



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 02:33 PM UTC

PDB ID : 9NL5 / pdb_00009nl5
EMDB ID : EMD-40921
Title : E. coli pre-elongation complex without an A-site tRNA with EQ2-EttA in Hydrolytic 1 conformation
Authors : Singh, S.; Hunt, J.F.
Deposited on : 2025-03-02
Resolution : 3.00 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

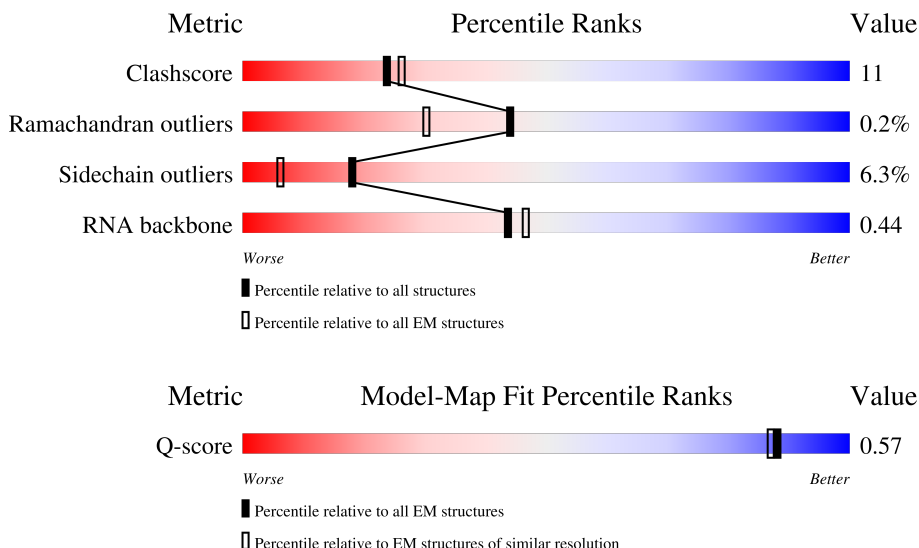
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



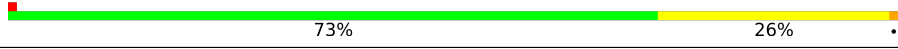
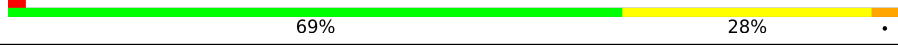
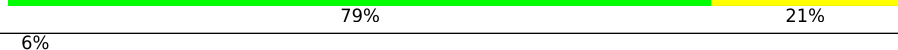
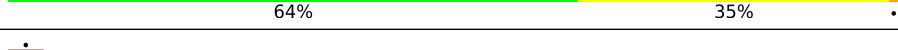
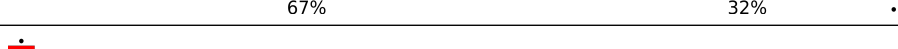
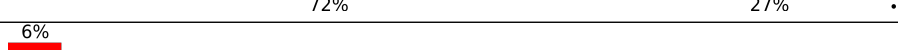
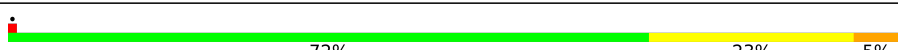
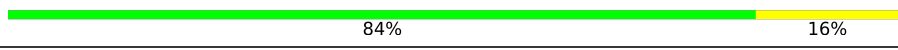
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	1	220	78% 70% 27% .
2	13	142	70% 28% .
3	14	122	75% 22% .

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Mol	Chain	Length	Quality of chain
4	15	143	
5	16	136	
6	17	120	
7	18	116	
8	19	114	
9	2	271	
10	20	117	
11	21	103	
12	22	110	
13	23	93	
14	24	102	
15	25	94	
16	27	85	
17	28	77	
18	29	63	
19	3	209	
20	30	58	
21	31	66	
22	32	56	
23	33	50	
24	34	46	
25	35	64	
26	36	38	
27	4	201	
28	5	177	

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Mol	Chain	Length	Quality of chain
29	6	176	
30	9	149	
31	E	551	
32	M	9	
33	R1	2903	
34	R2	119	
35	R3	1531	
36	T	76	
37	sb	218	
38	sc	206	
39	sd	205	
40	se	157	
41	sf	100	
42	sg	151	
43	sh	129	
44	si	127	
45	sj	98	
46	sk	116	
47	sl	123	
48	sm	112	
49	sn	100	
50	so	88	
51	sp	82	
52	sq	80	
53	sr	65	

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Mol	Chain	Length	Quality of chain
54	ss	79	11% 58% 37% 5%
55	st	85	• 66% 33% •
56	su	65	29% 49% 42% 8% •

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 149888 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 Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 2 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 3 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 4 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	15	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 5 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 6 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	18	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 8 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	2	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	20	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 11 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 12 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 14 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	24	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	25	94	Total	C	N	O	S		
			753	479	137	134	3	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	27	85	Total	C	N	O	S		
			642	396	130	114	2	0	0

- Molecule 17 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	28	77	Total	C	N	O	S		
			625	388	129	106	2	0	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	29	63	Total	C	N	O	S		
			509	313	99	95	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	3	209	Total	C	N	O	S		
			1565	979	288	294	4	0	0

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	30	58	Total	C	N	O	S		
			449	281	87	79	2	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	31	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 23 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	33	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 26 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 29 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 30 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	9	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 31 is a protein called EttA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	E	551	Total	C	N	O	S	0	0
			4352	2740	773	828	11		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	M	9	Total	C	N	O	P	0	0
			193	87	37	60	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	R1	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	R2	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R3	1531	Total	C	N	O	P	0	0
			32850	14652	6028	10640	1530		

- Molecule 36 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	T	76	Total	C	N	O	P	0	0
			1621	724	295	527	75		

- Molecule 37 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	sb	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 38 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	sc	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	sd	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 40 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	se	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 41 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	sf	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	sg	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	sh	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	si	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sj	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 46 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sk	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sl	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 48 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sm	112	Total	C	N	O	S	0	0
			867	537	173	154	3		

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	sn	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	so	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 51 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	sp	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	sq	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	sr	65	Total	C	N	O	S	0	0
			529	336	97	95	1		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	ss	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	st	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 56 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	su	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

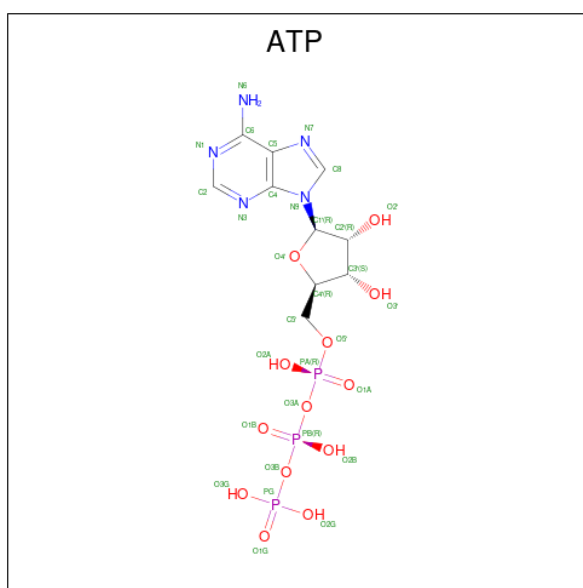
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	32	1	Total	Mg	0
			1	1	
57	33	1	Total	Mg	0
			1	1	
57	R1	83	Total	Mg	0
			83	83	
57	R2	1	Total	Mg	0
			1	1	
57	R3	38	Total	Mg	0
			38	38	
57	sn	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	36	1	Total	Zn	0
			1	1	

- Molecule 59 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
59	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
59	E	1	Total	C	N	O	P	0
			31	10	5	13	3	

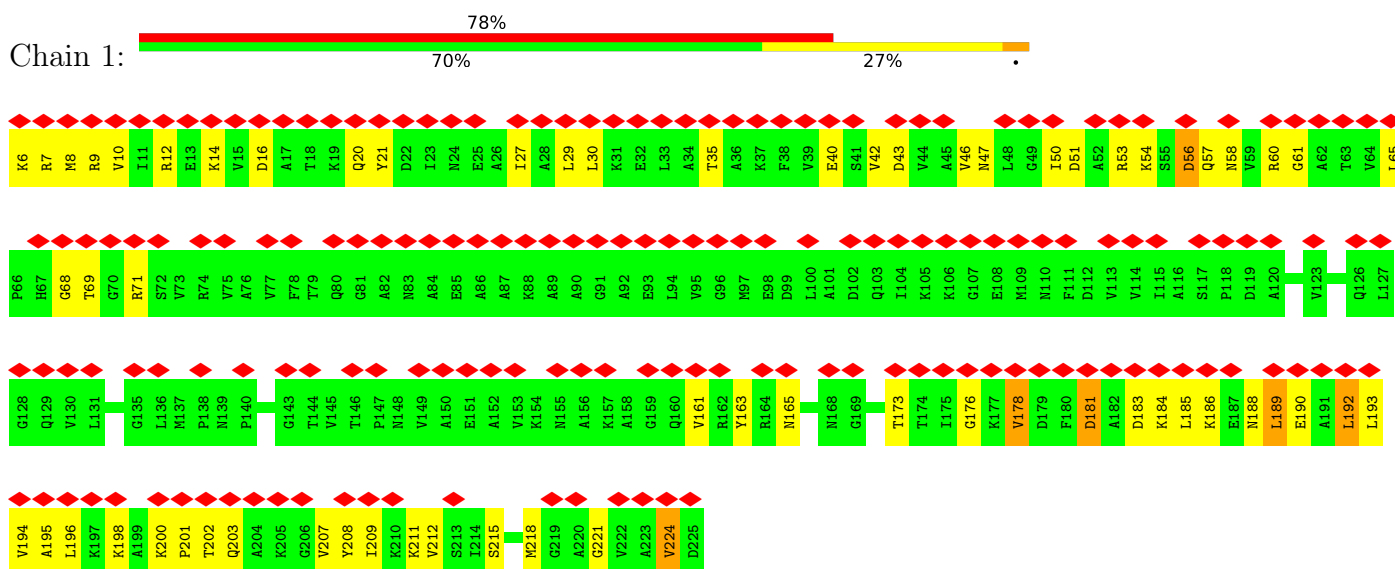
- Molecule 60 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
60	E	2	Total	Na	0
			2	2	

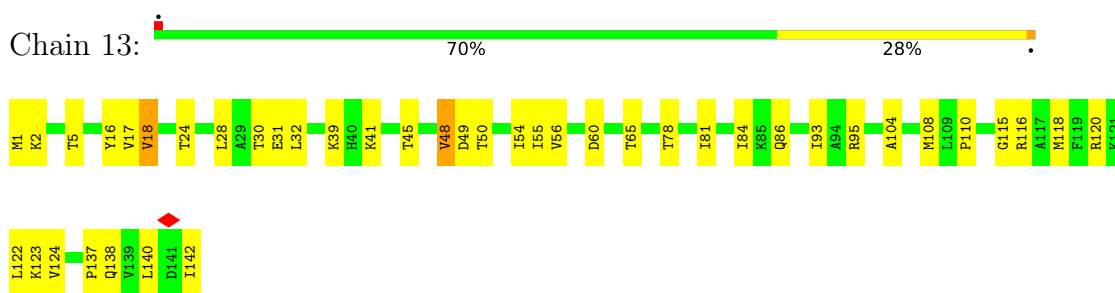
3 Residue-property plots

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

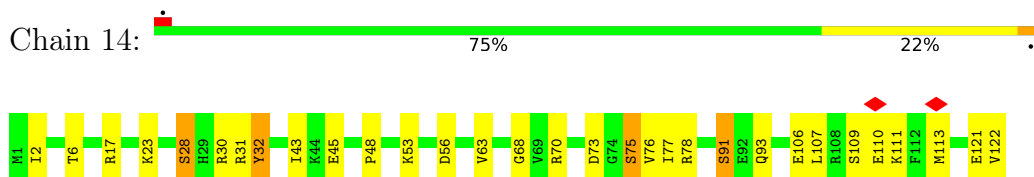
- Molecule 1: Large ribosomal subunit protein uL1



- Molecule 2: Large ribosomal subunit protein uL13

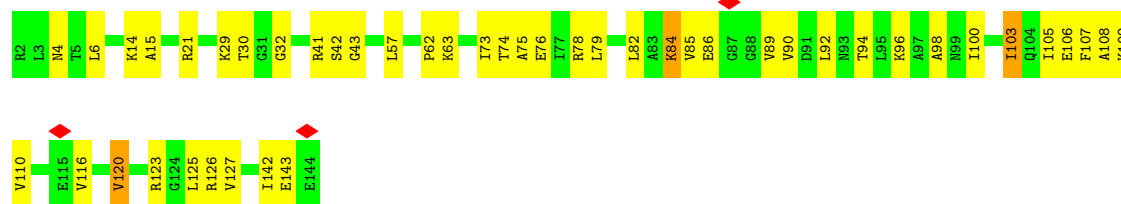


- Molecule 3: 50S ribosomal protein L14



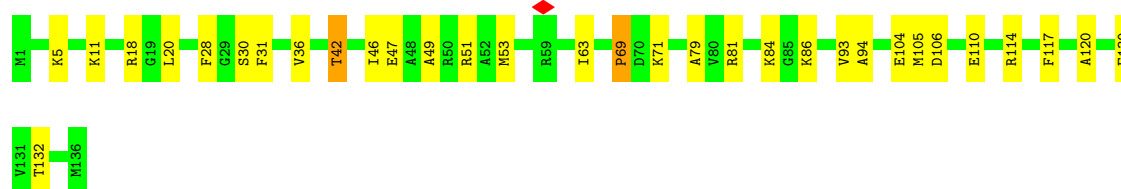
- Molecule 4: 50S ribosomal protein L15

Chain 15:  68% 30%



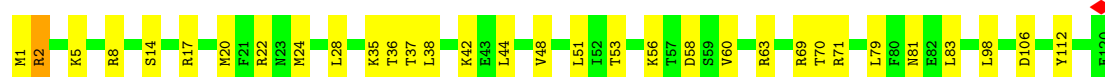
- Molecule 5: 50S ribosomal protein L16

Chain 16:  76% 22%



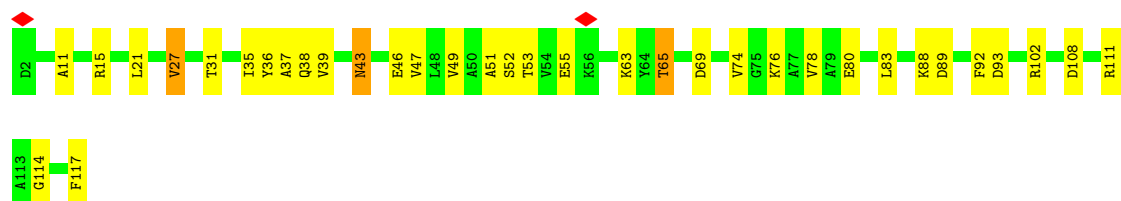
- Molecule 6: Large ribosomal subunit protein bL17

Chain 17:  73% 26%



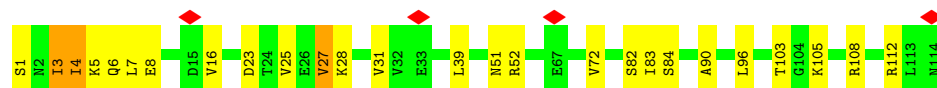
- Molecule 7: Large ribosomal subunit protein uL18

Chain 18:  69% 28%



- Molecule 8: 50S ribosomal protein L19

Chain 19:  77% 20%

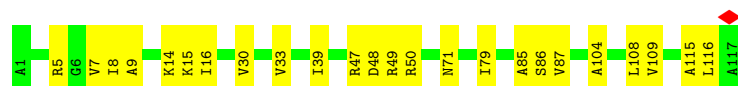
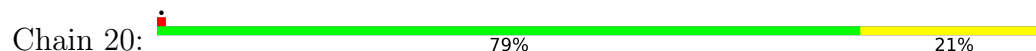


- Molecule 9: 50S ribosomal protein L2

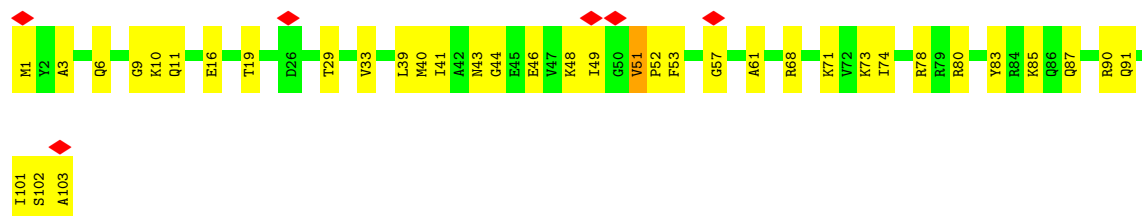
Chain 2:  71% 28%



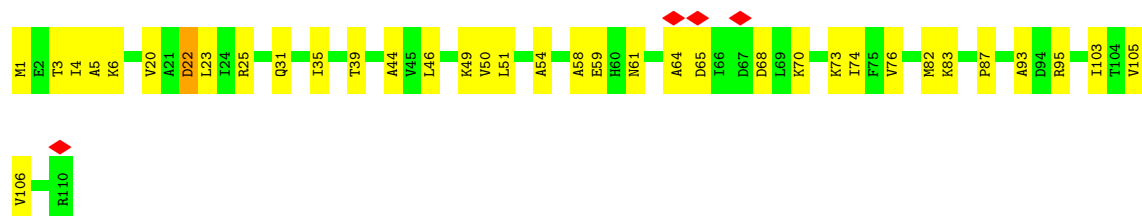
- Molecule 10: Large ribosomal subunit protein bL20



- Molecule 11: Large ribosomal subunit protein bL21



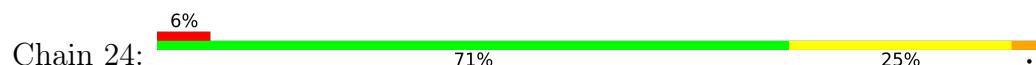
- Molecule 12: Large ribosomal subunit protein uL22

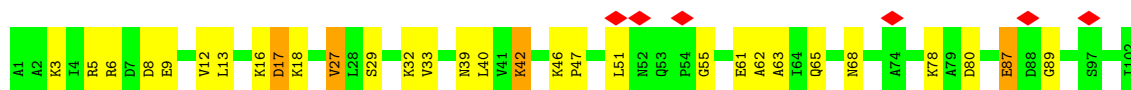


- Molecule 13: Large ribosomal subunit protein uL23



- Molecule 14: Large ribosomal subunit protein uL24





- Molecule 15: Large ribosomal subunit protein bL25



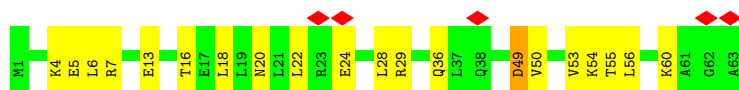
- Molecule 16: Large ribosomal subunit protein bL27



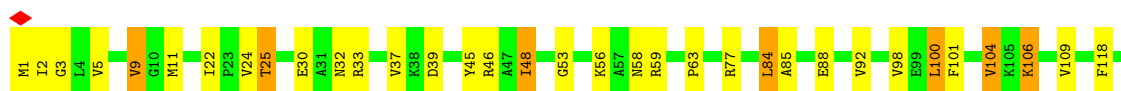
- Molecule 17: 50S ribosomal protein L28



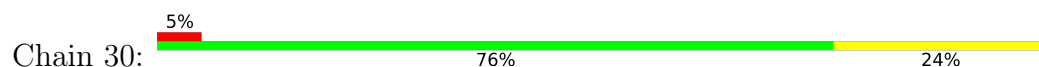
- Molecule 18: Large ribosomal subunit protein uL29

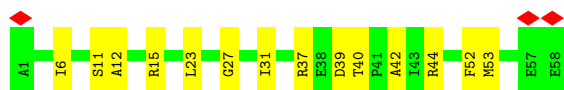


- Molecule 19: 50S ribosomal protein L3

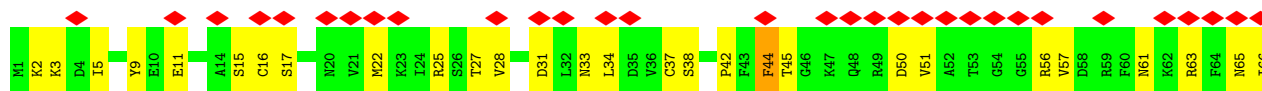


- Molecule 20: 50S ribosomal protein L30

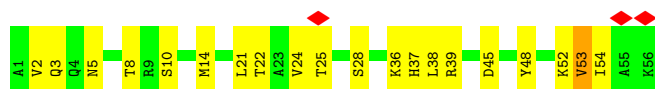




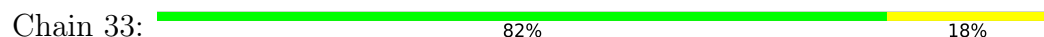
- Molecule 21: Large ribosomal subunit protein bL31



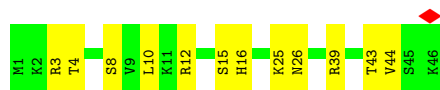
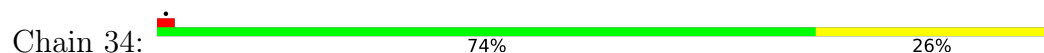
- Molecule 22: 50S ribosomal protein L32



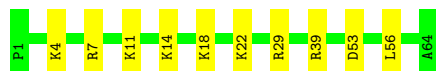
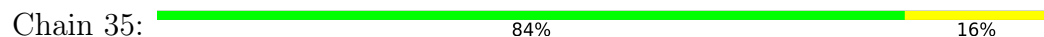
- Molecule 23: Large ribosomal subunit protein bL33



- Molecule 24: 50S ribosomal protein L34



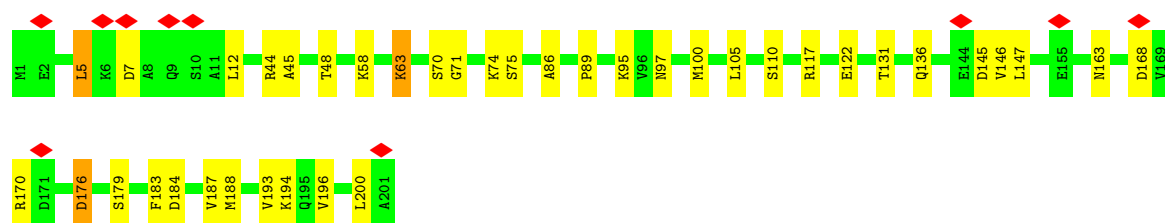
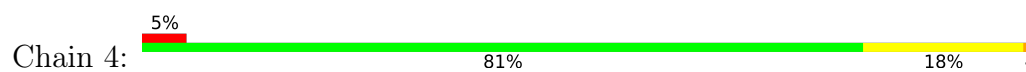
- Molecule 25: Large ribosomal subunit protein bL35



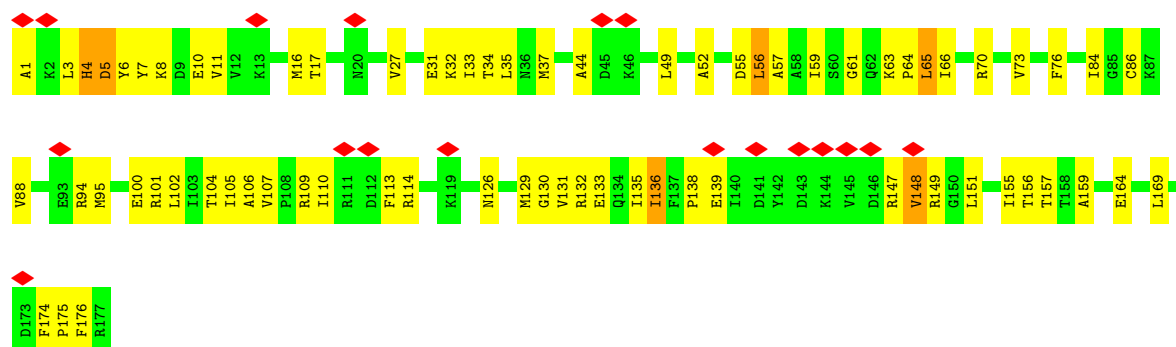
- Molecule 26: 50S ribosomal protein L36



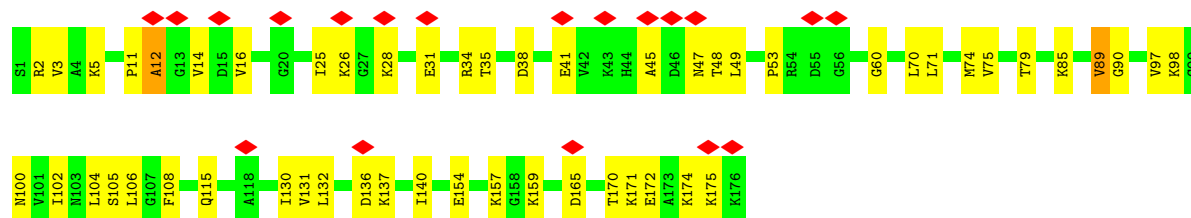
- Molecule 27: Large ribosomal subunit protein uL4



- Molecule 28: 50S ribosomal protein L5



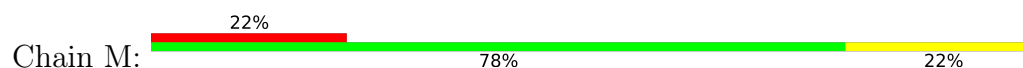
- Molecule 29: Large ribosomal subunit protein uL6



- Molecule 30: Large ribosomal subunit protein bL9

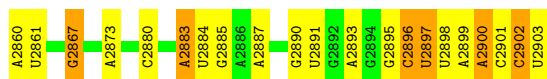


Chain E: 12% 67% 21%

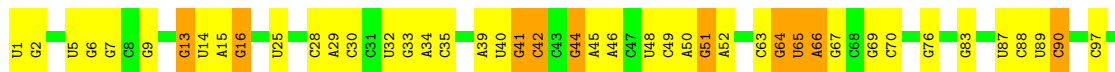




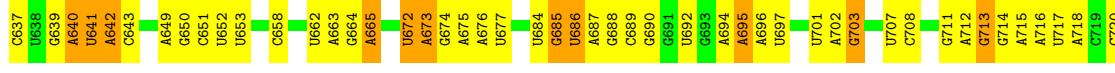
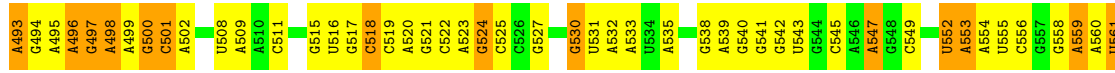
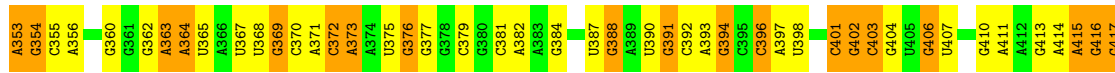
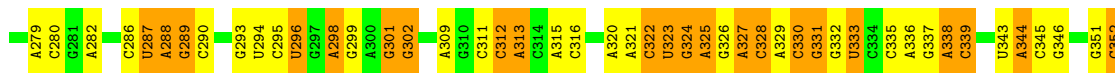
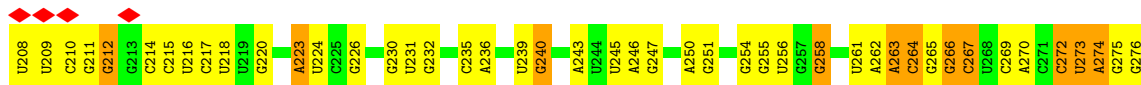
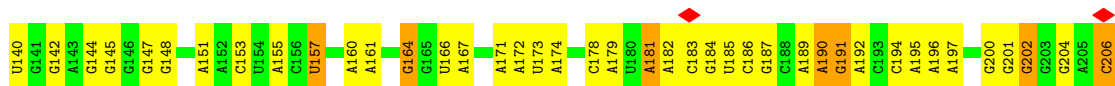
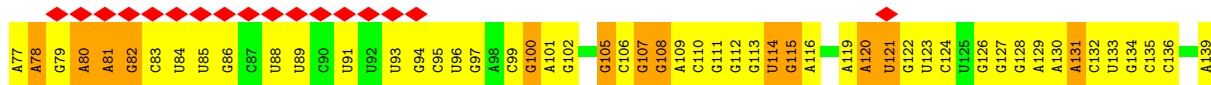
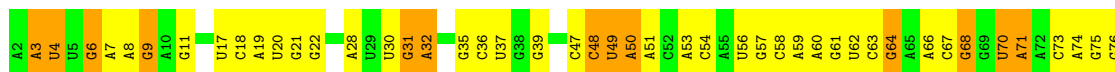
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U2779	C2683	A2589	C2498	G2409	G2315	U2233	G2157	C2096	G2021	U1915	A1809	G1718	A1590
G2780	U2684	A2590	G2411	G2410	G2316	G2234	A2158	A2097	U2022	A1916	A1809	G1719	A1597
U2783	G2685	G2592	A2502	G2413	G2319	G2235	G2159	U2098	G2024	U1917	U1812	G1720	A1598
U2784	U2688	G2595	U2504	A2423	A2322	G2236	C2160	G2100	G2025	A1918	G1814	G1721	G1601
C2785	U2689	A2598	G2505	G2423	G2323	U2240	C2161	A2101	U2026	A1919	G1815	G1722	U1602
U2786	U2690	A2602	U2506	C2424	G2324	G2241	A2162	G2102	G2029	C1924	A1816	G1723	U1603
C2788	G2699	U2610	G2507	A2425	G2325	U2242	C2164	C2104	A2030	A1927	C1816	C1728	C1604
C2789	U2701	C2610	G2508	A2426	G2326	U2243	G2165	U2105	A2031	A1928	U1817	U1729	A1608
G2793	G2702	U2609	U2514	C2427	A2327	U2244	U2167	G2107	G2032	G1929	U1818	C1730	A1609
C2794	A2706	C2610	C2515	G2428	G2328	G2245	A2168	A2108	A2033	U1930	A1829	G1731	A1608
U2795	A2706	U2611	A2518	A2429	G2329	G2246	A2169	U2109	G2035	G1931	G1835	G1732	A1609
U2796	G2709	U2613	U2519	A2430	G2330	A2247	A2170	G2110	G2036	U1932	C1836	G1733	A1610
U2797	G2710	U2614	C2520	A2431	G2331	G2248	U2171	U2111	A2037	G1933	C1837	G1734	A1614
U2798	C2711	U2615	A2529	G2432	A2332	U2249	U2172	U2112	G2038	A1936	C1838	G1738	G1622
U2799	G2712	C2616	G2533	G2433	A2333	G2251	A2173	U2113	U2039	A1937	G1842	A1746	A1632
G2801	G2714	G2617	U2534	A2434	A2334	G2252	C2174	A2114	G2040	A1938	C1843	U1747	G1633
G2802	C2715	G2618	G2535	U2440	A2340	C2258	C2175	G2115	A2041	U1943	G1847	A1756	A1634
G2803	C2716	U2618	G2536	U2441	G2341	U2261	A2176	G2116	A2042	A1952	A1848	A1757	A1635
G2804	G2717	C2626	G2537	C2442	G2342	U2262	C2177	A2117	G2043	A1953	U1855	U1758	U1636
G2805	G2718	U2629	U2538	G2443	A2343	C2263	C2178	A2118	C2044	G1954	U1856	A1759	A1637
U2808	G2719	U2630	C2538	G2444	G2347	C2268	C2179	G2120	C2045	U1956	U1857	G1764	C1638
A2809	A2720	G2630	G2543	G2447	C2350	A2268	U2180	U2121	A2051	U1963	U1858	A1764	C1639
A2810	U2721	C2636	G2544	A2448	G2351	G2271	U2181	G2122	C2055	U1964	U1859	C1771	G1645
G2811	A2726	U2637	G2545	U2449	C2352	G2272	U2182	G2123	G2056	G1965	C1870	U1772	U1646
G2812	G2727	G2638	U2546	C2452	G2355	U2273	U2183	G2124	G2057	C1966	C1871	A1773	U1647
G2813	U2728	A2639	A2547	G2453	U2356	A2273	U2187	G2125	A2058	C1967	C1872	U1776	U1648
G2814	G2729	G2640	U2548	G2454	G2357	A2274	U2188	A2126	G2059	C1968	A1871	G1776	G1649
C2815	U2732	G2641	U2554	G2455	A2358	G2279	U2189	G2127	A2062	C1969	C1873	U1779	A1652
G2816	A2733	C2646	G2555	U2456	G2359	G2280	U2190	G2128	A2063	A1970	C1874	U1782	C1656
U2817	G2738	C2649	G2556	U2457	G2360	A2281	U2191	U2130	G2064	U1980	C1879	A1783	C1657
G2818	U2739	U2650	C2557	G2458	G2361	G2282	U2192	U2131	C2065	A1981	U1880	A1784	G1659
A2820	A2741	G2651	U2560	G2459	C2362	C2283	U2193	U2132	C2066	U1982	U1881	A1785	G1664
G2822	U2742	G2655	U2561	U2460	A2377	G2286	U2194	G2133	A2070	U1991	U1882	A1786	A1664
A2823	G2744	A2660	U2562	C2466	G2380	A2287	A2198	A2134	A2071	C1997	U1883	C1788	G1667
G2830	A2748	G2661	U2563	G2467	G2383	A2288	G2204	G2135	C2072	C1997	A1884	A1789	G1674
G2831	G2751	A2662	A2564	A2476	U2384	U2291	G2208	U2136	A2072	C1997	A1889	C1790	C1675
G2834	G2755	G2663	A2565	U2477	C2385	U2292	C2208	U2137	C2073	C1997	U1889	A1791	G1678
U2839	C2762	A2664	U2566	A2478	G2386	A2293	A2211	U2138	U2074	C1997	U1890	C1792	A1679
G2840	U2765	G2665	U2567	G2479	U2389	A2297	U2212	G2140	U2075	G2002	U1891	A1793	G1682
U2845	A2765	C2667	A2572	G2481	G2391	G2304	U2213	G2144	U2079	C2006	U1898	U1796	U1683
G2846	G2772	G2668	C2573	U2484	C2395	U2305	U2214	C2145	A2080	C2006	U1899	U1799	U1683
U2847	G2773	U2669	G2574	G2485	G2396	C2306	G2215	C2146	U2081	G2010	A1900	A1800	U1714
G2848	C2774	C2486	A2577	G2486	U2402	G2307	G2216	U2147	A2082	G2011	A1901	A1801	G1715
U2849	U2775	U2578	U2578	C2489	U2403	G2308	G2217	U2148	U2086	G2012	C1902	U1796	U1716
G2857	G2776	G2674	C2579	U2489	U2404	C2310	G2224	U2149	G2087	A2013	G1906	G1799	
C2858	G2775	A2675	U2580	G2490	U2405	C2311	A2225	C2150	U2087	A2014	G1907	A1802	
G2859		C2676	A2606	U2312	A2406	U2312	G2226	U2151	G2093	U2016	A1912	A1803	
			A2407	C2313	G2230	U2230	U2231	A2154	A2094		A1913		

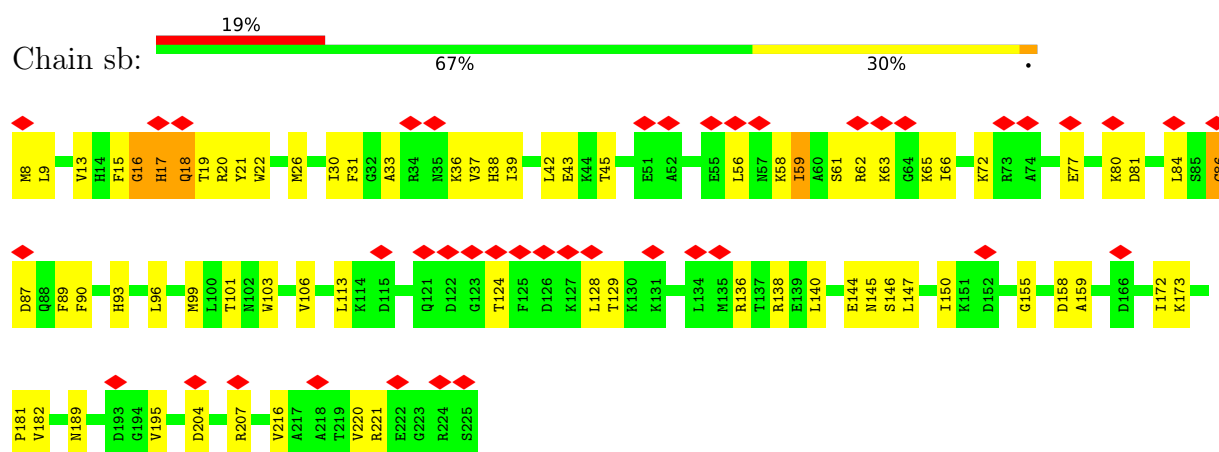


• Molecule 34: 5S ribosomal RNA

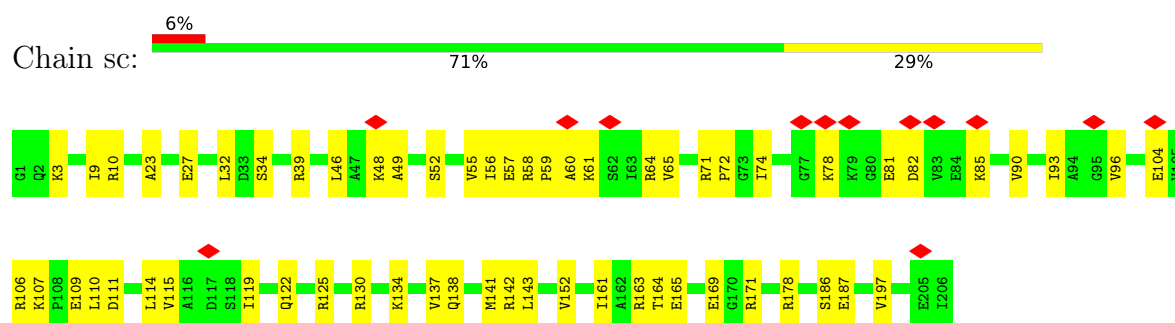


• Molecule 35: 16S ribosomal RNA

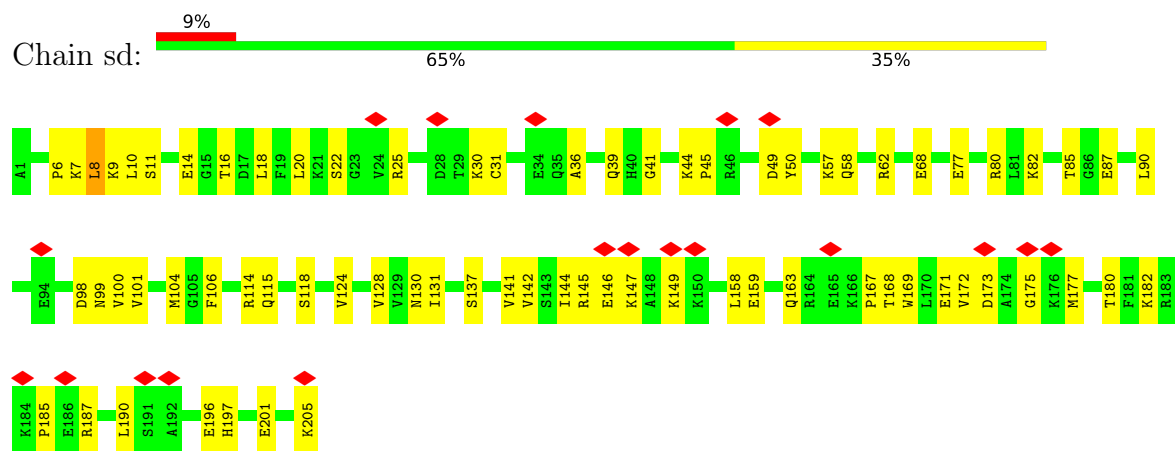




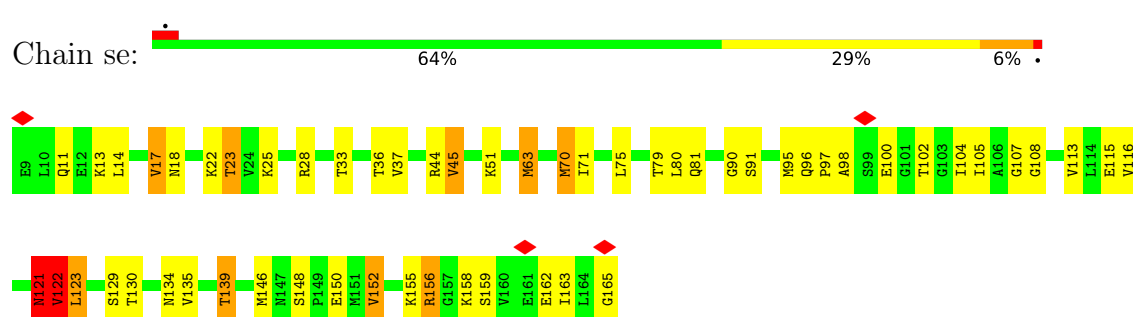
• Molecule 38: Small ribosomal subunit protein uS3



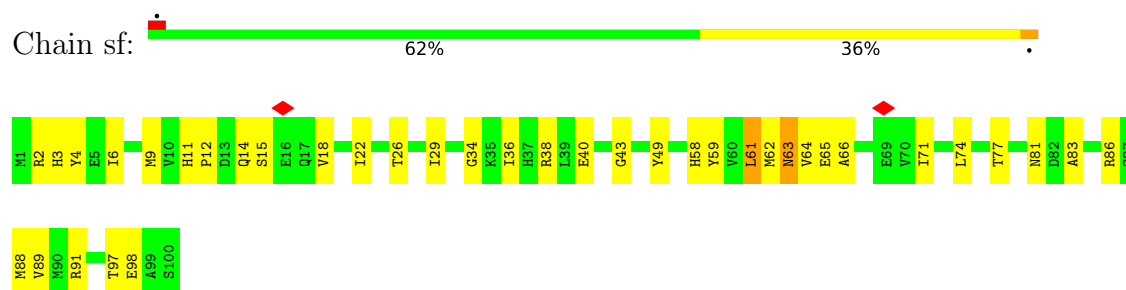
• Molecule 39: 30S ribosomal protein S4



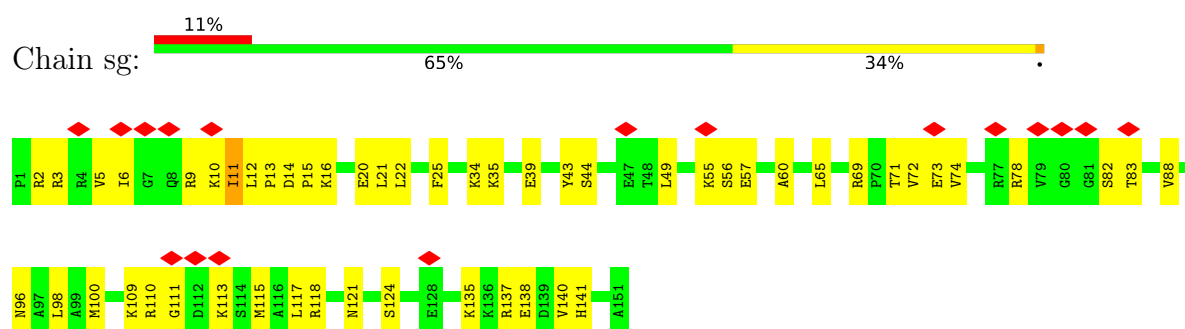
• Molecule 40: Small ribosomal subunit protein uS5



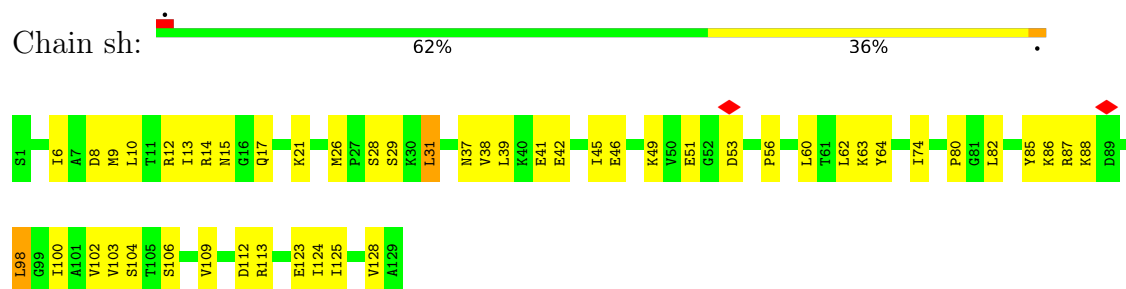
- Molecule 41: 30S ribosomal protein S6, non-modified isoform



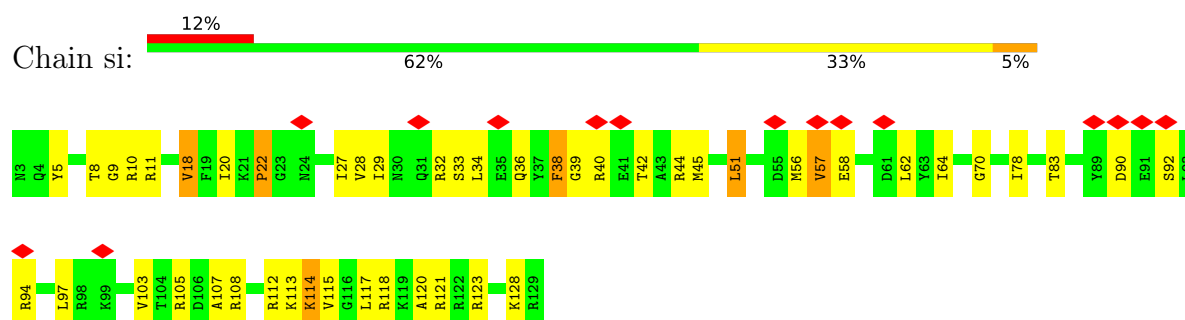
- Molecule 42: 30S ribosomal protein S7



- Molecule 43: 30S ribosomal protein S8

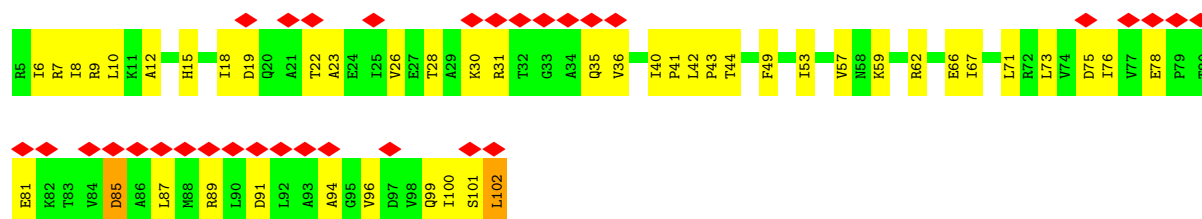


- Molecule 44: Small ribosomal subunit protein uS9



- Molecule 45: 30S ribosomal protein S10





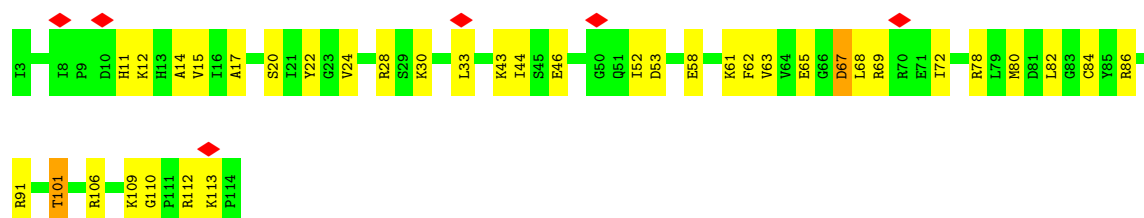
- Molecule 46: Small ribosomal subunit protein uS11



