



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 09:34 PM UTC

PDB ID : 6WDL / pdb_00006wdl
EMDB ID : EMD-21640
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Non-cognate Structure V-B1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 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

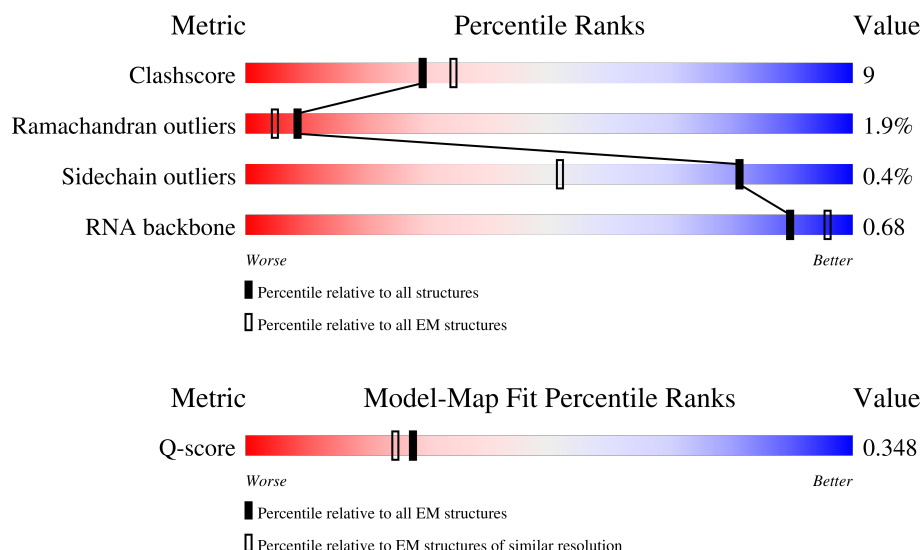
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



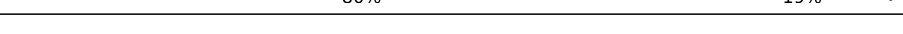
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	

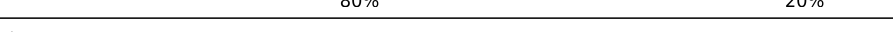
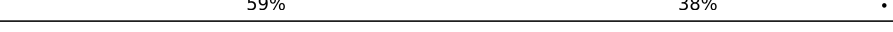
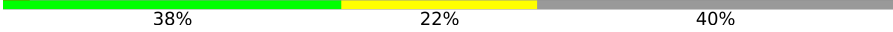
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	61%33%6%
55	5	77	71%27%
55	6	77	66%32%
56	4	18	78%22%
57	7	76	71%24%5%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150220 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		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

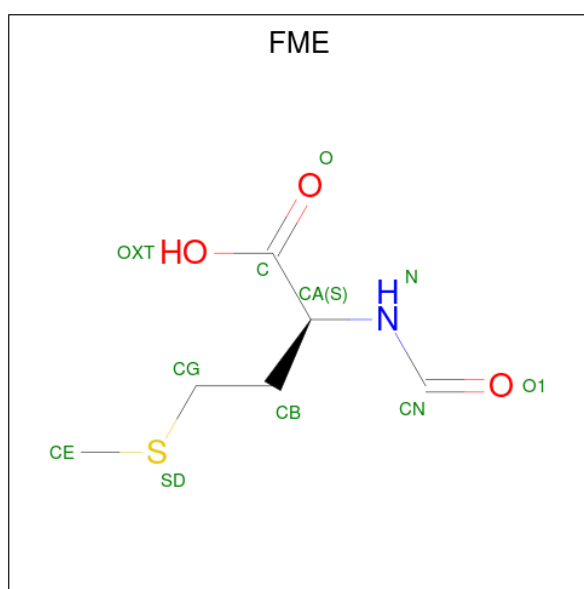
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	77	119	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

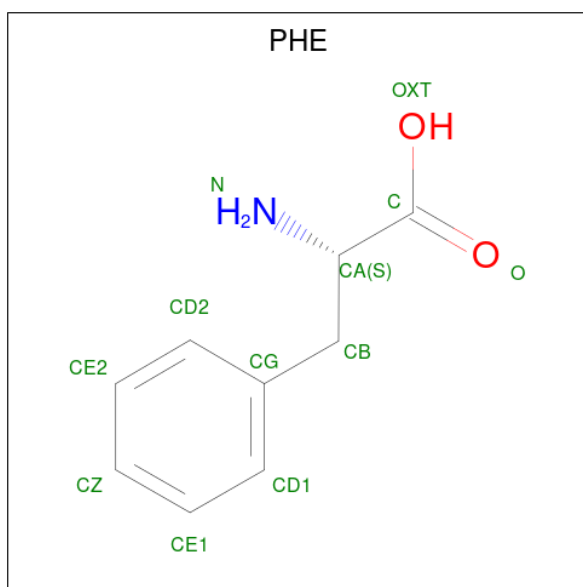
Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
58	1	1	Total	C	N	O	S	0
			8	5	1	1	1	

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).

