



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:28 AM UTC

PDB ID : 6WDG / pdb_00006wdg
EMDB ID : EMD-21635
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure VI-B)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.30 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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

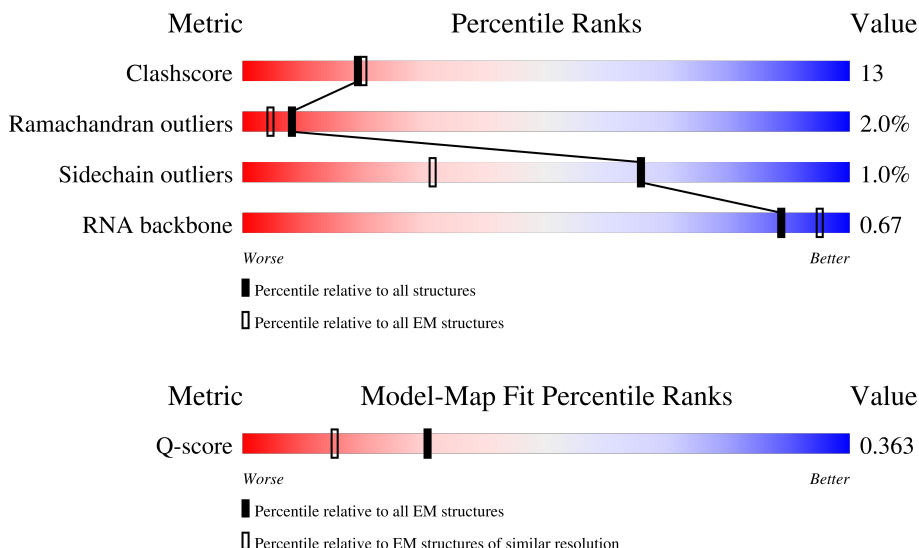
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



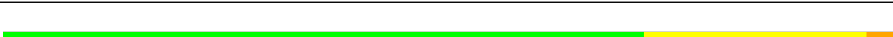
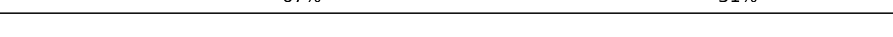
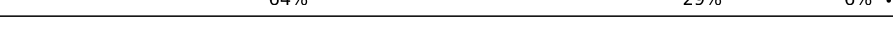
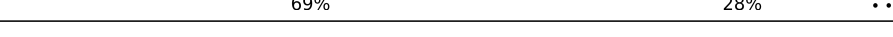
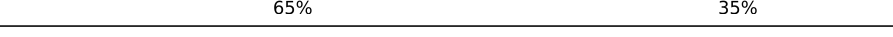
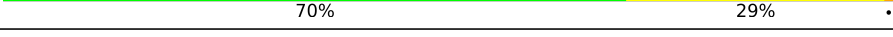
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	b	271	
2	c	209	
3	d	201	

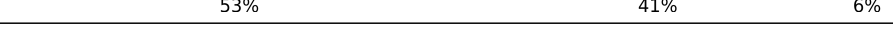
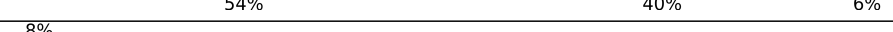
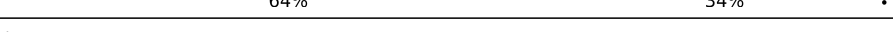
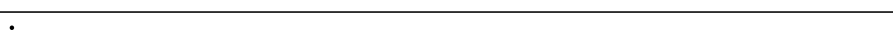
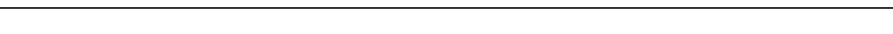
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	58%37%5%
55	5	77	40%38%21%
56	4	18	6%72%22%6%
57	7	76	54%36%11%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 148582 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	b	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	c	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	d	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	e	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	f	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	g	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	h	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	i	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	j	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	k	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	l	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	m	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	n	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	o	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	p	114	Total	C	N	O	S	0
			917	574	179	163	1	0

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	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	w	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	x	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	y	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	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

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

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

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

- Molecule 35 is a protein called 30S ribosomal protein S6.

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

- Molecule 36 is a protein called 30S ribosomal protein S7.

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

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

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

- Molecule 40 is a protein called 30S ribosomal protein S11.

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

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

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

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18.

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

- Molecule 48 is a protein called 30S ribosomal protein S19.

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

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

- Molecule 51 is a protein called 50S ribosomal protein L1.

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

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	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
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

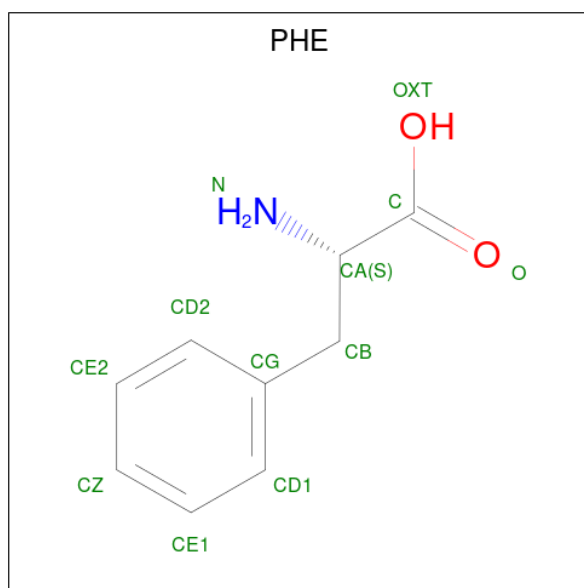
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^PPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
58	7	1	Total	C	N	O	0
			11	9	1	1	

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	7	1	10	6	1	2	1	0

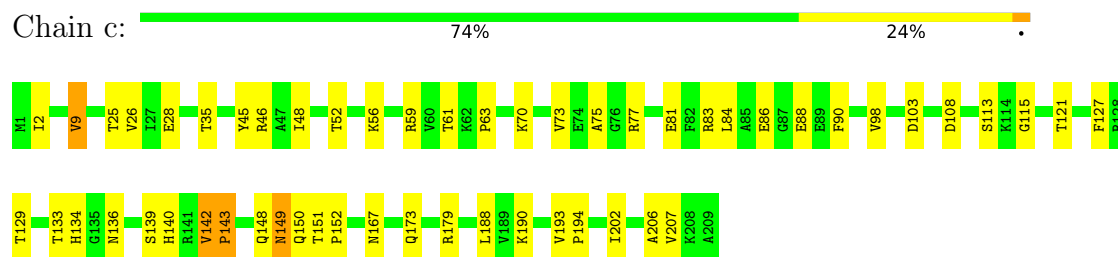
3 Residue-property plots

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.

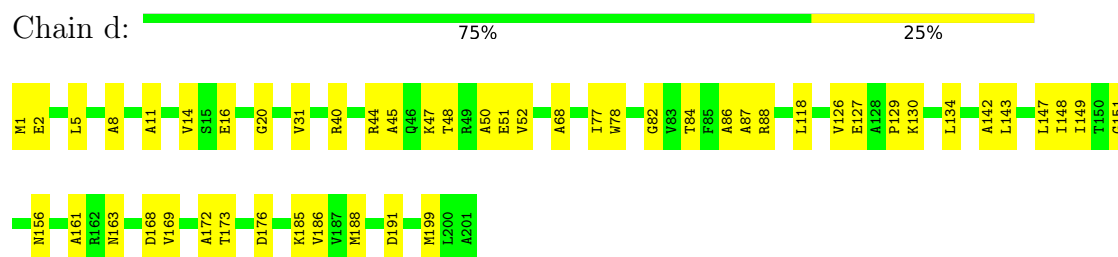
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

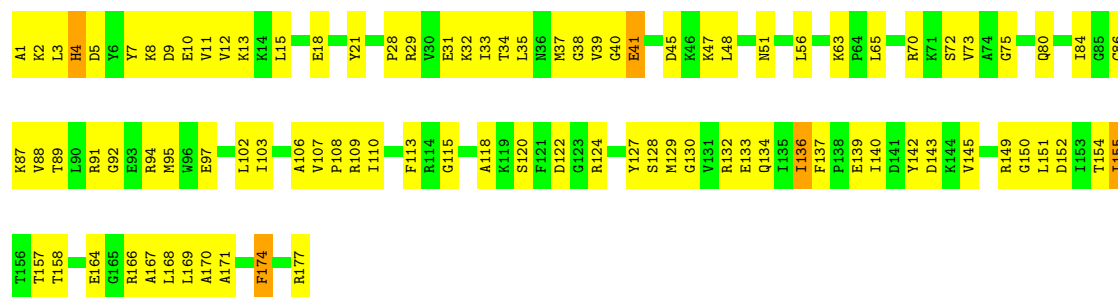


- Molecule 3: 50S ribosomal protein L4

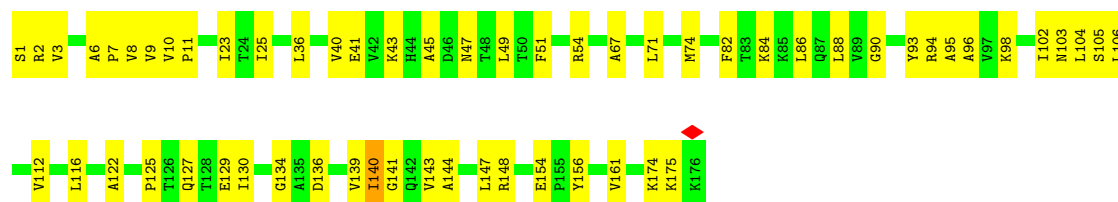


- Molecule 4: 50S ribosomal protein L5

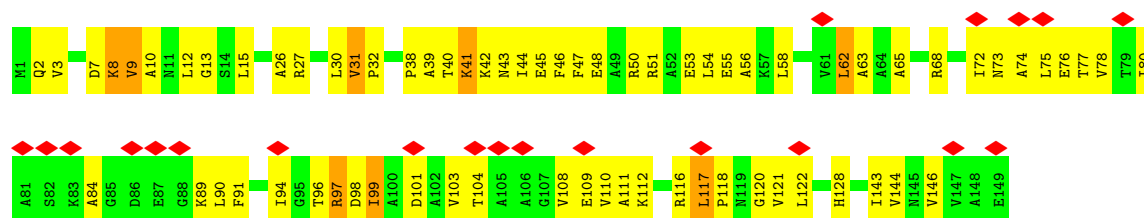




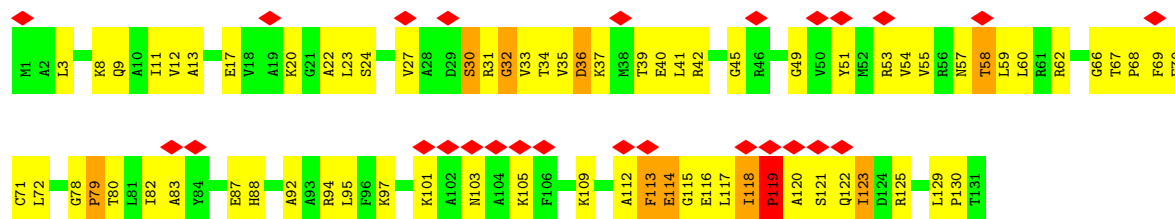
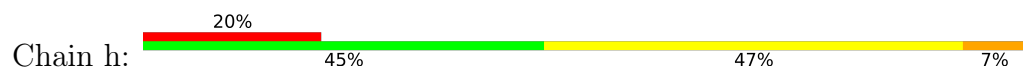
• Molecule 5: 50S ribosomal protein L6



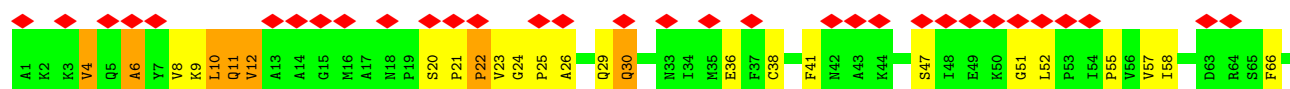
• Molecule 6: 50S ribosomal protein L9

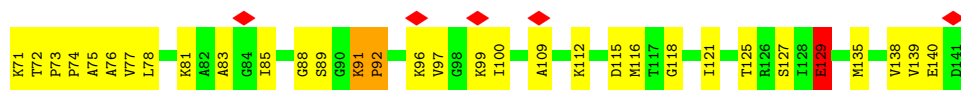


• Molecule 7: 50S ribosomal protein L10

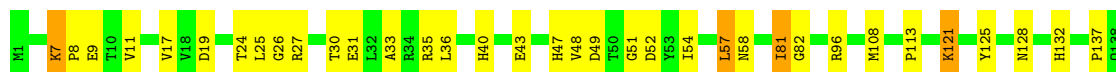


• Molecule 8: 50S ribosomal protein L11

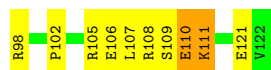




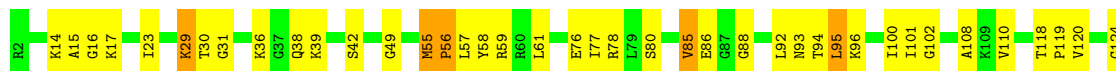
- Molecule 9: 50S ribosomal protein L13



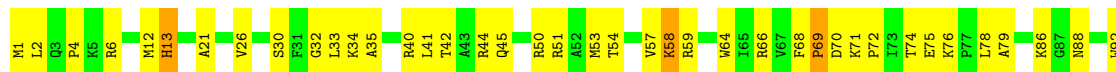
- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

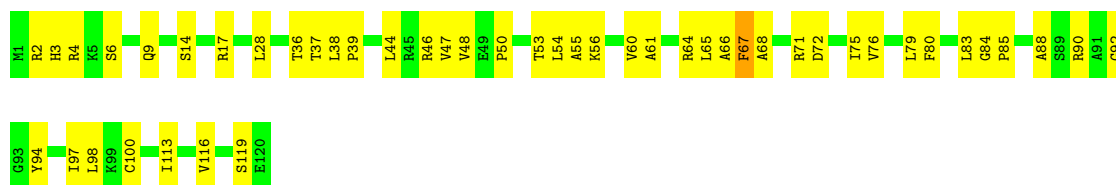


- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17

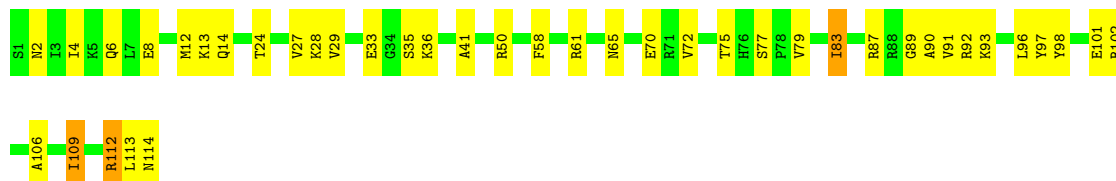




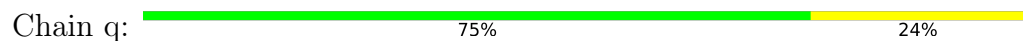
- Molecule 14: 50S ribosomal protein L18



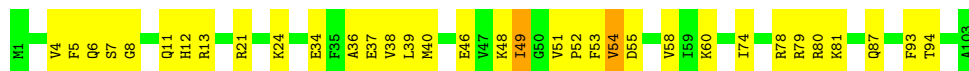
- Molecule 15: 50S ribosomal protein L19



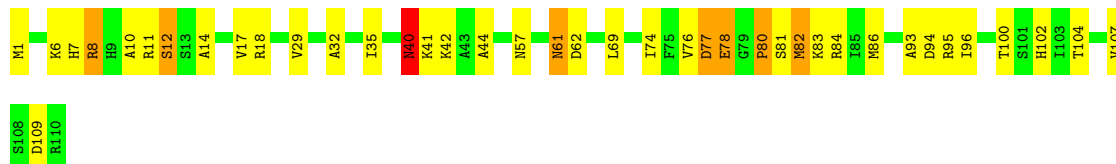
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23

Chain t:  74% 25%



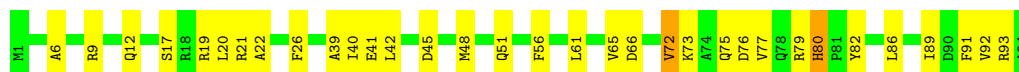
- Molecule 20: 50S ribosomal protein L24

Chain u:  69% 28%



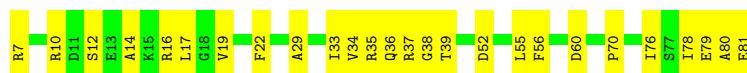
- Molecule 21: 50S ribosomal protein L25

Chain v:  65% 33%



- Molecule 22: 50S ribosomal protein L27

Chain w:  65% 35%



- Molecule 23: 50S ribosomal protein L28

Chain x:  70% 29%



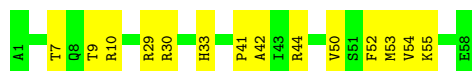
- Molecule 24: 50S ribosomal protein L29

Chain y:  57% 43%



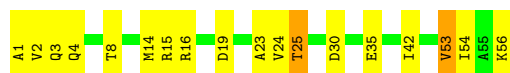
- Molecule 25: 50S ribosomal protein L30

Chain z:  76% 24%



- Molecule 26: 50S ribosomal protein L32

Chain B:  68% 29% .



- Molecule 27: 50S ribosomal protein L33

Chain C:  76% 24%



- Molecule 28: 50S ribosomal protein L34

Chain D:  61% 39%



- Molecule 29: 50S ribosomal protein L35

Chain E:  77% 20% .



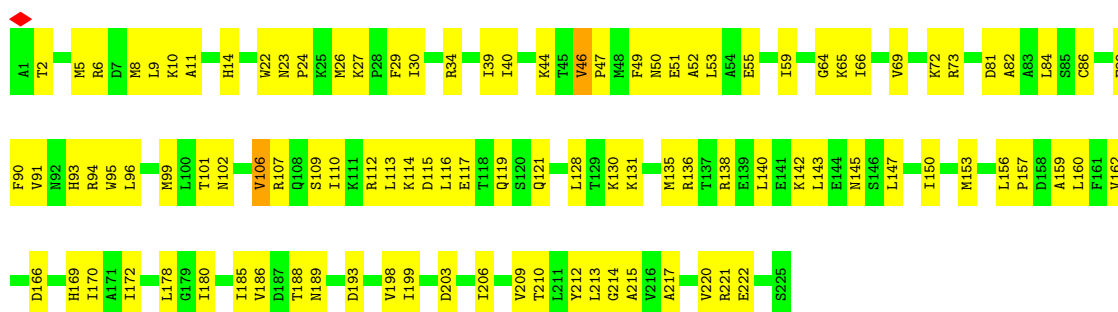
- Molecule 30: 50S ribosomal protein L36

Chain F:  66% 34%

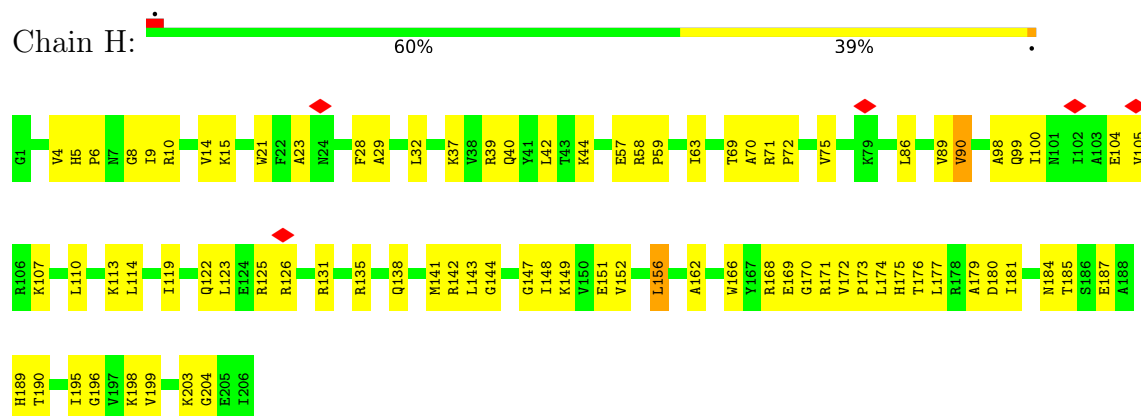


- Molecule 31: 30S ribosomal protein S2

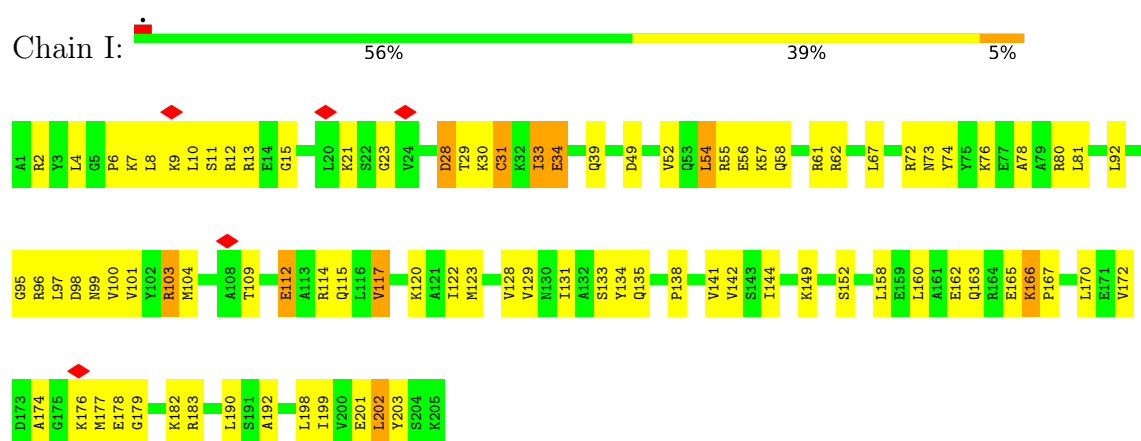
Chain G:  54% 45% .



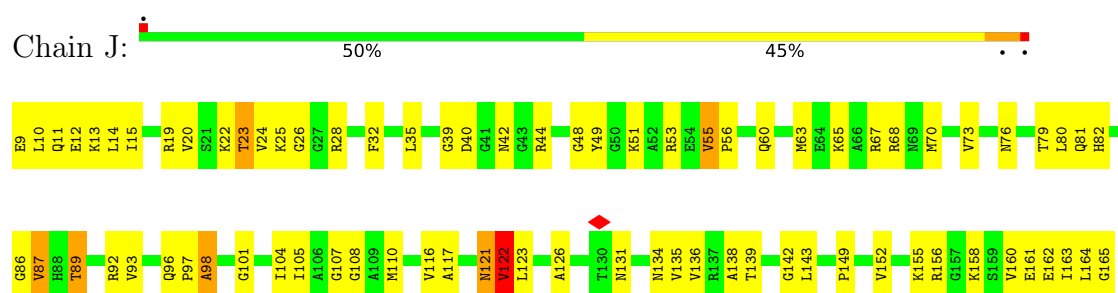
- Molecule 32: 30S ribosomal protein S3



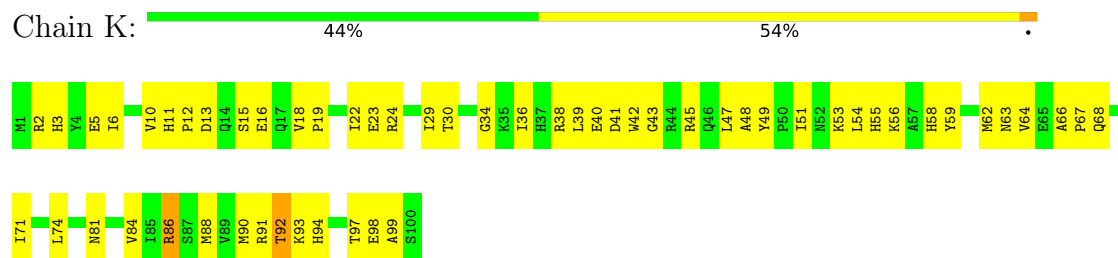
- Molecule 33: 30S ribosomal protein S4



- Molecule 34: 30S ribosomal protein S5

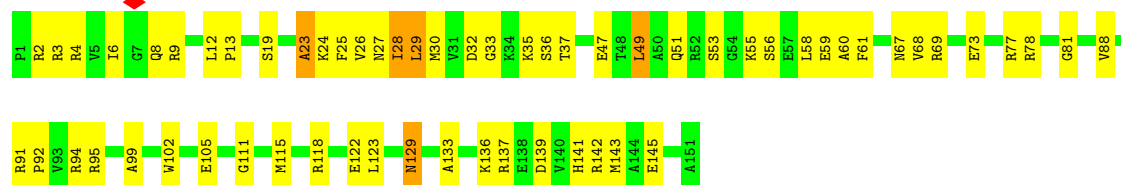


- Molecule 35: 30S ribosomal protein S6



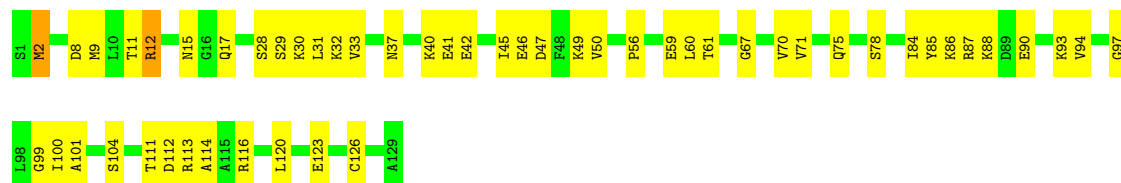
- Molecule 36: 30S ribosomal protein S7

Chain L: 



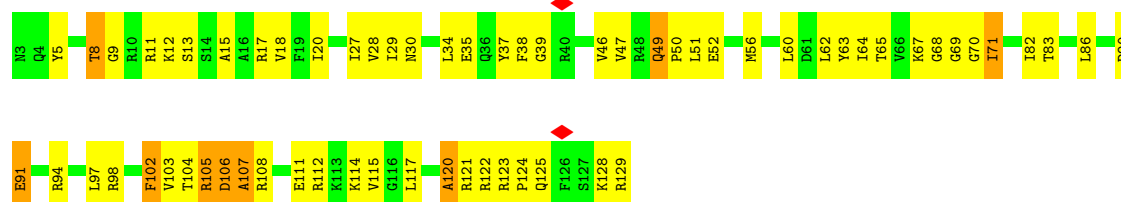
- Molecule 37: 30S ribosomal protein S8

Chain M: 



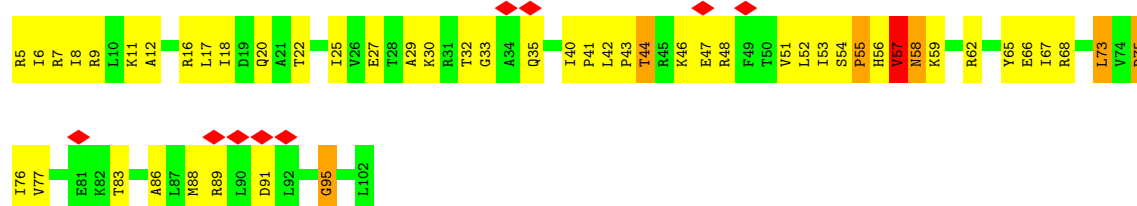
- Molecule 38: 30S ribosomal protein S9

Chain N: 



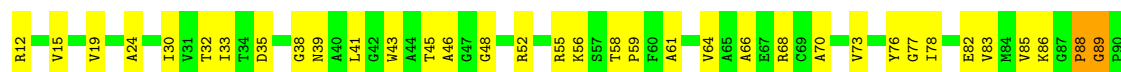
- Molecule 39: 30S ribosomal protein S10

Chain O: 



- Molecule 40: 30S ribosomal protein S11

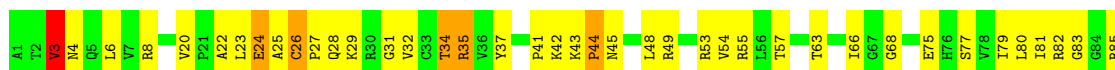
Chain P: 





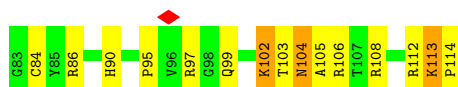
• Molecule 41: 30S ribosomal protein S12

Chain Q: 53% 41% 6%



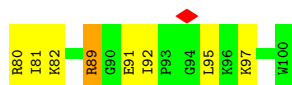
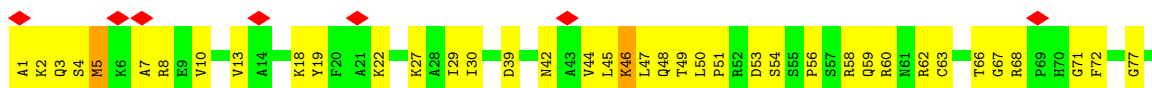
• Molecule 42: 30S ribosomal protein S13

Chain R: 54% 40% 6%



• Molecule 43: 30S ribosomal protein S14

Chain S: 8% 53% 44%



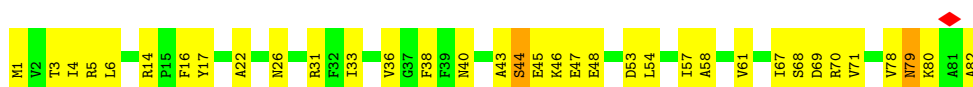
• Molecule 44: 30S ribosomal protein S15

Chain T: 64% 34% 2%



• Molecule 45: 30S ribosomal protein S16

Chain U: 57% 40% 3%



- Molecule 46: 30S ribosomal protein S17

Chain V:  58% 40%



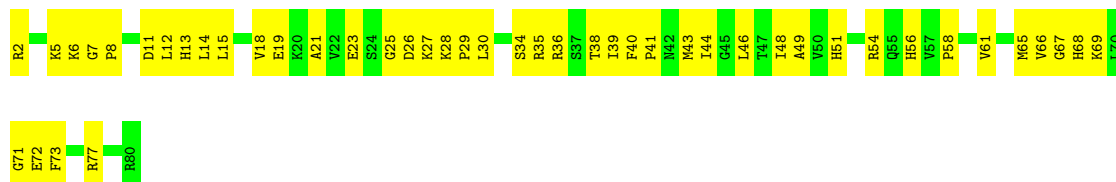
- Molecule 47: 30S ribosomal protein S18

Chain W:  74% 26%



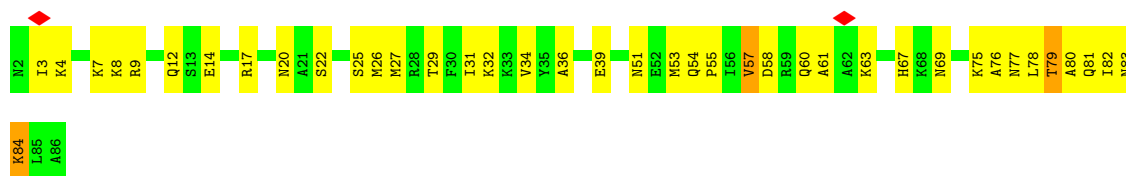
- Molecule 48: 30S ribosomal protein S19

Chain X:  42% 58%



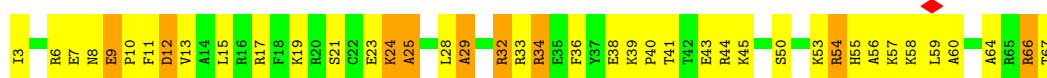
- Molecule 49: 30S ribosomal protein S20

Chain Y:  53% 44%

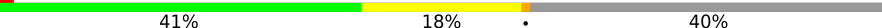


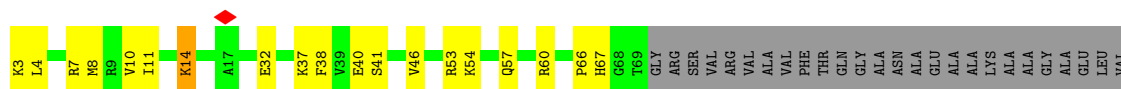
- Molecule 50: 30S ribosomal protein S21

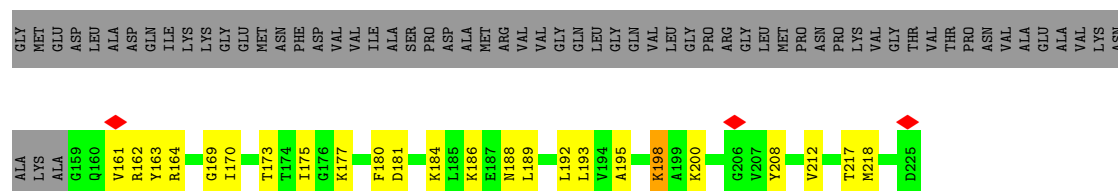
Chain Z:  37% 49% 14%



- Molecule 51: 50S ribosomal protein L1

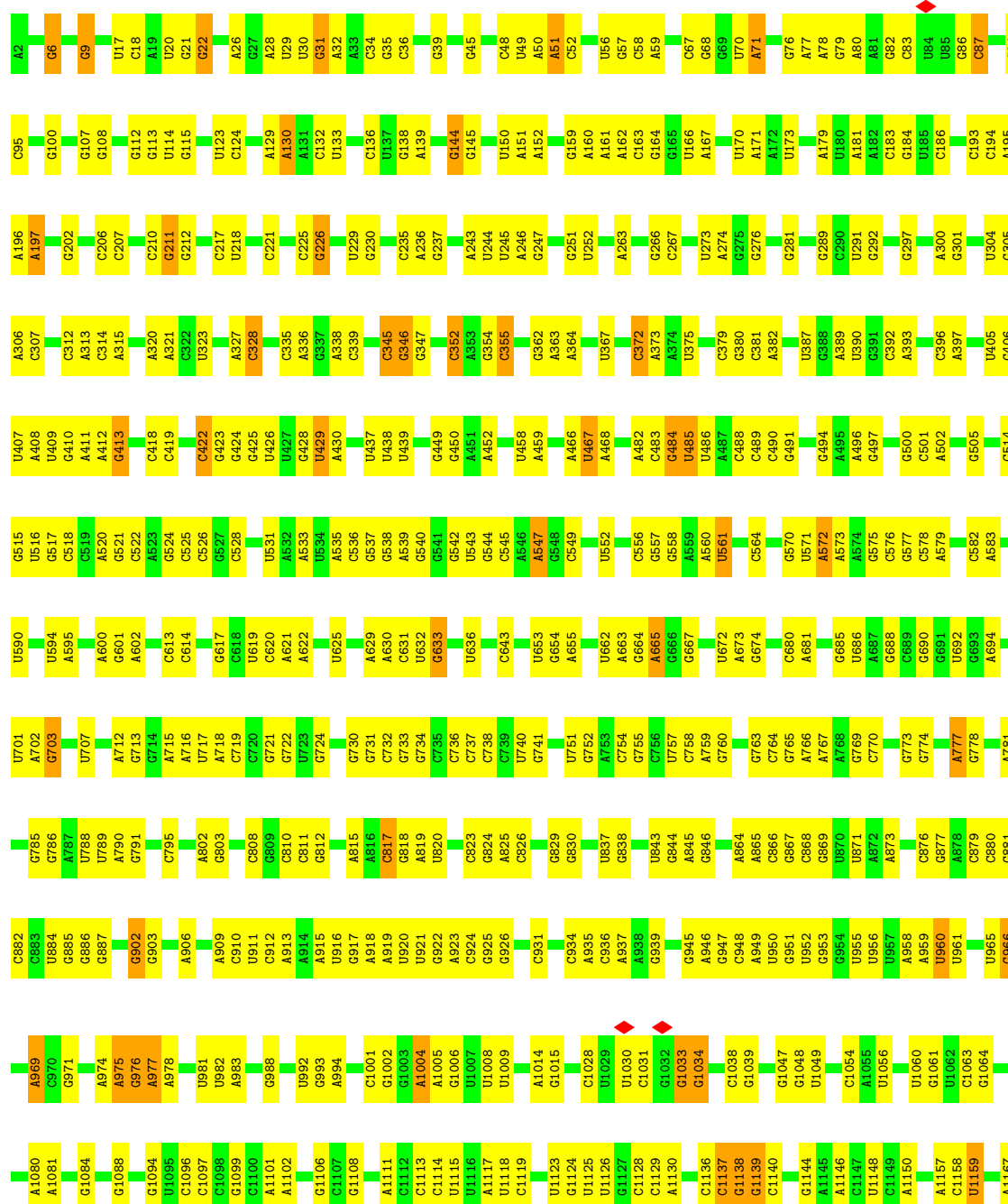
Chain a:  41% 18% 40%

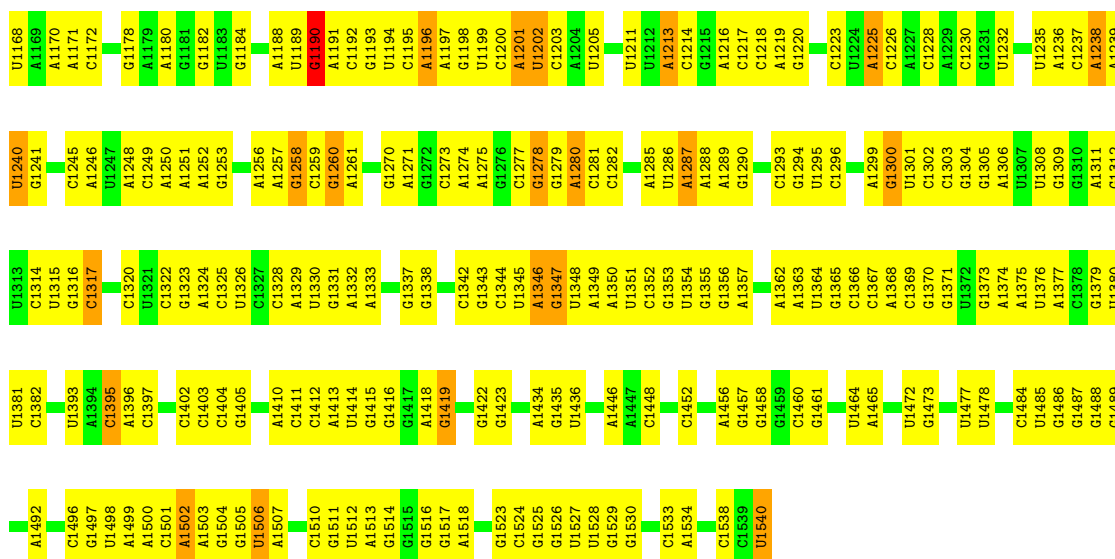




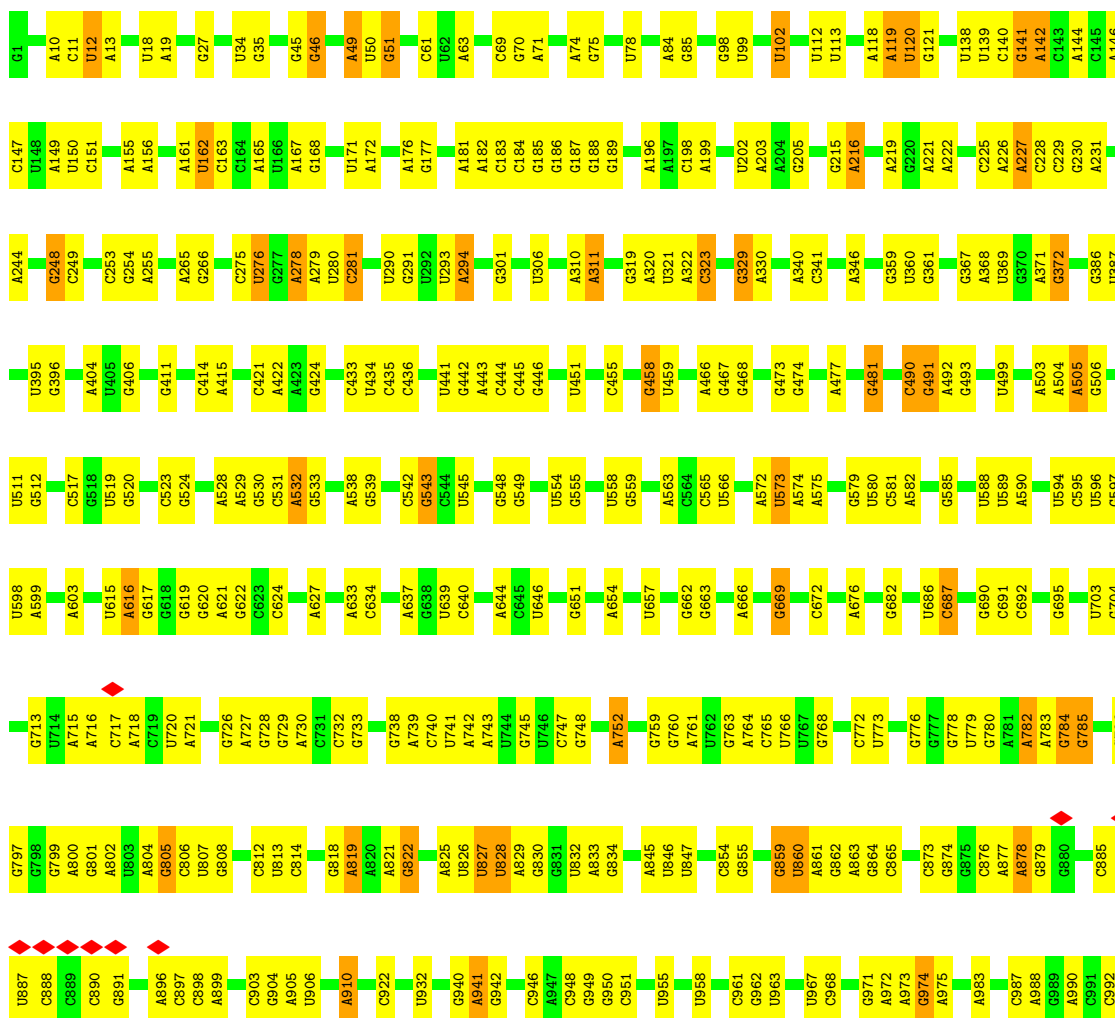
• Molecule 52: 16S ribosomal RNA

Chain 3: 53% 43% .

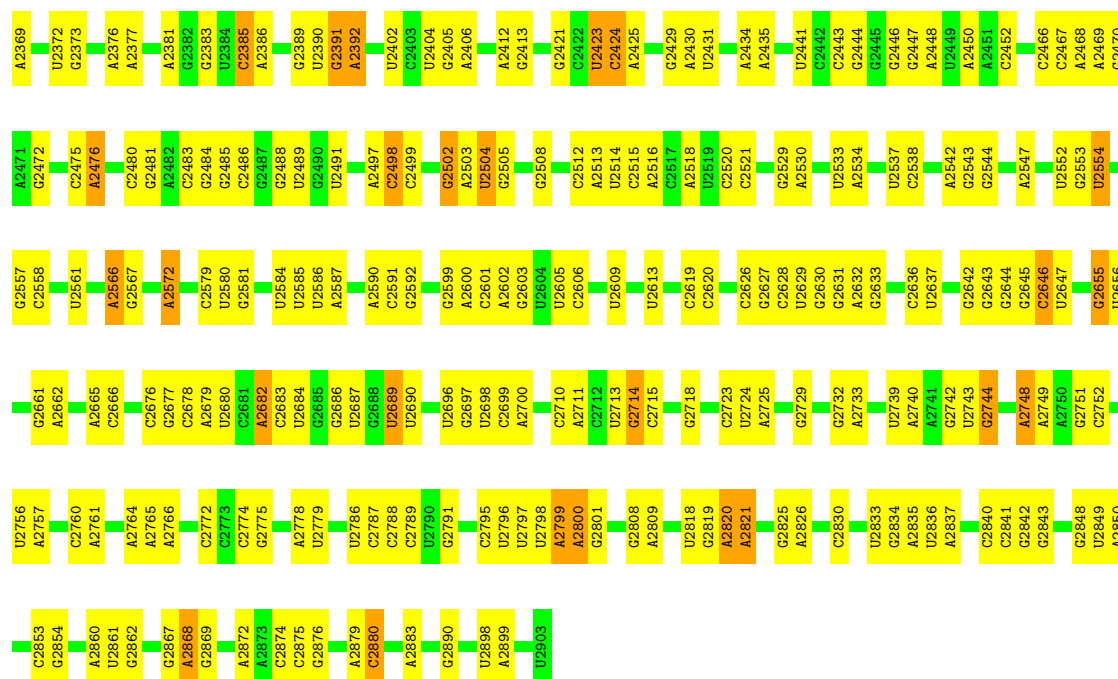




• Molecule 53: 23S ribosomal RNA

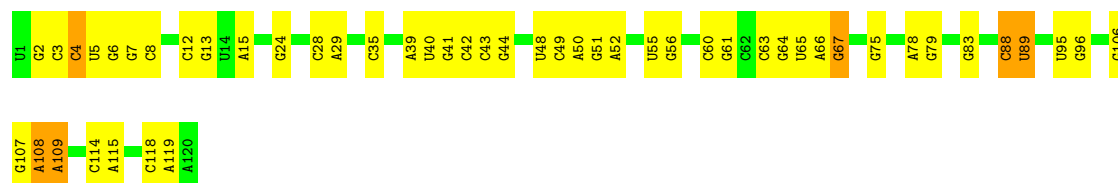


A2297	A2298	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	A2314	G2318	G2319	U2320	A2321	A2322	G2323	U2324	G2325	C2326	A2327	A2328	U2329	G2330	G2331	U2334	C2339	A2340	U2343	U2344	G2345	C2347	U2348	G2349	C2350	G2351	A2352	G2353	U2356	A2357	C2359	G2360	G2361	C2362	G2363	C2364	G2365	C2368
U2213	G2217	G2218	U2219	U2220	G2221	G2224	A2225	U2233	U2234	G2235	U2236	G2237	U2238	G2239	U2243	U2244	U2245	U2246	A2247	C2248	U2249	G2250	U2257	C2258	U2262	C2263	U2264	U2265	A2266	A2267	A2268	G2271	U2272	A2273	G2277	A2278	A2281	G2282	C2283	U2284	C2285	G2286	A2287	U2288	U2291	U2292	G2293	U2210	A2211	U2296
A2126	G2127	G2128	U2132	G2133	A2134	U2139	G2140	G2144	A2147	U2148	C2149	C2150	U2155	G2156	G2157	U2162	A2163	C2164	U2170	A2171	U2172	A2173	C2174	A2175	U2176	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2189	G2190	A2191	C2196	U2197	A2198	A2199	U2203	G2204	C2208	G2209	G2210	A2211	A2212				
G2040	U2041	A2042	C2043	U2044	G2045	G2049	G2053	A2054	C2055	G2056	A2060	G2061	A2062	C2063	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	C2078	U2079	U2086	G2087	A2088	G2093	C2096	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	
U1943	U1944	C1947	G1948	G1949	A1952	U1955	U1956	C1957	U1963	G1964	C1965	C1966	C1967	A1970	U1971	G1972	G1973	U1979	G1980	U1991	G1992	U1993	C1994	U1995	C1996	C1997	C2001	G2002	G2010	A2014	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	G2029	A2030	A2031	G2032	A2033	U2034	G2035	C2036				
A1829	G1842	C1843	G1846	A1847	A1854	U1855	U1856	G1857	G1862	G1863	A1871	A1872	G1873	C1874	G1875	A1876	G1877	G1878	G1884	G1888	U1891	U1892	C1893	A1900	A1901	G1906	G1907	C1908	G1909	U1910	U1911	A1912	A1913	C1914	U1917	A1918	A1919	C1920	C1924	C1925	U1926	G1930	U1931	A1932	G1933	A1936	A1937	A1938		
A1745	A1746	U1747	G1748	A1749	C1752	G1753	U1758	C1764	U1769	G1770	A1773	U1774	U1775	G1776	U1779	A1780	U1781	A1784	A1785	A1787	A1791	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	G1807	A1808	A1810	G1811	C1816	U1817	A1818	A1819	U1820	G1824	U1825	G1826	U1827	G1828					
C1639	A1640	A1641	G1642	C1643	C1644	G1645	C1646	U1648	G1651	U1657	C1658	G1663	A1664	A1665	G1666	C1670	U1671	G1674	C1675	A1676	A1677	A1678	A1679	U1680	G1681	C1682	G1683	G1684	A1690	C1691	U1692	U1693	C1694	G1695	G1696	G1715	U1720	G1721	U1729	C1730	U1736	G1737	G1738	A1739	G1740	A1744				
G1529	C1533	U1534	A1535	C1536	G1537	U1538	U1539	G1540	C1541	U1542	G1543	A1549	C1550	G1555	G1560	U1563	C1564	C1565	A1566	G1567	G1568	A1569	A1570	A1571	A1572	U1580	G1581	U1584	G1587	A1590	A1591	A1599	G1601	U1602	A1603	C1606	C1607	A1608	A1609	U1610	C1611	C1612	G1613	A1614	C1615	A1616	A1637	C1638		
U1415	U1416	C1417	G1418	A1419	U1420	G1421	G1424	G1425	G1432	A1433	A1434	G1435	G1441	U1442	U1443	G1444	G1445	C1446	C1447	G1448	C1451	A1452	A1453	C1454	C1461	G1475	U1476	G1482	A1490	G1491	A1494	C1498	G1501	C1507	A1508	A1509	U1510	A1515	G1524	A1525	C1526	G1527	A1528							
G1288	C1295	G1296	G1300	A1301	C1306	A1307	U1308	U1316	G1317	U1318	C1319	G1320	A1321	U1326	A1327	U1328	G1329	C1330	G1331	G1332	G1341	U1344	C1345	C1348	C1349	C1350	C1351	U1352	A1353	C1357	G1358	A1359	G1360	G1361	A1365	A1366	A1367	G1368	A1373	A1378	U1379	A1383	C1386	A1387						
U1083	A1084	A1085	A1088	C1092	G1093	U1097	A1098	C1102	A1103	U1105	G1106	G1107	G1110	A1111	G1112	G1122	C1123	G1124	A1127	G1128	A1129	U1130	G1131	U1132	A1133	C1135	G1138	G1139	C1140	U1141	U1142	A1143	C1146	A1147	C1153	G1154	G1157	A1169	C1170	U1174	A1175	C1176	G1177	C1178						
A996	G997	A1001	G1002	C1005	U1012	C1013	A1014	U1019	A1020	A1021	G1022	U1023	G1026	A1027	U1033	G1034	U1035	G1036	A1039	A1040	C1045	A1046	G1047	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1076	A1077	U1078	C1079	A1080	U1081	U1082	



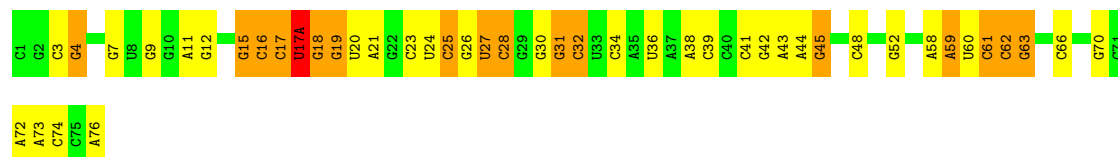
• Molecule 54: 5S ribosomal RNA

Chain 2: 58% 37% 5%



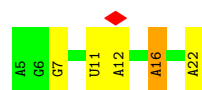
• Molecule 55: tRNA^{fMet}

Chain 5: 40% 38% 21% .



