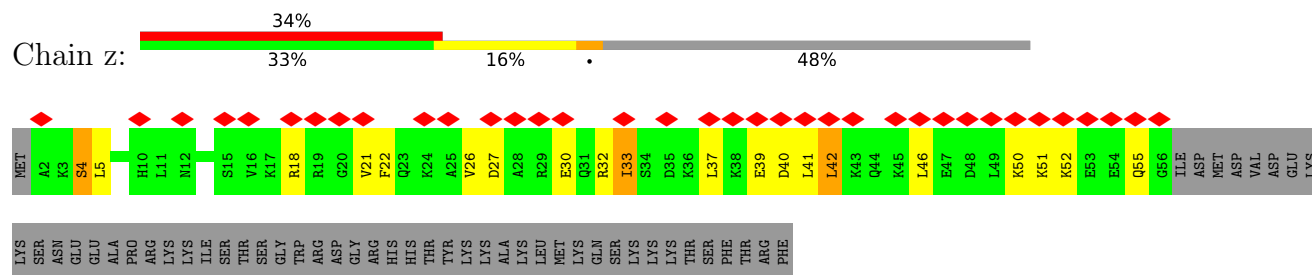
Chain x: 



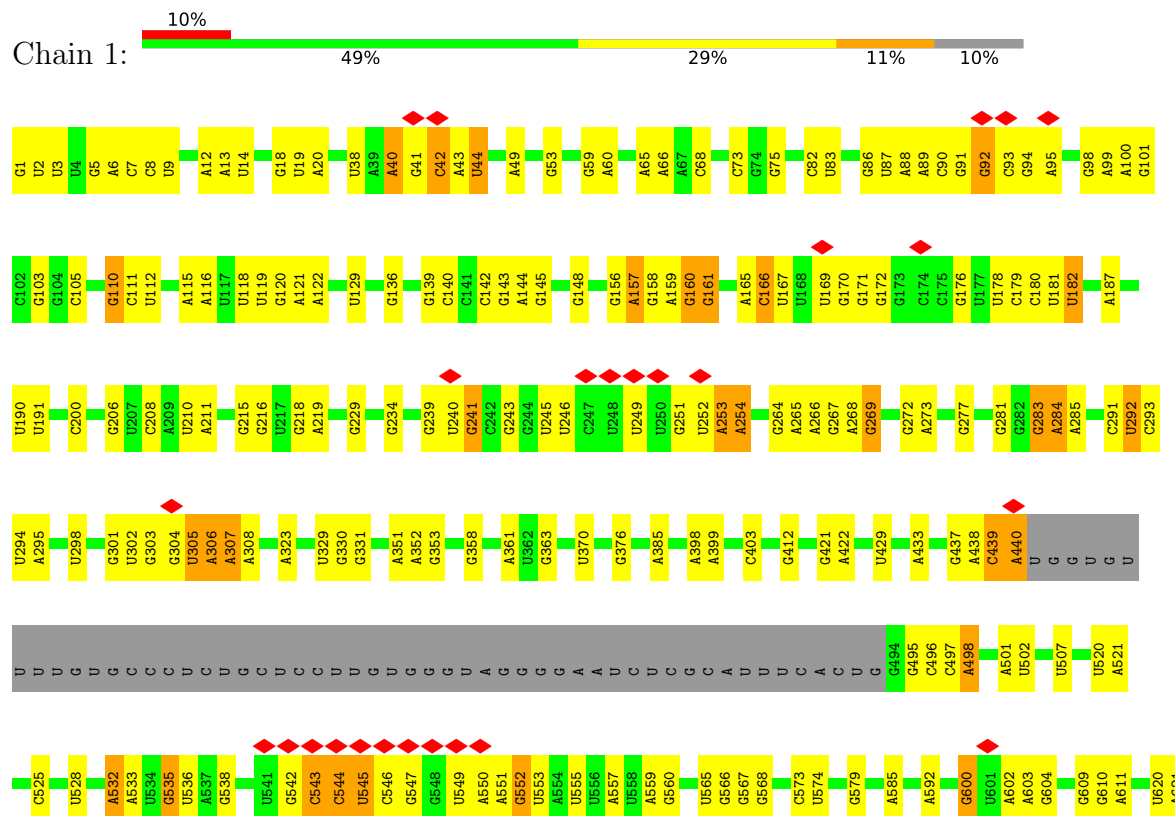
- Molecule 48: Eukaryotic translation initiation factor 6

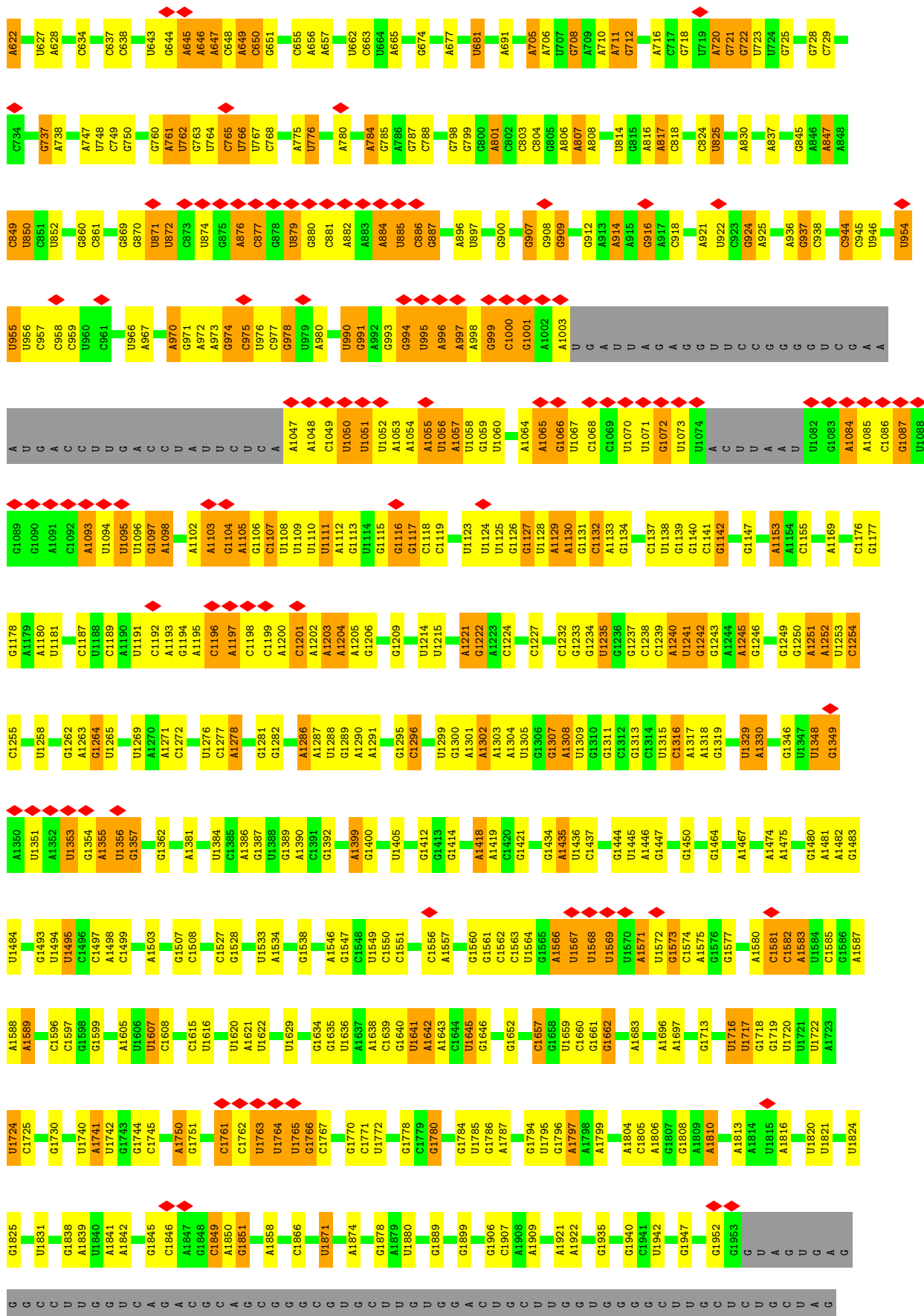


- Molecule 49: UPF0642 protein YBL028C

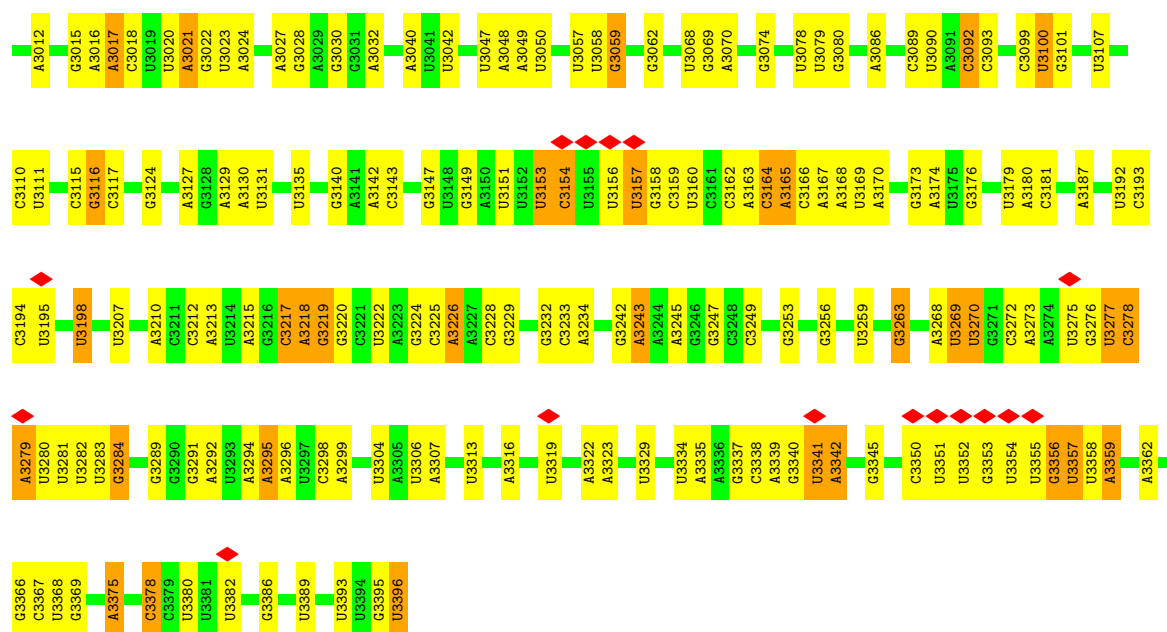


- Molecule 50: RDN25-1 rRNA

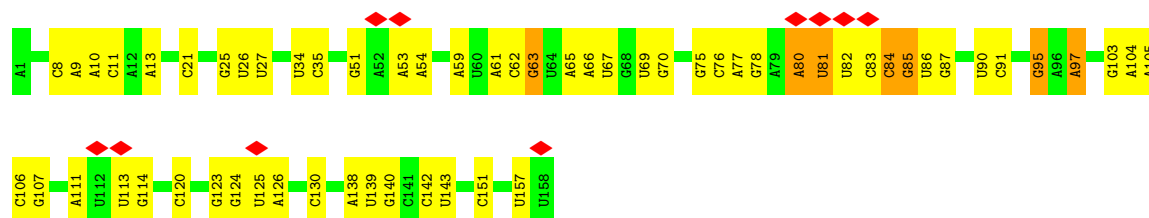




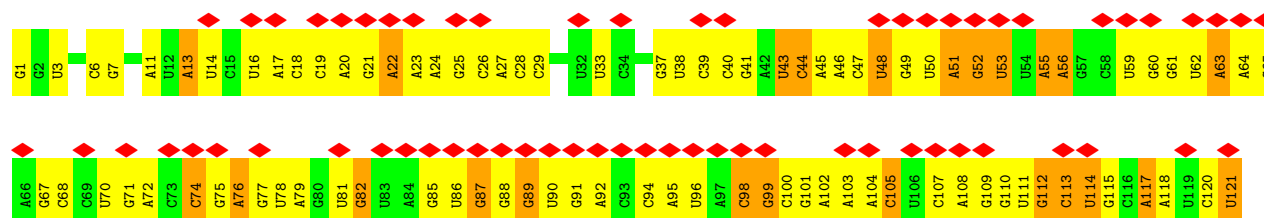
U2921	G2836	A2769	G2899	A2637	A2561	U	G2418	A2317	C2257	U2193	U	G
G2922	A2837	G2770	G2700	C2638	A2566	A	A2419	U2318	U2258	G2194	G	C
U2923	G2838	U2771	U2701	G2639	C2567	C	C2420	A2321	A2259	C2195	C	G
U2924	G2839	U2772	A2702	A2640	C2568	A	U2422	G2333	U2260	C2196	A	G
C2925	G2840	C2773	A2703	U2641	A2569	C	U2423	U2334	G2261	C2197	C	C
A2926	G2841	C2774	A2704	A2642	U2570	U	A2424	G2335	A2262	A2198	A	U
C2927	U2842	U2775	A2705	A2643	U2571	A	G2425	U2336	C2263	A2199	A	A
C2928	U2843	C2776	G2706	A2644	U2572	C	U2426	U2347	U2264	U2200	U	C
C2929	U2844	G2777	U2712	G2645	G2573	U	U2428	C2339	U2265	G2201	U	U
A2930	C2845	G2778	U2713	A2646	G2576	U	A2438	U2340	C2267	G2202	U	U
U2935	A2780	A2779	G2714	G2648	C2577	A	A2439	U2347	U2268	C2203	G	G
U2936	U2781	G2780	G2715	A2649	G2585	U	G2442	A2357	U2269	U2204	C	C
A2940	U2782	U2783	U2716	G2648	G2586	U	C2444	A2358	A2270	C2205	G	U
A	U2783	G2784	U2717	A2649	G2587	U	U2445	C2359	G2271	G2206	C	C
C	A2785	G2785	U2718	G2650	G2588	U	A	G2362	G2272	A2207	U	U
G2943	G2786	U2786	U2719	G2651	G2589	U	G	A2363	G2273	U2208	G	G
U2944	G2787	G2787	G2720	U2652	A2593	U	U	G2364	U2274	U2209	U	U
G2945	G2788	U2788	A2721	C2653	C2594	U	A	U2370	A2275	G2210	U	U
U2946	U2789	U2789	U2722	G2654	U2595	U	G	G2371	G2276	A2112	C	C
A2947	A2790	G2791	U2723	U2655	U2596	U	A	A	G2277	A2113	G	G
C2948	G2792	A2792	C2726	A2656	U2597	U	G	C2376	C2278	U2211	U	U
U2949	G2793	G2793	A2727	G2657	A2601	U	U	G2377	A2279	C2212	A	A
G2950	G2794	G2794	G2728	U2658	G2602	U	G	A	A2280	C2213	G	G
G2951	G2795	U2795	U2729	G2659	G2603	U	G	C	A	A2117	U	U
U2952	G2796	U2796	G2730	G2660	G2604	U	U	C	U	A2118	C	C
G2953	G2797	G2797	U2731	G2661	U2605	U	U	G	G	A2119	A	A
U2954	C2798	C2798	G2732	G2662	G2606	U	U	G	C	A2120	G	G
U2955	A2799	A2799	A2733	C2664	G2607	U	A	G2376	C	A2121	C	C
A2956	G2800	G2800	U2734	U2665	G2608	U	A	G2377	U	A2122	G	G
U2957	A2801	A2801	U2735	A2666	A2609	U	U	G	C	A2131	C	C
G2961	A2802	A2802	U2736	U2667	G2610	U	U	U2388	U	U2137	U	U
U2962	U2807	U2807	G2741	A2672	U2611	U	A	C2389	C	A2138	G	G
C2963	A2808	A2808	G2742	A2673	U2612	U	G	U	U	U2140	U	U
U2964	C2809	C2809	A2743	G2614	G2613	U	U	A2222	A	U2141	A	A
U2965	C2810	C2810	U2746	G2615	G2614	U	G	A2223	C	A2142	G	G
G2966	A2811	A2811	A2747	C	G	U	G	U2225	U	U2148	U	U
A2967	G2812	G2812	U2748	U	U	U	A	U2226	A	A2149	C	C
G2968	U2815	U2815	G2749	G2619	G2620	U	A	C2227	U	A2152	U	U
A2969	G2816	G2816	G2751	G2621	G2621	U	G	A2228	U	U2153	C	C
C2970	A2817	A2817	U2752	C2622	C2622	U	C	A2229	G	C2230	U	U
A2971	G2818	G2818	G2753	G2623	G2623	U	G	A2401	U	C2231	U	U
U2977	U2819	U2819	G2754	C2624	G2624	U	G	A2402	G	A2232	G	G
U2978	A2820	A2820	A2758	C2625	C2625	U	C	A2403	C	C2235	A	A
U2979	C2821	C2821	U2759	A2626	A2626	U	C	G2405	G	G2236	A	A
U2980	U2822	U2822	G2761	C2627	C2627	U	C	G2409	C	C2237	C	C
U2981	G2823	G2823	A2762	A2628	A2628	U	G	U2410	G	C2238	G	G
A2982	U2824	U2824	U2763	U2629	U2629	U	A	U2411	A	G2239	U	U
C2983	G2825	G2825	C2764	C2630	C2630	U	U	G2412	U	G2240	C	C
C2984	U2826	U2826	C2765	U2631	U2631	U	A	A2413	G	U2241	G	G
U2989	G2830	G2830	U2766	G2632	G2632	U	A	G2414	A	A2242	C	C
A2991	G2831	G2831	U2767	U2633	U2633	U	A	U2415	A	A2243	G	G
U2992	G2834	G2834	U2768	A2634	A2634	U	A	U2416	A	A2244	C	C
U2996	U2835	U2835		A2635	A2635	U	A	G2315	G	G2245	U	U
G2997				A2636	A2636	U	A	G2316	U	G2246	C	C
				A2695	A2695	U				G2247	C	C
				A2696	A2696	U				G2248	C	C
				A2697	A2697	U				G2249	C	C
				G2698	G2698	U				A2255	C	C
						U				A2256	C	C



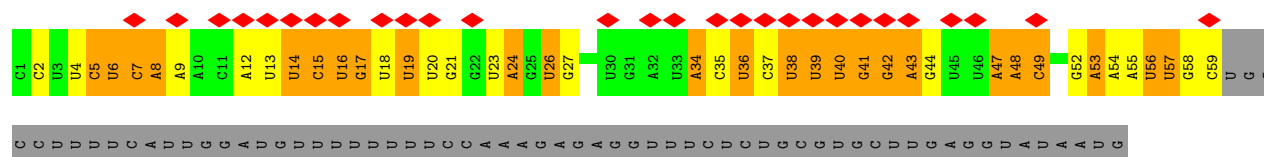
• Molecule 51: RDN5.8-1 rRNA



• Molecule 52: RDN5-2 rRNA



• Molecule 53: ITS2-1 miscRNA



C	A	A	G	U	A	C	G	G	U	C	G	U	U	U	U	A	G	U	U	U	U	A	C	C	A	A	C	U	G	C	G	C	U	A	A	U	C	U	U	U	U	U	U	U	U	U	U	U	U
U	G	A	A	C	G	U	U	A	U	C	G	A	U	A	A	G	A	A	G	A	G	A	G	C	G	U	C	U	A	G	C	G	C	A	A	A	U	G	U	U	U	C227	U228	U229	A230	A231	A232		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47025	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.208	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	412.02, 412.02, 412.02	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3734, 1.3734, 1.3734	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L	0.31	0/1508	0.59	0/2024
2	a	0.29	0/751	0.47	0/1013
3	A	0.34	0/1520	0.52	0/2043
4	B	0.34	0/3152	0.52	0/4239
5	C	0.34	0/2624	0.55	0/3553
6	D	0.21	0/2243	0.48	0/3025
7	E	0.28	0/1260	0.48	0/1694
8	F	0.33	0/1821	0.51	0/2451
9	G	0.30	0/1807	0.56	2/2439 (0.1%)
10	H	0.31	0/1514	0.45	0/2039
11	J	0.18	0/1357	0.49	0/1818
12	K	0.20	0/2077	0.53	2/2800 (0.1%)
13	M	0.30	0/1074	0.48	0/1446
14	N	0.34	0/1757	0.55	0/2354
15	O	0.37	0/1585	0.47	0/2128
16	P	0.32	0/1465	0.51	0/1968
17	Q	0.29	0/1050	0.46	0/1419
18	R	0.33	0/1275	0.45	0/1702
19	S	0.31	0/1473	0.54	0/1980
20	T	0.23	0/957	0.52	0/1285
21	U	0.26	0/843	0.47	0/1144
22	V	0.34	0/1018	0.48	0/1369
23	W	0.22	0/1918	0.49	0/2586
24	X	0.31	0/1116	0.46	0/1503
25	Y	0.31	0/1004	0.51	0/1341
26	Z	0.30	0/1118	0.57	0/1497
27	b	0.28	0/4211	0.52	0/5675
28	c	0.28	0/751	0.40	0/1008
29	d	0.34	0/870	0.48	0/1168
30	e	0.34	0/1028	0.45	0/1376
31	f	0.35	0/868	0.48	0/1168
32	g	0.38	0/891	0.54	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.31	0/978	0.49	0/1301
34	i	0.25	0/778	0.53	0/1034
35	j	0.34	0/685	0.48	0/908
36	k	0.28	0/610	0.50	0/815
37	m	0.30	0/3848	0.56	0/5181
38	n	0.25	0/3057	0.54	0/4127
39	o	0.23	0/1083	0.53	0/1440
40	p	0.36	0/701	0.51	0/934
41	q	0.21	0/1336	0.49	0/1788
42	r	0.32	0/1892	0.60	2/2528 (0.1%)
43	t	0.22	0/2333	0.54	0/3128
44	u	0.29	0/1218	0.56	2/1621 (0.1%)
45	v	0.22	0/2361	0.46	0/3153
46	w	0.23	0/1471	0.49	0/1980
47	x	0.22	0/3897	0.53	2/5282 (0.0%)
48	y	0.30	0/1872	0.50	0/2548
49	z	0.18	0/445	0.38	0/585
50	1	0.32	0/73234	0.39	0/114167
51	2	0.34	0/3746	0.37	0/5832
52	3	0.17	0/2883	0.36	0/4491
53	6	0.19	0/1527	0.43	0/2371
All	All	0.30	0/157861	0.45	10/229660 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	1
4	B	0	2
8	F	0	1
11	J	0	1
12	K	0	1
23	W	0	1
29	d	0	1
32	g	0	1
37	m	0	3
38	n	0	3
39	o	0	1
41	q	0	2
42	r	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	u	0	2
47	x	0	1
All	All	0	23

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	x	213	TRP	CA-C-N	10.43	135.50	121.74
47	x	213	TRP	C-N-CA	10.43	135.50	121.74
42	r	202	LYS	CA-C-N	6.52	132.00	121.83
42	r	202	LYS	C-N-CA	6.52	132.00	121.83
44	u	79	VAL	CA-C-N	5.62	132.28	121.54
44	u	79	VAL	C-N-CA	5.62	132.28	121.54
12	K	215	LYS	CA-C-N	5.57	132.19	121.54
12	K	215	LYS	C-N-CA	5.57	132.19	121.54
9	G	36	ILE	N-CA-C	-5.45	107.97	113.20
9	G	190	VAL	N-CA-C	-5.33	108.65	113.71

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	221	THR	Peptide
4	B	346	THR	Peptide
8	F	158	LYS	Peptide
11	J	167	TYR	Peptide
12	K	216	GLU	Peptide
1	L	46	ILE	Peptide
23	W	177	ALA	Peptide
29	d	86	LYS	Peptide
32	g	80	ARG	Peptide
37	m	240	LYS	Peptide
37	m	253	LYS	Peptide
37	m	417	GLU	Peptide
38	n	3	ILE	Peptide
38	n	375	ILE	Peptide
38	n	4	LYS	Peptide
39	o	158	MET	Peptide
41	q	200	ALA	Peptide
41	q	270	ASP	Peptide

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Mol	Chain	Res	Type	Group
42	r	15	GLY	Peptide
42	r	236	LYS	Peptide
44	u	78	PRO	Peptide
44	u	79	VAL	Peptide
47	x	207	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	1484	0	1539	34	0
2	a	735	0	776	17	0
3	A	1492	0	1548	35	0
4	B	3081	0	3165	64	0
5	C	2576	0	2692	42	0
6	D	2197	0	2157	82	0
7	E	1239	0	1326	22	0
8	F	1784	0	1862	27	0
9	G	1775	0	1870	41	0
10	H	1493	0	1566	32	0
11	J	1336	0	1370	54	0
12	K	2044	0	2133	79	0
13	M	1059	0	1154	20	0
14	N	1720	0	1779	40	0
15	O	1555	0	1659	4	0
16	P	1442	0	1485	28	0
17	Q	1035	0	1115	18	0
18	R	1258	0	1342	14	0
19	S	1437	0	1475	30	0
20	T	943	0	994	23	0
21	U	826	0	834	3	0
22	V	1003	0	1048	14	0
23	W	1885	0	1921	60	0
24	X	1100	0	1187	24	0
25	Y	993	0	1081	21	0
26	Z	1092	0	1155	22	0
27	b	4137	0	4199	114	0
28	c	743	0	797	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	d	856	0	904	18	0
30	e	1007	0	1074	9	0
31	f	850	0	880	16	0
32	g	881	0	945	19	0
33	h	969	0	1078	17	0
34	i	771	0	849	11	0
35	j	670	0	673	18	0
36	k	604	0	671	8	0
37	m	3774	0	3835	119	0
38	n	2988	0	3069	79	0
39	o	1064	0	1121	41	0
40	p	694	0	736	15	0
41	q	1313	0	1344	36	0
42	r	1860	0	1965	70	0
43	t	2306	0	2454	79	0
44	u	1196	0	1239	34	0
45	v	2318	0	2398	78	0
46	w	1448	0	1510	74	0
47	x	3807	0	3790	142	0
48	y	1849	0	1836	60	0
49	z	444	0	478	13	0
50	1	65427	0	32879	836	0
51	2	3353	0	1695	30	0
52	3	2579	0	1304	98	0
53	6	1370	0	692	47	0
54	b	32	0	12	3	0
54	m	32	0	12	2	0
55	b	1	0	0	0	0
55	m	1	0	0	0	0
56	j	1	0	0	0	0
56	p	1	0	0	0	0
56	u	1	0	0	0	0
All	All	147931	0	114672	2557	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 10.

