



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 04:02 AM UTC

PDB ID : 5UYN / pdb_00005uyn
EMDB ID : EMD-8618
Title : 70S ribosome bound with near-cognate ternary complex not base-paired to A site codon (Structure I-nc)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 4.00 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:

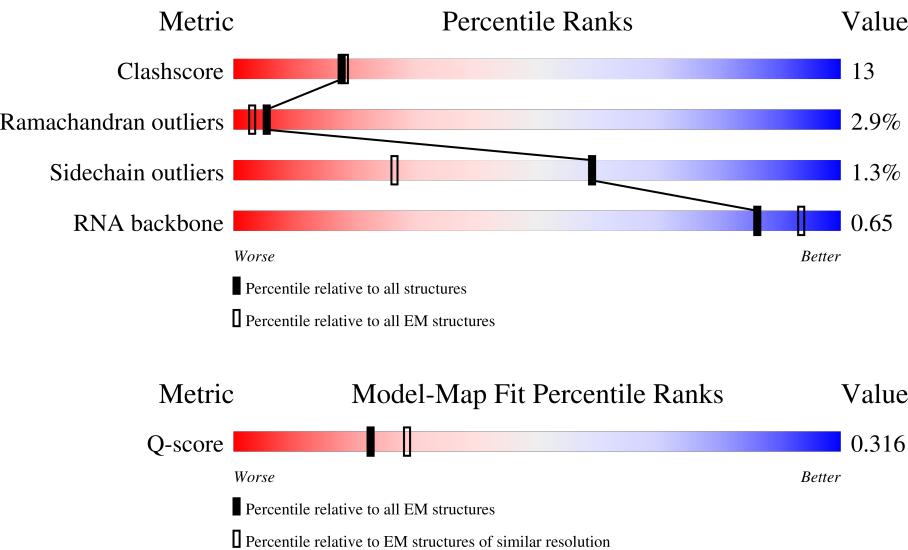
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.00 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	7587 (3.50 - 4.50)

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	04	271	
2	05	209	
3	06	201	

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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

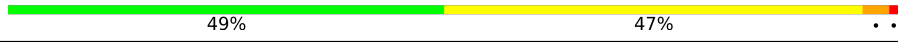
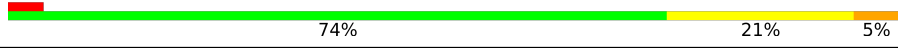
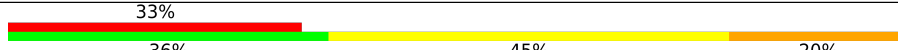
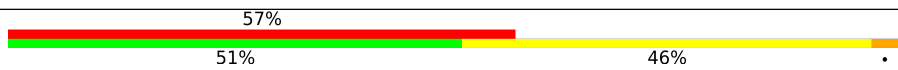
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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	223	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	17	
58	Y	76	
59	Z	392	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 153717 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	22	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

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

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

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

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	17	Total	C	N	O	P	0	0
			373	168	79	110	16		

- Molecule 58 is a RNA chain called tRNA^{Lys}.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Y	76	Total	C	N	O	P	S	0	0
			1618	723	282	536	76	1		

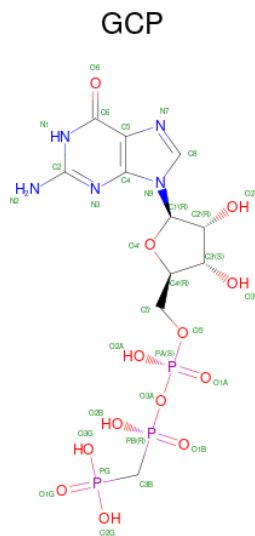
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	34	U8U	-	insertion	GB 558570689

- Molecule 59 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

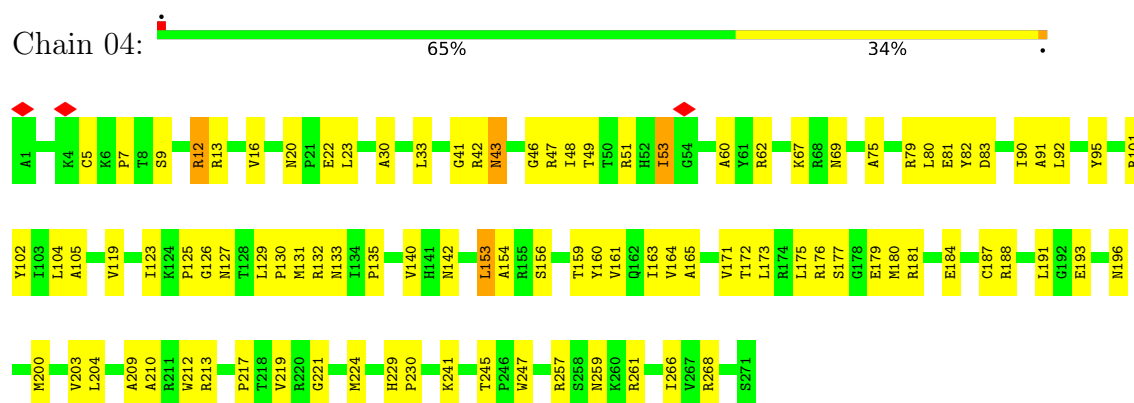


Mol	Chain	Residues	Atoms					AltConf
60	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

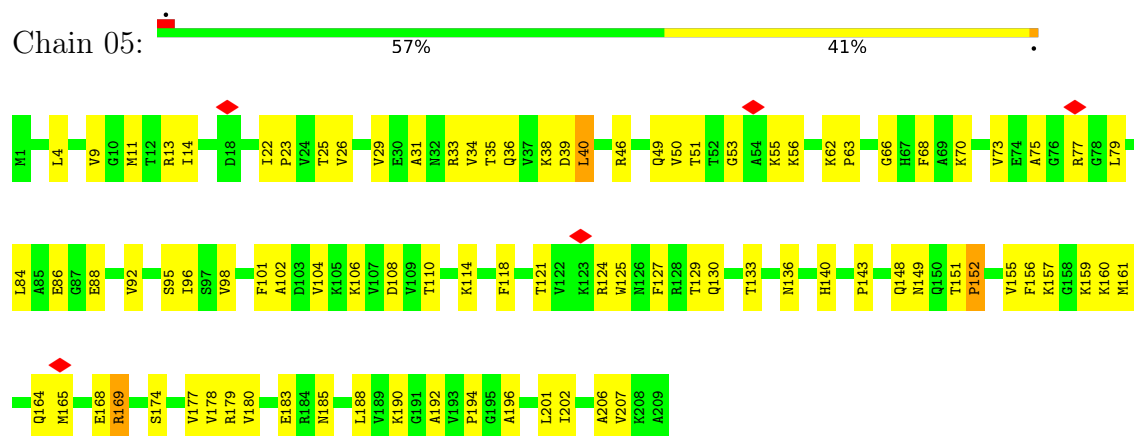
3 Residue-property plots

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.

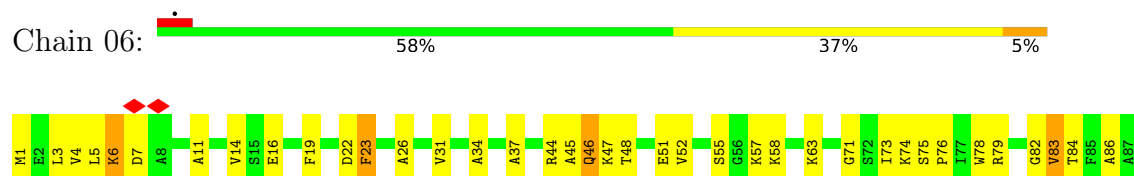
• Molecule 1: 50S ribosomal protein L2

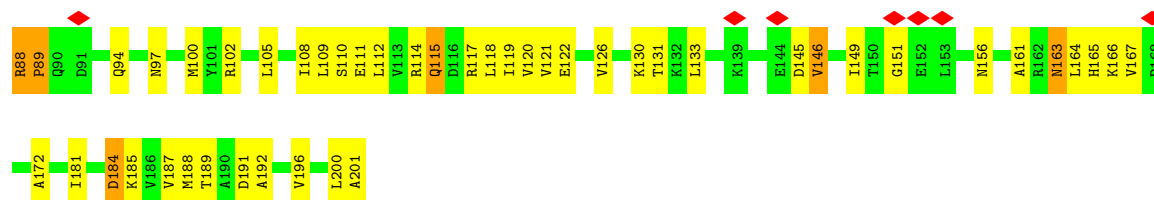


• Molecule 2: 50S ribosomal protein L3

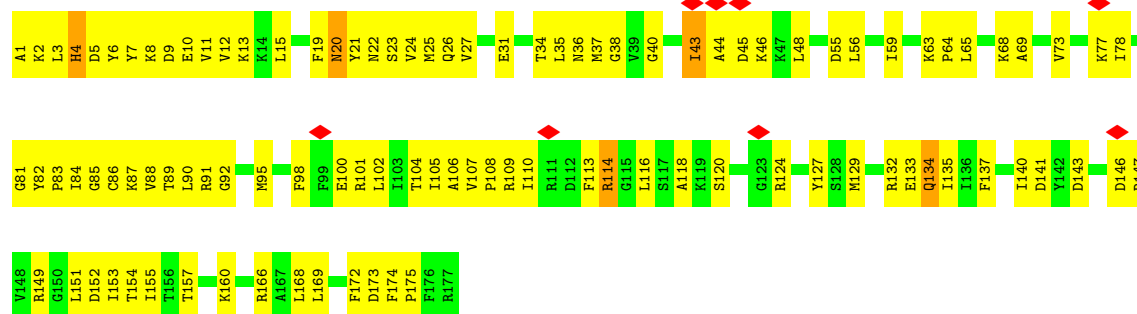


• Molecule 3: 50S ribosomal protein L4

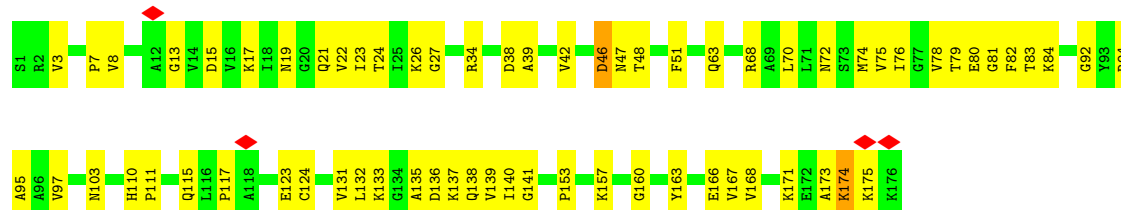




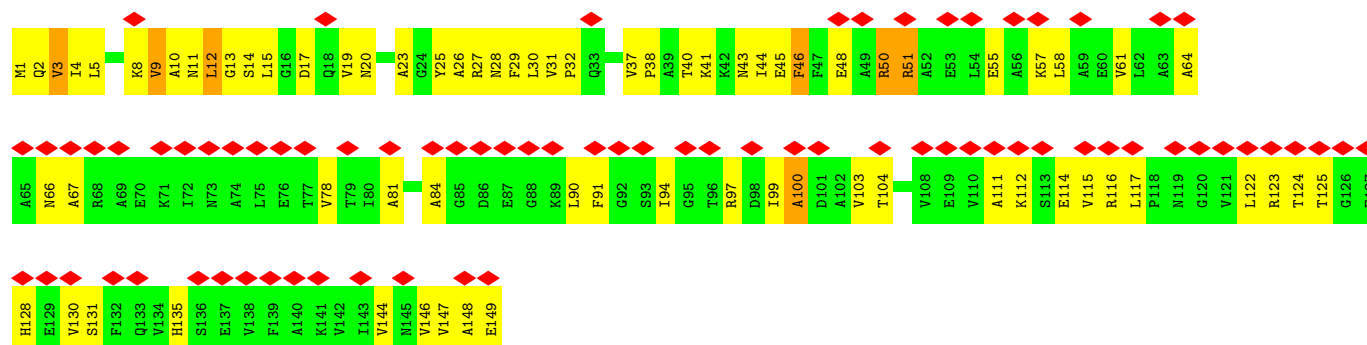
• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6

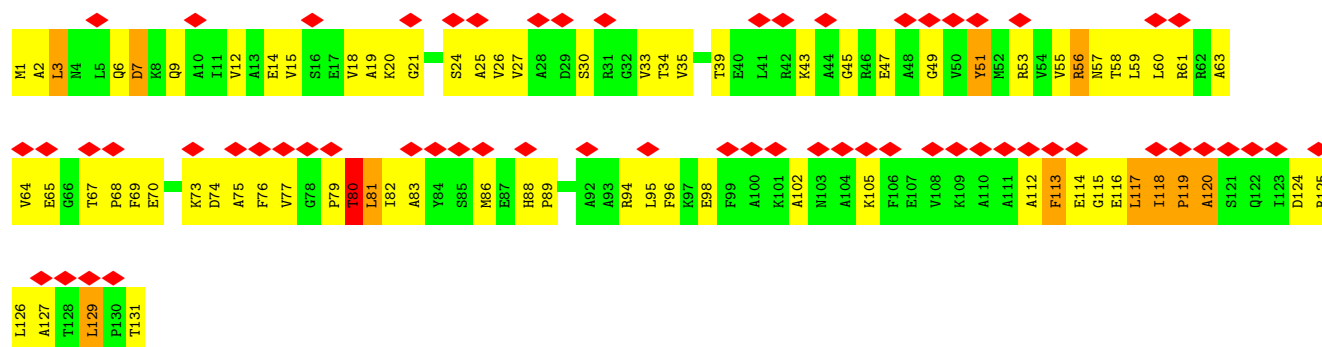


• Molecule 6: 50S ribosomal protein L9



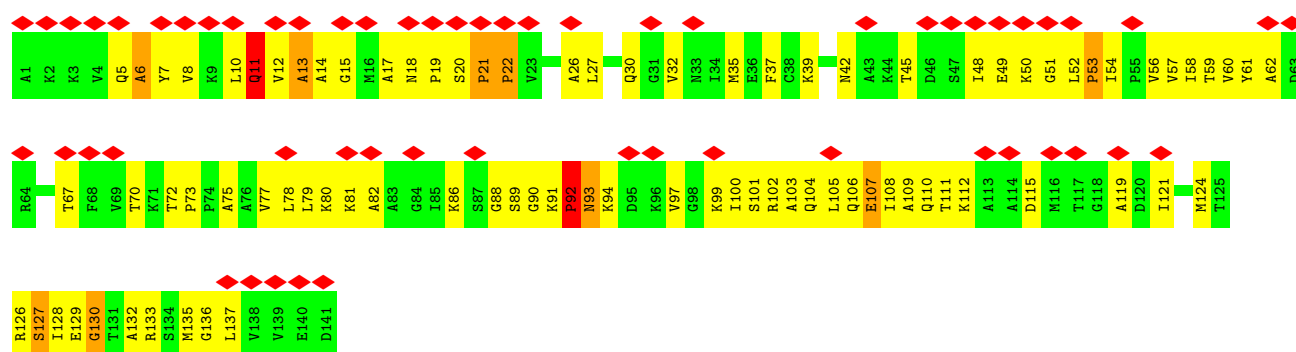
• Molecule 7: 50S ribosomal protein L10





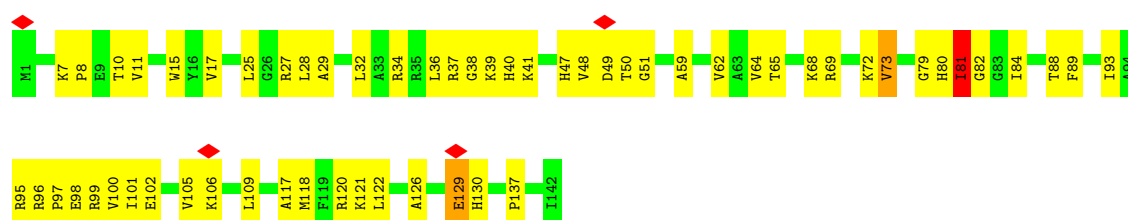
• Molecule 8: 50S ribosomal protein L11

Chain 11: 38% 40% 54% 6% •



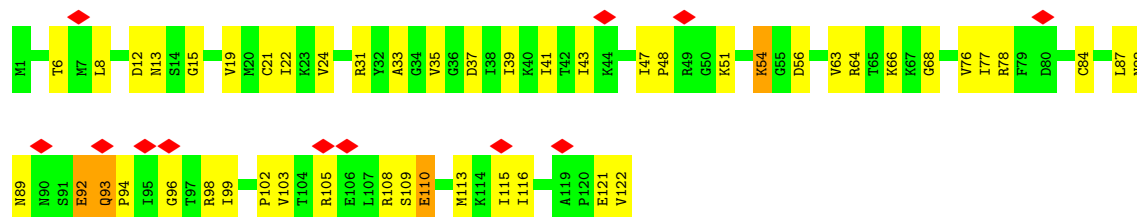
• Molecule 9: 50S ribosomal protein L13

Chain 12: 58% 39% ••

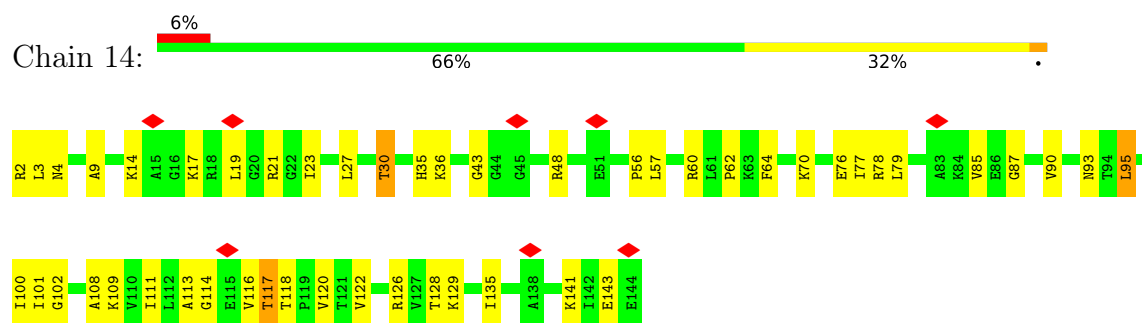


• Molecule 10: 50S ribosomal protein L14

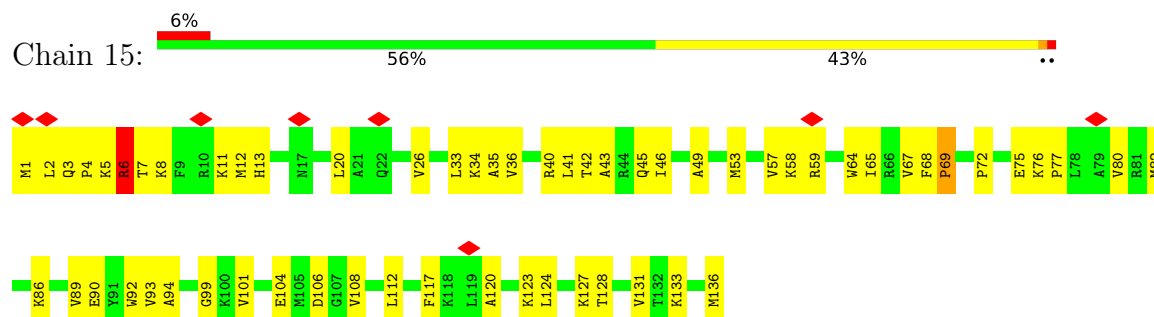
Chain 13: 10% 60% 37% •



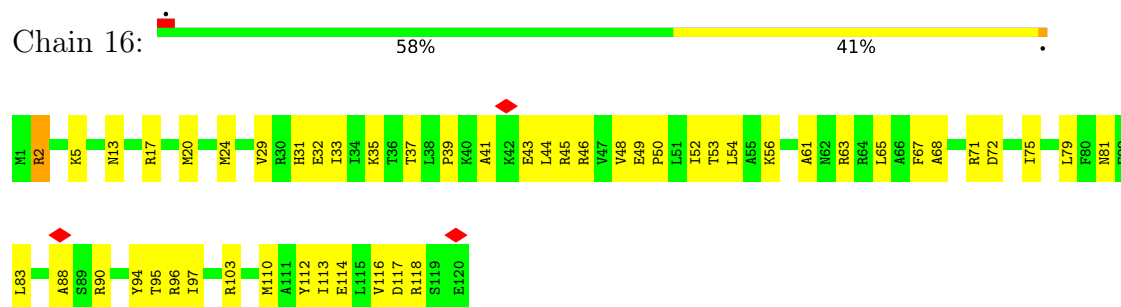
• Molecule 11: 50S ribosomal protein L15



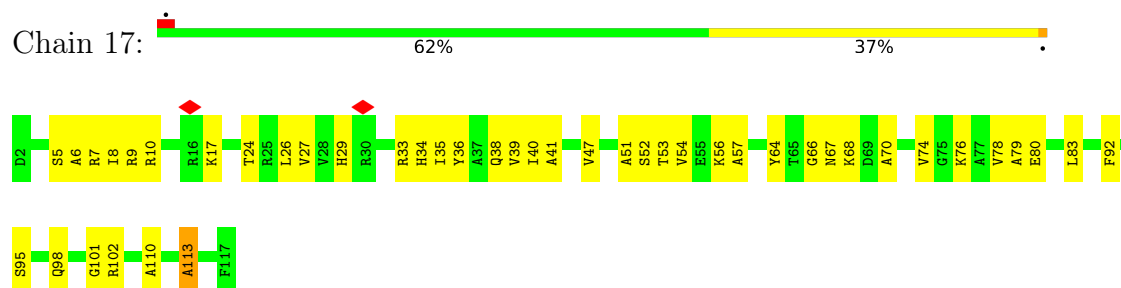
- Molecule 12: 50S ribosomal protein L16



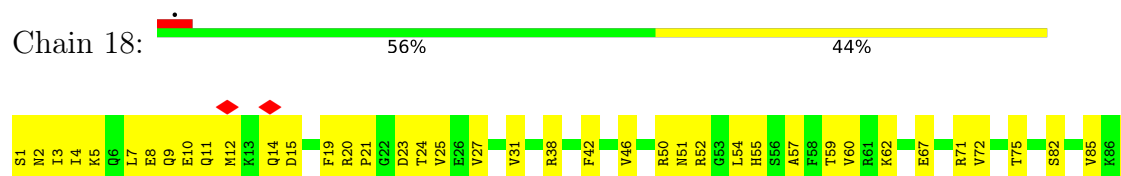
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

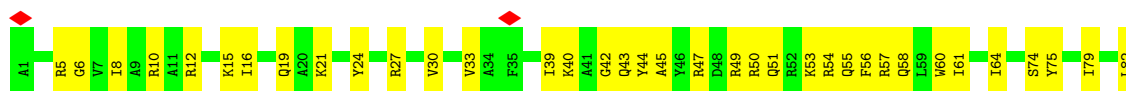


- Molecule 15: 50S ribosomal protein L19

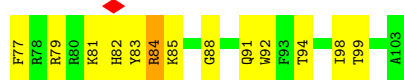
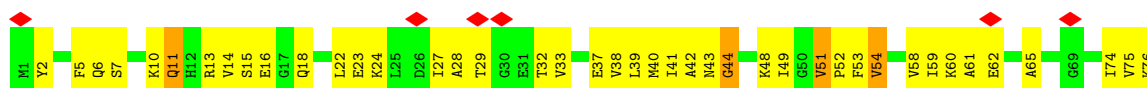




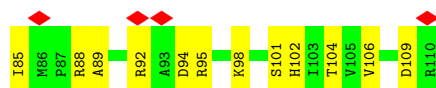
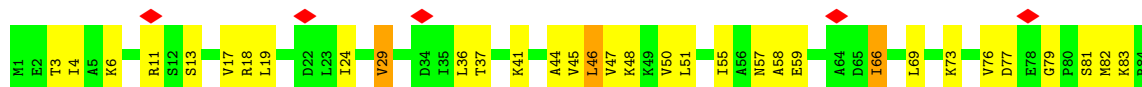
- Molecule 16: 50S ribosomal protein L20



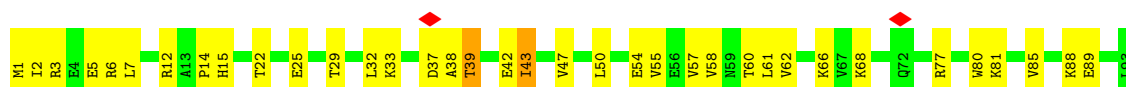
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

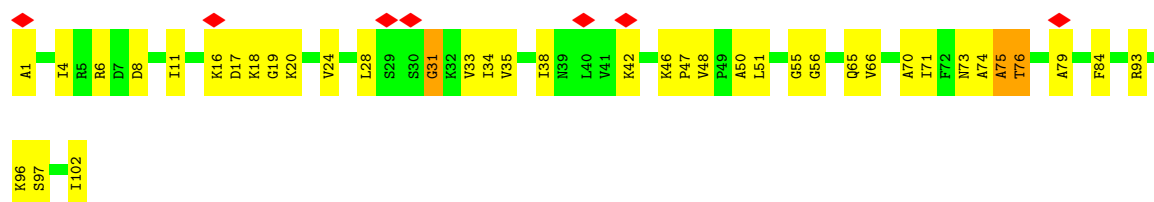


- Molecule 19: 50S ribosomal protein L23

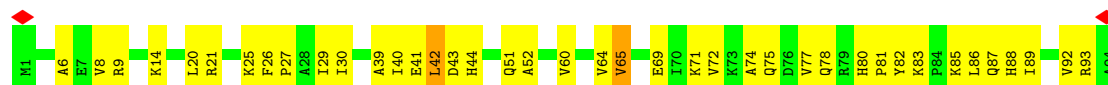


- Molecule 20: 50S ribosomal protein L24

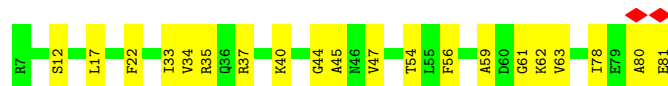
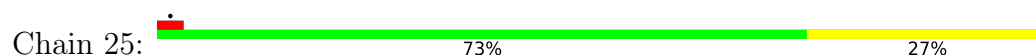




- Molecule 21: 50S ribosomal protein L25



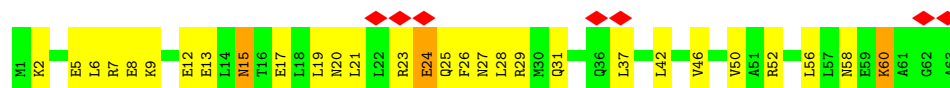
- Molecule 22: 50S ribosomal protein L27



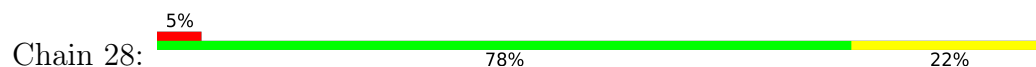
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

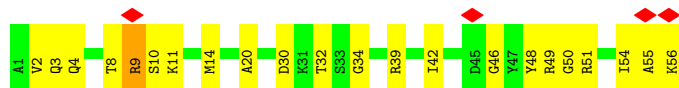


- Molecule 26: 50S ribosomal protein L31

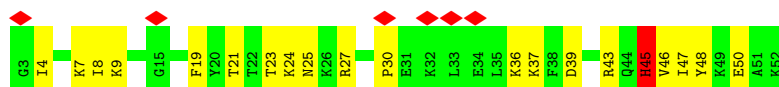




- Molecule 27: 50S ribosomal protein L32



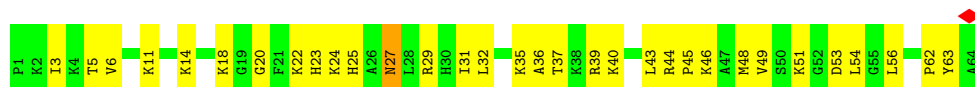
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35

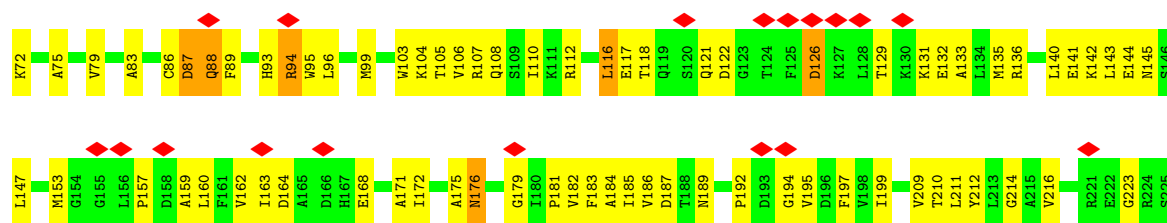


- Molecule 31: 50S ribosomal protein L36

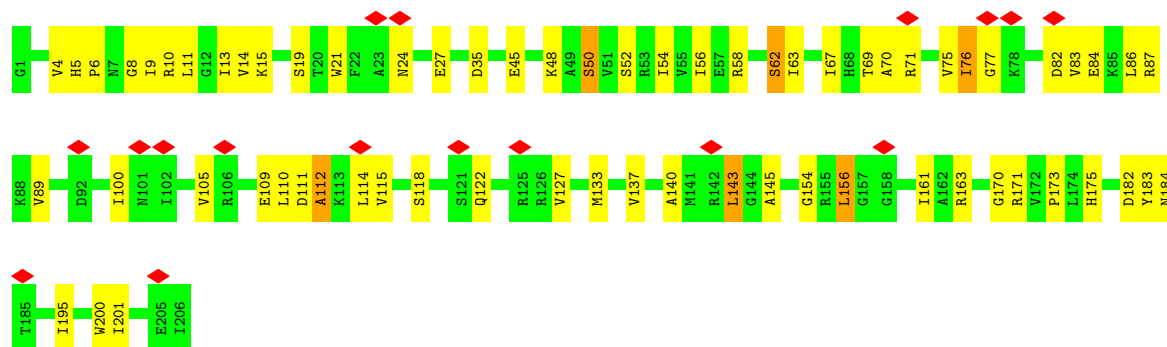


- Molecule 32: 30S ribosomal protein S2

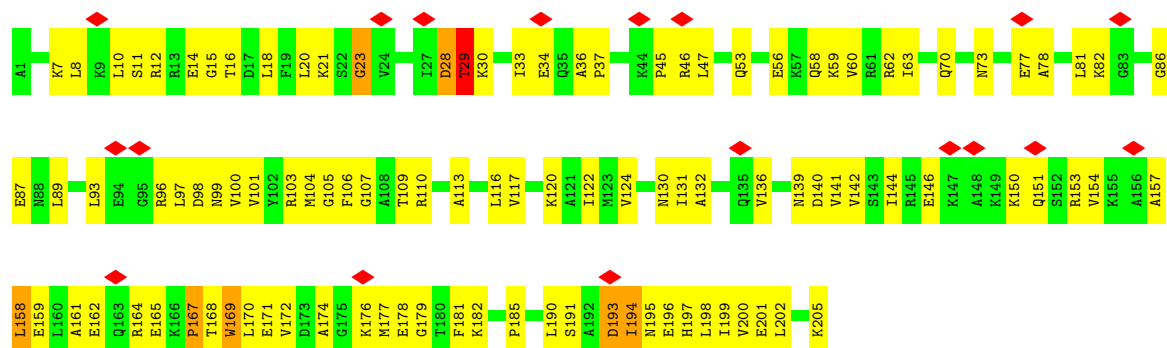




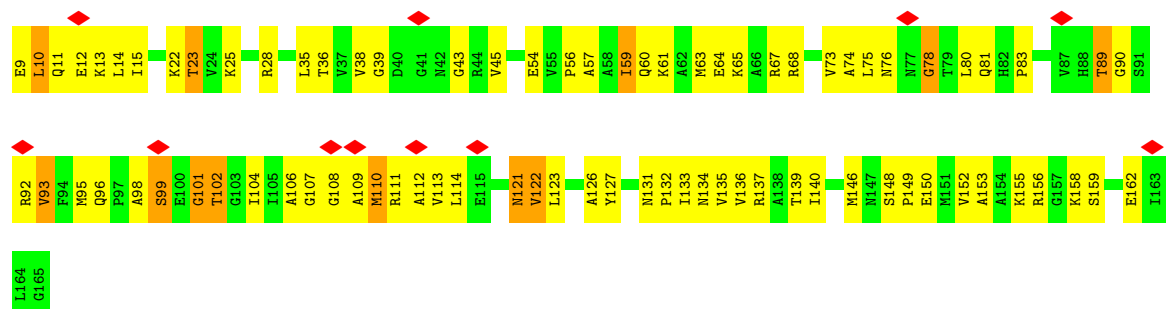
• Molecule 33: 30S ribosomal protein S3



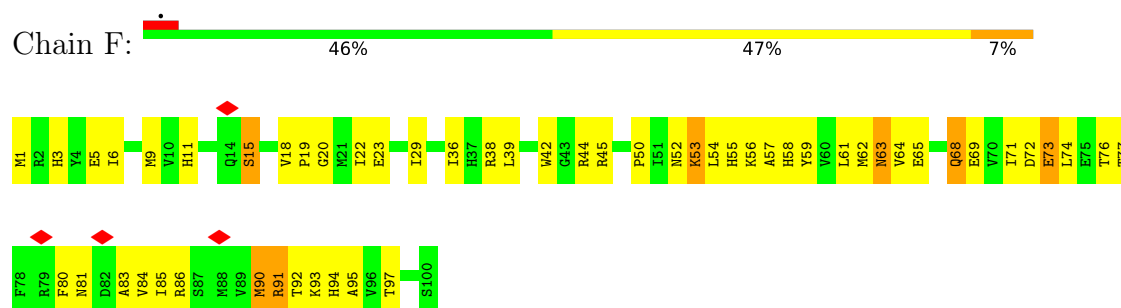
• Molecule 34: 30S ribosomal protein S4



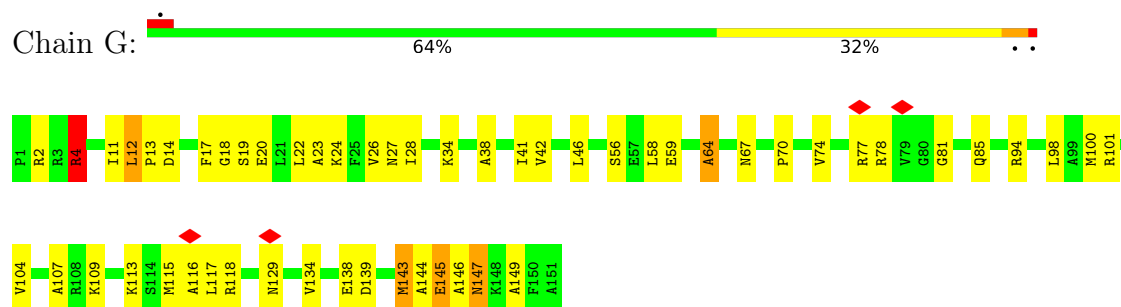
• Molecule 35: 30S ribosomal protein S5



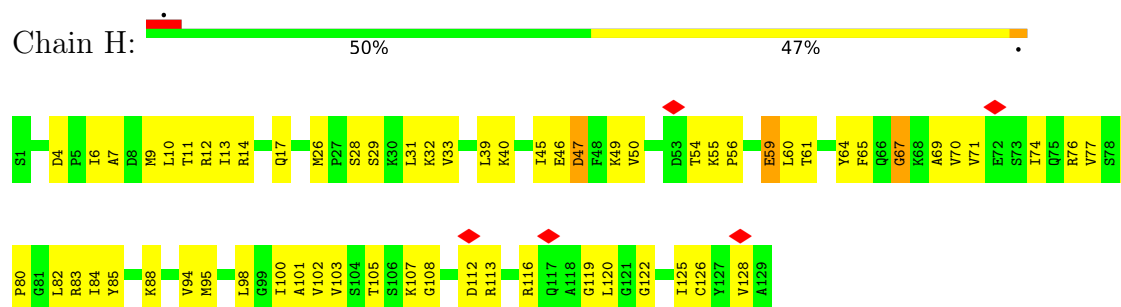
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8

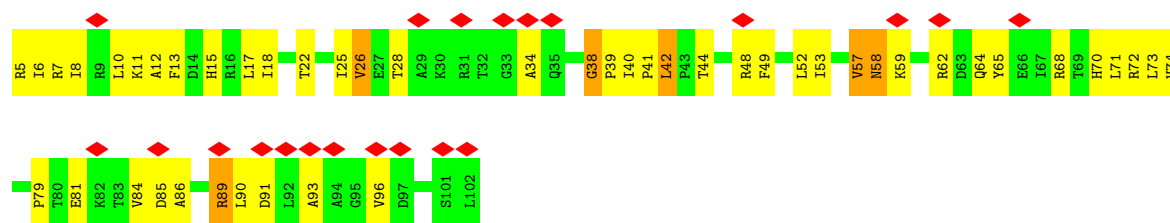


- Molecule 39: 30S ribosomal protein S9

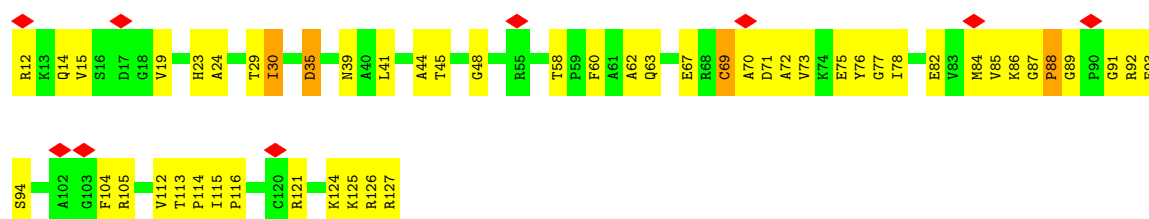


- Molecule 40: 30S ribosomal protein S10

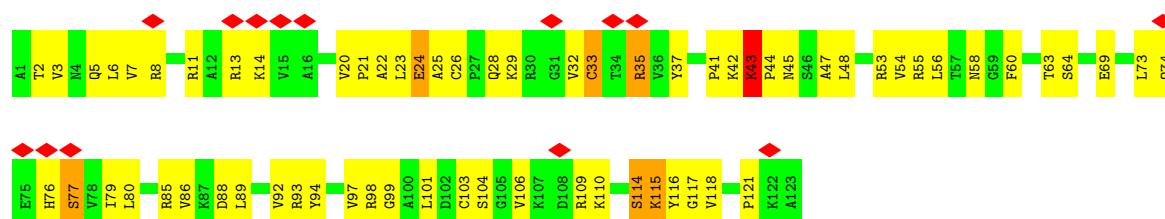




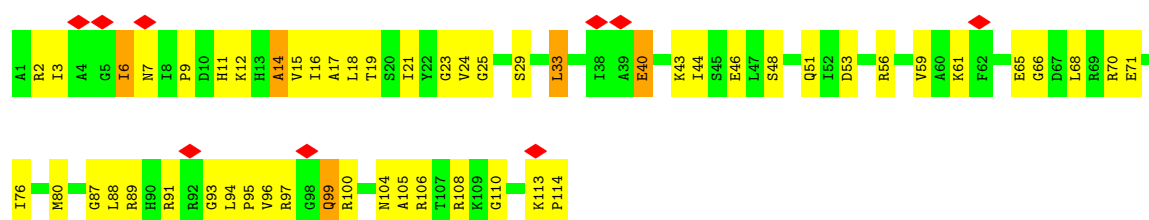
• Molecule 41: 30S ribosomal protein S11



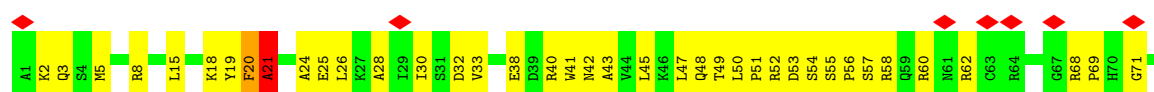
• Molecule 42: 30S ribosomal protein S12

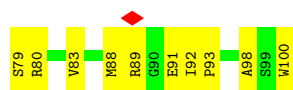


• Molecule 43: 30S ribosomal protein S13

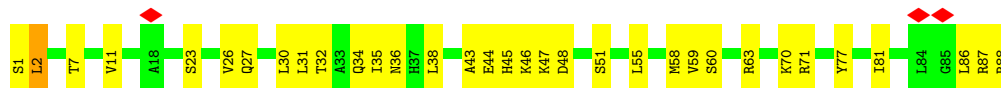


• Molecule 44: 30S ribosomal protein S14

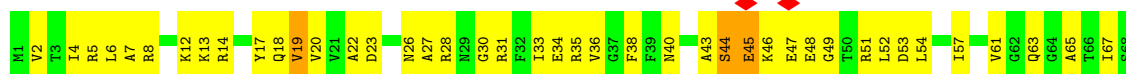




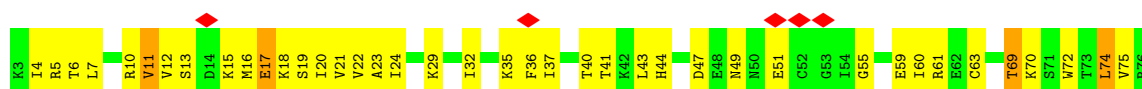
- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S18

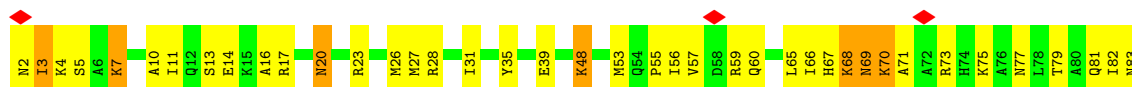


- Molecule 49: 30S ribosomal protein S19

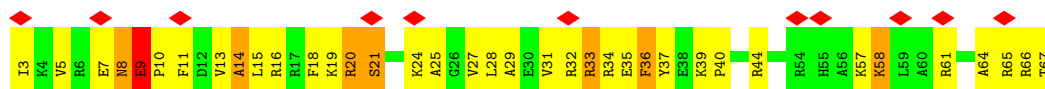
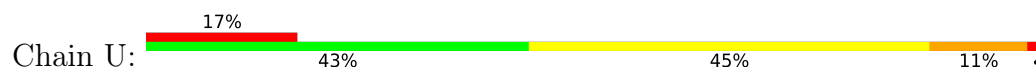




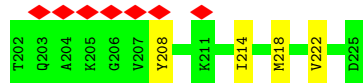
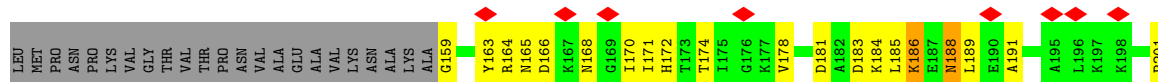
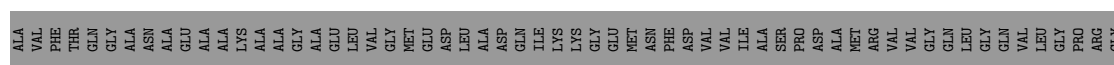
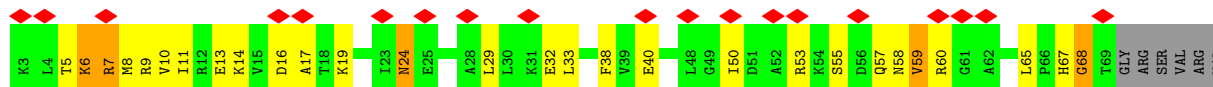
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21

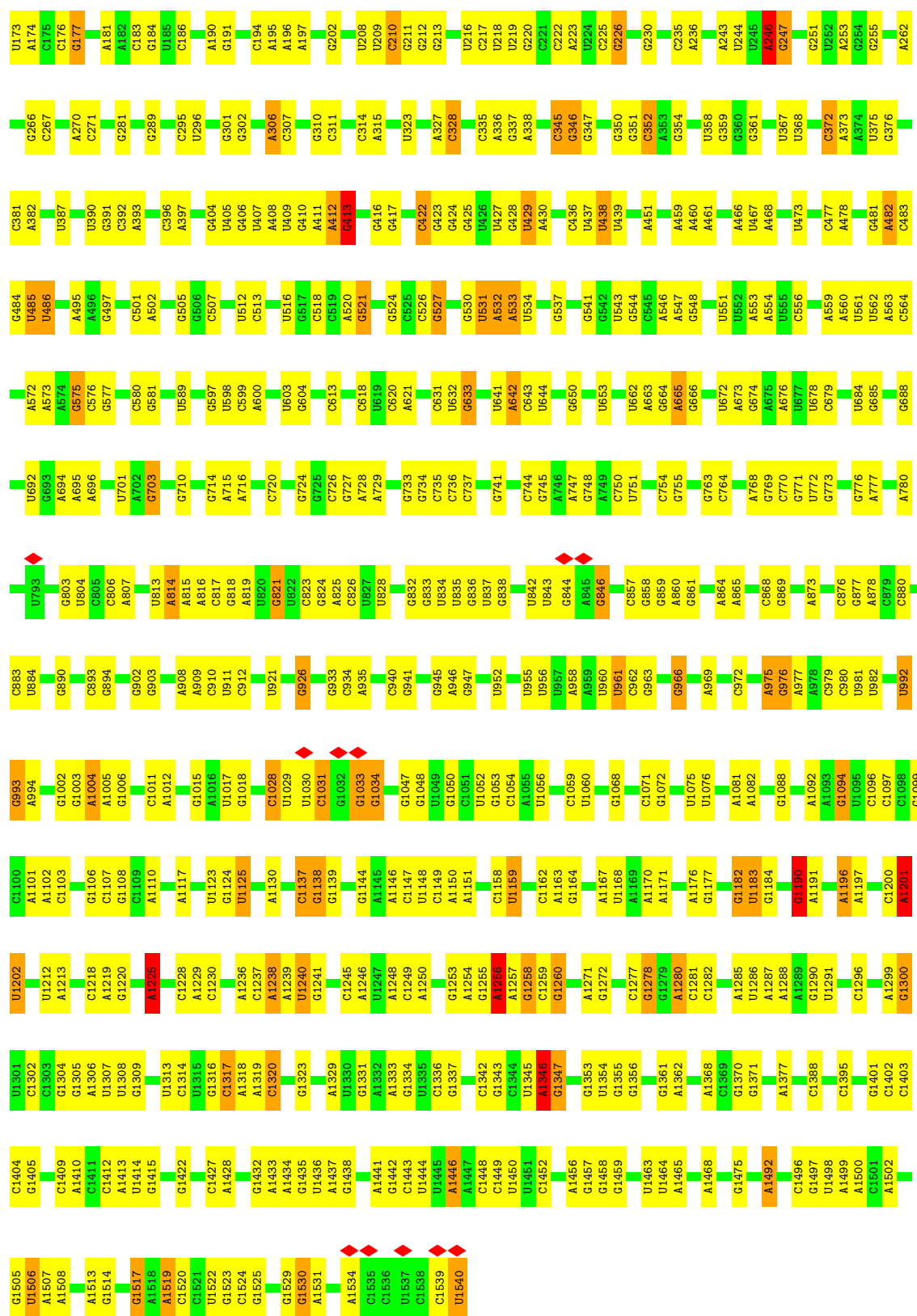


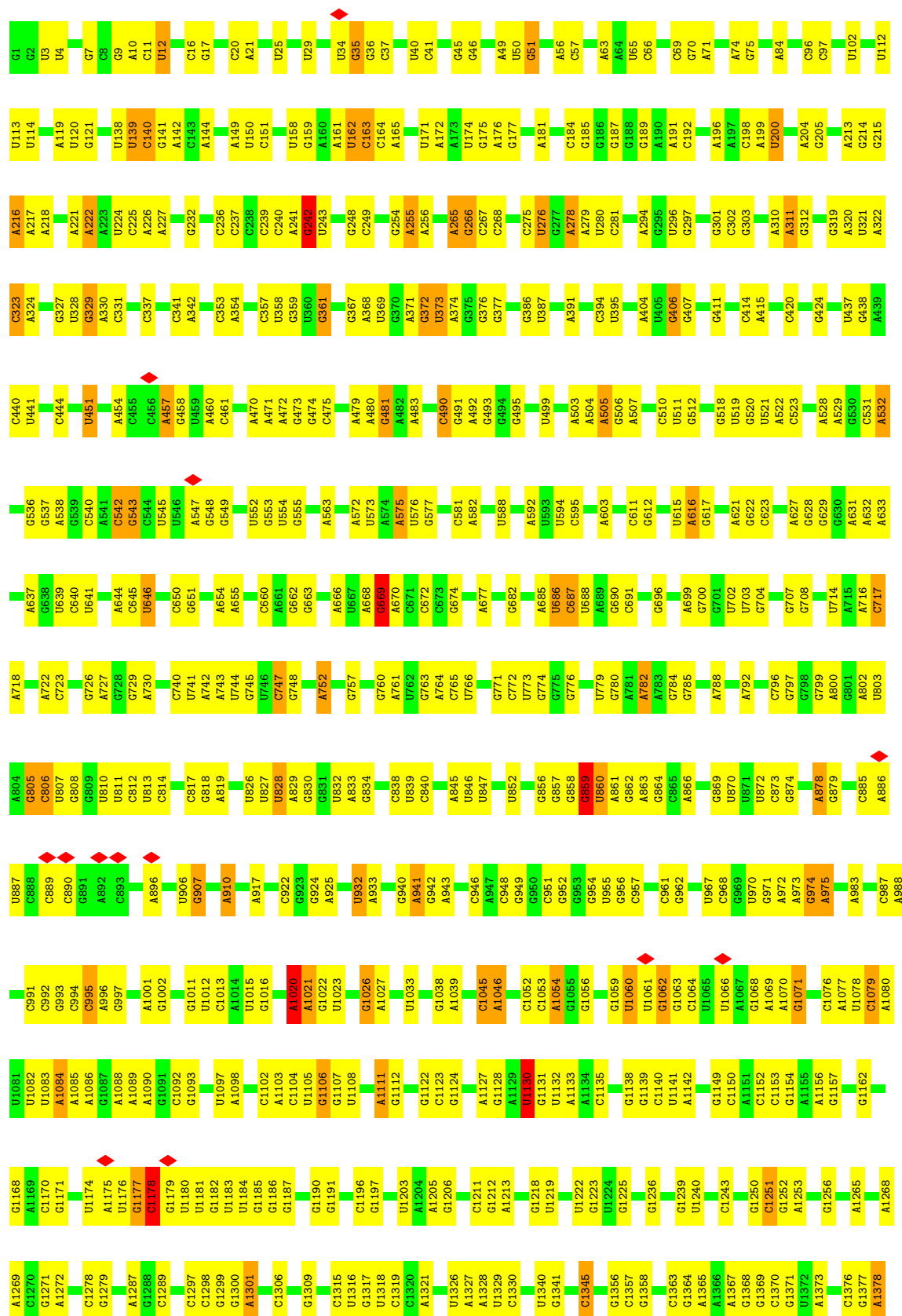
- Molecule 52: 50S ribosomal protein L1



- Molecule 53: 16S ribosomal RNA





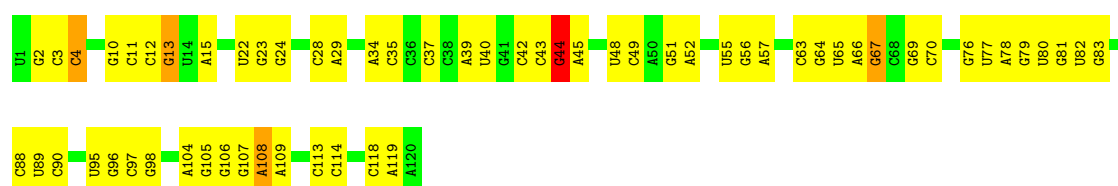


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U2613	A2516	G2429	U2343	U2262	U2181	U2106	U2017	U1883	A1784		A1689	A1580	A1474	G1380
A2614	C2517	A2430	U2344	C2263	U2182	G2107		A1884			G1695	G1581	U1475	A1383
U2615	U2519	U2431	G2345	U2265	A2183	A2108	A2020	A1885	U1796		G1696	A1583	U1476	
U2616	C2520	A2432	A2346	U2266	A2184	U2109	C2021	C1893	U1797		G1697	A1584		C1386
U2617	C2521		C2347	A2267	U2185	G2110	U2022	C1894	U1798				G1482	A1387
U2618	U2522		U2348	A2268	U2187	U2112	G2023	U1898	G1799		C1704	G1483	G1388	G1388
C2619		C2440	C2350	G2269	U2188	U2113	G2024	A1899	C1800		A1705	U1484	G1389	
	G2526	U2441	G2351	G2271	U2189	G2114	C2025	A1900	A1801		U1594	U1485	A1486	
C2626	C2527	C2442	G2352	G2272	G2190	G2115	U2028	A1901	A1802		A1603	U1394	A1395	
C2627	U2528	C2443	A2353	A2277	A2191	G2116	G2029	A1902	A1803		G1710		C1398	
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U2629	A2530	G2445	G2355		U2193	U2118	A2031	G1907	C1806		G1715	C1494	C1414	U1415
G2630			G2357	C2269	U2194	A2119	G2032	G1907	A1807		A1716	A1503	U1416	U1416
	U2533	A2448	C2358	C2283	U2195	G2120	A2033	A1913	A1808		A1717	C1498	C1417	C1417
G2633	A2534	C2452	C2359	G2286	U2196	U2122		C1924	A1809		G1718	A1504	G1418	G1418
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G2644	G2543		G2370	U2292	U2199	G2125	A2038	C1927	A1812		G1721	A1507	G1425	G1425
C2645	G2544	C2466	U2371	U2293	U2203	A2126	U2039	G1929	U1813			A1508	G1426	G1426
C2646		C2467	G2372	U2294	G2204	G2127	U2041	U1930	U1814			A1509	G1427	A1427
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		C2480	U2384	G2307	G2216	G2141	G2057	C1958	A1829			G1642		
C2676	C2677	G2481	C2385	G2308	U2220	A2142		U1963	G1831			G1645		
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C2681	G2581	U2492	A2391	G2316			C2064	U1970	G1757			A1535		
		U2493	U2393		G2230	C2153	C2065	U1971	U1758			C1536		
C2682		G2494	G2394	G2322	U2231	A2154	C2066	G1972	A1759			G1537		
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C2699			C2424	C2339	U2259	A2173	G2341	G2012	G1776			U1467		
				G2341	C2260	C2174		U2012	U1779			U1468		
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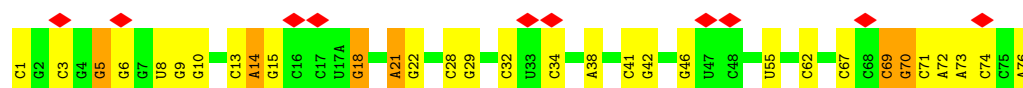
• Molecule 55: 5S ribosomal RNA

Chain 02: 49% 47% . .