• Molecule 56: mRNA

Chain 4: 6% 72% 22% 6%



• Molecule 57: tRNA^{Phe}

Chain 7: 54% 36% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19875	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	23.377	Depositor
Minimum map value	-14.097	Depositor
Average map value	0.117	Depositor
Map value standard deviation	0.965	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	b	0.30	0/2122	0.96	4/2852 (0.1%)
2	c	0.29	0/1586	0.95	1/2134 (0.0%)
3	d	0.29	0/1571	0.91	5/2113 (0.2%)
4	e	0.31	0/1435	0.94	6/1926 (0.3%)
5	f	0.31	0/1343	0.94	3/1816 (0.2%)
6	g	0.33	0/1122	1.05	11/1515 (0.7%)
7	h	0.36	0/1002	0.99	6/1350 (0.4%)
8	i	0.35	0/1046	1.05	8/1410 (0.6%)
9	j	0.30	0/1152	1.00	7/1551 (0.5%)
10	k	0.29	0/948	0.99	5/1268 (0.4%)
11	l	0.29	0/1054	1.00	5/1403 (0.4%)
12	m	0.30	0/1093	0.93	3/1460 (0.2%)
13	n	0.31	0/974	0.96	4/1301 (0.3%)
14	o	0.29	0/902	0.95	3/1209 (0.2%)
15	p	0.29	0/929	0.87	3/1242 (0.2%)
16	q	0.28	0/960	0.94	4/1278 (0.3%)
17	r	0.27	0/829	0.84	1/1107 (0.1%)
18	s	0.29	0/864	0.94	4/1156 (0.3%)
19	t	0.27	0/745	0.83	1/994 (0.1%)
20	u	0.30	0/788	0.92	3/1051 (0.3%)
21	v	0.29	0/766	0.89	4/1025 (0.4%)
22	w	0.28	0/582	0.91	1/769 (0.1%)
23	x	0.29	0/635	0.89	0/848
24	y	0.29	0/510	0.85	0/677
25	z	0.30	0/453	0.86	1/605 (0.2%)
26	B	0.29	0/450	0.87	1/599 (0.2%)
27	C	0.32	0/417	0.93	4/554 (0.7%)
28	D	0.31	0/380	0.98	0/498
29	E	0.30	0/513	1.02	2/676 (0.3%)
30	F	0.31	0/303	0.87	0/397
31	G	0.30	0/1788	0.98	12/2408 (0.5%)
32	H	0.33	0/1652	0.91	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.31	0/1665	0.99	10/2227 (0.4%)
34	J	0.33	0/1170	1.00	5/1573 (0.3%)
35	K	0.30	0/836	0.90	1/1128 (0.1%)
36	L	0.31	0/1196	1.01	7/1602 (0.4%)
37	M	0.30	0/989	0.95	4/1326 (0.3%)
38	N	0.33	0/1034	0.97	5/1375 (0.4%)
39	O	0.33	0/797	1.06	9/1077 (0.8%)
40	P	0.33	0/886	0.99	4/1195 (0.3%)
41	Q	0.33	0/969	1.02	7/1300 (0.5%)
42	R	0.33	0/893	1.05	5/1193 (0.4%)
43	S	0.33	0/817	0.94	5/1088 (0.5%)
44	T	0.29	0/722	0.95	3/964 (0.3%)
45	U	0.33	0/659	0.96	3/884 (0.3%)
46	V	0.32	0/658	0.94	1/881 (0.1%)
47	W	0.32	0/545	0.86	0/731
48	X	0.34	0/653	0.86	0/877
49	Y	0.29	0/671	0.99	5/888 (0.6%)
50	Z	0.32	0/551	0.97	5/728 (0.7%)
51	a	0.31	0/1034	0.87	3/1387 (0.2%)
52	3	0.43	0/36963	0.47	1/57662 (0.0%)
53	1	0.40	0/69796	0.47	2/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.42	0/1832	0.52	1/2855 (0.0%)
56	4	0.49	0/436	0.51	0/679
57	7	0.65	0/1809	0.56	0/2819
All	All	0.39	0/161367	0.64	203/241223 (0.1%)

There are no bond length outliers.