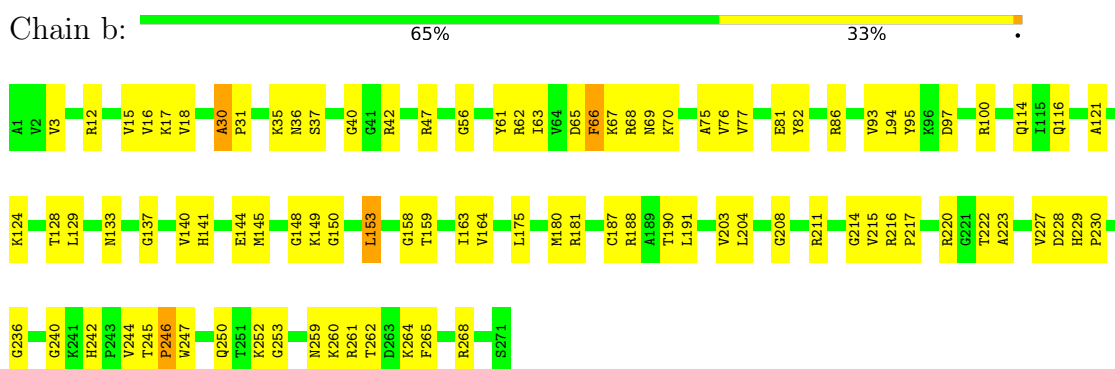


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
59	7	1	11	9	1	1	0

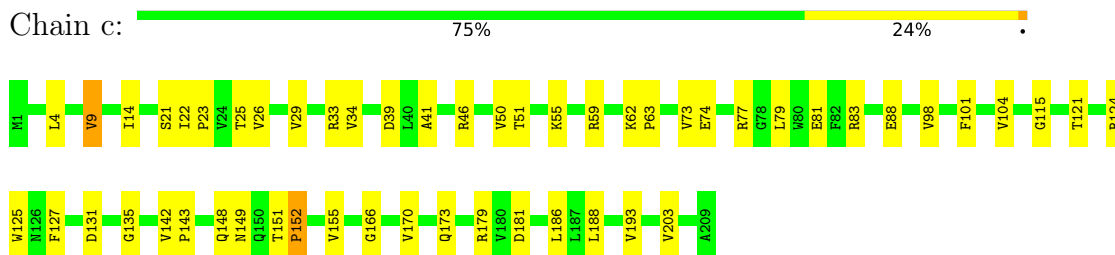
3 Residue-property plots

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.

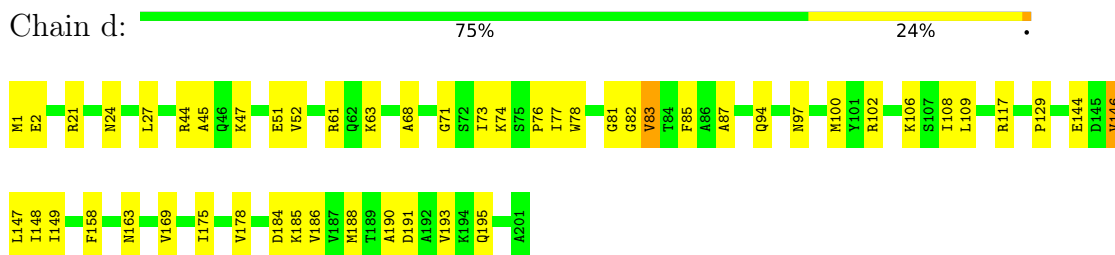
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