• Molecule 56: tRNA^{fMet}

Chain X: 13% 60% 32% 8%



• Molecule 56: tRNA^{fMet}

Chain W: 74% 21% 5%



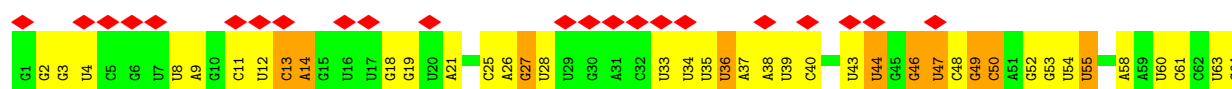
• Molecule 57: mRNA

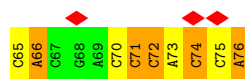
Chain V: 24% 76% 18% 6%



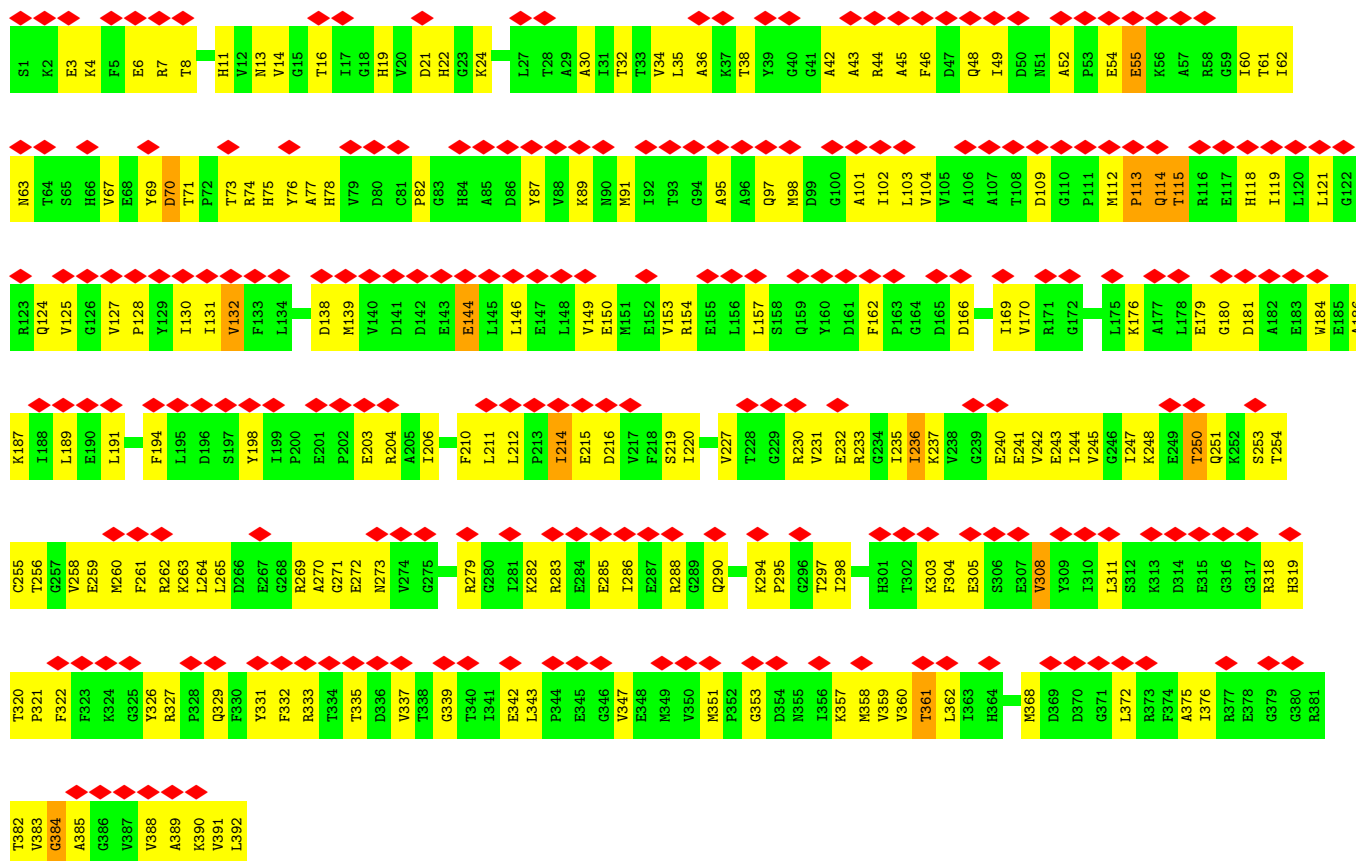
• Molecule 58: tRNA^{Lys}

Chain Y: 33% 36% 45% 20%





• Molecule 59: Elongation factor Tu 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	4629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	12.452	Depositor
Minimum map value	-6.336	Depositor
Average map value	-0.325	Depositor
Map value standard deviation	1.041	Depositor
Recommended contour level	2.79	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, U8U

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	04	0.36	0/2122	0.86	5/2852 (0.2%)
2	05	0.38	0/1586	0.87	3/2134 (0.1%)
3	06	0.38	0/1571	0.97	11/2113 (0.5%)
4	07	0.38	0/1435	0.89	5/1926 (0.3%)
5	08	0.39	0/1343	0.91	1/1816 (0.1%)
6	09	0.45	0/1122	1.04	6/1515 (0.4%)
7	10	0.47	0/1002	1.05	9/1350 (0.7%)
8	11	0.49	0/1046	1.07	9/1410 (0.6%)
9	12	0.38	0/1152	0.87	4/1551 (0.3%)
10	13	0.38	0/948	0.86	2/1268 (0.2%)
11	14	0.38	0/1054	0.95	4/1403 (0.3%)
12	15	0.36	0/1093	0.83	0/1460
13	16	0.37	0/974	0.88	3/1301 (0.2%)
14	17	0.36	0/902	0.85	2/1209 (0.2%)
15	18	0.37	0/929	0.84	0/1242
16	19	0.35	0/960	0.87	0/1278
17	20	0.39	0/829	0.92	4/1107 (0.4%)
18	21	0.37	0/864	0.93	2/1156 (0.2%)
19	22	0.36	0/745	0.86	2/994 (0.2%)
20	23	0.41	0/788	0.99	4/1051 (0.4%)
21	24	0.36	0/766	0.87	3/1025 (0.3%)
22	25	0.33	0/582	0.89	2/769 (0.3%)
23	26	0.32	0/635	0.79	1/848 (0.1%)
24	27	0.32	0/510	1.00	3/677 (0.4%)
25	28	0.36	0/453	0.86	0/605
26	29	0.36	0/532	0.92	2/709 (0.3%)
27	30	0.34	0/450	0.80	1/599 (0.2%)
28	31	0.43	0/417	0.91	2/554 (0.4%)
29	32	0.35	0/380	0.83	0/498
30	33	0.34	0/513	0.84	0/676
31	34	0.37	0/303	0.84	0/397
32	B	0.40	0/1736	0.98	10/2338 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.39	0/1652	0.87	4/2225 (0.2%)
34	D	0.37	0/1665	0.98	4/2227 (0.2%)
35	E	0.40	0/1170	0.91	3/1573 (0.2%)
36	F	0.43	0/836	0.89	4/1128 (0.4%)
37	G	0.38	0/1196	0.99	3/1602 (0.2%)
38	H	0.38	0/989	0.90	1/1326 (0.1%)
39	I	0.39	0/1034	1.02	5/1375 (0.4%)
40	J	0.42	0/797	0.95	4/1077 (0.4%)
41	K	0.41	0/886	0.87	1/1195 (0.1%)
42	L	0.39	0/969	1.02	6/1300 (0.5%)
43	M	0.38	0/893	0.90	1/1193 (0.1%)
44	N	0.36	0/817	0.88	4/1088 (0.4%)
45	O	0.35	0/722	0.90	1/964 (0.1%)
46	P	0.38	0/659	0.96	2/884 (0.2%)
47	Q	0.42	0/658	0.90	3/881 (0.3%)
48	R	0.41	0/545	0.98	3/731 (0.4%)
49	S	0.42	0/653	0.88	4/877 (0.5%)
50	T	0.34	0/671	0.99	5/888 (0.6%)
51	U	0.44	0/551	1.06	7/728 (1.0%)
52	03	0.44	0/1034	1.05	8/1387 (0.6%)
53	A	0.47	0/36963	0.55	11/57662 (0.0%)
54	01	0.47	0/69796	0.55	12/108888 (0.0%)
55	02	0.49	0/2872	0.55	1/4479 (0.0%)
56	W	0.49	0/1832	0.53	0/2855
56	X	0.51	0/1832	0.58	0/2855
57	V	0.50	0/421	0.61	0/657
58	Y	0.53	0/1780	0.59	1/2767 (0.0%)
59	Z	0.46	0/3085	0.96	14/4173 (0.3%)
All	All	0.45	0/166720	0.68	212/248816 (0.1%)

There are no bond length outliers.

All (212) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	09	51	ARG	N-CA-C	9.59	124.23	112.54
20	23	96	LYS	N-CA-C	-9.54	96.39	110.52
50	T	69	ASN	N-CA-C	-9.22	102.16	113.41
52	03	185	LEU	N-CA-C	-8.80	101.97	112.89
34	D	46	ARG	N-CA-C	-8.75	102.04	112.89
42	L	114	SER	N-CA-C	-8.01	102.13	112.23
52	03	191	ALA	N-CA-C	-7.91	103.42	113.23
45	O	43	ALA	N-CA-C	-7.73	103.11	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	25	40	LYS	N-CA-C	-7.72	102.95	111.36
11	14	14	LYS	N-CA-C	-7.71	105.03	114.75
33	C	143	LEU	N-CA-C	-7.62	104.50	113.88
39	I	59	LYS	N-CA-C	7.61	119.21	111.07
53	A	1190	G	C2'-C3'-O3'	7.58	120.87	109.50
6	09	67	ALA	N-CA-C	-7.54	103.15	111.36
20	23	76	THR	N-CA-C	-7.53	104.10	113.28
17	20	44	GLY	N-CA-C	-7.52	103.71	112.73
59	Z	250	THR	N-CA-C	7.40	120.71	110.35
21	24	80	HIS	N-CA-C	-7.36	100.15	110.31
37	G	143	MET	N-CA-C	-7.36	103.76	112.89
32	B	30	ILE	N-CA-C	7.29	118.66	108.23
54	01	1178	C	N1-C1'-C2'	7.29	122.94	112.00
1	04	153	LEU	N-CA-C	7.12	120.03	110.35
7	10	30	SER	N-CA-C	-7.08	104.24	113.17
8	11	62	ALA	N-CA-C	-7.07	104.63	113.18
59	Z	36	ALA	N-CA-C	-6.95	104.55	113.16
40	J	17	LEU	N-CA-C	-6.94	105.34	113.88
10	13	109	SER	N-CA-C	6.92	118.73	107.32
32	B	186	VAL	N-CA-C	6.81	119.52	108.97
33	C	89	VAL	N-CA-C	6.80	117.56	110.62
59	Z	308	VAL	N-CA-C	6.80	118.39	108.53
32	B	142	LYS	N-CA-C	-6.79	103.68	112.23
47	Q	11	VAL	N-CA-C	6.71	118.43	109.37
8	11	21	PRO	N-CA-C	6.70	118.88	110.70
51	U	37	TYR	N-CA-C	-6.70	105.06	113.23
59	Z	180	GLY	N-CA-C	6.69	123.91	115.21
32	B	176	ASN	N-CA-C	-6.69	104.94	113.23
20	23	75	ALA	N-CA-C	-6.68	103.80	112.68
48	R	66	LEU	N-CA-C	-6.67	105.30	113.50
17	20	14	VAL	N-CA-C	6.64	117.11	108.35
35	E	110	MET	N-CA-C	-6.56	103.33	112.45
51	U	44	ARG	N-CA-C	-6.55	103.97	112.23
50	T	7	LYS	N-CA-C	-6.55	104.55	112.54
32	B	21	TYR	N-CA-C	6.53	119.77	109.39
42	L	115	LYS	N-CA-C	-6.52	100.86	110.52
3	06	31	VAL	N-CA-C	6.50	116.64	110.53
32	B	62	ARG	N-CA-C	-6.50	105.38	113.38
42	L	43	LYS	N-CA-C	6.50	124.17	109.81
7	10	51	TYR	N-CA-C	6.44	119.12	111.33
8	11	127	SER	N-CA-C	-6.43	103.78	111.69
3	06	73	ILE	N-CA-C	-6.41	106.44	113.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	G	23	ALA	N-CA-C	-6.40	104.40	111.82
3	06	115	GLN	N-CA-C	-6.38	105.65	113.50
26	29	64	PHE	N-CA-C	-6.36	105.34	113.23
42	L	74	GLN	N-CA-C	6.34	117.98	107.20
59	Z	55	GLU	N-CA-C	-6.34	105.03	112.89
54	01	1020	A	C2'-C3'-O3'	6.33	119.00	109.50
53	A	1201	A	C2'-C3'-O3'	6.32	118.97	109.50
7	10	117	LEU	N-CA-C	6.30	119.82	108.48
14	17	113	ALA	N-CA-C	-6.25	105.69	113.38
3	06	146	VAL	N-CA-C	6.24	116.44	108.82
4	07	4	HIS	N-CA-C	-6.24	104.56	111.36
52	03	188	ASN	N-CA-C	-6.24	103.06	112.04
54	01	1818	U	N1-C1'-C2'	6.22	121.33	112.00
39	I	73	GLY	N-CA-C	-6.20	104.83	112.77
6	09	44	ILE	N-CA-C	-6.18	104.72	110.53
36	F	52	ASN	N-CA-C	-6.14	102.99	111.28
7	10	80	THR	N-CA-C	6.11	123.81	110.80
7	10	127	ALA	N-CA-C	-6.11	105.67	112.57
48	R	15	GLU	N-CA-C	-6.10	106.00	113.50
54	01	1130	U	C2'-C3'-O3'	6.09	122.83	113.70
32	B	187	ASP	N-CA-C	-6.08	101.00	110.42
19	22	43	ILE	N-CA-C	-6.06	104.39	111.00
59	Z	115	THR	N-CA-C	-6.06	104.24	111.69
3	06	110	SER	N-CA-C	-6.05	105.39	112.89
44	N	89	ARG	N-CA-C	-6.02	106.07	113.41
7	10	125	ARG	N-CA-C	-6.00	102.57	111.81
8	11	132	ALA	N-CA-C	-5.99	104.83	111.36
6	09	100	ALA	N-CA-C	-5.97	104.70	112.23
8	11	110	GLN	N-CA-C	-5.97	104.89	111.82
39	I	88	GLU	N-CA-C	-5.97	104.11	111.75
1	04	177	SER	N-CA-C	-5.96	105.77	113.16
32	B	214	GLY	N-CA-C	-5.95	105.39	113.37
37	G	77	ARG	N-CA-C	-5.94	103.41	111.55
48	R	69	TYR	N-CA-C	-5.93	104.76	112.23
13	16	67	PHE	N-CA-C	-5.92	106.40	113.97
4	07	134	GLN	N-CA-C	-5.91	105.38	112.59
3	06	46	GLN	N-CA-C	-5.91	101.78	110.52
53	A	438	U	C2'-C3'-O3'	5.91	122.56	113.70
28	31	30	PRO	N-CA-C	5.90	121.30	113.57
54	01	1378	A	C2'-C3'-O3'	5.90	118.35	109.50
3	06	88	ARG	N-CA-C	-5.89	101.08	109.62
54	01	242	G	N9-C1'-C2'	5.83	120.74	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	17	110	ALA	N-CA-C	-5.82	105.08	111.82
52	03	168	ASN	N-CA-C	-5.81	106.17	113.72
44	N	24	ALA	N-CA-C	-5.77	106.20	113.18
51	U	21	SER	N-CA-C	-5.77	106.00	113.16
42	L	7	VAL	N-CA-C	-5.76	104.72	111.00
41	K	69	CYS	N-CA-C	-5.76	106.29	113.38
9	12	79	GLY	N-CA-C	-5.76	107.38	115.32
53	A	1225	A	N9-C1'-C2'	5.75	120.63	112.00
5	08	13	GLY	N-CA-C	-5.75	107.12	114.37
4	07	77	LYS	N-CA-C	5.75	119.36	111.54
2	05	152	PRO	N-CA-C	-5.75	105.70	113.40
4	07	114	ARG	N-CA-C	-5.74	106.19	113.43
17	20	51	VAL	CA-C-N	-5.74	113.28	120.51
17	20	51	VAL	C-N-CA	-5.74	113.28	120.51
3	06	23	PHE	N-CA-C	5.72	118.00	109.59
3	06	16	GLU	N-CA-C	-5.72	106.14	113.23
47	Q	69	THR	N-CA-C	-5.70	101.93	108.49
50	T	70	LYS	N-CA-C	-5.70	104.68	111.69
52	03	186	LYS	N-CA-C	-5.69	105.83	112.89
51	U	9	GLU	N-CA-C	5.67	122.34	109.81
53	A	413	G	N9-C1'-C2'	5.66	120.50	112.00
54	01	859	G	C2'-C3'-O3'	5.65	122.18	113.70
23	26	65	THR	N-CA-C	-5.65	105.27	111.82
7	10	7	ASP	N-CA-C	-5.63	105.23	111.36
46	P	75	ILE	N-CA-C	-5.62	103.91	111.44
50	T	13	SER	N-CA-C	-5.61	105.32	111.82
34	D	45	PRO	N-CA-C	5.60	120.00	111.15
3	06	45	ALA	N-CA-C	5.59	116.70	107.20
40	J	26	VAL	N-CA-C	-5.59	103.95	111.44
59	Z	384	GLY	N-CA-C	5.57	118.72	110.42
24	27	58	ASN	N-CA-C	-5.57	105.99	112.89
52	03	7	ARG	N-CA-C	5.56	117.42	111.36
49	S	33	TRP	N-CA-C	-5.55	106.40	114.12
6	09	64	ALA	N-CA-C	-5.54	105.25	112.23
1	04	53	ILE	N-CA-C	5.53	117.37	108.85
33	C	76	ILE	N-CA-C	-5.53	104.55	112.35
27	30	9	ARG	N-CA-C	-5.52	105.42	111.82
1	04	12	ARG	N-CA-C	-5.50	105.83	112.54
40	J	6	ILE	N-CA-C	5.50	116.10	108.84
2	05	207	VAL	N-CA-C	-5.49	104.86	112.50
51	U	8	ASN	N-CA-C	5.49	122.49	110.80
11	14	43	GLY	N-CA-C	-5.49	107.75	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	10	65	GLU	N-CA-C	-5.46	105.87	112.54
49	S	27	LYS	N-CA-C	-5.46	101.67	110.14
13	16	68	ALA	N-CA-C	-5.46	105.72	112.38
44	N	20	PHE	N-CA-C	5.45	118.13	110.23
39	I	119	LYS	N-CA-C	5.44	116.79	107.28
53	A	1346	A	N9-C1'-C2'	5.42	120.12	112.00
18	21	29	VAL	N-CA-C	5.39	115.84	110.23
46	P	47	GLU	N-CA-C	5.39	116.84	111.07
26	29	50	ASP	N-CA-C	5.38	119.51	112.13
50	T	5	SER	N-CA-C	-5.37	106.00	112.54
54	01	2893	A	N9-C1'-C2'	5.37	120.05	112.00
3	06	6	LYS	N-CA-C	5.36	117.13	111.28
32	B	61	SER	N-CA-C	-5.36	106.69	113.18
51	U	33	ARG	N-CA-C	5.35	115.31	108.24
59	Z	144	GLU	N-CA-C	5.35	117.53	111.11
36	F	73	GLU	N-CA-C	-5.32	105.56	111.36
22	25	34	VAL	N-CA-C	5.30	115.54	108.11
18	21	24	ILE	N-CA-C	5.29	114.40	106.42
59	Z	132	VAL	N-CA-C	5.29	116.36	108.54
35	E	59	ILE	N-CA-C	5.28	116.00	110.62
8	11	11	GLN	N-CA-C	5.28	122.04	110.80
9	12	73	VAL	N-CA-C	5.26	116.29	108.23
53	A	345	C	N1-C1'-C2'	5.26	119.89	112.00
4	07	5	ASP	N-CA-C	-5.25	105.47	111.14
8	11	130	GLY	N-CA-C	-5.25	105.99	113.86
36	F	15	SER	N-CA-C	-5.24	106.15	112.54
34	D	110	ARG	N-CA-C	-5.23	106.40	112.89
51	U	58	LYS	N-CA-C	-5.22	106.41	112.89
11	14	35	HIS	N-CA-C	5.22	118.14	109.94
59	Z	286	ILE	N-CA-C	-5.22	102.35	109.55
19	22	60	THR	N-CA-C	5.22	116.91	109.14
54	01	669	G	N9-C1'-C2'	5.21	119.82	112.00
39	I	90	ASP	N-CA-C	5.21	121.89	110.80
8	11	107	GLU	N-CA-C	-5.20	105.70	111.36
9	12	81	ILE	N-CA-C	5.20	120.14	109.34
52	03	59	VAL	N-CA-C	5.19	116.85	108.85
54	01	2808	G	C2'-C3'-O3'	-5.19	105.92	113.70
32	B	88	GLN	N-CA-C	5.18	117.87	109.79
33	C	62	SER	N-CA-C	-5.18	101.78	109.96
42	L	24	GLU	N-CA-C	5.17	121.82	110.80
54	01	490	C	C2'-C3'-O3'	5.17	121.45	113.70
11	14	95	LEU	N-CA-C	-5.16	105.72	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	01	2286	G	N9-C1'-C2'	5.16	119.74	112.00
10	13	51	LYS	N-CA-C	-5.16	105.66	111.28
59	Z	54	GLU	N-CA-C	-5.15	106.51	112.89
55	02	44	G	N9-C1'-C2'	5.14	119.72	112.00
52	03	6	LYS	N-CA-C	5.14	119.79	111.37
2	05	70	LYS	N-CA-C	-5.12	107.42	113.97
58	Y	44	U	N1-C1'-C2'	5.12	119.68	112.00
6	09	46	PHE	N-CA-C	-5.12	107.01	113.20
24	27	60	LYS	N-CA-C	-5.12	106.55	112.89
35	E	101	GLY	N-CA-C	-5.12	106.80	115.34
36	F	90	MET	N-CA-C	5.11	117.30	109.95
21	24	42	LEU	N-CA-C	5.10	116.56	108.96
59	Z	170	VAL	N-CA-C	5.10	116.31	108.71
49	S	12	LEU	N-CA-C	-5.09	105.62	111.07
13	16	54	LEU	N-CA-C	-5.09	106.58	112.89
34	D	146	GLU	N-CA-C	5.09	117.23	111.02
53	A	246	A	C2'-C3'-O3'	5.07	117.11	109.50
59	Z	203	GLU	N-CA-C	5.07	117.55	108.17
43	M	71	GLU	N-CA-C	-5.06	105.84	111.36
20	23	31	GLY	N-CA-C	-5.06	108.08	115.72
53	A	1125	U	N1-C1'-C2'	5.06	119.59	112.00
1	04	30	ALA	N-CA-C	5.06	120.34	113.16
59	Z	179	GLU	N-CA-C	5.05	118.59	112.93
9	12	10	THR	N-CA-C	5.05	118.93	112.26
44	N	21	ALA	N-CA-C	-5.05	100.04	110.80
49	S	24	SER	N-CA-C	-5.05	107.15	113.72
28	31	43	ARG	N-CA-C	5.04	116.80	110.91
38	H	67	GLY	N-CA-C	-5.03	101.25	113.18
8	11	111	THR	N-CA-C	-5.03	105.71	111.14
47	Q	32	ILE	N-CA-C	5.03	115.88	111.56
21	24	52	ALA	N-CA-C	-5.02	106.93	113.16
7	10	56	ARG	N-CA-C	5.02	116.91	108.73
24	27	15	ASN	N-CA-C	-5.02	105.89	111.36
53	A	1256	A	N9-C1'-C2'	5.02	119.53	112.00
53	A	563	A	N9-C1'-C2'	5.01	119.51	112.00
40	J	38	GLY	N-CA-C	5.00	122.55	112.34

There are no chirality outliers.

There are no planarity outliers.

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	04	2083	0	2157	86	0
2	05	1565	0	1616	72	0
3	06	1552	0	1619	71	0
4	07	1411	0	1447	84	0
5	08	1323	0	1374	46	0
6	09	1111	0	1148	60	0
7	10	989	0	1025	58	0
8	11	1032	0	1088	74	0
9	12	1129	0	1162	46	0
10	13	939	0	1012	36	0
11	14	1045	0	1117	42	0
12	15	1074	0	1157	52	0
13	16	961	0	1000	41	0
14	17	892	0	923	31	0
15	18	917	0	965	45	0
16	19	947	0	1022	47	0
17	20	816	0	839	46	0
18	21	857	0	922	33	0
19	22	739	0	807	25	0
20	23	780	0	834	30	0
21	24	753	0	780	32	0
22	25	575	0	592	14	0
23	26	625	0	655	26	0
24	27	509	0	543	22	0
25	28	449	0	491	9	0
26	29	523	0	524	15	0
27	30	444	0	461	23	0
28	31	410	0	440	12	0
29	32	377	0	418	22	0
30	33	504	0	574	29	0
31	34	302	0	343	25	0
32	B	1705	0	1732	84	0
33	C	1625	0	1699	58	0
34	D	1643	0	1710	79	0
35	E	1157	0	1199	77	0
36	F	818	0	808	43	0
37	G	1182	0	1240	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	H	979	0	1034	52	0
39	I	1022	0	1070	60	0
40	J	787	0	828	37	0
41	K	870	0	878	44	0
42	L	955	0	1019	61	0
43	M	884	0	944	50	0
44	N	805	0	847	42	0
45	O	714	0	737	28	0
46	P	649	0	666	55	0
47	Q	649	0	691	36	0
48	R	536	0	552	37	0
49	S	638	0	665	39	0
50	T	665	0	714	38	0
51	U	545	0	579	32	0
52	03	1027	0	1092	43	0
53	A	33012	0	16618	465	0
54	01	62317	0	31346	878	0
55	02	2568	0	1303	54	0
56	W	1640	0	837	11	0
56	X	1640	0	837	20	0
57	V	373	0	187	2	0
58	Y	1618	0	821	37	0
59	Z	3029	0	3043	160	0
60	Z	32	0	14	1	0
All	All	153717	0	104765	3460	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 13.