All (203) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	10	ALA	N-CA-C	9.68	121.43	111.07
29	E	61	LEU	CA-C-N	9.41	128.76	118.97
29	E	61	LEU	C-N-CA	9.41	128.76	118.97
42	R	3	ILE	N-CA-C	9.41	121.28	108.11
9	j	121	LYS	N-CA-C	-9.12	101.93	113.23
1	b	213	ARG	N-CA-C	-8.38	101.67	112.23
31	G	11	ALA	N-CA-C	-8.29	103.31	113.50
11	l	95	LEU	N-CA-C	-7.94	101.42	112.45
11	l	23	ILE	N-CA-C	-7.90	105.78	113.53
40	P	125	LYS	N-CA-C	7.85	120.90	110.53
34	J	142	GLY	N-CA-C	-7.83	104.95	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	q	49	ARG	N-CA-C	-7.58	104.04	113.28
51	a	14	LYS	N-CA-C	-7.53	104.60	114.31
55	5	17(A)	U	C2'-C3'-O3'	7.44	120.67	109.50
36	L	28	ILE	N-CA-C	-7.24	104.31	113.22
39	O	86	ALA	N-CA-C	-7.16	105.07	113.88
12	m	57	VAL	N-CA-C	-7.09	105.44	112.17
21	v	80	HIS	N-CA-C	-7.08	100.87	109.72
8	i	129	GLU	N-CA-C	-7.07	103.62	111.82
13	n	119	SER	N-CA-C	-7.07	102.64	112.25
44	T	53	ARG	N-CA-C	-7.06	103.67	111.36
8	i	91	LYS	CA-C-N	6.92	128.49	119.84
8	i	91	LYS	C-N-CA	6.92	128.49	119.84
39	O	55	PRO	N-CA-C	-6.90	107.50	114.68
5	f	47	ASN	N-CA-C	-6.86	103.26	112.94
6	g	121	VAL	N-CA-C	-6.85	104.64	111.77
13	n	68	ALA	N-CA-C	-6.79	103.56	110.97
41	Q	115	LYS	N-CA-C	-6.76	100.47	110.48
41	Q	20	VAL	N-CA-C	6.76	114.84	108.15
38	N	106	ASP	N-CA-C	-6.75	102.62	111.74
49	Y	8	LYS	N-CA-C	-6.73	104.01	111.82
33	I	165	GLU	N-CA-C	6.69	119.43	111.33
3	d	82	GLY	N-CA-C	6.68	121.12	110.90
33	I	176	LYS	N-CA-C	-6.67	104.72	112.92
5	f	144	ALA	N-CA-C	-6.67	104.97	113.23
13	n	66	ALA	N-CA-C	-6.66	105.14	113.20
39	O	95	GLY	N-CA-C	-6.60	106.84	114.69
31	G	222	GLU	N-CA-C	-6.56	104.75	112.89
38	N	105	ARG	N-CA-C	-6.54	105.46	113.50
7	h	57	ASN	N-CA-C	-6.53	105.19	112.57
22	w	52	ASP	N-CA-C	-6.51	104.97	113.17
36	L	23	ALA	N-CA-C	-6.50	104.28	111.82
19	t	72	GLN	N-CA-C	-6.47	107.25	114.62
10	k	71	ARG	N-CA-C	-6.42	101.22	110.08
6	g	3	VAL	N-CA-C	6.39	117.68	109.30
34	J	82	HIS	N-CA-C	6.33	113.92	108.22
36	L	53	SER	N-CA-C	-6.32	106.54	114.56
53	1	1130	U	C2'-C3'-O3'	6.31	118.96	109.50
4	e	4	HIS	N-CA-C	-6.28	104.32	112.23
31	G	193	ASP	N-CA-C	6.26	118.11	111.28
9	j	128	ASN	N-CA-C	-6.26	105.59	112.72
33	I	103	ARG	N-CA-C	-6.25	105.14	112.89
33	I	117	VAL	N-CA-C	6.23	116.40	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	g	99	ILE	N-CA-C	-6.22	104.43	110.72
12	m	26	VAL	N-CA-C	-6.21	98.04	106.85
36	L	49	LEU	N-CA-C	-6.20	104.41	112.23
45	U	45	GLU	N-CA-C	-6.20	102.06	110.68
15	p	112	ARG	N-CA-C	6.20	117.83	111.14
38	N	47	VAL	N-CA-C	-6.18	105.61	113.22
11	l	55	MET	CA-C-N	6.17	127.55	119.84
11	l	55	MET	C-N-CA	6.17	127.55	119.84
49	Y	57	VAL	N-CA-C	6.16	116.83	110.36
37	M	12	ARG	N-CA-C	-6.14	105.62	113.23
39	O	54	SER	N-CA-C	6.12	119.79	110.50
26	B	53	VAL	N-CA-C	6.10	117.65	111.00
20	u	75	ALA	N-CA-C	-6.09	107.67	114.62
21	v	40	ILE	N-CA-C	6.09	116.63	108.11
41	Q	26	CYS	CA-C-N	6.09	127.45	119.84
41	Q	26	CYS	C-N-CA	6.09	127.45	119.84
14	o	20	GLU	N-CA-C	-6.07	105.84	113.18
46	V	75	VAL	N-CA-C	-6.00	105.97	111.67
43	S	89	ARG	N-CA-C	-5.99	105.80	113.23
39	O	44	THR	N-CA-C	5.97	118.91	109.96
52	3	1190	G	C2'-C3'-O3'	5.96	118.44	109.50
50	Z	17	ARG	N-CA-C	-5.95	105.86	113.23
1	b	215	VAL	N-CA-C	5.94	115.17	106.55
8	i	6	ALA	N-CA-C	5.94	119.04	109.83
15	p	14	GLN	N-CA-C	5.93	117.54	111.14
1	b	164	VAL	N-CA-C	5.92	116.56	110.82
10	k	51	LYS	N-CA-C	-5.91	105.34	112.54
10	k	92	GLU	N-CA-C	5.89	123.34	110.80
27	C	39	ASP	CA-C-N	5.88	125.42	119.19
27	C	39	ASP	C-N-CA	5.88	125.42	119.19
6	g	63	ALA	N-CA-C	-5.87	105.02	111.82
6	g	62	LEU	N-CA-C	-5.84	105.65	112.89
40	P	99	LEU	N-CA-C	-5.84	106.29	113.41
42	R	36	ALA	N-CA-C	-5.84	106.50	113.97
39	O	16	ARG	N-CA-C	5.80	118.55	111.82
33	I	166	LYS	CA-C-N	5.79	127.08	119.84
33	I	166	LYS	C-N-CA	5.79	127.08	119.84
3	d	31	VAL	N-CA-C	5.77	115.96	110.53
45	U	47	GLU	N-CA-C	5.76	117.56	111.28
43	S	5	MET	N-CA-C	-5.70	105.21	111.82
3	d	127	GLU	N-CA-C	5.70	117.57	111.36
31	G	214	GLY	N-CA-C	-5.69	107.61	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	l	59	ARG	N-CA-C	-5.68	107.60	114.75
44	T	57	ARG	N-CA-C	-5.66	104.74	111.03
49	Y	61	ALA	N-CA-C	-5.65	105.20	111.36
39	O	57	VAL	N-CA-C	5.64	121.08	109.34
34	J	117	ALA	N-CA-C	-5.63	105.52	112.90
4	e	136	ILE	N-CA-C	-5.62	104.18	112.04
27	C	42	VAL	N-CA-C	-5.59	106.87	113.42
4	e	170	ALA	N-CA-C	-5.59	105.18	112.23
35	K	24	ARG	N-CA-C	5.58	118.55	111.69
7	h	36	ASP	N-CA-C	-5.57	105.98	112.89
15	p	35	SER	N-CA-C	-5.56	107.50	114.56
32	H	156	LEU	N-CA-C	5.56	118.13	110.35
6	g	8	LYS	N-CA-C	5.56	119.59	112.26
50	Z	21	SER	N-CA-C	-5.56	106.86	113.97
33	I	33	ILE	N-CA-C	5.55	118.41	110.09
18	s	78	GLU	N-CA-C	5.54	118.39	110.24
44	T	70	LYS	N-CA-C	-5.54	105.16	111.14
33	I	112	GLU	N-CA-C	-5.53	105.40	111.82
40	P	56	LYS	N-CA-C	-5.53	105.27	112.23
10	k	32	TYR	N-CA-C	5.53	118.98	110.42
34	J	87	VAL	N-CA-C	5.53	116.83	109.37
31	G	130	LYS	N-CA-C	5.51	117.75	111.02
36	L	29	LEU	N-CA-C	-5.51	106.55	113.72
7	h	79	PRO	N-CA-C	5.51	119.89	111.34
16	q	80	ASN	N-CA-C	-5.48	105.46	111.82
7	h	51	TYR	N-CA-C	5.48	119.47	112.34
49	Y	84	LYS	N-CA-C	-5.48	105.39	111.36
10	k	111	LYS	N-CA-C	-5.48	105.72	112.90
42	R	71	GLU	N-CA-C	5.47	118.01	111.71
41	Q	3	VAL	N-CA-C	5.46	120.70	109.34
31	G	90	PHE	N-CA-C	5.46	117.70	109.41
43	S	29	ILE	N-CA-C	5.45	115.89	110.23
27	C	40	PRO	N-CA-C	5.43	120.69	113.57
38	N	62	LEU	N-CA-C	5.40	118.51	110.14
6	g	74	ALA	N-CA-C	5.39	117.16	111.28
9	j	96	ARG	CA-C-N	5.39	125.00	119.56
9	j	96	ARG	C-N-CA	5.39	125.00	119.56
31	G	106	VAL	N-CA-C	-5.39	104.36	111.09
43	S	46	LYS	N-CA-C	-5.38	106.22	112.89
21	v	22	ALA	N-CA-C	-5.38	106.56	113.23
32	H	177	LEU	N-CA-C	5.36	117.12	111.28
39	O	20	GLN	N-CA-C	-5.35	106.92	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	Y	79	THR	N-CA-C	-5.35	105.53	111.36
9	j	139	VAL	N-CA-C	5.34	115.98	109.30
14	o	56	LYS	N-CA-C	5.34	117.52	111.11
16	q	59	LEU	N-CA-C	-5.34	104.88	111.40
37	M	67	GLY	N-CA-C	-5.33	106.22	113.37
41	Q	122	LYS	N-CA-C	5.33	117.52	111.02
13	n	67	PHE	N-CA-C	-5.32	106.95	113.50
8	i	127	SER	N-CA-C	-5.32	105.53	112.23
8	i	11	GLN	N-CA-C	5.32	122.12	110.80
40	P	46	ALA	N-CA-C	-5.31	105.54	112.23
31	G	23	ASN	CA-C-N	5.31	126.48	119.84
31	G	23	ASN	C-N-CA	5.31	126.48	119.84
5	f	140	ILE	N-CA-C	-5.31	105.54	110.53
4	e	137	PHE	N-CA-C	-5.30	103.09	109.72
1	b	261	ARG	N-CA-C	-5.29	106.60	113.16
33	I	99	ASN	N-CA-C	-5.27	105.99	112.90
41	Q	43	LYS	N-CA-C	5.27	120.73	113.77
43	S	22	LYS	N-CA-C	-5.27	107.86	114.56
2	c	207	VAL	N-CA-C	-5.27	107.25	113.42
18	s	40	ASN	N-CA-C	5.26	117.67	108.52
7	h	105	LYS	N-CA-C	5.26	116.90	107.80
6	g	117	LEU	CA-C-N	5.25	124.76	119.19
6	g	117	LEU	C-N-CA	5.25	124.76	119.19
50	Z	66	ARG	N-CA-C	5.25	118.49	111.24
18	s	61	ASN	N-CA-C	5.25	117.08	111.36
18	s	82	MET	N-CA-C	-5.24	101.43	109.76
50	Z	54	ARG	N-CA-C	-5.24	105.25	111.69
53	l	1020	A	C2'-C3'-O3'	5.23	117.34	109.50
45	U	69	ASP	N-CA-C	5.23	117.65	111.33
7	h	30	SER	N-CA-C	-5.22	106.77	112.72
36	L	9	ARG	N-CA-C	5.22	116.83	110.41
50	Z	29	ALA	N-CA-C	-5.21	106.43	112.89
31	G	9	LEU	N-CA-C	-5.20	105.79	111.82
51	a	32	GLU	N-CA-C	-5.20	106.45	112.89
8	i	47	SER	N-CA-C	-5.19	106.86	114.39
32	H	8	GLY	N-CA-C	5.19	118.52	112.50
42	R	4	ALA	N-CA-C	5.19	121.86	110.80
39	O	77	VAL	N-CA-C	5.19	115.30	110.42
42	R	6	ILE	N-CA-C	-5.18	98.56	109.34
12	m	88	ASN	N-CA-C	5.17	117.20	110.53
21	v	48	MET	N-CA-C	-5.17	105.82	111.82
8	i	10	LEU	CB-CA-C	-5.15	107.10	114.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	G	217	ALA	N-CA-C	-5.15	106.51	112.89
3	d	176	ASP	CA-C-N	5.14	126.27	119.84
3	d	176	ASP	C-N-CA	5.14	126.27	119.84
4	e	5	ASP	N-CA-C	-5.14	105.76	111.36
6	g	30	LEU	N-CA-C	5.13	117.54	111.33
32	H	199	VAL	N-CA-C	5.13	115.29	108.11
37	M	9	MET	N-CA-C	-5.11	105.62	111.14
34	J	122	VAL	N-CA-C	5.10	119.96	109.34
33	I	73	ASN	N-CA-C	-5.10	105.80	111.36
9	j	7	LYS	CA-C-N	5.08	124.87	119.28
9	j	7	LYS	C-N-CA	5.08	124.87	119.28
25	z	42	ALA	N-CA-C	-5.08	105.83	111.36
14	o	10	ARG	N-CA-C	-5.06	107.28	113.50
20	u	29	SER	N-CA-C	5.05	116.48	110.97
31	G	49	PHE	N-CA-C	-5.05	105.48	111.69
32	H	90	VAL	N-CA-C	-5.04	105.65	113.16
36	L	8	GLN	N-CA-C	5.04	116.44	110.19
16	q	111	LYS	N-CA-C	-5.04	105.87	111.36
51	a	198	LYS	N-CA-C	-5.03	107.09	113.18
4	e	51	ASN	N-CA-C	-5.03	105.99	111.82
37	M	40	LYS	N-CA-C	-5.03	105.90	112.23
20	u	51	LEU	N-CA-C	5.02	121.50	110.80
17	r	49	ILE	N-CA-C	5.01	115.34	108.12
38	N	46	VAL	N-CA-C	-5.01	106.26	113.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	95	0
2	c	1565	0	1616	40	0
3	d	1552	0	1619	35	0
4	e	1411	0	1447	87	0
5	f	1323	0	1374	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	g	1111	0	1148	48	0
7	h	989	0	1025	77	0
8	i	1032	0	1088	56	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	45	0
11	l	1045	0	1117	39	0
12	m	1074	0	1157	43	0
13	n	961	0	1000	35	0
14	o	892	0	923	29	0
15	p	917	0	965	34	0
16	q	947	0	1022	26	0
17	r	816	0	839	37	0
18	s	857	0	922	30	0
19	t	739	0	807	22	0
20	u	780	0	834	24	0
21	v	753	0	780	22	0
22	w	575	0	592	25	0
23	x	625	0	655	16	0
24	y	509	0	543	23	0
25	z	449	0	491	16	0
26	B	444	0	461	15	0
27	C	410	0	440	10	0
28	D	377	0	418	21	0
29	E	504	0	574	15	0
30	F	302	0	343	9	0
31	G	1757	0	1787	68	0
32	H	1625	0	1699	73	0
33	I	1643	0	1710	90	0
34	J	1157	0	1199	62	0
35	K	818	0	808	50	0
36	L	1182	0	1240	55	0
37	M	979	0	1034	39	0
38	N	1022	0	1070	58	0
39	O	787	0	828	43	0
40	P	870	0	878	41	0
41	Q	955	0	1019	61	0
42	R	884	0	944	47	0
43	S	805	0	847	51	0
44	T	714	0	737	27	0
45	U	649	0	666	35	0
46	V	649	0	691	26	0
47	W	536	0	552	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	X	638	0	665	41	0
49	Y	665	0	714	29	0
50	Z	545	0	579	46	0
51	a	1027	0	1092	44	0
52	3	33012	0	16618	663	0
53	1	62317	0	31346	912	0
54	2	2568	0	1303	57	0
55	5	1640	0	837	53	0
56	4	388	0	196	4	0
57	7	1619	0	821	24	0
58	7	11	0	8	0	0
59	7	10	0	10	0	0
All	All	148582	0	100429	3185	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 (3185) 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)
7:h:23:LEU:HD22	7:h:118:ILE:HB	1.33	1.10
53:1:45:G:H5''	53:1:46:G:H5'	1.24	1.08
6:g:97:ARG:HH22	53:1:2220:U:H4'	1.18	1.06
6:g:84:ALA:HB2	6:g:90:LEU:HD23	1.41	1.02
53:1:2277:G:H2'	53:1:2278:A:H5''	1.40	1.02
7:h:34:THR:HG21	53:1:1057:A:H1'	1.43	1.00
55:5:27:U:H2'	55:5:28:C:H5''	1.42	1.00
7:h:118:ILE:CG2	7:h:119:PRO:HD3	1.93	0.99
4:e:63:LYS:O	54:2:42:C:H1'	1.64	0.97
6:g:97:ARG:NH2	53:1:2220:U:H4'	1.79	0.96
55:5:61:C:H3'	55:5:62:C:H5''	1.49	0.95
33:I:190:LEU:HD12	33:I:192:ALA:H	1.31	0.94
7:h:118:ILE:HG23	7:h:119:PRO:HD3	1.47	0.93
55:5:62:C:H2'	55:5:63:G:H5''	1.47	0.93
12:m:134:THR:HG21	21:v:79:ARG:HH22	1.31	0.93
1:b:23:LEU:HD11	1:b:82:TYR:HB2	1.49	0.92
32:H:9:ILE:HG23	32:H:10:ARG:HD3	1.49	0.92
55:5:3:C:H2'	55:5:4:G:H5''	1.50	0.92
55:5:28:C:H42	55:5:42:G:H1	1.18	0.92
28:D:42:LEU:HD23	28:D:43:THR:HG23	1.51	0.91
6:g:31:VAL:HG13	6:g:32:PRO:HD3	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1801:A:H5''	53:1:2203:U:H2'	1.52	0.91
12:m:12:MET:HA	53:1:910:A:H62	1.36	0.90
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	1.52	0.90
52:3:405:U:H3'	52:3:406:G:H5'	1.53	0.88
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.54	0.88
4:e:34:THR:HG21	53:1:2314:A:H5'	1.54	0.86
22:w:79:GLU:HG2	22:w:81:GLU:HG2	1.56	0.86
33:I:54:LEU:HA	33:I:57:LYS:HE2	1.58	0.85
53:1:1141:U:H4'	53:1:1142:A:O4'	1.76	0.85
4:e:139:GLU:HG2	4:e:140:ILE:HD12	1.59	0.85
37:M:88:LYS:HE2	37:M:116:ARG:HA	1.57	0.85
31:G:22:TRP:HE1	52:3:830:G:H5'	1.40	0.85
52:3:516:U:H3	52:3:533:A:H62	1.23	0.85
49:Y:20:ASN:HD21	52:3:323:U:H5''	1.41	0.85
40:P:30:ILE:HD13	40:P:45:THR:HG22	1.56	0.85
53:1:1053:C:H2'	53:1:1054:A:H5''	1.59	0.85
52:3:1306:A:H61	52:3:1331:G:H1'	1.42	0.84
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.58	0.84
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.60	0.84
53:1:1020:A:H1'	53:1:1021:A:OP2	1.77	0.84
8:i:129:GLU:HG3	8:i:139:VAL:HG21	1.60	0.83
33:I:10:LEU:HD23	33:I:62:ARG:HD2	1.59	0.83
53:1:542:C:H2'	53:1:543:G:H5''	1.60	0.83
53:1:2277:G:C2'	53:1:2278:A:H5''	2.08	0.83
57:7:72:C:H3'	57:7:73:A:H5''	1.60	0.83
20:u:33:VAL:HG13	20:u:66:VAL:HG12	1.61	0.83
32:H:63:ILE:HG23	32:H:98:ALA:HB2	1.61	0.83
54:2:3:C:H2'	54:2:4:C:H5''	1.59	0.82
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.62	0.82
53:1:821:A:H5''	53:1:822:G:H5''	1.62	0.82
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.61	0.81
52:3:664:G:H22	52:3:741:G:H1	1.26	0.81
41:Q:49:ARG:HG3	41:Q:89:LEU:HD11	1.61	0.80
8:i:10:LEU:HD23	53:1:1070:A:N1	1.97	0.80
53:1:1077:A:H2'	53:1:1078:U:H5'	1.63	0.80
42:R:22:TYR:HB3	42:R:65:GLU:HB2	1.61	0.80
45:U:6:LEU:HD11	45:U:17:TYR:HB3	1.63	0.80
53:1:275:C:H2'	53:1:276:U:H4'	1.63	0.80
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.64	0.80
8:i:6:ALA:HB1	8:i:30:GLN:HG2	1.61	0.80
57:7:71:G:H2'	57:7:72:C:H5''	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:113:LYS:H	42:R:114:PRO:HD2	1.47	0.80
57:7:31:A:H2'	57:7:32:U:H5'	1.63	0.80
29:E:18:LYS:HG3	53:1:651:G:H5'	1.64	0.79
32:H:171:ARG:HG2	52:3:1106:G:H5''	1.62	0.79
32:H:174:LEU:HD23	32:H:181:ILE:HD13	1.62	0.79
50:Z:8:ASN:HB3	50:Z:9:GLU:OE1	1.82	0.79
8:i:71:LYS:HE2	53:1:1059:G:H5'	1.65	0.79
12:m:45:GLN:HE21	53:1:2485:G:H5''	1.47	0.79
53:1:511:U:H2'	53:1:512:G:H5'	1.65	0.79
31:G:206:ILE:H	31:G:206:ILE:HD12	1.48	0.79
52:3:1130:A:H61	52:3:1144:G:H1'	1.47	0.79
34:J:24:VAL:HG22	34:J:25:LYS:H	1.48	0.78
2:c:46:ARG:HB3	2:c:84:LEU:HB2	1.63	0.78
4:e:87:LYS:HD2	53:1:2313:C:H5''	1.66	0.78
14:o:33:ARG:HB2	54:2:52:A:H62	1.48	0.78
31:G:116:LEU:HG	31:G:140:LEU:HD13	1.65	0.78
36:L:94:ARG:HH12	52:3:1376:U:H5''	1.48	0.78
55:5:17(A):U:H1'	55:5:18:G:OP1	1.84	0.78
45:U:16:PHE:CZ	52:3:625:U:H4'	2.19	0.77
53:1:215:G:H4'	53:1:216:A:H4'	1.65	0.77
55:5:3:C:C2'	55:5:4:G:H5''	2.14	0.77
10:k:102:PRO:HB3	10:k:121:GLU:HB3	1.67	0.77
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.65	0.76
15:p:29:VAL:HG13	15:p:79:VAL:HG22	1.67	0.76
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.67	0.76
42:R:26:LYS:HD3	42:R:27:THR:N	2.01	0.76
52:3:1033:G:H2'	52:3:1034:G:H5''	1.66	0.76
32:H:149:LYS:HG3	32:H:172:VAL:HG21	1.67	0.76
28:D:31:LEU:HG	28:D:42:LEU:HD21	1.67	0.76
38:N:115:VAL:HG23	52:3:1367:C:H5''	1.67	0.76
55:5:31:G:H1	55:5:39:C:H42	1.32	0.76
12:m:34:LYS:HG2	12:m:35:ALA:H	1.51	0.76
45:U:54:LEU:H	45:U:54:LEU:HD12	1.51	0.76
57:7:44:G:H2'	57:7:45:U:H4'	1.67	0.76
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.67	0.75
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.68	0.75
53:1:2112:G:H2'	53:1:2113:U:H5'	1.66	0.75
34:J:110:MET:HE2	34:J:126:ALA:HB2	1.67	0.75
38:N:20:ILE:HD11	38:N:60:LEU:HB3	1.68	0.75
52:3:1412:C:H2'	52:3:1413:A:C8	2.21	0.75
33:I:8:LEU:HD21	52:3:429:U:H5'	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:22:LYS:HG3	52:3:1081:A:H5'	1.68	0.75
34:J:55:VAL:HG13	34:J:56:PRO:HD3	1.67	0.75
35:K:98:GLU:HG3	35:K:99:ALA:H	1.51	0.75
39:O:29:ALA:O	39:O:33:GLY:HA3	1.86	0.75
42:R:79:LEU:HD11	42:R:86:ARG:HB2	1.67	0.75
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.69	0.75
8:i:118:GLY:HA2	53:1:1082:U:H5'	1.69	0.74
11:l:85:VAL:HG23	11:l:86:GLU:H	1.50	0.74
31:G:110:ILE:HG13	31:G:147:LEU:HD11	1.69	0.74
39:O:6:ILE:H	39:O:6:ILE:HD12	1.50	0.74
52:3:1513:A:H2'	52:3:1514:G:C8	2.22	0.74
2:c:151:THR:HB	2:c:152:PRO:HD3	1.68	0.74
13:n:2:ARG:HG2	13:n:2:ARG:O	1.86	0.74
37:M:45:ILE:HG12	37:M:60:LEU:HD22	1.69	0.74
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.68	0.74
48:X:14:LEU:HD11	48:X:34:SER:HB3	1.70	0.74
55:5:61:C:C3'	55:5:62:C:H5''	2.18	0.74
8:i:38:CYS:HA	8:i:41:PHE:HB3	1.67	0.74
39:O:88:MET:HG3	39:O:89:ARG:HG2	1.69	0.74
52:3:484:G:H4'	52:3:485:U:H5''	1.68	0.74
2:c:56:LYS:HE2	53:1:2830:C:H5''	1.70	0.74
21:v:75:GLN:HB2	21:v:92:VAL:HG23	1.69	0.74
42:R:95:PRO:HB2	42:R:99:GLN:HE21	1.53	0.74
53:1:1133:A:H4'	53:1:1134:A:H5''	1.69	0.74
2:c:9:VAL:HB	2:c:26:VAL:HG13	1.69	0.73
36:L:55:LYS:HB2	36:L:60:ALA:HB2	1.70	0.73
4:e:132:ARG:HE	53:1:2305:U:H4'	1.53	0.73
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.02	0.73
52:3:327:A:O2'	52:3:328:C:H4'	1.87	0.73
53:1:821:A:H5''	53:1:822:G:C5'	2.17	0.73
7:h:34:THR:HG21	53:1:1057:A:C1'	2.17	0.73
39:O:41:PRO:HG2	52:3:1150:A:C2	2.23	0.73
8:i:8:VAL:HG13	53:1:1097:U:O2'	1.89	0.73
36:L:30:MET:HE1	52:3:1373:G:O2'	1.88	0.73
51:a:53:ARG:HD2	55:5:62:C:H4'	1.71	0.73
17:r:78:ARG:HH12	53:1:990:A:H61	1.37	0.73
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.69	0.73
11:l:85:VAL:HG11	11:l:95:LEU:HD23	1.71	0.73
43:S:39:ASP:HA	43:S:42:ASN:HD21	1.54	0.73
42:R:24:VAL:HA	52:3:1329:A:H5''	1.69	0.72
50:Z:34:ARG:HB3	50:Z:36:PHE:CE1	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2286:G:H5''	53:1:2287:A:OP1	1.88	0.72
33:I:23:GLY:HA3	52:3:409:U:OP1	1.89	0.72
53:1:2063:C:O2'	57:7:76:A:H4'	1.89	0.72
32:H:57:GLU:HG3	32:H:59:PRO:HD3	1.72	0.72
41:Q:24:GLU:H	41:Q:24:GLU:CD	1.97	0.72
7:h:55:VAL:HA	53:1:1084:A:H4'	1.72	0.72
10:k:88:ASN:HB3	10:k:91:SER:O	1.90	0.72
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.71	0.72
36:L:49:LEU:HD22	36:L:123:LEU:HD13	1.69	0.72
53:1:713:G:H21	53:1:718:A:H62	1.37	0.72
8:i:9:LYS:O	53:1:1070:A:H2	1.72	0.72
55:5:15:G:H3'	55:5:16:C:C5'	2.20	0.71
57:7:49:C:H6	57:7:49:C:H5'	1.55	0.71
37:M:31:LEU:HD21	52:3:643:C:H5''	1.69	0.71
33:I:72:ARG:HH22	33:I:76:LYS:HD2	1.56	0.71
32:H:162:ALA:HB2	52:3:1056:U:H5'	1.73	0.71
33:I:58:GLN:O	33:I:62:ARG:HG2	1.91	0.71
18:s:69:LEU:HG	18:s:107:VAL:HG22	1.72	0.70
27:C:36:LYS:HE2	27:C:47:ILE:HG12	1.73	0.70
44:T:42:PHE:HB3	53:1:715:A:N3	2.06	0.70
46:V:12:VAL:HB	46:V:21:VAL:HG13	1.71	0.70
53:1:310:A:H2'	53:1:311:A:H5''	1.72	0.70
4:e:39:VAL:HG22	4:e:41:GLU:HB2	1.73	0.70
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.73	0.70
40:P:43:TRP:CZ2	52:3:686:U:H1'	2.26	0.70
49:Y:55:PRO:HA	52:3:194:C:H5'	1.73	0.70
21:v:45:ASP:OD2	53:1:1039:A:H4'	1.91	0.70
1:b:120:ASP:HB2	6:g:91:PHE:CZ	2.26	0.70
34:J:87:VAL:HG22	34:J:92:ARG:HD2	1.71	0.70
41:Q:120:ARG:NH1	52:3:500:G:H5'	2.06	0.70
52:3:1201:A:H1'	52:3:1202:U:OP2	1.92	0.70
57:7:7:A:O2'	57:7:49:C:H5''	1.90	0.70
14:o:100:HIS:HD2	54:2:48:U:H4'	1.56	0.70
49:Y:67:HIS:CE1	52:3:132:C:H4'	2.26	0.70
53:1:329:G:O4'	53:1:477:A:H1'	1.90	0.70
32:H:176:THR:HG22	52:3:1111:A:H61	1.55	0.70
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.74	0.69
40:P:32:THR:HG22	40:P:43:TRP:HB3	1.71	0.69
52:3:1513:A:H2'	52:3:1514:G:H8	1.56	0.69
53:1:1645:G:H5''	53:1:1646:C:H5'	1.74	0.69
53:1:1807:G:H2'	53:1:1808:A:H5'	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.72	0.69
15:p:112:ARG:HB3	15:p:114:ASN:HD22	1.57	0.69
23:x:3:VAL:HG22	23:x:10:ARG:HG3	1.74	0.69
28:D:24:THR:HG23	28:D:27:GLY:H	1.56	0.69
38:N:111:GLU:OE1	52:3:1348:U:H5''	1.92	0.69
14:o:32:PRO:HD2	54:2:29:A:OP2	1.93	0.69
54:2:3:C:C2'	54:2:4:C:H5''	2.23	0.69
55:5:62:C:C2'	55:5:63:G:H5''	2.21	0.69
12:m:41:LEU:HD13	12:m:96:ILE:HG13	1.74	0.69
1:b:94:LEU:HD21	53:1:1501:G:H4'	1.74	0.69
10:k:98:ARG:HD2	52:3:338:A:OP2	1.93	0.69
33:I:57:LYS:HD3	33:I:202:LEU:HD22	1.73	0.69
55:5:27:U:C2'	55:5:28:C:H5''	2.22	0.69
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.73	0.69
17:r:81:LYS:HD2	53:1:973:A:H5''	1.73	0.69
54:2:66:A:H5''	54:2:67:G:OP1	1.93	0.69
35:K:10:VAL:HG23	35:K:58:HIS:HB3	1.75	0.68
35:K:12:PRO:HA	35:K:15:SER:HB2	1.75	0.68
53:1:2391:G:H4'	53:1:2392:A:OP1	1.91	0.68
22:w:17:LEU:HD23	22:w:35:ARG:NH1	2.07	0.68
41:Q:120:ARG:NH2	52:3:500:G:H5'	2.08	0.68
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.28	0.68
51:a:218:MET:HE1	53:1:2128:G:H4'	1.74	0.68
52:3:1497:G:O2'	52:3:1498:U:H5'	1.93	0.68
28:D:25:LYS:HE3	53:1:1368:G:H5'	1.73	0.68
32:H:37:LYS:O	32:H:40:GLN:HG2	1.93	0.68
35:K:2:ARG:HB3	35:K:92:THR:HG21	1.75	0.68
52:3:959:A:H2'	52:3:960:U:H4'	1.75	0.68
40:P:127:ARG:HG3	50:Z:34:ARG:HH22	1.58	0.68
52:3:1158:C:H2'	52:3:1159:U:H4'	1.75	0.68
5:f:36:LEU:HD21	5:f:67:ALA:HB1	1.76	0.68
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.75	0.68
46:V:16:MET:HB3	46:V:19:SER:OG	1.94	0.68
52:3:701:U:H4'	52:3:703:G:H1'	1.76	0.68
35:K:2:ARG:HB3	35:K:92:THR:CG2	2.23	0.68
36:L:78:ARG:NH2	52:3:1382:C:H5'	2.09	0.68
51:a:54:LYS:HE3	55:5:63:G:O3'	1.93	0.68
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.74	0.68
34:J:155:LYS:HD2	34:J:156:ARG:HB2	1.76	0.68
18:s:32:ALA:O	18:s:35:ILE:HG22	1.93	0.68
53:1:2114:A:H61	53:1:2117:A:H62	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2800:A:H3'	53:1:2801:G:H5'	1.74	0.68
12:m:6:ARG:O	12:m:6:ARG:HD3	1.93	0.68
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.76	0.68
4:e:35:LEU:HB2	4:e:88:VAL:HB	1.76	0.67
7:h:23:LEU:HD22	7:h:118:ILE:CB	2.19	0.67
32:H:69:THR:HG21	32:H:75:VAL:HG21	1.75	0.67
49:Y:25:SER:OG	52:3:1458:G:H5''	1.94	0.67
53:1:1415:U:H2'	53:1:1416:G:H4'	1.76	0.67
10:k:35:VAL:HG11	10:k:106:GLU:HB2	1.77	0.67
32:H:189:HIS:HD2	52:3:1205:U:H4'	1.59	0.67
45:U:79:ASN:HB2	45:U:82:ALA:OXT	1.95	0.67
52:3:1259:C:H3'	52:3:1260:G:H5''	1.77	0.67
52:3:1306:A:N6	52:3:1331:G:H1'	2.08	0.67
31:G:170:ILE:H	31:G:170:ILE:HD12	1.59	0.67
26:B:8:THR:CG2	53:1:2020:A:H5'	2.25	0.67
36:L:24:LYS:NZ	52:3:1375:A:H5''	2.08	0.67
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.74	0.67
43:S:39:ASP:HA	43:S:42:ASN:ND2	2.10	0.67
51:a:10:VAL:O	51:a:14:LYS:HG3	1.95	0.67
47:W:39:VAL:HB	47:W:43:ILE:HD11	1.76	0.67
4:e:75:GLY:HA3	53:1:2310:C:O2	1.95	0.67
10:k:28:SER:OG	53:1:2566:A:N1	2.27	0.67
32:H:39:ARG:HH12	32:H:42:LEU:HD12	1.59	0.67
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.77	0.67
51:a:54:LYS:HD3	55:5:63:G:H4'	1.76	0.67
6:g:46:PHE:HB3	6:g:50:ARG:HH21	1.59	0.67
32:H:149:LYS:HE2	32:H:172:VAL:HB	1.76	0.67
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.59	0.67
22:w:38:GLY:HA2	53:1:2330:G:H21	1.60	0.67
53:1:310:A:C2'	53:1:311:A:H5''	2.24	0.67
53:1:441:U:O2'	53:1:442:G:H5'	1.95	0.67
53:1:962:G:H21	53:1:2250:G:H1	1.40	0.67
14:o:3:LYS:NZ	54:2:29:A:H5''	2.10	0.66
37:M:31:LEU:HD11	52:3:643:C:H5'	1.76	0.66
53:1:473:G:O2'	53:1:474:G:H5'	1.95	0.66
47:W:52:ARG:HB3	47:W:56:ARG:NH2	2.10	0.66
53:1:955:U:H3	53:1:962:G:H1	1.43	0.66
33:I:103:ARG:HD3	33:I:167:PRO:HG2	1.77	0.66
4:e:92:GLY:O	4:e:95:MET:HG2	1.96	0.66
53:1:676:A:H62	53:1:802:A:H61	1.43	0.66
53:1:1053:C:C2'	53:1:1054:A:H5''	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2296:U:H5''	53:1:2297:A:OP1	1.96	0.66
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.77	0.66
45:U:68:SER:OG	45:U:71:VAL:HG22	1.96	0.66
37:M:2:MET:HE2	37:M:8:ASP:HB2	1.78	0.66
52:3:988:G:H1'	52:3:1015:G:H22	1.61	0.66
45:U:14:ARG:HH12	52:3:617:G:H21	1.42	0.66
51:a:175:ILE:HB	51:a:188:ASN:HB3	1.78	0.66
53:1:2066:C:O2'	53:1:2067:G:H5'	1.96	0.66
57:7:71:G:C2'	57:7:72:C:H5''	2.26	0.66
17:r:34:GLU:HG3	17:r:60:LYS:HG2	1.76	0.66
53:1:1991:U:H2'	53:1:1992:G:H5''	1.78	0.66
53:1:2423:U:O2'	53:1:2425:A:H2'	1.96	0.66
55:5:25:C:H6	55:5:25:C:H5'	1.61	0.66
13:n:90:ARG:NH2	13:n:116:VAL:HG11	2.12	0.65
43:S:46:LYS:HD3	43:S:49:THR:HB	1.77	0.65
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.59	0.65
52:3:1412:C:H2'	52:3:1413:A:H8	1.59	0.65
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.76	0.65
36:L:115:MET:HE3	52:3:1240:U:C5	2.31	0.65
49:Y:14:GLU:O	49:Y:17:ARG:HG3	1.95	0.65
52:3:692:U:H2'	52:3:694:A:OP2	1.96	0.65
52:3:1236:A:H4'	52:3:1304:G:H4'	1.79	0.65
3:d:163:ASN:HB2	53:1:322:A:OP2	1.94	0.65
46:V:18:LYS:HD3	46:V:49:ASN:N	2.11	0.65
41:Q:57:THR:HG21	52:3:362:G:H5''	1.78	0.65
43:S:8:ARG:HG3	52:3:1217:C:OP1	1.97	0.65
53:1:2553:G:H3'	53:1:2554:U:H5''	1.78	0.65
5:f:94:ARG:H	5:f:105:SER:HB2	1.60	0.65
27:C:20:TYR:OH	53:1:2348:U:H5'	1.96	0.65
40:P:85:VAL:HG21	40:P:92:ARG:HG3	1.79	0.65
43:S:48:GLN:HB3	48:X:12:LEU:HD22	1.77	0.65
52:3:181:A:N6	52:3:194:C:H2'	2.11	0.65
11:l:93:ASN:C	11:l:95:LEU:H	2.05	0.65
14:o:3:LYS:HZ1	54:2:29:A:H5''	1.60	0.65
8:i:25:PRO:O	8:i:29:GLN:HG3	1.96	0.65
15:p:102:ARG:HH11	15:p:106:ALA:HB1	1.61	0.65
53:1:1077:A:C2'	53:1:1078:U:H5'	2.27	0.65
7:h:32:GLY:O	53:1:1055:G:H4'	1.96	0.65
41:Q:120:ARG:HH12	52:3:500:G:H5'	1.62	0.65
53:1:2600:A:O2'	53:1:2601:C:H5'	1.97	0.65
6:g:31:VAL:HG13	6:g:32:PRO:CD	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:39:GLN:OE1	53:1:715:A:H4'	1.97	0.64
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.80	0.64
4:e:115:GLY:HA3	4:e:177:ARG:HB2	1.78	0.64
43:S:4:SER:HB2	52:3:1216:A:H5''	1.80	0.64
50:Z:44:ARG:NH2	52:3:722:G:H5'	2.13	0.64
53:1:1872:A:H2'	53:1:1873:G:O4'	1.98	0.64
6:g:116:ARG:O	6:g:118:PRO:HD3	1.97	0.64
52:3:923:A:H61	52:3:1393:U:H3	1.43	0.64
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.78	0.64
42:R:16:ILE:HD13	52:3:1302:C:C5	2.33	0.64
53:1:2266:A:H4'	53:1:2267:A:N3	2.13	0.64
3:d:173:THR:HA	3:d:199:MET:HE1	1.79	0.64
41:Q:3:VAL:HA	41:Q:6:LEU:HD13	1.79	0.64
50:Z:29:ALA:HA	50:Z:32:ARG:NE	2.12	0.64
52:3:29:U:O2'	52:3:30:U:H5'	1.98	0.64
53:1:1664:A:H61	53:1:1996:C:H42	1.45	0.64
4:e:73:VAL:HG12	4:e:75:GLY:H	1.63	0.64
22:w:7:ARG:N	22:w:7:ARG:HH11	1.96	0.64
32:H:138:GLN:NE2	32:H:142:ARG:HD3	2.13	0.64
53:1:528:A:N1	53:1:2042:A:H2'	2.13	0.64
1:b:201:LEU:HD13	52:3:773:G:H5''	1.80	0.64
6:g:26:ALA:O	6:g:31:VAL:HG12	1.98	0.64
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.79	0.64
11:l:96:LYS:HG3	11:l:101:ILE:HD11	1.78	0.64
11:l:135:ILE:HD12	11:l:142:ILE:HD11	1.80	0.64
34:J:105:ILE:HD12	34:J:123:LEU:HD13	1.80	0.64
42:R:7:ASN:OD1	42:R:9:PRO:HD3	1.98	0.64
4:e:32:LYS:HD3	4:e:91:ARG:HH22	1.62	0.63
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.80	0.63
53:1:859:G:H1'	53:1:860:U:H5	1.63	0.63
10:k:108:ARG:HH22	52:3:345:C:H3'	1.63	0.63
37:M:45:ILE:HD11	37:M:60:LEU:HB3	1.79	0.63
51:a:37:LYS:HD3	53:1:2128:G:OP2	1.98	0.63
52:3:543:U:H2'	52:3:544:G:C8	2.34	0.63
5:f:136:ASP:HB3	5:f:139:VAL:HG22	1.81	0.63
41:Q:113:ARG:HB2	41:Q:118:VAL:HB	1.80	0.63
47:W:52:ARG:HB3	47:W:56:ARG:HH22	1.63	0.63
49:Y:29:THR:HA	49:Y:32:LYS:HE2	1.80	0.63
3:d:44:ARG:HD3	53:1:444:C:OP2	1.98	0.63
3:d:143:LEU:HD22	3:d:185:LYS:HG3	1.80	0.63
4:e:45:ASP:OD2	4:e:48:LEU:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:24:VAL:HG13	34:J:26:GLY:H	1.63	0.63
52:3:948:C:H2'	52:3:949:A:H8	1.62	0.63
52:3:1534:A:H61	56:4:11:U:H3	1.44	0.63
53:1:615:U:H5''	53:1:616:A:OP2	1.98	0.63
53:1:2281:A:O2'	53:1:2282:G:H5'	1.99	0.63
53:1:2743:U:C3'	53:1:2744:G:H5''	2.29	0.63
7:h:33:VAL:HG12	7:h:34:THR:H	1.63	0.63
24:y:2:LYS:NZ	53:1:102:U:H1'	2.12	0.63
37:M:101:ALA:HB3	37:M:112:ASP:HB3	1.80	0.63
52:3:1346:A:H2'	52:3:1347:G:H4'	1.80	0.63
36:L:25:PHE:O	36:L:28:ILE:HG12	1.99	0.63
36:L:47:GLU:O	36:L:51:GLN:HG2	1.99	0.63
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.80	0.63
52:3:1414:U:H2'	52:3:1415:G:H8	1.62	0.63
8:i:6:ALA:CB	8:i:30:GLN:HG2	2.29	0.63
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.81	0.63
44:T:55:LEU:O	44:T:59:VAL:HG23	1.99	0.63
53:1:161:A:H3'	53:1:162:U:H5''	1.81	0.63
53:1:215:G:C4'	53:1:216:A:H4'	2.29	0.63
53:1:639:U:H2'	53:1:640:C:C6	2.34	0.63
53:1:742:A:H2'	53:1:743:A:C8	2.33	0.63
53:1:2297:A:N1	53:1:2321:U:H5	1.97	0.63
2:c:48:ILE:HG23	2:c:84:LEU:HD21	1.81	0.63
9:j:27:ARG:NH1	53:1:1140:C:O3'	2.32	0.63
33:I:21:LYS:HE3	52:3:429:U:O2'	1.99	0.63
43:S:47:LEU:HG	52:3:1317:C:O2'	1.99	0.63
52:3:211:G:H2'	52:3:212:G:H5'	1.80	0.63
28:D:26:ASN:ND2	53:1:682:G:H5'	2.13	0.62
31:G:96:LEU:HD21	31:G:106:VAL:HG22	1.80	0.62
45:U:43:ALA:HB1	45:U:46:LYS:HE3	1.81	0.62
51:a:189:LEU:O	51:a:192:LEU:HG	1.98	0.62
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.79	0.62
12:m:51:ARG:HH12	53:1:2483:C:H4'	1.63	0.62
15:p:90:ALA:HB2	15:p:112:ARG:HG2	1.81	0.62
35:K:91:ARG:HG3	35:K:92:THR:H	1.64	0.62
38:N:28:VAL:HG23	38:N:63:TYR:HD1	1.63	0.62
31:G:34:ARG:HD2	31:G:39:ILE:HD11	1.80	0.62
7:h:97:LYS:HA	7:h:125:ARG:HH12	1.65	0.62
28:D:30:VAL:O	28:D:34:ARG:HG2	1.99	0.62
53:1:1418:G:H21	53:1:1580:A:H62	1.45	0.62
20:u:42:LYS:HE2	53:1:499:U:H5''	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:107:LYS:HB3	32:H:110:LEU:HD23	1.80	0.62
53:1:542:C:C2'	53:1:543:G:H5''	2.28	0.62
53:1:1300:G:H4'	53:1:1301:A:H5''	1.80	0.62
53:1:2743:U:H3'	53:1:2744:G:H5''	1.79	0.62
7:h:13:ALA:O	7:h:17:GLU:HG2	1.99	0.62
10:k:13:ASN:ND2	10:k:98:ARG:HG2	2.14	0.62
18:s:82:MET:HB3	18:s:84:ARG:NH2	2.13	0.62
32:H:171:ARG:CG	52:3:1106:G:H5''	2.29	0.62
34:J:149:PRO:HA	34:J:152:VAL:HG22	1.81	0.62
37:M:12:ARG:NH2	52:3:826:C:H5'	2.15	0.62
41:Q:68:GLY:O	52:3:521:G:H5'	2.00	0.62
52:3:1418:A:H3'	52:3:1419:G:H5''	1.81	0.62
53:1:49:A:H5'	53:1:51:G:O4'	1.99	0.62
39:O:12:ALA:HB3	39:O:18:ILE:HG21	1.81	0.62
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.82	0.62
1:b:269:ARG:HG2	1:b:270:ARG:N	2.15	0.62
7:h:37:LYS:HG3	7:h:41:LEU:HD12	1.81	0.62
24:y:19:LEU:HD22	24:y:23:ARG:HH12	1.63	0.62
33:I:104:MET:HE3	33:I:142:VAL:HG11	1.82	0.62
38:N:128:LYS:HE3	38:N:129:ARG:HH12	1.64	0.62
1:b:252:LYS:NZ	53:1:1825:U:H1'	2.15	0.62
41:Q:120:ARG:CZ	52:3:500:G:H5'	2.29	0.62
43:S:3:GLN:NE2	52:3:1047:G:H4'	2.15	0.62
43:S:66:THR:HG21	43:S:82:LYS:HE3	1.82	0.62
34:J:155:LYS:HD3	37:M:70:VAL:HG13	1.81	0.62
50:Z:11:PHE:O	50:Z:13:VAL:HG12	2.00	0.62
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.82	0.61
31:G:185:ILE:HG21	31:G:203:ASP:HB3	1.82	0.61
40:P:124:LYS:HG2	50:Z:34:ARG:NH1	2.15	0.61
53:1:2421:G:H2'	55:5:76:A:N6	2.15	0.61
57:7:17:C:O5'	57:7:18:G:H5''	2.00	0.61
18:s:94:ASP:OD2	53:1:2014:A:H5'	2.00	0.61
24:y:47:ARG:O	24:y:50:VAL:HG22	2.00	0.61
31:G:109:SER:HA	31:G:112:ARG:HD3	1.81	0.61
32:H:187:GLU:HA	32:H:196:GLY:HA2	1.81	0.61
34:J:23:THR:HA	34:J:28:ARG:HA	1.80	0.61
38:N:15:ALA:HB1	52:3:1148:U:O3'	2.00	0.61
52:3:211:G:C2'	52:3:212:G:H5'	2.30	0.61
5:f:98:LYS:HZ2	5:f:103:ASN:HB2	1.66	0.61
7:h:23:LEU:CD2	7:h:118:ILE:HB	2.19	0.61
46:V:48:GLU:HB2	46:V:51:GLU:OE2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:5:3:C:C3'	55:5:4:G:H5''	2.30	0.61
1:b:269:ARG:HG2	1:b:270:ARG:H	1.66	0.61
53:1:1300:G:H4'	53:1:1301:A:C5'	2.29	0.61
53:1:1680:U:H2'	53:1:1681:G:H5'	1.82	0.61
52:3:1464:U:H2'	52:3:1465:A:H8	1.66	0.61
55:5:61:C:H3'	55:5:62:C:C5'	2.29	0.61
4:e:34:THR:HG23	4:e:89:THR:HG22	1.82	0.61
34:J:108:GLY:H	52:3:9:G:C5'	2.14	0.61
38:N:49:GLN:N	38:N:50:PRO:HD2	2.14	0.61
53:1:1476:U:H3	53:1:1515:A:H62	1.48	0.61
5:f:104:LEU:HB2	5:f:112:VAL:HB	1.82	0.61
7:h:42:ARG:HH21	7:h:45:GLY:HA3	1.65	0.61
14:o:31:THR:HG21	54:2:28:C:OP1	2.00	0.61
21:v:72:VAL:HG11	21:v:91:PHE:HB3	1.81	0.61
25:z:30:ARG:O	25:z:33:HIS:HB2	2.01	0.61
54:2:65:U:H3'	54:2:108:A:H61	1.64	0.61
11:l:57:LEU:HD22	29:E:53:ASP:HB3	1.81	0.61
23:x:36:ARG:NH2	53:1:2199:A:OP1	2.33	0.61
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.83	0.61
11:l:118:THR:HG23	11:l:120:VAL:HG23	1.81	0.61
16:q:93:ILE:HD12	17:r:13:ARG:HB2	1.83	0.61
45:U:1:MET:HE2	52:3:136:C:H5'	1.83	0.61
53:1:2286:G:H4'	53:1:2287:A:O5'	2.01	0.61
53:1:2799:A:H2'	53:1:2800:A:H5'	1.83	0.61
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.16	0.60
3:d:2:GLU:HB3	3:d:11:ALA:HB1	1.83	0.60
52:3:1144:G:H21	52:3:1146:A:H62	1.48	0.60
26:B:54:ILE:HG23	26:B:56:LYS:H	1.66	0.60
36:L:35:LYS:HB2	52:3:1373:G:H5''	1.83	0.60
52:3:17:U:H2'	52:3:18:C:C6	2.36	0.60
52:3:483:C:H2'	52:3:484:G:C8	2.35	0.60
52:3:556:C:O2'	52:3:557:G:H5'	2.01	0.60
1:b:201:LEU:HD21	52:3:774:G:P	2.41	0.60
5:f:122:ALA:HB1	5:f:130:ILE:HD11	1.83	0.60
29:E:61:LEU:HD12	29:E:61:LEU:O	2.01	0.60
41:Q:120:ARG:HH22	52:3:500:G:H5'	1.64	0.60
53:1:752:A:O2'	53:1:1781:U:H5'	2.01	0.60
44:T:28:VAL:HB	44:T:80:LEU:HD21	1.82	0.60
53:1:293:U:H2'	53:1:294:A:H5''	1.83	0.60
53:1:554:U:H2'	53:1:555:G:O4'	2.02	0.60
2:c:61:THR:HB	2:c:63:PRO:HD2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:100:ILE:HG13	11:l:101:ILE:HG23	1.82	0.60
54:2:65:U:H3'	54:2:108:A:N6	2.17	0.60
36:L:24:LYS:HZ1	52:3:1375:A:H5''	1.67	0.60
53:1:1539:U:H2'	53:1:1540:G:H8	1.67	0.60
51:a:7:ARG:HE	51:a:11:ILE:HD11	1.67	0.60
4:e:128:SER:HB2	53:1:2303:G:O2'	2.01	0.60
6:g:40:THR:O	6:g:42:LYS:N	2.35	0.60
20:u:35:VAL:HG13	20:u:38:ILE:HG13	1.83	0.60
22:w:33:ILE:HG21	22:w:76:ILE:HG21	1.83	0.60
28:D:3:ARG:HD3	53:1:1613:G:H4'	1.82	0.60
51:a:170:ILE:HG12	53:1:2177:C:O2'	2.02	0.60
52:3:179:A:H61	52:3:196:A:H62	1.50	0.60
53:1:161:A:H62	53:1:165:A:H61	1.49	0.60
53:1:1796:U:H2'	53:1:1797:G:H8	1.67	0.60
42:R:23:GLY:O	52:3:1329:A:H4'	2.00	0.60
52:3:578:C:H2'	52:3:579:A:H8	1.67	0.60
53:1:1213:A:N6	53:1:1236:G:H1'	2.16	0.60
1:b:250:GLN:OE1	53:1:1843:C:H5'	2.02	0.60
34:J:156:ARG:HD3	37:M:42:GLU:HG3	1.83	0.60
41:Q:28:GLN:HB3	41:Q:80:LEU:HG	1.84	0.60
51:a:195:ALA:O	51:a:198:LYS:HG2	2.02	0.60
52:3:1379:G:O2'	52:3:1380:U:H5'	2.02	0.60
52:3:1422:G:O2'	52:3:1423:G:H5'	2.02	0.60
54:2:66:A:N1	54:2:107:G:H2'	2.17	0.60
55:5:17:C:H3'	55:5:17(A):U:H5'	1.82	0.60
12:m:34:LYS:HD3	12:m:99:GLY:HA2	1.84	0.59
26:B:30:ASP:HB3	26:B:35:GLU:H	1.66	0.59
53:1:1386:C:H2'	53:1:1387:A:H8	1.67	0.59
1:b:120:ASP:HB2	6:g:91:PHE:HZ	1.65	0.59
8:i:99:LYS:HD3	8:i:138:VAL:HG23	1.84	0.59
12:m:33:LEU:HD23	12:m:103:TYR:HD2	1.67	0.59
2:c:121:THR:HB	2:c:127:PHE:CD2	2.38	0.59
4:e:109:ARG:HH11	4:e:136:ILE:HA	1.67	0.59
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.85	0.59
13:n:53:THR:HG21	53:1:2840:C:H5''	1.84	0.59
21:v:51:GLN:OE1	21:v:86:LEU:HD11	2.02	0.59
31:G:113:LEU:O	31:G:117:GLU:HG3	2.01	0.59
33:I:12:ARG:HG2	33:I:33:ILE:HD12	1.84	0.59
53:1:807:U:H2'	53:1:808:G:H8	1.67	0.59
53:1:974:G:H1'	53:1:975:A:C8	2.37	0.59
1:b:137:GLY:HA3	52:3:712:A:H5'	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.83	0.59
52:3:129:A:H1'	52:3:130:A:C8	2.37	0.59
53:1:1956:U:H2'	53:1:1957:C:H5'	1.84	0.59
4:e:72:SER:HB2	4:e:80:GLN:N	2.17	0.59
5:f:140:ILE:HG13	5:f:141:GLY:N	2.16	0.59
10:k:98:ARG:HH21	52:3:339:C:H41	1.48	0.59
31:G:22:TRP:HE1	52:3:830:G:C5'	2.15	0.59
44:T:46:LYS:C	44:T:47:LYS:HD2	2.27	0.59
44:T:52:ARG:CZ	53:1:715:A:C6	2.85	0.59
52:3:876:C:H2'	52:3:877:G:H8	1.67	0.59
54:2:3:C:C3'	54:2:4:C:H5''	2.33	0.59
7:h:22:ALA:HB3	7:h:87:GLU:OE2	2.03	0.59
43:S:71:GLY:HA2	52:3:975:A:O2'	2.03	0.59
23:x:17:ARG:HE	23:x:23:ALA:HB2	1.67	0.59
31:G:135:MET:SD	31:G:136:ARG:N	2.76	0.59
43:S:81:ILE:H	43:S:81:ILE:HD12	1.67	0.59
52:3:77:A:H2'	52:3:78:A:C8	2.38	0.59
1:b:81:GLU:HB2	1:b:90:ILE:HG13	1.85	0.59
3:d:151:GLY:HA2	3:d:172:ALA:HB2	1.83	0.59
7:h:119:PRO:CD	7:h:120:ALA:H	2.16	0.59
19:t:44:LYS:HG3	19:t:55:VAL:HG21	1.85	0.59
37:M:85:TYR:CD1	37:M:123:GLU:HB3	2.38	0.59
41:Q:53:ARG:HA	41:Q:63:THR:HA	1.85	0.59
53:1:2156:G:H2'	53:1:2157:G:H5'	1.85	0.59
16:q:23:TYR:CD1	53:1:533:G:H5'	2.38	0.59
17:r:54:VAL:HG23	17:r:55:ASP:H	1.67	0.59
52:3:763:G:H2'	52:3:764:C:C6	2.38	0.59
52:3:881:G:H2'	52:3:882:C:O4'	2.02	0.59
53:1:2788:C:H2'	53:1:2789:C:C6	2.37	0.59
19:t:67:VAL:HA	19:t:76:ARG:HA	1.83	0.59
32:H:58:ARG:NH1	32:H:58:ARG:HB2	2.18	0.59
34:J:10:LEU:HA	34:J:44:ARG:HH22	1.67	0.59
35:K:92:THR:OG1	35:K:93:LYS:N	2.36	0.59
8:i:9:LYS:HD3	53:1:1061:U:P	2.43	0.58
12:m:12:MET:HA	53:1:910:A:N6	2.12	0.58
15:p:61:ARG:HG3	15:p:70:GLU:HG3	1.85	0.58
33:I:198:LEU:HA	33:I:201:GLU:HG2	1.85	0.58
34:J:55:VAL:HG13	34:J:56:PRO:CD	2.33	0.58
38:N:121:ARG:HD2	52:3:1348:U:H4'	1.83	0.58
40:P:115:ILE:HD12	40:P:116:PRO:HD2	1.85	0.58
49:Y:20:ASN:ND2	52:3:323:U:H5''	2.15	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:36:PHE:HB2	50:Z:40:PRO:HD3	1.85	0.58
52:3:1005:A:H2'	52:3:1006:G:O4'	2.03	0.58
52:3:1137:C:H4'	52:3:1138:G:N2	2.18	0.58
53:1:121:G:H4'	53:1:149:A:H5'	1.86	0.58
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.85	0.58
15:p:91:VAL:HG21	15:p:96:LEU:HD21	1.83	0.58
31:G:27:LYS:O	31:G:30:ILE:HG22	2.03	0.58
49:Y:36:ALA:O	49:Y:39:GLU:HG3	2.03	0.58
52:3:78:A:H2'	52:3:79:G:O4'	2.04	0.58
53:1:2030:A:N3	53:1:2499:C:H5''	2.18	0.58
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.68	0.58
17:r:74:ILE:HD13	53:1:992:C:H4'	1.84	0.58
33:I:6:PRO:HB2	33:I:9:LYS:HG3	1.85	0.58
36:L:142:ARG:HB3	36:L:143:MET:HE2	1.85	0.58
52:3:396:C:H2'	52:3:397:A:H5''	1.83	0.58
52:3:715:A:H2'	52:3:716:A:C8	2.39	0.58
52:3:1033:G:C2'	52:3:1034:G:H5''	2.32	0.58
53:1:1979:U:O2'	53:1:1980:G:H5'	2.03	0.58
55:5:25:C:H2'	55:5:26:G:O4'	2.04	0.58
34:J:35:LEU:HD21	34:J:136:VAL:HG21	1.84	0.58
45:U:16:PHE:CE1	52:3:625:U:H4'	2.38	0.58
52:3:1464:U:H2'	52:3:1465:A:C8	2.38	0.58
53:1:2220:U:H2'	53:1:2221:G:H8	1.68	0.58
3:d:126:VAL:O	3:d:156:ASN:ND2	2.37	0.58
38:N:68:GLY:HA2	52:3:1250:A:H5'	1.85	0.58
52:3:715:A:H2'	52:3:716:A:H8	1.68	0.58
32:H:63:ILE:HG23	32:H:98:ALA:CB	2.30	0.58
36:L:139:ASP:O	36:L:143:MET:HG2	2.03	0.58
52:3:70:U:H4'	52:3:71:A:H8	1.68	0.58
53:1:2196:C:O2'	53:1:2197:U:H5'	2.04	0.58
57:7:17:C:H5'	57:7:18:G:H3'	1.85	0.58
33:I:80:ARG:HH21	52:3:613:C:P	2.26	0.58
53:1:2698:U:H2'	53:1:2699:C:C6	2.39	0.58
22:w:36:GLN:NE2	22:w:39:THR:HA	2.18	0.58
23:x:9:LYS:HG2	53:1:396:G:OP1	2.04	0.58
28:D:26:ASN:CG	53:1:682:G:H5'	2.29	0.58
34:J:24:VAL:HG22	34:J:25:LYS:N	2.17	0.58
53:1:2163:A:H2'	53:1:2164:C:H5'	1.85	0.58
12:m:34:LYS:HE3	12:m:131:VAL:HG11	1.86	0.58
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.18	0.58
28:D:25:LYS:CE	53:1:1368:G:H5'	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:2:ARG:HH12	35:K:68:GLN:HE21	1.52	0.58
46:V:16:MET:HE2	52:3:276:G:H5''	1.86	0.58
48:X:49:ALA:HB2	48:X:58:PRO:HG3	1.86	0.58
53:1:873:C:H2'	53:1:874:G:C8	2.39	0.58
53:1:2144:G:H1'	53:1:2147:A:H61	1.69	0.58
8:i:71:LYS:HG2	8:i:72:THR:H	1.69	0.58
31:G:160:LEU:HD23	31:G:180:ILE:HG21	1.84	0.58
1:b:48:ILE:HG22	53:1:779:U:OP1	2.04	0.57
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.18	0.57
53:1:1278:C:H2'	53:1:1279:G:H8	1.68	0.57
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.86	0.57
6:g:78:VAL:HG21	6:g:103:VAL:HG12	1.85	0.57
6:g:128:HIS:HB2	6:g:144:VAL:HB	1.86	0.57
16:q:90:ASP:OD2	17:r:11:GLN:HG3	2.04	0.57
27:C:5:ARG:NH1	53:1:2285:C:OP2	2.36	0.57
34:J:39:GLY:HA3	34:J:116:VAL:HB	1.86	0.57
41:Q:24:GLU:CD	41:Q:24:GLU:N	2.61	0.57
52:3:346:G:H2'	52:3:347:G:H5'	1.85	0.57
12:m:58:LYS:O	12:m:59:ARG:HD2	2.04	0.57
33:I:9:LYS:HD2	52:3:428:G:H5''	1.86	0.57
36:L:30:MET:HE3	36:L:33:GLY:HA2	1.85	0.57
45:U:70:ARG:HD3	52:3:375:U:OP1	2.04	0.57
50:Z:50:SER:HA	50:Z:53:LYS:HG2	1.85	0.57
52:3:26:A:H61	52:3:558:G:H1'	1.69	0.57
52:3:1366:C:H2'	52:3:1367:C:C6	2.40	0.57
53:1:1373:A:C5'	53:1:2212:A:H1'	2.33	0.57
53:1:1810:A:H2'	53:1:1811:G:O4'	2.04	0.57
4:e:9:ASP:O	4:e:13:LYS:HG2	2.04	0.57
5:f:1:SER:HB3	53:1:2749:A:OP1	2.03	0.57
7:h:55:VAL:HA	53:1:1084:A:C4'	2.34	0.57
28:D:34:ARG:NH2	28:D:39:ARG:HD2	2.19	0.57
45:U:58:ALA:O	45:U:61:VAL:HG12	2.04	0.57
53:1:1386:C:H2'	53:1:1387:A:C8	2.40	0.57
53:1:1680:U:C2'	53:1:1681:G:H5'	2.34	0.57
53:1:2452:C:H42	53:1:2504:U:H3	1.53	0.57
54:2:106:G:H2'	54:2:107:G:O4'	2.04	0.57
17:r:21:ARG:HG3	17:r:93:PHE:CD2	2.39	0.57
45:U:54:LEU:HD23	45:U:80:LYS:NZ	2.19	0.57
51:a:192:LEU:HD12	51:a:193:LEU:N	2.19	0.57
53:1:1213:A:H62	53:1:1236:G:H1'	1.68	0.57
4:e:33:ILE:HD12	4:e:95:MET:HE3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:166:TRP:HE1	52:3:1193:G:P	2.28	0.57
40:P:127:ARG:HH12	52:3:795:C:H4'	1.69	0.57
46:V:13:SER:O	46:V:21:VAL:HG12	2.05	0.57
53:1:1874:C:H2'	53:1:1875:G:O4'	2.05	0.57
55:5:44:A:H2'	55:5:45:G:C8	2.39	0.57
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.20	0.57
36:L:102:TRP:HB3	36:L:136:LYS:HD2	1.86	0.57
37:M:11:THR:O	37:M:15:ASN:ND2	2.35	0.57
37:M:112:ASP:O	37:M:116:ARG:HG3	2.05	0.57
52:3:1252:A:H61	52:3:1285:A:H61	1.52	0.57
52:3:1395:C:H2'	52:3:1396:A:H8	1.69	0.57
52:3:1501:C:H5''	52:3:1502:A:OP2	2.05	0.57
53:1:45:G:C5'	53:1:46:G:H5'	2.17	0.57
53:1:523:C:H2'	53:1:524:G:H8	1.69	0.57
53:1:1357:C:H2'	53:1:1358:G:O4'	2.04	0.57
53:1:1609:A:H1'	53:1:1616:A:O4'	2.05	0.57
42:R:64:VAL:HG22	42:R:65:GLU:H	1.68	0.57
42:R:73:SER:O	42:R:77:LYS:HG2	2.04	0.57
6:g:73:ASN:ND2	6:g:76:GLU:HA	2.20	0.57
26:B:8:THR:HG21	53:1:2020:A:H5'	1.86	0.57
52:3:236:A:H2'	52:3:237:G:C8	2.40	0.57
52:3:245:U:O2'	52:3:246:A:H5'	2.05	0.57
52:3:876:C:H2'	52:3:877:G:C8	2.39	0.57
52:3:1370:G:H2'	52:3:1371:G:H8	1.70	0.57
53:1:2642:G:O2'	53:1:2643:G:H5'	2.05	0.57
21:v:6:ALA:HB3	21:v:65:VAL:HB	1.86	0.57
5:f:139:VAL:O	5:f:143:VAL:HG22	2.04	0.56
25:z:41:PRO:HA	25:z:44:ARG:HB2	1.87	0.56
32:H:171:ARG:HD2	52:3:1106:G:OP1	2.04	0.56
52:3:1280:A:O2'	52:3:1281:C:H5'	2.05	0.56
53:1:873:C:H2'	53:1:874:G:H8	1.69	0.56
53:1:1023:U:O2'	53:1:1122:G:H5'	2.05	0.56
53:1:2710:C:H2'	53:1:2711:A:C8	2.39	0.56
7:h:119:PRO:HD2	7:h:120:ALA:H	1.70	0.56
32:H:105:VAL:HG12	32:H:107:LYS:H	1.69	0.56
33:I:97:LEU:HD22	33:I:134:TYR:HB3	1.86	0.56
34:J:51:LYS:HG3	34:J:51:LYS:O	2.04	0.56
3:d:45:ALA:HA	3:d:87:ALA:O	2.06	0.56
6:g:40:THR:OG1	6:g:43:ASN:ND2	2.37	0.56
8:i:75:ALA:HA	8:i:78:LEU:HD12	1.86	0.56
10:k:76:VAL:HG22	15:p:72:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:21:TRP:HA	39:O:95:GLY:HA2	1.87	0.56
32:H:147:GLY:HA3	32:H:171:ARG:O	2.05	0.56
32:H:185:THR:HG22	32:H:198:LYS:HA	1.87	0.56
34:J:123:LEU:HD11	52:3:6:G:H2'	1.88	0.56
46:V:5:ARG:HE	52:3:636:U:H5''	1.71	0.56
53:1:669:G:H2'	53:1:669:G:N3	2.19	0.56
53:1:971:G:H2'	53:1:972:A:O4'	2.04	0.56
53:1:1060:U:H4'	53:1:1061:U:H5'	1.87	0.56
53:1:1509:A:H2'	53:1:1510:G:C8	2.40	0.56
53:1:1827:U:C2'	53:1:1828:G:H5'	2.35	0.56
53:1:2287:A:O2'	53:1:2288:A:H2'	2.05	0.56
5:f:104:LEU:HB3	5:f:106:LEU:HD23	1.86	0.56
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.05	0.56
15:p:33:GLU:HB2	15:p:36:LYS:HB2	1.88	0.56
36:L:56:SER:OG	36:L:59:GLU:HG2	2.05	0.56
41:Q:66:ILE:HD12	41:Q:66:ILE:N	2.20	0.56
52:3:34:C:H2'	52:3:35:G:H8	1.70	0.56
52:3:1218:C:H2'	52:3:1219:A:C8	2.41	0.56
53:1:414:C:H2'	53:1:415:A:C8	2.41	0.56
53:1:1300:G:C4'	53:1:1301:A:H5''	2.35	0.56
53:1:2327:A:H2'	53:1:2328:A:C8	2.41	0.56
53:1:2512:C:H2'	53:1:2513:A:O4'	2.06	0.56
8:i:58:ILE:H	8:i:58:ILE:HD12	1.69	0.56
10:k:63:VAL:HG23	10:k:64:ARG:H	1.68	0.56
16:q:57:ARG:O	16:q:61:ILE:HG12	2.06	0.56
18:s:83:LYS:HG2	18:s:95:ARG:HH12	1.70	0.56
55:5:30:G:H2'	55:5:31:G:O4'	2.05	0.56
57:7:37:A:H2'	57:7:38:A:O4'	2.05	0.56
5:f:51:PHE:CZ	5:f:71:LEU:HD12	2.41	0.56
15:p:83:ILE:HD12	15:p:83:ILE:N	2.20	0.56
19:t:2:ILE:HD11	53:1:144:A:H4'	1.86	0.56
20:u:13:LEU:HD11	20:u:70:ALA:HB2	1.86	0.56
32:H:180:ASP:HB3	32:H:204:GLY:H	1.71	0.56
35:K:15:SER:O	35:K:18:VAL:HG23	2.04	0.56
45:U:36:VAL:HG22	45:U:53:ASP:HB2	1.86	0.56
53:1:2190:G:H2'	53:1:2191:A:O4'	2.05	0.56
55:5:12:G:H1	55:5:23:C:H42	1.54	0.56
7:h:87:GLU:HB3	7:h:95:LEU:HD22	1.87	0.56
14:o:29:HIS:HB3	14:o:36:TYR:HB2	1.87	0.56
39:O:6:ILE:HD12	39:O:6:ILE:N	2.21	0.56
20:u:71:ILE:H	20:u:71:ILE:HD12	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:120:LYS:HE3	52:3:439:U:H5''	1.86	0.56
38:N:111:GLU:OE1	38:N:120:ALA:HB1	2.06	0.56
48:X:30:LEU:HB2	48:X:48:ILE:HG23	1.88	0.56
52:3:867:G:H2'	52:3:868:C:C6	2.39	0.56
52:3:948:C:H2'	52:3:949:A:C8	2.40	0.56
52:3:1376:U:H2'	52:3:1377:A:C8	2.41	0.56
52:3:1395:C:H2'	52:3:1396:A:C8	2.41	0.56
53:1:581:C:H2'	53:1:582:A:C8	2.40	0.56
53:1:1348:C:H2'	53:1:1349:C:H5'	1.87	0.56
53:1:1906:G:H2'	53:1:1907:G:O4'	2.06	0.56
53:1:2646:C:H2'	53:1:2647:U:O4'	2.04	0.56
53:1:2834:G:O2'	53:1:2835:A:H5'	2.06	0.56
10:k:71:ARG:NH2	10:k:105:ARG:HG2	2.21	0.56
15:p:98:TYR:O	15:p:101:GLU:HG2	2.06	0.56
29:E:31:ILE:O	29:E:31:ILE:HG13	2.06	0.56
31:G:113:LEU:HB2	31:G:143:LEU:HD23	1.87	0.56
40:P:32:THR:HG22	40:P:43:TRP:CB	2.36	0.56
52:3:1402:C:H2'	52:3:1403:C:O4'	2.06	0.56
53:1:579:G:H4'	53:1:2018:G:H5''	1.88	0.56
6:g:80:ILE:HD11	6:g:146:VAL:HG22	1.87	0.56
16:q:109:VAL:HG12	16:q:113:LYS:HE2	1.87	0.56
18:s:94:ASP:CG	53:1:2014:A:H5'	2.31	0.56
31:G:156:LEU:HD12	31:G:157:PRO:HD2	1.86	0.56
35:K:5:GLU:HA	35:K:63:ASN:HA	1.87	0.56
43:S:5:MET:SD	43:S:8:ARG:NH2	2.79	0.56
45:U:38:PHE:HZ	45:U:48:GLU:HG2	1.70	0.56
53:1:2480:C:H2'	53:1:2481:G:O4'	2.04	0.56
15:p:77:SER:OG	15:p:79:VAL:HG12	2.05	0.55
24:y:32:ALA:HB2	24:y:37:LEU:HD13	1.89	0.55
52:3:236:A:H2'	52:3:237:G:H8	1.71	0.55
52:3:955:U:H2'	52:3:956:U:O4'	2.06	0.55
52:3:1084:G:H5'	52:3:1102:A:OP2	2.05	0.55
53:1:2655:G:O2'	53:1:2656:U:H5	1.90	0.55
6:g:72:ILE:HD12	6:g:108:VAL:HG13	1.88	0.55
8:i:71:LYS:HG2	8:i:72:THR:N	2.21	0.55
10:k:108:ARG:NH2	52:3:346:G:OP1	2.39	0.55
52:3:77:A:H2'	52:3:78:A:H8	1.71	0.55
53:1:435:C:H2'	53:1:436:C:H5'	1.88	0.55
53:1:832:U:H2'	53:1:833:A:C8	2.41	0.55
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.88	0.55
7:h:34:THR:CG2	53:1:1057:A:H1'	2.29	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:72:ARG:NH2	33:I:76:LYS:HD2	2.20	0.55
39:O:41:PRO:HG2	52:3:1150:A:H2	1.69	0.55
42:R:9:PRO:HG2	42:R:44:ILE:CD1	2.35	0.55
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.35	0.55
32:H:143:LEU:O	32:H:143:LEU:HD23	2.06	0.55
46:V:26:ARG:NH2	52:3:237:G:H5''	2.22	0.55
52:3:113:G:H1'	52:3:354:G:H5'	1.88	0.55
52:3:202:G:H21	52:3:466:A:H61	1.53	0.55
2:c:28:GLU:HG3	2:c:28:GLU:O	2.06	0.55
7:h:80:THR:HA	53:1:1107:G:O2'	2.07	0.55
31:G:107:ARG:HA	31:G:110:ILE:HD12	1.88	0.55
32:H:107:LYS:HD2	32:H:143:LEU:HD22	1.88	0.55
43:S:68:ARG:HD2	52:3:1202:U:O4'	2.06	0.55
52:3:1414:U:H2'	52:3:1415:G:C8	2.41	0.55
2:c:56:LYS:HB2	2:c:59:ARG:HB2	1.89	0.55
18:s:29:VAL:HG23	18:s:69:LEU:O	2.07	0.55
32:H:149:LYS:HG3	32:H:172:VAL:CG2	2.36	0.55
35:K:3:HIS:O	35:K:92:THR:HG22	2.07	0.55
36:L:28:ILE:HG13	36:L:29:LEU:HD22	1.89	0.55
37:M:75:GLN:O	37:M:126:CYS:HB2	2.06	0.55
43:S:30:ILE:HD11	43:S:39:ASP:HB3	1.88	0.55
53:1:1394:U:H4'	53:1:1603:A:H4'	1.88	0.55
53:1:1507:C:H2'	53:1:1508:A:O4'	2.06	0.55
53:1:2128:G:H21	53:1:2173:A:H1'	1.71	0.55
53:1:2297:A:N6	53:1:2319:G:H1'	2.21	0.55
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.72	0.55
13:n:28:LEU:HD23	13:n:48:VAL:HG21	1.89	0.55
15:p:24:THR:HB	15:p:87:ARG:HB2	1.88	0.55
40:P:55:ARG:O	40:P:58:THR:HG22	2.06	0.55
43:S:1:ALA:HA	52:3:1203:C:OP1	2.06	0.55
52:3:578:C:H2'	52:3:579:A:C8	2.42	0.55
53:1:742:A:H2'	53:1:743:A:H8	1.71	0.55
5:f:23:ILE:HG22	5:f:25:ILE:HG13	1.88	0.55
14:o:10:ARG:HD3	53:1:2295:C:OP2	2.07	0.55
39:O:42:LEU:HD11	39:O:73:LEU:HB2	1.89	0.55
48:X:54:ARG:HB3	52:3:958:A:C2	2.42	0.55
51:a:4:LEU:HA	51:a:8:MET:SD	2.47	0.55
52:3:407:U:H2'	52:3:408:A:C8	2.42	0.55
53:1:278:A:H2'	53:1:278:A:N3	2.20	0.55
53:1:741:U:H2'	53:1:742:A:C8	2.41	0.55
53:1:1900:A:H1'	53:1:1970:A:H2'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:118:ILE:N	7:h:119:PRO:CD	2.70	0.55
11:l:61:LEU:O	29:E:12:ARG:HD3	2.07	0.55
25:z:52:PHE:CZ	25:z:53:MET:HE2	2.42	0.55
41:Q:82:ARG:HB2	52:3:552:U:H4'	1.89	0.55
41:Q:82:ARG:HG3	41:Q:95:HIS:HB2	1.89	0.55
53:1:1827:U:O2'	53:1:1828:G:H5'	2.06	0.55
7:h:55:VAL:HG22	53:1:1084:A:O5'	2.07	0.55
11:l:93:ASN:O	11:l:94:THR:OG1	2.23	0.55
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.71	0.55
40:P:19:VAL:HG22	40:P:82:GLU:OE1	2.07	0.55
40:P:88:PRO:HG2	40:P:89:GLY:H	1.71	0.55
53:1:226:A:H2'	53:1:227:A:O4'	2.06	0.55
53:1:598:U:H2'	53:1:599:A:C8	2.42	0.55
53:1:1856:U:H2'	53:1:1857:G:O4'	2.06	0.55
53:1:2029:G:O6	53:1:2032:G:H5''	2.06	0.55
53:1:2086:U:H2'	53:1:2087:G:C8	2.42	0.55
1:b:47:ARG:HD2	53:1:778:G:H5''	1.88	0.54
6:g:65:ALA:HA	6:g:68:ARG:HE	1.72	0.54
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.38	0.54
14:o:48:LEU:HD13	14:o:87:ILE:HD12	1.89	0.54
14:o:76:LYS:O	14:o:80:GLU:HG3	2.07	0.54
16:q:108:LEU:HA	17:r:48:LYS:HE2	1.89	0.54
21:v:19:ARG:NH2	54:2:95:U:OP2	2.39	0.54
28:D:26:ASN:HA	28:D:29:GLN:HE21	1.70	0.54
32:H:113:LYS:HE2	32:H:184:ASN:HB3	1.88	0.54
40:P:122:PRO:HB2	50:Z:33:ARG:HA	1.88	0.54
50:Z:44:ARG:CZ	52:3:722:G:H5'	2.37	0.54
50:Z:66:ARG:NH2	52:3:1099:G:H4'	2.22	0.54
52:3:974:A:H5''	52:3:975:A:H3'	1.89	0.54
53:1:290:U:H2'	53:1:291:G:H8	1.73	0.54
53:1:1186:G:H2'	53:1:1187:G:O4'	2.07	0.54
8:i:92:PRO:HG2	53:1:1076:C:O2	2.07	0.54
23:x:60:LYS:HZ3	53:1:372:G:C4'	2.20	0.54
40:P:15:VAL:HG12	40:P:76:TYR:HB3	1.89	0.54
43:S:5:MET:HE3	43:S:62:ARG:HH22	1.73	0.54
52:3:1342:C:H2'	52:3:1343:G:C8	2.43	0.54
53:1:580:U:H2'	53:1:581:C:C6	2.42	0.54
53:1:1417:C:H4'	53:1:1587:G:H21	1.73	0.54
53:1:2286:G:H4'	53:1:2287:A:O4'	2.06	0.54
2:c:190:LYS:HZ3	53:1:2729:G:H4'	1.73	0.54
9:j:57:LEU:O	9:j:58:ASN:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:M:111:THR:HG23	37:M:114:ALA:H	1.72	0.54
38:N:18:VAL:HG22	38:N:64:ILE:HG23	1.89	0.54
42:R:113:LYS:N	42:R:114:PRO:HD2	2.20	0.54
44:T:32:THR:O	44:T:35:ILE:HG22	2.07	0.54
53:1:2533:U:H2'	53:1:2534:A:O4'	2.08	0.54
6:g:117:LEU:HB3	6:g:120:GLY:O	2.07	0.54
7:h:58:THR:OG1	7:h:78:GLY:O	2.25	0.54
11:l:93:ASN:OD1	11:l:94:THR:HG23	2.07	0.54
12:m:34:LYS:HG2	12:m:35:ALA:N	2.20	0.54
31:G:131:LYS:NZ	52:3:1159:U:H5'	2.21	0.54
32:H:63:ILE:CG2	32:H:98:ALA:HB2	2.35	0.54
32:H:122:GLN:HG2	32:H:125:ARG:HH12	1.73	0.54
34:J:101:GLY:H	34:J:121:ASN:HB3	1.72	0.54
40:P:43:TRP:HZ2	52:3:686:U:H1'	1.71	0.54
41:Q:115:LYS:O	41:Q:116:TYR:HB2	2.07	0.54
51:a:40:GLU:HB3	51:a:217:THR:HG22	1.89	0.54
52:3:763:G:H2'	52:3:764:C:H6	1.72	0.54
52:3:1512:U:H2'	52:3:1513:A:C8	2.43	0.54
54:2:66:A:H4'	54:2:67:G:C8	2.43	0.54
20:u:6:ARG:HG2	20:u:7:ASP:OD2	2.07	0.54
31:G:147:LEU:HD23	31:G:147:LEU:O	2.07	0.54
33:I:6:PRO:HG2	52:3:428:G:OP2	2.07	0.54
46:V:5:ARG:NE	52:3:636:U:H5''	2.22	0.54
51:a:181:ASP:HB3	51:a:184:LYS:HD3	1.88	0.54
52:3:1397:C:H42	56:4:22:A:H2'	1.73	0.54
53:1:279:A:H2'	53:1:280:U:H5'	1.89	0.54
1:b:141:HIS:ND1	1:b:192:GLY:O	2.40	0.54
24:y:3:ALA:HA	24:y:6:LEU:HD12	1.90	0.54
40:P:91:GLY:C	40:P:93:GLU:H	2.15	0.54
50:Z:38:GLU:HB2	52:3:1526:G:OP2	2.07	0.54
53:1:1138:G:H2'	53:1:1139:G:O4'	2.08	0.54
10:k:109:SER:O	10:k:110:GLU:HG3	2.07	0.54
20:u:96:LYS:C	20:u:98:ASN:H	2.15	0.54
23:x:1:SER:O	23:x:3:VAL:N	2.40	0.54
53:1:45:G:H5''	53:1:46:G:C5'	2.16	0.54
53:1:807:U:H2'	53:1:808:G:C8	2.43	0.54
53:1:1912:A:H62	53:1:1917:U:H3	1.54	0.54
53:1:2210:U:H4'	53:1:2211:A:H2	1.72	0.54
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.22	0.54
8:i:115:ASP:HB2	8:i:116:MET:HE2	1.88	0.54
13:n:72:ASP:O	13:n:76:VAL:HG23	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:97:ILE:HD13	17:r:40:MET:HE1	1.90	0.54
33:I:13:ARG:HH21	52:3:542:G:H4'	1.73	0.54
35:K:6:ILE:HD13	35:K:74:LEU:HD21	1.89	0.54
37:M:31:LEU:HD11	52:3:643:C:C5'	2.38	0.54
53:1:367:G:H2'	53:1:368:A:O4'	2.07	0.54
1:b:204:LEU:HD12	1:b:204:LEU:H	1.72	0.54
10:k:25:LEU:HD21	10:k:59:LYS:HE2	1.88	0.54
11:l:55:MET:HG2	53:1:2392:A:C2	2.43	0.54
17:r:80:ARG:NH2	53:1:572:A:OP2	2.40	0.54
31:G:59:ILE:HG22	31:G:64:GLY:HA3	1.89	0.54
32:H:175:HIS:HD1	52:3:1108:G:H5'	1.71	0.54
52:3:1345:U:H4'	52:3:1346:A:H8	1.73	0.54
53:1:467:G:O2'	53:1:468:G:H5'	2.08	0.54
53:1:2277:G:C3'	53:1:2278:A:H5''	2.38	0.54
1:b:56:GLY:HA2	1:b:212:TRP:HA	1.90	0.54
7:h:118:ILE:HG23	7:h:119:PRO:CD	2.28	0.54
13:n:47:VAL:O	13:n:50:PRO:HD2	2.08	0.54
43:S:2:LYS:NZ	52:3:1216:A:OP1	2.37	0.54
50:Z:38:GLU:OE2	52:3:1527:U:H5	1.91	0.54
53:1:2372:U:H2'	53:1:2373:G:H8	1.72	0.54
7:h:67:THR:OG1	7:h:68:PRO:HD3	2.08	0.53
32:H:99:GLN:O	32:H:99:GLN:HG2	2.09	0.53
34:J:165:GLY:HA2	37:M:113:ARG:HD2	1.90	0.53
52:3:346:G:C2'	52:3:347:G:H5'	2.39	0.53
52:3:405:U:C3'	52:3:406:G:H5'	2.33	0.53
53:1:1971:U:H5'	53:1:1972:G:H5''	1.89	0.53
16:q:25:GLY:O	16:q:29:ARG:NH1	2.41	0.53
17:r:6:GLN:HG2	17:r:11:GLN:OE1	2.08	0.53
38:N:94:ARG:HA	38:N:97:LEU:HB3	1.91	0.53
50:Z:41:THR:HG22	50:Z:45:LYS:NZ	2.23	0.53