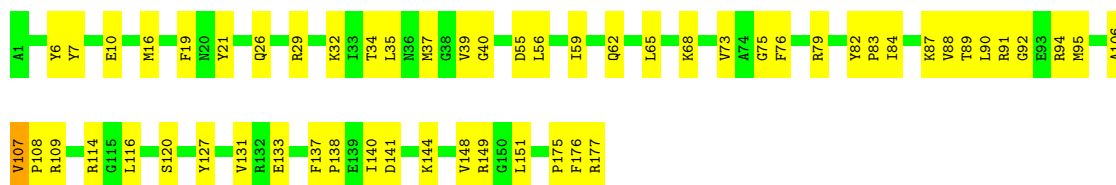


- Molecule 3: 50S ribosomal protein L4

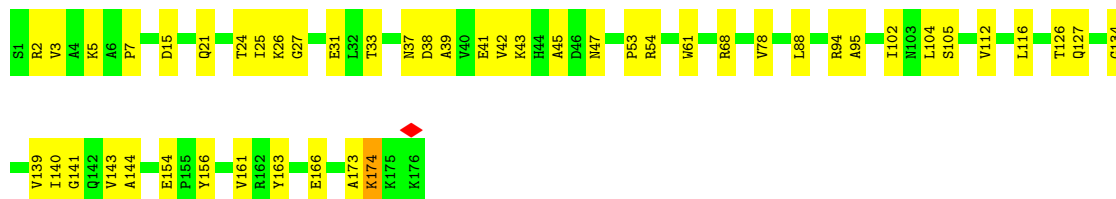


- Molecule 4: 50S ribosomal protein L5

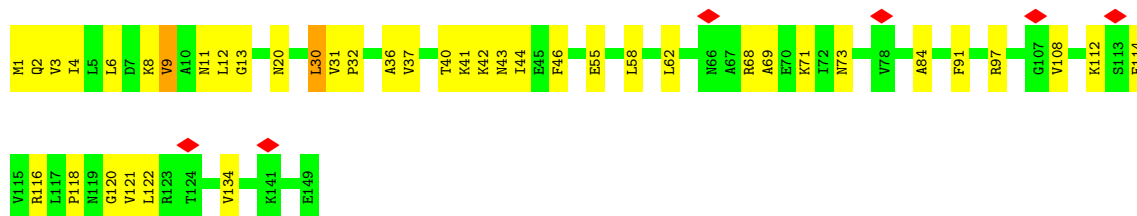




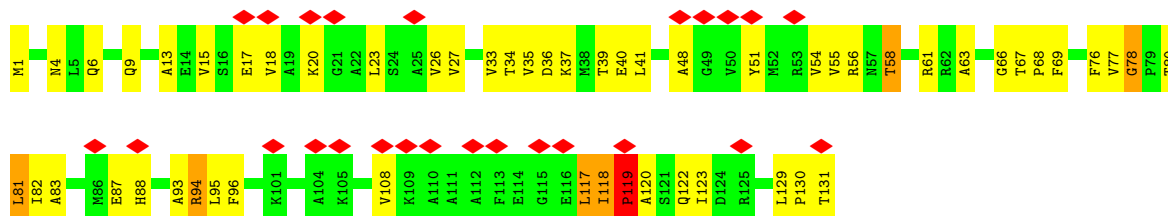
• Molecule 5: 50S ribosomal protein L6



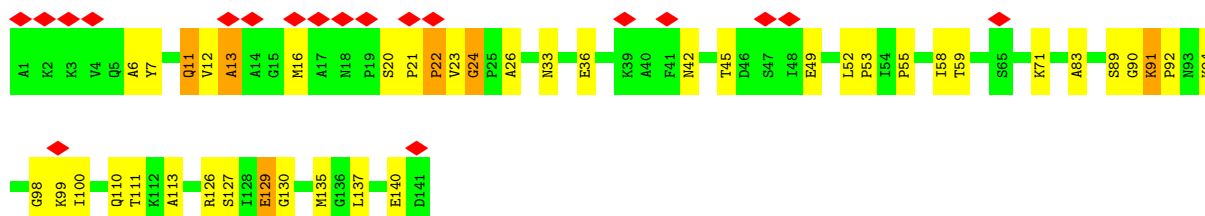
• Molecule 6: 50S ribosomal protein L9



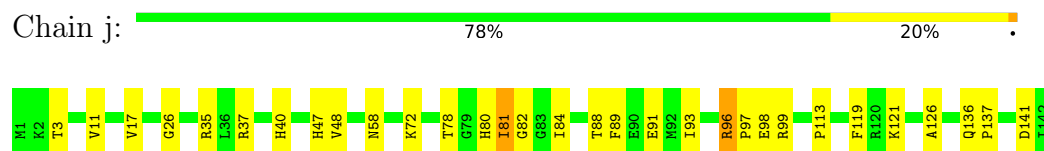
• Molecule 7: 50S ribosomal protein L10