All (2557) 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)
50:1:3222:U:H3	50:1:3263:G:H1	1.05	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:1001:G:C6	50:1:1050:U:O2	2.17	0.97
50:1:2426:U:H3	50:1:2603:G:H1	1.01	0.95
52:3:79:A:H62	52:3:101:G:H21	1.02	0.94
52:3:67:G:H1	52:3:111:U:H3	1.05	0.94
50:1:2137:U:OP2	50:1:2142:A:N6	2.01	0.92
50:1:976:U:H3	50:1:1107:C:N4	1.67	0.92
6:D:216:GLU:O	6:D:220:SER:HB3	1.70	0.91
27:b:187:ILE:HG23	27:b:188:THR:HG23	1.52	0.91
52:3:85:G:H1	52:3:95:A:H61	1.10	0.90
52:3:79:A:H62	52:3:101:G:N2	1.70	0.90
52:3:85:G:H1	52:3:95:A:N6	1.70	0.90
50:1:870:G:N2	50:1:871:U:O4	2.04	0.89
52:3:85:G:N1	52:3:95:A:N6	2.20	0.88
50:1:977:C:N3	50:1:1106:G:N2	2.20	0.88
23:W:137:ILE:HD12	23:W:186:TYR:HB3	1.56	0.88
50:1:437:G:H1	50:1:622:A:H61	1.18	0.87
50:1:993:G:H1	50:1:1056:U:H3	0.87	0.86
50:1:976:U:H3	50:1:1107:C:H42	0.87	0.86
46:w:28:ALA:HB2	46:w:61:LEU:HD21	1.58	0.85
50:1:1233:G:H1	50:1:1255:C:H5	1.25	0.84
6:D:83:LEU:HB3	6:D:88:ILE:HB	1.57	0.84
37:m:282:PRO:HB3	45:v:277:MET:HE1	1.57	0.84
50:1:993:G:N2	50:1:1056:U:O2	2.11	0.83
43:t:153:VAL:O	53:6:227:C:N4	2.11	0.83
52:3:79:A:N6	52:3:101:G:H21	1.76	0.83
37:m:240:LYS:O	37:m:242:VAL:N	2.10	0.82
12:K:184:ASP:HB2	53:6:7:C:H42	1.43	0.82
14:N:71:ARG:HD3	14:N:94:TYR:HB2	1.63	0.81
6:D:23:ARG:NH1	6:D:23:ARG:O	2.14	0.80
42:r:164:ARG:H	50:1:2727:A:H8	1.29	0.80
50:1:2770:G:H1	50:1:2788:C:H5	1.30	0.79
50:1:1493:G:N2	50:1:1493:G:OP2	2.14	0.79
51:2:8:C:H2'	51:2:9:A:H8	1.45	0.79
27:b:510:ARG:O	27:b:510:ARG:NH2	2.16	0.79
3:A:21:ARG:NH1	50:1:825:U:OP1	2.15	0.79
27:b:284:MET:HG3	27:b:316:GLU:HB2	1.65	0.79
50:1:1108:U:H2'	50:1:1109:U:H6	1.46	0.79
50:1:2409:G:O2'	50:1:2410:U:O2	2.01	0.79
50:1:2628:A:N6	50:1:2650:U:O2'	2.15	0.79
50:1:995:U:O4	50:1:997:A:N6	2.16	0.78
50:1:2720:G:O6	50:1:2736:A:N6	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:j:55:ARG:NH2	50:1:353:G:N7	2.32	0.78
37:m:381:ASP:OD1	37:m:406:ARG:NH2	2.17	0.78
50:1:1716:U:O2'	50:1:1717:U:O5'	2.02	0.78
24:X:73:MET:HE1	24:X:141:TYR:HD1	1.49	0.77
31:f:57:LYS:NZ	50:1:433:A:OP2	2.17	0.77
43:t:93:ILE:O	53:6:21:G:O2'	2.03	0.77
24:X:50:ALA:HB1	33:h:66:VAL:HG11	1.67	0.77
27:b:264:ILE:HG22	27:b:302:ARG:HH11	1.49	0.77
27:b:497:ARG:NH2	44:u:123:ASP:OD1	2.17	0.77
7:E:31:ARG:NH1	31:f:107:ILE:O	2.18	0.76
50:1:2917:G:H1	50:1:2929:C:H5	1.34	0.76
42:r:143:ARG:NH2	50:1:2874:G:N7	2.34	0.76
29:d:62:ARG:NH1	29:d:68:GLU:OE2	2.18	0.76
46:w:157:GLN:NE2	46:w:159:LEU:O	2.19	0.76
4:B:255:TRP:H	50:1:2943:G:HO2'	1.31	0.75
50:1:975:C:H4'	50:1:976:U:H5'	1.68	0.75
11:J:49:LYS:HB3	11:J:62:ASN:HA	1.67	0.75
46:w:148:LYS:N	50:1:2656:A:N7	2.33	0.75
6:D:211:LEU:HD22	6:D:219:PHE:HB2	1.67	0.75
50:1:2212:C:N4	50:1:2232:A:OP2	2.18	0.75
50:1:3099:C:H42	50:1:3135:U:H3	1.33	0.75
53:6:58:G:OP1	53:6:58:G:N2	2.20	0.75
10:H:62:ARG:NH2	50:1:3115:C:OP1	2.20	0.75
50:1:3020:U:H3'	50:1:3021:A:H5''	1.69	0.75
23:W:70:ARG:HD3	50:1:1282:G:H5''	1.68	0.75
17:Q:92:ARG:NH1	50:1:784:A:O2'	2.21	0.74
50:1:2721:A:H61	50:1:2735:U:H3	1.35	0.74
2:a:65:GLN:NE2	50:1:712:G:OP2	2.19	0.74
52:3:87:G:H2'	52:3:88:G:C8	2.22	0.74
37:m:400:ILE:HG13	37:m:428:ILE:HD11	1.69	0.74
11:J:28:ASP:HB3	11:J:32:ARG:HH21	1.53	0.74
20:T:119:ALA:HB1	20:T:124:VAL:HG21	1.70	0.74
37:m:416:TYR:N	37:m:417:GLU:HA	2.03	0.74
27:b:100:ARG:NH2	50:1:2860:U:OP2	2.20	0.74
47:x:297:HIS:HA	47:x:322:TRP:HB2	1.69	0.73
47:x:194:TRP:HE1	47:x:198:GLY:HA2	1.53	0.73
4:B:255:TRP:N	50:1:2943:G:O2'	2.13	0.73
4:B:216:ASP:HB3	4:B:278:ILE:HA	1.70	0.73
5:C:338:LYS:O	5:C:340:GLY:N	2.21	0.73
37:m:357:THR:HG23	50:1:2962:U:H5''	1.70	0.73
31:f:6:ARG:NH1	31:f:8:TYR:O	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:77:ARG:NH1	50:1:525:C:OP2	2.19	0.72
27:b:415:ASN:ND2	27:b:418:ASP:OD2	2.22	0.72
30:e:47:ARG:NH1	50:1:1147:G:OP1	2.21	0.72
44:u:73:GLN:OE1	44:u:75:ARG:NH2	2.22	0.72
50:1:1001:G:O6	50:1:1051:U:C4	2.42	0.72
53:6:40:U:H4'	53:6:41:G:H5'	1.71	0.72
50:1:2206:G:H21	50:1:2207:A:H1'	1.54	0.72
9:G:123:GLN:O	50:1:120:G:N2	2.21	0.72
23:W:156:PRO:HG2	23:W:179:LYS:HD2	1.70	0.72
25:Y:16:ARG:NH1	50:1:216:G:OP1	2.23	0.72
42:r:192:THR:HG21	50:1:2856:G:H21	1.53	0.72
50:1:2393:G:O2'	50:1:2982:A:N6	2.23	0.72
1:L:153:ASP:OD2	1:L:157:ARG:NH1	2.22	0.72
51:2:81:U:H3	51:2:83:C:H5	1.34	0.72
52:3:85:G:C6	52:3:95:A:N6	2.58	0.72
44:u:6:CYS:SG	44:u:9:CYS:N	2.62	0.72
27:b:264:ILE:O	27:b:302:ARG:NH1	2.23	0.72
5:C:292:SER:OG	5:C:294:GLU:OE1	2.06	0.71
50:1:2760:C:H6	50:1:2800:G:H22	1.35	0.71
16:P:131:ARG:NH2	50:1:880:G:OP2	2.24	0.71
42:r:164:ARG:HD3	50:1:2728:G:H5'	1.71	0.71
6:D:85:ARG:HH22	6:D:253:PHE:H	1.36	0.71
43:t:284:ASN:OD1	43:t:287:ARG:NH1	2.23	0.71
23:W:188:VAL:O	23:W:199:GLN:NE2	2.22	0.71
49:z:51:LYS:O	49:z:55:GLN:HG2	1.90	0.71
50:1:990:U:O2'	50:1:991:G:OP1	2.08	0.71
27:b:492:LYS:HZ1	44:u:137:ARG:HD3	1.56	0.71
46:w:149:GLY:H	50:1:2656:A:H62	1.38	0.70
50:1:545:U:H5''	50:1:546:C:H5'	1.73	0.70
17:Q:89:ASP:OD1	17:Q:90:ASP:N	2.24	0.70
6:D:41:LYS:NZ	6:D:44:TYR:O	2.23	0.70
24:X:85:GLN:OE1	24:X:115:ARG:NH2	2.23	0.70
50:1:2527:G:H2'	50:1:2528:G:C8	2.25	0.70
50:1:955:U:O4	50:1:966:U:N3	2.15	0.70
6:D:216:GLU:HA	6:D:219:PHE:HB3	1.73	0.70
52:3:81:U:O2	52:3:99:G:O6	2.10	0.70
11:J:165:GLN:HG3	11:J:166:LYS:H	1.56	0.70
45:v:182:ILE:HD12	45:v:203:VAL:HG12	1.74	0.70
50:1:1001:G:O6	50:1:1050:U:C2	2.44	0.70
50:1:1222:G:H1'	50:1:1286:A:H61	1.56	0.70
50:1:2689:A:O2'	50:1:2691:A:N6	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:258:LYS:NZ	52:3:120:C:OP2	2.24	0.70
50:1:2444:C:N4	50:1:2503:G:N3	2.40	0.70
20:T:92:ARG:HG3	46:w:177:ARG:HH22	1.57	0.70
31:f:19:SER:OG	50:1:1330:A:OP1	2.09	0.70
43:t:101:LEU:HD12	43:t:132:LYS:HG3	1.74	0.70
48:y:121:ILE:O	48:y:139:ARG:NH2	2.25	0.70
12:K:215:LYS:HD3	12:K:216:GLU:H	1.56	0.69
23:W:133:LEU:HD22	23:W:203:LEU:HD13	1.74	0.69
27:b:268:VAL:HG23	27:b:309:VAL:HG23	1.73	0.69
50:1:1567:U:H4'	50:1:1568:U:H5'	1.72	0.69
48:y:185:THR:OG1	48:y:214:GLU:OE2	2.10	0.69
4:B:92:TYR:HB2	4:B:157:VAL:HG22	1.75	0.69
50:1:2232:A:N3	50:1:2428:U:O2'	2.23	0.69
3:A:137:ILE:HD11	3:A:147:ARG:HD3	1.75	0.69
14:N:4:TYR:OH	50:1:148:G:OP2	2.08	0.69
2:a:74:ASN:HD21	50:1:705:A:H62	1.39	0.69
29:d:57:GLN:NE2	50:1:1474:A:O2'	2.25	0.69
40:p:46:THR:OG1	40:p:57:CYS:SG	2.49	0.69
50:1:2969:A:O2'	50:1:2970:C:O5'	2.10	0.69
38:n:172:LYS:HE3	38:n:264:LEU:HD13	1.74	0.69
9:G:100:GLU:HG3	9:G:104:GLU:HB2	1.73	0.69
47:x:494:TRP:HD1	47:x:495:SER:H	1.41	0.69
50:1:972:A:H2'	50:1:973:A:H8	1.57	0.69
47:x:57:GLU:HA	47:x:60:LEU:HD12	1.75	0.69
40:p:17:ARG:NH1	50:1:860:G:OP1	2.26	0.69
50:1:1001:G:O6	50:1:1050:U:O2	2.10	0.69
50:1:2929:C:O2'	50:1:2930:A:O5'	2.10	0.69
11:J:36:VAL:HG23	11:J:125:MET:HE1	1.75	0.68
9:G:98:ARG:NH2	9:G:188:THR:O	2.27	0.68
43:t:297:ARG:O	43:t:300:GLN:NE2	2.25	0.68
45:v:28:LYS:NZ	46:w:102:GLU:OE2	2.25	0.68
46:w:15:LYS:HE2	46:w:19:VAL:HG13	1.74	0.68
21:U:29:ASP:N	21:U:29:ASP:OD1	2.27	0.68
45:v:44:ASP:HB3	45:v:124:LEU:HD21	1.73	0.68
50:1:2761:G:H1	50:1:2799:A:H2	1.40	0.68
31:f:56:SER:O	31:f:63:LYS:NZ	2.26	0.68
50:1:2876:C:H1'	50:1:2877:G:H5'	1.76	0.68
18:R:62:ARG:NH1	50:1:3068:U:OP2	2.20	0.68
23:W:220:TYR:HD2	23:W:229:GLU:HB3	1.58	0.68
5:C:98:ARG:NH2	50:1:804:C:OP1	2.27	0.68
6:D:158:ARG:NH1	52:3:47:C:OP2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:70:ARG:NH1	53:6:2:C:O2	2.26	0.68
4:B:210:GLU:OE2	49:z:32:ARG:NH2	2.26	0.68
18:R:103:ARG:NH1	50:1:1722:U:OP2	2.27	0.68
33:h:31:LEU:HD21	33:h:43:LYS:HD3	1.76	0.68
40:p:44:LYS:NZ	40:p:59:CYS:SG	2.62	0.68
50:1:1187:C:H5	50:1:1319:G:H1	1.42	0.68
17:Q:79:LYS:NZ	50:1:729:C:O2'	2.28	0.67
37:m:50:ASN:HB3	37:m:56:ILE:HD11	1.76	0.67
42:r:230:MET:HE1	42:r:241:LYS:HD3	1.76	0.67
4:B:284:ARG:NH1	4:B:293:ASN:O	2.27	0.67
37:m:7:GLU:OE1	37:m:10:ARG:NH2	2.27	0.67
50:1:925:A:N6	50:1:2412:G:O2'	2.27	0.67
50:1:971:G:N1	50:1:1111:U:N3	2.42	0.67
5:C:8:VAL:HG23	5:C:151:VAL:HG12	1.76	0.67
6:D:68:THR:HG23	6:D:71:GLY:H	1.60	0.67
29:d:13:THR:OG1	29:d:72:ARG:NH1	2.28	0.67
48:y:106:ASN:HB3	48:y:147:LEU:HD23	1.76	0.67
50:1:2138:A:H3'	50:1:2139:A:H3'	1.77	0.67
41:q:200:ALA:O	41:q:202:VAL:N	2.27	0.67
48:y:163:PRO:HG3	48:y:185:THR:HG22	1.76	0.67
50:1:2761:G:OP2	50:1:2762:A:N6	2.27	0.67
35:j:2:GLY:N	50:1:2139:A:N7	2.42	0.67
37:m:8:LYS:O	37:m:12:ILE:HG12	1.95	0.67
16:P:116:HIS:HB3	16:P:149:VAL:HB	1.77	0.67
37:m:109:ARG:NH2	50:1:2731:U:OP2	2.27	0.67
45:v:103:ILE:HG12	45:v:113:MET:HG2	1.76	0.67
25:Y:110:HIS:CE1	51:2:83:C:H42	2.12	0.67
35:j:21:ARG:NH2	35:j:41:ALA:O	2.28	0.67
37:m:148:LYS:NZ	50:1:1242:G:N7	2.42	0.67
27:b:368:ALA:O	27:b:370:ASP:N	2.27	0.67
50:1:3340:G:O2'	50:1:3341:U:O4'	2.12	0.67
6:D:200:PHE:HB3	6:D:237:GLU:HG3	1.76	0.66
12:K:256:PRO:HA	12:K:259:PHE:HB2	1.77	0.66
23:W:67:MET:HG2	23:W:101:GLY:H	1.60	0.66
50:1:708:G:N2	50:1:711:A:OP2	2.26	0.66
13:M:124:ARG:NH2	50:1:3212:C:OP2	2.28	0.66
18:R:105:LEU:HD23	18:R:138:LEU:HD23	1.78	0.66
32:g:96:GLU:OE1	50:1:2555:G:N1	2.26	0.66
9:G:217:THR:O	9:G:221:ASN:ND2	2.24	0.66
37:m:373:PRO:HG2	50:1:2867:C:H2'	1.77	0.66
50:1:3042:U:OP2	50:1:3092:C:N4	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:174:ARG:NH1	50:1:712:G:OP1	2.29	0.66
26:Z:52:LYS:O	26:Z:65:ARG:NH1	2.28	0.66
41:q:204:PRO:HD2	41:q:207:LEU:HD12	1.77	0.66
2:a:58:MET:HE1	50:1:2775:U:H1'	1.76	0.66
14:N:124:ASP:OD2	14:N:125:SER:N	2.29	0.66
27:b:177:ASN:ND2	27:b:197:TYR:O	2.29	0.66
28:c:26:GLY:O	28:c:30:THR:OG1	2.14	0.66
45:v:151:HIS:HB3	45:v:154:TYR:HB2	1.78	0.66
50:1:2877:G:H1'	50:1:2878:G:H5''	1.78	0.66
37:m:340:VAL:HG13	50:1:2961:G:H5''	1.76	0.66
43:t:167:ARG:HE	43:t:270:PRO:HG3	1.61	0.66
47:x:174:ASP:OD1	47:x:500:ARG:NH2	2.29	0.66
50:1:924:G:N7	50:1:2810:C:O2'	2.24	0.66
17:Q:133:LYS:HB2	17:Q:135:GLN:HE21	1.60	0.66
23:W:52:VAL:HG11	23:W:213:PHE:HE2	1.59	0.66
27:b:500:GLN:NE2	50:1:1683:A:O2'	2.27	0.66
46:w:25:ASN:ND2	46:w:97:THR:OG1	2.28	0.66
4:B:129:ALA:O	50:1:3149:G:O2'	2.13	0.65
28:c:44:ILE:HG22	28:c:48:THR:HG21	1.77	0.65
50:1:1482:A:N6	50:1:1866:C:O2'	2.29	0.65
50:1:972:A:H2'	50:1:973:A:C8	2.30	0.65
52:3:82:G:H1	52:3:98:C:H41	1.42	0.65
38:n:367:VAL:HG22	38:n:389:SER:HA	1.79	0.65
42:r:7:ILE:H	50:1:2898:G:N2	1.94	0.65
6:D:226:TYR:HA	6:D:231:ILE:HD12	1.77	0.65
38:n:243:ILE:HD11	38:n:265:GLU:HG3	1.76	0.65
8:F:159:GLN:O	50:1:1362:G:H4'	1.96	0.65
10:H:48:VAL:HG23	10:H:49:ASN:H	1.62	0.65
27:b:99:SER:OG	50:1:2865:U:O4	2.15	0.65
52:3:75:G:N2	52:3:104:A:OP2	2.29	0.65
14:N:50:ARG:NH1	50:1:268:A:OP1	2.29	0.65
1:L:185:LYS:HG3	1:L:188:ARG:HH21	1.61	0.65
4:B:39:LYS:NZ	49:z:27:ASP:OD2	2.30	0.65
16:P:62:ARG:NH1	50:1:412:G:OP1	2.30	0.65
38:n:432:ILE:O	38:n:436:ILE:HG12	1.97	0.65
50:1:1084:A:H2'	50:1:1085:A:C8	2.32	0.65
6:D:58:LYS:NZ	52:3:49:G:O2'	2.29	0.65
27:b:268:VAL:HG11	27:b:305:LEU:HD22	1.79	0.65
46:w:17:ILE:O	46:w:32:ASN:ND2	2.30	0.65
13:M:37:GLU:OE2	13:M:74:ARG:NH1	2.30	0.65
50:1:3164:C:HO2'	50:1:3165:A:H8	1.46	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:24:ARG:NH2	52:3:13:A:O2'	2.30	0.64
27:b:250:VAL:HB	27:b:283:VAL:HG22	1.79	0.64
46:w:55:ARG:NH2	46:w:59:GLN:OE1	2.29	0.64
53:6:36:U:H2'	53:6:37:C:C6	2.32	0.64
18:R:62:ARG:NH2	50:1:3070:A:OP1	2.31	0.64
50:1:2427:U:H3	50:1:2602:G:H1	1.44	0.64
3:A:117:GLU:OE1	3:A:163:ARG:NH2	2.31	0.64
38:n:58:ALA:O	38:n:60:THR:OG1	2.15	0.64
50:1:845:G:H22	50:1:847:A:H3'	1.63	0.64
50:1:954:U:OP2	50:1:1116:G:O2'	2.16	0.64
50:1:1290:A:H2'	50:1:1291:A:C8	2.32	0.64
50:1:2626:A:OP2	50:1:2644:C:N4	2.30	0.64
6:D:184:ASP:HB3	6:D:186:GLU:HG2	1.80	0.64
23:W:131:ALA:HB1	23:W:133:LEU:HD13	1.80	0.64
50:1:2399:A:H2'	50:1:2400:G:O4'	1.96	0.64
16:P:16:SER:HB3	16:P:149:VAL:HG22	1.78	0.64
17:Q:99:THR:OG1	17:Q:100:THR:N	2.30	0.64
29:d:80:ASN:ND2	29:d:84:ASP:OD1	2.30	0.64
42:r:2:PRO:HA	42:r:6:TYR:CD2	2.32	0.64
45:v:89:LEU:HB3	45:v:101:THR:HB	1.80	0.64
30:e:6:HIS:ND1	30:e:7:PRO:O	2.29	0.64
38:n:428:GLN:HG2	38:n:429:PRO:HD2	1.79	0.64
50:1:2148:U:H2'	50:1:2149:A:C8	2.33	0.64
47:x:301:VAL:HG21	47:x:376:THR:HG21	1.80	0.64
50:1:1238:C:N3	50:1:1251:A:N6	2.44	0.64
50:1:2203:U:O2	50:1:2239:G:O6	2.16	0.64
6:D:148:ILE:HG12	6:D:151:GLN:HB3	1.79	0.63
6:D:235:SER:O	6:D:239:ILE:HG13	1.98	0.63
12:K:86:LYS:NZ	12:K:297:VAL:O	2.28	0.63
46:w:197:ARG:NH2	50:1:2796:G:O4'	2.32	0.63
6:D:28:THR:OG1	52:3:7:G:OP2	2.16	0.63
32:g:20:ILE:HD12	32:g:32:ALA:HB1	1.81	0.63
42:r:183:ASN:ND2	50:1:2857:C:O2	2.24	0.63
46:w:22:ASP:OD2	46:w:25:ASN:ND2	2.30	0.63
22:V:112:SER:O	22:V:132:ASN:ND2	2.30	0.63
43:t:132:LYS:NZ	53:6:8:A:OP1	2.28	0.63
43:t:139:PRO:HB3	43:t:180:THR:HG22	1.80	0.63
50:1:1899:G:O2'	50:1:2334:U:O4	2.15	0.63
50:1:2615:G:N1	50:1:2619:G:OP1	2.30	0.63
52:3:16:U:H2'	52:3:17:A:C8	2.32	0.63
10:H:168:ARG:NH1	50:1:2894:C:OP2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:350:THR:OG1	54:m:501:GTP:O3G	2.17	0.63
12:K:110:TRP:O	12:K:114:SER:OG	2.15	0.63
35:j:72:ARG:NH1	51:2:95:G:OP2	2.31	0.63
50:1:806:A:N6	50:1:937:G:O6	2.23	0.63
50:1:1281:G:H2'	50:1:1282:G:H8	1.64	0.63
5:C:286:VAL:HG11	17:Q:31:LYS:HE2	1.79	0.63
50:1:1646:G:O2'	50:1:1808:G:N2	2.31	0.63
29:d:10:ARG:NH1	29:d:12:TYR:OH	2.31	0.63
41:q:249:GLU:HG3	43:t:19:LEU:HD11	1.79	0.63
53:6:38:U:O2	53:6:42:G:N2	2.31	0.63
39:o:130:ASN:ND2	53:6:27:G:OP1	2.32	0.63
47:x:252:ALA:HB1	47:x:260:ILE:HD11	1.80	0.63
27:b:355:ASN:HA	27:b:358:LEU:HD23	1.81	0.63
39:o:117:LEU:HA	39:o:139:PHE:HA	1.80	0.63
50:1:2364:G:H1	50:1:2396:G:H21	1.44	0.63
50:1:2997:G:H1'	50:1:3396:U:H5'	1.80	0.63
27:b:249:CYS:SG	27:b:339:LEU:HB2	2.39	0.62
11:J:30:LEU:HD22	11:J:64:LYS:HE2	1.80	0.62
12:K:157:GLY:HA2	12:K:160:LEU:HD12	1.81	0.62
45:v:81:LYS:O	50:1:2698:G:N2	2.26	0.62
5:C:118:LYS:NZ	50:1:681:U:O4	2.28	0.62
39:o:158:MET:O	39:o:160:HIS:N	2.30	0.62
47:x:79:PHE:HD2	47:x:119:LEU:HD21	1.65	0.62
50:1:2608:G:H2'	50:1:2609:A:H8	1.64	0.62
4:B:238:LEU:HB2	4:B:246:LEU:HA	1.81	0.62
8:F:48:ASN:ND2	8:F:182:ASP:OD2	2.30	0.62
52:3:107:C:H2'	52:3:108:A:H8	1.64	0.62
33:h:27:GLU:OE2	33:h:43:LYS:NZ	2.32	0.62
37:m:289:SER:O	37:m:334:THR:OG1	2.14	0.62
41:q:434:PRO:O	41:q:436:ARG:NH1	2.32	0.62
44:u:78:PRO:HG3	48:y:81:LEU:HG	1.80	0.62
16:P:132:ALA:HB2	50:1:880:G:H5''	1.82	0.62
47:x:328:LEU:HD23	47:x:374:MET:HG3	1.81	0.62
53:6:41:G:N1	53:6:42:G:N3	2.47	0.62
6:D:39:GLN:N	6:D:41:LYS:HG2	2.14	0.62
30:e:105:ARG:NH2	50:1:1412:G:OP1	2.32	0.62
45:v:154:TYR:HE1	45:v:186:ILE:HG12	1.65	0.62
52:3:67:G:O6	52:3:111:U:O4	2.18	0.62
31:f:5:HIS:NE2	50:1:3219:G:O6	2.33	0.62
38:n:249:ASP:HB2	38:n:252:LYS:HD2	1.81	0.62
38:n:369:ARG:HE	38:n:390:GLU:HG2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:w:133:ILE:HG22	46:w:134:TYR:H	1.64	0.62
50:1:2222:A:H2'	50:1:2223:A:C8	2.35	0.62
39:o:128:THR:HG22	39:o:181:LYS:HG2	1.82	0.62
50:1:1329:U:O2'	50:1:1330:A:OP1	2.16	0.62
43:t:64:LYS:O	43:t:68:THR:OG1	2.15	0.61
12:K:36:ARG:HA	12:K:39:LYS:HG2	1.82	0.61
39:o:89:TYR:HA	39:o:168:PRO:HA	1.82	0.61
43:t:246:CYS:O	43:t:248:GLU:N	2.33	0.61
50:1:1551:C:HO2'	50:1:2170:U:HO2'	1.48	0.61
5:C:307:GLN:HE22	50:1:1346:G:H1'	1.65	0.61
38:n:369:ARG:NE	38:n:390:GLU:HG2	2.14	0.61
27:b:178:VAL:HG13	27:b:255:ASP:HB2	1.80	0.61
43:t:84:LYS:NZ	43:t:89:GLU:OE2	2.32	0.61
23:W:121:ARG:O	23:W:213:PHE:N	2.33	0.61
24:X:127:THR:HG22	24:X:128:ALA:H	1.64	0.61
25:Y:119:ILE:HG22	25:Y:124:GLY:HA3	1.81	0.61
37:m:413:GLU:HG2	37:m:418:ILE:HG22	1.83	0.61
11:J:59:ILE:HA	11:J:63:GLU:HG3	1.83	0.61
23:W:130:LYS:HB2	23:W:192:GLY:HA2	1.80	0.61
40:p:2:ALA:HB2	50:1:852:U:H5	1.66	0.61
45:v:46:MET:HB2	45:v:90:MET:HE2	1.82	0.61
47:x:365:LYS:HE2	47:x:368:GLY:HA2	1.81	0.61
48:y:222:PHE:HB3	48:y:224:LEU:HD23	1.83	0.61
3:A:97:ASN:HB2	3:A:100:ASN:HD21	1.65	0.61
5:C:317:PRO:C	5:C:319:LYS:H	2.09	0.61
50:1:1001:G:O6	50:1:1051:U:O4	2.18	0.61
50:1:2246:G:N2	50:1:2246:G:OP2	2.29	0.61
51:2:103:G:OP2	51:2:105:A:O2'	2.17	0.61
6:D:173:VAL:O	6:D:175:HIS:ND1	2.33	0.61
6:D:224:LYS:HD3	52:3:50:U:H4'	1.83	0.61
27:b:264:ILE:HG22	27:b:302:ARG:NH1	2.15	0.61
42:r:22:GLU:OE2	42:r:25:ARG:NH2	2.34	0.61
46:w:152:LYS:HD2	50:1:2625:C:H41	1.66	0.61
51:2:8:C:H2'	51:2:9:A:C8	2.30	0.61
52:3:82:G:H22	52:3:98:C:H5	1.47	0.61
12:K:108:LYS:HG2	12:K:109:PRO:HD3	1.82	0.61
37:m:119:GLU:O	37:m:120:GLU:HG2	2.01	0.61
37:m:239:CYS:HB2	37:m:372:PRO:HG2	1.83	0.61
43:t:284:ASN:ND2	50:1:1571:A:OP2	2.33	0.61
50:1:1222:G:H1'	50:1:1286:A:N6	2.16	0.61
16:P:155:GLU:N	16:P:155:GLU:OE1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:26:VAL:O	26:Z:93:LYS:NZ	2.34	0.61
31:f:49:ILE:HD11	31:f:71:VAL:HG22	1.83	0.61
41:q:200:ALA:HB2	51:2:120:C:H5''	1.81	0.61
48:y:215:LEU:HD23	48:y:218:ILE:HD11	1.83	0.61
50:1:1246:G:O2'	50:1:1264:G:OP2	2.17	0.61
50:1:2357:A:H2'	50:1:2358:A:H8	1.66	0.61
4:B:236:LYS:NZ	50:1:2340:U:OP1	2.34	0.60
19:S:109:ASP:OD2	19:S:113:ARG:NH1	2.32	0.60
38:n:108:ASN:N	38:n:108:ASN:OD1	2.34	0.60
10:H:20:ILE:HG12	10:H:25:VAL:HG22	1.83	0.60
10:H:72:LYS:NZ	10:H:76:ASP:OD2	2.33	0.60
5:C:99:MET:HE3	5:C:102:PRO:HA	1.83	0.60
24:X:46:TYR:HD2	33:h:75:TYR:HB3	1.65	0.60
50:1:1105:A:H2'	50:1:1106:G:C8	2.37	0.60
8:F:190:THR:O	8:F:190:THR:OG1	2.20	0.60
9:G:124:ASP:OD1	50:1:120:G:N2	2.35	0.60
52:3:112:G:H2'	52:3:113:C:C6	2.36	0.60
8:F:25:GLN:NE2	8:F:29:GLU:OE2	2.34	0.60
25:Y:74:TYR:OH	51:2:75:G:OP2	2.19	0.60
38:n:366:TYR:HD1	38:n:388:ILE:HG23	1.65	0.60
50:1:996:A:O2'	50:1:998:A:OP2	2.18	0.60
34:i:68:ARG:NH2	50:1:2218:G:OP1	2.35	0.60
38:n:96:ARG:NH1	38:n:98:GLU:OE2	2.32	0.60
42:r:174:PRO:HG2	42:r:177:LEU:HD13	1.83	0.60
47:x:285:LYS:HD2	47:x:328:LEU:HG	1.82	0.60
47:x:387:ASN:HB2	47:x:395:ILE:HD11	1.84	0.60
50:1:763:G:C2	50:1:764:U:H1'	2.36	0.60
50:1:2413:A:H62	50:1:2807:U:H3	1.48	0.60
12:K:271:ILE:HG22	12:K:276:ILE:HD11	1.84	0.60
23:W:14:GLN:O	42:r:72:LYS:NZ	2.24	0.60
44:u:16:GLY:O	50:1:3050:U:O2'	2.18	0.60
50:1:2717:U:HO2'	50:1:2718:U:H6	1.50	0.60
52:3:75:G:O2'	52:3:104:A:N6	2.35	0.60
52:3:78:U:H2'	52:3:79:A:H8	1.65	0.60
7:E:35:VAL:O	7:E:38:THR:OG1	2.18	0.60
37:m:160:LEU:O	37:m:164:THR:HG23	2.02	0.60
41:q:226:SER:HB3	41:q:229:PRO:HB3	1.84	0.60
52:3:52:G:O2'	52:3:53:U:O5'	2.18	0.60
5:C:282:SER:OG	17:Q:125:ASP:OD2	2.19	0.60
6:D:229:ASP:HB3	6:D:231:ILE:HD11	1.84	0.60
10:H:5:GLN:NE2	10:H:7:GLU:OE1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:416:TYR:H	37:m:417:GLU:HA	1.63	0.60
40:p:4:ARG:NH1	50:1:837:A:OP2	2.33	0.60
50:1:2571:U:H1'	50:1:2572:C:H5''	1.84	0.60
1:L:126:PHE:O	33:h:114:ARG:NH2	2.35	0.60
14:N:96:ARG:NH1	14:N:104:GLU:OE1	2.34	0.60
45:v:220:ARG:NH1	45:v:221:ILE:O	2.30	0.60
46:w:132:MET:HG2	46:w:143:PRO:HB3	1.84	0.60
32:g:15:THR:HG22	32:g:16:ARG:H	1.66	0.59
42:r:231:VAL:HG22	42:r:237:VAL:HG12	1.84	0.59
43:t:101:LEU:HD22	43:t:310:ILE:HD12	1.84	0.59
50:1:160:G:H2'	50:1:161:G:H8	1.66	0.59
52:3:78:U:H2'	52:3:79:A:C8	2.37	0.59
41:q:264:HIS:O	41:q:268:THR:OG1	2.13	0.59
45:v:144:GLN:HE21	46:w:57:ASN:HD22	1.50	0.59
50:1:1661:G:H2'	50:1:1662:G:C8	2.37	0.59
2:a:74:ASN:ND2	50:1:705:A:H62	1.99	0.59
6:D:211:LEU:HD21	6:D:218:ARG:HB2	1.83	0.59
9:G:90:THR:HA	9:G:214:LEU:HD21	1.84	0.59
12:K:293:TYR:CZ	39:o:200:MET:HG2	2.37	0.59
27:b:298:LEU:HD22	27:b:302:ARG:HG2	1.83	0.59
37:m:155:SER:O	37:m:156:ASN:ND2	2.35	0.59
47:x:130:LYS:HG3	47:x:515:HIS:HB2	1.84	0.59
47:x:301:VAL:HG11	47:x:374:MET:HE1	1.83	0.59
49:z:4:SER:OG	49:z:5:LEU:N	2.34	0.59
1:L:129:ASN:OD1	1:L:129:ASN:N	2.33	0.59
14:N:192:LYS:O	14:N:196:THR:OG1	2.15	0.59
33:h:26:LYS:O	33:h:30:GLU:HG3	2.01	0.59
33:h:31:LEU:HD11	33:h:43:LYS:HZ2	1.67	0.59
43:t:103:ILE:HG12	43:t:130:ARG:HG2	1.83	0.59
12:K:44:LEU:HD23	12:K:283:THR:HG23	1.83	0.59
48:y:234:GLY:HA2	48:y:237:ARG:NE	2.18	0.59
1:L:28:GLN:HB3	14:N:201:ARG:HH11	1.67	0.59
11:J:155:THR:OG1	11:J:156:LYS:N	2.32	0.59
23:W:1:MET:HE2	50:1:3115:C:H5'	1.83	0.59
38:n:28:SER:OG	38:n:31:ASP:OD2	2.20	0.59
43:t:28:ARG:O	43:t:32:GLU:HG2	2.01	0.59
50:1:627:U:H4'	50:1:1399:A:H1'	1.84	0.59
50:1:2639:G:H2'	50:1:2640:A:C8	2.37	0.59
52:3:88:G:H2'	52:3:89:G:C8	2.38	0.59
7:E:51:ARG:NH1	13:M:114:ASP:OD2	2.35	0.59
12:K:254:LEU:HD21	12:K:258:GLU:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:148:ARG:NH2	53:6:230:A:O2'	2.36	0.59
47:x:37:GLN:HA	47:x:43:ASP:HA	1.84	0.59
47:x:135:SER:OG	47:x:136:SER:O	2.20	0.59
47:x:296:SER:OG	47:x:297:HIS:N	2.36	0.59
50:1:158:G:H2'	50:1:159:A:H8	1.67	0.59
38:n:179:VAL:HG21	38:n:379:LEU:HD11	1.84	0.59
42:r:164:ARG:HD2	42:r:165:PRO:HD2	1.84	0.59
50:1:253:A:H2'	50:1:254:A:C8	2.38	0.59
50:1:807:A:H5'	50:1:2812:C:H4'	1.84	0.59
52:3:16:U:H2'	52:3:17:A:H8	1.68	0.59
6:D:43:LYS:HG3	6:D:44:TYR:H	1.67	0.59
11:J:17:LEU:HD13	11:J:129:VAL:HG22	1.84	0.59
26:Z:123:GLN:OE1	41:q:258:TYR:OH	2.20	0.59
37:m:418:ILE:HG21	37:m:421:TRP:CZ3	2.37	0.59
50:1:1:G:O5'	53:6:232:A:O2'	2.21	0.59
53:6:8:A:H2'	53:6:9:A:C8	2.37	0.58
11:J:32:ARG:HA	11:J:35:LYS:HE3	1.85	0.58
50:1:885:U:H2'	50:1:886:C:C6	2.39	0.58
50:1:1940:G:H21	50:1:3362:A:H8	1.51	0.58
50:1:2198:A:H2'	50:1:2199:G:C8	2.38	0.58
7:E:69:PHE:HB2	7:E:138:GLN:HE21	1.68	0.58
10:H:188:THR:O	10:H:188:THR:OG1	2.18	0.58
12:K:288:VAL:HG13	53:6:34:A:H4'	1.85	0.58
27:b:205:TYR:OH	42:r:9:ARG:NH2	2.35	0.58
45:v:28:LYS:NZ	45:v:163:ASP:OD2	2.32	0.58
50:1:2627:C:H2'	50:1:2651:G:H22	1.68	0.58
2:a:58:MET:HE3	50:1:2786:G:H21	1.68	0.58
9:G:144:GLU:OE2	14:N:6:TYR:OH	2.21	0.58
5:C:59:GLN:NE2	50:1:353:G:O6	2.36	0.58
38:n:27:VAL:HG23	38:n:28:SER:H	1.67	0.58
43:t:199:PRO:HG2	43:t:204:ILE:HD11	1.84	0.58
50:1:1103:A:H3'	50:1:1104:G:C2	2.39	0.58
50:1:2628:A:N6	50:1:2650:U:O2	2.37	0.58
50:1:2954:U:H1'	50:1:2955:U:H5''	1.84	0.58
1:L:75:PHE:O	1:L:76:THR:OG1	2.17	0.58
50:1:94:G:H3'	50:1:94:G:N3	2.19	0.58
50:1:600:G:N2	50:1:603:A:OP2	2.29	0.58
50:1:2969:A:O2'	50:1:2970:C:O4'	2.22	0.58
1:L:170:LEU:HB3	34:i:9:ILE:HD11	1.85	0.58
5:C:193:LYS:NZ	51:2:21:C:OP1	2.28	0.58
8:F:140:SER:OG	8:F:141:TYR:N	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:450:VAL:HG12	47:x:461:SER:HB3	1.86	0.58
50:1:3222:U:O4	50:1:3263:G:O6	2.22	0.58
9:G:137:ASN:HD22	14:N:3:ALA:H	1.51	0.58
12:K:217:PHE:HD1	12:K:218:SER:H	1.51	0.58
24:X:105:VAL:HG11	24:X:135:ILE:HD13	1.86	0.58
28:c:73:GLY:N	28:c:76:GLU:OE1	2.37	0.58
47:x:165:ASP:OD1	47:x:166:ASN:N	2.34	0.58
50:1:2528:G:C6	50:1:2529:A:C4	2.92	0.58
22:V:73:VAL:O	37:m:194:TRP:HB2	2.04	0.58
42:r:6:TYR:N	50:1:2898:G:H22	2.02	0.58
50:1:2609:A:H2'	50:1:2610:G:C8	2.39	0.58
50:1:3169:U:H3	50:1:3281:U:H3	1.52	0.58
50:1:3357:U:H2'	50:1:3358:U:H6	1.69	0.58
8:F:90:LYS:HG3	8:F:91:GLY:H	1.69	0.58
20:T:39:ILE:O	20:T:99:SER:OG	2.21	0.58
24:X:4:SER:O	24:X:7:ALA:N	2.33	0.58
27:b:188:THR:HG22	27:b:209:PHE:HB3	1.86	0.58
42:r:138:LYS:HA	42:r:146:SER:HA	1.86	0.58
50:1:845:G:N2	50:1:847:A:H3'	2.19	0.58
50:1:1240:A:N6	50:1:1241:U:O4	2.37	0.58
4:B:163:HIS:ND1	4:B:164:THR:O	2.35	0.57
11:J:141:ARG:HH21	11:J:144:CYS:HB2	1.69	0.57
23:W:34:LEU:HG	23:W:104:PHE:CZ	2.39	0.57
52:3:59:U:H2'	52:3:60:G:C8	2.39	0.57
4:B:187:SER:O	4:B:190:GLU:N	2.37	0.57
23:W:42:VAL:O	23:W:217:VAL:HG23	2.04	0.57
29:d:80:ASN:OD1	29:d:81:GLU:N	2.37	0.57
38:n:371:VAL:HB	38:n:376:LEU:HD12	1.84	0.57
51:2:83:C:H4'	51:2:85:G:H5''	1.86	0.57
5:C:92:ASN:HD21	50:1:803:C:H4'	1.68	0.57
19:S:132:THR:HG22	19:S:133:ALA:H	1.69	0.57
22:V:81:GLN:O	22:V:98:ASN:ND2	2.36	0.57
26:Z:107:ARG:NH1	50:1:1634:G:OP1	2.37	0.57
35:j:6:PRO:HD3	50:1:884:A:H3'	1.85	0.57
42:r:2:PRO:O	42:r:3:GLN:HG2	2.05	0.57
43:t:235:VAL:HG21	43:t:247:VAL:HG12	1.86	0.57
50:1:2815:G:H2'	50:1:2816:G:H5''	1.86	0.57
52:3:75:G:H1'	52:3:104:A:N6	2.19	0.57
12:K:166:ALA:HA	53:6:53:A:C2	2.38	0.57
19:S:84:ARG:HH21	19:S:115:ARG:HB3	1.70	0.57
43:t:82:GLU:HG2	43:t:185:PRO:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:494:TRP:CD1	47:x:495:SER:H	2.22	0.57
50:1:3:U:H1'	53:6:232:A:C8	2.39	0.57
50:1:2534:G:H1	50:1:2546:C:H42	1.50	0.57
50:1:3165:A:H2'	50:1:3166:C:H6	1.68	0.57
50:1:3169:U:H2'	50:1:3170:A:C8	2.39	0.57
8:F:138:TYR:CE2	8:F:233:GLU:HG2	2.39	0.57
25:Y:24:SER:OG	25:Y:75:ARG:NH1	2.37	0.57
38:n:177:ARG:HE	38:n:191:ASN:HD21	1.51	0.57
46:w:84:SER:OG	46:w:85:SER:N	2.37	0.57
47:x:209:THR:OG1	47:x:210:ILE:N	2.38	0.57
48:y:233:SER:O	48:y:237:ARG:HG2	2.04	0.57
38:n:57:THR:O	50:1:1810:A:O2'	2.22	0.57
50:1:3277:U:OP2	50:1:3278:C:N4	2.37	0.57
52:3:70:U:H2'	52:3:71:G:C8	2.39	0.57
52:3:107:C:H2'	52:3:108:A:C8	2.40	0.57
6:D:34:LYS:HA	6:D:37:VAL:HG12	1.85	0.57
20:T:65:TYR:HB3	20:T:75:ILE:HD11	1.85	0.57
31:f:15:SER:OG	31:f:16:TYR:N	2.36	0.57
43:t:318:LEU:O	43:t:322:ASN:HB3	2.04	0.57
50:1:1288:U:H2'	50:1:1289:G:H8	1.68	0.57
50:1:2809:C:C5	50:1:2810:C:H1'	2.39	0.57
6:D:153:THR:O	6:D:153:THR:OG1	2.23	0.57
10:H:92:TYR:HB3	10:H:179:ILE:HG12	1.87	0.57
43:t:143:PHE:HE2	43:t:318:LEU:HD21	1.69	0.57
47:x:417:ILE:HG13	47:x:431:GLY:HA2	1.87	0.57
50:1:2527:G:C2	50:1:2528:G:O6	2.58	0.57
14:N:14:LYS:HE2	50:1:269:G:H5''	1.87	0.57
14:N:187:ARG:HA	14:N:190:THR:HG22	1.87	0.57
45:v:37:SER:OG	45:v:92:SER:O	2.15	0.57
45:v:108:TYR:O	45:v:109:LYS:NZ	2.33	0.57
45:v:123:LYS:HZ1	45:v:229:ARG:HH11	1.53	0.57
45:v:188:GLY:HA3	46:w:36:LYS:HD2	1.86	0.57
50:1:1252:A:H2'	50:1:1253:U:O4'	2.04	0.57
50:1:3395:G:N2	50:1:3396:U:O4	2.35	0.57
47:x:76:PRO:HD2	47:x:126:VAL:HG21	1.87	0.57
47:x:250:ARG:HG2	47:x:264:ASP:HA	1.86	0.57
50:1:2137:U:O4	50:1:2142:A:H5'	2.05	0.57
12:K:265:LEU:HD12	12:K:266:ILE:HG13	1.87	0.56
39:o:205:GLU:HB3	39:o:209:LYS:NZ	2.20	0.56
42:r:236:LYS:O	42:r:237:VAL:HG13	2.05	0.56
44:u:32:CYS:SG	44:u:33:ARG:NH2	2.78	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:2227:C:H2'	50:1:2228:A:H8	1.69	0.56
50:1:2370:G:H5'	50:1:2371:G:H5'	1.87	0.56
50:1:2872:A:O2'	50:1:2874:G:N2	2.38	0.56
24:X:107:VAL:HG13	24:X:124:VAL:HG13	1.85	0.56
27:b:289:LYS:HB3	27:b:292:ILE:HD11	1.87	0.56
27:b:398:LEU:O	27:b:400:ARG:N	2.38	0.56
37:m:83:VAL:HG22	42:r:236:LYS:HB2	1.87	0.56
37:m:84:ILE:HG23	42:r:237:VAL:HG23	1.87	0.56
46:w:83:GLN:HB2	46:w:87:MET:HB2	1.88	0.56
3:A:9:ARG:NH1	50:1:912:G:OP2	2.37	0.56
4:B:296:THR:OG1	4:B:297:SER:N	2.34	0.56
27:b:478:TYR:HB3	27:b:481:PHE:HD1	1.70	0.56
27:b:511:LYS:HG3	27:b:512:SER:H	1.69	0.56
43:t:203:SER:HB3	43:t:318:LEU:HD12	1.86	0.56
43:t:211:ARG:NH2	43:t:272:LYS:O	2.38	0.56
46:w:76:SER:OG	46:w:77:VAL:N	2.39	0.56
53:6:17:G:H2'	53:6:18:U:C6	2.40	0.56
53:6:56:U:H4'	53:6:57:U:H5'	1.86	0.56
27:b:211:TYR:OH	27:b:337:GLU:OE1	2.23	0.56
48:y:101:LEU:HD23	48:y:101:LEU:H	1.70	0.56
50:1:19:U:H2'	50:1:20:A:C8	2.41	0.56
50:1:1696:A:H2'	50:1:1697:A:C8	2.40	0.56
50:1:2223:A:H2'	50:1:2224:A:C8	2.40	0.56
12:K:81:ILE:O	12:K:245:ASN:HA	2.05	0.56
18:R:23:TRP:HB3	18:R:51:VAL:HG23	1.87	0.56
19:S:73:LYS:NZ	19:S:97:VAL:O	2.31	0.56
38:n:15:PHE:HB3	38:n:62:PHE:HB3	1.86	0.56
47:x:232:ILE:HD13	47:x:255:SER:HB2	1.87	0.56
50:1:533:A:O2'	50:1:535:G:OP2	2.21	0.56
50:1:551:A:O2'	50:1:552:G:O5'	2.22	0.56
50:1:2951:G:H2'	50:1:2951:G:N3	2.20	0.56
9:G:189:LEU:HD12	9:G:190:VAL:HG23	1.88	0.56
35:j:72:ARG:O	35:j:76:ASN:ND2	2.39	0.56
37:m:218:VAL:O	37:m:222:SER:HB3	2.06	0.56
47:x:449:GLN:NE2	47:x:491:THR:HA	2.20	0.56
52:3:61:G:H2'	52:3:62:U:C6	2.40	0.56
6:D:36:LEU:HD13	6:D:50:ARG:HD2	1.87	0.56
11:J:53:THR:HG22	11:J:60:ARG:HA	1.88	0.56
38:n:211:SER:O	38:n:211:SER:OG	2.18	0.56
50:1:1047:A:H1'	50:1:1048:A:N7	2.21	0.56
50:1:2767:U:H2'	50:1:2768:U:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:66:ALA:HB2	50:1:2681:U:H4'	1.88	0.56
11:J:106:ILE:HG13	11:J:127:PHE:HE2	1.71	0.56
12:K:213:ALA:HB2	12:K:221:THR:HG21	1.87	0.56
23:W:70:ARG:O	23:W:74:GLN:HG2	2.06	0.56
23:W:177:ALA:O	23:W:179:LYS:N	2.38	0.56
50:1:907:G:OP1	50:1:909:G:O2'	2.20	0.56
50:1:2247:G:N1	50:1:2248:C:O2	2.38	0.56
50:1:2798:C:O2'	50:1:2799:A:O4'	2.23	0.56
53:6:5:C:N4	53:6:24:A:OP2	2.28	0.56
53:6:26:U:H2'	53:6:27:G:C8	2.40	0.56
3:A:69:TYR:OH	50:1:2557:A:OP1	2.22	0.56
23:W:91:GLN:OE1	23:W:91:GLN:N	2.35	0.56
23:W:175:ILE:HG22	23:W:180:ILE:HA	1.86	0.56
50:1:2841:G:H21	50:1:2847:A:H62	1.53	0.56
52:3:70:U:H2'	52:3:71:G:H8	1.69	0.56
1:L:27:ASP:OD1	1:L:27:ASP:N	2.39	0.55
3:A:140:ASN:ND2	3:A:143:GLU:O	2.39	0.55
19:S:101:ALA:O	19:S:105:THR:HG23	2.06	0.55
37:m:250:THR:O	37:m:250:THR:OG1	2.21	0.55
42:r:164:ARG:NH2	50:1:2726:C:O2	2.36	0.55
48:y:68:ARG:HH12	48:y:112:ASP:HB3	1.70	0.55
50:1:1093:A:H1'	50:1:1096:U:O4	2.06	0.55
50:1:2842:U:P	50:1:2844:C:H41	2.29	0.55
52:3:47:C:H2'	52:3:48:U:C6	2.40	0.55
1:L:15:ARG:NH1	1:L:16:LYS:O	2.39	0.55
9:G:145:ASN:H	9:G:146:LYS:HA	1.70	0.55
12:K:290:PRO:HB2	39:o:204:HIS:HE1	1.71	0.55
22:V:67:PRO:HA	22:V:70:ARG:HD3	1.87	0.55
47:x:185:HIS:NE2	47:x:203:THR:OG1	2.39	0.55
47:x:427:LYS:NZ	47:x:439:THR:OG1	2.39	0.55
52:3:24:A:H2'	52:3:25:G:C8	2.42	0.55
6:D:282:ARG:O	6:D:286:VAL:HG23	2.05	0.55
10:H:134:ILE:HG13	10:H:146:LEU:HG	1.87	0.55
28:c:99:ASP:N	28:c:99:ASP:OD1	2.39	0.55
32:g:81:CYS:HB2	32:g:84:CYS:HB2	1.87	0.55
37:m:423:ASP:O	37:m:426:GLU:N	2.34	0.55
50:1:160:G:H2'	50:1:161:G:C8	2.42	0.55
9:G:38:GLN:OE1	9:G:38:GLN:N	2.39	0.55
42:r:7:ILE:H	50:1:2898:G:H22	1.54	0.55
50:1:1202:A:H2'	50:1:1203:A:C2	2.41	0.55
50:1:2206:G:N2	50:1:2207:A:N3	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:2946:A:C2	50:1:2980:U:H3'	2.41	0.55
53:6:231:A:H1'	53:6:232:A:H5'	1.87	0.55
14:N:33:LYS:HD2	14:N:37:HIS:CE1	2.42	0.55
16:P:25:SER:O	16:P:29:THR:OG1	2.22	0.55
37:m:12:ILE:HD13	37:m:17:THR:HG21	1.89	0.55
41:q:452:LYS:NZ	50:1:2585:G:OP1	2.39	0.55
50:1:974:G:N2	50:1:1108:U:O4	2.36	0.55
50:1:2632:G:H2'	50:1:2633:U:C6	2.42	0.55
16:P:120:ASN:N	16:P:120:ASN:OD1	2.38	0.55
41:q:432:ARG:HB2	50:1:1566:A:C2	2.41	0.55
50:1:1464:G:N2	50:1:1467:A:OP2	2.39	0.55
50:1:2529:A:H2'	50:1:2530:G:H8	1.72	0.55
50:1:2531:C:H42	50:1:2547:A:N6	2.05	0.55
50:1:2693:C:H41	50:1:2700:G:H1	1.54	0.55
50:1:3057:U:O2'	50:1:3059:G:OP1	2.24	0.55
10:H:76:ASP:O	10:H:80:THR:HG23	2.06	0.55
27:b:227:ARG:O	27:b:229:THR:N	2.31	0.55
39:o:205:GLU:HB3	39:o:209:LYS:HZ3	1.71	0.55
41:q:394:LEU:HD11	43:t:20:LEU:HD23	1.89	0.55
46:w:184:ARG:NH1	46:w:184:ARG:HB2	2.22	0.55
47:x:136:SER:OG	47:x:137:SER:N	2.39	0.55
50:1:129:U:H3	50:1:139:G:H1	1.54	0.55
53:6:231:A:O2'	53:6:232:A:N3	2.30	0.55
4:B:34:LYS:HG3	4:B:35:ASP:H	1.72	0.55
16:P:69:ARG:HH21	50:1:2389:C:H1'	1.71	0.55
23:W:165:MET:HE3	23:W:173:THR:HG21	1.89	0.55
37:m:215:LEU:HD13	37:m:370:ILE:HD13	1.87	0.55
38:n:413:ASP:OD1	38:n:413:ASP:N	2.40	0.55
41:q:415:LEU:O	41:q:419:THR:HG23	2.06	0.55
45:v:69:PHE:CZ	45:v:236:ARG:HB3	2.42	0.55
47:x:421:SER:OG	47:x:422:PHE:N	2.38	0.55
50:1:91:G:OP2	50:1:92:G:O2'	2.25	0.55
52:3:76:A:OP1	52:3:103:A:N6	2.35	0.55
52:3:81:U:H2'	52:3:82:G:C8	2.42	0.55
16:P:69:ARG:NH2	50:1:2389:C:H1'	2.22	0.55
26:Z:61:LYS:O	26:Z:65:ARG:HG2	2.06	0.55
35:j:8:PHE:HD1	50:1:1845:G:H4'	1.71	0.55
38:n:104:ARG:NH1	50:1:142:C:OP1	2.33	0.55
47:x:185:HIS:NE2	47:x:203:THR:O	2.39	0.55
47:x:257:ASP:OD2	47:x:259:THR:OG1	2.23	0.55
50:1:1831:U:O2'	51:2:114:G:OP1	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:161:ASP:OD1	1:L:162:ASN:N	2.40	0.55
19:S:71:LYS:HE3	19:S:73:LYS:HG2	1.89	0.55
40:p:3:LYS:NZ	40:p:5:THR:O	2.32	0.55
45:v:70:GLU:OE2	52:3:100:C:O2'	2.24	0.55
4:B:198:HIS:CE1	49:z:41:LEU:HD22	2.43	0.54
12:K:88:PHE:HB2	12:K:241:GLY:O	2.06	0.54
12:K:173:PHE:HD2	12:K:174:ILE:HD13	1.72	0.54
16:P:36:ILE:HD11	16:P:44:ALA:HB1	1.88	0.54
50:1:876:A:N7	50:1:877:C:N4	2.53	0.54
6:D:223:PHE:HB3	6:D:226:TYR:HB2	1.87	0.54
16:P:141:SER:OG	16:P:142:SER:N	2.40	0.54
23:W:134:THR:HG23	23:W:191:GLU:HB2	1.89	0.54
43:t:99:PHE:CE2	53:6:8:A:H5''	2.41	0.54
45:v:209:TYR:HE2	45:v:222:GLU:HB2	1.72	0.54
47:x:264:ASP:HB3	47:x:267:SER:OG	2.07	0.54
50:1:1659:U:H2'	50:1:1660:C:C6	2.42	0.54
50:1:2655:U:H4'	50:1:2656:A:OP2	2.07	0.54
4:B:227:GLU:HG2	4:B:231:HIS:HD2	1.71	0.54
12:K:198:ALA:O	12:K:204:THR:OG1	2.25	0.54
50:1:646:A:H4'	50:1:647:A:OP1	2.07	0.54
50:1:1245:A:N7	50:1:1271:A:O2'	2.39	0.54
50:1:2240:G:H2'	50:1:2241:U:C6	2.42	0.54
53:6:43:A:N6	53:6:44:G:O6	2.39	0.54
10:H:80:THR:HA	10:H:83:THR:HG22	1.89	0.54
20:T:116:ARG:HH22	50:1:1096:U:P	2.31	0.54
38:n:408:THR:OG1	38:n:409:HIS:ND1	2.37	0.54
42:r:88:PRO:HD2	42:r:91:LEU:HB2	1.90	0.54
50:1:40:A:O2'	50:1:42:C:OP2	2.24	0.54
53:6:39:U:O2'	53:6:40:U:O2	2.23	0.54
14:N:56:LYS:NZ	14:N:145:ASP:OD2	2.41	0.54
23:W:183:ASP:OD1	23:W:183:ASP:N	2.33	0.54
42:r:93:ASP:OD2	47:x:256:LYS:NZ	2.36	0.54
47:x:433:ASP:OD2	47:x:435:LYS:NZ	2.40	0.54
47:x:482:LEU:HD13	47:x:513:TRP:CE3	2.43	0.54
50:1:291:C:H2'	50:1:292:U:O2	2.08	0.54
4:B:341:SER:O	4:B:343:TYR:N	2.40	0.54
6:D:33:ARG:NH1	52:3:7:G:O5'	2.41	0.54
12:K:186:ILE:HD12	53:6:6:U:H1'	1.89	0.54
14:N:194:GLN:NE2	50:1:99:A:OP1	2.39	0.54
43:t:99:PHE:HE2	53:6:8:A:H5''	1.71	0.54
50:1:567:G:H2'	50:1:568:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:882:A:O2'	50:1:884:A:OP1	2.26	0.54
6:D:196:ARG:HB2	47:x:177:THR:HG21	1.89	0.54
12:K:140:LEU:O	12:K:144:LEU:HB2	2.07	0.54
47:x:350:GLU:HG3	47:x:354:LYS:HZ1	1.73	0.54
48:y:197:MET:HB3	48:y:206:THR:HG22	1.90	0.54
50:1:542:G:H2'	50:1:543:C:C6	2.43	0.54
51:2:26:U:H2'	51:2:27:U:C6	2.43	0.54
2:a:117:ARG:NH2	50:1:718:G:OP1	2.40	0.54
12:K:79:GLN:HA	12:K:283:THR:HG22	1.89	0.54
42:r:16:LYS:O	42:r:17:ARG:HB2	2.07	0.54
50:1:2604:U:H2'	50:1:2605:G:O4'	2.08	0.54
1:L:62:THR:O	1:L:64:LYS:N	2.41	0.54
3:A:31:THR:OG1	3:A:123:ARG:NH2	2.33	0.54
4:B:67:PHE:CZ	22:V:88:ARG:HG3	2.43	0.54
16:P:14:SER:HB3	16:P:151:THR:HG23	1.88	0.54
50:1:2951:G:H5''	50:1:2952:G:N7	2.23	0.54
50:1:3334:U:H4'	50:1:3335:A:H5'	1.90	0.54
6:D:265:TYR:OH	52:3:121:U:OP2	2.17	0.54
38:n:157:ASN:O	38:n:161:LYS:HG2	2.08	0.54
50:1:880:G:H8	50:1:882:A:OP2	1.90	0.54
50:1:3016:A:HO2'	50:1:3017:A:H8	1.54	0.54
52:3:87:G:C2	52:3:95:A:C8	2.96	0.54
5:C:31:ARG:NH1	50:1:674:G:OP1	2.41	0.53
7:E:43:LEU:HD11	7:E:85:ILE:HG13	1.90	0.53
27:b:434:GLU:HA	27:b:441:VAL:HB	1.91	0.53
35:j:85:LYS:HB2	51:2:67:U:H5''	1.90	0.53
43:t:55:PHE:HB3	51:2:157:U:O4	2.09	0.53
44:u:74:ARG:HH22	48:y:74:THR:HG23	1.73	0.53
50:1:765:C:H4'	50:1:766:U:H5'	1.90	0.53
50:1:1097:G:H4'	50:1:1098:A:O5'	2.08	0.53
50:1:1117:G:H1	50:1:1142:G:H21	1.56	0.53
51:2:9:A:H2'	51:2:10:A:C8	2.43	0.53
14:N:85:THR:HG21	50:1:44:U:H5'	1.90	0.53
16:P:133:HIS:HB3	16:P:135:ARG:NH1	2.23	0.53
27:b:483:ALA:O	27:b:485:GLU:N	2.41	0.53
36:k:66:ILE:HD12	36:k:69:LEU:HD22	1.89	0.53
47:x:130:LYS:HB2	47:x:515:HIS:ND1	2.23	0.53
8:F:75:TYR:HB2	20:T:141:VAL:HG22	1.90	0.53
37:m:102:ASP:OD1	37:m:103:THR:N	2.41	0.53
37:m:238:ARG:HD3	37:m:240:LYS:HD2	1.90	0.53
37:m:455:ASN:O	37:m:459:ARG:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:430:ASP:HB3	47:x:435:LYS:H	1.74	0.53
49:z:26:VAL:O	49:z:30:GLU:HG2	2.09	0.53
50:1:885:U:O2'	50:1:1851:G:H5'	2.08	0.53
50:1:2657:A:N1	50:1:2713:U:C4	2.76	0.53
50:1:2728:G:N2	50:1:2730:G:OP2	2.41	0.53
4:B:67:PHE:HA	4:B:70:ARG:HD2	1.89	0.53
11:J:37:LEU:O	11:J:41:SER:OG	2.24	0.53
38:n:178:LYS:HB2	38:n:189:GLN:HB3	1.89	0.53
50:1:3283:U:H2'	50:1:3284:G:H8	1.72	0.53
1:L:95:ILE:HG21	1:L:116:LEU:HD21	1.91	0.53
37:m:338:LYS:NZ	50:1:2961:G:OP1	2.41	0.53
41:q:237:LEU:O	41:q:241:GLU:HG2	2.08	0.53
42:r:43:THR:HG22	50:1:1299:U:H5'	1.89	0.53
50:1:2262:A:H2'	50:1:2263:C:C6	2.44	0.53
3:A:132:ASN:ND2	50:1:2178:A:H5''	2.24	0.53
13:M:83:LYS:NZ	50:1:560:G:OP1	2.34	0.53
17:Q:123:THR:OG1	17:Q:125:ASP:OD1	2.26	0.53
46:w:98:ASP:OD2	46:w:98:ASP:N	2.38	0.53
50:1:2728:G:H4'	50:1:2729:U:OP1	2.08	0.53
27:b:302:ARG:HD2	27:b:305:LEU:HD12	1.90	0.53
41:q:226:SER:O	41:q:226:SER:OG	2.18	0.53
46:w:148:LYS:HE2	50:1:2653:C:N4	2.23	0.53
46:w:158:TRP:CD1	46:w:158:TRP:H	2.27	0.53
50:1:2657:A:N1	50:1:2713:U:O4	2.42	0.53
5:C:291:ASN:HD21	50:1:1349:G:H5'	1.74	0.53
23:W:92:LEU:H	23:W:92:LEU:HD23	1.74	0.53
37:m:31:ARG:NH2	50:1:2964:G:O2'	2.42	0.53
44:u:46:PRO:O	44:u:52:THR:HG21	2.08	0.53
45:v:141:PHE:HZ	45:v:165:PHE:HB2	1.73	0.53
50:1:2264:U:H2'	50:1:2265:C:C6	2.44	0.53
5:C:234:ASN:OD1	5:C:235:LEU:N	2.42	0.53
37:m:11:ARG:HB3	37:m:17:THR:HG22	1.91	0.53
45:v:81:LYS:HD2	50:1:2698:G:C2	2.43	0.53
2:a:77:LYS:O	2:a:79:TRP:N	2.42	0.53
4:B:346:THR:HG21	49:z:22:PHE:CD2	2.44	0.53
9:G:43:LYS:HD2	24:X:28:THR:HG21	1.90	0.53
9:G:140:VAL:HG21	14:N:3:ALA:HB2	1.91	0.53
25:Y:4:GLN:HB2	50:1:229:G:H5''	1.90	0.53
25:Y:110:HIS:HE1	51:2:83:C:H42	1.54	0.53
31:f:78:SER:O	31:f:78:SER:OG	2.24	0.53
37:m:87:ASP:N	37:m:87:ASP:OD1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:126:SER:HB2	47:x:399:THR:HB	1.91	0.53
39:o:194:LYS:H	39:o:194:LYS:HD2	1.73	0.53
50:1:2545:C:H4'	50:1:2546:C:OP1	2.09	0.53
50:1:2611:U:H2'	50:1:2612:U:C6	2.43	0.53
6:D:160:PHE:HA	6:D:163:LEU:HB3	1.92	0.52
12:K:81:ILE:HD11	12:K:248:LEU:HB2	1.91	0.52
12:K:225:ASN:O	12:K:229:VAL:HG23	2.09	0.52
23:W:132:PRO:HA	23:W:191:GLU:HG2	1.91	0.52
23:W:212:GLU:OE1	23:W:212:GLU:N	2.41	0.52
39:o:207:ARG:HH11	53:6:35:C:H5''	1.72	0.52
46:w:158:TRP:O	46:w:177:ARG:NH2	2.42	0.52
47:x:241:HIS:HA	47:x:353:GLN:HE22	1.73	0.52
48:y:9:ASN:ND2	50:1:3018:C:OP1	2.40	0.52
50:1:720:A:H1'	50:1:721:G:OP2	2.10	0.52
50:1:993:G:N2	50:1:1057:A:H2	2.07	0.52
50:1:3356:G:H2'	50:1:3357:U:C6	2.45	0.52
52:3:23:A:H2'	52:3:24:A:C8	2.44	0.52
1:L:73:ARG:NH1	50:1:110:G:OP2	2.42	0.52
12:K:230:TYR:HD2	12:K:231:MET:HE2	1.74	0.52
20:T:66:ASN:OD1	20:T:67:VAL:N	2.43	0.52
42:r:17:ARG:HB3	42:r:20:HIS:HB2	1.91	0.52
44:u:129:SER:O	44:u:131:PRO:HD3	2.10	0.52
47:x:228:HIS:CD2	47:x:261:LYS:HD2	2.44	0.52
47:x:438:SER:OG	47:x:439:THR:N	2.40	0.52
50:1:180:C:H2'	50:1:181:U:C6	2.44	0.52
50:1:737:G:H2'	50:1:738:A:H8	1.74	0.52
50:1:1051:U:H2'	50:1:1052:U:C6	2.44	0.52
50:1:1786:G:H2'	50:1:1787:A:C8	2.44	0.52
50:1:2359:C:H4'	50:1:2399:A:H4'	1.91	0.52
50:1:2393:G:O2'	50:1:2394:G:OP2	2.25	0.52
2:a:96:LYS:O	2:a:97:GLU:HG3	2.10	0.52
3:A:107:VAL:HB	3:A:111:THR:HG21	1.90	0.52
9:G:245:LYS:O	9:G:248:LYS:HG3	2.09	0.52
11:J:124:GLY:O	50:1:2674:A:N6	2.42	0.52
17:Q:86:THR:HG22	17:Q:105:ARG:HB2	1.91	0.52
38:n:378:PHE:O	38:n:382:SER:OG	2.24	0.52
39:o:92:ILE:HG12	39:o:138:GLU:HB2	1.91	0.52
45:v:53:LYS:HG3	45:v:56:ASP:O	2.10	0.52
50:1:1635:G:N2	50:1:1638:A:OP2	2.37	0.52
50:1:2981:U:O2'	50:1:2982:A:O5'	2.25	0.52
27:b:378:ILE:HB	27:b:383:LYS:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:65:VAL:HG12	32:g:66:SER:H	1.75	0.52
50:1:2141:U:H5''	50:1:2142:A:OP2	2.09	0.52
50:1:2442:G:H1	50:1:2505:U:H3	1.57	0.52
50:1:3298:C:C2	50:1:3299:A:C8	2.98	0.52
7:E:9:TRP:CE3	50:1:1353:U:H2'	2.44	0.52
23:W:88:ASN:HB3	23:W:91:GLN:HE22	1.75	0.52
37:m:188:GLU:O	37:m:192:ASN:ND2	2.34	0.52
39:o:194:LYS:HA	39:o:197:LYS:HZ3	1.75	0.52
50:1:2568:C:H2'	50:1:2569:A:C4	2.44	0.52
50:1:2921:U:C6	50:1:2923:U:H1'	2.44	0.52
50:1:3027:A:H2'	50:1:3028:G:O4'	2.09	0.52
50:1:3295:A:H2'	50:1:3296:A:C8	2.44	0.52