All (3460) 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)
54:01:45:G:H5''	54:01:46:G:H5'	1.37	1.06
12:15:45:GLN:HE21	54:01:2485:G:H5''	1.26	1.00
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.45	0.94
54:01:1045:C:H5'	54:01:1046:A:H5'	1.49	0.93
6:09:12:LEU:HD22	6:09:19:VAL:HG11	1.51	0.93
53:A:484:G:H4'	53:A:485:U:H5''	1.50	0.93
34:D:195:ASN:HD22	34:D:198:LEU:HG	1.34	0.92
40:J:40:ILE:HB	40:J:73:LEU:HB2	1.50	0.92
52:03:172:HIS:HB2	54:01:2123:G:H4'	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:405:U:H3'	53:A:406:G:H5'	1.51	0.91
32:B:176:ASN:HD21	32:B:194:GLY:HA3	1.37	0.90
44:N:5:MET:HE2	44:N:62:ARG:HH21	1.36	0.90
1:04:20:ASN:HD22	1:04:23:LEU:HG	1.36	0.89
30:33:18:LYS:HG3	54:01:651:G:H5'	1.56	0.88
41:K:126:ARG:HH22	53:A:692:U:H5''	1.39	0.87
42:L:69:GLU:HG2	53:A:521:G:H4'	1.57	0.87
36:F:38:ARG:HD3	36:F:97:THR:HA	1.57	0.87
2:05:33:ARG:HD3	2:05:73:VAL:HB	1.56	0.86
35:E:107:GLY:HA3	53:A:9:G:H5'	1.57	0.86
54:01:475:C:H4'	54:01:510:C:H5'	1.58	0.86
53:A:1259:C:H3'	53:A:1260:G:H5''	1.56	0.86
59:Z:24:LYS:HG2	59:Z:104:VAL:HB	1.55	0.86
59:Z:235:ILE:HG22	59:Z:269:ARG:HA	1.58	0.85
7:10:19:ALA:HA	7:10:70:GLU:HG3	1.58	0.85
58:Y:54:U:H3'	58:Y:55:U:H5''	1.59	0.85
3:06:146:VAL:HG12	3:06:185:LYS:HB2	1.59	0.85
35:E:54:GLU:HG2	35:E:56:PRO:HD2	1.59	0.85
3:06:88:ARG:HD3	3:06:89:PRO:HD2	1.60	0.84
4:07:48:LEU:HD21	4:07:147:ARG:HH12	1.42	0.84
32:B:99:MET:HA	32:B:106:VAL:HG21	1.59	0.83
53:A:813:U:H2'	53:A:814:A:H5''	1.59	0.83
7:10:94:ARG:HA	7:10:129:LEU:HD13	1.59	0.83
28:31:4:ILE:HG23	28:31:27:ARG:HH21	1.42	0.83
42:L:85:ARG:HA	42:L:93:ARG:HA	1.60	0.83
52:03:17:ALA:HB1	54:01:2105:U:H5''	1.61	0.82
18:21:66:ILE:H	18:21:66:ILE:HD12	1.44	0.82
36:F:6:ILE:HB	36:F:62:MET:HB2	1.61	0.82
47:Q:24:ILE:HD12	47:Q:43:LEU:HD12	1.58	0.82
21:24:25:LYS:HG2	21:24:43:ASP:HA	1.60	0.82
54:01:1177:G:H2'	54:01:1178:C:H4'	1.59	0.81
6:09:97:ARG:HG2	6:09:112:LYS:HD2	1.62	0.81
16:19:55:GLN:HA	16:19:58:GLN:HE21	1.43	0.81
12:15:49:ALA:HA	12:15:123:LYS:HG3	1.62	0.81
19:22:54:GLU:HB3	19:22:88:LYS:HD2	1.61	0.80
54:01:2584:U:H2'	54:01:2585:U:H2'	1.61	0.80
13:16:2:ARG:HA	13:16:5:LYS:HD2	1.62	0.80
9:12:73:VAL:HG22	9:12:88:THR:HG22	1.62	0.80
10:13:121:GLU:HG2	10:13:122:VAL:HG23	1.64	0.80
59:Z:206:ILE:HG22	59:Z:270:ALA:H	1.46	0.80
46:P:31:ARG:HB2	53:A:310:G:H5''	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:106:LYS:HE2	2:05:174:SER:HB3	1.63	0.79
54:01:1064:C:H41	54:01:1069:A:H5''	1.47	0.79
55:02:3:C:H2'	55:02:4:C:H5''	1.62	0.79
28:31:8:ILE:HD13	28:31:24:LYS:HE3	1.63	0.79
32:B:19:THR:HG23	32:B:20:ARG:H	1.45	0.79
36:F:81:ASN:HD22	36:F:84:VAL:H	1.30	0.79
54:01:2267:A:H5''	54:01:2268:A:H5'	1.65	0.79
48:R:11:ARG:HB2	48:R:47:ARG:HH12	1.47	0.79
8:11:91:LYS:HB3	8:11:94:LYS:HB2	1.65	0.79
35:E:152:VAL:HG11	38:H:98:LEU:HD13	1.64	0.78
38:H:77:VAL:HG23	38:H:126:CYS:HA	1.64	0.78
42:L:98:ARG:HH21	42:L:106:VAL:HG22	1.47	0.78
53:A:59:A:H5''	53:A:387:U:H5''	1.64	0.78
12:15:12:MET:HA	54:01:910:A:H62	1.48	0.78
16:19:5:ARG:HB2	16:19:8:ILE:HD11	1.64	0.78
53:A:769:G:H4'	53:A:1513:A:H4'	1.64	0.78
33:C:182:ASP:HB2	33:C:201:ILE:HB	1.66	0.78
14:17:40:ILE:HG12	14:17:47:VAL:HG12	1.64	0.78
20:23:24:VAL:HG22	20:23:35:VAL:HG22	1.65	0.78
20:23:47:PRO:HB3	20:23:55:GLY:H	1.47	0.78
59:Z:52:ALA:HB3	59:Z:55:GLU:HG3	1.66	0.78
11:14:95:LEU:HD22	11:14:100:ILE:HD11	1.66	0.77
12:15:64:TRP:HB2	12:15:104:GLU:HB2	1.66	0.77
41:K:127:ARG:HH22	53:A:1522:U:H5''	1.49	0.77
8:11:32:VAL:HG23	8:11:60:VAL:HG13	1.64	0.77
54:01:2127:G:H21	54:01:2173:A:H1'	1.48	0.77
22:25:44:GLY:H	22:25:47:VAL:HB	1.48	0.77
33:C:69:THR:HG21	33:C:75:VAL:HG21	1.64	0.77
52:03:53:ARG:HB3	56:X:62:C:H4'	1.64	0.77
51:U:7:GLU:HG3	51:U:15:LEU:HD13	1.67	0.77
54:01:2277:G:H2'	54:01:2278:A:H5''	1.66	0.77
6:09:8:LYS:HA	6:09:14:SER:HA	1.66	0.77
5:08:163:TYR:HB2	5:08:166:GLU:HB2	1.67	0.77
37:G:98:LEU:HA	37:G:101:ARG:HH12	1.49	0.77
1:04:164:VAL:HG11	1:04:180:MET:HE1	1.66	0.76
2:05:46:ARG:HG3	2:05:84:LEU:HB2	1.66	0.76
27:30:30:ASP:HB3	27:30:34:GLY:H	1.51	0.76
29:32:34:ARG:HH21	29:32:39:ARG:HD2	1.50	0.76
33:C:110:LEU:HG	33:C:143:LEU:HD23	1.66	0.76
33:C:112:ALA:HB1	33:C:184:ASN:HB2	1.67	0.76
35:E:23:THR:HA	35:E:28:ARG:HA	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:88:LYS:HE2	38:H:119:GLY:HA2	1.67	0.76
1:04:221:GLY:HA2	1:04:224:MET:HE3	1.67	0.76
37:G:26:VAL:HG22	37:G:42:VAL:HG21	1.67	0.76
38:H:102:VAL:HG12	38:H:125:ILE:HD12	1.68	0.76
53:A:1029:U:H2'	53:A:1031:C:H1'	1.68	0.76
59:Z:101:ALA:H	59:Z:130:ILE:HG12	1.50	0.76
3:06:117:ARG:HH21	3:06:184:ASP:HA	1.49	0.76
53:A:373:A:H61	53:A:391:G:H1'	1.50	0.76
8:11:42:ASN:HA	8:11:45:THR:HG22	1.66	0.75
10:13:76:VAL:H	15:18:72:VAL:HG22	1.50	0.75
59:Z:243:GLU:HG3	59:Z:295:PRO:HG3	1.68	0.75
11:14:111:ILE:H	11:14:111:ILE:HD12	1.50	0.75
13:16:29:VAL:HG13	13:16:83:LEU:HD11	1.68	0.75
13:16:44:LEU:HD23	13:16:113:ILE:HD13	1.67	0.75
38:H:46:GLU:HG3	38:H:47:ASP:H	1.50	0.75
10:13:21:CYS:HA	10:13:41:ILE:HG22	1.68	0.75
34:D:7:LYS:HE2	34:D:21:LYS:HG3	1.69	0.75
58:Y:13:C:H2'	58:Y:14:A:H5''	1.65	0.75
59:Z:248:LYS:HZ3	59:Z:251:GLN:HG2	1.51	0.75
59:Z:35:LEU:HD12	59:Z:69:TYR:HB2	1.69	0.75
4:07:10:GLU:HA	4:07:13:LYS:HE3	1.67	0.75
42:L:41:PRO:HB2	42:L:45:ASN:HB2	1.68	0.75
2:05:110:THR:HB	2:05:202:ILE:HB	1.69	0.74
32:B:117:GLU:HA	32:B:140:LEU:HD11	1.69	0.74
13:16:103:ARG:HB2	13:16:110:MET:HE3	1.68	0.74
11:14:48:ARG:HH11	54:01:666:A:H4'	1.52	0.74
16:19:108:LEU:HA	17:20:48:LYS:HE3	1.69	0.74
39:I:123:ARG:HB3	53:A:1343:G:H4'	1.68	0.74
52:03:6:LYS:HA	52:03:9:ARG:HH12	1.51	0.74
21:24:72:VAL:HG12	21:24:93:ARG:HA	1.70	0.74
39:I:23:GLY:H	39:I:60:LEU:HA	1.53	0.74
40:J:10:LEU:HD11	40:J:72:ARG:HB2	1.70	0.74
42:L:99:GLY:HA3	42:L:117:GLY:HA3	1.69	0.74
29:32:16:HIS:HA	29:32:21:ARG:HH22	1.53	0.73
15:18:52:ARG:HH22	54:01:2720:U:H5''	1.52	0.73
29:32:22:MET:HE1	29:32:28:ARG:HD3	1.69	0.73
59:Z:318:ARG:HH22	59:Z:322:PHE:HB3	1.52	0.73
10:13:110:GLU:H	10:13:113:MET:HE2	1.53	0.73
34:D:12:ARG:HD2	34:D:36:ALA:HB3	1.70	0.73
2:05:46:ARG:HB2	2:05:84:LEU:HD12	1.69	0.73
7:10:34:THR:HG22	54:01:1085:A:H61	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:33:LEU:HD13	12:15:117:PHE:HB3	1.69	0.73
31:34:12:ARG:HH12	54:01:1102:C:H4'	1.53	0.73
37:G:129:ASN:HA	37:G:134:VAL:HG11	1.69	0.73
46:P:6:LEU:HD11	46:P:70:ARG:HG2	1.71	0.73
59:Z:157:LEU:HB3	59:Z:162:PHE:HB2	1.70	0.73
8:11:106:GLN:HA	8:11:109:ALA:HB3	1.69	0.73
50:T:27:MET:HE3	50:T:57:VAL:HA	1.71	0.73
52:03:55:SER:HA	52:03:58:ASN:HD22	1.51	0.73
32:B:118:THR:HA	32:B:121:GLN:HE21	1.54	0.73
18:21:82:MET:HB2	18:21:98:LYS:HB2	1.70	0.73
59:Z:97:GLN:HA	59:Z:230:ARG:HD3	1.70	0.73
43:M:9:PRO:HG2	43:M:44:ILE:HG13	1.71	0.72
8:11:5:GLN:HG2	8:11:61:TYR:HD1	1.52	0.72
49:S:28:LYS:HE3	49:S:29:PRO:HD2	1.70	0.72
34:D:103:ARG:HD2	34:D:167:PRO:HG2	1.71	0.72
11:14:62:PRO:HB3	54:01:2393:U:H5''	1.71	0.72
26:29:20:ASN:HD21	26:29:39:LYS:HD3	1.54	0.72
17:20:49:ILE:HB	17:20:51:VAL:O	1.90	0.72
32:B:185:ILE:HA	32:B:199:ILE:HB	1.70	0.72
33:C:21:TRP:HB3	33:C:58:ARG:H	1.53	0.72
53:A:327:A:O2'	53:A:328:C:H4'	1.90	0.72
56:X:13:C:H2'	56:X:14:A:H5''	1.70	0.72
38:H:29:SER:HB2	53:A:589:U:H5''	1.72	0.72
51:U:16:ARG:HB2	51:U:19:LYS:HD3	1.71	0.72
7:10:6:GLN:HA	7:10:9:GLN:HB3	1.69	0.72
52:03:11:ILE:HG23	52:03:33:LEU:HD22	1.72	0.72
54:01:2427:C:H5''	54:01:2429:G:H5'	1.70	0.72
5:08:92:GLY:H	5:08:94:ARG:HH12	1.37	0.72
33:C:109:GLU:HB2	33:C:143:LEU:HD22	1.72	0.72
38:H:108:GLY:HA2	53:A:642:A:H1'	1.72	0.71
1:04:67:LYS:HD3	1:04:69:ASN:HD22	1.54	0.71
31:34:36:ARG:O	31:34:37:GLN:HB2	1.88	0.71
6:09:55:GLU:HA	6:09:58:LEU:HD12	1.71	0.71
50:T:67:HIS:HB3	53:A:262:A:H5'	1.73	0.71
4:07:21:TYR:HB3	4:07:26:GLN:HB3	1.71	0.71
9:12:7:LYS:HG2	54:01:538:A:H4'	1.70	0.71
15:18:46:VAL:HG22	15:18:60:VAL:HG22	1.72	0.71
52:03:8:MET:HE3	54:01:2174:C:H4'	1.72	0.71
2:05:133:THR:HG21	54:01:1993:U:H4'	1.72	0.71
8:11:78:LEU:HD21	8:11:108:ILE:HG21	1.72	0.71
9:12:37:ARG:HH21	9:12:118:MET:HE1	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:117:ALA:HA	9:12:120:ARG:NH2	2.06	0.71
59:Z:245:VAL:HA	59:Z:250:THR:HG22	1.71	0.71
52:03:10:VAL:HG12	52:03:14:LYS:HE3	1.72	0.71
28:31:36:LYS:HE2	28:31:45:HIS:HB3	1.73	0.71
54:01:275:C:H2'	54:01:276:U:H4'	1.73	0.71
32:B:163:ILE:HD11	32:B:209:VAL:HG11	1.70	0.71
38:H:101:ALA:HB3	38:H:112:ASP:HB3	1.73	0.71
4:07:91:ARG:HA	4:07:95:MET:HB3	1.71	0.71
42:L:98:ARG:HB2	42:L:116:TYR:HA	1.71	0.71
22:25:33:ILE:HD11	22:25:78:ILE:HD11	1.72	0.71
43:M:76:ILE:HG22	43:M:80:MET:HE2	1.73	0.71
47:Q:18:LYS:HD2	53:A:255:G:H4'	1.71	0.71
52:03:5:THR:HG21	54:01:2129:C:H5''	1.73	0.71
39:I:105:ARG:HH12	39:I:107:ALA:HA	1.56	0.70
55:02:65:U:H3'	55:02:108:A:H61	1.54	0.70
13:16:103:ARG:HH11	54:01:1287:A:H5'	1.56	0.70
45:O:88:ARG:H	45:O:88:ARG:HD2	1.54	0.70
21:24:8:VAL:HG23	21:24:65:VAL:HG21	1.73	0.70
37:G:24:LYS:HA	37:G:27:ASN:HD22	1.56	0.70
51:U:5:VAL:HG12	51:U:19:LYS:HZ3	1.57	0.70
31:34:19:ARG:HD2	31:34:24:ARG:HD2	1.73	0.70
38:H:77:VAL:HG12	38:H:84:ILE:HD12	1.71	0.70
43:M:48:SER:HB2	43:M:51:GLN:HG3	1.74	0.70
8:11:15:GLY:H	8:11:51:GLY:H	1.39	0.70
8:11:48:ILE:HG13	8:11:49:GLU:H	1.57	0.70
27:30:42:ILE:HG22	27:30:48:TYR:HB2	1.73	0.70
54:01:2553:G:H3'	54:01:2554:U:H5''	1.74	0.70
12:15:45:GLN:NE2	54:01:2485:G:H5''	2.06	0.70
14:17:64:TYR:HB3	14:17:67:ASN:ND2	2.07	0.70
36:F:71:ILE:HD12	36:F:74:LEU:HD12	1.71	0.70
51:U:5:VAL:HG12	51:U:19:LYS:NZ	2.06	0.70
53:A:664:G:H22	53:A:741:G:H1	1.39	0.70
20:23:73:ASN:ND2	20:23:75:ALA:HB3	2.06	0.69
31:34:2:LYS:HD2	31:34:4:ARG:HH12	1.56	0.69
59:Z:121:LEU:HD22	59:Z:375:ALA:HB1	1.74	0.69
59:Z:214:ILE:HD12	59:Z:290:GLN:HB2	1.74	0.69
9:12:72:LYS:HB3	9:12:89:PHE:HB2	1.74	0.69
54:01:729:G:H4'	54:01:763:G:H5'	1.74	0.69
6:09:26:ALA:HA	6:09:30:LEU:HB2	1.73	0.69
12:15:108:VAL:HB	12:15:112:LEU:HD23	1.73	0.69
3:06:47:LYS:HB2	3:06:51:GLU:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:38:VAL:O	17:20:53:PHE:HA	1.92	0.69
40:J:52:LEU:HB2	44:N:80:ARG:HD2	1.74	0.69
41:K:44:ALA:HB3	41:K:69:CYS:HB2	1.73	0.69
5:08:115:GLN:HG3	5:08:117:PRO:HD3	1.74	0.69
15:18:5:LYS:HE3	15:18:9:GLN:HB3	1.74	0.69
37:G:70:PRO:HG3	37:G:98:LEU:HD23	1.74	0.69
40:J:86:ALA:HA	40:J:90:LEU:HD12	1.74	0.69
52:03:174:THR:HB	54:01:2124:G:H5''	1.74	0.69
33:C:13:ILE:HG22	33:C:14:VAL:HG23	1.74	0.69
2:05:148:GLN:HB2	2:05:152:PRO:HG2	1.73	0.69
44:N:3:GLN:HG3	53:A:1047:G:H5''	1.75	0.69
54:01:799:G:H5''	54:01:800:A:H2'	1.75	0.69
2:05:156:PHE:HB3	9:12:81:ILE:HG13	1.75	0.69
38:H:10:LEU:HD22	38:H:74:ILE:HD11	1.74	0.69
58:Y:35:U:H2'	58:Y:36:U:H4'	1.73	0.69
49:S:71:GLY:HA3	53:A:1320:C:H1'	1.75	0.68
38:H:29:SER:HB3	38:H:32:LYS:HG2	1.75	0.68
2:05:35:THR:HG22	2:05:73:VAL:HG21	1.75	0.68
14:17:17:LYS:HZ2	54:01:2380:C:H5'	1.58	0.68
53:A:1345:U:H4'	53:A:1346:A:H8	1.58	0.68
3:06:181:ILE:HG23	11:14:2:ARG:HG3	1.75	0.68
35:E:80:LEU:HD13	35:E:122:VAL:HG11	1.75	0.68
58:Y:50:C:H1'	59:Z:327:ARG:HD3	1.76	0.68
50:T:26:MET:HB3	53:A:1458:G:H5'	1.75	0.68
8:11:89:SER:HB2	8:11:92:PRO:HG3	1.76	0.68
36:F:36:ILE:HA	36:F:64:VAL:HG23	1.76	0.68
42:L:101:LEU:HD12	42:L:101:LEU:H	1.57	0.68
10:13:63:VAL:HG23	10:13:64:ARG:H	1.57	0.67
1:04:95:TYR:HE2	1:04:101:ARG:HD2	1.59	0.67
12:15:35:ALA:HA	12:15:128:THR:HG22	1.74	0.67
45:O:23:SER:HB3	45:O:26:VAL:HG23	1.77	0.67
16:19:93:ILE:HG23	17:20:13:ARG:HB2	1.76	0.67
41:K:124:LYS:HA	51:U:34:ARG:H	1.58	0.67
53:A:1218:C:H2'	53:A:1219:A:C8	2.28	0.67
54:01:121:G:H4'	54:01:149:A:H5'	1.77	0.67
59:Z:368:MET:HB3	59:Z:391:VAL:HG21	1.74	0.67
12:15:42:THR:HG22	12:15:93:VAL:HG12	1.76	0.67
43:M:6:ILE:HG13	43:M:7:ASN:H	1.59	0.67
9:12:34:ARG:HG3	9:12:39:LYS:HB2	1.77	0.67
20:23:42:LYS:HE2	54:01:499:U:H5''	1.76	0.67
32:B:31:PHE:HB2	32:B:39:ILE:O	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:10:ARG:HH22	54:01:582:A:H4'	1.57	0.67
56:W:21:A:H61	56:W:46:G:H2'	1.60	0.67
32:B:66:ILE:HD12	32:B:159:ALA:HB3	1.76	0.67
2:05:157:LYS:HD2	9:12:80:HIS:HA	1.77	0.67
50:T:28:ARG:HA	50:T:31:ILE:HD12	1.76	0.67
14:17:33:ARG:HB2	55:02:52:A:N6	2.10	0.67
39:I:83:THR:HA	39:I:86:LEU:HD12	1.76	0.67
59:Z:55:GLU:HG2	59:Z:62:ILE:HG12	1.77	0.67
40:J:5:ARG:HG2	40:J:79:PRO:HD3	1.78	0.66
47:Q:29:LYS:HA	47:Q:36:PHE:HA	1.77	0.66
48:R:25:ILE:HA	48:R:28:LEU:HB3	1.77	0.66
54:01:2508:G:H1	54:01:2580:U:H3	1.41	0.66
36:F:81:ASN:ND2	36:F:84:VAL:HG23	2.09	0.66
47:Q:12:VAL:HB	47:Q:21:VAL:HG13	1.77	0.66
54:01:161:A:H3'	54:01:162:U:H5''	1.77	0.66
8:11:88:GLY:HA3	54:01:1063:G:H2'	1.76	0.66
32:B:60:ALA:HB3	32:B:223:GLY:HA3	1.77	0.66
32:B:96:LEU:H	32:B:99:MET:HE3	1.60	0.66
59:Z:212:LEU:HD12	59:Z:231:VAL:HG22	1.76	0.66
59:Z:335:THR:HG22	59:Z:337:VAL:HG23	1.77	0.66
3:06:79:ARG:HH22	54:01:471:A:H5''	1.61	0.66
7:10:33:VAL:HG12	7:10:35:VAL:H	1.59	0.66
14:17:51:ALA:HB3	14:17:78:VAL:HG22	1.76	0.66
59:Z:42:ALA:HB1	59:Z:69:TYR:HA	1.77	0.66
18:21:83:LYS:HG2	18:21:95:ARG:HH11	1.61	0.66
32:B:129:THR:HG22	32:B:131:LYS:H	1.61	0.66
11:14:79:LEU:H	11:14:113:ALA:HB3	1.60	0.66
14:17:26:LEU:HD13	14:17:39:VAL:HG22	1.77	0.66
26:29:61:ASN:O	26:29:65:ASN:HA	1.96	0.66
3:06:126:VAL:HG13	3:06:156:ASN:ND2	2.11	0.66
24:27:17:GLU:HA	24:27:20:ASN:HD22	1.61	0.66
41:K:30:ILE:HA	41:K:45:THR:HG22	1.78	0.66
46:P:5:ARG:HB2	53:A:376:G:H5''	1.77	0.66
5:08:3:VAL:HG21	54:01:2748:A:H5'	1.78	0.66
35:E:39:GLY:HA3	35:E:45:VAL:HG12	1.75	0.66
42:L:35:ARG:HH12	42:L:37:TYR:HB3	1.60	0.66
48:R:41:SER:HB3	48:R:51:GLN:HE21	1.59	0.66
20:23:1:ALA:HB1	54:01:337:C:H5''	1.77	0.65
45:O:71:ARG:NH2	53:A:754:C:H5'	2.11	0.65
59:Z:102:ILE:HD13	59:Z:191:LEU:HD21	1.78	0.65
53:A:225:C:H2'	53:A:226:G:H5''	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:188:LEU:HD21	15:18:7:LEU:HD11	1.78	0.65
3:06:3:LEU:HD12	3:06:14:VAL:HG11	1.79	0.65
3:06:164:LEU:HD12	3:06:164:LEU:H	1.61	0.65
16:19:90:ASP:OD2	17:20:11:GLN:HB2	1.96	0.65
42:L:32:VAL:HB	42:L:55:ARG:HB3	1.78	0.65
59:Z:35:LEU:HD22	59:Z:71:THR:HA	1.77	0.65
43:M:25:GLY:H	53:A:1329:A:H5''	1.62	0.65
53:A:112:G:H21	53:A:354:G:H5'	1.61	0.65
9:12:64:VAL:HB	9:12:68:LYS:HE3	1.77	0.65
42:L:23:LEU:HD23	42:L:29:LYS:HE3	1.77	0.65
15:18:105:LYS:O	15:18:108:ARG:HG2	1.96	0.65
35:E:156:ARG:HH22	38:H:100:ILE:HG23	1.61	0.65
3:06:58:LYS:HG2	3:06:71:GLY:HA2	1.77	0.65
33:C:69:THR:O	33:C:105:VAL:HG12	1.97	0.65
34:D:150:LYS:HA	34:D:154:VAL:HB	1.79	0.65
42:L:28:GLN:HE21	42:L:80:LEU:HD21	1.61	0.65
13:16:79:LEU:HD23	13:16:83:LEU:HD12	1.78	0.65
34:D:59:LYS:HE3	34:D:194:ILE:HG22	1.77	0.65
36:F:50:PRO:HG3	36:F:55:HIS:CE1	2.32	0.65
8:11:11:GLN:HB3	8:11:56:VAL:HG12	1.79	0.65
19:22:15:HIS:HB2	19:22:33:LYS:HG3	1.79	0.65
51:U:65:ARG:HG3	51:U:67:THR:HG22	1.78	0.65
53:A:520:A:H3'	53:A:521:G:H5''	1.78	0.64
53:A:1071:C:H2'	53:A:1072:G:H8	1.61	0.64
2:05:102:ALA:HA	2:05:180:VAL:HG21	1.79	0.64
14:17:17:LYS:NZ	54:01:2380:C:H5'	2.12	0.64
35:E:80:LEU:HD21	35:E:95:MET:HG3	1.79	0.64
2:05:33:ARG:HG3	2:05:51:THR:HG23	1.78	0.64
9:12:93:ILE:HD13	9:12:100:VAL:HG21	1.80	0.64
51:U:66:ARG:HD2	53:A:1099:G:H4'	1.78	0.64
21:24:77:VAL:HG23	21:24:89:ILE:HG12	1.78	0.64
46:P:27:ALA:HB3	46:P:30:GLY:HA3	1.77	0.64
14:17:34:HIS:HA	14:17:53:THR:OG1	1.98	0.64
16:19:44:TYR:HD1	16:19:47:ARG:HE	1.45	0.64
17:20:51:VAL:HB	17:20:52:PRO:HD2	1.80	0.64
6:09:45:GLU:HA	6:09:48:GLU:HB3	1.79	0.64
11:14:70:LYS:HD3	54:01:633:A:H5''	1.78	0.64
12:15:20:LEU:HD23	21:24:81:PRO:HG2	1.80	0.64
13:16:33:ILE:HD12	13:16:118:ARG:NH2	2.13	0.64
34:D:158:LEU:HD23	34:D:161:ALA:HB3	1.77	0.64
40:J:39:PRO:HD2	53:A:1123:U:H4'	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:T:69:ASN:HB2	53:A:262:A:H4'	1.79	0.64
54:01:2743:U:H2'	54:01:2744:G:H5''	1.79	0.64
1:04:81:GLU:HG3	1:04:102:TYR:HE1	1.62	0.64
11:14:116:VAL:HG21	11:14:135:ILE:HA	1.80	0.64
11:14:117:THR:HG22	11:14:118:THR:HG23	1.80	0.64
32:B:176:ASN:ND2	32:B:194:GLY:HA3	2.13	0.64
34:D:195:ASN:ND2	34:D:197:HIS:HB3	2.12	0.64
40:J:42:LEU:HD11	40:J:73:LEU:HG	1.78	0.64
50:T:73:ARG:HG2	50:T:77:ASN:ND2	2.13	0.64
53:A:208:U:H2'	53:A:210:C:H1'	1.80	0.64
59:Z:19:HIS:HB2	59:Z:115:THR:OG1	1.98	0.64
32:B:18:GLN:HE21	32:B:189:ASN:HD21	1.45	0.64
37:G:98:LEU:HA	37:G:101:ARG:NH1	2.12	0.64
48:R:12:PHE:H	48:R:47:ARG:HH12	1.46	0.64
2:05:4:LEU:HB2	2:05:101:PHE:HE2	1.63	0.64
3:06:4:VAL:HG12	3:06:11:ALA:HA	1.78	0.64
10:13:43:ILE:HD12	10:13:56:ASP:HB2	1.80	0.64
53:A:1496:C:H1'	53:A:1517:G:H22	1.63	0.64
46:P:7:ALA:HB3	46:P:18:GLN:HB2	1.80	0.63
53:A:396:C:H2'	53:A:397:A:H5''	1.79	0.63
7:10:124:ASP:HB3	7:10:126:LEU:HG	1.80	0.63
32:B:162:VAL:HB	32:B:184:ALA:HB2	1.80	0.63
35:E:159:SER:HB2	35:E:162:GLU:HB2	1.79	0.63
59:Z:282:LYS:HB2	59:Z:285:GLU:HG3	1.80	0.63
32:B:56:LEU:HD23	32:B:59:ILE:HD11	1.81	0.63
37:G:56:SER:HB3	37:G:59:GLU:HG2	1.80	0.63
42:L:26:CYS:SG	42:L:29:LYS:HG2	2.39	0.63
49:S:32:THR:HG23	49:S:50:VAL:HA	1.79	0.63
59:Z:176:LYS:HB3	59:Z:181:ASP:HB3	1.80	0.63
34:D:105:GLY:HA2	34:D:164:ARG:HH12	1.63	0.63
53:A:1506:U:O2'	53:A:1507:A:H5'	1.99	0.63
54:01:807:U:H2'	54:01:808:G:H8	1.63	0.63
55:02:37:C:H42	55:02:49:C:H1'	1.62	0.63
56:X:73:A:H2'	56:X:74:C:H5'	1.80	0.63
4:07:132:ARG:HH22	54:01:2306:C:H5'	1.61	0.63
34:D:100:VAL:O	34:D:104:MET:HG2	1.97	0.63
7:10:67:THR:HB	7:10:68:PRO:HD3	1.81	0.63
32:B:182:VAL:HG23	32:B:195:VAL:HA	1.81	0.63
34:D:96:ARG:HB2	34:D:99:ASN:HB2	1.80	0.63
1:04:7:PRO:HB3	1:04:13:ARG:HA	1.81	0.63
3:06:22:ASP:HA	3:06:114:ARG:HH12	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:19:LEU:HA	11:14:27:LEU:HD13	1.81	0.63
1:04:130:PRO:HG3	1:04:188:ARG:HE	1.63	0.63
46:P:4:ILE:HD12	46:P:67:ILE:HG13	1.81	0.63
49:S:72:GLU:HG2	53:A:1320:C:H4'	1.81	0.63
7:10:18:VAL:HA	7:10:86:MET:HE2	1.80	0.62
21:24:9:ARG:HH12	55:02:76:G:H5'	1.64	0.62
22:25:12:SER:HB2	54:01:2262:U:H5	1.64	0.62
33:C:175:HIS:ND1	53:A:1108:G:H5'	2.14	0.62
41:K:87:GLY:H	41:K:113:THR:HG22	1.63	0.62
52:03:218:MET:HE1	54:01:2128:G:H4'	1.80	0.62
32:B:172:ILE:HG23	32:B:182:VAL:HB	1.81	0.62
32:B:183:PHE:HB2	32:B:197:PHE:HB2	1.81	0.62
37:G:12:LEU:HG	37:G:13:PRO:HD2	1.81	0.62
46:P:67:ILE:H	46:P:67:ILE:HD12	1.64	0.62
3:06:117:ARG:NH1	11:14:2:ARG:HG2	2.15	0.62
59:Z:242:VAL:HA	59:Z:295:PRO:HD3	1.79	0.62
2:05:179:ARG:HB3	2:05:188:LEU:HD12	1.81	0.62
46:P:6:LEU:HD22	46:P:17:TYR:HB3	1.80	0.62
59:Z:321:PRO:HB3	59:Z:351:MET:HA	1.82	0.62
6:09:111:ALA:HB3	6:09:114:GLU:OE1	1.98	0.62
18:21:3:THR:HG21	18:21:58:ALA:HA	1.82	0.62
53:A:952:U:H5'	53:A:972:C:H41	1.65	0.62
6:09:1:MET:O	6:09:20:ASN:HA	1.98	0.62
1:04:42:ARG:HE	54:01:691:C:H1'	1.64	0.62
12:15:43:ALA:HA	12:15:46:ILE:HD12	1.80	0.62
30:33:36:ALA:HB3	30:33:39:ARG:HG3	1.81	0.62
31:34:2:LYS:HD2	31:34:4:ARG:NH1	2.14	0.62
32:B:11:ALA:HB2	32:B:211:LEU:HD13	1.82	0.62
42:L:109:ARG:NH1	53:A:537:G:H5''	2.13	0.62
59:Z:297:THR:HG23	59:Z:298:ILE:HG13	1.82	0.62
2:05:56:LYS:HZ1	54:01:2830:C:H5''	1.64	0.62
59:Z:248:LYS:NZ	59:Z:251:GLN:HG2	2.15	0.62
14:17:76:LYS:O	14:17:80:GLU:HG3	2.00	0.62
17:20:32:THR:HA	17:20:62:GLU:HA	1.82	0.62
1:04:156:SER:HB2	54:01:1818:U:H5'	1.82	0.62
4:07:69:ALA:H	4:07:82:TYR:H	1.47	0.62
15:18:1:SER:HA	54:01:2876:G:H5'	1.82	0.62
47:Q:43:LEU:HD21	53:A:236:A:H5''	1.81	0.62
54:01:948:C:H2'	54:01:949:G:H8	1.65	0.62
2:05:51:THR:HB	2:05:79:LEU:HD23	1.83	0.61
5:08:83:THR:HG23	5:08:133:LYS:HG2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:17:29:HIS:HB3	14:17:36:TYR:HB2	1.82	0.61
49:S:5:LYS:HG3	49:S:6:LYS:H	1.64	0.61
31:34:1:MET:HE3	31:34:34:LYS:HG2	1.82	0.61
39:I:94:ARG:HA	39:I:97:LEU:HB3	1.81	0.61
47:Q:61:ARG:HH12	47:Q:63:CYS:HB3	1.64	0.61
49:S:10:ILE:HG22	49:S:14:LEU:HD23	1.82	0.61
16:19:40:LYS:HA	16:19:43:GLN:NE2	2.15	0.61
41:K:86:LYS:HB2	41:K:112:VAL:HG23	1.83	0.61
4:07:98:PHE:HD1	4:07:101:ARG:HH11	1.46	0.61
17:20:11:GLN:HG2	17:20:39:LEU:HD22	1.81	0.61
32:B:162:VAL:HG21	32:B:172:ILE:HG12	1.83	0.61
37:G:144:ALA:O	37:G:146:ALA:N	2.34	0.61
39:I:8:THR:HG21	39:I:10:ARG:NH2	2.16	0.61
52:03:9:ARG:O	52:03:13:GLU:HG3	2.00	0.61
59:Z:304:PHE:HB2	59:Z:388:VAL:HG13	1.83	0.61
2:05:55:LYS:HE2	2:05:77:ARG:HA	1.83	0.61
7:10:19:ALA:HB2	7:10:69:PHE:HE2	1.65	0.61
9:12:17:VAL:HG23	9:12:137:PRO:HB2	1.83	0.61
17:20:24:LYS:HA	17:20:94:THR:OG1	2.00	0.61
54:01:807:U:H2'	54:01:808:G:C8	2.35	0.61
54:01:1476:U:H3	54:01:1515:A:H62	1.47	0.61
4:07:107:VAL:HB	4:07:108:PRO:HD3	1.83	0.61
17:20:76:LYS:HB2	17:20:85:LYS:HB3	1.81	0.61
39:I:10:ARG:HG3	39:I:105:ARG:NH2	2.16	0.61
41:K:115:ILE:HD13	51:U:27:VAL:HG23	1.82	0.61
46:P:36:VAL:HG23	46:P:53:ASP:HB3	1.83	0.61
54:01:2127:G:N2	54:01:2173:A:H1'	2.15	0.61
40:J:85:ASP:HB3	40:J:89:ARG:HH12	1.65	0.61
59:Z:320:THR:HB	59:Z:321:PRO:HD2	1.83	0.61
8:11:93:ASN:HB2	54:01:1077:A:C5'	2.31	0.61
39:I:44:ARG:H	39:I:44:ARG:HD2	1.66	0.61
40:J:22:THR:O	40:J:26:VAL:HG23	2.01	0.61
44:N:53:ASP:HA	44:N:58:ARG:HD3	1.83	0.61
46:P:22:ALA:HA	46:P:33:ILE:HD13	1.83	0.61
46:P:48:GLU:HG3	46:P:49:GLY:H	1.65	0.61
21:24:78:GLN:HE22	55:02:76:G:H21	1.49	0.61
25:28:45:GLY:HA3	54:01:852:U:H5'	1.83	0.61
31:34:7:VAL:HB	31:34:25:VAL:HG21	1.81	0.61
18:21:85:ILE:HG12	18:21:95:ARG:HG2	1.83	0.60
34:D:201:GLU:HB3	35:E:111:ARG:HH22	1.64	0.60
35:E:133:ILE:HD12	35:E:133:ILE:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:N:57:SER:HB3	53:A:979:C:H42	1.65	0.60
10:13:77:ILE:HG12	15:18:71:ARG:HG3	1.82	0.60
12:15:69:PRO:HA	12:15:94:ALA:HB2	1.83	0.60
33:C:24:ASN:HB3	33:C:27:GLU:HG2	1.83	0.60
39:I:113:LYS:HE2	39:I:118:ARG:O	2.01	0.60
53:A:412:A:O2'	53:A:413:G:H4'	2.00	0.60
9:12:129:GLU:HG2	9:12:130:HIS:H	1.66	0.60
34:D:58:GLN:O	34:D:62:ARG:HG2	2.01	0.60
36:F:29:ILE:HG21	36:F:64:VAL:HG21	1.83	0.60
53:A:352:C:H4'	53:A:354:G:OP1	2.01	0.60
54:01:2329:U:H2'	54:01:2330:G:C8	2.36	0.60
55:02:3:C:C2'	55:02:4:C:H5''	2.29	0.60
30:33:20:GLY:HA3	30:33:48:MET:HE1	1.82	0.60
33:C:118:SER:O	33:C:122:GLN:HG3	2.02	0.60
42:L:33:CYS:HA	42:L:54:VAL:HA	1.83	0.60
46:P:70:ARG:O	46:P:74:LEU:HG	2.02	0.60
54:01:1045:C:H5'	54:01:1046:A:C5'	2.28	0.60
54:01:1265:A:H61	54:01:2013:A:H3'	1.66	0.60
54:01:2296:U:H5''	54:01:2297:A:OP1	2.01	0.60
58:Y:76:A:H5''	59:Z:220:ILE:HD11	1.83	0.60
9:12:7:LYS:O	9:12:11:VAL:HG23	2.01	0.60
30:33:24:LYS:HE2	30:33:46:LYS:HE3	1.83	0.60
34:D:131:ILE:HG12	53:A:620:C:C2	2.37	0.60
36:F:85:ILE:HG22	36:F:86:ARG:HG2	1.84	0.60
47:Q:12:VAL:HG23	47:Q:23:ALA:H	1.66	0.60
54:01:2834:G:H2'	54:01:2879:A:H61	1.67	0.60
59:Z:237:LYS:H	59:Z:237:LYS:HD2	1.66	0.60
1:04:16:VAL:HB	1:04:203:VAL:HG22	1.81	0.60
15:18:2:ASN:ND2	54:01:2876:G:H4'	2.16	0.60
44:N:62:ARG:HH12	44:N:69:PRO:HD3	1.65	0.60
49:S:51:HIS:HA	49:S:56:HIS:HA	1.84	0.60
53:A:1005:A:H2'	53:A:1006:G:O4'	2.02	0.60
58:Y:43:U:H2'	58:Y:44:U:O4'	2.02	0.60
2:05:155:VAL:HG21	54:01:2618:G:H21	1.66	0.60
4:07:109:ARG:HH12	43:M:2:ARG:NH1	1.99	0.60
4:07:118:ALA:HB1	4:07:166:ARG:HE	1.66	0.60
4:07:133:GLU:HB3	4:07:135:ILE:HG12	1.84	0.60
12:15:45:GLN:HE21	54:01:2485:G:C5'	2.10	0.60
21:24:20:LEU:HD21	21:24:41:GLU:HG2	1.83	0.60
26:29:56:ARG:HG3	49:S:64:GLU:HA	1.83	0.60
40:J:41:PRO:HG3	53:A:1150:A:N3	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:24:LYS:HA	59:Z:104:VAL:HG11	1.82	0.60
6:09:117:LEU:HD22	6:09:122:LEU:HD11	1.84	0.60
43:M:3:ILE:HG22	43:M:56:ARG:HG2	1.83	0.60
46:P:52:LEU:HD22	46:P:78:VAL:HG11	1.83	0.60
54:01:972:A:H3'	54:01:973:A:H2'	1.84	0.60
54:01:1506:U:H2'	54:01:1507:C:C6	2.37	0.60
6:09:9:VAL:HB	6:09:13:GLY:HA3	1.84	0.60
53:A:531:U:H4'	53:A:532:A:H5'	1.83	0.60
41:K:85:VAL:HG21	51:U:16:ARG:HH22	1.67	0.60
11:14:23:ILE:HD12	11:14:23:ILE:H	1.67	0.59
22:25:59:ALA:HB3	22:25:78:ILE:HG22	1.83	0.59
26:29:11:GLU:HA	26:29:25:ARG:HA	1.84	0.59
35:E:131:ASN:HD22	35:E:132:PRO:HD2	1.65	0.59
41:K:35:ASP:OD2	41:K:39:ASN:HB2	2.03	0.59
49:S:69:LYS:HE3	53:A:1319:A:H5''	1.82	0.59
53:A:235:C:H2'	53:A:236:A:C8	2.37	0.59
54:01:528:A:N1	54:01:2042:A:H2'	2.16	0.59
1:04:259:ASN:ND2	1:04:261:ARG:HB3	2.16	0.59
3:06:84:THR:HG21	54:01:672:C:H5''	1.84	0.59
9:12:47:HIS:ND1	9:12:48:VAL:HG23	2.17	0.59
40:J:57:VAL:O	40:J:58:ASN:HB2	2.02	0.59
46:P:71:VAL:O	46:P:75:ILE:HG13	2.02	0.59
53:A:31:G:H21	53:A:46:G:H5''	1.67	0.59
54:01:1807:G:H2'	54:01:1808:A:H5'	1.84	0.59
1:04:22:GLU:HB3	1:04:80:LEU:HD12	1.84	0.59
7:10:60:LEU:HA	7:10:64:VAL:HB	1.83	0.59
9:12:25:LEU:HD13	9:12:62:VAL:HG21	1.84	0.59
35:E:101:GLY:H	35:E:121:ASN:CB	2.16	0.59
37:G:4:ARG:H	37:G:4:ARG:HD2	1.68	0.59
49:S:54:ARG:HB3	53:A:958:A:C2	2.38	0.59
49:S:62:THR:HG22	49:S:63:ASP:H	1.66	0.59
54:01:2452:C:H42	54:01:2504:U:H3	1.49	0.59
56:X:21:A:N6	56:X:46:G:H2'	2.17	0.59
56:X:71:C:H2'	56:X:72:A:C8	2.37	0.59
1:04:23:LEU:HD22	1:04:82:TYR:HB2	1.85	0.59
7:10:55:VAL:HG12	54:01:1084:A:H4'	1.84	0.59
12:15:26:VAL:HB	12:15:133:LYS:HB2	1.83	0.59
39:I:28:VAL:HB	39:I:63:TYR:HA	1.84	0.59
54:01:1363:C:H2'	54:01:1364:G:H8	1.65	0.59
1:04:42:ARG:HH12	1:04:48:ILE:HB	1.68	0.59
15:18:51:ASN:O	54:01:2845:U:H5''	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:22:1:MET:HE2	19:22:3:ARG:HB2	1.84	0.59
41:K:126:ARG:NH2	53:A:692:U:H5''	2.14	0.59
43:M:88:LEU:HD13	43:M:91:ARG:HH21	1.68	0.59
8:11:93:ASN:HB2	54:01:1077:A:H5''	1.84	0.59
36:F:81:ASN:HD22	36:F:84:VAL:HG23	1.68	0.59
50:T:35:TYR:O	50:T:39:GLU:HG2	2.02	0.59
52:03:65:LEU:HD22	52:03:188:ASN:HB3	1.84	0.59
8:11:126:ARG:HA	8:11:129:GLU:HB2	1.84	0.59
24:27:37:LEU:HD11	24:27:42:LEU:HD12	1.83	0.59
31:34:2:LYS:HB2	31:34:35:GLN:HB3	1.83	0.59
36:F:63:ASN:HD21	36:F:95:ALA:HB1	1.67	0.59
54:01:906:U:H2'	54:01:907:G:H5''	1.83	0.59
54:01:2111:U:H5'	54:01:2112:G:OP2	2.03	0.59
3:06:3:LEU:HB3	3:06:120:VAL:HG21	1.85	0.59
6:09:124:THR:HG22	6:09:125:THR:H	1.68	0.59
45:O:88:ARG:HD2	45:O:88:ARG:N	2.18	0.59
47:Q:69:THR:HG22	47:Q:70:LYS:H	1.68	0.59
48:R:52:ARG:HE	53:A:664:G:H5''	1.67	0.59
2:05:136:ASN:HA	54:01:2580:U:H5'	1.84	0.59
55:02:104:A:H2'	55:02:105:G:O4'	2.02	0.59
1:04:127:ASN:HB2	1:04:191:LEU:HD12	1.85	0.58
10:13:24:VAL:HG13	10:13:33:ALA:HB2	1.85	0.58
56:X:28:C:H2'	56:X:29:G:H8	1.67	0.58
45:O:35:ILE:HD13	45:O:59:VAL:HG22	1.86	0.58
50:T:67:HIS:CB	53:A:262:A:H5'	2.33	0.58
54:01:2105:U:H2'	54:01:2106:U:O4'	2.03	0.58
58:Y:13:C:C2'	58:Y:14:A:H5''	2.33	0.58
59:Z:35:LEU:HD13	59:Z:70:ASP:C	2.28	0.58
20:23:46:LYS:HA	54:01:483:A:H4'	1.85	0.58
54:01:2048:G:H2'	54:01:2049:G:H5''	1.85	0.58
59:Z:259:GLU:HG3	59:Z:263:LYS:O	2.03	0.58
20:23:18:LYS:HD2	20:23:19:GLY:N	2.18	0.58
48:R:17:VAL:HG22	48:R:18:GLN:H	1.69	0.58
54:01:991:C:H5'	54:01:1185:G:H2'	1.84	0.58
54:01:1316:U:H2'	54:01:1317:G:H8	1.69	0.58
54:01:1872:A:H2'	54:01:1873:G:O4'	2.04	0.58
58:Y:46:G:H3'	58:Y:47:U:H5''	1.85	0.58
5:08:7:PRO:HB2	5:08:48:THR:HB	1.85	0.58
8:11:79:LEU:HB3	8:11:137:LEU:HD13	1.85	0.58
18:21:4:ILE:HG22	18:21:106:VAL:HG13	1.84	0.58
59:Z:331:TYR:HA	59:Z:335:THR:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:11:7:TYR:HA	8:11:59:THR:HA	1.86	0.58
23:26:5:GLN:HB2	23:26:50:VAL:HG12	1.85	0.58
34:D:172:VAL:HG22	34:D:174:ALA:H	1.67	0.58
53:A:335:C:H2'	53:A:336:A:H8	1.69	0.58
59:Z:332:PHE:HB3	59:Z:372:LEU:HD21	1.85	0.58
5:08:171:LYS:HZ1	54:01:2530:A:H62	1.52	0.58
32:B:126:ASP:HA	32:B:133:ALA:HB2	1.85	0.58
36:F:5:GLU:HA	36:F:63:ASN:HA	1.84	0.58
2:05:56:LYS:NZ	54:01:2830:C:H5''	2.19	0.58
13:16:41:ALA:HB1	13:16:97:ILE:HD12	1.86	0.58
38:H:95:MET:O	38:H:98:LEU:HG	2.04	0.58
38:H:107:LYS:HG2	38:H:120:LEU:HD21	1.84	0.58
53:A:181:A:H61	53:A:194:C:H2'	1.69	0.58
2:05:121:THR:HG21	2:05:143:PRO:HB3	1.86	0.58
23:26:11:PRO:HB2	23:26:27:ARG:HH21	1.67	0.58
41:K:19:VAL:HG22	41:K:82:GLU:OE1	2.03	0.58
1:04:9:SER:O	1:04:12:ARG:HB3	2.04	0.58
11:14:62:PRO:HG2	30:33:24:LYS:HB3	1.86	0.58
39:I:11:ARG:NH2	39:I:108:ARG:HD3	2.19	0.58
45:O:48:ASP:OD2	45:O:51:SER:HB2	2.04	0.58
51:U:19:LYS:HB3	51:U:24:LYS:HD2	1.86	0.58
53:A:946:A:H2'	53:A:947:G:C8	2.39	0.58
55:02:65:U:H3'	55:02:108:A:N6	2.18	0.58
8:11:6:ALA:HB3	8:11:60:VAL:O	2.04	0.57
10:13:24:VAL:HA	10:13:39:ILE:HG22	1.85	0.57
10:13:48:PRO:HG3	53:A:1422:G:H5'	1.86	0.57
18:21:69:LEU:HD12	18:21:109:ASP:HA	1.86	0.57
19:22:47:VAL:HG21	19:22:85:VAL:HG11	1.86	0.57
26:29:11:GLU:HB2	26:29:25:ARG:HG2	1.86	0.57
36:F:19:PRO:O	36:F:23:GLU:HG3	2.03	0.57
41:K:23:HIS:HB3	41:K:30:ILE:HG23	1.85	0.57
53:A:1492:A:H2'	54:01:1913:A:N1	2.19	0.57
54:01:1570:A:H2'	54:01:1571:A:C8	2.39	0.57
17:20:40:MET:HE3	17:20:42:ALA:HB2	1.86	0.57
23:26:11:PRO:HB2	23:26:27:ARG:NH2	2.18	0.57
46:P:52:LEU:HB3	46:P:57:ILE:HD11	1.85	0.57
53:A:1033:G:H2'	53:A:1034:G:H4'	1.86	0.57
6:09:84:ALA:HB2	6:09:149:GLU:N	2.19	0.57
12:15:41:LEU:HD22	12:15:124:LEU:HD22	1.86	0.57
37:G:14:ASP:HB3	37:G:17:PHE:O	2.04	0.57
37:G:41:ILE:HG23	37:G:116:ALA:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:R:54:LEU:O	48:R:58:ILE:HG12	2.03	0.57
50:T:70:LYS:HA	50:T:73:ARG:NH1	2.20	0.57
54:01:2628:C:H3'	54:01:2629:U:H5'	1.86	0.57
59:Z:256:THR:HG21	59:Z:279:ARG:HE	1.68	0.57
10:13:33:ALA:HB1	10:13:37:ASP:HB2	1.85	0.57
12:15:40:ARG:HH11	12:15:93:VAL:HG11	1.70	0.57
40:J:48:ARG:HG2	44:N:100:TRP:HH2	1.69	0.57
46:P:4:ILE:HB	46:P:67:ILE:HA	1.86	0.57
52:03:67:HIS:NE2	52:03:184:LYS:HD2	2.18	0.57
4:07:2:LYS:HB3	4:07:100:GLU:OE1	2.04	0.57
21:24:64:VAL:HG22	21:24:69:GLU:HG2	1.86	0.57
35:E:80:LEU:HD11	35:E:95:MET:HE2	1.87	0.57
43:M:9:PRO:HG3	43:M:17:ALA:HB1	1.85	0.57
53:A:834:U:H2'	53:A:835:U:C6	2.39	0.57
54:01:296:U:H2'	54:01:297:G:C8	2.39	0.57
7:10:57:ASN:OD1	7:10:63:ALA:HB2	2.04	0.57
22:25:12:SER:OG	54:01:2261:C:H3'	2.04	0.57
33:C:8:GLY:HA2	33:C:11:LEU:HG	1.86	0.57
38:H:94:VAL:HG12	38:H:95:MET:HG3	1.86	0.57
54:01:511:U:H2'	54:01:512:G:H5'	1.86	0.57
59:Z:150:GLU:HA	59:Z:169:ILE:HG21	1.85	0.57
4:07:22:ASN:HD22	4:07:26:GLN:HE22	1.50	0.57
5:08:34:ARG:HH21	5:08:70:LEU:HD13	1.70	0.57
41:K:87:GLY:N	41:K:113:THR:HG22	2.19	0.57
49:S:36:ARG:HH21	53:A:1318:A:H1'	1.70	0.57
1:04:46:GLY:HA3	54:01:773:U:H5'	1.86	0.57
2:05:151:THR:HB	2:05:152:PRO:HD3	1.87	0.57
5:08:34:ARG:HD3	5:08:74:MET:SD	2.44	0.57
8:11:17:ALA:HB1	8:11:42:ASN:HD21	1.70	0.57
13:16:103:ARG:NH1	54:01:1287:A:H5'	2.19	0.57
18:21:79:GLY:H	18:21:101:SER:HA	1.69	0.57
19:22:22:THR:HA	19:22:25:GLU:HG2	1.86	0.57
36:F:45:ARG:HH22	48:R:25:ILE:HD11	1.69	0.57
39:I:105:ARG:NH1	39:I:107:ALA:HA	2.18	0.57
40:J:8:ILE:HB	40:J:74:VAL:HB	1.86	0.57
42:L:41:PRO:HD2	42:L:47:ALA:H	1.70	0.57
52:03:57:GLN:HA	52:03:201:PRO:HB2	1.87	0.57
54:01:310:A:H2'	54:01:311:A:H5''	1.85	0.57
56:W:69:C:H2'	56:W:70:G:H8	1.70	0.57
3:06:149:ILE:HD11	3:06:172:ALA:HA	1.86	0.57
8:11:101:SER:HB2	8:11:104:GLN:HG3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:14:23:ILE:HD13	17:20:84:ARG:NE	2.20	0.57
53:A:1414:U:H2'	53:A:1415:G:H8	1.67	0.57
4:07:55:ASP:O	4:07:59:ILE:HG13	2.05	0.57
4:07:104:THR:HG21	26:29:22:MET:SD	2.45	0.57
8:11:52:LEU:O	8:11:54:ILE:HG13	2.05	0.57
11:14:77:ILE:HD13	11:14:108:ALA:HB1	1.87	0.57
18:21:18:ARG:NH1	54:01:518:G:H4'	2.18	0.57
50:T:77:ASN:O	50:T:81:GLN:HG2	2.05	0.57
54:01:1367:A:H2'	54:01:1368:G:H5'	1.87	0.57
54:01:1418:G:H21	54:01:1580:A:H62	1.53	0.57
54:01:2354:C:H2'	54:01:2355:G:H8	1.68	0.57
5:08:21:GLN:NE2	5:08:38:ASP:HA	2.20	0.56
8:11:20:SER:HB3	8:11:21:PRO:HD3	1.87	0.56
8:11:100:ILE:HG22	8:11:101:SER:H	1.70	0.56
11:14:101:ILE:HG13	11:14:102:GLY:H	1.70	0.56
30:33:22:LYS:HA	30:33:48:MET:HA	1.86	0.56
37:G:14:ASP:H	37:G:19:SER:H	1.53	0.56
39:I:12:LYS:HA	39:I:109:GLN:OE1	2.03	0.56
49:S:35:ARG:HA	49:S:70:LEU:HB2	1.86	0.56
54:01:2114:A:H61	54:01:2117:A:H62	1.52	0.56
34:D:59:LYS:O	34:D:63:ILE:HG13	2.06	0.56
39:I:46:VAL:HA	39:I:49:GLN:HG3	1.87	0.56
48:R:47:ARG:H	48:R:47:ARG:HD2	1.70	0.56
53:A:663:A:H5'	53:A:836:G:OP1	2.06	0.56
54:01:1152:C:H2'	54:01:1153:C:H6	1.71	0.56
59:Z:214:ILE:HG23	59:Z:227:VAL:HG21	1.87	0.56
3:06:71:GLY:N	54:01:674:G:H5''	2.20	0.56
4:07:127:TYR:HD2	4:07:155:ILE:HD12	1.71	0.56
6:09:23:ALA:HB1	6:09:27:ARG:HH12	1.69	0.56
7:10:7:ASP:HB3	54:01:1046:A:H8	1.70	0.56
11:14:21:ARG:HA	54:01:811:U:H2'	1.87	0.56
14:17:68:LYS:HA	14:17:102:ARG:HG2	1.87	0.56
16:19:47:ARG:HH21	16:19:51:GLN:HE22	1.52	0.56
25:28:19:HIS:HD1	25:28:50:VAL:HG12	1.69	0.56
33:C:50:SER:HB2	33:C:71:ARG:HG3	1.87	0.56
34:D:107:GLY:HA2	34:D:157:ALA:HB1	1.88	0.56
53:A:501:C:H2'	53:A:502:A:C8	2.40	0.56
53:A:1299:A:H2'	53:A:1300:G:H4'	1.87	0.56
54:01:503:A:H4'	54:01:505:A:H5''	1.87	0.56
54:01:1077:A:H2'	54:01:1078:U:H5'	1.86	0.56
58:Y:46:G:H3'	58:Y:47:U:C5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:68:LYS:HB3	4:07:81:GLY:HA2	1.88	0.56
7:10:12:VAL:HA	7:10:15:VAL:HB	1.87	0.56
10:13:122:VAL:OXT	10:13:122:VAL:HG12	2.05	0.56
32:B:96:LEU:HD13	53:A:1103:C:H4'	1.87	0.56
39:I:51:LEU:HD13	39:I:56:MET:HG3	1.87	0.56
42:L:42:LYS:NZ	53:A:912:C:H5''	2.20	0.56
43:M:6:ILE:HG13	43:M:7:ASN:N	2.20	0.56
45:O:35:ILE:HG13	45:O:58:MET:HE2	1.87	0.56
54:01:1796:U:H2'	54:01:1797:G:H8	1.71	0.56
4:07:31:GLU:H	4:07:157:THR:HA	1.70	0.56
7:10:80:THR:HG22	54:01:1108:U:H4'	1.87	0.56
13:16:37:THR:HG23	13:16:103:ARG:HH21	1.70	0.56
18:21:89:ALA:O	18:21:92:ARG:HG2	2.04	0.56
23:26:70:LEU:HD13	23:26:77:TYR:HB3	1.87	0.56
24:27:2:LYS:HE2	54:01:102:U:H1'	1.88	0.56
30:33:40:LYS:HA	30:33:43:LEU:HD12	1.88	0.56
53:A:1308:U:H2'	53:A:1309:G:H8	1.71	0.56
3:06:102:ARG:NH1	3:06:201:ALA:HB3	2.20	0.56
4:07:91:ARG:HG2	55:02:43:C:O2'	2.06	0.56
12:15:64:TRP:HZ3	12:15:106:ASP:HB3	1.70	0.56
16:19:40:LYS:HA	16:19:43:GLN:HE21	1.69	0.56
17:20:6:GLN:HB2	17:20:37:GLU:HB3	1.86	0.56
54:01:1417:C:H4'	54:01:1587:G:H21	1.71	0.56
12:15:77:PRO:HB2	12:15:80:VAL:HG21	1.88	0.56
39:I:5:TYR:HB2	39:I:20:ILE:HG22	1.88	0.56
53:A:148:G:H1	53:A:174:A:H61	1.54	0.56
53:A:335:C:H2'	53:A:336:A:C8	2.41	0.56
54:01:996:A:H2'	54:01:997:G:H8	1.71	0.56
4:07:109:ARG:HH12	43:M:2:ARG:HH11	1.54	0.56
8:11:112:LYS:NZ	8:11:128:ILE:HG12	2.21	0.56
32:B:49:PHE:O	32:B:53:LEU:HG	2.06	0.56
35:E:101:GLY:H	35:E:121:ASN:HB3	1.70	0.56
54:01:828:U:H2'	54:01:829:A:C8	2.40	0.56
54:01:1023:U:O2'	54:01:1122:G:H5'	2.06	0.56
57:V:20:G:H2'	57:V:21:A:O4'	2.06	0.56
59:Z:149:VAL:O	59:Z:153:VAL:HG23	2.06	0.56
3:06:119:ILE:HB	3:06:187:VAL:HA	1.88	0.56
8:11:112:LYS:HA	8:11:115:ASP:HB2	1.88	0.56
53:A:1033:G:H3'	53:A:1034:G:H5''	1.88	0.56
54:01:740:C:H5'	54:01:1784:A:H2'	1.87	0.56
54:01:1857:G:N2	54:01:1884:G:H2'	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:121:THR:HB	2:05:127:PHE:HD2	1.71	0.56
32:B:37:VAL:HG22	32:B:38:HIS:H	1.70	0.56
33:C:171:ARG:HG2	33:C:173:PRO:HD3	1.88	0.56
58:Y:58:A:H4'	58:Y:60:U:H5	1.71	0.56
30:33:53:ASP:HB3	30:33:56:LEU:HD12	1.87	0.55
34:D:140:ASP:H	34:D:181:PHE:HB3	1.71	0.55
37:G:134:VAL:O	37:G:138:GLU:HG2	2.06	0.55
38:H:4:ASP:CG	38:H:80:PRO:HD3	2.31	0.55
54:01:310:A:C2'	54:01:311:A:H5''	2.34	0.55
54:01:1078:U:H4'	54:01:1079:C:H5''	1.87	0.55
3:06:6:LYS:HG2	3:06:121:VAL:HG12	1.88	0.55
6:09:116:ARG:HB2	6:09:131:SER:HB2	1.87	0.55
32:B:46:VAL:HB	32:B:47:PRO:HD3	1.88	0.55
34:D:33:ILE:HG13	34:D:34:GLU:N	2.21	0.55
43:M:104:ASN:O	43:M:105:ALA:HB3	2.06	0.55
54:01:581:C:H2'	54:01:582:A:C8	2.41	0.55
54:01:699:A:H2'	54:01:700:G:O4'	2.06	0.55
54:01:704:G:H2'	54:01:726:G:N2	2.21	0.55
54:01:971:G:H2'	54:01:972:A:O4'	2.07	0.55
1:04:91:ALA:HB2	1:04:105:ALA:HB2	1.88	0.55
20:23:73:ASN:HD21	20:23:75:ALA:HB3	1.70	0.55
24:27:7:ARG:O	24:27:8:GLU:HG3	2.06	0.55
24:27:56:LEU:O	24:27:60:LYS:HG2	2.05	0.55
29:32:12:ARG:NE	29:32:44:VAL:HG21	2.21	0.55
54:01:765:C:H2'	54:01:766:U:C6	2.41	0.55
54:01:2533:U:H2'	54:01:2534:A:O4'	2.06	0.55
6:09:4:ILE:HD12	6:09:17:ASP:O	2.05	0.55
6:09:43:ASN:HA	6:09:46:PHE:HB2	1.86	0.55
30:33:24:LYS:HG3	30:33:25:HIS:H	1.71	0.55
54:01:942:G:H2'	54:01:943:A:O4'	2.05	0.55
8:11:14:ALA:HB2	8:11:54:ILE:HD12	1.87	0.55
16:19:79:ILE:HD13	16:19:82:LEU:HD12	1.87	0.55
18:21:17:VAL:HG12	18:21:76:VAL:HG21	1.87	0.55
36:F:44:ARG:HA	36:F:58:HIS:HA	1.88	0.55
43:M:15:VAL:HG23	43:M:16:ILE:HD12	1.87	0.55
45:O:71:ARG:HH21	53:A:754:C:H5'	1.71	0.55
49:S:28:LYS:HB3	49:S:29:PRO:HD2	1.88	0.55
50:T:27:MET:HE1	50:T:66:ILE:HG13	1.88	0.55
58:Y:11:C:H2'	58:Y:12:U:C6	2.42	0.55
1:04:48:ILE:HD11	1:04:51:ARG:HA	1.88	0.55
2:05:190:LYS:HE2	54:01:2729:G:H4'	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:100:ALA:O	6:09:104:THR:HB	2.05	0.55
32:B:71:THR:HG22	32:B:72:LYS:H	1.71	0.55
48:R:12:PHE:H	48:R:47:ARG:NH1	2.04	0.55
53:A:823:C:H2'	53:A:824:G:H8	1.70	0.55
6:09:97:ARG:HH21	54:01:2220:U:H4'	1.72	0.55
7:10:88:HIS:HB2	7:10:89:PRO:HD3	1.88	0.55
13:16:48:VAL:HG12	13:16:52:ILE:HD11	1.89	0.55
18:21:36:LEU:HD13	18:21:48:LYS:HA	1.89	0.55
19:22:2:ILE:HD11	54:01:144:A:H4'	1.88	0.55
27:30:8:THR:CG2	54:01:2020:A:H5'	2.37	0.55
36:F:81:ASN:HD22	36:F:84:VAL:N	2.02	0.55
59:Z:95:ALA:HA	59:Z:98:MET:HE2	1.87	0.55
4:07:127:TYR:HE2	4:07:129:MET:HE2	1.72	0.55
6:09:2:GLN:HE21	6:09:20:ASN:HD22	1.54	0.55
7:10:67:THR:HG21	7:10:75:ALA:HB2	1.87	0.55
28:31:7:LYS:HA	28:31:23:THR:HA	1.88	0.55
43:M:53:ASP:HA	43:M:56:ARG:HH11	1.70	0.55
48:R:41:SER:HB3	48:R:51:GLN:NE2	2.22	0.55
54:01:265:A:H4'	54:01:266:G:OP1	2.06	0.55
54:01:932:U:H5'	54:01:933:A:C8	2.42	0.55
54:01:1178:C:H2'	54:01:1178:C:O2	2.07	0.55
54:01:1213:A:N6	54:01:1236:G:H1'	2.22	0.55
11:14:57:LEU:HD13	11:14:60:ARG:HH12	1.71	0.55
33:C:10:ARG:HA	33:C:13:ILE:HD13	1.89	0.55
35:E:13:LYS:NZ	35:E:112:ALA:HB1	2.22	0.55
45:O:55:LEU:O	45:O:59:VAL:HG23	2.06	0.55
48:R:35:SER:HB3	51:U:3:ILE:HG13	1.88	0.55
54:01:1020:A:H1'	54:01:1021:A:OP2	2.07	0.55
54:01:1357:C:H2'	54:01:1358:G:O4'	2.06	0.55
54:01:2515:C:H2'	54:01:2516:A:H8	1.70	0.55
1:04:5:CYS:HB3	1:04:12:ARG:HD2	1.89	0.55
4:07:40:GLY:HA2	4:07:84:ILE:HD11	1.89	0.55
20:23:84:PHE:HB2	54:01:297:G:H5''	1.88	0.55
29:32:26:ASN:O	29:32:30:VAL:HG23	2.05	0.55
54:01:241:A:H61	54:01:255:A:H3'	1.72	0.55
54:01:1107:G:H2'	54:01:1108:U:C6	2.42	0.55
54:01:1525:A:H2'	54:01:1526:C:O4'	2.07	0.55
54:01:2376:A:H2'	54:01:2377:A:O4'	2.07	0.55
59:Z:45:ALA:O	59:Z:49:ILE:HG13	2.07	0.55
12:15:5:LYS:C	12:15:6:ARG:HG3	2.32	0.54
12:15:34:LYS:HA	12:15:101:VAL:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:21:51:LEU:O	18:21:55:ILE:HG13	2.08	0.54
20:23:93:ARG:HB3	20:23:102:ILE:HD12	1.88	0.54
30:33:51:LYS:HA	30:33:54:LEU:HB2	1.88	0.54
53:A:1088:G:H21	53:A:1167:A:H61	1.55	0.54
54:01:2190:G:H2'	54:01:2191:A:C8	2.42	0.54
7:10:3:LEU:HD12	7:10:6:GLN:H	1.71	0.54
7:10:26:VAL:HG11	7:10:77:VAL:HG11	1.89	0.54
13:16:65:LEU:HD21	54:01:2870:C:H5''	1.87	0.54
13:16:94:TYR:O	13:16:116:VAL:HG23	2.07	0.54
32:B:29:PHE:HB3	32:B:40:ILE:HG23	1.89	0.54
41:K:88:PRO:HG2	41:K:89:GLY:H	1.73	0.54
44:N:25:GLU:HA	44:N:28:ALA:HB3	1.90	0.54
53:A:1524:C:H2'	53:A:1525:G:C8	2.42	0.54
54:01:1594:U:H2'	54:01:1595:C:C6	2.42	0.54
15:18:52:ARG:NH2	54:01:2720:U:H5''	2.20	0.54
20:23:33:VAL:HG13	20:23:66:VAL:HG22	1.88	0.54
22:25:63:VAL:HG22	22:25:78:ILE:HG12	1.90	0.54
32:B:75:ALA:HB1	32:B:163:ILE:HD13	1.88	0.54
47:Q:16:MET:HG3	47:Q:19:SER:OG	2.07	0.54
50:T:2:ASN:CG	50:T:3:ILE:H	2.15	0.54
53:A:946:A:H2'	53:A:947:G:H8	1.73	0.54
53:A:1259:C:H3'	53:A:1260:G:C5'	2.35	0.54
53:A:1316:G:H2'	53:A:1317:C:H5''	1.87	0.54
54:01:2724:U:H2'	54:01:2725:A:C8	2.41	0.54
6:09:81:ALA:HA	6:09:147:VAL:HB	1.89	0.54
7:10:35:VAL:O	7:10:39:THR:HG23	2.07	0.54
7:10:45:GLY:HA2	7:10:49:GLY:O	2.07	0.54
33:C:11:LEU:HA	33:C:15:LYS:HB2	1.88	0.54
59:Z:358:MET:HE1	59:Z:360:VAL:HG22	1.87	0.54
9:12:95:ARG:HG2	9:12:96:ARG:HG2	1.90	0.54
37:G:11:ILE:HG13	37:G:20:GLU:HG3	1.90	0.54
54:01:616:A:H2'	54:01:617:G:O4'	2.06	0.54
54:01:2039:U:H2'	54:01:2040:G:H8	1.73	0.54
1:04:79:ARG:HG2	1:04:92:LEU:HD23	1.90	0.54
1:04:140:VAL:HG12	1:04:191:LEU:HD23	1.89	0.54
2:05:124:ARG:HG3	2:05:165:MET:HB2	1.89	0.54
6:09:57:LYS:O	6:09:61:VAL:HG13	2.08	0.54
7:10:18:VAL:HG13	7:10:86:MET:HE2	1.89	0.54
10:13:113:MET:O	10:13:116:ILE:HG13	2.08	0.54
12:15:53:MET:HB2	12:15:120:ALA:HB2	1.90	0.54
19:22:68:LYS:HG3	19:22:77:ARG:NH2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:30:11:LYS:HA	27:30:14:MET:HE3	1.89	0.54
38:H:46:GLU:HB3	38:H:61:THR:HB	1.90	0.54
43:M:99:GLN:NE2	43:M:99:GLN:H	2.04	0.54
45:O:35:ILE:HG23	45:O:55:LEU:HD11	1.90	0.54
53:A:1170:A:H2'	53:A:1171:A:O4'	2.08	0.54
53:A:1230:C:H5'	56:W:30:G:H5''	1.90	0.54
16:19:47:ARG:HH21	16:19:51:GLN:NE2	2.05	0.54
16:19:82:LEU:HD22	16:19:87:VAL:HG11	1.89	0.54
16:19:105:PHE:O	16:19:109:VAL:HG23	2.08	0.54
29:32:10:LEU:O	29:32:14:ARG:HG2	2.07	0.54
36:F:68:GLN:O	36:F:71:ILE:HG22	2.07	0.54
41:K:19:VAL:HG23	41:K:35:ASP:O	2.08	0.54
53:A:715:A:H2'	53:A:716:A:C8	2.42	0.54
54:01:542:C:H2'	54:01:543:G:H5''	1.90	0.54
54:01:2210:U:H4'	54:01:2211:A:H2	1.72	0.54
2:05:31:ALA:HB1	2:05:95:SER:OG	2.08	0.54
16:19:12:ARG:O	16:19:16:ILE:HG12	2.07	0.54
53:A:3:A:H5'	53:A:613:C:H4'	1.88	0.54
54:01:112:U:H2'	54:01:113:U:H5'	1.89	0.54
56:X:28:C:H2'	56:X:29:G:C8	2.43	0.54
9:12:99:ARG:HA	9:12:102:GLU:HB3	1.88	0.54
18:21:55:ILE:O	18:21:59:GLU:HG2	2.07	0.54
33:C:56:ILE:HG22	33:C:63:ILE:HD11	1.90	0.54
35:E:93:VAL:HG11	35:E:139:THR:HG22	1.90	0.54
35:E:107:GLY:H	35:E:110:MET:HE2	1.71	0.54
39:I:79:ARG:NH1	39:I:102:PHE:HA	2.23	0.54
47:Q:10:ARG:C	47:Q:22:VAL:HG13	2.33	0.54
52:03:40:GLU:HB2	52:03:178:VAL:HG11	1.90	0.54
52:03:55:SER:HA	52:03:58:ASN:ND2	2.22	0.54
54:01:1068:G:H2'	54:01:1069:A:O4'	2.07	0.54
54:01:2185:U:H2'	54:01:2186:G:C8	2.43	0.54
20:23:70:ALA:HB3	20:23:79:ALA:HB1	1.90	0.54
46:P:70:ARG:HD3	53:A:375:U:OP1	2.08	0.54
54:01:327:G:H2'	54:01:328:U:O4'	2.08	0.54
54:01:373:U:H2'	54:01:374:A:H8	1.73	0.54
54:01:2884:U:H2'	54:01:2885:G:C8	2.43	0.54
2:05:11:MET:HG2	2:05:25:THR:HG23	1.89	0.53
3:06:145:ASP:HA	3:06:166:LYS:HB3	1.89	0.53
32:B:65:LYS:HD2	32:B:89:PHE:HE2	1.73	0.53
50:T:10:ALA:O	50:T:14:GLU:HG2	2.08	0.53
54:01:1105:U:H2'	54:01:1106:G:H5''	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2134:A:N6	54:01:2157:G:H4'	2.24	0.53
3:06:97:ASN:HB2	3:06:100:MET:HB2	1.89	0.53
7:10:21:GLY:HA3	7:10:86:MET:HE3	1.90	0.53
15:18:1:SER:HB2	15:18:4:ILE:HG13	1.89	0.53
18:21:83:LYS:HG2	18:21:95:ARG:NH1	2.23	0.53
24:27:52:ARG:O	24:27:56:LEU:HG	2.09	0.53
38:H:10:LEU:HD12	38:H:76:ARG:HB2	1.88	0.53
53:A:416:G:H2'	53:A:417:G:H8	1.73	0.53
53:A:813:U:C2'	53:A:814:A:H5''	2.34	0.53
53:A:1159:U:C5	53:A:1182:G:H2'	2.43	0.53
54:01:1141:U:H4'	54:01:1142:A:O4'	2.08	0.53
54:01:1858:A:H1'	54:01:1885:A:C2	2.44	0.53
54:01:2350:C:H2'	54:01:2351:G:O4'	2.08	0.53
59:Z:342:GLU:HB2	59:Z:359:VAL:O	2.09	0.53
1:04:257:ARG:HH12	1:04:259:ASN:H	1.54	0.53
3:06:118:LEU:HD11	3:06:188:MET:SD	2.48	0.53
4:07:73:VAL:HG22	4:07:78:ILE:HD11	1.89	0.53
7:10:118:ILE:HB	7:10:119:PRO:HD3	1.90	0.53
9:12:28:LEU:O	9:12:32:LEU:HG	2.07	0.53
15:18:12:MET:HE3	15:18:14:GLN:HE22	1.72	0.53
16:19:75:TYR:HE2	54:01:1153:C:H5'	1.73	0.53
19:22:14:PRO:HA	19:22:32:LEU:CB	2.38	0.53
33:C:19:SER:HB3	33:C:21:TRP:HE1	1.73	0.53
46:P:54:LEU:HA	46:P:57:ILE:HD12	1.91	0.53
48:R:31:TYR:HB3	48:R:54:LEU:HD21	1.90	0.53
49:S:30:LEU:HB2	49:S:48:ILE:HG22	1.90	0.53
50:T:27:MET:O	50:T:31:ILE:HG13	2.08	0.53
53:A:516:U:H3	53:A:533:A:H62	1.54	0.53
54:01:873:C:H2'	54:01:874:G:H8	1.73	0.53
54:01:2577:A:H2'	54:01:2614:A:H62	1.73	0.53
7:10:25:ALA:HB1	7:10:113:PHE:HB2	1.89	0.53
17:20:24:LYS:HD3	17:20:92:TRP:HB3	1.90	0.53
37:G:42:VAL:O	37:G:46:LEU:HD13	2.08	0.53
37:G:74:VAL:HG21	37:G:143:MET:HB3	1.91	0.53
43:M:89:ARG:HB2	43:M:96:VAL:HG22	1.90	0.53
1:04:181:ARG:HG3	1:04:266:ILE:HA	1.89	0.53
2:05:118:PHE:HB2	54:01:2823:A:OP1	2.08	0.53
3:06:149:ILE:CG2	3:06:188:MET:HG2	2.38	0.53
16:19:24:TYR:HE1	54:01:17:G:H4'	1.74	0.53
35:E:133:ILE:O	35:E:136:VAL:HG12	2.09	0.53
38:H:11:THR:HA	38:H:14:ARG:NH1	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:43:LYS:HB3	42:L:44:PRO:HD3	1.90	0.53
54:01:226:A:H2'	54:01:227:A:O4'	2.08	0.53
54:01:1060:U:H5'	54:01:1062:G:H5''	1.89	0.53
4:07:43:ILE:HD12	4:07:44:ALA:N	2.24	0.53
7:10:24:SER:HB2	7:10:116:GLU:HG2	1.91	0.53
7:10:61:ARG:HB3	54:01:1046:A:H4'	1.89	0.53
13:16:45:ARG:HG2	13:16:95:THR:HG21	1.90	0.53
42:L:98:ARG:CB	42:L:116:TYR:HA	2.39	0.53
51:U:13:VAL:HG13	51:U:15:LEU:HG	1.89	0.53
53:A:350:G:H2'	53:A:351:G:C8	2.43	0.53
54:01:171:U:H2'	54:01:172:A:C8	2.44	0.53
54:01:1683:U:H2'	54:01:1684:G:C8	2.44	0.53
54:01:2875:C:H2'	54:01:2876:G:C8	2.43	0.53
55:02:80:U:H2'	55:02:81:G:H8	1.73	0.53
5:08:157:LYS:HD2	54:01:2659:G:P	2.49	0.53
32:B:86:CYS:O	32:B:87:ASP:HB3	2.08	0.53
36:F:69:GLU:O	36:F:73:GLU:HG3	2.08	0.53
45:O:32:THR:HG22	45:O:36:ASN:HD21	1.74	0.53
54:01:1190:G:H2'	54:01:1191:G:C8	2.43	0.53
55:02:28:C:H2'	55:02:29:A:C8	2.44	0.53
56:X:13:C:C2'	56:X:14:A:H5''	2.38	0.53
15:18:25:VAL:HG22	15:18:85:VAL:HG22	1.89	0.53
16:19:10:ARG:NH2	54:01:582:A:H4'	2.24	0.53
21:24:6:ALA:CB	21:24:42:LEU:HB3	2.39	0.53
35:E:56:PRO:O	35:E:59:ILE:HG13	2.08	0.53
37:G:107:ALA:O	37:G:118:ARG:HD2	2.09	0.53
38:H:4:ASP:HB2	38:H:80:PRO:HG3	1.90	0.53
38:H:28:SER:HB3	38:H:56:PRO:HB2	1.89	0.53
38:H:29:SER:O	38:H:33:VAL:HG23	2.09	0.53
39:I:23:GLY:HA3	39:I:61:ASP:OD2	2.09	0.53
52:03:17:ALA:CB	54:01:2105:U:H5''	2.37	0.53
54:01:150:U:H2'	54:01:151:C:C6	2.44	0.53
54:01:760:G:H2'	54:01:761:A:O4'	2.09	0.53
56:X:14:A:H2'	56:X:15:G:O4'	2.09	0.53
59:Z:232:GLU:HG2	59:Z:333:ARG:HH22	1.74	0.53
2:05:121:THR:HB	2:05:127:PHE:CD2	2.43	0.53
7:10:96:PHE:HB3	7:10:129:LEU:HD11	1.91	0.53
9:12:73:VAL:HA	9:12:88:THR:HA	1.91	0.53
13:16:32:GLU:O	13:16:114:GLU:HB2	2.09	0.53
14:17:74:VAL:O	14:17:78:VAL:HG23	2.09	0.53
23:26:55:MET:SD	54:01:2091:C:H4'	2.48	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:94:ARG:HD2	32:B:94:ARG:N	2.24	0.53
33:C:109:GLU:HB3	33:C:140:ALA:HA	1.90	0.53
34:D:172:VAL:HG22	34:D:174:ALA:N	2.23	0.53
39:I:112:ARG:NH2	53:A:1368:A:H5''	2.23	0.53
42:L:5:GLN:HE21	53:A:880:C:H3'	1.74	0.53
42:L:13:ARG:HH11	42:L:14:LYS:H	1.56	0.53
46:P:75:ILE:HA	46:P:78:VAL:HG12	1.90	0.53
53:A:620:C:H2'	53:A:621:A:O4'	2.09	0.53
54:01:2771:C:H2'	54:01:2772:C:C6	2.44	0.53
56:X:70:G:H2'	56:X:71:C:O4'	2.08	0.53
59:Z:95:ALA:HB1	59:Z:125:VAL:HG11	1.90	0.53
8:11:35:MET:O	8:11:39:LYS:HG2	2.09	0.53
13:16:37:THR:HG22	13:16:110:MET:HE1	1.91	0.53
20:23:8:ASP:OD1	20:23:71:ILE:HG22	2.09	0.53
20:23:73:ASN:HD22	20:23:76:THR:H	1.56	0.53
23:26:30:PRO:HG2	23:26:32:LEU:HG	1.89	0.53
41:K:48:GLY:HA2	53:A:688:G:H5'	1.91	0.53
41:K:82:GLU:HB3	41:K:84:MET:HE3	1.91	0.53
42:L:69:GLU:OE2	53:A:537:G:H5'	2.09	0.53
48:R:19:GLU:HG2	48:R:53:GLN:HE22	1.73	0.53
53:A:77:A:H2'	53:A:78:A:C8	2.43	0.53
54:01:1316:U:H2'	54:01:1317:G:C8	2.44	0.53
54:01:1389:G:H5'	54:01:1526:C:H5''	1.91	0.53
54:01:2028:U:H2'	54:01:2029:G:O4'	2.08	0.53
54:01:2163:A:H2'	54:01:2164:C:H5'	1.90	0.53
1:04:200:MET:HE3	53:A:773:G:H4'	1.92	0.52
2:05:13:ARG:NH1	15:18:55:HIS:HA	2.24	0.52
3:06:48:THR:O	3:06:52:VAL:HG23	2.09	0.52
8:11:103:ALA:O	8:11:107:GLU:HG3	2.08	0.52
15:18:27:VAL:HG13	15:18:82:SER:O	2.09	0.52
41:K:124:LYS:NZ	53:A:780:A:H5''	2.24	0.52
48:R:40:PRO:HB2	48:R:42:ARG:HG2	1.91	0.52
54:01:457:A:H61	54:01:470:A:H5''	1.73	0.52
54:01:1662:U:H2'	54:01:1663:G:C8	2.44	0.52
54:01:2233:U:H2'	54:01:2234:G:H8	1.73	0.52
54:01:2469:A:H2'	54:01:2470:G:O4'	2.08	0.52
4:07:24:VAL:HG12	55:02:55:U:H4'	1.91	0.52
30:33:63:TYR:CE2	54:01:242:G:H5''	2.43	0.52
33:C:84:GLU:HG3	33:C:87:ARG:HH12	1.74	0.52
47:Q:61:ARG:NH1	47:Q:63:CYS:HB3	2.23	0.52
53:A:673:A:H2'	53:A:674:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1468:U:H2'	54:01:1522:A:N6	2.24	0.52
10:13:87:LEU:HD23	10:13:94:PRO:HA	1.90	0.52
15:18:99:LEU:O	15:18:99:LEU:HD23	2.08	0.52
32:B:112:ARG:O	32:B:116:LEU:HB2	2.09	0.52
33:C:13:ILE:H	33:C:13:ILE:HD12	1.74	0.52
33:C:19:SER:O	44:N:93:PRO:HG3	2.09	0.52
39:I:55:ASP:HB3	39:I:59:LYS:HG3	1.91	0.52
40:J:68:ARG:HB3	40:J:70:HIS:HE1	1.73	0.52
43:M:12:LYS:HB2	43:M:17:ALA:HB2	1.90	0.52
44:N:42:ASN:O	44:N:45:LEU:HB3	2.09	0.52
49:S:30:LEU:HD13	49:S:48:ILE:HG22	1.92	0.52
53:A:212:G:H2'	53:A:213:G:H8	1.74	0.52
53:A:1277:C:H2'	53:A:1278:G:H5''	1.91	0.52
54:01:2440:C:H5''	54:01:2587:A:H4'	1.91	0.52
59:Z:30:ALA:O	59:Z:34:VAL:HG23	2.08	0.52
4:07:24:VAL:O	4:07:27:VAL:HG12	2.09	0.52
49:S:35:ARG:HB3	49:S:71:GLY:HA2	1.90	0.52
53:A:559:A:H4'	53:A:560:A:H3'	1.92	0.52
53:A:1137:C:H5'	53:A:1138:G:H5'	1.92	0.52
54:01:2842:G:H2'	54:01:2843:G:O4'	2.09	0.52
55:02:77:U:H2'	55:02:78:A:H8	1.74	0.52
6:09:29:PHE:HB2	54:01:2198:A:C2	2.44	0.52
14:17:24:THR:HG23	14:17:41:ALA:HA	1.92	0.52
16:19:39:ILE:O	16:19:43:GLN:HG3	2.10	0.52
38:H:17:GLN:HE21	38:H:71:VAL:HB	1.74	0.52
41:K:116:PRO:HB3	53:A:676:A:H1'	1.91	0.52
53:A:372:C:N4	53:A:387:U:H2'	2.25	0.52
53:A:422:C:H4'	53:A:423:G:N2	2.25	0.52
54:01:275:C:H3'	54:01:276:U:H5''	1.92	0.52
54:01:1665:A:H2'	54:01:1666:G:O4'	2.09	0.52
59:Z:376:ILE:HD12	59:Z:384:GLY:HA3	1.91	0.52
3:06:131:THR:HG23	54:01:321:U:H5''	1.91	0.52
29:32:7:PRO:HB2	54:01:1309:G:H4'	1.92	0.52
32:B:19:THR:H	32:B:38:HIS:CD2	2.27	0.52
33:C:122:GLN:HB3	33:C:127:VAL:HG11	1.91	0.52
36:F:64:VAL:HG22	36:F:65:GLU:N	2.25	0.52
3:06:151:GLY:HA2	3:06:172:ALA:HB2	1.91	0.52
4:07:134:GLN:NE2	4:07:149:ARG:HB2	2.24	0.52
5:08:84:LYS:HD2	5:08:140:ILE:HB	1.92	0.52
43:M:66:GLY:O	43:M:70:ARG:HG2	2.10	0.52
54:01:2391:G:H4'	54:01:2392:A:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:32:THR:HG22	59:Z:69:TYR:HB3	1.92	0.52
59:Z:131:ILE:HD13	59:Z:194:PHE:HB3	1.92	0.52
5:08:27:GLY:HA3	5:08:78:VAL:HB	1.91	0.52
6:09:58:LEU:O	6:09:61:VAL:HG22	2.10	0.52
10:13:54:LYS:NZ	10:13:54:LYS:HB3	2.25	0.52
17:20:7:SER:HB3	17:20:10:LYS:HG3	1.91	0.52
34:D:164:ARG:HG2	34:D:165:GLU:N	2.25	0.52
53:A:162:A:H2'	53:A:163:C:O4'	2.10	0.52
53:A:1319:A:H61	53:A:1361:G:H21	1.58	0.52
54:01:1469:A:H2'	54:01:1470:A:C8	2.44	0.52
54:01:2818:U:H2'	54:01:2819:G:H8	1.75	0.52
59:Z:11:HIS:CE1	59:Z:77:ALA:HB2	2.44	0.52
4:07:65:LEU:HB3	4:07:87:LYS:HG3	1.92	0.52
8:11:109:ALA:HA	8:11:112:LYS:HZ2	1.75	0.52
10:13:13:ASN:ND2	10:13:98:ARG:HB2	2.25	0.52
17:20:81:LYS:HD2	54:01:973:A:H5''	1.92	0.52
41:K:15:VAL:HG12	41:K:76:TYR:HB3	1.91	0.52
45:O:70:LYS:HD3	45:O:77:TYR:CE2	2.45	0.52
46:P:20:VAL:HG23	46:P:35:ARG:HA	1.91	0.52
53:A:216:U:H2'	53:A:217:C:C6	2.44	0.52
53:A:270:A:H2'	53:A:271:C:C6	2.45	0.52
53:A:481:G:H1'	53:A:483:C:N4	2.25	0.52
54:01:704:G:H2'	54:01:726:G:H22	1.75	0.52
54:01:1494:A:H2	54:01:1579:A:H1'	1.75	0.52
54:01:1509:A:H2'	54:01:1510:G:C8	2.45	0.52
54:01:2006:C:H5''	54:01:2048:G:H5''	1.92	0.52
15:18:105:LYS:HE3	15:18:108:ARG:NH2	2.25	0.52
19:22:29:THR:HG23	19:22:85:VAL:C	2.35	0.52
31:34:4:ARG:HH11	31:34:4:ARG:HG3	1.75	0.52
32:B:212:TYR:O	32:B:216:VAL:HG23	2.10	0.52
39:I:109:GLN:O	53:A:1347:G:H5''	2.09	0.52
41:K:91:GLY:C	41:K:93:GLU:H	2.18	0.52
42:L:115:LYS:HE2	53:A:551:U:H5'	1.92	0.52
53:A:736:C:H2'	53:A:737:C:C6	2.45	0.52
53:A:1162:C:H2'	53:A:1163:A:C8	2.45	0.52
54:01:1469:A:H2'	54:01:1470:A:H8	1.75	0.52
54:01:2370:G:H2'	54:01:2371:G:O4'	2.08	0.52
7:10:24:SER:HB2	7:10:116:GLU:CG	2.40	0.51
34:D:98:ASP:OD2	34:D:132:ALA:HB1	2.09	0.51
35:E:153:ALA:O	35:E:158:LYS:HA	2.10	0.51
38:H:45:ILE:HG21	38:H:60:LEU:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:34:C:H2'	53:A:35:G:C8	2.45	0.51
54:01:1394:U:H4'	54:01:1603:A:H4'	1.92	0.51
3:06:63:LYS:HD2	54:01:2444:G:OP2	2.11	0.51
7:10:1:MET:HE3	7:10:2:ALA:H	1.75	0.51
8:11:59:THR:HB	8:11:67:THR:HG22	1.91	0.51
10:13:12:ASP:HB2	10:13:96:GLY:HA3	1.93	0.51
37:G:58:LEU:HD12	37:G:59:GLU:N	2.25	0.51
39:I:10:ARG:HG3	39:I:105:ARG:HH21	1.75	0.51
42:L:109:ARG:HH12	53:A:537:G:H5''	1.75	0.51
44:N:5:MET:HE2	44:N:62:ARG:NH2	2.16	0.51
46:P:26:ASN:HD22	46:P:31:ARG:HB3	1.74	0.51
48:R:33:THR:HG22	48:R:37:LYS:HB2	1.91	0.51
54:01:49:A:H5'	54:01:51:G:O4'	2.10	0.51
59:Z:303:LYS:O	59:Z:391:VAL:HG13	2.10	0.51
2:05:157:LYS:HA	54:01:2619:C:H4'	1.90	0.51
4:07:141:ASP:C	4:07:143:ASP:H	2.18	0.51
5:08:51:PHE:CE2	5:08:68:ARG:HA	2.45	0.51
6:09:1:MET:HB3	6:09:3:VAL:HG23	1.92	0.51
10:13:63:VAL:HG23	10:13:64:ARG:N	2.25	0.51
18:21:6:LYS:HE2	18:21:104:THR:HG23	1.92	0.51
19:22:62:VAL:HG22	19:22:81:LYS:HE2	1.91	0.51
33:C:109:GLU:HB2	33:C:143:LEU:CD2	2.40	0.51
46:P:71:VAL:HA	46:P:74:LEU:HB2	1.92	0.51
47:Q:44:HIS:O	47:Q:70:LYS:HA	2.10	0.51
59:Z:124:GLN:HG2	59:Z:385:ALA:HB1	1.92	0.51
17:20:60:LYS:HB2	17:20:60:LYS:NZ	2.26	0.51
35:E:155:LYS:HB3	38:H:70:VAL:HG13	1.93	0.51
52:03:181:ASP:OD2	52:03:183:ASP:HB2	2.11	0.51
53:A:1228:C:H2'	53:A:1229:A:C8	2.46	0.51
54:01:633:A:H1'	54:01:2403:C:H4'	1.92	0.51
56:X:5:G:H2'	56:X:6:G:O4'	2.10	0.51
59:Z:236:ILE:HD12	59:Z:236:ILE:O	2.10	0.51
3:06:94:GLN:HB2	54:01:660:C:H5''	1.91	0.51
5:08:157:LYS:HD3	54:01:2658:C:H5''	1.91	0.51
13:16:72:ASP:OD2	13:16:75:ILE:HG12	2.10	0.51
13:16:118:ARG:NH1	27:30:55:ALA:HB3	2.25	0.51
19:22:3:ARG:O	19:22:7:LEU:HG	2.11	0.51
20:23:93:ARG:HB2	20:23:102:ILE:HB	1.91	0.51
23:26:10:ARG:NH2	54:01:187:G:H4'	2.25	0.51
35:E:9:GLU:HG2	35:E:10:LEU:HG	1.92	0.51
38:H:105:THR:HA	38:H:122:GLY:HA3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:52:LEU:HD23	40:J:62:ARG:HG2	1.91	0.51
45:O:2:LEU:HG	45:O:7:THR:HG22	1.93	0.51
53:A:202:G:H21	53:A:466:A:H61	1.59	0.51
53:A:225:C:C2'	53:A:226:G:H5''	2.41	0.51
53:A:477:C:H2'	53:A:478:A:C8	2.45	0.51
53:A:1200:C:H5''	53:A:1201:A:H3'	1.93	0.51
54:01:1758:U:H5	54:01:2696:U:H5'	1.75	0.51
54:01:2800:A:H3'	54:01:2801:G:H5'	1.91	0.51