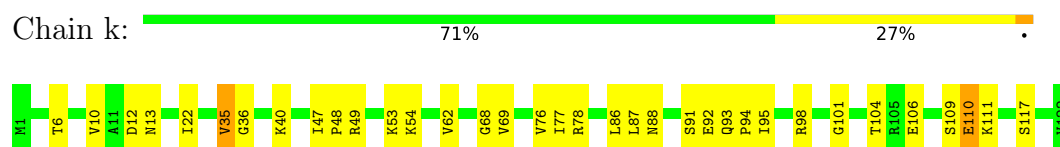
• Molecule 8: 50S ribosomal protein L11



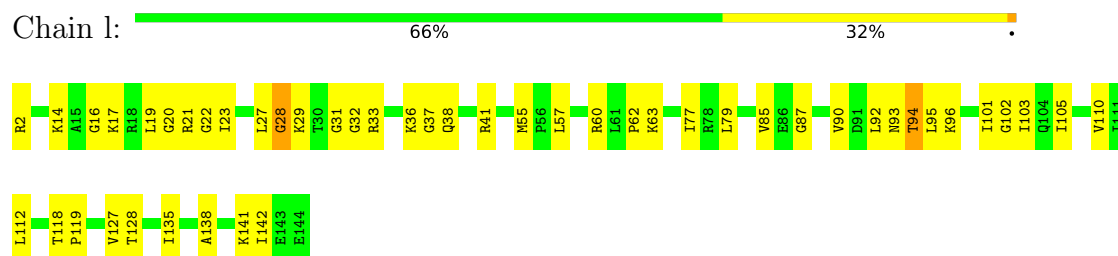
- Molecule 9: 50S ribosomal protein L13



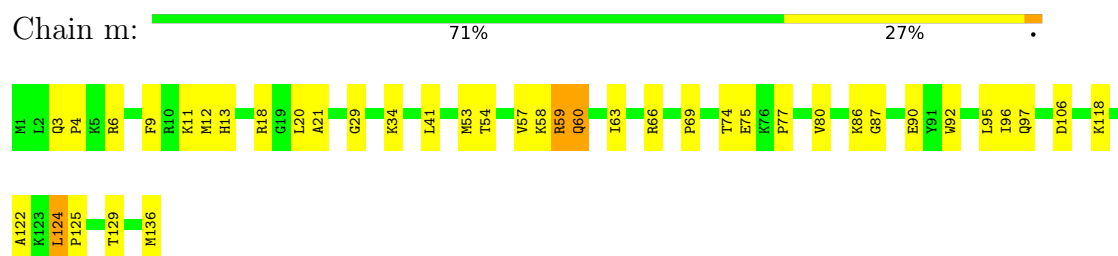
- Molecule 10: 50S ribosomal protein L14



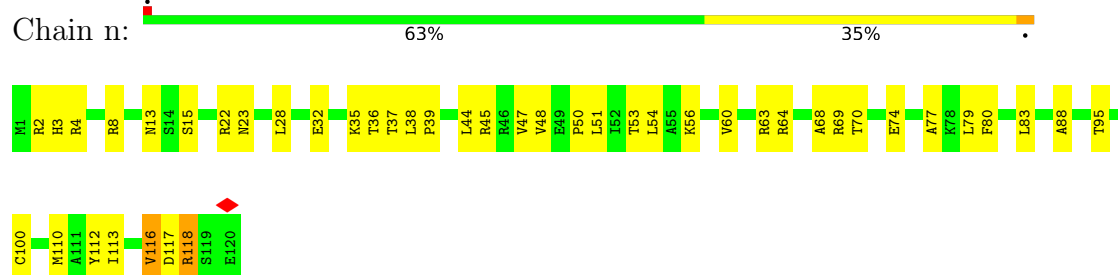
- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

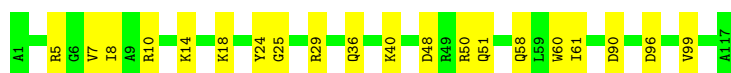
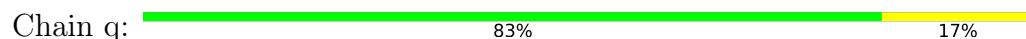