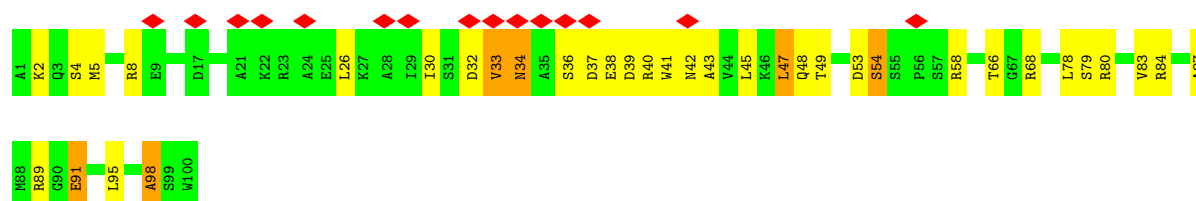
- Molecule 47: Small ribosomal subunit protein uS12



- Molecule 48: Small ribosomal subunit protein uS13



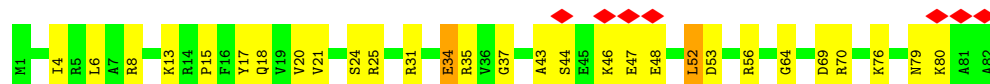
- Molecule 49: Small ribosomal subunit protein uS14



- Molecule 50: Small ribosomal subunit protein uS15



- Molecule 51: Small ribosomal subunit protein bS16



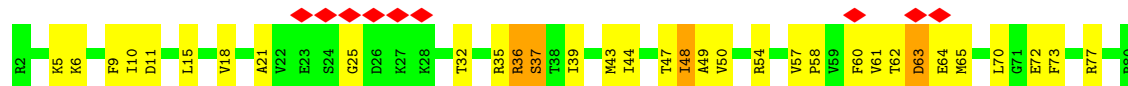
- Molecule 52: Small ribosomal subunit protein uS17



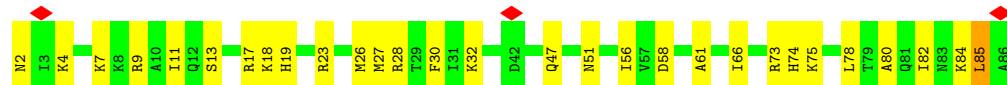
- Molecule 53: 30S ribosomal protein S18



- Molecule 54: 30S ribosomal protein S19



- Molecule 55: 30S ribosomal protein S20



- Molecule 56: Small ribosomal subunit protein bS21





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86261	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.969	Depositor
Minimum map value	-2.374	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	335.04, 335.04, 335.04	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.047, 1.047, 1.047	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.12	0/1361	0.33	0/1796
2	13	0.29	0/1152	0.33	0/1551
3	14	0.32	0/947	0.41	0/1268
4	15	0.30	0/1054	0.38	0/1403
5	16	0.30	0/1093	0.33	0/1460
6	17	0.32	0/973	0.42	0/1301
7	18	0.21	0/902	0.34	0/1209
8	19	0.30	0/929	0.35	0/1242
9	2	0.36	0/2121	0.40	0/2852
10	20	0.33	0/960	0.32	0/1278
11	21	0.27	0/829	0.44	0/1107
12	22	0.31	0/864	0.38	0/1156
13	23	0.25	0/744	0.40	0/994
14	24	0.24	0/787	0.44	1/1051 (0.1%)
15	25	0.24	0/766	0.33	0/1025
16	27	0.32	0/650	0.33	0/858
17	28	0.34	0/635	0.33	0/848
18	29	0.21	0/510	0.33	0/677
19	3	0.32	0/1586	0.41	0/2134
20	30	0.28	0/453	0.32	0/605
21	31	0.18	0/531	0.47	0/709
22	32	0.32	0/450	0.42	0/599
23	33	0.27	0/416	0.38	0/554
24	34	0.36	0/380	0.44	0/498
25	35	0.32	0/513	0.33	0/676
26	36	0.29	0/303	0.32	0/397
27	4	0.28	0/1571	0.37	0/2113
28	5	0.21	0/1434	0.36	0/1926
29	6	0.21	0/1343	0.41	1/1816 (0.1%)
30	9	0.17	0/1122	0.41	0/1515
31	E	0.22	0/4433	0.36	0/5983
32	M	0.21	0/216	0.32	0/334

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	R1	0.38	0/69797	0.35	0/108890
34	R2	0.27	0/2847	0.30	0/4440
35	R3	0.31	0/36782	0.36	1/57377 (0.0%)
36	T	0.24	0/1812	0.34	0/2824
37	sb	0.19	0/1735	0.41	2/2338 (0.1%)
38	sc	0.21	0/1651	0.32	0/2225
39	sd	0.21	0/1665	0.35	0/2227
40	se	0.27	0/1169	0.53	0/1573
41	sf	0.24	0/835	0.41	0/1128
42	sg	0.21	0/1195	0.39	0/1602
43	sh	0.25	0/989	0.36	0/1326
44	si	0.26	0/1034	0.63	1/1375 (0.1%)
45	sj	0.21	0/796	0.42	0/1077
46	sk	0.27	0/885	0.35	0/1195
47	sl	0.27	0/969	0.46	0/1300
48	sm	0.18	0/876	0.37	0/1172
49	sn	0.21	0/817	0.37	0/1088
50	so	0.26	0/722	0.36	0/964
51	sp	0.24	0/659	0.39	0/884
52	sq	0.26	0/657	0.41	0/881
53	sr	0.27	0/538	0.39	0/724
54	ss	0.19	0/652	0.35	0/877
55	st	0.22	0/671	0.31	0/888
56	su	0.28	0/550	0.67	0/728
All	All	0.32	0/162331	0.37	6/242038 (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
13	23	0	1
29	6	0	1
30	9	0	1
31	E	0	1
40	se	0	1
47	sl	0	1
56	su	0	1
All	All	0	7

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	si	22	PRO	CA-N-CD	-8.73	99.78	112.00
29	6	11	PRO	CA-N-CD	-6.27	103.22	112.00
35	R3	114	U	O3'-P-O5'	5.40	112.10	104.00
14	24	87	GLU	CB-CG-CD	5.36	121.71	112.60
37	sb	16	GLY	CA-C-N	5.14	131.36	121.54
37	sb	16	GLY	C-N-CA	5.14	131.36	121.54

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	23	37	ASP	Peptide
29	6	12	ALA	Peptide
30	9	8	LYS	Peptide
31	E	16	PRO	Peptide
40	se	121	ASN	Peptide
47	sl	86	VAL	Peptide
56	su	65	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1353	0	1159	45	0
2	13	1129	0	1162	27	0
3	14	938	0	1012	24	0
4	15	1045	0	1117	33	0
5	16	1074	0	1157	23	0
6	17	960	0	1000	26	0
7	18	892	0	923	22	0
8	19	917	0	965	17	0
9	2	2082	0	2157	53	0
10	20	947	0	1022	20	0
11	21	816	0	839	29	0
12	22	857	0	922	27	0
13	23	738	0	807	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	24	779	0	834	20	0
15	25	753	0	780	23	0
16	27	642	0	665	19	0
17	28	625	0	655	16	0
18	29	509	0	543	14	0
19	3	1565	0	1616	45	0
20	30	449	0	491	10	0
21	31	522	0	524	20	0
22	32	444	0	461	14	0
23	33	409	0	440	6	0
24	34	377	0	418	8	0
25	35	504	0	574	11	0
26	36	302	0	340	10	0
27	4	1552	0	1619	23	0
28	5	1410	0	1447	53	0
29	6	1323	0	1374	32	0
30	9	1111	0	1148	25	0
31	E	4352	0	4325	120	0
32	M	193	0	98	1	0
33	R1	62318	0	31345	864	0
34	R2	2546	0	1292	41	0
35	R3	32850	0	16533	626	0
36	T	1621	0	825	39	0
37	sb	1704	0	1732	51	0
38	sc	1624	0	1699	35	0
39	sd	1643	0	1710	50	0
40	se	1156	0	1199	48	0
41	sf	817	0	808	26	0
42	sg	1181	0	1240	31	0
43	sh	979	0	1034	34	0
44	si	1022	0	1070	44	0
45	sj	786	0	828	36	0
46	sk	869	0	878	35	0
47	sl	955	0	1019	33	0
48	sm	867	0	923	27	0
49	sn	805	0	847	29	0
50	so	714	0	737	15	0
51	sp	649	0	666	22	0
52	sq	648	0	691	33	0
53	sr	529	0	541	17	0
54	ss	637	0	665	27	0
55	st	665	0	714	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	su	544	0	579	33	0
57	32	1	0	0	0	0
57	33	1	0	0	0	0
57	R1	83	0	0	0	0
57	R2	1	0	0	0	0
57	R3	38	0	0	0	0
57	sn	1	0	0	0	0
58	36	1	0	0	0	0
59	E	62	0	24	6	0
60	E	2	0	0	0	0
All	All	149888	0	102193	2684	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 11.