1:04:204:LEU:HD22	1:04:209:ALA:HB1	1.93	0.51
3:06:19:PHE:HE1	3:06:109:LEU:HD23	1.75	0.51
7:10:56:ARG:CD	7:10:81:LEU:HG	2.41	0.51
8:11:21:PRO:HB2	8:11:22:PRO:HD3	1.92	0.51
34:D:131:ILE:H	34:D:131:ILE:HD12	1.76	0.51
34:D:164:ARG:HG2	34:D:165:GLU:H	1.75	0.51
42:L:35:ARG:NH1	42:L:37:TYR:HB3	2.25	0.51
45:O:23:SER:HB3	45:O:26:VAL:CG2	2.41	0.51
53:A:823:C:H2'	53:A:824:G:C8	2.45	0.51
54:01:2372:U:H2'	54:01:2373:G:C8	2.45	0.51
54:01:2808:G:H5'	54:01:2809:A:OP1	2.09	0.51
58:Y:63:U:H2'	58:Y:64:G:C8	2.45	0.51
39:I:20:ILE:HD11	39:I:60:LEU:HD22	1.93	0.51
39:I:70:GLY:HA3	53:A:1371:G:O3'	2.11	0.51
47:Q:59:GLU:HB2	47:Q:75:VAL:HB	1.93	0.51
48:R:12:PHE:O	48:R:14:ALA:N	2.44	0.51
53:A:1094:G:H2'	53:A:1094:G:N3	2.24	0.51
54:01:217:A:H2'	54:01:218:A:O4'	2.10	0.51
54:01:662:G:H2'	54:01:663:G:H8	1.75	0.51
54:01:1474:U:H2'	54:01:1475:G:H5'	1.91	0.51
54:01:1906:G:C3'	54:01:1907:G:H5''	2.40	0.51
6:09:1:MET:C	6:09:3:VAL:H	2.18	0.51
36:F:1:MET:HB2	36:F:65:GLU:HG2	1.93	0.51
48:R:47:ARG:HD2	48:R:47:ARG:N	2.25	0.51
53:A:171:A:H2'	53:A:172:A:C8	2.45	0.51
53:A:1052:U:H2'	53:A:1200:C:H41	1.74	0.51
53:A:1176:A:H2'	53:A:1177:G:O4'	2.10	0.51
54:01:311:A:H2	54:01:331:C:H3'	1.76	0.51
54:01:621:A:H2'	54:01:622:G:H5'	1.92	0.51
54:01:1704:C:H2'	54:01:1705:A:C8	2.46	0.51
54:01:1736:U:H2'	54:01:1737:G:O4'	2.11	0.51
54:01:1802:A:H2'	54:01:1803:A:C8	2.45	0.51
11:14:17:LYS:HD3	54:01:663:G:H5''	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:26:6:VAL:HG23	23:26:50:VAL:HG11	1.93	0.51
40:J:59:LYS:HE2	40:J:62:ARG:HH21	1.75	0.51
54:01:873:C:H2'	54:01:874:G:C8	2.45	0.51
56:W:69:C:H2'	56:W:70:G:C8	2.46	0.51
59:Z:16:THR:HG23	59:Z:78:HIS:CE1	2.46	0.51
1:04:119:VAL:HG12	1:04:130:PRO:HG2	1.93	0.51
35:E:35:LEU:HD11	35:E:136:VAL:HG11	1.93	0.51
51:U:65:ARG:HG3	51:U:67:THR:CG2	2.41	0.51
54:01:138:U:H3'	54:01:139:U:C5'	2.41	0.51
54:01:669:G:H2'	54:01:669:G:N3	2.26	0.51
58:Y:27:G:H2'	58:Y:28:U:O4'	2.11	0.51
2:05:14:ILE:HG23	15:18:11:GLN:HE22	1.76	0.50
8:11:80:LYS:HB3	8:11:86:LYS:HG3	1.91	0.50
11:14:101:ILE:HG13	11:14:102:GLY:N	2.25	0.50
24:27:9:LYS:HB3	24:27:12:GLU:HB2	1.93	0.50
28:31:7:LYS:HD3	54:01:2420:C:H5''	1.93	0.50
33:C:71:ARG:O	33:C:75:VAL:HG23	2.10	0.50
33:C:170:GLY:O	53:A:1106:G:H4'	2.11	0.50
34:D:18:LEU:HD22	34:D:63:ILE:HG12	1.93	0.50
35:E:22:LYS:O	53:A:921:U:H1'	2.10	0.50
47:Q:12:VAL:HG23	47:Q:23:ALA:N	2.26	0.50
47:Q:47:ASP:HB2	47:Q:51:GLU:OE2	2.11	0.50
49:S:39:ILE:HA	49:S:43:MET:SD	2.51	0.50
53:A:219:U:H2'	53:A:220:G:C8	2.47	0.50
53:A:219:U:H2'	53:A:220:G:H8	1.76	0.50
53:A:1256:A:H1'	53:A:1258:G:N9	2.26	0.50
54:01:65:U:H2'	54:01:66:C:C6	2.47	0.50
54:01:1092:C:H2'	54:01:1093:G:O4'	2.11	0.50
54:01:1906:G:H3'	54:01:1907:G:H5''	1.92	0.50
9:12:34:ARG:CG	9:12:39:LYS:HB2	2.40	0.50
21:24:75:GLN:HB2	21:24:92:VAL:HG23	1.93	0.50
31:34:38:GLY:OXT	54:01:1124:G:H1'	2.11	0.50
40:J:89:ARG:HG3	40:J:90:LEU:HG	1.92	0.50
44:N:47:LEU:HD21	53:A:1317:C:H4'	1.93	0.50
46:P:31:ARG:HH21	53:A:230:G:H5''	1.75	0.50
53:A:112:G:N2	53:A:354:G:H5'	2.26	0.50
53:A:701:U:H4'	53:A:703:G:H1'	1.93	0.50
53:A:868:C:H2'	53:A:869:G:O4'	2.11	0.50
53:A:1354:U:H2'	53:A:1355:G:H8	1.75	0.50
54:01:3:U:H2'	54:01:4:U:C6	2.46	0.50
54:01:996:A:H2'	54:01:997:G:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1026:G:H2'	54:01:1027:A:H8	1.75	0.50
54:01:1149:G:H2'	54:01:1150:C:C6	2.45	0.50
54:01:2039:U:H2'	54:01:2040:G:C8	2.47	0.50
54:01:2192:U:H2'	54:01:2193:G:H8	1.76	0.50
54:01:2270:A:H2'	54:01:2271:G:O4'	2.11	0.50
54:01:2277:G:C2'	54:01:2278:A:H5''	2.38	0.50
3:06:79:ARG:NH2	54:01:471:A:H5''	2.25	0.50
5:08:153:PRO:HB2	5:08:168:VAL:HG11	1.93	0.50
12:15:5:LYS:O	54:01:870:U:H5''	2.11	0.50
12:15:57:VAL:O	12:15:59:ARG:N	2.44	0.50
27:30:49:ARG:HG2	54:01:2884:U:C6	2.47	0.50
32:B:159:ALA:HA	32:B:181:PRO:HG2	1.92	0.50
40:J:44:THR:OG1	53:A:1151:A:H5''	2.11	0.50
47:Q:13:SER:H	47:Q:21:VAL:HG13	1.76	0.50
48:R:11:ARG:HB2	48:R:47:ARG:NH1	2.22	0.50
49:S:18:VAL:O	49:S:22:VAL:HG23	2.12	0.50
51:U:32:ARG:HG3	51:U:33:ARG:HG2	1.92	0.50
53:A:10:A:O2'	53:A:507:C:H4'	2.10	0.50
54:01:645:C:N4	54:01:2350:C:H1'	2.26	0.50
54:01:1856:U:H2'	54:01:1857:G:O4'	2.11	0.50
3:06:102:ARG:HH11	3:06:201:ALA:HB3	1.76	0.50
3:06:108:ILE:O	3:06:112:LEU:HG	2.11	0.50
4:07:46:LYS:HE3	4:07:83:PRO:HG2	1.94	0.50
26:29:14:ALA:HB2	26:29:32:LEU:HD23	1.93	0.50
41:K:112:VAL:HA	48:R:72:ARG:NH2	2.26	0.50
53:A:837:U:H2'	53:A:838:G:H8	1.76	0.50
54:01:1869:G:H3'	54:01:1870:C:H5''	1.94	0.50
59:Z:189:LEU:O	59:Z:189:LEU:HD23	2.11	0.50
4:07:23:SER:HB2	55:02:56:G:H5'	1.92	0.50
4:07:64:PRO:HB2	4:07:86:CYS:HB2	1.93	0.50
6:09:66:ASN:HB3	6:09:135:HIS:HB2	1.93	0.50
10:13:8:LEU:HB2	10:13:19:VAL:HG23	1.92	0.50
20:23:48:VAL:HG22	20:23:50:ALA:H	1.76	0.50
21:24:6:ALA:HB2	21:24:42:LEU:HB3	1.94	0.50
26:29:20:ASN:ND2	26:29:39:LYS:HD3	2.21	0.50
33:C:76:ILE:HG22	33:C:83:VAL:HG21	1.94	0.50
34:D:29:THR:C	34:D:30:LYS:HD2	2.36	0.50
39:I:16:ALA:HB2	39:I:66:VAL:HG23	1.93	0.50
39:I:57:VAL:HG12	39:I:58:GLU:HG2	1.94	0.50
53:A:1258:G:H2'	53:A:1259:C:C6	2.46	0.50
54:01:548:G:H2'	54:01:549:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2314:A:H2'	54:01:2315:G:C8	2.46	0.50
54:01:2637:U:H2'	54:01:2638:G:O4'	2.12	0.50
58:Y:39:U:H2'	58:Y:40:C:C6	2.46	0.50
59:Z:204:ARG:HB3	59:Z:270:ALA:HB1	1.93	0.50
8:11:14:ALA:HB3	8:11:50:LYS:HA	1.94	0.50
13:16:72:ASP:HB3	13:16:75:ILE:HB	1.94	0.50
23:26:67:LEU:O	23:26:71:ARG:HG2	2.12	0.50
31:34:24:ARG:NH2	31:34:36:ARG:HG3	2.26	0.50
34:D:124:VAL:HG23	34:D:141:VAL:O	2.12	0.50
44:N:20:PHE:O	44:N:21:ALA:CB	2.60	0.50
45:O:60:SER:O	45:O:63:ARG:HB3	2.12	0.50
46:P:44:SER:O	46:P:46:LYS:HG2	2.10	0.50
54:01:1869:G:H2'	54:01:1871:A:OP1	2.11	0.50
54:01:2345:G:N3	54:01:2381:A:H2'	2.26	0.50
54:01:2443:C:H2'	54:01:2444:G:C8	2.46	0.50
59:Z:153:VAL:O	59:Z:157:LEU:HG	2.12	0.50
1:04:204:LEU:HB3	1:04:209:ALA:HB3	1.93	0.50
3:06:14:VAL:HB	3:06:19:PHE:HD2	1.75	0.50
15:18:105:LYS:HD3	53:A:1433:A:OP1	2.12	0.50
16:19:56:PHE:HZ	54:01:536:G:H4'	1.76	0.50
24:27:23:ARG:O	24:27:25:GLN:N	2.45	0.50
27:30:4:GLN:O	54:01:2017:U:H4'	2.12	0.50
35:E:92:ARG:HB2	35:E:127:TYR:HB2	1.94	0.50
42:L:79:ILE:HG22	42:L:103:CYS:H	1.77	0.50
43:M:7:ASN:ND2	43:M:9:PRO:HD3	2.25	0.50
53:A:123:U:H5''	53:A:311:C:O2'	2.12	0.50
53:A:553:A:H2'	53:A:554:A:C8	2.47	0.50
54:01:716:A:H3'	54:01:717:C:H5''	1.92	0.50
54:01:1328:A:H2'	54:01:1330:C:C5	2.47	0.50
54:01:1345:C:H5'	54:01:1345:C:H6	1.77	0.50
54:01:1877:A:H2'	54:01:1878:G:O4'	2.12	0.50
59:Z:326:TYR:OH	59:Z:383:VAL:HG21	2.12	0.50
2:05:129:THR:HG23	2:05:140:HIS:O	2.12	0.50
21:24:9:ARG:HG2	21:24:41:GLU:HB2	1.94	0.50
23:26:7:THR:HG21	23:26:9:LYS:HZ1	1.76	0.50
32:B:71:THR:O	32:B:75:ALA:HB3	2.11	0.50
36:F:18:VAL:HB	36:F:19:PRO:HD3	1.92	0.50
42:L:106:VAL:HB	42:L:109:ARG:HG3	1.94	0.50
45:O:1:SER:C	45:O:34:GLN:HE22	2.20	0.50
46:P:23:ASP:HB3	46:P:26:ASN:OD1	2.11	0.50
50:T:23:ARG:NH2	50:T:60:GLN:HE22	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:239:C:H2'	54:01:240:C:O4'	2.12	0.50
54:01:1186:G:H2'	54:01:1187:G:O4'	2.12	0.50
54:01:1485:U:H2'	54:01:1486:U:C6	2.47	0.50
54:01:2629:U:O2'	54:01:2630:G:H5''	2.12	0.50
1:04:132:ARG:HB2	6:09:123:ARG:NH1	2.27	0.50
4:07:37:MET:HB3	4:07:56:LEU:HD11	1.93	0.50
20:23:17:ASP:HA	20:23:20:LYS:HE2	1.93	0.50
24:27:21:LEU:HD23	24:27:25:GLN:HG2	1.93	0.50
38:H:103:VAL:HG13	38:H:105:THR:HG23	1.92	0.50
39:I:10:ARG:HG3	39:I:105:ARG:CZ	2.42	0.50
40:J:57:VAL:O	40:J:58:ASN:CB	2.59	0.50
46:P:2:VAL:HG23	46:P:65:ALA:HA	1.93	0.50
51:U:20:ARG:H	51:U:20:ARG:HD2	1.76	0.50
53:A:243:A:H4'	53:A:244:U:H3'	1.93	0.50
54:01:1177:G:C2'	54:01:1178:C:H4'	2.36	0.50
54:01:1424:G:H2'	54:01:1425:G:O4'	2.12	0.50
54:01:1744:A:H3'	54:01:1745:A:H8	1.77	0.50
54:01:1775:U:H2'	54:01:1776:G:O4'	2.12	0.50
54:01:2427:C:C5'	54:01:2429:G:H5'	2.38	0.50
9:12:25:LEU:HB3	54:01:1140:C:OP1	2.12	0.49
10:13:99:ILE:HD13	10:13:115:ILE:HG23	1.95	0.49
11:14:78:ARG:CZ	11:14:113:ALA:HB1	2.42	0.49
19:22:15:HIS:H	19:22:32:LEU:HA	1.76	0.49
33:C:9:ILE:HG23	33:C:10:ARG:HG3	1.93	0.49
36:F:73:GLU:O	36:F:77:THR:HG23	2.12	0.49
36:F:81:ASN:ND2	36:F:83:ALA:H	2.10	0.49
39:I:10:ARG:HA	39:I:14:SER:O	2.12	0.49
42:L:98:ARG:HD2	42:L:103:CYS:SG	2.52	0.49
54:01:1563:U:H2'	54:01:1564:C:C6	2.46	0.49
54:01:1869:G:H3'	54:01:1870:C:C5'	2.41	0.49
54:01:2537:U:H2'	54:01:2538:C:C6	2.46	0.49
54:01:2682:A:H61	54:01:2728:U:H1'	1.76	0.49
55:02:51:G:H2'	55:02:52:A:O4'	2.12	0.49
59:Z:4:LYS:HG2	59:Z:264:LEU:HB2	1.94	0.49
3:06:1:MET:HB3	3:06:14:VAL:HG23	1.95	0.49
13:16:48:VAL:O	13:16:52:ILE:HG13	2.11	0.49
14:17:98:GLN:HE22	54:01:2293:G:H4'	1.76	0.49
18:21:89:ALA:HB3	54:01:747:C:H4'	1.93	0.49
24:27:42:LEU:O	24:27:46:VAL:HG23	2.11	0.49
38:H:100:ILE:HG13	38:H:128:VAL:HB	1.93	0.49
44:N:30:ILE:HG22	44:N:40:ARG:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:543:U:H2'	53:A:544:G:C8	2.46	0.49
53:A:662:U:H2'	53:A:663:A:C8	2.46	0.49
54:01:639:U:H2'	54:01:640:C:C6	2.47	0.49
54:01:862:G:H2'	54:01:863:A:O4'	2.11	0.49
54:01:1539:U:H2'	54:01:1540:G:H8	1.77	0.49
54:01:1611:C:H5'	54:01:1611:C:H6	1.77	0.49
54:01:1971:U:H5'	54:01:1972:G:H5''	1.93	0.49
54:01:2180:U:H2'	54:01:2181:U:O4'	2.12	0.49
2:05:34:VAL:HG22	2:05:50:VAL:HG12	1.93	0.49
10:13:68:GLY:HA3	10:13:78:ARG:HG2	1.94	0.49
18:21:29:VAL:HG11	18:21:55:ILE:HG12	1.94	0.49
22:25:22:PHE:HD2	54:01:922:C:H1'	1.77	0.49
30:33:37:THR:HA	30:33:40:LYS:HE3	1.93	0.49
34:D:105:GLY:O	34:D:158:LEU:HG	2.12	0.49
37:G:145:GLU:C	37:G:147:ASN:H	2.20	0.49
49:S:4:LEU:HD22	53:A:1318:A:H5''	1.94	0.49
49:S:36:ARG:NH2	53:A:1318:A:H1'	2.27	0.49
54:01:45:G:H5''	54:01:46:G:C5'	2.27	0.49
54:01:414:C:H5''	54:01:1879:C:O2'	2.13	0.49
54:01:838:C:H2'	54:01:839:U:C6	2.47	0.49
54:01:995:C:H6	54:01:995:C:H5'	1.77	0.49
54:01:2233:U:H2'	54:01:2234:G:C8	2.46	0.49
56:W:6:G:O2'	56:W:7:G:H5'	2.13	0.49
30:33:14:LYS:HD3	30:33:22:LYS:HE2	1.94	0.49
34:D:195:ASN:ND2	34:D:198:LEU:HG	2.16	0.49
34:D:195:ASN:HD21	34:D:197:HIS:HB3	1.78	0.49
34:D:196:GLU:HA	34:D:199:ILE:HD12	1.94	0.49
48:R:72:ARG:HA	48:R:72:ARG:HH11	1.78	0.49
51:U:8:ASN:HB3	51:U:9:GLU:OE2	2.11	0.49
53:A:1096:C:H2'	53:A:1097:C:C6	2.48	0.49
54:01:20:C:H2'	54:01:21:A:C8	2.48	0.49
54:01:752:A:H2'	54:01:1781:U:H5'	1.95	0.49
54:01:948:C:H2'	54:01:949:G:C8	2.47	0.49
54:01:1038:G:H2'	54:01:1039:A:C8	2.48	0.49
54:01:1318:U:H2'	54:01:1319:C:C6	2.48	0.49
54:01:1641:A:H2'	54:01:1642:G:O4'	2.12	0.49
59:Z:13:ASN:ND2	59:Z:204:ARG:HH12	2.10	0.49
6:09:23:ALA:HB1	6:09:27:ARG:HH22	1.76	0.49
7:10:56:ARG:HG3	7:10:82:ILE:O	2.12	0.49
34:D:96:ARG:O	34:D:100:VAL:HG23	2.12	0.49
45:O:31:LEU:O	45:O:35:ILE:HG13	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:R:59:LYS:HD3	53:A:734:G:O2'	2.13	0.49
54:01:171:U:H2'	54:01:172:A:H8	1.76	0.49
54:01:189:G:H2'	54:01:205:G:H22	1.77	0.49
54:01:1758:U:C5	54:01:2696:U:H5'	2.48	0.49
55:02:13:G:N7	55:02:70:C:H4'	2.28	0.49
16:19:93:ILE:O	16:19:97:ILE:HG13	2.13	0.49
23:26:25:LYS:HE2	23:26:25:LYS:HA	1.94	0.49
50:T:70:LYS:HG3	50:T:73:ARG:NH2	2.27	0.49
53:A:1524:C:H2'	53:A:1525:G:H8	1.77	0.49
54:01:1015:U:H2'	54:01:1016:G:C8	2.48	0.49
54:01:1438:U:H2'	54:01:1439:A:H8	1.78	0.49
55:02:3:C:C3'	55:02:4:C:H5''	2.43	0.49
55:02:48:U:H2'	55:02:49:C:C6	2.47	0.49
5:08:173:ALA:O	5:08:174:LYS:C	2.55	0.49
19:22:39:THR:O	19:22:43:ILE:HG13	2.13	0.49
20:23:73:ASN:O	20:23:74:ALA:HB3	2.11	0.49
25:28:19:HIS:NE2	55:02:82:U:H4'	2.28	0.49
31:34:4:ARG:O	31:34:37:GLN:HB3	2.13	0.49
34:D:53:GLN:HE22	53:A:8:A:H61	1.60	0.49
39:I:30:ASN:O	39:I:31:GLN:HB2	2.13	0.49
46:P:12:LYS:O	46:P:13:LYS:HB2	2.13	0.49
52:03:38:PHE:HB2	54:01:2126:A:H5'	1.95	0.49
53:A:770:C:H2'	53:A:771:G:H8	1.77	0.49
54:01:537:G:H22	54:01:555:G:H2'	1.77	0.49
54:01:581:C:H2'	54:01:582:A:H8	1.77	0.49
54:01:1468:U:H2'	54:01:1522:A:H61	1.78	0.49
58:Y:65:C:H2'	58:Y:66:A:C8	2.48	0.49
58:Y:74:C:H41	59:Z:283:ARG:NE	2.10	0.49
1:04:132:ARG:HD2	6:09:123:ARG:CZ	2.43	0.49
3:06:44:ARG:HD2	54:01:444:C:OP2	2.12	0.49
5:08:132:LEU:HD12	5:08:132:LEU:O	2.13	0.49
13:16:37:THR:HB	13:16:39:PRO:HD2	1.94	0.49
15:18:105:LYS:HB3	15:18:108:ARG:NH2	2.27	0.49
16:19:27:ARG:NH1	16:19:27:ARG:HB3	2.28	0.49
24:27:46:VAL:O	24:27:50:VAL:HG23	2.13	0.49
32:B:183:PHE:H	32:B:183:PHE:HD1	1.60	0.49
33:C:35:ASP:OD1	33:C:56:ILE:HG13	2.13	0.49
35:E:155:LYS:HD2	38:H:70:VAL:HA	1.95	0.49
51:U:13:VAL:HG22	51:U:14:ALA:N	2.28	0.49
52:03:6:LYS:HA	52:03:9:ARG:NH1	2.25	0.49
53:A:86:G:H4'	53:A:87:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1409:C:H2'	53:A:1410:A:C8	2.48	0.49
54:01:138:U:H3'	54:01:139:U:H5''	1.95	0.49
1:04:7:PRO:HG3	1:04:13:ARG:NH1	2.26	0.49
5:08:15:ASP:HB2	5:08:26:LYS:HE3	1.94	0.49
5:08:21:GLN:HE21	5:08:38:ASP:HA	1.78	0.49
8:11:30:GLN:HB3	8:11:60:VAL:HG11	1.95	0.49
13:16:24:MET:HE3	13:16:44:LEU:HD13	1.94	0.49
13:16:118:ARG:HH21	13:16:118:ARG:HG3	1.78	0.49
21:24:29:ILE:HG22	21:24:88:HIS:CE1	2.47	0.49
33:C:76:ILE:HA	33:C:83:VAL:HG23	1.94	0.49
35:E:93:VAL:HG13	35:E:110:MET:SD	2.53	0.49
42:L:28:GLN:HG3	42:L:80:LEU:HG	1.95	0.49
42:L:42:LYS:HG2	42:L:88:ASP:O	2.12	0.49
46:P:53:ASP:O	46:P:57:ILE:HG13	2.13	0.49
53:A:945:G:H2'	53:A:945:G:N3	2.28	0.49
54:01:213:A:H2'	54:01:214:G:C8	2.47	0.49
54:01:859:G:H1'	54:01:860:U:H5	1.77	0.49
54:01:1388:G:H2'	54:01:1389:G:C8	2.48	0.49
54:01:2146:C:H4'	54:01:2147:A:C5	2.48	0.49
54:01:2210:U:H4'	54:01:2211:A:C2	2.47	0.49
54:01:2244:U:H2'	54:01:2245:U:O4'	2.12	0.49
54:01:2298:A:H2'	54:01:2299:U:O4'	2.13	0.49
54:01:2519:U:H5'	54:01:2567:G:H21	1.78	0.49
59:Z:248:LYS:H	59:Z:290:GLN:NE2	2.11	0.49
8:11:10:LEU:HD21	8:11:26:ALA:HB1	1.94	0.49
11:14:141:LYS:HE2	11:14:143:GLU:HB3	1.94	0.49
15:18:38:ARG:HH21	15:18:38:ARG:HG3	1.77	0.49
24:27:9:LYS:O	24:27:13:GLU:HG2	2.13	0.49
35:E:133:ILE:HD12	35:E:133:ILE:N	2.27	0.49
39:I:125:GLN:HE22	53:A:1342:C:H1'	1.77	0.49
46:P:76:LYS:NZ	53:A:473:U:H5''	2.28	0.49
53:A:106:C:H2'	53:A:107:G:C8	2.47	0.49
53:A:505:G:H5'	53:A:534:U:H2'	1.95	0.49
54:01:1177:G:C5	54:01:1178:C:H1'	2.48	0.49
54:01:2774:C:H2'	54:01:2775:G:O4'	2.13	0.49
59:Z:112:MET:HB3	59:Z:113:PRO:HD2	1.95	0.49
4:07:101:ARG:HH21	26:29:26:SER:HA	1.78	0.48
6:09:46:PHE:HD1	6:09:50:ARG:HD2	1.78	0.48
9:12:37:ARG:HG3	9:12:118:MET:HE1	1.95	0.48
15:18:8:GLU:HA	15:18:54:LEU:HD22	1.94	0.48
21:24:9:ARG:HH12	55:02:76:G:C5'	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:33:3:ILE:HD11	54:01:592:A:C2	2.47	0.48
32:B:153:MET:HE1	32:B:157:PRO:HG3	1.94	0.48
32:B:162:VAL:HB	32:B:184:ALA:CB	2.42	0.48
35:E:106:ALA:HB1	35:E:110:MET:HE3	1.95	0.48
38:H:49:LYS:HD2	38:H:59:GLU:OE2	2.13	0.48
39:I:118:ARG:HH11	39:I:122:ARG:HG2	1.78	0.48
50:T:17:ARG:HB3	53:A:323:U:H5'	1.94	0.48
53:A:337:G:H2'	53:A:338:A:C8	2.48	0.48
53:A:1475:G:H4'	54:01:1689:A:H4'	1.95	0.48
54:01:1138:G:H2'	54:01:1139:G:O4'	2.13	0.48
54:01:1716:U:H2'	54:01:1717:A:H8	1.78	0.48
54:01:1837:C:H2'	54:01:1899:A:H61	1.78	0.48
54:01:2818:U:H2'	54:01:2819:G:C8	2.48	0.48
56:X:69:C:H2'	56:X:70:G:H5'	1.95	0.48
59:Z:247:ILE:HB	59:Z:290:GLN:HE21	1.78	0.48
1:04:51:ARG:HH22	54:01:1825:U:P	2.35	0.48
4:07:35:LEU:HD11	4:07:151:LEU:HD13	1.95	0.48
6:09:40:THR:HB	6:09:43:ASN:ND2	2.27	0.48
7:10:73:LYS:HD2	7:10:76:PHE:HD2	1.77	0.48
8:11:48:ILE:HG13	8:11:49:GLU:N	2.26	0.48
12:15:76:LYS:HD3	54:01:956:G:H5''	1.95	0.48
21:24:8:VAL:HG23	21:24:65:VAL:CG2	2.43	0.48
39:I:42:THR:HA	39:I:44:ARG:NH2	2.28	0.48
52:03:59:VAL:HG22	52:03:201:PRO:HD3	1.94	0.48
53:A:314:C:H2'	53:A:315:A:C8	2.48	0.48
53:A:603:U:H2'	53:A:604:G:H8	1.78	0.48
54:01:1957:C:H2'	54:01:1958:C:C6	2.48	0.48
54:01:2038:G:H2'	54:01:2039:U:O4'	2.13	0.48
54:01:2121:G:H2'	54:01:2122:U:O4'	2.13	0.48
54:01:2245:U:H5''	54:01:2246:G:H5'	1.95	0.48
54:01:2834:G:H2'	54:01:2879:A:N6	2.27	0.48
55:02:10:G:H2'	55:02:11:C:O4'	2.14	0.48
55:02:95:U:H2'	55:02:96:G:H8	1.79	0.48
59:Z:46:PHE:HA	59:Z:49:ILE:HD12	1.95	0.48
59:Z:339:GLY:HA2	59:Z:362:LEU:HA	1.94	0.48
1:04:75:ALA:HB2	1:04:95:TYR:CE1	2.48	0.48
14:17:33:ARG:HB2	55:02:52:A:H61	1.79	0.48
19:22:61:LEU:HD13	54:01:1340:U:H2'	1.94	0.48
35:E:14:LEU:HA	35:E:36:THR:HG22	1.95	0.48
36:F:3:HIS:N	36:F:92:THR:HG22	2.29	0.48
45:O:26:VAL:O	45:O:30:LEU:HD13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:R:52:ARG:NE	53:A:664:G:H5'	2.27	0.48
50:T:60:GLN:HB3	50:T:65:LEU:HD23	1.96	0.48
53:A:1028:C:H1'	53:A:1034:G:H1	1.78	0.48
53:A:1354:U:H2'	53:A:1355:G:C8	2.48	0.48
54:01:174:U:H2'	54:01:175:G:C8	2.48	0.48
54:01:992:C:H2'	54:01:993:G:H8	1.78	0.48
54:01:1152:C:H2'	54:01:1153:C:C6	2.48	0.48
54:01:1842:G:H1	54:01:1898:U:H3	1.61	0.48
58:Y:8:U:H5'	58:Y:49:G:H5'	1.94	0.48
2:05:114:LYS:NZ	2:05:196:ALA:HB2	2.29	0.48
7:10:119:PRO:O	7:10:120:ALA:HB3	2.13	0.48
13:16:13:ASN:HA	54:01:2002:G:O5'	2.14	0.48
18:21:73:LYS:HB2	18:21:106:VAL:HB	1.94	0.48
18:21:88:ARG:HG3	18:21:94:ASP:OD2	2.14	0.48
30:33:39:ARG:O	30:33:43:LEU:HG	2.13	0.48
32:B:96:LEU:H	32:B:99:MET:CE	2.26	0.48
43:M:94:LEU:HB3	43:M:95:PRO:HD2	1.94	0.48
47:Q:60:ILE:CG2	47:Q:72:TRP:HB3	2.44	0.48
48:R:11:ARG:NH2	48:R:15:GLU:HB2	2.28	0.48
52:03:10:VAL:HA	52:03:13:GLU:OE1	2.13	0.48
53:A:416:G:H2'	53:A:417:G:C8	2.48	0.48
53:A:1342:C:H2'	53:A:1343:G:C8	2.47	0.48
54:01:554:U:H2'	54:01:555:G:O4'	2.13	0.48
54:01:1298:C:H2'	54:01:1299:G:O4'	2.13	0.48
54:01:2432:A:H5'	56:X:76:A:O3'	2.13	0.48
5:08:140:ILE:HD12	5:08:141:GLY:N	2.28	0.48
7:10:81:LEU:HB2	54:01:1107:G:O2'	2.14	0.48
14:17:7:ARG:HA	14:17:10:ARG:NH2	2.28	0.48
17:20:43:ASN:CG	17:20:44:GLY:H	2.21	0.48
29:32:7:PRO:HG3	54:01:1612:C:H5'	1.94	0.48
32:B:18:GLN:HB2	32:B:38:HIS:HD2	1.77	0.48
35:E:155:LYS:HD2	38:H:70:VAL:HG13	1.96	0.48
36:F:91:ARG:HD2	36:F:93:LYS:HE3	1.95	0.48
42:L:48:LEU:HB2	53:A:520:A:OP1	2.13	0.48
46:P:6:LEU:HD12	53:A:375:U:H4'	1.95	0.48
53:A:1071:C:H2'	53:A:1072:G:C8	2.45	0.48
54:01:662:G:H2'	54:01:663:G:C8	2.49	0.48
54:01:1326:U:H2'	54:01:1327:A:H8	1.77	0.48
54:01:1744:A:H3'	54:01:1745:A:C8	2.49	0.48
54:01:1765:U:H2'	54:01:1766:G:C8	2.47	0.48
56:X:41:C:H2'	56:X:42:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:35:LEU:HD23	59:Z:38:THR:OG1	2.13	0.48
9:12:65:THR:H	9:12:68:LYS:CE	2.26	0.48
16:19:30:VAL:HG11	16:19:33:VAL:HG23	1.96	0.48
21:24:9:ARG:HD3	21:24:39:ALA:HB1	1.94	0.48
21:24:21:ARG:HA	21:24:25:LYS:O	2.13	0.48
24:27:26:PHE:HD1	24:27:29:ARG:HH11	1.60	0.48
33:C:161:ILE:HA	53:A:1056:U:OP1	2.14	0.48
35:E:149:PRO:HG2	35:E:150:GLU:OE2	2.14	0.48
42:L:80:LEU:HB3	42:L:97:VAL:HB	1.96	0.48
44:N:92:ILE:N	44:N:92:ILE:HD12	2.28	0.48
47:Q:35:LYS:O	47:Q:37:ILE:HG13	2.13	0.48
52:03:50:ILE:HG21	52:03:201:PRO:HG3	1.94	0.48
53:A:1052:U:H2'	53:A:1200:C:N4	2.29	0.48
53:A:1236:A:H4'	53:A:1304:G:H4'	1.95	0.48
54:01:1251:C:O2'	54:01:1252:G:H3'	2.14	0.48
54:01:1941:C:H2'	54:01:1942:C:O4'	2.14	0.48
55:02:63:C:H2'	55:02:64:G:H8	1.77	0.48
58:Y:76:A:H5''	59:Z:220:ILE:CD1	2.43	0.48
2:05:55:LYS:HG3	2:05:77:ARG:HB3	1.95	0.48
7:10:94:ARG:HG2	7:10:131:THR:HG22	1.96	0.48
22:25:17:LEU:HD21	22:25:37:ARG:NH2	2.28	0.48
29:32:14:ARG:HG3	54:01:771:G:OP1	2.14	0.48
29:32:34:ARG:HH21	29:32:39:ARG:CD	2.23	0.48
32:B:23:ASN:HB2	32:B:189:ASN:HA	1.96	0.48
32:B:132:GLU:O	32:B:136:ARG:HG2	2.13	0.48
35:E:113:VAL:HG11	35:E:139:THR:OG1	2.13	0.48
35:E:123:LEU:HD13	53:A:7:A:N7	2.28	0.48
40:J:12:ALA:HB2	40:J:96:VAL:HG22	1.96	0.48
42:L:3:VAL:HA	42:L:6:LEU:HD12	1.95	0.48
50:T:68:LYS:HA	50:T:71:ALA:HB3	1.96	0.48
54:01:576:U:H2'	54:01:577:G:C8	2.49	0.48
54:01:2041:U:H2'	54:01:2042:A:C8	2.49	0.48
54:01:2154:A:H2'	54:01:2155:U:C6	2.49	0.48
59:Z:70:ASP:HB3	59:Z:75:HIS:HA	1.95	0.48
1:04:176:ARG:HG2	54:01:1819:A:H3'	1.96	0.48
3:06:46:GLN:HB3	3:06:83:VAL:HG11	1.95	0.48
16:19:60:TRP:CE2	16:19:92:LYS:HA	2.48	0.48
27:30:46:GLY:HA3	27:30:54:ILE:CG2	2.44	0.48
32:B:209:VAL:HG23	32:B:210:THR:H	1.79	0.48
32:B:209:VAL:HG23	32:B:210:THR:N	2.29	0.48
39:I:10:ARG:HG3	39:I:105:ARG:NE	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:J:28:THR:HG22	40:J:86:ALA:HB1	1.95	0.48
43:M:14:ALA:HB1	43:M:33:LEU:HD11	1.95	0.48
46:P:38:PHE:HE1	46:P:51:ARG:HD2	1.79	0.48
51:U:25:ALA:HA	51:U:28:LEU:HB3	1.96	0.48
53:A:36:C:H2'	53:A:37:U:O4'	2.14	0.48
53:A:603:U:H2'	53:A:604:G:C8	2.49	0.48
54:01:158:U:H2'	54:01:159:G:O4'	2.13	0.48
54:01:974:G:H1'	54:01:975:A:C8	2.49	0.48
54:01:2030:A:N3	54:01:2499:C:H5''	2.28	0.48
54:01:2423:U:H5'	54:01:2424:C:H5'	1.96	0.48
54:01:2853:C:H2'	54:01:2854:G:H8	1.78	0.48
59:Z:67:VAL:HG22	59:Z:78:HIS:HB3	1.96	0.48
4:07:7:TYR:HA	4:07:11:VAL:HB	1.95	0.48
20:23:47:PRO:HB3	20:23:55:GLY:N	2.22	0.48
34:D:11:SER:O	34:D:15:GLY:N	2.47	0.48
34:D:82:LYS:HD2	34:D:82:LYS:N	2.28	0.48
35:E:149:PRO:HA	35:E:152:VAL:HG22	1.95	0.48
37:G:34:LYS:HE2	53:A:1290:G:H5'	1.96	0.48
47:Q:16:MET:HE2	47:Q:19:SER:HB2	1.96	0.48
54:01:967:U:H2'	54:01:968:C:C6	2.49	0.48
54:01:2064:C:H2'	54:01:2065:C:C6	2.49	0.48
54:01:2743:U:C2'	54:01:2744:G:H5''	2.43	0.48
59:Z:4:LYS:HA	59:Z:264:LEU:HB2	1.95	0.48
59:Z:184:TRP:CE3	59:Z:187:LYS:HG3	2.49	0.48
59:Z:304:PHE:CD2	59:Z:388:VAL:HG22	2.48	0.48
1:04:180:MET:HB2	1:04:268:ARG:HB2	1.96	0.48
3:06:5:LEU:HA	3:06:120:VAL:O	2.14	0.48
4:07:3:LEU:HA	4:07:6:TYR:HB3	1.96	0.48
5:08:97:VAL:HG23	5:08:124:CYS:SG	2.53	0.48
31:34:37:GLN:HG3	31:34:38:GLY:H	1.79	0.48
33:C:111:ASP:O	33:C:115:VAL:HG23	2.14	0.48
37:G:100:MET:O	37:G:104:VAL:HG23	2.14	0.48
39:I:88:GLU:HG2	39:I:89:TYR:N	2.27	0.48
42:L:86:VAL:HG23	42:L:88:ASP:H	1.79	0.48
48:R:33:THR:HG23	48:R:35:SER:H	1.78	0.48
53:A:129:A:H1'	53:A:130:A:N7	2.29	0.48
53:A:1048:G:H2'	53:A:1050:G:C8	2.48	0.48
54:01:492:A:H2'	54:01:493:G:O4'	2.14	0.48
54:01:817:C:H2'	54:01:818:G:O4'	2.14	0.48
54:01:1071:G:OP1	54:01:1071:G:H3'	2.14	0.48
54:01:1464:G:H2'	54:01:1465:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1535:A:H3'	54:01:1536:C:H5'	1.96	0.48
54:01:2093:G:N7	54:01:2225:A:H2'	2.29	0.48
54:01:2591:C:H2'	54:01:2592:G:H8	1.78	0.48
58:Y:73:A:H3'	58:Y:74:C:H4'	1.96	0.48
2:05:39:ASP:CG	2:05:40:LEU:H	2.22	0.47
14:17:79:ALA:O	14:17:83:LEU:HG	2.14	0.47
15:18:59:THR:HA	15:18:72:VAL:HA	1.96	0.47
28:31:39:ASP:HB2	28:31:46:VAL:HG23	1.96	0.47
34:D:10:LEU:HD13	34:D:62:ARG:HD2	1.95	0.47
38:H:12:ARG:CZ	53:A:826:C:H5'	2.44	0.47
39:I:38:PHE:HA	39:I:41:GLU:OE1	2.14	0.47
43:M:59:VAL:C	43:M:61:LYS:H	2.22	0.47
43:M:93:GLY:HA2	43:M:108:ARG:HH12	1.79	0.47
53:A:893:C:H2'	53:A:894:G:C8	2.49	0.47
53:A:994:A:H61	53:A:1047:G:H1'	1.79	0.47
53:A:1256:A:O2'	53:A:1257:A:H5''	2.14	0.47
54:01:69:C:H2'	54:01:70:G:C8	2.49	0.47
54:01:1645:G:H5''	54:01:1646:C:H5'	1.96	0.47
59:Z:101:ALA:C	59:Z:130:ILE:HG23	2.39	0.47
1:04:42:ARG:NH1	1:04:48:ILE:HB	2.29	0.47
1:04:47:ARG:HG2	54:01:773:U:O2'	2.14	0.47
1:04:245:THR:C	1:04:247:TRP:H	2.20	0.47
1:04:259:ASN:C	1:04:261:ARG:H	2.22	0.47
4:07:7:TYR:O	4:07:12:VAL:HG23	2.14	0.47
6:09:99:ILE:HG21	6:09:130:VAL:HG11	1.96	0.47
11:14:30:THR:HG23	54:01:810:U:H3	1.79	0.47
14:17:35:ILE:HB	14:17:102:ARG:NH2	2.29	0.47
22:25:35:ARG:HD2	22:25:54:THR:HG23	1.96	0.47
29:32:9:VAL:H	54:01:1309:G:H5''	1.79	0.47
33:C:69:THR:C	33:C:105:VAL:HG12	2.39	0.47
54:01:440:C:H2'	54:01:441:U:C6	2.48	0.47
54:01:1683:U:H2'	54:01:1684:G:H8	1.79	0.47
54:01:2364:C:H2'	54:01:2365:G:O4'	2.13	0.47
54:01:2859:G:H2'	54:01:2860:A:C8	2.49	0.47
54:01:2898:U:H2'	54:01:2899:A:C8	2.49	0.47
59:Z:13:ASN:HB3	59:Z:98:MET:HA	1.95	0.47
4:07:173:ASP:O	4:07:174:PHE:C	2.58	0.47
5:08:92:GLY:H	5:08:94:ARG:NH1	2.07	0.47
7:10:118:ILE:CB	7:10:119:PRO:HD3	2.43	0.47
14:17:64:TYR:HD2	14:17:67:ASN:HB3	1.79	0.47
16:19:64:ILE:HD13	16:19:94:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:29:46:GLY:HA2	26:29:49:ARG:HH21	1.78	0.47
42:L:28:GLN:NE2	42:L:80:LEU:HD21	2.29	0.47
54:01:184:C:H2'	54:01:185:G:C8	2.49	0.47
54:01:460:A:H2'	54:01:461:C:O4'	2.14	0.47
54:01:471:A:H2'	54:01:472:A:O4'	2.14	0.47
54:01:1268:A:H2'	54:01:1269:A:O4'	2.13	0.47
54:01:1370:C:H2'	54:01:1371:G:O4'	2.13	0.47
54:01:1747:U:H2'	54:01:1748:C:C6	2.49	0.47
54:01:1893:C:H2'	54:01:1894:C:H5'	1.95	0.47
54:01:2286:G:H5''	54:01:2287:A:OP1	2.15	0.47
54:01:2740:A:H2'	54:01:2741:A:C8	2.48	0.47
59:Z:308:VAL:HG21	59:Z:358:MET:HE2	1.95	0.47
4:07:45:ASP:HB3	4:07:48:LEU:HB2	1.97	0.47
4:07:105:ILE:HG13	4:07:106:ALA:N	2.29	0.47
10:13:102:PRO:HB3	10:13:121:GLU:OE1	2.15	0.47
12:15:34:LYS:HE3	12:15:131:VAL:HG21	1.97	0.47
13:16:96:ARG:HH22	27:30:51:ARG:NH2	2.13	0.47
17:20:27:ILE:HG13	17:20:33:VAL:HG11	1.97	0.47
33:C:154:GLY:HA3	33:C:195:ILE:HG12	1.96	0.47
34:D:171:GLU:HG3	34:D:172:VAL:H	1.80	0.47
35:E:12:GLU:HA	35:E:38:VAL:HG12	1.95	0.47
38:H:113:ARG:HA	38:H:116:ARG:HG2	1.95	0.47
39:I:49:GLN:N	39:I:50:PRO:HD2	2.29	0.47
53:A:910:C:H2'	53:A:911:U:C6	2.49	0.47
54:01:341:C:H2'	54:01:342:A:C8	2.49	0.47
54:01:1681:G:N3	54:01:1762:A:H2'	2.30	0.47
54:01:2455:G:H2'	54:01:2456:C:C6	2.49	0.47
58:Y:26:A:N6	58:Y:44:U:H3	2.13	0.47
59:Z:103:LEU:HB3	59:Z:132:VAL:HG13	1.97	0.47
2:05:53:GLY:HA3	2:05:77:ARG:HG2	1.97	0.47
3:06:189:THR:HG22	3:06:191:ASP:H	1.78	0.47
4:07:169:LEU:HD22	4:07:174:PHE:HE2	1.79	0.47
5:08:72:ASN:O	5:08:76:ILE:HG12	2.13	0.47
32:B:131:LYS:NZ	53:A:1159:U:H5'	2.30	0.47
35:E:76:ASN:C	35:E:78:GLY:H	2.22	0.47
36:F:15:SER:HA	36:F:18:VAL:HG23	1.97	0.47
37:G:13:PRO:HA	37:G:20:GLU:HA	1.96	0.47
39:I:48:ARG:HA	39:I:51:LEU:HD12	1.96	0.47
41:K:29:THR:HG21	41:K:62:ALA:HB2	1.95	0.47
44:N:50:LEU:HB3	44:N:51:PRO:HD2	1.96	0.47
50:T:55:PRO:HA	53:A:194:C:H5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:955:U:H3	54:01:962:G:H1	1.62	0.47
54:01:2122:U:H2'	54:01:2123:G:O4'	2.14	0.47
54:01:2475:C:H42	54:01:2529:G:H22	1.62	0.47
54:01:2853:C:H2'	54:01:2854:G:C8	2.49	0.47
9:12:105:VAL:HG11	9:12:122:LEU:HD22	1.96	0.47
18:21:46:LEU:O	18:21:50:VAL:HG23	2.15	0.47
27:30:46:GLY:HA3	27:30:54:ILE:HG21	1.96	0.47
29:32:30:VAL:O	29:32:34:ARG:HG2	2.14	0.47
34:D:60:VAL:HG21	34:D:199:ILE:HD11	1.95	0.47
41:K:73:VAL:HG21	41:K:104:PHE:HZ	1.80	0.47
43:M:113:LYS:H	43:M:114:PRO:HD2	1.80	0.47
44:N:30:ILE:HG21	44:N:43:ALA:CB	2.44	0.47
52:03:6:LYS:HG3	52:03:7:ARG:H	1.79	0.47
53:A:116:A:H2'	53:A:117:G:O4'	2.15	0.47
53:A:155:A:H2'	53:A:156:C:C6	2.50	0.47
54:01:2372:U:H2'	54:01:2373:G:H8	1.80	0.47
54:01:2633:G:H5''	54:01:2812:G:H5'	1.96	0.47
1:04:154:ALA:HB1	1:04:159:THR:HG22	1.96	0.47
3:06:48:THR:HG22	3:06:86:ALA:HB3	1.95	0.47
7:10:24:SER:O	7:10:115:GLY:HA2	2.15	0.47
14:17:5:SER:HA	14:17:8:ILE:HD12	1.96	0.47
23:26:11:PRO:HG3	23:26:30:PRO:HD2	1.96	0.47
27:30:3:GLN:HA	54:01:2615:U:C2	2.48	0.47
32:B:67:LEU:HB2	32:B:160:LEU:HD12	1.96	0.47
38:H:6:ILE:O	38:H:10:LEU:HG	2.14	0.47
39:I:82:ILE:O	39:I:86:LEU:HG	2.15	0.47
46:P:2:VAL:HA	46:P:23:ASP:HA	1.96	0.47
47:Q:11:VAL:HA	47:Q:22:VAL:HG22	1.96	0.47
53:A:70:U:H2'	53:A:94:G:C6	2.49	0.47
53:A:202:G:N2	53:A:466:A:H61	2.13	0.47
53:A:482:A:H2'	53:A:483:C:O4'	2.14	0.47
53:A:546:A:H4'	53:A:548:G:H4'	1.97	0.47
53:A:641:U:H4'	53:A:642:A:C8	2.49	0.47
53:A:643:C:H2'	53:A:644:U:C6	2.50	0.47
53:A:1004:A:H2'	53:A:1005:A:O4'	2.15	0.47
53:A:1434:A:H2'	53:A:1435:G:O4'	2.15	0.47
53:A:1539:C:O2'	53:A:1540:U:H5'	2.15	0.47
54:01:225:C:H2'	54:01:226:A:O4'	2.15	0.47
54:01:275:C:H2'	54:01:276:U:C4'	2.42	0.47
54:01:391:A:N3	54:01:391:A:H2'	2.29	0.47
54:01:1170:C:H2'	54:01:1171:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1524:G:H2'	54:01:1525:A:C8	2.49	0.47
54:01:2036:C:H2'	54:01:2037:A:H8	1.79	0.47
54:01:2343:U:H2'	54:01:2344:U:C6	2.49	0.47
54:01:2566:A:H4'	54:01:2567:G:H5''	1.97	0.47
54:01:2605:U:H2'	54:01:2606:C:C6	2.49	0.47
59:Z:11:HIS:N	59:Z:269:ARG:HH12	2.13	0.47
3:06:165:HIS:HB2	54:01:1205:A:C6	2.49	0.47
4:07:114:ARG:NH2	26:29:47:LYS:HA	2.30	0.47
5:08:39:ALA:HB3	5:08:63:GLN:HG2	1.97	0.47
7:10:67:THR:HG23	7:10:74:ASP:HB2	1.95	0.47
8:11:99:LYS:O	8:11:100:ILE:HD13	2.15	0.47
11:14:90:VAL:HB	11:14:122:VAL:HA	1.97	0.47
13:16:35:LYS:HB2	13:16:112:TYR:CE1	2.50	0.47
17:20:88:GLY:HA3	54:01:1225:G:OP1	2.15	0.47
28:31:21:THR:HG21	54:01:2419:U:H5''	1.95	0.47
30:33:63:TYR:CZ	54:01:242:G:H5''	2.50	0.47
33:C:75:VAL:O	33:C:82:ASP:HB2	2.14	0.47
34:D:7:LYS:HG2	53:A:430:A:OP2	2.15	0.47
34:D:14:GLU:C	34:D:16:THR:H	2.23	0.47
40:J:81:GLU:O	40:J:84:VAL:HG12	2.15	0.47
41:K:24:ALA:HB1	41:K:89:GLY:HA3	1.96	0.47
41:K:116:PRO:HB3	53:A:676:A:C1'	2.44	0.47
42:L:41:PRO:HD3	42:L:47:ALA:O	2.15	0.47
45:O:27:GLN:O	45:O:31:LEU:HG	2.15	0.47
47:Q:6:THR:O	47:Q:7:LEU:HD12	2.15	0.47
47:Q:60:ILE:HG22	47:Q:72:TRP:HE3	1.80	0.47
50:T:23:ARG:O	50:T:26:MET:HG3	2.14	0.47
52:03:16:ASP:HB3	52:03:19:LYS:HB3	1.97	0.47
54:01:702:U:H2'	54:01:703:U:C6	2.50	0.47
54:01:1765:U:H2'	54:01:1766:G:H8	1.79	0.47
54:01:2036:C:H2'	54:01:2037:A:C8	2.50	0.47
54:01:2589:A:H2'	54:01:2590:A:H8	1.79	0.47
55:02:2:G:H2'	55:02:3:C:C6	2.49	0.47
59:Z:214:ILE:HG23	59:Z:227:VAL:CG2	2.45	0.47
1:04:104:LEU:HD12	1:04:142:ASN:HD22	1.80	0.47
1:04:184:GLU:HB3	1:04:187:CYS:SG	2.55	0.47
3:06:26:ALA:HB1	11:14:9:ALA:HB2	1.97	0.47
11:14:23:ILE:HD12	11:14:23:ILE:N	2.28	0.47
12:15:41:LEU:HA	12:15:45:GLN:OE1	2.14	0.47
13:16:49:GLU:HB2	13:16:50:PRO:HD3	1.96	0.47
23:26:10:ARG:HH22	54:01:187:G:H4'	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:75:ALA:O	32:B:79:VAL:HG23	2.15	0.47
32:B:95:TRP:CZ2	32:B:171:ALA:HA	2.50	0.47
33:C:13:ILE:HD12	33:C:13:ILE:N	2.29	0.47
42:L:28:GLN:HG3	42:L:80:LEU:CG	2.45	0.47
42:L:117:GLY:HA2	53:A:35:G:O2'	2.15	0.47
45:O:88:ARG:NH2	54:01:714:U:H5''	2.29	0.47
53:A:12:U:H2'	53:A:13:U:H5''	1.96	0.47
53:A:1319:A:H4'	53:A:1320:C:H5	1.80	0.47
54:01:1190:G:H2'	54:01:1191:G:H8	1.79	0.47
54:01:2841:C:H2'	54:01:2842:G:C8	2.49	0.47
59:Z:242:VAL:HG22	59:Z:255:CYS:SG	2.55	0.47
1:04:132:ARG:HD2	6:09:123:ARG:NH2	2.30	0.47
2:05:201:LEU:C	2:05:202:ILE:HD12	2.39	0.47
4:07:34:THR:HB	4:07:154:THR:HB	1.96	0.47
4:07:43:ILE:HD12	4:07:44:ALA:H	1.80	0.47
5:08:8:VAL:HG23	5:08:51:PHE:HE2	1.80	0.47
8:11:80:LYS:HB3	8:11:86:LYS:HA	1.97	0.47
16:19:42:GLY:HA3	17:20:75:VAL:HG21	1.97	0.47
32:B:172:ILE:O	32:B:176:ASN:HB2	2.15	0.47
36:F:81:ASN:HD21	36:F:83:ALA:HB3	1.81	0.47
39:I:126:PHE:O	53:A:1342:C:H4'	2.15	0.47
42:L:114:SER:HB3	53:A:35:G:H21	1.80	0.47
43:M:97:ARG:HB2	43:M:99:GLN:OE1	2.15	0.47
44:N:26:LEU:O	44:N:30:ILE:HD12	2.15	0.47
53:A:459:A:H2'	53:A:460:A:C8	2.49	0.47
53:A:466:A:H2'	53:A:468:A:C8	2.50	0.47
53:A:1219:A:H2'	53:A:1220:G:C8	2.50	0.47
54:01:255:A:H2'	54:01:256:A:O4'	2.15	0.47
54:01:319:G:H2'	54:01:320:A:O4'	2.15	0.47
54:01:437:U:H2'	54:01:438:G:C8	2.50	0.47
54:01:1373:A:H4'	54:01:2212:A:C1'	2.45	0.47
54:01:2423:U:H5'	54:01:2424:C:C5'	2.45	0.47
54:01:2577:A:H2'	54:01:2614:A:N6	2.30	0.47
55:02:66:A:N1	55:02:107:G:H2'	2.30	0.47
59:Z:318:ARG:HG2	59:Z:319:HIS:H	1.80	0.47
7:10:80:THR:O	7:10:82:ILE:HG12	2.15	0.46
8:11:112:LYS:HZ3	8:11:128:ILE:HG12	1.79	0.46
11:14:78:ARG:HB3	11:14:113:ALA:CB	2.45	0.46
16:19:91:ARG:HD2	16:19:91:ARG:N	2.29	0.46
25:28:52:PHE:CD2	55:02:83:G:H4'	2.50	0.46
32:B:46:VAL:HA	32:B:49:PHE:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:76:ASN:HB2	35:E:81:GLN:OE1	2.15	0.46
35:E:131:ASN:O	35:E:135:VAL:HG22	2.15	0.46
35:E:156:ARG:NH2	38:H:100:ILE:HG23	2.30	0.46
53:A:1081:A:H2'	53:A:1082:A:C8	2.50	0.46
53:A:1319:A:H4'	53:A:1320:C:C5	2.51	0.46
54:01:222:A:N6	54:01:232:G:H1'	2.29	0.46
54:01:279:A:H61	54:01:361:G:H1'	1.79	0.46
54:01:1196:C:H2'	54:01:1197:G:C8	2.50	0.46
54:01:2206:C:H2'	54:01:2207:C:C6	2.50	0.46
54:01:2526:G:H2'	54:01:2527:C:C6	2.50	0.46
54:01:2737:G:H2'	54:01:2738:A:C8	2.49	0.46
55:02:78:A:H62	55:02:98:G:H21	1.61	0.46
59:Z:186:ALA:O	59:Z:189:LEU:HB3	2.15	0.46
3:06:23:PHE:H	3:06:114:ARG:HH12	1.62	0.46
4:07:63:LYS:HE2	26:29:5:ILE:HD12	1.97	0.46
6:09:94:ILE:HD12	6:09:122:LEU:HB3	1.96	0.46
14:17:79:ALA:HB3	14:17:113:ALA:HB3	1.98	0.46
22:25:45:ALA:O	22:25:47:VAL:HG23	2.15	0.46
31:34:5:ALA:HB3	54:01:2466:C:H5'	1.97	0.46
33:C:56:ILE:CG2	33:C:63:ILE:HD11	2.45	0.46
33:C:133:MET:O	33:C:137:VAL:HG23	2.15	0.46
46:P:19:VAL:HG22	46:P:36:VAL:HG13	1.97	0.46
53:A:31:G:N2	53:A:47:C:H5''	2.31	0.46
53:A:306:A:H2'	53:A:307:C:O4'	2.15	0.46
53:A:955:U:H2'	53:A:956:U:C6	2.51	0.46
53:A:1250:A:C2	53:A:1370:G:H1'	2.50	0.46
53:A:1432:G:H1'	53:A:1468:A:N6	2.30	0.46
54:01:414:C:H2'	54:01:415:A:C8	2.50	0.46
54:01:622:G:H2'	54:01:623:C:C6	2.51	0.46
54:01:1779:U:P	54:01:1780:A:H5'	2.55	0.46
54:01:2811:G:H2'	54:01:2812:G:C8	2.51	0.46
59:Z:304:PHE:HA	59:Z:390:LYS:O	2.15	0.46
2:05:46:ARG:HD3	2:05:86:GLU:HA	1.96	0.46
2:05:106:LYS:CE	2:05:174:SER:HB3	2.40	0.46
3:06:122:GLU:O	3:06:189:THR:HG23	2.16	0.46
11:14:56:PRO:O	11:14:60:ARG:HG3	2.15	0.46
11:14:118:THR:O	11:14:120:VAL:N	2.48	0.46
19:22:66:LYS:HE2	19:22:68:LYS:NZ	2.30	0.46
27:30:2:VAL:HG21	54:01:2057:G:H1'	1.98	0.46
34:D:104:MET:SD	34:D:170:LEU:HD22	2.55	0.46
46:P:36:VAL:CG2	46:P:53:ASP:HB3	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:40:ASN:HB3	46:P:43:ALA:HB2	1.96	0.46
47:Q:29:LYS:HB2	47:Q:36:PHE:CE1	2.49	0.46
48:R:58:ILE:O	48:R:62:ARG:HG3	2.15	0.46
49:S:62:THR:HG22	49:S:63:ASP:N	2.30	0.46
49:S:77:ARG:HH21	53:A:1225:A:H4'	1.80	0.46
51:U:29:ALA:HA	51:U:32:ARG:HD3	1.96	0.46
52:03:186:LYS:HA	52:03:189:LEU:HB3	1.97	0.46
53:A:1497:G:C2'	53:A:1498:U:H5'	2.46	0.46
56:X:1:C:H42	56:X:72:A:H61	1.63	0.46
58:Y:54:U:H3'	58:Y:55:U:C5'	2.40	0.46
1:04:132:ARG:C	1:04:133:ASN:HD22	2.24	0.46
2:05:29:VAL:HB	2:05:98:VAL:HG23	1.98	0.46
2:05:36:GLN:HB3	2:05:49:GLN:HB3	1.97	0.46
3:06:192:ALA:O	3:06:196:VAL:HG23	2.15	0.46
8:11:119:ALA:HB2	54:01:1082:U:H5''	1.98	0.46
9:12:15:TRP:HH2	54:01:7:G:H4'	1.80	0.46
9:12:29:ALA:HA	9:12:32:LEU:HD12	1.96	0.46
14:17:64:TYR:HB3	14:17:67:ASN:HD22	1.81	0.46
15:18:24:THR:HB	15:18:87:ARG:HB2	1.97	0.46
18:21:77:ASP:OD1	18:21:102:HIS:HB2	2.15	0.46
24:27:2:LYS:O	24:27:6:LEU:HB2	2.15	0.46
42:L:47:ALA:HB1	53:A:520:A:OP2	2.16	0.46
50:T:2:ASN:CG	50:T:3:ILE:N	2.74	0.46
53:A:24:U:H2'	53:A:25:C:C6	2.50	0.46
53:A:34:C:H2'	53:A:35:G:H8	1.81	0.46
53:A:976:G:N2	53:A:1362:A:H2'	2.29	0.46
53:A:992:U:H1'	53:A:993:G:C2	2.51	0.46
53:A:1011:C:H2'	53:A:1012:A:C8	2.51	0.46
53:A:1414:U:H2'	53:A:1415:G:C8	2.48	0.46
53:A:1522:U:H2'	53:A:1523:G:H8	1.81	0.46
54:01:215:G:H4'	54:01:216:A:H4'	1.97	0.46
55:02:39:A:H2'	55:02:40:U:C6	2.50	0.46
58:Y:2:G:H4'	59:Z:87:TYR:HE1	1.80	0.46
59:Z:112:MET:HB3	59:Z:113:PRO:CD	2.46	0.46
1:04:41:GLY:HA2	54:01:1813:G:O2'	2.16	0.46
1:04:153:LEU:HD22	1:04:175:LEU:HD22	1.98	0.46
1:04:159:THR:HG22	1:04:160:TYR:H	1.80	0.46
1:04:209:ALA:HA	1:04:212:TRP:NE1	2.31	0.46
12:15:75:GLU:HA	54:01:957:C:OP2	2.16	0.46
21:24:26:PHE:CZ	21:24:86:LEU:HD12	2.50	0.46
21:24:51:GLN:OE1	21:24:86:LEU:HD11	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:60:VAL:HG11	21:24:71:LYS:HE3	1.97	0.46
34:D:120:LYS:NZ	34:D:130:ASN:HD21	2.14	0.46
34:D:198:LEU:HA	34:D:201:GLU:OE1	2.16	0.46
36:F:9:MET:HB3	36:F:57:ALA:HB1	1.97	0.46
36:F:53:LYS:HE3	53:A:710:G:OP1	2.15	0.46
46:P:38:PHE:CE1	46:P:51:ARG:HD2	2.50	0.46
47:Q:11:VAL:HB	47:Q:55:GLY:H	1.80	0.46
52:O3:67:HIS:HB2	52:O3:188:ASN:ND2	2.31	0.46
53:A:86:G:H4'	53:A:87:C:C5	2.50	0.46
53:A:678:U:H2'	53:A:679:C:C6	2.51	0.46
53:A:1028:C:H1'	53:A:1034:G:N1	2.31	0.46
53:A:1147:C:H2'	53:A:1148:U:C6	2.50	0.46
53:A:1163:A:H2'	53:A:1164:G:C8	2.50	0.46
54:O1:594:U:H2'	54:O1:595:C:C6	2.51	0.46
54:O1:1182:G:H2'	54:O1:1183:U:O4'	2.16	0.46
54:O1:2011:U:H2'	54:O1:2012:G:O4'	2.15	0.46
59:Z:146:LEU:HD13	59:Z:149:VAL:HG21	1.97	0.46
59:Z:150:GLU:O	59:Z:154:ARG:HG3	2.15	0.46
3:O6:52:VAL:O	3:O6:74:LYS:HE3	2.16	0.46
4:O7:65:LEU:HD22	55:O2:42:C:C4	2.51	0.46
8:11:81:LYS:HA	8:11:86:LYS:HE3	1.97	0.46
11:14:30:THR:HG23	54:O1:810:U:N3	2.31	0.46
30:33:46:LYS:HD2	30:33:46:LYS:N	2.30	0.46
33:C:67:ILE:HD11	33:C:100:ILE:HD11	1.98	0.46
34:D:116:LEU:HD23	34:D:122:ILE:HD11	1.98	0.46
53:A:225:C:C3'	53:A:226:G:H5''	2.45	0.46
53:A:631:C:H5''	53:A:632:U:O4'	2.16	0.46
53:A:962:C:H2'	53:A:963:G:H8	1.80	0.46
53:A:1412:C:H2'	53:A:1413:A:C8	2.50	0.46
53:A:1463:U:H2'	53:A:1464:U:C6	2.51	0.46
53:A:1513:A:H2'	53:A:1514:G:C8	2.50	0.46
54:O1:2345:G:H5'	54:O1:2347:C:H5'	1.98	0.46
54:O1:2382:G:H5'	54:O1:2383:G:O5'	2.16	0.46
54:O1:2543:G:H2'	54:O1:2544:G:C8	2.50	0.46
54:O1:2687:U:H2'	54:O1:2688:G:O4'	2.15	0.46
54:O1:2743:U:C3'	54:O1:2744:G:H5''	2.45	0.46
3:O6:55:SER:HB2	54:O1:797:G:OP1	2.16	0.46
4:O7:127:TYR:CE2	4:O7:129:MET:HE2	2.50	0.46
8:11:8:VAL:O	8:11:57:VAL:HA	2.16	0.46
19:22:47:VAL:HB	19:22:55:VAL:HG21	1.96	0.46
21:24:82:TYR:CE2	21:24:83:LYS:HE3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:32:8:SER:HB3	54:01:686:U:O2	2.16	0.46
34:D:97:LEU:O	34:D:101:VAL:HG23	2.16	0.46
37:G:64:ALA:HA	37:G:67:ASN:HD22	1.81	0.46
38:H:79:ARG:HG3	38:H:82:LEU:H	1.80	0.46
41:K:127:ARG:NH2	53:A:1522:U:H5''	2.24	0.46
43:M:89:ARG:HH21	43:M:95:PRO:HG2	1.80	0.46
45:O:45:HIS:C	45:O:47:LYS:H	2.23	0.46
46:P:70:ARG:HH12	53:A:451:A:H5'	1.80	0.46
51:U:34:ARG:HD2	51:U:36:PHE:CE2	2.51	0.46
53:A:77:A:H2'	53:A:78:A:H8	1.79	0.46
53:A:392:C:H2'	53:A:393:A:C8	2.50	0.46
53:A:598:U:H2'	53:A:599:C:C6	2.51	0.46
53:A:728:A:H2'	53:A:729:A:C8	2.51	0.46
53:A:1336:C:H4'	53:A:1337:G:O4'	2.16	0.46
54:01:184:C:H2'	54:01:185:G:H8	1.80	0.46
54:01:320:A:H4'	54:01:322:A:N7	2.31	0.46
54:01:696:G:H1	54:01:766:U:H3	1.64	0.46
54:01:780:G:H2'	54:01:782:A:N7	2.30	0.46
54:01:1526:C:H2'	54:01:1527:G:O4'	2.15	0.46
54:01:2055:C:H5'	54:01:2056:G:O5'	2.16	0.46
54:01:2395:C:O2	56:X:76:A:H5'	2.15	0.46
59:Z:101:ALA:O	59:Z:130:ILE:HG23	2.16	0.46
59:Z:115:THR:O	59:Z:119:ILE:HG13	2.15	0.46
4:07:153:ILE:HD12	4:07:153:ILE:N	2.30	0.46
16:19:113:LYS:HA	16:19:116:LEU:HB3	1.98	0.46
23:26:36:ARG:HD2	23:26:45:PHE:HB3	1.97	0.46
29:32:24:THR:HG23	29:32:27:GLY:H	1.81	0.46
35:E:113:VAL:HG13	35:E:114:LEU:CD1	2.46	0.46
35:E:131:ASN:ND2	35:E:132:PRO:HD2	2.31	0.46
46:P:14:ARG:HH12	53:A:618:C:H1'	1.81	0.46
53:A:235:C:H2'	53:A:236:A:H8	1.81	0.46
53:A:246:A:H4'	53:A:247:G:H4'	1.97	0.46
53:A:396:C:C2'	53:A:397:A:H5''	2.46	0.46
53:A:744:C:H2'	53:A:745:G:C8	2.51	0.46
53:A:1333:A:H2'	53:A:1334:G:O4'	2.16	0.46
54:01:519:U:H2'	54:01:520:G:C8	2.50	0.46
54:01:687:C:H2'	54:01:688:U:O4'	2.15	0.46
54:01:1111:A:O2'	54:01:1112:G:H4'	2.15	0.46
54:01:2348:U:H2'	54:01:2349:G:C8	2.51	0.46
55:02:77:U:H2'	55:02:78:A:C8	2.51	0.46
59:Z:7:ARG:HE	59:Z:265:LEU:HD11	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:153:LEU:HD13	1:04:175:LEU:HD21	1.98	0.46
2:05:4:LEU:HD21	2:05:96:ILE:HG22	1.96	0.46
2:05:164:GLN:HE22	54:01:2822:G:H5''	1.79	0.46
3:06:19:PHE:CE1	3:06:109:LEU:HD23	2.51	0.46
4:07:90:LEU:HD12	4:07:90:LEU:O	2.15	0.46
5:08:171:LYS:NZ	54:01:2530:A:H62	2.14	0.46
8:11:72:THR:CG2	8:11:73:PRO:HD2	2.46	0.46
12:15:64:TRP:HE1	54:01:873:C:H4'	1.81	0.46
23:26:39:VAL:HG22	23:26:63:ILE:HG12	1.98	0.46
47:Q:11:VAL:HG13	47:Q:20:ILE:HD11	1.98	0.46
49:S:35:ARG:HB3	49:S:71:GLY:CA	2.46	0.46
53:A:212:G:H2'	53:A:213:G:C8	2.51	0.46
53:A:1500:A:H5''	53:A:1508:A:H5''	1.97	0.46
54:01:267:C:H2'	54:01:268:C:C6	2.51	0.46
54:01:834:G:H1'	54:01:2358:A:N3	2.31	0.46
54:01:1437:C:H2'	54:01:1438:U:C6	2.51	0.46
54:01:2048:G:C3'	54:01:2049:G:H5''	2.45	0.46
54:01:2264:C:H2'	54:01:2265:U:O4'	2.16	0.46
2:05:192:ALA:HB1	54:01:2680:U:H1'	1.98	0.46
2:05:194:PRO:HA	54:01:2680:U:H5'	1.97	0.46
17:20:15:SER:O	17:20:18:GLN:HG2	2.16	0.46
17:20:91:GLN:HE22	54:01:1162:G:N2	2.15	0.46
19:22:12:ARG:HB2	19:22:33:LYS:O	2.16	0.46
20:23:65:GLN:HG3	54:01:328:U:H4'	1.98	0.46
27:30:32:THR:OG1	27:30:50:GLY:HA2	2.16	0.46
30:33:3:ILE:HD11	54:01:592:A:H2	1.80	0.46
30:33:5:THR:HG22	30:33:6:VAL:N	2.30	0.46
34:D:113:ALA:O	34:D:117:VAL:HG23	2.16	0.46
38:H:9:MET:HA	38:H:26:MET:SD	2.56	0.46
38:H:45:ILE:HD13	38:H:60:LEU:HD13	1.98	0.46
48:R:21:ASP:CG	48:R:22:TYR:H	2.24	0.46
53:A:144:G:H2'	53:A:145:G:O4'	2.16	0.46
53:A:684:U:H2'	53:A:685:G:O4'	2.16	0.46
53:A:1296:C:H4'	53:A:1302:C:N4	2.31	0.46
54:01:481:G:H2'	54:01:507:A:N1	2.30	0.46
54:01:631:A:H2'	54:01:632:A:O4'	2.16	0.46
54:01:1564:C:H2'	54:01:1565:C:O4'	2.16	0.46
54:01:1675:C:H2'	54:01:1676:A:O4'	2.15	0.46
54:01:2893:A:H1'	54:01:2894:G:C6	2.51	0.46
1:04:83:ASP:HB2	1:04:90:ILE:HD13	1.98	0.45
1:04:219:VAL:HG21	54:01:782:A:N7	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:168:GLU:O	2:05:169:ARG:HB2	2.16	0.45
5:08:123:GLU:HB2	5:08:131:VAL:HB	1.98	0.45
7:10:80:THR:HA	54:01:1108:U:C5'	2.47	0.45
8:11:6:ALA:HB3	8:11:60:VAL:C	2.41	0.45
10:13:63:VAL:HG22	10:13:84:CYS:HA	1.97	0.45
10:13:105:ARG:CZ	15:18:31:VAL:HG21	2.46	0.45
30:33:5:THR:HG23	30:33:62:PRO:HD2	1.97	0.45
32:B:163:ILE:HG22	32:B:168:GLU:OE1	2.15	0.45
35:E:104:ILE:HD11	35:E:114:LEU:HD23	1.97	0.45
52:03:163:TYR:HD2	52:03:171:ILE:HD13	1.81	0.45
53:A:501:C:H2'	53:A:502:A:H8	1.79	0.45
54:01:717:C:H2'	54:01:718:A:O4'	2.17	0.45
54:01:1443:U:H2'	54:01:1444:G:H8	1.81	0.45
54:01:1857:G:H1'	54:01:1885:A:N6	2.31	0.45
54:01:2692:G:H5''	54:01:2870:C:O2'	2.16	0.45
1:04:42:ARG:HG2	1:04:42:ARG:HH11	1.81	0.45
2:05:62:LYS:HB2	2:05:63:PRO:HD3	1.98	0.45
3:06:149:ILE:HG21	3:06:188:MET:HE3	1.97	0.45
3:06:161:ALA:HB1	3:06:167:VAL:HG12	1.98	0.45
4:07:68:LYS:HE3	4:07:83:PRO:HD3	1.98	0.45
5:08:84:LYS:HD3	5:08:132:LEU:HD11	1.98	0.45
8:11:15:GLY:N	8:11:51:GLY:H	2.10	0.45
8:11:56:VAL:HA	8:11:70:THR:HA	1.97	0.45
9:12:15:TRP:CH2	54:01:7:G:H4'	2.50	0.45
9:12:69:ARG:HA	9:12:89:PHE:HD2	1.80	0.45
12:15:13:HIS:HE1	54:01:2265:U:H4'	1.82	0.45
16:19:15:LYS:O	16:19:19:GLN:HG3	2.15	0.45
20:23:28:LEU:HD21	20:23:34:ILE:HD11	1.97	0.45
25:28:21:ALA:O	25:28:24:LEU:HB3	2.16	0.45
37:G:4:ARG:H	37:G:4:ARG:CD	2.29	0.45
37:G:149:ALA:HA	41:K:60:PHE:HB3	1.99	0.45
49:S:5:LYS:HG3	49:S:6:LYS:N	2.29	0.45
53:A:50:A:N6	53:A:361:G:H4'	2.31	0.45
53:A:747:A:H2'	53:A:748:G:O4'	2.16	0.45
53:A:1497:G:O2'	53:A:1498:U:H5'	2.16	0.45
54:01:189:G:H2'	54:01:205:G:N2	2.31	0.45
54:01:1045:C:C5'	54:01:1046:A:H5'	2.34	0.45
54:01:1278:C:H2'	54:01:1279:G:H8	1.81	0.45
54:01:1297:C:OP1	54:01:2710:C:H4'	2.17	0.45
54:01:2710:C:H2'	54:01:2711:A:C8	2.51	0.45
54:01:2808:G:H2'	54:01:2890:G:O6	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:106:G:H2'	55:02:107:G:O4'	2.16	0.45
59:Z:216:ASP:OD1	59:Z:288:ARG:HG3	2.15	0.45
3:06:22:ASP:HA	3:06:114:ARG:NH1	2.29	0.45
4:07:89:THR:O	55:02:43:C:H1'	2.16	0.45
4:07:140:ILE:HD12	4:07:140:ILE:N	2.31	0.45
6:09:51:ARG:HG2	6:09:55:GLU:OE1	2.16	0.45
9:12:97:PRO:HG2	9:12:98:GLU:OE2	2.16	0.45
10:13:22:ILE:HG12	10:13:41:ILE:HA	1.98	0.45
12:15:11:LYS:HD3	12:15:86:LYS:HG2	1.98	0.45
12:15:36:VAL:HG13	21:24:82:TYR:CD2	2.52	0.45
13:16:79:LEU:C	13:16:81:ASN:H	2.25	0.45
16:19:85:ALA:HB3	16:19:87:VAL:HG23	1.98	0.45
23:26:60:LYS:HD2	54:01:372:G:C5	2.51	0.45
33:C:70:ALA:HB2	33:C:114:LEU:HD13	1.99	0.45
39:I:5:TYR:HB2	39:I:20:ILE:CG2	2.46	0.45
51:U:64:ALA:C	51:U:66:ARG:H	2.23	0.45
53:A:543:U:H2'	53:A:544:G:H8	1.81	0.45
54:01:163:C:H2'	54:01:164:C:O4'	2.16	0.45
54:01:184:C:H4'	54:01:217:A:C2	2.51	0.45
54:01:644:A:H2'	54:01:645:C:C4'	2.47	0.45
54:01:704:G:H1'	54:01:727:A:H61	1.80	0.45
54:01:2339:C:H2'	54:01:2340:A:C8	2.51	0.45
54:01:2421:G:H2'	56:X:76:A:N6	2.31	0.45
54:01:2554:U:H2'	54:01:2555:U:C6	2.52	0.45
54:01:2893:A:H4'	54:01:2894:G:C4	2.51	0.45
59:Z:11:HIS:NE2	59:Z:273:ASN:HB3	2.32	0.45
59:Z:97:GLN:HG3	59:Z:230:ARG:HB2	1.97	0.45
59:Z:259:GLU:OE2	59:Z:262:ARG:HA	2.17	0.45
1:04:176:ARG:NE	1:04:176:ARG:HA	2.31	0.45
4:07:45:ASP:O	4:07:48:LEU:HB3	2.17	0.45
4:07:109:ARG:HH22	43:M:2:ARG:HD3	1.82	0.45
8:11:88:GLY:CA	54:01:1063:G:H2'	2.44	0.45
8:11:101:SER:HB2	8:11:104:GLN:CG	2.47	0.45
12:15:3:GLN:HG3	12:15:92:TRP:CE2	2.52	0.45
12:15:12:MET:HG2	12:15:72:PRO:HG2	1.99	0.45
17:20:6:GLN:HB2	17:20:37:GLU:CB	2.46	0.45
17:20:61:ALA:HA	17:20:99:THR:H	1.81	0.45
22:25:61:GLY:HA3	22:25:80:ALA:HA	1.99	0.45
33:C:48:LYS:HD2	33:C:48:LYS:N	2.32	0.45
34:D:23:GLY:H	34:D:109:THR:CG2	2.29	0.45
36:F:3:HIS:H	36:F:92:THR:HG22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:85:TYR:CG	53:A:598:U:H4'	2.51	0.45
42:L:110:LYS:NZ	42:L:121:PRO:HB3	2.31	0.45
43:M:25:GLY:N	53:A:1329:A:H5''	2.29	0.45
43:M:43:LYS:HB2	43:M:46:GLU:HB2	1.98	0.45
44:N:68:ARG:HD2	53:A:1202:U:H1'	1.99	0.45
52:O3:29:LEU:HD23	52:O3:222:VAL:HG22	1.98	0.45
53:A:424:G:H2'	53:A:425:G:O4'	2.17	0.45
53:A:1443:C:H2'	53:A:1444:U:O4'	2.17	0.45
54:O1:473:G:O2'	54:O1:474:G:H5'	2.16	0.45
54:O1:668:A:H2'	54:O1:670:A:H62	1.82	0.45
54:O1:1827:U:O2'	54:O1:1828:G:H5'	2.17	0.45
55:O2:66:A:H5''	55:O2:67:G:OP1	2.16	0.45
59:Z:254:THR:HB	59:Z:279:ARG:HB3	1.99	0.45
4:O7:92:GLY:O	4:O7:95:MET:HG2	2.16	0.45
6:O9:78:VAL:O	6:O9:144:VAL:HG13	2.15	0.45
8:11:54:ILE:HG22	8:11:70:THR:OG1	2.16	0.45
13:16:96:ARG:HH22	27:30:51:ARG:HH21	1.63	0.45
17:20:51:VAL:HB	17:20:52:PRO:CD	2.45	0.45
19:22:43:ILE:O	19:22:47:VAL:HG23	2.16	0.45
32:B:27:LYS:HB3	32:B:28:PRO:HD3	1.99	0.45
35:E:15:ILE:HD12	35:E:15:ILE:N	2.32	0.45
36:F:20:GLY:HA2	36:F:23:GLU:OE1	2.17	0.45
42:L:8:ARG:HH12	53:A:880:C:H5''	1.81	0.45
43:M:87:GLY:O	43:M:91:ARG:HG3	2.16	0.45
46:P:26:ASN:HD21	46:P:31:ARG:CZ	2.30	0.45
53:A:195:A:H2'	53:A:196:A:C8	2.51	0.45
53:A:301:G:H2'	53:A:302:G:C8	2.50	0.45
53:A:302:G:H21	53:A:556:C:H4'	1.82	0.45
53:A:672:U:H2'	53:A:673:A:C8	2.52	0.45
53:A:763:G:H2'	53:A:764:C:C6	2.52	0.45
53:A:770:C:H2'	53:A:771:G:C8	2.52	0.45
54:O1:940:G:C3'	54:O1:941:A:H5''	2.47	0.45
54:O1:1060:U:H5''	54:O1:1061:U:H5'	1.99	0.45
54:O1:1105:U:C2'	54:O1:1106:G:H5''	2.46	0.45
55:O2:97:C:H2'	55:O2:98:G:O4'	2.15	0.45
58:Y:33:U:H2'	58:Y:35:U:OP2	2.17	0.45
59:Z:42:ALA:CB	59:Z:69:TYR:HA	2.46	0.45
59:Z:244:ILE:HD11	59:Z:253:SER:HB2	1.98	0.45
1:O4:259:ASN:HD21	1:O4:261:ARG:HB3	1.79	0.45
4:O7:35:LEU:HB3	4:O7:88:VAL:HB	1.98	0.45
6:O9:117:LEU:HD21	6:O9:130:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:129:GLU:HG2	9:12:130:HIS:N	2.32	0.45
17:20:58:VAL:O	17:20:58:VAL:HG13	2.17	0.45
28:31:4:ILE:HG22	28:31:25:ASN:OD1	2.17	0.45
32:B:9:LEU:HD21	32:B:12:GLY:HA2	1.98	0.45
34:D:100:VAL:HG21	34:D:136:VAL:HG21	1.98	0.45
38:H:120:LEU:HA	53:A:600:A:H5'	1.99	0.45
41:K:91:GLY:O	41:K:93:GLU:N	2.48	0.45
43:M:21:ILE:HB	43:M:24:VAL:HG12	1.98	0.45
46:P:71:VAL:HA	46:P:74:LEU:HD12	1.99	0.45
51:U:57:LYS:HE2	51:U:57:LYS:HA	1.98	0.45
53:A:1033:G:H2'	53:A:1034:G:C4'	2.46	0.45
53:A:1059:C:H2'	53:A:1060:U:C6	2.51	0.45
54:01:279:A:H2'	54:01:280:U:H5'	1.97	0.45
54:01:553:G:H2'	54:01:554:U:O4'	2.17	0.45
54:01:813:U:H2'	54:01:814:C:C6	2.52	0.45
54:01:826:U:H2'	54:01:828:U:O4'	2.17	0.45
54:01:861:A:H2'	54:01:862:G:O4'	2.16	0.45
54:01:2123:G:H1'	54:01:2176:A:H2	1.82	0.45
1:04:165:ALA:HB3	1:04:172:THR:HB	1.98	0.45
3:06:57:LYS:NZ	54:01:796:C:H5''	2.31	0.45
3:06:130:LYS:HB2	3:06:133:LEU:HD12	1.99	0.45
6:09:11:ASN:HD22	6:09:12:LEU:HG	1.82	0.45
6:09:78:VAL:HG21	6:09:103:VAL:HA	1.97	0.45
12:15:1:MET:C	12:15:2:LEU:HD12	2.41	0.45
12:15:65:ILE:HG22	12:15:67:VAL:H	1.81	0.45
16:19:53:LYS:HE3	54:01:994:C:H3'	1.99	0.45
31:34:3:VAL:HG21	54:01:2539:C:H5'	1.97	0.45
33:C:6:PRO:HG2	33:C:200:TRP:HE1	1.81	0.45
41:K:63:GLN:HB2	41:K:94:SER:OG	2.17	0.45
43:M:7:ASN:HB2	43:M:21:ILE:HG12	1.99	0.45
53:A:531:U:H4'	53:A:532:A:C5'	2.45	0.45
53:A:580:C:H2'	53:A:581:G:O4'	2.17	0.45
53:A:981:U:H2'	53:A:982:U:C5	2.52	0.45
54:01:236:C:H2'	54:01:237:C:C6	2.51	0.45
54:01:278:A:H2'	54:01:278:A:N3	2.32	0.45
54:01:1153:C:H2'	54:01:1154:G:O4'	2.16	0.45
54:01:2128:G:H2'	54:01:2129:C:O4'	2.16	0.45
54:01:2339:C:H2'	54:01:2340:A:H8	1.82	0.45
54:01:2718:G:H21	54:01:2847:U:H5'	1.81	0.45
54:01:2743:U:H2'	54:01:2744:G:C5'	2.46	0.45
55:02:66:A:H4'	55:02:67:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:104:THR:HA	26:29:38:SER:HB3	1.99	0.45
5:08:136:ASP:OD2	5:08:138:GLN:HB3	2.17	0.45
8:11:77:VAL:HA	8:11:80:LYS:HE2	1.98	0.45
11:14:4:ASN:O	54:01:1243:C:H1'	2.17	0.45
13:16:61:ALA:O	13:16:65:LEU:HD13	2.17	0.45
32:B:93:HIS:HB2	32:B:145:ASN:O	2.16	0.45
36:F:18:VAL:HG11	36:F:58:HIS:CD2	2.52	0.45
44:N:56:PRO:HD2	53:A:1317:C:OP1	2.16	0.45
53:A:390:U:H2'	53:A:391:G:H8	1.82	0.45
53:A:828:U:H3	53:A:859:G:H1'	1.82	0.45
53:A:842:U:H5''	53:A:846:G:C6	2.51	0.45
53:A:1402:C:H2'	53:A:1403:C:O4'	2.17	0.45
53:A:1435:G:H2'	53:A:1436:U:C6	2.52	0.45
54:01:1089:A:H2	54:01:1090:A:H62	1.64	0.45
54:01:1130:U:N3	54:01:2025:C:H5''	2.32	0.45
54:01:1368:G:H2'	54:01:1369:G:C8	2.52	0.45
54:01:2041:U:H2'	54:01:2042:A:H8	1.82	0.45
54:01:2075:U:H1'	54:01:2597:G:H21	1.82	0.45
54:01:2197:U:O2'	54:01:2198:A:H5''	2.17	0.45
54:01:2302:U:H2'	54:01:2303:G:C8	2.52	0.45
54:01:2646:C:H2'	54:01:2647:U:O4'	2.16	0.45
1:04:33:LEU:HD11	1:04:60:ALA:CB	2.47	0.45
2:05:125:TRP:CG	2:05:160:LYS:HB3	2.51	0.45
4:07:109:ARG:HH22	43:M:2:ARG:CD	2.30	0.45
12:15:123:LYS:HE2	12:15:123:LYS:HA	1.98	0.45
16:19:55:GLN:O	16:19:58:GLN:HG2	2.17	0.45
18:21:11:ARG:HD3	18:21:11:ARG:N	2.32	0.45
19:22:50:LEU:HD23	24:27:26:PHE:CZ	2.52	0.45
31:34:17:VAL:CG1	31:34:19:ARG:HG3	2.47	0.45
32:B:141:GLU:HA	32:B:144:GLU:HB2	1.98	0.45
38:H:39:LEU:HB3	38:H:45:ILE:HD12	1.97	0.45
41:K:105:ARG:HB3	41:K:105:ARG:NH1	2.32	0.45
44:N:52:ARG:HE	53:A:1219:A:H5''	1.82	0.45
54:01:35:G:H2'	54:01:36:G:O4'	2.15	0.45
54:01:296:U:H2'	54:01:297:G:H8	1.81	0.45
54:01:802:A:H2'	54:01:803:U:O4'	2.17	0.45
54:01:1222:U:H2'	54:01:1223:G:C8	2.52	0.45
54:01:2328:A:H2'	54:01:2329:U:C6	2.52	0.45
54:01:2411:A:H2'	54:01:2412:A:C8	2.52	0.45
54:01:2556:C:H2'	54:01:2557:G:O4'	2.17	0.45
54:01:2781:A:H5''	54:01:2782:G:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:210:PHE:HB3	59:Z:294:LYS:HB2	1.99	0.45
3:06:71:GLY:H	54:01:674:G:H5''	1.82	0.45
4:07:38:GLY:HA2	4:07:85:GLY:HA2	1.98	0.45
9:12:28:LEU:HG	9:12:32:LEU:HD11	1.98	0.45
21:24:30:ILE:HG13	21:24:40:ILE:HG13	1.98	0.45
29:32:8:SER:HA	54:01:1309:G:H5''	1.98	0.45
34:D:144:ILE:HD13	34:D:177:MET:HB3	1.98	0.45
39:I:27:ILE:N	39:I:27:ILE:HD12	2.32	0.45
44:N:32:ASP:CG	44:N:33:VAL:H	2.25	0.45
45:O:34:GLN:HB3	45:O:58:MET:HE1	1.99	0.45
52:03:29:LEU:O	52:03:33:LEU:HG	2.16	0.45
53:A:1148:U:H2'	53:A:1149:C:O4'	2.17	0.45
53:A:1163:A:H2'	53:A:1164:G:H8	1.82	0.45
53:A:1182:G:H5'	53:A:1183:U:OP1	2.16	0.45
53:A:1228:C:H2'	53:A:1229:A:H8	1.82	0.45
53:A:1464:U:H2'	53:A:1465:A:C8	2.52	0.45
54:01:376:G:H2'	54:01:377:G:H8	1.82	0.45
54:01:1097:U:H2'	54:01:1098:A:O4'	2.17	0.45
54:01:1111:A:C2	54:01:1112:G:H1'	2.52	0.45
54:01:2356:U:H2'	54:01:2357:G:C8	2.52	0.45
54:01:2788:C:H2'	54:01:2789:C:C6	2.52	0.45
59:Z:44:ARG:HG3	59:Z:67:VAL:HB	1.98	0.45
59:Z:342:GLU:HG3	59:Z:361:THR:OG1	2.17	0.45
6:09:124:THR:HG22	6:09:125:THR:N	2.31	0.44
17:20:83:TYR:CZ	54:01:1187:G:H5''	2.52	0.44
24:27:24:GLU:HA	24:27:28:LEU:HG	1.98	0.44
24:27:25:GLN:HE21	24:27:50:VAL:HG21	1.82	0.44
29:32:26:ASN:CG	54:01:682:G:H5'	2.42	0.44
30:33:32:LEU:HD23	30:33:35:LYS:HD2	1.98	0.44
37:G:11:ILE:HD13	37:G:24:LYS:HD3	1.99	0.44
43:M:33:LEU:HD22	43:M:40:GLU:HA	1.99	0.44
44:N:49:THR:OG1	49:S:12:LEU:HD11	2.17	0.44
45:O:32:THR:HG22	45:O:36:ASN:ND2	2.33	0.44
51:U:9:GLU:HB2	51:U:10:PRO:HD3	1.98	0.44
53:A:1144:G:H21	53:A:1146:A:H62	1.65	0.44
54:01:198:C:H4'	54:01:2243:U:H4'	1.98	0.44
54:01:1434:A:H2'	54:01:1435:G:C8	2.52	0.44
54:01:2156:G:H2'	54:01:2157:G:H5'	1.98	0.44
54:01:2443:C:H2'	54:01:2444:G:H8	1.81	0.44
54:01:2480:C:H2'	54:01:2481:G:O4'	2.16	0.44
54:01:2626:C:H2'	54:01:2627:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2795:C:H2'	54:01:2796:U:O4'	2.17	0.44
59:Z:212:LEU:HD23	59:Z:212:LEU:O	2.17	0.44
59:Z:248:LYS:HG3	59:Z:290:GLN:HE22	1.81	0.44
2:05:9:VAL:O	2:05:26:VAL:HB	2.17	0.44
2:05:13:ARG:HH11	15:18:55:HIS:HA	1.82	0.44
6:09:9:VAL:C	6:09:11:ASN:H	2.25	0.44
17:20:65:ALA:O	17:20:94:THR:HG23	2.17	0.44
19:22:38:ALA:HA	19:22:42:GLU:OE1	2.17	0.44
20:23:16:LYS:HB2	54:01:329:G:H1	1.82	0.44
22:25:62:LYS:HE3	22:25:81:GLU:HG3	1.99	0.44
33:C:161:ILE:HD12	33:C:161:ILE:O	2.17	0.44
38:H:9:MET:O	38:H:13:ILE:HG13	2.18	0.44
41:K:121:ARG:HG3	51:U:35:GLU:OE1	2.16	0.44
42:L:64:SER:HB3	42:L:94:TYR:HB2	1.99	0.44
47:Q:4:ILE:HD12	47:Q:4:ILE:O	2.18	0.44
47:Q:29:LYS:HB2	47:Q:36:PHE:CD1	2.52	0.44
53:A:358:U:H2'	53:A:359:G:H8	1.82	0.44
53:A:410:G:H2'	53:A:429:U:C4	2.52	0.44
54:01:523:C:H4'	54:01:540:C:O2	2.18	0.44
54:01:543:G:H5'	54:01:543:G:H8	1.82	0.44
54:01:2881:U:H2'	54:01:2882:A:H8	1.82	0.44
59:Z:231:VAL:O	59:Z:271:GLY:N	2.51	0.44
59:Z:321:PRO:HD3	59:Z:351:MET:SD	2.57	0.44
1:04:47:ARG:NH2	54:01:774:G:H5''	2.31	0.44
6:09:3:VAL:HG13	6:09:37:VAL:C	2.43	0.44
10:13:6:THR:HG23	54:01:1666:G:O3'	2.17	0.44
12:15:82:MET:HE2	54:01:962:G:H21	1.81	0.44
14:17:27:VAL:HG13	14:17:95:SER:OG	2.18	0.44
32:B:162:VAL:HG12	32:B:164:ASP:H	1.82	0.44
36:F:38:ARG:HB2	36:F:63:ASN:HB3	1.98	0.44
49:S:35:ARG:HD2	49:S:51:HIS:O	2.18	0.44
54:01:832:U:H2'	54:01:833:A:C8	2.52	0.44
54:01:1239:G:H2'	54:01:1240:U:O4'	2.17	0.44
54:01:1827:U:H2'	54:01:1828:G:O4'	2.17	0.44
54:01:2214:C:H2'	54:01:2215:C:O4'	2.18	0.44
54:01:2393:U:H2'	54:01:2394:C:O4'	2.18	0.44
54:01:2705:A:H2'	54:01:2706:A:O4'	2.18	0.44
54:01:2881:U:H2'	54:01:2882:A:C8	2.53	0.44
58:Y:74:C:N3	59:Z:219:SER:HB2	2.32	0.44
59:Z:166:ASP:HB3	59:Z:198:TYR:CE1	2.53	0.44