- Molecule 15: 50S ribosomal protein L19



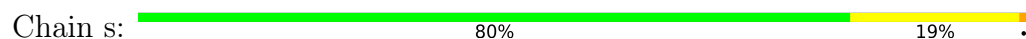
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25





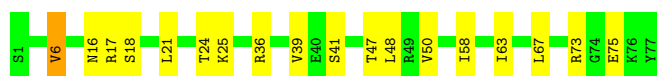
- Molecule 22: 50S ribosomal protein L27

Chain w: 85% 13%



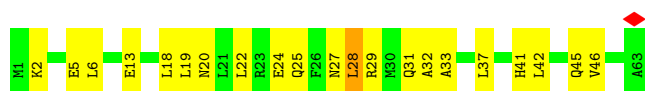
- Molecule 23: 50S ribosomal protein L28

Chain x: 77% 22%



- Molecule 24: 50S ribosomal protein L29

Chain y: 67% 32%



- Molecule 25: 50S ribosomal protein L30

Chain z: 81% 19%



- Molecule 26: 50S ribosomal protein L32

Chain B: 71% 29%



- Molecule 27: 50S ribosomal protein L33

Chain C: 78% 22%

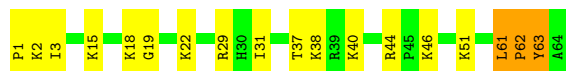


- Molecule 28: 50S ribosomal protein L34

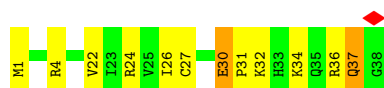
Chain D: 72% 28%



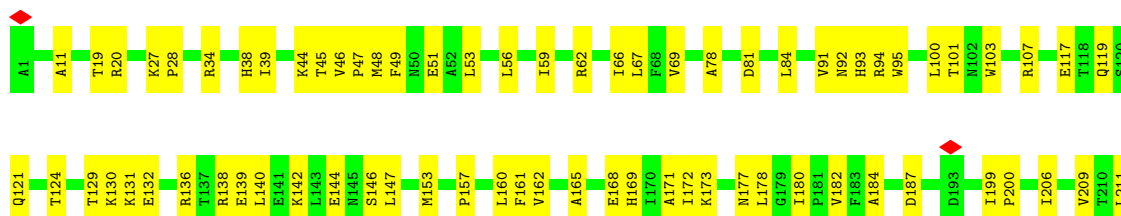
- Molecule 29: 50S ribosomal protein L35



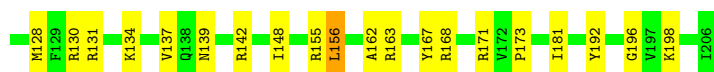
- Molecule 30: 50S ribosomal protein L36



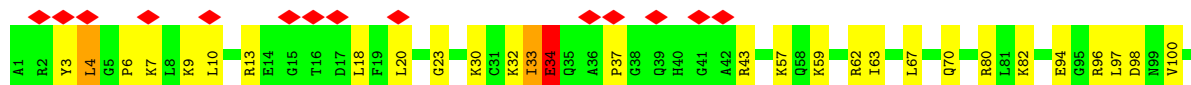
- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3