52:3:34:C:H2'	52:3:35:G:C8	2.43	0.53
53:1:2238:G:H2'	53:1:2238:G:N3	2.22	0.53
53:1:2799:A:C2'	53:1:2800:A:H5'	2.38	0.53
2:c:133:THR:OG1	2:c:134:HIS:N	2.40	0.53
11:l:92:LEU:HD12	11:l:93:ASN:N	2.23	0.53
14:o:33:ARG:HB2	54:2:52:A:N6	2.21	0.53
22:w:17:LEU:HD21	22:w:37:ARG:HH21	1.73	0.53
22:w:19:VAL:HG22	22:w:34:VAL:HG22	1.90	0.53
33:I:33:ILE:HG13	33:I:34:GLU:N	2.24	0.53
42:R:84:CYS:HB2	48:X:72:GLU:HB3	1.90	0.53
50:Z:56:ALA:O	50:Z:59:LEU:HG	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:974:A:H5'	52:3:976:G:OP1	2.08	0.53
53:1:1285:A:H2'	53:1:1286:A:H5'	1.90	0.53
53:1:2508:G:H1	53:1:2580:U:H3	1.56	0.53
53:1:2605:U:H2'	53:1:2606:C:C6	2.43	0.53
53:1:2798:U:H4'	53:1:2799:A:C4	2.44	0.53
5:f:143:VAL:O	5:f:147:LEU:HG	2.08	0.53
7:h:33:VAL:HG12	7:h:34:THR:N	2.24	0.53
15:p:28:LYS:HA	15:p:41:ALA:HA	1.89	0.53
17:r:49:ILE:HG22	17:r:54:VAL:HA	1.89	0.53
31:G:91:VAL:HG11	31:G:95:TRP:HE3	1.73	0.53
35:K:29:ILE:CG2	35:K:66:ALA:HB2	2.39	0.53
38:N:105:ARG:HD2	52:3:1117:A:O3'	2.07	0.53
38:N:122:ARG:NH1	38:N:123:ARG:O	2.41	0.53
39:O:48:ARG:HA	39:O:66:GLU:HA	1.89	0.53
40:P:58:THR:OG1	40:P:59:PRO:HD2	2.09	0.53
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.09	0.53
45:U:33:ILE:H	45:U:33:ILE:HD12	1.73	0.53
45:U:36:VAL:CG2	45:U:53:ASP:HB2	2.38	0.53
51:a:218:MET:HG3	53:1:2174:C:O2'	2.09	0.53
53:1:2514:U:H2'	53:1:2515:C:C6	2.43	0.53
57:7:43:C:H2'	57:7:44:G:C8	2.43	0.53
39:O:8:ILE:O	39:O:73:LEU:HD13	2.09	0.53
48:X:27:LYS:HG2	48:X:28:LYS:H	1.74	0.53
53:1:717:C:H2'	53:1:718:A:H5'	1.89	0.53
53:1:1326:U:H2'	53:1:1327:A:H8	1.73	0.53
53:1:2313:C:H2'	53:1:2314:A:C8	2.44	0.53
17:r:38:VAL:HG13	17:r:54:VAL:CG2	2.39	0.53
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.90	0.53
32:H:168:ARG:HH12	52:3:1106:G:H4'	1.74	0.53
42:R:106:ARG:HE	42:R:112:ARG:HH21	1.55	0.53
53:1:1352:U:O2'	53:1:1353:A:H5'	2.09	0.53
4:e:31:GLU:OE1	4:e:157:THR:HA	2.08	0.53
12:m:64:TRP:HE1	53:1:873:C:H4'	1.72	0.53
24:y:21:LEU:HA	24:y:25:GLN:CB	2.39	0.53
31:G:94:ARG:HD2	52:3:1099:G:OP1	2.08	0.53
34:J:105:ILE:CD1	34:J:123:LEU:HD13	2.38	0.53
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.90	0.53
40:P:58:THR:HG23	40:P:61:ALA:H	1.73	0.53
45:U:14:ARG:NH1	52:3:617:G:H21	2.06	0.53
51:a:66:PRO:HG2	51:a:67:HIS:ND1	2.24	0.53
52:3:946:A:H2'	52:3:947:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:150:U:H2'	53:1:151:C:C6	2.43	0.53
53:1:687:C:H6	53:1:687:C:H5'	1.73	0.53
55:5:32:C:H1'	55:5:38:A:H61	1.74	0.53
1:b:176:ARG:HH21	53:1:1820:U:H5	1.55	0.53
31:G:81:ASP:HA	31:G:84:LEU:HG	1.91	0.53
31:G:110:ILE:O	31:G:114:LYS:HG2	2.09	0.53
46:V:18:LYS:HD3	46:V:49:ASN:H	1.74	0.53
52:3:721:G:H4'	52:3:722:G:O4'	2.09	0.53
52:3:823:C:H2'	52:3:824:G:C8	2.43	0.53
52:3:1477:U:H2'	52:3:1478:U:C6	2.43	0.53
53:1:1319:C:O2'	53:1:1320:C:H5'	2.09	0.53
53:1:1443:U:H2'	53:1:1444:G:C8	2.44	0.53
53:1:2023:C:H2'	53:1:2024:G:H8	1.73	0.53
3:d:134:LEU:HD21	3:d:161:ALA:HB2	1.89	0.53
8:i:9:LYS:HD3	53:1:1061:U:OP1	2.09	0.53
11:l:101:ILE:HG13	11:l:102:GLY:H	1.74	0.53
15:p:4:ILE:O	15:p:8:GLU:HG2	2.08	0.53
35:K:48:ALA:HB1	47:W:68:PRO:HG3	1.90	0.53
44:T:74:VAL:HG11	46:V:82:VAL:HG21	1.91	0.53
52:3:1330:U:H2'	52:3:1331:G:O4'	2.09	0.53
53:1:184:C:H2'	53:1:185:G:H8	1.74	0.53
53:1:876:C:H2'	53:1:877:A:O4'	2.09	0.53
53:1:1103:A:H2'	53:1:1103:A:N3	2.23	0.53
53:1:2328:A:H2'	53:1:2329:U:C6	2.44	0.53
4:e:37:MET:SD	4:e:56:LEU:HG	2.49	0.53
8:i:12:VAL:HG13	53:1:1061:U:O2	2.09	0.53
9:j:27:ARG:HE	53:1:1012:U:H3	1.57	0.53
33:I:39:GLN:HA	52:3:426:U:H4'	1.90	0.53
38:N:121:ARG:CZ	52:3:1345:U:H5''	2.39	0.53
43:S:60:ARG:HG2	52:3:981:U:H4'	1.91	0.53
51:a:41:SER:HB2	53:1:2124:G:O2'	2.09	0.53
53:1:1111:A:H2'	53:1:1111:A:N3	2.24	0.53
53:1:2066:C:C2'	53:1:2067:G:H5'	2.39	0.53
53:1:2073:C:O2'	53:1:2074:U:H5'	2.09	0.53
55:5:11:A:H61	55:5:24:U:H3	1.57	0.53
1:b:252:LYS:HZ2	53:1:1825:U:H1'	1.73	0.52
4:e:87:LYS:CD	53:1:2313:C:H5''	2.37	0.52
6:g:8:LYS:O	6:g:9:VAL:C	2.52	0.52
39:O:57:VAL:O	39:O:58:ASN:HB2	2.08	0.52
41:Q:6:LEU:HB3	46:V:33:TYR:CZ	2.45	0.52
52:3:971:G:H1'	52:3:1365:G:O2'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:189:G:H2'	53:1:205:G:N2	2.25	0.52
53:1:2180:U:H2'	53:1:2181:U:O4'	2.09	0.52
53:1:2537:U:H2'	53:1:2538:C:C6	2.43	0.52
53:1:2756:U:H4'	53:1:2757:A:OP1	2.09	0.52
12:m:66:ARG:NH1	12:m:104:GLU:OE2	2.38	0.52
16:q:116:LEU:O	16:q:116:LEU:HD23	2.09	0.52
33:I:98:ASP:O	33:I:101:VAL:HG12	2.09	0.52
48:X:11:ASP:HB3	48:X:14:LEU:HG	1.91	0.52
52:3:1342:C:H2'	52:3:1343:G:H8	1.74	0.52
53:1:760:G:H2'	53:1:761:A:O4'	2.08	0.52
53:1:2389:G:H5''	53:1:2390:U:O4'	2.09	0.52
53:1:2808:G:H2'	53:1:2890:G:O6	2.09	0.52
55:5:32:C:H1'	55:5:38:A:N6	2.24	0.52
1:b:145:MET:HE1	1:b:152:GLN:HB2	1.92	0.52
4:e:134:GLN:NE2	4:e:149:ARG:O	2.42	0.52
10:k:63:VAL:HG12	10:k:107:LEU:HD11	1.91	0.52
52:3:392:C:H2'	52:3:393:A:H8	1.75	0.52
52:3:915:A:H2'	52:3:916:U:H5'	1.91	0.52
53:1:738:G:O2'	53:1:739:A:H5'	2.09	0.52
53:1:1078:U:H5''	53:1:1079:C:H5''	1.91	0.52
53:1:2875:C:H2'	53:1:2876:G:C8	2.44	0.52
33:I:6:PRO:HA	52:3:430:A:O5'	2.08	0.52
47:W:11:ARG:HG2	52:3:845:A:O2'	2.09	0.52
52:3:560:A:H4'	52:3:561:U:H5'	1.91	0.52
53:1:1026:G:H2'	53:1:1027:A:H8	1.74	0.52
53:1:2197:U:O2'	53:1:2198:A:H5''	2.08	0.52
3:d:68:ALA:HA	53:1:1255:U:C6	2.44	0.52
4:e:32:LYS:HD3	4:e:91:ARG:NH2	2.25	0.52
8:i:109:ALA:HA	8:i:112:LYS:HZ3	1.74	0.52
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.40	0.52
32:H:40:GLN:O	32:H:44:LYS:HG2	2.10	0.52
38:N:64:ILE:HD12	38:N:64:ILE:N	2.24	0.52
49:Y:3:ILE:HG23	49:Y:3:ILE:O	2.09	0.52
51:a:37:LYS:HB2	53:1:2127:G:O3'	2.10	0.52
53:1:395:U:H2'	53:1:396:G:C8	2.45	0.52
53:1:1307:A:H2'	53:1:1308:A:H5'	1.92	0.52
53:1:2244:U:H2'	53:1:2245:U:O4'	2.10	0.52
55:5:24:U:H2'	55:5:25:C:H5'	1.92	0.52
1:b:225:ASN:ND2	53:1:784:G:O4'	2.43	0.52
4:e:154:THR:HG23	4:e:154:THR:O	2.09	0.52
31:G:116:LEU:HD21	31:G:140:LEU:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:107:LYS:HZ3	32:H:143:LEU:HB3	1.74	0.52
42:R:105:ALA:HA	52:3:948:C:OP1	2.09	0.52
45:U:40:ASN:CG	45:U:43:ALA:HB2	2.35	0.52
48:X:5:LYS:HZ3	48:X:6:LYS:HG2	1.73	0.52
52:3:1137:C:H5'	52:3:1138:G:H5'	1.89	0.52
53:1:580:U:H2'	53:1:581:C:H6	1.74	0.52
7:h:119:PRO:CD	7:h:120:ALA:N	2.72	0.52
8:i:89:SER:HB3	8:i:135:MET:HA	1.91	0.52
10:k:35:VAL:HG22	10:k:69:VAL:HG23	1.91	0.52
38:N:18:VAL:HG13	38:N:64:ILE:HG13	1.92	0.52
39:O:40:ILE:O	39:O:42:LEU:HD12	2.09	0.52
52:3:45:G:H5''	52:3:307:C:O2'	2.10	0.52
53:1:542:C:H2'	53:1:543:G:C5'	2.37	0.52
53:1:619:G:H3'	53:1:620:G:H21	1.74	0.52
53:1:890:C:H2'	53:1:891:G:H5'	1.91	0.52
53:1:967:U:H2'	53:1:968:C:C6	2.44	0.52
53:1:1215:G:O2'	53:1:1216:G:H5'	2.10	0.52
1:b:130:PRO:HB2	1:b:133:ASN:OD1	2.10	0.52
8:i:74:PRO:HA	53:1:1060:U:P	2.50	0.52
11:l:101:ILE:HG13	11:l:102:GLY:N	2.25	0.52
11:l:135:ILE:CD1	11:l:142:ILE:HD11	2.40	0.52
31:G:86:CYS:HB2	31:G:220:VAL:HG11	1.91	0.52
44:T:24:THR:HG21	44:T:69:LEU:HD21	1.92	0.52
46:V:30:HIS:ND1	46:V:31:PRO:HD2	2.24	0.52
52:3:297:G:H4'	52:3:557:G:H4'	1.91	0.52
52:3:902:G:H2'	52:3:903:G:H8	1.75	0.52
53:1:1794:A:H2'	53:1:1795:C:C6	2.44	0.52
53:1:2156:G:C2'	53:1:2157:G:H5'	2.39	0.52
1:b:224:MET:SD	1:b:229:HIS:HB2	2.50	0.52
2:c:108:ASP:OD2	2:c:206:ALA:HA	2.10	0.52
19:t:47:VAL:HG13	19:t:51:PHE:HD2	1.75	0.52
29:E:6:VAL:HG23	29:E:9:ALA:HB3	1.91	0.52
33:I:54:LEU:HD23	33:I:55:ARG:HE	1.73	0.52
36:L:27:ASN:HA	36:L:30:MET:HB2	1.90	0.52
50:Z:39:LYS:HB3	50:Z:43:GLU:OE1	2.10	0.52
52:3:352:C:H4'	52:3:354:G:OP1	2.10	0.52
53:1:1053:C:C3'	53:1:1054:A:H5''	2.39	0.52
53:1:2019:A:H2	53:1:2035:G:H22	1.58	0.52
53:1:2248:C:C2'	53:1:2249:U:H5'	2.39	0.52
53:1:2329:U:H2'	53:1:2330:G:C8	2.45	0.52
53:1:2515:C:H2'	53:1:2516:A:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:59:ARG:NH2	53:1:2830:C:H3'	2.25	0.52
5:f:174:LYS:HE3	5:f:175:LYS:NZ	2.25	0.52
16:q:90:ASP:HB3	53:1:997:G:H5'	1.91	0.52
19:t:47:VAL:HG13	19:t:51:PHE:CD2	2.45	0.52
20:u:86:PHE:C	20:u:88:ASP:H	2.16	0.52
27:C:26:LYS:O	27:C:26:LYS:HD3	2.10	0.52
32:H:156:LEU:H	32:H:156:LEU:HD12	1.75	0.52
33:I:67:LEU:HD11	52:3:547:A:OP2	2.10	0.52
34:J:158:LYS:N	34:J:158:LYS:HD2	2.25	0.52
41:Q:101:LEU:HD12	41:Q:101:LEU:H	1.74	0.52
52:3:810:C:O2'	52:3:811:C:H5'	2.10	0.52
52:3:1316:G:H2'	52:3:1317:C:H5''	1.92	0.52
53:1:1752:C:H2'	53:1:1753:G:C8	2.45	0.52
53:1:2498:C:O2'	53:1:2499:C:H5'	2.10	0.52
55:5:27:U:H2'	55:5:28:C:C5'	2.28	0.52
5:f:154:GLU:OE2	5:f:156:TYR:HB2	2.10	0.51
7:h:122:GLN:CD	7:h:122:GLN:N	2.68	0.51
17:r:5:PHE:CE1	17:r:12:HIS:HB2	2.46	0.51
24:y:27:ASN:O	24:y:31:GLN:HG3	2.10	0.51
31:G:135:MET:HA	31:G:138:ARG:NH1	2.24	0.51
33:I:78:ALA:HA	33:I:81:LEU:HD12	1.91	0.51
34:J:73:VAL:HG21	34:J:143:LEU:HG	1.91	0.51
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.09	0.51
48:X:28:LYS:HE3	48:X:29:PRO:HD2	1.91	0.51
52:3:1170:A:H2'	52:3:1171:A:O4'	2.10	0.51
52:3:1256:A:H1'	52:3:1258:G:C4	2.45	0.51
52:3:1270:G:H2'	52:3:1271:A:C8	2.44	0.51
52:3:1308:U:H2'	52:3:1309:G:C8	2.45	0.51
53:1:1528:A:H2'	53:1:1529:G:O4'	2.10	0.51
10:k:35:VAL:O	10:k:62:VAL:HG23	2.09	0.51
15:p:112:ARG:C	15:p:113:LEU:HD23	2.35	0.51
35:K:49:TYR:OH	35:K:86:ARG:NH1	2.43	0.51
51:a:195:ALA:HA	51:a:198:LYS:HE2	1.92	0.51
53:1:481:G:H1'	53:1:506:G:N2	2.25	0.51
53:1:1306:C:H41	53:1:1606:C:H2'	1.75	0.51
53:1:1307:A:C2'	53:1:1308:A:H5'	2.40	0.51
53:1:2111:U:H5'	53:1:2112:G:OP2	2.10	0.51
2:c:88:GLU:OE1	2:c:88:GLU:N	2.43	0.51
5:f:84:LYS:HE2	5:f:141:GLY:HA2	1.92	0.51
16:q:91:ARG:N	16:q:91:ARG:HD2	2.25	0.51
25:z:29:ARG:NH2	53:1:1183:U:H4'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:4:VAL:HB	52:3:1190:G:OP2	2.10	0.51
48:X:18:VAL:HG13	48:X:19:GLU:N	2.26	0.51
48:X:54:ARG:HD3	52:3:958:A:C4	2.46	0.51
53:1:1344:U:H3'	53:1:1345:C:H5'	1.91	0.51
4:e:129:MET:C	53:1:2304:G:H4'	2.35	0.51
8:i:73:PRO:HG2	8:i:78:LEU:CD2	2.40	0.51
8:i:99:LYS:HG3	8:i:140:GLU:HB2	1.92	0.51
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.91	0.51
12:m:13:HIS:O	12:m:71:LYS:NZ	2.44	0.51
33:I:12:ARG:HH22	52:3:428:G:H3'	1.75	0.51
41:Q:109:ARG:NH1	52:3:537:G:H5''	2.25	0.51
52:3:70:U:H5''	52:3:71:A:OP1	2.10	0.51
52:3:673:A:H2'	52:3:674:G:C8	2.45	0.51
52:3:865:A:H2'	52:3:866:C:C6	2.46	0.51
52:3:912:C:O2'	52:3:913:A:H5'	2.10	0.51
52:3:1506:U:O2'	52:3:1507:A:H5'	2.10	0.51
53:1:2853:C:H2'	53:1:2854:G:C8	2.46	0.51
10:k:6:THR:HG23	53:1:1666:G:H4'	1.92	0.51
15:p:93:LYS:HA	53:1:2848:G:H5''	1.93	0.51
41:Q:109:ARG:HH11	52:3:537:G:H5''	1.75	0.51
44:T:47:LYS:NZ	52:3:808:C:OP1	2.44	0.51
48:X:19:GLU:O	48:X:23:GLU:HG2	2.11	0.51
53:1:2795:C:H2'	53:1:2796:U:O4'	2.10	0.51
1:b:35:LYS:NZ	53:1:1353:A:O3'	2.43	0.51
3:d:77:ILE:HG13	3:d:78:TRP:CD1	2.45	0.51
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.40	0.51
12:m:42:THR:HG22	12:m:93:VAL:HG12	1.93	0.51
13:n:79:LEU:HD23	13:n:83:LEU:HD12	1.92	0.51
19:t:1:MET:HG3	19:t:3:ARG:H	1.76	0.51
45:U:31:ARG:NH2	52:3:230:G:H5''	2.26	0.51
52:3:982:U:H4'	52:3:983:A:O5'	2.11	0.51
53:1:2472:G:H2'	53:1:2475:C:H42	1.76	0.51
54:2:3:C:H3'	54:2:4:C:H5''	1.93	0.51
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.91	0.51
4:e:87:LYS:HD2	53:1:2313:C:C5'	2.38	0.51
10:k:40:LYS:HD2	10:k:57:VAL:HG12	1.93	0.51
11:l:17:LYS:HD3	53:1:663:G:H5''	1.93	0.51
33:I:170:LEU:HA	33:I:182:LYS:H	1.74	0.51
34:J:14:LEU:HD23	34:J:14:LEU:H	1.76	0.51
37:M:50:VAL:HG22	37:M:50:VAL:O	2.11	0.51
52:3:114:U:O2'	52:3:115:G:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:536:C:H2'	52:3:537:G:C8	2.46	0.51
53:1:596:U:H2'	53:1:597:G:H8	1.76	0.51
53:1:2087:G:H2'	53:1:2088:A:H8	1.76	0.51
53:1:2343:U:O2'	53:1:2344:U:H5'	2.10	0.51
53:1:2819:G:H2'	53:1:2821:A:N7	2.25	0.51
1:b:250:GLN:OE1	53:1:1842:G:O2'	2.29	0.51
6:g:15:LEU:HD21	6:g:56:ALA:HB1	1.93	0.51
7:h:80:THR:HA	53:1:1107:G:HO2'	1.75	0.51
39:O:40:ILE:HD11	52:3:1124:G:H4'	1.91	0.51
53:1:189:G:H2'	53:1:205:G:H22	1.75	0.51
1:b:59:GLN:HA	53:1:1568:G:H5'	1.93	0.51
14:o:29:HIS:NE2	54:2:7:G:H5''	2.26	0.51
19:t:18:GLU:O	19:t:22:THR:HG23	2.11	0.51
19:t:68:LYS:HG3	19:t:77:ARG:CZ	2.41	0.51
21:v:42:LEU:HD21	21:v:91:PHE:HE2	1.76	0.51
33:I:2:ARG:NH2	52:3:407:U:H5'	2.26	0.51
33:I:160:LEU:HD23	33:I:163:GLN:OE1	2.11	0.51
39:O:51:VAL:HG22	39:O:52:LEU:N	2.26	0.51
41:Q:45:ASN:ND2	52:3:528:C:H41	2.08	0.51
53:1:225:C:H2'	53:1:226:A:O4'	2.11	0.51
53:1:2246:G:H2'	53:1:2247:A:C8	2.46	0.51
1:b:143:VAL:HG22	1:b:153:LEU:HB2	1.91	0.51
8:i:58:ILE:HD12	8:i:58:ILE:N	2.26	0.51
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.46	0.51
32:H:10:ARG:HH22	32:H:181:ILE:HB	1.75	0.51
32:H:86:LEU:O	32:H:90:VAL:HG22	2.10	0.51
33:I:6:PRO:HG3	52:3:430:A:H4'	1.93	0.51
42:R:28:ARG:CZ	42:R:62:PHE:HB2	2.41	0.51
45:U:70:ARG:HD2	52:3:452:A:H1'	1.93	0.51
48:X:61:VAL:HA	48:X:65:MET:SD	2.51	0.51
53:1:503:A:H4'	53:1:505:A:H5''	1.92	0.51
53:1:1475:G:O2'	53:1:1476:U:H6	1.94	0.51
1:b:200:MET:HB2	53:1:1820:U:O2	2.12	0.50
1:b:201:LEU:HD22	52:3:773:G:H5''	1.93	0.50
18:s:94:ASP:OD1	53:1:2014:A:H5'	2.11	0.50
34:J:40:ASP:OD2	34:J:42:ASN:HB2	2.11	0.50
34:J:89:THR:HB	52:3:864:A:H5''	1.93	0.50
39:O:9:ARG:NH1	39:O:11:LYS:HE2	2.26	0.50
46:V:13:SER:H	46:V:21:VAL:CG1	2.23	0.50
47:W:37:LYS:HB3	52:3:719:C:H1'	1.93	0.50
52:3:665:A:O4'	52:3:733:G:H1'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:55:U:O2'	54:2:56:G:H5'	2.11	0.50
4:e:84:ILE:HB	53:1:2312:U:H5'	1.92	0.50
8:i:83:ALA:HB2	8:i:100:ILE:HD11	1.93	0.50
32:H:86:LEU:HA	32:H:89:VAL:CG2	2.41	0.50
38:N:51:LEU:HD22	38:N:56:MET:HG3	1.92	0.50
43:S:44:VAL:O	43:S:48:GLN:NE2	2.45	0.50
52:3:304:U:O2'	52:3:305:G:H5'	2.12	0.50
52:3:570:G:H5'	52:3:820:U:O4'	2.11	0.50
52:3:1211:U:H4'	52:3:1213:A:N3	2.26	0.50
53:1:395:U:H2'	53:1:396:G:H8	1.75	0.50
53:1:2679:A:O2'	53:1:2680:U:H5'	2.10	0.50
2:c:194:PRO:HA	53:1:2680:U:H5'	1.93	0.50
7:h:8:LYS:HA	7:h:11:ILE:HG22	1.94	0.50
19:t:61:LEU:C	19:t:61:LEU:HD12	2.37	0.50
25:z:50:VAL:HG12	25:z:54:VAL:HG13	1.92	0.50
28:D:5:PHE:O	28:D:7:PRO:HD3	2.11	0.50
34:J:86:GLY:O	34:J:138:ALA:HB1	2.11	0.50
36:L:2:ARG:H	36:L:4:ARG:NH2	2.09	0.50
38:N:105:ARG:HH11	38:N:107:ALA:HA	1.77	0.50
49:Y:77:ASN:O	49:Y:81:GLN:HG2	2.11	0.50
50:Z:7:GLU:HG3	50:Z:15:LEU:HD12	1.92	0.50
52:3:410:G:H2'	52:3:429:U:C4	2.46	0.50
52:3:539:A:H2'	52:3:540:G:C8	2.47	0.50
52:3:543:U:H2'	52:3:544:G:H8	1.76	0.50
53:1:310:A:O2'	53:1:311:A:H5''	2.12	0.50
53:1:854:C:H2'	53:1:855:G:H8	1.76	0.50
53:1:1013:C:H2'	53:1:1014:A:H8	1.76	0.50
53:1:1035:U:H2'	53:1:1036:G:H8	1.75	0.50
53:1:1675:C:H2'	53:1:1676:A:O4'	2.11	0.50
53:1:2467:C:H2'	53:1:2468:A:O4'	2.11	0.50
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.92	0.50
7:h:8:LYS:O	7:h:11:ILE:HG22	2.11	0.50
14:o:68:LYS:HE3	54:2:49:C:O3'	2.11	0.50
18:s:86:MET:HB2	18:s:96:ILE:HD13	1.93	0.50
40:P:126:ARG:HH12	52:3:692:U:H5''	1.76	0.50
42:R:103:THR:O	42:R:106:ARG:NH1	2.45	0.50
44:T:1:SER:OG	52:3:740:U:OP1	2.29	0.50
45:U:54:LEU:HD23	45:U:80:LYS:HZ1	1.74	0.50
49:Y:80:ALA:HA	49:Y:83:ASN:HD21	1.76	0.50
52:3:1301:U:O2	52:3:1301:U:H2'	2.11	0.50
1:b:119:VAL:O	1:b:119:VAL:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:124:GLY:C	11:l:125:LEU:HD12	2.36	0.50
12:m:1:MET:HE1	12:m:44:ARG:HG2	1.93	0.50
28:D:24:THR:HG23	28:D:27:GLY:N	2.24	0.50
48:X:71:GLY:HA3	52:3:1320:C:O2	2.11	0.50
53:1:804:A:H2'	53:1:806:C:C4	2.46	0.50
4:e:103:ILE:HG22	4:e:107:VAL:HG21	1.93	0.50
10:k:34:GLY:H	10:k:37:ASP:CG	2.20	0.50
16:q:88:GLU:N	16:q:88:GLU:OE2	2.44	0.50
18:s:41:LYS:HB2	18:s:44:ALA:HB2	1.94	0.50
32:H:107:LYS:HD3	32:H:110:LEU:HB3	1.94	0.50
33:I:162:GLU:HA	33:I:166:LYS:HD3	1.94	0.50
41:Q:8:ARG:NH2	52:3:880:C:OP1	2.36	0.50
52:3:49:U:O2'	52:3:50:A:H2'	2.12	0.50
52:3:825:A:H2'	52:3:826:C:C6	2.46	0.50
52:3:1413:A:H2	52:3:1487:G:H22	1.57	0.50
53:1:1991:U:C2'	53:1:1992:G:H5''	2.41	0.50
53:1:2853:C:H2'	53:1:2854:G:H8	1.77	0.50
10:k:69:VAL:HG22	10:k:70:ARG:N	2.27	0.50
22:w:39:THR:H	53:1:2331:G:H4'	1.76	0.50
31:G:96:LEU:HD23	31:G:99:MET:HG2	1.94	0.50
36:L:115:MET:HG2	52:3:1240:U:OP1	2.11	0.50
42:R:103:THR:OG1	42:R:104:ASN:N	2.44	0.50
52:3:422:C:H5'	52:3:423:G:N3	2.26	0.50
52:3:946:A:H2'	52:3:947:G:H8	1.77	0.50
53:1:433:C:O2'	53:1:434:U:H5'	2.12	0.50
53:1:948:C:H2'	53:1:949:G:H8	1.77	0.50
53:1:1796:U:H2'	53:1:1797:G:C8	2.47	0.50
53:1:2760:C:O2'	53:1:2761:A:H5'	2.11	0.50
55:5:30:G:H2'	55:5:31:G:C1'	2.42	0.50
6:g:8:LYS:HD3	6:g:8:LYS:N	2.27	0.50
12:m:42:THR:HA	12:m:93:VAL:HG12	1.93	0.50
16:q:91:ARG:HD2	16:q:91:ARG:H	1.77	0.50
22:w:12:SER:OG	53:1:2262:U:H5	1.95	0.50
25:z:9:THR:OG1	25:z:10:ARG:N	2.45	0.50
27:C:9:LYS:O	27:C:51:ALA:HB3	2.12	0.50
32:H:57:GLU:O	32:H:63:ILE:HD12	2.12	0.50
33:I:2:ARG:NH1	52:3:405:U:OP2	2.44	0.50
36:L:78:ARG:NH2	52:3:1382:C:C5'	2.75	0.50
41:Q:80:LEU:HD11	52:3:363:A:H4'	1.92	0.50
52:3:235:C:H2'	52:3:236:A:C8	2.46	0.50
52:3:372:C:N4	52:3:387:U:H2'	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1277:C:H2'	52:3:1278:G:H5''	1.93	0.50
53:1:69:C:O2'	53:1:70:G:H5'	2.11	0.50
53:1:2243:U:H2'	53:1:2244:U:C6	2.46	0.50
2:c:52:THR:HG23	2:c:77:ARG:HH22	1.77	0.50
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.92	0.50
18:s:80:PRO:O	18:s:100:THR:HG22	2.12	0.50
29:E:3:ILE:HG22	53:1:666:A:H1'	1.92	0.50
33:I:6:PRO:HA	52:3:430:A:P	2.52	0.50
33:I:96:ARG:HB3	33:I:98:ASP:OD1	2.12	0.50
33:I:122:ILE:HA	33:I:144:ILE:HA	1.93	0.50
36:L:3:ARG:NH2	52:3:931:C:H5''	2.27	0.50
52:3:235:C:H2'	52:3:236:A:H8	1.76	0.50
52:3:252:U:O2	52:3:252:U:H2'	2.11	0.50
52:3:662:U:H2'	52:3:663:A:C8	2.46	0.50
52:3:1237:C:OP1	52:3:1238:A:H1'	2.11	0.50
52:3:1395:C:O2'	52:3:1396:A:H5'	2.12	0.50
52:3:1497:G:C2'	52:3:1498:U:H5'	2.42	0.50
53:1:2404:U:H2'	53:1:2405:G:O4'	2.11	0.50
57:7:31:A:C2'	57:7:32:U:H5'	2.38	0.50
5:f:2:ARG:HD3	53:1:2751:G:C4	2.47	0.49
5:f:82:PHE:HB2	5:f:140:ILE:HG21	1.94	0.49
6:g:143:ILE:HD12	6:g:143:ILE:N	2.26	0.49
7:h:39:THR:HG23	7:h:40:GLU:CD	2.37	0.49
8:i:121:ILE:O	8:i:125:THR:HG23	2.12	0.49
13:n:53:THR:HG22	13:n:94:TYR:OH	2.12	0.49
15:p:2:ASN:O	15:p:6:GLN:HG3	2.12	0.49
32:H:119:ILE:O	32:H:123:LEU:HG	2.11	0.49
35:K:42:TRP:HB2	35:K:59:TYR:HB2	1.94	0.49
43:S:42:ASN:HA	43:S:45:LEU:HG	1.94	0.49
48:X:36:ARG:HB3	52:3:1320:C:N4	2.27	0.49
53:1:511:U:C2'	53:1:512:G:H5'	2.39	0.49
53:1:1111:A:O2'	53:1:1112:G:H4'	2.11	0.49
53:1:1278:C:H2'	53:1:1279:G:C8	2.46	0.49
53:1:1736:U:H2'	53:1:1737:G:O4'	2.12	0.49
53:1:2291:U:H2'	53:1:2292:U:C6	2.47	0.49
53:1:2475:C:C2'	53:1:2476:A:H5'	2.41	0.49
55:5:3:C:H3'	55:5:4:G:H5''	1.93	0.49
5:f:90:GLY:HA3	5:f:93:TYR:CD2	2.47	0.49
6:g:143:ILE:HD12	6:g:143:ILE:H	1.75	0.49
7:h:45:GLY:HA2	7:h:49:GLY:HA2	1.94	0.49
10:k:88:ASN:ND2	10:k:91:SER:OG	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:77:ASP:OD1	18:s:102:HIS:HB2	2.12	0.49
32:H:107:LYS:O	32:H:110:LEU:HG	2.12	0.49
37:M:93:LYS:HG2	37:M:97:GLY:N	2.27	0.49
40:P:41:LEU:O	52:3:685:G:H4'	2.12	0.49
41:Q:29:LYS:HA	52:3:363:A:H5'	1.93	0.49
42:R:2:ARG:O	42:R:56:ARG:NH2	2.45	0.49
46:V:64:ARG:HG3	52:3:130:A:C8	2.47	0.49
48:X:49:ALA:HA	48:X:58:PRO:HA	1.94	0.49
52:3:1219:A:H2'	52:3:1220:G:C8	2.47	0.49
53:1:878:A:H2'	53:1:879:G:H5'	1.94	0.49
53:1:1083:U:H2'	53:1:1085:A:OP2	2.12	0.49
53:1:1563:U:H2'	53:1:1564:C:C6	2.47	0.49
53:1:2183:A:H2'	53:1:2184:A:C8	2.47	0.49
53:1:2699:C:H2'	53:1:2700:A:C8	2.47	0.49
1:b:62:ARG:HD2	1:b:83:ASP:OD1	2.12	0.49
1:b:75:ALA:HB1	1:b:93:VAL:HG12	1.95	0.49
1:b:206:LYS:HB3	53:1:729:G:N7	2.27	0.49
2:c:150:GLN:NE2	53:1:574:A:C2	2.80	0.49
18:s:17:VAL:HB	18:s:76:VAL:HG11	1.93	0.49
20:u:94:PHE:HB2	20:u:100:GLU:O	2.12	0.49
31:G:186:VAL:HG21	31:G:198:VAL:HG13	1.94	0.49
40:P:82:GLU:HB3	40:P:107:THR:HB	1.93	0.49
41:Q:119:LYS:HD2	52:3:36:C:H5''	1.94	0.49
47:W:31:TYR:O	47:W:39:VAL:HG22	2.13	0.49
49:Y:60:GLN:HA	49:Y:63:LYS:HB2	1.93	0.49
50:Z:67:THR:HB	52:3:1088:G:O2'	2.12	0.49
53:1:290:U:H2'	53:1:291:G:C8	2.47	0.49
53:1:346:A:H2'	53:1:346:A:N3	2.27	0.49
13:n:4:ARG:HD2	53:1:2874:C:OP1	2.12	0.49
16:q:82:LEU:HD22	16:q:87:VAL:HB	1.95	0.49
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.47	0.49
39:O:6:ILE:HG22	39:O:8:ILE:HD11	1.93	0.49
45:U:38:PHE:CZ	45:U:48:GLU:HG2	2.48	0.49
52:3:1123:U:O2'	52:3:1124:G:H5'	2.12	0.49
53:1:1020:A:C1'	53:1:1021:A:OP2	2.56	0.49
53:1:2834:G:H2'	53:1:2879:A:H61	1.77	0.49
8:i:71:LYS:HE2	53:1:1059:G:C5'	2.41	0.49
17:r:54:VAL:HG23	17:r:55:ASP:N	2.27	0.49
33:I:123:MET:HB2	33:I:128:VAL:HG22	1.94	0.49
52:3:225:C:H2'	52:3:226:G:O4'	2.12	0.49
52:3:966:G:C2	55:5:34:C:H5'	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1139:G:O2'	53:1:1140:C:H5'	2.11	0.49
7:h:54:VAL:O	7:h:54:VAL:HG22	2.12	0.49
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.43	0.49
10:k:13:ASN:ND2	52:3:339:C:OP2	2.45	0.49
19:t:80:TRP:N	19:t:80:TRP:CD1	2.81	0.49
31:G:93:HIS:C	31:G:94:ARG:HD3	2.37	0.49
33:I:74:TYR:CD1	33:I:92:LEU:HD21	2.48	0.49
41:Q:113:ARG:NH2	41:Q:120:ARG:HG3	2.27	0.49
46:V:45:VAL:HG21	46:V:60:ILE:HG21	1.94	0.49
48:X:35:ARG:HB3	48:X:71:GLY:HA3	1.95	0.49
52:3:70:U:H2'	52:3:94:G:O6	2.13	0.49
53:1:741:U:H2'	53:1:742:A:H8	1.77	0.49
53:1:799:G:H5''	53:1:800:A:H2'	1.94	0.49
53:1:995:C:H6	53:1:995:C:H5'	1.78	0.49
53:1:1947:C:H2'	53:1:1948:G:H8	1.76	0.49
54:2:51:G:H2'	54:2:52:A:O4'	2.13	0.49
4:e:39:VAL:HG22	4:e:41:GLU:H	1.77	0.49
4:e:140:ILE:HG22	4:e:142:TYR:H	1.78	0.49
7:h:31:ARG:O	53:1:1055:G:H5'	2.13	0.49
10:k:40:LYS:NZ	53:1:2561:U:O3'	2.41	0.49
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.93	0.49
31:G:117:GLU:O	31:G:121:GLN:HG2	2.12	0.49
32:H:190:THR:HG21	32:H:195:ILE:HD12	1.93	0.49
36:L:78:ARG:NH2	36:L:81:GLY:HA2	2.28	0.49
37:M:42:GLU:HG2	37:M:100:ILE:HG21	1.94	0.49
42:R:114:PRO:HG2	52:3:1228:C:OP1	2.13	0.49
53:1:1664:A:H2'	53:1:1664:A:N3	2.28	0.49
53:1:2385:C:H2'	53:1:2386:A:C8	2.47	0.49
1:b:164:VAL:HG21	1:b:174:ARG:HB2	1.93	0.49
7:h:60:LEU:HD11	7:h:79:PRO:HB3	1.94	0.49
9:j:11:VAL:HG13	9:j:11:VAL:O	2.12	0.49
31:G:131:LYS:HZ3	52:3:1159:U:H5'	1.76	0.49
33:I:96:ARG:O	33:I:100:VAL:HG23	2.13	0.49
34:J:162:GLU:O	37:M:113:ARG:NH1	2.46	0.49
35:K:41:ASP:OD1	35:K:58:HIS:NE2	2.46	0.49
35:K:91:ARG:NH2	52:3:738:C:OP1	2.46	0.49
42:R:27:THR:HG21	52:3:1328:C:H5''	1.94	0.49
48:X:43:MET:HG3	48:X:46:LEU:HD12	1.95	0.49
52:3:314:C:H2'	52:3:315:A:C8	2.48	0.49
52:3:405:U:H3'	52:3:406:G:C5'	2.35	0.49
53:1:703:U:H2'	53:1:704:G:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2636:C:H2'	53:1:2637:U:H6	1.76	0.49
8:i:36:GLU:HG3	8:i:66:PHE:HZ	1.78	0.49
17:r:37:GLU:HB3	17:r:53:PHE:CE1	2.48	0.49
18:s:8:ARG:HH11	18:s:8:ARG:HB2	1.77	0.49
18:s:11:ARG:O	18:s:12:SER:HB3	2.12	0.49
19:t:61:LEU:HB3	53:1:1341:G:H4'	1.95	0.49
52:3:572:A:H5''	52:3:917:G:H4'	1.94	0.49
52:3:766:A:H2'	52:3:767:A:O4'	2.12	0.49
52:3:1323:G:H2'	52:3:1324:A:H8	1.77	0.49
53:1:765:C:H2'	53:1:766:U:C6	2.48	0.49
53:1:2139:U:H2'	53:1:2140:G:C8	2.48	0.49
54:2:5:U:H2'	54:2:6:G:H8	1.76	0.49
55:5:15:G:H3'	55:5:16:C:H5'	1.95	0.49
2:c:70:LYS:HD2	53:1:2786:U:H5'	1.94	0.49
4:e:37:MET:HG3	4:e:56:LEU:HD21	1.95	0.49
13:n:54:LEU:HD21	13:n:65:LEU:HB3	1.94	0.49
17:r:24:LYS:HA	17:r:94:THR:OG1	2.13	0.49
20:u:71:ILE:HD12	20:u:71:ILE:N	2.28	0.49
36:L:49:LEU:HD13	36:L:123:LEU:HB3	1.94	0.49
38:N:29:ILE:HG12	38:N:30:ASN:ND2	2.28	0.49
51:a:46:VAL:HG13	51:a:212:VAL:HG12	1.95	0.49
52:3:1287:A:H2	52:3:1353:G:H1'	1.77	0.49
53:1:2149:U:H2'	53:1:2150:C:O4'	2.13	0.49
3:d:148:ILE:HB	3:d:169:VAL:HG22	1.94	0.48
4:e:122:ASP:OD2	4:e:124:ARG:HB2	2.13	0.48
9:j:24:THR:OG1	9:j:27:ARG:HB2	2.13	0.48
22:w:17:LEU:HD23	22:w:35:ARG:HH12	1.77	0.48
32:H:10:ARG:NH1	32:H:179:ALA:O	2.45	0.48
33:I:109:THR:CG2	52:3:408:A:H5''	2.43	0.48
34:J:67:ARG:O	34:J:70:MET:HG2	2.12	0.48
39:O:29:ALA:O	39:O:33:GLY:CA	2.59	0.48
39:O:62:ARG:NH2	52:3:1366:C:O2'	2.46	0.48
52:3:654:G:H2'	52:3:655:A:O4'	2.13	0.48
52:3:1273:C:H2'	52:3:1274:A:O4'	2.12	0.48
53:1:572:A:H5''	53:1:573:U:OP2	2.13	0.48
53:1:1434:A:H2'	53:1:1435:G:C8	2.48	0.48
53:1:1443:U:H2'	53:1:1444:G:H8	1.76	0.48
53:1:1979:U:C2'	53:1:1980:G:H5'	2.43	0.48
53:1:2155:U:H2'	53:1:2156:G:H5'	1.95	0.48
53:1:2443:C:O2'	53:1:2444:G:H5'	2.12	0.48
1:b:57:HIS:ND1	53:1:1567:G:H5'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:43:GLU:OE1	9:j:43:GLU:N	2.44	0.48
21:v:65:VAL:HG22	21:v:66:ASP:OD1	2.13	0.48
21:v:72:VAL:HG12	21:v:73:LYS:H	1.77	0.48
52:3:82:G:H2'	52:3:83:C:O4'	2.13	0.48
53:1:729:G:H4'	53:1:763:G:C5'	2.43	0.48
53:1:1001:A:H2'	53:1:1002:G:O4'	2.14	0.48
53:1:1601:G:C2'	53:1:1602:U:H5'	2.43	0.48
53:1:1965:C:H5''	53:1:1966:A:H2'	1.95	0.48
53:1:2743:U:H2'	53:1:2744:G:H5''	1.93	0.48
5:f:96:ALA:H	5:f:103:ASN:HB3	1.78	0.48
12:m:97:GLN:OE1	12:m:97:GLN:N	2.44	0.48
13:n:60:VAL:HG13	13:n:61:ALA:H	1.79	0.48
18:s:40:ASN:O	18:s:41:LYS:HD2	2.13	0.48
31:G:206:ILE:O	31:G:209:VAL:HG22	2.13	0.48
33:I:33:ILE:HG23	33:I:34:GLU:HG3	1.95	0.48
33:I:112:GLU:O	33:I:115:GLN:HB3	2.13	0.48
34:J:11:GLN:HB2	34:J:39:GLY:O	2.14	0.48
36:L:19:SER:HB2	36:L:58:LEU:HD11	1.95	0.48
49:Y:22:SER:OG	52:3:1458:G:H4'	2.13	0.48
49:Y:51:ASN:HA	49:Y:54:GLN:NE2	2.27	0.48
52:3:354:G:C2'	52:3:355:C:H5'	2.43	0.48
52:3:1033:G:C3'	52:3:1034:G:H5''	2.43	0.48
53:1:458:G:HO2'	53:1:459:U:H5	1.60	0.48
53:1:779:U:H2'	53:1:780:G:C8	2.48	0.48
53:1:1061:U:H4'	53:1:1070:A:N3	2.28	0.48
53:1:1146:C:H2'	53:1:1147:A:H8	1.78	0.48
53:1:1451:C:H4'	53:1:1452:G:C4	2.48	0.48
54:2:5:U:H2'	54:2:6:G:C8	2.48	0.48
17:r:38:VAL:HG13	17:r:54:VAL:HG22	1.95	0.48
26:B:8:THR:HG22	53:1:2020:A:H5'	1.94	0.48
34:J:19:ARG:HB3	34:J:32:PHE:CE1	2.49	0.48
42:R:64:VAL:HG22	42:R:65:GLU:N	2.28	0.48
45:U:67:ILE:HG13	45:U:68:SER:N	2.28	0.48
48:X:15:LEU:O	48:X:18:VAL:HG12	2.13	0.48
48:X:77:ARG:HH22	52:3:1322:C:P	2.37	0.48
52:3:418:C:H2'	52:3:419:C:C6	2.49	0.48
53:1:1176:U:H2'	53:1:1177:G:C8	2.49	0.48
53:1:2001:C:H1'	53:1:2689:U:C4	2.49	0.48
53:1:2055:C:H5'	53:1:2056:G:O5'	2.13	0.48
53:1:2469:A:H2'	53:1:2470:G:O4'	2.13	0.48
53:1:2488:G:H2'	53:1:2489:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:66:PHE:HB3	1:b:150:GLY:O	2.14	0.48
1:b:235:GLU:HB2	53:1:2599:G:N7	2.28	0.48
1:b:268:ARG:NH1	1:b:269:ARG:O	2.46	0.48
4:e:38:GLY:O	53:1:2306:C:N4	2.46	0.48
9:j:30:THR:HG21	53:1:1005:C:O2'	2.13	0.48
9:j:31:GLU:HG2	9:j:142:ILE:HG12	1.94	0.48
15:p:70:GLU:OE1	15:p:70:GLU:N	2.46	0.48
16:q:10:ARG:HH21	53:1:1216:G:H5''	1.78	0.48
36:L:23:ALA:O	36:L:26:VAL:HG12	2.13	0.48
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.95	0.48
52:3:67:C:H2'	52:3:68:G:C8	2.48	0.48
52:3:411:A:N9	52:3:413:G:H1'	2.29	0.48
52:3:1213:A:O2'	52:3:1214:C:H2'	2.14	0.48
52:3:1347:G:HO2'	52:3:1348:U:H5	1.60	0.48
53:1:466:A:H2'	53:1:467:G:H5'	1.95	0.48
53:1:898:C:H2'	53:1:899:A:O4'	2.14	0.48
53:1:2248:C:H2'	53:1:2249:U:H5'	1.94	0.48
53:1:2297:A:N1	53:1:2321:U:C5	2.81	0.48
53:1:2808:G:H2'	53:1:2890:G:C6	2.49	0.48
1:b:42:ARG:HH11	1:b:42:ARG:HG2	1.78	0.48
11:l:38:GLN:HG3	53:1:805:G:H5''	1.95	0.48
28:D:12:ARG:CZ	28:D:44:VAL:HG21	2.42	0.48
33:I:13:ARG:NH2	52:3:542:G:H4'	2.28	0.48
37:M:104:SER:HB3	37:M:123:GLU:OE2	2.13	0.48
52:3:86:G:H4'	52:3:87:C:C5	2.48	0.48
52:3:731:G:O2'	52:3:732:C:H5'	2.14	0.48
53:1:1683:U:H2'	53:1:1684:G:H8	1.78	0.48
53:1:2628:C:H3'	53:1:2629:U:H5'	1.96	0.48
54:2:49:C:H2'	54:2:50:A:C8	2.48	0.48
1:b:96:LYS:HB2	53:1:1490:A:H62	1.77	0.48
1:b:120:ASP:HB2	6:g:91:PHE:CE1	2.48	0.48
2:c:48:ILE:O	2:c:81:GLU:HG3	2.14	0.48
5:f:9:VAL:O	5:f:11:PRO:HD3	2.13	0.48
7:h:71:CYS:HB3	7:h:117:LEU:CD1	2.43	0.48
9:j:81:ILE:CD1	53:1:2514:U:H5''	2.44	0.48
13:n:84:GLY:N	13:n:85:PRO:HD2	2.29	0.48
32:H:147:GLY:HA2	32:H:170:GLY:HA3	1.96	0.48
42:R:3:ILE:HG13	42:R:56:ARG:HG2	1.96	0.48
50:Z:64:ALA:C	50:Z:66:ARG:H	2.21	0.48
52:3:20:U:H2'	52:3:21:G:O4'	2.14	0.48
52:3:56:U:H2'	52:3:57:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:423:G:H2'	52:3:424:G:H5'	1.95	0.48
52:3:1201:A:C1'	52:3:1202:U:OP2	2.61	0.48
52:3:1349:A:H2'	52:3:1350:A:O4'	2.12	0.48
52:3:1404:C:H2'	52:3:1405:G:C8	2.48	0.48
53:1:176:A:O2'	53:1:177:G:H5'	2.13	0.48
53:1:818:G:C2'	53:1:819:A:H5''	2.43	0.48
53:1:1744:A:H3'	53:1:1745:A:H8	1.78	0.48
53:1:2030:A:C2	53:1:2499:C:H5''	2.48	0.48
53:1:2446:G:H2'	53:1:2447:G:H5''	1.95	0.48
55:5:7:G:H1	55:5:66:C:H42	1.62	0.48
55:5:26:G:C2'	55:5:27:U:OP1	2.61	0.48
4:e:9:ASP:HB2	4:e:10:GLU:OE1	2.13	0.48
15:p:27:VAL:HG21	15:p:58:PHE:HZ	1.77	0.48
22:w:16:ARG:HG2	53:1:2356:U:O3'	2.14	0.48
31:G:65:LYS:HD3	31:G:89:PHE:CE2	2.49	0.48
34:J:12:GLU:HG3	34:J:63:MET:HE2	1.96	0.48
35:K:2:ARG:HB3	35:K:92:THR:HG22	1.96	0.48
38:N:28:VAL:O	38:N:63:TYR:HA	2.12	0.48
38:N:69:GLY:N	52:3:1250:A:H4'	2.28	0.48
51:a:60:ARG:NH1	51:a:164:ARG:HG3	2.29	0.48
52:3:437:U:H2'	52:3:438:U:O4'	2.14	0.48
53:1:481:G:H1'	53:1:506:G:H21	1.78	0.48
53:1:783:A:H2'	53:1:784:G:H5'	1.95	0.48
53:1:1854:A:N6	53:1:1888:G:H1'	2.28	0.48
3:d:48:THR:O	3:d:52:VAL:HG23	2.12	0.48
6:g:45:GLU:HA	6:g:48:GLU:HG2	1.95	0.48
6:g:109:GLU:H	6:g:109:GLU:CD	2.22	0.48
11:l:78:ARG:NH2	11:l:80:SER:OG	2.47	0.48
12:m:1:MET:HE1	12:m:44:ARG:HA	1.95	0.48
31:G:102:ASN:O	31:G:106:VAL:HG23	2.13	0.48
32:H:100:ILE:HD12	32:H:100:ILE:N	2.29	0.48
36:L:141:HIS:O	36:L:145:GLU:HG3	2.14	0.48
43:S:60:ARG:CZ	52:3:981:U:H1'	2.44	0.48
44:T:39:GLN:NE2	53:1:715:A:O2'	2.47	0.48
19:t:33:LYS:HE3	19:t:80:TRP:CE3	2.48	0.48
29:E:3:ILE:HD12	29:E:62:PRO:HG2	1.95	0.48
33:I:8:LEU:HD11	52:3:429:U:OP1	2.14	0.48
36:L:4:ARG:HD3	36:L:4:ARG:N	2.28	0.48
39:O:91:ASP:OD2	39:O:91:ASP:N	2.47	0.48
42:R:97:ARG:HB2	42:R:99:GLN:OE1	2.14	0.48
43:S:53:ASP:O	43:S:54:SER:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:X:13:HIS:CE1	52:3:1014:A:H4'	2.49	0.48
52:3:1484:C:H2'	52:3:1485:U:C6	2.49	0.48
53:1:558:U:H2'	53:1:559:G:H8	1.79	0.48
53:1:832:U:H2'	53:1:833:A:H8	1.79	0.48
53:1:1146:C:H2'	53:1:1147:A:C8	2.49	0.48
53:1:2636:C:H2'	53:1:2637:U:C6	2.48	0.48
1:b:107:LYS:N	1:b:193:GLU:O	2.46	0.47
2:c:115:GLY:HA3	2:c:167:ASN:HB2	1.96	0.47
7:h:23:LEU:HD11	7:h:92:ALA:HA	1.96	0.47
10:k:43:ILE:HD12	10:k:56:ASP:HB2	1.96	0.47
26:B:4:GLN:O	53:1:2017:U:H4'	2.14	0.47
32:H:72:PRO:HD3	32:H:104:GLU:OE1	2.14	0.47
34:J:98:ALA:HB2	34:J:123:LEU:HD23	1.96	0.47
38:N:125:GLN:HG3	52:3:1232:U:OP1	2.14	0.47
39:O:7:ARG:HD3	39:O:75:ASP:OD1	2.13	0.47
53:1:987:C:H2'	53:1:988:A:O4'	2.14	0.47
53:1:1019:U:H3	53:1:1142:A:H62	1.62	0.47
53:1:1045:C:P	53:1:1047:G:H5'	2.54	0.47
53:1:1078:U:C5'	53:1:1079:C:H5''	2.44	0.47
7:h:92:ALA:HB1	7:h:129:LEU:HD22	1.95	0.47
11:l:127:VAL:HG22	11:l:131:ALA:HB3	1.96	0.47
22:w:14:ALA:HB1	53:1:2271:G:OP1	2.14	0.47
22:w:79:GLU:CG	22:w:81:GLU:HG2	2.37	0.47
34:J:108:GLY:H	52:3:9:G:H5'	1.78	0.47
46:V:11:VAL:HG11	46:V:20:ILE:HD11	1.96	0.47
49:Y:75:LYS:HE2	52:3:186:C:H1'	1.95	0.47
52:3:537:G:H2'	52:3:538:G:H8	1.79	0.47
52:3:1001:C:H2'	52:3:1002:G:C8	2.48	0.47
53:1:112:U:H2'	53:1:113:U:H5'	1.95	0.47
53:1:828:U:H2'	53:1:829:A:C8	2.49	0.47
53:1:1571:A:H2'	53:1:1572:A:C8	2.49	0.47
53:1:2350:C:H2'	53:1:2351:G:O4'	2.14	0.47
53:1:2423:U:H5'	53:1:2424:C:C5'	2.43	0.47
57:7:34:G:H2'	57:7:35:A:C8	2.49	0.47
57:7:61:C:H5'	57:7:61:C:H6	1.79	0.47
2:c:142:VAL:HG13	2:c:143:PRO:HD2	1.96	0.47
3:d:149:ILE:HD11	3:d:172:ALA:HA	1.95	0.47
13:n:60:VAL:HG13	13:n:61:ALA:N	2.29	0.47
14:o:53:THR:HB	14:o:65:THR:OG1	2.14	0.47
15:p:97:TYR:HB2	53:1:2718:G:OP1	2.13	0.47
33:I:2:ARG:HH12	52:3:406:G:H4'	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:69:ARG:HA	36:L:99:ALA:HB2	1.96	0.47
43:S:1:ALA:HB1	52:3:1049:U:O4	2.13	0.47
52:3:335:C:H2'	52:3:336:A:H8	1.80	0.47
52:3:379:C:H2'	52:3:380:G:C8	2.49	0.47
52:3:392:C:H2'	52:3:393:A:C8	2.49	0.47
52:3:482:A:H2'	52:3:483:C:H5'	1.96	0.47
52:3:514:C:H2'	52:3:515:G:C8	2.49	0.47
52:3:945:G:H1'	52:3:1337:G:H1'	1.95	0.47
52:3:1001:C:H2'	52:3:1002:G:H8	1.79	0.47
52:3:1308:U:H2'	52:3:1309:G:H8	1.80	0.47
54:2:108:A:H5'	54:2:109:A:O5'	2.14	0.47
4:e:34:THR:OG1	53:1:2314:A:H4'	2.14	0.47
4:e:84:ILE:HG21	53:1:2311:A:O2'	2.14	0.47
4:e:142:TYR:HA	4:e:145:VAL:HG12	1.97	0.47
6:g:12:LEU:HD12	6:g:13:GLY:N	2.30	0.47
9:j:125:TYR:OH	9:j:132:HIS:NE2	2.39	0.47
14:o:108:ASP:HA	14:o:111:ARG:HD2	1.95	0.47
20:u:73:ASN:HD22	20:u:76:THR:H	1.62	0.47
21:v:77:VAL:HG23	21:v:89:ILE:HG12	1.96	0.47
22:w:22:PHE:CD2	53:1:922:C:H1'	2.49	0.47
33:I:170:LEU:C	33:I:170:LEU:HD12	2.40	0.47
34:J:87:VAL:CG2	34:J:92:ARG:HD2	2.43	0.47
36:L:122:GLU:OE1	36:L:122:GLU:N	2.47	0.47
38:N:29:ILE:HG13	38:N:64:ILE:O	2.14	0.47
52:3:229:U:H2'	52:3:230:G:C8	2.49	0.47
52:3:320:A:H2'	52:3:321:A:C8	2.48	0.47
52:3:1516:G:H2'	52:3:1518:A:OP2	2.14	0.47
53:1:167:A:H2'	53:1:168:G:O4'	2.14	0.47
53:1:1295:C:H2'	53:1:1296:G:H8	1.78	0.47
53:1:2117:A:H61	53:1:2170:A:H61	1.63	0.47
1:b:18:VAL:O	1:b:18:VAL:HG13	2.14	0.47
1:b:156:SER:OG	53:1:1818:U:H5'	2.15	0.47
4:e:34:THR:CG2	53:1:2314:A:H5'	2.36	0.47
4:e:63:LYS:NZ	54:2:42:C:P	2.87	0.47
7:h:112:ALA:O	7:h:113:PHE:C	2.56	0.47
9:j:35:ARG:HA	9:j:40:HIS:HD2	1.80	0.47
9:j:108:MET:HE2	53:1:1138:G:H21	1.79	0.47
16:q:91:ARG:NH2	53:1:1153:C:OP1	2.48	0.47
32:H:110:LEU:C	32:H:110:LEU:HD12	2.39	0.47
39:O:56:HIS:ND1	39:O:57:VAL:HG13	2.29	0.47
53:1:1857:G:N2	53:1:1884:G:H2'	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1972:G:H2'	53:1:1973:G:H8	1.79	0.47
53:1:2450:A:OP1	53:1:2497:A:H2'	2.14	0.47
1:b:231:HIS:O	1:b:232:GLY:O	2.32	0.47
7:h:24:SER:O	7:h:116:GLU:HB2	2.14	0.47
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.96	0.47
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.97	0.47
11:l:76:GLU:C	11:l:77:ILE:HD12	2.40	0.47
13:n:9:GLN:HE21	53:1:2002:G:H5'	1.79	0.47
13:n:97:ILE:C	13:n:98:LEU:HD12	2.40	0.47
27:C:5:ARG:HG3	53:1:2284:A:P	2.55	0.47
33:I:80:ARG:HE	52:3:613:C:P	2.38	0.47
43:S:72:PHE:CE1	43:S:77:GLY:HA2	2.50	0.47
50:Z:23:GLU:OE2	50:Z:24:LYS:N	2.48	0.47
52:3:1302:C:O2'	52:3:1303:C:H5'	2.15	0.47
53:1:340:A:H2'	53:1:341:C:O4'	2.15	0.47
53:1:1420:A:H5'	53:1:1421:G:OP2	2.15	0.47
53:1:2144:G:H1'	53:1:2147:A:N6	2.29	0.47
3:d:16:GLU:OE2	3:d:20:GLY:HA3	2.14	0.47
4:e:94:ARG:NH2	54:2:43:C:O3'	2.48	0.47
5:f:140:ILE:HG13	5:f:141:GLY:H	1.78	0.47
8:i:99:LYS:HE3	8:i:140:GLU:CB	2.45	0.47
17:r:46:GLU:CD	17:r:46:GLU:N	2.72	0.47
31:G:5:MET:HA	31:G:8:MET:HB2	1.95	0.47
31:G:14:HIS:HA	31:G:40:ILE:HG22	1.95	0.47
32:H:144:GLY:O	32:H:203:LYS:NZ	2.48	0.47
34:J:24:VAL:HG13	34:J:26:GLY:N	2.30	0.47
35:K:11:HIS:CD2	35:K:12:PRO:HD2	2.48	0.47
36:L:91:ARG:O	36:L:95:ARG:HG3	2.13	0.47
36:L:115:MET:HE3	52:3:1240:U:H5	1.76	0.47
40:P:111:ASP:HB3	50:Z:3:ILE:HA	1.96	0.47
41:Q:23:LEU:HB3	41:Q:26:CYS:SG	2.55	0.47
41:Q:32:VAL:HG12	41:Q:34:THR:HG22	1.95	0.47
41:Q:109:ARG:HA	52:3:538:G:OP1	2.15	0.47
42:R:22:TYR:HE2	42:R:68:LEU:HD22	1.79	0.47
50:Z:54:ARG:O	50:Z:58:LYS:HG3	2.15	0.47
52:3:107:G:H2'	52:3:108:G:O4'	2.14	0.47
52:3:424:G:O2'	52:3:425:G:H5'	2.14	0.47
52:3:482:A:C2'	52:3:483:C:H5'	2.45	0.47
52:3:950:U:H2'	52:3:951:G:C8	2.50	0.47
52:3:1323:G:H2'	52:3:1324:A:C8	2.49	0.47
52:3:1325:C:O2'	52:3:1326:U:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:729:G:H4'	53:1:763:G:H5'	1.97	0.47
53:1:2086:U:H2'	53:1:2087:G:H8	1.79	0.47
53:1:2257:U:O2'	53:1:2258:C:H5'	2.15	0.47
53:1:2266:A:H4'	53:1:2267:A:C2	2.48	0.47
53:1:2361:G:O2'	53:1:2362:C:H5'	2.15	0.47
53:1:2699:C:H2'	53:1:2700:A:H8	1.79	0.47
53:1:2786:U:O2'	53:1:2787:C:H5'	2.15	0.47
54:2:49:C:H2'	54:2:50:A:H8	1.80	0.47
55:5:26:G:H2'	55:5:27:U:OP1	2.14	0.47
55:5:59:A:C2'	55:5:60:U:H5'	2.45	0.47
1:b:264:LYS:NZ	53:1:2224:G:H5'	2.29	0.47
3:d:68:ALA:HA	53:1:1255:U:C5	2.49	0.47
6:g:75:LEU:HG	6:g:77:THR:H	1.80	0.47
15:p:109:ILE:HD12	15:p:109:ILE:H	1.80	0.47
33:I:199:ILE:O	33:I:202:LEU:HG	2.14	0.47
40:P:66:ALA:CB	40:P:98:ALA:HB3	2.44	0.47
41:Q:82:ARG:NH2	52:3:552:U:H5'	2.30	0.47
43:S:4:SER:CB	52:3:1216:A:H5''	2.43	0.47
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.48	0.47
52:3:945:G:H2'	52:3:945:G:N3	2.29	0.47
52:3:1004:A:H2'	52:3:1005:A:O4'	2.15	0.47
52:3:1472:U:H2'	52:3:1473:G:C8	2.50	0.47
52:3:1527:U:H2'	52:3:1528:U:C6	2.50	0.47
53:1:548:G:H2'	53:1:549:G:O4'	2.15	0.47
53:1:565:C:H4'	53:1:1253:A:N6	2.30	0.47
53:1:1570:A:H2'	53:1:1571:A:C8	2.49	0.47
53:1:2682:A:O2'	53:1:2683:C:H5'	2.14	0.47
12:m:2:LEU:HB3	12:m:68:PHE:CE1	2.50	0.47
12:m:102:LEU:HD11	12:m:126:ILE:HD11	1.97	0.47
24:y:1:MET:HA	24:y:4:LYS:NZ	2.29	0.47
24:y:3:ALA:HB1	24:y:7:ARG:HH21	1.79	0.47
31:G:22:TRP:CZ2	52:3:829:G:H4'	2.49	0.47
33:I:141:VAL:HG21	33:I:178:GLU:HG2	1.97	0.47
36:L:24:LYS:O	36:L:28:ILE:HG23	2.15	0.47
37:M:29:SER:HB3	37:M:32:LYS:HD2	1.97	0.47
44:T:34:GLN:O	44:T:38:LEU:HD23	2.15	0.47
49:Y:79:THR:O	49:Y:82:ILE:HG22	2.15	0.47
50:Z:23:GLU:O	50:Z:25:ALA:N	2.46	0.47
52:3:320:A:H2'	52:3:321:A:H8	1.80	0.47
53:1:319:G:H2'	53:1:320:A:O4'	2.14	0.47
53:1:825:A:H2'	53:1:826:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1666:G:C2'	53:1:1667:G:H5'	2.45	0.47
53:1:1936:A:H2	53:1:1943:U:H3	1.63	0.47
53:1:2208:C:H2'	53:1:2209:G:H8	1.79	0.47
53:1:2836:U:H2'	53:1:2837:A:H8	1.80	0.47
25:z:7:THR:HG23	25:z:55:LYS:HB3	1.97	0.47
31:G:51:GLU:O	31:G:55:GLU:HG2	2.15	0.47
35:K:43:GLY:HA2	35:K:58:HIS:CE1	2.49	0.47
35:K:88:MET:HE2	35:K:90:MET:SD	2.55	0.47
37:M:87:ARG:HB2	37:M:90:GLU:OE2	2.15	0.47
38:N:27:ILE:HB	38:N:34:LEU:HD23	1.97	0.47
38:N:65:THR:HG23	38:N:65:THR:O	2.15	0.47
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.97	0.47
49:Y:27:MET:O	49:Y:31:ILE:HD12	2.15	0.47
52:3:26:A:N6	52:3:558:G:H1'	2.29	0.47
52:3:31:G:H5'	52:3:306:A:C2	2.50	0.47
52:3:730:G:H2'	52:3:731:G:H5'	1.97	0.47
53:1:1013:C:H2'	53:1:1014:A:C8	2.50	0.47
53:1:1110:G:H2'	53:1:1111:A:H8	1.80	0.47
53:1:1432:G:H2'	53:1:1433:A:C8	2.50	0.47
53:1:2247:A:O2'	53:1:2248:C:H5'	2.15	0.47
2:c:150:GLN:NE2	53:1:574:A:H2	2.13	0.46
4:e:7:TYR:O	4:e:12:VAL:HG23	2.14	0.46
8:i:10:LEU:HB3	8:i:11:GLN:H	1.46	0.46
9:j:113:PRO:HD2	53:1:558:U:P	2.55	0.46
18:s:14:ALA:HB2	18:s:78:GLU:HB3	1.97	0.46
30:F:16:ILE:HD13	30:F:25:VAL:HG22	1.97	0.46
31:G:29:PHE:O	31:G:40:ILE:HD12	2.15	0.46
32:H:69:THR:OG1	32:H:70:ALA:N	2.48	0.46
38:N:12:LYS:HE3	52:3:1371:G:OP1	2.14	0.46
38:N:49:GLN:N	38:N:50:PRO:CD	2.79	0.46
41:Q:32:VAL:HB	41:Q:55:ARG:HB3	1.97	0.46
48:X:30:LEU:HD13	48:X:48:ILE:HG12	1.97	0.46
50:Z:41:THR:O	50:Z:45:LYS:HG3	2.15	0.46
52:3:1256:A:O2'	52:3:1257:A:H5''	2.15	0.46
53:1:732:C:H2'	53:1:733:G:O4'	2.13	0.46
53:1:1092:C:H2'	53:1:1093:G:O4'	2.15	0.46
55:5:3:C:H3'	55:5:4:G:C5'	2.44	0.46
4:e:151:LEU:HD12	4:e:152:ASP:N	2.30	0.46
5:f:23:ILE:HD12	5:f:23:ILE:N	2.30	0.46
11:l:77:ILE:HD13	11:l:108:ALA:HB1	1.96	0.46
12:m:74:THR:OG1	12:m:75:GLU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:40:MET:HG3	17:r:48:LYS:HA	1.96	0.46
17:r:79:ARG:NH1	53:1:572:A:OP2	2.48	0.46
27:C:29:LYS:NZ	53:1:2286:G:H3'	2.30	0.46
35:K:38:ARG:HD3	35:K:97:THR:HA	1.97	0.46
37:M:120:LEU:HA	52:3:600:A:H5'	1.97	0.46
42:R:113:LYS:H	42:R:114:PRO:CD	2.23	0.46
47:W:62:ARG:NH1	52:3:718:A:N6	2.63	0.46
48:X:38:THR:HG22	48:X:39:ILE:H	1.80	0.46
50:Z:23:GLU:C	50:Z:25:ALA:H	2.22	0.46
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.78	0.46
52:3:1218:C:H2'	52:3:1219:A:H8	1.78	0.46
53:1:184:C:H2'	53:1:185:G:C8	2.49	0.46
53:1:1565:C:O2'	53:1:1566:A:H2'	2.15	0.46
53:1:1657:U:H2'	53:1:1658:C:C6	2.51	0.46
53:1:2282:G:H4'	53:1:2389:G:O2'	2.15	0.46
53:1:2849:U:H4'	53:1:2868:A:C2	2.50	0.46
4:e:65:LEU:HD23	4:e:65:LEU:C	2.40	0.46
5:f:125:PRO:HG2	5:f:129:GLU:HB3	1.97	0.46
6:g:7:ASP:C	6:g:8:LYS:HD3	2.40	0.46
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.30	0.46
11:l:39:LYS:HE2	11:l:39:LYS:HB3	1.79	0.46
16:q:57:ARG:NH1	53:1:1154:G:OP2	2.49	0.46
17:r:46:GLU:CD	17:r:46:GLU:H	2.23	0.46
31:G:169:HIS:HA	31:G:172:ILE:HG12	1.98	0.46
33:I:4:LEU:HD21	52:3:406:G:OP1	2.15	0.46
38:N:65:THR:OG1	38:N:67:LYS:NZ	2.44	0.46
40:P:124:LYS:NZ	52:3:1524:C:OP2	2.41	0.46
41:Q:26:CYS:HB2	52:3:363:A:C5	2.49	0.46
52:3:163:C:H2'	52:3:164:G:O4'	2.15	0.46
52:3:1347:G:N2	52:3:1374:A:OP2	2.44	0.46
52:3:1488:G:H2'	52:3:1489:G:H8	1.79	0.46
53:1:818:G:O2'	53:1:819:A:H5''	2.15	0.46
53:1:2162:G:H2'	53:1:2163:A:H8	1.79	0.46
53:1:2339:C:H2'	53:1:2340:A:H8	1.80	0.46
2:c:136:ASN:ND2	2:c:139:SER:O	2.37	0.46
3:d:1:MET:N	3:d:14:VAL:O	2.48	0.46
37:M:37:ASN:O	37:M:41:GLU:HG3	2.15	0.46
52:3:521:G:O2'	52:3:522:C:H5'	2.15	0.46
52:3:1329:A:O2'	52:3:1330:U:H5'	2.15	0.46
53:1:279:A:C2'	53:1:280:U:H5'	2.44	0.46
53:1:974:G:N3	53:1:974:G:H2'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2197:U:H1'	53:1:2198:A:C8	2.49	0.46
53:1:2233:U:H2'	53:1:2234:G:H8	1.79	0.46
53:1:2339:C:H2'	53:1:2340:A:C8	2.50	0.46
53:1:2475:C:H2'	53:1:2476:A:H5'	1.98	0.46
1:b:97:ASP:HB3	53:1:1490:A:C8	2.50	0.46
7:h:33:VAL:HB	7:h:35:VAL:HG22	1.98	0.46
10:k:63:VAL:HG23	10:k:64:ARG:N	2.30	0.46
11:l:93:ASN:C	11:l:95:LEU:N	2.72	0.46
15:p:13:LYS:HD3	15:p:75:THR:O	2.15	0.46
15:p:92:ARG:NH2	53:1:2849:U:OP1	2.48	0.46
24:y:2:LYS:HD2	53:1:78:U:OP2	2.16	0.46
33:I:122:ILE:O	33:I:128:VAL:HG13	2.15	0.46
40:P:115:ILE:HG23	40:P:115:ILE:O	2.15	0.46
41:Q:87:LYS:HE3	52:3:526:C:OP1	2.16	0.46
45:U:16:PHE:CE2	52:3:625:U:H4'	2.49	0.46
51:a:37:LYS:HB3	53:1:2127:G:H5'	1.95	0.46
52:3:244:U:O4	52:3:906:A:H1'	2.16	0.46
52:3:494:G:O2'	52:3:496:A:H1'	2.16	0.46
52:3:680:C:H2'	52:3:681:A:H8	1.80	0.46
52:3:1096:C:H2'	52:3:1097:C:C6	2.50	0.46
53:1:2093:G:N7	53:1:2225:A:H2'	2.30	0.46
53:1:2485:G:O2'	53:1:2486:C:H5'	2.15	0.46
54:2:2:G:H2'	54:2:3:C:C6	2.50	0.46
2:c:35:THR:HG22	2:c:73:VAL:HG21	1.96	0.46
2:c:129:THR:OG1	2:c:140:HIS:O	2.32	0.46
6:g:101:ASP:O	6:g:104:THR:HG22	2.15	0.46
16:q:30:VAL:HG13	53:1:580:U:O3'	2.15	0.46
18:s:35:ILE:HD11	26:B:23:ALA:HB1	1.97	0.46
20:u:50:ALA:O	20:u:51:LEU:HG	2.16	0.46
21:v:45:ASP:CG	53:1:1039:A:H4'	2.40	0.46
22:w:7:ARG:O	22:w:10:ARG:NH2	2.48	0.46
22:w:17:LEU:HD21	22:w:37:ARG:NH2	2.30	0.46
25:z:50:VAL:O	25:z:54:VAL:HG22	2.16	0.46
31:G:142:LYS:HA	31:G:145:ASN:HD22	1.81	0.46
33:I:8:LEU:HD22	33:I:31:CYS:SG	2.56	0.46
42:R:52:ILE:HA	42:R:55:LEU:HD12	1.97	0.46
44:T:46:LYS:NZ	53:1:716:A:H1'	2.31	0.46
47:W:50:TYR:O	47:W:54:LEU:N	2.49	0.46
52:3:70:U:H4'	52:3:71:A:C8	2.48	0.46
52:3:195:A:H2'	52:3:196:A:C8	2.51	0.46
52:3:291:U:O2'	52:3:292:G:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:823:C:H2'	52:3:824:G:H8	1.81	0.46
53:1:538:A:H2'	53:1:539:G:O4'	2.15	0.46
53:1:1295:C:H2'	53:1:1296:G:C8	2.50	0.46
53:1:1991:U:H2'	53:1:1992:G:C5'	2.46	0.46
53:1:2368:C:H2'	53:1:2369:A:H8	1.80	0.46
5:f:3:VAL:HG11	53:1:2748:A:H4'	1.97	0.46
5:f:8:VAL:HB	5:f:49:LEU:HD12	1.98	0.46
5:f:41:GLU:OE2	5:f:43:LYS:NZ	2.48	0.46
10:k:10:VAL:HG21	10:k:16:ALA:C	2.40	0.46
19:t:33:LYS:HG2	19:t:80:TRP:CZ3	2.51	0.46
24:y:40:SER:HB2	53:1:61:C:O4'	2.15	0.46
31:G:53:LEU:HD11	31:G:215:ALA:HB1	1.97	0.46
32:H:58:ARG:HB2	32:H:58:ARG:HH11	1.79	0.46
33:I:95:GLY:HA3	33:I:135:GLN:HE22	1.81	0.46
34:J:20:VAL:HG11	52:3:1080:A:H4'	1.96	0.46
38:N:128:LYS:HE3	38:N:129:ARG:HH22	1.80	0.46
43:S:8:ARG:HD3	52:3:1218:C:OP2	2.15	0.46
52:3:396:C:C2'	52:3:397:A:H5''	2.45	0.46
52:3:483:C:H3'	52:3:484:G:H2'	1.98	0.46
52:3:613:C:H2'	52:3:614:C:C6	2.51	0.46
52:3:911:U:H2'	52:3:912:C:C6	2.51	0.46
52:3:915:A:C2'	52:3:916:U:H5'	2.46	0.46
52:3:1347:G:O2'	52:3:1348:U:C5	2.68	0.46
52:3:1354:U:H2'	52:3:1355:G:H8	1.81	0.46
53:1:306:U:H3	53:1:310:A:H62	1.64	0.46
53:1:414:C:H2'	53:1:415:A:H8	1.79	0.46
53:1:1683:U:H2'	53:1:1684:G:C8	2.51	0.46
53:1:1720:U:H2'	53:1:1721:G:O4'	2.16	0.46
53:1:1748:C:H2'	53:1:1749:A:C8	2.50	0.46
53:1:2475:C:H42	53:1:2529:G:H22	1.63	0.46
53:1:2836:U:H2'	53:1:2837:A:C8	2.50	0.46
12:m:108:VAL:HG21	12:m:113:ALA:HB2	1.98	0.46
12:m:136:MET:HE3	21:v:76:ASP:HA	1.98	0.46
14:o:33:ARG:O	14:o:34:HIS:CB	2.63	0.46
28:D:25:LYS:HD3	53:1:1367:A:O2'	2.16	0.46
42:R:56:ARG:O	42:R:59:VAL:HG12	2.15	0.46
43:S:97:LYS:HE2	52:3:1189:U:OP1	2.16	0.46
52:3:501:C:H2'	52:3:502:A:C8	2.50	0.46
52:3:571:U:H2'	52:3:572:A:H5''	1.97	0.46
52:3:1418:A:H3'	52:3:1419:G:C5'	2.45	0.46
53:1:248:G:N3	53:1:2431:U:H4'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1258:U:H2'	53:1:1259:G:C8	2.51	0.46
53:1:1956:U:C2'	53:1:1957:C:H5'	2.46	0.46
53:1:2297:A:H62	53:1:2319:G:H1'	1.80	0.46
53:1:2364:C:H2'	53:1:2365:G:O4'	2.16	0.46
53:1:2743:U:C2'	53:1:2744:G:H5''	2.46	0.46
21:v:20:LEU:HD11	21:v:41:GLU:HG3	1.98	0.46
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.50	0.46
29:E:38:LYS:HA	29:E:41:ARG:NH2	2.31	0.46
31:G:26:MET:HG3	31:G:188:THR:HA	1.98	0.46
31:G:115:ASP:O	31:G:119:GLN:HG2	2.16	0.46
36:L:24:LYS:HZ2	52:3:1375:A:H5''	1.81	0.46
41:Q:68:GLY:H	52:3:522:C:P	2.39	0.46
43:S:66:THR:CG2	52:3:1203:C:H4'	2.46	0.46
52:3:396:C:C3'	52:3:397:A:H5''	2.46	0.46
52:3:406:G:H2'	52:3:407:U:C6	2.51	0.46
52:3:423:G:C2'	52:3:424:G:H5'	2.46	0.46
52:3:810:C:H2'	52:3:811:C:O4'	2.16	0.46
52:3:817:C:H5'	52:3:820:U:OP2	2.15	0.46
52:3:879:C:O2'	52:3:880:C:H5'	2.16	0.46
52:3:950:U:H2'	52:3:951:G:H8	1.81	0.46
52:3:978:A:H4'	52:3:1322:C:N3	2.31	0.46
53:1:112:U:C2'	53:1:113:U:H5'	2.46	0.46
53:1:532:A:H2'	53:1:532:A:N3	2.31	0.46
53:1:1639:C:O2'	53:1:1640:A:H5'	2.15	0.46
53:1:1769:U:O2'	53:1:1770:G:H5'	2.16	0.46
53:1:2134:A:N6	53:1:2157:G:H4'	2.31	0.46
55:5:16:C:H1'	55:5:61:C:OP1	2.16	0.46
57:7:73:A:O5'	57:7:74:C:H5''	2.16	0.46
7:h:114:GLU:C	7:h:115:GLY:O	2.58	0.46
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.41	0.46
14:o:100:HIS:CD2	54:2:48:U:H4'	2.45	0.46
17:r:49:ILE:O	17:r:49:ILE:HG13	2.15	0.46
28:D:22:MET:HE1	28:D:31:LEU:HD22	1.96	0.46
31:G:210:THR:O	31:G:213:LEU:HG	2.16	0.46
32:H:151:GLU:HB3	32:H:198:LYS:HB2	1.97	0.46
33:I:72:ARG:HH12	33:I:76:LYS:HD2	1.81	0.46
42:R:19:THR:HG22	42:R:25:GLY:O	2.16	0.46
43:S:53:ASP:HA	43:S:58:ARG:HD3	1.98	0.46
51:a:170:ILE:HD12	51:a:170:ILE:N	2.31	0.46
52:3:243:A:H4'	52:3:244:U:H3'	1.98	0.46
52:3:467:U:H5'	52:3:468:A:OP2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1270:G:H2'	52:3:1271:A:H8	1.81	0.46
52:3:1271:A:H5'	52:3:1314:C:H5''	1.98	0.46
52:3:1278:G:OP1	52:3:1279:G:H5'	2.16	0.46
53:1:596:U:H2'	53:1:597:G:C8	2.50	0.46
53:1:864:G:O2'	53:1:865:C:H5'	2.16	0.46
53:1:1079:C:H2'	53:1:1080:A:C8	2.50	0.46
53:1:1373:A:H5''	53:1:2212:A:H1'	1.97	0.46
53:1:1994:C:O2'	53:1:1995:U:H5'	2.16	0.46
53:1:2236:U:H2'	53:1:2237:G:O4'	2.16	0.46
53:1:2345:G:N3	53:1:2381:A:H2'	2.31	0.46
53:1:2543:G:H2'	53:1:2544:G:C8	2.51	0.46
4:e:70:ARG:HD2	53:1:2298:A:OP1	2.15	0.45
4:e:132:ARG:NE	53:1:2305:U:H4'	2.26	0.45
9:j:52:ASP:O	9:j:54:ILE:HG13	2.16	0.45
10:k:18:ARG:HG2	10:k:18:ARG:HH11	1.81	0.45
14:o:49:VAL:CG2	14:o:85:LYS:HG3	2.47	0.45
14:o:111:ARG:HG2	14:o:117:PHE:OXT	2.15	0.45
30:F:5:ALA:HB3	53:1:2466:C:H5'	1.97	0.45
38:N:5:TYR:HB2	38:N:20:ILE:CG2	2.47	0.45
39:O:53:ILE:HD13	52:3:1060:U:O3'	2.17	0.45
43:S:56:PRO:HA	43:S:59:GLN:HG2	1.98	0.45
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.51	0.45
52:3:123:U:H2'	52:3:124:C:C6	2.51	0.45
52:3:1289:A:H2'	52:3:1290:G:H5'	1.98	0.45
53:1:1441:G:H2'	53:1:1442:U:C6	2.51	0.45
53:1:1590:A:H2'	53:1:1591:A:C8	2.51	0.45
53:1:1609:A:H1'	53:1:1616:A:C1'	2.46	0.45
53:1:2329:U:H2'	53:1:2330:G:H8	1.80	0.45
1:b:242:HIS:O	1:b:244:VAL:HG13	2.15	0.45
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.15	0.45
4:e:39:VAL:CG2	4:e:41:GLU:HB2	2.45	0.45
4:e:87:LYS:NZ	53:1:2313:C:H5''	2.31	0.45
4:e:152:ASP:HB2	53:1:2304:G:O2'	2.16	0.45
7:h:71:CYS:HB3	7:h:117:LEU:HD11	1.98	0.45
8:i:99:LYS:HE3	8:i:140:GLU:HG2	1.97	0.45
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.84	0.45
32:H:141:MET:HE2	32:H:169:GLU:HG2	1.97	0.45
52:3:21:G:H2'	52:3:22:G:C8	2.51	0.45
52:3:1368:A:O2'	52:3:1369:C:H5'	2.15	0.45
53:1:859:G:O2'	53:1:860:U:C6	2.68	0.45
53:1:1663:G:O2'	53:1:2686:G:H4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1779:U:OP2	53:1:1784:A:N6	2.49	0.45
53:1:2106:U:H2'	53:1:2107:G:C8	2.51	0.45
53:1:2220:U:H2'	53:1:2221:G:C8	2.49	0.45
53:1:2515:C:H2'	53:1:2516:A:C8	2.51	0.45
7:h:33:VAL:HG13	53:1:1056:G:P	2.56	0.45
7:h:58:THR:HG21	7:h:82:ILE:H	1.81	0.45
11:l:77:ILE:HD12	11:l:77:ILE:N	2.31	0.45
13:n:9:GLN:NE2	53:1:2002:G:H5''	2.31	0.45
18:s:74:ILE:HG23	18:s:74:ILE:O	2.16	0.45
33:I:172:VAL:HA	33:I:179:GLY:HA2	1.98	0.45
34:J:104:ILE:O	34:J:104:ILE:HG13	2.16	0.45
36:L:91:ARG:HB2	36:L:94:ARG:HG2	1.98	0.45
48:X:66:VAL:HG23	48:X:67:GLY:H	1.80	0.45
52:3:51:A:H4'	52:3:52:C:H5''	1.99	0.45
52:3:123:U:OP1	52:3:312:C:H5'	2.15	0.45
52:3:407:U:H2'	52:3:408:A:H8	1.80	0.45
52:3:1157:A:N6	52:3:1178:G:H1'	2.31	0.45
53:1:12:U:O2'	53:1:13:A:H5'	2.16	0.45
53:1:458:G:O2'	53:1:459:U:H5	1.99	0.45
53:1:1434:A:H2'	53:1:1435:G:H8	1.81	0.45
53:1:1444:G:H2'	53:1:1445:G:H8	1.82	0.45
53:1:2661:G:H2'	53:1:2662:A:O4'	2.15	0.45
2:c:194:PRO:HA	53:1:2680:U:C5'	2.46	0.45
3:d:5:LEU:HD23	3:d:8:ALA:HB3	1.97	0.45
10:k:34:GLY:O	10:k:62:VAL:HG21	2.16	0.45
13:n:79:LEU:O	13:n:80:PHE:HB2	2.16	0.45
31:G:113:LEU:HB2	31:G:143:LEU:CD2	2.46	0.45
34:J:160:VAL:O	34:J:163:ILE:HG12	2.16	0.45
38:N:117:LEU:HA	38:N:124:PRO:HD3	1.98	0.45
46:V:5:ARG:HH21	52:3:636:U:P	2.39	0.45
53:1:202:U:H2'	53:1:203:A:O4'	2.17	0.45
53:1:1326:U:H2'	53:1:1327:A:C8	2.50	0.45
53:1:1564:C:H2'	53:1:1565:C:O4'	2.16	0.45
53:1:2024:G:OP2	53:1:2034:U:H4'	2.16	0.45
7:h:113:PHE:C	7:h:115:GLY:H	2.25	0.45
26:B:14:MET:SD	53:1:2045:C:H5''	2.56	0.45
33:I:123:MET:HA	33:I:128:VAL:HA	1.99	0.45
48:X:77:ARG:HD2	52:3:1225:A:H1'	1.99	0.45
50:Z:36:PHE:C	50:Z:38:GLU:H	2.25	0.45
52:3:620:C:H2'	52:3:621:A:O4'	2.17	0.45
53:1:1539:U:H2'	53:1:1540:G:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1678:A:H2'	53:1:1679:A:O4'	2.17	0.45
53:1:2412:A:H2'	53:1:2413:G:O4'	2.16	0.45
53:1:2557:G:H2'	53:1:2558:C:C6	2.51	0.45
1:b:229:HIS:C	1:b:231:HIS:H	2.24	0.45
4:e:127:TYR:HB3	4:e:155:ILE:HG23	1.97	0.45
5:f:51:PHE:CE1	5:f:71:LEU:HD12	2.52	0.45
11:l:14:LYS:O	11:l:15:ALA:HB3	2.16	0.45
13:n:36:THR:OG1	13:n:37:THR:N	2.49	0.45
17:r:6:GLN:HE21	17:r:11:GLN:NE2	2.15	0.45
32:H:147:GLY:O	32:H:148:ILE:HD13	2.17	0.45
35:K:47:LEU:HG	35:K:56:LYS:H	1.81	0.45
40:P:24:ALA:HB1	40:P:89:GLY:HA3	1.99	0.45
40:P:126:ARG:HH22	52:3:692:U:H5''	1.81	0.45
43:S:68:ARG:HE	52:3:1202:U:H5'	1.82	0.45
51:a:66:PRO:HD2	51:a:188:ASN:OD1	2.16	0.45
52:3:1410:A:H2'	52:3:1411:C:C6	2.51	0.45
52:3:1418:A:H2	53:1:1948:G:H21	1.64	0.45
53:1:768:G:N2	53:1:1379:U:H1'	2.31	0.45
53:1:2126:A:H2'	53:1:2162:G:C2	2.52	0.45
53:1:2676:C:H2'	53:1:2677:G:C8	2.52	0.45
53:1:2696:U:H2'	53:1:2697:G:C8	2.51	0.45
53:1:2861:U:H2'	53:1:2862:G:H8	1.82	0.45
4:e:37:MET:HB2	4:e:86:CYS:SG	2.57	0.45
7:h:92:ALA:HB3	7:h:130:PRO:HD2	1.99	0.45
9:j:108:MET:HE2	53:1:1138:G:N2	2.32	0.45
13:n:3:HIS:CG	53:1:2820:A:H4'	2.52	0.45
20:u:88:ASP:OD2	20:u:90:LYS:NZ	2.49	0.45
20:u:100:GLU:HB3	20:u:101:THR:H	1.58	0.45
33:I:49:ASP:O	33:I:52:VAL:HG22	2.16	0.45
34:J:107:GLY:HA3	52:3:9:G:H5'	1.97	0.45
36:L:68:VAL:C	36:L:137:ARG:HD3	2.42	0.45
36:L:92:PRO:HA	36:L:95:ARG:HG3	1.99	0.45
41:Q:31:GLY:HA3	41:Q:54:VAL:CG1	2.46	0.45
42:R:97:ARG:HG3	42:R:97:ARG:HH11	1.82	0.45
44:T:73:ASP:OD2	44:T:76:ARG:HG3	2.17	0.45
52:3:517:G:H2'	52:3:531:U:C5	2.52	0.45
52:3:1346:A:H2'	52:3:1346:A:N3	2.30	0.45
52:3:1353:G:O2'	52:3:1354:U:H5'	2.17	0.45
53:1:594:U:H2'	53:1:595:C:C6	2.52	0.45
53:1:2105:U:H2'	53:1:2106:U:O4'	2.17	0.45
6:g:41:LYS:HA	6:g:44:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:20:LYS:HG3	7:h:88:HIS:CE1	2.51	0.45
8:i:99:LYS:CD	8:i:138:VAL:HG23	2.46	0.45
10:k:76:VAL:HG22	15:p:72:VAL:CG2	2.47	0.45