5:08:81:GLY:HA2	5:08:135:ALA:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:5:LYS:O	15:18:9:GLN:HG2	2.18	0.44
16:19:6:GLY:HA3	54:01:29:U:H5''	1.99	0.44
17:20:2:TYR:O	17:20:42:ALA:HB3	2.18	0.44
23:26:7:THR:OG1	23:26:9:LYS:HG3	2.18	0.44
34:D:20:LEU:HD21	34:D:62:ARG:O	2.17	0.44
45:O:7:THR:O	45:O:11:VAL:HG23	2.18	0.44
46:P:22:ALA:HA	46:P:33:ILE:CD1	2.46	0.44
53:A:1054:C:H5'	53:A:1196:A:N3	2.32	0.44
53:A:1201:A:H1'	53:A:1202:U:OP2	2.17	0.44
54:01:704:G:H1'	54:01:727:A:N6	2.33	0.44
54:01:779:U:H2'	54:01:780:G:C8	2.52	0.44
54:01:1052:C:H2'	54:01:1053:C:C6	2.53	0.44
1:04:41:GLY:HA3	1:04:53:ILE:HD11	1.98	0.44
4:07:102:LEU:O	4:07:106:ALA:HB3	2.17	0.44
5:08:17:LYS:HB2	5:08:24:THR:HB	2.00	0.44
5:08:79:THR:HG22	5:08:80:GLU:OE2	2.17	0.44
10:13:31:ARG:HH22	54:01:2676:C:P	2.41	0.44
14:17:26:LEU:HB3	14:17:92:PHE:HA	1.98	0.44
15:18:5:LYS:HA	15:18:8:GLU:HB2	1.99	0.44
32:B:182:VAL:O	32:B:195:VAL:HG13	2.18	0.44
34:D:77:GLU:O	34:D:81:LEU:HG	2.17	0.44
37:G:22:LEU:O	37:G:26:VAL:HG23	2.17	0.44
39:I:51:LEU:HD13	39:I:56:MET:HE2	2.00	0.44
40:J:57:VAL:HG22	40:J:58:ASN:N	2.32	0.44
43:M:99:GLN:H	43:M:99:GLN:HE21	1.65	0.44
43:M:113:LYS:N	43:M:114:PRO:HD2	2.32	0.44
46:P:78:VAL:O	46:P:79:ASN:O	2.36	0.44
48:R:40:PRO:HB3	53:A:720:C:H5''	2.00	0.44
50:T:48:LYS:HB2	50:T:48:LYS:NZ	2.32	0.44
53:A:31:G:H5'	53:A:306:A:C2	2.53	0.44
54:01:367:G:H2'	54:01:368:A:O4'	2.17	0.44
54:01:575:A:O2'	54:01:576:U:H5'	2.18	0.44
54:01:740:C:H5''	54:01:1784:A:OP1	2.17	0.44
54:01:2220:U:H2'	54:01:2221:G:H8	1.82	0.44
55:02:22:U:H2'	55:02:23:G:C8	2.51	0.44
59:Z:176:LYS:HB3	59:Z:181:ASP:CB	2.47	0.44
3:06:34:ALA:HA	3:06:94:GLN:NE2	2.33	0.44
9:12:11:VAL:HG11	9:12:49:ASP:O	2.18	0.44
11:14:109:LYS:HA	11:14:126:ARG:O	2.16	0.44
12:15:8:LYS:HD2	54:01:869:G:H1'	1.99	0.44
12:15:75:GLU:HB2	12:15:90:GLU:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:18:23:ASP:HA	15:18:89:GLY:H	1.81	0.44
20:23:31:GLY:O	20:23:66:VAL:HG23	2.17	0.44
21:24:44:HIS:NE2	21:24:85:LYS:HB2	2.32	0.44
31:34:17:VAL:HG12	31:34:19:ARG:HG3	1.98	0.44
43:M:106:ARG:HD3	43:M:110:GLY:O	2.18	0.44
47:Q:13:SER:O	47:Q:20:ILE:HG13	2.17	0.44
53:A:714:G:H5'	53:A:776:G:H5'	1.98	0.44
53:A:1075:U:H2'	53:A:1076:U:C6	2.52	0.44
54:01:9:G:H1'	54:01:2895:G:N2	2.32	0.44
54:01:1056:G:H4'	54:01:1086:A:H8	1.83	0.44
54:01:1536:C:H4'	54:01:1537:G:C2	2.52	0.44
54:01:2031:A:H3'	54:01:2031:A:OP2	2.17	0.44
54:01:2380:C:H2'	54:01:2381:A:C8	2.52	0.44
54:01:2476:A:H2'	54:01:2477:U:O4'	2.17	0.44
55:02:118:C:H2'	55:02:119:A:C8	2.53	0.44
58:Y:37:A:H2'	58:Y:38:A:O4'	2.17	0.44
59:Z:260:MET:HE2	59:Z:272:GLU:OE2	2.17	0.44
1:04:132:ARG:HG3	1:04:133:ASN:ND2	2.33	0.44
2:05:133:THR:CG2	54:01:1993:U:H4'	2.44	0.44
2:05:183:GLU:CD	2:05:183:GLU:H	2.25	0.44
3:06:6:LYS:HG3	3:06:7:ASP:N	2.33	0.44
8:11:27:LEU:HD13	8:11:58:ILE:HG21	1.99	0.44
11:14:78:ARG:NH1	11:14:113:ALA:HB1	2.33	0.44
20:23:73:ASN:ND2	20:23:76:THR:H	2.16	0.44
31:34:7:VAL:HB	31:34:25:VAL:CG2	2.47	0.44
31:34:12:ARG:HH21	31:34:12:ARG:HG3	1.83	0.44
38:H:31:LEU:HD13	53:A:643:C:H5''	1.99	0.44
39:I:105:ARG:HG2	53:A:1117:A:O2'	2.17	0.44
40:J:49:PHE:HB2	40:J:65:TYR:O	2.18	0.44
42:L:8:ARG:HH22	53:A:880:C:H5''	1.83	0.44
42:L:109:ARG:HB2	42:L:118:VAL:HG11	1.99	0.44
44:N:62:ARG:NH1	44:N:69:PRO:HD3	2.31	0.44
49:S:13:HIS:O	49:S:17:LYS:HE2	2.17	0.44
49:S:33:TRP:HA	49:S:51:HIS:HB3	2.00	0.44
52:03:67:HIS:CD2	52:03:184:LYS:HB3	2.53	0.44
54:01:1373:A:H4'	54:01:2212:A:H1'	1.99	0.44
54:01:2195:U:H2'	54:01:2196:C:C6	2.53	0.44
54:01:2704:C:H2'	54:01:2705:A:O4'	2.18	0.44
2:05:108:ASP:OD2	2:05:206:ALA:HA	2.18	0.44
5:08:136:ASP:OD2	5:08:139:VAL:HG23	2.17	0.44
7:10:14:GLU:O	7:10:18:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:11:130:GLY:HA2	8:11:133:ARG:HH11	1.82	0.44
11:14:3:LEU:HD23	54:01:1203:U:H5'	1.99	0.44
21:24:21:ARG:HE	21:24:87:GLN:HA	1.82	0.44
32:B:37:VAL:HG22	32:B:38:HIS:N	2.33	0.44
39:I:80:HIS:NE2	39:I:105:ARG:HA	2.33	0.44
40:J:70:HIS:HB3	40:J:72:ARG:HH12	1.82	0.44
41:K:67:GLU:HA	41:K:70:ALA:HB2	2.00	0.44
47:Q:5:ARG:HB2	47:Q:5:ARG:CZ	2.47	0.44
53:A:113:G:H1'	53:A:354:G:H5''	1.99	0.44
53:A:295:C:H2'	53:A:296:U:O4'	2.18	0.44
53:A:695:A:H2'	53:A:696:A:C8	2.52	0.44
53:A:1285:A:H4'	53:A:1286:U:H5''	2.00	0.44
54:01:56:A:H2'	54:01:57:C:O4'	2.18	0.44
54:01:96:C:H2'	54:01:97:C:C6	2.53	0.44
54:01:992:C:H2'	54:01:993:G:C8	2.52	0.44
54:01:2329:U:H2'	54:01:2330:G:H8	1.81	0.44
54:01:2514:U:H2'	54:01:2515:C:C6	2.53	0.44
54:01:2848:G:O2'	54:01:2849:U:H5'	2.17	0.44
56:X:18:G:H1	56:X:55:U:H6	1.66	0.44
58:Y:52:G:H2'	58:Y:53:G:H8	1.82	0.44
1:04:179:GLU:HG3	1:04:268:ARG:O	2.18	0.44
1:04:224:MET:SD	1:04:229:HIS:HB2	2.58	0.44
3:06:117:ARG:HH12	11:14:2:ARG:HG2	1.80	0.44
11:14:23:ILE:HG13	17:20:82:HIS:CE1	2.52	0.44
14:17:36:TYR:HA	14:17:52:SER:HB3	2.00	0.44
15:18:102:ARG:NH2	54:01:1755:A:H5'	2.32	0.44
15:18:102:ARG:C	15:18:107:ALA:HB2	2.43	0.44
16:19:56:PHE:CZ	54:01:536:G:H4'	2.52	0.44
16:19:75:TYR:CE2	54:01:1153:C:H5'	2.52	0.44
19:22:33:LYS:NZ	19:22:33:LYS:HB3	2.32	0.44
20:23:35:VAL:HB	20:23:38:ILE:HG13	1.99	0.44
23:26:22:ASN:HA	54:01:200:U:OP1	2.16	0.44
29:32:16:HIS:HA	29:32:21:ARG:NH2	2.28	0.44
32:B:25:LYS:HB3	32:B:192:PRO:HD2	2.00	0.44
33:C:110:LEU:CD2	33:C:145:ALA:HB2	2.46	0.44
34:D:56:GLU:HG2	34:D:198:LEU:HB2	2.00	0.44
35:E:80:LEU:HD13	35:E:122:VAL:CG1	2.46	0.44
37:G:24:LYS:HA	37:G:27:ASN:ND2	2.27	0.44
38:H:83:ARG:NH2	53:A:644:U:H4'	2.33	0.44
44:N:68:ARG:HD3	44:N:79:SER:OG	2.17	0.44
46:P:76:LYS:HZ1	53:A:473:U:H5''	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S:52:ASN:CG	49:S:53:GLY:H	2.26	0.44
53:A:575:G:O2'	53:A:821:G:H5'	2.17	0.44
53:A:825:A:H2'	53:A:826:C:C6	2.52	0.44
53:A:1437:A:H2'	53:A:1438:G:H8	1.83	0.44
54:01:2441:U:H2'	54:01:2442:C:C6	2.53	0.44
58:Y:2:G:H2'	58:Y:3:G:C8	2.53	0.44
7:10:51:TYR:O	7:10:53:ARG:HG2	2.18	0.43
8:11:130:GLY:HA2	8:11:133:ARG:NH1	2.33	0.43
9:12:59:ALA:HB3	9:12:126:ALA:HA	1.99	0.43
13:16:43:GLU:OE2	13:16:46:ARG:HD3	2.18	0.43
13:16:53:THR:HG21	54:01:2840:C:H5''	2.00	0.43
13:16:90:ARG:HB2	13:16:90:ARG:NH1	2.33	0.43
14:17:38:GLN:OE1	14:17:47:VAL:HG11	2.18	0.43
35:E:110:MET:HA	35:E:139:THR:HG21	2.00	0.43
35:E:148:SER:HB2	35:E:149:PRO:HD2	2.00	0.43
40:J:22:THR:HA	40:J:25:ILE:HG22	2.00	0.43
45:O:34:GLN:CG	45:O:58:MET:HE1	2.48	0.43
46:P:26:ASN:ND2	46:P:31:ARG:HB3	2.33	0.43
47:Q:11:VAL:CG1	47:Q:20:ILE:HD11	2.47	0.43
48:R:33:THR:CG2	48:R:37:LYS:HB2	2.48	0.43
49:S:5:LYS:C	49:S:6:LYS:HD2	2.43	0.43
53:A:1102:A:H2'	53:A:1103:C:C6	2.53	0.43
53:A:1441:A:H2'	53:A:1442:G:H5'	2.00	0.43
54:01:722:A:H2'	54:01:723:C:O4'	2.18	0.43
54:01:2159:G:H2'	54:01:2160:C:O4'	2.18	0.43
54:01:2801:G:H2'	54:01:2802:G:C8	2.53	0.43
1:04:131:MET:HE3	1:04:187:CYS:HB2	2.00	0.43
4:07:116:LEU:HD23	4:07:127:TYR:OH	2.18	0.43
6:09:11:ASN:CG	6:09:12:LEU:H	2.26	0.43
11:14:77:ILE:N	11:14:77:ILE:HD12	2.33	0.43
17:20:77:PHE:HD1	17:20:84:ARG:HB3	1.84	0.43
18:21:19:LEU:HD11	27:30:20:ALA:HA	1.99	0.43
21:24:51:GLN:HE22	21:24:86:LEU:HD21	1.82	0.43
30:33:44:ARG:N	30:33:45:PRO:HD2	2.33	0.43
33:C:70:ALA:HB2	33:C:114:LEU:CD1	2.48	0.43
34:D:86:GLY:H	35:E:102:THR:HG21	1.83	0.43
34:D:142:VAL:O	34:D:179:GLY:N	2.51	0.43
34:D:151:GLN:C	34:D:153:ARG:H	2.26	0.43
35:E:137:ARG:O	35:E:140:ILE:HG22	2.18	0.43
40:J:12:ALA:HB2	40:J:96:VAL:HA	2.00	0.43
44:N:41:TRP:HZ3	49:S:8:PRO:HD2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:147:G:H2'	53:A:148:G:C8	2.53	0.43
53:A:149:A:H1'	53:A:1446:A:C2	2.53	0.43
53:A:532:A:H3'	53:A:533:A:H5'	2.01	0.43
54:01:457:A:N6	54:01:470:A:H5''	2.31	0.43
54:01:726:G:H2'	54:01:1432:G:O2'	2.18	0.43
54:01:940:G:H3'	54:01:941:A:H5''	2.00	0.43
54:01:970:U:H2'	54:01:971:G:H8	1.82	0.43
54:01:2412:A:H2'	54:01:2413:G:O4'	2.18	0.43
54:01:2429:G:H5''	54:01:2430:A:OP2	2.18	0.43
59:Z:138:ASP:O	59:Z:139:MET:HE2	2.18	0.43
59:Z:237:LYS:HD3	59:Z:240:GLU:HB2	2.00	0.43
1:04:7:PRO:O	54:01:1695:G:H1'	2.19	0.43
1:04:126:GLY:C	1:04:127:ASN:HD22	2.26	0.43
1:04:159:THR:HG22	1:04:160:TYR:N	2.32	0.43
9:12:27:ARG:HG2	9:12:27:ARG:HH11	1.83	0.43
10:13:76:VAL:HG12	15:18:72:VAL:CG2	2.48	0.43
13:16:39:PRO:HG2	54:01:1651:G:H4'	1.99	0.43
14:17:70:ALA:O	14:17:74:VAL:HG23	2.19	0.43
15:18:3:ILE:N	15:18:3:ILE:HD12	2.34	0.43
24:27:7:ARG:C	24:27:8:GLU:HG3	2.43	0.43
39:I:41:GLU:OE2	53:A:1291:U:H4'	2.18	0.43
39:I:78:ILE:O	39:I:82:ILE:HG13	2.19	0.43
41:K:19:VAL:HG13	41:K:82:GLU:HB2	2.01	0.43
47:Q:40:THR:HG22	47:Q:41:THR:N	2.33	0.43
49:S:5:LYS:HA	53:A:1313:U:OP2	2.18	0.43
52:03:60:ARG:HD3	52:03:164:ARG:HB2	1.99	0.43
53:A:106:C:H2'	53:A:107:G:H8	1.83	0.43
53:A:665:A:O4'	53:A:733:G:H1'	2.18	0.43
54:01:11:C:H2'	54:01:12:U:H5''	2.00	0.43
54:01:792:A:H2'	54:01:2440:C:O2	2.18	0.43
54:01:1111:A:C2'	54:01:1112:G:H4'	2.48	0.43
54:01:2170:A:H2'	54:01:2171:A:O4'	2.17	0.43
54:01:2215:C:H2'	54:01:2216:G:H8	1.83	0.43
54:01:2636:C:H2'	54:01:2637:U:C6	2.53	0.43
55:02:56:G:H4'	55:02:57:A:H8	1.84	0.43
1:04:135:PRO:HG2	36:F:80:PHE:HD1	1.83	0.43
4:07:1:ALA:HB3	4:07:4:HIS:HB2	1.99	0.43
8:11:12:VAL:O	8:11:13:ALA:C	2.61	0.43
8:11:121:ILE:HA	8:11:124:MET:HE3	2.00	0.43
9:12:84:ILE:HG23	9:12:84:ILE:O	2.18	0.43
10:13:108:ARG:HG2	10:13:113:MET:HE1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:4:PRO:HB2	12:15:7:THR:CG2	2.48	0.43
14:17:6:ALA:O	14:17:9:ARG:HG3	2.18	0.43
16:19:51:GLN:HA	16:19:54:ARG:HG2	2.00	0.43
19:22:57:VAL:HG22	19:22:58:VAL:N	2.32	0.43
20:23:4:ILE:HD12	20:23:4:ILE:N	2.33	0.43
25:28:5:LYS:NZ	25:28:34:THR:HG21	2.33	0.43
27:30:10:SER:HA	54:01:16:C:O3'	2.18	0.43
32:B:68:PHE:CD2	32:B:83:ALA:HB2	2.54	0.43
34:D:195:ASN:CG	34:D:197:HIS:HB3	2.44	0.43
35:E:13:LYS:HZ1	35:E:112:ALA:HB1	1.82	0.43
37:G:85:GLN:CD	56:X:32:C:H4'	2.44	0.43
37:G:113:LYS:HB2	37:G:117:LEU:HD23	2.00	0.43
38:H:11:THR:HA	38:H:14:ARG:HH12	1.83	0.43
43:M:15:VAL:O	43:M:19:THR:HG23	2.18	0.43
46:P:36:VAL:HG13	46:P:36:VAL:O	2.18	0.43
53:A:392:C:H2'	53:A:393:A:H8	1.83	0.43
54:01:532:A:H2'	54:01:532:A:N3	2.34	0.43
54:01:1655:A:H2'	54:01:1656:C:O4'	2.19	0.43
54:01:2131:U:OP1	54:01:2134:A:H5'	2.19	0.43
55:02:12:C:H1'	55:02:15:A:C2	2.52	0.43
1:04:33:LEU:HD11	1:04:60:ALA:HB1	2.00	0.43
4:07:110:ILE:O	4:07:113:PHE:HB2	2.19	0.43
6:09:3:VAL:HG22	6:09:38:PRO:HA	2.01	0.43
8:11:78:LEU:HD21	8:11:108:ILE:HD13	1.99	0.43
9:12:69:ARG:HA	9:12:89:PHE:CD2	2.53	0.43
15:18:90:ALA:HB2	15:18:112:ARG:HA	1.99	0.43
30:33:40:LYS:HA	30:33:43:LEU:HB2	1.99	0.43
34:D:8:LEU:O	34:D:11:SER:HB3	2.18	0.43
37:G:78:ARG:HH21	37:G:81:GLY:H	1.65	0.43
40:J:64:GLN:HB3	44:N:98:ALA:HB3	2.01	0.43
42:L:101:LEU:H	42:L:101:LEU:CD1	2.27	0.43
43:M:11:HIS:HB3	43:M:43:LYS:HD2	2.00	0.43
46:P:69:ASP:HA	46:P:72:ALA:HB3	1.99	0.43
47:Q:60:ILE:HG22	47:Q:72:TRP:HB3	2.01	0.43
48:R:11:ARG:HB2	48:R:47:ARG:HH22	1.83	0.43
51:U:66:ARG:CD	53:A:1099:G:H4'	2.47	0.43
53:A:860:A:H2'	53:A:861:G:O4'	2.18	0.43
53:A:1492:A:H2'	54:01:1913:A:C2	2.53	0.43
54:01:479:A:H4'	54:01:480:A:H5'	2.00	0.43
54:01:2192:U:H2'	54:01:2193:G:C8	2.53	0.43
54:01:2538:C:H2'	54:01:2539:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2809:A:H2'	54:01:2810:A:C8	2.53	0.43
1:04:161:VAL:HG11	1:04:173:LEU:HD13	2.01	0.43
4:07:124:ARG:NH2	54:01:2316:G:H4'	2.33	0.43
4:07:124:ARG:HD3	4:07:160:LYS:O	2.19	0.43
8:11:10:LEU:HB3	8:11:11:GLN:H	1.33	0.43
12:15:75:GLU:OE2	54:01:957:C:H5'	2.19	0.43
31:34:36:ARG:O	31:34:37:GLN:CB	2.64	0.43
33:C:4:VAL:HB	53:A:1190:G:OP2	2.18	0.43
35:E:54:GLU:HB3	35:E:57:ALA:HB3	2.00	0.43
35:E:101:GLY:H	35:E:121:ASN:HB2	1.83	0.43
39:I:43:ALA:HB1	39:I:46:VAL:HG11	2.01	0.43
41:K:73:VAL:HG21	41:K:104:PHE:CZ	2.53	0.43
44:N:18:LYS:HE3	44:N:19:TYR:CE2	2.53	0.43
50:T:11:ILE:O	50:T:14:GLU:HB2	2.18	0.43
51:U:39:LYS:N	51:U:40:PRO:CD	2.82	0.43
52:03:29:LEU:HA	52:03:32:GLU:OE1	2.18	0.43
53:A:103:U:H5'	53:A:151:A:H1'	2.01	0.43
53:A:961:U:H2'	53:A:962:C:O4'	2.18	0.43
54:01:2131:U:O5'	54:01:2133:G:H4'	2.18	0.43
54:01:2478:A:C2	54:01:2529:G:H2'	2.54	0.43
54:01:2580:U:H2'	54:01:2581:G:H5'	1.99	0.43
54:01:2861:U:H2'	54:01:2862:G:C8	2.53	0.43
59:Z:14:VAL:HG21	59:Z:76:TYR:HB3	2.01	0.43
1:04:204:LEU:HD21	1:04:213:ARG:HH21	1.84	0.43
2:05:23:PRO:HB3	54:01:2682:A:C2	2.53	0.43
2:05:33:ARG:CG	2:05:51:THR:HG23	2.48	0.43
2:05:110:THR:CG2	2:05:169:ARG:HE	2.32	0.43
5:08:138:GLN:NE2	54:01:2746:U:H1'	2.33	0.43
6:09:5:LEU:HD22	6:09:13:GLY:CA	2.49	0.43
14:17:52:SER:OG	14:17:54:VAL:HG12	2.19	0.43
15:18:50:ARG:HB3	15:18:57:ALA:HB3	2.00	0.43
32:B:22:TRP:CD1	32:B:22:TRP:H	2.35	0.43
32:B:143:LEU:O	32:B:147:LEU:HB2	2.19	0.43
33:C:6:PRO:HD2	33:C:183:TYR:CE2	2.54	0.43
33:C:58:ARG:HG3	33:C:62:SER:O	2.19	0.43
34:D:169:TRP:CD1	34:D:185:PRO:HG3	2.53	0.43
39:I:6:TYR:OH	53:A:1148:U:H5'	2.18	0.43
39:I:11:ARG:HG2	39:I:76:GLY:HA3	2.01	0.43
39:I:67:LYS:HA	39:I:74:GLN:HE21	1.84	0.43
43:M:89:ARG:NH2	43:M:94:LEU:HB3	2.34	0.43
45:O:77:TYR:O	45:O:81:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:R:31:TYR:CB	48:R:54:LEU:HD21	2.49	0.43
54:01:839:U:H2'	54:01:840:C:C6	2.54	0.43
54:01:1427:A:H4'	54:01:1428:C:O5'	2.18	0.43
54:01:2108:A:H2'	54:01:2109:U:H5'	1.99	0.43
54:01:2247:A:H2'	54:01:2248:C:C6	2.53	0.43
55:02:113:C:H2'	55:02:114:C:C6	2.53	0.43
58:Y:71:C:H2'	58:Y:72:C:H5'	2.01	0.43
59:Z:19:HIS:CD2	59:Z:114:GLN:HB2	2.53	0.43
2:05:159:LYS:O	2:05:161:MET:HG3	2.19	0.43
4:07:116:LEU:HD12	4:07:116:LEU:N	2.34	0.43
17:20:74:ILE:HG12	54:01:992:C:H4'	2.01	0.43
20:23:4:ILE:HG23	20:23:8:ASP:OD2	2.18	0.43
27:30:10:SER:O	27:30:14:MET:HG3	2.19	0.43
33:C:83:VAL:HA	33:C:86:LEU:HD12	2.01	0.43
34:D:176:LYS:HE2	34:D:178:GLU:HB2	2.00	0.43
41:K:86:LYS:HG3	41:K:114:PRO:HD3	2.00	0.43
43:M:23:GLY:HA2	43:M:68:LEU:HD22	2.00	0.43
43:M:88:LEU:HD12	43:M:91:ARG:HE	1.83	0.43
49:S:33:TRP:O	53:A:1220:G:H4'	2.19	0.43
50:T:53:MET:HA	50:T:56:ILE:HG22	1.99	0.43
53:A:832:G:H2'	53:A:833:G:O4'	2.19	0.43
54:01:358:U:H2'	54:01:359:G:C8	2.54	0.43
54:01:856:G:H2'	54:01:857:G:C8	2.54	0.43
54:01:1386:C:H1'	54:01:1470:A:H1'	2.01	0.43
54:01:1451:C:H4'	54:01:1452:G:C8	2.54	0.43
54:01:1474:U:C2'	54:01:1475:G:H5'	2.49	0.43
54:01:1639:C:O2'	54:01:1640:A:H5'	2.18	0.43
54:01:2652:C:H2'	54:01:2653:U:O4'	2.19	0.43
2:05:13:ARG:NH2	54:01:2683:C:H4'	2.33	0.43
4:07:24:VAL:HG13	4:07:25:MET:HE2	2.00	0.43
4:07:137:PHE:HB2	4:07:140:ILE:HD13	2.01	0.43
5:08:51:PHE:CZ	5:08:68:ARG:HA	2.54	0.43
5:08:167:VAL:O	5:08:167:VAL:HG13	2.19	0.43
7:10:81:LEU:HD12	54:01:1107:G:H1'	2.00	0.43
8:11:79:LEU:HA	8:11:82:ALA:HB3	2.01	0.43
12:15:13:HIS:HB3	54:01:954:G:OP1	2.19	0.43
15:18:19:PHE:HD2	15:18:23:ASP:HB2	1.84	0.43
16:19:89:ILE:HG13	17:20:49:ILE:HD11	2.01	0.43
18:21:13:SER:O	18:21:17:VAL:HG23	2.19	0.43
23:26:7:THR:HG21	23:26:9:LYS:NZ	2.34	0.43
25:28:8:GLN:HB2	25:28:28:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:31:24:LYS:NZ	28:31:50:GLU:HG3	2.33	0.43
30:33:45:PRO:C	30:33:46:LYS:HD2	2.44	0.43
33:C:54:ILE:HG22	33:C:67:ILE:HA	1.99	0.43
33:C:82:ASP:O	33:C:86:LEU:HG	2.18	0.43
34:D:101:VAL:HG13	34:D:106:PHE:HD2	1.83	0.43
35:E:107:GLY:HA3	53:A:9:G:C5'	2.38	0.43
35:E:131:ASN:HD22	35:E:132:PRO:CD	2.30	0.43
40:J:40:ILE:HG21	40:J:73:LEU:HD12	2.01	0.43
40:J:53:ILE:HG12	53:A:1060:U:H5''	2.00	0.43
42:L:76:HIS:O	42:L:77:SER:C	2.62	0.43
46:P:20:VAL:HG23	46:P:34:GLU:C	2.43	0.43
49:S:14:LEU:O	49:S:18:VAL:HG23	2.18	0.43
51:U:18:PHE:HA	51:U:21:SER:HB3	2.01	0.43
53:A:803:G:H2'	53:A:804:U:O4'	2.18	0.43
54:01:575:A:H5'	54:01:2500:U:H5'	2.01	0.43
54:01:1306:C:H41	54:01:1606:C:H2'	1.84	0.43
54:01:1689:A:H61	54:01:1697:G:H2'	1.83	0.43
54:01:1717:A:H2'	54:01:1718:G:O4'	2.19	0.43
54:01:2591:C:H2'	54:01:2592:G:C8	2.53	0.43
54:01:2732:G:H3'	54:01:2733:A:O4'	2.19	0.43
58:Y:38:A:H2'	58:Y:39:U:O4'	2.18	0.43
59:Z:342:GLU:OE1	59:Z:361:THR:HG23	2.19	0.43
2:05:51:THR:HG21	2:05:68:PHE:HE1	1.82	0.43
4:07:105:ILE:HG13	4:07:106:ALA:H	1.83	0.43
4:07:114:ARG:HH11	43:M:70:ARG:CZ	2.31	0.43
7:10:80:THR:HA	54:01:1108:U:H5'	2.01	0.43
8:11:127:SER:HA	54:01:1080:A:H1'	2.01	0.43
10:13:64:ARG:HE	15:18:67:GLU:CD	2.27	0.43
24:27:15:ASN:O	24:27:19:LEU:HG	2.18	0.43
27:30:8:THR:HG22	54:01:2020:A:H5'	2.01	0.43
27:30:30:ASP:HB3	27:30:34:GLY:N	2.27	0.43
32:B:23:ASN:H	32:B:189:ASN:HA	1.83	0.43
32:B:51:GLU:O	32:B:55:GLU:HG2	2.19	0.43
47:Q:17:GLU:OE2	53:A:255:G:H1'	2.18	0.43
53:A:12:U:H4'	53:A:526:C:H4'	2.00	0.43
53:A:56:U:H2'	53:A:57:G:C8	2.54	0.43
53:A:1401:G:H2'	53:A:1402:C:O4'	2.19	0.43
54:01:889:C:H2'	54:01:890:C:O4'	2.19	0.43
54:01:1306:C:N4	54:01:1606:C:H2'	2.34	0.43
54:01:1709:U:H2'	54:01:1710:G:C8	2.54	0.43
54:01:1830:C:H2'	54:01:1831:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1906:G:H2'	54:01:1907:G:O4'	2.19	0.43
54:01:2802:G:H2'	54:01:2803:G:C8	2.54	0.43
54:01:2811:G:H2'	54:01:2812:G:H8	1.83	0.43
55:02:34:A:N6	55:02:44:G:H2'	2.33	0.43
59:Z:19:HIS:CD2	59:Z:112:MET:HB2	2.53	0.43
1:04:241:LYS:O	54:01:1902:C:H4'	2.19	0.42
5:08:23:ILE:HD11	5:08:42:VAL:HG11	2.00	0.42
8:11:75:ALA:O	8:11:79:LEU:N	2.51	0.42
8:11:92:PRO:HA	8:11:136:GLY:CA	2.49	0.42
9:12:36:LEU:O	9:12:51:GLY:HA3	2.19	0.42
11:14:76:GLU:C	11:14:77:ILE:HD12	2.43	0.42
12:15:49:ALA:HB2	12:15:123:LYS:HB2	2.00	0.42
17:20:88:GLY:H	54:01:1225:G:H5'	1.84	0.42
34:D:176:LYS:O	34:D:177:MET:HB2	2.19	0.42
35:E:110:MET:O	35:E:114:LEU:HD13	2.19	0.42
38:H:64:TYR:HD1	38:H:69:ALA:HA	1.84	0.42
39:I:47:VAL:C	39:I:50:PRO:HD2	2.44	0.42
42:L:11:ARG:HG3	53:A:562:U:H1'	2.01	0.42
44:N:80:ARG:O	44:N:83:VAL:HG12	2.18	0.42
46:P:18:GLN:NE2	46:P:35:ARG:HE	2.17	0.42
53:A:404:G:H2'	53:A:405:U:C6	2.54	0.42
53:A:599:C:H2'	53:A:600:A:H8	1.83	0.42
53:A:643:C:H2'	53:A:644:U:H6	1.83	0.42
53:A:864:A:H2'	53:A:865:A:C8	2.54	0.42
53:A:1449:C:H2'	53:A:1450:U:O4'	2.19	0.42
54:01:164:C:H2'	54:01:165:A:O4'	2.19	0.42
54:01:741:U:H2'	54:01:742:A:H8	1.84	0.42
54:01:805:G:H5'	54:01:806:C:C5	2.54	0.42
54:01:1300:G:H4'	54:01:1301:A:C5'	2.49	0.42
54:01:2074:U:H2'	54:01:2075:U:C6	2.54	0.42
54:01:2124:G:H2'	54:01:2125:G:O4'	2.19	0.42
54:01:2187:U:H2'	54:01:2188:U:C6	2.55	0.42
54:01:2215:C:H2'	54:01:2216:G:C8	2.54	0.42
54:01:2327:A:H2'	54:01:2328:A:C8	2.53	0.42
58:Y:63:U:H2'	58:Y:64:G:H8	1.82	0.42
4:07:169:LEU:HA	4:07:172:PHE:HD2	1.84	0.42
6:09:12:LEU:HD13	6:09:19:VAL:HG21	2.02	0.42
12:15:4:PRO:HB2	12:15:7:THR:HG22	2.00	0.42
14:17:56:LYS:HG3	14:17:57:ALA:N	2.34	0.42
15:18:52:ARG:HB2	15:18:55:HIS:HB2	2.01	0.42
19:22:80:TRP:CD1	19:22:80:TRP:H	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:24:20:LEU:HD23	21:24:27:PRO:HD3	2.01	0.42
23:26:6:VAL:HG23	23:26:50:VAL:CG1	2.49	0.42
32:B:23:ASN:HD22	32:B:24:PRO:HD2	1.85	0.42
37:G:38:ALA:O	37:G:42:VAL:HG23	2.18	0.42
43:M:18:LEU:HB2	43:M:29:SER:OG	2.19	0.42
48:R:21:ASP:OD2	48:R:23:LYS:HG3	2.19	0.42
52:03:24:ASN:HD22	52:03:24:ASN:HA	1.60	0.42
52:03:166:ASP:HB3	54:01:2122:U:H4'	2.02	0.42
52:03:214:ILE:HG13	52:03:222:VAL:O	2.17	0.42
53:A:768:A:H2'	53:A:769:G:O4'	2.19	0.42
53:A:1124:G:H1'	53:A:1125:U:H5	1.84	0.42
53:A:1306:A:H2'	53:A:1307:U:O4'	2.18	0.42
54:01:176:A:O2'	54:01:177:G:H5'	2.19	0.42
54:01:302:C:H2'	54:01:303:G:H8	1.85	0.42
54:01:987:C:H2'	54:01:988:A:O4'	2.18	0.42
54:01:2048:G:C2'	54:01:2049:G:H5''	2.48	0.42
54:01:2287:A:O2'	54:01:2288:A:H2'	2.20	0.42
54:01:2331:G:H2'	54:01:2332:C:C6	2.54	0.42
58:Y:76:A:N3	59:Z:259:GLU:HB3	2.34	0.42
59:Z:89:LYS:HE2	59:Z:331:TYR:CE1	2.54	0.42
1:04:213:ARG:HH11	1:04:213:ARG:HG3	1.85	0.42
4:07:36:ASN:OD1	4:07:87:LYS:HB3	2.19	0.42
4:07:40:GLY:HA3	54:01:2307:G:O6	2.19	0.42
7:10:47:GLU:OE1	7:10:95:LEU:HD11	2.19	0.42
8:11:18:ASN:N	8:11:19:PRO:CD	2.83	0.42
8:11:127:SER:HB2	54:01:1080:A:H1'	2.02	0.42
15:18:42:PHE:CZ	15:18:62:LYS:HB3	2.54	0.42
16:19:30:VAL:HG12	16:19:33:VAL:H	1.83	0.42
23:26:29:LEU:HB2	54:01:2230:G:O3'	2.20	0.42
32:B:23:ASN:HD22	32:B:24:PRO:CD	2.32	0.42
35:E:64:GLU:O	35:E:68:ARG:HG2	2.20	0.42
37:G:14:ASP:N	37:G:19:SER:H	2.15	0.42
40:J:53:ILE:HG12	53:A:1060:U:C5'	2.49	0.42
47:Q:74:LEU:HD11	47:Q:77:VAL:HG22	2.01	0.42
53:A:460:A:H2'	53:A:461:A:C8	2.54	0.42
53:A:908:A:H2'	53:A:909:A:C8	2.55	0.42
53:A:1404:C:H2'	53:A:1405:G:C8	2.53	0.42
54:01:37:C:H4'	54:01:451:U:OP1	2.19	0.42
54:01:215:G:C4'	54:01:216:A:H4'	2.49	0.42
54:01:1183:U:O2'	54:01:1184:U:H5'	2.20	0.42
54:01:1454:C:H2'	54:01:1455:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1507:C:H2'	54:01:1508:A:C4'	2.49	0.42
54:01:2543:G:H21	54:01:2646:C:H5''	1.83	0.42
55:02:48:U:H2'	55:02:49:C:H6	1.84	0.42
55:02:82:U:H2'	55:02:83:G:C8	2.54	0.42
58:Y:73:A:H2'	58:Y:74:C:H4'	2.00	0.42
1:04:43:ASN:ND2	1:04:49:THR:HG22	2.33	0.42
6:09:122:LEU:HD22	6:09:128:HIS:CE1	2.54	0.42
11:14:93:ASN:C	11:14:95:LEU:H	2.28	0.42
17:20:74:ILE:N	17:20:74:ILE:HD12	2.35	0.42
32:B:75:ALA:HB1	32:B:163:ILE:CD1	2.49	0.42
32:B:105:THR:O	32:B:108:GLN:HG3	2.19	0.42
37:G:109:LYS:O	37:G:118:ARG:HD3	2.19	0.42
39:I:49:GLN:N	39:I:50:PRO:CD	2.82	0.42
42:L:20:VAL:HG21	53:A:553:A:OP1	2.19	0.42
50:T:20:ASN:HD22	50:T:20:ASN:HA	1.56	0.42
50:T:59:ARG:NH1	53:A:177:G:H5'	2.35	0.42
53:A:1280:A:O2'	53:A:1281:C:H5'	2.19	0.42
54:01:677:A:O2'	54:01:2071:A:H5'	2.20	0.42
54:01:729:G:H4'	54:01:763:G:C5'	2.47	0.42
54:01:1438:U:H2'	54:01:1439:A:C8	2.54	0.42
54:01:1494:A:C2	54:01:1579:A:H1'	2.54	0.42
59:Z:19:HIS:HB3	59:Z:22:HIS:ND1	2.35	0.42
59:Z:311:LEU:CD1	59:Z:382:THR:HB	2.49	0.42
4:07:102:LEU:O	4:07:107:VAL:HG23	2.20	0.42
4:07:169:LEU:HA	4:07:172:PHE:CD2	2.54	0.42
6:09:25:TYR:O	6:09:29:PHE:HB3	2.19	0.42
8:11:127:SER:OG	8:11:128:ILE:HD12	2.20	0.42
16:19:5:ARG:HD2	54:01:1251:C:OP2	2.19	0.42
30:33:23:HIS:HD2	30:33:49:VAL:HG22	1.85	0.42
32:B:104:LYS:O	32:B:108:GLN:HG2	2.20	0.42
34:D:89:LEU:O	34:D:93:LEU:HG	2.20	0.42
37:G:2:ARG:HB3	53:A:933:G:OP2	2.19	0.42
45:O:23:SER:O	45:O:27:GLN:HG3	2.19	0.42
52:03:68:GLY:HA2	52:03:159:GLY:HA2	2.01	0.42
53:A:222:C:H2'	53:A:223:A:C8	2.53	0.42
53:A:1237:C:OP1	53:A:1238:A:H1'	2.19	0.42
54:01:96:C:H2'	54:01:97:C:H6	1.84	0.42
54:01:615:U:H5''	54:01:616:A:OP2	2.19	0.42
54:01:740:C:H5'	54:01:1784:A:C2'	2.49	0.42
54:01:1376:C:H2'	54:01:1377:G:O4'	2.19	0.42
54:01:1981:A:H5''	54:01:1982:U:OP2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2108:A:C2'	54:01:2109:U:H5'	2.49	0.42
59:Z:32:THR:HB	59:Z:43:ALA:HA	2.01	0.42
59:Z:73:THR:HG22	59:Z:74:ARG:HG3	2.02	0.42
3:06:149:ILE:HG21	3:06:188:MET:HG2	2.01	0.42
5:08:95:ALA:HA	5:08:103:ASN:O	2.19	0.42
9:12:40:HIS:CE1	9:12:41:LYS:HG3	2.54	0.42
15:18:52:ARG:CB	15:18:55:HIS:HB2	2.49	0.42
21:24:14:LYS:HE3	55:02:98:G:H22	1.84	0.42
32:B:121:GLN:HG3	32:B:122:ASP:N	2.33	0.42
34:D:168:THR:C	34:D:170:LEU:H	2.28	0.42
35:E:39:GLY:HA2	35:E:45:VAL:HA	2.01	0.42
35:E:67:ARG:HG2	35:E:67:ARG:HH11	1.84	0.42
37:G:24:LYS:O	37:G:28:ILE:HG13	2.19	0.42
38:H:10:LEU:HD22	38:H:74:ILE:CD1	2.44	0.42
39:I:17:ARG:HB2	39:I:65:THR:OG1	2.20	0.42
39:I:79:ARG:HH12	39:I:102:PHE:HA	1.84	0.42
39:I:105:ARG:HH11	39:I:105:ARG:HG3	1.85	0.42
40:J:11:LYS:HB3	40:J:71:LEU:HG	2.01	0.42
41:K:124:LYS:HZ3	53:A:780:A:H5''	1.85	0.42
42:L:88:ASP:HB3	42:L:89:LEU:HD12	2.01	0.42
50:T:16:ALA:HB3	53:A:323:U:H4'	2.01	0.42
53:A:96:U:H2'	53:A:97:G:H8	1.85	0.42
53:A:427:U:H4'	53:A:541:G:H5''	2.00	0.42
53:A:750:C:H2'	53:A:751:U:C6	2.55	0.42
53:A:1308:U:H2'	53:A:1309:G:C8	2.52	0.42
54:01:1068:G:H2'	54:01:1069:A:C1'	2.50	0.42
54:01:1123:C:H2'	54:01:1124:G:C8	2.54	0.42
54:01:1130:U:C2	54:01:2025:C:H5''	2.53	0.42
54:01:1463:C:H2'	54:01:1464:G:C8	2.55	0.42
54:01:1581:G:H2'	54:01:1582:C:C6	2.55	0.42
54:01:1609:A:H1'	54:01:1616:A:C1'	2.50	0.42
54:01:2457:U:H3	54:01:2494:G:H1	1.67	0.42
54:01:2521:C:H2'	54:01:2522:U:C6	2.54	0.42
54:01:2808:G:H2'	54:01:2890:G:C6	2.54	0.42
58:Y:25:C:C2	58:Y:26:A:H1'	2.54	0.42
1:04:200:MET:HB2	54:01:1820:U:C1'	2.50	0.42
7:10:102:ALA:HA	7:10:105:LYS:HB3	2.02	0.42
13:16:63:ARG:NH2	54:01:1454:C:H5'	2.34	0.42
14:17:68:LYS:HE3	55:02:49:C:H4'	2.00	0.42
15:18:20:ARG:HB3	15:18:21:PRO:HD2	2.01	0.42
16:19:24:TYR:CE1	54:01:17:G:H4'	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:49:ARG:HH21	17:20:74:ILE:HG13	1.85	0.42
18:21:79:GLY:C	54:01:25:U:H4'	2.45	0.42
18:21:81:SER:O	18:21:83:LYS:HD3	2.19	0.42
19:22:2:ILE:HB	19:22:5:GLU:HB3	2.02	0.42
32:B:183:PHE:CB	32:B:197:PHE:HB2	2.48	0.42
35:E:74:ALA:O	35:E:146:MET:HE3	2.20	0.42
35:E:123:LEU:HD13	53:A:7:A:C8	2.55	0.42
39:I:56:MET:O	39:I:57:VAL:C	2.61	0.42
39:I:94:ARG:HE	39:I:103:VAL:HG11	1.84	0.42
40:J:48:ARG:HG2	44:N:100:TRP:CH2	2.51	0.42
48:R:13:THR:HB	48:R:20:ILE:HD11	2.01	0.42
49:S:18:VAL:HG11	49:S:43:MET:HG2	2.02	0.42
51:U:58:LYS:HA	51:U:61:ARG:HB3	2.01	0.42
53:A:25:C:H5'	53:A:524:G:H1'	2.01	0.42
53:A:211:G:H2'	53:A:212:G:H5'	2.02	0.42
53:A:526:C:H2'	53:A:527:G:H4'	2.02	0.42
53:A:857:C:H2'	53:A:858:G:O4'	2.19	0.42
53:A:926:G:H22	57:V:15:A:H2'	1.84	0.42
54:01:552:U:H2'	54:01:553:G:H8	1.85	0.42
54:01:742:A:H2'	54:01:743:A:C8	2.54	0.42
54:01:1168:G:H1	54:01:1181:U:H3	1.68	0.42
54:01:1368:G:H2'	54:01:1369:G:H8	1.84	0.42
54:01:2141:G:H2'	54:01:2142:A:H8	1.84	0.42
54:01:2810:A:H2'	54:01:2811:G:O4'	2.19	0.42
58:Y:50:C:H6	58:Y:50:C:H5'	1.85	0.42
59:Z:91:MET:HG3	59:Z:118:HIS:HD2	1.84	0.42
59:Z:125:VAL:HG13	59:Z:127:VAL:HG23	2.01	0.42
59:Z:343:LEU:HB3	59:Z:347:VAL:O	2.19	0.42
2:05:22:ILE:HA	2:05:23:PRO:HD3	1.87	0.42
4:07:4:HIS:CD2	4:07:8:LYS:HE3	2.54	0.42
5:08:19:ASN:HB3	5:08:22:VAL:HB	2.01	0.42
6:09:28:ASN:C	6:09:32:PRO:HG3	2.45	0.42
7:10:117:LEU:HD23	7:10:120:ALA:HA	2.00	0.42
9:12:8:PRO:HD2	54:01:538:A:O2'	2.20	0.42
11:14:64:PHE:CE1	30:33:23:HIS:HA	2.54	0.42
12:15:64:TRP:CB	12:15:104:GLU:HB2	2.43	0.42
13:16:31:HIS:C	13:16:33:ILE:H	2.26	0.42
17:20:7:SER:OG	17:20:22:LEU:HD22	2.20	0.42
28:31:46:VAL:HG12	28:31:47:ILE:N	2.34	0.42
34:D:131:ILE:HG21	53:A:620:C:O2	2.20	0.42
36:F:22:ILE:HG23	36:F:62:MET:HE3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:8:ARG:HH12	53:A:880:C:C5'	2.32	0.42
44:N:15:LEU:CD2	44:N:54:SER:HB3	2.49	0.42
46:P:79:ASN:O	46:P:81:ALA:N	2.52	0.42
50:T:82:ILE:O	50:T:86:ALA:HB2	2.19	0.42
53:A:1342:C:H2'	53:A:1343:G:H8	1.85	0.42
54:01:310:A:O2'	54:01:311:A:H2'	2.19	0.42
54:01:772:C:H5''	54:01:1356:G:H5'	2.02	0.42
54:01:1465:G:H2'	54:01:1466:U:O4'	2.20	0.42
54:01:2589:A:H2'	54:01:2590:A:C8	2.55	0.42
54:01:2815:C:H2'	54:01:2816:G:H8	1.83	0.42
59:Z:109:ASP:HB3	59:Z:112:MET:SD	2.60	0.42
59:Z:261:PHE:O	59:Z:262:ARG:HB2	2.20	0.42
6:09:99:ILE:HD12	6:09:115:VAL:HG11	2.02	0.42
7:10:43:LYS:HD2	7:10:98:GLU:OE1	2.20	0.42
18:21:37:THR:HA	18:21:48:LYS:NZ	2.34	0.42
22:25:12:SER:HB2	54:01:2262:U:C5	2.50	0.42
24:27:17:GLU:HA	24:27:20:ASN:ND2	2.31	0.42
26:29:12:ILE:HD11	26:29:32:LEU:HD22	2.02	0.42
29:32:3:ARG:HD3	29:32:4:THR:H	1.85	0.42
34:D:171:GLU:HB2	34:D:182:LYS:NZ	2.35	0.42
34:D:200:VAL:HG21	35:E:102:THR:HG22	2.01	0.42
35:E:83:PRO:HB3	35:E:96:GLN:HG3	2.02	0.42
36:F:44:ARG:HB2	36:F:58:HIS:ND1	2.35	0.42
41:K:23:HIS:HB3	41:K:30:ILE:CG2	2.50	0.42
42:L:20:VAL:O	42:L:22:ALA:N	2.52	0.42
42:L:98:ARG:NH2	42:L:106:VAL:HG22	2.25	0.42
43:M:21:ILE:HB	43:M:24:VAL:CG1	2.50	0.42
49:S:5:LYS:HB2	49:S:6:LYS:HD2	2.01	0.42
53:A:67:C:H2'	53:A:68:G:C8	2.54	0.42
53:A:79:G:H2'	53:A:80:A:O4'	2.19	0.42
53:A:692:U:H2'	53:A:694:A:OP2	2.20	0.42
53:A:726:C:H2'	53:A:727:G:C8	2.54	0.42
53:A:814:A:H2'	53:A:816:A:O5'	2.20	0.42
53:A:1248:A:H2'	53:A:1249:C:C6	2.55	0.42
54:01:510:C:OP1	54:01:510:C:H3'	2.20	0.42
54:01:645:C:O2'	54:01:646:U:H5'	2.20	0.42
54:01:796:C:H2'	54:01:797:G:C8	2.55	0.42
54:01:1001:A:H2'	54:01:1002:G:O4'	2.20	0.42
54:01:1798:U:O2'	54:01:1802:A:H1'	2.20	0.42
54:01:2248:C:H2'	54:01:2249:U:H5'	2.00	0.42
59:Z:391:VAL:C	59:Z:392:LEU:HD22	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:62:ARG:HH11	1:04:62:ARG:HG3	1.85	0.42
1:04:129:LEU:N	1:04:129:LEU:HD23	2.35	0.42
1:04:247:TRP:CD2	54:01:1805:A:H5''	2.54	0.42
2:05:98:VAL:HG11	2:05:185:ASN:HA	2.01	0.42
7:10:112:ALA:O	7:10:113:PHE:C	2.63	0.42
23:26:63:ILE:O	23:26:66:VAL:HB	2.19	0.42
29:32:21:ARG:O	29:32:27:GLY:HA3	2.20	0.42
29:32:22:MET:HE3	29:32:28:ARG:HH11	1.84	0.42
32:B:96:LEU:HD13	53:A:1103:C:C5'	2.50	0.42
34:D:172:VAL:HA	34:D:179:GLY:HA2	2.01	0.42
42:L:25:ALA:HB2	53:A:554:A:H5'	2.01	0.42
46:P:70:ARG:HH12	53:A:451:A:C5'	2.33	0.42
50:T:75:LYS:C	53:A:186:C:H4'	2.45	0.42
51:U:13:VAL:HG22	51:U:14:ALA:H	1.85	0.42
53:A:73:C:H2'	53:A:74:A:C8	2.54	0.42
54:01:224:U:H2'	54:01:225:C:O4'	2.19	0.42
54:01:536:G:H2'	54:01:537:G:O4'	2.19	0.42
54:01:1426:G:H1'	54:01:1572:A:N6	2.35	0.42
54:01:2155:U:H2'	54:01:2156:G:O4'	2.20	0.42
55:02:63:C:H2'	55:02:64:G:C8	2.54	0.42
55:02:95:U:H2'	55:02:96:G:C8	2.55	0.42
12:15:4:PRO:HG3	12:15:68:PHE:HE2	1.85	0.41
17:20:5:PHE:HB3	17:20:59:ILE:HD12	2.01	0.41
25:28:40:THR:HG23	25:28:43:ILE:H	1.84	0.41
27:30:11:LYS:NZ	54:01:2616:C:H5''	2.35	0.41
27:30:54:ILE:HG13	27:30:56:LYS:HB2	2.01	0.41
28:31:9:LYS:HG3	28:31:19:PHE:CD2	2.54	0.41
34:D:70:GLN:HA	34:D:73:ASN:HD22	1.85	0.41
34:D:78:ALA:HA	34:D:81:LEU:HD12	2.02	0.41
35:E:59:ILE:O	35:E:63:MET:HG2	2.19	0.41
35:E:59:ILE:HD12	35:E:60:GLN:N	2.35	0.41
42:L:56:LEU:HD12	42:L:60:PHE:HB3	2.02	0.41
50:T:67:HIS:C	50:T:69:ASN:H	2.28	0.41
53:A:436:C:H2'	53:A:437:U:C6	2.53	0.41
53:A:485:U:H5'	53:A:486:U:OP2	2.20	0.41
53:A:530:G:H2'	53:A:530:G:N3	2.34	0.41
53:A:883:C:H2'	53:A:884:U:C6	2.55	0.41
53:A:1271:A:H5'	53:A:1314:C:H5''	2.01	0.41
54:01:368:A:C2'	54:01:369:U:H5'	2.50	0.41
54:01:406:G:H2'	54:01:407:G:C8	2.55	0.41
54:01:690:G:O2'	54:01:691:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:741:U:H2'	54:01:742:A:C8	2.55	0.41
54:01:744:U:H2'	54:01:745:G:O4'	2.20	0.41
54:01:2183:A:H2'	54:01:2184:A:C8	2.54	0.41
54:01:2231:U:H2'	54:01:2232:C:C6	2.55	0.41
54:01:2358:A:H2'	54:01:2359:C:O4'	2.20	0.41
1:04:160:TYR:HB3	1:04:193:GLU:HG2	2.03	0.41
6:09:2:GLN:HG2	6:09:20:ASN:HD22	1.85	0.41
8:11:92:PRO:HD2	54:01:1076:C:O2'	2.20	0.41
8:11:103:ALA:HA	8:11:106:GLN:HB3	2.03	0.41
12:15:20:LEU:N	12:15:20:LEU:HD12	2.36	0.41
12:15:86:LYS:HD3	54:01:955:U:H5''	2.01	0.41
17:20:79:ARG:NH2	54:01:572:A:H5'	2.35	0.41
18:21:94:ASP:OD1	54:01:2014:A:H4'	2.20	0.41
31:34:24:ARG:HG2	31:34:36:ARG:HG3	2.01	0.41
32:B:103:TRP:CH2	32:B:107:ARG:HD3	2.55	0.41
35:E:92:ARG:O	35:E:93:VAL:C	2.64	0.41
35:E:93:VAL:HA	35:E:126:ALA:HA	2.01	0.41
35:E:149:PRO:O	35:E:152:VAL:HG22	2.20	0.41
38:H:40:LYS:HA	38:H:45:ILE:O	2.20	0.41
39:I:114:LYS:HD3	39:I:120:ALA:O	2.20	0.41
41:K:41:LEU:HD13	41:K:78:ILE:HD11	2.01	0.41
50:T:67:HIS:CG	53:A:262:A:H5'	2.55	0.41
52:03:218:MET:HG2	54:01:2174:C:H1'	2.01	0.41
53:A:1002:G:H2'	53:A:1003:G:C8	2.55	0.41
53:A:1092:A:N1	53:A:1110:A:H5''	2.36	0.41
53:A:1254:A:H4'	53:A:1356:G:O3'	2.19	0.41
54:01:139:U:H5'	54:01:140:C:OP1	2.19	0.41
54:01:611:C:H2'	54:01:612:G:O4'	2.20	0.41
54:01:906:U:H2'	54:01:907:G:O4'	2.20	0.41
54:01:1367:A:C2'	54:01:1368:G:H5'	2.50	0.41
54:01:1380:G:H1'	54:01:1569:A:N6	2.34	0.41
59:Z:6:GLU:HG2	59:Z:8:THR:HG23	2.02	0.41
59:Z:318:ARG:NH2	59:Z:322:PHE:HB3	2.28	0.41
1:04:163:ILE:HA	1:04:173:LEU:HD23	2.02	0.41
3:06:109:LEU:HA	3:06:112:LEU:HG	2.01	0.41
3:06:163:ASN:HB2	54:01:322:A:OP2	2.20	0.41
5:08:75:VAL:HA	5:08:78:VAL:HG22	2.02	0.41
6:09:9:VAL:O	6:09:11:ASN:N	2.53	0.41
8:11:10:LEU:HD21	8:11:26:ALA:CB	2.50	0.41
8:11:92:PRO:HB2	54:01:1077:A:O4'	2.21	0.41
13:16:56:LYS:NZ	13:16:88:ALA:HA	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:16:96:ARG:HB3	13:16:114:GLU:OE2	2.20	0.41
16:19:112:ALA:O	16:19:116:LEU:HB2	2.20	0.41
20:23:18:LYS:HD2	20:23:18:LYS:C	2.45	0.41
26:29:59:ARG:O	26:29:63:ARG:HG3	2.20	0.41
31:34:25:VAL:HB	31:34:35:GLN:HG3	2.02	0.41
32:B:42:LEU:O	32:B:46:VAL:HG23	2.20	0.41
32:B:160:LEU:HD22	32:B:175:ALA:CB	2.51	0.41
37:G:115:MET:HB2	53:A:1240:U:OP1	2.19	0.41
40:J:68:ARG:HB3	40:J:70:HIS:CE1	2.54	0.41
44:N:30:ILE:HD13	44:N:43:ALA:HB2	2.02	0.41
44:N:38:GLU:O	44:N:41:TRP:HB3	2.20	0.41
44:N:60:ARG:HA	44:N:60:ARG:HD2	1.91	0.41
50:T:56:ILE:O	50:T:60:GLN:HG2	2.19	0.41
52:03:165:ASN:HA	52:03:171:ILE:HG12	2.02	0.41
53:A:41:G:H2'	53:A:42:G:C8	2.54	0.41
53:A:123:U:H2'	53:A:124:C:C6	2.54	0.41
53:A:512:U:H2'	53:A:513:C:C6	2.55	0.41
53:A:599:C:H2'	53:A:600:A:C8	2.54	0.41
53:A:940:C:H2'	53:A:941:G:C8	2.55	0.41
53:A:1245:C:H2'	53:A:1246:A:C8	2.56	0.41
53:A:1456:A:H2'	53:A:1457:G:O4'	2.21	0.41
53:A:1458:G:H2'	53:A:1459:G:H8	1.83	0.41
54:01:629:G:H5''	54:01:650:C:O2'	2.19	0.41
54:01:878:A:H2'	54:01:879:G:O4'	2.19	0.41
54:01:1077:A:C2'	54:01:1078:U:H5'	2.49	0.41
54:01:1561:C:H2'	54:01:1562:U:C6	2.55	0.41
54:01:2248:C:C2'	54:01:2249:U:H5'	2.50	0.41
54:01:2805:C:H2'	54:01:2806:C:C6	2.55	0.41
58:Y:71:C:H2'	58:Y:72:C:C5'	2.50	0.41
59:Z:184:TRP:HA	59:Z:187:LYS:HG2	2.01	0.41
3:06:75:SER:HB3	3:06:78:TRP:CD1	2.55	0.41
4:07:82:TYR:CD1	4:07:83:PRO:HD2	2.55	0.41
8:11:53:PRO:O	8:11:73:PRO:HB3	2.20	0.41
8:11:100:ILE:HG13	8:11:105:LEU:HD21	2.01	0.41
10:13:15:GLY:O	10:13:47:ILE:HG12	2.21	0.41
33:C:5:HIS:HB3	44:N:88:MET:HE3	2.02	0.41
36:F:90:MET:HE1	48:R:22:TYR:OH	2.20	0.41
37:G:94:ARG:HD2	53:A:1377:A:OP1	2.20	0.41
42:L:53:ARG:HA	42:L:63:THR:HA	2.02	0.41
44:N:53:ASP:C	44:N:55:SER:H	2.29	0.41
45:O:44:GLU:O	45:O:45:HIS:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:T:4:LYS:HZ2	53:A:61:G:P	2.44	0.41
53:A:49:U:O2'	53:A:50:A:H2'	2.20	0.41
53:A:160:A:H2'	53:A:161:A:O4'	2.20	0.41
54:01:521:U:H2'	54:01:522:A:C8	2.56	0.41
54:01:685:A:H5''	54:01:788:A:H62	1.85	0.41
54:01:872:U:H2'	54:01:873:C:C6	2.55	0.41
54:01:1127:A:H2'	54:01:1128:G:H5''	2.03	0.41
54:01:1139:G:O2'	54:01:1140:C:H5'	2.20	0.41
54:01:2028:U:H3	54:01:2033:A:H62	1.67	0.41
54:01:2565:A:C2'	54:01:2566:A:H5'	2.51	0.41
54:01:2644:G:H3'	54:01:2645:G:H21	1.85	0.41
54:01:2644:G:H3'	54:01:2645:G:N2	2.35	0.41
56:W:47:U:H3'	56:W:48:C:C5'	2.50	0.41
58:Y:18:G:H4'	58:Y:60:U:C2	2.55	0.41
59:Z:97:GLN:NE2	59:Z:215:GLU:HG3	2.36	0.41
59:Z:244:ILE:N	59:Z:244:ILE:HD12	2.36	0.41
3:06:46:GLN:O	3:06:86:ALA:HB1	2.21	0.41
3:06:163:ASN:ND2	54:01:323:C:H5''	2.35	0.41
5:08:110:HIS:HA	5:08:111:PRO:HD3	1.92	0.41
5:08:153:PRO:HA	5:08:160:GLY:HA3	2.02	0.41
6:09:1:MET:C	6:09:3:VAL:N	2.78	0.41
8:11:37:PHE:HE1	8:11:58:ILE:HG13	1.86	0.41
13:16:79:LEU:CD2	13:16:83:LEU:HD12	2.48	0.41
17:20:27:ILE:HG22	17:20:28:ALA:N	2.35	0.41
20:23:11:ILE:HG13	20:23:20:LYS:O	2.21	0.41
32:B:86:CYS:SG	32:B:88:GLN:HG2	2.60	0.41
34:D:10:LEU:HD22	34:D:62:ARG:HD2	2.02	0.41
35:E:14:LEU:C	35:E:15:ILE:HD12	2.45	0.41
36:F:9:MET:HG2	36:F:59:TYR:CD1	2.55	0.41
36:F:42:TRP:CZ3	36:F:61:LEU:HB2	2.55	0.41
38:H:7:ALA:HB2	38:H:76:ARG:HG2	2.01	0.41
38:H:50:VAL:HG22	38:H:50:VAL:O	2.21	0.41
43:M:16:ILE:HG21	53:A:1302:C:C6	2.55	0.41
52:03:170:ILE:HD12	54:01:2121:G:N2	2.36	0.41
53:A:806:C:H2'	53:A:807:A:C8	2.56	0.41
53:A:876:C:H2'	53:A:877:G:H8	1.85	0.41
53:A:1030:U:H3'	53:A:1031:C:H5'	2.02	0.41
53:A:1271:A:H2'	53:A:1272:G:C8	2.55	0.41
54:01:191:A:H2'	54:01:192:C:C6	2.56	0.41
54:01:232:G:H22	54:01:420:C:H5''	1.86	0.41
54:01:796:C:H2'	54:01:797:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:951:C:H2'	54:01:952:G:H8	1.85	0.41
54:01:1086:A:H4'	54:01:1103:A:N1	2.36	0.41
54:01:1443:U:H2'	54:01:1444:G:C8	2.56	0.41
54:01:2354:C:H2'	54:01:2355:G:C8	2.52	0.41
54:01:2492:U:H2'	54:01:2493:U:C6	2.55	0.41
59:Z:35:LEU:HD13	59:Z:70:ASP:N	2.35	0.41
59:Z:62:ILE:HG13	59:Z:63:ASN:N	2.35	0.41
2:05:39:ASP:HA	2:05:46:ARG:HA	2.03	0.41
2:05:66:GLY:HA3	54:01:2787:C:H5'	2.02	0.41
7:10:34:THR:HG22	54:01:1085:A:N6	2.27	0.41
8:11:89:SER:HA	8:11:135:MET:O	2.21	0.41
11:14:62:PRO:HA	54:01:2393:U:O3'	2.20	0.41
12:15:136:MET:HE1	21:24:74:ALA:O	2.20	0.41
18:21:57:ASN:HD21	54:01:495:G:H1'	1.85	0.41
19:22:6:ARG:HD3	19:22:6:ARG:C	2.46	0.41
20:23:8:ASP:O	20:23:24:VAL:HG23	2.20	0.41
35:E:61:LYS:HG2	35:E:65:LYS:HE2	2.03	0.41
35:E:158:LYS:HD3	35:E:158:LYS:N	2.35	0.41
36:F:64:VAL:HG22	36:F:65:GLU:H	1.85	0.41
37:G:85:GLN:NE2	56:X:32:C:H4'	2.35	0.41
46:P:57:ILE:O	46:P:61:VAL:HG23	2.20	0.41
53:A:1015:G:H1'	53:A:1218:C:O2'	2.20	0.41
53:A:1048:G:H2'	53:A:1050:G:H8	1.84	0.41
53:A:1288:A:O2'	53:A:1353:G:H5'	2.20	0.41
54:01:1218:G:O2'	54:01:1219:U:H5'	2.20	0.41
54:01:2693:G:H2'	54:01:2694:G:C8	2.56	0.41
54:01:2698:U:H2'	54:01:2699:C:C6	2.56	0.41
54:01:2858:C:H2'	54:01:2859:G:O4'	2.21	0.41
59:Z:32:THR:HB	59:Z:42:ALA:O	2.20	0.41
59:Z:61:THR:O	59:Z:82:PRO:HB3	2.20	0.41
59:Z:95:ALA:HB3	59:Z:125:VAL:HG21	2.03	0.41
59:Z:357:LYS:HB3	59:Z:357:LYS:NZ	2.35	0.41
3:06:37:ALA:CB	3:06:94:GLN:HE21	2.34	0.41
6:09:84:ALA:HB2	6:09:148:ALA:C	2.45	0.41
7:10:56:ARG:HG2	54:01:1107:G:H5'	2.02	0.41
10:13:33:ALA:HB1	10:13:37:ASP:CB	2.50	0.41
10:13:88:ASN:N	10:13:92:GLU:O	2.51	0.41
13:16:29:VAL:HB	13:16:75:ILE:HD12	2.03	0.41
16:19:50:ARG:HG2	54:01:1156:A:C5	2.55	0.41
18:21:44:ALA:HA	18:21:47:VAL:HG12	2.01	0.41
29:32:12:ARG:O	29:32:16:HIS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:42:LEU:HD23	32:B:42:LEU:H	1.86	0.41
32:B:69:VAL:HG12	32:B:168:GLU:OE2	2.20	0.41
42:L:86:VAL:HG23	42:L:89:LEU:H	1.86	0.41
48:R:69:TYR:HB2	48:R:73:HIS:NE2	2.35	0.41
51:U:7:GLU:CG	51:U:15:LEU:HD13	2.45	0.41
53:A:132:C:H5'	53:A:262:A:O2'	2.21	0.41
53:A:597:G:H2'	53:A:598:U:H5'	2.02	0.41
53:A:1305:G:H22	53:A:1331:G:H2'	1.85	0.41
53:A:1502:A:H8	53:A:1505:G:H22	1.65	0.41
54:01:204:A:O3'	54:01:205:G:H4'	2.20	0.41
54:01:807:U:H4'	54:01:2445:G:O3'	2.20	0.41
54:01:1053:C:H3'	54:01:1054:A:H5''	2.03	0.41
54:01:1449:G:H2'	54:01:1450:G:O4'	2.21	0.41
54:01:1510:G:H2'	54:01:1511:G:O4'	2.21	0.41
54:01:2287:A:C2'	54:01:2288:A:H2'	2.51	0.41
54:01:2292:U:H2'	54:01:2293:G:C8	2.55	0.41
54:01:2441:U:H2'	54:01:2442:C:H6	1.86	0.41
54:01:2676:C:H2'	54:01:2677:G:C8	2.55	0.41
54:01:2732:G:O2'	54:01:2733:A:H5'	2.21	0.41
55:02:66:A:C2	55:02:107:G:H2'	2.55	0.41
60:Z:401:GCP:H2'	60:Z:401:GCP:H8	1.89	0.41
1:04:257:ARG:NH1	1:04:259:ASN:H	2.17	0.41
3:06:109:LEU:HD22	3:06:200:LEU:HD21	2.01	0.41
12:15:82:MET:HE2	54:01:962:G:N2	2.36	0.41
16:19:57:ARG:O	16:19:61:ILE:HG13	2.20	0.41
23:26:15:ASN:HA	23:26:24:THR:O	2.21	0.41
27:30:39:ARG:HD3	54:01:2886:A:N1	2.36	0.41
29:32:12:ARG:CZ	29:32:44:VAL:HG21	2.51	0.41
31:34:19:ARG:NH2	31:34:26:ILE:HD13	2.36	0.41
33:C:171:ARG:HB2	53:A:1106:G:H5''	2.01	0.41
34:D:36:ALA:N	34:D:37:PRO:HD3	2.35	0.41
34:D:191:SER:C	34:D:193:ASP:H	2.28	0.41
35:E:43:GLY:O	35:E:73:VAL:N	2.54	0.41
41:K:124:LYS:HA	51:U:34:ARG:N	2.32	0.41
42:L:26:CYS:CB	42:L:29:LYS:HE2	2.50	0.41
42:L:73:LEU:N	42:L:73:LEU:HD12	2.35	0.41
51:U:31:VAL:O	51:U:31:VAL:HG22	2.20	0.41
53:A:1144:G:N2	53:A:1146:A:H62	2.18	0.41
53:A:1427:C:H2'	53:A:1428:A:C8	2.56	0.41
54:01:707:G:H2'	54:01:708:G:O4'	2.21	0.41
54:01:1083:U:H2'	54:01:1085:A:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1695:G:N3	54:01:1695:G:H3'	2.36	0.41
54:01:1769:U:H4'	54:01:1958:C:H5''	2.02	0.41
54:01:1810:A:H2'	54:01:1811:G:O4'	2.20	0.41
54:01:2342:C:O2'	54:01:2374:C:H5''	2.21	0.41
54:01:2677:G:H2'	54:01:2678:C:C6	2.55	0.41
56:W:3:C:H2'	56:W:4:G:C8	2.55	0.41
59:Z:258:VAL:HG12	59:Z:265:LEU:HB3	2.03	0.41
59:Z:262:ARG:HH11	59:Z:262:ARG:HG3	1.86	0.41
3:06:105:LEU:O	3:06:109:LEU:HD13	2.20	0.41
3:06:163:ASN:HD21	54:01:323:C:H5''	1.86	0.41
3:06:164:LEU:HD12	3:06:164:LEU:N	2.31	0.41
4:07:19:PHE:O	4:07:20:ASN:C	2.64	0.41
5:08:138:GLN:HE22	54:01:2746:U:H1'	1.85	0.41
7:10:20:LYS:HB2	7:10:88:HIS:HE1	1.85	0.41
7:10:27:VAL:CG1	7:10:83:ALA:HB3	2.51	0.41
9:12:38:GLY:HA3	9:12:50:THR:C	2.46	0.41
9:12:106:LYS:HA	9:12:109:LEU:HD12	2.02	0.41
10:13:66:LYS:NZ	10:13:66:LYS:HB3	2.35	0.41
10:13:92:GLU:O	10:13:93:GLN:C	2.64	0.41
10:13:103:VAL:O	10:13:122:VAL:HB	2.21	0.41
12:15:82:MET:HB2	54:01:2496:C:OP1	2.21	0.41
12:15:99:GLY:HA2	21:24:82:TYR:HB3	2.03	0.41
15:18:7:LEU:HA	15:18:10:GLU:OE1	2.21	0.41
17:20:16:GLU:HA	17:20:98:ILE:HB	2.02	0.41
23:26:20:ALA:HB3	23:26:22:ASN:OD1	2.20	0.41
24:27:5:GLU:HA	24:27:8:GLU:OE1	2.21	0.41
28:31:37:LYS:HB2	28:31:48:TYR:CE2	2.56	0.41
32:B:15:PHE:CD2	32:B:39:ILE:HG12	2.56	0.41
33:C:76:ILE:HG13	33:C:77:GLY:N	2.36	0.41
33:C:156:LEU:HD21	33:C:163:ARG:HG3	2.03	0.41
34:D:53:GLN:HB3	34:D:202:LEU:HD12	2.03	0.41
35:E:113:VAL:HG13	35:E:114:LEU:HD13	2.03	0.41
36:F:36:ILE:CA	36:F:64:VAL:HG23	2.48	0.41
38:H:54:THR:HG23	38:H:55:LYS:HG3	2.02	0.41
40:J:15:HIS:O	40:J:18:ILE:HG22	2.21	0.41
43:M:16:ILE:HD12	43:M:16:ILE:H	1.85	0.41
43:M:100:ARG:HH11	43:M:100:ARG:HG3	1.86	0.41
43:M:104:ASN:O	43:M:105:ALA:CB	2.69	0.41
44:N:26:LEU:HD22	44:N:47:LEU:HD13	2.03	0.41
47:Q:59:GLU:CB	47:Q:75:VAL:HB	2.51	0.41
50:T:70:LYS:HA	50:T:73:ARG:HH12	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:10:VAL:O	52:03:14:LYS:HG3	2.20	0.41
52:03:50:ILE:C	52:03:50:ILE:HD12	2.46	0.41
53:A:27:G:H2'	53:A:28:A:O4'	2.19	0.41
53:A:51:A:H4'	53:A:52:C:H5''	2.03	0.41
53:A:56:U:H2'	53:A:57:G:H8	1.86	0.41
53:A:70:U:H5''	53:A:71:A:OP1	2.20	0.41
53:A:407:U:H2'	53:A:408:A:C8	2.56	0.41
53:A:632:U:H3'	53:A:633:G:H5'	2.02	0.41
53:A:772:U:H2'	53:A:773:G:C8	2.56	0.41
53:A:1017:U:H2'	53:A:1018:G:C8	2.55	0.41
53:A:1255:G:O2'	53:A:1258:G:H1'	2.20	0.41
54:01:353:C:H2'	54:01:354:A:H8	1.85	0.41
54:01:357:C:H2'	54:01:358:U:C6	2.56	0.41
54:01:640:C:H2'	54:01:641:U:C6	2.55	0.41
54:01:1441:G:H4'	54:01:1628:G:C5'	2.51	0.41
54:01:1484:U:H3	54:01:1505:A:H61	1.67	0.41
54:01:1635:A:H2'	54:01:1636:U:O4'	2.21	0.41
54:01:1878:G:H2'	54:01:1879:C:O4'	2.20	0.41
54:01:1924:C:H2'	54:01:1925:C:C6	2.56	0.41
54:01:2114:A:H2'	54:01:2114:A:N3	2.36	0.41
54:01:2158:A:H4'	54:01:2159:G:O4'	2.20	0.41
54:01:2287:A:H2'	54:01:2288:A:H2'	2.01	0.41
54:01:2322:A:H2'	54:01:2323:G:O4'	2.21	0.41
54:01:2564:A:C2	54:01:2647:U:H4'	2.55	0.41
54:01:2813:A:H2'	54:01:2814:A:C8	2.55	0.41
55:02:3:C:H3'	55:02:4:C:H5''	2.03	0.41
55:02:79:G:H2'	55:02:80:U:O4'	2.21	0.41
56:W:20:U:H3'	56:W:21:A:H5'	2.02	0.41
59:Z:45:ALA:HB3	59:Z:48:GLN:HG2	2.03	0.41
59:Z:127:VAL:HG11	59:Z:130:ILE:HD11	2.02	0.41
59:Z:176:LYS:HD2	59:Z:184:TRP:CD1	2.55	0.41
59:Z:211:LEU:HB3	59:Z:233:ARG:HG2	2.03	0.41
59:Z:305:GLU:HB2	59:Z:389:ALA:HB3	2.02	0.41
2:05:177:VAL:HG22	2:05:178:VAL:N	2.36	0.41
6:09:8:LYS:O	6:09:9:VAL:C	2.64	0.41
6:09:94:ILE:CD1	6:09:146:VAL:HG21	2.51	0.41
8:11:93:ASN:HD22	8:11:93:ASN:HA	1.53	0.41
11:14:79:LEU:HD12	11:14:114:GLY:H	1.85	0.41
15:18:23:ASP:OD1	15:18:88:ARG:HA	2.21	0.41
34:D:159:GLU:O	34:D:162:GLU:HG2	2.20	0.41
34:D:205:LYS:HD2	53:A:8:A:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:89:THR:HB	35:E:134:ASN:OD1	2.21	0.41
39:I:18:VAL:HG13	39:I:64:ILE:HG12	2.03	0.41
42:L:23:LEU:HD22	42:L:58:ASN:ND2	2.35	0.41
46:P:43:ALA:O	46:P:44:SER:C	2.63	0.41
47:Q:6:THR:C	47:Q:7:LEU:HD12	2.46	0.41
49:S:19:GLU:O	49:S:23:GLU:HG2	2.21	0.41
53:A:1506:U:HO2'	53:A:1507:A:H5'	1.83	0.41
54:01:1710:G:H2'	54:01:1711:A:C8	2.56	0.41
54:01:1881:C:H2'	54:01:1882:U:C6	2.56	0.41
54:01:2345:G:H21	54:01:2381:A:H3'	1.86	0.41
54:01:2389:G:H5''	54:01:2390:U:O4'	2.21	0.41
54:01:2801:G:H2'	54:01:2802:G:H8	1.87	0.41
54:01:2898:U:H2'	54:01:2899:A:H8	1.84	0.41
59:Z:11:HIS:HB2	59:Z:269:ARG:NH1	2.36	0.41
59:Z:16:THR:HG22	59:Z:102:ILE:HB	2.03	0.41
59:Z:60:ILE:O	59:Z:60:ILE:HG13	2.19	0.41
59:Z:372:LEU:O	59:Z:388:VAL:HG23	2.20	0.41
59:Z:376:ILE:HG22	59:Z:383:VAL:HG23	2.03	0.41
1:04:204:LEU:HD13	1:04:210:ALA:HB2	2.03	0.40
4:07:43:ILE:H	4:07:43:ILE:HG13	1.61	0.40
5:08:166:GLU:OE2	5:08:168:VAL:HG22	2.21	0.40
6:09:43:ASN:HA	6:09:46:PHE:HD2	1.85	0.40
7:10:47:GLU:CD	7:10:95:LEU:HD21	2.45	0.40
7:10:129:LEU:H	7:10:129:LEU:HG	1.66	0.40
9:12:65:THR:H	9:12:68:LYS:HE3	1.85	0.40
16:19:27:ARG:HB3	16:19:27:ARG:HH11	1.85	0.40
16:19:45:ALA:O	16:19:49:ARG:HG3	2.21	0.40
17:20:49:ILE:HG22	17:20:54:VAL:N	2.36	0.40
23:26:4:CYS:O	23:26:8:GLY:HA2	2.21	0.40
30:33:27:ASN:O	30:33:35:LYS:HE2	2.21	0.40
32:B:106:VAL:O	32:B:110:ILE:HG13	2.20	0.40
32:B:141:GLU:O	32:B:144:GLU:HB3	2.21	0.40
33:C:19:SER:HB2	44:N:91:GLU:O	2.21	0.40
33:C:52:SER:HB3	33:C:114:LEU:HG	2.02	0.40
33:C:171:ARG:HG3	53:A:1107:C:P	2.61	0.40
34:D:56:GLU:O	34:D:60:VAL:HG23	2.21	0.40
34:D:205:LYS:HB3	53:A:8:A:N7	2.36	0.40
36:F:72:ASP:O	36:F:76:THR:HG23	2.22	0.40
38:H:79:ARG:HD2	53:A:878:A:P	2.61	0.40
39:I:49:GLN:C	39:I:51:LEU:H	2.28	0.40
40:J:7:ARG:HH11	40:J:7:ARG:HG2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:99:GLY:N	42:L:103:CYS:O	2.46	0.40
43:M:76:ILE:O	43:M:80:MET:HG3	2.20	0.40
44:N:71:GLY:HA2	53:A:975:A:O2'	2.20	0.40
46:P:20:VAL:HG23	46:P:34:GLU:O	2.21	0.40
46:P:61:VAL:C	46:P:63:GLN:H	2.30	0.40
53:A:346:G:H2'	53:A:347:G:H5'	2.02	0.40
53:A:381:C:H2'	53:A:382:A:O4'	2.21	0.40
53:A:409:U:H2'	53:A:410:G:O4'	2.21	0.40
53:A:902:G:O2'	53:A:903:G:H5'	2.21	0.40
54:01:40:U:H2'	54:01:41:C:C6	2.56	0.40
54:01:1637:A:H5'	54:01:1760:C:O2'	2.20	0.40
54:01:1665:A:H8	54:01:1665:A:H5'	1.87	0.40
54:01:1806:C:H2'	54:01:1807:G:O4'	2.21	0.40
54:01:2220:U:H2'	54:01:2221:G:C8	2.56	0.40
55:02:69:G:H2'	55:02:70:C:H5'	2.03	0.40
56:W:34:C:H2'	56:W:35:A:C8	2.56	0.40
3:06:105:LEU:HA	3:06:108:ILE:HG12	2.03	0.40
5:08:82:PHE:CE2	5:08:137:LYS:HB2	2.57	0.40
6:09:5:LEU:HD12	6:09:5:LEU:H	1.86	0.40
7:10:57:ASN:C	7:10:59:LEU:H	2.28	0.40
9:12:105:VAL:O	9:12:109:LEU:HG	2.21	0.40
9:12:109:LEU:HD22	9:12:118:MET:SD	2.61	0.40
17:20:10:LYS:HZ1	17:20:23:GLU:HB2	1.87	0.40
18:21:41:LYS:O	18:21:45:VAL:HG23	2.20	0.40
21:24:75:GLN:HG2	21:24:92:VAL:HG23	2.04	0.40
27:30:9:ARG:HH21	27:30:9:ARG:HG3	1.87	0.40
35:E:98:ALA:O	35:E:99:SER:C	2.64	0.40
44:N:58:ARG:HA	53:A:980:C:H1'	2.02	0.40
48:R:59:LYS:HD3	53:A:735:C:H5'	2.03	0.40
49:S:50:VAL:O	49:S:57:VAL:HG12	2.21	0.40
50:T:23:ARG:NH1	53:A:176:C:H5''	2.37	0.40
50:T:79:THR:HA	50:T:82:ILE:HG12	2.03	0.40
53:A:81:A:H2'	53:A:82:G:C8	2.56	0.40
53:A:166:U:H2'	53:A:167:A:C8	2.57	0.40
53:A:1306:A:N6	53:A:1331:G:H1'	2.35	0.40
54:01:1268:A:H62	54:01:2012:G:H21	1.69	0.40
54:01:1414:C:H2'	54:01:1415:U:O4'	2.20	0.40
54:01:1417:C:H2'	54:01:1418:G:O4'	2.21	0.40
54:01:1859:U:H2'	54:01:1860:G:H8	1.86	0.40
54:01:2066:C:O2'	54:01:2067:G:H5'	2.21	0.40
54:01:2467:C:H2'	54:01:2468:A:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:311:LEU:HD11	59:Z:382:THR:HB	2.03	0.40
2:05:35:THR:O	2:05:92:VAL:HG13	2.22	0.40
2:05:36:GLN:OE1	2:05:38:LYS:HE3	2.22	0.40
4:07:15:LEU:HD11	4:07:168:LEU:HD12	2.03	0.40
4:07:35:LEU:HD12	4:07:152:ASP:O	2.22	0.40
8:11:27:LEU:HD23	8:11:27:LEU:H	1.86	0.40
18:21:55:ILE:HG13	18:21:55:ILE:H	1.77	0.40
24:27:27:ASN:O	24:27:31:GLN:N	2.52	0.40
30:33:29:ARG:HD3	30:33:29:ARG:HA	1.85	0.40
31:34:13:ASN:HB3	31:34:28:SER:OG	2.20	0.40
36:F:3:HIS:O	36:F:92:THR:HA	2.21	0.40
41:K:71:ASP:O	41:K:72:ALA:HB3	2.21	0.40
53:A:70:U:H4'	53:A:71:A:H8	1.85	0.40
53:A:641:U:H4'	53:A:642:A:H8	1.86	0.40
53:A:1081:A:H2'	53:A:1082:A:H8	1.87	0.40
53:A:1158:C:H2'	53:A:1159:U:H4'	2.03	0.40
53:A:1239:A:H62	53:A:1299:A:H2	1.69	0.40
54:01:341:C:H2'	54:01:342:A:H8	1.85	0.40
54:01:394:C:H2'	54:01:395:U:O4'	2.21	0.40
54:01:437:U:H2'	54:01:438:G:H8	1.86	0.40
54:01:864:G:H21	54:01:866:A:H62	1.70	0.40
54:01:1706:C:C2	54:01:1757:A:H5'	2.57	0.40
54:01:1716:U:H2'	54:01:1717:A:C8	2.56	0.40
54:01:2156:G:C2'	54:01:2157:G:H5'	2.52	0.40
54:01:2758:A:H2'	54:01:2759:G:O4'	2.21	0.40
56:W:61:C:H2'	56:W:62:C:C6	2.56	0.40
59:Z:248:LYS:C	59:Z:248:LYS:HD2	2.46	0.40
59:Z:335:THR:CG2	59:Z:337:VAL:HG23	2.48	0.40
2:05:77:ARG:HG3	2:05:77:ARG:NH2	2.37	0.40
2:05:114:LYS:HZ2	2:05:196:ALA:HB2	1.87	0.40
2:05:130:GLN:HG3	54:01:2511:U:H4'	2.02	0.40
4:07:65:LEU:HD22	55:02:42:C:C5	2.57	0.40
4:07:120:SER:HB2	4:07:127:TYR:CE1	2.56	0.40
7:10:59:LEU:C	7:10:61:ARG:H	2.28	0.40
9:12:101:ILE:O	9:12:105:VAL:HG23	2.21	0.40
9:12:118:MET:HA	9:12:121:LYS:HG2	2.03	0.40
15:18:102:ARG:O	15:18:107:ALA:HB2	2.22	0.40
16:19:74:SER:HB2	54:01:1011:G:OP1	2.22	0.40
17:20:41:ILE:HG13	17:20:54:VAL:HG21	2.04	0.40
22:25:56:PHE:CE1	54:01:2365:G:H4'	2.56	0.40
30:33:11:LYS:HB2	30:33:11:LYS:NZ	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:D:190:LEU:O	34:D:191:SER:HB3	2.22	0.40
35:E:108:GLY:O	35:E:109:ALA:HB3	2.21	0.40
37:G:149:ALA:HB1	41:K:58:THR:OG1	2.21	0.40
48:R:29:LYS:O	48:R:32:ILE:HG13	2.21	0.40
53:A:190:A:H2'	53:A:191:G:O4'	2.21	0.40
53:A:218:U:H2'	53:A:219:U:O4'	2.22	0.40
53:A:368:U:OP2	59:Z:256:THR:HG21	2.21	0.40
53:A:966:G:C2	56:W:34:C:H5'	2.57	0.40
53:A:1068:G:O5'	53:A:1388:C:H5'	2.22	0.40
53:A:1519:A:H3'	53:A:1520:C:O4'	2.21	0.40
54:01:924:G:H2'	54:01:925:A:C8	2.56	0.40
54:01:1507:C:C2'	54:01:1508:A:H4'	2.52	0.40
54:01:1662:U:H2'	54:01:1663:G:H8	1.84	0.40
54:01:2323:G:H2'	54:01:2324:U:O4'	2.21	0.40
54:01:2752:C:H2'	54:01:2753:A:O4'	2.20	0.40
59:Z:241:GLU:HG3	59:Z:254:THR:N	2.36	0.40
59:Z:283:ARG:C	59:Z:283:ARG:HD3	2.47	0.40
1:04:62:ARG:HD2	1:04:83:ASP:HA	2.03	0.40
1:04:140:VAL:O	1:04:161:VAL:N	2.49	0.40
1:04:165:ALA:O	1:04:171:VAL:HG13	2.22	0.40
1:04:176:ARG:HB3	54:01:1819:A:H2'	2.04	0.40
1:04:229:HIS:ND1	1:04:230:PRO:HD2	2.36	0.40
3:06:111:GLU:OE2	3:06:115:GLN:HG2	2.22	0.40
6:09:5:LEU:HD22	6:09:13:GLY:HA2	2.03	0.40
6:09:31:VAL:N	6:09:32:PRO:HD2	2.37	0.40
8:11:8:VAL:HB	8:11:10:LEU:HD13	2.04	0.40
13:16:17:ARG:O	13:16:20:MET:HG3	2.21	0.40
17:20:7:SER:N	17:20:10:LYS:O	2.55	0.40
23:26:60:LYS:HD2	54:01:372:G:C4	2.57	0.40
25:28:50:VAL:O	25:28:54:VAL:HG22	2.22	0.40
31:34:30:GLU:HA	31:34:31:PRO:HD3	1.97	0.40
32:B:132:GLU:O	32:B:135:MET:HB3	2.22	0.40
34:D:172:VAL:HG23	34:D:178:GLU:C	2.46	0.40
35:E:108:GLY:C	35:E:110:MET:H	2.30	0.40
40:J:13:PHE:CE2	44:N:93:PRO:HB2	2.56	0.40
41:K:67:GLU:O	41:K:70:ALA:HB3	2.21	0.40
42:L:63:THR:O	42:L:92:VAL:HG13	2.22	0.40
44:N:5:MET:HG2	44:N:8:ARG:HH21	1.87	0.40
46:P:8:ARG:HG2	46:P:28:ARG:NH2	2.36	0.40
50:T:7:LYS:O	50:T:10:ALA:HB3	2.21	0.40
53:A:427:U:H2'	53:A:428:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1530:G:H2'	53:A:1531:A:C8	2.57	0.40
54:01:242:G:N2	54:01:254:G:H2'	2.37	0.40
54:01:917:A:H5''	54:01:2268:A:H61	1.86	0.40
54:01:1720:U:H2'	54:01:1721:G:O4'	2.21	0.40
54:01:1796:U:H2'	54:01:1797:G:C8	2.55	0.40
58:Y:53:G:H5''	59:Z:320:THR:OG1	2.21	0.40
59:Z:102:ILE:O	59:Z:104:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	04	269/271 (99%)	229 (85%)	37 (14%)	3 (1%)	11	44
2	05	207/209 (99%)	173 (84%)	30 (14%)	4 (2%)	6	34
3	06	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	8	38
4	07	175/177 (99%)	147 (84%)	26 (15%)	2 (1%)	11	44
5	08	174/176 (99%)	152 (87%)	18 (10%)	4 (2%)	5	31
6	09	147/149 (99%)	117 (80%)	22 (15%)	8 (5%)	1	18
7	10	129/131 (98%)	93 (72%)	26 (20%)	10 (8%)	1	12
8	11	139/141 (99%)	111 (80%)	19 (14%)	9 (6%)	1	15
9	12	140/142 (99%)	124 (89%)	14 (10%)	2 (1%)	9	39
10	13	120/122 (98%)	95 (79%)	20 (17%)	5 (4%)	2	21
11	14	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	20
12	15	134/136 (98%)	120 (90%)	10 (8%)	4 (3%)	3	26
13	16	118/120 (98%)	100 (85%)	16 (14%)	2 (2%)	7	36
14	17	114/116 (98%)	99 (87%)	13 (11%)	2 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	18	112/114 (98%)	97 (87%)	12 (11%)	3 (3%)	4	28
16	19	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	14	48
17	20	101/103 (98%)	78 (77%)	21 (21%)	2 (2%)	6	33
18	21	108/110 (98%)	92 (85%)	15 (14%)	1 (1%)	14	48
19	22	91/93 (98%)	72 (79%)	17 (19%)	2 (2%)	5	31
20	23	100/102 (98%)	85 (85%)	11 (11%)	4 (4%)	2	21
21	24	92/94 (98%)	79 (86%)	12 (13%)	1 (1%)	11	44
22	25	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
23	26	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
24	27	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	37
25	28	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	29	64/66 (97%)	44 (69%)	20 (31%)	0	100	100
27	30	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
28	31	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	5	32
29	32	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
30	33	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	25
31	34	36/38 (95%)	28 (78%)	6 (17%)	2 (6%)	1	17
32	B	216/218 (99%)	174 (81%)	35 (16%)	7 (3%)	3	25
33	C	204/206 (99%)	186 (91%)	15 (7%)	3 (2%)	8	38
34	D	203/205 (99%)	167 (82%)	28 (14%)	8 (4%)	2	22
35	E	155/157 (99%)	123 (79%)	21 (14%)	11 (7%)	1	14
36	F	98/100 (98%)	79 (81%)	11 (11%)	8 (8%)	0	11
37	G	149/151 (99%)	124 (83%)	20 (13%)	5 (3%)	3	24
38	H	127/129 (98%)	113 (89%)	11 (9%)	3 (2%)	4	30
39	I	125/127 (98%)	93 (74%)	27 (22%)	5 (4%)	2	21
40	J	96/98 (98%)	67 (70%)	22 (23%)	7 (7%)	1	13
41	K	114/116 (98%)	89 (78%)	20 (18%)	5 (4%)	2	20
42	L	121/123 (98%)	85 (70%)	28 (23%)	8 (7%)	1	15
43	M	112/114 (98%)	93 (83%)	15 (13%)	4 (4%)	2	23
44	N	98/100 (98%)	84 (86%)	12 (12%)	2 (2%)	6	33
45	O	86/88 (98%)	77 (90%)	6 (7%)	3 (4%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	P	80/82 (98%)	62 (78%)	14 (18%)	4 (5%)	1	18
47	Q	78/80 (98%)	63 (81%)	13 (17%)	2 (3%)	4	29
48	R	63/65 (97%)	52 (82%)	8 (13%)	3 (5%)	2	19
49	S	77/79 (98%)	64 (83%)	11 (14%)	2 (3%)	4	29
50	T	83/85 (98%)	75 (90%)	6 (7%)	2 (2%)	4	30
51	U	63/65 (97%)	38 (60%)	21 (33%)	4 (6%)	1	15
52	03	130/223 (58%)	105 (81%)	23 (18%)	2 (2%)	8	38
59	Z	390/392 (100%)	337 (86%)	49 (13%)	4 (1%)	12	45
All	All	6366/6563 (97%)	5298 (83%)	882 (14%)	186 (3%)	5	26