All (2684) 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)
33:R1:136:G:N1	33:R1:142:A:H2	1.39	1.17
33:R1:136:G:N1	33:R1:142:A:C2	2.11	1.15
33:R1:156:A:C2	33:R1:169:G:N1	2.24	1.06
33:R1:156:A:H2	33:R1:169:G:N1	1.54	1.03
33:R1:2099:U:H3	33:R1:2190:G:H1	1.01	0.96
35:R3:1130:A:HO2'	35:R3:1131:G:H8	1.05	0.94
19:3:5:VAL:H	19:3:32:ASN:HD21	1.14	0.94
33:R1:2848:G:O2'	33:R1:2867:G:N2	1.99	0.93
33:R1:160:A:H8	33:R1:2217:G:H21	1.10	0.93
33:R1:290:U:H3	33:R1:350:G:H1	1.09	0.92
33:R1:1171:G:H1	33:R1:1176:U:H3	1.09	0.90
35:R3:119:A:H2	35:R3:287:U:H3	1.18	0.90
33:R1:1847:G:HO2'	33:R1:1848:A:H8	0.97	0.90
33:R1:2073:C:H5	33:R1:2436:G:H1	1.21	0.89
4:15:78:ARG:NH1	33:R1:627:A:OP1	2.07	0.87
33:R1:882:G:H1	33:R1:894:U:H3	1.20	0.87
6:17:2:ARG:HA	6:17:5:LYS:HD3	1.56	0.86
33:R1:2701:U:H5''	33:R1:2702:G:H5''	1.57	0.86
33:R1:805:G:N2	33:R1:829:A:OP1	2.09	0.86
33:R1:414:C:H5	33:R1:2409:G:H1	1.19	0.85
33:R1:1936:A:H2	33:R1:1943:U:H3	1.25	0.85
33:R1:2545:G:H21	33:R1:2565:A:H8	1.22	0.84
33:R1:2324:U:H3'	33:R1:2325:G:H5''	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:406:G:H1	35:R3:436:C:H5	1.23	0.84
11:21:51:VAL:HG22	11:21:52:PRO:HD2	1.58	0.83
15:25:32:GLY:HA3	15:25:93:ARG:HB2	1.60	0.83
35:R3:71:A:N6	35:R3:99:C:O2'	2.12	0.82
37:sb:96:LEU:H	37:sb:99:MET:HE3	1.44	0.82
43:sh:6:ILE:HD11	43:sh:31:LEU:HD13	1.61	0.82
4:15:30:THR:HG23	33:R1:810:U:H3	1.44	0.82
10:20:5:ARG:NH2	33:R1:585:G:N7	2.29	0.81
35:R3:332:G:O2'	35:R3:333:U:O2	1.98	0.81
3:14:121:GLU:HG2	3:14:122:VAL:HG23	1.62	0.81
37:sb:99:MET:HA	37:sb:106:VAL:HG21	1.61	0.80
1:1:181:ASP:H	1:1:184:LYS:HD2	1.45	0.80
12:22:59:GLU:HA	12:22:64:ALA:HA	1.64	0.79
6:17:17:ARG:NH2	33:R1:2002:G:OP1	2.14	0.79
35:R3:686:U:H1'	46:sk:43:TRP:HE1	1.45	0.79
33:R1:2602:A:H62	36:T:76:A:HO3'	1.26	0.79
16:27:14:ARG:NH1	33:R1:2279:G:N7	2.31	0.79
1:1:47:ASN:ND2	33:R1:2177:C:O2'	2.15	0.79
31:E:87:ARG:HB2	31:E:156:TRP:HB3	1.65	0.79
35:R3:990:C:H5	35:R3:1215:G:H1	1.28	0.79
6:17:2:ARG:HG2	33:R1:1653:G:H3'	1.65	0.78
19:3:169:ARG:HG2	33:R1:2773:C:H5'	1.66	0.78
1:1:211:LYS:HD3	33:R1:2177:C:H4'	1.65	0.78
33:R1:1045:C:H4'	33:R1:1046:A:H5''	1.63	0.78
33:R1:136:G:O6	33:R1:142:A:N1	2.16	0.78
35:R3:1367:C:OP2	44:si:113:LYS:NZ	2.16	0.78
35:R3:689:C:OP2	46:sk:52:ARG:NH2	2.17	0.77
33:R1:158:U:O2	33:R1:167:A:N6	2.17	0.77
35:R3:673:A:H2'	35:R3:674:G:C8	2.20	0.77
3:14:70:ARG:NH2	33:R1:2683:C:O2	2.18	0.77
30:9:132:PHE:HB2	30:9:140:ALA:HB3	1.68	0.76
48:sm:11:HIS:O	48:sm:11:HIS:ND1	2.16	0.76
40:se:156:ARG:NH2	43:sh:42:GLU:OE1	2.19	0.76
42:sg:113:LYS:HB2	42:sg:117:LEU:HD22	1.66	0.76
25:35:4:LYS:NZ	33:R1:253:C:OP2	2.19	0.76
50:so:17:ASP:OD1	50:so:18:ALA:N	2.19	0.76
36:T:53:G:N2	36:T:63:G:N7	2.34	0.76
49:sn:36:SER:HB2	49:sn:40:ARG:HE	1.49	0.76
34:R2:112:G:O2'	34:R2:113:C:O2	2.04	0.76
35:R3:999:C:H3'	35:R3:1000:A:H4'	1.67	0.75
21:31:11:GLU:HG2	21:31:25:ARG:HG2	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:439:U:O2'	39:sd:118:SER:O	2.04	0.75
56:su:19:LYS:HD2	56:su:19:LYS:O	1.85	0.75
35:R3:1397:C:OP2	40:se:28:ARG:NH2	2.20	0.75
33:R1:962:G:H21	33:R1:2250:G:H1	1.35	0.75
33:R1:2602:A:N6	36:T:76:A:HO3'	1.84	0.75
1:1:51:ASP:HB3	1:1:54:LYS:HG2	1.69	0.74
33:R1:76:C:H5	33:R1:110:G:H1	1.34	0.74
37:sb:59:ILE:HG22	37:sb:62:ARG:HH21	1.50	0.74
35:R3:962:C:H5	35:R3:973:G:H1	1.32	0.74
9:2:79:ARG:NH1	9:2:81:GLU:OE2	2.21	0.74
40:se:98:ALA:HB3	40:se:122:VAL:HA	1.69	0.74
8:19:52:ARG:NH2	33:R1:2720:U:OP1	2.21	0.74
31:E:155:ASP:OD1	31:E:155:ASP:N	2.21	0.74
38:sc:34:SER:OG	38:sc:58:ARG:NH2	2.21	0.74
19:3:77:ARG:NH1	19:3:200:ASP:OD1	2.20	0.74
2:13:81:ILE:HD12	33:R1:2514:U:H5''	1.69	0.73
19:3:30:GLU:O	19:3:185:ASN:ND2	2.21	0.73
33:R1:199:A:O2'	33:R1:200:U:O2	2.06	0.73
33:R1:371:A:H2	33:R1:402:A:H62	1.37	0.73
3:14:17:ARG:HB2	3:14:45:GLU:HG2	1.71	0.73
21:31:2:LYS:HB3	21:31:5:ILE:HG12	1.68	0.73
35:R3:1228:C:OP2	48:sm:109:LYS:NZ	2.22	0.73
40:se:37:VAL:HG21	40:se:113:VAL:HG12	1.69	0.73
48:sm:22:TYR:HB3	48:sm:65:GLU:HG3	1.71	0.73
33:R1:475:C:O2	33:R1:479:A:N6	2.21	0.73
28:5:104:THR:HG22	28:5:105:ILE:HG23	1.70	0.72
39:sd:90:LEU:HD13	39:sd:190:LEU:HD11	1.72	0.72
33:R1:197:A:N6	33:R1:2430:A:O2'	2.22	0.72
33:R1:1802:A:H2'	33:R1:1803:A:C8	2.23	0.72
38:sc:141:MET:HG3	38:sc:169:GLU:HG2	1.70	0.72
35:R3:1087:G:H21	56:su:65:ARG:HD3	1.55	0.72
33:R1:1450:G:N2	33:R1:1452:G:O6	2.17	0.72
33:R1:1558:C:H4'	33:R1:1559:U:H5''	1.70	0.72
33:R1:2249:U:H3'	33:R1:2250:G:H5''	1.71	0.72
17:28:11:PRO:HB3	17:28:29:LEU:HD23	1.72	0.72
39:sd:85:THR:H	40:se:102:THR:HG21	1.54	0.72
48:sm:24:VAL:HG22	48:sm:28:ARG:HD2	1.71	0.72
35:R3:456:A:H62	35:R3:476:U:H3	1.38	0.72
37:sb:66:ILE:HD12	37:sb:159:ALA:HB3	1.72	0.72
33:R1:2062:A:N6	33:R1:2503:A:N7	2.38	0.71
22:32:14:MET:HE3	33:R1:2045:C:H5''	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:se:79:THR:HB	40:se:121:ASN:HD22	1.55	0.71
47:sl:109:ARG:HB3	47:sl:118:VAL:HG21	1.71	0.71
19:3:59:ARG:NH2	33:R1:2831:G:OP2	2.23	0.71
33:R1:704:G:O2'	33:R1:726:G:N2	2.20	0.71
28:5:147:ARG:HG2	28:5:148:VAL:H	1.56	0.71
33:R1:156:A:H2	33:R1:169:G:H1	0.80	0.71
35:R3:261:U:OP2	55:st:73:ARG:NH2	2.22	0.71
3:14:109:SER:O	3:14:111:LYS:N	2.24	0.71
33:R1:695:G:H5''	33:R1:1380:G:H4'	1.71	0.71
35:R3:687:A:N6	35:R3:703:G:O2'	2.24	0.71
33:R1:947:A:HO2'	33:R1:984:A:H2	1.38	0.70
54:ss:39:ILE:HG23	54:ss:43:MET:HE2	1.73	0.70
35:R3:1031:C:OP1	35:R3:1032:G:N2	2.24	0.70
35:R3:1118:U:H1'	35:R3:1179:A:C4	2.25	0.70
41:sf:11:HIS:HB3	41:sf:14:GLN:HG2	1.73	0.70
28:5:33:ILE:HG12	28:5:95:MET:HG2	1.72	0.70
35:R3:108:G:H5'	35:R3:109:A:H5''	1.73	0.70
31:E:309:ASN:OD1	31:E:485:ASN:ND2	2.25	0.70
35:R3:266:G:H3'	52:sq:68:LYS:HB2	1.73	0.70
35:R3:427:U:H5''	35:R3:428:G:H2'	1.72	0.70
35:R3:1363:A:O2'	35:R3:1365:G:N7	2.24	0.70
37:sb:56:LEU:HD12	37:sb:59:ILE:HD11	1.74	0.70
1:1:194:VAL:HG12	1:1:198:LYS:HE3	1.73	0.70
34:R2:5:U:H2'	34:R2:6:G:H8	1.56	0.70
35:R3:57:G:H1	35:R3:355:C:H5	1.38	0.70
38:sc:82:ASP:HA	38:sc:85:LYS:HE2	1.72	0.70
33:R1:134:G:H1	33:R1:144:A:H2	1.38	0.70
40:se:80:LEU:HD22	40:se:122:VAL:HG21	1.73	0.70
17:28:18:SER:OG	33:R1:2080:A:O5'	2.09	0.70
33:R1:156:A:N1	33:R1:169:G:O6	2.25	0.70
35:R3:343:U:O2'	35:R3:346:G:O6	2.09	0.70
33:R1:2602:A:N6	36:T:76:A:O3'	2.20	0.69
33:R1:2682:A:H61	33:R1:2728:U:H1'	1.57	0.69
40:se:155:LYS:HG3	40:se:156:ARG:HG3	1.74	0.69
3:14:28:SER:OG	33:R1:2566:A:N1	2.24	0.69
52:sq:30:HIS:HB3	52:sq:34:GLY:H	1.57	0.69
24:34:43:THR:OG1	24:34:44:VAL:N	2.17	0.69
34:R2:1:U:H2'	34:R2:2:G:H8	1.57	0.69
35:R3:127:G:O3'	52:sq:5:ARG:NH2	2.24	0.69
6:17:2:ARG:NE	6:17:2:ARG:O	2.25	0.69
28:5:3:LEU:HD22	28:5:100:GLU:HB2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:354:ILE:HD11	31:E:495:MET:HE2	1.74	0.69
33:R1:415:A:H62	33:R1:2408:U:H3	1.39	0.69
46:sk:126:ARG:CD	56:su:33:ARG:HH22	2.04	0.69
9:2:145:MET:HE2	9:2:153:LEU:HD21	1.74	0.69
1:1:6:LYS:N	33:R1:2130:U:OP1	2.25	0.69
29:6:34:ARG:HH12	29:6:70:LEU:HD22	1.56	0.69
33:R1:2144:G:N3	33:R1:2148:G:N2	2.41	0.69
55:st:58:ASP:OD1	55:st:75:LYS:NZ	2.22	0.69
56:su:9:GLU:HB3	56:su:10:PRO:HD3	1.73	0.69
2:13:17:VAL:HG23	2:13:137:PRO:HB2	1.74	0.69
2:13:81:ILE:HG22	19:3:156:PHE:HB3	1.74	0.68
13:23:89:GLU:N	13:23:89:GLU:OE2	2.26	0.68
31:E:41:ASN:ND2	31:E:476:ASP:OD1	2.26	0.68
35:R3:1011:C:H2'	35:R3:1012:A:C8	2.29	0.68
56:su:7:GLU:N	56:su:7:GLU:OE2	2.26	0.68
6:17:53:THR:HA	6:17:56:LYS:HD2	1.74	0.68
33:R1:1906:G:N2	33:R1:1924:C:O2	2.18	0.68
30:9:29:PHE:O	30:9:33:GLN:HB2	1.93	0.68
35:R3:1317:C:H4'	49:sn:47:LEU:HG	1.76	0.68
21:31:28:VAL:HG22	28:5:139:GLU:HG3	1.76	0.68
39:sd:144:ILE:HD12	39:sd:177:MET:HB2	1.75	0.68
33:R1:1417:C:O2'	33:R1:1587:G:O2'	2.10	0.68
12:22:83:LYS:HB3	12:22:95:ARG:HE	1.57	0.68
15:25:55:GLU:N	15:25:55:GLU:OE2	2.26	0.68
18:29:5:GLU:HB3	18:29:56:LEU:HD22	1.74	0.68
34:R2:5:U:H2'	34:R2:6:G:C8	2.29	0.68
35:R3:1356:G:H2'	35:R3:1357:A:C8	2.28	0.68
39:sd:36:ALA:HB3	39:sd:41:GLY:HA2	1.73	0.68
33:R1:413:C:O2'	33:R1:414:C:O2	2.09	0.68
35:R3:522:C:OP2	47:sl:65:TYR:OH	2.12	0.68
18:29:13:GLU:OE2	18:29:60:LYS:NZ	2.27	0.68
35:R3:781:A:OP1	46:sk:124:LYS:NZ	2.25	0.68
45:sj:81:GLU:OE1	45:sj:81:GLU:N	2.26	0.68
28:5:70:ARG:NH1	33:R1:2298:A:OP1	2.27	0.68
33:R1:848:C:H2'	33:R1:849:A:H8	1.58	0.68
33:R1:1179:G:H5''	33:R1:1180:U:H6	1.57	0.68
16:27:15:ASP:OD1	33:R1:2263:C:N4	2.27	0.68
35:R3:1447:A:H5''	35:R3:1448:C:H5	1.58	0.68
9:2:47:ARG:HD3	33:R1:778:G:H5''	1.77	0.67
33:R1:136:G:C2	33:R1:142:A:H2	2.09	0.67
33:R1:358:U:H2'	33:R1:359:G:H8	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1918:A:O2'	33:R1:1919:A:N7	2.27	0.67
47:sl:35:ARG:H	47:sl:75:GLU:HG3	1.59	0.67
3:14:43:ILE:HD12	3:14:56:ASP:HB2	1.76	0.67
33:R1:45:G:H5''	33:R1:46:G:H5'	1.75	0.67
35:R3:407:U:H3	35:R3:435:A:H62	1.42	0.67
16:27:40:GLN:NE2	16:27:57:HIS:O	2.26	0.67
33:R1:84:A:N1	33:R1:98:G:O2'	2.26	0.67
33:R1:136:G:C6	33:R1:142:A:N1	2.62	0.67
33:R1:1858:A:N6	33:R1:1884:G:O2'	2.28	0.67
22:32:45:ASP:OD1	22:32:52:LYS:NZ	2.28	0.67
23:33:27:ARG:HH21	31:E:17:PRO:HG2	1.59	0.67
1:1:184:LYS:O	1:1:188:ASN:ND2	2.27	0.67
39:sd:49:ASP:OD1	39:sd:50:TYR:N	2.27	0.67
10:20:49:ARG:NH1	33:R1:993:G:OP1	2.26	0.67
35:R3:254:G:OP1	52:sq:67:SER:OG	2.12	0.67
35:R3:1149:C:OP1	44:si:10:ARG:NE	2.27	0.67
52:sq:26:ARG:NH1	52:sq:41:THR:OG1	2.27	0.67
7:18:46:GLU:N	7:18:46:GLU:OE2	2.25	0.67
28:5:16:MET:HE2	28:5:16:MET:HA	1.77	0.67
33:R1:880:G:H1	33:R1:895:U:H3	1.41	0.67
33:R1:1171:G:O6	33:R1:1176:U:O4	2.13	0.67
31:E:203:ARG:HG2	31:E:547:ARG:HG2	1.75	0.67
26:36:32:LYS:HD3	33:R1:2478:A:H5'	1.76	0.67
33:R1:2848:G:HO2'	33:R1:2867:G:H22	1.41	0.67
35:R3:1368:A:OP1	44:si:112:ARG:NH2	2.28	0.67
46:sk:26:PHE:O	46:sk:57:SER:OG	2.11	0.67
5:16:84:LYS:NZ	33:R1:2250:G:OP1	2.28	0.67
33:R1:1779:U:H5	33:R1:1784:A:N7	1.92	0.67
33:R1:695:G:O2'	33:R1:696:G:O5'	2.13	0.66
33:R1:1326:U:HO2'	33:R1:2010:G:HO2'	1.43	0.66
11:21:10:LYS:NZ	33:R1:994:C:O2	2.27	0.66
35:R3:1186:G:HO2'	35:R3:1187:G:H8	1.44	0.66
40:se:23:THR:HA	40:se:28:ARG:HA	1.77	0.66
33:R1:1912:A:HO2'	35:R3:1494:G:HO2'	1.43	0.66
35:R3:718:A:H5'	46:sk:118:ASN:HB2	1.77	0.66
26:36:34:LYS:NZ	33:R1:2743:U:OP1	2.29	0.66
29:6:2:ARG:HA	29:6:5:LYS:HE3	1.76	0.66
40:se:152:VAL:HG12	40:se:155:LYS:HE2	1.78	0.66
10:20:5:ARG:HD2	33:R1:1250:G:H5''	1.77	0.66
19:3:56:LYS:HE3	33:R1:2830:C:H5''	1.76	0.66
33:R1:879:G:H1	33:R1:898:C:H42	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:sq:48:GLU:OE2	52:sq:48:GLU:N	2.17	0.66
13:23:30:ILE:HG12	13:23:87:LEU:HD11	1.78	0.66
19:3:25:THR:OG1	19:3:191:GLY:O	2.13	0.66
28:5:59:ILE:O	28:5:101:ARG:NH2	2.22	0.66
35:R3:114:U:H1'	35:R3:353:A:H1'	1.77	0.66
40:se:135:VAL:O	40:se:139:THR:OG1	2.13	0.66
17:28:71:ARG:NH1	17:28:77:TYR:OH	2.27	0.66
35:R3:946:A:H2'	35:R3:947:G:C8	2.30	0.66
41:sf:12:PRO:O	41:sf:15:SER:OG	2.08	0.66
33:R1:1597:A:H5''	33:R1:1598:A:H5'	1.77	0.66
33:R1:2328:A:H2'	33:R1:2329:U:C6	2.31	0.66
42:sg:110:ARG:HH12	42:sg:121:ASN:HD22	1.44	0.66
19:3:46:ARG:NH1	19:3:85:ALA:O	2.27	0.65
9:2:220:ARG:NH1	33:R1:1789:A:OP2	2.30	0.65
12:22:49:LYS:NZ	33:R1:491:G:O6	2.29	0.65
33:R1:1172:C:O2'	33:R1:1174:U:O4'	2.14	0.65
33:R1:195:A:H61	33:R1:198:C:H3'	1.60	0.65
49:sn:30:ILE:HG21	49:sn:43:ALA:HB3	1.78	0.65
25:35:14:LYS:HB2	25:35:22:LYS:HE2	1.77	0.65
33:R1:388:G:N2	33:R1:390:U:O2'	2.30	0.65
21:31:63:ARG:NH2	35:R3:1312:G:OP2	2.29	0.65
28:5:130:GLY:HA3	33:R1:2305:U:H5''	1.79	0.65
36:T:58:A:O2'	36:T:60:C:OP2	2.14	0.65
46:sk:30:ILE:HG12	46:sk:45:THR:HG22	1.78	0.65
3:14:23:LYS:NZ	33:R1:2561:U:O2	2.30	0.65
3:14:63:VAL:HG12	3:14:107:LEU:HD11	1.79	0.65
33:R1:1054:A:H2'	33:R1:1055:G:H8	1.62	0.65
35:R3:338:A:H3'	35:R3:339:C:H5''	1.79	0.65
5:16:20:LEU:HD13	15:25:81:PRO:HG2	1.79	0.65
28:5:44:ALA:HB1	31:E:416:LYS:HB2	1.79	0.65
35:R3:664:G:H22	35:R3:741:G:H1	1.45	0.65
9:2:60:ALA:O	9:2:62:ARG:NH1	2.29	0.65
19:3:148:GLN:HB2	19:3:152:PRO:HG2	1.78	0.65
33:R1:131:A:H61	33:R1:147:C:H42	1.45	0.65
33:R1:2774:C:O2'	33:R1:2775:G:O5'	2.15	0.65
40:se:152:VAL:HG21	43:sh:98:LEU:HG	1.79	0.65
48:sm:84:CYS:HB2	54:ss:72:GLU:HG2	1.78	0.65
11:21:1:MET:HE2	11:21:43:ASN:HB3	1.80	0.64
31:E:133:GLN:O	31:E:133:GLN:NE2	2.26	0.64
35:R3:523:A:C2	47:sl:87:LYS:HB3	2.31	0.64
35:R3:545:C:H5'	39:sd:68:GLU:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:4:45:ALA:HB2	27:4:89:PRO:HD3	1.77	0.64
20:30:11:SER:HB2	33:R1:988:A:H5''	1.80	0.64
35:R3:35:G:N2	47:sl:114:SER:OG	2.30	0.64
35:R3:402:G:H5''	35:R3:621:A:H1'	1.79	0.64
51:sp:46:LYS:HD3	51:sp:46:LYS:H	1.63	0.64
6:17:22:ARG:HG3	6:17:70:THR:HA	1.78	0.64
9:2:257:ARG:NH1	9:2:263:ASP:OD1	2.30	0.64
33:R1:2774:C:HO2'	33:R1:2775:G:H8	1.45	0.64
37:sb:124:THR:OG1	37:sb:136:ARG:NH2	2.30	0.64
40:se:165:GLY:O	43:sh:113:ARG:NH1	2.30	0.64
52:sq:16:MET:HG3	52:sq:19:SER:HB2	1.79	0.64
1:1:7:ARG:H	1:1:7:ARG:HD3	1.62	0.64
33:R1:157:C:H2'	33:R1:158:U:H5'	1.79	0.64
33:R1:356:G:H2'	33:R1:357:C:C6	2.33	0.64
45:sj:7:ARG:HA	45:sj:75:ASP:HA	1.79	0.64
45:sj:85:ASP:O	45:sj:89:ARG:NH2	2.28	0.64
47:sl:98:ARG:HB2	47:sl:116:TYR:HA	1.79	0.64
8:19:105:LYS:HG2	35:R3:1432:G:H5''	1.79	0.64
33:R1:412:A:H2'	33:R1:413:C:H5'	1.80	0.64
33:R1:2774:C:O2'	33:R1:2775:G:H8	1.80	0.64
35:R3:115:G:H8	35:R3:115:G:OP1	1.79	0.64
12:22:5:ALA:O	33:R1:494:G:O2'	2.14	0.64
35:R3:946:A:H2'	35:R3:947:G:H8	1.61	0.64
35:R3:1014:A:N1	35:R3:1218:C:O2'	2.31	0.64
35:R3:1081:A:OP2	40:se:51:LYS:NZ	2.31	0.64
35:R3:82:G:H1'	35:R3:88:U:H3	1.63	0.64
35:R3:744:C:H2'	35:R3:745:G:C8	2.33	0.64
35:R3:157:U:H3	35:R3:164:G:H1	1.46	0.64
38:sc:23:ALA:HB1	38:sc:27:GLU:HG2	1.78	0.64
49:sn:36:SER:O	49:sn:36:SER:OG	2.16	0.64
21:31:37:CYS:SG	21:31:38:SER:N	2.71	0.63
33:R1:856:G:H2'	33:R1:857:G:C8	2.32	0.63
35:R3:1151:A:H2'	35:R3:1152:A:C8	2.33	0.63
39:sd:8:LEU:HD23	39:sd:31:CYS:HB3	1.78	0.63
39:sd:98:ASP:OD1	39:sd:99:ASN:N	2.31	0.63
1:1:43:ASP:OD2	33:R1:2123:G:N2	2.31	0.63
35:R3:70:U:H1'	35:R3:71:A:H2	1.62	0.63
41:sf:6:ILE:HG12	41:sf:89:VAL:HG22	1.80	0.63
48:sm:28:ARG:HH21	48:sm:62:PHE:HB2	1.63	0.63
30:9:14:SER:N	30:9:17:ASP:OD2	2.31	0.63
51:sp:43:ALA:HA	51:sp:46:LYS:HZ3	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:2162:G:H4'	33:R1:2171:A:H2'	1.81	0.63
35:R3:126:G:OP1	35:R3:605:U:O2'	2.13	0.63
35:R3:258:G:OP1	55:st:84:LYS:NZ	2.31	0.63
35:R3:321:A:H62	35:R3:332:G:H1	1.46	0.63
35:R3:963:G:N2	45:sj:57:VAL:HG11	2.13	0.63
35:R3:562:U:H1'	47:sl:11:ARG:HG3	1.81	0.63
35:R3:1233:G:OP1	44:si:118:ARG:NH2	2.30	0.63
52:sq:13:SER:HB3	52:sq:21:VAL:HB	1.79	0.63
33:R1:1869:G:H22	33:R1:1872:A:H5''	1.63	0.63
33:R1:2562:U:H2'	33:R1:2563:U:H5'	1.80	0.63
33:R1:2668:G:O2'	33:R1:2669:G:O5'	2.12	0.63
43:sh:10:LEU:HD22	43:sh:74:ILE:HD11	1.81	0.63
35:R3:1060:U:OP1	49:sn:84:ARG:NH2	2.24	0.63
44:si:34:LEU:O	44:si:39:GLY:N	2.24	0.63
10:20:49:ARG:NH2	11:21:73:LYS:O	2.31	0.63
31:E:233:ASP:OD2	31:E:254:ARG:NH2	2.32	0.63
31:E:357:PRO:O	31:E:362:LYS:NZ	2.31	0.63
33:R1:219:A:N3	33:R1:234:U:O2'	2.29	0.63
35:R3:981:U:OP1	49:sn:8:ARG:NH1	2.31	0.63
49:sn:38:GLU:O	49:sn:42:ASN:ND2	2.27	0.63
33:R1:134:G:N1	33:R1:144:A:C2	2.57	0.62
35:R3:107:G:N7	55:st:9:ARG:NH2	2.46	0.62
47:sl:86:VAL:HG21	47:sl:89:LEU:HD12	1.80	0.62
4:15:127:VAL:HG21	4:15:142:ILE:HD13	1.82	0.62
31:E:457:LYS:O	31:E:460:GLN:NE2	2.32	0.62
33:R1:1779:U:OP2	33:R1:1784:A:N6	2.26	0.62
35:R3:58:C:O2'	35:R3:388:G:N2	2.29	0.62
33:R1:2144:G:N2	33:R1:2146:C:O2	2.32	0.62
42:sg:14:ASP:OD2	42:sg:43:TYR:OH	2.10	0.62
42:sg:56:SER:OG	42:sg:57:GLU:N	2.33	0.62
35:R3:1151:A:P	45:sj:43:PRO:HA	2.38	0.62
41:sf:86:ARG:NH1	53:sr:63:TYR:O	2.32	0.62
46:sk:126:ARG:HD2	56:su:33:ARG:HH22	1.62	0.62
50:so:42:PHE:HB3	50:so:52:ARG:HH21	1.65	0.62
28:5:169:LEU:HD12	28:5:174:PHE:CD1	2.34	0.62
33:R1:721:A:H2'	33:R1:722:A:C8	2.35	0.62
33:R1:2668:G:O2'	33:R1:2669:G:O4'	2.17	0.62
35:R3:263:A:OP1	55:st:73:ARG:NH1	2.32	0.62
35:R3:1150:A:H4'	45:sj:43:PRO:HB3	1.80	0.62
4:15:74:THR:HG23	4:15:107:PHE:HB2	1.81	0.62
35:R3:477:C:H2'	35:R3:478:A:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:375:PRO:HG2	31:E:378:GLY:HA2	1.81	0.62
35:R3:311:C:OP1	51:sp:31:ARG:NH2	2.20	0.62
28:5:61:GLY:O	28:5:94:ARG:NH2	2.33	0.62
33:R1:281:C:H41	33:R1:359:G:H22	1.47	0.62
33:R1:2140:G:H2'	33:R1:2141:G:C8	2.34	0.62
51:sp:46:LYS:H	51:sp:46:LYS:CD	2.13	0.62
53:sr:15:GLU:N	53:sr:15:GLU:OE2	2.32	0.62
56:su:4:LYS:H	56:su:4:LYS:HD2	1.65	0.62
9:2:259:ASN:OD1	9:2:262:THR:OG1	2.11	0.62
14:24:68:ASN:ND2	33:R1:329:G:OP2	2.33	0.62
17:28:42:GLU:OE1	17:28:44:ARG:NE	2.27	0.62
35:R3:1452:C:O2'	35:R3:1453:G:N2	2.33	0.62
3:14:78:ARG:NH2	33:R1:2685:G:OP1	2.33	0.61
33:R1:136:G:H1	33:R1:142:A:H2	0.67	0.61
35:R3:1412:C:H2'	35:R3:1413:A:C8	2.34	0.61
53:sr:70:THR:OG1	53:sr:71:ASP:N	2.32	0.61
35:R3:1004:A:H2'	35:R3:1005:A:H5''	1.81	0.61
40:se:96:GLN:O	40:se:122:VAL:HB	2.00	0.61
33:R1:2029:G:N1	33:R1:2033:A:OP2	2.30	0.61
35:R3:1347:G:O6	44:si:11:ARG:NH2	2.33	0.61
48:sm:53:ASP:OD1	48:sm:53:ASP:N	2.33	0.61
8:19:23:ASP:OD1	8:19:112:ARG:NH2	2.34	0.61
31:E:529:GLU:OE2	42:sg:135:LYS:NZ	2.33	0.61
33:R1:827:U:O2'	33:R1:2068:U:N3	2.32	0.61
35:R3:928:G:H1	35:R3:1389:C:H5	1.47	0.61
11:21:16:GLU:OE1	11:21:101:ILE:N	2.33	0.61
33:R1:151:C:H2'	33:R1:152:A:C8	2.35	0.61
33:R1:1108:U:O2	33:R1:1109:C:N4	2.33	0.61
35:R3:57:G:N2	35:R3:388:G:O6	2.32	0.61
48:sm:63:VAL:HG13	48:sm:67:ASP:HB2	1.83	0.61
55:st:47:GLN:NE2	55:st:51:ASN:OD1	2.34	0.61
1:1:195:ALA:HA	1:1:198:LYS:HD2	1.83	0.61
31:E:404:VAL:HG13	31:E:453:LEU:HD12	1.83	0.61
42:sg:137:ARG:NH2	42:sg:138:GLU:OE2	2.32	0.61
5:16:110:GLU:OE2	5:16:114:ARG:NH2	2.34	0.61
31:E:169:ARG:NH2	31:E:188:GLN:O	2.34	0.61
33:R1:411:G:OP2	33:R1:2406:A:O2'	2.19	0.61
3:14:106:GLU:N	3:14:106:GLU:OE2	2.28	0.61
31:E:116:ALA:HB1	31:E:120:LYS:HD2	1.83	0.61
27:4:97:ASN:HB2	27:4:100:MET:HG3	1.83	0.61
31:E:388:LEU:HD21	31:E:467:LEU:HD13	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1103:A:H3'	33:R1:1104:C:H5''	1.82	0.61
41:sf:49:TYR:OH	53:sr:62:ARG:O	2.19	0.61
8:19:90:ALA:HB2	8:19:112:ARG:HA	1.83	0.61
33:R1:388:G:O2'	33:R1:390:U:OP2	2.17	0.61
33:R1:414:C:OP1	33:R1:1879:C:O2'	2.19	0.61
33:R1:1171:G:N1	33:R1:1176:U:N3	2.27	0.61
33:R1:1721:G:N2	33:R1:1738:G:O2'	2.17	0.61
33:R1:1847:G:H21	33:R1:1848:A:H62	1.49	0.61
35:R3:373:A:O2'	35:R3:451:A:N7	2.34	0.61
20:30:40:THR:HG22	20:30:42:ALA:H	1.66	0.60
37:sb:17:HIS:CG	37:sb:37:VAL:HG13	2.36	0.60
16:27:19:LYS:NZ	33:R1:2261:C:OP1	2.30	0.60
28:5:33:ILE:HD12	28:5:155:ILE:HG12	1.82	0.60
31:E:391:VAL:HA	31:E:458:LEU:HD23	1.82	0.60
33:R1:2176:A:H2'	33:R1:2177:C:C4	2.37	0.60
33:R1:639:U:H2'	33:R1:640:C:C6	2.36	0.60
33:R1:1179:G:H5'	33:R1:1180:U:H5''	1.83	0.60
35:R3:309:A:O2'	35:R3:607:A:N1	2.33	0.60
4:15:29:LYS:O	4:15:30:THR:OG1	2.19	0.60
31:E:552:ARG:NH2	33:R1:2168:G:O6	2.35	0.60
40:se:159:SER:HB3	40:se:162:GLU:HB2	1.83	0.60
5:16:53:MET:HG3	5:16:120:ALA:HB2	1.83	0.60
31:E:327:SER:O	31:E:379:THR:OG1	2.20	0.60
33:R1:962:G:N2	33:R1:2250:G:H1	2.00	0.60
38:sc:39:ARG:NH1	49:sn:91:GLU:HG3	2.16	0.60
27:4:163:ASN:ND2	33:R1:320:A:N3	2.49	0.60
31:E:194:ASP:OD1	31:E:358:ASN:ND2	2.35	0.60
33:R1:2174:C:H2'	33:R1:2175:C:C6	2.37	0.60
6:17:42:LYS:NZ	33:R1:2817:U:OP1	2.34	0.60
15:25:65:VAL:HG23	15:25:66:ASP:H	1.66	0.60
31:E:107:VAL:HG22	31:E:121:LEU:HD12	1.83	0.60
33:R1:1204:A:H4'	33:R1:1205:A:H5''	1.83	0.60
35:R3:17:U:H2'	35:R3:18:C:C6	2.36	0.60
35:R3:1013:G:N1	35:R3:1016:A:OP2	2.35	0.60
1:1:202:THR:OG1	1:1:203:GLN:NE2	2.34	0.60
9:2:233:GLY:HA3	33:R1:2598:A:H5''	1.81	0.60
31:E:405:TRP:O	31:E:409:SER:OG	2.17	0.60
33:R1:324:A:OP2	33:R1:1205:A:N6	2.34	0.60
35:R3:1129:C:H1'	35:R3:1130:A:H2	1.67	0.60
46:sk:55:ARG:O	46:sk:58:THR:OG1	2.20	0.60
9:2:139:THR:OG1	9:2:162:GLN:OE1	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:577:G:O2'	33:R1:1254:A:OP1	2.18	0.60
33:R1:1900:A:H1'	33:R1:1970:A:H2'	1.82	0.60
33:R1:221:A:N1	33:R1:265:A:O2'	2.35	0.60
33:R1:2134:A:N7	33:R1:2156:G:N2	2.50	0.60
35:R3:976:G:OP2	35:R3:1358:U:O2'	2.19	0.60
35:R3:1005:A:H2'	35:R3:1006:G:C5	2.36	0.60
35:R3:1356:G:H2'	35:R3:1357:A:H8	1.66	0.60
39:sd:145:ARG:HH21	39:sd:147:LYS:HD2	1.65	0.60
54:ss:62:THR:HB	54:ss:65:MET:HE3	1.83	0.60
35:R3:677:U:H3	35:R3:713:G:H22	1.50	0.59
54:ss:47:THR:HG22	54:ss:60:PHE:HD1	1.67	0.59
33:R1:993:G:H2'	33:R1:994:C:H5''	1.83	0.59
35:R3:878:A:H5''	43:sh:80:PRO:HG2	1.84	0.59
46:sk:15:VAL:HG12	46:sk:76:TYR:HB3	1.83	0.59
48:sm:11:HIS:O	48:sm:43:LYS:NZ	2.35	0.59
32:M:6:U:H3	36:T:34:A:H62	1.49	0.59
33:R1:153:U:H2'	33:R1:154:U:O4'	2.02	0.59
33:R1:1051:G:H22	33:R1:1110:G:H1	1.48	0.59
35:R3:744:C:H2'	35:R3:745:G:H8	1.67	0.59
6:17:8:ARG:NH1	33:R1:1652:A:OP1	2.31	0.59
22:32:48:TYR:OH	33:R1:2883:A:OP1	2.16	0.59
33:R1:156:A:N1	33:R1:169:G:C6	2.71	0.59
36:T:23:A:H2'	36:T:24:G:C8	2.38	0.59
38:sc:52:SER:OG	38:sc:111:ASP:OD2	2.20	0.59
44:si:51:LEU:HB2	44:si:56:MET:HB2	1.83	0.59
33:R1:2124:G:O2'	33:R1:2125:G:O4'	2.20	0.59
35:R3:545:C:OP1	39:sd:57:LYS:NZ	2.35	0.59
8:19:105:LYS:HE3	35:R3:1432:G:H3'	1.85	0.59
33:R1:2591:C:H2'	33:R1:2592:G:C8	2.37	0.59
2:13:18:VAL:HG12	2:13:140:LEU:HB3	1.84	0.59
31:E:405:TRP:NE1	31:E:424:SER:OG	2.35	0.59
33:R1:1038:G:H2'	33:R1:1039:A:C8	2.38	0.59
33:R1:1149:G:H2'	33:R1:1150:C:C6	2.37	0.59
38:sc:72:PRO:HG3	38:sc:104:GLU:HB2	1.83	0.59
43:sh:8:ASP:O	43:sh:12:ARG:HG2	2.03	0.59
55:st:28:ARG:O	55:st:32:LYS:HG3	2.03	0.59
2:13:65:THR:OG1	33:R1:1141:U:OP2	2.19	0.59
4:15:4:ASN:OD1	33:R1:1203:U:O2'	2.21	0.59
8:19:6:GLN:HG2	19:3:184:ARG:HH12	1.68	0.59
17:28:69:GLU:N	17:28:69:GLU:OE2	2.36	0.59
18:29:4:LYS:HG3	18:29:7:ARG:HH12	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:1081:A:H5'	40:se:22:LYS:HG3	1.85	0.59
45:sj:15:HIS:HA	45:sj:18:ILE:HG22	1.84	0.59
48:sm:80:MET:HG2	48:sm:91:ARG:HG2	1.85	0.59
36:T:23:A:H2'	36:T:24:G:H8	1.66	0.58
37:sb:124:THR:HG23	37:sb:128:LEU:HD21	1.84	0.58
19:3:196:ALA:O	19:3:199:SER:OG	2.17	0.58
31:E:49:LEU:HD13	31:E:215:ILE:HD11	1.85	0.58
33:R1:134:G:H22	33:R1:144:A:H2	1.51	0.58
33:R1:1176:U:O2'	33:R1:1178:C:N4	2.36	0.58
33:R1:1720:U:H2'	33:R1:1721:G:O4'	2.02	0.58
35:R3:451:A:H1'	35:R3:452:A:C2	2.38	0.58
35:R3:1014:A:C2	35:R3:1015:G:H1'	2.37	0.58
21:31:44:PHE:HD1	21:31:45:THR:HG23	1.68	0.58
33:R1:500:G:N1	33:R1:503:A:OP2	2.31	0.58
35:R3:1150:A:O2'	35:R3:1151:A:O5'	2.20	0.58
52:sq:50:ASN:OD1	52:sq:50:ASN:N	2.27	0.58
15:25:69:GLU:OE1	15:25:69:GLU:N	2.34	0.58
31:E:196:GLU:OE2	31:E:196:GLU:N	2.35	0.58
54:ss:49:ALA:HA	54:ss:58:PRO:HA	1.85	0.58
33:R1:161:A:H61	33:R1:2218:G:H4'	1.68	0.58
33:R1:590:A:H62	33:R1:667:U:H3	1.51	0.58
35:R3:235:C:H2'	35:R3:236:A:C8	2.38	0.58
17:28:56:ARG:NH2	33:R1:400:G:N7	2.50	0.58
33:R1:1432:G:H2'	33:R1:1433:A:C8	2.39	0.58
33:R1:1912:A:O2'	35:R3:1494:G:O2'	2.15	0.58
35:R3:492:C:H5'	35:R3:493:A:OP2	2.03	0.58
37:sb:65:LYS:HB3	37:sb:89:PHE:HE2	1.68	0.58
2:13:30:THR:HG21	33:R1:1005:C:O2'	2.03	0.58
33:R1:319:G:H1	33:R1:323:C:H5	1.49	0.58
35:R3:362:G:H5'	47:sl:57:THR:HG21	1.85	0.58
35:R3:441:A:H61	35:R3:493:A:H61	1.51	0.58
35:R3:1011:C:H2'	35:R3:1012:A:H8	1.66	0.58
39:sd:6:PRO:HB2	39:sd:9:LYS:HB2	1.86	0.58
43:sh:45:ILE:HD12	43:sh:46:GLU:O	2.04	0.58
5:16:81:ARG:HH21	16:27:5:LYS:HG3	1.67	0.58
31:E:351:ILE:HG22	31:E:508:ALA:HA	1.85	0.58
33:R1:878:A:H3'	33:R1:879:G:H8	1.67	0.58
34:R2:29:A:H2'	34:R2:30:C:C6	2.39	0.58
35:R3:115:G:O2'	35:R3:289:G:H5'	2.03	0.58
37:sb:86:CYS:HB3	37:sb:221:ARG:HG3	1.84	0.58
40:se:105:ILE:HG13	40:se:105:ILE:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:29:54:LYS:HD3	33:R1:72:U:H5'	1.85	0.58
35:R3:1118:U:OP1	44:si:105:ARG:NE	2.35	0.58
9:2:209:ALA:HA	9:2:212:TRP:CE2	2.39	0.58
9:2:35:LYS:NZ	9:2:37:SER:OG	2.37	0.57
33:R1:2123:G:H2'	33:R1:2124:G:C5	2.39	0.57
35:R3:473:U:H2'	35:R3:474:G:C8	2.38	0.57
35:R3:1005:A:H5'	35:R3:1006:G:N7	2.19	0.57
36:T:75:C:H3'	36:T:76:A:H5''	1.85	0.57
39:sd:197:HIS:O	39:sd:201:GLU:HG2	2.04	0.57
19:3:45:TYR:OH	33:R1:2636:C:O2'	2.21	0.57
35:R3:685:G:H2'	35:R3:686:U:C6	2.39	0.57
35:R3:1323:G:H2'	35:R3:1324:A:C8	2.39	0.57
36:T:43:G:H2'	36:T:44:G:C8	2.39	0.57
41:sf:61:LEU:HD13	53:sr:23:LYS:HD3	1.86	0.57
8:19:105:LYS:O	8:19:108:ARG:NH1	2.35	0.57
9:2:226:PRO:HD3	9:2:233:GLY:H	1.68	0.57
22:32:39:ARG:NH1	33:R1:2885:G:N7	2.49	0.57
33:R1:1090:A:H2'	33:R1:1091:G:C8	2.38	0.57
33:R1:2243:U:H2'	33:R1:2244:U:C6	2.39	0.57
9:2:4:LYS:HD3	9:2:16:VAL:HG22	1.86	0.57
31:E:361:GLY:N	59:E:602:ATP:O1B	2.31	0.57
37:sb:13:VAL:HG11	37:sb:207:ARG:HE	1.69	0.57
41:sf:40:GLU:HB2	41:sf:61:LEU:HD23	1.85	0.57
42:sg:55:LYS:HB2	42:sg:60:ALA:HB2	1.86	0.57
48:sm:12:LYS:HB2	48:sm:17:ALA:HB2	1.86	0.57
51:sp:79:ASN:OD1	51:sp:79:ASN:N	2.37	0.57
19:3:1:MET:HG3	19:3:100:LEU:HD11	1.85	0.57
33:R1:1386:C:H2'	33:R1:1387:A:C8	2.40	0.57
35:R3:672:U:H2'	35:R3:673:A:C8	2.40	0.57
56:su:36:PHE:HD2	56:su:38:GLU:HG3	1.69	0.57
29:6:174:LYS:HD3	33:R1:2529:G:H4'	1.87	0.57
33:R1:64:A:H2'	33:R1:65:U:C6	2.40	0.57
33:R1:881:G:H2'	33:R1:882:G:C8	2.39	0.57
33:R1:2123:G:H2'	33:R1:2124:G:C8	2.40	0.57
33:R1:2124:G:H2'	33:R1:2125:G:C8	2.39	0.57
35:R3:992:U:O2'	35:R3:1043:G:O6	2.14	0.57
37:sb:9:LEU:HD23	37:sb:42:LEU:HB2	1.86	0.57
25:35:4:LYS:HD3	33:R1:242:G:N7	2.20	0.57
33:R1:156:A:H2	33:R1:169:G:C2	2.19	0.57
33:R1:593:U:H2'	33:R1:594:U:C6	2.40	0.57
35:R3:1348:U:H4'	44:si:121:ARG:HD2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:sk:91:GLY:O	46:sk:95:THR:OG1	2.19	0.57
1:1:56:ASP:N	1:1:56:ASP:OD1	2.33	0.57
1:1:207:VAL:HG22	1:1:209:ILE:H	1.69	0.57
5:16:31:PHE:HD1	5:16:132:THR:HG22	1.69	0.57
8:19:6:GLN:OE1	19:3:184:ARG:NH2	2.38	0.57
31:E:262:GLU:OE1	31:E:265:ARG:NH2	2.38	0.57
31:E:318:ARG:NH2	35:R3:1300:G:OP2	2.37	0.57
33:R1:265:A:N1	33:R1:427:U:O2'	2.34	0.57
33:R1:890:C:H3'	33:R1:891:G:H4'	1.85	0.57
33:R1:1028:A:H2'	33:R1:1029:A:C8	2.40	0.57
35:R3:106:C:H2'	35:R3:107:G:H5'	1.86	0.57
35:R3:838:G:O2'	35:R3:839:C:O5'	2.23	0.57
7:18:37:ALA:HB3	7:18:78:VAL:HG21	1.87	0.57
22:32:8:THR:HG23	33:R1:2020:A:H5'	1.87	0.57
26:36:2:LYS:NZ	33:R1:2478:A:OP2	2.30	0.57
33:R1:1327:A:N6	33:R1:1647:U:O2	2.37	0.57
33:R1:1353:A:H2'	33:R1:1354:A:C8	2.39	0.57
33:R1:2638:G:H1'	33:R1:2778:A:H61	1.69	0.57
35:R3:1345:U:OP1	44:si:121:ARG:NH1	2.34	0.57
39:sd:124:VAL:HG22	39:sd:142:VAL:HG22	1.87	0.57
43:sh:42:GLU:HG3	43:sh:100:ILE:HD13	1.86	0.57
51:sp:44:SER:H	51:sp:46:LYS:NZ	2.03	0.57
14:24:6:ARG:NH2	33:R1:84:A:O2'	2.37	0.56
21:31:34:LEU:HD12	28:5:109:ARG:HH12	1.70	0.56
33:R1:279:A:N6	33:R1:361:G:H1'	2.19	0.56
33:R1:675:A:N3	33:R1:2443:C:O2'	2.38	0.56
33:R1:2140:G:H2'	33:R1:2141:G:H8	1.70	0.56
35:R3:206:C:C5	35:R3:207:C:H1'	2.38	0.56
33:R1:858:G:HO2'	33:R1:2268:A:HO2'	1.51	0.56
33:R1:895:U:H4'	33:R1:896:A:H2	1.70	0.56
34:R2:2:G:O6	34:R2:119:A:N6	2.38	0.56
35:R3:717:U:H4'	46:sk:118:ASN:HD22	1.70	0.56
47:sl:30:ARG:O	47:sl:57:THR:OG1	2.23	0.56
50:so:63:ARG:NE	50:so:67:ASP:OD1	2.34	0.56
1:1:7:ARG:NH2	1:1:218:MET:SD	2.78	0.56
9:2:231:HIS:HA	9:2:241:LYS:HE3	1.87	0.56
29:6:108:PHE:O	33:R1:2666:C:N4	2.39	0.56
33:R1:2183:A:H2'	33:R1:2184:A:C8	2.40	0.56
34:R2:32:U:H2'	34:R2:33:G:H8	1.71	0.56
35:R3:587:G:N2	35:R3:754:C:OP2	2.35	0.56
37:sb:87:ASP:OD1	37:sb:87:ASP:N	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:sh:37:ASN:O	43:sh:41:GLU:HG2	2.06	0.56
1:1:65:LEU:HD21	1:1:68:GLY:HA2	1.87	0.56
19:3:5:VAL:N	19:3:32:ASN:HD21	1.94	0.56
19:3:155:VAL:HG21	33:R1:2618:G:H21	1.69	0.56
33:R1:947:A:O2'	33:R1:984:A:H2	1.89	0.56
35:R3:254:G:O4'	52:sq:16:MET:HE2	2.06	0.56
35:R3:1071:C:H2'	35:R3:1072:G:H8	1.71	0.56
33:R1:729:G:H5''	33:R1:730:A:H5''	1.88	0.56
33:R1:2291:U:H2'	33:R1:2292:U:C6	2.41	0.56
34:R2:64:G:O2'	34:R2:65:U:OP1	2.22	0.56
35:R3:136:C:O2'	51:sp:64:GLY:O	2.18	0.56
35:R3:381:C:H2'	35:R3:382:A:O4'	2.06	0.56
35:R3:727:G:N2	35:R3:730:G:OP2	2.35	0.56
35:R3:1031:C:H4'	35:R3:1033:G:N3	2.21	0.56
35:R3:1124:G:N2	35:R3:1125:U:O4	2.32	0.56
33:R1:657:U:H2'	33:R1:658:U:C6	2.41	0.56
33:R1:2430:A:H2'	33:R1:2430:A:N3	2.20	0.56
35:R3:9:G:H5'	40:se:107:GLY:HA3	1.87	0.56
4:15:75:ALA:HB2	4:15:105:ILE:HD12	1.86	0.56
17:28:27:ARG:NH2	33:R1:1365:A:OP1	2.33	0.56
29:6:53:PRO:HB3	29:6:60:GLY:HA3	1.88	0.56
9:2:241:LYS:O	33:R1:1902:C:H4'	2.06	0.56
33:R1:645:C:H2'	33:R1:647:G:N7	2.20	0.56
33:R1:2638:G:H1'	33:R1:2778:A:N6	2.21	0.56
35:R3:636:U:H5'	52:sq:5:ARG:HH11	1.70	0.56
47:sl:86:VAL:HG23	47:sl:87:LYS:H	1.71	0.56
1:1:58:ASN:HD22	1:1:165:ASN:HD22	1.54	0.56
6:17:24:MET:HG2	33:R1:1277:G:O2'	2.06	0.56
21:31:5:ILE:HD12	28:5:63:LYS:HD3	1.88	0.56
35:R3:1010:U:H2'	35:R3:1011:C:C6	2.41	0.56
39:sd:101:VAL:HG13	39:sd:106:PHE:HB2	1.88	0.56
45:sj:8:ILE:HD11	45:sj:87:LEU:HD21	1.88	0.56
47:sl:35:ARG:HB3	47:sl:53:ARG:HB2	1.86	0.56
19:3:48:ILE:HG23	19:3:84:LEU:HD21	1.88	0.56
23:33:10:LEU:HB3	23:33:48:TYR:HB3	1.85	0.56
33:R1:458:G:O2'	33:R1:469:G:O6	2.23	0.56
34:R2:7:G:H1	34:R2:113:C:H5	1.53	0.56
35:R3:518:C:O2'	35:R3:530:G:N2	2.39	0.56
35:R3:855:U:OP2	35:R3:871:U:N3	2.32	0.56
35:R3:1507:A:H2'	35:R3:1508:A:C8	2.41	0.56
37:sb:93:HIS:CD2	37:sb:145:ASN:HB2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:sc:107:LYS:HB3	38:sc:110:LEU:HB2	1.88	0.56
44:si:117:LEU:HD22	44:si:123:ARG:HG2	1.87	0.56
54:ss:65:MET:HB2	54:ss:73:PHE:CZ	2.41	0.56
21:31:42:PRO:O	28:5:114:ARG:NH2	2.38	0.55
31:E:151:LEU:HD11	31:E:550:TYR:OH	2.06	0.55
33:R1:1028:A:N3	33:R1:2486:C:O2'	2.34	0.55
35:R3:524:G:H2'	35:R3:525:C:C6	2.41	0.55
35:R3:542:G:OP1	39:sd:9:LYS:NZ	2.21	0.55
35:R3:1270:G:H2'	35:R3:1271:A:C8	2.41	0.55
39:sd:141:VAL:HG12	39:sd:180:THR:HG22	1.88	0.55
9:2:34:GLU:OE1	33:R1:1816:C:N4	2.29	0.55
33:R1:742:A:H2'	33:R1:743:A:C8	2.40	0.55
33:R1:1170:C:O2'	33:R1:1171:G:H8	1.90	0.55
35:R3:1122:U:HO2'	35:R3:1123:U:H6	1.52	0.55
37:sb:77:GLU:H	37:sb:77:GLU:CD	2.14	0.55
41:sf:9:MET:HE3	41:sf:59:TYR:OH	2.06	0.55
12:22:82:MET:HE1	33:R1:1322:A:H5''	1.86	0.55
29:6:85:LYS:HG2	29:6:131:VAL:HG22	1.89	0.55
33:R1:948:C:O2	33:R1:984:A:O2'	2.19	0.55
35:R3:112:G:H22	35:R3:315:A:H2	1.53	0.55
35:R3:441:A:H61	35:R3:493:A:N6	2.04	0.55
44:si:5:TYR:HB2	44:si:20:ILE:HG22	1.88	0.55
28:5:57:ALA:HB2	28:5:64:PRO:HD3	1.86	0.55
31:E:415:MET:HE1	31:E:460:GLN:HB2	1.89	0.55
33:R1:1443:U:H2'	33:R1:1444:G:H8	1.70	0.55
35:R3:80:A:N6	35:R3:89:U:O4	2.40	0.55
38:sc:9:ILE:HG23	38:sc:10:ARG:HG3	1.89	0.55
49:sn:41:TRP:O	49:sn:45:LEU:HG	2.07	0.55
18:29:36:GLN:OE1	18:29:36:GLN:N	2.39	0.55
33:R1:882:G:N2	33:R1:894:U:O2	2.36	0.55
33:R1:2646:C:OP2	33:R1:2732:G:O2'	2.25	0.55
54:ss:21:ALA:O	54:ss:25:GLY:N	2.39	0.55
4:15:110:VAL:HB	4:15:127:VAL:HG12	1.88	0.55
19:3:181:ASP:OD2	19:3:184:ARG:HD2	2.06	0.55
31:E:196:GLU:H	31:E:196:GLU:CD	2.13	0.55
33:R1:1064:C:H3'	33:R1:1065:U:H3'	1.88	0.55
34:R2:7:G:H22	34:R2:113:C:H5	1.53	0.55
35:R3:1127:G:H1	35:R3:1145:A:H61	1.54	0.55
35:R3:1238:A:H2	35:R3:1241:G:N3	2.05	0.55
35:R3:1297:G:H4'	35:R3:1298:U:O5'	2.07	0.55
42:sg:71:THR:HG22	42:sg:72:VAL:HG13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:20:50:ARG:NH2	33:R1:993:G:OP2	2.38	0.55
31:E:46:SER:OG	59:E:601:ATP:O2B	2.25	0.55
35:R3:1252:A:H61	35:R3:1285:A:H62	1.54	0.55
9:2:143:VAL:HB	9:2:153:LEU:HB2	1.89	0.55
19:3:151:THR:OG1	33:R1:2032:G:N2	2.40	0.55
33:R1:1223:G:N2	33:R1:1226:A:OP2	2.32	0.55
33:R1:1428:C:C5	33:R1:1569:A:H5''	2.41	0.55
33:R1:2291:U:H5'	33:R1:2380:C:H1'	1.88	0.55
33:R1:2638:G:HO2'	33:R1:2639:A:H8	1.55	0.55
44:si:18:VAL:HB	44:si:64:ILE:HD13	1.87	0.55
9:2:106:PRO:HD2	9:2:109:LEU:HD22	1.89	0.55
14:24:87:GLU:O	14:24:89:GLY:N	2.39	0.55
22:32:2:VAL:HG13	33:R1:2015:A:C6	2.42	0.55
22:32:37:HIS:ND1	22:32:38:LEU:O	2.40	0.55
33:R1:181:A:H1'	33:R1:435:C:H5'	1.88	0.55
35:R3:769:G:H4'	35:R3:1513:A:H4'	1.88	0.55
35:R3:932:C:H4'	42:sg:3:ARG:NH2	2.22	0.55
35:R3:1273:C:H2'	35:R3:1274:A:O4'	2.07	0.55
37:sb:113:LEU:HD11	37:sb:144:GLU:HG2	1.88	0.55
39:sd:87:GLU:HG2	39:sd:187:ARG:HB2	1.87	0.55
41:sf:9:MET:HE3	41:sf:59:TYR:CZ	2.42	0.55
49:sn:26:LEU:HD12	49:sn:47:LEU:HD13	1.88	0.55
52:sq:16:MET:HB3	52:sq:19:SER:O	2.07	0.55
5:16:5:LYS:HG2	33:R1:871:U:OP1	2.06	0.55
28:5:105:ILE:O	28:5:109:ARG:NH2	2.40	0.55
33:R1:1639:C:H4'	33:R1:2700:A:OP1	2.07	0.55
35:R3:404:G:OP2	39:sd:114:ARG:NH1	2.39	0.55
35:R3:1151:A:OP2	45:sj:44:THR:N	2.30	0.55
36:T:45:G:O2'	36:T:46:G:H5'	2.05	0.55
2:13:116:ARG:NH2	33:R1:528:A:OP2	2.34	0.54
31:E:66:GLN:NE2	31:E:67:PRO:HD2	2.23	0.54
31:E:100:ALA:O	31:E:104:LEU:HD23	2.06	0.54
35:R3:28:A:O2'	35:R3:296:U:OP1	2.22	0.54
35:R3:1071:C:H2'	35:R3:1072:G:C8	2.42	0.54
9:2:75:ALA:HB1	9:2:93:VAL:HG13	1.89	0.54
13:23:64:LYS:HA	13:23:79:ASP:HB2	1.89	0.54
20:30:27:GLY:HA3	20:30:37:ARG:HH21	1.72	0.54
21:31:31:ASP:OD1	21:31:31:ASP:N	2.37	0.54
31:E:13:LYS:NZ	31:E:58:ASP:OD1	2.39	0.54
34:R2:13:G:H8	34:R2:69:G:H21	1.52	0.54
35:R3:331:G:O2'	55:st:2:ASN:ND2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:696:A:H2'	35:R3:697:U:H6	1.72	0.54
35:R3:990:C:O2'	35:R3:991:U:H5''	2.07	0.54
35:R3:1218:C:H2'	35:R3:1219:A:C8	2.43	0.54
51:sp:4:ILE:HG12	51:sp:21:VAL:HG22	1.89	0.54
2:13:122:LEU:HG	2:13:124:VAL:HG23	1.90	0.54
6:17:24:MET:HE2	6:17:44:LEU:HD22	1.89	0.54
28:5:106:ALA:HB1	28:5:136:ILE:HD12	1.89	0.54
33:R1:257:C:H3'	33:R1:258:G:H8	1.73	0.54
34:R2:32:U:H2'	34:R2:33:G:C8	2.42	0.54
35:R3:1002:G:N7	35:R3:1038:C:N4	2.54	0.54
35:R3:1477:U:H2'	35:R3:1478:U:C6	2.41	0.54
36:T:68:C:HO2'	36:T:69:A:H8	1.54	0.54
47:sl:78:VAL:O	47:sl:102:ASP:HB2	2.08	0.54
49:sn:79:SER:OG	49:sn:80:ARG:N	2.39	0.54
52:sq:61:ARG:HG2	52:sq:75:VAL:HG22	1.90	0.54
33:R1:976:G:HO2'	33:R1:1155:A:HO2'	1.54	0.54
33:R1:2313:C:H2'	33:R1:2314:A:H8	1.72	0.54
35:R3:330:C:O2'	35:R3:331:G:H5'	2.07	0.54
35:R3:555:U:H2'	35:R3:556:C:C6	2.42	0.54
55:st:82:ILE:HA	55:st:85:LEU:HD23	1.88	0.54
1:1:221:GLY:N	33:R1:2175:C:O2'	2.36	0.54
19:3:33:ARG:NH2	19:3:53:GLY:O	2.39	0.54
28:5:56:LEU:HD13	28:5:88:VAL:HG23	1.88	0.54
31:E:85:THR:H	31:E:88:GLU:HB2	1.71	0.54
33:R1:1019:U:H3	33:R1:1142:A:H62	1.56	0.54
35:R3:1010:U:H2'	35:R3:1011:C:H6	1.71	0.54
35:R3:1052:U:O2'	35:R3:1055:A:OP2	2.18	0.54
35:R3:1144:G:N2	35:R3:1146:A:H62	2.05	0.54
35:R3:1346:A:N1	35:R3:1374:A:H5''	2.22	0.54
37:sb:31:PHE:O	37:sb:39:ILE:N	2.40	0.54
44:si:8:THR:OG1	44:si:9:GLY:N	2.40	0.54
44:si:45:MET:SD	44:si:45:MET:N	2.80	0.54
46:sk:93:GLU:OE2	46:sk:97:ARG:NH1	2.41	0.54
24:34:10:LEU:HD23	33:R1:770:G:H5''	1.90	0.54
31:E:156:TRP:H	31:E:156:TRP:CD1	2.25	0.54
31:E:376:ASP:OD1	31:E:376:ASP:N	2.37	0.54
33:R1:639:U:H2'	33:R1:640:C:H6	1.72	0.54
35:R3:1077:G:N2	35:R3:1080:A:OP2	2.36	0.54
35:R3:1530:G:H2'	35:R3:1531:A:C8	2.42	0.54
44:si:83:THR:HG23	44:si:97:LEU:HD22	1.90	0.54
4:15:123:ARG:NH1	4:15:143:GLU:OE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:6:70:LEU:O	29:6:74:MET:HG3	2.08	0.54
33:R1:1171:G:H2'	33:R1:1172:C:O4'	2.06	0.54
45:sj:28:THR:HA	45:sj:31:ARG:HG3	1.87	0.54
45:sj:35:GLN:HB3	45:sj:78:GLU:CD	2.33	0.54
19:3:1:MET:HG2	19:3:2:ILE:N	2.21	0.54
30:9:50:ARG:HH11	30:9:51:ARG:HA	1.73	0.54
35:R3:751:U:H2'	35:R3:752:G:O4'	2.07	0.54
56:su:36:PHE:HB3	56:su:39:LYS:H	1.72	0.54
1:1:215:SER:HB2	1:1:221:GLY:HA2	1.89	0.54
2:13:16:TYR:HB3	2:13:140:LEU:HB2	1.90	0.54
4:15:76:GLU:HG2	33:R1:636:G:H1	1.72	0.54
6:17:28:LEU:HD23	6:17:48:VAL:HG11	1.90	0.54
13:23:6:ARG:HH22	13:23:37:ASP:HB3	1.71	0.54
17:28:9:LYS:NZ	33:R1:397:U:OP2	2.28	0.54
33:R1:387:U:H4'	33:R1:388:G:H5'	1.90	0.54
33:R1:2899:A:H2'	33:R1:2900:A:C8	2.43	0.54
26:36:30:GLU:OE2	26:36:32:LYS:HB2	2.07	0.54
28:5:7:TYR:HA	28:5:11:VAL:HG23	1.89	0.54
30:9:5:LEU:HD12	30:9:17:ASP:H	1.73	0.54
33:R1:2130:U:H1'	33:R1:2159:G:H22	1.73	0.54
34:R2:48:U:H2'	34:R2:49:C:C6	2.42	0.54
35:R3:745:G:H2'	35:R3:746:A:C8	2.43	0.54
31:E:128:LEU:O	31:E:131:ILE:HG22	2.09	0.53
35:R3:275:G:H5'	52:sq:15:LYS:HG3	1.89	0.53
35:R3:908:A:H2'	35:R3:909:A:C8	2.43	0.53
35:R3:958:A:O2'	35:R3:959:A:O5'	2.21	0.53
35:R3:1087:G:H21	56:su:65:ARG:CD	2.19	0.53
54:ss:5:LYS:HD2	54:ss:6:LYS:HE3	1.89	0.53
2:13:60:ASP:OD1	2:13:60:ASP:N	2.41	0.53
11:21:102:SER:OG	11:21:103:ALA:N	2.40	0.53
33:R1:849:A:H2'	33:R1:850:U:H6	1.74	0.53
33:R1:1178:C:C5	33:R1:1179:G:H1'	2.43	0.53
33:R1:2064:C:H2'	33:R1:2065:C:C6	2.43	0.53
35:R3:617:G:H4'	51:sp:46:LYS:HE3	1.90	0.53
35:R3:1062:U:H2'	35:R3:1063:C:C6	2.44	0.53
35:R3:1513:A:H2'	35:R3:1514:G:C8	2.43	0.53
29:6:90:GLY:HA2	29:6:159:LYS:HZ2	1.73	0.53
33:R1:1410:G:H2'	33:R1:1411:U:C6	2.43	0.53
34:R2:39:A:N1	34:R2:44:G:N1	2.57	0.53
36:T:28:C:H2'	36:T:29:U:H6	1.73	0.53
45:sj:101:SER:OG	45:sj:102:LEU:N	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:24:51:LEU:H	14:24:51:LEU:HD12	1.73	0.53
31:E:326:VAL:HG12	31:E:380:ILE:HG13	1.90	0.53
33:R1:279:A:H61	33:R1:361:G:H1'	1.73	0.53
35:R3:321:A:H2	35:R3:328:C:O2'	1.92	0.53
35:R3:356:A:N3	35:R3:368:U:O2'	2.36	0.53
35:R3:1270:G:O2'	35:R3:1271:A:OP1	2.23	0.53
36:T:25:C:O2'	36:T:26:A:H8	1.91	0.53
33:R1:644:A:H2'	33:R1:645:C:O4'	2.09	0.53
33:R1:1213:A:H62	33:R1:1236:G:H1'	1.72	0.53
33:R1:1645:G:H5''	33:R1:1646:C:H5'	1.90	0.53
33:R1:1794:A:H2'	33:R1:1795:C:C6	2.44	0.53
33:R1:1796:U:H2'	33:R1:1797:G:H8	1.74	0.53
35:R3:613:C:H2'	35:R3:614:C:C6	2.44	0.53
39:sd:149:LYS:HA	39:sd:177:MET:HE1	1.91	0.53
43:sh:9:MET:HG3	43:sh:26:MET:SD	2.49	0.53
46:sk:12:ARG:C	46:sk:13:LYS:HE2	2.34	0.53
9:2:179:GLU:OE2	33:R1:1799:G:O2'	2.16	0.53
16:27:37:ILE:HG22	16:27:38:VAL:HG23	1.90	0.53
27:4:145:ASP:HB3	27:4:184:ASP:HB2	1.90	0.53
33:R1:1542:U:H2'	33:R1:1543:G:O4'	2.08	0.53
33:R1:2023:C:H5'	33:R1:2617:U:H4'	1.90	0.53
33:R1:2115:G:H1'	33:R1:2117:A:H62	1.72	0.53
35:R3:147:G:H2'	35:R3:148:G:C8	2.43	0.53
37:sb:17:HIS:HB3	37:sb:38:HIS:H	1.74	0.53
12:22:65:ASP:OD1	12:22:68:ASP:HB2	2.09	0.53
13:23:9:LYS:O	13:23:12:ARG:NH1	2.42	0.53
29:6:97:VAL:HG22	29:6:102:ILE:HD13	1.91	0.53
31:E:169:ARG:HH22	31:E:189:PRO:HA	1.73	0.53
33:R1:1837:C:O2'	33:R1:1927:A:N3	2.40	0.53
33:R1:2139:U:O2	33:R1:2152:G:O6	2.27	0.53
4:15:108:ALA:HB3	4:15:125:LEU:HD22	1.90	0.53
4:15:109:LYS:HG3	4:15:126:ARG:O	2.09	0.53
10:20:87:VAL:HG22	11:21:49:ILE:HG23	1.90	0.53
27:4:48:THR:HG22	27:4:86:ALA:HB3	1.90	0.53
33:R1:828:U:H2'	33:R1:829:A:C8	2.44	0.53
33:R1:2637:U:H2'	33:R1:2638:G:O4'	2.09	0.53
35:R3:9:G:H4'	40:se:108:GLY:H	1.74	0.53
35:R3:1013:G:C2	35:R3:1015:G:H5''	2.42	0.53
39:sd:10:LEU:HD13	39:sd:62:ARG:HD2	1.89	0.53
5:16:47:GLU:OE2	5:16:51:ARG:NH1	2.41	0.53
9:2:160:TYR:HB3	9:2:193:GLU:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:282:A:N6	33:R1:283:G:O6	2.42	0.53
33:R1:2097:A:H2'	33:R1:2098:U:C6	2.44	0.53
35:R3:106:C:C2'	35:R3:107:G:H5'	2.39	0.53
12:22:23:LEU:HB3	12:22:35:ILE:HD11	1.91	0.53
12:22:83:LYS:HB3	12:22:95:ARG:NE	2.23	0.53
31:E:333:TYR:OH	31:E:373:GLU:OE2	2.26	0.53
33:R1:813:U:H2'	33:R1:814:C:C6	2.44	0.53
33:R1:1889:A:H2'	33:R1:1890:A:C8	2.44	0.53
35:R3:376:G:OP1	35:R3:376:G:H4'	2.09	0.53
35:R3:393:A:C2'	35:R3:394:G:H5'	2.39	0.53
44:si:34:LEU:O	44:si:38:PHE:N	2.42	0.53
8:19:51:ASN:O	33:R1:2845:U:H5''	2.09	0.52
27:4:44:ARG:HH22	33:R1:1248:G:P	2.32	0.52
31:E:85:THR:HA	31:E:159:LYS:HA	1.90	0.52
33:R1:2111:U:H2'	33:R1:2145:C:O2	2.09	0.52
1:1:161:VAL:HG11	1:1:173:THR:HG23	1.91	0.52
9:2:246:PRO:HG2	9:2:247:TRP:CZ3	2.44	0.52
28:5:65:LEU:HD13	34:R2:42:C:C5	2.45	0.52
31:E:337:LEU:HD11	31:E:340:ASP:HB2	1.89	0.52
33:R1:347:A:H2'	33:R1:348:A:C8	2.44	0.52
33:R1:1434:A:H2'	33:R1:1435:G:C8	2.44	0.52
33:R1:1494:A:H2'	33:R1:1495:A:C8	2.45	0.52
35:R3:235:C:H2'	35:R3:236:A:H8	1.73	0.52
35:R3:658:C:H1'	50:so:21:THR:HG21	1.91	0.52
35:R3:859:G:OP2	35:R3:869:G:N1	2.34	0.52
42:sg:25:PHE:HD1	42:sg:100:MET:HG2	1.74	0.52
42:sg:73:GLU:HG3	42:sg:74:VAL:N	2.23	0.52
43:sh:21:LYS:O	43:sh:64:TYR:OH	2.17	0.52
6:17:98:LEU:HD22	22:32:53:VAL:HG21	1.91	0.52
11:21:39:LEU:O	11:21:49:ILE:HB	2.09	0.52
17:28:1:SER:OG	33:R1:1366:A:OP1	2.20	0.52
22:32:3:GLN:NE2	33:R1:2016:U:O2	2.42	0.52
31:E:362:LYS:N	59:E:602:ATP:O1B	2.39	0.52
33:R1:150:U:H3	33:R1:175:G:H1	1.56	0.52
35:R3:78:A:H61	35:R3:80:A:H62	1.56	0.52
35:R3:113:G:N2	35:R3:353:A:H8	2.07	0.52
35:R3:1290:G:OP1	42:sg:34:LYS:NZ	2.43	0.52
36:T:43:G:H2'	36:T:44:G:H8	1.74	0.52
40:se:37:VAL:HG12	40:se:116:VAL:HG21	1.91	0.52
41:sf:22:ILE:O	41:sf:26:THR:OG1	2.23	0.52
44:si:64:ILE:HD12	44:si:78:ILE:HG23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:15:30:THR:HG23	33:R1:810:U:N3	2.19	0.52
12:22:35:ILE:O	12:22:39:THR:HG23	2.09	0.52
31:E:89:SER:O	31:E:175:ARG:NH1	2.35	0.52
33:R1:2137:U:H2'	33:R1:2138:G:C8	2.44	0.52
35:R3:113:G:H21	35:R3:353:A:H8	1.56	0.52
35:R3:612:C:H2'	35:R3:613:C:H6	1.74	0.52
35:R3:939:G:H2'	35:R3:940:C:C6	2.45	0.52
14:24:42:LYS:O	33:R1:480:A:O2'	2.28	0.52
15:25:42:LEU:HD13	15:25:47:VAL:HG21	1.92	0.52
31:E:37:VAL:HG12	31:E:45:LYS:HG2	1.92	0.52
31:E:79:GLN:OE1	31:E:79:GLN:N	2.39	0.52
31:E:299:SER:OG	31:E:300:THR:N	2.43	0.52
33:R1:1213:A:N6	33:R1:1236:G:H1'	2.23	0.52
33:R1:1883:U:H2'	33:R1:1884:G:O4'	2.09	0.52
34:R2:40:U:N3	34:R2:44:G:OP2	2.39	0.52
7:18:88:LYS:HE3	7:18:89:ASP:OD1	2.10	0.52
20:30:23:LEU:HD11	20:30:53:MET:SD	2.49	0.52
33:R1:157:C:C2'	33:R1:158:U:H5'	2.38	0.52
33:R1:1548:A:H2'	33:R1:1549:A:C8	2.44	0.52
33:R1:2116:G:N2	33:R1:2162:G:OP1	2.39	0.52
35:R3:64:G:OP1	35:R3:382:A:N6	2.39	0.52
35:R3:463:U:O2'	35:R3:464:U:O4'	2.25	0.52
41:sf:9:MET:SD	41:sf:86:ARG:HB2	2.49	0.52
4:15:41:ARG:NH2	33:R1:807:U:OP2	2.43	0.52
4:15:85:VAL:HG11	4:15:90:VAL:HG22	1.91	0.52
9:2:75:ALA:HB2	9:2:95:TYR:CD1	2.45	0.52
33:R1:2006:C:O2'	33:R1:2823:A:N3	2.42	0.52
33:R1:2514:U:H2'	33:R1:2515:C:C6	2.44	0.52
33:R1:2899:A:H2'	33:R1:2900:A:H8	1.75	0.52
35:R3:1124:G:O2'	35:R3:1145:A:N6	2.43	0.52
35:R3:1187:G:H2'	35:R3:1188:A:C8	2.45	0.52