10:k:87:LEU:HG	10:k:92:GLU:O	2.17	0.45
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.99	0.45
19:t:67:VAL:O	19:t:67:VAL:HG13	2.16	0.45
23:x:69:GLU:O	23:x:73:ARG:N	2.49	0.45
26:B:15:ARG:NH1	53:1:1264:A:OP1	2.50	0.45
30:F:25:VAL:HB	30:F:35:GLN:HG2	1.97	0.45
31:G:65:LYS:NZ	31:G:153:MET:HA	2.32	0.45
38:N:56:MET:SD	38:N:56:MET:C	3.00	0.45
41:Q:28:GLN:HA	41:Q:81:ILE:O	2.16	0.45
43:S:27:LYS:HD2	43:S:47:LEU:HD13	1.98	0.45
45:U:3:THR:OG1	45:U:4:ILE:N	2.50	0.45
52:3:939:G:H21	52:3:1375:A:H2	1.64	0.45
52:3:1415:G:H2'	52:3:1416:G:H8	1.82	0.45
53:1:182:A:O2'	53:1:183:C:H5'	2.17	0.45
53:1:854:C:H2'	53:1:855:G:C8	2.52	0.45
53:1:2185:U:H2'	53:1:2186:G:C8	2.52	0.45
53:1:2189:U:H2'	53:1:2190:G:H8	1.81	0.45
53:1:2739:U:O2'	53:1:2740:A:H5'	2.16	0.45
1:b:23:LEU:HD23	1:b:24:HIS:O	2.16	0.45
1:b:74:PRO:O	1:b:96:LYS:HG2	2.17	0.45
2:c:59:ARG:HH22	53:1:2830:C:H3'	1.82	0.45
6:g:84:ALA:HB1	6:g:90:LEU:HA	1.98	0.45
7:h:68:PRO:HA	7:h:72:LEU:HD23	1.99	0.45
16:q:93:ILE:O	16:q:97:ILE:HG13	2.16	0.45
17:r:54:VAL:CG2	17:r:55:ASP:H	2.27	0.45
28:D:3:ARG:HG3	28:D:4:THR:H	1.81	0.45
30:F:8:LYS:NZ	53:1:2467:C:OP1	2.43	0.45
31:G:66:ILE:HA	31:G:159:ALA:HB3	1.98	0.45
33:I:33:ILE:C	33:I:34:GLU:HG3	2.41	0.45
33:I:142:VAL:HG12	33:I:179:GLY:O	2.17	0.45
35:K:5:GLU:OE2	35:K:63:ASN:ND2	2.50	0.45
35:K:91:ARG:NH1	52:3:738:C:OP2	2.50	0.45
38:N:8:THR:OG1	38:N:9:GLY:N	2.41	0.45
40:P:125:LYS:HG2	40:P:126:ARG:N	2.32	0.45
45:U:43:ALA:O	45:U:44:SER:OG	2.29	0.45
51:a:169:GLY:C	51:a:170:ILE:HD12	2.41	0.45
52:3:1344:C:O2'	52:3:1345:U:H5'	2.17	0.45
53:1:890:C:C2'	53:1:891:G:H5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1748:C:H2'	53:1:1749:A:H8	1.82	0.45
53:1:2372:U:H2'	53:1:2373:G:C8	2.52	0.45
53:1:2841:C:H2'	53:1:2842:G:C8	2.51	0.45
1:b:23:LEU:HD11	1:b:82:TYR:CB	2.36	0.45
1:b:52:HIS:CE1	1:b:218:THR:HG23	2.52	0.45
12:m:42:THR:N	12:m:45:GLN:OE1	2.48	0.45
18:s:1:MET:HG2	18:s:62:ASP:OD2	2.17	0.45
23:x:31:ASN:HD22	23:x:52:ALA:HB2	1.80	0.45
33:I:28:ASP:O	33:I:30:LYS:N	2.49	0.45
36:L:32:ASP:OD1	52:3:1351:U:H5'	2.16	0.45
39:O:47:GLU:HB3	39:O:67:ILE:HB	1.99	0.45
41:Q:42:LYS:HG3	41:Q:44:PRO:HD2	1.99	0.45
44:T:50:HIS:ND1	52:3:667:G:H4'	2.32	0.45
44:T:68:TYR:HB2	52:3:754:C:H4'	1.98	0.45
45:U:54:LEU:HA	45:U:57:ILE:HD12	1.97	0.45
46:V:56:ASP:N	46:V:56:ASP:OD1	2.48	0.45
47:W:49:LYS:HE3	47:W:49:LYS:HB2	1.81	0.45
48:X:2:ARG:HE	52:3:1311:A:H62	1.65	0.45
48:X:40:PHE:HB2	48:X:43:MET:HE1	1.99	0.45
50:Z:64:ALA:HB1	50:Z:66:ARG:CZ	2.47	0.45
51:a:37:LYS:CB	53:1:2127:G:H5'	2.47	0.45
52:3:123:U:H2'	52:3:124:C:H6	1.81	0.45
52:3:1251:A:H2'	52:3:1252:A:C8	2.52	0.45
52:3:1304:G:H21	52:3:1333:A:H62	1.63	0.45
52:3:1456:A:H2'	52:3:1457:G:O4'	2.17	0.45
53:1:186:G:H2'	53:1:187:G:H8	1.82	0.45
53:1:941:A:H2'	53:1:942:G:O4'	2.17	0.45
53:1:1444:G:H2'	53:1:1445:G:C8	2.51	0.45
53:1:1535:A:H3'	53:1:1536:C:H5'	1.99	0.45
54:2:60:C:H2'	54:2:61:G:H8	1.81	0.45
1:b:97:ASP:HB3	53:1:1490:A:H8	1.82	0.44
9:j:113:PRO:HD2	53:1:558:U:OP2	2.17	0.44
11:l:49:GLY:HA3	11:l:58:TYR:HE1	1.82	0.44
18:s:83:LYS:HG2	18:s:95:ARG:NH1	2.31	0.44
20:u:96:LYS:O	20:u:98:ASN:N	2.50	0.44
21:v:17:SER:OG	21:v:21:ARG:NH2	2.50	0.44
23:x:6:VAL:HG23	23:x:50:VAL:HG12	2.00	0.44
25:z:7:THR:HG22	25:z:55:LYS:O	2.17	0.44
25:z:29:ARG:HD2	25:z:33:HIS:HE1	1.81	0.44
29:E:7:ARG:NH2	53:1:244:A:OP2	2.44	0.44
30:F:15:LYS:HE3	30:F:26:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:52:ALA:HB2	31:G:199:ILE:HD11	1.99	0.44
32:H:23:ALA:HB1	32:H:28:PHE:HA	1.98	0.44
33:I:158:LEU:HD11	33:I:174:ALA:HB1	1.98	0.44
36:L:36:SER:OG	36:L:37:THR:N	2.50	0.44
37:M:17:GLN:HE21	37:M:71:VAL:H	1.65	0.44
40:P:83:VAL:HB	40:P:109:ILE:HA	1.99	0.44
41:Q:4:ASN:HB3	52:3:880:C:OP2	2.17	0.44
41:Q:48:LEU:HD13	52:3:520:A:P	2.57	0.44
51:a:184:LYS:O	51:a:188:ASN:ND2	2.50	0.44
52:3:1199:U:H2'	52:3:1200:C:H5'	1.99	0.44
52:3:1460:C:H2'	52:3:1461:G:C8	2.52	0.44
53:1:821:A:H5''	53:1:822:G:H5'	1.94	0.44
53:1:2208:C:H2'	53:1:2209:G:C8	2.52	0.44
54:2:88:C:H5''	54:2:89:U:OP1	2.17	0.44
1:b:257:ARG:NH1	53:1:1799:G:OP1	2.51	0.44
7:h:36:ASP:O	7:h:39:THR:HG22	2.17	0.44
34:J:96:GLN:HA	34:J:97:PRO:HD2	1.80	0.44
43:S:81:ILE:HD12	43:S:81:ILE:N	2.32	0.44
52:3:225:C:H2'	52:3:226:G:H5''	2.00	0.44
52:3:600:A:H2'	52:3:601:G:C8	2.52	0.44
52:3:621:A:H2'	52:3:622:A:C8	2.52	0.44
52:3:785:G:O2'	52:3:786:G:H5'	2.18	0.44
52:3:902:G:H2'	52:3:903:G:C8	2.52	0.44
52:3:920:U:H2'	52:3:921:U:C6	2.52	0.44
52:3:1258:G:H2'	52:3:1259:C:C6	2.51	0.44
52:3:1352:C:H2'	52:3:1353:G:C8	2.51	0.44
53:1:1268:A:H2'	53:1:1269:A:O4'	2.16	0.44
53:1:1360:G:H2'	53:1:1361:G:H5'	2.00	0.44
53:1:2358:A:H2'	53:1:2359:C:O4'	2.18	0.44
53:1:2665:A:O2'	53:1:2666:C:H5'	2.17	0.44
53:1:2898:U:H2'	53:1:2899:A:C8	2.52	0.44
55:5:52:G:H1	55:5:62:C:H42	1.65	0.44
1:b:7:PRO:HB3	1:b:13:ARG:CB	2.47	0.44
7:h:62:ARG:NH2	53:1:1047:G:OP2	2.44	0.44
15:p:89:GLY:O	15:p:112:ARG:NH1	2.50	0.44
28:D:25:LYS:O	28:D:29:GLN:HG3	2.18	0.44
34:J:80:LEU:HG	34:J:122:VAL:HG11	1.99	0.44
41:Q:49:ARG:NE	41:Q:88:ASP:OD2	2.45	0.44
45:U:33:ILE:HD12	45:U:33:ILE:N	2.32	0.44
47:W:36:GLY:O	47:W:62:ARG:NH2	2.50	0.44
52:3:1139:G:H5''	52:3:1140:C:H5	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1171:A:H2'	52:3:1172:C:C6	2.52	0.44
53:1:589:U:H2'	53:1:590:A:C8	2.53	0.44
53:1:1105:U:C2'	53:1:1106:G:H5''	2.47	0.44
4:e:39:VAL:HG13	4:e:40:GLY:N	2.33	0.44
4:e:87:LYS:NZ	53:1:2314:A:P	2.90	0.44
4:e:129:MET:SD	4:e:130:GLY:N	2.90	0.44
15:p:91:VAL:HG21	15:p:96:LEU:CD2	2.47	0.44
19:t:56:GLU:HB2	19:t:86:THR:O	2.17	0.44
21:v:12:GLN:NE2	54:2:75:G:OP1	2.43	0.44
22:w:14:ALA:O	22:w:16:ARG:NH1	2.50	0.44
24:y:23:ARG:O	24:y:27:ASN:HB2	2.17	0.44
38:N:37:TYR:HD2	38:N:38:PHE:HD1	1.65	0.44
40:P:86:LYS:HE3	52:3:707:U:OP1	2.18	0.44
41:Q:53:ARG:NH1	52:3:1412:C:OP1	2.51	0.44
52:3:411:A:C4	52:3:413:G:H1'	2.52	0.44
52:3:537:G:H2'	52:3:538:G:C8	2.52	0.44
53:1:796:C:H2'	53:1:797:G:C8	2.51	0.44
53:1:1932:A:H2'	53:1:1933:G:O4'	2.17	0.44
53:1:2774:C:H2'	53:1:2775:G:O4'	2.18	0.44
3:d:130:LYS:HD3	53:1:321:U:OP2	2.17	0.44
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.82	0.44
8:i:76:ALA:HB1	8:i:135:MET:SD	2.57	0.44
22:w:70:PRO:HB3	54:2:12:C:C4	2.52	0.44
32:H:152:VAL:HB	32:H:156:LEU:HD21	1.98	0.44
35:K:13:ASP:O	35:K:16:GLU:OE2	2.35	0.44
35:K:39:LEU:HD12	35:K:39:LEU:HA	1.84	0.44
35:K:47:LEU:HB2	35:K:55:HIS:HB3	1.99	0.44
35:K:51:ILE:C	35:K:53:LYS:H	2.26	0.44
35:K:71:ILE:O	35:K:74:LEU:HB3	2.17	0.44
36:L:67:ASN:ND2	36:L:129:ASN:HD22	2.15	0.44
37:M:30:LYS:HB2	52:3:590:U:OP1	2.18	0.44
38:N:123:ARG:NH2	52:3:1343:G:H5''	2.32	0.44
41:Q:120:ARG:HH22	52:3:500:G:C5'	2.29	0.44
43:S:42:ASN:HA	43:S:45:LEU:CD2	2.48	0.44
43:S:63:CYS:O	43:S:67:GLY:HA2	2.18	0.44
51:a:163:TYR:HB3	51:a:173:THR:HG22	1.99	0.44
52:3:484:G:H4'	52:3:485:U:C5'	2.42	0.44
52:3:680:C:H2'	52:3:681:A:C8	2.52	0.44
53:1:819:A:C4	53:1:1189:A:C2	3.06	0.44
53:1:861:A:H2'	53:1:862:G:O4'	2.18	0.44
53:1:1071:G:OP1	53:1:1071:G:H3'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2182:U:H2'	53:1:2183:A:C8	2.52	0.44
55:5:19:G:H5'	55:5:20:U:H5	1.82	0.44
1:b:7:PRO:O	53:1:1695:G:H1'	2.17	0.44
1:b:164:VAL:HG21	1:b:180:MET:HE1	1.98	0.44
5:f:103:ASN:C	5:f:104:LEU:HD12	2.42	0.44
7:h:59:LEU:HB3	7:h:62:ARG:HB3	2.00	0.44
17:r:6:GLN:HG2	17:r:11:GLN:CD	2.43	0.44
17:r:74:ILE:HB	17:r:87:GLN:HB3	2.00	0.44
24:y:8:GLU:N	24:y:8:GLU:OE1	2.51	0.44
33:I:61:ARG:HH12	52:3:545:C:P	2.41	0.44
37:M:46:GLU:HB3	37:M:61:THR:OG1	2.17	0.44
39:O:32:THR:O	39:O:83:THR:OG1	2.33	0.44
42:R:102:LYS:HG3	52:3:1226:C:N4	2.33	0.44
43:S:7:ALA:HB1	52:3:994:A:O2'	2.17	0.44
46:V:70:LYS:HE2	46:V:70:LYS:HB3	1.83	0.44
49:Y:53:MET:HE2	49:Y:57:VAL:HG11	1.99	0.44
52:3:112:G:H4'	52:3:389:A:H4'	1.99	0.44
52:3:166:U:H2'	52:3:167:A:C8	2.52	0.44
52:3:505:G:P	52:3:535:A:H5'	2.58	0.44
52:3:629:A:H2'	52:3:630:A:O4'	2.18	0.44
52:3:868:C:H2'	52:3:869:G:O4'	2.18	0.44
52:3:1088:G:H21	52:3:1167:A:H61	1.64	0.44
53:1:598:U:H2'	53:1:599:A:H8	1.82	0.44
53:1:2655:G:O2'	53:1:2656:U:C5	2.69	0.44
55:5:36:U:H3	56:4:16:A:H61	1.65	0.44
1:b:65:ASP:OD1	1:b:101:ARG:NH1	2.50	0.44
3:d:149:ILE:HG21	3:d:188:MET:HG2	1.99	0.44
9:j:49:ASP:OD2	9:j:121:LYS:NZ	2.44	0.44
14:o:29:HIS:CD2	54:2:7:G:H5''	2.53	0.44
17:r:36:ALA:HA	17:r:58:VAL:HA	2.00	0.44
19:t:50:LEU:N	19:t:50:LEU:HD22	2.33	0.44
31:G:110:ILE:CG1	31:G:147:LEU:HD11	2.43	0.44
33:I:58:GLN:OE1	33:I:61:ARG:HD3	2.17	0.44
33:I:138:PRO:HB3	33:I:183:ARG:HA	1.99	0.44
37:M:33:VAL:O	37:M:37:ASN:ND2	2.51	0.44
39:O:55:PRO:HA	43:S:81:ILE:HG12	1.99	0.44
44:T:44:GLU:O	44:T:45:HIS:HB2	2.18	0.44
45:U:36:VAL:HG22	45:U:36:VAL:O	2.18	0.44
50:Z:32:ARG:HG3	50:Z:33:ARG:HG2	2.00	0.44
50:Z:59:LEU:C	50:Z:59:LEU:HD12	2.43	0.44
52:3:28:A:H2'	52:3:29:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:273:U:H2'	52:3:274:A:H5'	2.00	0.44
52:3:363:A:H2'	52:3:364:A:O4'	2.18	0.44
52:3:976:G:H22	52:3:1362:A:H2'	1.83	0.44
52:3:1128:C:O2'	52:3:1129:C:H5'	2.18	0.44
52:3:1356:G:H2'	52:3:1357:A:C8	2.52	0.44
53:1:729:G:H2'	53:1:1775:U:H1'	2.00	0.44
53:1:2121:G:H2'	53:1:2122:U:O4'	2.17	0.44
53:1:2591:C:H2'	53:1:2592:G:C8	2.53	0.44
54:2:3:C:H3'	54:2:4:C:C5'	2.48	0.44
57:7:69:G:H2'	57:7:70:G:C8	2.52	0.44
1:b:179:GLU:OE2	1:b:269:ARG:HA	2.17	0.44
4:e:87:LYS:NZ	53:1:2313:C:O3'	2.50	0.44
5:f:86:LEU:HD12	5:f:86:LEU:N	2.33	0.44
7:h:121:SER:OG	7:h:122:GLN:N	2.49	0.44
8:i:30:GLN:CD	8:i:30:GLN:H	2.25	0.44
10:k:109:SER:O	10:k:111:LYS:N	2.50	0.44
14:o:38:GLN:OE1	14:o:47:VAL:HG11	2.18	0.44
24:y:2:LYS:HZ2	53:1:102:U:H1'	1.82	0.44
31:G:166:ASP:OD1	31:G:189:ASN:ND2	2.50	0.44
36:L:94:ARG:NH1	52:3:1376:U:H5''	2.25	0.44
37:M:94:VAL:HG12	37:M:99:GLY:HA3	2.00	0.44
39:O:27:GLU:HA	39:O:30:LYS:HE3	2.00	0.44
42:R:15:VAL:O	42:R:19:THR:HG23	2.18	0.44
42:R:102:LYS:HD2	42:R:102:LYS:C	2.43	0.44
46:V:61:ARG:NH1	46:V:73:THR:OG1	2.51	0.44
48:X:41:PRO:O	48:X:44:ILE:HG13	2.18	0.44
52:3:206:C:H2'	52:3:207:C:O4'	2.17	0.44
52:3:428:G:H4'	52:3:429:U:O5'	2.18	0.44
52:3:922:G:H2'	52:3:923:A:C8	2.53	0.44
52:3:1245:C:H2'	52:3:1246:A:C8	2.52	0.44
53:1:84:A:N1	53:1:99:U:H5'	2.33	0.44
53:1:519:U:H2'	53:1:520:G:C8	2.53	0.44
53:1:1045:C:H5'	53:1:1046:A:H5''	2.00	0.44
53:1:1251:C:O2'	53:1:1252:G:H3'	2.17	0.44
53:1:1775:U:H2'	53:1:1776:G:O4'	2.18	0.44
53:1:1947:C:H2'	53:1:1948:G:C8	2.52	0.44
53:1:1955:U:C4	53:1:2552:U:H1'	2.53	0.44
54:2:95:U:H2'	54:2:96:G:C8	2.52	0.44
1:b:204:LEU:HB3	1:b:209:ALA:HB3	1.99	0.44
1:b:228:ASP:OD2	53:1:780:G:N1	2.38	0.44
4:e:107:VAL:HA	4:e:110:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:110:VAL:HG22	6:g:111:ALA:N	2.33	0.44
11:l:55:MET:HA	11:l:56:PRO:HD3	1.82	0.44
11:l:127:VAL:HG22	11:l:128:THR:N	2.33	0.44
12:m:50:ARG:O	12:m:54:THR:HG23	2.18	0.44
15:p:8:GLU:O	15:p:12:MET:HG3	2.18	0.44
31:G:101:THR:HG22	31:G:178:LEU:HD11	2.00	0.44
34:J:48:GLY:HA3	34:J:65:LYS:HB3	1.99	0.44
35:K:29:ILE:HG23	35:K:66:ALA:HB2	1.99	0.44
40:P:61:ALA:O	40:P:64:VAL:HG22	2.17	0.44
41:Q:4:ASN:ND2	52:3:880:C:OP1	2.51	0.44
44:T:3:SER:O	44:T:7:THR:HG23	2.18	0.44
47:W:41:SER:O	47:W:45:GLY:N	2.42	0.44
50:Z:57:LYS:HD2	50:Z:60:ALA:HB3	2.00	0.44
53:1:27:G:N2	53:1:512:G:H1'	2.33	0.44
53:1:1637:A:H2'	53:1:1638:C:C6	2.53	0.44
53:1:2060:A:O4'	53:1:2502:G:H1'	2.18	0.44
53:1:2318:G:H2'	53:1:2319:G:O4'	2.18	0.44
53:1:2861:U:H2'	53:1:2862:G:C8	2.53	0.44
55:5:73:A:N3	55:5:73:A:H2'	2.33	0.44
7:h:27:VAL:HG23	7:h:83:ALA:HB3	2.00	0.43
8:i:51:GLY:O	8:i:52:LEU:HD23	2.18	0.43
27:C:6:GLU:OE1	27:C:26:LYS:HB2	2.18	0.43
27:C:36:LYS:HE3	27:C:36:LYS:HB2	1.85	0.43
32:H:131:ARG:HG3	32:H:135:ARG:NH2	2.32	0.43
33:I:129:VAL:HA	52:3:619:U:O2	2.17	0.43
36:L:102:TRP:O	36:L:105:GLU:HG2	2.18	0.43
43:S:2:LYS:HD3	52:3:1049:U:H2'	2.00	0.43
52:3:79:G:O2'	52:3:80:A:H5'	2.18	0.43
52:3:193:C:H2'	52:3:194:C:C6	2.53	0.43
52:3:1064:G:H1'	52:3:1190:G:N2	2.33	0.43
52:3:1230:C:H5'	55:5:30:G:H5''	2.00	0.43
53:1:1909:C:H2'	53:1:1910:G:H8	1.82	0.43
53:1:2579:C:O2'	53:1:2580:U:H5'	2.17	0.43
3:d:151:GLY:HA3	3:d:191:ASP:OD2	2.17	0.43
7:h:31:ARG:HB3	7:h:109:LYS:HD2	1.99	0.43
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.18	0.43
7:h:66:GLY:HA2	7:h:69:PHE:HE2	1.83	0.43
10:k:31:ARG:N	10:k:31:ARG:HD2	2.33	0.43
13:n:72:ASP:HB3	13:n:75:ILE:HG12	2.00	0.43
19:t:33:LYS:HG2	19:t:80:TRP:HZ3	1.83	0.43
20:u:6:ARG:N	53:1:85:G:OP1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:52:PHE:CD2	54:2:83:G:H4'	2.52	0.43
29:E:43:LEU:HD21	53:1:2362:C:OP2	2.18	0.43
32:H:29:ALA:HA	32:H:32:LEU:HB3	1.99	0.43
33:I:144:ILE:HD11	33:I:149:LYS:HG3	2.00	0.43
34:J:10:LEU:HB3	34:J:12:GLU:OE1	2.18	0.43
34:J:15:ILE:HD12	34:J:15:ILE:N	2.33	0.43
38:N:106:ASP:O	38:N:108:ARG:N	2.50	0.43
41:Q:83:GLY:H	52:3:552:U:H4'	1.83	0.43
43:S:66:THR:HG22	52:3:1203:C:H4'	1.99	0.43
46:V:14:ASP:HA	46:V:20:ILE:HG13	1.98	0.43
52:3:769:G:O2'	52:3:770:C:H5'	2.17	0.43
52:3:1259:C:H3'	52:3:1260:G:C5'	2.47	0.43
52:3:1295:U:H2'	52:3:1296:C:C6	2.53	0.43
52:3:1502:A:H8	52:3:1505:G:H22	1.62	0.43
53:1:171:U:H2'	53:1:172:A:H8	1.83	0.43
53:1:1367:A:H2'	53:1:1368:G:H5'	2.00	0.43
53:1:1424:G:H2'	53:1:1425:G:O4'	2.18	0.43
53:1:1877:A:H2'	53:1:1878:G:O4'	2.18	0.43
53:1:2323:G:O2'	53:1:2324:U:H5'	2.18	0.43
2:c:2:ILE:HD13	2:c:90:PHE:CE2	2.52	0.43
4:e:28:PRO:HB2	4:e:168:LEU:HD11	2.01	0.43
5:f:6:ALA:HA	5:f:7:PRO:HD3	1.85	0.43
7:h:114:GLU:O	7:h:115:GLY:O	2.36	0.43
12:m:78:LEU:HD12	12:m:79:ALA:H	1.84	0.43
17:r:7:SER:OG	17:r:8:GLY:N	2.49	0.43
33:I:117:VAL:HG12	33:I:122:ILE:HD13	1.99	0.43
34:J:12:GLU:HG3	34:J:63:MET:CE	2.49	0.43
34:J:76:ASN:HB2	34:J:81:GLN:NE2	2.33	0.43
34:J:79:THR:OG1	34:J:80:LEU:N	2.51	0.43
37:M:86:LYS:HB3	37:M:90:GLU:HB3	1.99	0.43
50:Z:11:PHE:C	50:Z:12:ASP:OD1	2.61	0.43
52:3:76:G:H2'	52:3:77:A:O4'	2.18	0.43
52:3:757:U:H2'	52:3:758:C:O4'	2.18	0.43
52:3:837:U:H2'	52:3:838:G:H8	1.84	0.43
52:3:994:A:C4	52:3:1216:A:H4'	2.53	0.43
52:3:1038:C:H2'	52:3:1039:G:H8	1.82	0.43
52:3:1060:U:H2'	52:3:1061:G:H8	1.82	0.43
53:1:827:U:H4'	53:1:828:U:C5	2.53	0.43
53:1:996:A:H2'	53:1:997:G:H8	1.82	0.43
53:1:2053:G:O2'	53:1:2054:A:H5'	2.18	0.43
57:7:41:C:O2'	57:7:42:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:94:ILE:HG12	6:g:98:ASP:H	1.83	0.43
7:h:39:THR:HG23	7:h:40:GLU:OE1	2.18	0.43
7:h:94:ARG:HD3	7:h:94:ARG:N	2.33	0.43
7:h:97:LYS:O	7:h:101:LYS:HG2	2.19	0.43
8:i:88:GLY:HA3	53:1:1063:G:O2'	2.17	0.43
10:k:6:THR:O	10:k:20:MET:HA	2.17	0.43
10:k:26:GLY:O	10:k:30:ARG:HD2	2.18	0.43
18:s:81:SER:O	18:s:83:LYS:HD3	2.18	0.43
21:v:42:LEU:HD21	21:v:91:PHE:CE2	2.52	0.43
26:B:1:ALA:H3	53:1:2056:G:N2	2.16	0.43
28:D:44:VAL:HG13	28:D:44:VAL:O	2.19	0.43
31:G:2:THR:OG1	31:G:50:ASN:ND2	2.50	0.43
37:M:12:ARG:CZ	52:3:826:C:H5'	2.48	0.43
38:N:114:LYS:HD2	38:N:117:LEU:HD22	1.99	0.43
44:T:45:HIS:O	44:T:47:LYS:N	2.52	0.43
45:U:5:ARG:HA	45:U:68:SER:HB3	2.00	0.43
47:W:38:ILE:H	47:W:38:ILE:HD12	1.83	0.43
52:3:217:C:H2'	52:3:218:U:C6	2.53	0.43
52:3:1114:C:H2'	52:3:1115:U:O4'	2.19	0.43
53:1:1590:A:H2'	53:1:1591:A:H8	1.82	0.43
53:1:2267:A:H5''	53:1:2268:A:H5'	2.00	0.43
53:1:2655:G:HO2'	53:1:2656:U:H5	1.66	0.43
54:2:39:A:H2'	54:2:40:U:C6	2.53	0.43
3:d:147:LEU:HD13	3:d:168:ASP:HB3	2.01	0.43
4:e:15:LEU:HD23	4:e:18:GLU:HB2	2.01	0.43
4:e:151:LEU:HD12	4:e:151:LEU:C	2.43	0.43
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.49	0.43
8:i:4:VAL:O	8:i:4:VAL:HG13	2.18	0.43
15:p:29:VAL:HG13	15:p:79:VAL:O	2.19	0.43
18:s:18:ARG:NH2	53:1:517:C:O2'	2.48	0.43
29:E:42:HIS:HE1	53:1:2351:G:N7	2.16	0.43
31:G:46:VAL:N	31:G:47:PRO:HD2	2.34	0.43
31:G:82:ALA:HB2	31:G:213:LEU:HB2	2.00	0.43
33:I:144:ILE:HD11	33:I:177:MET:SD	2.58	0.43
35:K:54:LEU:HG	35:K:55:HIS:H	1.83	0.43
37:M:49:LYS:O	37:M:59:GLU:HG2	2.18	0.43
43:S:3:GLN:NE2	52:3:994:A:C2	2.85	0.43
43:S:82:LYS:NZ	52:3:1203:C:H1'	2.34	0.43
48:X:51:HIS:HB2	48:X:56:HIS:CD2	2.53	0.43
52:3:304:U:H2'	52:3:305:G:C8	2.53	0.43
52:3:781:A:OP1	52:3:1523:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:909:A:H2'	52:3:910:C:O4'	2.18	0.43
4:e:169:LEU:HD13	4:e:169:LEU:HA	1.88	0.43
24:y:17:GLU:HA	24:y:20:ASN:HD22	1.83	0.43
26:B:16:ARG:HA	26:B:19:ASP:OD2	2.17	0.43
27:C:29:LYS:NZ	53:1:2286:G:OP1	2.51	0.43
33:I:2:ARG:HH21	52:3:407:U:H5'	1.83	0.43
34:J:63:MET:O	34:J:67:ARG:HD3	2.19	0.43
35:K:30:THR:HA	35:K:34:GLY:O	2.19	0.43
35:K:38:ARG:NH2	35:K:40:GLU:OE1	2.43	0.43
39:O:59:LYS:HA	39:O:59:LYS:HD2	1.87	0.43
42:R:114:PRO:OXT	52:3:1228:C:H5''	2.18	0.43
52:3:389:A:H3'	52:3:390:U:H6	1.84	0.43
52:3:422:C:H5'	52:3:423:G:C2	2.53	0.43
53:1:784:G:H5'	53:1:785:G:OP1	2.18	0.43
53:1:1433:A:O2'	53:1:1434:A:H5'	2.18	0.43
53:1:1785:A:N1	53:1:1787:A:H1'	2.34	0.43
53:1:2190:G:N3	53:1:2191:A:H1'	2.33	0.43
53:1:2263:C:O2'	53:1:2264:C:H5'	2.19	0.43
53:1:2590:A:H2'	53:1:2591:C:C6	2.54	0.43
53:1:2626:C:O2'	53:1:2627:G:H5'	2.18	0.43
1:b:163:ILE:HG23	1:b:171:VAL:CG1	2.48	0.43
5:f:148:ARG:HA	5:f:161:VAL:CG1	2.48	0.43
9:j:36:LEU:O	9:j:51:GLY:HA3	2.19	0.43
13:n:56:LYS:NZ	13:n:88:ALA:HA	2.33	0.43
17:r:49:ILE:HB	17:r:51:VAL:O	2.18	0.43
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.82	0.43
25:z:10:ARG:HH21	25:z:10:ARG:HG3	1.83	0.43
25:z:29:ARG:HD2	25:z:33:HIS:CE1	2.54	0.43
31:G:69:VAL:HB	31:G:162:VAL:HG13	2.01	0.43
33:I:33:ILE:HG13	33:I:34:GLU:H	1.83	0.43
35:K:81:ASN:HB3	35:K:84:VAL:HG12	2.00	0.43
41:Q:82:ARG:CZ	52:3:552:U:H5'	2.48	0.43
43:S:3:GLN:HG3	52:3:1048:G:OP1	2.19	0.43
49:Y:80:ALA:HA	49:Y:83:ASN:ND2	2.32	0.43
51:a:186:LYS:O	51:a:189:LEU:HG	2.18	0.43
53:1:492:A:H2'	53:1:493:G:O4'	2.18	0.43
53:1:1239:G:H2'	53:1:1240:U:O4'	2.19	0.43
53:1:2345:G:H5'	53:1:2347:C:H5'	2.00	0.43
3:d:48:THR:C	3:d:50:ALA:H	2.26	0.43
5:f:8:VAL:HB	5:f:49:LEU:HB2	2.01	0.43
15:p:112:ARG:HD2	15:p:114:ASN:ND2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.52	0.43
31:G:22:TRP:HZ2	52:3:829:G:H4'	1.84	0.43
37:M:78:SER:HB2	37:M:84:ILE:HG12	2.01	0.43
41:Q:88:ASP:C	41:Q:89:LEU:HD12	2.43	0.43
42:R:9:PRO:HG2	42:R:44:ILE:HD11	2.00	0.43
43:S:92:ILE:N	43:S:92:ILE:HD12	2.33	0.43
52:3:1008:U:H2'	52:3:1009:U:O4'	2.18	0.43
52:3:1069:C:O2'	52:3:1192:C:H1'	2.18	0.43
52:3:1496:C:H2'	52:3:1497:G:O4'	2.19	0.43
53:1:155:A:H2'	53:1:156:A:C8	2.54	0.43
53:1:323:C:H2'	53:1:1205:A:N6	2.34	0.43
53:1:1026:G:H2'	53:1:1027:A:C8	2.53	0.43
53:1:2529:G:H5''	53:1:2530:A:H5''	2.00	0.43
57:7:26:A:H61	57:7:44:G:H1	1.67	0.43
6:g:38:PRO:O	6:g:43:ASN:ND2	2.52	0.43
6:g:97:ARG:HG3	6:g:112:LYS:HE2	2.00	0.43
10:k:63:VAL:HG12	10:k:107:LEU:CD1	2.49	0.43
12:m:45:GLN:H	12:m:45:GLN:HG3	1.67	0.43
23:x:11:PRO:HG3	23:x:30:PRO:HD2	2.00	0.43
29:E:6:VAL:HG23	29:E:6:VAL:O	2.18	0.43
40:P:78:ILE:H	40:P:78:ILE:HD12	1.83	0.43
47:W:38:ILE:HD12	47:W:38:ILE:N	2.34	0.43
48:X:2:ARG:HG3	52:3:1312:G:O6	2.19	0.43
49:Y:67:HIS:NE2	52:3:132:C:O3'	2.50	0.43
52:3:524:G:H2'	52:3:525:C:C6	2.54	0.43
52:3:1225:A:H2'	52:3:1225:A:N3	2.34	0.43
52:3:1538:C:H42	56:4:7:G:H1	1.67	0.43
53:1:690:G:H2'	53:1:691:C:C6	2.54	0.43
53:1:948:C:H2'	53:1:949:G:C8	2.53	0.43
53:1:1775:U:C2'	53:1:1776:G:H5'	2.49	0.43
53:1:2070:A:H2'	53:1:2071:A:O4'	2.18	0.43
53:1:2850:A:C2	53:1:2869:G:H4'	2.54	0.43
54:2:95:U:H2'	54:2:96:G:H8	1.83	0.43
55:5:41:C:H2'	55:5:42:G:C8	2.54	0.43
5:f:102:ILE:HD11	5:f:116:LEU:HD21	2.01	0.43
8:i:74:PRO:O	8:i:78:LEU:N	2.46	0.43
14:o:33:ARG:O	14:o:34:HIS:HB2	2.18	0.43
19:t:54:GLU:CG	19:t:88:LYS:HD2	2.49	0.43
30:F:3:VAL:O	30:F:3:VAL:HG13	2.18	0.43
31:G:6:ARG:HH12	31:G:10:LYS:HG3	1.84	0.43
33:I:8:LEU:C	33:I:8:LEU:HD12	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:10:LEU:CD2	33:I:62:ARG:HD2	2.41	0.43
36:L:6:ILE:H	36:L:6:ILE:HG13	1.63	0.43
40:P:48:GLY:O	40:P:68:ARG:NH1	2.52	0.43
40:P:126:ARG:NH1	52:3:692:U:H5''	2.34	0.43
49:Y:4:LYS:O	49:Y:7:LYS:HG2	2.19	0.43
52:3:335:C:H2'	52:3:336:A:C8	2.54	0.43
52:3:631:C:H3'	52:3:632:U:H5'	2.00	0.43
52:3:965:U:H1'	52:3:969:A:N3	2.33	0.43
52:3:1038:C:H2'	52:3:1039:G:C8	2.54	0.43
53:1:624:C:O2'	53:1:657:U:H5''	2.19	0.43
53:1:1695:G:H2'	53:1:1696:G:O4'	2.19	0.43
53:1:2360:G:H2'	53:1:2361:G:H5'	2.01	0.43
57:7:57:G:H2'	57:7:58:A:H5'	2.00	0.43
1:b:216:ARG:HG3	1:b:216:ARG:NH1	2.34	0.42
1:b:222:THR:HG23	53:1:1826:G:OP1	2.19	0.42
8:i:55:PRO:HB3	53:1:1061:U:C5	2.54	0.42
8:i:57:VAL:O	8:i:57:VAL:HG13	2.19	0.42
8:i:85:ILE:HD12	8:i:97:VAL:HG12	2.01	0.42
12:m:53:MET:HE1	12:m:103:TYR:CG	2.54	0.42
17:r:39:LEU:O	17:r:49:ILE:HG23	2.19	0.42
30:F:17:VAL:HG13	30:F:19:ARG:HG3	2.00	0.42
35:K:11:HIS:CG	35:K:12:PRO:HD2	2.54	0.42
35:K:22:ILE:HG13	35:K:23:GLU:N	2.34	0.42
40:P:70:ALA:O	40:P:73:VAL:HG22	2.19	0.42
44:T:35:ILE:HD11	44:T:59:VAL:HG22	1.99	0.42
50:Z:29:ALA:HA	50:Z:32:ARG:CZ	2.48	0.42
52:3:56:U:H2'	52:3:57:G:C8	2.53	0.42
52:3:545:C:O2'	52:3:549:C:H5''	2.19	0.42
52:3:736:C:H2'	52:3:737:C:C6	2.53	0.42
52:3:1118:U:H2'	52:3:1119:C:C6	2.53	0.42
52:3:1354:U:H2'	52:3:1355:G:C8	2.54	0.42
53:1:1105:U:H2'	53:1:1106:G:H5''	2.01	0.42
53:1:2376:A:H2'	53:1:2377:A:O4'	2.19	0.42
53:1:2818:U:H2'	53:1:2819:G:H8	1.84	0.42
54:2:48:U:H2'	54:2:49:C:C6	2.54	0.42
55:5:59:A:H2'	55:5:60:U:H5'	2.01	0.42
3:d:86:ALA:O	3:d:88:ARG:NH2	2.52	0.42
4:e:1:ALA:H1	4:e:97:GLU:HA	1.83	0.42
7:h:53:ARG:HD2	7:h:55:VAL:HG23	2.01	0.42
10:k:22:ILE:HD12	53:1:1952:A:C2	2.55	0.42
11:l:29:LYS:O	11:l:30:THR:OG1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:21:ALA:HB2	12:m:97:GLN:HB2	1.99	0.42
24:y:1:MET:HG3	24:y:4:LYS:HE2	2.00	0.42
32:H:131:ARG:HG3	32:H:135:ARG:HH21	1.83	0.42
41:Q:4:ASN:HB3	52:3:880:C:P	2.59	0.42
41:Q:26:CYS:SG	41:Q:29:LYS:HD3	2.59	0.42
41:Q:87:LYS:HE3	52:3:526:C:P	2.58	0.42
42:R:73:SER:O	42:R:76:ILE:HG22	2.19	0.42
42:R:90:HIS:HA	42:R:108:ARG:NH2	2.33	0.42
43:S:2:LYS:HD2	52:3:1048:G:H5''	1.99	0.42
43:S:89:ARG:HB2	43:S:91:GLU:HG2	2.01	0.42
52:3:59:A:H1'	52:3:354:G:N2	2.34	0.42
52:3:1195:C:H5''	52:3:1196:A:OP2	2.19	0.42
53:1:141:G:H3'	53:1:142:A:O4'	2.20	0.42
53:1:230:G:O2'	53:1:231:A:H5'	2.18	0.42
53:1:275:C:H3'	53:1:276:U:H5''	2.01	0.42
53:1:360:U:H2'	53:1:361:G:O4'	2.18	0.42
53:1:466:A:C2'	53:1:467:G:H5'	2.49	0.42
53:1:473:G:C2'	53:1:474:G:H5'	2.49	0.42
53:1:833:A:H2'	53:1:834:G:C8	2.55	0.42
53:1:1078:U:H4'	53:1:1079:C:H5''	2.00	0.42
53:1:1542:U:H2'	53:1:1543:G:O4'	2.19	0.42
53:1:2266:A:H4'	53:1:2267:A:C4	2.53	0.42
53:1:2860:A:H2'	53:1:2861:U:H5'	2.00	0.42
54:2:28:C:H2'	54:2:29:A:C8	2.54	0.42
1:b:211:ARG:HA	1:b:211:ARG:HD2	1.85	0.42
2:c:148:GLN:HB2	2:c:152:PRO:HG2	2.02	0.42
4:e:102:LEU:O	4:e:106:ALA:HB3	2.19	0.42
7:h:9:GLN:O	7:h:12:VAL:HG12	2.20	0.42
10:k:1:MET:N	10:k:65:THR:HG21	2.34	0.42
15:p:29:VAL:CG1	15:p:79:VAL:HG22	2.44	0.42
21:v:80:HIS:HE1	21:v:82:TYR:CE1	2.36	0.42
25:z:10:ARG:HB2	25:z:53:MET:HB2	2.01	0.42
33:I:2:ARG:NH1	52:3:406:G:H4'	2.34	0.42
33:I:109:THR:HG21	52:3:408:A:H5''	2.00	0.42
35:K:42:TRP:HE3	35:K:45:ARG:NH2	2.17	0.42
35:K:66:ALA:HB1	35:K:67:PRO:CD	2.43	0.42
38:N:98:ARG:HG3	38:N:103:VAL:HG21	2.00	0.42
38:N:128:LYS:CE	38:N:129:ARG:HH12	2.31	0.42
41:Q:86:VAL:HG21	41:Q:89:LEU:HD13	2.01	0.42
42:R:28:ARG:NH2	42:R:62:PHE:HB2	2.33	0.42
44:T:52:ARG:NH2	53:1:715:A:N1	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:69:ASN:HB3	52:3:263:A:OP1	2.19	0.42
51:a:4:LEU:HD23	51:a:4:LEU:H	1.84	0.42
52:3:458:U:H2'	52:3:459:A:C8	2.55	0.42
52:3:594:U:H2'	52:3:595:A:O4'	2.19	0.42
52:3:837:U:H2'	52:3:838:G:C8	2.54	0.42
53:1:18:U:H2'	53:1:19:A:C8	2.53	0.42
53:1:119:A:H4'	53:1:120:U:H5'	2.00	0.42
53:1:293:U:C2'	53:1:294:A:H5''	2.49	0.42
53:1:740:C:O2'	53:1:741:U:H5'	2.19	0.42
53:1:2619:C:O2'	53:1:2620:C:H5'	2.19	0.42
57:7:34:G:H2'	57:7:35:A:H8	1.82	0.42
57:7:50:U:H2'	57:7:51:U:O4'	2.20	0.42
1:b:200:MET:HB2	53:1:1820:U:C2	2.55	0.42
2:c:59:ARG:HA	2:c:59:ARG:HD2	1.87	0.42
4:e:63:LYS:O	54:2:42:C:C1'	2.52	0.42
4:e:84:ILE:CB	53:1:2312:U:H5'	2.50	0.42
5:f:40:VAL:O	5:f:54:ARG:NH2	2.52	0.42
7:h:69:PHE:HB2	7:h:70:GLU:OE1	2.20	0.42
7:h:103:ASN:HD22	7:h:103:ASN:HA	1.73	0.42
12:m:72:PRO:HD3	12:m:92:TRP:CZ3	2.55	0.42
13:n:2:ARG:O	13:n:2:ARG:NH1	2.53	0.42
16:q:24:TYR:CG	16:q:25:GLY:N	2.88	0.42
21:v:72:VAL:HG13	21:v:93:ARG:HA	2.01	0.42
24:y:44:LYS:HA	24:y:47:ARG:HH12	1.84	0.42
28:D:34:ARG:CZ	28:D:39:ARG:HD2	2.50	0.42
32:H:39:ARG:NH1	32:H:42:LEU:HD12	2.30	0.42
35:K:6:ILE:HB	35:K:62:MET:HB2	2.02	0.42
36:L:67:ASN:HD22	36:L:129:ASN:HD22	1.67	0.42
38:N:121:ARG:NH1	52:3:1345:U:H5''	2.35	0.42
39:O:56:HIS:CE1	39:O:57:VAL:HG13	2.54	0.42
40:P:12:ARG:N	40:P:12:ARG:HD2	2.34	0.42
51:a:186:LYS:HA	51:a:189:LEU:HG	2.00	0.42
52:3:312:C:H2'	52:3:313:A:C8	2.55	0.42
52:3:977:A:H3'	52:3:977:A:N3	2.35	0.42
53:1:323:C:H2'	53:1:1205:A:H61	1.85	0.42
53:1:1421:G:H1'	53:1:1494:A:H61	1.83	0.42
53:1:1670:C:H2'	53:1:1671:U:H5'	2.01	0.42
53:1:1948:G:O2'	53:1:1949:G:H5'	2.20	0.42
53:1:2542:A:H5''	53:1:2766:A:O2'	2.19	0.42
53:1:2724:U:H2'	53:1:2725:A:C8	2.54	0.42
1:b:259:ASN:C	1:b:261:ARG:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:21:TYR:OH	4:e:164:GLU:OE2	2.37	0.42
4:e:150:GLY:O	53:1:2305:U:N3	2.52	0.42
7:h:59:LEU:HD21	53:1:1047:G:C8	2.55	0.42
12:m:32:GLY:O	12:m:131:VAL:HG22	2.19	0.42
13:n:98:LEU:CD2	26:B:53:VAL:HG11	2.50	0.42
22:w:29:ALA:N	22:w:60:ASP:OD2	2.52	0.42
31:G:113:LEU:HA	31:G:116:LEU:HB3	2.00	0.42
32:H:126:ARG:HD2	32:H:126:ARG:N	2.35	0.42
33:I:131:ILE:HG22	33:I:133:SER:H	1.85	0.42
34:J:14:LEU:C	34:J:15:ILE:HD12	2.44	0.42
38:N:34:LEU:C	38:N:34:LEU:HD12	2.44	0.42
39:O:22:THR:HA	39:O:25:ILE:HG12	2.01	0.42
45:U:6:LEU:HD21	45:U:17:TYR:HB3	2.01	0.42
46:V:13:SER:H	46:V:21:VAL:HG13	1.83	0.42
52:3:150:U:H3	52:3:171:A:H62	1.68	0.42
52:3:439:U:O2	52:3:439:U:H2'	2.20	0.42
53:1:198:C:O2'	53:1:199:A:H5'	2.19	0.42
53:1:676:A:H62	53:1:802:A:N6	2.15	0.42
53:1:772:C:O2'	53:1:773:U:H5'	2.19	0.42
53:1:864:G:H2'	53:1:865:C:C6	2.54	0.42
53:1:1039:A:H2'	53:1:1040:A:C8	2.55	0.42
53:1:1123:C:H2'	53:1:1124:G:H8	1.84	0.42
53:1:2368:C:H2'	53:1:2369:A:C8	2.54	0.42
1:b:224:MET:HE2	53:1:782:A:C2	2.55	0.42
7:h:125:ARG:HD2	7:h:125:ARG:HA	1.95	0.42
8:i:36:GLU:HG3	8:i:66:PHE:CZ	2.55	0.42
10:k:69:VAL:HG22	10:k:70:ARG:H	1.84	0.42
16:q:24:TYR:HE2	53:1:2020:A:H4'	1.85	0.42
18:s:6:LYS:HB3	18:s:6:LYS:HE2	1.80	0.42
20:u:14:THR:HG23	53:1:310:A:H5''	2.00	0.42
26:B:24:VAL:HG23	26:B:25:THR:N	2.35	0.42
33:I:74:TYR:HD1	33:I:92:LEU:HD21	1.84	0.42
34:J:9:GLU:O	34:J:44:ARG:NH2	2.53	0.42
34:J:13:LYS:HZ2	34:J:116:VAL:HG11	1.85	0.42
35:K:53:LYS:HA	35:K:53:LYS:HE2	2.01	0.42
36:L:3:ARG:HH21	52:3:931:C:H5''	1.85	0.42
39:O:56:HIS:CG	39:O:57:VAL:H	2.38	0.42
40:P:91:GLY:C	40:P:93:GLU:N	2.78	0.42
41:Q:79:ILE:HD12	41:Q:96:THR:HB	2.02	0.42
45:U:78:VAL:O	45:U:79:ASN:O	2.36	0.42
48:X:5:LYS:NZ	48:X:6:LYS:HG2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Y:57:VAL:HG23	49:Y:58:ASP:N	2.35	0.42
50:Z:6:ARG:HB2	50:Z:6:ARG:HH11	1.84	0.42
51:a:161:VAL:HG12	51:a:162:ARG:N	2.35	0.42
52:3:701:U:C4'	52:3:703:G:H1'	2.48	0.42
52:3:788:U:H2'	52:3:789:U:O4'	2.19	0.42
52:3:881:G:O2'	52:3:882:C:H5'	2.20	0.42
52:3:918:A:H2'	52:3:919:A:O4'	2.19	0.42
52:3:1238:A:H2'	52:3:1239:A:H5'	2.01	0.42
52:3:1434:A:H2'	52:3:1435:G:O4'	2.19	0.42
53:1:633:A:H2'	53:1:634:C:H5'	2.01	0.42
53:1:2040:G:H2'	53:1:2041:U:O4'	2.20	0.42
53:1:2322:A:H2'	53:1:2323:G:O4'	2.19	0.42
54:2:63:C:H2'	54:2:64:G:C8	2.55	0.42
54:2:88:C:OP1	54:2:88:C:H3'	2.20	0.42
2:c:98:VAL:HG22	2:c:98:VAL:O	2.20	0.42
3:d:118:LEU:HD11	3:d:188:MET:SD	2.60	0.42
4:e:38:GLY:O	53:1:2307:G:N1	2.53	0.42
4:e:133:GLU:HB2	4:e:136:ILE:HG23	2.02	0.42
5:f:82:PHE:N	5:f:134:GLY:O	2.50	0.42
10:k:109:SER:C	10:k:110:GLU:HG3	2.44	0.42
17:r:39:LEU:HD12	17:r:49:ILE:HD13	2.02	0.42
20:u:40:LEU:HD21	20:u:61:GLU:OE2	2.20	0.42
21:v:9:ARG:HD3	21:v:39:ALA:HB1	2.01	0.42
33:I:56:GLU:OE2	33:I:198:LEU:HB2	2.20	0.42
34:J:135:VAL:O	34:J:139:THR:HG23	2.19	0.42
38:N:104:THR:HG22	52:3:1180:A:OP1	2.20	0.42
40:P:52:ARG:NH2	52:3:690:G:O6	2.53	0.42
48:X:49:ALA:CB	48:X:58:PRO:HG3	2.49	0.42
51:a:177:LYS:HB2	51:a:180:PHE:CD2	2.55	0.42
52:3:1510:C:H2'	52:3:1511:G:H8	1.84	0.42
53:1:445:C:O2'	53:1:446:G:H5'	2.20	0.42
53:1:1378:A:H1'	53:1:1379:U:C5	2.54	0.42
53:1:2217:G:O2'	53:1:2218:G:H5'	2.20	0.42
53:1:2581:G:H2'	53:1:2581:G:N3	2.35	0.42
1:b:184:GLU:OE1	1:b:185:ALA:N	2.53	0.42
1:b:201:LEU:HD21	52:3:773:G:O3'	2.19	0.42
1:b:227:VAL:HG12	53:1:2073:C:H5''	2.02	0.42
4:e:110:ILE:HB	4:e:113:PHE:HB2	2.02	0.42
8:i:89:SER:O	8:i:91:LYS:N	2.52	0.42
11:l:16:GLY:HA2	53:1:662:G:O3'	2.20	0.42
11:l:135:ILE:HG22	11:l:140:GLY:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:47:VAL:C	13:n:50:PRO:HD2	2.44	0.42
19:t:32:LEU:HD12	19:t:32:LEU:O	2.20	0.42
22:w:22:PHE:HD2	53:1:922:C:H1'	1.85	0.42
22:w:56:PHE:CZ	53:1:2365:G:H4'	2.55	0.42
34:J:55:VAL:N	34:J:56:PRO:HD2	2.35	0.42
36:L:73:GLU:O	36:L:88:VAL:N	2.53	0.42
41:Q:100:ALA:O	41:Q:101:LEU:C	2.62	0.42
51:a:66:PRO:HG2	51:a:67:HIS:CE1	2.54	0.42
51:a:200:LYS:NZ	51:a:208:TYR:HB2	2.35	0.42
52:3:132:C:O2'	52:3:133:U:H5'	2.19	0.42
52:3:422:C:H5''	52:3:423:G:O5'	2.20	0.42
52:3:449:G:H2'	52:3:450:G:O4'	2.20	0.42
52:3:717:U:H2'	52:3:734:G:OP2	2.19	0.42
52:3:764:C:H2'	52:3:765:G:O4'	2.20	0.42
52:3:886:G:H2'	52:3:887:G:H8	1.85	0.42
52:3:1125:U:H2'	52:3:1126:U:H2'	2.02	0.42
53:1:2537:U:H2'	53:1:2538:C:H6	1.82	0.42
53:1:2825:G:H2'	53:1:2826:A:H5'	2.01	0.42
54:2:118:C:H2'	54:2:119:A:C8	2.54	0.42
4:e:4:HIS:CD2	4:e:8:LYS:HE3	2.55	0.42
4:e:143:ASP:HB2	42:R:69:ARG:HD2	2.02	0.42
6:g:53:GLU:O	6:g:54:LEU:HD22	2.19	0.42
7:h:31:ARG:HD2	7:h:31:ARG:C	2.45	0.42
19:t:51:PHE:HE1	24:y:30:MET:HE2	1.84	0.42
24:y:28:LEU:HD13	24:y:42:LEU:HB3	2.02	0.42
28:D:25:LYS:CG	28:D:26:ASN:N	2.83	0.42
38:N:11:ARG:NH2	38:N:108:ARG:HH21	2.17	0.42
40:P:35:ASP:OD1	40:P:39:ASN:N	2.53	0.42
41:Q:80:LEU:HD12	41:Q:80:LEU:HA	1.91	0.42
45:U:70:ARG:CD	52:3:452:A:H1'	2.50	0.42
51:a:3:LYS:HD2	53:1:2108:A:OP2	2.20	0.42
52:3:601:G:H2'	52:3:602:A:C8	2.55	0.42
52:3:672:U:H2'	52:3:673:A:H8	1.84	0.42
52:3:960:U:O2'	52:3:1223:C:H4'	2.20	0.42
52:3:1526:G:H2'	52:3:1527:U:C6	2.54	0.42
53:1:435:C:C2'	53:1:436:C:H5'	2.48	0.42
53:1:2677:G:H2'	53:1:2678:C:C6	2.54	0.42
3:d:40:ARG:HD2	53:1:443:A:C5	2.55	0.42
16:q:5:ARG:NH1	53:1:585:G:N7	2.62	0.42
35:K:18:VAL:HG21	35:K:58:HIS:CD2	2.54	0.42
39:O:18:ILE:O	39:O:22:THR:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:802:A:H2'	52:3:803:G:O4'	2.20	0.42
52:3:1299:A:H2'	52:3:1300:G:H4'	2.01	0.42
53:1:621:A:H2'	53:1:622:G:H5'	2.02	0.42
53:1:759:G:H2'	53:1:760:G:H8	1.85	0.42
53:1:1601:G:O2'	53:1:1602:U:H5'	2.19	0.42
53:1:2586:U:H2'	53:1:2587:A:C8	2.54	0.42
53:1:2632:A:O2'	53:1:2633:G:H5'	2.19	0.42
55:5:42:G:H2'	55:5:43:A:O4'	2.20	0.42
3:d:118:LEU:HD12	3:d:186:VAL:O	2.20	0.41
4:e:103:ILE:HG21	4:e:174:PHE:HE1	1.85	0.41
6:g:27:ARG:HE	23:x:55:MET:HE2	1.84	0.41
7:h:114:GLU:O	7:h:122:GLN:C	2.63	0.41
19:t:55:VAL:HG12	19:t:87:LEU:HD23	2.02	0.41
23:x:9:LYS:CE	23:x:53:LYS:HE2	2.50	0.41
25:z:30:ARG:NH1	53:1:1184:U:OP2	2.53	0.41
31:G:128:LEU:HD23	31:G:136:ARG:HH12	1.85	0.41
34:J:165:GLY:O	37:M:113:ARG:NH1	2.52	0.41
36:L:25:PHE:CD1	36:L:28:ILE:HD11	2.55	0.41
37:M:29:SER:HB3	37:M:32:LYS:CD	2.50	0.41
41:Q:87:LYS:HE2	52:3:913:A:OP2	2.20	0.41
48:X:66:VAL:HG23	48:X:67:GLY:N	2.35	0.41
49:Y:81:GLN:O	49:Y:84:LYS:HB3	2.20	0.41
52:3:886:G:H2'	52:3:887:G:C8	2.54	0.41
52:3:1195:C:H2'	52:3:1197:A:O4'	2.20	0.41
52:3:1332:A:H2'	52:3:1333:A:C8	2.56	0.41
52:3:1486:G:H2'	52:3:1487:G:C8	2.55	0.41
53:1:281:C:H42	53:1:359:G:H1	1.68	0.41
53:1:715:A:H2'	53:1:716:A:C8	2.54	0.41
53:1:903:C:H2'	53:1:904:G:C8	2.55	0.41
53:1:905:A:O2'	53:1:906:U:H5'	2.20	0.41
53:1:1182:G:H2'	53:1:1183:U:O4'	2.19	0.41
53:1:1300:G:H4'	53:1:1301:A:H5'	2.00	0.41
53:1:1667:G:H22	53:1:1992:G:H5'	1.84	0.41
53:1:1745:A:H2'	53:1:1746:A:H8	1.85	0.41
53:1:2421:G:H2'	55:5:76:A:H62	1.85	0.41
53:1:2644:G:H3'	53:1:2645:G:N2	2.34	0.41
53:1:2686:G:H2'	53:1:2687:U:C6	2.55	0.41
1:b:81:GLU:HG3	1:b:102:TYR:HE1	1.85	0.41
1:b:229:HIS:HA	1:b:230:PRO:HD3	1.97	0.41
1:b:231:HIS:CG	1:b:239:PHE:HE1	2.38	0.41
4:e:87:LYS:HZ2	53:1:2314:A:P	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:120:SER:HA	53:1:2303:G:H4'	2.02	0.41
6:g:2:GLN:O	6:g:39:ALA:HB2	2.20	0.41
13:n:64:ARG:O	13:n:67:PHE:HB3	2.20	0.41
14:o:81:ARG:H	14:o:81:ARG:HG2	1.71	0.41
16:q:111:LYS:HG2	17:r:48:LYS:HD2	2.02	0.41
18:s:41:LYS:O	18:s:44:ALA:HB3	2.20	0.41
24:y:16:THR:HA	24:y:19:LEU:HD12	2.02	0.41
26:B:2:VAL:HG22	26:B:3:GLN:N	2.35	0.41
42:R:40:GLU:H	42:R:40:GLU:HG2	1.67	0.41
43:S:10:VAL:O	43:S:13:VAL:HG12	2.20	0.41
48:X:8:PRO:HB3	48:X:38:THR:HG21	2.01	0.41
52:3:225:C:C3'	52:3:226:G:H5''	2.50	0.41
52:3:759:A:H2'	52:3:760:G:H5'	2.01	0.41
53:1:281:C:N4	53:1:359:G:H1	2.18	0.41
53:1:368:A:C2'	53:1:369:U:H5'	2.50	0.41
53:1:713:G:N2	53:1:718:A:H62	2.10	0.41
53:1:745:G:O2'	53:1:748:G:H1'	2.20	0.41
53:1:1127:A:H2'	53:1:1128:G:H5''	2.01	0.41
53:1:1351:C:H2'	53:1:1352:U:C6	2.55	0.41
53:1:2123:G:H2'	53:1:2124:G:C8	2.55	0.41
53:1:2584:U:H2'	53:1:2585:U:H2'	2.01	0.41
53:1:2644:G:H3'	53:1:2645:G:H21	1.84	0.41
55:5:62:C:H2'	55:5:63:G:C5'	2.34	0.41
3:d:47:LYS:HB3	3:d:51:GLU:HG2	2.01	0.41
8:i:91:LYS:NZ	53:1:1076:C:O5'	2.53	0.41
9:j:9:GLU:OE2	53:1:539:G:H5'	2.20	0.41
14:o:82:ALA:HB1	14:o:87:ILE:HB	2.02	0.41
17:r:53:PHE:O	17:r:54:VAL:C	2.63	0.41
33:I:11:SER:O	33:I:15:GLY:N	2.53	0.41
33:I:114:ARG:HA	33:I:117:VAL:HG22	2.02	0.41
34:J:60:GLN:HA	34:J:63:MET:HG2	2.02	0.41
34:J:131:ASN:HD22	34:J:134:ASN:H	1.69	0.41
35:K:18:VAL:HB	35:K:19:PRO:HD3	2.02	0.41
39:O:17:LEU:HD13	39:O:17:LEU:HA	1.95	0.41
44:T:52:ARG:NH2	53:1:715:A:C6	2.88	0.41
52:3:501:C:H1'	52:3:549:C:O2'	2.20	0.41
52:3:789:U:H2'	52:3:791:G:OP2	2.21	0.41
52:3:790:A:H5'	55:5:39:C:OP1	2.19	0.41
52:3:1293:C:H2'	52:3:1294:G:C8	2.55	0.41
52:3:1315:U:H2'	52:3:1316:G:O4'	2.20	0.41
52:3:1332:A:H2'	52:3:1333:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1485:U:H2'	52:3:1486:G:C8	2.56	0.41
53:1:1447:C:H2'	53:1:1448:G:H8	1.85	0.41
53:1:1611:C:H6	53:1:1611:C:H5'	1.85	0.41
53:1:1775:U:H2'	53:1:1776:G:H5'	2.02	0.41
53:1:2590:A:H2'	53:1:2591:C:H6	1.85	0.41
53:1:2630:G:H2'	53:1:2631:G:H8	1.86	0.41
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.85	0.41
6:g:122:LEU:HD13	6:g:122:LEU:HA	1.96	0.41
7:h:123:ILE:HG23	7:h:123:ILE:O	2.19	0.41
11:l:29:LYS:HE2	53:1:566:U:H5''	2.01	0.41
12:m:74:THR:HG21	12:m:86:LYS:HD2	2.01	0.41
13:n:9:GLN:HE21	53:1:2002:G:C5'	2.34	0.41
16:q:91:ARG:O	16:q:92:LYS:C	2.63	0.41
17:r:4:VAL:O	17:r:39:LEU:N	2.43	0.41
32:H:14:VAL:HG23	32:H:15:LYS:H	1.85	0.41
33:I:80:ARG:NH2	52:3:614:C:OP2	2.52	0.41
36:L:2:ARG:HD3	52:3:1380:U:C4	2.56	0.41
39:O:53:ILE:CG1	52:3:1060:U:H5''	2.48	0.41
44:T:42:PHE:CB	53:1:715:A:H1'	2.50	0.41
45:U:22:ALA:HA	45:U:33:ILE:HD12	2.01	0.41
51:a:54:LYS:HB2	51:a:57:GLN:HE21	1.84	0.41
52:3:138:G:H2'	52:3:139:A:C8	2.55	0.41
52:3:406:G:O2'	52:3:407:U:H5'	2.19	0.41
52:3:632:U:H3'	52:3:633:G:H5'	2.01	0.41
52:3:765:G:H3'	52:3:812:G:H22	1.85	0.41
52:3:1435:G:H2'	52:3:1436:U:C6	2.55	0.41
52:3:1488:G:H2'	52:3:1489:G:C8	2.55	0.41
53:1:760:G:C2'	53:1:761:A:H5'	2.51	0.41
53:1:765:C:H2'	53:1:766:U:H6	1.85	0.41
53:1:1093:G:H21	53:1:1098:A:H62	1.68	0.41
53:1:1549:A:H2'	53:1:1550:C:C6	2.55	0.41
53:1:1642:G:O2'	53:1:1643:G:H5'	2.20	0.41
53:1:1827:U:H2'	53:1:1828:G:O4'	2.20	0.41
53:1:1846:G:H2'	53:1:1847:A:O4'	2.21	0.41
53:1:1972:G:H2'	53:1:1973:G:C8	2.56	0.41
53:1:2818:U:H2'	53:1:2819:G:C8	2.56	0.41
53:1:2841:C:H2'	53:1:2842:G:H8	1.85	0.41
1:b:13:ARG:NH1	53:1:1693:U:O2	2.54	0.41
1:b:42:ARG:N	1:b:42:ARG:HD2	2.35	0.41
2:c:129:THR:HG22	53:1:1997:C:P	2.61	0.41
3:d:44:ARG:NH2	53:1:1248:G:OP1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:129:PRO:O	53:1:321:U:H5'	2.21	0.41
4:e:35:LEU:N	4:e:88:VAL:O	2.51	0.41
8:i:23:VAL:HG13	8:i:26:ALA:HB3	2.01	0.41
9:j:81:ILE:HG23	9:j:82:GLY:N	2.35	0.41
11:l:42:SER:OG	53:1:672:C:H5	2.04	0.41
12:m:69:PRO:O	12:m:70:ASP:CG	2.64	0.41
23:x:13:THR:HG21	53:1:188:G:H5'	2.02	0.41
30:F:1:MET:HB3	30:F:34:LYS:HE3	2.01	0.41
33:I:190:LEU:HD12	33:I:192:ALA:N	2.14	0.41
36:L:133:ALA:O	36:L:136:LYS:HG2	2.20	0.41
40:P:119:GLY:HA2	52:3:716:A:N3	2.35	0.41
44:T:26:VAL:O	44:T:30:LEU:N	2.52	0.41
47:W:43:ILE:HG13	47:W:44:THR:HG23	2.02	0.41
49:Y:9:ARG:NE	49:Y:12:GLN:OE1	2.53	0.41
52:3:197:A:C6	52:3:221:C:H4'	2.56	0.41
52:3:488:C:O2'	52:3:489:C:H5'	2.19	0.41
52:3:1248:A:O2'	52:3:1249:C:H5'	2.20	0.41
52:3:1499:A:O2'	52:3:1500:A:H5'	2.20	0.41
52:3:1502:A:H5'	52:3:1504:G:N7	2.36	0.41
53:1:171:U:H2'	53:1:172:A:C8	2.55	0.41
53:1:779:U:H2'	53:1:780:G:H8	1.85	0.41
53:1:833:A:H2'	53:1:834:G:H8	1.85	0.41
53:1:940:G:H2'	53:1:941:A:C4'	2.51	0.41
53:1:2114:A:N6	53:1:2117:A:H62	2.15	0.41
53:1:2245:U:H5''	53:1:2246:G:H5'	2.03	0.41
53:1:2732:G:O2'	53:1:2733:A:H5'	2.21	0.41
53:1:2751:G:O2'	53:1:2752:C:H5'	2.19	0.41
5:f:93:TYR:CD1	5:f:106:LEU:HA	2.55	0.41
5:f:95:ALA:N	5:f:127:GLN:O	2.50	0.41
6:g:55:GLU:OE1	6:g:58:LEU:HD21	2.21	0.41
7:h:55:VAL:HA	53:1:1084:A:C5'	2.51	0.41
12:m:76:LYS:HA	12:m:76:LYS:HD2	1.93	0.41
13:n:6:SER:OG	13:n:46:ARG:NH2	2.54	0.41
13:n:92:GLY:O	53:1:2880:C:H1'	2.21	0.41
33:I:33:ILE:O	33:I:34:GLU:HG3	2.20	0.41
33:I:182:LYS:HB2	33:I:182:LYS:HE3	1.85	0.41
36:L:92:PRO:HA	36:L:95:ARG:CD	2.51	0.41
39:O:33:GLY:HA2	39:O:83:THR:HG21	2.02	0.41
39:O:46:LYS:HG2	39:O:68:ARG:HG2	2.02	0.41
46:V:17:GLU:O	46:V:18:LYS:HB2	2.20	0.41
52:3:51:A:H4'	52:3:52:C:C5'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:159:G:H1'	52:3:162:A:N6	2.36	0.41
52:3:959:A:H2'	52:3:960:U:C4'	2.47	0.41
52:3:1063:C:H2'	52:3:1064:G:C8	2.56	0.41
52:3:1167:A:H2'	52:3:1167:A:N3	2.36	0.41
53:1:69:C:H2'	53:1:70:G:C8	2.55	0.41
53:1:644:A:H61	53:1:2349:G:H21	1.67	0.41
53:1:704:G:H2'	53:1:726:G:H22	1.85	0.41
53:1:1066:U:H2'	53:1:1068:G:OP2	2.20	0.41
53:1:1316:U:H2'	53:1:1317:G:H8	1.86	0.41
53:1:2283:C:H2'	53:1:2284:A:O4'	2.20	0.41
53:1:2842:G:O2'	53:1:2843:G:H5'	2.21	0.41
54:2:60:C:H2'	54:2:61:G:C8	2.56	0.41
54:2:63:C:H2'	54:2:64:G:H8	1.86	0.41
1:b:70:LYS:HE3	1:b:73:ILE:HD12	2.02	0.41
1:b:176:ARG:HG2	53:1:1819:A:H3'	2.02	0.41
4:e:15:LEU:HA	4:e:18:GLU:HB2	2.01	0.41
4:e:33:ILE:CD1	4:e:95:MET:HE3	2.49	0.41
6:g:90:LEU:HD11	6:g:146:VAL:HG11	2.01	0.41
8:i:78:LEU:HA	8:i:81:LYS:HE3	2.03	0.41
10:k:76:VAL:H	15:p:72:VAL:HG22	1.85	0.41
18:s:7:HIS:CD2	18:s:10:ALA:HB2	2.56	0.41
34:J:53:ARG:HD3	34:J:53:ARG:HA	1.89	0.41
38:N:114:LYS:HE3	38:N:120:ALA:O	2.20	0.41
39:O:41:PRO:HG2	52:3:1150:A:N3	2.35	0.41
46:V:77:VAL:HG13	46:V:77:VAL:O	2.21	0.41
52:3:160:A:H2'	52:3:161:A:O4'	2.19	0.41
52:3:952:U:H2'	52:3:953:G:H8	1.86	0.41
52:3:1193:G:O2'	52:3:1194:U:H5'	2.21	0.41
52:3:1403:C:H6	52:3:1403:C:O5'	2.03	0.41
53:1:490:C:H4'	53:1:491:G:OP2	2.21	0.41
53:1:720:U:H2'	53:1:721:A:H8	1.86	0.41
53:1:950:G:H2'	53:1:951:C:C6	2.56	0.41
53:1:1169:A:H2'	53:1:1170:C:O4'	2.20	0.41
53:1:2126:A:H2'	53:1:2162:G:N2	2.36	0.41
53:1:2174:C:O2'	53:1:2175:C:H5'	2.20	0.41
53:1:2443:C:H2'	53:1:2444:G:C8	2.55	0.41
54:2:114:C:H2'	54:2:115:A:C8	2.56	0.41
2:c:45:TYR:HB2	2:c:83:ARG:HH11	1.85	0.41
4:e:63:LYS:NZ	54:2:42:C:OP2	2.52	0.41
8:i:96:LYS:HE3	8:i:138:VAL:HG11	2.03	0.41
11:l:85:VAL:HG23	11:l:86:GLU:N	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:30:SER:HA	12:m:133:LYS:HB2	2.03	0.41
18:s:93:ALA:HB2	53:1:1614:A:N1	2.36	0.41
29:E:6:VAL:HG21	29:E:60:CYS:HB2	2.01	0.41
31:G:220:VAL:HG13	31:G:221:ARG:N	2.36	0.41
32:H:70:ALA:HB2	32:H:114:LEU:HD13	2.02	0.41
39:O:12:ALA:HB3	39:O:18:ILE:CG2	2.50	0.41
39:O:44:THR:HG21	39:O:68:ARG:HB3	2.02	0.41
40:P:66:ALA:HB3	40:P:98:ALA:CB	2.51	0.41
42:R:32:ILE:HD13	42:R:58:GLU:HG3	2.02	0.41
46:V:57:VAL:HG12	46:V:58:VAL:N	2.36	0.41
47:W:62:ARG:HH11	52:3:718:A:N6	2.18	0.41
48:X:25:GLY:O	48:X:27:LYS:N	2.54	0.41
52:3:58:C:O2'	52:3:59:A:H5'	2.21	0.41
52:3:243:A:C2	52:3:245:U:H2'	2.56	0.41
52:3:751:U:C2'	52:3:752:G:H5'	2.51	0.41
52:3:1245:C:H2'	52:3:1246:A:H8	1.84	0.41
53:1:691:C:O2'	53:1:692:C:H5'	2.20	0.41
53:1:768:G:H22	53:1:1379:U:H1'	1.86	0.41
53:1:1258:U:H2'	53:1:1259:G:H8	1.85	0.41
53:1:1773:A:N7	53:1:1829:A:H1'	2.36	0.41
53:1:1862:G:O2'	53:1:1863:G:H5'	2.21	0.41
54:2:78:A:H2'	54:2:79:G:O4'	2.20	0.41
1:b:52:HIS:CD2	53:1:1824:G:OP2	2.74	0.41
1:b:229:HIS:C	1:b:231:HIS:N	2.79	0.41
4:e:47:LYS:HB2	4:e:47:LYS:HE3	1.88	0.41
5:f:88:LEU:HD23	5:f:93:TYR:HB3	2.03	0.41
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.88	0.41
12:m:30:SER:O	12:m:133:LYS:N	2.53	0.41
13:n:56:LYS:HZ2	13:n:88:ALA:HA	1.86	0.41
14:o:40:ILE:HD13	54:2:8:C:O2'	2.21	0.41
15:p:50:ARG:NH1	53:1:2684:U:OP2	2.54	0.41
16:q:34:ALA:O	16:q:38:VAL:HG23	2.21	0.41
16:q:55:GLN:NE2	53:1:559:G:N3	2.69	0.41
18:s:74:ILE:HA	18:s:104:THR:O	2.21	0.41
20:u:31:GLY:O	20:u:66:VAL:HG13	2.21	0.41
30:F:36:ARG:HD2	53:1:2742:G:OP1	2.20	0.41
32:H:71:ARG:HA	32:H:72:PRO:HD2	1.96	0.41
33:I:80:ARG:HH22	52:3:614:C:P	2.44	0.41
33:I:98:ASP:OD1	33:I:98:ASP:N	2.52	0.41
36:L:35:LYS:HB2	52:3:1373:G:C5'	2.50	0.41
38:N:67:LYS:HA	38:N:67:LYS:HD3	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:85:ARG:HA	41:Q:93:ARG:HA	2.02	0.41
42:R:26:LYS:HE2	42:R:30:LYS:HZ1	1.86	0.41
43:S:97:LYS:HE2	52:3:1188:A:O3'	2.21	0.41
48:X:7:GLY:HA2	48:X:8:PRO:HD3	1.84	0.41
48:X:68:HIS:HB3	48:X:69:LYS:H	1.77	0.41
49:Y:34:VAL:HG11	49:Y:78:LEU:HD21	2.02	0.41
49:Y:78:LEU:HD12	49:Y:78:LEU:HA	1.88	0.41
50:Z:6:ARG:CB	50:Z:6:ARG:NH1	2.84	0.41
50:Z:66:ARG:HG3	52:3:1099:G:H1'	2.02	0.41
51:a:7:ARG:O	51:a:11:ILE:HG13	2.21	0.41
52:3:151:A:H2'	52:3:152:A:O4'	2.20	0.41
52:3:300:A:H2'	52:3:301:G:O4'	2.21	0.41
52:3:974:A:C5'	52:3:975:A:H3'	2.50	0.41
52:3:1235:U:O2'	52:3:1305:G:H5'	2.21	0.41
52:3:1238:A:C2'	52:3:1239:A:H5'	2.51	0.41
52:3:1376:U:H2'	52:3:1377:A:H8	1.84	0.41
53:1:118:A:OP2	53:1:119:A:H5''	2.21	0.41
53:1:146:A:H2'	53:1:147:C:C6	2.56	0.41
53:1:616:A:H2'	53:1:617:G:O4'	2.20	0.41
53:1:813:U:H2'	53:1:814:C:C6	2.56	0.41
53:1:1739:A:H2'	53:1:1740:G:O4'	2.21	0.41
53:1:2078:C:O2'	53:1:2079:U:H5'	2.21	0.41
53:1:2352:A:H2'	53:1:2353:G:H5'	2.02	0.41
53:1:2689:U:O2	53:1:2713:U:H5''	2.20	0.41
53:1:2714:G:O2'	53:1:2715:C:H5'	2.21	0.41
1:b:6:LYS:O	1:b:8:THR:HG23	2.21	0.41
2:c:83:ARG:NH2	53:1:2637:U:H5''	2.36	0.41
3:d:50:ALA:HB2	53:1:801:G:C8	2.56	0.41
3:d:130:LYS:HA	53:1:321:U:OP2	2.20	0.41
3:d:142:ALA:O	3:d:143:LEU:HD23	2.21	0.41
4:e:2:LYS:HG3	4:e:3:LEU:N	2.35	0.41
6:g:27:ARG:NE	23:x:55:MET:HE2	2.35	0.41
6:g:96:THR:HA	6:g:99:ILE:HD12	2.03	0.41
10:k:107:LEU:O	10:k:109:SER:N	2.54	0.41
20:u:88:ASP:HB3	20:u:90:LYS:HG2	2.03	0.41
33:I:202:LEU:HD12	33:I:203:TYR:CD2	2.56	0.41
34:J:161:GLU:O	34:J:164:LEU:HD23	2.21	0.41
38:N:82:ILE:O	38:N:86:LEU:HG	2.20	0.41
38:N:112:ARG:HH12	38:N:114:LYS:HA	1.85	0.41
52:3:582:C:H2'	52:3:583:A:C8	2.56	0.41
52:3:924:C:H2'	52:3:925:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1113:C:H2'	52:3:1114:C:C6	2.55	0.41
52:3:1338:G:H1'	55:5:42:G:H5'	2.03	0.41
52:3:1347:G:O2'	52:3:1348:U:H5	2.04	0.41
52:3:1524:C:H2'	52:3:1525:G:C8	2.56	0.41
53:1:11:C:H2'	53:1:12:U:H5''	2.02	0.41
53:1:862:G:H2'	53:1:863:A:O4'	2.20	0.41
53:1:1690:A:H2'	53:1:1691:C:O4'	2.21	0.41
53:1:2723:C:H2'	53:1:2724:U:O4'	2.21	0.41
57:7:25:C:H2'	57:7:26:A:C8	2.56	0.41
1:b:48:ILE:HG23	1:b:48:ILE:O	2.21	0.40
1:b:149:LYS:HD3	53:1:2204:G:H4'	2.03	0.40
5:f:95:ALA:HA	5:f:103:ASN:O	2.21	0.40
12:m:40:ARG:NH1	53:1:958:U:OP1	2.51	0.40
23:x:16:ASN:HB3	23:x:24:THR:OG1	2.21	0.40
31:G:72:LYS:HD3	31:G:73:ARG:N	2.36	0.40
35:K:10:VAL:CG2	35:K:58:HIS:HB3	2.47	0.40
38:N:17:ARG:CZ	52:3:1129:C:H4'	2.50	0.40
42:R:18:LEU:HD23	42:R:18:LEU:O	2.22	0.40
52:3:1305:G:H22	52:3:1331:G:H2'	1.87	0.40
52:3:1540:U:O2	52:3:1540:U:H3'	2.22	0.40
53:1:1657:U:H2'	53:1:1658:C:H6	1.86	0.40
53:1:1917:U:C2'	53:1:1918:A:H5'	2.51	0.40
53:1:2484:G:O2'	53:1:2485:G:H5'	2.21	0.40
55:5:19:G:H5'	55:5:20:U:C5	2.56	0.40
2:c:202:ILE:HD12	2:c:202:ILE:N	2.36	0.40
4:e:11:VAL:HG13	4:e:171:ALA:HB1	2.03	0.40
4:e:110:ILE:O	4:e:113:PHE:HB2	2.21	0.40
5:f:25:ILE:HD12	5:f:74:MET:HE2	2.02	0.40
7:h:30:SER:OG	7:h:109:LYS:HD3	2.21	0.40
8:i:74:PRO:HB2	8:i:77:VAL:HG23	2.02	0.40
9:j:17:VAL:HG13	9:j:137:PRO:HB2	2.02	0.40
11:l:118:THR:HA	11:l:119:PRO:HD3	1.88	0.40
14:o:101:GLY:HA3	54:2:49:C:OP1	2.21	0.40
19:t:54:GLU:HG3	19:t:88:LYS:HD2	2.03	0.40
20:u:98:ASN:O	20:u:99:SER:C	2.64	0.40
32:H:5:HIS:HA	32:H:6:PRO:HD3	1.91	0.40
33:I:4:LEU:HD22	52:3:406:G:H5''	2.02	0.40
34:J:65:LYS:HA	34:J:68:ARG:HH11	1.87	0.40
35:K:18:VAL:N	35:K:19:PRO:CD	2.84	0.40
35:K:36:ILE:HD12	35:K:64:VAL:HG22	2.02	0.40
38:N:71:ILE:HD11	52:3:1289:A:H61	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:54:GLY:O	44:T:57:ARG:HB3	2.21	0.40
48:X:21:ALA:HA	48:X:27:LYS:HD2	2.02	0.40
50:Z:38:GLU:OE2	52:3:1527:U:C5	2.72	0.40
52:3:490:C:H2'	52:3:491:G:H8	1.85	0.40
52:3:777:A:H2'	52:3:778:G:O4'	2.20	0.40
52:3:923:A:N6	52:3:1393:U:H3	2.14	0.40
52:3:1288:A:O2'	52:3:1353:G:H5'	2.21	0.40
53:1:490:C:O2'	53:1:491:G:P	2.80	0.40
53:1:727:A:O2'	53:1:728:G:H5'	2.21	0.40
53:1:1103:A:H2'	53:1:1104:C:OP1	2.21	0.40
53:1:1287:A:O2'	53:1:1288:G:H5'	2.22	0.40
53:1:1525:A:H2'	53:1:1526:C:O4'	2.21	0.40
53:1:1744:A:H3'	53:1:1745:A:C8	2.56	0.40
53:1:1924:C:H3'	53:1:1925:C:C5'	2.51	0.40
53:1:2071:A:H2'	53:1:2072:C:C6	2.57	0.40
53:1:2713:U:H3'	53:1:2714:G:H5''	2.04	0.40
53:1:2849:U:H4'	53:1:2868:A:N1	2.36	0.40
57:7:25:C:H2'	57:7:26:A:H8	1.86	0.40
1:b:184:GLU:OE2	1:b:186:ASP:HB2	2.22	0.40
2:c:56:LYS:HE3	53:1:2830:C:O3'	2.21	0.40
4:e:29:ARG:H	4:e:158:THR:HG22	1.86	0.40
10:k:61:VAL:O	10:k:61:VAL:HG13	2.20	0.40
13:n:14:SER:HA	13:n:17:ARG:NH1	2.36	0.40
14:o:31:THR:HG21	54:2:28:C:P	2.62	0.40
23:x:56:ARG:NH2	53:1:372:G:O6	2.55	0.40
24:y:37:LEU:HD21	24:y:39:GLN:O	2.21	0.40
25:z:52:PHE:CG	54:2:83:G:H4'	2.56	0.40
36:L:61:PHE:HD1	36:L:123:LEU:HD21	1.87	0.40
36:L:77:ARG:HA	36:L:77:ARG:HD2	1.86	0.40
38:N:108:ARG:HB3	52:3:1347:G:O4'	2.20	0.40
41:Q:22:ALA:HB2	41:Q:94:TYR:CE1	2.56	0.40
43:S:18:LYS:HE3	43:S:19:TYR:CE2	2.55	0.40
44:T:84:LEU:HD12	44:T:84:LEU:HA	1.90	0.40
45:U:26:ASN:ND2	45:U:31:ARG:H	2.19	0.40
51:a:217:THR:OG1	53:1:2124:G:N2	2.55	0.40
53:1:1077:A:C3'	53:1:1078:U:H5'	2.51	0.40
53:1:1102:C:H2'	53:1:1103:A:O4'	2.20	0.40
53:1:1239:G:O2'	53:1:1240:U:H5'	2.21	0.40
53:1:1802:A:O2'	53:1:1803:A:H5'	2.22	0.40
53:1:1919:A:H2'	53:1:1920:C:H5'	2.03	0.40
53:1:2087:G:H2'	53:1:2088:A:C8	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2520:C:O2'	53:1:2521:C:H5'	2.20	0.40
1:b:164:VAL:CG2	1:b:174:ARG:HB2	2.52	0.40
7:h:23:LEU:HD21	7:h:118:ILE:HD13	2.04	0.40
9:j:19:ASP:HA	9:j:57:LEU:HD12	2.04	0.40
9:j:33:ALA:HA	9:j:36:LEU:HD12	2.02	0.40
14:o:98:GLN:O	14:o:100:HIS:N	2.55	0.40
15:p:102:ARG:NH1	15:p:106:ALA:HB1	2.33	0.40
22:w:55:LEU:HD12	22:w:76:ILE:HD12	2.03	0.40
32:H:173:PRO:HB2	32:H:176:THR:OG1	2.21	0.40
38:N:98:ARG:NH2	52:3:1178:G:C8	2.89	0.40
38:N:128:LYS:HE3	38:N:129:ARG:NH1	2.34	0.40
41:Q:35:ARG:HG2	41:Q:37:TYR:HD1	1.87	0.40
43:S:80:ARG:HG3	43:S:81:ILE:HD12	2.04	0.40
50:Z:19:LYS:HA	50:Z:19:LYS:HD3	1.87	0.40
50:Z:24:LYS:HB2	50:Z:24:LYS:HE3	1.87	0.40
50:Z:55:HIS:HA	50:Z:58:LYS:HD2	2.04	0.40
51:a:53:ARG:HB3	55:5:62:C:O3'	2.21	0.40
51:a:192:LEU:HD12	51:a:192:LEU:C	2.46	0.40
52:3:151:A:H62	52:3:170:U:H3	1.69	0.40
52:3:381:C:H2'	52:3:382:A:O4'	2.22	0.40
52:3:884:U:H4'	52:3:885:G:H5''	2.03	0.40
52:3:936:C:H2'	52:3:937:A:O4'	2.21	0.40
53:1:2185:U:H2'	53:1:2186:G:H8	1.86	0.40
1:b:106:PRO:HG2	1:b:109:LEU:HD13	2.04	0.40
4:e:15:LEU:HD21	4:e:167:ALA:HB1	2.03	0.40
4:e:118:ALA:O	4:e:166:ARG:NH2	2.47	0.40
6:g:51:ARG:N	6:g:51:ARG:HD2	2.37	0.40
10:k:70:ARG:CG	10:k:76:VAL:HG12	2.50	0.40
11:l:110:VAL:HB	11:l:127:VAL:HG23	2.04	0.40
14:o:81:ARG:HA	14:o:84:GLU:HG3	2.03	0.40
24:y:50:VAL:O	24:y:54:LYS:HG3	2.21	0.40
31:G:44:LYS:C	31:G:47:PRO:HD2	2.46	0.40
31:G:107:ARG:O	31:G:110:ILE:HB	2.22	0.40
32:H:21:TRP:CZ3	32:H:23:ALA:HB2	2.56	0.40
33:I:6:PRO:HB2	33:I:9:LYS:CG	2.52	0.40
35:K:54:LEU:HD12	35:K:54:LEU:HA	1.84	0.40
37:M:45:ILE:HD12	37:M:45:ILE:HA	1.90	0.40
41:Q:24:GLU:O	41:Q:25:ALA:HB3	2.21	0.40
42:R:82:LEU:HG	48:X:73:PHE:HE2	1.87	0.40
42:R:97:ARG:HG3	42:R:97:ARG:NH1	2.36	0.40
48:X:58:PRO:HB2	53:1:888:C:N3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:144:G:O2'	52:3:145:G:H5'	2.22	0.40
53:1:253:C:H2'	53:1:254:G:O4'	2.20	0.40
53:1:962:G:O2'	53:1:963:U:H5'	2.22	0.40
53:1:1229:C:H2'	53:1:1230:A:H8	1.87	0.40
53:1:1536:C:H4'	53:1:1537:G:C2	2.56	0.40
53:1:2272:U:H5''	53:1:2273:A:OP1	2.21	0.40
53:1:2296:U:H4'	53:1:2297:A:O5'	2.21	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	b	269/271 (99%)	233 (87%)	33 (12%)	3 (1%)	11	39
2	c	207/209 (99%)	173 (84%)	29 (14%)	5 (2%)	4	24
3	d	199/201 (99%)	180 (90%)	19 (10%)	0	100	100
4	e	175/177 (99%)	158 (90%)	17 (10%)	0	100	100
5	f	174/176 (99%)	156 (90%)	17 (10%)	1 (1%)	21	52
6	g	147/149 (99%)	125 (85%)	18 (12%)	4 (3%)	4	22
7	h	129/131 (98%)	100 (78%)	22 (17%)	7 (5%)	1	10
8	i	139/141 (99%)	114 (82%)	21 (15%)	4 (3%)	3	21
9	j	140/142 (99%)	125 (89%)	14 (10%)	1 (1%)	18	49
10	k	120/122 (98%)	93 (78%)	22 (18%)	5 (4%)	2	14
11	l	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	14
12	m	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	5	26
13	n	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	45
14	o	114/116 (98%)	101 (89%)	10 (9%)	3 (3%)	4	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	p	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
16	q	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
17	r	101/103 (98%)	86 (85%)	14 (14%)	1 (1%)	12	40
18	s	108/110 (98%)	93 (86%)	13 (12%)	2 (2%)	6	28
19	t	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
20	u	100/102 (98%)	82 (82%)	15 (15%)	3 (3%)	3	20
21	v	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	w	73/75 (97%)	65 (89%)	7 (10%)	1 (1%)	9	33
23	x	75/77 (97%)	69 (92%)	4 (5%)	2 (3%)	4	22
24	y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	B	54/56 (96%)	48 (89%)	5 (9%)	1 (2%)	6	28
27	C	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
28	D	44/46 (96%)	36 (82%)	8 (18%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	31
30	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
31	G	223/225 (99%)	202 (91%)	19 (8%)	2 (1%)	14	43
32	H	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
33	I	203/205 (99%)	181 (89%)	18 (9%)	4 (2%)	6	27
34	J	155/157 (99%)	123 (79%)	25 (16%)	7 (4%)	2	13
35	K	98/100 (98%)	73 (74%)	22 (22%)	3 (3%)	3	20
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	49
37	M	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	31
38	N	125/127 (98%)	101 (81%)	16 (13%)	8 (6%)	1	8
39	O	96/98 (98%)	78 (81%)	13 (14%)	5 (5%)	1	11
40	P	114/116 (98%)	88 (77%)	20 (18%)	6 (5%)	1	10
41	Q	121/123 (98%)	94 (78%)	19 (16%)	8 (7%)	1	7
42	R	112/114 (98%)	99 (88%)	8 (7%)	5 (4%)	2	13
43	S	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
44	T	86/88 (98%)	74 (86%)	11 (13%)	1 (1%)	10	37
45	U	80/82 (98%)	68 (85%)	10 (12%)	2 (2%)	4	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	V	78/80 (98%)	60 (77%)	13 (17%)	5 (6%)	1	8
47	W	63/65 (97%)	54 (86%)	9 (14%)	0	100	100
48	X	77/79 (98%)	65 (84%)	11 (14%)	1 (1%)	9	35
49	Y	83/85 (98%)	76 (92%)	6 (7%)	1 (1%)	10	37
50	Z	63/65 (97%)	39 (62%)	18 (29%)	6 (10%)	0	3
51	a	130/223 (58%)	119 (92%)	11 (8%)	0	100	100
All	All	5919/6112 (97%)	5078 (86%)	720 (12%)	121 (2%)	8	27