All (186) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	06	83	VAL
3	06	184	ASP
5	08	46	ASP
5	08	174	LYS
6	09	9	VAL
6	09	10	ALA
6	09	41	LYS
6	09	50	ARG
7	10	80	THR
7	10	113	PHE
8	11	11	GLN
9	12	81	ILE
10	13	35	VAL
11	14	36	LYS
11	14	128	THR
12	15	58	LYS
17	20	54	VAL
19	22	39	THR
20	23	6	ARG
24	27	24	GLU
31	34	37	GLN
32	B	18	GLN
32	B	19	THR
32	B	87	ASP
32	B	126	ASP
35	E	122	VAL

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Mol	Chain	Res	Type
37	G	4	ARG
37	G	145	GLU
39	I	57	VAL
39	I	90	ASP
40	J	34	ALA
40	J	58	ASN
40	J	93	ALA
41	K	125	LYS
42	L	43	LYS
43	M	14	ALA
46	P	45	GLU
46	P	79	ASN
47	Q	17	GLU
48	R	13	THR
48	R	19	GLU
50	T	68	LYS
51	U	36	PHE
2	05	169	ARG
5	08	175	LYS
6	09	3	VAL
7	10	3	LEU
11	14	85	VAL
13	16	2	ARG
13	16	71	ARG
15	18	15	ASP
15	18	113	LEU
18	21	66	ILE
20	23	56	GLY
28	31	45	HIS
30	33	27	ASN
32	B	17	HIS
34	D	29	THR
34	D	47	LEU
34	D	169	TRP
35	E	25	LYS
35	E	89	THR
35	E	93	VAL
35	E	102	THR
35	E	121	ASN
36	F	91	ARG
37	G	18	GLY
37	G	64	ALA