37:sb:15:PHE:CD1	37:sb:17:HIS:CE1	2.98	0.52
37:sb:16:GLY:C	37:sb:17:HIS:CG	2.88	0.52
37:sb:96:LEU:N	37:sb:99:MET:HE3	2.21	0.52
49:sn:38:GLU:OE1	49:sn:38:GLU:HA	2.09	0.52
5:16:30:SER:OG	5:16:106:ASP:OD1	2.28	0.52
29:6:12:ALA:O	29:6:14:VAL:N	2.42	0.52
33:R1:287:G:H2'	33:R1:288:U:C6	2.44	0.52
33:R1:1808:A:H3'	33:R1:1809:A:C8	2.45	0.52
33:R1:2051:A:H5'	33:R1:2578:G:O4'	2.10	0.52
35:R3:508:U:H1'	35:R3:509:A:H2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:1226:C:H2'	48:sm:101:THR:HB	1.91	0.52
38:sc:60:ALA:O	38:sc:61:LYS:HD3	2.10	0.52
38:sc:104:GLU:OE1	38:sc:106:ARG:NH2	2.42	0.52
6:17:20:MET:O	6:17:24:MET:HG3	2.09	0.52
7:18:36:TYR:OH	34:R2:28:C:OP1	2.25	0.52
35:R3:1314:C:H2'	35:R3:1315:U:C6	2.45	0.52
35:R3:1516:G:H2'	35:R3:1518:A:OP2	2.09	0.52
16:27:43:THR:H	33:R1:2331:G:H4'	1.75	0.52
33:R1:1028:A:N6	33:R1:1125:G:H2'	2.25	0.52
33:R1:2329:U:H2'	33:R1:2330:G:C8	2.45	0.52
35:R3:611:C:H5'	35:R3:612:C:OP2	2.10	0.52
46:sk:12:ARG:HB2	46:sk:13:LYS:HD3	1.92	0.52
9:2:203:VAL:HG13	33:R1:1792:G:H5'	1.91	0.51
16:27:83:GLU:O	16:27:85:GLU:N	2.44	0.51
33:R1:12:U:O2	33:R1:2626:C:H4'	2.10	0.51
33:R1:882:G:O6	33:R1:894:U:O4	2.27	0.51
33:R1:1441:G:H2'	33:R1:1442:U:C6	2.44	0.51
33:R1:1540:G:H2'	33:R1:1541:C:C6	2.46	0.51
33:R1:2233:U:H2'	33:R1:2234:G:C8	2.45	0.51
35:R3:404:G:O2'	35:R3:498:A:N1	2.35	0.51
35:R3:1228:C:OP1	48:sm:106:ARG:NH2	2.44	0.51
36:T:28:C:H2'	36:T:29:U:C6	2.44	0.51
51:sp:24:SER:O	51:sp:24:SER:OG	2.26	0.51
9:2:12:ARG:HD2	33:R1:728:G:H4'	1.91	0.51
20:30:12:ALA:HA	20:30:15:ARG:HG3	1.92	0.51
33:R1:1108:U:H2'	33:R1:1109:C:N3	2.25	0.51
33:R1:1410:G:H2'	33:R1:1411:U:H6	1.74	0.51
33:R1:1733:G:H2'	33:R1:1734:G:H8	1.75	0.51
33:R1:2700:A:H2'	33:R1:2701:U:H6	1.76	0.51
35:R3:79:G:H2'	35:R3:81:A:C4	2.46	0.51
1:1:8:MET:O	1:1:12:ARG:HG2	2.11	0.51
9:2:32:LEU:HD11	9:2:101:ARG:HA	1.93	0.51
14:24:3:LYS:NZ	33:R1:337:C:OP2	2.40	0.51
33:R1:1386:C:H2'	33:R1:1387:A:H8	1.74	0.51
33:R1:1405:U:H2'	33:R1:1406:U:C6	2.45	0.51
33:R1:1563:U:H2'	33:R1:1564:C:C6	2.45	0.51
33:R1:2011:U:H2'	33:R1:2012:G:O4'	2.10	0.51
35:R3:3:A:N3	35:R3:613:C:O2'	2.43	0.51
2:13:120:ARG:HD3	33:R1:2780:G:OP2	2.11	0.51
29:6:100:ASN:N	29:6:100:ASN:OD1	2.44	0.51
33:R1:514:A:N3	33:R1:581:C:O2'	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:581:C:H2'	33:R1:582:A:C8	2.46	0.51
33:R1:2155:U:H2'	33:R1:2156:G:O4'	2.11	0.51
33:R1:2654:A:N1	33:R1:2665:A:H5''	2.25	0.51
35:R3:6:G:H4'	35:R3:298:A:H4'	1.92	0.51
1:1:16:ASP:O	1:1:21:TYR:OH	2.25	0.51
12:22:73:LYS:HB2	12:22:106:VAL:HB	1.91	0.51
33:R1:1052:C:N4	33:R1:1107:G:O6	2.43	0.51
33:R1:1443:U:H2'	33:R1:1444:G:C8	2.45	0.51
35:R3:210:C:O2'	35:R3:211:G:OP2	2.24	0.51
35:R3:966:G:O2'	44:si:128:LYS:O	2.28	0.51
37:sb:8:MET:O	37:sb:8:MET:HG2	2.09	0.51
8:19:83:ILE:O	8:19:83:ILE:HG22	2.11	0.51
29:6:165:ASP:OD1	29:6:165:ASP:N	2.37	0.51
33:R1:2025:C:H2'	33:R1:2026:U:C6	2.45	0.51
35:R3:580:C:H2'	35:R3:581:G:O4'	2.11	0.51
35:R3:587:G:H22	35:R3:754:C:P	2.33	0.51
35:R3:1318:A:H1'	54:ss:36:ARG:NH1	2.26	0.51
56:su:23:GLU:O	56:su:25:ALA:N	2.44	0.51
1:1:46:VAL:HG23	1:1:212:VAL:HG22	1.92	0.51
13:23:8:LEU:HD22	18:29:22:LEU:HA	1.92	0.51
24:34:39:ARG:NH2	33:R1:468:G:N7	2.56	0.51
35:R3:375:U:H2'	35:R3:376:G:O4'	2.10	0.51
47:sl:45:ASN:ND2	47:sl:88:ASP:OD2	2.44	0.51
50:so:73:ASP:OD1	50:so:73:ASP:N	2.43	0.51
33:R1:1209:U:O2'	33:R1:1237:A:N1	2.37	0.51
33:R1:2086:U:H2'	33:R1:2087:G:C8	2.46	0.51
33:R1:2328:A:H2'	33:R1:2329:U:H6	1.75	0.51
35:R3:463:U:H2'	35:R3:464:U:C6	2.46	0.51
35:R3:867:G:O2'	35:R3:873:A:N1	2.35	0.51
37:sb:77:GLU:OE1	37:sb:77:GLU:N	2.35	0.51
37:sb:172:ILE:HG12	37:sb:182:VAL:HG11	1.93	0.51
42:sg:13:PRO:HA	42:sg:20:GLU:HG3	1.92	0.51
53:sr:46:THR:OG1	53:sr:51:GLN:OE1	2.29	0.51
33:R1:1:G:H2'	33:R1:2:G:H8	1.74	0.51
33:R1:2123:G:H2'	33:R1:2124:G:C4	2.46	0.51
33:R1:2273:A:H2'	33:R1:2274:A:C8	2.45	0.51
35:R3:321:A:C2'	35:R3:322:C:H5'	2.41	0.51
37:sb:58:LYS:O	37:sb:61:SER:OG	2.28	0.51
38:sc:122:GLN:OE1	38:sc:125:ARG:NH2	2.44	0.51
27:4:170:ARG:NH2	27:4:176:ASP:OD2	2.44	0.51
33:R1:1179:G:H5''	33:R1:1180:U:C6	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:2178:C:H2'	33:R1:2179:C:C6	2.45	0.51
33:R1:2788:C:H2'	33:R1:2789:C:C6	2.46	0.51
34:R2:7:G:H1	34:R2:113:C:H41	1.58	0.51
35:R3:223:A:H2'	35:R3:224:U:C6	2.45	0.51
35:R3:256:U:H3	35:R3:270:A:N6	2.08	0.51
35:R3:460:A:H2'	35:R3:461:A:C8	2.46	0.51
35:R3:908:A:H2'	35:R3:909:A:H8	1.76	0.51
35:R3:923:A:OP1	40:se:25:LYS:HE2	2.11	0.51
49:sn:89:ARG:NH1	49:sn:91:GLU:OE2	2.35	0.51
1:1:50:ILE:HB	1:1:57:GLN:HB3	1.93	0.50
31:E:399:ASP:N	31:E:407:GLU:OE2	2.42	0.50
33:R1:177:G:H3'	33:R1:178:G:H8	1.76	0.50
33:R1:580:U:H2'	33:R1:581:C:C6	2.45	0.50
33:R1:632:A:H2'	33:R1:633:A:C8	2.46	0.50
33:R1:1000:A:H2'	33:R1:1001:A:C8	2.47	0.50
33:R1:2661:G:O2'	33:R1:2662:A:O5'	2.29	0.50
35:R3:560:A:H5''	35:R3:561:U:H3'	1.94	0.50
35:R3:723:U:H2'	35:R3:855:U:H4'	1.93	0.50
4:15:57:LEU:HD22	25:35:53:ASP:HB3	1.94	0.50
4:15:79:LEU:HD13	4:15:116:VAL:HG12	1.93	0.50
11:21:43:ASN:OD1	11:21:44:GLY:N	2.43	0.50
11:21:49:ILE:HG13	11:21:53:PHE:N	2.25	0.50
19:3:149:ASN:HB3	33:R1:2572:A:OP2	2.11	0.50
28:5:131:VAL:HG23	28:5:133:GLU:H	1.76	0.50
31:E:13:LYS:HD2	31:E:59:ILE:HG22	1.93	0.50
33:R1:241:A:N1	33:R1:255:A:H5''	2.27	0.50
33:R1:859:G:H4'	33:R1:860:U:O5'	2.11	0.50
33:R1:1531:C:H2'	33:R1:1532:A:C8	2.47	0.50
33:R1:2101:A:H2'	33:R1:2102:G:H8	1.77	0.50
33:R1:2639:A:N6	33:R1:2775:G:O2'	2.44	0.50
35:R3:239:U:H5''	35:R3:240:G:OP2	2.10	0.50
35:R3:337:G:H2'	35:R3:338:A:C8	2.47	0.50
35:R3:462:G:N2	35:R3:471:U:O2	2.43	0.50
35:R3:862:C:H2'	35:R3:863:U:H5'	1.93	0.50
35:R3:875:U:O2'	43:sh:14:ARG:NH1	2.35	0.50
35:R3:928:G:H22	35:R3:1389:C:H5	1.60	0.50
35:R3:1142:G:C8	35:R3:1143:G:C8	2.99	0.50
36:T:33:U:H5	36:T:36:C:OP2	1.94	0.50
38:sc:109:GLU:HB2	38:sc:143:LEU:HD12	1.91	0.50
45:sj:19:ASP:HA	45:sj:22:THR:HG22	1.94	0.50
28:5:1:ALA:HB3	28:5:4:HIS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:330:ARG:NH1	31:E:340:ASP:OD2	2.44	0.50
33:R1:368:A:H2'	33:R1:369:U:H1'	1.93	0.50
33:R1:848:C:H2'	33:R1:849:A:C8	2.42	0.50
35:R3:519:C:H2'	35:R3:520:A:O4'	2.12	0.50
36:T:51:C:H2'	36:T:52:G:C2	2.46	0.50
51:sp:6:LEU:HB3	51:sp:17:TYR:HB3	1.93	0.50
54:ss:50:VAL:HG11	54:ss:70:LEU:HB3	1.92	0.50
1:1:51:ASP:N	1:1:57:GLN:OE1	2.38	0.50
7:18:35:ILE:HG23	7:18:74:VAL:HG11	1.94	0.50
33:R1:833:A:H2'	33:R1:834:G:C8	2.45	0.50
33:R1:1020:A:N1	33:R1:1141:U:O2'	2.33	0.50
35:R3:438:U:O2'	35:R3:439:U:O5'	2.23	0.50
35:R3:1132:C:H2'	35:R3:1133:G:C8	2.47	0.50
43:sh:85:TYR:CE1	43:sh:123:GLU:HG3	2.46	0.50
19:3:58:ASN:OD1	19:3:59:ARG:N	2.45	0.50
21:31:22:MET:N	21:31:22:MET:SD	2.84	0.50
31:E:218:ASP:OD1	31:E:221:PHE:HB3	2.11	0.50
33:R1:84:A:N7	33:R1:101:A:H2	2.09	0.50
33:R1:191:A:H2'	33:R1:192:C:C6	2.47	0.50
33:R1:195:A:N6	33:R1:198:C:H3'	2.25	0.50
33:R1:1790:C:H2'	33:R1:1791:A:C5	2.47	0.50
33:R1:2126:A:C2	33:R1:2127:G:H1'	2.47	0.50
35:R3:59:A:H5''	35:R3:387:U:H5''	1.92	0.50
35:R3:131:A:N1	35:R3:231:U:H5	2.10	0.50
35:R3:662:U:H2'	35:R3:663:A:C8	2.46	0.50
35:R3:714:G:H2'	35:R3:715:A:C8	2.46	0.50
35:R3:753:A:H4'	35:R3:754:C:O5'	2.11	0.50
43:sh:26:MET:HE3	43:sh:60:LEU:HD13	1.94	0.50
9:2:224:MET:HG2	33:R1:782:A:C2	2.47	0.50
11:21:80:ARG:NH1	33:R1:572:A:OP2	2.26	0.50
22:32:24:VAL:O	22:32:25:THR:HG22	2.11	0.50
29:6:104:LEU:HB3	29:6:106:LEU:HD13	1.93	0.50
33:R1:357:C:H2'	33:R1:358:U:C2	2.47	0.50
33:R1:1847:G:N2	33:R1:1848:A:H62	2.10	0.50
42:sg:15:PRO:HG3	44:si:45:MET:HE3	1.94	0.50
45:sj:40:ILE:HG22	45:sj:42:LEU:HD23	1.94	0.50
50:so:68:TYR:CE1	50:so:72:LYS:HE3	2.46	0.50
31:E:234:ARG:NH1	31:E:302:TYR:O	2.45	0.50
33:R1:851:C:H2'	33:R1:852:U:C6	2.47	0.50
33:R1:2847:U:H2'	33:R1:2848:G:O4'	2.11	0.50
36:T:68:C:O2'	36:T:69:A:H8	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sr:17:VAL:HG13	53:sr:50:TYR:OH	2.12	0.50
7:18:63:LYS:HE3	34:R2:51:G:OP1	2.12	0.50
9:2:120:ASP:OD1	9:2:120:ASP:N	2.39	0.50
14:24:87:GLU:O	14:24:87:GLU:OE1	2.30	0.50
21:31:65:ASN:C	21:31:65:ASN:ND2	2.70	0.50
27:4:136:GLN:OE1	27:4:136:GLN:HA	2.11	0.50
31:E:69:ILE:HG13	31:E:69:ILE:O	2.12	0.50
33:R1:879:G:H22	33:R1:898:C:H42	1.59	0.50
35:R3:1393:U:O2'	35:R3:1501:C:O2'	2.27	0.50
36:T:63:G:C2	36:T:64:U:H1'	2.47	0.50
36:T:66:A:H2'	36:T:67:U:C6	2.47	0.50
52:sq:3:LYS:NZ	52:sq:4:ILE:H	2.10	0.50
56:su:32:ARG:HH12	56:su:33:ARG:CZ	2.25	0.50
2:13:45:THR:HB	2:13:48:VAL:HG13	1.92	0.50
19:3:101:PHE:HA	19:3:104:VAL:HG13	1.94	0.50
29:6:100:ASN:ND2	29:6:115:GLN:OE1	2.44	0.50
33:R1:99:U:H5''	33:R1:100:U:H5'	1.93	0.50
33:R1:1292:G:H2'	33:R1:1293:C:C6	2.47	0.50
33:R1:1496:A:H2'	33:R1:1498:C:C5	2.46	0.50
33:R1:2901:C:H2'	33:R1:2902:C:C6	2.46	0.50
35:R3:696:A:H2'	35:R3:697:U:C6	2.47	0.50
40:se:18:ASN:OD1	40:se:33:THR:OG1	2.29	0.50
53:sr:40:PRO:HG2	53:sr:43:ILE:HD12	1.92	0.50
54:ss:48:ILE:HD11	54:ss:70:LEU:HD13	1.94	0.50
5:16:63:ILE:HG12	5:16:105:MET:HG3	1.94	0.49
10:20:104:ALA:HA	11:21:46:GLU:HG3	1.94	0.49
28:5:110:ILE:HB	28:5:113:PHE:HB2	1.93	0.49
33:R1:1236:G:O2'	33:R1:1237:A:O5'	2.29	0.49
33:R1:1484:U:H2'	33:R1:1485:U:H6	1.77	0.49
33:R1:2230:G:H2'	33:R1:2231:U:C6	2.46	0.49
35:R3:363:A:H2'	35:R3:364:A:C8	2.47	0.49
35:R3:520:A:O2'	47:sl:69:GLU:OE1	2.24	0.49
54:ss:18:VAL:HG21	54:ss:43:MET:SD	2.52	0.49
1:1:27:ILE:HD12	1:1:30:LEU:HD22	1.93	0.49
16:27:77:ARG:NH1	33:R1:2333:A:OP1	2.25	0.49
33:R1:1219:U:H2'	33:R1:1220:G:C8	2.48	0.49
35:R3:181:A:H61	35:R3:194:C:H2'	1.77	0.49
46:sk:44:ALA:HB3	46:sk:69:CYS:HB2	1.94	0.49
27:4:188:MET:HE2	27:4:193:VAL:HG22	1.93	0.49
33:R1:849:A:H2'	33:R1:850:U:C6	2.47	0.49
33:R1:1198:U:H2'	33:R1:1199:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:142:G:O2'	35:R3:196:A:N1	2.37	0.49
35:R3:200:G:H2'	35:R3:201:G:H8	1.78	0.49
35:R3:216:U:H2'	35:R3:217:C:H6	1.77	0.49
35:R3:344:A:H5''	35:R3:345:C:H5	1.77	0.49
35:R3:718:A:H2	53:sr:37:LYS:HD2	1.78	0.49
35:R3:738:C:O2'	35:R3:739:C:H6	1.95	0.49
43:sh:28:SER:HB3	43:sh:56:PRO:HB2	1.92	0.49
28:5:35:LEU:HB3	28:5:56:LEU:HD21	1.95	0.49
31:E:399:ASP:OD2	31:E:402:LYS:NZ	2.46	0.49
31:E:468:LEU:HB3	31:E:471:PRO:HG3	1.93	0.49
33:R1:1183:U:H2'	33:R1:1184:U:C6	2.46	0.49
33:R1:1447:C:O2'	33:R1:1544:A:N3	2.39	0.49
33:R1:2176:A:H2'	33:R1:2177:C:C5	2.47	0.49
35:R3:516:U:O2'	35:R3:519:C:H5	1.96	0.49
35:R3:890:G:O2'	35:R3:906:A:N6	2.45	0.49
1:1:21:TYR:HE2	1:1:29:LEU:HD22	1.76	0.49
5:16:49:ALA:HB1	5:16:120:ALA:HB1	1.93	0.49
20:30:11:SER:OG	20:30:12:ALA:N	2.46	0.49
33:R1:52:A:H2'	33:R1:53:A:C8	2.48	0.49
33:R1:1171:G:O6	33:R1:1176:U:C4	2.66	0.49
34:R2:34:A:C6	34:R2:44:G:C8	3.01	0.49
34:R2:39:A:C6	34:R2:44:G:N1	2.79	0.49
35:R3:74:A:H2'	35:R3:75:G:O4'	2.11	0.49
48:sm:43:LYS:HB2	48:sm:46:GLU:OE1	2.12	0.49
49:sn:36:SER:HB2	49:sn:40:ARG:NE	2.24	0.49
4:15:21:ARG:HA	33:R1:811:U:H2'	1.94	0.49
10:20:8:ILE:HG13	10:20:9:ALA:N	2.28	0.49
13:23:48:GLN:HG3	13:23:55:VAL:HG23	1.93	0.49
33:R1:1814:G:OP2	33:R1:1815:A:O2'	2.21	0.49
35:R3:642:A:C5	43:sh:106:SER:HA	2.47	0.49
35:R3:672:U:H2'	35:R3:673:A:H8	1.76	0.49
35:R3:1306:A:OP2	35:R3:1306:A:H8	1.94	0.49
35:R3:1410:A:H2'	35:R3:1411:C:C6	2.47	0.49
44:si:32:ARG:HB2	44:si:36:GLN:HG3	1.94	0.49
47:sl:31:GLY:HA3	47:sl:54:VAL:HG12	1.95	0.49
9:2:99:GLU:OE2	9:2:101:ARG:NE	2.46	0.49
9:2:149:LYS:HD3	33:R1:2204:G:H4'	1.94	0.49
11:21:48:LYS:HD3	11:21:49:ILE:H	1.77	0.49
17:28:37:PHE:HZ	17:28:55:MET:HG2	1.78	0.49
19:3:39:ASP:OD1	19:3:39:ASP:N	2.37	0.49
26:36:25:VAL:HB	26:36:35:GLN:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:305:C:H2'	33:R1:306:U:C6	2.48	0.49
33:R1:2291:U:OP1	33:R1:2380:C:O2'	2.29	0.49
33:R1:2439:A:N6	33:R1:2585:U:O2'	2.46	0.49
33:R1:2689:U:OP1	33:R1:2719:G:N1	2.34	0.49
35:R3:1120:C:H2'	35:R3:1121:U:C6	2.47	0.49
35:R3:1439:G:HO2'	35:R3:1440:U:H6	1.58	0.49
39:sd:58:GLN:O	39:sd:62:ARG:HG2	2.13	0.49
52:sq:30:HIS:H	52:sq:35:LYS:H	1.61	0.49
5:16:79:ALA:HA	33:R1:2494:G:O2'	2.12	0.49
9:2:170:TYR:HB3	9:2:182:LYS:HD2	1.93	0.49
15:25:26:PHE:HE2	15:25:89:ILE:HG13	1.77	0.49
33:R1:813:U:H2'	33:R1:814:C:H6	1.77	0.49
33:R1:878:A:H3'	33:R1:879:G:C8	2.47	0.49
33:R1:1536:C:H4'	33:R1:1537:G:C4	2.47	0.49
33:R1:2146:C:O2'	33:R1:2147:A:O5'	2.27	0.49
33:R1:2168:G:N3	33:R1:2168:G:H2'	2.28	0.49
33:R1:2700:A:H2'	33:R1:2701:U:C6	2.47	0.49
35:R3:211:G:O2'	35:R3:212:G:OP2	2.30	0.49
35:R3:403:C:OP1	39:sd:131:ILE:HG23	2.12	0.49
35:R3:779:C:H2'	35:R3:780:A:O4'	2.13	0.49
35:R3:1037:C:H2'	35:R3:1038:C:C5	2.47	0.49
37:sb:103:TRP:CH2	37:sb:155:GLY:HA2	2.47	0.49
52:sq:58:VAL:HG12	52:sq:77:VAL:HG22	1.94	0.49
2:13:110:PRO:O	2:13:115:GLY:HA3	2.13	0.49
3:14:73:ASP:OD1	3:14:75:SER:OG	2.31	0.49
15:25:51:GLN:OE1	15:25:57:TYR:OH	2.31	0.49
35:R3:232:G:H21	35:R3:263:A:H8	1.60	0.49
35:R3:324:G:N1	35:R3:327:A:OP2	2.42	0.49
35:R3:470:C:O2'	35:R3:471:U:H5''	2.13	0.49
35:R3:1391:U:H2'	35:R3:1392:G:C8	2.48	0.49
37:sb:19:THR:OG1	37:sb:20:ARG:N	2.46	0.49
48:sm:58:GLU:HA	48:sm:61:LYS:HE2	1.94	0.49
2:13:95:ARG:NH2	33:R1:2640:G:OP1	2.46	0.49
19:3:11:MET:HE2	33:R1:2682:A:C8	2.48	0.49
22:32:2:VAL:HG11	33:R1:2016:U:H1'	1.95	0.49
28:5:32:LYS:HG3	28:5:156:THR:HB	1.94	0.49
31:E:221:PHE:O	31:E:225:VAL:HG22	2.13	0.49
33:R1:832:U:H2'	33:R1:833:A:C8	2.48	0.49
33:R1:1857:G:H22	33:R1:1884:G:H2'	1.78	0.49
33:R1:2064:C:H2'	33:R1:2065:C:H6	1.77	0.49
33:R1:2846:G:H2'	33:R1:2847:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:2898:U:H2'	33:R1:2899:A:H8	1.78	0.49
35:R3:470:C:HO2'	35:R3:471:U:H6	1.60	0.49
35:R3:558:G:OP2	35:R3:559:A:O2'	2.30	0.49
35:R3:1012:A:C6	35:R3:1013:G:C6	3.01	0.49
41:sf:3:HIS:NE2	41:sf:65:GLU:OE1	2.46	0.49
41:sf:36:ILE:HD13	41:sf:64:VAL:HG23	1.93	0.49
45:sj:12:ALA:HB3	45:sj:18:ILE:HB	1.95	0.49
6:17:106:ASP:OD1	6:17:106:ASP:N	2.44	0.48
33:R1:274:C:H5	33:R1:363:G:H22	1.61	0.48
33:R1:980:A:N7	33:R1:1136:G:H5'	2.27	0.48
33:R1:1048:A:N6	33:R1:1111:A:H1'	2.28	0.48
33:R1:1416:G:H2'	33:R1:1417:C:C6	2.48	0.48
33:R1:1746:A:H2'	33:R1:1747:U:C6	2.48	0.48
33:R1:1891:G:HO2'	33:R1:2235:G:HO2'	1.58	0.48
35:R3:634:C:H2'	35:R3:635:A:H8	1.77	0.48
35:R3:1187:G:OP1	44:si:114:LYS:HD3	2.13	0.48
37:sb:26:MET:HA	37:sb:26:MET:HE3	1.95	0.48
38:sc:39:ARG:HH11	49:sn:91:GLU:HG3	1.77	0.48
3:14:32:TYR:OH	33:R1:2726:A:H5'	2.12	0.48
7:18:31:THR:O	7:18:102:ARG:NH2	2.38	0.48
7:18:39:VAL:N	7:18:49:VAL:O	2.32	0.48
9:2:224:MET:SD	9:2:229:HIS:HB2	2.53	0.48
29:6:157:LYS:HB2	29:6:159:LYS:HG3	1.94	0.48
33:R1:412:A:C2'	33:R1:413:C:H5'	2.43	0.48
35:R3:836:G:H1	35:R3:850:U:H5	1.61	0.48
39:sd:171:GLU:HG2	39:sd:182:LYS:HD3	1.93	0.48
26:36:30:GLU:HG3	26:36:32:LYS:H	1.78	0.48
33:R1:1074:G:N1	33:R1:1075:C:H1'	2.29	0.48
33:R1:1469:A:H2'	33:R1:1470:A:C8	2.48	0.48
33:R1:2174:C:O2'	33:R1:2175:C:OP1	2.28	0.48
33:R1:2191:A:H2'	33:R1:2192:U:C6	2.48	0.48
35:R3:974:A:OP1	49:sn:68:ARG:NH1	2.41	0.48
35:R3:1048:G:O2'	35:R3:1050:G:OP1	2.32	0.48
36:T:65:C:H2'	36:T:66:A:H8	1.78	0.48
38:sc:130:ARG:O	38:sc:134:LYS:HG2	2.14	0.48
33:R1:1152:C:H2'	33:R1:1153:C:H6	1.78	0.48
33:R1:1534:U:O2'	33:R1:1537:G:O6	2.30	0.48
33:R1:1636:U:H2'	33:R1:1637:A:C8	2.48	0.48
33:R1:2116:G:H22	33:R1:2162:G:P	2.36	0.48
33:R1:2458:G:O2'	33:R1:2460:U:O4	2.31	0.48
33:R1:2783:U:H2'	33:R1:2784:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:20:U:H2'	35:R3:21:G:O4'	2.13	0.48
35:R3:396:C:H5'	35:R3:397:A:OP2	2.13	0.48
35:R3:674:G:H2'	35:R3:675:A:H8	1.78	0.48
39:sd:159:GLU:O	39:sd:163:GLN:NE2	2.46	0.48
40:se:80:LEU:HG	40:se:146:MET:SD	2.53	0.48
40:se:148:SER:OG	40:se:150:GLU:OE1	2.31	0.48
51:sp:18:GLN:HG2	51:sp:35:ARG:HE	1.79	0.48
5:16:18:ARG:HG2	34:R2:90:C:H5'	1.95	0.48
9:2:44:ASN:N	33:R1:1812:U:O2'	2.41	0.48
19:3:25:THR:HG21	19:3:193:VAL:HG22	1.95	0.48
21:31:11:GLU:N	21:31:25:ARG:HE	2.11	0.48
31:E:329:LEU:HD23	31:E:342:LEU:HD23	1.96	0.48
33:R1:645:C:H2'	33:R1:647:G:C8	2.48	0.48
33:R1:1796:U:H2'	33:R1:1797:G:C8	2.48	0.48
33:R1:2590:A:H2'	33:R1:2591:C:H6	1.78	0.48
35:R3:73:C:H2'	35:R3:74:A:C8	2.48	0.48
35:R3:499:A:H61	35:R3:547:A:H5''	1.78	0.48
35:R3:736:C:H2'	35:R3:737:C:H6	1.78	0.48
35:R3:737:C:C2'	35:R3:738:C:H5'	2.43	0.48
35:R3:950:U:H2'	35:R3:951:G:C8	2.48	0.48
35:R3:1388:C:H2'	35:R3:1389:C:O2	2.13	0.48
48:sm:14:ALA:HB3	48:sm:33:LEU:HD21	1.94	0.48
49:sn:32:ASP:OD2	49:sn:34:ASN:N	2.46	0.48
2:13:41:LYS:NZ	2:13:50:THR:O	2.35	0.48
6:17:1:MET:O	6:17:2:ARG:HG3	2.13	0.48
7:18:102:ARG:HG3	34:R2:49:C:OP1	2.13	0.48
9:2:10:PRO:O	33:R1:729:G:N2	2.47	0.48
16:27:25:ARG:NH2	33:R1:2355:G:OP1	2.40	0.48
25:35:56:LEU:HD11	33:R1:834:G:H5'	1.96	0.48
27:4:117:ARG:NH2	27:4:183:PHE:O	2.45	0.48
31:E:476:ASP:O	31:E:480:LEU:HB2	2.13	0.48
33:R1:499:U:H2'	33:R1:500:G:O4'	2.13	0.48
33:R1:2014:A:H2'	33:R1:2015:A:C8	2.48	0.48
35:R3:415:A:C4	35:R3:416:G:C8	3.01	0.48
35:R3:863:U:O2'	35:R3:865:A:OP2	2.28	0.48
37:sb:42:LEU:HA	37:sb:45:THR:HB	1.95	0.48
47:sl:86:VAL:HG23	47:sl:87:LYS:N	2.29	0.48
54:ss:61:VAL:HA	54:ss:65:MET:SD	2.53	0.48
9:2:139:THR:HG23	9:2:160:TYR:HB2	1.94	0.48
15:25:80:HIS:ND1	15:25:83:LYS:HB2	2.28	0.48
33:R1:1056:G:H4'	33:R1:1057:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1433:A:H2'	33:R1:1434:A:O4'	2.14	0.48
33:R1:1484:U:H2'	33:R1:1485:U:C6	2.48	0.48
33:R1:2246:G:H2'	33:R1:2247:A:C8	2.48	0.48
33:R1:2315:G:O2'	33:R1:2316:G:H8	1.97	0.48
33:R1:2803:G:H2'	33:R1:2804:U:H6	1.78	0.48
35:R3:195:A:H2'	35:R3:196:A:C8	2.49	0.48
35:R3:266:G:N2	35:R3:269:C:OP2	2.46	0.48
35:R3:676:A:H5''	46:sk:114:PRO:HB3	1.94	0.48
35:R3:1130:A:O2'	35:R3:1131:G:O5'	2.31	0.48
35:R3:1317:C:OP1	49:sn:54:SER:HB3	2.13	0.48
37:sb:16:GLY:O	37:sb:17:HIS:ND1	2.47	0.48
38:sc:71:ARG:HB3	38:sc:71:ARG:HH11	1.78	0.48
40:se:81:GLN:HG2	40:se:146:MET:HE3	1.94	0.48
41:sf:38:ARG:HB2	41:sf:63:ASN:HB3	1.95	0.48
45:sj:23:ALA:HA	45:sj:26:VAL:HG12	1.94	0.48
47:sl:48:LEU:HD12	47:sl:48:LEU:HA	1.71	0.48
53:sr:71:ASP:OD2	56:su:4:LYS:HE2	2.13	0.48
54:ss:9:PHE:HE2	54:ss:36:ARG:HD2	1.78	0.48
6:17:48:VAL:HA	6:17:51:LEU:HD12	1.96	0.48
15:25:51:GLN:OE1	15:25:79:ARG:NH2	2.47	0.48
29:6:26:LYS:HD3	29:6:31:GLU:HB2	1.96	0.48
33:R1:740:C:H5'	33:R1:1784:A:H3'	1.95	0.48
33:R1:1070:A:N6	33:R1:1096:A:N3	2.61	0.48
33:R1:2099:U:O4	33:R1:2190:G:O6	2.30	0.48
35:R3:862:C:N4	35:R3:863:U:O4	2.46	0.48
35:R3:1187:G:H5'	44:si:114:LYS:HZ2	1.79	0.48
36:T:42:G:H3'	36:T:43:G:H5''	1.94	0.48
42:sg:11:ILE:HG23	42:sg:20:GLU:HG2	1.95	0.48
48:sm:65:GLU:O	48:sm:69:ARG:HG3	2.14	0.48
17:28:28:PHE:HB3	33:R1:396:G:H1'	1.96	0.48
18:29:20:ASN:HB3	18:29:50:VAL:HG22	1.95	0.48
23:33:22:THR:OG1	23:33:23:THR:N	2.47	0.48
27:4:176:ASP:OD2	27:4:179:SER:OG	2.30	0.48
28:5:10:GLU:HG3	28:5:11:VAL:N	2.28	0.48
33:R1:81:G:O2'	33:R1:295:G:O2'	2.29	0.48
33:R1:500:G:H2'	33:R1:502:A:H2	1.78	0.48
33:R1:979:A:H5'	33:R1:980:A:H5''	1.96	0.48
33:R1:1278:C:H2'	33:R1:1279:G:H8	1.79	0.48
33:R1:2331:G:O2'	33:R1:2336:A:N1	2.45	0.48
33:R1:2898:U:H2'	33:R1:2899:A:C8	2.48	0.48
35:R3:559:A:H4'	35:R3:560:A:H3'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:632:U:H5''	35:R3:633:G:C8	2.49	0.48
35:R3:862:C:C2'	35:R3:863:U:H5'	2.44	0.48
35:R3:1270:G:H2'	35:R3:1271:A:H8	1.79	0.48
37:sb:33:ALA:N	37:sb:37:VAL:O	2.46	0.48
39:sd:7:LYS:HB3	39:sd:20:LEU:HB3	1.96	0.48
44:si:113:LYS:HE2	44:si:118:ARG:O	2.13	0.48
3:14:70:ARG:HG2	3:14:70:ARG:HH11	1.78	0.48
7:18:11:ALA:O	7:18:15:ARG:HB2	2.14	0.48
9:2:99:GLU:OE1	33:R1:1491:G:O2'	2.29	0.48
33:R1:1327:A:H2'	33:R1:1328:A:O4'	2.14	0.48
33:R1:1361:G:H2'	33:R1:1362:C:C6	2.48	0.48
10:20:50:ARG:HH22	33:R1:993:G:P	2.37	0.47
13:23:11:LEU:HD22	13:23:32:LEU:HD13	1.96	0.47
19:3:22:ILE:HG23	19:3:190:LYS:HG3	1.95	0.47
30:9:11:ASN:HD22	33:R1:2095:A:H5'	1.78	0.47
31:E:74:LEU:HB2	31:E:176:LEU:HD22	1.95	0.47
31:E:432:ASN:HB3	31:E:452:ARG:NH1	2.29	0.47
33:R1:5:A:H2'	33:R1:6:A:C8	2.49	0.47
33:R1:143:C:H3'	33:R1:144:A:H8	1.79	0.47
33:R1:228:C:N4	33:R1:2407:A:N3	2.61	0.47
33:R1:248:G:H5'	33:R1:250:G:N7	2.29	0.47
33:R1:1394:U:H2'	33:R1:1395:A:O4'	2.14	0.47
33:R1:1416:G:H2'	33:R1:1417:C:H6	1.79	0.47
33:R1:1884:G:H8	33:R1:1884:G:OP2	1.97	0.47
35:R3:49:U:O4	35:R3:365:U:H5	1.97	0.47
35:R3:635:A:H2'	35:R3:636:U:C6	2.49	0.47
35:R3:643:C:H4'	43:sh:31:LEU:HD11	1.95	0.47
35:R3:723:U:O5'	56:su:48:LYS:HD2	2.14	0.47
35:R3:737:C:O2'	35:R3:738:C:H5'	2.13	0.47
35:R3:1102:A:O2'	35:R3:1103:C:H5'	2.14	0.47
47:sl:113:ARG:HB3	47:sl:118:VAL:HB	1.96	0.47
8:19:1:SER:O	8:19:5:LYS:HG3	2.15	0.47
30:9:6:LEU:O	30:9:15:LEU:HG	2.14	0.47
31:E:64:ARG:NH2	33:R1:1859:U:O2'	2.47	0.47
33:R1:1064:C:H4'	33:R1:1065:U:OP2	2.13	0.47
33:R1:2156:G:OP2	33:R1:2157:G:N1	2.47	0.47
34:R2:34:A:C5	34:R2:44:G:C8	3.02	0.47
35:R3:1124:G:O4'	45:sj:40:ILE:HD11	2.14	0.47
12:22:46:LEU:O	12:22:50:VAL:HG12	2.14	0.47
17:28:30:PRO:HB2	17:28:32:LEU:HD13	1.96	0.47
19:3:11:MET:HB2	19:3:24:VAL:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:3:98:VAL:C	19:3:100:LEU:H	2.22	0.47
28:5:55:ASP:OD1	28:5:149:ARG:NH2	2.42	0.47
29:6:16:VAL:HG22	29:6:25:ILE:HG13	1.96	0.47
30:9:5:LEU:HD21	30:9:19:VAL:HG21	1.95	0.47
31:E:86:VAL:HB	31:E:156:TRP:HA	1.96	0.47
33:R1:1589:U:H2'	33:R1:1590:A:H8	1.79	0.47
33:R1:1721:G:H22	33:R1:1738:G:HO2'	1.52	0.47
33:R1:1727:C:H2'	33:R1:1728:C:H6	1.79	0.47
33:R1:1754:A:N1	33:R1:2716:C:O2'	2.42	0.47
35:R3:73:C:H2'	35:R3:74:A:H8	1.78	0.47
35:R3:1063:C:OP2	35:R3:1064:G:O2'	2.20	0.47
35:R3:1088:G:H2'	35:R3:1089:G:O4'	2.15	0.47
35:R3:1235:U:H2'	35:R3:1236:A:O4'	2.14	0.47
35:R3:1315:U:H2'	35:R3:1316:G:O4'	2.14	0.47
37:sb:17:HIS:C	37:sb:19:THR:H	2.22	0.47
51:sp:46:LYS:HG2	51:sp:47:GLU:OE2	2.15	0.47
55:st:61:ALA:HA	55:st:66:ILE:O	2.15	0.47
15:25:9:ARG:NH2	34:R2:76:G:OP1	2.46	0.47
27:4:5:LEU:HD21	27:4:12:LEU:HD13	1.96	0.47
33:R1:570:G:H2'	33:R1:2030:A:N7	2.29	0.47
33:R1:1152:C:H2'	33:R1:1153:C:C6	2.48	0.47
33:R1:2071:A:H2'	33:R1:2072:C:C6	2.49	0.47
33:R1:2304:G:H22	33:R1:2312:U:H3	1.62	0.47
33:R1:2391:G:O6	33:R1:2425:A:H8	1.97	0.47
33:R1:2502:G:H5''	33:R1:2503:A:H5''	1.97	0.47
33:R1:2809:A:H2'	33:R1:2810:A:C8	2.50	0.47
35:R3:439:U:O2	35:R3:439:U:H2'	2.14	0.47
39:sd:201:GLU:CD	40:se:104:ILE:H	2.21	0.47
42:sg:111:GLY:HA2	42:sg:118:ARG:HE	1.79	0.47
46:sk:63:GLN:O	46:sk:67:GLU:HG3	2.14	0.47
5:16:71:LYS:HB3	5:16:93:VAL:O	2.14	0.47
33:R1:603:A:N1	33:R1:625:G:O2'	2.40	0.47
33:R1:897:C:H2'	33:R1:898:C:H5	1.80	0.47
33:R1:2124:G:H21	33:R1:2174:C:H41	1.61	0.47
33:R1:2155:U:H3'	33:R1:2156:G:H8	1.79	0.47
33:R1:2233:U:H2'	33:R1:2234:G:H8	1.80	0.47
35:R3:57:G:N1	35:R3:355:C:H5	2.11	0.47
35:R3:332:G:O2'	35:R3:333:U:O5'	2.32	0.47
35:R3:715:A:H2'	35:R3:716:A:C8	2.50	0.47
35:R3:961:U:OP2	35:R3:1223:C:O2'	2.23	0.47
35:R3:1162:C:H2'	35:R3:1163:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:69:THR:HG23	1:1:71:ARG:H	1.80	0.47
18:29:55:THR:HG21	33:R1:76:C:O2'	2.15	0.47
21:31:3:LYS:HD3	21:31:3:LYS:HA	1.80	0.47
31:E:495:MET:HE2	31:E:495:MET:HB3	1.79	0.47
33:R1:95:A:H2'	33:R1:96:C:O4'	2.15	0.47
33:R1:918:A:H5''	34:R2:97:C:O2'	2.15	0.47
33:R1:2038:G:H2'	33:R1:2039:U:O4'	2.14	0.47
35:R3:56:U:H2'	35:R3:57:G:C8	2.50	0.47
35:R3:379:C:H5	35:R3:384:G:H1	1.62	0.47
46:sk:105:ARG:HG2	46:sk:105:ARG:HH11	1.80	0.47
14:24:6:ARG:HB2	33:R1:85:G:OP2	2.15	0.47
21:31:27:THR:O	21:31:27:THR:OG1	2.28	0.47
28:5:151:LEU:N	33:R1:2305:U:O2	2.48	0.47
29:6:174:LYS:HE3	29:6:175:LYS:HE3	1.97	0.47
33:R1:159:G:H1'	33:R1:2208:C:O2'	2.14	0.47
33:R1:181:A:H2'	33:R1:182:A:C8	2.50	0.47
33:R1:278:A:H8	33:R1:279:A:C8	2.32	0.47
33:R1:349:U:H2'	33:R1:350:G:C8	2.50	0.47
33:R1:1269:A:H2'	33:R1:1270:C:C6	2.50	0.47
34:R2:15:A:H3'	34:R2:16:G:H8	1.79	0.47
34:R2:25:U:O2	34:R2:117:G:O2'	2.27	0.47
34:R2:116:G:H2'	34:R2:117:G:H5''	1.96	0.47
35:R3:4:U:H2'	35:R3:4:U:O2	2.13	0.47
35:R3:50:A:O2'	35:R3:360:G:N2	2.48	0.47
35:R3:166:U:H2'	35:R3:167:A:C8	2.50	0.47
35:R3:612:C:H2'	35:R3:613:C:C6	2.49	0.47
35:R3:875:U:H1'	43:sh:15:ASN:HD21	1.79	0.47
35:R3:1008:U:H2'	35:R3:1009:U:C6	2.49	0.47
35:R3:1037:C:H2'	35:R3:1038:C:C4	2.50	0.47
36:T:63:G:H2'	36:T:64:U:O4'	2.15	0.47
41:sf:88:MET:HE1	53:sr:60:ARG:HG2	1.97	0.47
43:sh:38:VAL:HG21	43:sh:109:VAL:HG12	1.96	0.47
43:sh:82:LEU:HD11	52:sq:34:GLY:O	2.15	0.47
45:sj:66:GLU:HG2	49:sn:98:ALA:HB2	1.97	0.47
46:sk:28:ASN:OD1	46:sk:29:THR:N	2.47	0.47
46:sk:92:ARG:NH2	46:sk:111:ASP:OD2	2.38	0.47
7:18:43:ASN:HD22	7:18:46:GLU:CD	2.22	0.47
11:21:74:ILE:HB	11:21:87:GLN:HB3	1.97	0.47
19:3:150:GLN:HB3	33:R1:2572:A:N7	2.29	0.47
27:4:188:MET:HE1	27:4:196:VAL:HG11	1.96	0.47
28:5:65:LEU:HB2	34:R2:42:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:9:96:THR:HG23	30:9:117:LEU:HD11	1.97	0.47
31:E:548:ILE:O	31:E:549:LYS:HB2	2.14	0.47
33:R1:419:U:H2'	33:R1:420:C:C6	2.50	0.47
33:R1:839:U:H2'	33:R1:840:C:C6	2.50	0.47
33:R1:1570:A:H2'	33:R1:1571:A:C8	2.49	0.47
33:R1:1727:C:H2'	33:R1:1728:C:C6	2.50	0.47
33:R1:2081:U:H2'	33:R1:2082:A:H8	1.80	0.47
35:R3:35:G:O2'	47:sl:114:SER:O	2.28	0.47
49:sn:32:ASP:OD2	49:sn:33:VAL:N	2.48	0.47
4:15:85:VAL:HG13	4:15:86:GLU:N	2.30	0.47
7:18:76:LYS:O	7:18:80:GLU:HG2	2.14	0.47
13:23:33:LYS:HG2	13:23:80:TRP:CE3	2.50	0.47
28:5:56:LEU:HD12	28:5:86:CYS:SG	2.54	0.47
31:E:219:ARG:HB2	31:E:244:TYR:CG	2.50	0.47
31:E:234:ARG:HE	31:E:304:LYS:HG3	1.80	0.47
31:E:240:TRP:CD1	31:E:247:TRP:HB2	2.50	0.47
33:R1:1:G:H2'	33:R1:2:G:C8	2.50	0.47
33:R1:1071:G:O2'	33:R1:1088:A:O3'	2.33	0.47
33:R1:1187:G:N2	33:R1:1188:U:O4	2.47	0.47
35:R3:564:C:P	47:sl:11:ARG:HH21	2.38	0.47
35:R3:1253:G:H2'	35:R3:1254:A:H8	1.80	0.47
36:T:25:C:C2	36:T:26:A:C8	3.03	0.47
41:sf:43:GLY:HA2	41:sf:58:HIS:CE1	2.49	0.47
44:si:90:ASP:O	44:si:92:SER:N	2.48	0.47
46:sk:126:ARG:HD2	56:su:33:ARG:NH2	2.30	0.47
2:13:55:ILE:HA	2:13:123:LYS:HB2	1.97	0.47
13:23:64:LYS:NZ	33:R1:1601:G:OP1	2.48	0.47
28:5:102:LEU:HD12	28:5:106:ALA:HB3	1.96	0.47
33:R1:232:G:H8	33:R1:232:G:OP2	1.98	0.47
33:R1:1682:G:H2'	33:R1:1683:U:C6	2.50	0.47
35:R3:37:U:H4'	35:R3:501:C:OP1	2.15	0.47
35:R3:707:U:H2'	35:R3:708:C:C6	2.49	0.47
35:R3:963:G:H21	45:sj:57:VAL:HG11	1.77	0.47
35:R3:1251:A:H2'	35:R3:1252:A:C8	2.50	0.47
35:R3:1439:G:O2'	35:R3:1440:U:H6	1.97	0.47
35:R3:1526:G:OP1	56:su:37:TYR:HB3	2.15	0.47
39:sd:167:PRO:HB3	39:sd:169:TRP:CZ3	2.50	0.47
15:25:38:LEU:HB3	15:25:40:ILE:HD13	1.95	0.46
15:25:83:LYS:HB3	15:25:85:LYS:HZ3	1.80	0.46
31:E:313:ILE:HG13	31:E:486:ALA:HB1	1.96	0.46
33:R1:586:A:N1	33:R1:809:G:O2'	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:933:A:H5''	33:R1:934:U:OP2	2.14	0.46
33:R1:1266:G:O2'	33:R1:2012:G:O6	2.29	0.46
33:R1:1954:G:O2'	33:R1:1956:U:O4	2.17	0.46
33:R1:2055:C:H2'	33:R1:2504:U:H4'	1.96	0.46
33:R1:2176:A:H2'	33:R1:2177:C:C2	2.50	0.46
33:R1:2455:G:H2'	33:R1:2456:C:C6	2.49	0.46
35:R3:464:U:N3	35:R3:467:U:OP1	2.40	0.46
35:R3:497:G:H2'	35:R3:498:A:C8	2.49	0.46
44:si:22:PRO:HD2	44:si:22:PRO:O	2.15	0.46
45:sj:42:LEU:HB2	45:sj:71:LEU:HD23	1.97	0.46
56:su:16:ARG:O	56:su:19:LYS:HB3	2.15	0.46
56:su:27:VAL:O	56:su:31:VAL:HG23	2.15	0.46
7:18:53:THR:HB	7:18:65:THR:HB	1.97	0.46
9:2:164:VAL:HG21	9:2:180:MET:HE1	1.97	0.46
20:30:39:ASP:OD2	20:30:44:ARG:NH2	2.47	0.46
31:E:85:THR:N	31:E:88:GLU:HB2	2.31	0.46
31:E:128:LEU:O	31:E:132:ILE:HG12	2.15	0.46
33:R1:827:U:O2'	33:R1:2068:U:C2	2.69	0.46
33:R1:2834:G:H1'	33:R1:2883:A:N6	2.30	0.46
35:R3:58:C:C2'	35:R3:388:G:H22	2.27	0.46
35:R3:79:G:O2'	35:R3:80:A:N7	2.48	0.46
35:R3:516:U:H5	35:R3:533:A:N7	2.14	0.46
35:R3:600:A:OP1	43:sh:87:ARG:HG3	2.15	0.46
35:R3:686:U:O4	35:R3:703:G:H2'	2.14	0.46
35:R3:1149:C:O2'	35:R3:1150:A:H5'	2.15	0.46
42:sg:14:ASP:OD1	42:sg:22:LEU:HD23	2.16	0.46
2:13:39:LYS:NZ	33:R1:1007:C:OP1	2.43	0.46
17:28:38:TRP:CD1	30:9:32:PRO:HA	2.50	0.46
28:5:135:ILE:HD12	28:5:136:ILE:N	2.30	0.46
31:E:382:LEU:HD22	31:E:386:VAL:HG11	1.96	0.46
33:R1:1275:A:N1	33:R1:1295:C:O2'	2.42	0.46
35:R3:984:C:H2'	35:R3:985:C:H6	1.80	0.46
37:sb:18:GLN:HG2	37:sb:189:ASN:CG	2.40	0.46
52:sq:6:THR:OG1	52:sq:60:ILE:O	2.27	0.46
6:17:35:LYS:HB2	6:17:112:TYR:CE1	2.50	0.46
6:17:69:ARG:O	6:17:70:THR:OG1	2.29	0.46
7:18:27:VAL:HA	7:18:93:ASP:HB3	1.97	0.46
14:24:32:LYS:HB3	14:24:63:ALA:HB1	1.97	0.46
30:9:30:LEU:HB3	30:9:36:ALA:HB3	1.96	0.46
31:E:110:LEU:HD22	31:E:121:LEU:HD21	1.97	0.46
33:R1:160:A:H8	33:R1:2217:G:N2	1.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:358:U:H2'	33:R1:359:G:C8	2.43	0.46
33:R1:528:A:C2	33:R1:2043:C:H4'	2.50	0.46
33:R1:2074:U:H2'	33:R1:2075:U:C6	2.50	0.46
33:R1:2100:G:H2'	33:R1:2101:A:H8	1.79	0.46
33:R1:2101:A:H2'	33:R1:2102:G:C8	2.50	0.46
35:R3:466:A:O2'	35:R3:467:U:H5''	2.16	0.46
35:R3:1319:A:O2'	35:R3:1323:G:N7	2.48	0.46
45:sj:49:PHE:HE1	45:sj:67:ILE:HG13	1.80	0.46
3:14:109:SER:O	3:14:109:SER:OG	2.29	0.46
20:30:11:SER:CB	33:R1:988:A:H5''	2.43	0.46
28:5:109:ARG:HH21	28:5:138:PRO:HD3	1.81	0.46
33:R1:134:G:C6	33:R1:144:A:N1	2.83	0.46
33:R1:832:U:H2'	33:R1:833:A:H8	1.80	0.46
33:R1:2774:C:O2'	33:R1:2775:G:C8	2.59	0.46
34:R2:110:C:H2'	34:R2:111:U:O4'	2.16	0.46
35:R3:189:A:H2'	35:R3:190:A:C8	2.51	0.46
35:R3:674:G:H2'	35:R3:675:A:C8	2.50	0.46
35:R3:821:G:H2'	35:R3:822:U:C6	2.50	0.46
35:R3:1186:G:O2'	35:R3:1187:G:H8	1.96	0.46
36:T:73:A:H5'	36:T:74:C:O5'	2.16	0.46
39:sd:82:LYS:HE3	39:sd:82:LYS:HB3	1.71	0.46
42:sg:9:ARG:O	42:sg:10:LYS:HG2	2.14	0.46
44:si:33:SER:OG	44:si:34:LEU:N	2.49	0.46
46:sk:66:ALA:HB2	46:sk:95:THR:HG23	1.96	0.46
11:21:68:ARG:HB2	11:21:90:ARG:HH21	1.79	0.46
27:4:200:LEU:HD23	27:4:200:LEU:HA	1.82	0.46
31:E:516:ASP:O	31:E:519:LYS:HG2	2.16	0.46
33:R1:931:U:H5''	33:R1:932:U:OP2	2.15	0.46
33:R1:1486:U:H2'	33:R1:1487:U:C6	2.50	0.46
33:R1:2107:G:C4	33:R1:2108:A:C8	3.04	0.46
33:R1:2134:A:C4	33:R1:2157:G:H4'	2.50	0.46
35:R3:254:G:O2'	52:sq:17:GLU:O	2.33	0.46
35:R3:335:C:H2'	35:R3:336:A:C8	2.51	0.46
35:R3:464:U:H3	35:R3:467:U:P	2.38	0.46
35:R3:1112:C:O2	38:sc:178:ARG:HG2	2.16	0.46
35:R3:1305:G:H4'	35:R3:1306:A:O5'	2.15	0.46
35:R3:1435:G:H2'	35:R3:1436:U:C6	2.50	0.46
43:sh:88:LYS:HE3	43:sh:88:LYS:HB3	1.67	0.46
51:sp:69:ASP:OD1	51:sp:70:ARG:N	2.49	0.46
9:2:97:ASP:OD2	9:2:98:GLY:N	2.49	0.46
16:27:12:ASN:HA	16:27:14:ARG:NH2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:290:U:O4	33:R1:350:G:O6	2.33	0.46
33:R1:857:G:H2'	33:R1:858:G:O4'	2.16	0.46
33:R1:1486:U:H2'	33:R1:1487:U:H6	1.80	0.46
34:R2:1:U:H2'	34:R2:2:G:C8	2.43	0.46
35:R3:466:A:C4	35:R3:468:A:C8	3.03	0.46
35:R3:713:G:H2'	35:R3:714:G:C8	2.51	0.46
35:R3:1118:U:H1'	35:R3:1179:A:C5	2.51	0.46
35:R3:1191:A:OP1	38:sc:3:LYS:HD2	2.15	0.46
41:sf:4:TYR:CD1	41:sf:71:ILE:HG13	2.51	0.46
46:sk:125:LYS:NZ	56:su:35:GLU:HA	2.30	0.46
47:sl:70:GLY:O	47:sl:98:ARG:NH2	2.42	0.46
19:3:37:VAL:HG23	19:3:92:VAL:HG13	1.98	0.46
31:E:6:TYR:HB2	31:E:183:MET:HE1	1.98	0.46
33:R1:598:U:H2'	33:R1:599:A:H8	1.80	0.46
33:R1:1656:C:H2'	33:R1:1657:U:H6	1.81	0.46
33:R1:2795:C:H2'	33:R1:2796:U:O4'	2.16	0.46
35:R3:835:U:OP1	53:sr:52:ARG:NH2	2.46	0.46
35:R3:1330:U:H2'	35:R3:1331:G:O4'	2.15	0.46
56:su:32:ARG:O	56:su:33:ARG:HD2	2.16	0.46
7:18:83:LEU:HD11	7:18:114:GLY:HA3	1.98	0.46
28:5:84:ILE:HD11	33:R1:2311:A:N3	2.31	0.46
28:5:132:ARG:O	28:5:133:GLU:HG3	2.15	0.46
33:R1:1219:U:H2'	33:R1:1220:G:H8	1.81	0.46
33:R1:1224:U:H2'	33:R1:1225:G:C8	2.51	0.46
33:R1:2098:U:H2'	33:R1:2099:U:O4'	2.16	0.46
33:R1:2831:G:N2	33:R1:2884:U:OP2	2.46	0.46
35:R3:35:G:H2'	35:R3:36:C:C6	2.51	0.46
35:R3:1253:G:H2'	35:R3:1254:A:C8	2.50	0.46
10:20:47:ARG:NE	10:20:48:ASP:OD2	2.46	0.46
33:R1:980:A:N3	33:R1:2037:A:O2'	2.43	0.46
33:R1:1357:C:H2'	33:R1:1358:G:O4'	2.16	0.46
33:R1:1429:G:H2'	33:R1:1430:G:H8	1.81	0.46
33:R1:1564:C:H2'	33:R1:1565:C:C6	2.51	0.46
33:R1:2067:G:H3'	33:R1:2068:U:H4'	1.98	0.46
33:R1:2783:U:H2'	33:R1:2784:U:H6	1.80	0.46
35:R3:276:G:H5'	52:sq:16:MET:SD	2.56	0.46
36:T:5:G:H2'	36:T:6:A:H8	1.81	0.46
39:sd:187:ARG:NH1	39:sd:187:ARG:O	2.49	0.46
13:23:38:ALA:HB1	13:23:43:ILE:HD11	1.98	0.45
33:R1:453:A:O2'	33:R1:454:A:OP1	2.27	0.45
33:R1:739:A:H1'	33:R1:740:C:H5	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1880:U:H2'	33:R1:1881:C:C6	2.51	0.45
33:R1:2106:U:H2'	33:R1:2107:G:O4'	2.15	0.45
33:R1:2489:U:H2'	33:R1:2490:G:O4'	2.16	0.45
33:R1:2557:G:H2'	33:R1:2558:C:C6	2.51	0.45
35:R3:564:C:OP2	47:sl:11:ARG:NH2	2.43	0.45
35:R3:570:G:H2'	35:R3:571:U:C6	2.51	0.45
35:R3:649:A:H2'	35:R3:650:G:O4'	2.16	0.45
35:R3:911:U:H2'	35:R3:912:C:C6	2.51	0.45
35:R3:921:U:O2	40:se:23:THR:HG23	2.16	0.45
35:R3:1120:C:H2'	35:R3:1121:U:H6	1.80	0.45
35:R3:1229:A:OP2	48:sm:112:ARG:HD3	2.17	0.45
35:R3:1447:A:H5''	35:R3:1448:C:C5	2.46	0.45
38:sc:152:VAL:HG22	38:sc:197:VAL:HG22	1.98	0.45
42:sg:49:LEU:HD21	42:sg:60:ALA:HB1	1.97	0.45
12:22:1:MET:HE1	12:22:58:ALA:HB1	1.97	0.45
14:24:5:ARG:N	14:24:8:ASP:OD2	2.41	0.45
29:6:137:LYS:O	29:6:140:ILE:HG13	2.17	0.45
33:R1:207:A:H2'	33:R1:208:C:O4'	2.15	0.45
33:R1:897:C:H2'	33:R1:898:C:C5	2.51	0.45
33:R1:1071:G:H2'	33:R1:1089:A:H2'	1.97	0.45
33:R1:1604:C:O2'	33:R1:1610:A:N1	2.40	0.45
33:R1:2649:C:H2'	33:R1:2650:U:H6	1.80	0.45
35:R3:417:G:H1'	35:R3:418:C:H5'	1.98	0.45
35:R3:453:G:O2'	35:R3:454:G:OP1	2.25	0.45
35:R3:1286:U:H2'	35:R3:1287:A:H5'	1.99	0.45
35:R3:1450:U:H2'	35:R3:1452:C:H1'	1.97	0.45
40:se:75:LEU:HA	40:se:146:MET:HE1	1.97	0.45
42:sg:98:LEU:HD23	42:sg:98:LEU:HA	1.83	0.45
50:so:2:LEU:HD12	50:so:2:LEU:HA	1.79	0.45
12:22:5:ALA:HB2	12:22:54:ALA:HB2	1.98	0.45
19:3:46:ARG:NH2	19:3:88:GLU:O	2.48	0.45
28:5:139:GLU:OE1	28:5:139:GLU:N	2.48	0.45
31:E:41:ASN:HD21	31:E:475:LEU:HA	1.80	0.45
33:R1:1794:A:H2'	33:R1:1795:C:H6	1.81	0.45
33:R1:2411:A:H2'	33:R1:2412:A:C8	2.51	0.45
35:R3:115:G:P	35:R3:115:G:O4'	2.75	0.45
35:R3:322:C:O2'	35:R3:323:U:OP2	2.30	0.45
35:R3:636:U:H2'	35:R3:637:C:H6	1.80	0.45
35:R3:1323:G:H2'	35:R3:1324:A:H8	1.80	0.45
38:sc:130:ARG:NH2	38:sc:165:GLU:OE2	2.48	0.45
46:sk:12:ARG:C	46:sk:14:GLN:H	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:sl:67:GLY:O	47:sl:98:ARG:NH1	2.43	0.45
49:sn:53:ASP:HA	49:sn:58:ARG:HG3	1.98	0.45
4:15:84:LYS:HB2	4:15:84:LYS:HE3	1.68	0.45
9:2:2:VAL:HG12	9:2:18:VAL:HG22	1.98	0.45
11:21:49:ILE:HG13	11:21:53:PHE:H	1.81	0.45
14:24:87:GLU:C	14:24:89:GLY:H	2.24	0.45
30:9:89:LYS:HG3	30:9:123:ARG:HB2	1.98	0.45
33:R1:580:U:H2'	33:R1:581:C:H6	1.81	0.45
33:R1:2103:C:H2'	33:R1:2104:C:O2	2.16	0.45
35:R3:322:C:O3'	55:st:17:ARG:HG2	2.14	0.45
35:R3:945:G:C2	35:R3:946:A:C8	3.04	0.45
35:R3:1051:C:O2'	35:R3:1052:U:O5'	2.32	0.45
35:R3:1428:A:H2'	35:R3:1429:A:O4'	2.16	0.45
36:T:5:G:H2'	36:T:6:A:C8	2.51	0.45
49:sn:37:ASP:OD1	49:sn:37:ASP:N	2.39	0.45
1:1:60:ARG:HG2	1:1:61:GLY:N	2.31	0.45
11:21:9:GLY:O	33:R1:996:A:H1'	2.16	0.45
13:23:39:THR:HG22	13:23:42:GLU:HG3	1.98	0.45
16:27:18:ALA:O	16:27:20:ARG:NH1	2.47	0.45
33:R1:285:G:H2'	33:R1:286:U:C6	2.51	0.45
33:R1:1871:A:H5''	33:R1:1872:A:OP2	2.17	0.45
33:R1:2100:G:H2'	33:R1:2101:A:C8	2.51	0.45
35:R3:315:A:C5	35:R3:330:C:H5'	2.51	0.45
35:R3:736:C:O2'	41:sf:89:VAL:O	2.33	0.45
35:R3:985:C:H2'	35:R3:986:U:C6	2.51	0.45
35:R3:1133:G:H1	35:R3:1142:G:N2	2.14	0.45
37:sb:17:HIS:NE2	37:sb:39:ILE:HD13	2.31	0.45
43:sh:9:MET:O	43:sh:13:ILE:HG13	2.17	0.45
43:sh:112:ASP:N	43:sh:112:ASP:OD1	2.49	0.45
51:sp:34:GLU:OE2	51:sp:56:ARG:HD3	2.17	0.45
52:sq:22:VAL:HG11	52:sq:60:ILE:HD13	1.98	0.45
56:su:48:LYS:HB3	56:su:48:LYS:HE2	1.77	0.45
11:21:51:VAL:HG22	11:21:52:PRO:CD	2.40	0.45
11:21:57:GLY:HA2	11:21:102:SER:C	2.42	0.45
14:24:65:GLN:HG2	33:R1:328:U:H4'	1.98	0.45
27:4:168:ASP:OD2	27:4:170:ARG:NH1	2.49	0.45
29:6:26:LYS:HE2	29:6:31:GLU:HG3	1.98	0.45
29:6:89:VAL:HG22	29:6:159:LYS:HA	1.97	0.45
33:R1:784:G:H5'	33:R1:785:G:OP1	2.16	0.45
33:R1:1181:U:H2'	33:R1:1182:G:C8	2.52	0.45
33:R1:1181:U:H2'	33:R1:1182:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1932:A:H2'	33:R1:1933:G:O4'	2.16	0.45
33:R1:2405:G:O2'	33:R1:2411:A:N6	2.47	0.45
35:R3:31:G:O2'	35:R3:48:C:N4	2.50	0.45
35:R3:635:A:H2'	35:R3:636:U:H6	1.81	0.45
35:R3:1144:G:H21	35:R3:1146:A:H62	1.63	0.45
35:R3:1463:U:H2'	35:R3:1464:U:C6	2.51	0.45
39:sd:8:LEU:HD21	39:sd:30:LYS:HG3	1.99	0.45
55:st:18:LYS:HE2	55:st:18:LYS:HB2	1.75	0.45
5:16:11:LYS:HD3	5:16:86:LYS:HD3	1.98	0.45
9:2:266:ILE:HG21	9:2:269:ARG:HE	1.81	0.45
10:20:85:ALA:HB2	10:20:115:ALA:HB2	1.98	0.45
11:21:33:VAL:HG13	11:21:61:ALA:HB3	1.98	0.45
12:22:93:ALA:HB2	33:R1:1614:A:N1	2.32	0.45
19:3:149:ASN:OD1	19:3:150:GLN:N	2.48	0.45
28:5:113:PHE:HZ	28:5:175:PRO:HB2	1.81	0.45
30:9:80:ILE:HD11	30:9:99:ILE:HA	1.99	0.45
33:R1:1321:A:C4	33:R1:1322:A:C8	3.05	0.45
33:R1:1437:C:O2'	33:R1:1516:G:O2'	2.28	0.45
35:R3:1036:A:H2'	35:R3:1037:C:C2	2.51	0.45
35:R3:1259:C:O2'	35:R3:1283:U:O2	2.28	0.45
41:sf:81:ASN:OD1	41:sf:83:ALA:N	2.48	0.45
49:sn:78:LEU:HB2	49:sn:83:VAL:HG23	1.98	0.45
3:14:48:PRO:HB3	35:R3:1422:G:H4'	1.99	0.45
19:3:2:ILE:HG13	19:3:3:GLY:H	1.82	0.45
27:4:95:LYS:O	33:R1:659:G:O2'	2.32	0.45
33:R1:1222:U:H2'	33:R1:1223:G:C8	2.52	0.45
33:R1:1538:G:H8	33:R1:1538:G:OP2	2.00	0.45
33:R1:2247:A:H2'	33:R1:2248:C:H6	1.81	0.45
35:R3:131:A:H2'	35:R3:132:C:C6	2.51	0.45
35:R3:509:A:C8	35:R3:543:U:O2'	2.69	0.45
38:sc:59:PRO:HB3	45:sj:94:ALA:HB1	1.99	0.45
38:sc:90:VAL:O	38:sc:93:ILE:HG22	2.15	0.45
39:sd:196:GLU:OE1	39:sd:196:GLU:N	2.48	0.45
40:se:14:LEU:HD21	40:se:17:VAL:HG13	1.98	0.45
43:sh:104:SER:HB2	43:sh:125:ILE:HD11	1.98	0.45
44:si:33:SER:HB3	44:si:36:GLN:NE2	2.32	0.45
52:sq:16:MET:CG	52:sq:19:SER:HB2	2.46	0.45
55:st:26:MET:O	55:st:30:PHE:HD1	1.99	0.45
7:18:117:PHE:O	33:R1:2377:A:O2'	2.24	0.45
10:20:48:ASP:OD1	33:R1:534:U:O2'	2.26	0.45
19:3:122:VAL:HG21	19:3:129:THR:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:E:355:ILE:HG22	31:E:504:LEU:HD13	1.97	0.45
33:R1:858:G:O2'	33:R1:2268:A:O2'	2.27	0.45
33:R1:1054:A:H2'	33:R1:1055:G:C8	2.47	0.45
33:R1:2537:U:H2'	33:R1:2538:C:C6	2.52	0.45
33:R1:2543:G:H2'	33:R1:2544:G:C8	2.52	0.45
34:R2:32:U:C2	34:R2:51:G:N2	2.85	0.45
35:R3:35:G:N3	47:sl:114:SER:OG	2.50	0.45
35:R3:595:A:H8	35:R3:595:A:OP2	2.00	0.45
35:R3:1287:A:H2'	35:R3:1288:A:C8	2.52	0.45
44:si:120:ALA:O	44:si:121:ARG:HG3	2.16	0.45
54:ss:11:ASP:H	54:ss:37:SER:HB3	1.81	0.45
5:16:117:PHE:HD2	5:16:130:PHE:HD2	1.65	0.45
6:17:79:LEU:C	6:17:81:ASN:H	2.25	0.45
11:21:41:ILE:HD11	11:21:57:GLY:HA3	1.98	0.45
17:28:30:PRO:HG2	17:28:32:LEU:HD22	1.99	0.45
18:29:4:LYS:H	18:29:4:LYS:HE2	1.81	0.45
28:5:31:GLU:HG3	28:5:32:LYS:HG2	1.97	0.45
31:E:323:VAL:HG11	31:E:493:CYS:SG	2.57	0.45
33:R1:191:A:H2'	33:R1:192:C:H6	1.82	0.45
33:R1:373:U:H2'	33:R1:374:A:H8	1.82	0.45
33:R1:714:U:H1'	33:R1:717:C:H5	1.81	0.45
33:R1:1589:U:H2'	33:R1:1590:A:C8	2.52	0.45
33:R1:2162:G:H2'	33:R1:2163:A:O4'	2.17	0.45
33:R1:2241:A:H2'	33:R1:2242:G:C8	2.52	0.45
33:R1:2497:A:OP2	33:R1:2497:A:H8	2.00	0.45
35:R3:552:U:O4	35:R3:553:A:N6	2.50	0.45
35:R3:607:A:H2'	35:R3:608:A:C8	2.52	0.45
35:R3:881:G:P	47:sl:8:ARG:HH22	2.40	0.45
35:R3:1233:G:H5'	44:si:118:ARG:NH2	2.32	0.45
35:R3:1291:U:O2'	44:si:40:ARG:HD2	2.16	0.45
45:sj:10:LEU:O	45:sj:71:LEU:HA	2.17	0.45
52:sq:27:PHE:CE1	52:sq:38:LYS:HG3	2.52	0.45
14:24:47:PRO:HB3	14:24:55:GLY:HA3	1.98	0.44
15:25:75:GLN:HB2	15:25:92:VAL:HG22	1.99	0.44
24:34:16:HIS:HB2	24:34:44:VAL:HG21	1.98	0.44
27:4:63:LYS:HE3	33:R1:2444:G:OP2	2.16	0.44
31:E:66:GLN:HE21	31:E:67:PRO:HD2	1.82	0.44
33:R1:634:C:H2'	33:R1:635:C:C6	2.52	0.44
33:R1:642:U:O2'	33:R1:644:A:N7	2.45	0.44
33:R1:2177:C:H5	33:R1:2178:C:C6	2.35	0.44
33:R1:2803:G:H2'	33:R1:2804:U:C6	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:264:C:O2'	52:sq:65:PRO:O	2.32	0.44
35:R3:390:U:H2'	35:R3:391:G:H8	1.82	0.44
35:R3:473:U:OP2	51:sp:76:LYS:HE2	2.17	0.44
35:R3:1008:U:H2'	35:R3:1009:U:H6	1.82	0.44
35:R3:1179:A:H5''	44:si:103:VAL:HG12	1.99	0.44
35:R3:1228:C:H5'	48:sm:113:LYS:O	2.17	0.44
36:T:22:G:H2'	36:T:23:A:H8	1.82	0.44
45:sj:12:ALA:HB2	45:sj:96:VAL:HG22	1.98	0.44
8:19:105:LYS:HA	8:19:108:ARG:HD3	1.99	0.44
12:22:31:GLN:O	12:22:35:ILE:HG23	2.17	0.44
19:3:190:LYS:HE2	33:R1:2729:G:H5'	1.99	0.44
21:31:56:ARG:HD3	21:31:56:ARG:HA	1.78	0.44
27:4:58:LYS:HG3	27:4:71:GLY:HA2	1.97	0.44
28:5:6:TYR:O	28:5:10:GLU:HG2	2.17	0.44
30:9:9:VAL:HG11	30:9:12:LEU:HB3	1.99	0.44
33:R1:141:G:H2'	33:R1:142:A:O4'	2.18	0.44
33:R1:1201:U:H2'	33:R1:1202:G:H8	1.82	0.44
33:R1:1536:C:O2'	33:R1:1537:G:N2	2.50	0.44
33:R1:2102:G:H2'	33:R1:2103:C:C6	2.53	0.44
33:R1:2193:G:H2'	33:R1:2194:U:C6	2.53	0.44
34:R2:104:A:H2'	34:R2:105:G:O4'	2.16	0.44
35:R3:301:G:HO2'	35:R3:302:G:P	2.40	0.44
35:R3:447:G:N1	35:R3:486:U:OP1	2.37	0.44
35:R3:780:A:H5''	46:sk:124:LYS:HD3	2.00	0.44
37:sb:80:LYS:NZ	37:sb:84:LEU:HD12	2.33	0.44
1:1:185:LEU:O	1:1:189:LEU:HD12	2.17	0.44
9:2:211:ARG:HD2	9:2:211:ARG:HA	1.63	0.44
11:21:6:GLN:HG3	11:21:11:GLN:HG3	2.00	0.44
13:23:8:LEU:O	18:29:29:ARG:NH2	2.50	0.44
31:E:45:LYS:NZ	59:E:601:ATP:O2G	2.50	0.44
33:R1:780:G:H2'	33:R1:782:A:N7	2.32	0.44
33:R1:1915:U:H4'	33:R1:1916:A:H5'	2.00	0.44
33:R1:2340:A:H5'	34:R2:41:G:H21	1.83	0.44
33:R1:2639:A:H2'	33:R1:2640:G:O4'	2.17	0.44
35:R3:640:A:O2'	35:R3:641:U:OP1	2.34	0.44
35:R3:1496:C:H2'	35:R3:1497:G:O4'	2.18	0.44
38:sc:78:LYS:O	38:sc:81:GLU:HG2	2.17	0.44
39:sd:14:GLU:HG3	39:sd:18:LEU:HD11	1.99	0.44
40:se:90:GLY:O	40:se:129:SER:N	2.47	0.44
47:sl:107:LYS:HB2	47:sl:107:LYS:HE2	1.65	0.44
51:sp:44:SER:H	51:sp:46:LYS:HZ2	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2:20:ASN:HB3	9:2:23:LEU:HG	1.99	0.44
14:24:27:VAL:HB	14:24:33:VAL:HG12	1.99	0.44
15:25:20:LEU:HD23	15:25:20:LEU:HA	1.80	0.44
29:6:154:GLU:HG2	29:6:157:LYS:H	1.81	0.44
31:E:234:ARG:H	31:E:234:ARG:HG2	1.67	0.44
31:E:415:MET:HE2	31:E:415:MET:HB3	1.80	0.44