All (121) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA
6	g	41	LYS
7	h	118	ILE
8	i	92	PRO
10	k	35	VAL
10	k	110	GLU
11	l	36	LYS
14	o	34	HIS
20	u	51	LEU
23	x	2	ARG
33	I	7	LYS
33	I	29	THR
33	I	34	GLU
34	J	93	VAL
38	N	90	ASP
38	N	107	ALA
39	O	57	VAL
41	Q	27	PRO
42	R	6	ILE
42	R	7	ASN
44	T	46	LYS
45	U	79	ASN
46	V	49	ASN
46	V	81	ALA
50	Z	32	ARG
50	Z	34	ARG
1	b	260	LYS
6	g	97	ARG

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Mol	Chain	Res	Type
7	h	32	GLY
7	h	113	PHE
7	h	119	PRO
9	j	81	ILE
10	k	89	ASN
11	l	31	GLY
11	l	85	VAL
12	m	13	HIS
14	o	99	TYR
17	r	54	VAL
29	E	31	ILE
34	J	122	VAL
38	N	13	SER
38	N	71	ILE
38	N	91	GLU
40	P	77	GLY
40	P	89	GLY
41	Q	101	LEU
42	R	4	ALA
42	R	104	ASN
46	V	53	GLY
48	X	26	ASP
50	Z	12	ASP
50	Z	24	LYS
2	c	75	ALA
2	c	149	ASN
7	h	58	THR
10	k	92	GLU
11	l	29	LYS
12	m	69	PRO
13	n	71	ARG
14	o	116	GLN
18	s	12	SER
20	u	97	SER
20	u	99	SER
22	w	80	ALA
26	B	25	THR
34	J	49	TYR
34	J	98	ALA
34	J	121	ASN
35	K	86	ARG
35	K	94	HIS