20:T:119:ALA:HA	20:T:124:VAL:HG11	1.92	0.52
25:Y:11:ASP:OD1	25:Y:13:ARG:N	2.42	0.52
27:b:396:ARG:NH2	48:y:40:ALA:O	2.42	0.52
35:j:19:CYS:SG	35:j:20:ASN:N	2.82	0.52
45:v:133:PHE:HE1	45:v:180:HIS:HB3	1.74	0.52
50:1:2112:U:H2'	50:1:2113:A:H5''	1.91	0.52
50:1:2699:G:H2'	50:1:2700:G:O4'	2.09	0.52
7:E:18:LEU:H	7:E:18:LEU:HD12	1.74	0.52
34:i:42:SER:O	34:i:46:GLU:HG3	2.10	0.52
37:m:208:SER:O	37:m:208:SER:OG	2.25	0.52
38:n:125:PHE:O	38:n:129:ILE:HG13	2.10	0.52
43:t:216:TYR:OH	43:t:237:GLU:OE1	2.20	0.52
50:1:998:A:H2'	50:1:999:G:C5	2.45	0.52
50:1:2724:U:H5	50:1:2732:G:H1	1.57	0.52
50:1:2830:G:H2'	50:1:2831:G:C8	2.45	0.52
50:1:2838:A:N6	50:1:2850:G:O2'	2.32	0.52
12:K:183:ASP:HB3	12:K:186:ILE:HG22	1.92	0.52
19:S:171:PHE:HA	19:S:172:TYR:C	2.34	0.52
27:b:169:THR:HB	27:b:217:GLN:HG3	1.91	0.52
35:j:69:HIS:O	35:j:73:ARG:HG3	2.10	0.52
38:n:181:VAL:HB	38:n:456:HIS:HE1	1.75	0.52
39:o:92:ILE:HD13	39:o:173:ILE:HG23	1.91	0.52
43:t:183:VAL:HA	43:t:186:LEU:HD12	1.91	0.52
47:x:9:SER:H	47:x:12:GLN:HB2	1.75	0.52
50:1:2543:U:C2	50:1:2544:U:H5	2.28	0.52
8:F:156:ILE:C	8:F:158:LYS:H	2.17	0.52
9:G:190:VAL:HG12	9:G:192:GLN:HG2	1.91	0.52
14:N:190:THR:O	14:N:194:GLN:HG2	2.09	0.52
27:b:195:GLN:HB2	27:b:197:TYR:HE1	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:443:HIS:CE1	47:x:463:SER:HB3	2.45	0.52
50:1:439:C:O2'	50:1:440:A:N7	2.42	0.52
50:1:3154:C:O2'	50:1:3157:U:H5''	2.10	0.52
6:D:236:LEU:HA	6:D:239:ILE:HD12	1.91	0.52
36:k:58:ASP:OD2	36:k:60:GLY:N	2.43	0.52
44:u:79:VAL:HA	48:y:85:ARG:HG2	1.91	0.52
47:x:418:VAL:HG21	47:x:459:LEU:HD21	1.93	0.52
47:x:455:ASP:OD1	47:x:455:ASP:N	2.42	0.52
50:1:900:G:H1'	50:1:1589:A:N6	2.25	0.52
50:1:2667:A:H8	50:1:2668:U:C6	2.27	0.52
1:L:122:LYS:HE3	33:h:119:LYS:HG2	1.92	0.51
2:a:75:LEU:HD22	2:a:78:LEU:HD22	1.92	0.51
3:A:37:ARG:NH2	50:1:2526:C:OP1	2.42	0.51
9:G:24:ASN:OD1	9:G:24:ASN:N	2.44	0.51
10:H:49:ASN:O	10:H:51:GLN:N	2.42	0.51
26:Z:126:LYS:HD2	41:q:271:ASP:HB3	1.92	0.51
37:m:6:LYS:NZ	50:1:2421:U:OP2	2.38	0.51
39:o:172:LYS:O	39:o:174:GLU:HG2	2.10	0.51
6:D:40:HIS:CG	6:D:43:LYS:HG2	2.45	0.51
11:J:86:VAL:HG11	11:J:111:ASP:HB2	1.92	0.51
20:T:128:LEU:N	50:1:1095:U:O2	2.43	0.51
27:b:25:THR:O	27:b:29:THR:OG1	2.27	0.51
27:b:357:VAL:HG13	48:y:244:TYR:HB2	1.92	0.51
31:f:40:ASP:N	31:f:40:ASP:OD1	2.43	0.51
33:h:67:ARG:NH2	51:2:97:A:OP1	2.43	0.51
37:m:158:GLU:HG2	37:m:159:ASP:N	2.25	0.51
39:o:214:SER:N	39:o:215:GLY:HA2	2.24	0.51
41:q:394:LEU:HD13	43:t:23:ARG:HG2	1.92	0.51
42:r:203:ASN:ND2	42:r:214:VAL:O	2.43	0.51
44:u:8:PHE:HB3	44:u:36:CYS:HB3	1.92	0.51
44:u:22:VAL:HG22	44:u:28:GLU:HG2	1.91	0.51
50:1:1214:U:H2'	50:1:1215:U:C6	2.44	0.51
50:1:2506:U:H2'	50:1:2507:C:C5	2.45	0.51
50:1:2609:A:H2'	50:1:2610:G:H8	1.74	0.51
50:1:3234:A:H2	50:1:3253:G:H1	1.56	0.51
4:B:289:ASP:N	4:B:289:ASP:OD1	2.44	0.51
5:C:49:ALA:HB1	5:C:105:THR:HG23	1.92	0.51
5:C:283:THR:HG22	5:C:285:ASP:H	1.75	0.51
27:b:149:TYR:O	27:b:153:VAL:HG23	2.09	0.51
27:b:284:MET:HE1	27:b:335:ALA:HB2	1.92	0.51
32:g:74:ARG:HG2	32:g:75:ALA:N	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:161:THR:HG22	47:x:171:TRP:HE1	1.76	0.51
47:x:261:LYS:HG2	47:x:273:THR:HG22	1.91	0.51
47:x:463:SER:OG	47:x:464:LYS:N	2.42	0.51
50:1:971:G:N1	50:1:1111:U:C2	2.79	0.51
50:1:1301:A:O2'	50:1:1302:A:H5'	2.10	0.51
50:1:1778:G:O2'	50:1:1780:G:OP2	2.28	0.51
50:1:2404:A:H62	50:1:2817:A:N6	2.07	0.51
4:B:255:TRP:N	50:1:2943:G:HO2'	2.05	0.51
10:H:48:VAL:HG23	10:H:49:ASN:N	2.24	0.51
12:K:132:ILE:H	12:K:132:ILE:HD12	1.75	0.51
20:T:92:ARG:HB2	20:T:95:HIS:HD2	1.75	0.51
38:n:56:SER:OG	38:n:57:THR:N	2.43	0.51
46:w:137:ALA:N	46:w:138:SER:O	2.43	0.51
47:x:342:THR:HB	47:x:344:LYS:HE2	1.92	0.51
50:1:2267:C:H1'	50:1:2268:U:H3	1.76	0.51
50:1:2760:C:H2'	50:1:2761:G:C8	2.45	0.51
3:A:54:ARG:NH1	50:1:2176:U:OP1	2.36	0.51
4:B:221:THR:O	4:B:221:THR:OG1	2.22	0.51
4:B:221:THR:HG23	4:B:273:HIS:O	2.10	0.51
6:D:178:ASN:HD21	50:1:2746:A:H5'	1.75	0.51
6:D:286:VAL:HA	6:D:289:LYS:HE2	1.91	0.51
8:F:234:GLU:O	8:F:237:ASN:ND2	2.44	0.51
15:O:119:VAL:HG11	19:S:167:ARG:HD3	1.91	0.51
19:S:170:THR:O	19:S:170:THR:OG1	2.27	0.51
20:T:89:LEU:HD12	46:w:161:GLU:HA	1.91	0.51
41:q:264:HIS:CE1	41:q:268:THR:HG21	2.46	0.51
45:v:71:ASP:OD2	45:v:72:MET:N	2.43	0.51
45:v:120:ASP:OD1	45:v:120:ASP:N	2.36	0.51
50:1:1106:G:N1	50:1:1107:C:N4	2.58	0.51
2:a:77:LYS:C	2:a:79:TRP:H	2.17	0.51
47:x:494:TRP:HA	47:x:501:VAL:HG22	1.91	0.51
50:1:656:A:H2'	50:1:657:A:C8	2.46	0.51
50:1:2113:A:H61	50:1:3062:G:H21	1.59	0.51
50:1:2684:C:H2'	50:1:2685:C:C6	2.45	0.51
50:1:2784:G:H2'	50:1:2785:A:H8	1.76	0.51
4:B:216:ASP:OD1	4:B:339:ARG:HB3	2.10	0.51
9:G:185:ARG:O	9:G:188:THR:OG1	2.28	0.51
11:J:45:PRO:HA	11:J:69:VAL:HG22	1.93	0.51
12:K:290:PRO:HB2	39:o:204:HIS:CE1	2.45	0.51
20:T:45:ASN:OD1	20:T:45:ASN:N	2.43	0.51
22:V:15:LEU:HD22	22:V:51:ALA:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:139:GLU:HB3	23:W:185:PRO:HD3	1.92	0.51
25:Y:25:SER:OG	51:2:91:C:O2'	2.23	0.51
46:w:147:TYR:HA	50:1:2656:A:C8	2.46	0.51
47:x:173:CYS:O	47:x:500:ARG:NH1	2.44	0.51
50:1:1126:G:H2'	50:1:1127:G:O4'	2.10	0.51
50:1:2667:A:O2'	50:1:2691:A:H5'	2.11	0.51
52:3:29:C:O2'	52:3:52:G:N2	2.42	0.51
12:K:144:LEU:HB3	12:K:149:ILE:O	2.09	0.51
25:Y:113:LYS:HG3	51:2:84:C:O2	2.11	0.51
45:v:9:ASN:ND2	45:v:10:ALA:H	2.08	0.51
47:x:182:LEU:HD21	47:x:213:TRP:CD1	2.45	0.51
50:1:997:A:N6	50:1:1053:A:N1	2.58	0.51
50:1:1001:G:C6	50:1:1051:U:C4	2.98	0.51
50:1:1048:A:H2'	50:1:1049:C:O4'	2.10	0.51
50:1:2278:C:H5	50:1:2315:G:H22	1.58	0.51
50:1:2657:A:C6	50:1:2658:G:C6	2.99	0.51
52:3:72:A:H2'	52:3:74:C:C5	2.46	0.51
4:B:108:GLU:HB2	4:B:137:TYR:CD2	2.45	0.51
4:B:269:GLN:NE2	4:B:270:ARG:O	2.43	0.51
12:K:88:PHE:CE2	12:K:244:LEU:HD11	2.46	0.51
12:K:215:LYS:HD3	12:K:216:GLU:N	2.26	0.51
21:U:19:VAL:HG12	21:U:105:LEU:HD13	1.93	0.51
32:g:46:ASP:OD2	32:g:88:ARG:NH2	2.43	0.51
38:n:421:VAL:HG12	38:n:423:GLY:H	1.76	0.51
45:v:39:ASN:N	45:v:39:ASN:OD1	2.44	0.51
47:x:514:THR:OG1	47:x:515:HIS:N	2.44	0.51
50:1:2727:A:H3'	50:1:2729:U:C2	2.46	0.51
3:A:136:ILE:HD13	3:A:148:VAL:HG12	1.92	0.51
11:J:24:GLY:HA2	11:J:65:ILE:HA	1.92	0.51
26:Z:53:VAL:HG21	26:Z:62:VAL:HG23	1.93	0.51
47:x:355:LYS:O	47:x:359:ASN:ND2	2.25	0.51
50:1:1067:U:H2'	50:1:1068:C:H6	1.76	0.51
50:1:2743:A:N6	50:1:2751:G:O6	2.44	0.51
6:D:175:HIS:HA	50:1:2747:A:H5'	1.94	0.50
27:b:229:THR:HG21	37:m:156:ASN:HA	1.91	0.50
37:m:124:ASP:N	37:m:125:GLU:OE2	2.42	0.50
44:u:56:ARG:HB3	44:u:61:LYS:HB2	1.92	0.50
47:x:281:VAL:HA	47:x:296:SER:HA	1.92	0.50
47:x:324:ASN:ND2	47:x:379:ASP:OD1	2.44	0.50
50:1:2357:A:H2'	50:1:2358:A:C8	2.46	0.50
16:P:28:ASN:O	16:P:32:THR:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:123:ASP:CG	23:W:213:PHE:HB2	2.36	0.50
27:b:51:LYS:O	27:b:55:GLU:HG3	2.11	0.50
37:m:85:SER:HA	42:r:236:LYS:HB3	1.93	0.50
47:x:11:LYS:O	47:x:15:GLU:HG2	2.11	0.50
50:1:885:U:H2'	50:1:886:C:H6	1.76	0.50
50:1:2503:G:H1'	50:1:2504:U:C5	2.47	0.50
50:1:2683:U:H2'	50:1:2684:C:C6	2.46	0.50
52:3:100:C:H2'	52:3:101:G:O4'	2.10	0.50
6:D:37:VAL:HA	6:D:48:LYS:NZ	2.26	0.50
12:K:123:VAL:HG13	12:K:152:ASP:H	1.76	0.50
14:N:6:TYR:CE1	34:i:40:VAL:HG22	2.47	0.50
37:m:157:LEU:O	37:m:161:VAL:HG23	2.12	0.50
46:w:128:ARG:NH1	50:1:2754:G:OP2	2.44	0.50
50:1:2096:A:H2'	50:1:2097:U:C6	2.47	0.50
50:1:2529:A:C4	50:1:2530:G:C8	2.99	0.50
50:1:2923:U:H2'	50:1:2924:U:H3'	1.92	0.50
50:1:2929:C:O2'	50:1:2930:A:O4'	2.29	0.50
1:L:23:LYS:HE3	1:L:25:HIS:HE1	1.77	0.50
1:L:128:ARG:HE	33:h:112:PRO:HG3	1.77	0.50
10:H:113:GLU:HG3	10:H:123:ILE:HG23	1.94	0.50
27:b:175:TYR:CD1	27:b:270:LEU:HD22	2.46	0.50
34:i:3:VAL:O	34:i:12:ASN:HB3	2.11	0.50
38:n:430:GLN:HE22	38:n:456:HIS:HA	1.77	0.50
50:1:2635:A:H4'	50:1:2636:A:C2	2.47	0.50
50:1:2749:G:H2'	50:1:2750:U:C6	2.46	0.50
50:1:3192:U:H2'	50:1:3193:C:C6	2.46	0.50
6:D:141:PRO:HD2	46:w:86:VAL:HG11	1.92	0.50
9:G:196:ALA:O	9:G:197:VAL:HG13	2.11	0.50
18:R:74:ARG:NH2	50:1:1942:U:OP2	2.33	0.50
22:V:104:ASN:O	22:V:106:LYS:N	2.44	0.50
26:Z:124:ALA:HB1	41:q:266:MET:HB2	1.94	0.50
31:f:35:VAL:HG13	31:f:40:ASP:HB2	1.92	0.50
38:n:16:ILE:HD11	38:n:68:ILE:HD12	1.93	0.50
43:t:187:LEU:HA	43:t:190:ILE:HG12	1.93	0.50
45:v:203:VAL:HG23	45:v:203:VAL:O	2.11	0.50
50:1:1108:U:H2'	50:1:1109:U:C6	2.36	0.50
50:1:1140:G:H2'	50:1:1141:C:C6	2.46	0.50
4:B:108:GLU:O	4:B:108:GLU:HG2	2.10	0.50
10:H:176:LEU:HD22	42:r:17:ARG:HA	1.92	0.50
13:M:23:ILE:O	13:M:30:GLY:N	2.39	0.50
27:b:388:TYR:CE1	27:b:395:ARG:HD2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:420:TYR:HB2	48:y:86:ASN:O	2.11	0.50
37:m:418:ILE:HG21	37:m:421:TRP:HZ3	1.76	0.50
1:L:168:ARG:O	1:L:172:LEU:HG	2.11	0.50
12:K:215:LYS:HD3	12:K:216:GLU:HB2	1.94	0.50
24:X:21:LYS:HB2	50:1:2:U:H5'	1.93	0.50
43:t:290:LYS:O	43:t:293:GLU:HG2	2.12	0.50
45:v:9:ASN:HA	50:1:2694:A:H5''	1.94	0.50
45:v:181:VAL:HG13	45:v:204:TYR:HB2	1.92	0.50
46:w:133:ILE:O	46:w:141:TRP:HE3	1.94	0.50
48:y:20:THR:OG1	48:y:21:ASN:N	2.45	0.50
50:1:307:A:H2'	50:1:308:A:C8	2.47	0.50
50:1:2729:U:H4'	50:1:2730:G:OP1	2.12	0.50
50:1:2841:G:N2	50:1:2844:C:O2'	2.45	0.50
52:3:37:G:N1	52:3:41:G:C2	2.80	0.50
53:6:6:U:O2	53:6:6:U:H2'	2.11	0.50
5:C:334:PHE:HA	5:C:339:LEU:HD12	1.93	0.50
12:K:124:LEU:HB2	12:K:177:PHE:CD2	2.47	0.50
27:b:8:ILE:HB	27:b:154:ARG:HG3	1.94	0.50
47:x:135:SER:HB2	47:x:513:TRP:CZ3	2.47	0.50
47:x:142:HIS:CD2	47:x:169:ARG:HG3	2.47	0.50
47:x:383:MET:SD	47:x:419:SER:OG	2.57	0.50
50:1:1355:A:H4'	50:1:1356:U:O5'	2.11	0.50
50:1:2752:U:H2'	50:1:2753:G:C8	2.46	0.50
5:C:36:HIS:O	5:C:40:THR:HG23	2.12	0.50
7:E:60:ASP:OD2	7:E:62:THR:OG1	2.30	0.50
12:K:250:ASN:OD1	12:K:251:LEU:N	2.45	0.50
20:T:40:VAL:HG21	20:T:96:ILE:HD11	1.93	0.50
27:b:456:LEU:HD21	44:u:99:ILE:HD12	1.94	0.50
41:q:397:LYS:NZ	41:q:410:LYS:HB3	2.27	0.50
43:t:265:ASN:HA	43:t:268:LEU:HD12	1.94	0.50
44:u:66:ASP:OD2	44:u:103:ARG:NH1	2.44	0.50
45:v:154:TYR:HA	45:v:157:ILE:HG12	1.94	0.50
50:1:1084:A:H2'	50:1:1085:A:H8	1.73	0.50
6:D:172:TYR:CD2	47:x:134:ARG:HD2	2.47	0.49
19:S:77:VAL:HG22	19:S:126:VAL:HG23	1.93	0.49
38:n:160:GLN:O	38:n:164:ASN:ND2	2.34	0.49
47:x:351:GLU:HA	47:x:354:LYS:HG2	1.94	0.49
48:y:6:GLN:HE21	48:y:11:ASN:HD21	1.60	0.49
50:1:1234:G:H2'	50:1:1235:U:C5	2.47	0.49
50:1:2940:A:H3'	50:1:2943:G:H5''	1.93	0.49
50:1:3291:G:H2'	50:1:3292:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:143:ILE:HG23	9:G:175:VAL:HG21	1.94	0.49
11:J:107:ASP:OD1	11:J:108:GLU:N	2.41	0.49
27:b:282:SER:HB2	27:b:338:LYS:HZ2	1.76	0.49
33:h:49:LYS:NZ	51:2:63:G:O2'	2.45	0.49
37:m:224:VAL:HG12	37:m:254:HIS:CD2	2.46	0.49
39:o:205:GLU:HA	39:o:208:ILE:HD12	1.94	0.49
43:t:231:ASP:OD1	43:t:232:ASN:N	2.45	0.49
45:v:28:LYS:HZ3	46:w:102:GLU:CD	2.19	0.49
48:y:75:GLN:N	48:y:75:GLN:OE1	2.45	0.49
50:1:885:U:H4'	50:1:1851:G:H4'	1.94	0.49
52:3:72:A:H2'	52:3:74:C:H5	1.77	0.49
4:B:357:LYS:HB3	44:u:1:MET:HE2	1.94	0.49
8:F:25:GLN:HA	8:F:29:GLU:HB2	1.94	0.49
15:O:60:LYS:HE2	50:1:1307:G:H5'	1.94	0.49
22:V:45:ARG:HG2	22:V:48:ARG:HH21	1.78	0.49
23:W:20:ARG:NH1	50:1:1221:A:N7	2.60	0.49
45:v:81:LYS:HB3	50:1:2698:G:N3	2.28	0.49
47:x:37:GLN:O	47:x:120:LEU:HA	2.12	0.49
50:1:2428:U:H5	50:1:2601:A:N1	2.09	0.49
50:1:3165:A:H2'	50:1:3166:C:C6	2.46	0.49
53:6:13:U:O2'	53:6:14:U:H5''	2.13	0.49
5:C:207:VAL:HB	5:C:227:THR:HG22	1.95	0.49
9:G:114:ALA:O	9:G:118:GLU:HG3	2.12	0.49
12:K:218:SER:O	12:K:221:THR:HG23	2.12	0.49
37:m:346:ILE:HD12	37:m:389:ARG:HH21	1.77	0.49
42:r:148:LYS:NZ	42:r:169:GLU:O	2.45	0.49
42:r:160:GLY:HA3	50:1:2730:G:N7	2.27	0.49
47:x:225:LEU:HD22	47:x:263:TRP:CE3	2.48	0.49
48:y:26:VAL:HG21	48:y:35:TYR:HD2	1.78	0.49
50:1:68:C:OP2	50:1:301:G:N2	2.44	0.49
50:1:1049:C:H2'	50:1:1050:U:C2	2.48	0.49
50:1:2678:A:H2'	50:1:2679:A:N3	2.27	0.49
1:L:107:GLU:OE1	1:L:107:GLU:N	2.44	0.49
5:C:197:ARG:NH1	50:1:1381:A:OP1	2.46	0.49
50:1:602:A:H2'	50:1:603:A:C8	2.47	0.49
50:1:2215:A:H2'	50:1:2216:G:O4'	2.13	0.49
6:D:268:GLU:OE2	6:D:271:LYS:HD3	2.12	0.49
7:E:94:GLU:OE1	7:E:94:GLU:N	2.44	0.49
8:F:184:LEU:HD21	8:F:202:LEU:HD21	1.95	0.49
37:m:149:ARG:HB2	37:m:149:ARG:NH2	2.27	0.49
37:m:313:ARG:O	50:1:2728:G:O2'	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:447:TYR:O	38:n:448:LEU:HG	2.12	0.49
41:q:219:GLU:OE1	41:q:219:GLU:N	2.45	0.49
42:r:88:PRO:O	42:r:92:LEU:HG	2.12	0.49
42:r:241:LYS:HE2	42:r:261:VAL:HG12	1.95	0.49
47:x:208:ASN:HD22	47:x:231:TRP:HA	1.78	0.49
50:1:2376:G:H2'	50:1:2377:G:C8	2.46	0.49
50:1:2413:A:N6	50:1:2807:U:H3	2.11	0.49
50:1:3218:A:H5''	50:1:3219:G:C4	2.47	0.49
52:3:74:C:H2'	52:3:75:G:C8	2.47	0.49
53:6:39:U:O2'	53:6:40:U:H5''	2.12	0.49
2:a:96:LYS:NZ	2:a:142:GLY:O	2.45	0.49
3:A:134:VAL:HG23	3:A:149:ARG:O	2.13	0.49
16:P:18:ARG:NH2	16:P:147:GLU:OE1	2.46	0.49
27:b:358:LEU:O	27:b:362:HIS:HB3	2.13	0.49
14:N:160:GLU:HG2	14:N:161:ALA:N	2.28	0.49
24:X:127:THR:HG22	24:X:128:ALA:N	2.26	0.49
37:m:52:LYS:H	37:m:53:GLY:HA2	1.78	0.49
43:t:260:SER:O	43:t:262:SER:N	2.46	0.49
50:1:1277:C:HO2'	50:1:1278:A:C5'	2.25	0.49
50:1:1308:A:O2'	50:1:1311:G:OP1	2.22	0.49
50:1:1348:U:O2	50:1:1349:G:N2	2.46	0.49
50:1:3234:A:H2	50:1:3253:G:H22	1.61	0.49
3:A:37:ARG:HG3	3:A:38:HIS:CD2	2.48	0.49
7:E:75:PRO:HA	7:E:138:GLN:NE2	2.28	0.49
20:T:116:ARG:NH2	50:1:1096:U:OP2	2.39	0.49
26:Z:5:LEU:HD11	28:c:35:ARG:HD2	1.95	0.49
28:c:40:LYS:NZ	28:c:94:GLU:OE2	2.46	0.49
29:d:84:ASP:OD2	29:d:86:LYS:N	2.46	0.49
33:h:107:LYS:NZ	50:1:112:U:OP1	2.46	0.49
40:p:49:ARG:NH1	40:p:68:ALA:O	2.46	0.49
41:q:391:ASP:O	41:q:421:ARG:HD2	2.12	0.49
43:t:76:LYS:O	43:t:80:ILE:HG13	2.13	0.49
50:1:877:C:O2	50:1:882:A:N6	2.43	0.49
50:1:2535:A:H2'	50:1:2536:A:O4'	2.12	0.49
50:1:3341:U:H1'	50:1:3342:A:H5'	1.94	0.49
18:R:136:ARG:NH1	50:1:1947:G:OP1	2.45	0.49
27:b:292:ILE:HG21	54:b:701:GTP:HN21	1.78	0.49
27:b:436:LEU:HD22	44:u:93:MET:HE3	1.94	0.49
27:b:485:GLU:HA	27:b:488:ASP:HB2	1.95	0.49
42:r:173:ARG:NH1	42:r:212:LEU:O	2.45	0.49
44:u:119:ASP:OD1	44:u:122:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:y:168:GLN:OE1	48:y:168:GLN:N	2.38	0.49
50:1:543:C:H3'	50:1:544:C:C6	2.48	0.49
50:1:737:G:H2'	50:1:738:A:C8	2.48	0.49
50:1:775:A:H2'	50:1:776:U:C6	2.48	0.49
50:1:2528:G:H8	50:1:2528:G:OP2	1.96	0.49
50:1:3322:A:H2'	50:1:3323:A:C8	2.47	0.49
5:C:209:TYR:O	5:C:230:VAL:HG23	2.13	0.48
6:D:40:HIS:HB3	6:D:41:LYS:HA	1.95	0.48
11:J:12:LEU:HD11	11:J:159:THR:HB	1.95	0.48
41:q:249:GLU:O	41:q:253:ILE:HG12	2.13	0.48
46:w:97:THR:HB	46:w:99:LEU:HD13	1.95	0.48
47:x:90:ASP:OD1	47:x:90:ASP:N	2.46	0.48
47:x:316:LEU:HD23	47:x:386:TRP:CD2	2.48	0.48
50:1:2537:U:O4	50:1:2542:U:N3	2.46	0.48
50:1:2622:C:HO2'	50:1:2623:G:H8	1.60	0.48
50:1:2841:G:H3'	50:1:2843:U:OP2	2.13	0.48
50:1:3015:G:O2'	50:1:3016:A:H5'	2.13	0.48
52:3:114:U:H2'	52:3:115:G:H8	1.78	0.48
5:C:237:GLN:O	5:C:246:ARG:NH1	2.44	0.48
9:G:150:LEU:HD12	9:G:176:PRO:O	2.13	0.48
10:H:78:MET:O	10:H:82:VAL:HG23	2.12	0.48
11:J:16:LYS:HZ2	11:J:16:LYS:C	2.21	0.48
35:j:48:ASN:HB2	50:1:53:G:P	2.53	0.48
45:v:110:ILE:HG13	45:v:113:MET:HE3	1.95	0.48
46:w:131:LYS:HE3	50:1:2715:A:N7	2.27	0.48
47:x:31:ASN:OD1	47:x:31:ASN:N	2.45	0.48
47:x:61:GLU:HG2	47:x:77:TYR:H	1.78	0.48
50:1:994:G:H22	50:1:1054:A:H61	1.60	0.48
50:1:2643:A:O2'	50:1:2645:G:OP1	2.31	0.48
6:D:77:ALA:O	6:D:108:ARG:NH1	2.45	0.48
7:E:165:LEU:HB2	31:f:6:ARG:O	2.13	0.48
18:R:125:LYS:NZ	50:1:1724:U:O4	2.45	0.48
43:t:231:ASP:HB3	43:t:234:ILE:HG13	1.96	0.48
48:y:20:THR:HG21	48:y:23:TYR:CZ	2.48	0.48
48:y:146:ILE:HG22	48:y:147:LEU:H	1.79	0.48
48:y:221:ILE:HA	48:y:230:GLU:OE2	2.13	0.48
50:1:8:C:H2'	50:1:9:U:C6	2.47	0.48
52:3:76:A:N6	52:3:103:A:OP2	2.45	0.48
1:L:61:PRO:O	1:L:62:THR:OG1	2.32	0.48
3:A:133:TYR:HB3	3:A:168:VAL:HG12	1.95	0.48
10:H:128:VAL:HA	10:H:157:ASN:HD21	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:67:ILE:HD12	24:X:121:LYS:HG3	1.96	0.48
37:m:423:ASP:OD2	37:m:425:THR:OG1	2.32	0.48
38:n:202:PRO:HB3	41:q:415:LEU:HD11	1.96	0.48
43:t:221:GLU:C	43:t:223:GLU:H	2.21	0.48
50:1:2702:A:O2'	50:1:2703:A:OP2	2.29	0.48
50:1:2799:A:H2'	50:1:2800:G:C8	2.49	0.48
50:1:3233:C:H2'	50:1:3234:A:C8	2.49	0.48
6:D:14:SER:HB2	52:3:68:C:OP1	2.12	0.48
12:K:296:ASP:N	12:K:296:ASP:OD1	2.46	0.48
37:m:358:LEU:HD23	37:m:362:ILE:O	2.13	0.48
45:v:241:SER:O	45:v:245:VAL:HG23	2.13	0.48
46:w:16:PRO:HB2	46:w:17:ILE:HD12	1.95	0.48
47:x:61:GLU:OE1	47:x:76:PRO:HB3	2.13	0.48
47:x:363:ILE:HA	47:x:366:LYS:HD3	1.95	0.48
50:1:1766:G:H2'	50:1:1767:C:C6	2.49	0.48
6:D:105:ILE:O	6:D:109:THR:OG1	2.26	0.48
11:J:28:ASP:OD2	11:J:31:THR:OG1	2.26	0.48
12:K:227:LYS:O	12:K:231:MET:HG2	2.13	0.48
32:g:42:PRO:HB2	32:g:51:LEU:HD21	1.94	0.48
42:r:146:SER:OG	42:r:147:TRP:N	2.43	0.48
42:r:187:PRO:HG2	42:r:261:VAL:HG22	1.94	0.48
48:y:25:LEU:HD22	48:y:51:THR:HG21	1.94	0.48
50:1:1001:G:C6	50:1:1051:U:N3	2.80	0.48
50:1:1203:A:C2	50:1:1300:G:H2'	2.49	0.48
50:1:1224:C:H2'	50:1:1224:C:O2	2.13	0.48
50:1:1249:G:C2	50:1:1250:G:C5	3.02	0.48
50:1:1657:C:O2'	50:1:1797:A:OP2	2.21	0.48
50:1:2503:G:O2'	50:1:2504:U:OP2	2.29	0.48
50:1:2655:U:H3'	50:1:2657:A:OP2	2.13	0.48
6:D:57:ASN:HB2	52:3:27:A:OP2	2.14	0.48
17:Q:144:ARG:NH1	50:1:976:U:OP2	2.45	0.48
23:W:15:THR:OG1	23:W:16:ASP:N	2.47	0.48
37:m:261:LYS:HB3	37:m:264:LEU:HD12	1.96	0.48
37:m:286:PHE:HE2	37:m:334:THR:HG21	1.79	0.48
38:n:374:ASP:OD2	38:n:374:ASP:N	2.47	0.48
46:w:67:SER:O	46:w:67:SER:OG	2.30	0.48
46:w:133:ILE:HD11	46:w:144:LYS:HD2	1.95	0.48
47:x:196:PRO:O	47:x:337:GLY:HA3	2.14	0.48
50:1:1201:C:N4	50:1:2824:G:O6	2.47	0.48
50:1:1824:U:C2	50:1:1825:G:C8	3.01	0.48
50:1:3375:A:O2'	50:1:3378:C:OP2	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:43:LYS:HG3	6:D:44:TYR:N	2.29	0.48
11:J:105:GLY:HA3	50:1:2674:A:C8	2.49	0.48
27:b:323:GLN:HG2	54:b:701:GTP:C6	2.48	0.48
32:g:65:VAL:HG12	32:g:66:SER:N	2.29	0.48
37:m:239:CYS:HB3	37:m:323:TYR:HE1	1.79	0.48
37:m:333:ASN:OD1	37:m:340:VAL:N	2.37	0.48
37:m:455:ASN:OD1	37:m:459:ARG:NH2	2.47	0.48
41:q:249:GLU:CD	41:q:252:ARG:HH11	2.21	0.48
43:t:142:LEU:HD22	43:t:196:ILE:HG22	1.96	0.48
45:v:40:LYS:NZ	52:3:70:U:H4'	2.29	0.48
45:v:144:GLN:NE2	46:w:54:THR:HG22	2.29	0.48
45:v:204:TYR:CD2	45:v:223:LEU:HD23	2.49	0.48
46:w:38:ASP:OD1	46:w:49:LYS:NZ	2.47	0.48
47:x:107:LYS:HE2	47:x:108:PRO:HD3	1.94	0.48
50:1:1568:U:H4'	50:1:1569:U:O5'	2.14	0.48
50:1:2506:U:H2'	50:1:2507:C:C6	2.48	0.48
50:1:2568:C:O2'	50:1:2569:A:O4'	2.30	0.48
50:1:3162:C:H2'	50:1:3163:A:C8	2.49	0.48
52:3:43:U:H2'	52:3:44:C:C6	2.48	0.48
10:H:109:ALA:HB3	10:H:111:PHE:CE1	2.49	0.48
12:K:227:LYS:HA	12:K:231:MET:HE3	1.96	0.48
16:P:167:ARG:O	31:f:60:ARG:HG3	2.14	0.48
23:W:220:TYR:OH	23:W:222:ASP:HB2	2.14	0.48
27:b:197:TYR:CZ	27:b:200:THR:HA	2.48	0.48
29:d:80:ASN:H	29:d:88:PRO:HB2	1.79	0.48
43:t:236:GLU:HB2	43:t:245:ILE:HG23	1.95	0.48
47:x:79:PHE:CD2	47:x:119:LEU:HD21	2.48	0.48
50:1:1645:U:H2'	50:1:1646:G:H5'	1.95	0.48
50:1:3099:C:N4	50:1:3135:U:H3	2.08	0.48
50:1:3225:C:H2'	50:1:3226:A:O4'	2.14	0.48
52:3:52:G:H4'	52:3:53:U:OP1	2.13	0.48
8:F:118:LYS:HD2	8:F:191:VAL:HG11	1.95	0.48
12:K:202:VAL:HG11	12:K:247:HIS:CE1	2.49	0.48
12:K:222:LEU:HA	12:K:225:ASN:HD21	1.79	0.48
18:R:154:ALA:HA	18:R:157:GLU:OE2	2.14	0.48
36:k:32:ASN:OD1	36:k:36:LYS:N	2.42	0.48
42:r:154:HIS:NE2	42:r:249:PRO:O	2.47	0.48
47:x:34:ILE:HD11	47:x:119:LEU:HB2	1.95	0.48
50:1:710:A:H2'	50:1:711:A:C8	2.49	0.48
50:1:1250:G:H2'	50:1:1251:A:C8	2.49	0.48
50:1:2238:G:O2'	50:1:2239:G:H5''	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:3194:C:O2'	50:1:3195:U:H2'	2.14	0.48
4:B:140:ASP:OD1	4:B:140:ASP:N	2.47	0.47
5:C:361:HIS:O	19:S:28:ARG:NH2	2.47	0.47
6:D:277:LEU:CD1	6:D:282:ARG:HG3	2.44	0.47
11:J:106:ILE:HG13	11:J:127:PHE:CE2	2.48	0.47
24:X:39:LYS:HG2	50:1:13:A:H4'	1.95	0.47
27:b:175:TYR:CD2	27:b:176:PRO:HD2	2.49	0.47
41:q:214:VAL:HG12	41:q:215:LYS:H	1.79	0.47
48:y:19:LEU:HB3	48:y:198:VAL:HB	1.94	0.47
50:1:655:C:H2'	50:1:656:A:C8	2.48	0.47
50:1:1132:C:H2'	50:1:1133:A:C8	2.48	0.47
53:6:56:U:O2'	53:6:57:U:O5'	2.30	0.47
1:L:15:ARG:HH12	50:1:798:G:H4'	1.78	0.47
3:A:146:THR:OG1	3:A:160:SER:OG	2.31	0.47
4:B:137:TYR:O	4:B:139:GLN:N	2.43	0.47
12:K:166:ALA:HA	53:6:53:A:H2	1.78	0.47
19:S:26:ARG:HH11	20:T:150:THR:HB	1.78	0.47
36:k:7:ASP:HB3	36:k:10:GLN:HG2	1.96	0.47
42:r:153:LYS:HD3	42:r:153:LYS:HA	1.71	0.47
48:y:101:LEU:HD12	48:y:107:VAL:HG11	1.95	0.47
50:1:86:G:O2'	50:1:98:G:O6	2.29	0.47
50:1:1067:U:H2'	50:1:1068:C:C6	2.49	0.47
19:S:117:ARG:HG3	19:S:118:PHE:H	1.78	0.47
27:b:368:ALA:HA	48:y:178:GLN:HE22	1.78	0.47
27:b:469:TYR:CE1	44:u:102:LYS:HG2	2.49	0.47
28:c:23:TYR:OH	28:c:83:LYS:NZ	2.48	0.47
43:t:52:LYS:HA	43:t:52:LYS:HD2	1.66	0.47
46:w:143:PRO:O	46:w:149:GLY:HA2	2.14	0.47
46:w:147:TYR:CE2	46:w:148:LYS:HE3	2.49	0.47
47:x:124:ARG:HB2	47:x:126:VAL:HG22	1.96	0.47
50:1:1784:G:H2'	50:1:1785:U:O4'	2.14	0.47
50:1:2227:C:H2'	50:1:2228:A:C8	2.48	0.47
50:1:2658:G:O2'	50:1:2659:G:O5'	2.30	0.47
50:1:2716:U:C2'	50:1:2717:U:H5'	2.44	0.47
6:D:85:ARG:HH22	6:D:253:PHE:N	2.07	0.47
9:G:70:LYS:HB3	9:G:70:LYS:HE3	1.46	0.47
11:J:158:ASP:O	11:J:161:SER:OG	2.27	0.47
27:b:260:CYS:O	27:b:262:PHE:N	2.44	0.47
35:j:10:LYS:NZ	50:1:818:C:OP1	2.37	0.47
36:k:5:ILE:HD11	36:k:52:TYR:CD2	2.49	0.47
41:q:230:ASN:HD22	41:q:232:LYS:HE3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:188:GLU:HG2	42:r:189:LEU:HD12	1.95	0.47
43:t:137:GLY:HA2	43:t:138:LYS:HB3	1.97	0.47
46:w:133:ILE:HG22	46:w:134:TYR:N	2.29	0.47
46:w:158:TRP:H	46:w:158:TRP:HD1	1.62	0.47
48:y:142:ILE:HD11	48:y:152:CYS:HB2	1.95	0.47
50:1:2778:G:C2'	50:1:2779:A:H5'	2.44	0.47
3:A:80:GLU:HG3	40:p:66:GLY:HA2	1.97	0.47
12:K:278:SER:HB3	12:K:280:PHE:CZ	2.50	0.47
13:M:20:VAL:O	13:M:66:THR:OG1	2.28	0.47
27:b:327:ASN:O	27:b:330:GLU:HG2	2.14	0.47
29:d:84:ASP:OD2	29:d:87:ASN:N	2.36	0.47
44:u:79:VAL:HG12	44:u:80:ARG:HB2	1.96	0.47
45:v:129:LYS:HE3	45:v:129:LYS:HB3	1.56	0.47
47:x:507:ASP:OD1	47:x:507:ASP:N	2.43	0.47
50:1:139:G:H2'	50:1:140:C:C6	2.50	0.47
50:1:166:C:H2'	50:1:167:U:C6	2.50	0.47
50:1:869:G:O2'	50:1:870:G:H5'	2.14	0.47
50:1:1000:C:O3'	50:1:1001:G:H8	1.96	0.47
50:1:1112:A:H2'	50:1:1113:G:C8	2.49	0.47
50:1:2362:C:H2'	50:1:2363:A:O4'	2.15	0.47
50:1:2655:U:H5	50:1:2712:U:C4	2.32	0.47
53:6:14:U:O2	53:6:16:U:H5''	2.14	0.47
6:D:102:GLY:O	6:D:105:ILE:HG22	2.15	0.47
12:K:190:LEU:N	12:K:191:PRO:HD2	2.29	0.47
12:K:239:PRO:HD2	12:K:244:LEU:HG	1.97	0.47
23:W:20:ARG:NH2	50:1:1221:A:H62	2.13	0.47
27:b:289:LYS:HZ1	54:b:701:GTP:H1'	1.79	0.47
38:n:388:ILE:HD11	38:n:393:MET:HE3	1.96	0.47
42:r:229:GLY:HA2	47:x:444:VAL:HG12	1.96	0.47
43:t:25:ASN:O	43:t:29:THR:HG23	2.14	0.47
43:t:229:LEU:HD23	43:t:229:LEU:HA	1.73	0.47
49:z:39:GLU:HA	49:z:42:LEU:HD12	1.97	0.47
50:1:1277:C:O2'	50:1:1278:A:O5'	2.32	0.47
50:1:1390:A:N6	50:1:1418:A:O2'	2.48	0.47
50:1:2213:A:H2'	50:1:2214:A:C8	2.49	0.47
50:1:3337:G:H2'	50:1:3338:C:C6	2.49	0.47
53:6:20:U:H2'	53:6:21:G:C8	2.49	0.47
53:6:56:U:HO2'	53:6:57:U:C5'	2.27	0.47
1:L:22:VAL:HG12	14:N:197:LEU:HD23	1.96	0.47
6:D:23:ARG:HA	6:D:23:ARG:HD2	1.63	0.47
6:D:64:ILE:HG22	6:D:75:LEU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:85:ARG:NH2	6:D:253:PHE:H	2.07	0.47
11:J:32:ARG:O	11:J:35:LYS:HG2	2.14	0.47
11:J:32:ARG:O	11:J:36:VAL:HG13	2.15	0.47
11:J:150:ASN:HA	11:J:153:LYS:HB2	1.97	0.47
27:b:129:LYS:HE3	27:b:129:LYS:HB3	1.57	0.47
36:k:12:LEU:O	36:k:15:THR:OG1	2.33	0.47
37:m:336:ARG:HG2	37:m:340:VAL:HG21	1.95	0.47
38:n:379:LEU:HD23	38:n:379:LEU:HA	1.73	0.47
40:p:49:ARG:HB2	40:p:55:TRP:CZ3	2.49	0.47
41:q:416:LEU:O	41:q:420:VAL:HG23	2.15	0.47
42:r:10:HIS:CD2	42:r:14:HIS:HD2	2.31	0.47
43:t:221:GLU:O	43:t:223:GLU:N	2.48	0.47
44:u:84:GLU:O	44:u:88:THR:HG23	2.14	0.47
47:x:231:TRP:CH2	47:x:256:LYS:HD3	2.50	0.47
47:x:446:SER:O	47:x:463:SER:OG	2.26	0.47
50:1:100:A:H2'	50:1:101:G:N3	2.29	0.47
50:1:241:G:H2'	50:1:241:G:N3	2.29	0.47
50:1:649:A:H2'	50:1:650:C:H6	1.79	0.47
50:1:1605:A:O2'	50:1:1607:U:OP2	2.29	0.47
50:1:2113:A:H61	50:1:3062:G:N2	2.11	0.47
50:1:2203:U:O2	50:1:2239:G:C6	2.68	0.47
50:1:2528:G:C5	50:1:2529:A:C8	3.03	0.47
50:1:2661:G:H2'	50:1:2662:G:H8	1.80	0.47
50:1:2789:U:H2'	50:1:2790:A:O4'	2.15	0.47
50:1:2946:A:H2	50:1:2980:U:H3'	1.80	0.47
50:1:3322:A:H2'	50:1:3323:A:H8	1.80	0.47
52:3:22:A:H2'	52:3:23:A:C8	2.50	0.47
4:B:173:GLN:O	4:B:175:LYS:N	2.48	0.47
26:Z:42:LEU:HD12	26:Z:74:VAL:HG22	1.96	0.47
37:m:2:GLY:HA3	37:m:3:THR:HA	1.48	0.47
39:o:207:ARG:HH11	53:6:35:C:C5'	2.28	0.47
48:y:118:HIS:CE1	48:y:146:ILE:HG21	2.49	0.47
50:1:1549:U:H2'	50:1:1550:C:H6	1.80	0.47
52:3:49:G:N2	52:3:50:U:O4	2.48	0.47
3:A:146:THR:HG1	3:A:160:SER:HG	1.62	0.47
4:B:212:ASN:ND2	4:B:353:GLU:OE1	2.47	0.47
22:V:121:GLU:H	22:V:121:GLU:CD	2.23	0.47
24:X:33:ARG:HH11	50:1:1580:A:H2	1.62	0.47
35:j:56:ARG:NH2	50:1:363:G:OP2	2.47	0.47
37:m:417:GLU:O	37:m:418:ILE:HB	2.13	0.47
43:t:232:ASN:HB3	43:t:246:CYS:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:747:A:H2'	50:1:748:U:C6	2.49	0.47
50:1:799:G:H2'	50:1:801:A:H62	1.80	0.47
50:1:2210:G:H2'	50:1:2211:U:C6	2.49	0.47
52:3:13:A:H5'	52:3:14:U:H5	1.78	0.47
19:S:78:TRP:CD1	19:S:125:LYS:HZ1	2.33	0.47
24:X:133:LEU:HA	24:X:133:LEU:HD23	1.70	0.47
25:Y:100:HIS:CE1	25:Y:102:SER:HG	2.32	0.47
27:b:175:TYR:HD1	27:b:270:LEU:HD22	1.80	0.47
27:b:379:PRO:HG2	27:b:382:VAL:HG22	1.97	0.47
38:n:9:ARG:HG2	38:n:13:ARG:HH11	1.80	0.47
38:n:142:PHE:HZ	38:n:218:MET:HE3	1.80	0.47
45:v:275:ILE:HD13	45:v:275:ILE:HA	1.79	0.47
4:B:240:ARG:CZ	4:B:241:LYS:HB2	2.46	0.46
5:C:347:THR:OG1	50:1:520:U:O4	2.31	0.46
6:D:113:LEU:HD23	6:D:113:LEU:HA	1.72	0.46
27:b:385:LEU:HD21	48:y:43:GLY:HA3	1.96	0.46
28:c:47:ASN:ND2	28:c:74:ASN:OD1	2.42	0.46
37:m:290:ILE:H	37:m:290:ILE:HG13	1.37	0.46
40:p:74:ALA:O	40:p:78:THR:HG23	2.15	0.46
43:t:135:TYR:CZ	43:t:137:GLY:HA3	2.49	0.46
45:v:87:MET:HB2	45:v:103:ILE:HB	1.96	0.46
46:w:73:THR:HB	46:w:75:GLU:OE1	2.15	0.46
50:1:885:U:O2'	50:1:1850:A:O2'	2.27	0.46
50:1:1203:A:H2	50:1:1300:G:H2'	1.79	0.46
50:1:2528:G:C8	50:1:2529:A:C8	3.03	0.46
50:1:2874:G:H2'	50:1:2875:U:O4'	2.15	0.46
4:B:20:LYS:NZ	50:1:3140:G:OP1	2.48	0.46
23:W:34:LEU:HG	23:W:104:PHE:HZ	1.79	0.46
23:W:141:ILE:HG12	23:W:181:THR:HG22	1.97	0.46
24:X:75:LYS:HE2	24:X:123:TYR:CD1	2.50	0.46
41:q:237:LEU:HA	41:q:240:LYS:HG2	1.96	0.46
47:x:172:ASP:OD2	47:x:175:THR:HG22	2.14	0.46
50:1:2205:U:H3'	50:1:2206:G:C8	2.51	0.46
52:3:27:A:H2'	52:3:28:C:O4'	2.15	0.46
53:6:47:A:H2'	53:6:48:A:H5'	1.98	0.46
10:H:17:THR:HG23	10:H:28:VAL:HB	1.97	0.46
10:H:23:ARG:NH2	10:H:39:LYS:O	2.49	0.46
30:e:101:SER:HB3	50:1:1389:G:H5''	1.97	0.46
37:m:238:ARG:HE	37:m:238:ARG:HB2	1.51	0.46
37:m:314:LYS:O	37:m:314:LYS:HG2	2.15	0.46
37:m:423:ASP:O	37:m:425:THR:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:364:VAL:HB	38:n:406:LYS:O	2.15	0.46
42:r:164:ARG:HB2	50:1:2729:U:OP1	2.16	0.46
43:t:217:LYS:HZ1	43:t:222:ALA:HA	1.80	0.46
46:w:21:TYR:CE1	46:w:64:GLN:HG3	2.51	0.46
47:x:325:HIS:HD2	47:x:408:VAL:HG12	1.80	0.46
48:y:221:ILE:HD12	48:y:230:GLU:OE2	2.14	0.46
49:z:18:ARG:NH2	50:1:3100:U:H5''	2.30	0.46
50:1:649:A:HO2'	50:1:650:C:P	2.37	0.46
50:1:954:U:O4	50:1:1115:G:H8	1.99	0.46
50:1:1744:G:H2'	50:1:1745:C:H6	1.81	0.46
50:1:1761:C:H1'	50:1:1763:U:OP2	2.15	0.46
9:G:30:THR:O	9:G:30:THR:OG1	2.28	0.46
12:K:228:LYS:O	12:K:232:ASN:HB2	2.16	0.46
17:Q:55:SER:OG	17:Q:56:LYS:N	2.48	0.46
20:T:41:ASP:OD1	20:T:41:ASP:N	2.47	0.46
28:c:78:GLY:HA2	28:c:87:VAL:HG12	1.98	0.46
32:g:41:ARG:HG2	32:g:56:THR:HG21	1.98	0.46
47:x:55:ILE:HD11	47:x:59:GLN:HB3	1.98	0.46
48:y:157:GLN:O	48:y:180:PRO:HD2	2.15	0.46
50:1:1054:A:H2'	50:1:1055:A:H8	1.80	0.46
50:1:2101:C:O2'	50:1:2102:U:O5'	2.28	0.46
50:1:2953:U:OP1	50:1:2954:U:H5''	2.15	0.46
52:3:74:C:O2'	52:3:105:C:N3	2.46	0.46
4:B:57:VAL:HG12	4:B:358:TRP:HB3	1.98	0.46
5:C:339:LEU:HA	5:C:339:LEU:HD23	1.73	0.46
11:J:82:ARG:HG2	11:J:112:LEU:HB2	1.97	0.46
46:w:56:ASP:O	46:w:59:GLN:HB3	2.15	0.46
47:x:330:THR:O	47:x:334:LEU:HG	2.16	0.46
50:1:760:G:O2'	50:1:761:A:OP2	2.33	0.46
50:1:1659:U:H2'	50:1:1660:C:H6	1.80	0.46
50:1:2652:U:O2'	50:1:2653:C:O5'	2.25	0.46
50:1:2858:U:O2'	50:1:2859:U:OP1	2.25	0.46
52:3:19:C:H2'	52:3:20:A:C8	2.50	0.46
2:a:77:LYS:C	2:a:79:TRP:N	2.73	0.46
10:H:21:LYS:HB2	50:1:3198:U:C2	2.51	0.46
11:J:137:ARG:HD3	52:3:28:C:OP1	2.16	0.46
13:M:8:LYS:HB2	13:M:9:ALA:HB2	1.97	0.46
24:X:73:MET:HE1	24:X:141:TYR:CD1	2.40	0.46
25:Y:60:ARG:HD3	25:Y:60:ARG:HA	1.59	0.46
27:b:161:PRO:HD3	42:r:3:GLN:O	2.16	0.46
27:b:169:THR:OG1	27:b:170:LEU:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:301:GLU:OE1	27:b:301:GLU:N	2.49	0.46
39:o:107:LEU:HD23	39:o:137:LEU:HD11	1.98	0.46
46:w:23:LEU:HD21	46:w:64:GLN:HB3	1.96	0.46
50:1:649:A:H2'	50:1:650:C:C6	2.51	0.46
50:1:1740:U:H4'	50:1:1741:A:H5''	1.97	0.46
50:1:2240:G:H2'	50:1:2241:U:H6	1.81	0.46
50:1:2627:C:H2'	50:1:2651:G:N2	2.30	0.46
50:1:3164:C:O2'	50:1:3165:A:H8	1.98	0.46
52:3:39:C:H2'	52:3:40:C:C6	2.51	0.46
1:L:109:PHE:O	1:L:113:VAL:HG23	2.16	0.46
5:C:9:HIS:ND1	5:C:14:GLU:O	2.49	0.46
5:C:260:GLN:O	5:C:270:SER:HB3	2.16	0.46
12:K:166:ALA:O	12:K:168:GLU:N	2.49	0.46
13:M:76:ALA:HB1	13:M:80:THR:OG1	2.16	0.46
23:W:196:ASP:OD2	23:W:198:ARG:HG2	2.16	0.46
37:m:31:ARG:NH2	50:1:2966:G:O6	2.49	0.46
38:n:18:ARG:HE	38:n:29:LEU:HD11	1.81	0.46
47:x:264:ASP:N	47:x:271:GLN:HE22	2.14	0.46
50:1:543:C:H2'	50:1:544:C:O4'	2.15	0.46
50:1:921:A:N6	50:1:1846:C:OP2	2.48	0.46
50:1:1137:C:H2'	50:1:1138:U:C6	2.50	0.46
50:1:1596:C:H2'	50:1:1597:C:C6	2.51	0.46
4:B:108:GLU:HB2	4:B:137:TYR:CE2	2.51	0.46
6:D:22:ARG:H	6:D:22:ARG:HG2	1.56	0.46
8:F:110:ARG:O	8:F:113:SER:OG	2.22	0.46
11:J:65:ILE:HD13	50:1:2681:U:H5'	1.97	0.46
23:W:108:ASP:N	23:W:108:ASP:OD1	2.48	0.46
27:b:179:GLY:O	27:b:288:ASN:ND2	2.49	0.46
38:n:18:ARG:NH1	50:1:1566:A:OP2	2.49	0.46
38:n:148:THR:H	38:n:151:VAL:HG12	1.81	0.46
43:t:47:LYS:O	43:t:47:LYS:HD3	2.16	0.46
50:1:293:C:H2'	50:1:294:U:O4'	2.16	0.46
50:1:2883:U:H2'	50:1:2884:C:C6	2.50	0.46
52:3:75:G:H1'	52:3:104:A:H62	1.81	0.46
3:A:106:SER:O	3:A:106:SER:OG	2.21	0.46
12:K:214:ASN:HA	12:K:215:LYS:HA	1.73	0.46
39:o:93:ILE:HD12	39:o:166:VAL:HA	1.98	0.46
39:o:94:TYR:O	39:o:164:VAL:HA	2.16	0.46
45:v:102:PHE:HB2	45:v:114:ILE:CG2	2.46	0.46
47:x:255:SER:OG	47:x:256:LYS:N	2.49	0.46
48:y:95:GLN:HE21	48:y:128:LEU:HD21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:283:G:H2'	50:1:284:A:C8	2.50	0.46
50:1:655:C:H2'	50:1:656:A:H8	1.80	0.46
50:1:722:G:H2'	50:1:723:U:H6	1.80	0.46
50:1:2723:U:O2'	50:1:2724:U:O2	2.30	0.46
8:F:216:VAL:HG23	8:F:216:VAL:O	2.15	0.46
23:W:41:TRP:CD2	23:W:220:TYR:HB2	2.50	0.46
23:W:190:THR:HG22	23:W:191:GLU:H	1.81	0.46
27:b:459:GLU:OE2	44:u:103:ARG:NH2	2.45	0.46
42:r:4:ASN:HB2	42:r:9:ARG:HH22	1.80	0.46
45:v:19:ARG:HD3	45:v:19:ARG:HA	1.75	0.46
45:v:179:GLN:O	45:v:206:LEU:HD23	2.16	0.46
45:v:187:GLN:N	45:v:198:ASN:O	2.49	0.46
46:w:30:ASP:OD1	46:w:32:ASN:HB2	2.16	0.46
46:w:64:GLN:HE22	47:x:19:PRO:HB3	1.81	0.46
47:x:187:ASN:HB3	47:x:207:ASP:H	1.81	0.46
47:x:282:SER:OG	47:x:283:CYS:N	2.49	0.46
50:1:182:U:H3	50:1:234:G:H1	1.64	0.46
50:1:1065:A:H5'	50:1:1066:G:C8	2.51	0.46
50:1:1254:C:H2'	50:1:1255:C:O2	2.16	0.46
50:1:3283:U:H2'	50:1:3284:G:C8	2.50	0.46
51:2:10:A:H2'	51:2:11:C:C6	2.51	0.46
5:C:163:LYS:HE3	50:1:208:C:OP2	2.17	0.45
13:M:133:LYS:HA	13:M:133:LYS:HD2	1.60	0.45
42:r:237:VAL:HG11	47:x:444:VAL:HG21	1.98	0.45
43:t:200:SER:O	43:t:204:ILE:HG12	2.17	0.45
48:y:123:ARG:NH1	48:y:126:GLU:OE2	2.49	0.45
50:1:1641:U:O2'	50:1:1642:A:H3'	2.16	0.45
50:1:2119:A:O5'	50:1:2119:A:H8	1.99	0.45
50:1:2569:A:HO2'	50:1:2570:U:P	2.38	0.45
52:3:27:A:H1'	52:3:56:A:H61	1.81	0.45
4:B:84:VAL:HG22	4:B:162:VAL:HB	1.98	0.45
12:K:190:LEU:HD23	12:K:190:LEU:HA	1.78	0.45
16:P:65:SER:HB3	50:1:1447:G:OP1	2.17	0.45
17:Q:43:PRO:O	17:Q:47:VAL:HG23	2.16	0.45
22:V:84:SER:HA	22:V:94:TYR:HB3	1.98	0.45
23:W:91:GLN:HB2	23:W:228:VAL:HG11	1.98	0.45
27:b:70:ASN:HA	50:1:2863:G:O6	2.17	0.45
27:b:511:LYS:HG3	27:b:512:SER:N	2.31	0.45
30:e:82:LEU:HD21	30:e:112:ALA:HB2	1.97	0.45
38:n:176:VAL:HG21	38:n:382:SER:HB2	1.99	0.45
38:n:383:CYS:SG	38:n:436:ILE:HD12	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:v:223:LEU:HD11	46:w:58:VAL:HG21	1.98	0.45
47:x:154:HIS:HB2	47:x:339:PHE:CE1	2.50	0.45
47:x:185:HIS:CE1	47:x:205:SER:HB2	2.52	0.45
47:x:411:SER:HB3	47:x:416:TYR:HB2	1.98	0.45
50:1:1317:A:O2'	50:1:1318:A:H3'	2.16	0.45
50:1:2245:C:H2'	50:1:2245:C:O2	2.16	0.45
51:2:81:U:N3	51:2:83:C:H5	2.10	0.45
11:J:33:ALA:O	11:J:36:VAL:HG22	2.17	0.45
12:K:128:LYS:HB2	12:K:183:ASP:OD1	2.16	0.45
23:W:18:LYS:HD3	23:W:18:LYS:HA	1.76	0.45
24:X:19:ASN:OD1	50:1:1:G:O2'	2.31	0.45
27:b:274:ILE:C	27:b:276:PRO:HD2	2.42	0.45
31:f:72:THR:HG22	50:1:585:A:H4'	1.98	0.45
45:v:53:LYS:NZ	45:v:164:PHE:O	2.33	0.45
50:1:885:U:HO2'	50:1:1850:A:HO2'	1.59	0.45
50:1:2841:G:N2	50:1:2847:A:H62	2.13	0.45
12:K:123:VAL:HG11	12:K:150:LYS:O	2.17	0.45
13:M:7:VAL:O	13:M:7:VAL:HG12	2.15	0.45
26:Z:51:LEU:HB2	26:Z:65:ARG:HD2	1.97	0.45
28:c:27:TYR:O	28:c:31:VAL:HG23	2.16	0.45
37:m:422:LYS:O	37:m:426:GLU:HB3	2.16	0.45
43:t:98:ASP:HB2	43:t:184:TYR:CZ	2.52	0.45
48:y:61:ARG:NH1	48:y:195:ALA:HA	2.31	0.45
50:1:2266:U:O4	50:1:2267:C:N4	2.49	0.45
50:1:2636:A:H5''	50:1:2637:A:H5'	1.99	0.45
50:1:3232:G:C6	50:1:3256:G:C6	3.04	0.45
50:1:3358:U:C2	50:1:3359:A:C8	3.04	0.45
4:B:260:VAL:HG21	4:B:266:ARG:HH21	1.81	0.45
6:D:220:SER:OG	6:D:221:GLU:N	2.49	0.45
19:S:81:TYR:CD1	19:S:110:MET:HE1	2.52	0.45
21:U:89:LEU:O	21:U:92:TRP:HB2	2.16	0.45
23:W:74:GLN:HE22	23:W:96:CYS:HB3	1.82	0.45
24:X:86:VAL:HG11	24:X:95:ILE:HG12	1.98	0.45
27:b:168:ARG:HH12	27:b:214:LEU:HD22	1.81	0.45
37:m:437:ARG:HD3	37:m:437:ARG:HA	1.80	0.45
38:n:207:GLU:HG2	38:n:208:ASN:H	1.80	0.45
41:q:249:GLU:OE2	41:q:252:ARG:NH1	2.36	0.45
45:v:123:LYS:NZ	45:v:229:ARG:HH11	2.15	0.45
47:x:77:TYR:HB2	47:x:79:PHE:CE1	2.51	0.45
50:1:1124:U:H2'	50:1:1125:U:C6	2.52	0.45
50:1:2242:A:O2'	50:1:2243:A:H5''	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:2683:U:C2	50:1:2684:C:C5	3.05	0.45
3:A:113:VAL:HG12	3:A:166:ILE:HD13	1.99	0.45
4:B:364:LYS:HD2	50:1:3049:A:H4'	1.97	0.45
6:D:262:LYS:HA	6:D:265:TYR:HD2	1.82	0.45
11:J:33:ALA:O	11:J:37:LEU:HG	2.16	0.45
19:S:171:PHE:HA	19:S:172:TYR:O	2.17	0.45
23:W:169:PHE:HB3	23:W:171:ILE:HD12	1.98	0.45
33:h:62:GLN:O	33:h:66:VAL:HG23	2.16	0.45
34:i:26:ILE:HG21	50:1:157:A:C8	2.52	0.45
42:r:46:LYS:NZ	50:1:2908:G:OP1	2.46	0.45
46:w:45:ARG:HA	46:w:45:ARG:NE	2.31	0.45
47:x:449:GLN:HE21	47:x:491:THR:HA	1.81	0.45
50:1:2692:A:N6	50:1:2693:C:H42	2.15	0.45
4:B:227:GLU:HG2	4:B:231:HIS:CD2	2.52	0.45
6:D:107:ARG:NH1	6:D:169:GLY:O	2.50	0.45
10:H:49:ASN:N	10:H:49:ASN:OD1	2.50	0.45
12:K:221:THR:O	12:K:225:ASN:ND2	2.50	0.45
16:P:85:ALA:O	16:P:89:LYS:HG3	2.16	0.45
22:V:2:SER:OG	22:V:3:GLY:N	2.47	0.45
30:e:33:ARG:NH1	50:1:944:C:H4'	2.32	0.45
33:h:118:ILE:HG22	33:h:119:LYS:N	2.32	0.45
37:m:359:MET:HG3	37:m:362:ILE:HD13	1.98	0.45
39:o:193:VAL:O	39:o:197:LYS:HG3	2.17	0.45
43:t:173:THR:HG22	43:t:272:LYS:HA	1.97	0.45
46:w:148:LYS:HE2	50:1:2653:C:H41	1.80	0.45
47:x:32:VAL:O	47:x:52:PRO:HD2	2.17	0.45
50:1:1176:C:H2'	50:1:1177:G:N2	2.32	0.45
50:1:1549:U:H2'	50:1:1550:C:C6	2.51	0.45
50:1:2576:G:H2'	50:1:2577:C:C6	2.52	0.45
50:1:2762:A:H5''	50:1:2763:U:O5'	2.16	0.45
3:A:97:ASN:HB2	3:A:100:ASN:ND2	2.32	0.45
11:J:35:LYS:HE2	11:J:35:LYS:HB3	1.84	0.45
11:J:145:LYS:HE3	11:J:145:LYS:HB2	1.90	0.45
11:J:166:LYS:HE2	11:J:166:LYS:HB2	1.84	0.45
23:W:30:VAL:O	23:W:34:LEU:HD12	2.17	0.45
23:W:50:THR:HG21	50:1:1232:C:H1'	1.97	0.45
37:m:417:GLU:OE1	37:m:417:GLU:N	2.50	0.45
39:o:193:VAL:HG22	39:o:194:LYS:HE3	1.98	0.45
42:r:62:ARG:HE	42:r:62:ARG:HB2	1.59	0.45
47:x:158:ARG:HA	47:x:158:ARG:HD3	1.72	0.45
50:1:1771:C:H2'	50:1:1772:U:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:2152:A:H2'	50:1:2153:U:C6	2.52	0.45
52:3:22:A:H2'	52:3:23:A:H8	1.82	0.45
5:C:270:SER:O	5:C:270:SER:OG	2.33	0.45
6:D:55:PHE:CE2	6:D:60:ILE:HD12	2.52	0.45
7:E:137:ASP:O	7:E:141:VAL:HG12	2.17	0.45
13:M:20:VAL:HG22	13:M:66:THR:OG1	2.16	0.45
16:P:126:ARG:HA	16:P:140:GLU:HG2	1.99	0.45
27:b:318:MET:HE3	27:b:334:LYS:HD2	1.98	0.45
32:g:84:CYS:HA	32:g:87:GLU:HG2	1.99	0.45
38:n:126:PRO:HA	38:n:129:ILE:HD12	1.98	0.45
42:r:87:LEU:HB3	42:r:91:LEU:HB3	1.99	0.45
46:w:194:GLN:HB3	50:1:2758:A:OP1	2.17	0.45
48:y:18:LYS:HE2	48:y:18:LYS:HB2	1.77	0.45
48:y:223:ARG:HG3	48:y:230:GLU:OE1	2.17	0.45
50:1:656:A:H2'	50:1:657:A:H8	1.80	0.45
50:1:787:G:H2'	50:1:788:C:H6	1.82	0.45
50:1:994:G:O2'	50:1:996:A:N6	2.50	0.45
50:1:1124:U:H5	50:1:1134:G:H1	1.64	0.45
50:1:2278:C:H41	50:1:2315:G:H1	1.65	0.45
50:1:2657:A:C6	50:1:2713:U:O4	2.69	0.45
50:1:2761:G:O2'	50:1:2762:A:O5'	2.27	0.45
8:F:33:ARG:O	8:F:37:ASN:ND2	2.49	0.45
9:G:188:THR:HG22	38:n:96:ARG:HD2	1.99	0.45
12:K:267:SER:O	12:K:271:ILE:HG23	2.17	0.45
23:W:20:ARG:NH2	50:1:1221:A:N7	2.63	0.45
23:W:216:LYS:HB2	23:W:216:LYS:HE3	1.74	0.45
27:b:265:GLU:O	27:b:268:VAL:HG12	2.17	0.45
27:b:290:THR:HG23	27:b:295:PRO:HD2	1.99	0.45
37:m:149:ARG:HB2	37:m:149:ARG:HH21	1.82	0.45
37:m:208:SER:O	37:m:210:ARG:N	2.49	0.45
38:n:366:TYR:CD1	38:n:388:ILE:HG23	2.48	0.45
38:n:449:PRO:HA	38:n:451:GLU:H	1.81	0.45
43:t:171:THR:OG1	43:t:172:ASN:N	2.49	0.45
43:t:258:GLY:O	43:t:260:SER:N	2.47	0.45
45:v:213:GLN:NE2	46:w:9:LEU:HB3	2.32	0.45
45:v:229:ARG:NH2	46:w:47:GLU:HG3	2.32	0.45
47:x:194:TRP:HD1	47:x:195:SER:O	2.00	0.45
50:1:12:A:H2'	50:1:13:A:C8	2.52	0.45
50:1:761:A:O2'	50:1:762:U:OP1	2.31	0.45
50:1:2681:U:H2'	50:1:2682:C:O4'	2.17	0.45
50:1:2982:A:O2'	50:1:2984:C:OP2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:3116:G:N3	50:1:3116:G:H2'	2.31	0.45
1:L:23:LYS:HE3	1:L:25:HIS:CE1	2.52	0.44
4:B:355:SER:O	4:B:355:SER:OG	2.35	0.44
7:E:69:PHE:HB2	7:E:138:GLN:NE2	2.33	0.44
9:G:136:LEU:O	9:G:140:VAL:HG23	2.16	0.44
9:G:158:ASP:HB2	9:G:159:PRO:HD3	1.99	0.44
12:K:237:LYS:O	12:K:238:LEU:HD23	2.17	0.44
26:Z:95:VAL:O	26:Z:100:THR:HG21	2.17	0.44
27:b:71:ILE:HG23	27:b:72:ASN:H	1.82	0.44
27:b:434:GLU:O	27:b:435:ILE:HG12	2.17	0.44
33:h:101:THR:OG1	33:h:102:GLU:N	2.48	0.44
34:i:54:GLU:O	34:i:58:ILE:HG12	2.18	0.44
37:m:121:LYS:HB3	37:m:121:LYS:HE2	1.71	0.44
42:r:136:VAL:HG13	42:r:149:ARG:NH2	2.32	0.44
43:t:90:THR:HB	43:t:93:ILE:HD13	1.99	0.44
44:u:77:VAL:HA	44:u:78:PRO:HD3	1.70	0.44
45:v:41:ASN:HB3	45:v:122:PHE:CZ	2.53	0.44
46:w:187:LEU:HD22	50:1:2623:G:H4'	1.99	0.44
50:1:171:G:H2'	50:1:172:G:H8	1.82	0.44
50:1:497:C:H2'	50:1:498:A:O4'	2.17	0.44
50:1:998:A:H2'	50:1:999:G:N7	2.32	0.44
50:1:1288:U:H2'	50:1:1289:G:C8	2.48	0.44
51:2:139:U:H2'	51:2:140:G:C8	2.52	0.44