33:R1:286:U:H3	33:R1:354:A:N6	2.14	0.44
33:R1:286:U:H2'	33:R1:287:G:C8	2.52	0.44
33:R1:851:C:H2'	33:R1:852:U:H6	1.82	0.44
33:R1:1063:G:H2'	33:R1:1063:G:N3	2.32	0.44
33:R1:1771:C:H2'	33:R1:1772:A:C8	2.53	0.44
33:R1:2258:C:O2'	33:R1:2427:C:OP2	2.32	0.44
35:R3:393:A:H2'	35:R3:394:G:H5'	1.98	0.44
35:R3:673:A:O3'	41:sf:86:ARG:NH2	2.50	0.44
35:R3:685:G:O2'	35:R3:686:U:OP1	2.25	0.44
39:sd:169:TRP:CD1	39:sd:185:PRO:HG3	2.53	0.44
40:se:79:THR:OG1	40:se:97:PRO:O	2.35	0.44
41:sf:2:ARG:HG2	41:sf:91:ARG:NH1	2.33	0.44
3:14:70:ARG:HG2	3:14:70:ARG:NH1	2.33	0.44
18:29:24:GLU:O	18:29:28:LEU:HB2	2.18	0.44
31:E:219:ARG:HG2	31:E:220:TYR:N	2.33	0.44
31:E:548:ILE:HG23	33:R1:2112:G:O2'	2.18	0.44
33:R1:576:U:H2'	33:R1:577:G:C8	2.53	0.44
33:R1:1169:A:H2'	33:R1:1170:C:C6	2.52	0.44
33:R1:1270:C:H5''	33:R1:1271:G:O5'	2.17	0.44
33:R1:2591:C:H2'	33:R1:2592:G:H8	1.77	0.44
35:R3:471:U:H3'	35:R3:472:U:H5''	1.99	0.44
39:sd:77:GLU:HA	39:sd:80:ARG:HG2	1.99	0.44
47:sl:81:ILE:HG23	47:sl:94:TYR:HB3	2.00	0.44
55:st:78:LEU:HA	55:st:78:LEU:HD12	1.72	0.44
3:14:30:ARG:HD2	33:R1:2674:G:H4'	2.00	0.44
12:22:20:VAL:HG11	12:22:44:ALA:HA	1.98	0.44
14:24:12:VAL:HB	14:24:17:ASP:O	2.18	0.44
31:E:51:ILE:HG12	31:E:59:ILE:HG21	2.00	0.44
33:R1:149:A:N1	33:R1:176:A:N1	2.65	0.44
33:R1:700:G:O2'	33:R1:1632:A:N3	2.38	0.44
35:R3:160:A:H2'	35:R3:161:A:O4'	2.18	0.44
35:R3:457:G:H1	35:R3:475:C:H42	1.66	0.44
35:R3:500:G:H4'	35:R3:501:C:OP1	2.18	0.44
35:R3:868:C:H2'	35:R3:869:G:O4'	2.18	0.44
48:sm:30:LYS:HE2	48:sm:30:LYS:HB3	1.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:15:14:LYS:HG3	4:15:15:ALA:H	1.83	0.44
14:24:9:GLU:OE1	14:24:9:GLU:HA	2.18	0.44
29:6:34:ARG:NH1	29:6:70:LEU:HD22	2.29	0.44
31:E:82:PRO:HA	31:E:160:ILE:HG22	1.99	0.44
33:R1:1048:A:C5	33:R1:1111:A:H8	2.36	0.44
33:R1:1171:G:C6	33:R1:1176:U:N3	2.83	0.44
33:R1:1527:G:N1	33:R1:1544:A:OP2	2.41	0.44
33:R1:2120:G:H2'	33:R1:2121:G:C8	2.52	0.44
33:R1:2190:G:H2'	33:R1:2191:A:H8	1.81	0.44
35:R3:500:G:H2'	35:R3:501:C:C6	2.52	0.44
35:R3:861:G:H2'	35:R3:862:C:O4'	2.16	0.44
35:R3:1402:C:H2'	35:R3:1403:C:O4'	2.18	0.44
50:so:32:THR:HG21	50:so:84:LEU:HG	1.99	0.44
51:sp:8:ARG:CZ	51:sp:15:PRO:HB3	2.48	0.44
52:sq:10:ARG:HG3	52:sq:57:VAL:HG22	1.98	0.44
11:21:83:TYR:OH	11:21:85:LYS:HE3	2.18	0.44
12:22:93:ALA:HB2	33:R1:1614:A:C2	2.53	0.44
16:27:1:MET:HE2	16:27:1:MET:HB2	1.89	0.44
19:3:106:LYS:HG3	19:3:174:SER:HA	2.00	0.44
33:R1:58:G:O2'	33:R1:73:A:N1	2.48	0.44
33:R1:106:C:H2'	33:R1:107:G:H8	1.82	0.44
33:R1:2137:U:H2'	33:R1:2138:G:H8	1.82	0.44
33:R1:2148:G:H2'	33:R1:2149:U:C5	2.52	0.44
35:R3:363:A:HO2'	35:R3:364:A:P	2.39	0.44
35:R3:592:G:H2'	35:R3:593:U:C6	2.52	0.44
35:R3:639:G:O2'	35:R3:640:A:H5'	2.18	0.44
35:R3:757:U:H2'	35:R3:758:C:O4'	2.17	0.44
35:R3:1042:A:H2'	35:R3:1043:G:C8	2.53	0.44
35:R3:1121:U:H2'	35:R3:1122:U:C6	2.53	0.44
36:T:53:G:C4	36:T:62:C:C2	3.05	0.44
36:T:69:A:H2'	36:T:70:C:O4'	2.18	0.44
39:sd:49:ASP:OD1	39:sd:49:ASP:C	2.60	0.44
48:sm:65:GLU:OE2	48:sm:65:GLU:N	2.47	0.44
4:15:32:GLY:HA2	33:R1:1190:G:H5''	2.00	0.44
4:15:62:PRO:HB2	25:35:29:ARG:HH21	1.83	0.44
5:16:105:MET:HE3	5:16:117:PHE:CE1	2.53	0.44
11:21:73:LYS:HB3	11:21:73:LYS:HE3	1.70	0.44
23:33:33:LEU:HD12	23:33:33:LEU:HA	1.84	0.44
27:4:176:ASP:HB2	27:4:179:SER:H	1.83	0.44
28:5:109:ARG:HD2	28:5:136:ILE:HA	2.00	0.44
31:E:404:VAL:HG23	31:E:440:LYS:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1980:G:O2'	33:R1:1982:U:OP2	2.36	0.44
35:R3:107:G:H5''	35:R3:379:C:OP1	2.18	0.44
35:R3:494:G:O2'	35:R3:496:A:H1'	2.17	0.44
35:R3:619:U:H5	39:sd:130:ASN:H	1.66	0.44
35:R3:883:C:O2'	35:R3:884:U:H5'	2.18	0.44
35:R3:1226:C:O2'	48:sm:101:THR:O	2.20	0.44
35:R3:1412:C:H2'	35:R3:1413:A:H8	1.81	0.44
38:sc:48:LYS:H	38:sc:48:LYS:HG2	1.54	0.44
42:sg:11:ILE:HG13	42:sg:12:LEU:H	1.82	0.44
49:sn:87:ALA:HB2	49:sn:95:LEU:HD23	2.00	0.44
55:st:74:HIS:O	55:st:78:LEU:HB2	2.18	0.44
7:18:108:ASP:O	7:18:112:GLU:HG3	2.18	0.43
10:20:108:LEU:HD23	10:20:108:LEU:HA	1.88	0.43
13:23:39:THR:CG2	13:23:42:GLU:HG3	2.48	0.43
15:25:28:ALA:N	15:25:40:ILE:O	2.48	0.43
18:29:49:ASP:O	18:29:53:VAL:HG23	2.17	0.43
29:6:3:VAL:HG21	33:R1:2748:A:H5'	1.99	0.43
29:6:45:ALA:C	29:6:47:ASN:H	2.26	0.43
33:R1:64:A:H2'	33:R1:65:U:H6	1.82	0.43
33:R1:370:G:O2'	33:R1:424:G:OP1	2.30	0.43
33:R1:1842:G:H2'	33:R1:1843:C:C6	2.52	0.43
33:R1:2129:C:N3	33:R1:2160:C:N4	2.64	0.43
33:R1:2773:C:C2'	33:R1:2774:C:H5'	2.48	0.43
33:R1:2810:A:H2'	33:R1:2811:G:O4'	2.17	0.43
35:R3:110:C:H2'	35:R3:111:G:O4'	2.17	0.43
35:R3:527:G:O2'	35:R3:535:A:N1	2.40	0.43
35:R3:736:C:H2'	35:R3:737:C:C6	2.53	0.43
35:R3:1057:G:O2'	38:sc:187:GLU:OE2	2.30	0.43
35:R3:1439:G:O2'	35:R3:1440:U:O4'	2.34	0.43
36:T:57:G:C5	36:T:58:A:H2	2.36	0.43
40:se:45:VAL:O	40:se:71:ILE:HG22	2.17	0.43
46:sk:105:ARG:HG2	46:sk:105:ARG:NH1	2.32	0.43
3:14:2:ILE:HD12	3:14:6:THR:HG21	1.98	0.43
3:14:31:ARG:HH22	33:R1:2676:C:P	2.42	0.43
9:2:121:ALA:HB3	9:2:129:LEU:HD22	2.00	0.43
9:2:155:ARG:HB2	33:R1:1818:U:H2'	1.99	0.43
9:2:244:VAL:HA	9:2:251:THR:H	1.83	0.43
14:24:46:LYS:HB2	14:24:46:LYS:HE3	1.72	0.43
31:E:47:THR:OG1	59:E:601:ATP:O2A	2.32	0.43
33:R1:279:A:H2'	33:R1:280:U:H5'	2.01	0.43
33:R1:608:A:H2'	33:R1:609:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:723:C:H2'	33:R1:724:U:O4'	2.18	0.43
33:R1:1340:U:C5	33:R1:1603:A:C8	3.07	0.43
33:R1:1873:G:H2'	33:R1:1874:C:C6	2.53	0.43
33:R1:2112:G:H2'	33:R1:2112:G:N3	2.32	0.43
33:R1:2124:G:N2	33:R1:2174:C:H41	2.16	0.43
33:R1:2457:U:H5	33:R1:2494:G:O6	2.01	0.43
35:R3:330:C:O2'	35:R3:331:G:N2	2.27	0.43
35:R3:1150:A:O2'	35:R3:1151:A:P	2.76	0.43
35:R3:1175:G:H2'	35:R3:1176:A:H8	1.82	0.43
35:R3:1318:A:H1'	54:ss:36:ARG:HH11	1.83	0.43
35:R3:1512:U:H2'	35:R3:1513:A:C8	2.53	0.43
37:sb:17:HIS:O	37:sb:19:THR:N	2.51	0.43
40:se:45:VAL:O	40:se:71:ILE:N	2.51	0.43
48:sm:68:LEU:O	48:sm:72:ILE:HG12	2.18	0.43
5:16:42:THR:HA	5:16:93:VAL:HA	1.99	0.43
6:17:58:ASP:OD1	6:17:63:ARG:NE	2.37	0.43
7:18:111:ARG:NE	7:18:117:PHE:OXT	2.52	0.43
9:2:13:ARG:NH2	33:R1:1693:U:O2'	2.51	0.43
33:R1:279:A:C2'	33:R1:280:U:H5'	2.48	0.43
33:R1:1963:U:O5'	33:R1:1963:U:H6	2.02	0.43
33:R1:2146:C:O2'	33:R1:2147:A:H8	2.00	0.43
35:R3:501:C:OP2	47:sl:113:ARG:NH2	2.34	0.43
35:R3:950:U:H2'	35:R3:951:G:H8	1.82	0.43
35:R3:1099:G:H1'	56:su:65:ARG:HH11	1.82	0.43
35:R3:1187:G:H2'	35:R3:1188:A:H8	1.82	0.43
35:R3:1220:G:O3'	54:ss:35:ARG:HD3	2.19	0.43
39:sd:201:GLU:HG2	39:sd:201:GLU:H	1.65	0.43
45:sj:9:ARG:HG2	45:sj:99:GLN:HB2	1.99	0.43
47:sl:55:ARG:NH2	47:sl:61:GLU:OE2	2.51	0.43
4:15:73:ILE:HD12	4:15:106:GLU:OE1	2.18	0.43
10:20:116:LEU:HA	10:20:116:LEU:HD23	1.79	0.43
21:31:56:ARG:HG2	54:ss:64:GLU:OE1	2.18	0.43
31:E:5:VAL:N	31:E:29:PHE:O	2.26	0.43
33:R1:278:A:C8	33:R1:279:A:C8	3.06	0.43
33:R1:394:C:H2'	33:R1:395:U:O4'	2.19	0.43
33:R1:2244:U:O2	33:R1:2434:A:H2'	2.18	0.43
33:R1:2329:U:H2'	33:R1:2330:G:H8	1.84	0.43
33:R1:2411:A:H2'	33:R1:2412:A:H8	1.84	0.43
33:R1:2533:U:H2'	33:R1:2534:A:O4'	2.18	0.43
33:R1:2812:G:H2'	33:R1:2813:A:C8	2.53	0.43
35:R3:129:A:H2	35:R3:232:G:H22	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:216:U:H2'	35:R3:217:C:C6	2.54	0.43
35:R3:368:U:H5'	35:R3:369:G:H5''	2.00	0.43
35:R3:746:A:H2'	35:R3:747:A:C8	2.53	0.43
35:R3:1410:A:H2'	35:R3:1411:C:H6	1.83	0.43
37:sb:33:ALA:HB3	37:sb:37:VAL:HB	2.00	0.43
38:sc:57:GLU:HG3	38:sc:64:ARG:HE	1.83	0.43
40:se:95:MET:HE3	40:se:95:MET:HB2	1.76	0.43
46:sk:52:ARG:HE	46:sk:52:ARG:HB2	1.58	0.43
47:sl:55:ARG:HE	47:sl:61:GLU:HG2	1.83	0.43
50:so:13:GLU:HG3	50:so:14:PHE:CD1	2.54	0.43
52:sq:16:MET:HE3	52:sq:16:MET:HA	2.00	0.43
2:13:104:ALA:O	2:13:108:MET:HG3	2.17	0.43
3:14:70:ARG:NH1	33:R1:2684:U:O4'	2.51	0.43
4:15:96:LYS:HE2	4:15:103:ILE:HA	2.01	0.43
6:17:60:VAL:HG21	33:R1:1455:G:H5'	2.00	0.43
12:22:3:THR:O	12:22:3:THR:OG1	2.25	0.43
21:31:16:CYS:SG	21:31:17:SER:N	2.90	0.43
24:34:26:ASN:CG	33:R1:682:G:H5'	2.43	0.43
28:5:4:HIS:O	28:5:8:LYS:HG3	2.18	0.43
29:6:16:VAL:HG11	29:6:49:LEU:HD11	2.00	0.43
30:9:42:LYS:HA	30:9:45:GLU:HG3	2.01	0.43
31:E:526:ASN:OD1	31:E:529:GLU:HG2	2.18	0.43
33:R1:276:U:O2'	33:R1:277:G:OP1	2.32	0.43
33:R1:1427:A:H4'	33:R1:1428:C:O4'	2.19	0.43
33:R1:2281:A:O2'	33:R1:2282:G:H5'	2.18	0.43
35:R3:406:G:H21	39:sd:115:GLN:HE22	1.66	0.43
35:R3:900:A:H2'	35:R3:901:A:C8	2.53	0.43
35:R3:959:A:H5''	35:R3:960:U:OP2	2.18	0.43
35:R3:1003:G:O3'	35:R3:1004:A:H4'	2.18	0.43
35:R3:1246:A:H2'	35:R3:1247:U:C6	2.53	0.43
55:st:80:ALA:O	55:st:84:LYS:HD3	2.19	0.43
2:13:24:THR:HG21	33:R1:1141:U:OP1	2.19	0.43
13:23:79:ASP:OD2	13:23:79:ASP:C	2.62	0.43
17:28:14:GLY:HA3	17:28:28:PHE:HE1	1.84	0.43
24:34:12:ARG:HG2	24:34:44:VAL:HG11	2.01	0.43
26:36:4:ARG:HB2	33:R1:2466:C:OP1	2.18	0.43
33:R1:27:G:N2	33:R1:512:G:H1'	2.33	0.43
33:R1:57:C:H2'	33:R1:58:G:O4'	2.19	0.43
33:R1:596:U:H2'	33:R1:597:G:H8	1.83	0.43
33:R1:654:A:H3'	33:R1:654:A:N3	2.33	0.43
33:R1:858:G:N3	33:R1:2268:A:H2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1539:U:H2'	33:R1:1540:G:C8	2.54	0.43
33:R1:2327:A:H2'	33:R1:2328:A:C8	2.53	0.43
33:R1:2577:A:H2'	33:R1:2614:A:N6	2.34	0.43
33:R1:2895:G:H2'	33:R1:2896:C:C6	2.54	0.43
35:R3:343:U:O3'	35:R3:344:A:H8	2.02	0.43
35:R3:414:A:C4	35:R3:415:A:C8	3.06	0.43
35:R3:427:U:H3'	35:R3:428:G:H8	1.83	0.43
35:R3:718:A:C2	53:sr:37:LYS:HD2	2.54	0.43
35:R3:1001:C:O2	35:R3:1040:U:N3	2.51	0.43
40:se:156:ARG:HA	40:se:158:LYS:NZ	2.33	0.43
48:sm:46:GLU:CD	48:sm:46:GLU:N	2.77	0.43
50:so:87:ARG:HD2	50:so:87:ARG:HA	1.67	0.43
26:36:2:LYS:HE2	26:36:32:LYS:O	2.19	0.43
27:4:194:LYS:HE2	27:4:194:LYS:HA	2.01	0.43
28:5:33:ILE:HG12	28:5:95:MET:CG	2.45	0.43
28:5:73:VAL:HG21	28:5:76:PHE:HD2	1.83	0.43
29:6:2:ARG:H	29:6:2:ARG:HG2	1.46	0.43
30:9:62:LEU:HD23	30:9:62:LEU:HA	1.84	0.43
33:R1:609:A:H2'	33:R1:610:C:O4'	2.19	0.43
33:R1:667:U:H2'	33:R1:668:A:O4'	2.19	0.43
33:R1:1064:C:H5''	33:R1:1066:U:OP2	2.18	0.43
33:R1:1292:G:H2'	33:R1:1293:C:H6	1.83	0.43
33:R1:1478:G:H1	33:R1:1513:U:H3	1.67	0.43
33:R1:2128:G:H2'	33:R1:2129:C:H6	1.83	0.43
33:R1:2134:A:N3	33:R1:2157:G:H4'	2.34	0.43
33:R1:2813:A:H2'	33:R1:2814:A:C8	2.54	0.43
35:R3:108:G:H5'	35:R3:109:A:C5'	2.43	0.43
35:R3:686:U:H2'	35:R3:687:A:C8	2.54	0.43
35:R3:945:G:H21	35:R3:1334:G:H4'	1.84	0.43
35:R3:982:U:H4'	35:R3:983:A:O4'	2.19	0.43
38:sc:115:VAL:O	38:sc:119:ILE:HG13	2.19	0.43
40:se:80:LEU:HB2	40:se:122:VAL:HG11	2.01	0.43
41:sf:74:LEU:O	41:sf:77:THR:OG1	2.35	0.43
54:ss:10:ILE:HG21	54:ss:15:LEU:HD12	2.01	0.43
5:16:28:PHE:HB2	5:16:104:GLU:OE2	2.18	0.43
9:2:256:THR:OG1	33:R1:1797:G:O2'	2.33	0.43
14:24:13:LEU:O	14:24:18:LYS:HD2	2.19	0.43
15:25:50:MET:HE3	15:25:50:MET:HB2	1.83	0.43
15:25:77:VAL:HG23	15:25:89:ILE:HG12	1.99	0.43
31:E:552:ARG:HH12	33:R1:2168:G:H1	1.67	0.43
33:R1:969:G:H2'	33:R1:970:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:2175:C:N4	33:R1:2176:A:C6	2.86	0.43
35:R3:120:A:H4'	35:R3:121:U:OP1	2.18	0.43
35:R3:1318:A:O2'	54:ss:36:ARG:HD3	2.18	0.43
37:sb:17:HIS:HD2	37:sb:38:HIS:O	2.02	0.43
42:sg:69:ARG:NH2	42:sg:96:ASN:OD1	2.52	0.43
44:si:57:VAL:HG23	44:si:58:GLU:H	1.84	0.43
50:so:78:THR:HB	50:so:79:GLN:NE2	2.34	0.43
2:13:56:VAL:HB	2:13:124:VAL:HA	2.01	0.43
4:15:43:GLY:N	33:R1:671:C:OP1	2.45	0.43
9:2:186:ASP:OD1	9:2:186:ASP:N	2.52	0.43
31:E:141:ASN:OD1	31:E:141:ASN:N	2.48	0.43
33:R1:704:G:H1'	33:R1:727:A:N6	2.33	0.43
33:R1:947:A:H2'	33:R1:948:C:C6	2.54	0.43
33:R1:2146:C:HO2'	33:R1:2147:A:P	2.41	0.43
33:R1:2655:G:O2'	33:R1:2664:G:O6	2.31	0.43
33:R1:2665:A:O2'	33:R1:2666:C:OP1	2.36	0.43
33:R1:2794:C:H2'	33:R1:2795:C:C6	2.54	0.43
35:R3:273:U:O2'	35:R3:274:A:H5''	2.18	0.43
35:R3:604:G:H2'	35:R3:605:U:O4'	2.18	0.43
35:R3:1379:G:O2'	35:R3:1380:U:H5'	2.19	0.43
37:sb:63:LYS:HE2	37:sb:63:LYS:HB2	1.87	0.43
38:sc:71:ARG:O	38:sc:74:ILE:HG22	2.18	0.43
40:se:158:LYS:HA	40:se:158:LYS:HD3	1.77	0.43
44:si:42:THR:HB	44:si:44:ARG:HH21	1.83	0.43
1:1:208:TYR:CE1	1:1:209:ILE:HG12	2.54	0.43
3:14:91:SER:O	3:14:93:GLN:N	2.52	0.43
10:20:86:SER:HB3	11:21:52:PRO:HD3	2.00	0.43
12:22:87:PRO:HB3	33:R1:1614:A:C6	2.54	0.43
16:27:9:SER:OG	16:27:10:THR:N	2.52	0.43
22:32:28:SER:O	22:32:36:LYS:HA	2.19	0.43
33:R1:1170:C:HO2'	33:R1:1171:G:H8	1.67	0.43
33:R1:2589:A:H2'	33:R1:2590:A:C8	2.53	0.43
33:R1:2698:U:O2'	33:R1:2699:C:H5'	2.18	0.43
35:R3:265:G:N2	35:R3:267:C:H5'	2.34	0.43
35:R3:390:U:H2'	35:R3:391:G:C8	2.54	0.43
36:T:66:A:H2'	36:T:67:U:H6	1.83	0.43
52:sq:20:ILE:HG21	52:sq:52:CYS:SG	2.59	0.43
55:st:27:MET:HG3	55:st:56:ILE:HG22	2.01	0.43
8:19:7:LEU:HD11	19:3:186:LEU:HD21	2.01	0.42
20:30:52:PHE:CG	34:R2:83:G:H4'	2.54	0.42
28:5:157:THR:HG23	28:5:159:ALA:H	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:6:98:LYS:HG3	29:6:98:LYS:O	2.18	0.42
31:E:103:ARG:NE	31:E:106:GLU:OE1	2.52	0.42
33:R1:274:C:H41	33:R1:363:G:H21	1.67	0.42
33:R1:645:C:O2'	33:R1:646:U:H5'	2.18	0.42
33:R1:783:A:O2'	33:R1:1779:U:O2	2.26	0.42
33:R1:1296:G:OP1	33:R1:2709:G:O2'	2.34	0.42
33:R1:1856:U:H2'	33:R1:1857:G:O4'	2.19	0.42
35:R3:110:C:O2'	51:sp:25:ARG:O	2.30	0.42
35:R3:468:A:H2'	35:R3:468:A:N3	2.33	0.42
35:R3:606:G:N2	35:R3:632:U:OP1	2.24	0.42
35:R3:692:U:O2'	35:R3:694:A:N7	2.38	0.42
35:R3:933:G:O6	42:sg:2:ARG:NH2	2.52	0.42
35:R3:958:A:H8	35:R3:985:C:O2'	2.02	0.42
35:R3:992:U:H1'	35:R3:993:G:N2	2.34	0.42
35:R3:1118:U:H3'	35:R3:1119:C:H6	1.83	0.42
35:R3:1240:U:OP1	42:sg:115:MET:HB2	2.19	0.42
35:R3:1452:C:H4'	35:R3:1453:G:C2	2.54	0.42
38:sc:56:ILE:HG12	38:sc:65:VAL:HG13	2.01	0.42
56:su:11:PHE:HB3	56:su:13:VAL:H	1.84	0.42
56:su:23:GLU:H	56:su:23:GLU:HG2	1.64	0.42
1:1:42:VAL:HG22	1:1:176:GLY:H	1.83	0.42
19:3:121:THR:HB	19:3:127:PHE:CD2	2.54	0.42
25:35:7:ARG:HD2	25:35:7:ARG:HA	1.79	0.42
30:9:94:ILE:HG22	30:9:98:ASP:OD2	2.19	0.42
33:R1:315:G:H2'	33:R1:316:C:C6	2.54	0.42
33:R1:1190:G:H2'	33:R1:1191:G:C8	2.54	0.42
33:R1:1239:G:H2'	33:R1:1240:U:O4'	2.17	0.42
33:R1:1378:A:O2'	33:R1:1380:G:N7	2.44	0.42
33:R1:1678:A:H2'	33:R1:1679:A:O4'	2.19	0.42
33:R1:2070:A:H2'	33:R1:2071:A:O4'	2.19	0.42
33:R1:2567:G:H2'	33:R1:2568:U:C6	2.54	0.42
33:R1:2804:U:H2'	33:R1:2805:C:H6	1.84	0.42
35:R3:553:A:H2'	35:R3:554:A:H8	1.83	0.42
35:R3:575:G:O2'	35:R3:821:G:OP2	2.28	0.42
35:R3:966:G:C2	36:T:34:A:H5'	2.54	0.42
37:sb:84:LEU:HG	37:sb:90:PHE:HE1	1.84	0.42
38:sc:138:GLN:O	38:sc:142:ARG:HG2	2.19	0.42
40:se:156:ARG:HE	40:se:156:ARG:HB2	1.48	0.42
44:si:51:LEU:HD13	44:si:56:MET:HG3	2.00	0.42
46:sk:125:LYS:HZ1	56:su:35:GLU:HA	1.84	0.42
56:su:65:ARG:HA	56:su:65:ARG:HD2	1.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2:145:MET:CE	9:2:153:LEU:HD21	2.46	0.42
10:20:16:ILE:HD13	10:20:16:ILE:HA	1.86	0.42
29:6:108:PHE:HB3	33:R1:2667:C:H1'	2.00	0.42
30:9:66:ASN:HB3	30:9:134:VAL:HG11	2.02	0.42
31:E:38:LEU:HA	31:E:38:LEU:HD23	1.74	0.42
31:E:151:LEU:HD11	31:E:550:TYR:CZ	2.54	0.42
31:E:500:ASP:HB3	31:E:503:PHE:HB3	2.01	0.42
33:R1:1857:G:N2	33:R1:1884:G:H2'	2.33	0.42
33:R1:1906:G:N1	33:R1:1924:C:N3	2.38	0.42
33:R1:2040:G:H2'	33:R1:2041:U:O4'	2.20	0.42
33:R1:2831:G:O2'	33:R1:2884:U:OP1	2.33	0.42
35:R3:312:C:H2'	35:R3:313:A:C8	2.54	0.42
35:R3:634:C:H2'	35:R3:635:A:C8	2.53	0.42
35:R3:676:A:H2'	35:R3:677:U:H6	1.84	0.42
35:R3:1074:G:O2'	37:sb:101:THR:OG1	2.36	0.42
37:sb:147:LEU:HA	37:sb:150:ILE:HD11	2.00	0.42
41:sf:29:ILE:HG21	41:sf:64:VAL:CG2	2.49	0.42
41:sf:29:ILE:HG22	41:sf:34:GLY:HA3	2.01	0.42
42:sg:35:LYS:O	42:sg:39:GLU:HG2	2.19	0.42
45:sj:7:ARG:HH11	45:sj:73:LEU:HD11	1.85	0.42
45:sj:30:LYS:HE3	45:sj:30:LYS:HB3	1.89	0.42
52:sq:42:LYS:HE3	52:sq:42:LYS:HB3	1.81	0.42
5:16:81:ARG:NH2	16:27:5:LYS:HG3	2.32	0.42
7:18:52:SER:O	7:18:55:GLU:HG3	2.19	0.42
31:E:164:SER:HB2	59:E:602:ATP:O1G	2.19	0.42
33:R1:1050:A:O2'	33:R1:1051:G:P	2.78	0.42
33:R1:1167:C:H2'	33:R1:1168:G:O4'	2.20	0.42
33:R1:1328:A:H2'	33:R1:1330:C:C5	2.53	0.42
33:R1:2224:G:H4'	33:R1:2226:C:C2	2.55	0.42
33:R1:2469:A:N6	33:R1:2481:G:O2'	2.42	0.42
33:R1:2595:G:N2	33:R1:2598:A:OP2	2.35	0.42
33:R1:2804:U:H2'	33:R1:2805:C:C6	2.54	0.42
35:R3:32:A:N1	35:R3:552:U:H5	2.17	0.42
35:R3:62:U:H5	35:R3:105:G:O6	2.02	0.42
35:R3:287:U:H2'	35:R3:288:A:H5'	2.01	0.42
35:R3:401:C:H2'	35:R3:402:G:H5'	2.01	0.42
35:R3:918:A:H2'	35:R3:919:A:C8	2.54	0.42
35:R3:1170:A:H2'	35:R3:1171:A:O4'	2.19	0.42
46:sk:125:LYS:HB3	46:sk:125:LYS:HE3	1.66	0.42
48:sm:78:ARG:O	48:sm:82:LEU:HB2	2.20	0.42
3:14:68:GLY:HA3	3:14:78:ARG:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:15:63:LYS:HG2	25:35:11:LYS:HB3	2.00	0.42
8:19:4:ILE:O	8:19:8:GLU:HG3	2.20	0.42
9:2:3:VAL:HG22	9:2:17:LYS:HB2	2.00	0.42
12:22:74:ILE:HD13	12:22:105:VAL:HG22	2.02	0.42
15:25:28:ALA:HB3	15:25:40:ILE:HG22	2.01	0.42
22:32:8:THR:HB	22:32:10:SER:H	1.83	0.42
24:34:3:ARG:HD3	24:34:3:ARG:HA	1.79	0.42
27:4:131:THR:HG21	33:R1:320:A:H2'	2.01	0.42
33:R1:30:G:O2'	33:R1:1214:A:N3	2.47	0.42
33:R1:44:A:H2'	33:R1:45:G:O4'	2.20	0.42
35:R3:8:A:C6	39:sd:205:LYS:HB3	2.54	0.42
35:R3:456:A:N6	35:R3:476:U:H3	2.10	0.42
35:R3:553:A:H2'	35:R3:554:A:C8	2.55	0.42
35:R3:957:U:H2'	35:R3:959:A:OP2	2.19	0.42
35:R3:1143:G:H2'	35:R3:1144:G:H8	1.84	0.42
35:R3:1371:G:O3'	44:si:70:GLY:HA3	2.20	0.42
39:sd:146:GLU:HA	39:sd:149:LYS:HD2	2.01	0.42
42:sg:109:LYS:O	42:sg:110:ARG:HG2	2.20	0.42
44:si:27:ILE:HG23	44:si:62:LEU:HB2	2.02	0.42
2:13:93:ILE:HD13	2:13:93:ILE:HA	1.89	0.42
10:20:14:LYS:HB3	10:20:14:LYS:HE2	1.78	0.42
11:21:51:VAL:HG13	11:21:52:PRO:O	2.20	0.42
15:25:76:ASP:OD1	15:25:77:VAL:N	2.52	0.42
17:28:37:PHE:CZ	17:28:55:MET:HG2	2.54	0.42
31:E:15:VAL:HG23	31:E:19:ARG:HB3	2.01	0.42
31:E:378:GLY:O	31:E:379:THR:OG1	2.38	0.42
33:R1:203:A:OP2	33:R1:204:A:O2'	2.30	0.42
33:R1:528:A:C2	33:R1:2042:A:H2'	2.54	0.42
33:R1:533:G:H2'	33:R1:534:U:C6	2.55	0.42
33:R1:698:C:O2'	33:R1:734:A:N6	2.48	0.42
33:R1:886:A:H3'	33:R1:886:A:N3	2.34	0.42
33:R1:1370:C:H2'	33:R1:1371:G:O4'	2.20	0.42
33:R1:1485:U:H2'	33:R1:1486:U:H6	1.85	0.42
33:R1:2126:A:H2	33:R1:2127:G:H1'	1.83	0.42
33:R1:2545:G:H2'	33:R1:2546:U:O4'	2.19	0.42
33:R1:2896:C:O2'	33:R1:2897:U:O5'	2.36	0.42
35:R3:757:U:O2'	35:R3:879:C:O2	2.36	0.42
35:R3:766:A:OP2	35:R3:812:G:N2	2.52	0.42
50:so:88:ARG:HD3	50:so:88:ARG:HA	1.83	0.42
56:su:34:ARG:HH11	56:su:34:ARG:HG3	1.84	0.42
13:23:61:LEU:HD12	33:R1:1341:G:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:9:68:ARG:O	30:9:72:ILE:HG13	2.19	0.42
31:E:169:ARG:HB3	31:E:169:ARG:HH11	1.84	0.42
33:R1:955:U:H5	33:R1:962:G:H1	1.68	0.42
33:R1:1086:A:H3'	33:R1:1086:A:N3	2.35	0.42
33:R1:1733:G:H2'	33:R1:1734:G:C8	2.53	0.42
33:R1:2177:C:H3'	33:R1:2178:C:H5''	2.02	0.42
33:R1:2412:A:H2'	33:R1:2413:G:O4'	2.20	0.42
33:R1:2688:G:H1'	33:R1:2721:A:N6	2.34	0.42
33:R1:2740:A:H2'	33:R1:2741:A:C8	2.54	0.42
35:R3:834:U:H2'	35:R3:835:U:C6	2.54	0.42
35:R3:984:C:H2'	35:R3:985:C:C6	2.55	0.42
35:R3:1058:G:H2'	35:R3:1059:C:O4'	2.19	0.42
35:R3:1149:C:O2'	35:R3:1150:A:OP1	2.30	0.42
35:R3:1260:G:OP1	35:R3:1284:C:O2'	2.32	0.42
35:R3:1316:G:N1	35:R3:1319:A:OP2	2.50	0.42
36:T:67:U:H2'	36:T:68:C:C6	2.54	0.42
37:sb:17:HIS:CD2	37:sb:39:ILE:HA	2.55	0.42
40:se:80:LEU:HD13	40:se:122:VAL:HG11	2.01	0.42
44:si:29:ILE:N	44:si:32:ARG:O	2.28	0.42
46:sk:23:HIS:HB3	46:sk:30:ILE:HB	2.02	0.42
52:sq:56:ASP:HB2	52:sq:79:GLU:O	2.20	0.42
1:1:200:LYS:HG2	1:1:201:PRO:HD2	2.02	0.42
3:14:77:ILE:O	3:14:77:ILE:HG22	2.20	0.42
6:17:36:THR:OG1	6:17:37:THR:N	2.53	0.42
7:18:69:ASP:OD2	7:18:69:ASP:N	2.51	0.42
26:36:16:ILE:HD13	26:36:25:VAL:HG22	2.02	0.42
33:R1:306:U:H2'	33:R1:307:G:O4'	2.19	0.42
33:R1:638:G:H2'	33:R1:639:U:O4'	2.20	0.42
33:R1:668:A:H2'	33:R1:670:A:H62	1.85	0.42
33:R1:1505:A:H2'	33:R1:1506:U:C6	2.55	0.42
33:R1:1838:C:N4	33:R1:1898:U:H2'	2.35	0.42
33:R1:2081:U:H2'	33:R1:2082:A:C8	2.54	0.42
34:R2:66:A:H61	34:R2:107:G:H3'	1.84	0.42
35:R3:402:G:O2'	35:R3:403:C:H6	2.02	0.42
43:sh:46:GLU:HG3	43:sh:63:LYS:HB2	2.02	0.42
1:1:53:ARG:HB3	1:1:54:LYS:HE2	2.01	0.42
5:16:53:MET:HE2	5:16:53:MET:HB2	1.80	0.42
13:23:30:ILE:HG22	13:23:32:LEU:HG	2.01	0.42
31:E:188:GLN:HE22	31:E:474:ASP:HA	1.85	0.42
31:E:327:SER:HB3	31:E:379:THR:HB	2.02	0.42
33:R1:6:A:H2'	33:R1:7:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1263:U:H2'	33:R1:1264:A:C8	2.55	0.42
33:R1:1919:A:N1	35:R3:1495:U:O2'	2.50	0.42
33:R1:2113:U:H2'	33:R1:2114:A:C8	2.54	0.42
34:R2:32:U:C2	34:R2:33:G:C8	3.08	0.42
35:R3:67:C:H2'	35:R3:68:G:C8	2.54	0.42
35:R3:157:U:O4	35:R3:164:G:O6	2.38	0.42
35:R3:593:U:H2'	35:R3:594:U:C6	2.55	0.42
35:R3:711:G:O2'	35:R3:712:A:H5'	2.20	0.42
35:R3:811:C:O2'	35:R3:901:A:N1	2.52	0.42
35:R3:1223:C:OP2	54:ss:77:ARG:NH2	2.52	0.42
43:sh:86:LYS:HB2	43:sh:124:ILE:HD11	2.02	0.42
46:sk:126:ARG:CG	56:su:33:ARG:HH22	2.32	0.42
50:so:29:ALA:HA	50:so:84:LEU:HD21	2.02	0.42
1:1:186:LYS:HE3	1:1:190:GLU:HB2	2.00	0.42
1:1:208:TYR:CD1	1:1:209:ILE:HG23	2.54	0.42
4:15:89:VAL:O	4:15:94:THR:HG21	2.19	0.42
7:18:51:ALA:HB3	7:18:78:VAL:HG22	2.02	0.42
11:21:71:LYS:HG3	11:21:90:ARG:HG3	2.01	0.42
12:22:61:ASN:ND2	33:R1:495:G:O2'	2.51	0.42
15:25:90:ASP:N	15:25:90:ASP:OD2	2.52	0.42
27:4:147:LEU:HD11	27:4:170:ARG:HD2	2.02	0.42
33:R1:134:G:O6	33:R1:144:A:N1	2.52	0.42
33:R1:709:U:H2'	33:R1:710:U:C6	2.55	0.42
33:R1:1090:A:H61	33:R1:1101:U:H3	1.67	0.42
33:R1:1297:C:OP1	33:R1:2710:C:H4'	2.19	0.42
33:R1:1717:A:H2'	33:R1:1718:G:O4'	2.20	0.42
34:R2:45:A:C4	34:R2:46:A:C8	3.08	0.42
35:R3:246:A:C2	35:R3:282:A:C5	3.08	0.42
35:R3:728:A:H2'	35:R3:729:A:C8	2.54	0.42
35:R3:1219:A:H2'	35:R3:1220:G:C8	2.54	0.42
37:sb:9:LEU:HD21	37:sb:43:GLU:HG2	2.01	0.42
45:sj:7:ARG:HG3	45:sj:101:SER:HB3	2.02	0.42
54:ss:5:LYS:HG3	54:ss:6:LYS:HG2	2.01	0.42
25:35:18:LYS:HB2	33:R1:651:G:OP1	2.20	0.41
30:9:8:LYS:HB2	30:9:9:VAL:H	1.73	0.41
31:E:387:LYS:HB3	31:E:463:GLY:HA2	2.02	0.41
33:R1:558:U:H2'	33:R1:559:G:H8	1.85	0.41
33:R1:588:U:H2'	33:R1:589:U:C6	2.55	0.41
33:R1:687:C:H5	33:R1:787:C:H5''	1.85	0.41
33:R1:742:A:H2'	33:R1:743:A:H8	1.83	0.41
33:R1:1540:G:H2'	33:R1:1541:C:H6	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:2128:G:H1	33:R1:2160:C:N4	2.18	0.41
33:R1:2508:G:H1	33:R1:2580:U:H5	1.67	0.41
33:R1:2636:C:H2'	33:R1:2637:U:C6	2.55	0.41
33:R1:2751:G:H2'	33:R1:2751:G:N3	2.35	0.41
33:R1:2809:A:OP2	33:R1:2890:G:N1	2.26	0.41
35:R3:187:G:C2	35:R3:191:G:C6	3.08	0.41
35:R3:223:A:H2'	35:R3:224:U:H6	1.85	0.41
35:R3:335:C:H2'	35:R3:336:A:H8	1.83	0.41
35:R3:344:A:H5''	35:R3:345:C:C5	2.55	0.41
35:R3:352:C:O2'	35:R3:354:G:OP1	2.31	0.41
35:R3:721:G:H4'	35:R3:722:G:O4'	2.20	0.41
35:R3:1155:A:H2'	35:R3:1156:G:O4'	2.20	0.41
35:R3:1171:A:H2'	35:R3:1172:C:H6	1.84	0.41
35:R3:1179:A:OP2	44:si:94:ARG:NH2	2.52	0.41
37:sb:138:ARG:HB3	37:sb:138:ARG:HH11	1.85	0.41
39:sd:169:TRP:NE1	39:sd:185:PRO:HG3	2.35	0.41
45:sj:40:ILE:HB	45:sj:73:LEU:HB3	2.01	0.41
50:so:22:GLY:O	50:so:27:GLN:NE2	2.41	0.41
1:1:20:GLN:OE1	1:1:20:GLN:N	2.53	0.41
11:21:3:ALA:HA	11:21:40:MET:O	2.20	0.41
24:34:4:THR:HG22	33:R1:687:C:H1'	2.01	0.41
31:E:404:VAL:HG22	31:E:445:LEU:HD11	2.02	0.41
33:R1:286:U:H3	33:R1:354:A:H61	1.66	0.41
33:R1:743:A:O2'	33:R1:1659:G:OP1	2.33	0.41
33:R1:1130:U:C2	33:R1:2025:C:H5''	2.55	0.41
33:R1:1341:G:OP1	33:R1:1397:U:N3	2.47	0.41
33:R1:1842:G:H2'	33:R1:1843:C:H6	1.85	0.41
33:R1:2147:A:C5	33:R1:2148:G:H1'	2.55	0.41
33:R1:2572:A:OP1	33:R1:2574:G:H4'	2.20	0.41
35:R3:100:G:H2'	35:R3:101:A:H8	1.85	0.41
35:R3:592:G:H2'	35:R3:593:U:H6	1.86	0.41
35:R3:692:U:H1'	35:R3:695:A:N7	2.35	0.41
35:R3:958:A:H5'	54:ss:54:ARG:NH1	2.34	0.41
35:R3:983:A:H5'	35:R3:984:C:OP2	2.20	0.41
35:R3:999:C:C3'	35:R3:1000:A:H4'	2.45	0.41
35:R3:1101:A:H4'	35:R3:1102:A:O5'	2.19	0.41
35:R3:1122:U:O2'	35:R3:1123:U:H6	2.03	0.41
35:R3:1228:C:H2'	35:R3:1229:A:H8	1.85	0.41
40:se:100:GLU:O	40:se:102:THR:HG23	2.20	0.41
43:sh:17:GLN:HG2	43:sh:62:LEU:HD13	2.02	0.41
43:sh:86:LYS:HD3	43:sh:86:LYS:HA	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:sn:48:GLN:NE2	54:ss:10:ILE:O	2.53	0.41
52:sq:56:ASP:HB2	52:sq:80:LYS:HA	2.03	0.41
18:29:4:LYS:H	18:29:4:LYS:CE	2.34	0.41
26:36:24:ARG:NH2	26:36:36:ARG:HG3	2.35	0.41
27:4:7:ASP:HB2	27:4:122:GLU:CD	2.44	0.41
33:R1:159:G:H22	33:R1:2216:G:N2	2.18	0.41
33:R1:439:A:H2'	33:R1:440:C:O4'	2.21	0.41
33:R1:569:U:H2'	33:R1:570:G:O4'	2.20	0.41
33:R1:898:C:H2'	33:R1:899:A:O4'	2.20	0.41
33:R1:1005:C:H1'	33:R1:1012:U:N3	2.35	0.41
33:R1:1534:U:O2	33:R1:1536:C:O2'	2.38	0.41
35:R3:144:G:H2'	35:R3:145:G:C8	2.55	0.41
35:R3:201:G:H2'	35:R3:202:G:O4'	2.20	0.41
35:R3:325:A:H2'	35:R3:326:G:O4'	2.21	0.41
35:R3:515:G:H3'	35:R3:516:U:O2	2.20	0.41
35:R3:838:G:C6	35:R3:849:G:C6	3.08	0.41
35:R3:1060:U:H4'	45:sj:53:ILE:HG13	2.02	0.41
35:R3:1330:U:C4	35:R3:1331:G:C6	3.08	0.41
42:sg:78:ARG:HA	42:sg:82:SER:HB2	2.01	0.41
47:sl:42:LYS:HB2	47:sl:88:ASP:HB2	2.02	0.41
49:sn:2:LYS:O	49:sn:5:MET:N	2.44	0.41
51:sp:80:LYS:HA	51:sp:80:LYS:HD2	1.79	0.41
53:sr:35:SER:HA	53:sr:71:ASP:HB2	2.02	0.41
7:18:92:PHE:HB2	7:18:117:PHE:CD2	2.55	0.41
13:23:82:LYS:NZ	33:R1:1340:U:OP2	2.54	0.41
16:27:18:ALA:HB1	33:R1:2271:G:OP1	2.20	0.41
31:E:331:LYS:HD3	31:E:368:MET:HE1	2.03	0.41
33:R1:1589:U:C2	33:R1:1590:A:C8	3.08	0.41
35:R3:665:A:H1'	35:R3:733:G:H5'	2.02	0.41
35:R3:1063:C:H3'	35:R3:1064:G:H2'	2.02	0.41
35:R3:1102:A:C6	35:R3:1103:C:N4	2.88	0.41
37:sb:17:HIS:ND1	37:sb:37:VAL:HG13	2.35	0.41
40:se:13:LYS:HE3	40:se:115:GLU:OE2	2.20	0.41
40:se:104:ILE:HA	40:se:121:ASN:O	2.20	0.41
45:sj:66:GLU:HG2	49:sn:98:ALA:CB	2.50	0.41
47:sl:121:PRO:O	47:sl:122:LYS:HB3	2.19	0.41
56:su:64:ALA:HB1	56:su:66:ARG:HH12	1.85	0.41
1:1:40:GLU:HG3	1:1:178:VAL:HB	2.03	0.41
1:1:212:VAL:HB	1:1:224:VAL:HG22	2.03	0.41
5:16:42:THR:O	5:16:46:ILE:HG12	2.20	0.41
12:22:4:ILE:HG22	12:22:106:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:6:136:ASP:OD2	29:6:136:ASP:C	2.64	0.41
29:6:171:LYS:HG2	29:6:172:GLU:H	1.85	0.41
31:E:392:ASP:OD1	31:E:392:ASP:N	2.52	0.41
33:R1:257:C:H5'	33:R1:258:G:OP2	2.20	0.41
33:R1:1588:G:H2'	33:R1:1589:U:C6	2.56	0.41
33:R1:1916:A:H2'	33:R1:1917:U:O2	2.20	0.41
33:R1:2395:C:H2'	33:R1:2396:G:O4'	2.20	0.41
33:R1:2503:A:N3	33:R1:2503:A:H5'	2.35	0.41
34:R2:14:U:OP2	34:R2:70:C:O2'	2.34	0.41
35:R3:105:G:H2'	35:R3:106:C:O4'	2.19	0.41
35:R3:107:G:O2'	35:R3:108:G:OP2	2.32	0.41
35:R3:185:U:H2'	35:R3:186:C:C6	2.55	0.41
35:R3:590:U:H2'	35:R3:591:U:C6	2.55	0.41
35:R3:827:U:H2'	35:R3:870:U:O4	2.21	0.41
35:R3:925:G:H1'	35:R3:1502:A:C4	2.56	0.41
35:R3:935:A:O2'	35:R3:1383:C:O2	2.38	0.41
36:T:22:G:O2'	36:T:23:A:H5'	2.20	0.41
36:T:44:G:O2'	36:T:45:G:H5'	2.20	0.41
37:sb:158:ASP:O	37:sb:181:PRO:HD2	2.21	0.41
50:so:70:LYS:HG3	50:so:74:VAL:HG13	2.02	0.41
1:1:16:ASP:N	1:1:16:ASP:OD1	2.53	0.41
1:1:21:TYR:N	1:1:21:TYR:HD1	2.19	0.41
2:13:17:VAL:HG22	2:13:55:ILE:HB	2.01	0.41
4:15:14:LYS:HG3	4:15:15:ALA:N	2.35	0.41
5:16:69:PRO:HA	5:16:94:ALA:HB2	2.02	0.41
6:17:69:ARG:C	6:17:71:ARG:H	2.28	0.41
12:22:25:ARG:HG3	12:22:74:ILE:HG22	2.02	0.41
13:23:54:GLU:CD	13:23:54:GLU:H	2.29	0.41
16:27:11:ARG:O	16:27:14:ARG:NH2	2.53	0.41
19:3:46:ARG:HB3	19:3:84:LEU:HD12	2.02	0.41
28:5:159:ALA:HB1	28:5:164:GLU:HB2	2.03	0.41
30:9:43:ASN:HA	30:9:46:PHE:HD2	1.86	0.41
31:E:286:LYS:HD2	31:E:286:LYS:HA	1.90	0.41
33:R1:308:G:H2'	33:R1:309:A:C8	2.56	0.41
33:R1:518:G:H2'	33:R1:519:U:C6	2.56	0.41
33:R1:598:U:H2'	33:R1:599:A:C8	2.55	0.41
33:R1:688:U:C2'	33:R1:689:A:H5'	2.51	0.41
33:R1:881:G:H2'	33:R1:882:G:H8	1.83	0.41
33:R1:1201:U:H2'	33:R1:1202:G:C8	2.56	0.41
33:R1:1429:G:H2'	33:R1:1430:G:C8	2.55	0.41
33:R1:1858:A:H61	33:R1:1884:G:H1'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:R1:1930:G:O2'	33:R1:1968:G:O6	2.30	0.41
33:R1:2099:U:O2	33:R1:2190:G:N2	2.42	0.41
33:R1:2102:G:H1	33:R1:2187:U:H3	1.68	0.41
33:R1:2452:C:H2'	33:R1:2453:A:C8	2.56	0.41
33:R1:2590:A:H2'	33:R1:2591:C:C6	2.56	0.41
35:R3:123:U:H2'	35:R3:124:C:C6	2.55	0.41
35:R3:178:C:H2'	35:R3:179:A:H8	1.85	0.41
35:R3:722:G:H3'	35:R3:722:G:N3	2.36	0.41
35:R3:1425:U:H2'	35:R3:1426:G:H8	1.85	0.41
35:R3:1464:U:H2'	35:R3:1465:A:H8	1.84	0.41
37:sb:19:THR:HG23	37:sb:21:TYR:O	2.21	0.41
37:sb:22:TRP:HE3	37:sb:30:ILE:HD11	1.84	0.41
38:sc:143:LEU:HA	38:sc:143:LEU:HD23	1.81	0.41
43:sh:49:LYS:HB3	43:sh:51:GLU:OE1	2.21	0.41
44:si:20:ILE:O	44:si:20:ILE:HG23	2.21	0.41
33:R1:2313:C:H2'	33:R1:2314:A:C8	2.53	0.41
33:R1:2547:A:H2'	33:R1:2548:U:C6	2.55	0.41
35:R3:131:A:O2'	35:R3:262:A:H8	2.02	0.41
35:R3:690:G:O6	46:sk:52:ARG:NH1	2.53	0.41
35:R3:1117:A:O2'	44:si:107:ALA:HB2	2.20	0.41
35:R3:1320:C:H2'	35:R3:1321:U:C6	2.56	0.41
35:R3:1399:C:H4'	35:R3:1400:C:H5''	2.02	0.41
35:R3:1446:A:O2'	35:R3:1447:A:O5'	2.31	0.41
39:sd:44:LYS:HA	39:sd:45:PRO:HD3	1.95	0.41
41:sf:18:VAL:HG11	41:sf:58:HIS:CD2	2.55	0.41
41:sf:29:ILE:HG23	41:sf:66:ALA:HB2	2.02	0.41
42:sg:65:LEU:O	42:sg:69:ARG:HG2	2.21	0.41
45:sj:26:VAL:HG23	45:sj:36:VAL:HG21	2.03	0.41
46:sk:33:ILE:HD12	46:sk:69:CYS:SG	2.61	0.41
49:sn:39:ASP:OD1	49:sn:39:ASP:N	2.37	0.41
1:1:9:ARG:HG2	1:1:12:ARG:NH2	2.36	0.41
6:17:106:ASP:OD2	33:R1:1649:G:O2'	2.29	0.41
10:20:30:VAL:HG12	10:20:33:VAL:H	1.86	0.41
31:E:48:LEU:HA	31:E:51:ILE:HD12	2.02	0.41
33:R1:910:A:H2'	33:R1:911:A:C8	2.56	0.41
33:R1:1024:G:O2'	33:R1:1144:A:O2'	2.39	0.41
33:R1:1171:G:N2	33:R1:1176:U:O2	2.43	0.41
33:R1:2802:G:H2'	33:R1:2803:G:H8	1.85	0.41
33:R1:2895:G:O2'	33:R1:2896:C:H5'	2.21	0.41
35:R3:272:C:N4	35:R3:273:U:O4	2.54	0.41
35:R3:617:G:C5'	51:sp:46:LYS:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:sb:20:ARG:HA	37:sb:36:LYS:O	2.21	0.41
38:sc:52:SER:HB2	38:sc:114:LEU:HG	2.03	0.41
43:sh:38:VAL:HG11	43:sh:102:VAL:HG22	2.03	0.41
52:sq:3:LYS:HD2	52:sq:3:LYS:HA	1.75	0.41
55:st:23:ARG:HA	55:st:26:MET:HE2	2.02	0.41
1:1:190:GLU:O	1:1:194:VAL:HG23	2.21	0.41
2:13:1:MET:CG	2:13:2:LYS:H	2.34	0.41
6:17:24:MET:HB2	6:17:44:LEU:HD13	2.02	0.41
9:2:154:ALA:HA	9:2:159:THR:HG22	2.02	0.41
11:21:78:ARG:HE	11:21:78:ARG:HB2	1.70	0.41
14:24:39:ASN:HB3	14:24:62:ALA:HB3	2.03	0.41
15:25:31:TYR:O	15:25:92:VAL:HA	2.21	0.41
15:25:69:GLU:N	15:25:69:GLU:CD	2.79	0.41
20:30:11:SER:HB2	20:30:31:ILE:HD11	2.02	0.41
23:33:29:LYS:HE2	33:R1:2286:G:H5'	2.03	0.41
23:33:33:LEU:HD21	33:R1:2286:G:C5	2.56	0.41
28:5:37:MET:SD	28:5:52:ALA:HB1	2.60	0.41
28:5:131:VAL:HG22	28:5:151:LEU:H	1.86	0.41
28:5:174:PHE:O	28:5:176:PHE:N	2.53	0.41
30:9:8:LYS:H	30:9:8:LYS:HG3	1.53	0.41
30:9:145:ASN:OD1	30:9:146:VAL:N	2.53	0.41
31:E:136:ASP:HB3	31:E:143:GLN:OE1	2.21	0.41
33:R1:257:C:H3'	33:R1:258:G:C8	2.55	0.41
33:R1:285:G:H2'	33:R1:286:U:H6	1.86	0.41
33:R1:285:G:C6	33:R1:356:G:O6	2.74	0.41
33:R1:357:C:H2'	33:R1:358:U:N1	2.36	0.41
33:R1:685:A:H5''	33:R1:788:A:H62	1.85	0.41
33:R1:721:A:H2'	33:R1:722:A:H8	1.82	0.41
33:R1:1344:U:O2	33:R1:1385:A:H5'	2.21	0.41
33:R1:1722:A:H2'	33:R1:1723:G:O4'	2.21	0.41
33:R1:1881:C:H2'	33:R1:1882:U:O4'	2.21	0.41
33:R1:2661:G:O2'	33:R1:2662:A:C8	2.63	0.41
33:R1:2663:G:H2'	33:R1:2664:G:O4'	2.21	0.41
33:R1:2846:G:H2'	33:R1:2847:U:H6	1.85	0.41
33:R1:2857:G:N2	33:R1:2860:A:OP2	2.34	0.41
35:R3:142:G:N3	35:R3:196:A:H2	2.18	0.41
35:R3:298:A:H2'	35:R3:299:G:O4'	2.21	0.41
35:R3:388:G:N2	35:R3:388:G:OP1	2.49	0.41
35:R3:417:G:O2'	35:R3:418:C:H6	2.03	0.41
35:R3:493:A:H5'	35:R3:494:G:OP2	2.21	0.41
35:R3:545:C:H5'	39:sd:68:GLU:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:734:G:O2'	53:sr:59:LYS:HD3	2.21	0.41
35:R3:763:G:H2'	35:R3:764:C:C6	2.55	0.41
35:R3:1150:A:C2	45:sj:41:PRO:HG2	2.56	0.41
35:R3:1171:A:H2'	35:R3:1172:C:C6	2.56	0.41
35:R3:1260:G:H4'	35:R3:1283:U:O2'	2.21	0.41
35:R3:1456:A:H2'	35:R3:1457:G:O4'	2.20	0.41
37:sb:72:LYS:NZ	37:sb:204:ASP:HB3	2.36	0.41
39:sd:100:VAL:O	39:sd:104:MET:HG3	2.20	0.41
45:sj:6:ILE:HD11	45:sj:76:ILE:HD12	2.01	0.41
52:sq:10:ARG:HA	52:sq:57:VAL:HA	2.02	0.41
53:sr:9:PHE:HB3	53:sr:10:CYS:H	1.63	0.41
53:sr:55:ALA:O	53:sr:59:LYS:HG3	2.20	0.41
55:st:19:HIS:O	55:st:23:ARG:HG2	2.20	0.41
1:1:192:LEU:HD13	1:1:196:LEU:HD23	2.03	0.41
3:14:109:SER:N	3:14:113:MET:HE1	2.36	0.41
9:2:33:LEU:HD12	9:2:33:LEU:HA	1.89	0.41
14:24:40:LEU:HD23	14:24:61:GLU:HG3	2.03	0.41
21:31:57:VAL:O	21:31:61:ASN:N	2.47	0.41
30:9:94:ILE:O	30:9:94:ILE:HG13	2.21	0.41
33:R1:500:G:H2'	33:R1:502:A:C2	2.55	0.41
33:R1:1581:G:H2'	33:R1:1582:C:C6	2.56	0.41
35:R3:3:A:H8	35:R3:3:A:OP2	2.04	0.41
35:R3:286:C:H2'	35:R3:287:U:C6	2.57	0.41
35:R3:321:A:H5''	35:R3:328:C:C4	2.56	0.41
35:R3:410:G:OP2	39:sd:25:ARG:HG3	2.20	0.41
35:R3:636:U:H2'	35:R3:637:C:C6	2.56	0.41
35:R3:938:A:N3	35:R3:1376:U:O2'	2.37	0.41
35:R3:1092:A:H5''	42:sg:3:ARG:NH1	2.36	0.41
35:R3:1329:A:C5	35:R3:1330:U:C5	3.09	0.41
38:sc:106:ARG:H	38:sc:106:ARG:HG2	1.67	0.41
39:sd:169:TRP:CE2	39:sd:185:PRO:HG3	2.56	0.41
45:sj:59:LYS:O	45:sj:62:ARG:HD2	2.21	0.41
49:sn:5:MET:HE3	49:sn:5:MET:HB3	1.93	0.41
2:13:31:GLU:HG2	2:13:142:ILE:HG13	2.02	0.40
2:13:32:LEU:HD22	2:13:54:ILE:HG21	2.03	0.40
2:13:49:ASP:HB2	2:13:118:MET:HG2	2.02	0.40
4:15:98:ALA:HB3	4:15:100:ILE:HD12	2.03	0.40
8:19:3:ILE:HG13	19:3:9:VAL:HG11	2.02	0.40
9:2:44:ASN:H	33:R1:1812:U:HO2'	1.63	0.40
12:22:74:ILE:CD1	12:22:105:VAL:HG22	2.50	0.40
13:23:34:VAL:HG23	13:23:81:LYS:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:29:6:LEU:HA	18:29:56:LEU:HD11	2.03	0.40
19:3:118:PHE:HB2	33:R1:2823:A:OP1	2.22	0.40
31:E:81:ASN:HB3	31:E:84:HIS:CG	2.56	0.40
31:E:412:LEU:HD22	31:E:412:LEU:H	1.86	0.40
33:R1:716:A:H2'	33:R1:717:C:O4'	2.22	0.40
33:R1:2064:C:H5''	36:T:75:C:O2'	2.20	0.40
33:R1:2562:U:C2'	33:R1:2563:U:H5'	2.50	0.40
35:R3:100:G:C4	35:R3:101:A:C8	3.09	0.40
35:R3:294:U:H2'	35:R3:295:C:C6	2.55	0.40
35:R3:640:A:H2'	35:R3:641:U:C2	2.56	0.40
35:R3:1096:C:H2'	35:R3:1097:C:H6	1.86	0.40
35:R3:1294:G:H2'	35:R3:1295:U:C6	2.56	0.40
35:R3:1469:C:H2'	35:R3:1470:U:O4'	2.21	0.40
38:sc:46:LEU:HB3	38:sc:49:ALA:HB3	2.03	0.40
54:ss:44:ILE:HD13	54:ss:63:ASP:HA	2.02	0.40
10:20:71:ASN:HB3	10:20:109:VAL:HG11	2.02	0.40
12:22:6:LYS:HA	12:22:103:ILE:O	2.22	0.40
13:23:54:GLU:HB2	13:23:88:LYS:HD2	2.02	0.40
16:27:5:LYS:NZ	33:R1:2252:G:N7	2.69	0.40
21:31:15:SER:O	21:31:33:ASN:HA	2.21	0.40
25:35:39:ARG:NE	33:R1:2362:C:OP1	2.52	0.40
28:5:49:LEU:HG	28:5:66:ILE:HD12	2.04	0.40
31:E:136:ASP:OD1	31:E:139:ASN:HB2	2.21	0.40
31:E:194:ASP:OD1	31:E:194:ASP:N	2.52	0.40
33:R1:365:U:H2'	33:R1:366:C:C6	2.56	0.40
33:R1:753:A:H2'	33:R1:754:U:C6	2.56	0.40
33:R1:2667:C:C2'	33:R1:2668:G:H5'	2.52	0.40
35:R3:8:A:C5	39:sd:205:LYS:HB3	2.57	0.40
35:R3:320:A:C2	35:R3:333:U:H5	2.38	0.40
35:R3:640:A:HO2'	35:R3:641:U:P	2.43	0.40
35:R3:1102:A:C2'	35:R3:1103:C:H5'	2.51	0.40
35:R3:1120:C:C2	35:R3:1121:U:C5	3.08	0.40
35:R3:1486:G:H2'	35:R3:1487:G:O4'	2.21	0.40
39:sd:11:SER:OG	39:sd:16:THR:O	2.37	0.40
39:sd:173:ASP:C	39:sd:175:GLY:H	2.29	0.40
44:si:90:ASP:C	44:si:92:SER:H	2.29	0.40
56:su:24:LYS:NZ	56:su:25:ALA:HB2	2.36	0.40
56:su:57:LYS:HE3	56:su:57:LYS:HB3	1.80	0.40
1:1:21:TYR:N	1:1:21:TYR:CD1	2.88	0.40
1:1:183:ASP:OD1	1:1:183:ASP:N	2.55	0.40
2:13:78:THR:HB	33:R1:2641:G:H5''	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:15:82:LEU:HD13	4:15:120:VAL:HG11	2.03	0.40
8:19:27:VAL:HA	8:19:82:SER:O	2.22	0.40
10:20:79:ILE:HD13	10:20:79:ILE:HA	1.86	0.40
16:27:24:LYS:HA	16:27:24:LYS:HD3	1.95	0.40
33:R1:128:C:H2'	33:R1:129:C:C6	2.55	0.40
33:R1:138:U:O2'	33:R1:140:C:N4	2.55	0.40
33:R1:596:U:H2'	33:R1:597:G:C8	2.56	0.40
33:R1:1231:U:H2'	33:R1:1232:G:H8	1.86	0.40
33:R1:2079:U:H2'	33:R1:2080:A:O4'	2.21	0.40
33:R1:2144:G:H1'	33:R1:2148:G:H21	1.85	0.40
33:R1:2323:G:O2'	33:R1:2324:U:H5'	2.20	0.40
33:R1:2554:U:H2'	33:R1:2555:U:C6	2.57	0.40
34:R2:106:G:H2'	34:R2:107:G:O4'	2.21	0.40
35:R3:362:G:N1	35:R3:365:U:OP2	2.50	0.40
35:R3:920:U:H2'	35:R3:921:U:C6	2.56	0.40
35:R3:1107:C:OP1	38:sc:171:ARG:HG3	2.21	0.40
35:R3:1162:C:H2'	35:R3:1163:A:C8	2.56	0.40
35:R3:1208:C:H5'	35:R3:1209:C:OP2	2.21	0.40
35:R3:1309:G:P	48:sm:86:ARG:HH21	2.44	0.40
36:T:53:G:N2	36:T:62:C:O2'	2.55	0.40
42:sg:16:LYS:HG3	42:sg:43:TYR:CZ	2.56	0.40
42:sg:49:LEU:HD23	42:sg:49:LEU:C	2.46	0.40
46:sk:12:ARG:NE	46:sk:75:GLU:OE2	2.41	0.40
51:sp:37:GLY:HA3	51:sp:52:LEU:HA	2.02	0.40
55:st:4:LYS:O	55:st:7:LYS:HD2	2.20	0.40
56:su:15:LEU:HA	56:su:15:LEU:HD13	1.81	0.40
4:15:42:SER:OG	33:R1:672:C:OP2	2.29	0.40
4:15:79:LEU:HD23	4:15:79:LEU:HA	1.84	0.40
6:17:79:LEU:HD23	6:17:83:LEU:HD12	2.03	0.40
12:22:22:ASP:OD1	12:22:22:ASP:N	2.53	0.40
19:3:63:PRO:O	33:R1:2786:U:O2'	2.35	0.40
25:35:53:ASP:OD1	33:R1:2359:C:O2'	2.29	0.40
29:6:28:LYS:NZ	29:6:79:THR:O	2.29	0.40
31:E:199:ALA:O	31:E:202:GLU:HG2	2.22	0.40
33:R1:81:G:H2'	33:R1:82:U:O4'	2.22	0.40
33:R1:134:G:N1	33:R1:144:A:H2	2.08	0.40
33:R1:979:A:H5'	33:R1:980:A:C5'	2.52	0.40
33:R1:1090:A:N6	33:R1:1101:U:H3	2.20	0.40
33:R1:1536:C:H4'	33:R1:1537:G:C2	2.57	0.40
33:R1:2176:A:H2'	33:R1:2177:C:C6	2.56	0.40
35:R3:18:C:H4'	35:R3:1078:U:O2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:R3:19:A:OP1	40:se:134:ASN:ND2	2.54	0.40
35:R3:107:G:H2'	35:R3:108:G:H21	1.85	0.40
35:R3:264:C:H2'	35:R3:265:G:O4'	2.21	0.40
35:R3:864:A:H2'	35:R3:865:A:C8	2.56	0.40
35:R3:1263:C:H2'	35:R3:1264:U:C6	2.57	0.40
40:se:44:ARG:HG2	40:se:70:MET:CG	2.51	0.40
40:se:98:ALA:HB2	40:se:123:LEU:HG	2.04	0.40
43:sh:39:LEU:HD21	43:sh:128:VAL:HG21	2.04	0.40
45:sj:57:VAL:HG23	45:sj:57:VAL:O	2.22	0.40
54:ss:9:PHE:CE2	54:ss:36:ARG:HD2	2.56	0.40
54:ss:44:ILE:HA	54:ss:61:VAL:HG12	2.04	0.40
8:19:28:LYS:HE3	8:19:28:LYS:HB3	1.84	0.40
12:22:23:LEU:HD11	22:32:21:LEU:HB2	2.03	0.40
28:5:5:ASP:OD1	28:5:5:ASP:N	2.53	0.40
28:5:135:ILE:H	28:5:135:ILE:HG13	1.67	0.40
30:9:99:ILE:HD13	30:9:130:VAL:HG11	2.03	0.40
31:E:219:ARG:HB2	31:E:244:TYR:CD2	2.57	0.40
31:E:434:LYS:HE2	31:E:434:LYS:HB3	1.79	0.40
33:R1:29:U:H2'	33:R1:30:G:C8	2.57	0.40
33:R1:438:G:H2'	33:R1:439:A:C8	2.57	0.40
33:R1:1444:G:H2'	33:R1:1445:G:H8	1.87	0.40
33:R1:2107:G:C6	33:R1:2183:A:C6	3.09	0.40
33:R1:2126:A:H2'	33:R1:2127:G:H4'	2.03	0.40
33:R1:2246:G:H2'	33:R1:2247:A:H8	1.85	0.40
35:R3:49:U:O2'	35:R3:50:A:H2'	2.21	0.40
35:R3:139:A:H2'	35:R3:140:U:C6	2.57	0.40
35:R3:371:A:H2'	35:R3:372:C:O4'	2.21	0.40
35:R3:720:C:H2'	35:R3:721:G:C8	2.56	0.40
35:R3:875:U:O2'	43:sh:14:ARG:HD2	2.22	0.40
35:R3:1004:A:C2'	35:R3:1005:A:H5''	2.51	0.40
35:R3:1127:G:H1	35:R3:1145:A:N6	2.18	0.40
35:R3:1347:G:O5'	44:si:108:ARG:HB2	2.22	0.40
40:se:36:THR:HG21	40:se:63:MET:HE2	2.04	0.40
40:se:130:THR:HA	40:se:135:VAL:HG11	2.04	0.40
44:si:28:VAL:HG12	44:si:62:LEU:O	2.21	0.40
48:sm:106:ARG:NH1	48:sm:110:GLY:O	2.54	0.40
56:su:24:LYS:C	56:su:24:LYS:HD2	2.47	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	218/220 (99%)	197 (90%)	21 (10%)	0	100	100
2	13	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
3	14	120/122 (98%)	112 (93%)	7 (6%)	1 (1%)	16	50
4	15	141/143 (99%)	127 (90%)	14 (10%)	0	100	100
5	16	134/136 (98%)	128 (96%)	5 (4%)	1 (1%)	18	53
6	17	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
7	18	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
8	19	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
9	2	269/271 (99%)	243 (90%)	26 (10%)	0	100	100
10	20	115/117 (98%)	115 (100%)	0	0	100	100
11	21	101/103 (98%)	91 (90%)	9 (9%)	1 (1%)	12	45
12	22	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
13	23	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
14	24	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
15	25	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
16	27	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
17	28	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
18	29	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
19	3	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
20	30	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
21	31	64/66 (97%)	55 (86%)	9 (14%)	0	100	100
22	32	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
23	33	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
24	34	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
25	35	62/64 (97%)	60 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	36	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
27	4	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
28	5	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
29	6	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
30	9	147/149 (99%)	128 (87%)	17 (12%)	2 (1%)	9	36
31	E	549/551 (100%)	508 (92%)	39 (7%)	2 (0%)	30	65
37	sb	216/218 (99%)	188 (87%)	27 (12%)	1 (0%)	24	60
38	sc	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
39	sd	203/205 (99%)	185 (91%)	18 (9%)	0	100	100
40	se	155/157 (99%)	133 (86%)	20 (13%)	2 (1%)	9	38
41	sf	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
42	sg	149/151 (99%)	135 (91%)	13 (9%)	1 (1%)	18	53
43	sh	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
44	si	125/127 (98%)	100 (80%)	24 (19%)	1 (1%)	16	50
45	sj	96/98 (98%)	83 (86%)	12 (12%)	1 (1%)	12	45
46	sk	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
47	sl	121/123 (98%)	95 (78%)	26 (22%)	0	100	100
48	sm	110/112 (98%)	97 (88%)	13 (12%)	0	100	100
49	sn	98/100 (98%)	84 (86%)	13 (13%)	1 (1%)	12	45
50	so	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
51	sp	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
52	sq	78/80 (98%)	64 (82%)	14 (18%)	0	100	100
53	sr	63/65 (97%)	60 (95%)	3 (5%)	0	100	100
54	ss	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
55	st	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
56	su	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	7	34
All	All	6353/6455 (98%)	5789 (91%)	549 (9%)	15 (0%)	44	76