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Mol	Chain	Res	Type
36	L	129	ASN
38	N	8	THR
38	N	102	PHE
39	O	35	GLN
39	O	75	ASP
40	P	126	ARG
41	Q	3	VAL
41	Q	35	ARG
41	Q	77	SER
46	V	17	GLU
50	Z	25	ALA
2	c	113	SER
10	k	26	GLY
12	m	58	LYS
34	J	89	THR
35	K	92	THR
38	N	120	ALA
40	P	92	ARG
41	Q	75	GLU
45	U	44	SER
50	Z	9	GLU
7	h	114	GLU
8	i	30	GLN
18	s	80	PRO
31	G	24	PRO
33	I	152	SER
34	J	23	THR
37	M	2	MET
37	M	47	ASP
39	O	58	ASN
42	R	113	LYS
49	Y	76	ALA
2	c	86	GLU
6	g	9	VAL
6	g	89	LYS
11	l	88	GLY
40	P	38	GLY
46	V	15	LYS
1	b	248	GLY
2	c	143	PRO
11	l	56	PRO
39	O	43	PRO

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Mol	Chain	Res	Type
40	P	88	PRO
41	Q	44	PRO
8	i	22	PRO
8	i	4	VAL
31	G	150	ILE
41	Q	41	PRO
7	h	123	ILE
23	x	6	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	212 (98%)	4 (2%)	50	68
2	c	164/164 (100%)	161 (98%)	3 (2%)	51	70
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	81
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	68
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	80
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	70
7	h	100/100 (100%)	98 (98%)	2 (2%)	48	68
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	70
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	78
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	78
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	66
15	p	99/99 (100%)	96 (97%)	3 (3%)	36	61
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	76
17	r	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	s	93/93 (100%)	89 (96%)	4 (4%)	26	54
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	74
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	74
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	185 (100%)	1 (0%)	81	83
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	168 (98%)	4 (2%)	44	66
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	79
35	K	87/87 (100%)	87 (100%)	0	100	100
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	104 (100%)	0	100	100
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	68
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	66
40	P	89/89 (100%)	87 (98%)	2 (2%)	45	66
41	Q	103/103 (100%)	101 (98%)	2 (2%)	50	68
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	76
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	73
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	70
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4859 (99%)	49 (1%)	65	76

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	18	VAL
1	b	33	LEU
1	b	184	GLU
1	b	203	VAL
2	c	9	VAL
2	c	103	ASP
2	c	142	VAL
3	d	84	THR
4	e	41	GLU
4	e	155	ILE
4	e	174	PHE
5	f	10	VAL
6	g	31	VAL
6	g	62	LEU
7	h	3	LEU
7	h	119	PRO
8	i	12	VAL
8	i	129	GLU
9	j	57	LEU
12	m	135	VAL
14	o	31	THR
14	o	32	PRO
15	p	65	ASN
15	p	83	ILE
15	p	109	ILE
16	q	94	LEU
18	s	8	ARG
18	s	40	ASN
18	s	77	ASP
18	s	109	ASP
19	t	72	GLN
21	v	72	VAL
31	G	46	VAL

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Mol	Chain	Res	Type
33	I	28	ASP
33	I	31	CYS
33	I	54	LEU
33	I	202	LEU
34	J	55	VAL
38	N	49	GLN
38	N	52	GLU
39	O	73	LEU
39	O	76	ILE
40	P	33	ILE
40	P	127	ARG
41	Q	24	GLU
41	Q	34	THR
42	R	102	LYS
46	V	27	PHE
50	Z	28	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (124) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	45	ASN
1	b	52	HIS
1	b	59	GLN
1	b	85	ASN
1	b	89	ASN
1	b	152	GLN
1	b	225	ASN
2	c	36	GLN
2	c	136	ASN
2	c	150	GLN
2	c	173	GLN
3	d	41	GLN
3	d	90	GLN
3	d	97	ASN
3	d	136	GLN
3	d	156	ASN
5	f	37	ASN
5	f	103	ASN
6	g	43	ASN
6	g	66	ASN
6	g	128	HIS

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Mol	Chain	Res	Type
6	g	135	HIS
6	g	145	ASN
7	h	6	GLN
7	h	103	ASN
7	h	122	GLN
8	i	11	GLN
8	i	29	GLN
9	j	40	HIS
9	j	58	ASN
9	j	135	GLN
10	k	88	ASN
10	k	89	ASN
11	l	4	ASN
11	l	35	HIS
11	l	54	GLN
11	l	104	GLN
12	m	17	ASN
13	n	3	HIS
13	n	9	GLN
13	n	62	ASN
13	n	107	ASN
14	o	29	HIS
14	o	100	HIS
14	o	104	GLN
15	p	114	ASN
16	q	36	GLN
16	q	80	ASN
17	r	6	GLN
17	r	66	HIS
17	r	86	GLN
18	s	15	GLN
18	s	40	ASN
19	t	59	ASN
20	u	45	GLN
20	u	52	ASN
20	u	65	GLN
20	u	68	ASN
20	u	73	ASN
21	v	49	ASN
21	v	87	GLN
22	w	8	ASN
22	w	46	ASN

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Mol	Chain	Res	Type
23	x	15	ASN
24	y	15	ASN
24	y	20	ASN
24	y	27	ASN
26	B	5	ASN
28	D	26	ASN
28	D	29	GLN
29	E	27	ASN
29	E	42	HIS
30	F	13	ASN
31	G	14	HIS
31	G	17	HIS
31	G	18	GLN
31	G	50	ASN
31	G	57	ASN
31	G	121	GLN
31	G	145	ASN
31	G	169	HIS
32	H	122	GLN
32	H	139	ASN
33	I	99	ASN
33	I	115	GLN
33	I	119	HIS
33	I	139	ASN
33	I	151	GLN
33	I	197	HIS
34	J	11	GLN
34	J	18	ASN
34	J	72	ASN
34	J	82	HIS
34	J	131	ASN
35	K	11	HIS
35	K	68	GLN
36	L	27	ASN
36	L	67	ASN
37	M	3	GLN
37	M	66	GLN
38	N	30	ASN
39	O	35	GLN
40	P	14	GLN
40	P	39	ASN
40	P	118	ASN

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Mol	Chain	Res	Type
41	Q	4	ASN
41	Q	45	ASN
41	Q	58	ASN
42	R	99	GLN
43	S	34	ASN
44	T	49	HIS
45	U	40	ASN
45	U	79	ASN
47	W	73	HIS
48	X	13	HIS
49	Y	69	ASN
49	Y	81	GLN
49	Y	83	ASN
50	Z	55	HIS
50	Z	63	ASN
51	a	20	GLN
51	a	57	GLN
51	a	203	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	143 (9%)	2 (0%)
53	1	2902/2903 (99%)	326 (11%)	11 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	24 (31%)	1 (1%)
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4727/4733 (99%)	520 (11%)	15 (0%)

All (520) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A

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Mol	Chain	Res	Type
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G
52	3	130	A
52	3	144	G
52	3	173	U
52	3	183	C
52	3	184	G
52	3	197	A
52	3	210	C
52	3	211	G
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	328	C
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	373	A
52	3	412	A
52	3	413	G
52	3	422	C
52	3	429	U
52	3	467	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A

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Mol	Chain	Res	Type
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	653	U
52	3	665	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	713	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	902	G
52	3	926	G
52	3	934	C
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1054	C

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Mol	Chain	Res	Type
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1253	G
52	3	1258	G
52	3	1260	G
52	3	1261	A
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1381	U
52	3	1395	C
52	3	1419	G
52	3	1446	A
52	3	1448	C
52	3	1452	C

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Mol	Chain	Res	Type
52	3	1492	A
52	3	1502	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	46	G
53	1	49	A
53	1	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	98	G
53	1	102	U
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	219	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C

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Mol	Chain	Res	Type
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	329	G
53	1	330	A
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	422	A
53	1	424	G
53	1	451	U
53	1	455	C
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	563	A
53	1	573	U
53	1	575	A
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A

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Mol	Chain	Res	Type
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A
53	1	995	C
53	1	1012	U
53	1	1013	C
53	1	1021	A

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Mol	Chain	Res	Type
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1103	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1174	U
53	1	1175	A
53	1	1177	G
53	1	1178	C
53	1	1180	U
53	1	1206	G
53	1	1211	C
53	1	1212	G
53	1	1238	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1301	A
53	1	1321	A

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Mol	Chain	Res	Type
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A

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Mol	Chain	Res	Type
53	1	1780	A
53	1	1791	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1913	A
53	1	1914	C
53	1	1925	C
53	1	1926	U
53	1	1930	G
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1972	G
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2036	C
53	1	2043	C
53	1	2049	G
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U

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Mol	Chain	Res	Type
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2126	A
53	1	2132	U
53	1	2133	G
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2239	G
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2434	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A

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Mol	Chain	Res	Type
53	1	2491	U
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2797	U
53	1	2799	A
53	1	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2883	A
54	2	4	C

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Mol	Chain	Res	Type
54	2	13	G
54	2	15	A
54	2	24	G
54	2	35	C
54	2	41	G
54	2	44	G
54	2	67	G
54	2	89	U
54	2	108	A
54	2	109	A
55	5	4	G
55	5	9	G
55	5	15	G
55	5	16	C
55	5	17	C
55	5	17(A)	U
55	5	18	G
55	5	19	G
55	5	21	A
55	5	25	C
55	5	27	U
55	5	28	C
55	5	31	G
55	5	32	C
55	5	45	G
55	5	48	C
55	5	58	A
55	5	59	A
55	5	61	C
55	5	62	C
55	5	63	G
55	5	70	G
55	5	72	A
55	5	74	C
56	4	12	A
56	4	16	A
57	7	17	C
57	7	21	A
57	7	22	G
57	7	45	U
57	7	46	G
57	7	47	U

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Mol	Chain	Res	Type
57	7	48	C
57	7	49	C
57	7	59	U
57	7	61	C
57	7	72	C
57	7	73	A
57	7	74	C
57	7	76	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	1190	G
52	3	1201	A
53	1	227	A
53	1	421	C
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
54	2	88	C
55	5	17(A)	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are 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	PHE	7	101	59,57	10,11,12	0.43	0	8,13,15	0.60	0
59	FME	7	102	58	8,9,10	1.41	1 (12%)	8,9,11	1.36	1 (12%)

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	PHE	7	101	59,57	-	2/5/6/8	0/1/1/1
59	FME	7	102	58	-	3/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	7	102	FME	CN-N	3.73	1.45	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	7	102	FME	O1-CN-N	-2.05	120.01	125.32

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	7	101	PHE	N-CA-CB-CG
58	7	101	PHE	C-CA-CB-CG
59	7	102	FME	O1-CN-N-CA
59	7	102	FME	CB-CG-SD-CE
59	7	102	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

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.