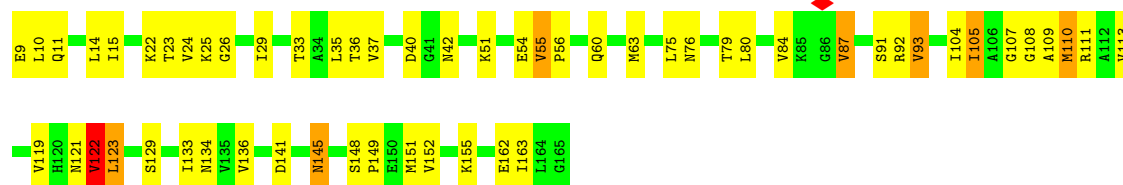


- Molecule 33: 30S ribosomal protein S4

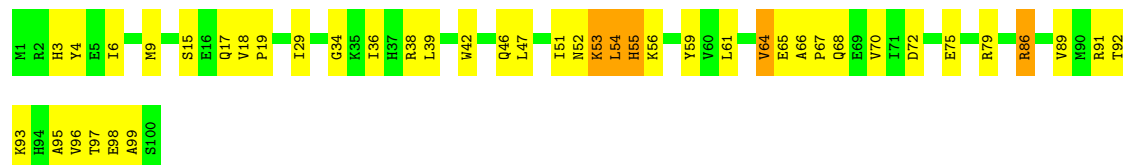




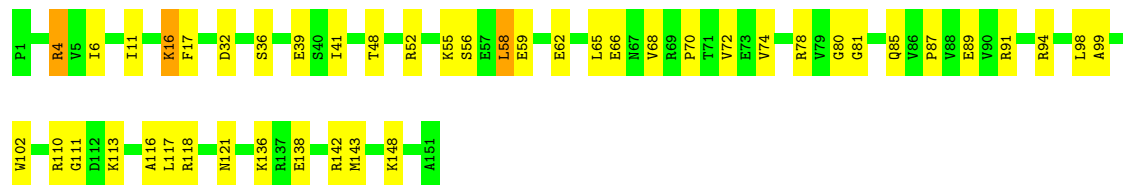
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6



- Molecule 36: 30S ribosomal protein S7

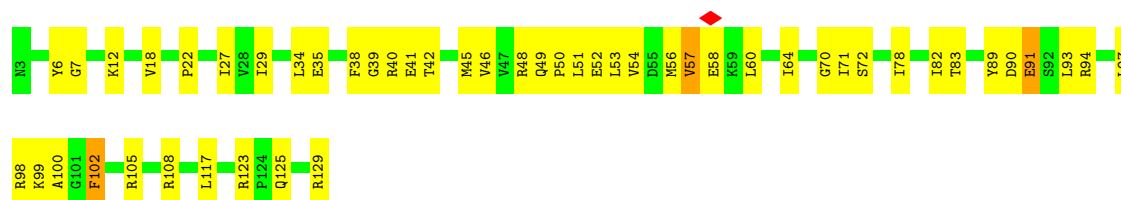


- Molecule 37: 30S ribosomal protein S8

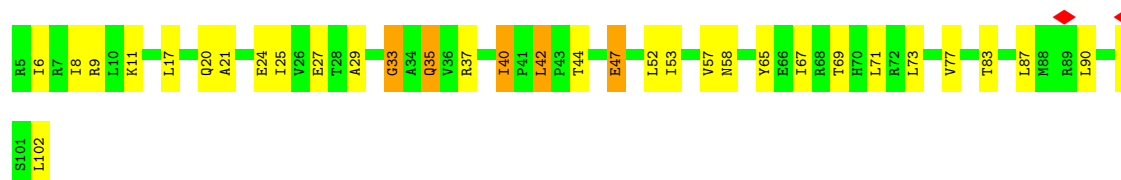


- Molecule 38: 30S ribosomal protein S9





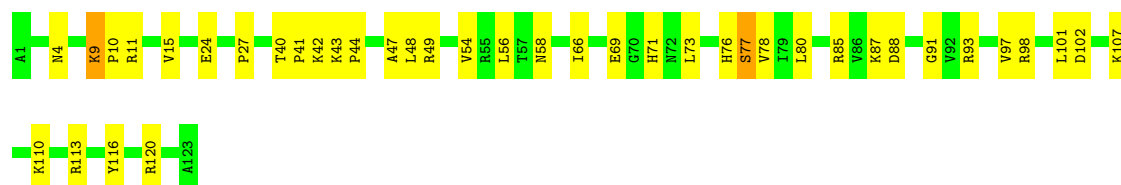
- Molecule 39: 30S ribosomal protein S10



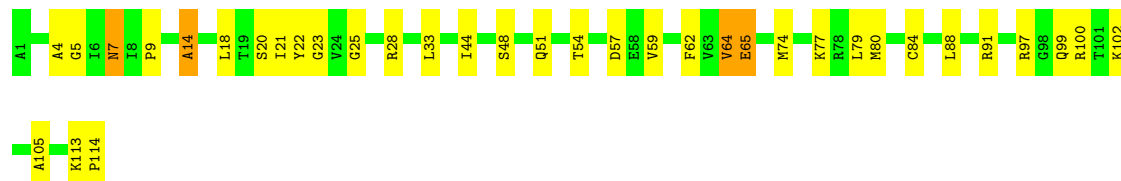
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