3:A:117:GLU:HB2	3:A:162:ALA:HB1	1.99	0.44
6:D:35:ARG:HD3	6:D:35:ARG:HA	1.72	0.44
27:b:170:LEU:HA	27:b:248:SER:HB2	1.98	0.44
27:b:258:GLU:OE1	27:b:258:GLU:N	2.44	0.44
27:b:512:SER:O	27:b:512:SER:OG	2.28	0.44
37:m:278:SER:HA	37:m:281:ARG:O	2.17	0.44
37:m:285:ALA:HB3	45:v:280:GLN:HE21	1.82	0.44
37:m:422:LYS:HE3	37:m:422:LYS:HB3	1.75	0.44
38:n:41:ILE:HD12	38:n:71:LEU:HD22	1.99	0.44
43:t:216:TYR:CE1	43:t:234:ILE:HG23	2.52	0.44
45:v:22:LYS:HD2	45:v:22:LYS:HA	1.58	0.44
48:y:7:PHE:O	48:y:8:GLU:C	2.59	0.44
50:1:565:U:H2'	50:1:566:G:H8	1.81	0.44
50:1:970:A:H2'	50:1:971:G:O4'	2.17	0.44
50:1:1481:A:N3	50:1:1858:A:O2'	2.48	0.44
50:1:2623:G:H2'	50:1:2624:G:C8	2.52	0.44
50:1:2625:C:N3	50:1:2656:A:C4	2.85	0.44
50:1:2781:U:H2'	50:1:2782:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:2866:U:O3'	50:1:2867:C:H4'	2.17	0.44
50:1:3218:A:H5''	50:1:3219:G:C5	2.52	0.44
2:a:87:ARG:O	2:a:91:LEU:HG	2.17	0.44
4:B:210:GLU:HG2	49:z:33:ILE:HD11	1.98	0.44
4:B:348:ARG:HA	4:B:348:ARG:HD3	1.62	0.44
6:D:186:GLU:H	6:D:186:GLU:CD	2.25	0.44
16:P:127:ARG:HB3	16:P:139:TYR:O	2.17	0.44
27:b:229:THR:HA	27:b:232:MET:HG2	1.99	0.44
37:m:302:LEU:HD11	45:v:275:ILE:HG23	1.98	0.44
38:n:448:LEU:HD12	38:n:448:LEU:O	2.17	0.44
42:r:161:PHE:HZ	50:1:2727:A:C6	2.36	0.44
42:r:214:VAL:HG12	42:r:216:THR:HG23	2.00	0.44
47:x:379:ASP:OD1	47:x:379:ASP:N	2.50	0.44
50:1:115:A:H2'	50:1:265:A:N3	2.33	0.44
50:1:358:G:N2	50:1:361:A:OP2	2.44	0.44
50:1:824:C:O2'	50:1:825:U:H5'	2.18	0.44
50:1:914:A:O3'	50:1:916:G:N2	2.50	0.44
50:1:1444:G:H2'	50:1:1445:U:O4'	2.17	0.44
50:1:2203:U:C2	50:1:2239:G:O6	2.70	0.44
50:1:2402:A:H4'	50:1:2403:G:C8	2.53	0.44
50:1:2883:U:H2'	50:1:2884:C:H6	1.81	0.44
50:1:3153:U:H1'	50:1:3154:C:H6	1.82	0.44
1:L:18:TRP:HZ3	14:N:195:ASN:ND2	2.15	0.44
11:J:138:VAL:HG22	11:J:141:ARG:HH12	1.82	0.44
13:M:46:ILE:HD13	13:M:58:ILE:HG21	1.98	0.44
14:N:108:ARG:NH2	50:1:1547:G:OP1	2.43	0.44
25:Y:115:ARG:O	25:Y:119:ILE:HG13	2.17	0.44
27:b:171:LEU:HD23	27:b:248:SER:OG	2.18	0.44
27:b:226:ASP:CG	27:b:227:ARG:H	2.24	0.44
38:n:196:GLU:OE2	38:n:198:ARG:NH1	2.51	0.44
47:x:135:SER:HB2	47:x:513:TRP:CE3	2.52	0.44
47:x:321:HIS:HD2	47:x:379:ASP:HB2	1.82	0.44
50:1:542:G:C6	50:1:550:A:C6	3.06	0.44
50:1:973:A:H3'	50:1:974:G:O4'	2.17	0.44
50:1:2113:A:N6	50:1:3062:G:H21	2.15	0.44
50:1:2423:U:H2'	50:1:2424:A:H8	1.81	0.44
50:1:2778:G:H2'	50:1:2779:A:H5'	1.99	0.44
51:2:80:A:O2'	51:2:81:U:H2'	2.17	0.44
52:3:71:G:C6	52:3:72:A:C6	3.05	0.44
4:B:261:MET:HE2	4:B:261:MET:HB3	1.65	0.44
6:D:277:LEU:HD23	52:3:62:U:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:43:PRO:HB2	50:1:728:G:H5'	2.00	0.44
27:b:511:LYS:HD2	27:b:513:LEU:HD12	1.99	0.44
44:u:117:GLU:O	44:u:121:LEU:HG	2.18	0.44
50:1:1107:C:H2'	50:1:1108:U:C2	2.53	0.44
8:F:156:ILE:HG23	8:F:161:VAL:HG21	2.00	0.44
11:J:28:ASP:O	11:J:31:THR:OG1	2.35	0.44
11:J:74:PRO:O	11:J:78:GLU:HG3	2.18	0.44
11:J:114:ILE:HD12	11:J:114:ILE:HA	1.83	0.44
12:K:126:ILE:HD13	12:K:160:LEU:HD11	2.00	0.44
27:b:175:TYR:O	27:b:178:VAL:HG23	2.18	0.44
42:r:45:TRP:HA	42:r:48:LYS:HG3	1.99	0.44
46:w:49:LYS:HD3	46:w:49:LYS:HA	1.71	0.44
47:x:487:ASP:OD2	47:x:488:GLU:HG2	2.17	0.44
50:1:2095:G:O6	50:1:2096:A:N6	2.50	0.44
50:1:3217:C:C5	50:1:3220:G:H1'	2.52	0.44
52:3:3:U:O2'	52:3:25:G:N3	2.50	0.44
52:3:55:A:H2'	52:3:56:A:O4'	2.18	0.44
1:L:56:PRO:HG3	1:L:74:GLY:O	2.18	0.44
6:D:282:ARG:NH2	52:3:63:A:OP2	2.51	0.44
8:F:53:LYS:O	8:F:57:THR:HG23	2.17	0.44
9:G:163:VAL:HG12	9:G:166:LEU:HD12	2.00	0.44
9:G:216:SER:OG	53:6:52:G:N2	2.41	0.44
11:J:109:HIS:CD2	11:J:123:PHE:H	2.36	0.44
20:T:143:THR:O	20:T:143:THR:OG1	2.23	0.44
32:g:29:ILE:HD11	32:g:31:ARG:HH21	1.83	0.44
32:g:105:VAL:O	32:g:109:THR:OG1	2.36	0.44
37:m:358:LEU:HG	37:m:359:MET:HG2	1.98	0.44
44:u:76:ASN:ND2	48:y:96:ARG:HD2	2.32	0.44
47:x:24:ILE:HB	47:x:26:PRO:HG3	1.98	0.44
47:x:323:VAL:HA	47:x:378:SER:HB2	1.98	0.44
48:y:57:ARG:HE	48:y:57:ARG:HB2	1.55	0.44
48:y:177:LEU:O	48:y:179:VAL:HG23	2.18	0.44
50:1:1717:U:H2'	50:1:1718:G:C8	2.53	0.44
50:1:1719:G:H2'	50:1:1720:U:O4'	2.18	0.44
50:1:2528:G:OP2	50:1:2528:G:H2'	2.18	0.44
50:1:2724:U:O2	50:1:2724:U:H2'	2.17	0.44
50:1:3058:U:O2	50:1:3058:U:H2'	2.18	0.44
50:1:3339:A:O2'	50:1:3340:G:H5'	2.17	0.44
51:2:78:G:H8	51:2:78:G:O5'	2.00	0.44
10:H:62:ARG:HH22	23:W:1:MET:HG2	1.82	0.44
12:K:119:LYS:HD2	12:K:119:LYS:HA	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:8:LYS:HD3	13:M:9:ALA:HB2	1.98	0.44
14:N:140:LYS:HB3	14:N:144:ARG:NH1	2.33	0.44
16:P:182:ILE:HG23	50:1:3217:C:N3	2.32	0.44
28:c:50:VAL:O	28:c:54:SER:OG	2.25	0.44
37:m:215:LEU:HD12	37:m:321:ILE:HD12	2.00	0.44
39:o:136:PHE:HE1	39:o:167:LEU:HD11	1.82	0.44
43:t:217:LYS:HB2	43:t:223:GLU:OE1	2.18	0.44
43:t:314:ILE:HA	43:t:317:LEU:HB3	1.99	0.44
46:w:133:ILE:CG1	46:w:144:LYS:HB3	2.48	0.44
47:x:472:ASP:OD1	47:x:475:THR:HG22	2.17	0.44
50:1:501:A:H2'	50:1:502:U:C6	2.52	0.44
50:1:2258:U:H2'	50:1:2259:A:C8	2.53	0.44
50:1:3366:G:H2'	50:1:3367:C:C6	2.53	0.44
52:3:13:A:C4	52:3:112:G:C6	3.06	0.44
52:3:67:G:H2'	52:3:68:C:O4'	2.18	0.44
52:3:77:G:H1'	52:3:78:U:C5	2.53	0.44
5:C:22:LEU:HA	5:C:23:PRO:HD3	1.87	0.44
5:C:181:VAL:O	5:C:182:LEU:HG	2.18	0.44
6:D:215:ASP:OD1	6:D:216:GLU:N	2.51	0.44
7:E:63:LEU:HB2	7:E:79:VAL:HG12	2.00	0.44
12:K:168:GLU:HG2	12:K:169:ALA:H	1.83	0.44
12:K:260:VAL:HG13	12:K:261:ASP:H	1.83	0.44
14:N:204:LYS:HE2	50:1:82:C:O3'	2.18	0.44
15:O:156:LEU:HD22	50:1:3243:A:C8	2.53	0.44
17:Q:57:ILE:HD12	17:Q:57:ILE:HA	1.81	0.44
27:b:302:ARG:NH2	27:b:305:LEU:HB2	2.33	0.44
32:g:38:LEU:HD21	50:1:1741:A:O2'	2.18	0.44
37:m:274:VAL:HG23	37:m:283:THR:HG22	2.00	0.44
38:n:360:PHE:O	38:n:363:PHE:HB2	2.18	0.44
42:r:18:LEU:HA	42:r:18:LEU:HD12	1.72	0.44
42:r:128:ILE:HG23	42:r:132:GLU:OE2	2.17	0.44
47:x:25:ILE:HG22	47:x:102:TYR:HD2	1.83	0.44
47:x:275:SER:O	47:x:275:SER:OG	2.29	0.44
48:y:6:GLN:HG3	48:y:208:LEU:HB2	1.99	0.44
50:1:1196:C:O2'	50:1:1197:A:H5''	2.18	0.44
50:1:2222:A:H8	50:1:2222:A:O5'	2.01	0.44
50:1:2688:U:H4'	50:1:2689:A:H5''	2.00	0.44
50:1:2768:U:H2'	50:1:2769:A:C8	2.53	0.44
50:1:3159:C:H2'	50:1:3160:U:C6	2.53	0.44
5:C:58:HIS:HD1	5:C:90:PHE:HE1	1.65	0.43
7:E:98:VAL:C	7:E:100:LYS:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:146:LYS:HD2	9:G:173:MET:HB3	1.99	0.43
12:K:34:ARG:O	12:K:38:ILE:HG12	2.18	0.43
12:K:201:LYS:NZ	53:6:49:C:OP2	2.47	0.43
14:N:5:LYS:HG3	34:i:40:VAL:HG11	2.00	0.43
19:S:34:GLU:O	19:S:38:LYS:HG3	2.17	0.43
22:V:45:ARG:HD2	22:V:46:LEU:H	1.81	0.43
26:Z:61:LYS:HD3	26:Z:61:LYS:HA	1.77	0.43
26:Z:83:THR:HG22	32:g:93:PHE:CZ	2.53	0.43
34:i:20:MET:HB3	34:i:20:MET:HE2	1.63	0.43
37:m:418:ILE:HA	37:m:418:ILE:HD12	1.64	0.43
43:t:168:LEU:HA	43:t:168:LEU:HD23	1.72	0.43
46:w:26:LEU:HD22	46:w:65:LEU:HD21	1.99	0.43
47:x:451:ALA:HB3	47:x:460:VAL:HG13	1.99	0.43
5:C:299:ILE:HD13	5:C:299:ILE:HA	1.81	0.43
6:D:196:ARG:HD3	47:x:177:THR:HB	2.00	0.43
37:m:94:SER:O	37:m:98:GLU:HG2	2.17	0.43
37:m:99:THR:C	37:m:100:GLN:HG2	2.43	0.43
37:m:189:ASP:OD2	37:m:194:TRP:NE1	2.48	0.43
38:n:139:LEU:HD23	38:n:139:LEU:HA	1.83	0.43
38:n:428:GLN:OE1	38:n:453:LEU:HD11	2.18	0.43
42:r:137:ILE:HD11	42:r:150:MET:HE3	2.00	0.43
42:r:145:LYS:HA	42:r:145:LYS:HD3	1.60	0.43
44:u:137:ARG:O	44:u:141:ILE:HG13	2.17	0.43
47:x:458:LEU:HB2	47:x:494:TRP:HH2	1.84	0.43
50:1:887:G:H8	50:1:887:G:OP2	2.02	0.43
50:1:1072:G:H2'	50:1:1073:U:H6	1.83	0.43
50:1:2228:A:H2'	50:1:2229:A:H8	1.83	0.43
50:1:2622:C:O2'	50:1:2623:G:H8	2.01	0.43
2:a:75:LEU:HD13	2:a:118:ILE:HD13	1.99	0.43
4:B:248:LYS:NZ	50:1:1889:G:H5'	2.33	0.43
7:E:20:LYS:HA	7:E:20:LYS:HD3	1.85	0.43
11:J:21:ILE:HD12	11:J:33:ALA:HB1	1.99	0.43
12:K:177:PHE:HB3	12:K:180:ILE:HD11	1.99	0.43
23:W:55:GLU:HA	23:W:58:THR:HG22	2.01	0.43
23:W:194:LYS:HA	23:W:194:LYS:HD3	1.64	0.43
24:X:33:ARG:HD3	50:1:1580:A:C2	2.52	0.43
25:Y:5:SER:OG	25:Y:7:ASP:OD2	2.35	0.43
29:d:84:ASP:HB3	29:d:87:ASN:ND2	2.33	0.43
37:m:41:MET:HE3	42:r:147:TRP:CZ3	2.52	0.43
37:m:224:VAL:HG23	37:m:318:VAL:HG13	2.00	0.43
38:n:191:ASN:HA	38:n:196:GLU:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:x:344:LYS:HB2	47:x:344:LYS:HE3	1.76	0.43
48:y:1:MET:N	48:y:224:LEU:HD12	2.33	0.43
48:y:72:VAL:HG23	48:y:96:ARG:HA	2.00	0.43
50:1:1621:A:H2'	50:1:1622:U:C6	2.54	0.43
50:1:2809:C:H2'	50:1:2810:C:H4'	2.00	0.43
52:3:59:U:H2'	52:3:60:G:H8	1.79	0.43
53:6:15:C:O2'	53:6:16:U:OP1	2.28	0.43
2:a:96:LYS:C	2:a:98:THR:H	2.26	0.43
7:E:76:LEU:HD23	7:E:76:LEU:HA	1.88	0.43
30:e:33:ARG:NH1	50:1:944:C:O2'	2.52	0.43
37:m:228:VAL:HG21	37:m:328:LYS:HG2	2.00	0.43
41:q:407:ARG:HD2	43:t:246:CYS:SG	2.59	0.43
43:t:221:GLU:C	43:t:223:GLU:N	2.76	0.43
47:x:293:TYR:CD1	47:x:303:VAL:HG22	2.52	0.43
50:1:542:G:O6	50:1:550:A:N6	2.51	0.43
50:1:2528:G:C6	50:1:2529:A:C5	3.07	0.43
50:1:2953:U:H5'	50:1:2954:U:C6	2.54	0.43
52:3:19:C:C2	52:3:61:G:N2	2.86	0.43
4:B:4:ARG:HD3	4:B:6:TYR:O	2.18	0.43
7:E:100:LYS:NZ	7:E:137:ASP:OD1	2.50	0.43
8:F:132:PRO:HA	8:F:229:PHE:CD2	2.53	0.43
13:M:4:ASP:OD1	13:M:4:ASP:N	2.51	0.43
19:S:24:LEU:HD23	19:S:24:LEU:HA	1.79	0.43
25:Y:118:LEU:O	25:Y:122:LYS:HG3	2.18	0.43
26:Z:111:LYS:HA	26:Z:114:VAL:HG22	2.01	0.43
38:n:148:THR:OG1	38:n:149:ASN:N	2.51	0.43
42:r:182:ALA:HA	42:r:255:VAL:HG13	1.99	0.43
45:v:138:LYS:HB2	45:v:138:LYS:HE2	1.81	0.43
45:v:286:GLN:NE2	50:1:2277:C:H42	2.16	0.43
47:x:332:TYR:O	47:x:336:ILE:HG23	2.19	0.43
50:1:306:A:H2'	50:1:307:A:H8	1.82	0.43
50:1:824:C:O2'	50:1:1534:A:N3	2.50	0.43
50:1:881:C:O2'	50:1:1849:C:H1'	2.18	0.43
50:1:1480:G:O2'	50:1:1871:U:O4	2.29	0.43
50:1:1764:U:H4'	50:1:1765:U:H5''	1.99	0.43
50:1:2571:U:O2'	50:1:2572:C:OP2	2.29	0.43
50:1:2731:U:O2'	50:1:2733:A:N7	2.51	0.43
51:2:9:A:H2'	51:2:10:A:H8	1.83	0.43
2:a:100:PRO:HG2	2:a:123:VAL:HG12	1.99	0.43
10:H:21:LYS:N	50:1:3198:U:O2	2.52	0.43
11:J:80:LEU:HD12	11:J:129:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:75:LYS:HG2	12:K:284:ASN:HD21	1.83	0.43
16:P:69:ARG:NH1	50:1:2992:U:H1'	2.33	0.43
22:V:136:VAL:HG12	22:V:137:VAL:HG23	2.01	0.43
26:Z:34:LYS:HB2	26:Z:34:LYS:HE2	1.88	0.43
42:r:164:ARG:N	50:1:2727:A:H8	2.07	0.43
45:v:140:MET:HE1	46:w:62:ILE:HD11	2.01	0.43
50:1:532:A:O2'	50:1:533:A:H5'	2.18	0.43
50:1:958:C:H5'	50:1:959:C:H5''	2.00	0.43
50:1:1355:A:H5'	50:1:1357:G:H1'	2.01	0.43
50:1:2505:U:C2	50:1:2506:U:C5	3.06	0.43
50:1:2819:A:O2'	50:1:2820:A:OP2	2.33	0.43
52:3:81:U:H2'	52:3:82:G:H8	1.82	0.43
1:L:165:SER:C	1:L:167:PHE:H	2.26	0.43
6:D:234:ASP:OD1	6:D:234:ASP:N	2.51	0.43
8:F:31:ALA:HA	8:F:34:LYS:HG2	2.00	0.43
20:T:76:ILE:HA	20:T:76:ILE:HD13	1.81	0.43
30:e:11:LYS:O	30:e:12:LYS:HB2	2.19	0.43
38:n:430:GLN:NE2	38:n:456:HIS:HA	2.33	0.43
39:o:101:GLY:HA3	43:t:66:LEU:HD21	2.01	0.43
45:v:200:LEU:HD13	45:v:202:ARG:NH2	2.33	0.43
46:w:193:LYS:HB2	46:w:193:LYS:HE3	1.87	0.43
47:x:138:ALA:HB1	47:x:509:MET:HB3	1.99	0.43
47:x:224:ALA:HB3	47:x:226:ARG:CZ	2.49	0.43
50:1:2768:U:H3	50:1:2790:A:H61	1.67	0.43
50:1:3357:U:H2'	50:1:3358:U:C6	2.51	0.43
52:3:90:U:H2'	52:3:91:G:O4'	2.19	0.43
11:J:80:LEU:HD23	11:J:81:GLU:N	2.33	0.43
12:K:289:LEU:O	12:K:291:LEU:HD12	2.19	0.43
13:M:137:LYS:HE2	13:M:137:LYS:HB3	1.80	0.43
23:W:142:VAL:HG23	23:W:157:MET:HB3	2.01	0.43
23:W:165:MET:HA	23:W:169:PHE:HB2	2.01	0.43
38:n:101:SER:O	38:n:105:LEU:HD12	2.18	0.43
43:t:192:PRO:HG2	43:t:193:TYR:CE2	2.54	0.43
46:w:132:MET:HA	46:w:143:PRO:HA	2.00	0.43
47:x:348:THR:HB	47:x:351:GLU:HG2	1.99	0.43
47:x:383:MET:HE1	47:x:429:TRP:HE1	1.82	0.43
50:1:532:A:H2'	50:1:533:A:C8	2.53	0.43
50:1:543:C:OP2	50:1:544:C:N4	2.52	0.43
50:1:3306:U:H2'	50:1:3307:A:H5''	2.01	0.43
53:6:16:U:H5'	53:6:16:U:O2	2.18	0.43
1:L:80:VAL:HG12	1:L:116:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:81:THR:O	4:B:81:THR:OG1	2.32	0.43
6:D:39:GLN:H	6:D:41:LYS:HG2	1.82	0.43
27:b:187:ILE:HD11	27:b:332:ARG:HG3	2.01	0.43
32:g:4:ARG:HD3	50:1:1858:A:H1'	2.00	0.43
35:j:39:TYR:CD1	35:j:40:PRO:HA	2.54	0.43
38:n:377:GLU:O	38:n:381:LEU:HG	2.18	0.43
39:o:208:ILE:O	39:o:211:LEU:HG	2.19	0.43
43:t:21:ARG:HE	43:t:21:ARG:HB2	1.70	0.43
47:x:191:CYS:SG	47:x:235:LEU:HG	2.59	0.43
50:1:87:U:H2'	50:1:88:A:H8	1.83	0.43
50:1:2522:G:H2'	50:1:2522:G:N3	2.34	0.43
50:1:3277:U:H5''	50:1:3278:C:C5	2.54	0.43
52:3:37:G:O2'	52:3:38:U:O4'	2.28	0.43
4:B:240:ARG:NH2	4:B:241:LYS:HD3	2.34	0.43
12:K:265:LEU:HD12	12:K:266:ILE:N	2.34	0.43
14:N:36:ILE:HD13	14:N:106:VAL:HG12	1.99	0.43
17:Q:93:ILE:HG22	50:1:784:A:N1	2.34	0.43
20:T:63:VAL:O	20:T:75:ILE:HD12	2.19	0.43
26:Z:9:LYS:HB2	26:Z:9:LYS:HE2	1.89	0.43
27:b:104:LEU:O	27:b:108:VAL:HG23	2.19	0.43
27:b:282:SER:HB2	27:b:338:LYS:NZ	2.34	0.43
32:g:73:SER:O	32:g:73:SER:OG	2.31	0.43
35:j:15:SER:HB2	50:1:817:A:C8	2.54	0.43
37:m:108:LEU:HD22	37:m:310:HIS:CE1	2.54	0.43
41:q:240:LYS:NZ	41:q:244:GLU:OE1	2.49	0.43
41:q:440:LYS:HB3	50:1:1577:G:OP1	2.19	0.43
42:r:164:ARG:CD	50:1:2728:G:H5'	2.44	0.43
44:u:82:ASN:HB3	44:u:85:LEU:HB3	2.00	0.43
45:v:141:PHE:HB2	46:w:27:ALA:HB2	2.01	0.43
46:w:142:VAL:HG23	46:w:142:VAL:O	2.18	0.43
48:y:215:LEU:HD23	48:y:215:LEU:HA	1.92	0.43
50:1:1119:C:N3	50:1:1140:G:N1	2.67	0.43
50:1:2278:C:O2'	50:1:2279:A:O5'	2.36	0.43
51:2:65:A:H2'	51:2:66:A:H8	1.84	0.43
52:3:3:U:H4'	52:3:25:G:N2	2.34	0.43
19:S:26:ARG:HH22	19:S:28:ARG:HD2	1.84	0.42
27:b:252:TYR:HB3	27:b:285:VAL:HG22	2.01	0.42
32:g:87:GLU:HG3	32:g:88:ARG:N	2.33	0.42
43:t:142:LEU:HD12	43:t:179:LEU:HB2	2.00	0.42
47:x:366:LYS:HD2	47:x:366:LYS:HA	1.86	0.42
48:y:158:GLY:HA3	48:y:221:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:573:C:H2'	50:1:574:U:C6	2.54	0.42
50:1:1138:U:H2'	50:1:1139:G:H8	1.83	0.42
50:1:1615:C:H2'	50:1:1616:U:C6	2.54	0.42
50:1:2228:A:H2'	50:1:2229:A:C8	2.54	0.42
50:1:2717:U:O2'	50:1:2718:U:H6	2.02	0.42
50:1:3016:A:N3	50:1:3017:A:C8	2.87	0.42
51:2:53:A:C4	51:2:54:A:C8	3.07	0.42
52:3:109:G:C2	52:3:110:G:C8	3.06	0.42
4:B:228:GLY:O	4:B:232:ARG:HB2	2.19	0.42
27:b:183:PHE:CZ	27:b:187:ILE:HD12	2.55	0.42
42:r:17:ARG:HA	42:r:17:ARG:HD2	1.88	0.42
42:r:204:PRO:O	42:r:205:GLN:HG2	2.19	0.42
50:1:1057:A:O2'	50:1:1058:U:H5''	2.19	0.42
50:1:1286:A:H2'	50:1:1286:A:OP2	2.19	0.42
50:1:1921:A:H2'	50:1:1922:A:C8	2.54	0.42
50:1:2862:U:H4'	50:1:2863:G:H5''	2.01	0.42
50:1:3279:A:H2'	50:1:3279:A:N3	2.33	0.42
4:B:198:HIS:NE2	49:z:41:LEU:HD13	2.34	0.42
4:B:308:MET:HE2	50:1:3329:U:H5''	2.00	0.42
19:S:45:LEU:HD22	19:S:45:LEU:HA	1.85	0.42
23:W:121:ARG:HA	23:W:121:ARG:HD2	1.89	0.42
23:W:222:ASP:OD1	23:W:223:ASN:N	2.51	0.42
29:d:20:LEU:HD12	29:d:67:VAL:HG21	2.01	0.42
37:m:230:ASP:OD1	37:m:261:LYS:HD2	2.19	0.42
37:m:246:MET:HB3	37:m:246:MET:HE3	1.71	0.42
37:m:286:PHE:CE1	37:m:299:LEU:HD12	2.54	0.42
38:n:148:THR:O	38:n:151:VAL:HG12	2.19	0.42
38:n:407:VAL:HG23	38:n:407:VAL:O	2.19	0.42
39:o:214:SER:OG	39:o:215:GLY:HA2	2.19	0.42
50:1:272:G:H2'	50:1:273:A:H8	1.85	0.42
50:1:1194:G:H2'	50:1:1195:A:C8	2.54	0.42
50:1:1563:C:H2'	50:1:1564:U:C6	2.54	0.42
50:1:1652:G:C2	50:1:1804:A:C2	3.07	0.42
50:1:3047:U:O2'	50:1:3048:A:H5'	2.18	0.42
3:A:180:LEU:HD11	40:p:26:VAL:HG21	2.00	0.42
4:B:206:ASP:OD1	4:B:206:ASP:N	2.49	0.42
6:D:54:ARG:NE	52:3:6:C:OP1	2.52	0.42
7:E:165:LEU:HD23	7:E:165:LEU:HA	1.86	0.42
11:J:40:LEU:HD21	11:J:82:ARG:HH22	1.84	0.42
37:m:77:TRP:HA	42:r:242:TYR:CD2	2.54	0.42
37:m:124:ASP:OD1	47:x:399:THR:OG1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:71:LEU:O	38:n:74:GLU:HB2	2.19	0.42
38:n:148:THR:H	38:n:151:VAL:CG1	2.33	0.42
39:o:90:SER:HB3	39:o:168:PRO:O	2.20	0.42
43:t:57:ARG:O	43:t:59:GLU:N	2.52	0.42
45:v:61:ASN:OD1	45:v:62:ARG:HG3	2.19	0.42
46:w:75:GLU:OE1	46:w:75:GLU:N	2.52	0.42
46:w:146:GLY:N	50:1:2656:A:N1	2.57	0.42
47:x:34:ILE:HD11	47:x:119:LEU:HD13	2.01	0.42
48:y:146:ILE:H	48:y:146:ILE:HG12	1.64	0.42
50:1:1316:C:H5''	50:1:1317:A:H5''	2.01	0.42
50:1:2404:A:H2'	50:1:2404:A:N3	2.34	0.42
51:2:69:U:H2'	51:2:70:G:O4'	2.19	0.42
52:3:61:G:C2	52:3:62:U:C2	3.07	0.42
4:B:173:GLN:NE2	4:B:175:LYS:O	2.50	0.42
8:F:203:TRP:CD1	8:F:204:PRO:HD2	2.54	0.42
10:H:96:HIS:CD2	50:1:3024:A:H5''	2.55	0.42
14:N:7:LEU:HD23	14:N:7:LEU:HA	1.91	0.42
17:Q:39:ARG:NH2	50:1:1348:U:OP1	2.52	0.42
23:W:22:ASN:O	23:W:26:ILE:HG13	2.19	0.42
27:b:278:PHE:CD1	27:b:283:VAL:HG21	2.54	0.42
27:b:389:ASP:OD2	27:b:389:ASP:N	2.39	0.42
30:e:33:ARG:HH11	50:1:944:C:H4'	1.84	0.42
37:m:328:LYS:NZ	37:m:367:CYS:O	2.51	0.42
37:m:346:ILE:HD12	37:m:389:ARG:NH2	2.35	0.42
38:n:380:ILE:HD13	38:n:380:ILE:HA	1.77	0.42
39:o:103:HIS:N	39:o:106:GLU:OE1	2.47	0.42
43:t:74:ARG:HH22	43:t:192:PRO:HG3	1.85	0.42
44:u:44:ARG:NE	50:1:2112:U:OP1	2.53	0.42
47:x:288:GLY:HA3	47:x:360:TYR:OH	2.19	0.42
47:x:321:HIS:CD2	47:x:379:ASP:HB2	2.54	0.42
50:1:1295:G:H2'	50:1:1296:C:C6	2.54	0.42
50:1:1494:U:H4'	50:1:1495:U:O5'	2.20	0.42
50:1:2630:C:H2'	50:1:2631:U:C6	2.53	0.42
51:2:142:C:H2'	51:2:143:U:C6	2.54	0.42
52:3:117:A:H2'	52:3:118:A:H8	1.84	0.42
4:B:104:THR:HG22	50:1:3147:G:O2'	2.18	0.42
12:K:298:LEU:HD23	12:K:301:LEU:HD11	2.01	0.42
14:N:86:ASN:O	14:N:87:GLN:HB2	2.20	0.42
19:S:137:ARG:NH2	50:1:1214:U:OP2	2.51	0.42
24:X:91:ASN:ND2	24:X:94:GLN:HE21	2.17	0.42
27:b:258:GLU:H	27:b:258:GLU:CD	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:445:ASP:OD1	37:m:448:GLY:N	2.50	0.42
42:r:186:HIS:HB3	42:r:188:GLU:O	2.19	0.42
44:u:23:ARG:HG2	44:u:24:ASN:N	2.35	0.42
45:v:268:MET:HE3	45:v:268:MET:HB2	1.90	0.42
47:x:214:ASP:OD2	47:x:218:GLY:N	2.52	0.42
48:y:119:PRO:HA	48:y:139:ARG:HB3	2.02	0.42
50:1:1072:G:C6	50:1:1087:G:C5	3.07	0.42
50:1:2569:A:O2'	50:1:2570:U:OP2	2.25	0.42
50:1:2596:U:H2'	50:1:2597:U:C6	2.54	0.42
5:C:258:LEU:HD12	5:C:258:LEU:HA	1.85	0.42
6:D:179:ARG:HD3	6:D:179:ARG:HA	1.76	0.42
9:G:97:TYR:OH	9:G:204:ARG:N	2.42	0.42
12:K:281:ILE:HG13	12:K:291:LEU:HD13	2.01	0.42
16:P:125:GLN:HB2	16:P:141:SER:HB3	2.02	0.42
18:R:133:LYS:HE2	18:R:133:LYS:HB2	1.78	0.42
19:S:83:SER:HA	19:S:84:ARG:HA	1.74	0.42
31:f:68:TRP:HZ2	50:1:3275:U:H5'	1.85	0.42
38:n:49:LYS:HE2	38:n:57:THR:HG22	2.01	0.42
38:n:437:ASN:HD21	38:n:459:PRO:HD3	1.84	0.42
41:q:214:VAL:O	41:q:215:LYS:C	2.63	0.42
45:v:277:MET:HE3	45:v:277:MET:HB2	1.57	0.42
46:w:145:TRP:HA	50:1:2656:A:H61	1.85	0.42
48:y:67:ARG:HG2	48:y:68:ARG:N	2.32	0.42
48:y:67:ARG:HD2	48:y:112:ASP:OD2	2.19	0.42
50:1:2603:G:H2'	50:1:2604:U:C6	2.54	0.42
50:1:3089:C:H2'	50:1:3090:U:O4'	2.20	0.42
5:C:328:ASN:OD1	8:F:48:ASN:ND2	2.52	0.42
9:G:137:ASN:ND2	14:N:3:ALA:H	2.17	0.42
13:M:55:ARG:HD3	19:S:70:THR:HB	2.02	0.42
13:M:121:MET:HE1	50:1:3215:A:H5'	2.01	0.42
13:M:124:ARG:HH11	13:M:124:ARG:HB3	1.85	0.42
14:N:4:TYR:OH	14:N:49:ARG:NH2	2.41	0.42
20:T:57:TYR:OH	20:T:78:LYS:NZ	2.53	0.42
23:W:188:VAL:HG22	23:W:189:CYS:SG	2.59	0.42
24:X:57:LEU:HD12	24:X:57:LEU:HA	1.83	0.42
38:n:91:THR:OG1	50:1:1573:G:O6	2.35	0.42
39:o:88:GLU:HG2	39:o:89:TYR:H	1.85	0.42
39:o:152:MET:HE3	39:o:152:MET:HB3	1.82	0.42
42:r:170:ARG:NH2	50:1:2727:A:OP1	2.53	0.42
43:t:135:TYR:HE2	43:t:181:LYS:HA	1.84	0.42
47:x:503:SER:OG	47:x:504:GLY:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:954:U:H5	50:1:1115:G:H1'	1.84	0.42
50:1:2667:A:C8	50:1:2668:U:C6	3.08	0.42
52:3:20:A:H2'	52:3:21:G:C8	2.55	0.42
1:L:16:LYS:HE2	1:L:18:TRP:CZ3	2.55	0.42
5:C:312:VAL:HG21	50:1:610:G:C8	2.54	0.42
12:K:134:LYS:HB3	12:K:134:LYS:HE3	1.80	0.42
16:P:53:ASP:O	16:P:54:HIS:HB2	2.19	0.42
26:Z:17:ARG:O	26:Z:17:ARG:HG3	2.19	0.42
27:b:290:THR:HG21	27:b:319:THR:HG23	2.01	0.42
27:b:433:PRO:O	27:b:434:GLU:HG2	2.20	0.42
37:m:229:LEU:HD23	37:m:234:PRO:HB2	2.02	0.42
37:m:414:ARG:HG2	45:v:297:PHE:O	2.20	0.42
39:o:194:LYS:HG3	39:o:197:LYS:NZ	2.35	0.42
43:t:286:LEU:HA	43:t:286:LEU:HD23	1.76	0.42
45:v:87:MET:HE3	45:v:87:MET:HB3	1.86	0.42
45:v:157:ILE:HG13	45:v:158:LYS:N	2.34	0.42
46:w:50:ILE:O	46:w:54:THR:HG23	2.20	0.42
46:w:189:LYS:HD2	46:w:189:LYS:HA	1.77	0.42
48:y:95:GLN:NE2	48:y:128:LEU:HD21	2.35	0.42
48:y:123:ARG:HA	48:y:123:ARG:HD3	1.69	0.42
50:1:2528:G:O2'	50:1:2529:A:O5'	2.38	0.42
50:1:2900:A:O2'	50:1:2901:G:OP1	2.33	0.42
52:3:99:G:H2'	52:3:99:G:N3	2.34	0.42
9:G:200:LEU:HD12	9:G:200:LEU:HA	1.78	0.42
14:N:94:TYR:O	14:N:96:ARG:N	2.53	0.42
18:R:23:TRP:O	18:R:50:ILE:HA	2.20	0.42
23:W:41:TRP:CE3	23:W:220:TYR:HB2	2.55	0.42
27:b:69:PRO:HD2	27:b:91:TYR:OH	2.20	0.42
27:b:495:TRP:CH2	44:u:137:ARG:HB2	2.55	0.42
37:m:191:GLU:HG3	37:m:192:ASN:N	2.35	0.42
38:n:177:ARG:O	38:n:178:LYS:HD3	2.20	0.42
39:o:211:LEU:HB2	39:o:216:ILE:HD11	2.02	0.42
46:w:133:ILE:HG13	46:w:144:LYS:HB3	2.02	0.42
47:x:265:THR:O	47:x:268:ARG:NE	2.53	0.42
50:1:1794:G:O2'	50:1:1796:G:N2	2.52	0.42
50:1:2333:C:H2'	50:1:2334:U:O4'	2.19	0.42
50:1:2633:U:H2'	50:1:2634:U:O4'	2.20	0.42
50:1:2686:A:H2'	50:1:2686:A:N3	2.35	0.42
3:A:155:LYS:HB2	3:A:155:LYS:HE3	1.69	0.41
23:W:53:LEU:HA	23:W:53:LEU:HD23	1.74	0.41
27:b:229:THR:CG2	37:m:156:ASN:HD22	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:255:ASP:OD2	27:b:257:SER:OG	2.27	0.41
27:b:453:LEU:HD23	27:b:456:LEU:HD23	2.01	0.41
31:f:30:ILE:HB	31:f:81:VAL:HG23	2.00	0.41
34:i:83:ALA:O	34:i:87:VAL:HG23	2.20	0.41
37:m:72:GLN:O	37:m:77:TRP:HZ3	2.02	0.41
37:m:307:SER:O	37:m:361:ARG:NH2	2.53	0.41
38:n:418:LYS:HG2	38:n:419:ASN:HA	2.02	0.41
39:o:178:LYS:NZ	39:o:179:TYR:O	2.32	0.41
45:v:153:VAL:HG23	45:v:154:TYR:HD2	1.85	0.41
47:x:151:PHE:CD2	47:x:495:SER:HA	2.56	0.41
47:x:177:THR:HG22	47:x:178:PRO:HD2	2.01	0.41
47:x:374:MET:HB3	47:x:386:TRP:HB2	2.01	0.41
50:1:179:C:H2'	50:1:180:C:H6	1.83	0.41
50:1:305:U:H1'	50:1:306:A:H8	1.85	0.41
50:1:998:A:N6	50:1:1053:A:N6	2.67	0.41
5:C:233:LEU:HD23	5:C:233:LEU:HA	1.79	0.41
6:D:45:ASN:HB2	45:v:173:GLN:HE22	1.85	0.41
6:D:224:LYS:NZ	52:3:51:A:OP1	2.53	0.41
17:Q:86:THR:HG22	17:Q:105:ARG:CB	2.49	0.41
25:Y:23:PRO:HG2	25:Y:26:GLN:HG3	2.01	0.41
25:Y:109:LEU:HD22	25:Y:115:ARG:HD3	2.01	0.41
26:Z:135:ARG:HB3	26:Z:135:ARG:HH21	1.85	0.41
35:j:5:THR:HG22	35:j:6:PRO:HD3	2.02	0.41
49:z:50:LYS:HA	49:z:50:LYS:HD3	1.69	0.41
50:1:301:G:H2'	50:1:302:U:O4'	2.20	0.41
50:1:538:G:H1	50:1:553:U:H3	1.68	0.41
50:1:1538:G:H21	50:1:1583:A:H62	1.68	0.41
50:1:1805:C:H2'	50:1:1806:A:H8	1.85	0.41
50:1:2198:A:N6	50:1:2246:G:H8	2.18	0.41
50:1:2238:G:H21	50:1:2239:G:H1'	1.86	0.41
50:1:2526:C:H2'	50:1:2527:G:C8	2.54	0.41
6:D:104:LEU:HD13	6:D:247:ILE:HG23	2.02	0.41
6:D:203:HIS:HA	6:D:206:GLN:HG2	2.02	0.41
6:D:286:VAL:HA	6:D:289:LYS:CE	2.50	0.41
9:G:62:LYS:HD3	14:N:29:GLU:HG3	2.02	0.41
10:H:168:ARG:HE	10:H:168:ARG:HB3	1.52	0.41
11:J:141:ARG:NH2	11:J:144:CYS:HB2	2.33	0.41
14:N:17:ASP:HA	14:N:20:ARG:HG2	2.02	0.41
14:N:203:ARG:HD3	14:N:203:ARG:HA	1.85	0.41
16:P:135:ARG:HD2	50:1:879:U:C5	2.55	0.41
16:P:180:LYS:HA	16:P:180:LYS:HD2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:16:ARG:HG2	17:Q:53:PHE:HB3	2.03	0.41
38:n:208:ASN:OD1	38:n:208:ASN:N	2.52	0.41
39:o:134:TYR:CZ	53:6:56:U:H5''	2.55	0.41
43:t:100:ILE:HG13	43:t:309:VAL:HG13	2.01	0.41
43:t:215:ILE:HB	43:t:269:GLN:HE22	1.85	0.41
45:v:200:LEU:HD22	45:v:231:ASP:OD2	2.20	0.41
46:w:66:LEU:HD23	46:w:66:LEU:HA	1.83	0.41
50:1:2195:C:O2'	50:1:2196:C:OP2	2.38	0.41
50:1:2269:U:H1'	50:1:2270:A:P	2.60	0.41
50:1:2426:U:H2'	50:1:2427:U:C6	2.55	0.41
50:1:2657:A:H8	50:1:2657:A:O5'	2.03	0.41
1:L:89:TYR:O	1:L:92:THR:OG1	2.37	0.41
3:A:28:LYS:HD3	3:A:123:ARG:HD2	2.03	0.41
4:B:5:LYS:NZ	50:1:2878:G:H3'	2.35	0.41
4:B:251:CYS:HB3	50:1:2880:U:O2	2.20	0.41
6:D:262:LYS:HE3	52:3:1:G:N7	2.34	0.41
9:G:24:ASN:N	9:G:25:PRO:HD3	2.34	0.41
16:P:133:HIS:HA	50:1:880:G:C6	2.55	0.41
19:S:93:GLU:OE1	19:S:135:VAL:HG13	2.20	0.41
19:S:110:MET:HB3	19:S:110:MET:HE3	1.82	0.41
23:W:73:LEU:O	23:W:77:LEU:HG	2.20	0.41
27:b:129:LYS:HD2	27:b:133:LEU:HD22	2.02	0.41
27:b:432:MET:HE1	27:b:445:LEU:HD13	2.02	0.41
37:m:467:LEU:HD23	37:m:467:LEU:HA	1.95	0.41
40:p:38:ASP:OD1	40:p:38:ASP:N	2.54	0.41
45:v:40:LYS:HZ2	52:3:70:U:H4'	1.85	0.41
47:x:175:THR:HG23	47:x:177:THR:OG1	2.20	0.41
50:1:720:A:H2'	50:1:720:A:N3	2.36	0.41
50:1:2683:U:H2'	50:1:2684:C:H6	1.86	0.41
52:3:75:G:C6	52:3:76:A:C6	3.08	0.41
53:6:5:C:H41	53:6:24:A:P	2.40	0.41
4:B:187:SER:O	4:B:189:SER:N	2.52	0.41
4:B:231:HIS:CD2	4:B:270:ARG:HE	2.38	0.41
10:H:34:LEU:HD23	10:H:34:LEU:HA	1.84	0.41
10:H:142:ASP:OD2	10:H:142:ASP:N	2.53	0.41
12:K:123:VAL:HG11	12:K:151:VAL:HA	2.02	0.41
19:S:149:LYS:HE2	19:S:149:LYS:HB3	1.72	0.41
26:Z:6:LYS:HD3	26:Z:6:LYS:HA	1.82	0.41
33:h:14:LYS:HB2	33:h:14:LYS:HE3	1.79	0.41
47:x:377:ALA:HA	47:x:383:MET:HG2	2.02	0.41
48:y:236:LEU:O	48:y:240:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:144:A:H2'	50:1:145:G:O4'	2.20	0.41
50:1:662:U:H2'	50:1:663:C:C6	2.55	0.41
50:1:1001:G:C6	50:1:1050:U:C2	3.00	0.41
50:1:1277:C:C2	50:1:1278:A:C8	3.09	0.41
50:1:1308:A:C8	50:1:1308:A:OP2	2.73	0.41
50:1:1581:C:H4'	50:1:1582:C:OP1	2.20	0.41
50:1:1640:G:O2'	50:1:1641:U:H5'	2.20	0.41
50:1:2653:C:H1'	50:1:2655:U:P	2.61	0.41
50:1:3281:U:H2'	50:1:3282:U:C6	2.56	0.41
52:3:18:C:H2'	52:3:19:C:H6	1.86	0.41
6:D:289:LYS:O	6:D:293:LEU:HG	2.20	0.41
9:G:45:ASN:HB2	24:X:26:VAL:HG23	2.03	0.41
9:G:49:TYR:HB3	50:1:2523:A:O2'	2.21	0.41
10:H:38:LEU:HD23	10:H:38:LEU:HA	1.84	0.41
11:J:19:LEU:HD22	11:J:125:MET:HB3	2.03	0.41
12:K:275:GLN:O	12:K:297:VAL:HG11	2.20	0.41
19:S:117:ARG:HG2	19:S:119:ARG:HH21	1.85	0.41
23:W:50:THR:N	23:W:51:PRO:HD2	2.35	0.41
29:d:31:ARG:O	29:d:35:GLU:HG2	2.20	0.41
36:k:42:LYS:NZ	50:1:1750:A:OP2	2.42	0.41
37:m:338:LYS:O	37:m:340:VAL:HG23	2.20	0.41
37:m:355:TYR:C	37:m:356:ILE:HD12	2.45	0.41
38:n:39:LYS:HD2	38:n:39:LYS:HA	1.72	0.41
45:v:42:LEU:HD21	45:v:90:MET:HB3	2.02	0.41
50:1:651:G:O2'	50:1:1435:A:OP1	2.39	0.41
50:1:921:A:H61	50:1:1846:C:P	2.43	0.41
50:1:1129:A:O2'	50:1:1130:A:OP1	2.33	0.41
50:1:1276:U:O2'	50:1:1277:C:H5'	2.21	0.41
50:1:1290:A:H2'	50:1:1291:A:H8	1.82	0.41
50:1:2140:U:O5'	50:1:2140:U:H6	2.04	0.41
50:1:2224:A:H3'	50:1:2225:U:H6	1.84	0.41
50:1:2608:G:H2'	50:1:2609:A:C8	2.50	0.41
52:3:45:A:H2'	52:3:46:A:C8	2.55	0.41
3:A:50:HIS:CD2	50:1:1795:U:H2'	2.56	0.41
3:A:177:LYS:HB2	40:p:29:LEU:HD12	2.02	0.41
4:B:334:ARG:HG2	4:B:335:ILE:H	1.86	0.41
6:D:196:ARG:HH21	6:D:200:PHE:HE2	1.69	0.41
11:J:35:LYS:HD2	11:J:120:ILE:HG22	2.02	0.41
12:K:138:ASP:OD2	12:K:139:ASP:N	2.53	0.41
14:N:98:LEU:HD12	14:N:128:LYS:HD2	2.02	0.41
15:O:156:LEU:HD22	50:1:3243:A:N7	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:43:LYS:HE3	20:T:97:LYS:HE2	2.03	0.41
26:Z:73:LYS:HG2	26:Z:74:VAL:O	2.21	0.41
28:c:77:LEU:O	28:c:81:VAL:HG23	2.21	0.41
37:m:74:ASP:OD2	37:m:75:ARG:N	2.54	0.41
37:m:104:TYR:OH	50:1:2269:U:O2	2.36	0.41
42:r:86:ALA:HA	47:x:188:TRP:CZ3	2.55	0.41
45:v:172:LEU:HB3	46:w:89:LEU:HD23	2.02	0.41
45:v:253:LYS:O	45:v:254:GLN:HG3	2.21	0.41
50:1:627:U:H2'	50:1:628:A:C8	2.56	0.41
50:1:748:U:H2'	50:1:749:C:C6	2.56	0.41
50:1:877:C:H1'	50:1:880:G:H1'	2.02	0.41
50:1:1138:U:H2'	50:1:1139:G:C8	2.55	0.41
50:1:1204:A:H2'	50:1:1205:A:O4'	2.20	0.41
50:1:2654:C:H4'	50:1:2655:U:H5'	2.03	0.41
50:1:2878:G:O2'	50:1:2879:C:OP2	2.33	0.41
3:A:57:PRO:HD2	3:A:170:ALA:HB3	2.03	0.41
4:B:232:ARG:HA	4:B:270:ARG:HD2	2.01	0.41
4:B:250:ALA:HB1	50:1:2947:G:C2	2.55	0.41
6:D:21:ARG:HD3	52:3:112:G:O6	2.21	0.41
8:F:90:LYS:HD2	8:F:220:PHE:CE1	2.56	0.41
11:J:21:ILE:HD11	11:J:125:MET:SD	2.61	0.41
12:K:271:ILE:HA	12:K:276:ILE:HD11	2.03	0.41
50:1:550:A:H2'	50:1:551:A:H8	1.86	0.41
50:1:966:U:H2'	50:1:967:A:C8	2.55	0.41
50:1:977:C:C2	50:1:1106:G:N2	2.87	0.41
50:1:978:G:N2	50:1:1103:A:O2'	2.54	0.41
50:1:1497:C:H2'	50:1:1498:A:H8	1.85	0.41
50:1:2661:G:H2'	50:1:2662:G:C8	2.56	0.41
50:1:2667:A:H1'	50:1:2691:A:H5'	2.03	0.41
50:1:2968:G:O2'	50:1:2969:A:H5'	2.21	0.41
52:3:37:G:H21	52:3:44:C:H42	1.69	0.41
3:A:178:PRO:HD2	40:p:26:VAL:HG22	2.03	0.41
4:B:284:ARG:HB3	4:B:323:MET:HE2	2.03	0.41
6:D:17:GLN:NE2	45:v:61:ASN:HD22	2.19	0.41
9:G:246:MET:HE3	9:G:246:MET:HB2	1.86	0.41
10:H:87:LYS:C	10:H:88:TYR:HD1	2.29	0.41
11:J:65:ILE:HD11	50:1:2680:A:H1'	2.02	0.41
11:J:122:ILE:HD13	11:J:122:ILE:HA	1.98	0.41
14:N:93:LYS:HE3	50:1:277:G:H1'	2.03	0.41
14:N:185:ALA:HA	14:N:188:ARG:HG2	2.03	0.41
22:V:68:GLU:OE1	22:V:68:GLU:N	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:70:ARG:HD2	23:W:98:GLY:O	2.20	0.41
25:Y:31:LEU:HD21	25:Y:78:PHE:HD1	1.85	0.41
27:b:73:ASP:OD1	27:b:73:ASP:N	2.54	0.41
27:b:214:LEU:HD23	27:b:214:LEU:HA	1.91	0.41
29:d:80:ASN:N	29:d:88:PRO:HB2	2.36	0.41
37:m:35:ARG:NH2	50:1:2965:U:OP2	2.54	0.41
37:m:175:GLN:HA	37:m:178:ASP:OD1	2.21	0.41
37:m:306:PHE:CE1	45:v:275:ILE:HD11	2.55	0.41
39:o:92:ILE:HA	39:o:138:GLU:HB2	2.02	0.41
41:q:424:GLN:NE2	41:q:431:THR:HG23	2.36	0.41
42:r:117:LYS:HE3	42:r:117:LYS:HB2	1.75	0.41
42:r:188:GLU:C	42:r:190:GLY:H	2.28	0.41
42:r:207:PRO:O	42:r:211:GLN:HG3	2.21	0.41
43:t:40:LYS:HE3	43:t:40:LYS:HB3	1.79	0.41
43:t:214:ILE:HD13	43:t:214:ILE:HA	1.95	0.41
43:t:259:GLU:O	43:t:260:SER:OG	2.34	0.41
44:u:10:SER:HB3	44:u:53:LYS:HB2	2.02	0.41
46:w:92:LEU:H	46:w:92:LEU:HD12	1.86	0.41
47:x:230:LYS:O	47:x:255:SER:OG	2.21	0.41
48:y:146:ILE:O	48:y:147:LEU:HB2	2.21	0.41
48:y:162:HIS:O	48:y:165:THR:OG1	2.36	0.41
50:1:645:A:OP2	50:1:1153:A:N6	2.51	0.41
50:1:722:G:H2'	50:1:723:U:C6	2.55	0.41
50:1:849:C:H2'	50:1:850:U:C6	2.55	0.41
50:1:870:G:HO2'	50:1:872:U:H6	1.67	0.41
50:1:993:G:N2	50:1:1057:A:C2	2.86	0.41
50:1:1112:A:H2'	50:1:1113:G:H8	1.85	0.41
50:1:1716:U:HO2'	50:1:1717:U:P	2.40	0.41
50:1:2097:U:H2'	50:1:2098:C:C6	2.56	0.41
50:1:2202:C:H2'	50:1:2203:U:H6	1.86	0.41
50:1:2438:A:H2'	50:1:2439:A:C8	2.55	0.41
50:1:2528:G:C5	50:1:2529:A:C5	3.09	0.41
50:1:2536:A:C2	50:1:2537:U:H5	2.39	0.41
50:1:3110:C:H2'	50:1:3111:U:C6	2.55	0.41
50:1:3269:U:H4'	50:1:3270:U:O5'	2.20	0.41
1:L:21:ARG:HD2	14:N:196:THR:HG23	2.03	0.41
3:A:92:LYS:HB2	3:A:92:LYS:HE2	1.92	0.41
7:E:145:LEU:HD12	7:E:145:LEU:HA	1.76	0.41
11:J:103:GLY:C	50:1:2673:A:H4'	2.45	0.41
12:K:281:ILE:HB	12:K:289:LEU:HD12	2.03	0.41
18:R:82:LYS:HE2	18:R:82:LYS:HB3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:12:ARG:HG3	19:S:22:PRO:HB2	2.03	0.41
24:X:46:TYR:CD2	33:h:75:TYR:HB3	2.49	0.41
27:b:253:PHE:HD1	27:b:253:PHE:HA	1.75	0.41
28:c:74:ASN:OD1	28:c:74:ASN:N	2.53	0.41
29:d:53:PRO:O	29:d:57:GLN:HG3	2.21	0.41
32:g:30:LEU:HD23	32:g:30:LEU:HA	1.84	0.41
37:m:284:LEU:HD21	37:m:298:SER:HB2	2.03	0.41
37:m:418:ILE:HD11	37:m:430:ILE:HG22	2.03	0.41
38:n:142:PHE:CZ	38:n:218:MET:HE3	2.55	0.41
38:n:449:PRO:HA	38:n:451:GLU:N	2.35	0.41
39:o:130:ASN:OD1	39:o:130:ASN:N	2.54	0.41
43:t:146:ARG:HG2	43:t:171:THR:HA	2.02	0.41
44:u:44:ARG:HD2	44:u:49:LEU:HD11	2.03	0.41
45:v:110:ILE:HD13	45:v:110:ILE:HA	1.81	0.41
46:w:61:LEU:HA	46:w:61:LEU:HD23	1.73	0.41
47:x:336:ILE:HG13	47:x:337:GLY:N	2.36	0.41
50:1:1189:C:H42	50:1:1315:U:HO2'	1.59	0.41
50:1:1528:G:O2'	50:1:1588:A:N3	2.46	0.41
50:1:3016:A:O2'	50:1:3017:A:H8	2.03	0.41
52:3:56:A:N3	52:3:56:A:H2'	2.36	0.41
3:A:19:HIS:CD2	3:A:19:HIS:N	2.89	0.40
3:A:112:ILE:HD13	40:p:79:VAL:HG22	2.03	0.40
5:C:35:VAL:HG11	5:C:244:LEU:HD21	2.03	0.40
6:D:220:SER:O	6:D:224:LYS:HG3	2.21	0.40
7:E:52:VAL:HG11	7:E:65:ILE:HD12	2.02	0.40
8:F:156:ILE:HG22	8:F:172:ASN:ND2	2.36	0.40
9:G:75:ILE:C	9:G:77:GLN:H	2.29	0.40
9:G:146:LYS:HB2	9:G:146:LYS:HE2	1.80	0.40
9:G:168:ALA:HB3	34:i:47:ILE:HD11	2.04	0.40
11:J:36:VAL:HA	11:J:39:GLN:NE2	2.35	0.40
20:T:56:PHE:HD1	20:T:56:PHE:HA	1.64	0.40
25:Y:12:ARG:HG3	50:1:215:G:OP1	2.19	0.40
27:b:34:ARG:HG3	50:1:2821:C:OP2	2.21	0.40
35:j:8:PHE:CD1	50:1:1845:G:H4'	2.53	0.40
37:m:95:ALA:HA	37:m:98:GLU:HG2	2.04	0.40
37:m:188:GLU:HA	37:m:191:GLU:HG2	2.02	0.40
37:m:382:ILE:HD13	37:m:382:ILE:HA	1.95	0.40
38:n:96:ARG:HG2	50:1:6:A:H4'	2.02	0.40
39:o:139:PHE:HB2	39:o:140:VAL:H	1.68	0.40
43:t:58:ALA:O	43:t:62:VAL:HG23	2.21	0.40
49:z:21:VAL:HG13	49:z:22:PHE:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1:171:G:H2'	50:1:172:G:C8	2.56	0.40
50:1:824:C:C2'	50:1:825:U:H5'	2.50	0.40
50:1:1108:U:C2	50:1:1109:U:H5	2.40	0.40
50:1:1295:G:H2'	50:1:1296:C:H6	1.87	0.40
50:1:1850:A:H8	50:1:1850:A:OP1	2.03	0.40
50:1:2784:G:H2'	50:1:2785:A:C8	2.53	0.40
3:A:68:LYS:HG2	3:A:69:TYR:N	2.36	0.40
4:B:136:LYS:HE3	4:B:136:LYS:HB2	1.86	0.40
5:C:22:LEU:HA	5:C:22:LEU:HD23	1.91	0.40
5:C:220:ARG:HH12	25:Y:4:GLN:HG3	1.86	0.40
7:E:130:ILE:H	7:E:130:ILE:HG13	1.66	0.40
8:F:156:ILE:HG12	8:F:161:VAL:HG21	2.02	0.40
12:K:227:LYS:HB2	12:K:227:LYS:HE2	1.88	0.40
12:K:259:PHE:HD1	12:K:259:PHE:HA	1.74	0.40
27:b:260:CYS:C	27:b:262:PHE:H	2.26	0.40
29:d:11:GLU:OE2	29:d:74:ARG:NE	2.48	0.40
29:d:20:LEU:HD11	29:d:32:ALA:HB2	2.03	0.40
35:j:75:LYS:HE3	35:j:75:LYS:HB3	1.89	0.40
38:n:44:ARG:HG3	38:n:64:TYR:CE2	2.57	0.40
45:v:43:HIS:O	45:v:46:MET:HE3	2.20	0.40
47:x:350:GLU:O	47:x:354:LYS:NZ	2.55	0.40
48:y:74:THR:OG1	48:y:98:GLU:HA	2.20	0.40
48:y:226:ASP:HA	48:y:227:ALA:HA	1.73	0.40
50:1:994:G:H21	50:1:995:U:H3	1.69	0.40
50:1:1264:G:H4'	50:1:1265:U:OP1	2.20	0.40
50:1:2751:G:O2'	50:1:2752:U:OP2	2.29	0.40
50:1:2929:C:O2'	50:1:2930:A:H8	2.03	0.40
50:1:3164:C:C2	50:1:3165:A:C8	3.09	0.40
53:6:18:U:H2'	53:6:19:U:C6	2.56	0.40
1:L:27:ASP:O	1:L:31:LYS:HB2	2.21	0.40
8:F:222:HIS:O	8:F:225:GLN:N	2.51	0.40
9:G:214:LEU:HD12	9:G:214:LEU:HA	1.89	0.40
11:J:101:ASN:HB2	11:J:128:TYR:OH	2.21	0.40
18:R:89:LEU:HD12	18:R:90:PRO:HD2	2.03	0.40
18:R:102:LEU:HD22	18:R:138:LEU:HD22	2.04	0.40
27:b:227:ARG:HD2	27:b:227:ARG:HA	1.78	0.40
27:b:487:ASP:O	27:b:491:GLU:HG3	2.22	0.40
29:d:47:ASP:OD2	29:d:47:ASP:N	2.53	0.40
37:m:275:LYS:NZ	50:1:2271:A:OP1	2.54	0.40
37:m:413:GLU:HG2	37:m:418:ILE:CG2	2.51	0.40
39:o:94:TYR:HB2	39:o:136:PHE:CE1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:q:259:LYS:HA	41:q:259:LYS:HD2	1.87	0.40
41:q:384:GLY:O	41:q:386:LYS:N	2.54	0.40
45:v:206:LEU:HD23	45:v:206:LEU:H	1.86	0.40
47:x:382:THR:HG21	47:x:397:ARG:NH2	2.35	0.40
50:1:178:U:H2'	50:1:179:C:H6	1.87	0.40
50:1:305:U:O2'	50:1:306:A:OP2	2.37	0.40
50:1:787:G:H2'	50:1:788:C:C6	2.56	0.40
50:1:945:C:H2'	50:1:946:U:C6	2.56	0.40
50:1:1250:G:C2	50:1:1251:A:C5	3.10	0.40
50:1:2196:C:H2'	50:1:2242:A:N6	2.37	0.40
50:1:2788:C:O2	50:1:2788:C:H2'	2.22	0.40
6:D:196:ARG:NH1	47:x:178:PRO:O	2.54	0.40
8:F:158:LYS:HA	8:F:158:LYS:HD3	1.81	0.40
10:H:44:THR:HG22	10:H:56:ALA:HB3	2.03	0.40
10:H:141:LYS:HD2	10:H:141:LYS:HA	1.90	0.40
12:K:110:TRP:CH2	12:K:178:SER:HB3	2.56	0.40
14:N:104:GLU:HG2	14:N:160:GLU:HG3	2.04	0.40
19:S:91:TYR:OH	19:S:93:GLU:OE2	2.35	0.40
38:n:380:ILE:HG21	38:n:387:VAL:HG22	2.04	0.40
39:o:157:LEU:O	39:o:158:MET:C	2.64	0.40
43:t:132:LYS:HE2	43:t:132:LYS:HB3	1.92	0.40
44:u:3:ILE:HD13	44:u:3:ILE:HG21	1.87	0.40
47:x:81:CYS:SG	47:x:119:LEU:HD12	2.61	0.40
50:1:330:G:C2	50:1:331:G:C8	3.10	0.40
50:1:886:C:H3'	50:1:887:G:C8	2.56	0.40
50:1:1059:G:H2'	50:1:1060:U:C6	2.56	0.40
50:1:1348:U:H4'	50:1:1349:G:OP1	2.22	0.40
50:1:1621:A:H2'	50:1:1622:U:H6	1.86	0.40
50:1:2690:G:N3	50:1:2690:G:H2'	2.35	0.40
53:6:53:A:O2'	53:6:55:A:N6	2.55	0.40
1:L:139:LEU:HD23	1:L:139:LEU:HA	1.89	0.40
1:L:170:LEU:HD21	2:a:147:LEU:HD13	2.04	0.40
3:A:117:GLU:HG2	3:A:124:GLY:H	1.86	0.40
12:K:149:ILE:HD13	12:K:230:TYR:CD2	2.56	0.40
13:M:89:ALA:HB1	13:M:92:GLU:OE1	2.21	0.40
14:N:63:ARG:NH2	14:N:131:GLU:OE2	2.39	0.40
19:S:152:LEU:HD23	19:S:152:LEU:HA	1.79	0.40
20:T:57:TYR:CD1	20:T:89:LEU:HD21	2.57	0.40
25:Y:32:SER:O	25:Y:101:PRO:HB2	2.22	0.40
26:Z:87:LEU:HD23	26:Z:88:ASP:N	2.36	0.40
27:b:229:THR:HA	27:b:232:MET:CG	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:298:LEU:HD23	27:b:299:ASP:H	1.86	0.40
27:b:406:ASN:H	27:b:407:GLY:HA3	1.86	0.40
28:c:14:LEU:HA	28:c:17:VAL:HG12	2.04	0.40
29:d:87:ASN:HA	29:d:88:PRO:HA	1.80	0.40
36:k:30:LYS:O	36:k:37:PRO:HA	2.20	0.40
37:m:344:ALA:O	54:m:501:GTP:H5'	2.21	0.40
47:x:225:LEU:HD21	47:x:268:ARG:HA	2.03	0.40
50:1:761:A:HO2'	50:1:762:U:P	2.44	0.40
50:1:871:U:H5''	50:1:2142:A:H2'	2.04	0.40
50:1:1112:A:C6	50:1:1113:G:C6	3.09	0.40
50:1:1498:A:H2'	50:1:1499:C:C6	2.56	0.40
50:1:2666:C:H1'	50:1:2691:A:N3	2.37	0.40
50:1:3295:A:H2'	50:1:3296:A:H8	1.85	0.40
52:3:45:A:C2	52:3:46:A:C5	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	183/199 (92%)	157 (86%)	25 (14%)	1 (0%)	24	58
2	a	91/149 (61%)	79 (87%)	11 (12%)	1 (1%)	11	42
3	A	191/254 (75%)	172 (90%)	19 (10%)	0	100	100
4	B	384/387 (99%)	330 (86%)	51 (13%)	3 (1%)	16	48
5	C	332/362 (92%)	282 (85%)	47 (14%)	3 (1%)	14	46
6	D	270/297 (91%)	246 (91%)	24 (9%)	0	100	100
7	E	152/176 (86%)	136 (90%)	16 (10%)	0	100	100
8	F	220/244 (90%)	204 (93%)	16 (7%)	0	100	100
9	G	225/256 (88%)	196 (87%)	29 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	H	186/191 (97%)	169 (91%)	16 (9%)	1 (0%)	24	58
11	J	165/174 (95%)	136 (82%)	29 (18%)	0	100	100
12	K	249/376 (66%)	217 (87%)	30 (12%)	2 (1%)	16	48
13	M	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
14	N	201/204 (98%)	185 (92%)	14 (7%)	2 (1%)	12	44
15	O	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
16	P	181/184 (98%)	163 (90%)	18 (10%)	0	100	100
17	Q	132/186 (71%)	120 (91%)	12 (9%)	0	100	100
18	R	154/189 (82%)	145 (94%)	9 (6%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	T	115/160 (72%)	98 (85%)	17 (15%)	0	100	100
21	U	102/121 (84%)	90 (88%)	12 (12%)	0	100	100
22	V	134/137 (98%)	124 (92%)	10 (8%)	0	100	100
23	W	232/236 (98%)	209 (90%)	22 (10%)	1 (0%)	30	61
24	X	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
25	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
26	Z	133/136 (98%)	113 (85%)	18 (14%)	2 (2%)	8	36
27	b	505/647 (78%)	430 (85%)	72 (14%)	3 (1%)	21	55
28	c	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
29	d	103/113 (91%)	91 (88%)	12 (12%)	0	100	100
30	e	123/130 (95%)	113 (92%)	10 (8%)	0	100	100
31	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
32	g	110/121 (91%)	103 (94%)	7 (6%)	0	100	100
33	h	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	46
34	i	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
35	j	83/88 (94%)	75 (90%)	8 (10%)	0	100	100
36	k	74/78 (95%)	67 (90%)	7 (10%)	0	100	100
37	m	465/486 (96%)	389 (84%)	70 (15%)	6 (1%)	9	39
38	n	360/605 (60%)	311 (86%)	46 (13%)	3 (1%)	16	48
39	o	127/220 (58%)	110 (87%)	16 (13%)	1 (1%)	16	48
40	p	89/92 (97%)	80 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	q	154/455 (34%)	128 (83%)	24 (16%)	2 (1%)	9	39
42	r	224/261 (86%)	188 (84%)	33 (15%)	3 (1%)	9	39
43	t	283/322 (88%)	238 (84%)	42 (15%)	3 (1%)	11	42
44	u	140/199 (70%)	126 (90%)	14 (10%)	0	100	100
45	v	283/344 (82%)	265 (94%)	18 (6%)	0	100	100
46	w	178/203 (88%)	158 (89%)	20 (11%)	0	100	100
47	x	476/515 (92%)	422 (89%)	54 (11%)	0	100	100
48	y	242/245 (99%)	213 (88%)	29 (12%)	0	100	100
49	z	53/106 (50%)	51 (96%)	2 (4%)	0	100	100
All	All	9279/11058 (84%)	8226 (89%)	1015 (11%)	38 (0%)	31	61