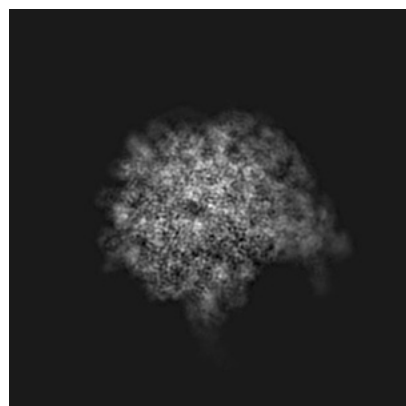
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21635. These allow visual inspection of the internal detail of the map and identification of artifacts.

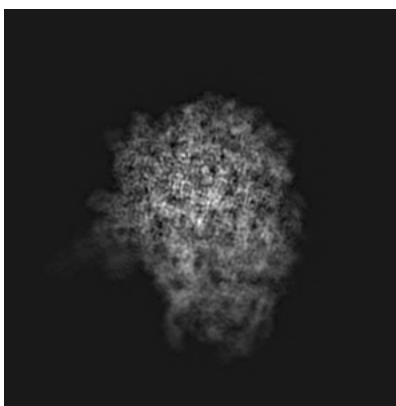
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

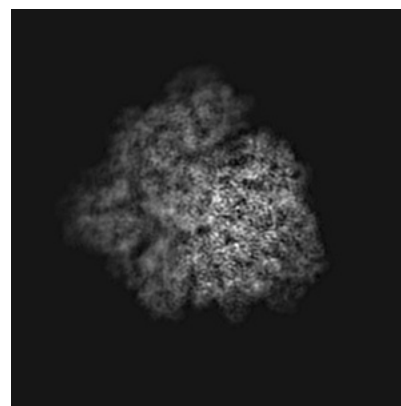
6.1.1 Primary map



X

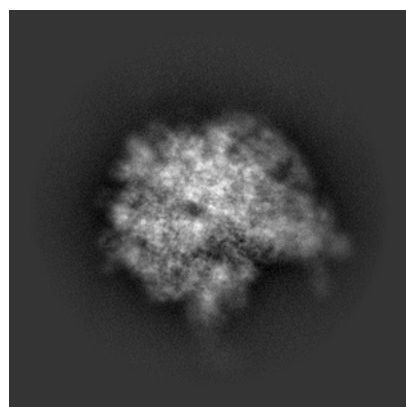


Y

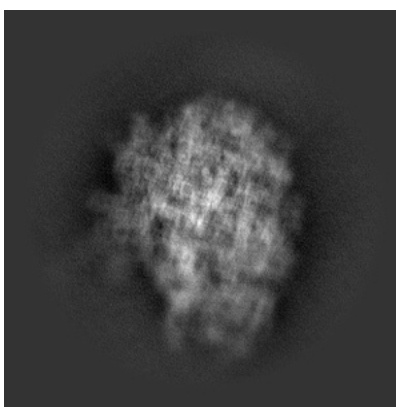


Z

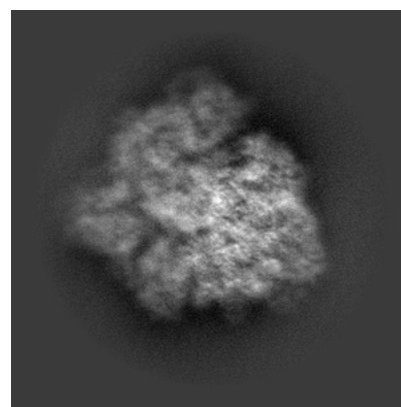
6.1.2 Raw map



X



Y

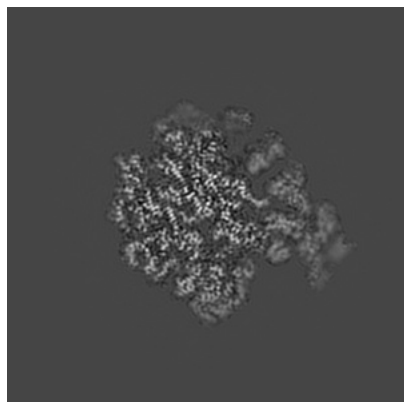


Z

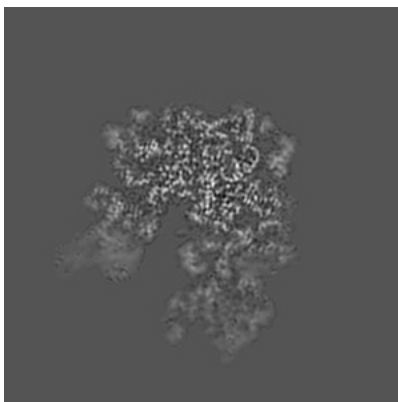
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

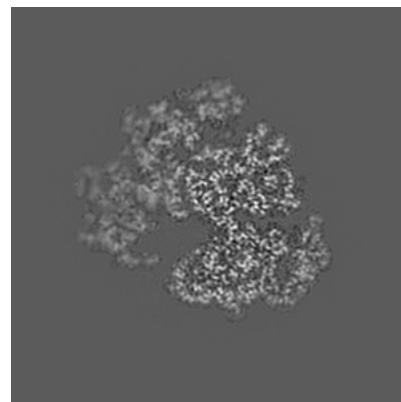
6.2.1 Primary map



X Index: 144

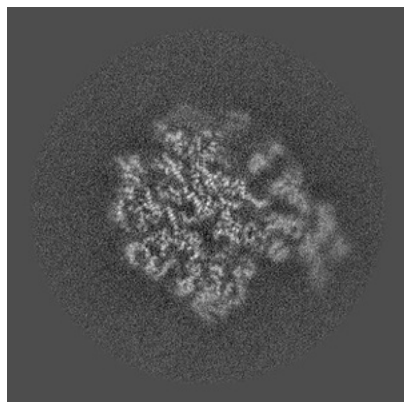


Y Index: 144

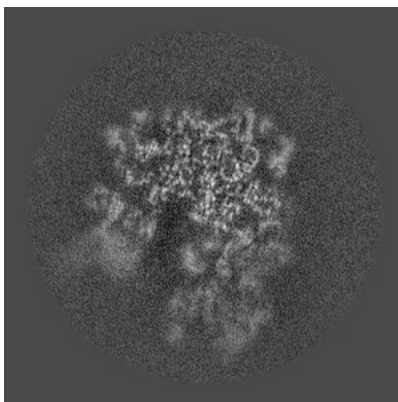


Z Index: 144

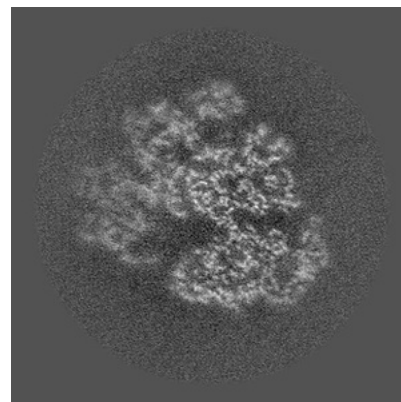
6.2.2 Raw map



X Index: 144



Y Index: 144

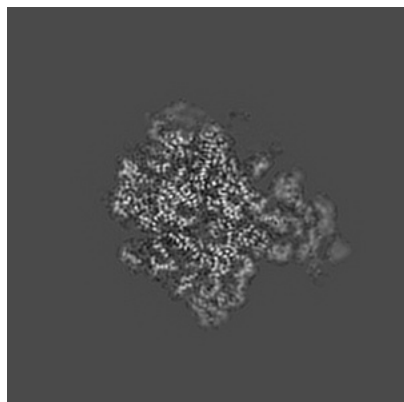


Z Index: 144

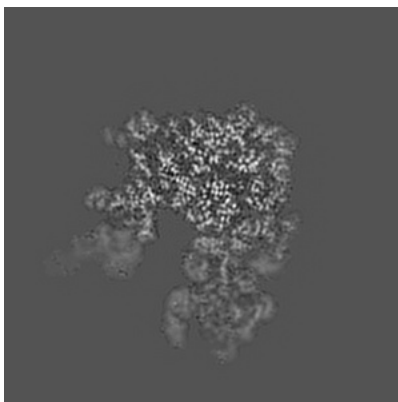
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

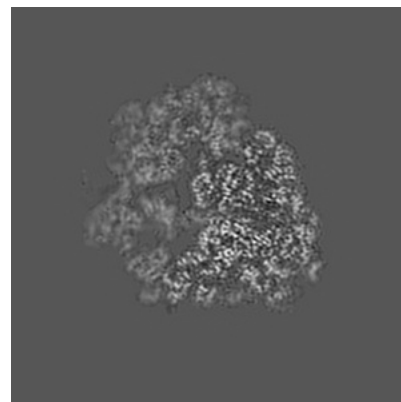
6.3.1 Primary map



X Index: 148

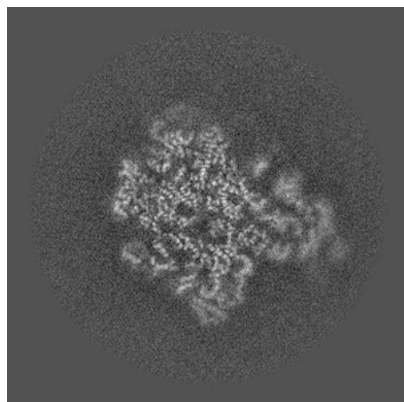


Y Index: 149

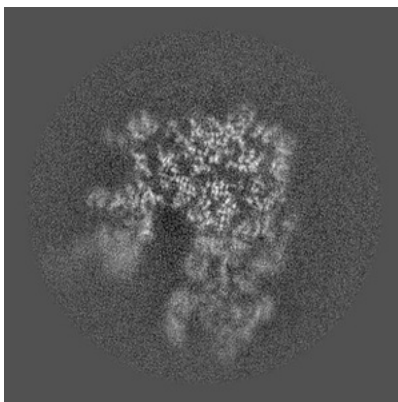


Z Index: 135

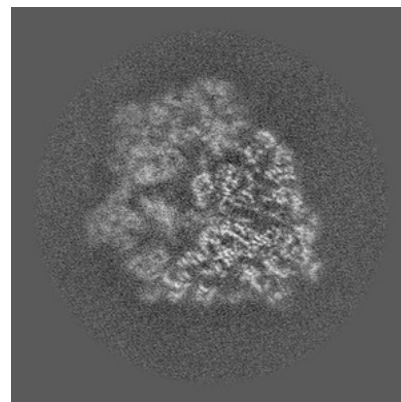
6.3.2 Raw map



X Index: 148



Y Index: 149

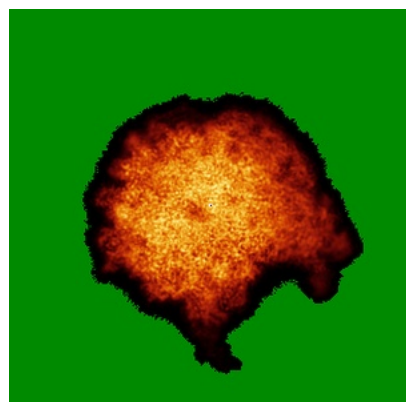


Z Index: 135

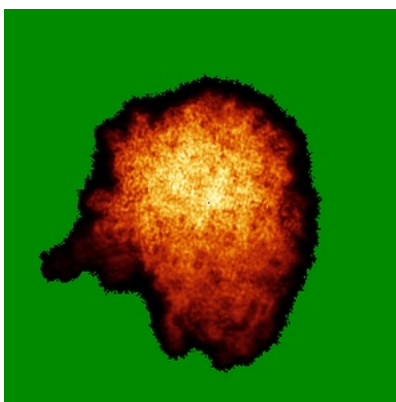
The images above show the largest variance slices of the map in three orthogonal directions.

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

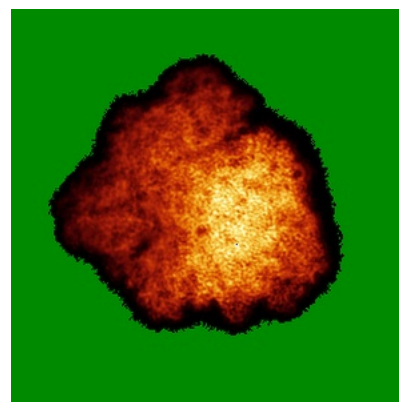
6.4.1 Primary map



X

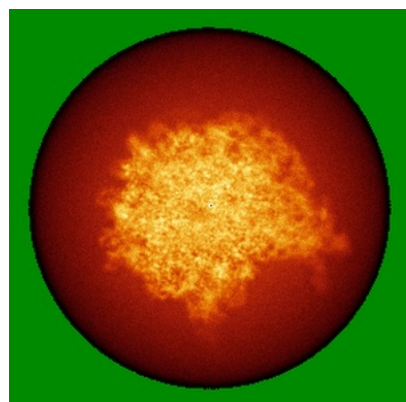


Y

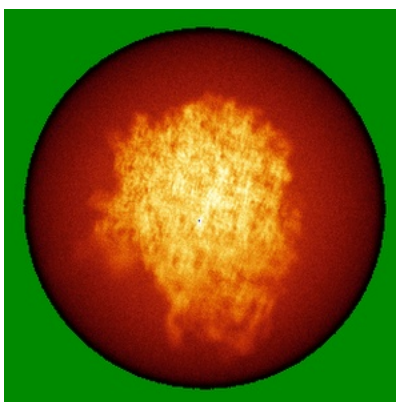


Z

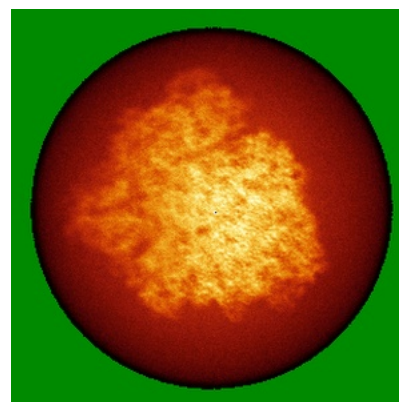
6.4.2 Raw map



X



Y

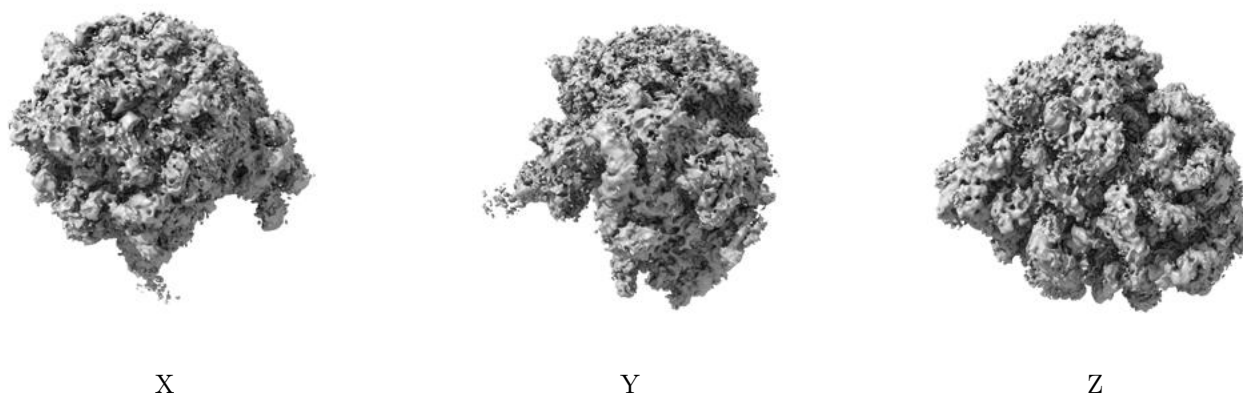


Z

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.

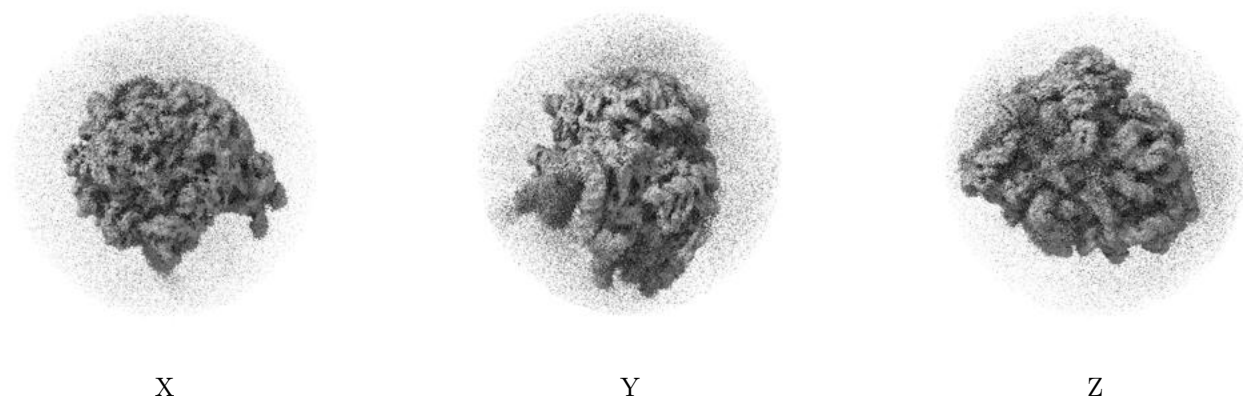
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

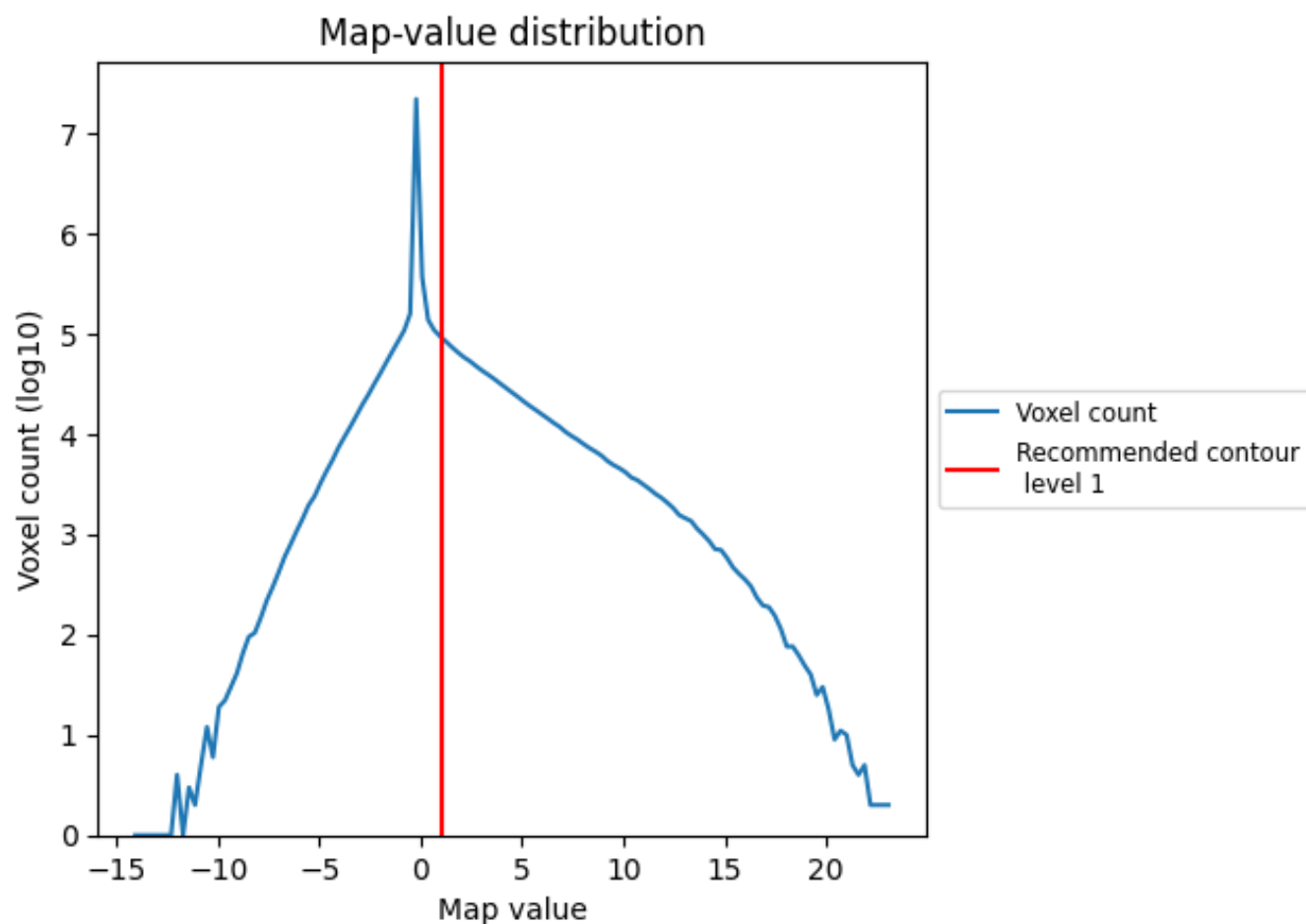
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

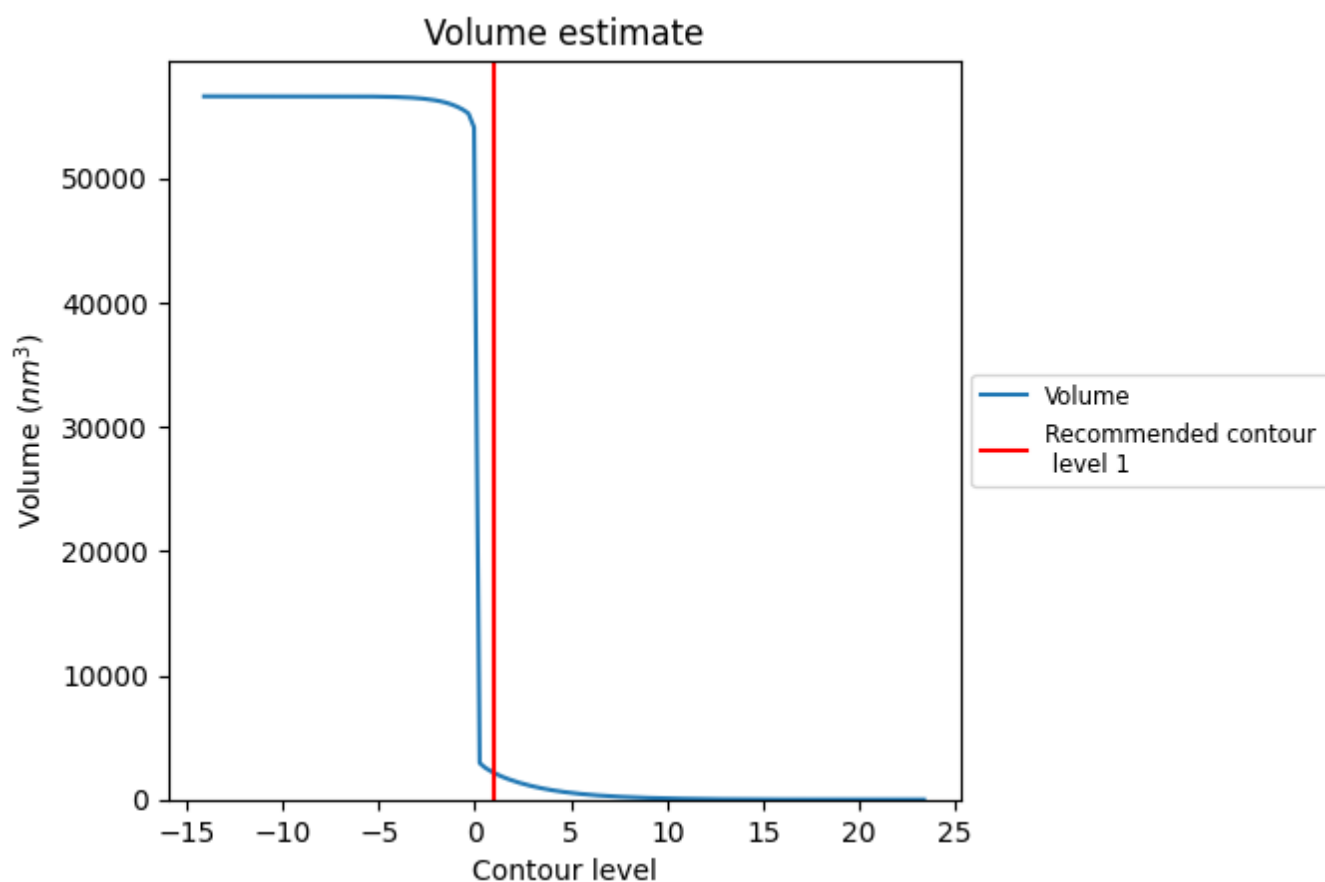
This section contains the results of statistical analysis of the map.

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.

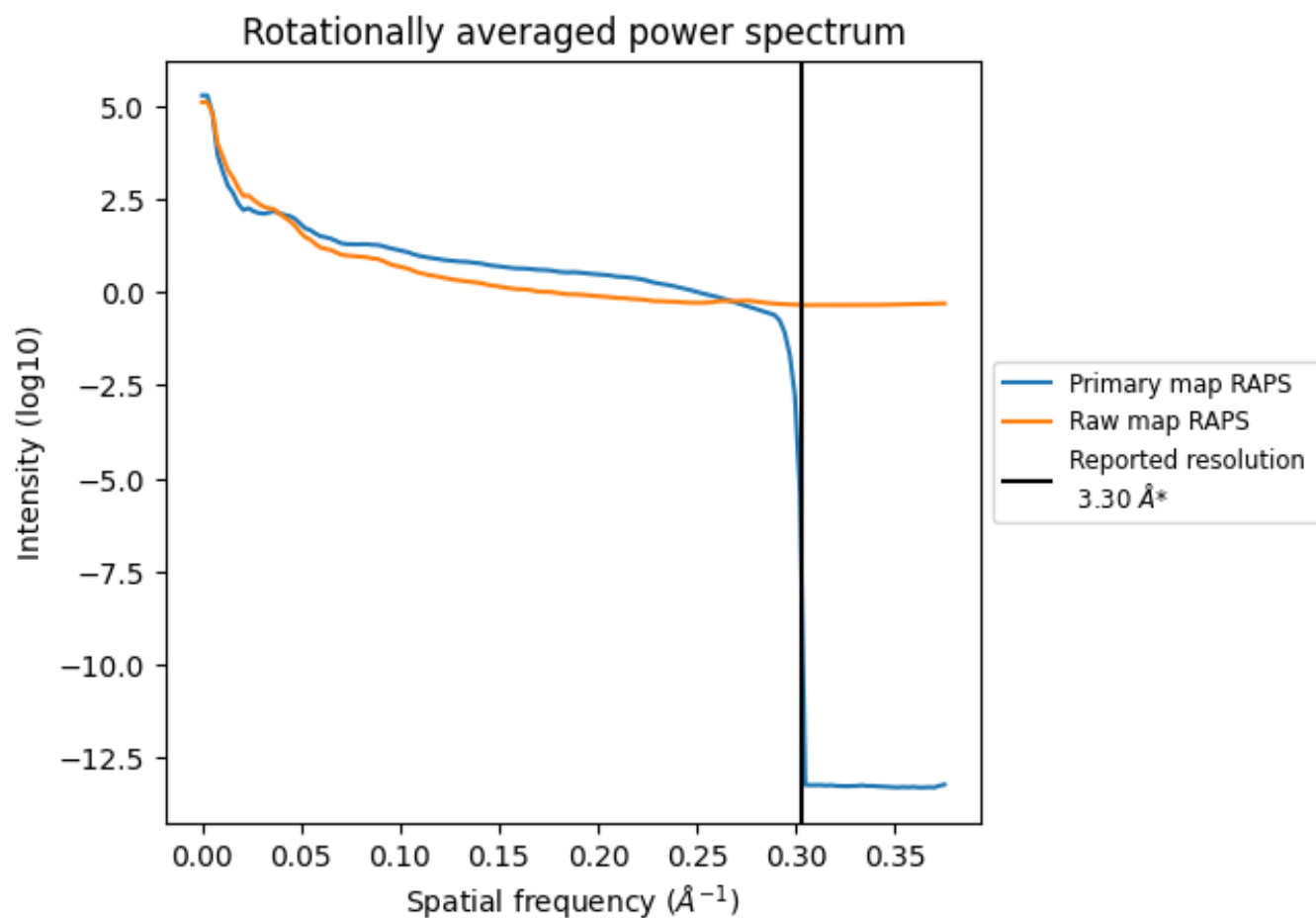
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2148 nm^3 ; this corresponds to an approximate mass of 1940 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 ⓘ

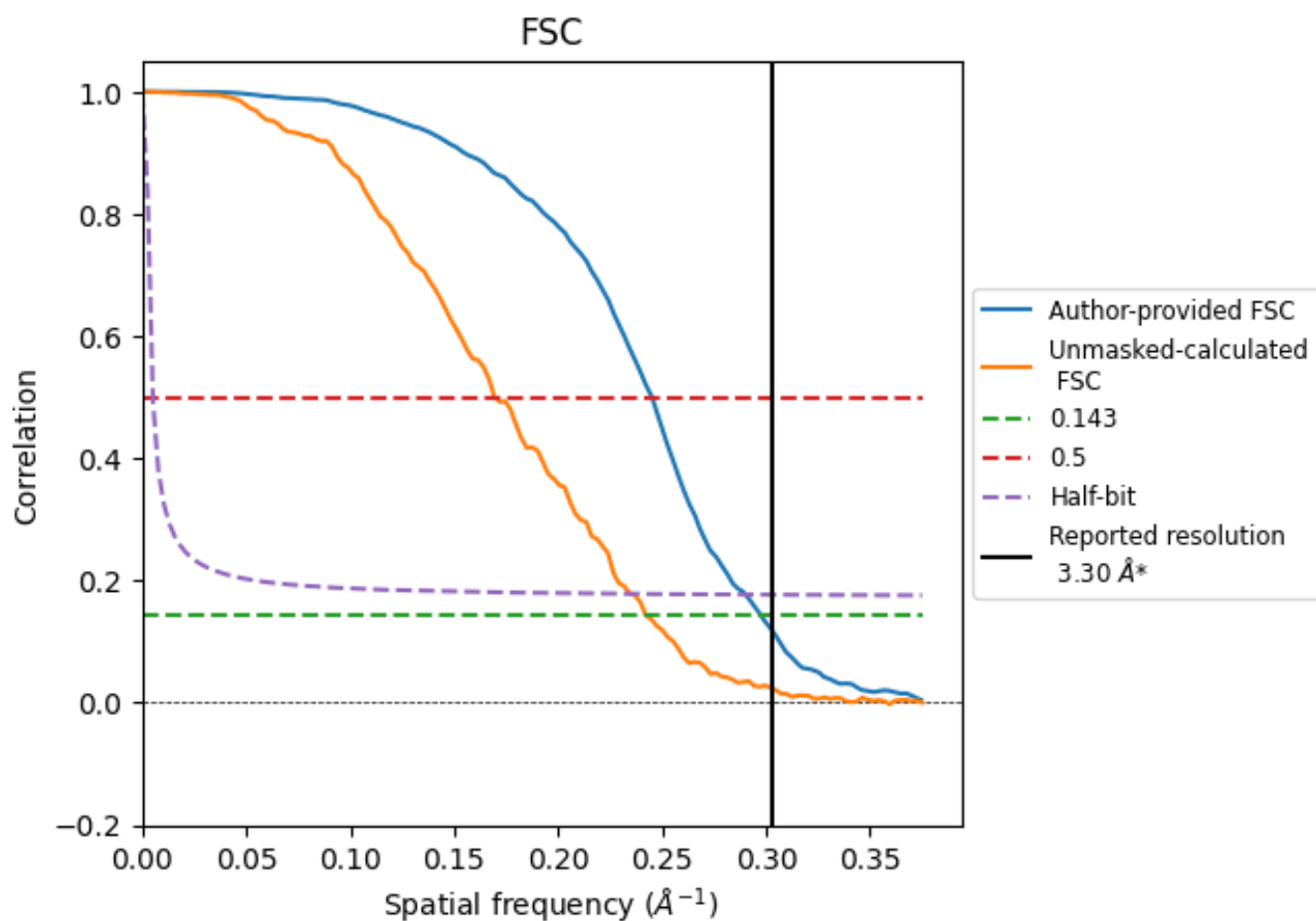


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.36	4.08	3.45
Unmasked-calculated*	4.13	5.89	4.26

*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 4.13 differs from the reported value 3.3 by more than 10 %

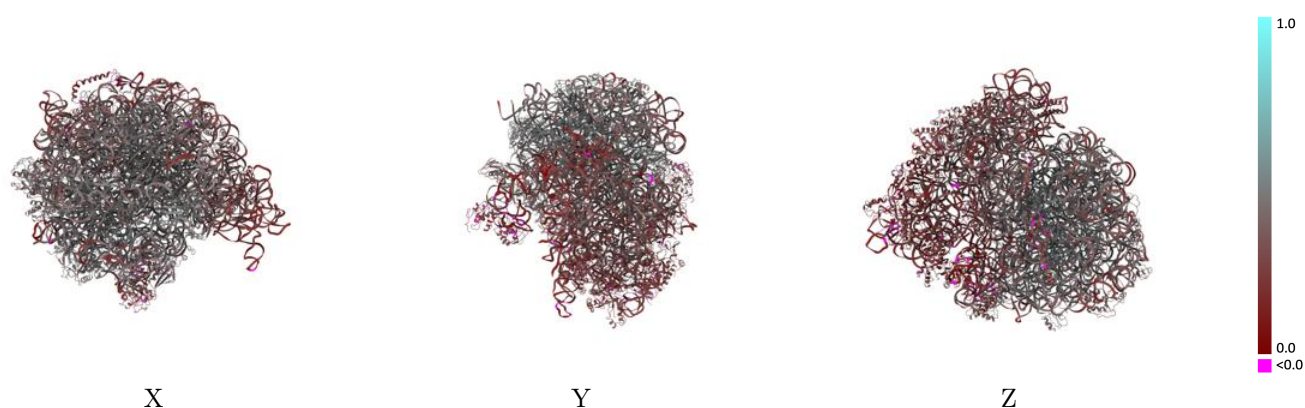
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-21635 and PDB model 6WDG. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

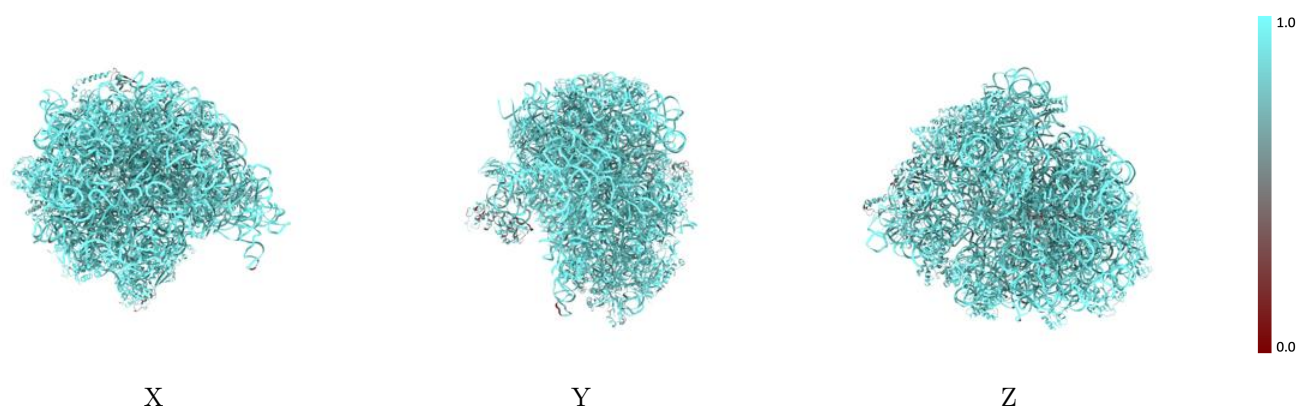
This section was not generated.

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



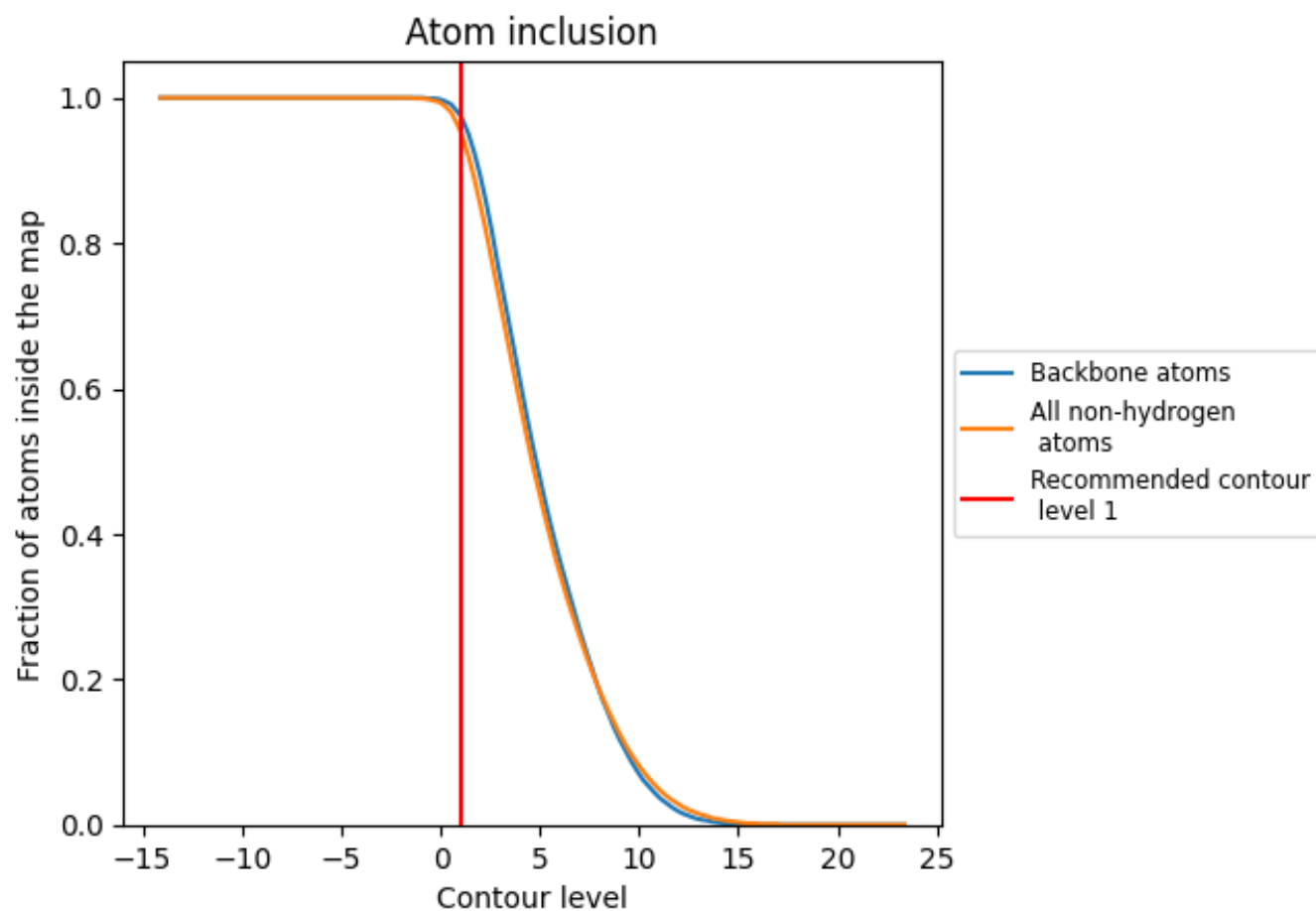
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.3630
1	 0.9790	 0.4080
2	 0.9860	 0.3620
3	 0.9660	 0.2890
4	 0.8630	 0.2300
5	 0.9710	 0.2360
7	 0.9570	 0.2520
B	 0.9700	 0.4740
C	 0.8480	 0.4140
D	 0.9630	 0.4860
E	 0.9800	 0.5080
F	 0.8770	 0.4470
G	 0.8740	 0.2800
H	 0.8200	 0.2450
I	 0.8700	 0.2590
J	 0.9210	 0.3350
K	 0.9670	 0.3500
L	 0.9150	 0.2370
M	 0.9130	 0.3490
N	 0.8580	 0.2050
O	 0.7570	 0.2490
P	 0.9460	 0.3660
Q	 0.9360	 0.3900
R	 0.9050	 0.2570
S	 0.7950	 0.2330
T	 0.9640	 0.3670
U	 0.9040	 0.3360
V	 0.9430	 0.3520
W	 0.9380	 0.3400
X	 0.9310	 0.2300
Y	 0.9010	 0.2800
Z	 0.8900	 0.2880
a	 0.9100	 0.1860
b	 0.9690	 0.4860
c	 0.9670	 0.4890



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Chain	Atom inclusion	Q-score
d	 0.9590	 0.4480
e	 0.9350	 0.3080
f	 0.9600	 0.3870
g	 0.7890	 0.2690
h	 0.7090	 0.1550
i	 0.6440	 0.1660
j	 0.9580	 0.4740
k	 0.9510	 0.4810
l	 0.9590	 0.4660
m	 0.9670	 0.4710
n	 0.9710	 0.4790
o	 0.9590	 0.4020
p	 0.9630	 0.4690
q	 0.9530	 0.4780
r	 0.9600	 0.4500
s	 0.9340	 0.4740
t	 0.9540	 0.4480
u	 0.9540	 0.4200
v	 0.9680	 0.4400
w	 0.9540	 0.4890
x	 0.9700	 0.4840
y	 0.9480	 0.3830
z	 0.9680	 0.4610