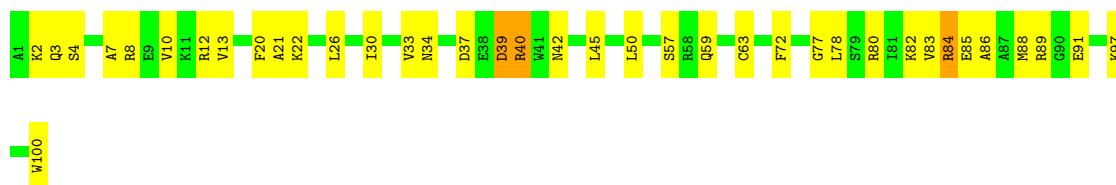


- Molecule 42: 30S ribosomal protein S13

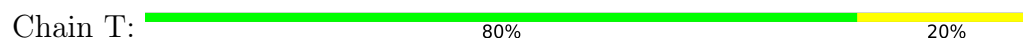


- Molecule 43: 30S ribosomal protein S14

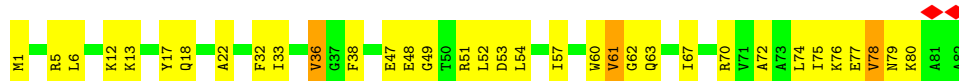




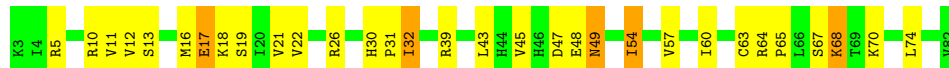
- Molecule 44: 30S ribosomal protein S15



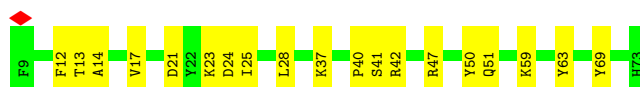
- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17



- Molecule 47: 30S ribosomal protein S18



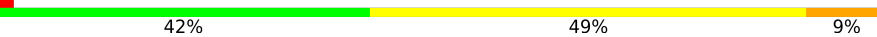
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20

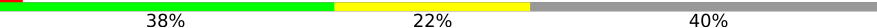


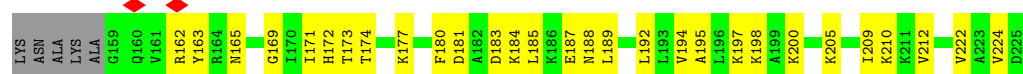
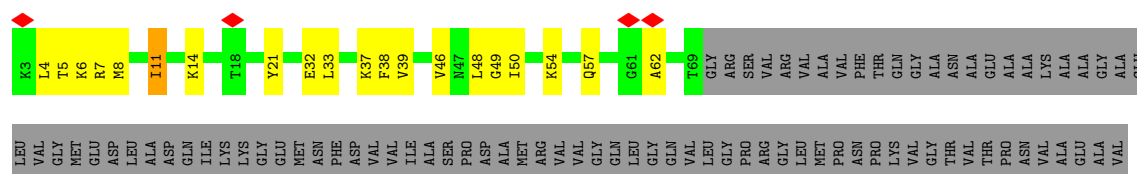
- Molecule 50: 30S ribosomal protein S21

Chain Z: 