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	339	LEU
12	K	216	GLU
26	Z	102	GLU
37	m	241	SER
1	L	63	VAL
2	a	78	LEU
14	N	95	GLN
27	b	399	ALA
27	b	484	SER
37	m	78	PHE
37	m	209	LYS
37	m	418	ILE
37	m	424	ALA
41	q	201	SER
43	t	58	ALA
43	t	222	ALA
43	t	247	VAL
5	C	4	PRO
12	K	167	TYR
27	b	369	ARG
37	m	240	LYS
38	n	455	PRO
41	q	406	LEU
42	r	17	ARG
42	r	147	TRP

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Mol	Chain	Res	Type
4	B	342	LEU
5	C	268	ALA
23	W	178	GLY
33	h	92	LEU
38	n	6	LYS
42	r	146	SER
10	H	50	ASN
39	o	159	GLY
4	B	188	ILE
14	N	146	ALA
38	n	55	GLY
4	B	239	PRO
26	Z	104	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	147/159 (92%)	128 (87%)	19 (13%)	4	19
2	a	76/119 (64%)	63 (83%)	13 (17%)	2	10
3	A	152/196 (78%)	136 (90%)	16 (10%)	6	27
4	B	322/323 (100%)	282 (88%)	40 (12%)	4	21
5	C	273/289 (94%)	248 (91%)	25 (9%)	8	32
6	D	226/245 (92%)	212 (94%)	14 (6%)	16	47
7	E	134/153 (88%)	122 (91%)	12 (9%)	9	33
8	F	186/205 (91%)	169 (91%)	17 (9%)	9	32
9	G	186/208 (89%)	168 (90%)	18 (10%)	8	31
10	H	168/171 (98%)	152 (90%)	16 (10%)	8	31
11	J	145/150 (97%)	136 (94%)	9 (6%)	16	47
12	K	234/346 (68%)	213 (91%)	21 (9%)	9	33
13	M	108/109 (99%)	97 (90%)	11 (10%)	7	28
14	N	175/176 (99%)	161 (92%)	14 (8%)	11	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	160/162 (99%)	154 (96%)	6 (4%)	29	60
16	P	145/146 (99%)	126 (87%)	19 (13%)	4	19
17	Q	110/151 (73%)	96 (87%)	14 (13%)	4	20
18	R	129/154 (84%)	120 (93%)	9 (7%)	14	43
19	S	155/156 (99%)	138 (89%)	17 (11%)	6	25
20	T	102/137 (74%)	87 (85%)	15 (15%)	3	14
21	U	91/107 (85%)	76 (84%)	15 (16%)	2	10
22	V	104/105 (99%)	96 (92%)	8 (8%)	12	40
23	W	211/213 (99%)	187 (89%)	24 (11%)	5	23
24	X	117/118 (99%)	105 (90%)	12 (10%)	7	27
25	Y	109/110 (99%)	101 (93%)	8 (7%)	13	42
26	Z	115/116 (99%)	105 (91%)	10 (9%)	9	35
27	b	457/573 (80%)	414 (91%)	43 (9%)	8	31
28	c	81/88 (92%)	71 (88%)	10 (12%)	4	21
29	d	92/97 (95%)	82 (89%)	10 (11%)	6	25
30	e	108/111 (97%)	95 (88%)	13 (12%)	5	22
31	f	90/91 (99%)	85 (94%)	5 (6%)	19	50
32	g	95/103 (92%)	81 (85%)	14 (15%)	3	14
33	h	104/105 (99%)	90 (86%)	14 (14%)	4	18
34	i	81/82 (99%)	75 (93%)	6 (7%)	13	41
35	j	69/71 (97%)	61 (88%)	8 (12%)	5	23
36	k	67/69 (97%)	61 (91%)	6 (9%)	9	33
37	m	413/428 (96%)	369 (89%)	44 (11%)	6	26
38	n	329/548 (60%)	288 (88%)	41 (12%)	4	20
39	o	114/199 (57%)	101 (89%)	13 (11%)	5	23
40	p	71/72 (99%)	64 (90%)	7 (10%)	7	29
41	q	147/420 (35%)	133 (90%)	14 (10%)	8	31
42	r	203/229 (89%)	183 (90%)	20 (10%)	7	29
43	t	256/287 (89%)	233 (91%)	23 (9%)	9	33
44	u	126/180 (70%)	118 (94%)	8 (6%)	16	46
45	v	258/309 (84%)	234 (91%)	24 (9%)	8	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	w	161/179 (90%)	149 (92%)	12 (8%)	12	40
47	x	428/451 (95%)	386 (90%)	42 (10%)	7	30
48	y	210/211 (100%)	187 (89%)	23 (11%)	6	25
49	z	48/95 (50%)	41 (85%)	7 (15%)	3	15
All	All	8088/9522 (85%)	7279 (90%)	809 (10%)	9	29