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	14	110	GLU
31	E	17	PRO

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Mol	Chain	Res	Type
40	se	122	VAL
42	sg	11	ILE
45	sj	100	ILE
11	21	51	VAL
30	9	8	LYS
44	si	57	VAL
30	9	9	VAL
56	su	24	LYS
31	E	548	ILE
37	sb	18	GLN
40	se	121	ASN
49	sn	98	ALA
5	16	69	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	1	106/171 (62%)	95 (90%)	11 (10%)	7	28
2	13	116/116 (100%)	109 (94%)	7 (6%)	17	50
3	14	103/103 (100%)	97 (94%)	6 (6%)	18	51
4	15	102/102 (100%)	97 (95%)	5 (5%)	22	56
5	16	109/109 (100%)	107 (98%)	2 (2%)	51	77
6	17	100/100 (100%)	97 (97%)	3 (3%)	36	69
7	18	86/86 (100%)	80 (93%)	6 (7%)	14	44
8	19	99/99 (100%)	88 (89%)	11 (11%)	6	25
9	2	216/216 (100%)	207 (96%)	9 (4%)	26	61
10	20	89/89 (100%)	86 (97%)	3 (3%)	32	66
11	21	84/84 (100%)	81 (96%)	3 (4%)	31	65
12	22	93/93 (100%)	89 (96%)	4 (4%)	26	60
13	23	80/80 (100%)	80 (100%)	0	100	100
14	24	83/83 (100%)	76 (92%)	7 (8%)	10	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	25	78/78 (100%)	74 (95%)	4 (5%)	21	55
16	27	63/63 (100%)	58 (92%)	5 (8%)	11	39
17	28	67/67 (100%)	65 (97%)	2 (3%)	36	69
18	29	55/55 (100%)	52 (94%)	3 (6%)	19	53
19	3	164/164 (100%)	151 (92%)	13 (8%)	11	39
20	30	48/48 (100%)	47 (98%)	1 (2%)	47	75
21	31	59/59 (100%)	54 (92%)	5 (8%)	10	36
22	32	47/47 (100%)	43 (92%)	4 (8%)	10	36
23	33	45/45 (100%)	43 (96%)	2 (4%)	25	60
24	34	38/38 (100%)	35 (92%)	3 (8%)	11	39
25	35	51/51 (100%)	51 (100%)	0	100	100
26	36	34/34 (100%)	33 (97%)	1 (3%)	37	70
27	4	165/165 (100%)	155 (94%)	10 (6%)	17	49
28	5	148/148 (100%)	136 (92%)	12 (8%)	11	38
29	6	137/137 (100%)	126 (92%)	11 (8%)	11	38
30	9	114/114 (100%)	106 (93%)	8 (7%)	14	44
31	E	460/463 (99%)	423 (92%)	37 (8%)	11	38
37	sb	180/180 (100%)	169 (94%)	11 (6%)	17	49
38	sc	170/170 (100%)	162 (95%)	8 (5%)	23	58
39	sd	172/172 (100%)	164 (95%)	8 (5%)	23	58
40	se	119/119 (100%)	106 (89%)	13 (11%)	6	26
41	sf	87/87 (100%)	82 (94%)	5 (6%)	18	52
42	sg	124/124 (100%)	115 (93%)	9 (7%)	13	42
43	sh	104/104 (100%)	99 (95%)	5 (5%)	23	57
44	si	105/105 (100%)	100 (95%)	5 (5%)	23	57
45	sj	86/86 (100%)	83 (96%)	3 (4%)	32	65
46	sk	89/89 (100%)	88 (99%)	1 (1%)	65	83
47	sl	103/103 (100%)	88 (85%)	15 (15%)	3	15
48	sm	91/91 (100%)	85 (93%)	6 (7%)	15	46
49	sn	83/83 (100%)	75 (90%)	8 (10%)	8	31
50	so	76/76 (100%)	71 (93%)	5 (7%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	sp	65/65 (100%)	59 (91%)	6 (9%)	8	33
52	sq	74/74 (100%)	72 (97%)	2 (3%)	39	71
53	sr	55/56 (98%)	53 (96%)	2 (4%)	31	65
54	ss	70/70 (100%)	64 (91%)	6 (9%)	10	36
55	st	65/65 (100%)	62 (95%)	3 (5%)	24	58
56	su	55/55 (100%)	44 (80%)	11 (20%)	1	7
All	All	5212/5281 (99%)	4882 (94%)	330 (6%)	18	48