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Mol	Chain	Res	Type
37	G	147	ASN
40	J	38	GLY
40	J	89	ARG
42	L	77	SER
44	N	21	ALA
46	P	44	SER
46	P	80	LYS
51	U	14	ALA
52	03	208	TYR
59	Z	3	GLU
1	04	43	ASN
2	05	75	ALA
2	05	149	ASN
4	07	20	ASN
6	09	90	LEU
6	09	91	PHE
7	10	114	GLU
7	10	118	ILE
8	11	6	ALA
10	13	89	ASN
10	13	110	GLU
11	14	117	THR
20	23	51	LEU
31	34	2	LYS
32	B	94	ARG
32	B	179	GLY
33	C	112	ALA
34	D	23	GLY
34	D	167	PRO
35	E	78	GLY
35	E	90	GLY
35	E	99	SER
36	F	56	LYS
38	H	47	ASP
39	I	102	PHE
39	I	125	GLN
41	K	14	GLN
41	K	92	ARG
42	L	24	GLU
42	L	33	CYS
43	M	65	GLU
45	O	87	ARG

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Mol	Chain	Res	Type
51	U	11	PHE
52	03	68	GLY
2	05	104	VAL
3	06	89	PRO
7	10	79	PRO
7	10	120	ALA
8	11	13	ALA
8	11	92	PRO
8	11	97	VAL
12	15	6	ARG
12	15	69	PRO
15	18	75	THR
16	19	21	LYS
17	20	29	THR
19	22	89	GLU
20	23	97	SER
30	33	31	ILE
33	C	50	SER
34	D	28	ASP
34	D	193	ASP
35	E	11	GLN
36	F	39	LEU
36	F	63	ASN
38	H	67	GLY
39	I	91	GLU
40	J	42	LEU
42	L	21	PRO
42	L	35	ARG
42	L	104	SER
43	M	40	GLU
44	N	2	LYS
45	O	46	LYS
48	R	18	GLN
51	U	9	GLU
5	08	47	ASN
7	10	58	THR
7	10	81	LEU
8	11	90	GLY
8	11	102	ARG
9	12	82	GLY
10	13	92	GLU
11	14	129	LYS

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Mol	Chain	Res	Type
34	D	194	ILE
36	F	53	LYS
36	F	54	LEU
36	F	68	GLN
36	F	94	HIS
38	H	65	PHE
42	L	2	THR
45	O	2	LEU
50	T	3	ILE
4	07	175	PRO
6	09	15	LEU
11	14	87	GLY
33	C	45	GLU
35	E	23	THR
47	Q	15	LYS
59	Z	128	PRO
8	11	22	PRO
7	10	119	PRO
14	17	66	GLY
14	17	101	GLY
41	K	77	GLY
41	K	88	PRO
49	S	48	ILE
49	S	53	GLY
1	04	123	ILE
8	11	53	PRO
59	Z	214	ILE
1	04	125	PRO
12	15	89	VAL
59	Z	353	GLY
10	13	93	GLN
21	24	65	VAL
40	J	57	VAL
43	M	6	ILE

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	04	216/216 (100%)	214 (99%)	2 (1%)	70	76
2	05	164/164 (100%)	162 (99%)	2 (1%)	63	73
3	06	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	07	148/148 (100%)	145 (98%)	3 (2%)	48	66
5	08	137/137 (100%)	136 (99%)	1 (1%)	76	79
6	09	114/114 (100%)	113 (99%)	1 (1%)	70	76
7	10	100/100 (100%)	99 (99%)	1 (1%)	68	76
8	11	109/109 (100%)	107 (98%)	2 (2%)	51	68
9	12	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	13	103/103 (100%)	102 (99%)	1 (1%)	68	76
11	14	102/102 (100%)	101 (99%)	1 (1%)	68	76
12	15	109/109 (100%)	107 (98%)	2 (2%)	51	68
13	16	100/100 (100%)	99 (99%)	1 (1%)	68	76
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	82 (98%)	2 (2%)	43	63
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	22	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	23	83/83 (100%)	83 (100%)	0	100	100
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	55 (100%)	0	100	100
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	44 (98%)	1 (2%)	45	65
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	34 (100%)	0	100	100
32	B	180/180 (100%)	178 (99%)	2 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	C	170/170 (100%)	169 (99%)	1 (1%)	78	81
34	D	172/172 (100%)	167 (97%)	5 (3%)	37	58
35	E	119/119 (100%)	117 (98%)	2 (2%)	53	68
36	F	87/87 (100%)	86 (99%)	1 (1%)	65	74
37	G	124/124 (100%)	121 (98%)	3 (2%)	43	63
38	H	104/104 (100%)	103 (99%)	1 (1%)	68	76
39	I	105/105 (100%)	104 (99%)	1 (1%)	68	76
40	J	86/86 (100%)	85 (99%)	1 (1%)	63	73
41	K	89/89 (100%)	85 (96%)	4 (4%)	24	47
42	L	103/103 (100%)	103 (100%)	0	100	100
43	M	92/92 (100%)	90 (98%)	2 (2%)	45	65
44	N	83/83 (100%)	82 (99%)	1 (1%)	63	73
45	O	76/76 (100%)	74 (97%)	2 (3%)	40	61
46	P	65/65 (100%)	63 (97%)	2 (3%)	35	56
47	Q	74/74 (100%)	72 (97%)	2 (3%)	39	60
48	R	56/56 (100%)	56 (100%)	0	100	100
49	S	70/70 (100%)	68 (97%)	2 (3%)	37	58
50	T	65/65 (100%)	62 (95%)	3 (5%)	24	47
51	U	55/55 (100%)	54 (98%)	1 (2%)	51	68
52	03	110/174 (63%)	109 (99%)	1 (1%)	70	76
59	Z	324/325 (100%)	316 (98%)	8 (2%)	42	62
All	All	5285/5350 (99%)	5216 (99%)	69 (1%)	59	72

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	04	196	ASN
1	04	217	PRO
2	05	40	LEU
2	05	88	GLU
3	06	163	ASN
4	07	9	ASP
4	07	43	ILE
4	07	146	ASP
5	08	46	ASP

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Mol	Chain	Res	Type
6	09	12	LEU
7	10	129	LEU
8	11	92	PRO
8	11	93	ASN
9	12	129	GLU
10	13	54	LYS
11	14	30	THR
12	15	6	ARG
12	15	127	LYS
13	16	117	ASP
17	20	11	GLN
17	20	84	ARG
18	21	46	LEU
19	22	37	ASP
28	31	45	HIS
32	B	23	ASN
32	B	116	LEU
33	C	156	LEU
34	D	28	ASP
34	D	29	THR
34	D	87	GLU
34	D	139	ASN
34	D	158	LEU
35	E	10	LEU
35	E	75	LEU
36	F	11	HIS
37	G	4	ARG
37	G	12	LEU
37	G	139	ASP
38	H	59	GLU
39	I	88	GLU
40	J	91	ASP
41	K	12	ARG
41	K	30	ILE
41	K	35	ASP
41	K	75	GLU
43	M	33	LEU
43	M	99	GLN
44	N	48	GLN
45	O	38	LEU
45	O	86	LEU
46	P	19	VAL

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Mol	Chain	Res	Type
46	P	45	GLU
47	Q	49	ASN
47	Q	74	LEU
49	S	10	ILE
49	S	42	ASN
50	T	20	ASN
50	T	48	LYS
50	T	83	ASN
51	U	20	ARG
52	03	24	ASN
59	Z	21	ASP
59	Z	70	ASP
59	Z	113	PRO
59	Z	114	GLN
59	Z	144	GLU
59	Z	236	ILE
59	Z	329	GLN
59	Z	361	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (138) such sidechains are listed below:

Mol	Chain	Res	Type
1	04	14	HIS
1	04	20	ASN
1	04	36	ASN
1	04	69	ASN
1	04	85	ASN
1	04	127	ASN
1	04	133	ASN
1	04	196	ASN
1	04	199	HIS
2	05	32	ASN
2	05	94	GLN
2	05	148	GLN
2	05	173	GLN
2	05	185	ASN
3	06	90	GLN
3	06	94	GLN
3	06	115	GLN
3	06	163	ASN
4	07	22	ASN
5	08	21	GLN

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Mol	Chain	Res	Type
5	08	63	GLN
5	08	100	ASN
5	08	138	GLN
6	09	2	GLN
6	09	11	ASN
6	09	20	ASN
6	09	43	ASN
6	09	145	ASN
7	10	4	ASN
7	10	88	HIS
7	10	103	ASN
8	11	42	ASN
8	11	93	ASN
9	12	58	ASN
9	12	128	ASN
11	14	54	GLN
11	14	99	ASN
12	15	3	GLN
12	15	17	ASN
13	16	23	ASN
13	16	62	ASN
13	16	107	ASN
14	17	19	GLN
14	17	104	GLN
15	18	2	ASN
15	18	11	GLN
15	18	14	GLN
15	18	40	GLN
16	19	43	GLN
16	19	51	GLN
16	19	55	GLN
16	19	58	GLN
16	19	65	ASN
17	20	91	GLN
18	21	7	HIS
18	21	57	ASN
20	23	65	GLN
20	23	68	ASN
20	23	73	ASN
21	24	5	ASN
21	24	78	GLN
22	25	8	ASN

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Mol	Chain	Res	Type
22	25	72	ASN
23	26	15	ASN
23	26	19	HIS
24	27	20	ASN
24	27	31	GLN
24	27	39	GLN
24	27	41	HIS
24	27	58	ASN
25	28	8	GLN
27	30	4	GLN
27	30	5	ASN
28	31	45	HIS
29	32	29	GLN
32	B	23	ASN
32	B	38	HIS
32	B	102	ASN
32	B	121	GLN
32	B	176	ASN
32	B	189	ASN
33	C	24	ASN
33	C	138	GLN
33	C	139	ASN
34	D	53	GLN
34	D	73	ASN
34	D	130	ASN
34	D	139	ASN
34	D	195	ASN
34	D	197	HIS
35	E	76	ASN
35	E	131	ASN
35	E	147	ASN
36	F	17	GLN
36	F	55	HIS
36	F	81	ASN
37	G	27	ASN
37	G	67	ASN
37	G	147	ASN
38	H	17	GLN
39	I	74	GLN
39	I	125	GLN
40	J	64	GLN
41	K	14	GLN

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Mol	Chain	Res	Type
41	K	27	ASN
41	K	63	GLN
42	L	4	ASN
42	L	45	ASN
42	L	72	ASN
43	M	99	GLN
44	N	48	GLN
45	O	36	ASN
46	P	18	GLN
46	P	26	ASN
46	P	79	ASN
47	Q	8	GLN
47	Q	44	HIS
48	R	53	GLN
49	S	42	ASN
49	S	55	GLN
50	T	20	ASN
50	T	51	ASN
50	T	69	ASN
51	U	8	ASN
51	U	55	HIS
52	03	20	GLN
52	03	24	ASN
52	03	57	GLN
52	03	203	GLN
59	Z	13	ASN
59	Z	19	HIS
59	Z	66	HIS
59	Z	90	ASN
59	Z	97	GLN
59	Z	124	GLN
59	Z	159	GLN
59	Z	290	GLN
59	Z	329	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	150 (9%)	7 (0%)
54	01	2902/2903 (99%)	348 (11%)	12 (0%)
55	02	119/120 (99%)	11 (9%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	W	76/77 (98%)	8 (10%)	0
56	X	76/77 (98%)	14 (18%)	0
57	V	16/17 (94%)	2 (12%)	0
58	Y	75/76 (98%)	22 (29%)	0
All	All	4802/4809 (99%)	555 (11%)	20 (0%)

All (555) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	9	G
53	A	31	G
53	A	32	A
53	A	39	G
53	A	51	A
53	A	71	A
53	A	82	G
53	A	85	U
53	A	87	C
53	A	95	C
53	A	100	G
53	A	116	A
53	A	121	U
53	A	130	A
53	A	144	G
53	A	173	U
53	A	177	G
53	A	183	C
53	A	184	G
53	A	197	A
53	A	209	U
53	A	210	C
53	A	226	G
53	A	247	G
53	A	251	G
53	A	253	A
53	A	266	G
53	A	267	C
53	A	281	G
53	A	289	G
53	A	306	A
53	A	328	C

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Mol	Chain	Res	Type
53	A	345	C
53	A	346	G
53	A	352	C
53	A	367	U
53	A	372	C
53	A	411	A
53	A	412	A
53	A	413	G
53	A	422	C
53	A	429	U
53	A	439	U
53	A	467	U
53	A	482	A
53	A	485	U
53	A	486	U
53	A	495	A
53	A	497	G
53	A	518	C
53	A	521	G
53	A	527	G
53	A	531	U
53	A	532	A
53	A	533	A
53	A	547	A
53	A	561	U
53	A	564	C
53	A	572	A
53	A	573	A
53	A	575	G
53	A	576	C
53	A	577	G
53	A	633	G
53	A	642	A
53	A	650	G
53	A	653	U
53	A	665	A
53	A	666	G
53	A	703	G
53	A	724	G
53	A	755	G
53	A	777	A
53	A	814	A

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Mol	Chain	Res	Type
53	A	815	A
53	A	817	C
53	A	818	G
53	A	819	A
53	A	821	G
53	A	843	U
53	A	844	G
53	A	846	G
53	A	873	A
53	A	890	G
53	A	926	G
53	A	934	C
53	A	935	A
53	A	960	U
53	A	961	U
53	A	966	G
53	A	969	A
53	A	975	A
53	A	976	G
53	A	977	A
53	A	992	U
53	A	993	G
53	A	1004	A
53	A	1028	C
53	A	1031	C
53	A	1033	G
53	A	1034	G
53	A	1053	G
53	A	1094	G
53	A	1101	A
53	A	1130	A
53	A	1137	C
53	A	1138	G
53	A	1139	G
53	A	1159	U
53	A	1168	U
53	A	1183	U
53	A	1184	G
53	A	1191	A
53	A	1196	A
53	A	1197	A
53	A	1202	U

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Mol	Chain	Res	Type
53	A	1212	U
53	A	1213	A
53	A	1225	A
53	A	1238	A
53	A	1240	U
53	A	1241	G
53	A	1253	G
53	A	1256	A
53	A	1258	G
53	A	1260	G
53	A	1278	G
53	A	1280	A
53	A	1282	C
53	A	1287	A
53	A	1300	G
53	A	1317	C
53	A	1320	C
53	A	1323	G
53	A	1346	A
53	A	1347	G
53	A	1395	C
53	A	1446	A
53	A	1448	C
53	A	1452	C
53	A	1492	A
53	A	1499	A
53	A	1506	U
53	A	1517	G
53	A	1519	A
53	A	1529	G
53	A	1530	G
53	A	1534	A
53	A	1540	U
54	01	10	A
54	01	12	U
54	01	34	U
54	01	35	G
54	01	50	U
54	01	51	G
54	01	63	A
54	01	71	A
54	01	74	A