All (809) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	10	LEU
1	L	13	HIS
1	L	15	ARG
1	L	18	TRP
1	L	19	GLN
1	L	22	VAL
1	L	24	VAL
1	L	27	ASP
1	L	54	LEU
1	L	58	VAL
1	L	69	VAL
1	L	121	SER
1	L	122	LYS
1	L	124	ILE
1	L	125	VAL
1	L	129	ASN
1	L	175	SER
1	L	176	GLU
1	L	188	ARG
2	a	73	LEU
2	a	75	LEU
2	a	76	ASP
2	a	80	THR
2	a	95	SER
2	a	97	GLU
2	a	118	ILE
2	a	123	VAL
2	a	131	SER
2	a	133	LEU
2	a	136	GLU
2	a	138	ILE
2	a	145	VAL

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Mol	Chain	Res	Type
3	A	8	GLN
3	A	10	LYS
3	A	17	THR
3	A	29	LEU
3	A	31	THR
3	A	36	GLU
3	A	61	VAL
3	A	101	VAL
3	A	116	VAL
3	A	126	LEU
3	A	130	SER
3	A	142	ASP
3	A	147	ARG
3	A	157	VAL
3	A	175	VAL
3	A	195	SER
4	B	35	ASP
4	B	71	GLU
4	B	85	VAL
4	B	89	VAL
4	B	90	VAL
4	B	101	SER
4	B	103	THR
4	B	104	THR
4	B	105	VAL
4	B	111	SER
4	B	113	GLU
4	B	114	VAL
4	B	126	LYS
4	B	140	ASP
4	B	157	VAL
4	B	160	VAL
4	B	161	LEU
4	B	171	LEU
4	B	173	GLN
4	B	188	ILE
4	B	198	HIS
4	B	211	GLN
4	B	218	ILE
4	B	237	LYS
4	B	240	ARG
4	B	242	THR

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Mol	Chain	Res	Type
4	B	251	CYS
4	B	261	MET
4	B	264	VAL
4	B	274	SER
4	B	283	TYR
4	B	296	THR
4	B	301	THR
4	B	325	LYS
4	B	335	ILE
4	B	336	VAL
4	B	347	SER
4	B	354	VAL
4	B	372	THR
4	B	382	THR
5	C	6	VAL
5	C	7	THR
5	C	16	THR
5	C	27	SER
5	C	52	VAL
5	C	60	THR
5	C	133	SER
5	C	134	LEU
5	C	138	ARG
5	C	163	LYS
5	C	181	VAL
5	C	193	LYS
5	C	222	VAL
5	C	227	THR
5	C	235	LEU
5	C	256	THR
5	C	267	VAL
5	C	287	THR
5	C	292	SER
5	C	293	SER
5	C	295	ILE
5	C	299	ILE
5	C	333	VAL
5	C	349	THR
5	C	356	THR
6	D	27	LYS
6	D	41	LYS
6	D	53	VAL

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Mol	Chain	Res	Type
6	D	61	ILE
6	D	81	HIS
6	D	109	THR
6	D	115	LEU
6	D	153	THR
6	D	155	THR
6	D	227	LEU
6	D	231	ILE
6	D	274	GLN
6	D	275	THR
6	D	293	LEU
7	E	2	SER
7	E	15	VAL
7	E	21	THR
7	E	38	THR
7	E	52	VAL
7	E	58	LEU
7	E	62	THR
7	E	89	THR
7	E	96	VAL
7	E	101	PHE
7	E	103	VAL
7	E	174	LEU
8	F	26	VAL
8	F	63	ILE
8	F	74	SER
8	F	77	VAL
8	F	86	VAL
8	F	93	ASN
8	F	104	GLN
8	F	111	ILE
8	F	124	LEU
8	F	129	LEU
8	F	142	SER
8	F	143	THR
8	F	156	ILE
8	F	182	ASP
8	F	189	ILE
8	F	190	THR
8	F	208	SER
9	G	24	ASN
9	G	26	LEU