All (330) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	10	VAL
1	1	14	LYS
1	1	35	THR
1	1	56	ASP
1	1	163	TYR
1	1	178	VAL
1	1	181	ASP
1	1	189	LEU
1	1	192	LEU
1	1	193	LEU
1	1	224	VAL
2	13	5	THR
2	13	18	VAL
2	13	28	LEU
2	13	48	VAL
2	13	84	ILE
2	13	86	GLN
2	13	138	GLN
3	14	28	SER
3	14	32	TYR
3	14	53	LYS
3	14	75	SER
3	14	76	VAL
3	14	91	SER
4	15	6	LEU
4	15	84	LYS
4	15	92	LEU
4	15	103	ILE
4	15	120	VAL

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Mol	Chain	Res	Type
5	16	36	VAL
5	16	42	THR
6	17	2	ARG
6	17	14	SER
6	17	38	LEU
7	18	21	LEU
7	18	27	VAL
7	18	38	GLN
7	18	43	ASN
7	18	47	VAL
7	18	65	THR
8	19	3	ILE
8	19	4	ILE
8	19	16	VAL
8	19	25	VAL
8	19	27	VAL
8	19	31	VAL
8	19	39	LEU
8	19	72	VAL
8	19	84	SER
8	19	96	LEU
8	19	103	THR
9	2	19	VAL
9	2	50	THR
9	2	93	VAL
9	2	119	VAL
9	2	129	LEU
9	2	191	LEU
9	2	222	THR
9	2	251	THR
9	2	270	ARG
10	20	7	VAL
10	20	15	LYS
10	20	39	ILE
11	21	19	THR
11	21	29	THR
11	21	91	GLN
12	22	22	ASP
12	22	51	LEU
12	22	70	LYS
12	22	76	VAL
14	24	16	LYS

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Mol	Chain	Res	Type
14	24	17	ASP
14	24	27	VAL
14	24	29	SER
14	24	42	LYS
14	24	78	LYS
14	24	80	ASP
15	25	20	LEU
15	25	40	ILE
15	25	42	LEU
15	25	64	VAL
16	27	21	LEU
16	27	43	THR
16	27	51	VAL
16	27	82	ILE
16	27	83	GLU
17	28	32	LEU
17	28	34	SER
18	29	16	THR
18	29	18	LEU
18	29	49	ASP
19	3	9	VAL
19	3	25	THR
19	3	48	ILE
19	3	84	LEU
19	3	100	LEU
19	3	104	VAL
19	3	106	LYS
19	3	109	VAL
19	3	150	GLN
19	3	151	THR
19	3	177	VAL
19	3	199	SER
19	3	203	VAL
20	30	6	ILE
21	31	9	TYR
21	31	44	PHE
21	31	50	ASP
21	31	51	VAL
21	31	66	ILE
22	32	5	ASN
22	32	22	THR
22	32	53	VAL

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Mol	Chain	Res	Type
22	32	54	ILE
23	33	16	THR
23	33	26	LYS
24	34	8	SER
24	34	15	SER
24	34	25	LYS
26	36	6	SER
27	4	5	LEU
27	4	63	LYS
27	4	70	SER
27	4	74	LYS
27	4	75	SER
27	4	105	LEU
27	4	110	SER
27	4	146	VAL
27	4	176	ASP
27	4	187	VAL
28	5	4	HIS
28	5	5	ASP
28	5	17	THR
28	5	27	VAL
28	5	34	THR
28	5	56	LEU
28	5	65	LEU
28	5	107	VAL
28	5	126	ASN
28	5	129	MET
28	5	136	ILE
28	5	148	VAL
29	6	35	THR
29	6	38	ASP
29	6	41	GLU
29	6	48	THR
29	6	71	LEU
29	6	75	VAL
29	6	89	VAL
29	6	105	SER
29	6	130	ILE
29	6	132	LEU
29	6	170	THR
30	9	5	LEU
30	9	9	VAL

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Mol	Chain	Res	Type
30	9	12	LEU
30	9	19	VAL
30	9	77	THR
30	9	110	VAL
30	9	117	LEU
30	9	147	VAL
31	E	46	SER
31	E	58	ASP
31	E	69	ILE
31	E	91	GLU
31	E	95	SER
31	E	97	VAL
31	E	107	VAL
31	E	110	LEU
31	E	141	ASN
31	E	142	VAL
31	E	155	ASP
31	E	157	ASP
31	E	160	ILE
31	E	163	LEU
31	E	173	LEU
31	E	174	CYS
31	E	182	ASP
31	E	216	THR
31	E	218	ASP
31	E	224	ASN
31	E	274	GLU
31	E	285	SER
31	E	300	THR
31	E	301	GLU
31	E	337	LEU
31	E	364	THR
31	E	376	ASP
31	E	380	ILE
31	E	381	THR
31	E	398	MET
31	E	403	THR
31	E	412	LEU
31	E	424	SER
31	E	437	ASP
31	E	461	VAL
31	E	513	ASP

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Mol	Chain	Res	Type
31	E	529	GLU
37	sb	17	HIS
37	sb	59	ILE
37	sb	81	ASP
37	sb	86	CYS
37	sb	129	THR
37	sb	140	LEU
37	sb	146	SER
37	sb	173	LYS
37	sb	195	VAL
37	sb	216	VAL
37	sb	220	VAL
38	sc	32	LEU
38	sc	55	VAL
38	sc	96	VAL
38	sc	137	VAL
38	sc	161	ILE
38	sc	163	ARG
38	sc	164	THR
38	sc	186	SER
39	sd	8	LEU
39	sd	22	SER
39	sd	39	GLN
39	sd	128	VAL
39	sd	137	SER
39	sd	158	LEU
39	sd	168	THR
39	sd	172	VAL
40	se	11	GLN
40	se	17	VAL
40	se	23	THR
40	se	45	VAL
40	se	63	MET
40	se	70	MET
40	se	91	SER
40	se	122	VAL
40	se	123	LEU
40	se	139	THR
40	se	152	VAL
40	se	156	ARG
40	se	163	ILE
41	sf	61	LEU

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Mol	Chain	Res	Type
41	sf	62	MET
41	sf	63	ASN
41	sf	97	THR
41	sf	98	GLU
42	sg	5	VAL
42	sg	6	ILE
42	sg	21	LEU
42	sg	44	SER
42	sg	83	THR
42	sg	88	VAL
42	sg	124	SER
42	sg	140	VAL
42	sg	141	HIS
43	sh	29	SER
43	sh	31	LEU
43	sh	53	ASP
43	sh	98	LEU
43	sh	103	VAL
44	si	18	VAL
44	si	38	PHE
44	si	51	LEU
44	si	114	LYS
44	si	115	VAL
45	sj	85	ASP
45	sj	91	ASP
45	sj	102	LEU
46	sk	54	SER
47	sl	2	THR
47	sl	3	VAL
47	sl	14	LYS
47	sl	15	VAL
47	sl	34	THR
47	sl	39	THR
47	sl	46	SER
47	sl	48	LEU
47	sl	53	ARG
47	sl	54	VAL
47	sl	57	THR
47	sl	58	ASN
47	sl	63	THR
47	sl	78	VAL
47	sl	111	GLN

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Mol	Chain	Res	Type
48	sm	15	VAL
48	sm	20	SER
48	sm	44	ILE
48	sm	52	ILE
48	sm	67	ASP
48	sm	101	THR
49	sn	4	SER
49	sn	33	VAL
49	sn	34	ASN
49	sn	47	LEU
49	sn	49	THR
49	sn	54	SER
49	sn	66	THR
49	sn	91	GLU
50	so	2	LEU
50	so	39	GLN
50	so	61	GLN
50	so	74	VAL
50	so	86	LEU
51	sp	13	LYS
51	sp	20	VAL
51	sp	34	GLU
51	sp	48	GLU
51	sp	52	LEU
51	sp	53	ASP
52	sq	50	ASN
52	sq	75	VAL
53	sr	9	PHE
53	sr	70	THR
54	ss	32	THR
54	ss	36	ARG
54	ss	37	SER
54	ss	48	ILE
54	ss	57	VAL
54	ss	63	ASP
55	st	11	ILE
55	st	13	SER
55	st	85	LEU
56	su	15	LEU
56	su	22	CYS
56	su	23	GLU
56	su	27	VAL

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Mol	Chain	Res	Type
56	su	28	LEU
56	su	30	GLU
56	su	36	PHE
56	su	55	HIS
56	su	62	GLU
56	su	63	ASN
56	su	65	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	58	ASN
1	1	172	HIS
2	13	47	HIS
2	13	58	ASN
2	13	80	HIS
2	13	128	ASN
3	14	29	HIS
3	14	88	ASN
3	14	93	GLN
4	15	104	GLN
5	16	22	GLN
6	17	81	ASN
9	2	24	HIS
9	2	85	ASN
9	2	152	GLN
10	20	80	ASN
11	21	12	HIS
12	22	31	GLN
15	25	75	GLN
16	27	57	HIS
18	29	25	GLN
19	3	32	ASN
26	36	13	ASN
27	4	9	GLN
27	4	195	GLN
30	9	20	ASN
30	9	33	GLN
31	E	41	ASN
31	E	66	GLN
31	E	191	ASN
31	E	400	ASN

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Mol	Chain	Res	Type
31	E	460	GLN
31	E	473	ASN
37	sb	17	HIS
37	sb	18	GLN
37	sb	50	ASN
38	sc	24	ASN
38	sc	68	HIS
39	sd	125	ASN
39	sd	135	GLN
39	sd	163	GLN
40	se	121	ASN
41	sf	11	HIS
41	sf	58	HIS
42	sg	121	ASN
43	sh	15	ASN
46	sk	118	ASN
47	sl	111	GLN
51	sp	9	HIS
51	sp	26	ASN
53	sr	30	ASN
55	st	2	ASN
55	st	19	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	M	8/9 (88%)	1 (12%)	0
33	R1	2902/2903 (99%)	688 (23%)	23 (0%)
34	R2	118/119 (99%)	26 (22%)	1 (0%)
35	R3	1528/1531 (99%)	450 (29%)	30 (1%)
36	T	75/76 (98%)	30 (40%)	0
All	All	4631/4638 (99%)	1195 (25%)	54 (1%)

All (1195) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
32	M	9	A
33	R1	2	G
33	R1	5	A
33	R1	10	A
33	R1	11	C

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Mol	Chain	Res	Type
33	R1	12	U
33	R1	27	G
33	R1	29	U
33	R1	34	U
33	R1	35	G
33	R1	36	G
33	R1	46	G
33	R1	51	G
33	R1	60	G
33	R1	62	U
33	R1	63	A
33	R1	71	A
33	R1	72	U
33	R1	73	A
33	R1	74	A
33	R1	75	G
33	R1	78	U
33	R1	79	C
33	R1	80	G
33	R1	83	A
33	R1	84	A
33	R1	85	G
33	R1	87	U
33	R1	88	G
33	R1	96	C
33	R1	102	U
33	R1	110	G
33	R1	118	A
33	R1	119	A
33	R1	120	U
33	R1	125	A
33	R1	136	G
33	R1	139	U
33	R1	140	C
33	R1	143	C
33	R1	144	A
33	R1	146	A
33	R1	152	A
33	R1	154	U
33	R1	155	A
33	R1	156	A
33	R1	158	U

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Mol	Chain	Res	Type
33	R1	159	G
33	R1	162	U
33	R1	163	C
33	R1	164	C
33	R1	176	A
33	R1	178	G
33	R1	181	A
33	R1	196	A
33	R1	199	A
33	R1	200	U
33	R1	203	A
33	R1	213	A
33	R1	215	G
33	R1	216	A
33	R1	218	A
33	R1	222	A
33	R1	224	U
33	R1	227	A
33	R1	228	C
33	R1	230	G
33	R1	233	A
33	R1	239	C
33	R1	248	G
33	R1	249	C
33	R1	256	A
33	R1	257	C
33	R1	258	G
33	R1	261	G
33	R1	265	A
33	R1	266	G
33	R1	272	A
33	R1	274	C
33	R1	275	C
33	R1	276	U
33	R1	277	G
33	R1	280	U
33	R1	281	C
33	R1	282	A
33	R1	285	G
33	R1	286	U
33	R1	304	U
33	R1	311	A

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Mol	Chain	Res	Type
33	R1	326	G
33	R1	329	G
33	R1	330	A
33	R1	345	A
33	R1	348	A
33	R1	352	A
33	R1	353	C
33	R1	354	A
33	R1	355	U
33	R1	359	G
33	R1	361	G
33	R1	365	U
33	R1	369	U
33	R1	371	A
33	R1	372	G
33	R1	373	U
33	R1	380	G
33	R1	383	C
33	R1	386	G
33	R1	387	U
33	R1	388	G
33	R1	389	G
33	R1	395	U
33	R1	396	G
33	R1	399	U
33	R1	401	A
33	R1	404	A
33	R1	405	U
33	R1	406	G
33	R1	407	G
33	R1	411	G
33	R1	412	A
33	R1	413	C
33	R1	414	C
33	R1	424	G
33	R1	428	A
33	R1	443	A
33	R1	447	A
33	R1	452	G
33	R1	454	A
33	R1	456	C
33	R1	477	A

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Mol	Chain	Res	Type
33	R1	478	A
33	R1	480	A
33	R1	481	G
33	R1	489	G
33	R1	490	C
33	R1	491	G
33	R1	503	A
33	R1	504	A
33	R1	505	A
33	R1	506	G
33	R1	509	C
33	R1	527	C
33	R1	528	A
33	R1	529	A
33	R1	530	G
33	R1	531	C
33	R1	532	A
33	R1	533	G
33	R1	534	U
33	R1	541	A
33	R1	543	G
33	R1	545	U
33	R1	546	U
33	R1	547	A
33	R1	548	G
33	R1	549	G
33	R1	550	C
33	R1	554	U
33	R1	555	G
33	R1	563	A
33	R1	571	U
33	R1	573	U
33	R1	575	A
33	R1	580	U
33	R1	581	C
33	R1	591	U
33	R1	601	C
33	R1	603	A
33	R1	614	A
33	R1	615	U
33	R1	622	G
33	R1	627	A

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Mol	Chain	Res	Type
33	R1	637	A
33	R1	645	C
33	R1	646	U
33	R1	647	G
33	R1	653	U
33	R1	654	A
33	R1	655	A
33	R1	668	A
33	R1	685	A
33	R1	686	U
33	R1	688	U
33	R1	689	A
33	R1	696	G
33	R1	704	G
33	R1	705	A
33	R1	711	G
33	R1	712	G
33	R1	713	G
33	R1	717	C
33	R1	730	A
33	R1	738	G
33	R1	740	C
33	R1	746	U
33	R1	747	U
33	R1	762	U
33	R1	775	G
33	R1	776	G
33	R1	782	A
33	R1	784	G
33	R1	785	G
33	R1	789	A
33	R1	791	C
33	R1	792	A
33	R1	805	G
33	R1	806	C
33	R1	812	C
33	R1	819	A
33	R1	827	U
33	R1	829	A
33	R1	830	G
33	R1	831	G
33	R1	845	A

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Mol	Chain	Res	Type
33	R1	846	U
33	R1	847	U
33	R1	856	G
33	R1	858	G
33	R1	859	G
33	R1	860	U
33	R1	869	G
33	R1	870	U
33	R1	871	U
33	R1	872	U
33	R1	875	G
33	R1	877	A
33	R1	878	A
33	R1	882	G
33	R1	886	A
33	R1	887	U
33	R1	888	C
33	R1	889	C
33	R1	891	G
33	R1	892	A
33	R1	896	A
33	R1	897	C
33	R1	898	C
33	R1	901	C
33	R1	902	C
33	R1	904	G
33	R1	907	G
33	R1	910	A
33	R1	914	G
33	R1	915	C
33	R1	931	U
33	R1	932	U
33	R1	933	A
33	R1	941	A
33	R1	946	C
33	R1	958	U
33	R1	961	C
33	R1	971	G
33	R1	973	A
33	R1	974	G
33	R1	975	A
33	R1	979	A

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Mol	Chain	Res	Type
33	R1	980	A
33	R1	983	A
33	R1	988	A
33	R1	989	G
33	R1	994	C
33	R1	995	C
33	R1	996	A
33	R1	999	U
33	R1	1005	C
33	R1	1012	U
33	R1	1013	C
33	R1	1021	A
33	R1	1022	G
33	R1	1026	G
33	R1	1033	U
33	R1	1045	C
33	R1	1046	A
33	R1	1050	A
33	R1	1051	G
33	R1	1052	C
33	R1	1060	U
33	R1	1061	U
33	R1	1062	G
33	R1	1064	C
33	R1	1065	U
33	R1	1066	U
33	R1	1067	A
33	R1	1070	A
33	R1	1071	G
33	R1	1072	C
33	R1	1073	A
33	R1	1075	C
33	R1	1077	A
33	R1	1078	U
33	R1	1079	C
33	R1	1083	U
33	R1	1084	A
33	R1	1085	A
33	R1	1087	G
33	R1	1088	A
33	R1	1094	U
33	R1	1095	A

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Mol	Chain	Res	Type
33	R1	1096	A
33	R1	1103	A
33	R1	1104	C
33	R1	1106	G
33	R1	1109	C
33	R1	1110	G
33	R1	1111	A
33	R1	1112	G
33	R1	1114	C
33	R1	1115	G
33	R1	1116	G
33	R1	1128	G
33	R1	1130	U
33	R1	1132	U
33	R1	1134	A
33	R1	1135	C
33	R1	1141	U
33	R1	1157	G
33	R1	1166	G
33	R1	1171	G
33	R1	1173	U
33	R1	1174	U
33	R1	1175	A
33	R1	1176	U
33	R1	1179	G
33	R1	1180	U
33	R1	1182	G
33	R1	1186	G
33	R1	1195	G
33	R1	1205	A
33	R1	1206	G
33	R1	1213	A
33	R1	1214	A
33	R1	1237	A
33	R1	1238	G
33	R1	1247	A
33	R1	1248	G
33	R1	1250	G
33	R1	1253	A
33	R1	1256	G
33	R1	1271	G
33	R1	1272	A

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Mol	Chain	Res	Type
33	R1	1281	G
33	R1	1287	A
33	R1	1300	G
33	R1	1301	A
33	R1	1311	G
33	R1	1321	A
33	R1	1323	C
33	R1	1329	U
33	R1	1341	G
33	R1	1345	C
33	R1	1352	U
33	R1	1365	A
33	R1	1367	A
33	R1	1368	G
33	R1	1379	U
33	R1	1383	A
33	R1	1386	C
33	R1	1392	A
33	R1	1393	A
33	R1	1395	A
33	R1	1416	G
33	R1	1419	A
33	R1	1428	C
33	R1	1432	G
33	R1	1452	G
33	R1	1453	A
33	R1	1459	G
33	R1	1461	C
33	R1	1481	U
33	R1	1482	G
33	R1	1493	C
33	R1	1494	A
33	R1	1497	U
33	R1	1503	A
33	R1	1509	A
33	R1	1515	A
33	R1	1519	G
33	R1	1523	U
33	R1	1524	G
33	R1	1531	C
33	R1	1532	A
33	R1	1534	U

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Mol	Chain	Res	Type
33	R1	1535	A
33	R1	1536	C
33	R1	1537	G
33	R1	1554	U
33	R1	1559	U
33	R1	1566	A
33	R1	1569	A
33	R1	1578	U
33	R1	1582	C
33	R1	1583	A
33	R1	1584	U
33	R1	1608	A
33	R1	1610	A
33	R1	1622	G
33	R1	1634	A
33	R1	1647	U
33	R1	1648	U
33	R1	1649	G
33	R1	1664	A
33	R1	1667	G
33	R1	1674	G
33	R1	1675	C
33	R1	1693	U
33	R1	1714	U
33	R1	1715	G
33	R1	1730	C
33	R1	1732	C
33	R1	1738	G
33	R1	1757	A
33	R1	1759	A
33	R1	1764	C
33	R1	1773	A
33	R1	1776	G
33	R1	1782	U
33	R1	1784	A
33	R1	1786	A
33	R1	1788	C
33	R1	1799	G
33	R1	1800	C
33	R1	1801	A
33	R1	1808	A
33	R1	1812	U

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Mol	Chain	Res	Type
33	R1	1816	C
33	R1	1829	A
33	R1	1835	G
33	R1	1838	C
33	R1	1855	U
33	R1	1868	C
33	R1	1869	G
33	R1	1870	C
33	R1	1872	A
33	R1	1873	G
33	R1	1884	G
33	R1	1891	G
33	R1	1900	A
33	R1	1906	G
33	R1	1912	A
33	R1	1913	A
33	R1	1914	C
33	R1	1915	U
33	R1	1916	A
33	R1	1919	A
33	R1	1927	A
33	R1	1929	G
33	R1	1930	G
33	R1	1937	A
33	R1	1938	A
33	R1	1952	A
33	R1	1955	U
33	R1	1965	C
33	R1	1966	A
33	R1	1967	C
33	R1	1970	A
33	R1	1971	U
33	R1	1972	G
33	R1	1980	G
33	R1	1991	U
33	R1	1997	C
33	R1	2022	U
33	R1	2023	C
33	R1	2030	A
33	R1	2031	A
33	R1	2033	A
33	R1	2035	G

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Mol	Chain	Res	Type
33	R1	2036	C
33	R1	2043	C
33	R1	2055	C
33	R1	2056	G
33	R1	2058	A
33	R1	2059	A
33	R1	2061	G
33	R1	2062	A
33	R1	2064	C
33	R1	2069	G
33	R1	2072	C
33	R1	2079	U
33	R1	2080	A
33	R1	2093	G
33	R1	2096	C
33	R1	2099	U
33	R1	2107	G
33	R1	2109	U
33	R1	2111	U
33	R1	2112	G
33	R1	2113	U
33	R1	2115	G
33	R1	2116	G
33	R1	2117	A
33	R1	2118	U
33	R1	2119	A
33	R1	2120	G
33	R1	2122	U
33	R1	2123	G
33	R1	2124	G
33	R1	2125	G
33	R1	2126	A
33	R1	2128	G
33	R1	2131	U
33	R1	2132	U
33	R1	2133	G
33	R1	2134	A
33	R1	2135	A
33	R1	2137	U
33	R1	2145	C
33	R1	2146	C
33	R1	2147	A

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Mol	Chain	Res	Type
33	R1	2148	G
33	R1	2150	C
33	R1	2153	C
33	R1	2157	G
33	R1	2158	A
33	R1	2161	C
33	R1	2164	C
33	R1	2166	U
33	R1	2168	G
33	R1	2170	A
33	R1	2171	A
33	R1	2172	U
33	R1	2173	A
33	R1	2174	C
33	R1	2175	C
33	R1	2176	A
33	R1	2177	C
33	R1	2178	C
33	R1	2179	C
33	R1	2181	U
33	R1	2182	U
33	R1	2184	A
33	R1	2188	U
33	R1	2189	U
33	R1	2198	A
33	R1	2204	G
33	R1	2211	A
33	R1	2213	U
33	R1	2214	C
33	R1	2225	A
33	R1	2226	C
33	R1	2238	G
33	R1	2239	G
33	R1	2250	G
33	R1	2279	G
33	R1	2283	C
33	R1	2287	A
33	R1	2288	A
33	R1	2291	U
33	R1	2292	U
33	R1	2297	A
33	R1	2305	U

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Mol	Chain	Res	Type
33	R1	2306	C
33	R1	2308	G
33	R1	2309	A
33	R1	2310	C
33	R1	2311	A
33	R1	2316	G
33	R1	2319	G
33	R1	2322	A
33	R1	2325	G
33	R1	2333	A
33	R1	2336	A
33	R1	2345	G
33	R1	2347	C
33	R1	2350	C
33	R1	2354	C
33	R1	2357	G
33	R1	2359	C
33	R1	2361	G
33	R1	2377	A
33	R1	2383	G
33	R1	2385	C
33	R1	2389	G
33	R1	2391	G
33	R1	2402	U
33	R1	2403	C
33	R1	2406	A
33	R1	2423	U
33	R1	2424	C
33	R1	2425	A
33	R1	2429	G
33	R1	2430	A
33	R1	2434	A
33	R1	2435	A
33	R1	2436	G
33	R1	2439	A
33	R1	2441	U
33	R1	2447	G
33	R1	2448	A
33	R1	2468	A
33	R1	2470	G
33	R1	2476	A
33	R1	2478	A

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Mol	Chain	Res	Type
33	R1	2484	G
33	R1	2494	G
33	R1	2497	A
33	R1	2498	C
33	R1	2502	G
33	R1	2503	A
33	R1	2504	U
33	R1	2505	G
33	R1	2506	U
33	R1	2518	A
33	R1	2520	C
33	R1	2529	G
33	R1	2547	A
33	R1	2554	U
33	R1	2560	A
33	R1	2562	U
33	R1	2563	U
33	R1	2564	A
33	R1	2565	A
33	R1	2566	A
33	R1	2567	G
33	R1	2572	A
33	R1	2573	C
33	R1	2585	U
33	R1	2586	U
33	R1	2602	A
33	R1	2609	U
33	R1	2610	C
33	R1	2613	U
33	R1	2615	U
33	R1	2629	U
33	R1	2630	G
33	R1	2646	C
33	R1	2650	U
33	R1	2660	A
33	R1	2662	A
33	R1	2663	G
33	R1	2664	G
33	R1	2666	C
33	R1	2669	G
33	R1	2671	G
33	R1	2682	A

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Mol	Chain	Res	Type
33	R1	2689	U
33	R1	2690	U
33	R1	2700	A
33	R1	2701	U
33	R1	2706	A
33	R1	2714	G
33	R1	2716	C
33	R1	2718	G
33	R1	2720	U
33	R1	2726	A
33	R1	2732	G
33	R1	2733	A
33	R1	2738	A
33	R1	2739	U
33	R1	2744	G
33	R1	2748	A
33	R1	2755	C
33	R1	2762	C
33	R1	2765	A
33	R1	2772	C
33	R1	2773	C
33	R1	2774	C
33	R1	2775	G
33	R1	2778	A
33	R1	2779	U
33	R1	2793	C
33	R1	2798	U
33	R1	2800	A
33	R1	2808	G
33	R1	2814	A
33	R1	2815	C
33	R1	2816	G
33	R1	2817	U
33	R1	2818	U
33	R1	2820	A
33	R1	2821	A
33	R1	2840	C
33	R1	2847	U
33	R1	2848	G
33	R1	2849	U
33	R1	2859	G
33	R1	2861	U

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Mol	Chain	Res	Type
33	R1	2867	G
33	R1	2873	A
33	R1	2880	C
33	R1	2883	A
33	R1	2887	A
33	R1	2891	U
33	R1	2893	A
33	R1	2896	C
33	R1	2897	U
33	R1	2900	A
33	R1	2902	C
33	R1	2903	U
34	R2	9	G
34	R2	13	G
34	R2	16	G
34	R2	35	C
34	R2	41	G
34	R2	42	C
34	R2	44	G
34	R2	50	A
34	R2	51	G
34	R2	52	A
34	R2	63	C
34	R2	64	G
34	R2	65	U
34	R2	66	A
34	R2	67	G
34	R2	87	U
34	R2	88	C
34	R2	89	U
34	R2	90	C
34	R2	108	A
34	R2	109	A
34	R2	112	G
34	R2	113	C
34	R2	114	C
34	R2	117	G
34	R2	119	A
35	R3	3	A
35	R3	4	U
35	R3	6	G
35	R3	7	A

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Mol	Chain	Res	Type
35	R3	9	G
35	R3	11	G
35	R3	22	G
35	R3	30	U
35	R3	31	G
35	R3	32	A
35	R3	39	G
35	R3	47	C
35	R3	48	C
35	R3	49	U
35	R3	50	A
35	R3	51	A
35	R3	53	A
35	R3	54	C
35	R3	60	A
35	R3	61	G
35	R3	63	C
35	R3	64	G
35	R3	66	A
35	R3	68	G
35	R3	70	U
35	R3	71	A
35	R3	76	G
35	R3	77	A
35	R3	78	A
35	R3	80	A
35	R3	81	A
35	R3	82	G
35	R3	83	C
35	R3	84	U
35	R3	85	U
35	R3	86	G
35	R3	91	U
35	R3	93	U
35	R3	94	G
35	R3	95	C
35	R3	96	U
35	R3	97	G
35	R3	100	G
35	R3	102	G
35	R3	105	G
35	R3	107	G

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Mol	Chain	Res	Type
35	R3	108	G
35	R3	115	G
35	R3	116	A
35	R3	120	A
35	R3	121	U
35	R3	122	G
35	R3	128	G
35	R3	130	A
35	R3	131	A
35	R3	133	U
35	R3	134	G
35	R3	135	C
35	R3	151	A
35	R3	153	C
35	R3	155	A
35	R3	157	U
35	R3	164	G
35	R3	171	A
35	R3	172	A
35	R3	173	U
35	R3	174	A
35	R3	181	A
35	R3	182	A
35	R3	183	C
35	R3	184	G
35	R3	190	A
35	R3	191	G
35	R3	192	A
35	R3	197	A
35	R3	202	G
35	R3	204	G
35	R3	206	C
35	R3	207	C
35	R3	208	U
35	R3	209	U
35	R3	212	G
35	R3	214	C
35	R3	215	C
35	R3	218	U
35	R3	220	G
35	R3	223	A
35	R3	226	G

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Mol	Chain	Res	Type
35	R3	230	G
35	R3	240	G
35	R3	243	A
35	R3	245	U
35	R3	247	G
35	R3	250	A
35	R3	251	G
35	R3	255	G
35	R3	258	G
35	R3	263	A
35	R3	264	C
35	R3	266	G
35	R3	267	C
35	R3	272	C
35	R3	273	U
35	R3	274	A
35	R3	279	A
35	R3	280	C
35	R3	287	U
35	R3	289	G
35	R3	290	C
35	R3	293	G
35	R3	296	U
35	R3	298	A
35	R3	302	G
35	R3	313	A
35	R3	316	C
35	R3	322	C
35	R3	323	U
35	R3	324	G
35	R3	325	A
35	R3	327	A
35	R3	328	C
35	R3	329	A
35	R3	330	C
35	R3	331	G
35	R3	333	U
35	R3	338	A
35	R3	339	C
35	R3	344	A
35	R3	351	G
35	R3	352	C

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Mol	Chain	Res	Type
35	R3	353	A
35	R3	354	G
35	R3	363	A
35	R3	364	A
35	R3	367	U
35	R3	369	G
35	R3	370	C
35	R3	372	C
35	R3	373	A
35	R3	376	G
35	R3	377	G
35	R3	388	G
35	R3	391	G
35	R3	392	C
35	R3	394	G
35	R3	396	C
35	R3	398	U
35	R3	401	C
35	R3	402	G
35	R3	403	C
35	R3	406	G
35	R3	411	A
35	R3	413	G
35	R3	415	A
35	R3	416	G
35	R3	417	G
35	R3	418	C
35	R3	421	U
35	R3	422	C
35	R3	423	G
35	R3	425	G
35	R3	427	U
35	R3	428	G
35	R3	429	U
35	R3	437	U
35	R3	438	U
35	R3	440	C
35	R3	451	A
35	R3	454	G
35	R3	456	A
35	R3	465	A
35	R3	466	A

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Mol	Chain	Res	Type
35	R3	467	U
35	R3	468	A
35	R3	470	C
35	R3	472	U
35	R3	473	U
35	R3	479	U
35	R3	480	U
35	R3	482	A
35	R3	484	G
35	R3	487	A
35	R3	492	C
35	R3	493	A
35	R3	495	A
35	R3	496	A
35	R3	497	G
35	R3	498	A
35	R3	501	C
35	R3	502	A
35	R3	511	C
35	R3	517	G
35	R3	518	C
35	R3	521	G
35	R3	524	G
35	R3	530	G
35	R3	531	U
35	R3	532	A
35	R3	538	G
35	R3	539	A
35	R3	540	G
35	R3	541	G
35	R3	547	A
35	R3	549	C
35	R3	552	U
35	R3	553	A
35	R3	559	A
35	R3	562	U
35	R3	564	C
35	R3	566	G
35	R3	572	A
35	R3	573	A
35	R3	576	C
35	R3	577	G

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Mol	Chain	Res	Type
35	R3	579	A
35	R3	589	U
35	R3	596	A
35	R3	597	G
35	R3	607	A
35	R3	610	U
35	R3	611	C
35	R3	612	C
35	R3	613	C
35	R3	628	G
35	R3	630	A
35	R3	632	U
35	R3	633	G
35	R3	640	A
35	R3	641	U
35	R3	642	A
35	R3	651	C
35	R3	652	U
35	R3	653	U
35	R3	665	A
35	R3	673	A
35	R3	684	U
35	R3	686	U
35	R3	688	G
35	R3	695	A
35	R3	701	U
35	R3	702	A
35	R3	703	G
35	R3	713	G
35	R3	721	G
35	R3	723	U
35	R3	724	G
35	R3	731	G
35	R3	734	G
35	R3	738	C
35	R3	739	C
35	R3	743	A
35	R3	749	A
35	R3	754	C
35	R3	755	G
35	R3	774	G
35	R3	777	A

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Mol	Chain	Res	Type
35	R3	779	C
35	R3	781	A
35	R3	787	A
35	R3	791	G
35	R3	792	A
35	R3	793	U
35	R3	794	A
35	R3	815	A
35	R3	817	C
35	R3	818	G
35	R3	819	A
35	R3	829	G
35	R3	832	G
35	R3	838	G
35	R3	839	C
35	R3	840	C
35	R3	841	C
35	R3	843	U
35	R3	844	G
35	R3	846	G
35	R3	849	G
35	R3	850	U
35	R3	851	G
35	R3	863	U
35	R3	864	A
35	R3	870	U
35	R3	871	U
35	R3	872	A
35	R3	876	C
35	R3	877	G
35	R3	878	A
35	R3	902	G
35	R3	914	A
35	R3	926	G
35	R3	933	G
35	R3	935	A
35	R3	947	G
35	R3	958	A
35	R3	959	A
35	R3	960	U
35	R3	961	U
35	R3	966	G

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Mol	Chain	Res	Type
35	R3	969	A
35	R3	975	A
35	R3	976	G
35	R3	977	A
35	R3	990	C
35	R3	991	U
35	R3	992	U
35	R3	1000	A
35	R3	1001	C
35	R3	1002	G
35	R3	1003	G
35	R3	1004	A
35	R3	1006	G
35	R3	1007	U
35	R3	1008	U
35	R3	1009	U
35	R3	1015	G
35	R3	1017	U
35	R3	1020	G
35	R3	1024	G
35	R3	1027	C
35	R3	1028	C
35	R3	1031	C
35	R3	1032	G
35	R3	1033	G
35	R3	1037	C
35	R3	1039	G
35	R3	1040	U
35	R3	1045	C
35	R3	1049	U
35	R3	1050	G
35	R3	1052	U
35	R3	1053	G
35	R3	1054	C
35	R3	1065	U
35	R3	1084	G
35	R3	1085	U
35	R3	1094	G
35	R3	1095	U
35	R3	1101	A
35	R3	1103	C
35	R3	1104	G

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Mol	Chain	Res	Type
35	R3	1108	G
35	R3	1113	C
35	R3	1114	C
35	R3	1118	U
35	R3	1119	C
35	R3	1123	U
35	R3	1125	U
35	R3	1126	U
35	R3	1129	C
35	R3	1130	A
35	R3	1131	G
35	R3	1133	G
35	R3	1134	G
35	R3	1137	C
35	R3	1138	G
35	R3	1139	G
35	R3	1140	C
35	R3	1142	G
35	R3	1145	A
35	R3	1150	A
35	R3	1151	A
35	R3	1152	A
35	R3	1157	A
35	R3	1158	C
35	R3	1159	U
35	R3	1168	U
35	R3	1169	A
35	R3	1182	G
35	R3	1184	G
35	R3	1187	G
35	R3	1196	A
35	R3	1197	A
35	R3	1200	C
35	R3	1201	A
35	R3	1208	C
35	R3	1209	C
35	R3	1212	U
35	R3	1213	A
35	R3	1227	A
35	R3	1228	C
35	R3	1238	A
35	R3	1240	U

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Mol	Chain	Res	Type
35	R3	1255	G
35	R3	1257	A
35	R3	1258	G
35	R3	1260	G
35	R3	1261	A
35	R3	1262	C
35	R3	1267	C
35	R3	1268	G
35	R3	1271	A
35	R3	1275	A
35	R3	1280	A
35	R3	1285	A
35	R3	1286	U
35	R3	1287	A
35	R3	1297	G
35	R3	1298	U
35	R3	1300	G
35	R3	1302	C
35	R3	1305	G
35	R3	1306	A
35	R3	1312	G
35	R3	1315	U
35	R3	1332	A
35	R3	1336	C
35	R3	1346	A
35	R3	1353	G
35	R3	1363	A
35	R3	1368	A
35	R3	1370	G
35	R3	1376	U
35	R3	1378	C
35	R3	1389	C
35	R3	1396	A
35	R3	1398	A
35	R3	1400	C
35	R3	1404	C
35	R3	1405	G
35	R3	1409	C
35	R3	1419	G
35	R3	1422	G
35	R3	1429	A
35	R3	1437	A

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Mol	Chain	Res	Type
35	R3	1440	U
35	R3	1441	A
35	R3	1442	G
35	R3	1443	C
35	R3	1446	A
35	R3	1448	C
35	R3	1451	U
35	R3	1452	C
35	R3	1455	G
35	R3	1473	G
35	R3	1474	U
35	R3	1475	G
35	R3	1487	G
35	R3	1491	G
35	R3	1492	A
35	R3	1493	A
35	R3	1494	G
35	R3	1497	G
35	R3	1499	A
35	R3	1502	A
35	R3	1506	U
35	R3	1517	G
35	R3	1519	A
35	R3	1520	C
35	R3	1529	G
35	R3	1530	G
36	T	8	U
36	T	13	C
36	T	16	C
36	T	17	U
36	T	18	G
36	T	19	G
36	T	20	G
36	T	21	A
36	T	24	G
36	T	25	C
36	T	26	A
36	T	42	G
36	T	43	G
36	T	44	G
36	T	46	G
36	T	47	U

Continued on next page...

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Mol	Chain	Res	Type
36	T	51	C
36	T	57	G
36	T	58	A
36	T	59	U
36	T	60	C
36	T	61	C
36	T	62	C
36	T	63	G
36	T	65	C
36	T	66	A
36	T	69	A
36	T	70	C
36	T	74	C
36	T	76	A

All (54) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	R1	198	C
33	R1	271	G
33	R1	276	U
33	R1	446	G
33	R1	453	A
33	R1	479	A
33	R1	784	G
33	R1	859	G
33	R1	903	C
33	R1	1020	A
33	R1	1050	A
33	R1	1236	G
33	R1	1915	U
33	R1	2115	G
33	R1	2146	C
33	R1	2174	C
33	R1	2178	C
33	R1	2663	G
33	R1	2665	A
33	R1	2699	C
33	R1	2839	G
33	R1	2846	G
33	R1	2896	C
34	R2	64	G

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Mol	Chain	Res	Type
35	R3	94	G
35	R3	95	C
35	R3	120	A
35	R3	288	A
35	R3	301	G
35	R3	312	C
35	R3	363	A
35	R3	416	G
35	R3	428	G
35	R3	453	G
35	R3	497	G
35	R3	500	G
35	R3	561	U
35	R3	588	G
35	R3	612	C
35	R3	640	A
35	R3	672	U
35	R3	685	G
35	R3	753	A
35	R3	837	U
35	R3	870	U
35	R3	1003	G
35	R3	1064	G
35	R3	1125	U
35	R3	1137	C
35	R3	1149	C
35	R3	1150	A
35	R3	1270	G
35	R3	1297	G
35	R3	1305	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 130 ligands modelled in this entry, 128 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
59	ATP	E	601	60	32,33,33	0.53	0	48,52,52	0.36	0
59	ATP	E	602	60	32,33,33	0.50	0	48,52,52	0.28	0

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
59	ATP	E	601	60	-	2/22/38/38	0/3/3/3
59	ATP	E	602	60	-	6/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

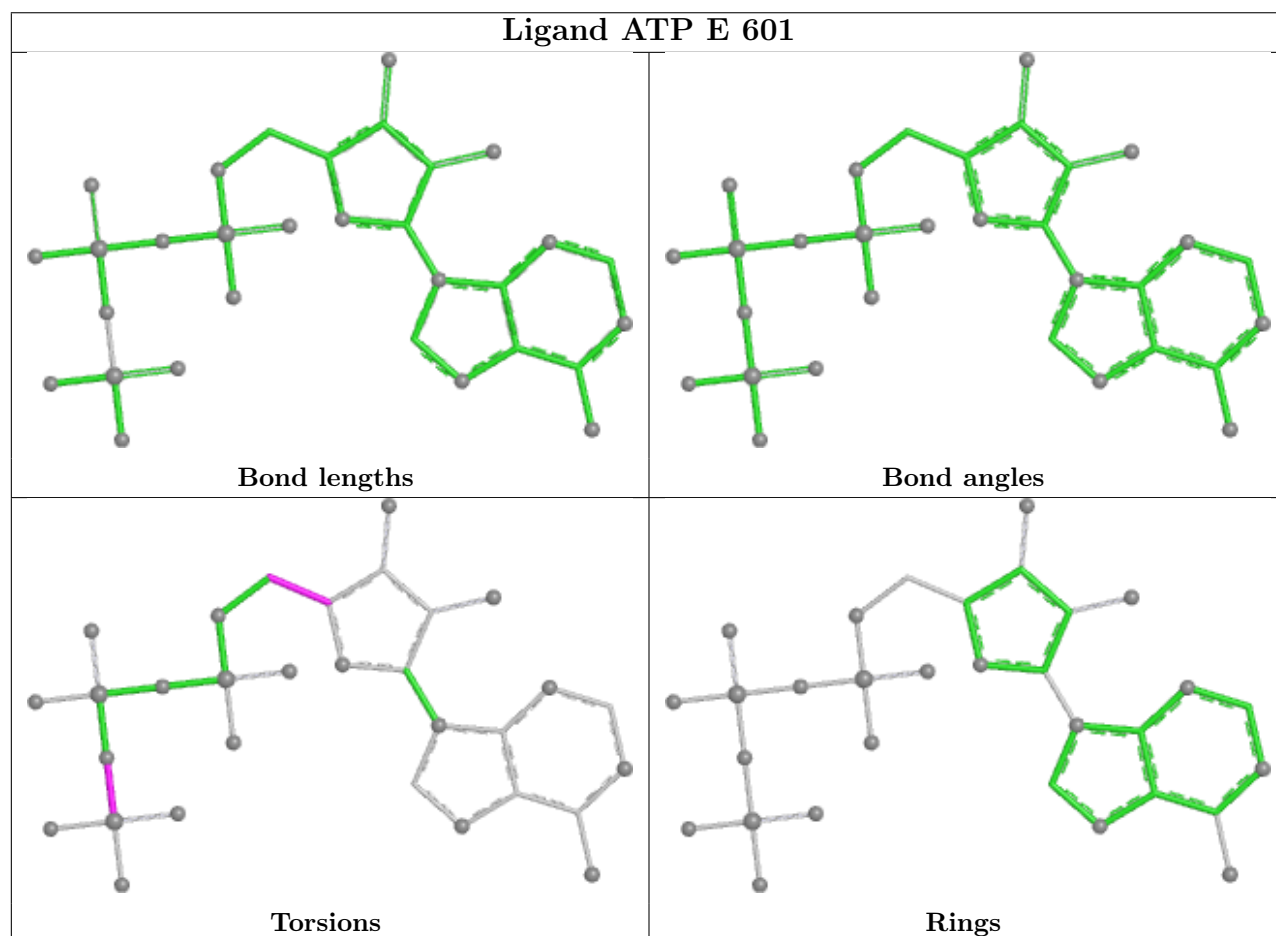
Mol	Chain	Res	Type	Atoms
59	E	602	ATP	C5'-O5'-PA-O3A
59	E	602	ATP	O4'-C4'-C5'-O5'
59	E	602	ATP	C3'-C4'-C5'-O5'
59	E	602	ATP	PB-O3A-PA-O5'
59	E	602	ATP	C5'-O5'-PA-O1A
59	E	601	ATP	PB-O3B-PG-O3G
59	E	602	ATP	PB-O3A-PA-O1A
59	E	601	ATP	O4'-C4'-C5'-O5'

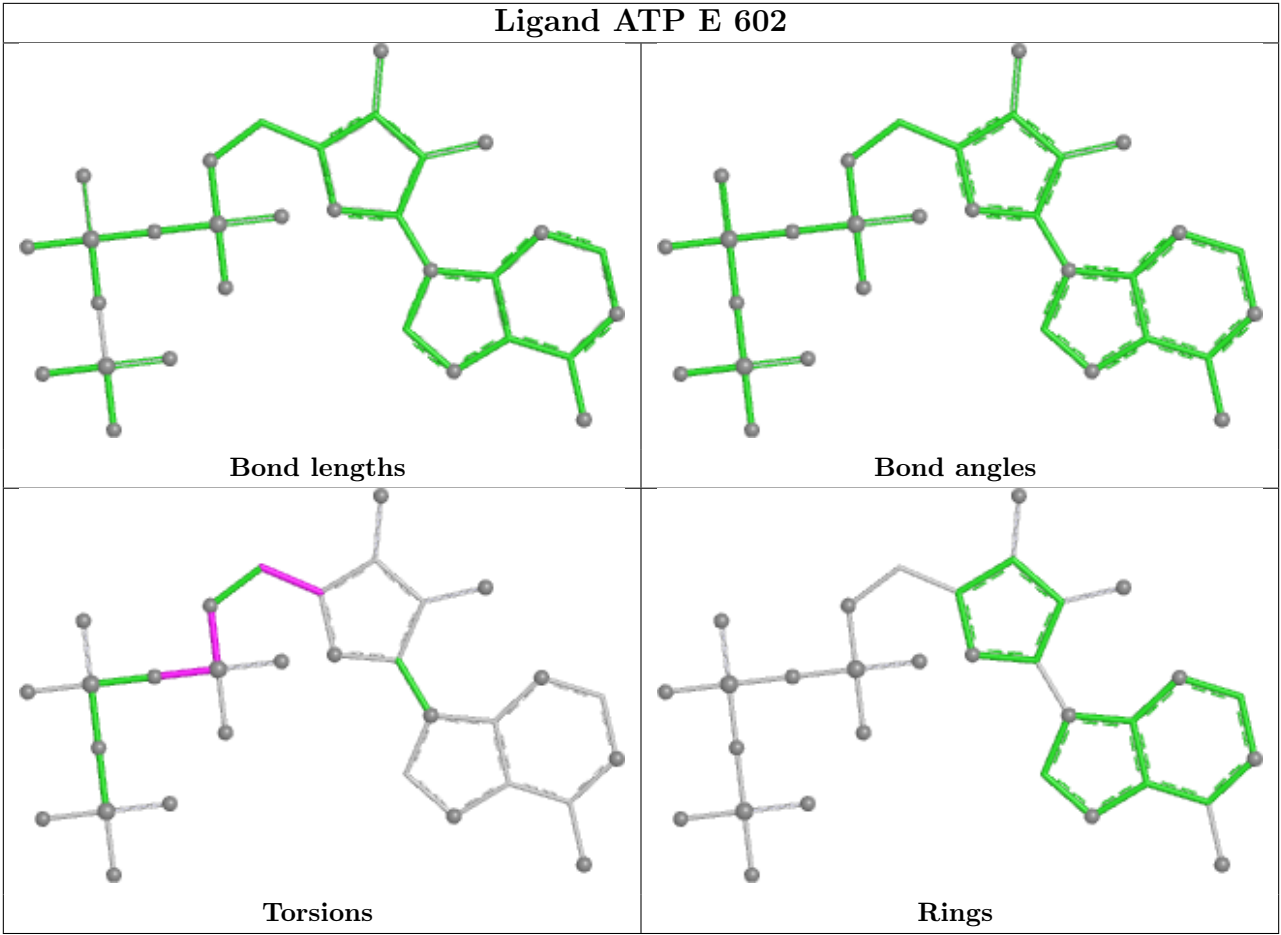
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	E	601	ATP	3	0
59	E	602	ATP	3	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.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
35	R3	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R3	460:A	O3'	461:A	P	5.02
1	R3	210:C	O3'	211:G	P	3.87

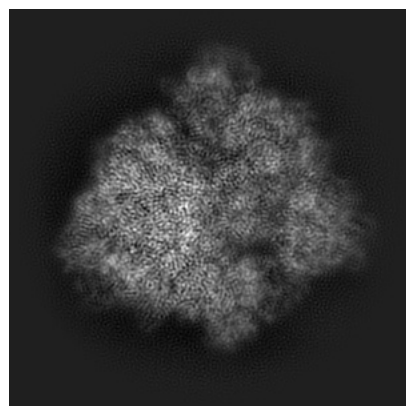
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40921. These allow visual inspection of the internal detail of the map and identification of artifacts.