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Mol	Chain	Res	Type
54	01	75	G
54	01	84	A
54	01	114	U
54	01	119	A
54	01	120	U
54	01	139	U
54	01	140	C
54	01	141	G
54	01	142	A
54	01	162	U
54	01	163	C
54	01	181	A
54	01	196	A
54	01	199	A
54	01	200	U
54	01	216	A
54	01	221	A
54	01	222	A
54	01	242	G
54	01	243	U
54	01	248	G
54	01	249	C
54	01	255	A
54	01	266	G
54	01	276	U
54	01	278	A
54	01	281	C
54	01	294	A
54	01	301	G
54	01	311	A
54	01	312	G
54	01	323	C
54	01	324	A
54	01	329	G
54	01	330	A
54	01	361	G
54	01	371	A
54	01	372	G
54	01	373	U
54	01	386	G
54	01	387	U
54	01	404	A

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Mol	Chain	Res	Type
54	01	406	G
54	01	411	G
54	01	424	G
54	01	451	U
54	01	454	A
54	01	457	A
54	01	458	G
54	01	481	G
54	01	491	G
54	01	504	A
54	01	505	A
54	01	506	G
54	01	529	A
54	01	531	C
54	01	532	A
54	01	542	C
54	01	543	G
54	01	545	U
54	01	547	A
54	01	563	A
54	01	573	U
54	01	575	A
54	01	588	U
54	01	603	A
54	01	616	A
54	01	627	A
54	01	628	G
54	01	637	A
54	01	646	U
54	01	654	A
54	01	655	A
54	01	669	G
54	01	686	U
54	01	687	C
54	01	717	C
54	01	730	A
54	01	747	C
54	01	748	G
54	01	752	A
54	01	757	G
54	01	764	A
54	01	776	G

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Mol	Chain	Res	Type
54	01	782	A
54	01	784	G
54	01	785	G
54	01	805	G
54	01	806	C
54	01	812	C
54	01	819	A
54	01	827	U
54	01	828	U
54	01	830	G
54	01	845	A
54	01	846	U
54	01	847	U
54	01	858	G
54	01	860	U
54	01	878	A
54	01	885	C
54	01	886	A
54	01	887	U
54	01	896	A
54	01	907	G
54	01	910	A
54	01	932	U
54	01	941	A
54	01	946	C
54	01	961	C
54	01	974	G
54	01	975	A
54	01	983	A
54	01	995	C
54	01	1012	U
54	01	1013	C
54	01	1021	A
54	01	1022	G
54	01	1026	G
54	01	1033	U
54	01	1045	C
54	01	1046	A
54	01	1054	A
54	01	1059	G
54	01	1060	U
54	01	1062	G

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Mol	Chain	Res	Type
54	01	1066	U
54	01	1070	A
54	01	1071	G
54	01	1079	C
54	01	1084	A
54	01	1088	A
54	01	1104	C
54	01	1106	G
54	01	1111	A
54	01	1131	G
54	01	1132	U
54	01	1133	A
54	01	1135	C
54	01	1157	G
54	01	1174	U
54	01	1175	A
54	01	1176	U
54	01	1177	G
54	01	1178	C
54	01	1179	G
54	01	1180	U
54	01	1206	G
54	01	1211	C
54	01	1212	G
54	01	1250	G
54	01	1251	C
54	01	1253	A
54	01	1256	G
54	01	1271	G
54	01	1272	A
54	01	1289	C
54	01	1301	A
54	01	1315	C
54	01	1321	A
54	01	1329	U
54	01	1341	G
54	01	1345	C
54	01	1365	A
54	01	1378	A
54	01	1379	U
54	01	1383	A
54	01	1395	A

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Mol	Chain	Res	Type
54	01	1398	C
54	01	1416	G
54	01	1419	A
54	01	1420	A
54	01	1428	C
54	01	1454	C
54	01	1461	C
54	01	1482	G
54	01	1490	A
54	01	1493	C
54	01	1498	C
54	01	1504	A
54	01	1515	A
54	01	1524	G
54	01	1533	C
54	01	1535	A
54	01	1536	C
54	01	1537	G
54	01	1555	G
54	01	1560	G
54	01	1569	A
54	01	1584	U
54	01	1608	A
54	01	1611	C
54	01	1616	A
54	01	1647	U
54	01	1648	U
54	01	1654	A
54	01	1665	A
54	01	1674	G
54	01	1715	G
54	01	1729	U
54	01	1730	C
54	01	1732	C
54	01	1738	G
54	01	1758	U
54	01	1764	C
54	01	1773	A
54	01	1780	A
54	01	1800	C
54	01	1801	A
54	01	1802	A

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Mol	Chain	Res	Type
54	01	1808	A
54	01	1816	C
54	01	1829	A
54	01	1866	A
54	01	1871	A
54	01	1901	A
54	01	1906	G
54	01	1907	G
54	01	1913	A
54	01	1929	G
54	01	1930	G
54	01	1931	U
54	01	1938	A
54	01	1955	U
54	01	1963	U
54	01	1967	C
54	01	1970	A
54	01	1971	U
54	01	1972	G
54	01	1991	U
54	01	1993	U
54	01	1997	C
54	01	2006	C
54	01	2021	C
54	01	2022	U
54	01	2023	C
54	01	2030	A
54	01	2031	A
54	01	2033	A
54	01	2036	C
54	01	2043	C
54	01	2049	G
54	01	2052	A
54	01	2055	C
54	01	2056	G
54	01	2060	A
54	01	2061	G
54	01	2062	A
54	01	2069	G
54	01	2072	C
54	01	2095	A
54	01	2110	G

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Mol	Chain	Res	Type
54	01	2111	U
54	01	2112	G
54	01	2115	G
54	01	2118	U
54	01	2119	A
54	01	2132	U
54	01	2133	G
54	01	2145	C
54	01	2147	A
54	01	2162	G
54	01	2164	C
54	01	2172	U
54	01	2173	A
54	01	2198	A
54	01	2199	A
54	01	2203	U
54	01	2204	G
54	01	2211	A
54	01	2212	A
54	01	2225	A
54	01	2239	G
54	01	2250	G
54	01	2259	U
54	01	2278	A
54	01	2283	C
54	01	2287	A
54	01	2297	A
54	01	2305	U
54	01	2309	A
54	01	2325	G
54	01	2327	A
54	01	2334	U
54	01	2335	A
54	01	2350	C
54	01	2382	G
54	01	2383	G
54	01	2385	C
54	01	2392	A
54	01	2402	U
54	01	2423	U
54	01	2424	C
54	01	2427	C

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Mol	Chain	Res	Type
54	01	2429	G
54	01	2430	A
54	01	2435	A
54	01	2441	U
54	01	2448	A
54	01	2476	A
54	01	2484	G
54	01	2498	C
54	01	2502	G
54	01	2503	A
54	01	2505	G
54	01	2518	A
54	01	2529	G
54	01	2547	A
54	01	2554	U
54	01	2567	G
54	01	2602	A
54	01	2609	U
54	01	2613	U
54	01	2629	U
54	01	2646	C
54	01	2655	G
54	01	2682	A
54	01	2689	U
54	01	2690	U
54	01	2714	G
54	01	2744	G
54	01	2748	A
54	01	2764	A
54	01	2765	A
54	01	2778	A
54	01	2779	U
54	01	2791	G
54	01	2794	C
54	01	2797	U
54	01	2799	A
54	01	2800	A
54	01	2801	G
54	01	2809	A
54	01	2820	A
54	01	2833	U
54	01	2867	G

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Mol	Chain	Res	Type
54	01	2868	A
54	01	2880	C
54	01	2884	U
55	02	4	C
55	02	13	G
55	02	24	G
55	02	35	C
55	02	44	G
55	02	45	A
55	02	67	G
55	02	89	U
55	02	90	C
55	02	108	A
55	02	109	A
56	X	3	C
56	X	5	G
56	X	8	U
56	X	9	G
56	X	10	G
56	X	14	A
56	X	18	G
56	X	21	A
56	X	22	G
56	X	34	C
56	X	38	A
56	X	67	C
56	X	69	C
56	X	70	G
57	V	12	A
57	V	20	G
56	W	9	G
56	W	19	G
56	W	20	U
56	W	47	U
56	W	48	C
56	W	59	A
56	W	61	C
56	W	76	A
58	Y	4	U
58	Y	9	A
58	Y	13	C
58	Y	14	A

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Mol	Chain	Res	Type
58	Y	19	G
58	Y	21	A
58	Y	27	G
58	Y	36	U
58	Y	46	G
58	Y	47	U
58	Y	48	C
58	Y	49	G
58	Y	50	C
58	Y	55	U
58	Y	61	C
58	Y	66	A
58	Y	70	C
58	Y	71	C
58	Y	72	C
58	Y	74	C
58	Y	75	C
58	Y	76	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	246	A
53	A	438	U
53	A	1182	G
53	A	1190	G
53	A	1201	A
53	A	1300	G
53	A	1347	G
54	01	242	G
54	01	265	A
54	01	372	G
54	01	490	C
54	01	859	G
54	01	1020	A
54	01	1130	U
54	01	1378	A
54	01	1930	G
54	01	2326	C
54	01	2391	G
54	01	2808	G
55	02	88	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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$
58	U8U	Y	34	58	20,24,25	1.24	2 (10%)	22,34,37	1.00	2 (9%)

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
58	U8U	Y	34	58	-	3/10/28/29	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	Y	34	U8U	C6-N1	3.84	1.44	1.38
58	Y	34	U8U	C4-C5	2.58	1.51	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Y	34	U8U	C2'-C1'-N1	2.56	120.36	113.25
58	Y	34	U8U	C5-C6-N1	2.01	125.64	122.94

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	Y	34	U8U	N-C-C5-C4
58	Y	34	U8U	C5-C-N-CA
58	Y	34	U8U	N-C-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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
60	GCP	Z	401	-	32,34,34	1.76	5 (15%)	49,54,54	2.57	15 (30%)

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
60	GCP	Z	401	-	-	9/19/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	Z	401	GCP	PA-O3A	-5.68	1.53	1.59
60	Z	401	GCP	PB-O3A	-4.16	1.53	1.58
60	Z	401	GCP	C1'-N9	3.16	1.56	1.47
60	Z	401	GCP	PB-O2B	-2.13	1.51	1.56
60	Z	401	GCP	C2'-C3'	2.13	1.59	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	Z	401	GCP	C1'-N9-C4	8.23	150.81	126.49
60	Z	401	GCP	C1'-N9-C8	-7.81	104.54	126.73
60	Z	401	GCP	O1G-PG-C3B	-7.37	95.29	111.37
60	Z	401	GCP	O2B-PB-O1B	3.86	122.50	109.95
60	Z	401	GCP	O5'-PA-O1A	-3.75	94.07	108.94
60	Z	401	GCP	O4'-C1'-C2'	-3.72	98.65	106.62
60	Z	401	GCP	O2A-PA-O3A	-3.60	97.55	107.27
60	Z	401	GCP	O3'-C3'-C4'	-3.47	101.12	111.08
60	Z	401	GCP	O3G-PG-O1G	3.10	120.41	112.39
60	Z	401	GCP	PB-O3A-PA	2.73	141.27	132.37
60	Z	401	GCP	C2'-C1'-N9	2.65	120.62	113.25
60	Z	401	GCP	C3'-C2'-C1'	-2.60	96.55	101.46
60	Z	401	GCP	O2G-PG-C3B	2.50	112.47	106.40
60	Z	401	GCP	O2A-PA-O1A	2.41	123.65	112.44
60	Z	401	GCP	O4'-C4'-C5'	2.26	116.59	109.33

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	Z	401	GCP	PB-C3B-PG-O1G
60	Z	401	GCP	PB-C3B-PG-O2G
60	Z	401	GCP	PG-C3B-PB-O1B
60	Z	401	GCP	O4'-C4'-C5'-O5'
60	Z	401	GCP	C3'-C4'-C5'-O5'
60	Z	401	GCP	PB-C3B-PG-O3G
60	Z	401	GCP	C5'-O5'-PA-O3A
60	Z	401	GCP	C5'-O5'-PA-O1A
60	Z	401	GCP	C5'-O5'-PA-O2A

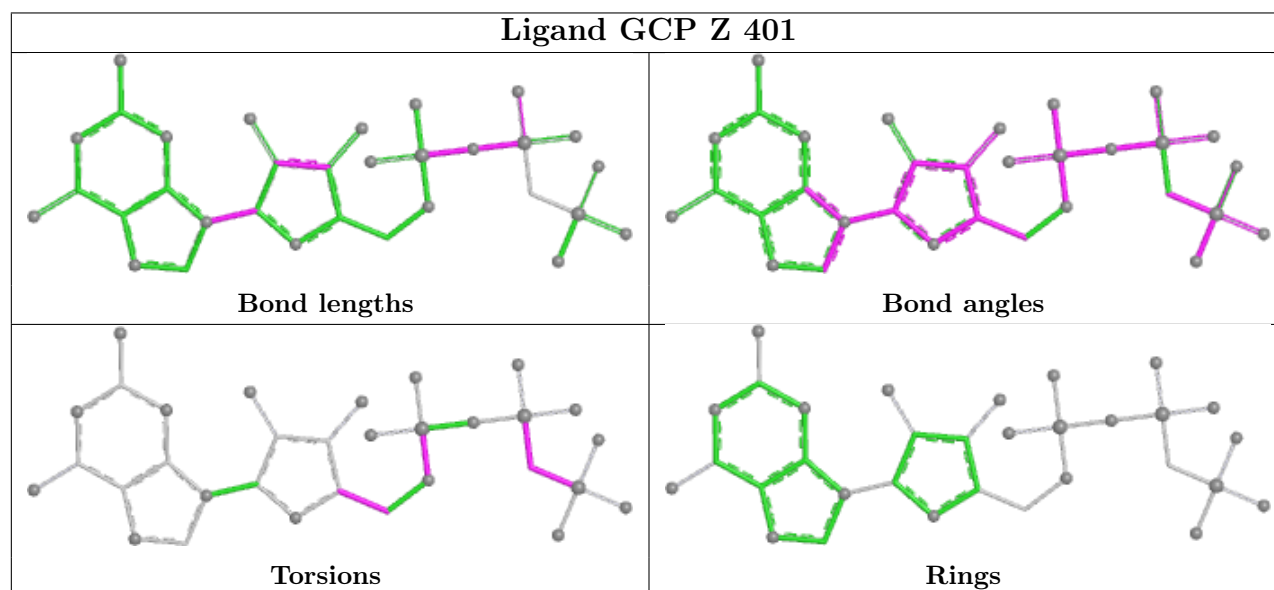
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Z	401	GCP	1	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

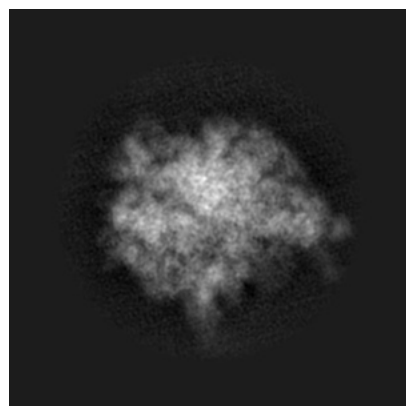
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8618. These allow visual inspection of the internal detail of the map and identification of artifacts.

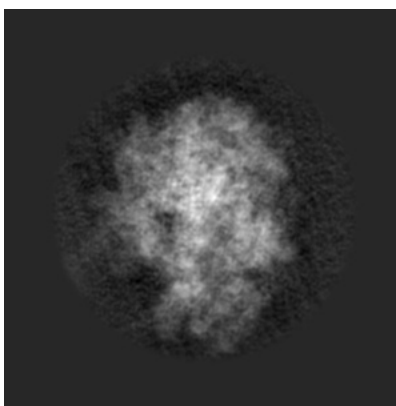
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

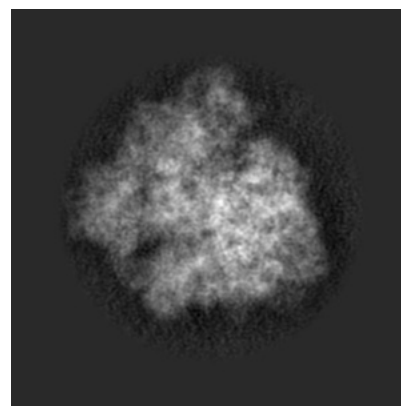
6.1.1 Primary map



X

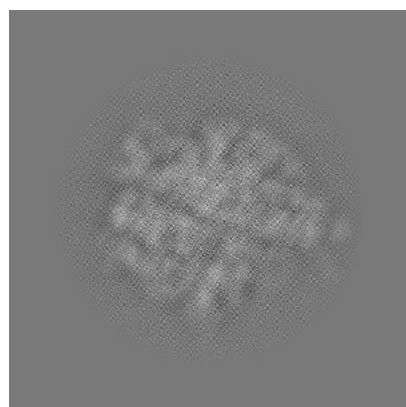


Y

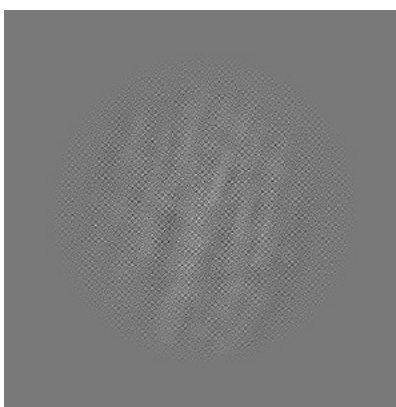


Z

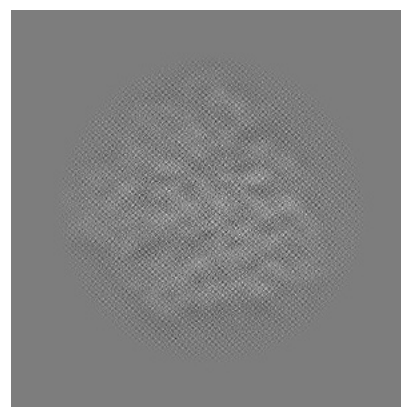
6.1.2 Raw map



X



Y

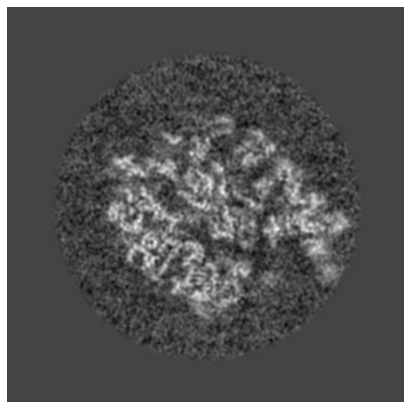


Z

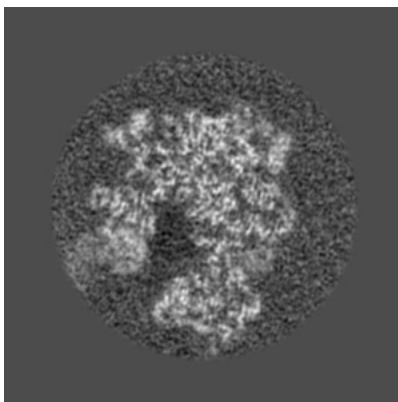
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

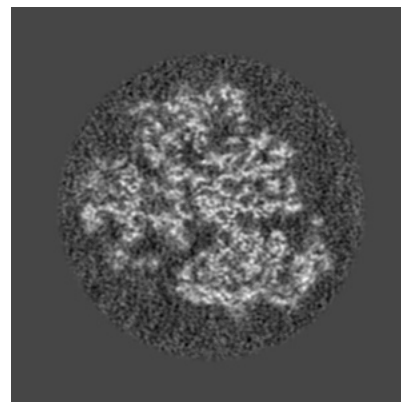
6.2.1 Primary map



X Index: 240

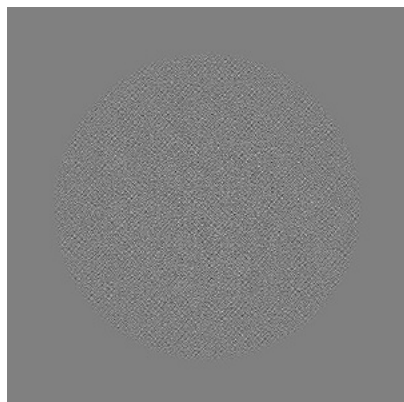


Y Index: 240

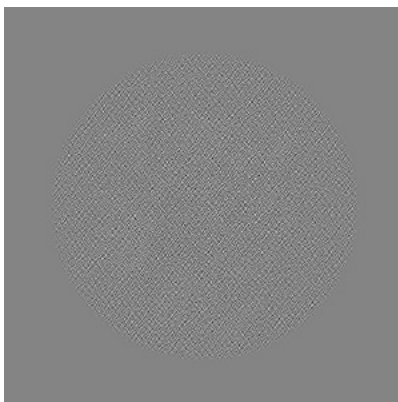


Z Index: 240

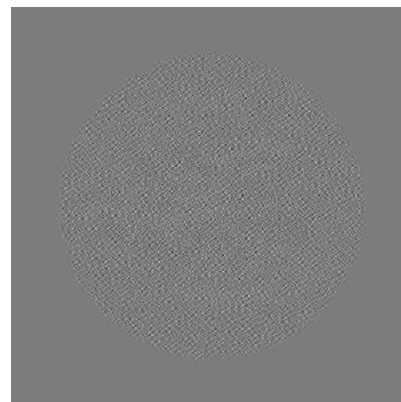
6.2.2 Raw map



X Index: 240



Y Index: 240

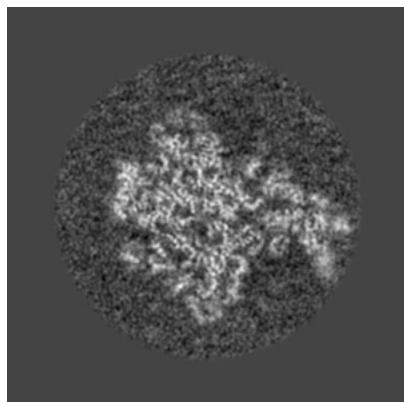


Z Index: 240

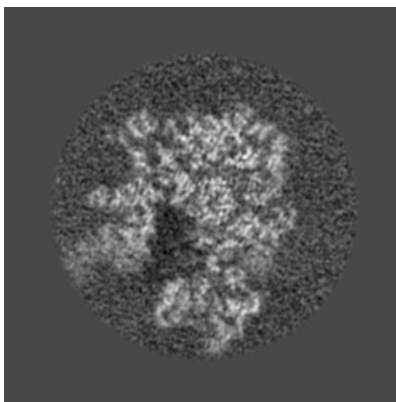
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

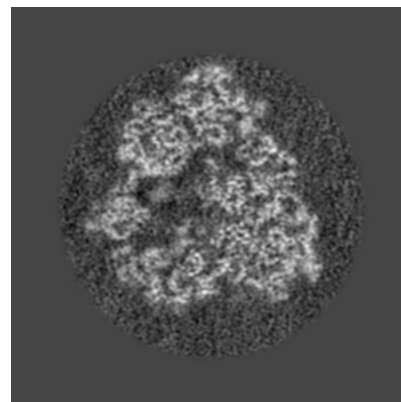
6.3.1 Primary map



X Index: 251

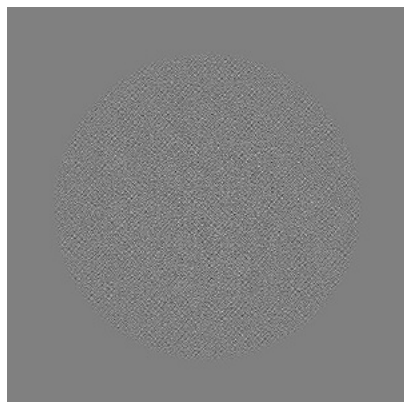


Y Index: 244

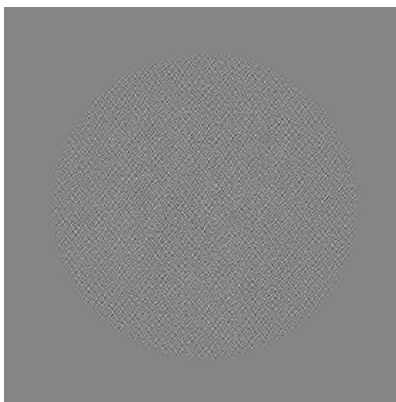


Z Index: 219

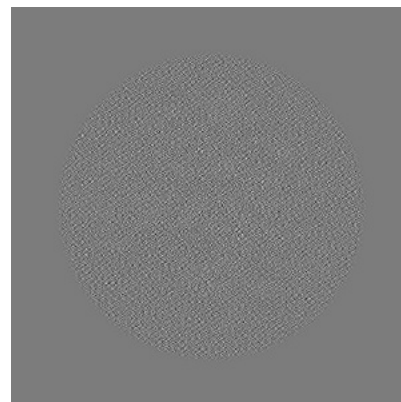
6.3.2 Raw map



X Index: 240



Y Index: 234

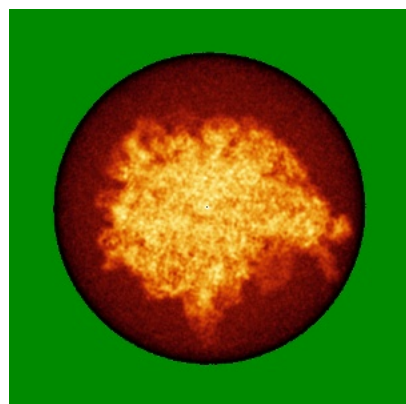


Z Index: 252

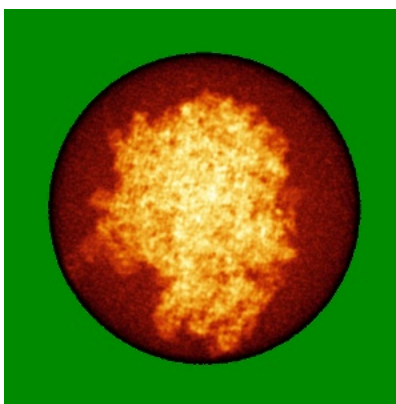
The images above show the largest variance slices of the map in three orthogonal directions.

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

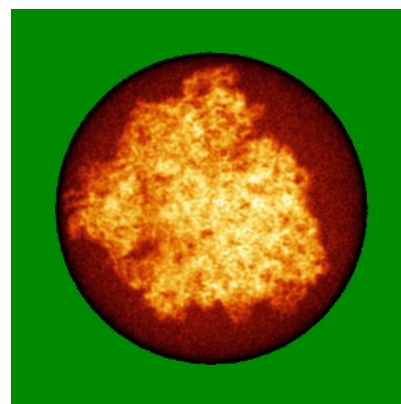
6.4.1 Primary map



X

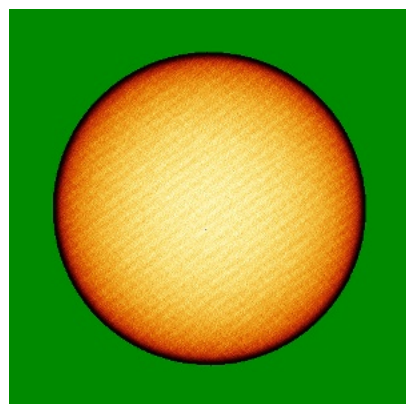


Y

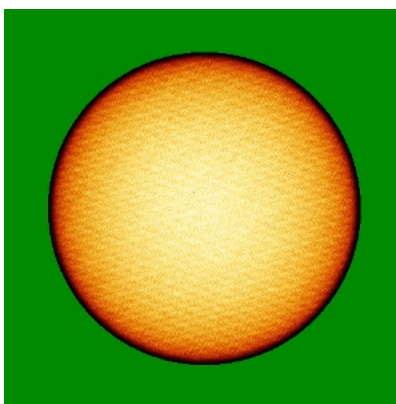


Z

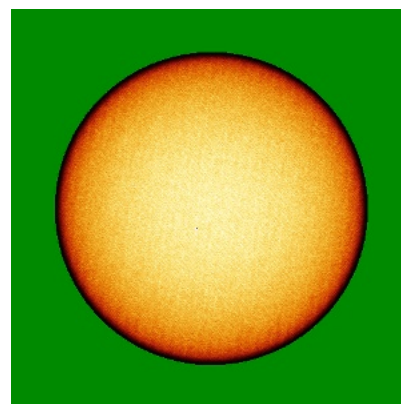
6.4.2 Raw map



X



Y



Z

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

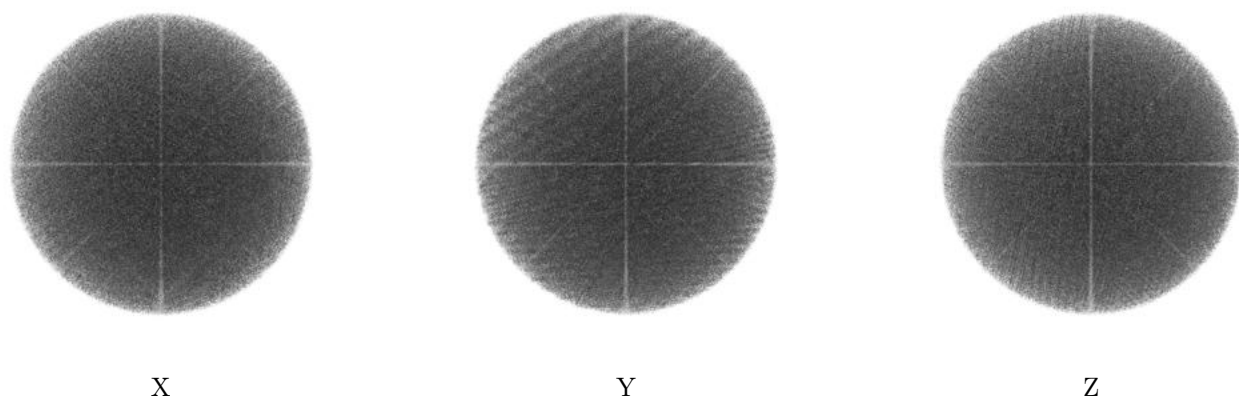
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.79. 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.

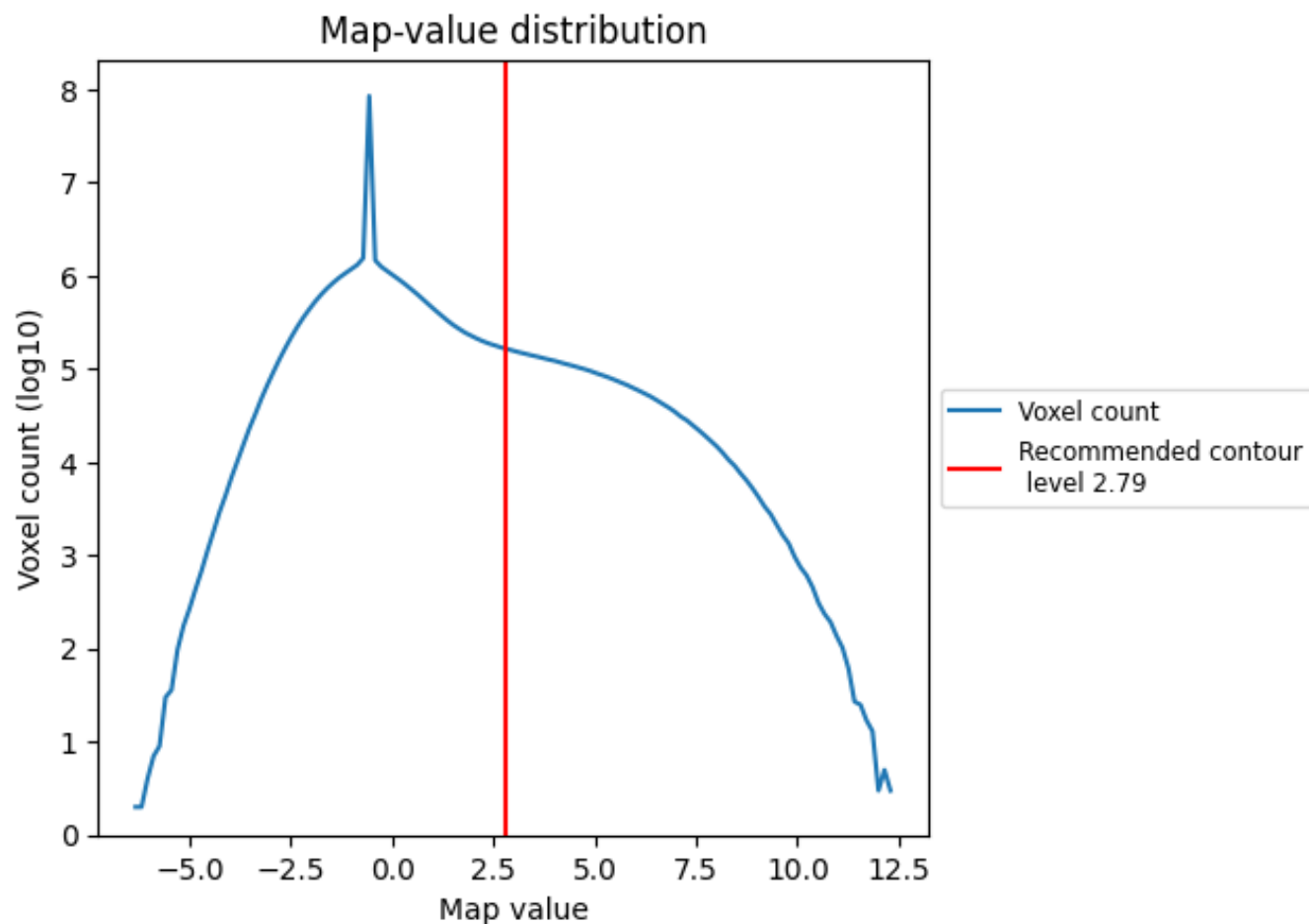
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

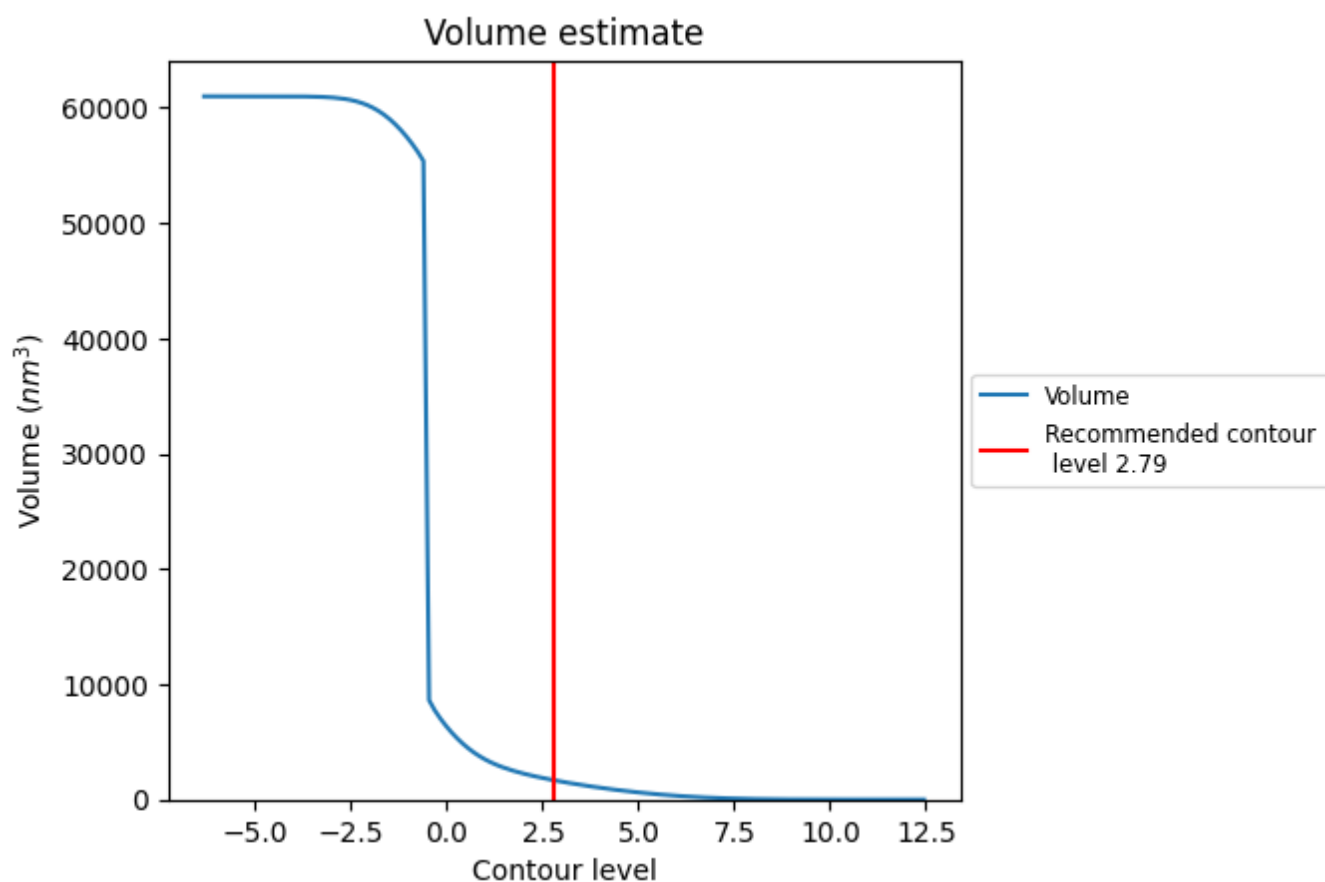
This section contains the results of statistical analysis of the map.

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.

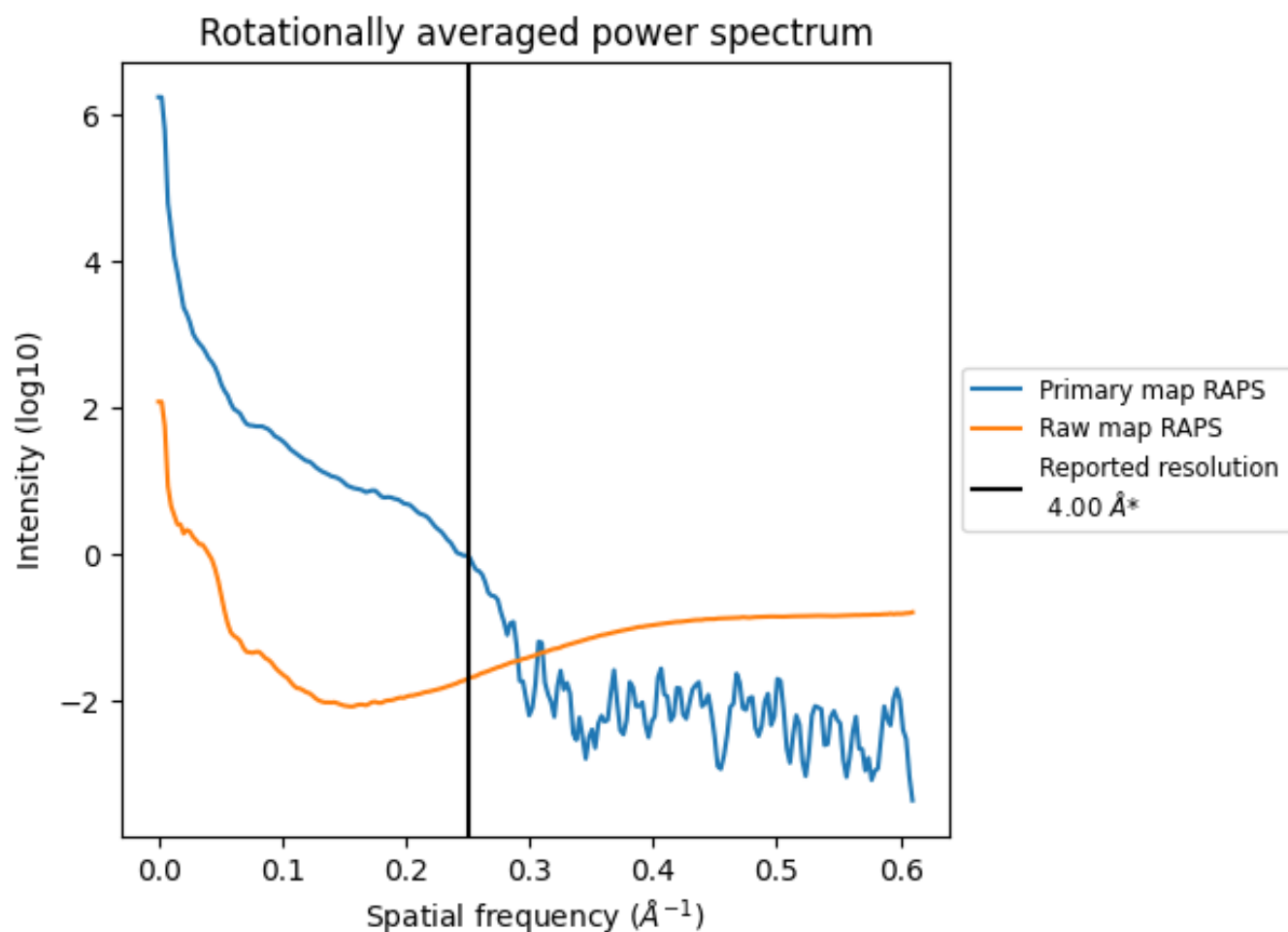
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1679 nm³; this corresponds to an approximate mass of 1517 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 ⓘ

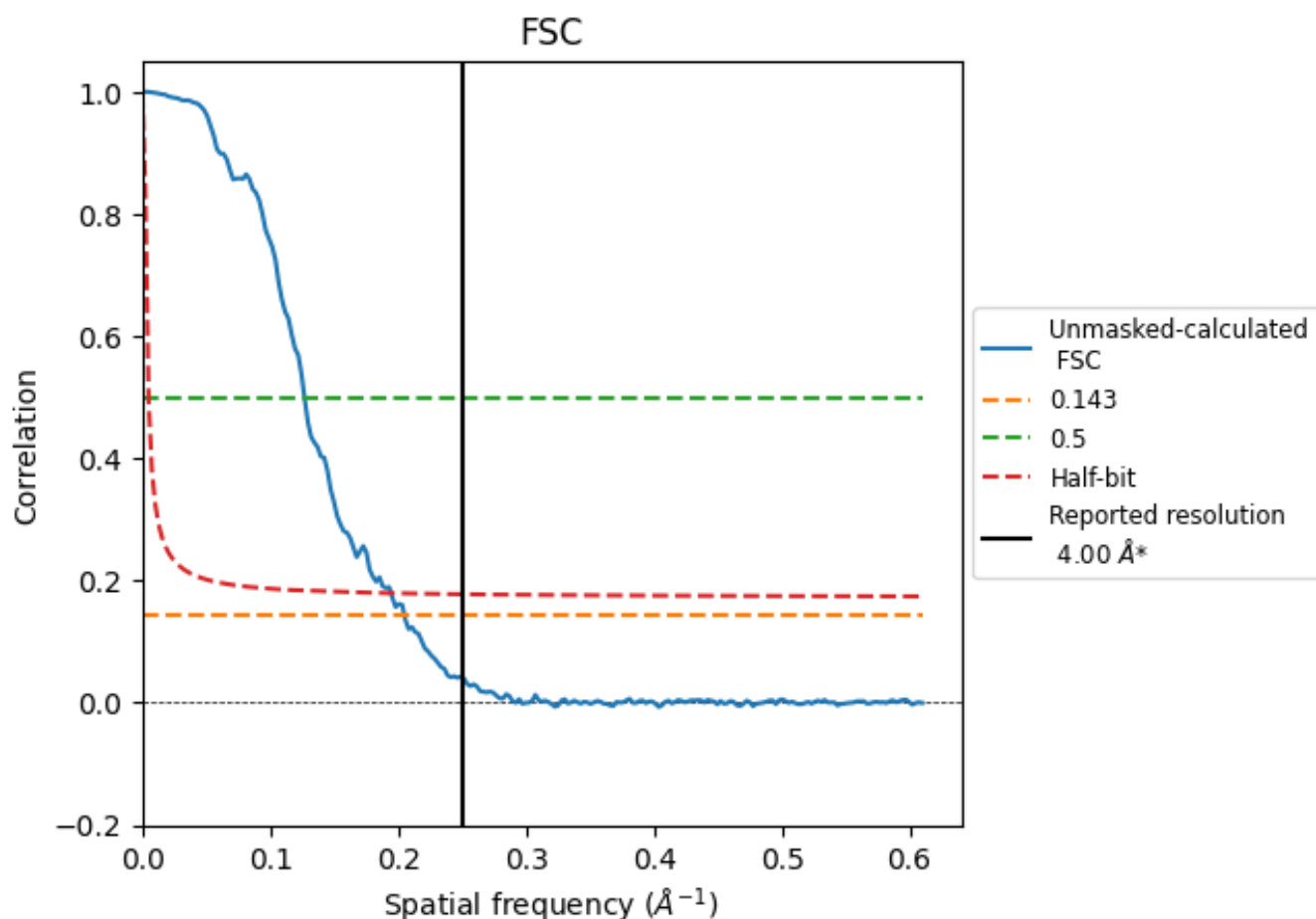


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

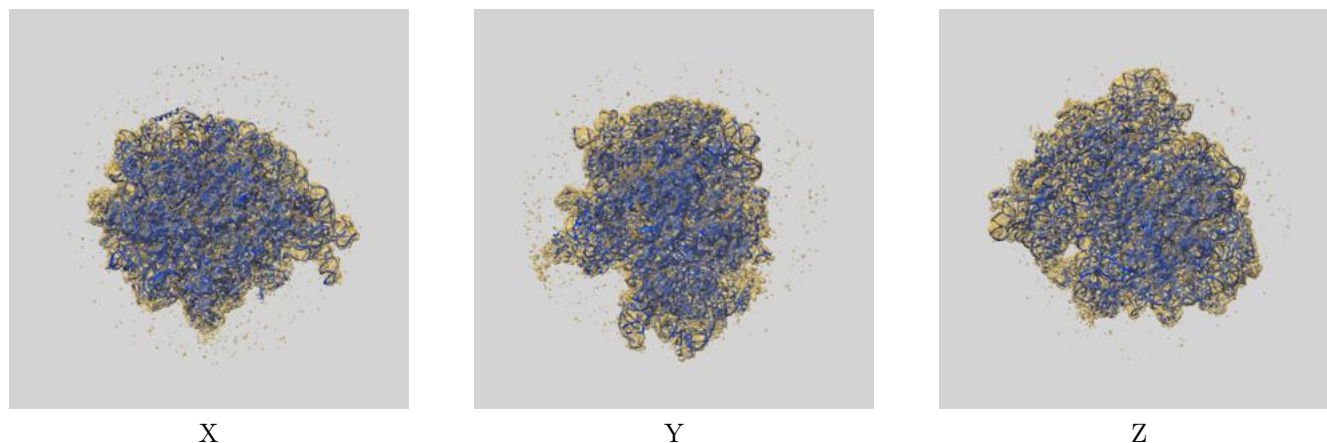
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.88	7.88	5.14

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.88 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8618 and PDB model 5UYN. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



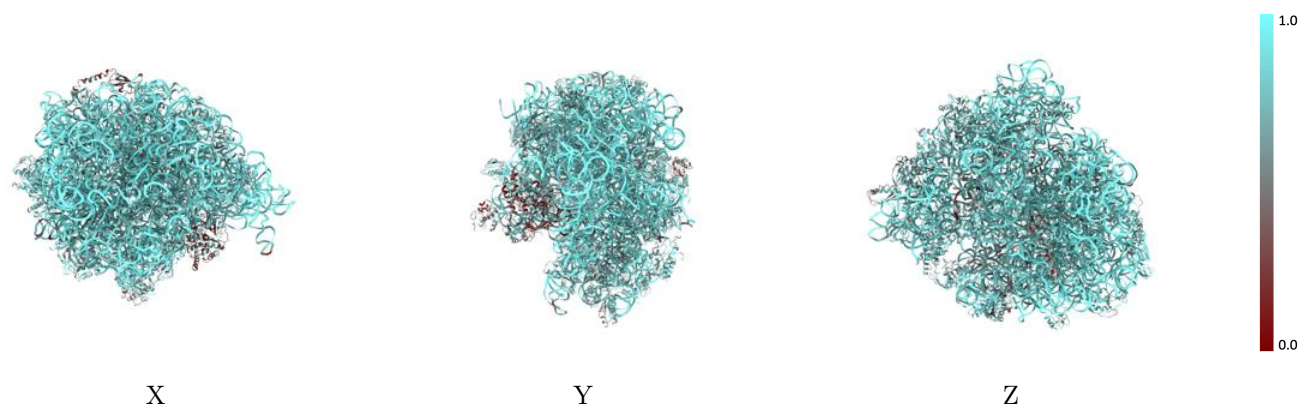
The images above show the 3D surface view of the map at the recommended contour level 2.79 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



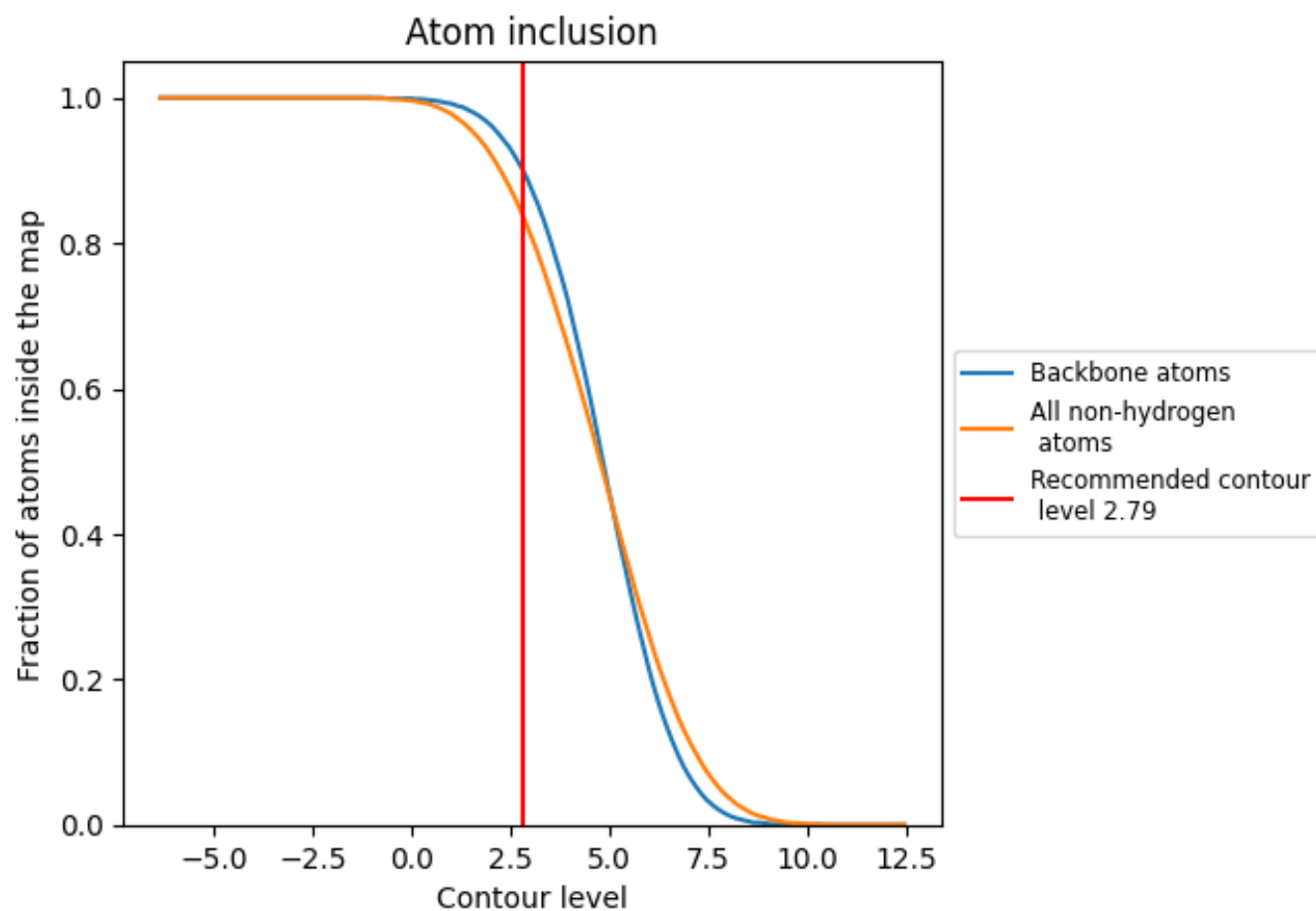
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.79).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.79) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.3160
01	 0.9270	 0.3300
02	 0.9360	 0.3190
03	 0.5890	 0.2000
04	 0.7880	 0.3640
05	 0.7680	 0.3660
06	 0.7440	 0.3180
07	 0.7550	 0.3010
08	 0.7980	 0.3200
09	 0.4200	 0.2620
10	 0.4410	 0.1700
11	 0.5460	 0.2060
12	 0.7500	 0.3500
13	 0.6630	 0.3550
14	 0.7580	 0.3250
15	 0.6810	 0.3550
16	 0.7980	 0.3280
17	 0.7990	 0.3150
18	 0.7190	 0.3290
19	 0.7660	 0.3220
20	 0.7140	 0.3100
21	 0.7050	 0.3190
22	 0.7650	 0.3240
23	 0.7550	 0.2910
24	 0.7910	 0.3420
25	 0.7660	 0.3600
26	 0.7470	 0.3400
27	 0.7240	 0.2610
28	 0.7300	 0.3210
29	 0.7270	 0.2810
30	 0.7710	 0.3410
31	 0.6770	 0.2940
32	 0.8080	 0.3360
33	 0.7960	 0.3450
34	 0.7940	 0.3580



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Chain	Atom inclusion	Q-score
A	 0.9160	 0.3230
B	 0.6690	 0.2810
C	 0.6830	 0.3300
D	 0.7080	 0.2920
E	 0.7010	 0.3320
F	 0.7590	 0.3060
G	 0.7320	 0.2930
H	 0.7530	 0.3280
I	 0.7600	 0.2830
J	 0.5910	 0.2730
K	 0.7330	 0.3170
L	 0.7420	 0.3390
M	 0.7200	 0.2950
N	 0.7020	 0.3020
O	 0.7940	 0.3270
P	 0.8170	 0.3300
Q	 0.7160	 0.3060
R	 0.7510	 0.2930
S	 0.7600	 0.2950
T	 0.7550	 0.2940
U	 0.6330	 0.2610
V	 0.6170	 0.2090
W	 0.8310	 0.2930
X	 0.6590	 0.1740
Y	 0.5180	 0.1620
Z	 0.3720	 0.2160