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Mol	Chain	Res	Type
9	G	36	ILE
9	G	47	SER
9	G	65	LEU
9	G	67	ILE
9	G	71	VAL
9	G	77	GLN
9	G	83	ASP
9	G	85	ASN
9	G	86	THR
9	G	151	VAL
9	G	163	VAL
9	G	164	VAL
9	G	166	LEU
9	G	197	VAL
9	G	203	VAL
9	G	206	GLU
10	H	6	THR
10	H	17	THR
10	H	33	THR
10	H	35	THR
10	H	44	THR
10	H	53	ILE
10	H	55	VAL
10	H	65	VAL
10	H	73	SER
10	H	93	VAL
10	H	132	VAL
10	H	138	THR
10	H	144	ILE
10	H	181	VAL
10	H	184	LYS
10	H	188	THR
11	J	12	LEU
11	J	18	VAL
11	J	40	LEU
11	J	65	ILE
11	J	80	LEU
11	J	99	THR
11	J	112	LEU
11	J	122	ILE
11	J	155	THR
12	K	43	GLU

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Mol	Chain	Res	Type
12	K	45	ILE
12	K	78	LEU
12	K	84	ASN
12	K	88	PHE
12	K	89	THR
12	K	91	THR
12	K	99	LEU
12	K	102	VAL
12	K	116	THR
12	K	132	ILE
12	K	142	ASP
12	K	186	ILE
12	K	188	THR
12	K	215	LYS
12	K	217	PHE
12	K	219	LEU
12	K	248	LEU
12	K	260	VAL
12	K	272	LYS
12	K	280	PHE
13	M	8	LYS
13	M	20	VAL
13	M	38	ILE
13	M	39	ILE
13	M	63	VAL
13	M	64	VAL
13	M	91	CYS
13	M	98	SER
13	M	120	VAL
13	M	122	VAL
13	M	135	LEU
14	N	8	GLU
14	N	18	VAL
14	N	35	VAL
14	N	61	ILE
14	N	80	THR
14	N	97	SER
14	N	106	VAL
14	N	109	ARG
14	N	143	ARG
14	N	147	ARG
14	N	155	VAL

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Mol	Chain	Res	Type
14	N	159	ARG
14	N	195	ASN
14	N	198	SER
15	O	34	VAL
15	O	40	GLU
15	O	67	THR
15	O	119	VAL
15	O	129	LEU
15	O	151	ASP
16	P	7	THR
16	P	9	THR
16	P	16	SER
16	P	22	LEU
16	P	29	THR
16	P	36	ILE
16	P	51	VAL
16	P	58	ILE
16	P	65	SER
16	P	87	SER
16	P	110	THR
16	P	115	SER
16	P	117	ILE
16	P	119	VAL
16	P	120	ASN
16	P	129	THR
16	P	133	HIS
16	P	139	TYR
16	P	176	ILE
17	Q	32	LEU
17	Q	50	LYS
17	Q	59	ARG
17	Q	64	VAL
17	Q	79	LYS
17	Q	81	VAL
17	Q	83	VAL
17	Q	84	VAL
17	Q	99	THR
17	Q	104	LEU
17	Q	115	VAL
17	Q	122	ILE
17	Q	129	VAL
17	Q	136	ASN

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Mol	Chain	Res	Type
18	R	14	VAL
18	R	22	VAL
18	R	44	LEU
18	R	49	THR
18	R	51	VAL
18	R	55	VAL
18	R	69	SER
18	R	84	THR
18	R	150	GLN
19	S	8	GLN
19	S	16	THR
19	S	45	LEU
19	S	48	LEU
19	S	53	LYS
19	S	63	GLN
19	S	70	THR
19	S	79	VAL
19	S	87	THR
19	S	89	ASN
19	S	94	ILE
19	S	120	SER
19	S	140	VAL
19	S	156	VAL
19	S	159	SER
19	S	160	THR
19	S	170	THR
20	T	36	VAL
20	T	41	ASP
20	T	45	ASN
20	T	54	HIS
20	T	56	PHE
20	T	63	VAL
20	T	68	THR
20	T	76	ILE
20	T	99	SER
20	T	106	LEU
20	T	126	VAL
20	T	141	VAL
20	T	143	THR
20	T	150	THR
20	T	151	LEU
21	U	29	ASP

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Mol	Chain	Res	Type
21	U	37	LEU
21	U	41	ILE
21	U	43	VAL
21	U	47	VAL
21	U	55	THR
21	U	56	VAL
21	U	59	ASP
21	U	62	VAL
21	U	63	VAL
21	U	64	THR
21	U	76	LEU
21	U	91	ASP
21	U	96	VAL
21	U	105	LEU
22	V	4	ASN
22	V	7	GLN
22	V	19	VAL
22	V	27	ASP
22	V	63	LYS
22	V	73	VAL
22	V	93	LEU
22	V	137	VAL
23	W	9	LEU
23	W	10	VAL
23	W	11	THR
23	W	15	THR
23	W	25	ARG
23	W	34	LEU
23	W	45	LEU
23	W	52	VAL
23	W	72	VAL
23	W	83	GLU
23	W	96	CYS
23	W	105	THR
23	W	108	ASP
23	W	134	THR
23	W	149	ILE
23	W	158	ILE
23	W	161	LEU
23	W	164	THR
23	W	175	ILE
23	W	183	ASP

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Mol	Chain	Res	Type
23	W	190	THR
23	W	220	TYR
23	W	228	VAL
23	W	230	SER
24	X	14	VAL
24	X	26	VAL
24	X	33	ARG
24	X	34	LEU
24	X	40	LEU
24	X	51	VAL
24	X	57	LEU
24	X	63	ILE
24	X	88	MET
24	X	104	GLU
24	X	113	LEU
24	X	119	THR
25	Y	7	ASP
25	Y	25	SER
25	Y	42	GLN
25	Y	54	ASP
25	Y	57	LEU
25	Y	95	VAL
25	Y	102	SER
25	Y	126	LEU
26	Z	9	LYS
26	Z	24	VAL
26	Z	42	LEU
26	Z	46	ILE
26	Z	53	VAL
26	Z	72	ILE
26	Z	89	VAL
26	Z	99	GLU
26	Z	100	THR
26	Z	132	SER
27	b	5	TRP
27	b	22	LEU
27	b	29	THR
27	b	39	ILE
27	b	58	VAL
27	b	71	ILE
27	b	73	ASP
27	b	115	LEU

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Mol	Chain	Res	Type
27	b	116	LEU
27	b	117	LYS
27	b	129	LYS
27	b	138	THR
27	b	145	ASP
27	b	157	ILE
27	b	166	ASN
27	b	169	THR
27	b	170	LEU
27	b	181	SER
27	b	187	ILE
27	b	192	VAL
27	b	203	SER
27	b	210	ASP
27	b	229	THR
27	b	247	ARG
27	b	248	SER
27	b	264	ILE
27	b	298	LEU
27	b	309	VAL
27	b	358	LEU
27	b	369	ARG
27	b	375	THR
27	b	398	LEU
27	b	411	VAL
27	b	414	VAL
27	b	420	TYR
27	b	435	ILE
27	b	440	ASN
27	b	453	LEU
27	b	456	LEU
27	b	479	ASP
27	b	484	SER
27	b	488	ASP
27	b	502	THR
28	c	11	ASN
28	c	16	LEU
28	c	18	ILE
28	c	33	SER
28	c	44	ILE
28	c	54	SER
28	c	86	ARG

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Mol	Chain	Res	Type
28	c	87	VAL
28	c	97	ASP
28	c	100	ILE
29	d	8	VAL
29	d	13	THR
29	d	46	THR
29	d	47	ASP
29	d	64	VAL
29	d	96	VAL
29	d	98	VAL
29	d	100	SER
29	d	106	THR
29	d	107	VAL
30	e	16	LYS
30	e	21	HIS
30	e	26	HIS
30	e	55	ILE
30	e	62	LYS
30	e	67	SER
30	e	69	SER
30	e	73	THR
30	e	76	VAL
30	e	88	HIS
30	e	91	THR
30	e	120	THR
30	e	126	LEU
31	f	9	VAL
31	f	40	ASP
31	f	52	VAL
31	f	71	VAL
31	f	100	ILE
32	g	6	THR
32	g	15	THR
32	g	23	VAL
32	g	33	GLN
32	g	35	VAL
32	g	36	LYS
32	g	38	LEU
32	g	47	CYS
32	g	51	LEU
32	g	56	THR
32	g	71	THR

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Mol	Chain	Res	Type
32	g	73	SER
32	g	81	CYS
32	g	109	THR
33	h	11	THR
33	h	33	VAL
33	h	38	ARG
33	h	44	ILE
33	h	46	THR
33	h	48	ARG
33	h	50	SER
33	h	84	LYS
33	h	85	THR
33	h	86	ARG
33	h	92	LEU
33	h	100	VAL
33	h	101	THR
33	h	109	ILE
34	i	3	VAL
34	i	9	ILE
34	i	17	VAL
34	i	18	THR
34	i	37	THR
34	i	97	SER
35	j	5	THR
35	j	11	ARG
35	j	13	ASN
35	j	44	THR
35	j	59	THR
35	j	67	LEU
35	j	71	SER
35	j	80	THR
36	k	5	ILE
36	k	8	ILE
36	k	31	LEU
36	k	33	LYS
36	k	45	VAL
36	k	72	THR
37	m	13	ARG
37	m	30	TYR
37	m	32	ASP
37	m	41	MET
37	m	65	THR

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Mol	Chain	Res	Type
37	m	83	VAL
37	m	84	ILE
37	m	87	ASP
37	m	116	SER
37	m	118	LEU
37	m	132	LEU
37	m	133	ASP
37	m	134	THR
37	m	139	ASP
37	m	166	GLU
37	m	176	VAL
37	m	191	GLU
37	m	207	GLN
37	m	226	ILE
37	m	250	THR
37	m	255	LEU
37	m	287	HIS
37	m	290	ILE
37	m	291	THR
37	m	299	LEU
37	m	307	SER
37	m	312	ASP
37	m	313	ARG
37	m	326	THR
37	m	332	ILE
37	m	341	CYS
37	m	385	ARG
37	m	388	VAL
37	m	394	THR
37	m	409	VAL
37	m	418	ILE
37	m	425	THR
37	m	430	ILE
37	m	438	LEU
37	m	449	VAL
37	m	452	GLN
37	m	454	LEU
37	m	462	ILE
37	m	466	VAL
38	n	2	ARG
38	n	4	LYS
38	n	17	THR

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Mol	Chain	Res	Type
38	n	27	VAL
38	n	35	LEU
38	n	51	LYS
38	n	56	SER
38	n	60	THR
38	n	61	THR
38	n	64	TYR
38	n	68	ILE
38	n	76	VAL
38	n	77	LEU
38	n	91	THR
38	n	105	LEU
38	n	108	ASN
38	n	111	SER
38	n	113	THR
38	n	118	ILE
38	n	148	THR
38	n	151	VAL
38	n	175	LEU
38	n	176	VAL
38	n	200	LEU
38	n	208	ASN
38	n	217	ILE
38	n	220	THR
38	n	228	LEU
38	n	242	LEU
38	n	248	LEU
38	n	259	LEU
38	n	265	GLU
38	n	367	VAL
38	n	371	VAL
38	n	376	LEU
38	n	382	SER
38	n	390	GLU
38	n	394	ASP
38	n	416	VAL
38	n	427	ILE
38	n	442	VAL
39	o	95	VAL
39	o	100	HIS
39	o	107	LEU
39	o	120	VAL

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Mol	Chain	Res	Type
39	o	130	ASN
39	o	139	PHE
39	o	140	VAL
39	o	157	LEU
39	o	164	VAL
39	o	176	LEU
39	o	187	LYS
39	o	193	VAL
39	o	196	LEU
40	p	16	VAL
40	p	17	ARG
40	p	38	ASP
40	p	41	PHE
40	p	56	THR
40	p	58	SER
40	p	89	MET
41	q	193	SER
41	q	194	THR
41	q	195	THR
41	q	206	THR
41	q	209	ILE
41	q	214	VAL
41	q	230	ASN
41	q	241	GLU
41	q	269	LEU
41	q	389	VAL
41	q	391	ASP
41	q	395	GLU
41	q	409	LEU
41	q	446	THR
42	r	7	ILE
42	r	35	ILE
42	r	71	SER
42	r	85	ASP
42	r	120	VAL
42	r	133	MET
42	r	145	LYS
42	r	157	VAL
42	r	171	ILE
42	r	189	LEU
42	r	193	VAL
42	r	195	LEU

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Mol	Chain	Res	Type
42	r	198	LEU
42	r	221	ILE
42	r	232	THR
42	r	237	VAL
42	r	245	VAL
42	r	250	ASP
42	r	255	VAL
42	r	258	VAL
43	t	44	GLN
43	t	61	ILE
43	t	93	ILE
43	t	97	LYS
43	t	103	ILE
43	t	128	LEU
43	t	129	ILE
43	t	133	THR
43	t	166	LEU
43	t	183	VAL
43	t	189	VAL
43	t	208	ILE
43	t	215	ILE
43	t	227	ILE
43	t	229	LEU
43	t	239	LEU
43	t	245	ILE
43	t	247	VAL
43	t	256	THR
43	t	262	SER
43	t	263	VAL
43	t	289	ILE
43	t	306	THR
44	u	3	ILE
44	u	6	CYS
44	u	9	CYS
44	u	63	LEU
44	u	68	THR
44	u	90	LEU
44	u	126	LEU
44	u	127	VAL
45	v	33	ILE
45	v	37	SER
45	v	39	ASN

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Mol	Chain	Res	Type
45	v	41	ASN
45	v	47	VAL
45	v	62	ARG
45	v	73	SER
45	v	98	ASN
45	v	116	LEU
45	v	120	ASP
45	v	126	SER
45	v	129	LYS
45	v	135	VAL
45	v	181	VAL
45	v	199	VAL
45	v	221	ILE
45	v	224	VAL
45	v	226	ILE
45	v	239	THR
45	v	267	ILE
45	v	275	ILE
45	v	277	MET
45	v	293	LEU
45	v	296	LYS
46	w	13	VAL
46	w	19	VAL
46	w	41	SER
46	w	56	ASP
46	w	72	THR
46	w	74	THR
46	w	97	THR
46	w	127	GLU
46	w	138	SER
46	w	151	ASN
46	w	159	LEU
46	w	179	LEU
47	x	3	THR
47	x	11	LYS
47	x	17	GLN
47	x	24	ILE
47	x	25	ILE
47	x	31	ASN
47	x	40	ASP
47	x	71	SER
47	x	90	ASP

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Mol	Chain	Res	Type
47	x	126	VAL
47	x	133	THR
47	x	142	HIS
47	x	145	THR
47	x	151	PHE
47	x	155	THR
47	x	157	SER
47	x	177	THR
47	x	179	MET
47	x	200	VAL
47	x	223	ASP
47	x	265	THR
47	x	281	VAL
47	x	300	THR
47	x	344	LYS
47	x	347	SER
47	x	371	GLU
47	x	375	VAL
47	x	404	LEU
47	x	405	VAL
47	x	418	VAL
47	x	421	SER
47	x	424	ASN
47	x	438	SER
47	x	457	ARG
47	x	460	VAL
47	x	466	THR
47	x	468	LEU
47	x	473	VAL
47	x	482	LEU
47	x	492	VAL
47	x	496	VAL
47	x	503	SER
48	y	3	THR
48	y	20	THR
48	y	22	THR
48	y	28	VAL
48	y	52	THR
48	y	59	ILE
48	y	67	ARG
48	y	72	VAL
48	y	88	LEU

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Mol	Chain	Res	Type
48	y	92	VAL
48	y	101	LEU
48	y	117	VAL
48	y	120	ASP
48	y	146	ILE
48	y	165	THR
48	y	169	ASP
48	y	192	VAL
48	y	198	VAL
48	y	217	VAL
48	y	224	LEU
48	y	226	ASP
48	y	232	ILE
48	y	239	THR
49	z	4	SER
49	z	33	ILE
49	z	37	LEU
49	z	40	ASP
49	z	42	LEU
49	z	46	LEU
49	z	52	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (167) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	25	HIS
1	L	103	ASN
1	L	120	GLN
2	a	62	HIS
2	a	74	ASN
3	A	19	HIS
3	A	38	HIS
3	A	50	HIS
3	A	83	HIS
3	A	115	ASN
3	A	132	ASN
4	B	212	ASN
4	B	231	HIS
5	C	114	ASN
5	C	116	ASN
5	C	221	ASN
5	C	243	HIS

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Mol	Chain	Res	Type
5	C	260	GLN
6	D	17	GLN
6	D	111	GLN
6	D	297	GLN
8	F	166	ASN
8	F	172	ASN
9	G	24	ASN
9	G	79	GLN
9	G	85	ASN
9	G	95	ASN
9	G	137	ASN
9	G	138	HIS
9	G	145	ASN
9	G	155	ASN
10	H	50	ASN
10	H	59	ASN
10	H	125	ASN
10	H	157	ASN
11	J	68	HIS
11	J	90	GLN
11	J	95	ASN
11	J	109	HIS
11	J	150	ASN
12	K	214	ASN
12	K	247	HIS
12	K	295	GLN
13	M	41	GLN
13	M	126	GLN
14	N	37	HIS
14	N	90	ASN
15	O	42	ASN
15	O	55	HIS
15	O	72	HIS
16	P	55	GLN
16	P	96	GLN
16	P	118	GLN
16	P	133	HIS
17	Q	15	HIS
17	Q	126	GLN
17	Q	135	GLN
17	Q	145	ASN
18	R	34	GLN

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Mol	Chain	Res	Type
18	R	118	HIS
19	S	62	ASN
19	S	63	GLN
19	S	142	GLN
19	S	154	HIS
20	T	90	ASN
20	T	95	HIS
20	T	98	HIS
20	T	131	GLN
21	U	25	ASN
23	W	14	GLN
23	W	22	ASN
23	W	74	GLN
23	W	88	ASN
24	X	94	GLN
25	Y	4	GLN
25	Y	81	GLN
25	Y	110	HIS
26	Z	36	HIS
26	Z	57	HIS
27	b	152	GLN
27	b	177	ASN
27	b	333	ASN
27	b	406	ASN
27	b	465	ASN
27	b	500	GLN
28	c	75	ASN
29	d	15	ASN
29	d	56	ASN
29	d	57	GLN
29	d	87	ASN
30	e	35	GLN
30	e	52	GLN
31	f	42	GLN
32	g	11	ASN
33	h	62	GLN
34	i	63	ASN
35	j	30	GLN
35	j	76	ASN
37	m	28	ASN
37	m	111	ASN
37	m	146	GLN

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Mol	Chain	Res	Type
37	m	156	ASN
37	m	187	GLN
37	m	207	GLN
37	m	276	HIS
37	m	315	GLN
37	m	452	GLN
38	n	149	ASN
38	n	160	GLN
38	n	189	GLN
38	n	430	GLN
38	n	437	ASN
39	o	103	HIS
39	o	153	ASN
39	o	160	HIS
39	o	204	HIS
40	p	34	HIS
41	q	222	HIS
41	q	228	ASN
41	q	264	HIS
41	q	381	HIS
41	q	424	GLN
41	q	451	HIS
42	r	4	ASN
42	r	14	HIS
42	r	40	GLN
42	r	70	GLN
43	t	25	ASN
43	t	91	GLN
43	t	154	ASN
43	t	157	ASN
43	t	182	ASN
43	t	232	ASN
43	t	233	ASN
43	t	252	HIS
43	t	265	ASN
43	t	269	GLN
44	u	7	HIS
44	u	17	HIS
44	u	37	HIS
44	u	45	ASN
44	u	76	ASN
44	u	110	ASN

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Mol	Chain	Res	Type
44	u	130	ASN
45	v	9	ASN
45	v	82	ASN
45	v	144	GLN
45	v	173	GLN
45	v	198	ASN
45	v	286	GLN
46	w	91	GLN
46	w	151	ASN
46	w	195	GLN
47	x	12	GLN
47	x	154	HIS
47	x	208	ASN
47	x	297	HIS
47	x	321	HIS
47	x	353	GLN
47	x	402	GLN
47	x	443	HIS
47	x	449	GLN
48	y	11	ASN
48	y	79	GLN
48	y	106	ASN
48	y	156	ASN
48	y	187	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	1	3048/3396 (89%)	815 (26%)	64 (2%)
51	2	157/158 (99%)	32 (20%)	1 (0%)
52	3	120/121 (99%)	33 (27%)	1 (0%)
53	6	63/232 (27%)	33 (52%)	2 (3%)
All	All	3388/3907 (86%)	913 (26%)	68 (2%)

All (913) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	1	5	G
50	1	7	C
50	1	14	U
50	1	18	G

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Mol	Chain	Res	Type
50	1	38	U
50	1	40	A
50	1	41	G
50	1	42	C
50	1	43	A
50	1	44	U
50	1	49	A
50	1	59	G
50	1	60	A
50	1	65	A
50	1	66	A
50	1	73	C
50	1	75	G
50	1	83	U
50	1	89	A
50	1	90	C
50	1	92	G
50	1	93	C
50	1	95	A
50	1	103	G
50	1	105	C
50	1	110	G
50	1	111	C
50	1	116	A
50	1	118	U
50	1	119	U
50	1	121	A
50	1	122	A
50	1	136	G
50	1	143	G
50	1	156	G
50	1	157	A
50	1	161	G
50	1	165	A
50	1	166	C
50	1	170	G
50	1	176	G
50	1	182	U
50	1	187	A
50	1	190	U
50	1	191	U
50	1	200	C

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Mol	Chain	Res	Type
50	1	206	G
50	1	210	U
50	1	211	A
50	1	218	G
50	1	219	A
50	1	240	U
50	1	241	G
50	1	243	G
50	1	245	U
50	1	246	U
50	1	249	U
50	1	251	G
50	1	252	U
50	1	253	A
50	1	254	A
50	1	264	G
50	1	266	A
50	1	267	G
50	1	269	G
50	1	281	G
50	1	283	G
50	1	284	A
50	1	285	A
50	1	292	U
50	1	295	A
50	1	298	U
50	1	303	G
50	1	304	G
50	1	305	U
50	1	306	A
50	1	307	A
50	1	323	A
50	1	329	U
50	1	351	A
50	1	352	A
50	1	370	U
50	1	376	G
50	1	385	A
50	1	398	A
50	1	399	A
50	1	403	C
50	1	421	G

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Mol	Chain	Res	Type
50	1	422	A
50	1	429	U
50	1	438	A
50	1	439	C
50	1	440	A
50	1	495	G
50	1	496	C
50	1	498	A
50	1	507	U
50	1	521	A
50	1	528	U
50	1	532	A
50	1	535	G
50	1	536	U
50	1	543	C
50	1	544	C
50	1	545	U
50	1	547	G
50	1	549	U
50	1	552	G
50	1	555	U
50	1	557	A
50	1	559	A
50	1	579	G
50	1	592	A
50	1	600	G
50	1	604	G
50	1	609	G
50	1	611	A
50	1	620	U
50	1	621	A
50	1	622	A
50	1	634	C
50	1	637	C
50	1	638	C
50	1	643	U
50	1	644	G
50	1	645	A
50	1	646	A
50	1	647	A
50	1	648	C
50	1	650	C

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Mol	Chain	Res	Type
50	1	665	A
50	1	677	A
50	1	681	U
50	1	691	A
50	1	705	A
50	1	706	A
50	1	708	G
50	1	711	A
50	1	712	G
50	1	716	A
50	1	720	A
50	1	721	G
50	1	722	G
50	1	725	G
50	1	737	G
50	1	750	G
50	1	762	U
50	1	765	C
50	1	766	U
50	1	767	U
50	1	768	C
50	1	776	U
50	1	780	A
50	1	784	A
50	1	785	G
50	1	801	A
50	1	807	A
50	1	808	A
50	1	814	U
50	1	816	A
50	1	817	A
50	1	825	U
50	1	830	A
50	1	847	A
50	1	849	C
50	1	850	U
50	1	861	C
50	1	871	U
50	1	872	U
50	1	874	U
50	1	876	A
50	1	877	C

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Mol	Chain	Res	Type
50	1	879	U
50	1	884	A
50	1	885	U
50	1	886	C
50	1	887	G
50	1	896	A
50	1	897	U
50	1	907	G
50	1	908	G
50	1	909	G
50	1	914	A
50	1	916	G
50	1	918	C
50	1	922	U
50	1	924	G
50	1	936	A
50	1	938	C
50	1	944	C
50	1	954	U
50	1	955	U
50	1	956	U
50	1	957	C
50	1	970	A
50	1	974	G
50	1	975	C
50	1	978	G
50	1	980	A
50	1	991	G
50	1	994	G
50	1	995	U
50	1	996	A
50	1	997	A
50	1	999	G
50	1	1000	C
50	1	1001	G
50	1	1003	A
50	1	1050	U
50	1	1051	U
50	1	1055	A
50	1	1056	U
50	1	1057	A
50	1	1064	A

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Mol	Chain	Res	Type
50	1	1065	A
50	1	1066	G
50	1	1070	U
50	1	1071	U
50	1	1072	G
50	1	1084	A
50	1	1086	C
50	1	1087	G
50	1	1093	A
50	1	1094	U
50	1	1095	U
50	1	1097	G
50	1	1098	A
50	1	1102	A
50	1	1103	A
50	1	1104	G
50	1	1105	A
50	1	1107	C
50	1	1110	U
50	1	1111	U
50	1	1116	G
50	1	1117	G
50	1	1118	C
50	1	1123	U
50	1	1127	G
50	1	1128	U
50	1	1129	A
50	1	1130	A
50	1	1131	G
50	1	1132	C
50	1	1142	G
50	1	1153	A
50	1	1155	C
50	1	1169	A
50	1	1178	G
50	1	1180	A
50	1	1181	U
50	1	1191	U
50	1	1192	C
50	1	1193	A
50	1	1196	C
50	1	1197	A

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Mol	Chain	Res	Type
50	1	1198	C
50	1	1199	C
50	1	1200	A
50	1	1201	C
50	1	1203	A
50	1	1204	A
50	1	1206	G
50	1	1209	G
50	1	1221	A
50	1	1222	G
50	1	1227	C
50	1	1235	U
50	1	1237	G
50	1	1239	C
50	1	1240	A
50	1	1241	U
50	1	1242	G
50	1	1243	G
50	1	1245	A
50	1	1251	A
50	1	1252	A
50	1	1254	C
50	1	1258	U
50	1	1262	G
50	1	1263	A
50	1	1264	G
50	1	1269	U
50	1	1272	C
50	1	1278	A
50	1	1286	A
50	1	1287	A
50	1	1296	C
50	1	1302	A
50	1	1303	A
50	1	1304	A
50	1	1305	U
50	1	1307	G
50	1	1308	A
50	1	1309	U
50	1	1313	G
50	1	1316	C
50	1	1330	A

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Mol	Chain	Res	Type
50	1	1348	U
50	1	1349	G
50	1	1351	U
50	1	1353	U
50	1	1354	G
50	1	1355	A
50	1	1356	U
50	1	1357	G
50	1	1384	U
50	1	1386	A
50	1	1387	G
50	1	1392	G
50	1	1399	A
50	1	1400	G
50	1	1405	U
50	1	1414	G
50	1	1418	A
50	1	1419	A
50	1	1421	G
50	1	1434	G
50	1	1435	A
50	1	1436	U
50	1	1437	C
50	1	1446	A
50	1	1450	G
50	1	1475	A
50	1	1483	G
50	1	1484	U
50	1	1495	U
50	1	1503	A
50	1	1507	G
50	1	1508	C
50	1	1527	C
50	1	1533	U
50	1	1546	A
50	1	1556	C
50	1	1557	A
50	1	1560	G
50	1	1561	G
50	1	1562	C
50	1	1566	A
50	1	1567	U

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Mol	Chain	Res	Type
50	1	1568	U
50	1	1569	U
50	1	1571	A
50	1	1572	U
50	1	1573	G
50	1	1575	A
50	1	1581	C
50	1	1582	C
50	1	1583	A
50	1	1585	C
50	1	1587	A
50	1	1589	A
50	1	1599	G
50	1	1607	U
50	1	1608	C
50	1	1620	U
50	1	1629	U
50	1	1636	U
50	1	1639	C
50	1	1641	U
50	1	1642	A
50	1	1643	A
50	1	1645	U
50	1	1657	C
50	1	1662	G
50	1	1713	G
50	1	1716	U
50	1	1717	U
50	1	1724	U
50	1	1725	C
50	1	1730	G
50	1	1741	A
50	1	1742	U
50	1	1750	A
50	1	1751	G
50	1	1761	C
50	1	1762	C
50	1	1763	U
50	1	1764	U
50	1	1765	U
50	1	1766	G
50	1	1770	G

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Mol	Chain	Res	Type
50	1	1780	G
50	1	1797	A
50	1	1799	A
50	1	1810	A
50	1	1813	A
50	1	1816	A
50	1	1820	U
50	1	1821	U
50	1	1838	G
50	1	1839	A
50	1	1841	A
50	1	1842	A
50	1	1849	C
50	1	1851	G
50	1	1871	U
50	1	1874	A
50	1	1878	G
50	1	1880	U
50	1	1906	G
50	1	1907	C
50	1	1909	A
50	1	1935	G
50	1	1952	G
50	1	2102	U
50	1	2112	U
50	1	2117	A
50	1	2121	G
50	1	2122	G
50	1	2131	A
50	1	2139	A
50	1	2158	A
50	1	2163	C
50	1	2169	G
50	1	2170	U
50	1	2174	G
50	1	2184	U
50	1	2194	G
50	1	2195	C
50	1	2196	C
50	1	2197	C
50	1	2198	A
50	1	2201	G

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Mol	Chain	Res	Type
50	1	2204	C
50	1	2205	U
50	1	2206	G
50	1	2207	A
50	1	2208	A
50	1	2209	U
50	1	2210	G
50	1	2218	G
50	1	2219	A
50	1	2222	A
50	1	2224	A
50	1	2237	C
50	1	2239	G
50	1	2242	A
50	1	2243	A
50	1	2247	G
50	1	2248	C
50	1	2249	G
50	1	2255	A
50	1	2256	A
50	1	2257	C
50	1	2258	U
50	1	2261	G
50	1	2262	A
50	1	2264	U
50	1	2268	U
50	1	2269	U
50	1	2270	A
50	1	2273	G
50	1	2274	U
50	1	2276	G
50	1	2277	C
50	1	2278	C
50	1	2279	A
50	1	2316	G
50	1	2318	U
50	1	2321	A
50	1	2334	U
50	1	2336	U
50	1	2339	C
50	1	2347	U
50	1	2371	G

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Mol	Chain	Res	Type
50	1	2385	G
50	1	2388	U
50	1	2393	G
50	1	2396	G
50	1	2397	A
50	1	2398	A
50	1	2401	A
50	1	2402	A
50	1	2403	G
50	1	2404	A
50	1	2405	C
50	1	2410	U
50	1	2413	A
50	1	2415	C
50	1	2416	U
50	1	2417	U
50	1	2418	G
50	1	2419	A
50	1	2443	A
50	1	2445	A
50	1	2502	A
50	1	2503	G
50	1	2506	U
50	1	2507	C
50	1	2514	U
50	1	2515	A
50	1	2522	G
50	1	2523	A
50	1	2528	G
50	1	2529	A
50	1	2530	G
50	1	2531	C
50	1	2532	U
50	1	2533	G
50	1	2534	G
50	1	2538	U
50	1	2539	C
50	1	2540	A
50	1	2541	U
50	1	2542	U
50	1	2543	U
50	1	2544	U

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Mol	Chain	Res	Type
50	1	2545	C
50	1	2546	C
50	1	2547	A
50	1	2548	C
50	1	2549	G
50	1	2550	U
50	1	2551	U
50	1	2552	C
50	1	2553	U
50	1	2561	A
50	1	2566	C
50	1	2568	C
50	1	2569	A
50	1	2570	U
50	1	2571	U
50	1	2572	C
50	1	2573	G
50	1	2585	G
50	1	2586	G
50	1	2593	A
50	1	2594	C
50	1	2605	G
50	1	2606	G
50	1	2607	G
50	1	2608	G
50	1	2613	U
50	1	2614	G
50	1	2620	G
50	1	2621	G
50	1	2623	G
50	1	2625	C
50	1	2626	A
50	1	2627	C
50	1	2628	A
50	1	2629	U
50	1	2632	G
50	1	2633	U
50	1	2635	A
50	1	2638	C
50	1	2640	A
50	1	2642	A
50	1	2644	C

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Mol	Chain	Res	Type
50	1	2645	G
50	1	2648	G
50	1	2649	A
50	1	2650	U
50	1	2651	G
50	1	2652	U
50	1	2653	C
50	1	2654	C
50	1	2655	U
50	1	2656	A
50	1	2659	G
50	1	2665	U
50	1	2666	C
50	1	2668	U
50	1	2672	G
50	1	2673	A
50	1	2674	A
50	1	2677	G
50	1	2678	A
50	1	2682	C
50	1	2687	G
50	1	2688	U
50	1	2689	A
50	1	2690	G
50	1	2691	A
50	1	2693	C
50	1	2694	A
50	1	2695	A
50	1	2696	A
50	1	2697	A
50	1	2698	G
50	1	2700	G
50	1	2701	U
50	1	2702	A
50	1	2703	A
50	1	2704	A
50	1	2706	G
50	1	2713	U
50	1	2714	G
50	1	2715	A
50	1	2717	U
50	1	2718	U

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Mol	Chain	Res	Type
50	1	2719	U
50	1	2720	G
50	1	2721	A
50	1	2724	U
50	1	2725	U
50	1	2726	C
50	1	2727	A
50	1	2728	G
50	1	2729	U
50	1	2730	G
50	1	2731	U
50	1	2732	G
50	1	2734	A
50	1	2741	C
50	1	2751	G
50	1	2752	U
50	1	2754	G
50	1	2758	A
50	1	2759	U
50	1	2760	C
50	1	2762	A
50	1	2764	C
50	1	2765	C
50	1	2766	U
50	1	2771	U
50	1	2772	C
50	1	2773	C
50	1	2774	C
50	1	2777	G
50	1	2778	G
50	1	2779	A
50	1	2786	G
50	1	2789	U
50	1	2791	G
50	1	2793	G
50	1	2794	G
50	1	2795	U
50	1	2796	G
50	1	2797	C
50	1	2798	C
50	1	2800	G
50	1	2801	A

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Mol	Chain	Res	Type
50	1	2802	A
50	1	2808	A
50	1	2809	C
50	1	2810	C
50	1	2811	A
50	1	2816	G
50	1	2817	A
50	1	2819	A
50	1	2820	A
50	1	2822	U
50	1	2824	G
50	1	2826	U
50	1	2834	G
50	1	2836	C
50	1	2838	A
50	1	2840	C
50	1	2842	U
50	1	2843	U
50	1	2846	U
50	1	2847	A
50	1	2849	C
50	1	2858	U
50	1	2859	U
50	1	2861	U
50	1	2863	G
50	1	2864	A
50	1	2865	U
50	1	2866	U
50	1	2867	C
50	1	2868	U
50	1	2869	U
50	1	2872	A
50	1	2873	U
50	1	2874	G
50	1	2875	U
50	1	2876	C
50	1	2877	G
50	1	2878	G
50	1	2879	C
50	1	2887	A
50	1	2897	A
50	1	2898	G

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Mol	Chain	Res	Type
50	1	2899	C
50	1	2900	A
50	1	2901	G
50	1	2904	U
50	1	2921	U
50	1	2923	U
50	1	2925	C
50	1	2926	A
50	1	2928	C
50	1	2930	A
50	1	2935	U
50	1	2936	A
50	1	2945	G
50	1	2946	A
50	1	2947	G
50	1	2948	C
50	1	2949	U
50	1	2952	G
50	1	2953	U
50	1	2954	U
50	1	2955	U
50	1	2956	A
50	1	2957	G
50	1	2970	C
50	1	2971	A
50	1	2977	G
50	1	2978	U
50	1	2979	U
50	1	2980	U
50	1	2981	U
50	1	2982	A
50	1	2983	C
50	1	2984	C
50	1	2990	G
50	1	2996	U
50	1	2997	G
50	1	3012	A
50	1	3017	A
50	1	3021	A
50	1	3022	G
50	1	3023	U
50	1	3030	G

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Mol	Chain	Res	Type
50	1	3032	A
50	1	3040	A
50	1	3059	G
50	1	3069	G
50	1	3074	G
50	1	3078	U
50	1	3079	U
50	1	3080	G
50	1	3086	A
50	1	3092	C
50	1	3093	C
50	1	3100	U
50	1	3101	G
50	1	3107	U
50	1	3116	G
50	1	3117	C
50	1	3124	G
50	1	3127	A
50	1	3129	A
50	1	3130	A
50	1	3131	U
50	1	3142	A
50	1	3143	C
50	1	3151	U
50	1	3153	U
50	1	3154	C
50	1	3156	U
50	1	3157	U
50	1	3158	G
50	1	3164	C
50	1	3165	A
50	1	3167	A
50	1	3168	A
50	1	3173	G
50	1	3174	A
50	1	3176	G
50	1	3179	U
50	1	3180	A
50	1	3181	C
50	1	3187	A
50	1	3198	U
50	1	3207	U

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Mol	Chain	Res	Type
50	1	3210	A
50	1	3213	A
50	1	3217	C
50	1	3218	A
50	1	3219	G
50	1	3224	G
50	1	3226	A
50	1	3228	C
50	1	3229	G
50	1	3242	G
50	1	3243	A
50	1	3245	A
50	1	3247	G
50	1	3249	C
50	1	3259	U
50	1	3263	G
50	1	3268	A
50	1	3270	U
50	1	3272	C
50	1	3273	A
50	1	3276	G
50	1	3277	U
50	1	3278	C
50	1	3279	A
50	1	3280	U
50	1	3284	G
50	1	3289	G
50	1	3294	A
50	1	3295	A
50	1	3304	U
50	1	3313	U
50	1	3316	A
50	1	3319	U
50	1	3341	U
50	1	3342	A
50	1	3345	G
50	1	3350	C
50	1	3351	U
50	1	3352	U
50	1	3353	G
50	1	3354	U
50	1	3355	U

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Mol	Chain	Res	Type
50	1	3356	G
50	1	3357	U
50	1	3359	A
50	1	3368	U
50	1	3369	G
50	1	3375	A
50	1	3378	C
50	1	3380	U
50	1	3382	U
50	1	3386	G
50	1	3389	U
50	1	3393	U
50	1	3396	U
51	2	13	A
51	2	25	G
51	2	34	U
51	2	35	C
51	2	51	G
51	2	59	A
51	2	61	A
51	2	62	C
51	2	63	G
51	2	76	C
51	2	77	A
51	2	80	A
51	2	81	U
51	2	82	U
51	2	84	C
51	2	85	G
51	2	86	U
51	2	87	G
51	2	90	U
51	2	95	G
51	2	97	A
51	2	104	A
51	2	106	C
51	2	107	G
51	2	111	A
51	2	113	U
51	2	124	G
51	2	125	U
51	2	126	A

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Mol	Chain	Res	Type
51	2	130	C
51	2	138	A
51	2	151	C
52	3	11	A
52	3	13	A
52	3	22	A
52	3	26	C
52	3	33	U
52	3	43	U
52	3	44	C
52	3	48	U
52	3	51	A
52	3	53	U
52	3	55	A
52	3	56	A
52	3	63	A
52	3	64	A
52	3	65	G
52	3	74	C
52	3	76	A
52	3	82	G
52	3	86	U
52	3	87	G
52	3	89	G
52	3	92	A
52	3	94	C
52	3	96	U
52	3	98	C
52	3	99	G
52	3	102	A
52	3	105	C
52	3	112	G
52	3	113	C
52	3	114	U
52	3	117	A
52	3	121	U
53	6	4	U
53	6	5	C
53	6	6	U
53	6	7	C
53	6	8	A
53	6	12	A

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Mol	Chain	Res	Type
53	6	14	U
53	6	15	C
53	6	16	U
53	6	17	G
53	6	19	U
53	6	23	U
53	6	24	A
53	6	26	U
53	6	34	A
53	6	36	U
53	6	38	U
53	6	39	U
53	6	40	U
53	6	41	G
53	6	42	G
53	6	43	A
53	6	47	A
53	6	48	A
53	6	49	C
53	6	53	A
53	6	54	A
53	6	56	U
53	6	57	U
53	6	59	C
53	6	230	A
53	6	231	A
53	6	232	A

All (68) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	89	A
50	1	160	G
50	1	169	U
50	1	239	G
50	1	305	U
50	1	637	C
50	1	643	U
50	1	647	A
50	1	649	A
50	1	720	A
50	1	761	A

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Mol	Chain	Res	Type
50	1	765	C
50	1	784	A
50	1	849	C
50	1	937	G
50	1	990	U
50	1	1064	A
50	1	1097	G
50	1	1102	A
50	1	1103	A
50	1	1128	U
50	1	1129	A
50	1	1241	U
50	1	1302	A
50	1	1307	G
50	1	1329	U
50	1	1355	A
50	1	1556	C
50	1	1567	U
50	1	1568	U
50	1	1574	C
50	1	1581	C
50	1	1589	A
50	1	1607	U
50	1	1716	U
50	1	2101	C
50	1	2209	U
50	1	2269	U
50	1	2277	C
50	1	2317	A
50	1	2537	U
50	1	2541	U
50	1	2545	C
50	1	2569	A
50	1	2593	A
50	1	2624	G
50	1	2625	C
50	1	2651	G
50	1	2652	U
50	1	2655	U
50	1	2689	A
50	1	2727	A
50	1	2728	G