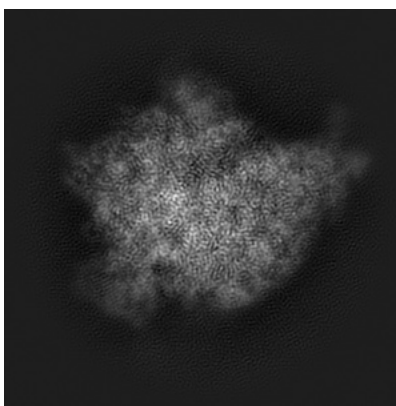
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

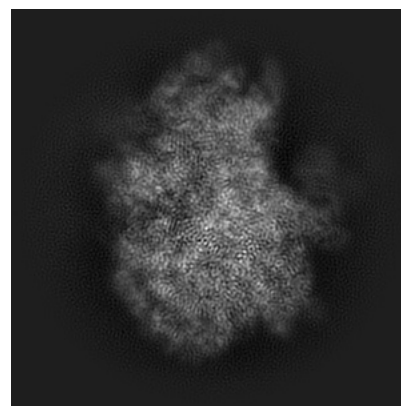
6.1.1 Primary map



X

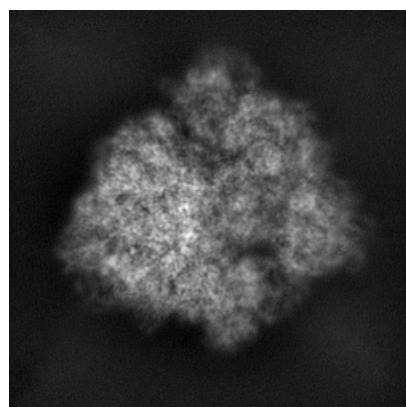


Y

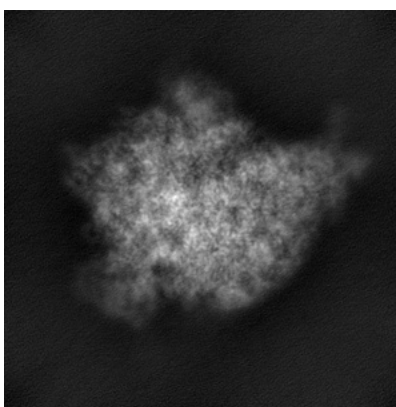


Z

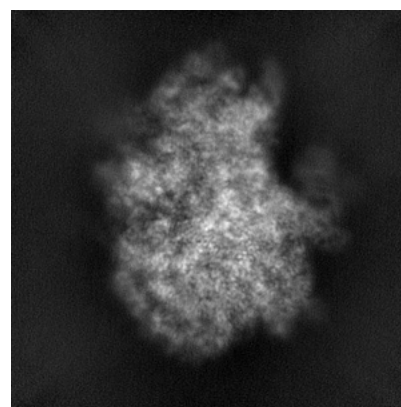
6.1.2 Raw map



X



Y

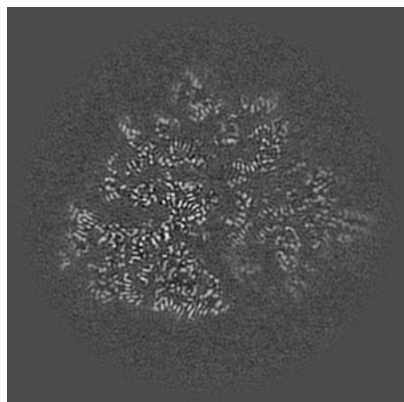


Z

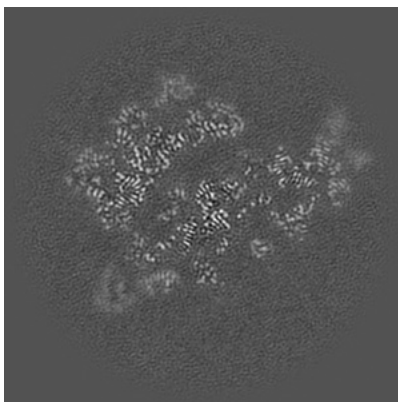
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

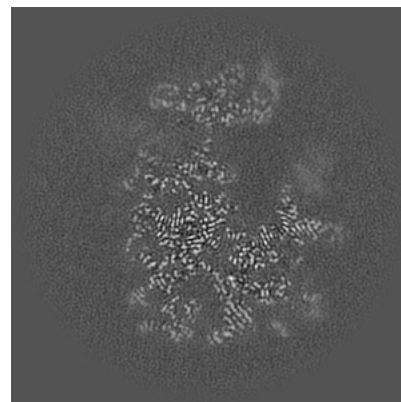
6.2.1 Primary map



X Index: 160

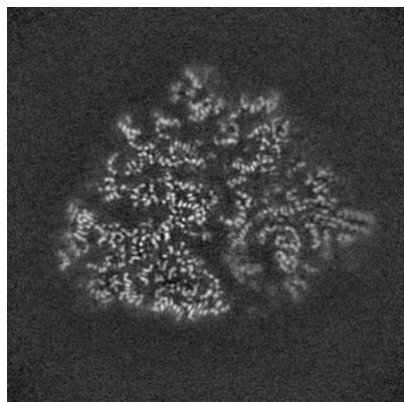


Y Index: 160

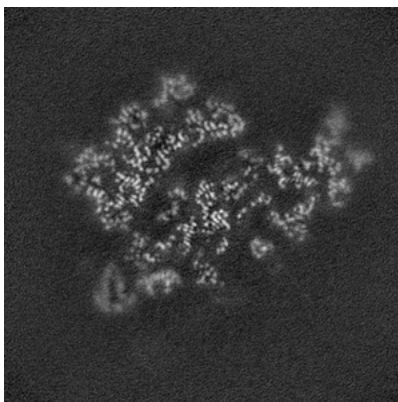


Z Index: 160

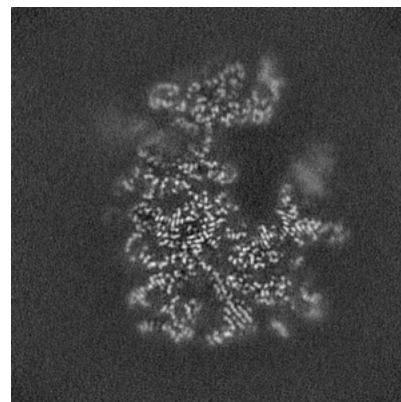
6.2.2 Raw map



X Index: 160



Y Index: 160

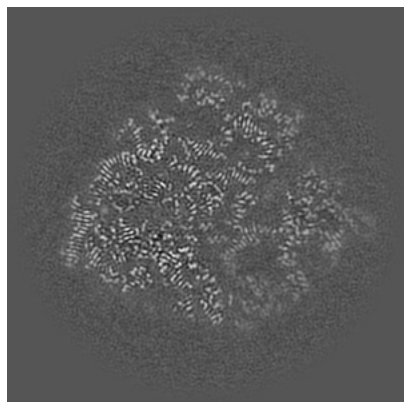


Z Index: 160

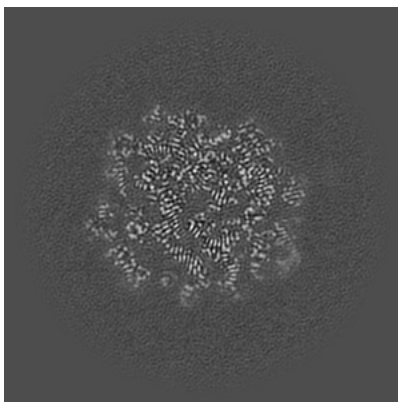
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

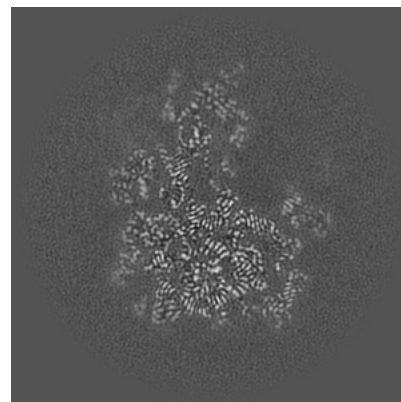
6.3.1 Primary map



X Index: 167

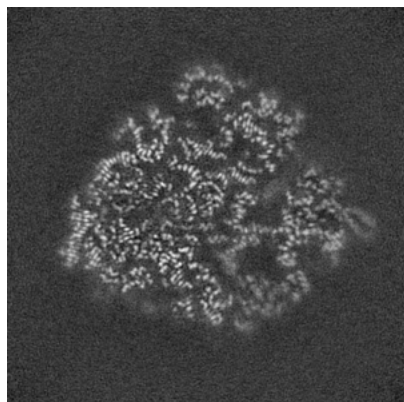


Y Index: 118

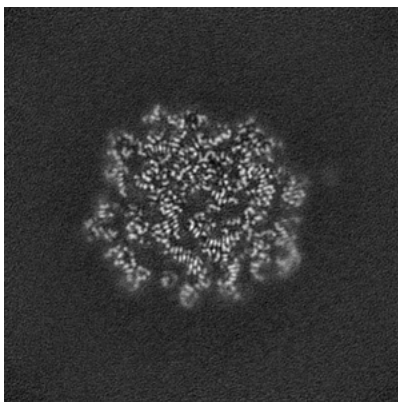


Z Index: 177

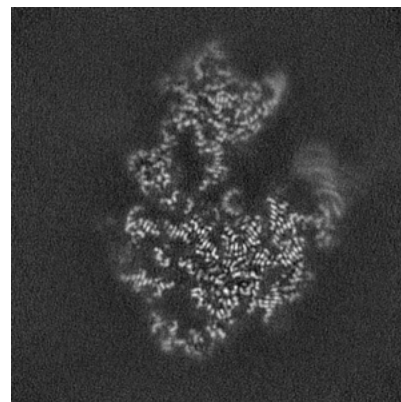
6.3.2 Raw map



X Index: 167



Y Index: 118

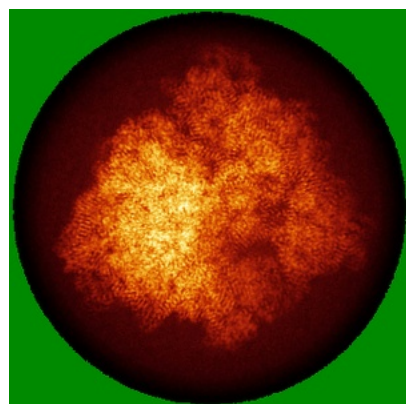


Z Index: 140

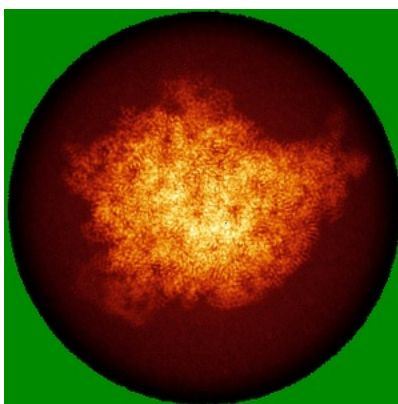
The images above show the largest variance slices of the map in three orthogonal directions.

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

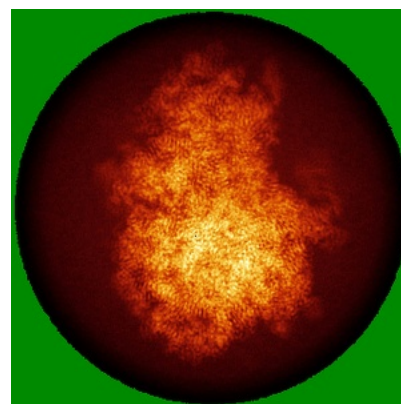
6.4.1 Primary map



X

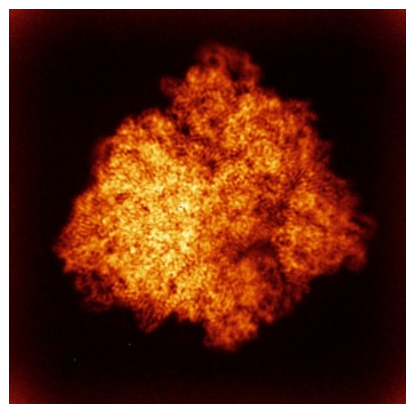


Y

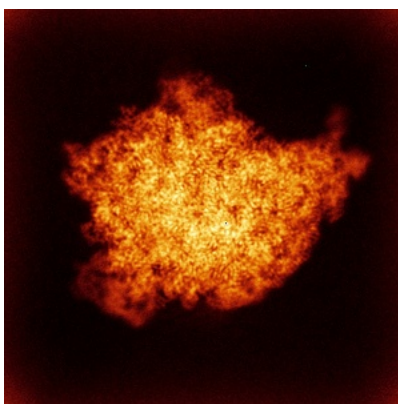


Z

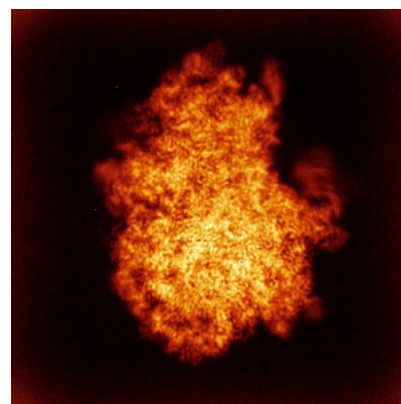
6.4.2 Raw map



X



Y

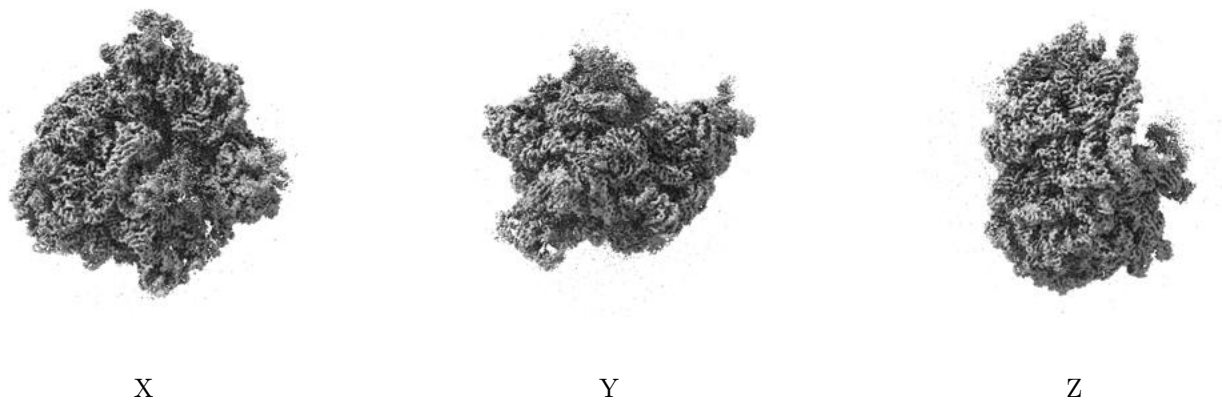


Z

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

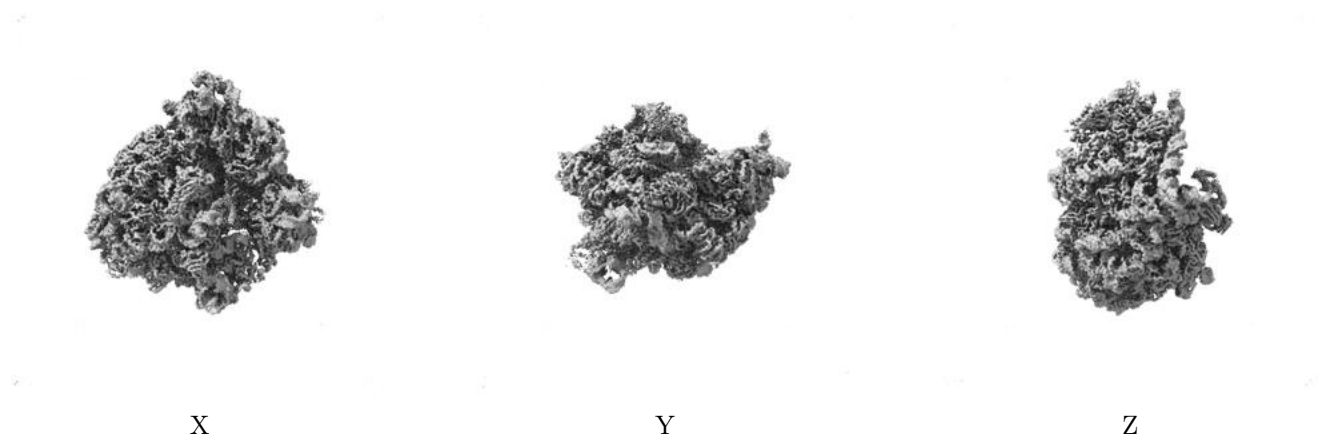
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

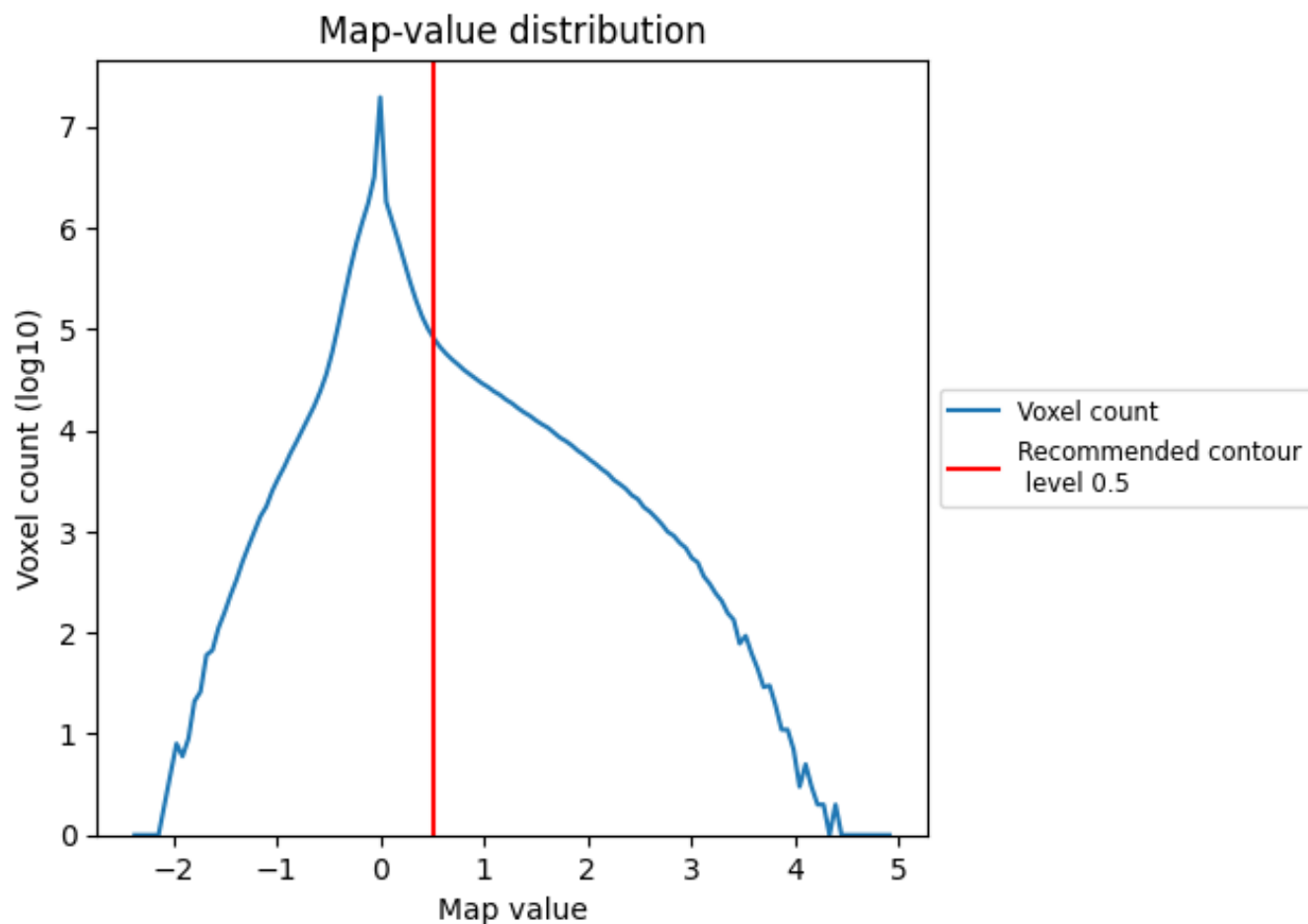
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

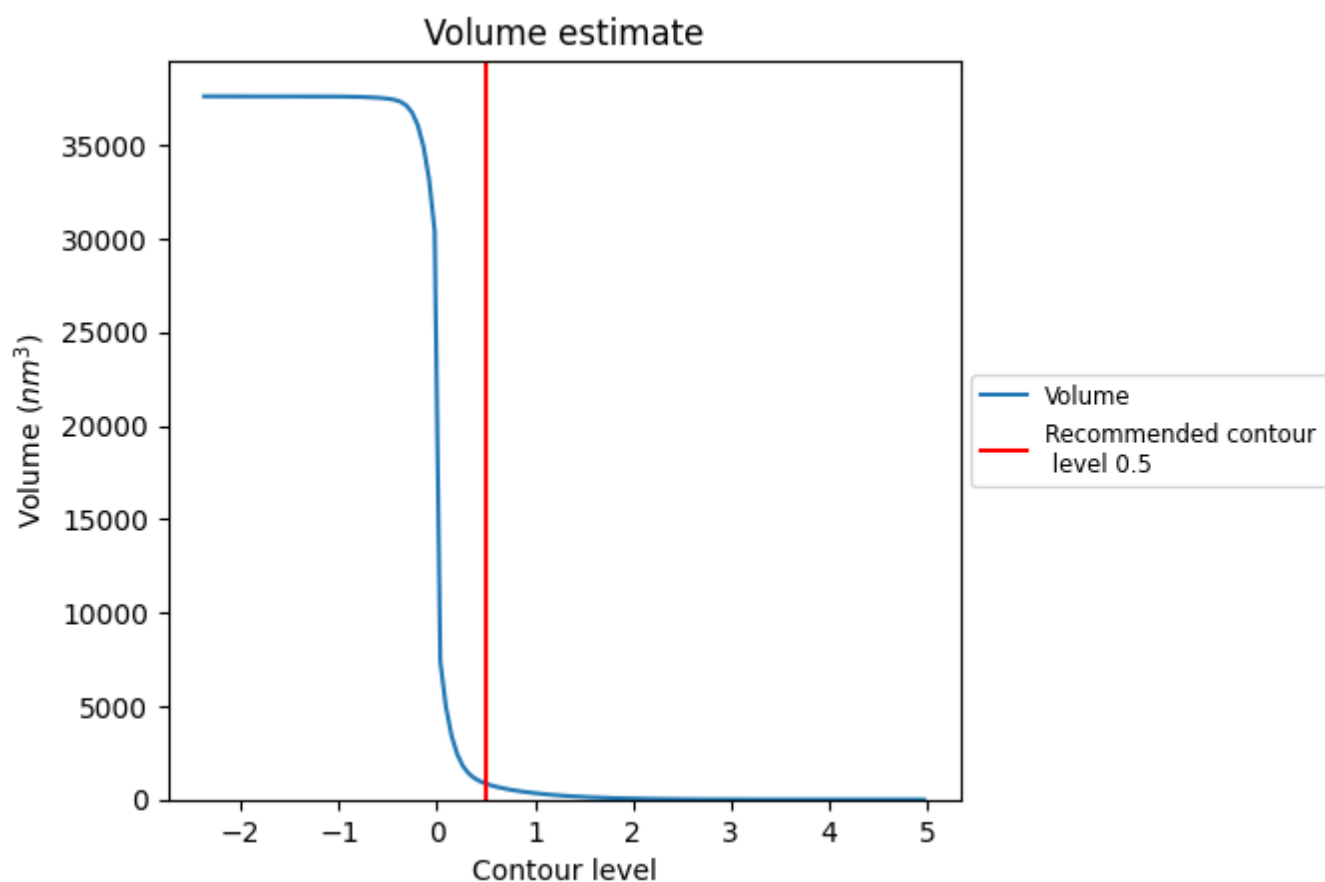
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

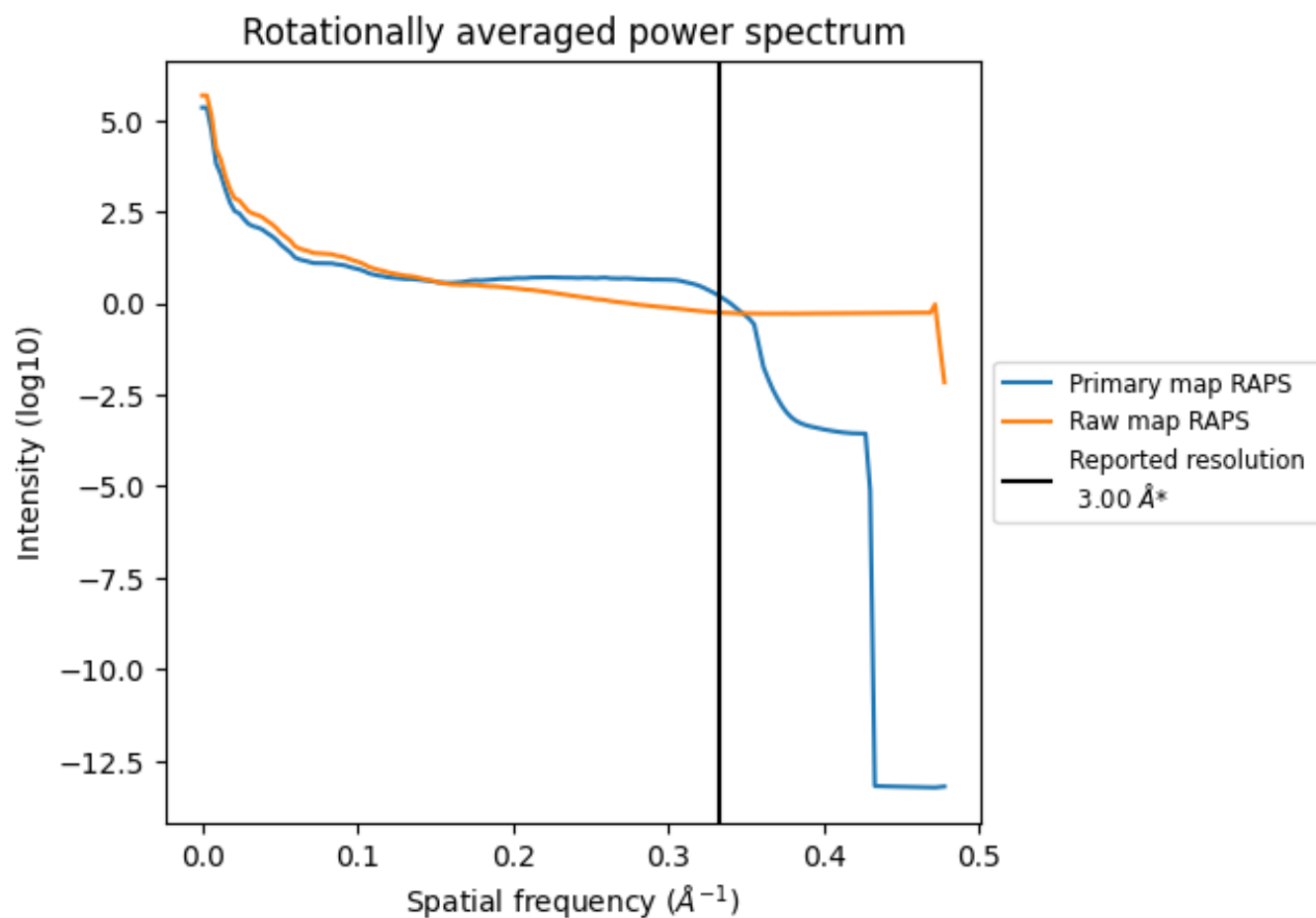
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 851 nm³; this corresponds to an approximate mass of 768 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

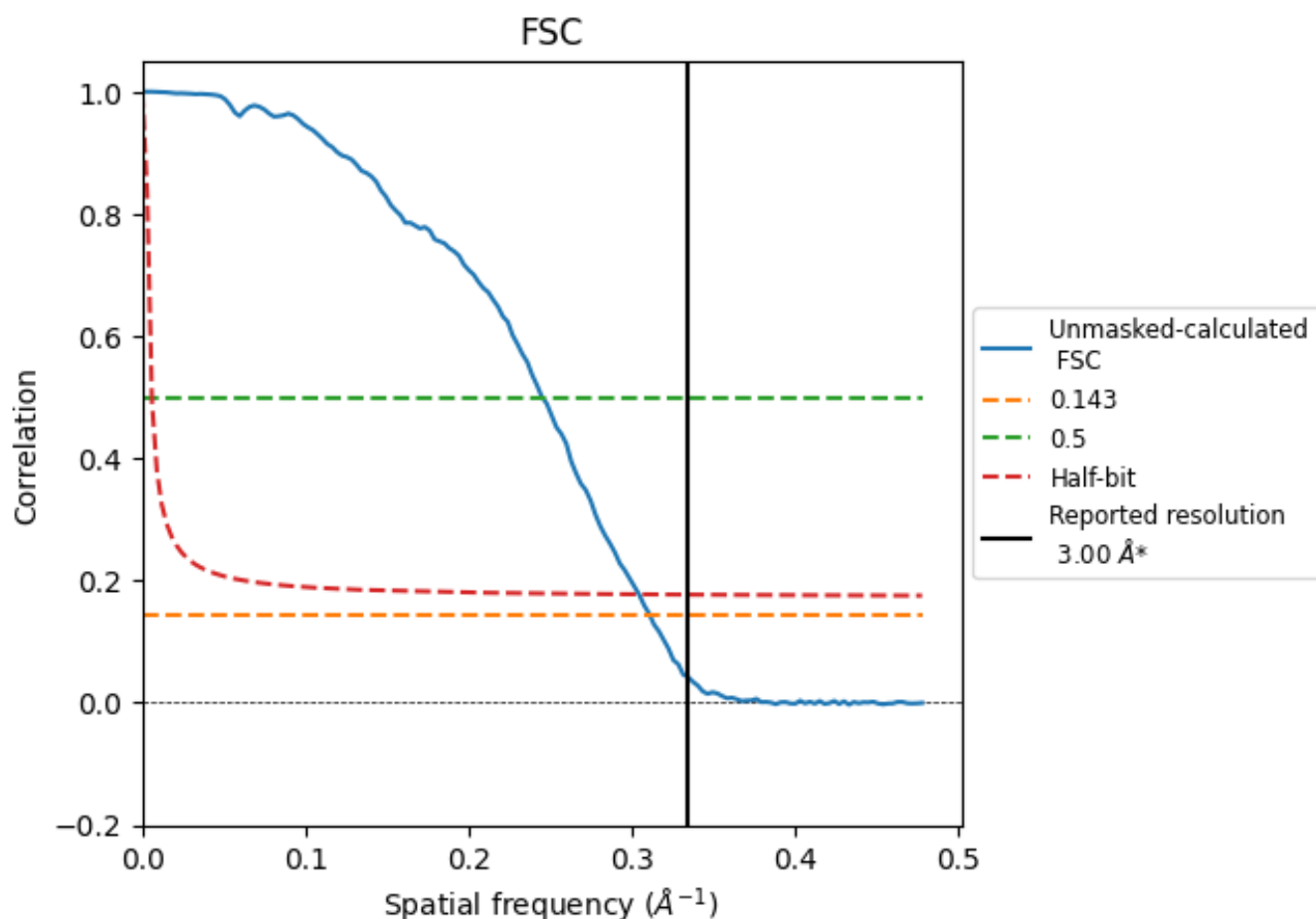


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

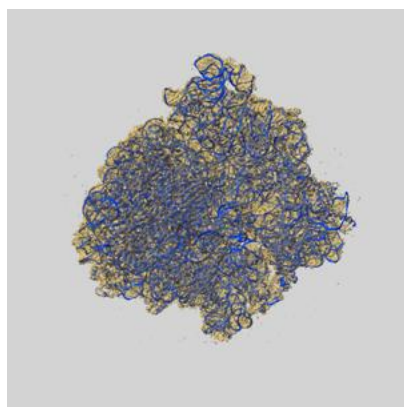
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.22	4.08	3.29

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

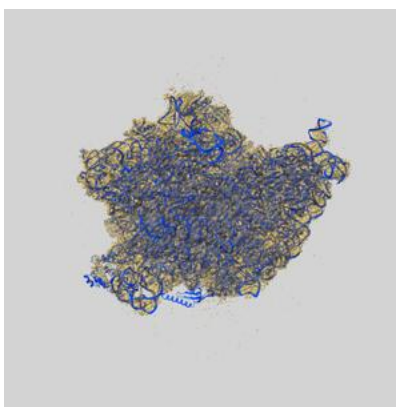
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40921 and PDB model 9NL5. Per-residue inclusion information can be found in section [3](#) on page [16](#).

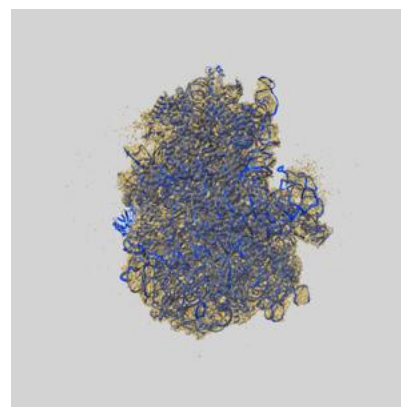
9.1 Map-model overlay [i](#)



X



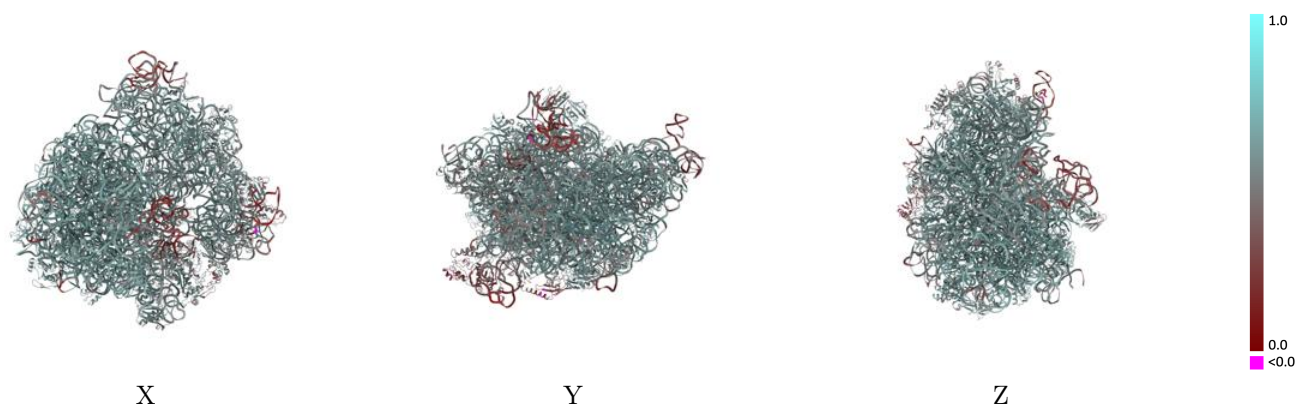
Y



Z

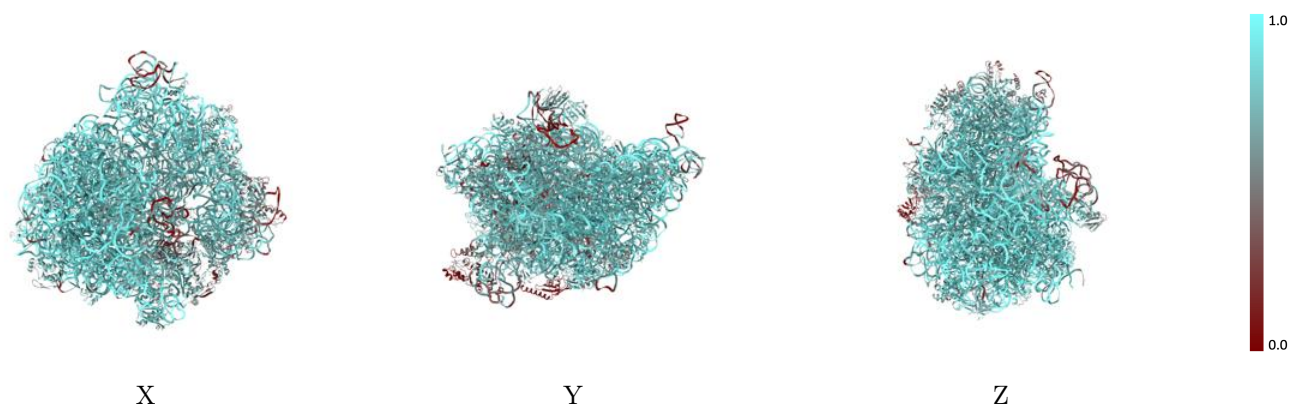
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



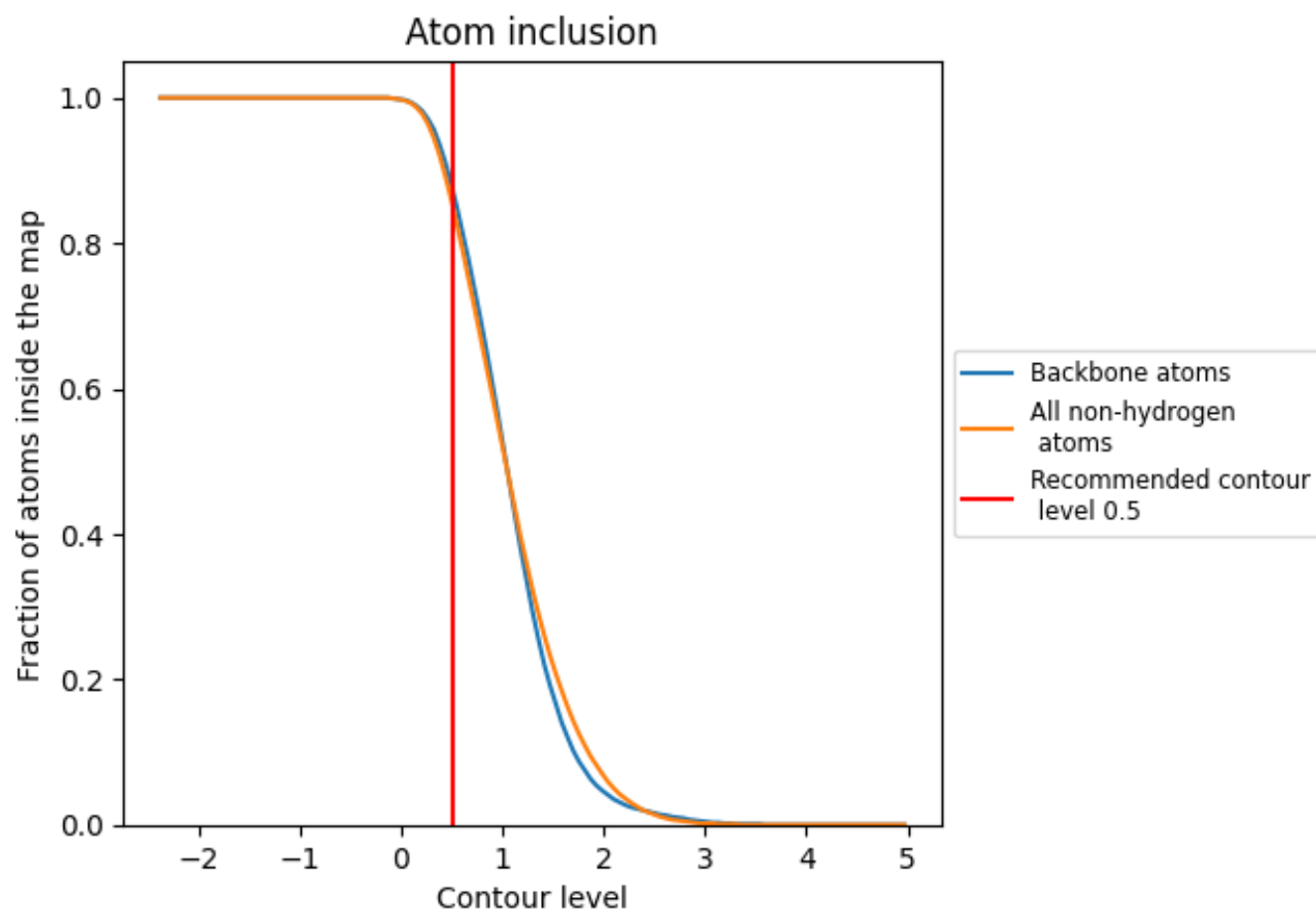
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8570	 0.5700
1	 0.2330	 0.3310
13	 0.8910	 0.6110
14	 0.8630	 0.6160
15	 0.8640	 0.6030
16	 0.8720	 0.6160
17	 0.9050	 0.6130
18	 0.7680	 0.5680
19	 0.8480	 0.6060
2	 0.9210	 0.6300
20	 0.9140	 0.6250
21	 0.8340	 0.5900
22	 0.8620	 0.6040
23	 0.8260	 0.5960
24	 0.7610	 0.5640
25	 0.7820	 0.5830
27	 0.8770	 0.6120
28	 0.9050	 0.6240
29	 0.7300	 0.5630
3	 0.8970	 0.6180
30	 0.8580	 0.5970
31	 0.3990	 0.4300
32	 0.8600	 0.6030
33	 0.8560	 0.6020
34	 0.9440	 0.6380
35	 0.9180	 0.6330
36	 0.8840	 0.6210
4	 0.7850	 0.5860
5	 0.6740	 0.5170
6	 0.6790	 0.5260
9	 0.2230	 0.3520
E	 0.6950	 0.5450
M	 0.6630	 0.5300
R1	 0.9230	 0.5850
R2	 0.9090	 0.5540



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Chain	Atom inclusion	Q-score
R3	 0.8970	 0.5620
T	 0.7270	 0.4900
sb	 0.6020	 0.4960
sc	 0.7140	 0.5600
sd	 0.7230	 0.5550
se	 0.8020	 0.5720
sf	 0.7840	 0.5590
sg	 0.6870	 0.5360
sh	 0.8220	 0.5980
si	 0.6870	 0.5260
sj	 0.5660	 0.4990
sk	 0.8140	 0.5890
sl	 0.8090	 0.5790
sm	 0.7070	 0.5340
sn	 0.7190	 0.5290
so	 0.8260	 0.5820
sp	 0.7640	 0.5660
sq	 0.7780	 0.5720
sr	 0.8200	 0.5750
ss	 0.6710	 0.5270
st	 0.7880	 0.5620
su	 0.5380	 0.4600