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Mol	Chain	Res	Type
50	1	2758	A
50	1	2801	A
50	1	2808	A
50	1	2819	A
50	1	2857	C
50	1	2866	U
50	1	2875	U
50	1	2900	A
50	1	3218	A
50	1	3269	U
50	1	3350	C
51	2	123	G
52	3	52	G
53	6	16	U
53	6	56	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
54	GTP	b	701	55	33,34,34	0.92	0	50,54,54	1.59	8 (16%)
54	GTP	m	501	-	33,34,34	0.92	2 (6%)	50,54,54	1.73	8 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	GTP	b	701	55	-	3/22/38/38	0/3/3/3
54	GTP	m	501	-	-	8/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	m	501	GTP	O4'-C4'	-2.04	1.40	1.45
54	m	501	GTP	C2-N3	2.03	1.38	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	m	501	GTP	C5-C4-N3	-5.39	119.82	128.39
54	b	701	GTP	C5-C4-N3	-4.72	120.88	128.39
54	m	501	GTP	C2-N3-C4	4.70	120.40	112.30
54	b	701	GTP	C2-N3-C4	4.54	120.12	112.30
54	m	501	GTP	N9-C4-N3	3.66	133.26	125.95
54	m	501	GTP	C2-N1-C6	-3.25	119.22	125.11
54	m	501	GTP	N9-C8-N7	-3.03	107.78	113.40
54	b	701	GTP	C2-N1-C6	-2.86	119.93	125.11
54	b	701	GTP	N9-C4-N3	2.85	131.66	125.95
54	m	501	GTP	C8-N7-C5	2.83	109.30	104.26
54	b	701	GTP	N9-C8-N7	-2.78	108.25	113.40
54	m	501	GTP	C5-C6-N1	2.72	120.16	113.25
54	b	701	GTP	C8-N7-C5	2.58	108.86	104.26
54	b	701	GTP	C5-C6-N1	2.49	119.58	113.25
54	m	501	GTP	O6-C6-C5	-2.41	120.18	126.53
54	b	701	GTP	O6-C6-C5	-2.38	120.24	126.53

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	m	501	GTP	O4'-C4'-C5'-O5'
54	m	501	GTP	C3'-C4'-C5'-O5'
54	b	701	GTP	C3'-C4'-C5'-O5'
54	b	701	GTP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
54	m	501	GTP	PB-O3B-PG-O1G
54	b	701	GTP	C5'-O5'-PA-O1A
54	m	501	GTP	C5'-O5'-PA-O1A
54	m	501	GTP	PB-O3A-PA-O1A
54	m	501	GTP	PB-O3B-PG-O2G
54	m	501	GTP	PB-O3B-PG-O3G
54	m	501	GTP	PB-O3A-PA-O2A

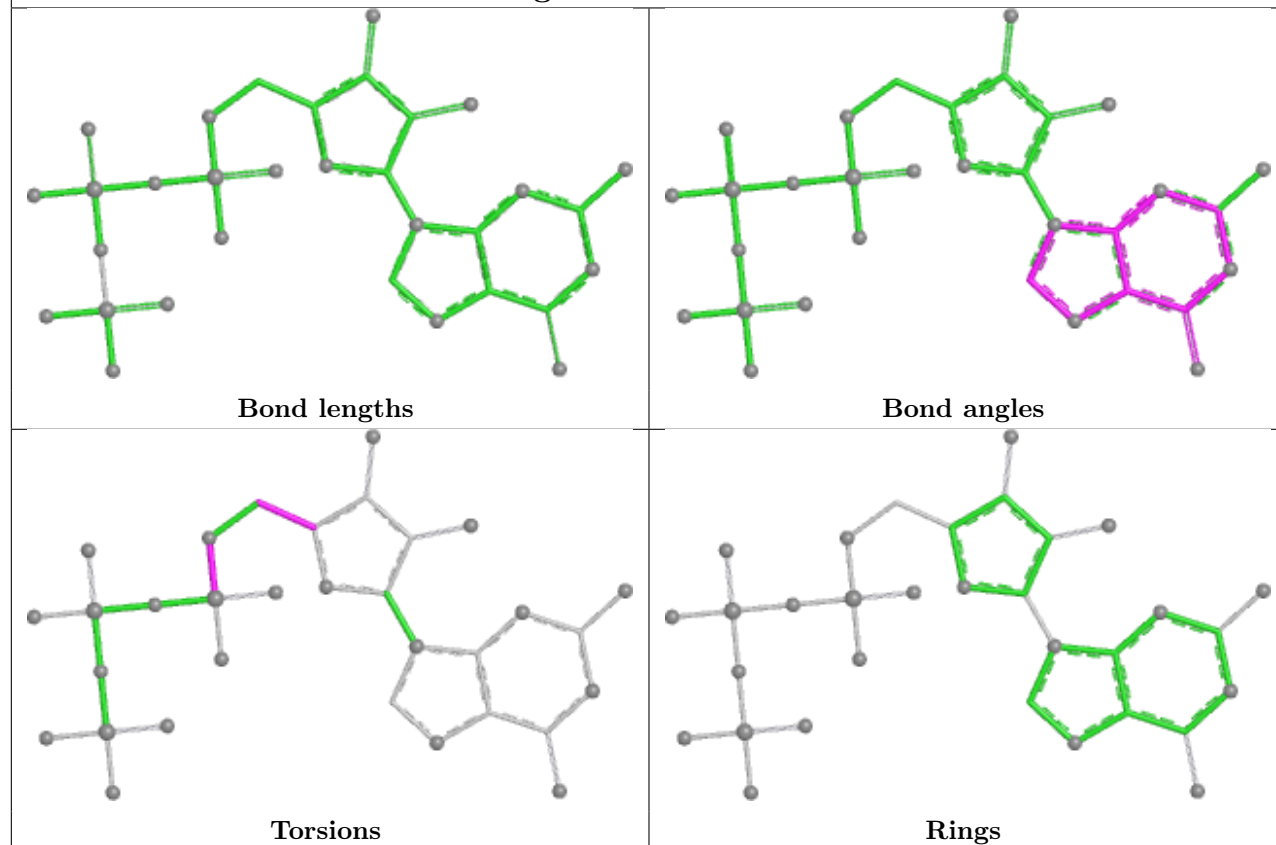
There are no ring outliers.

2 monomers are involved in 5 short contacts:

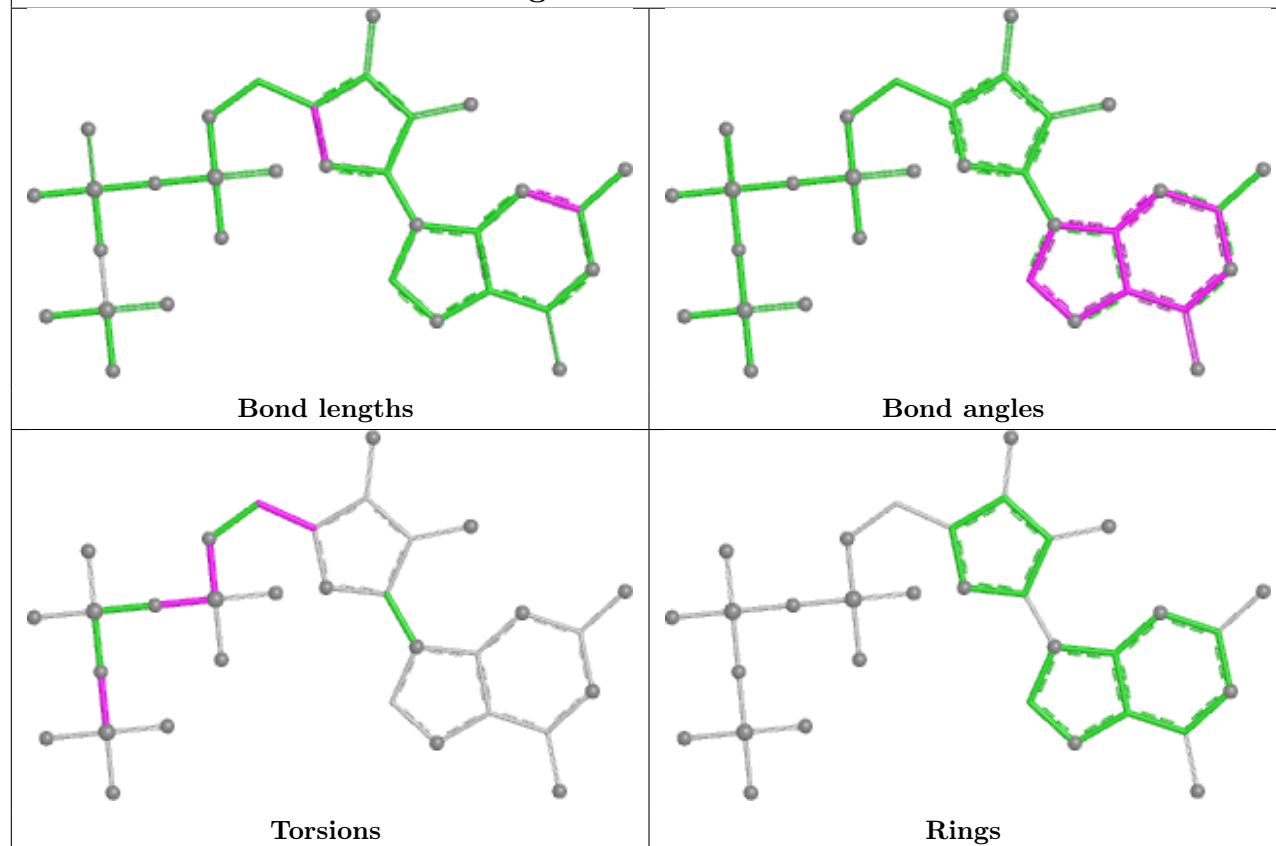
Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	b	701	GTP	3	0
54	m	501	GTP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP b 701



Ligand GTP m 501



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

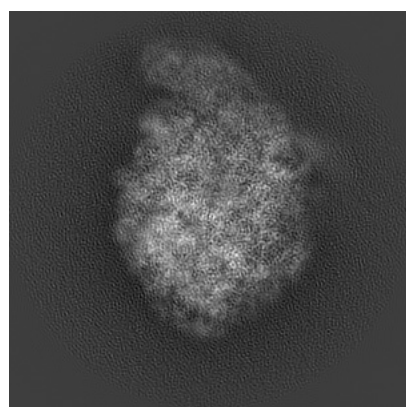
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30174. These allow visual inspection of the internal detail of the map and identification of artifacts.

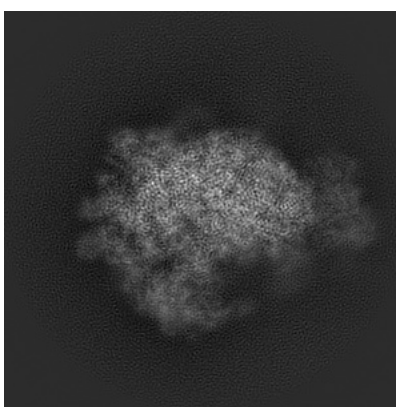
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

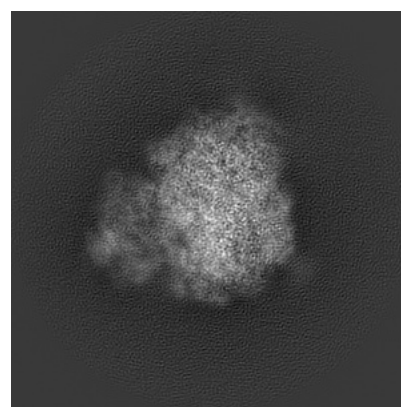
6.1.1 Primary map



X



Y

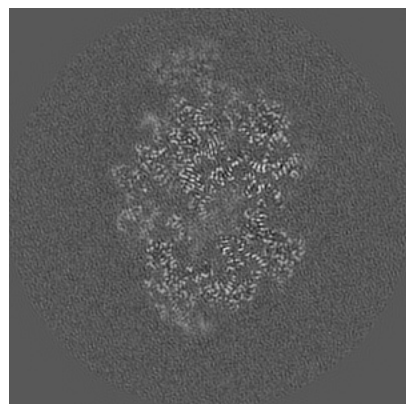


Z

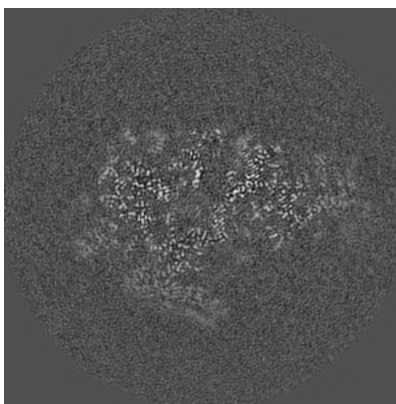
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

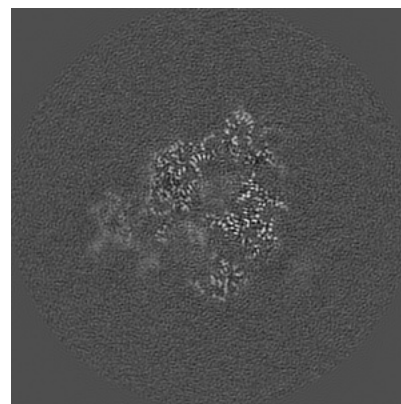
6.2.1 Primary map



X Index: 150



Y Index: 150

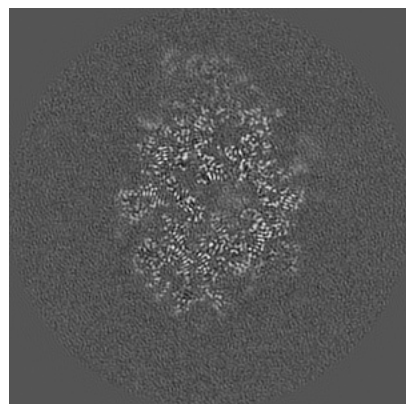


Z Index: 150

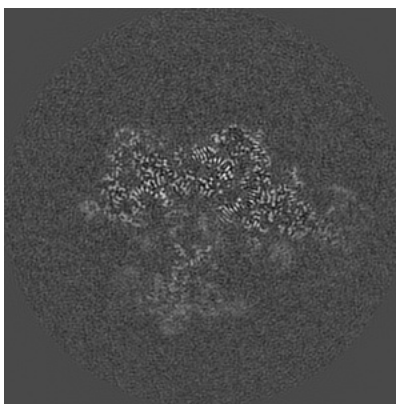
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

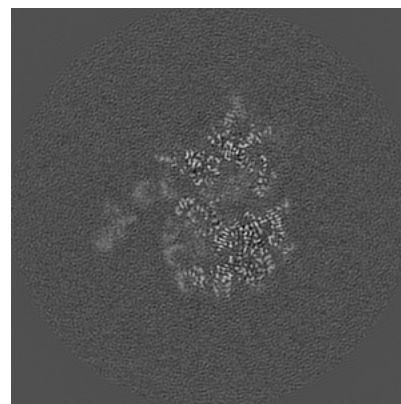
6.3.1 Primary map



X Index: 162



Y Index: 133

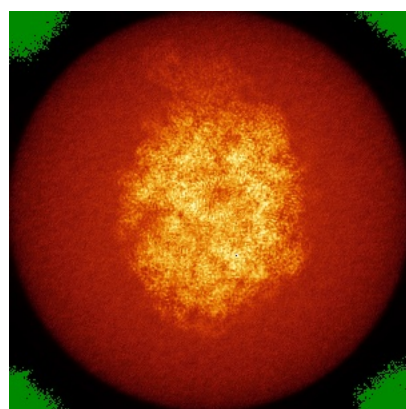


Z Index: 162

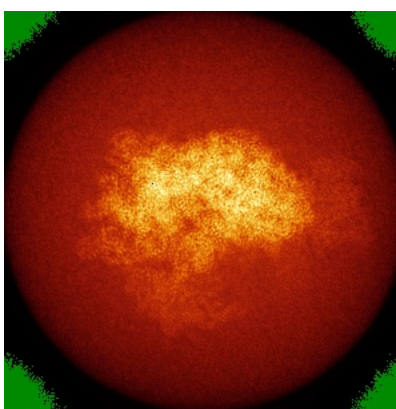
The images above show the largest variance slices of the map in three orthogonal directions.

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

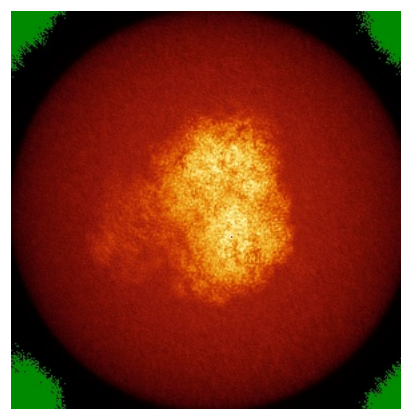
6.4.1 Primary map



X



Y

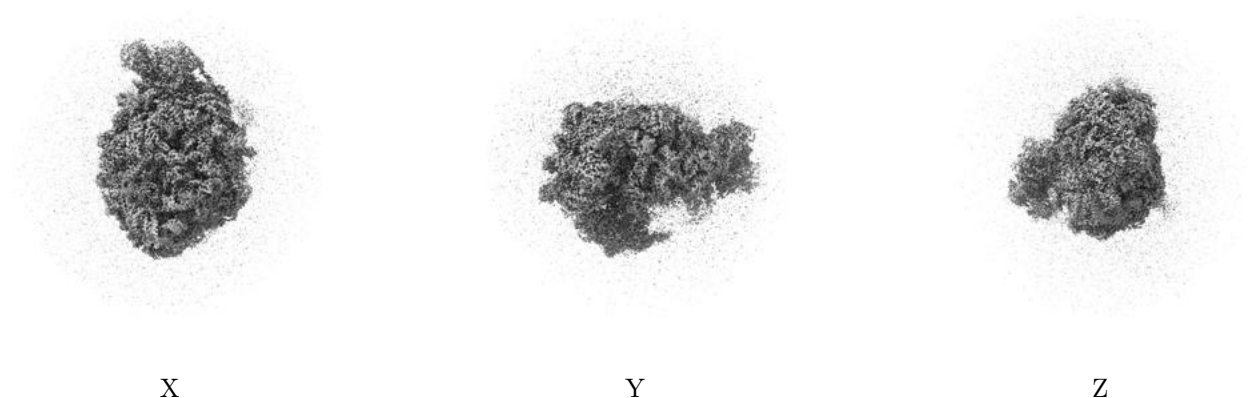


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

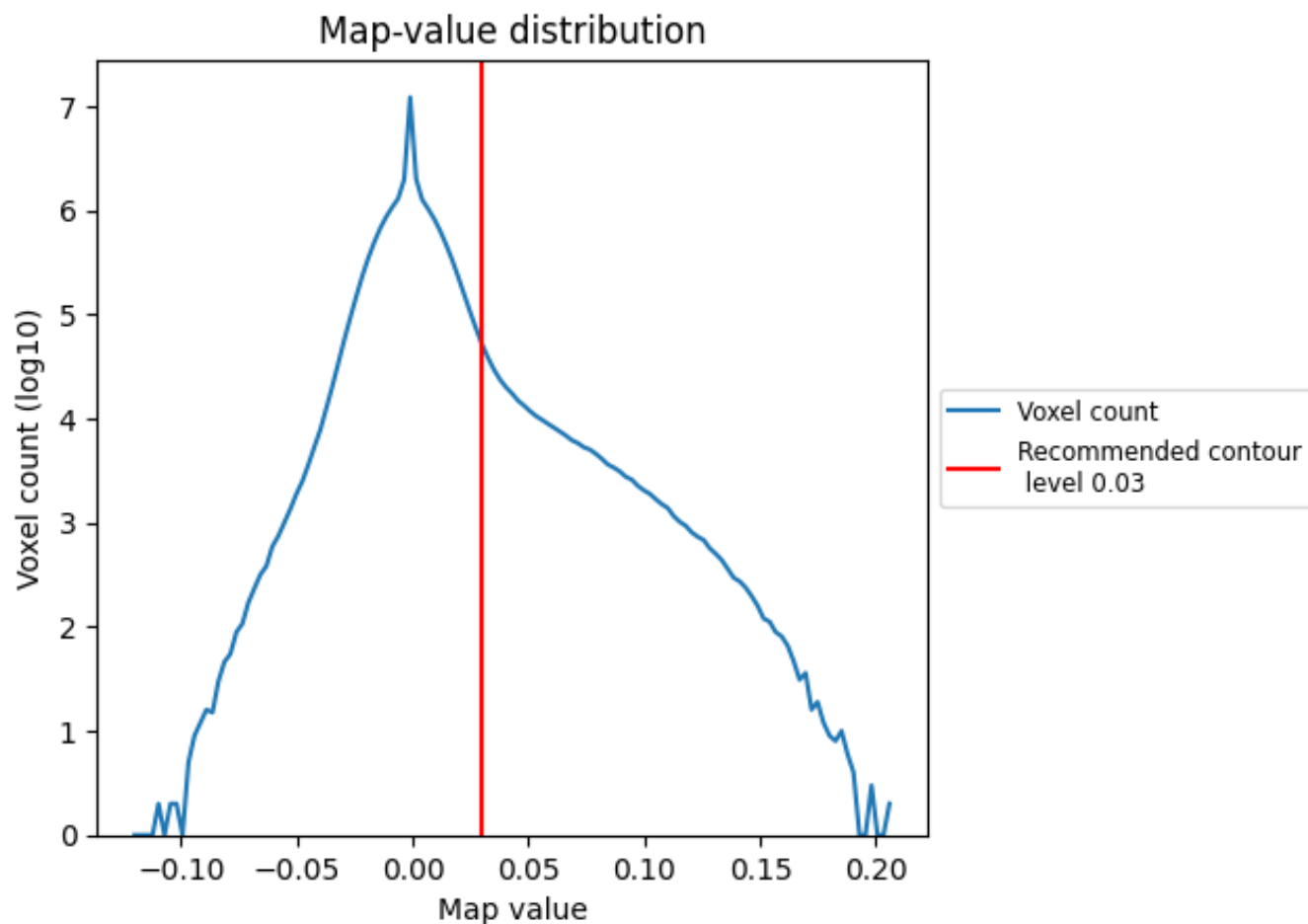
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

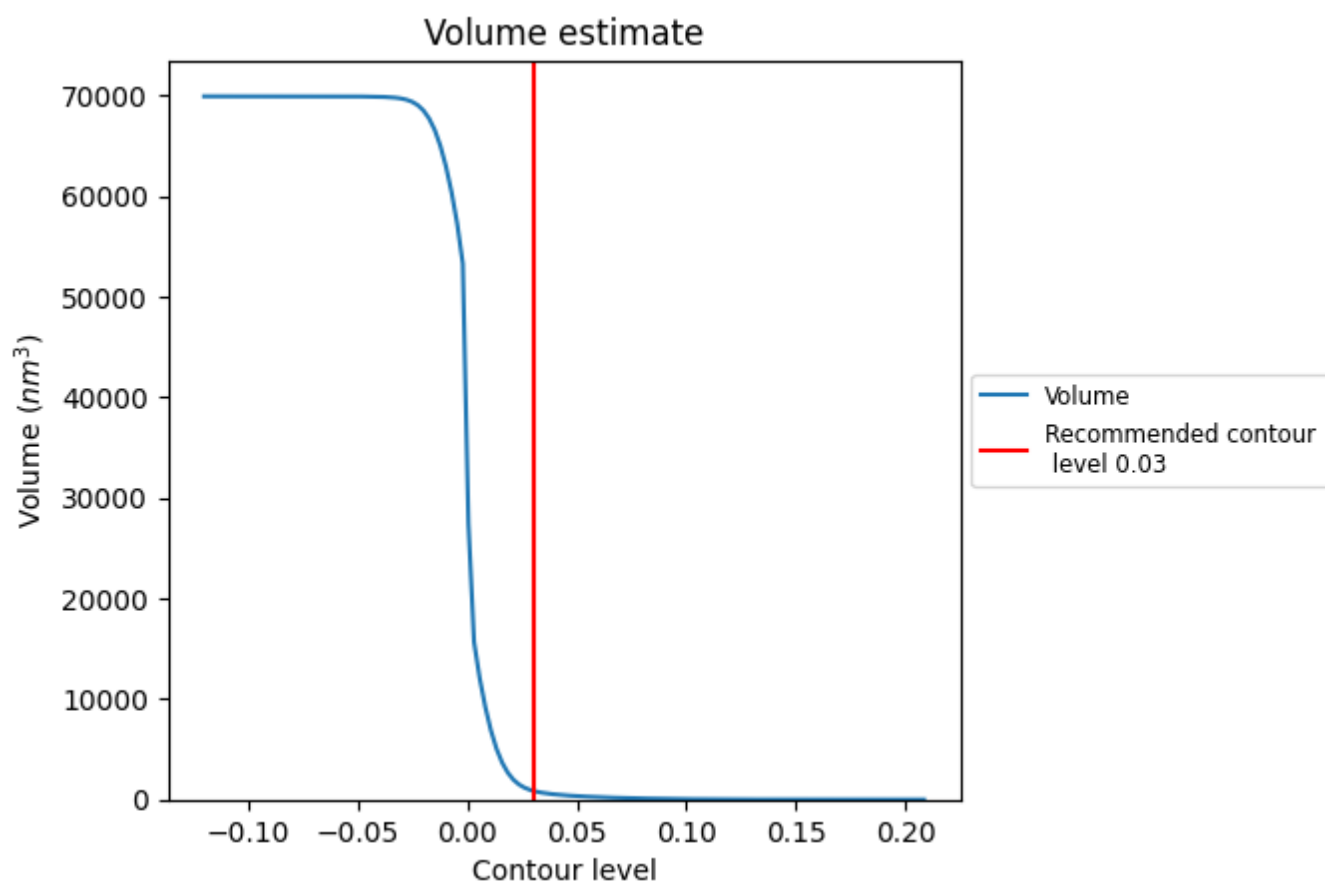
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

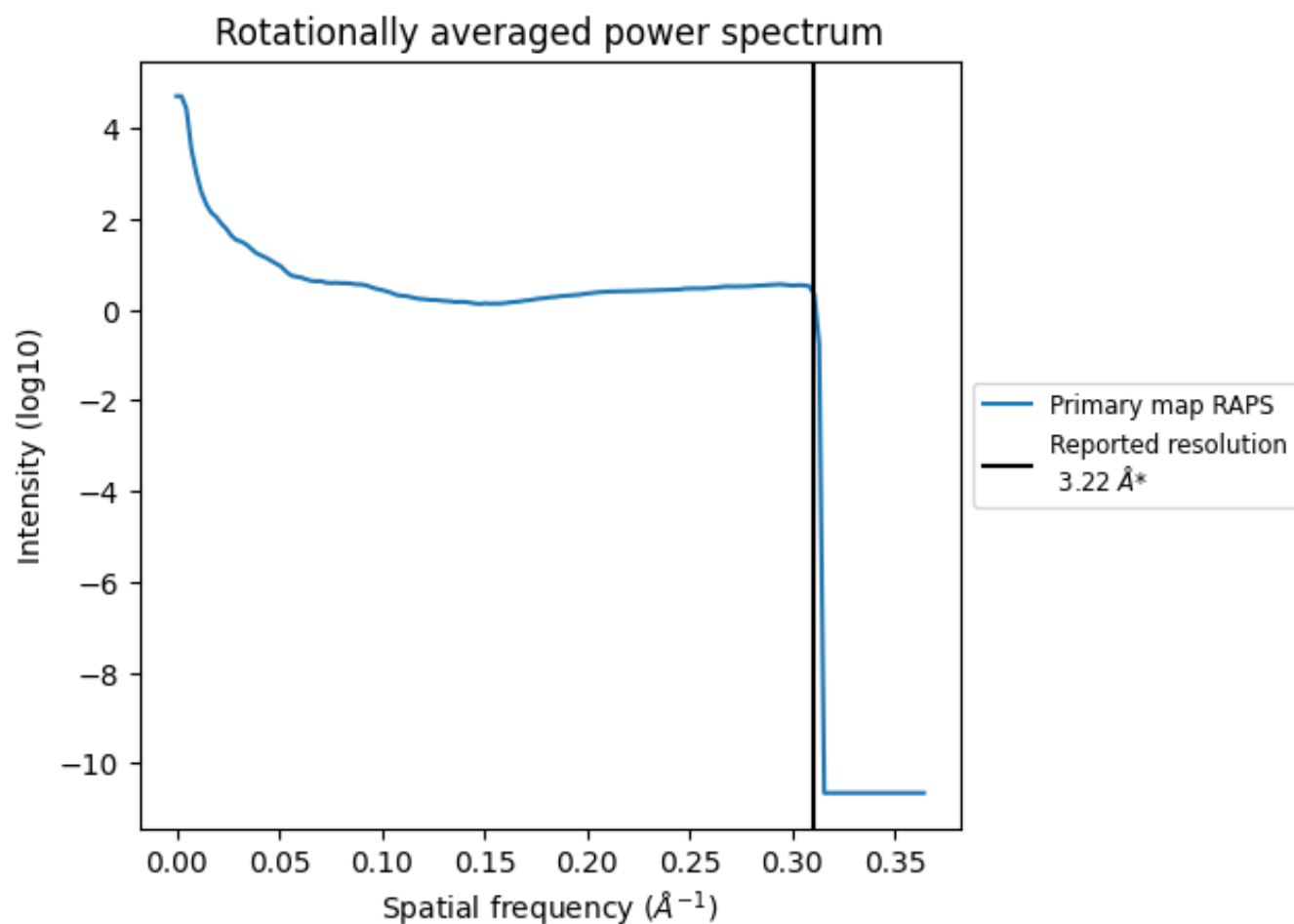
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 879 nm³; this corresponds to an approximate mass of 794 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 0.311 Å⁻¹

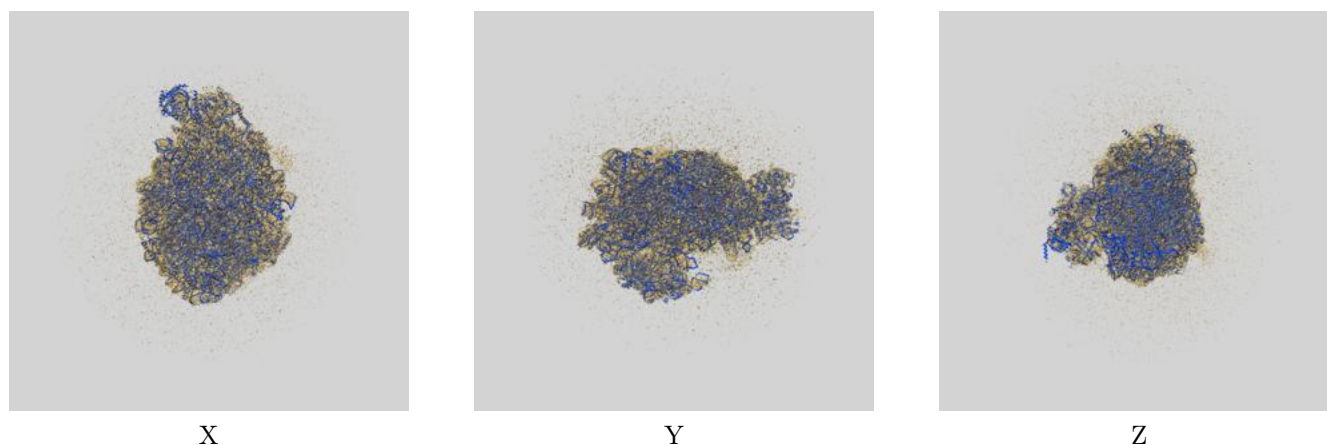
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

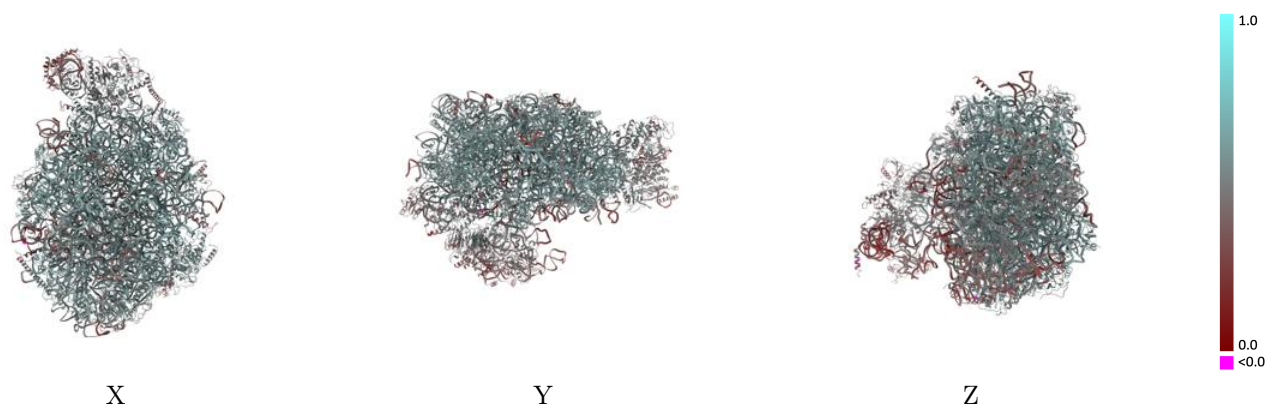
This section contains information regarding the fit between EMDB map EMD-30174 and PDB model 7BTB. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



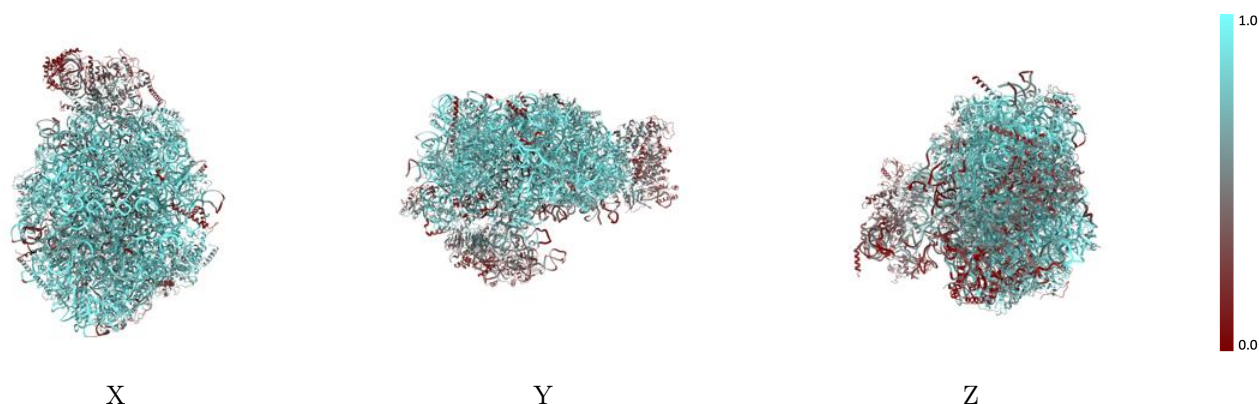
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



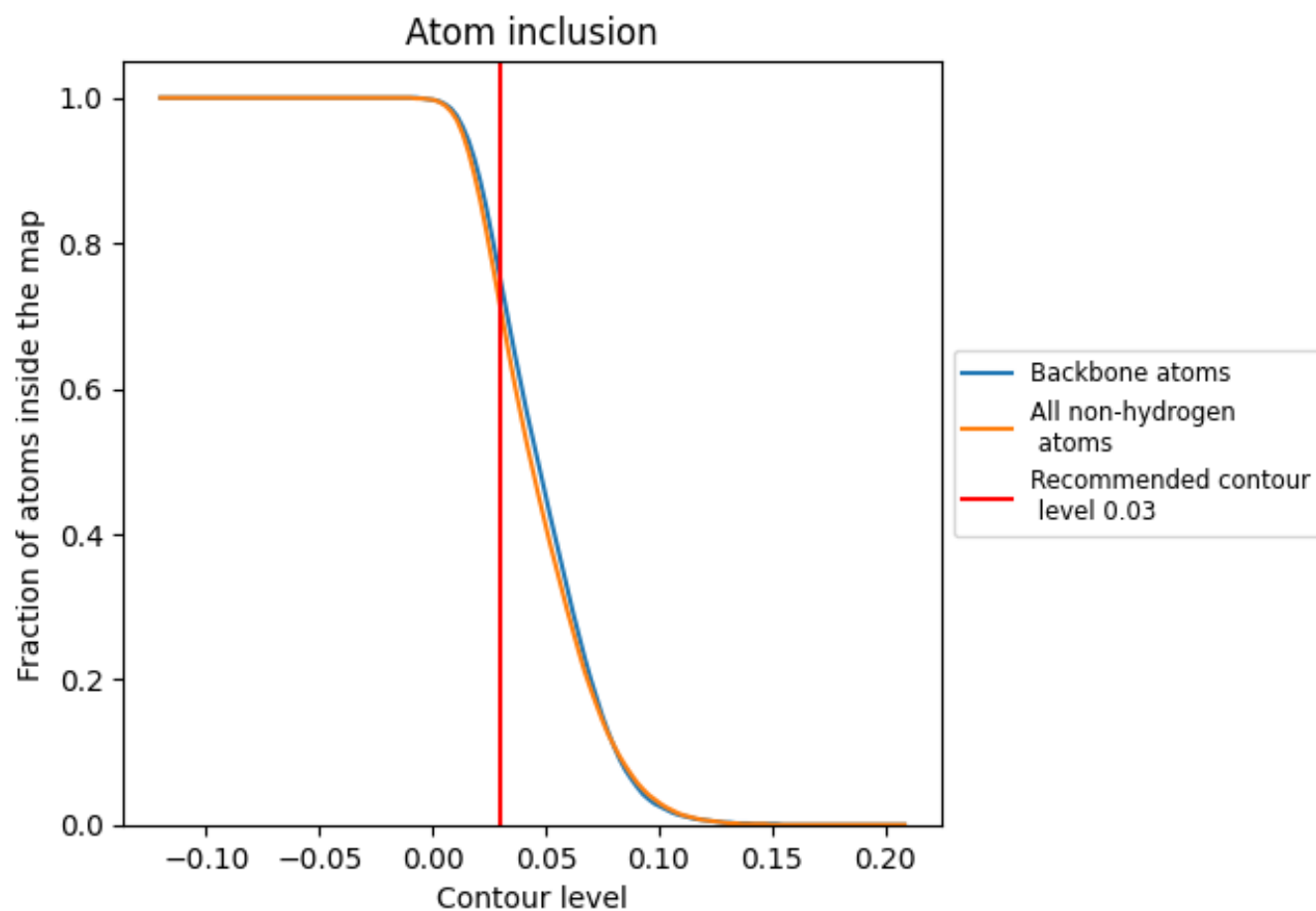
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7110	 0.5100
1	 0.8040	 0.5140
2	 0.8900	 0.5560
3	 0.3970	 0.2790
6	 0.4140	 0.3910
A	 0.8090	 0.5840
B	 0.8060	 0.5650
C	 0.7910	 0.5630
D	 0.2930	 0.3840
E	 0.7340	 0.5370
F	 0.8030	 0.5620
G	 0.7080	 0.5340
H	 0.8120	 0.5680
J	 0.1700	 0.3260
K	 0.2040	 0.4020
L	 0.7400	 0.5360
M	 0.8010	 0.5580
N	 0.7700	 0.5650
O	 0.8500	 0.5860
P	 0.7340	 0.5480
Q	 0.7600	 0.5520
R	 0.7990	 0.5600
S	 0.7320	 0.5350
T	 0.5200	 0.4760
U	 0.6560	 0.5090
V	 0.8210	 0.5790
W	 0.4070	 0.4260
X	 0.7970	 0.5710
Y	 0.8060	 0.5730
Z	 0.7780	 0.5560
a	 0.7180	 0.5340
b	 0.6150	 0.5010
c	 0.7500	 0.5470
d	 0.7960	 0.5680
e	 0.8180	 0.5740



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Chain	Atom inclusion	Q-score
f	 0.8690	 0.6000
g	 0.8000	 0.5670
h	 0.7890	 0.5530
i	 0.6310	 0.5020
j	 0.7640	 0.5670
k	 0.6750	 0.5310
m	 0.7100	 0.5360
n	 0.5060	 0.4950
o	 0.3810	 0.4530
p	 0.8130	 0.5690
q	 0.4080	 0.4910
r	 0.7590	 0.5550
t	 0.3730	 0.4630
u	 0.7060	 0.5380
v	 0.3920	 0.4360
w	 0.4820	 0.4560
x	 0.4330	 0.4390
y	 0.7380	 0.5430
z	 0.3430	 0.4870