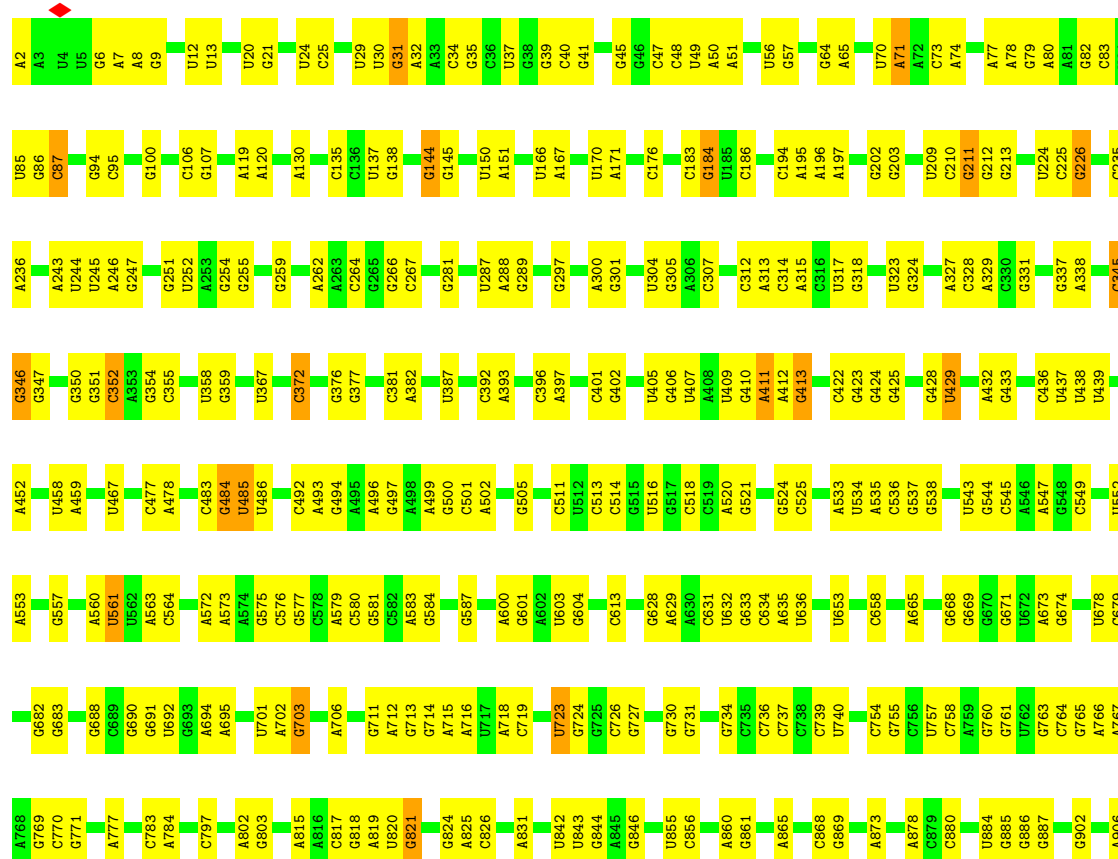
• Molecule 51: 50S ribosomal protein L1

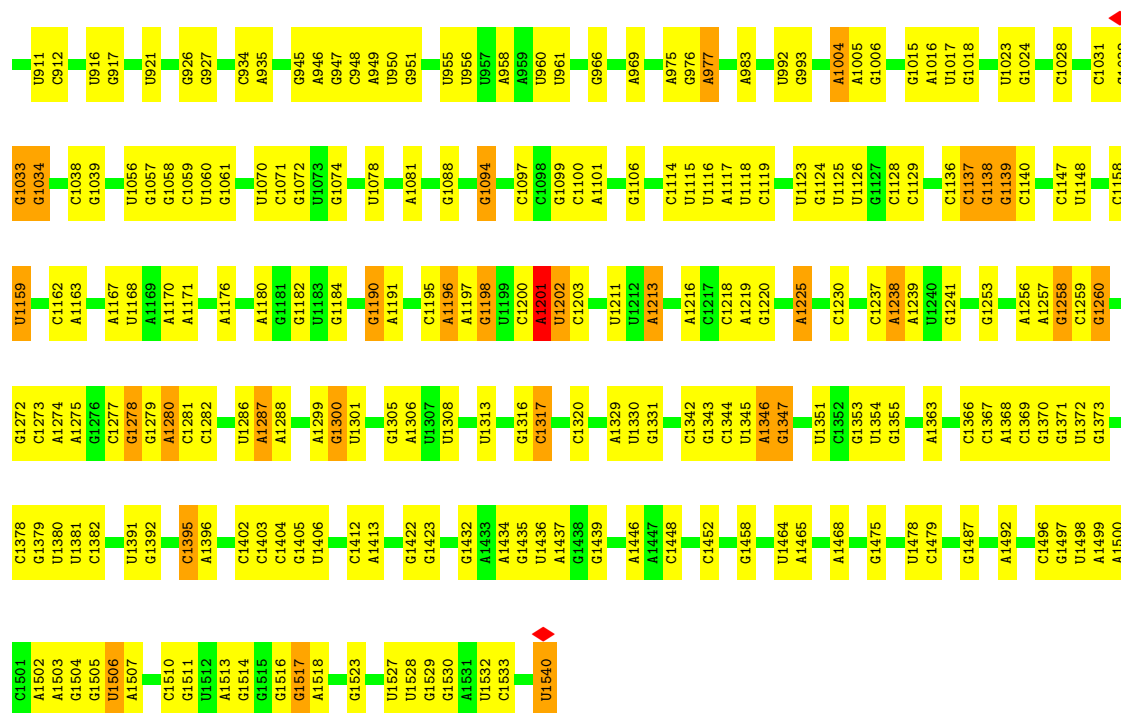
Chain a: 



• Molecule 52: 16S ribosomal RNA

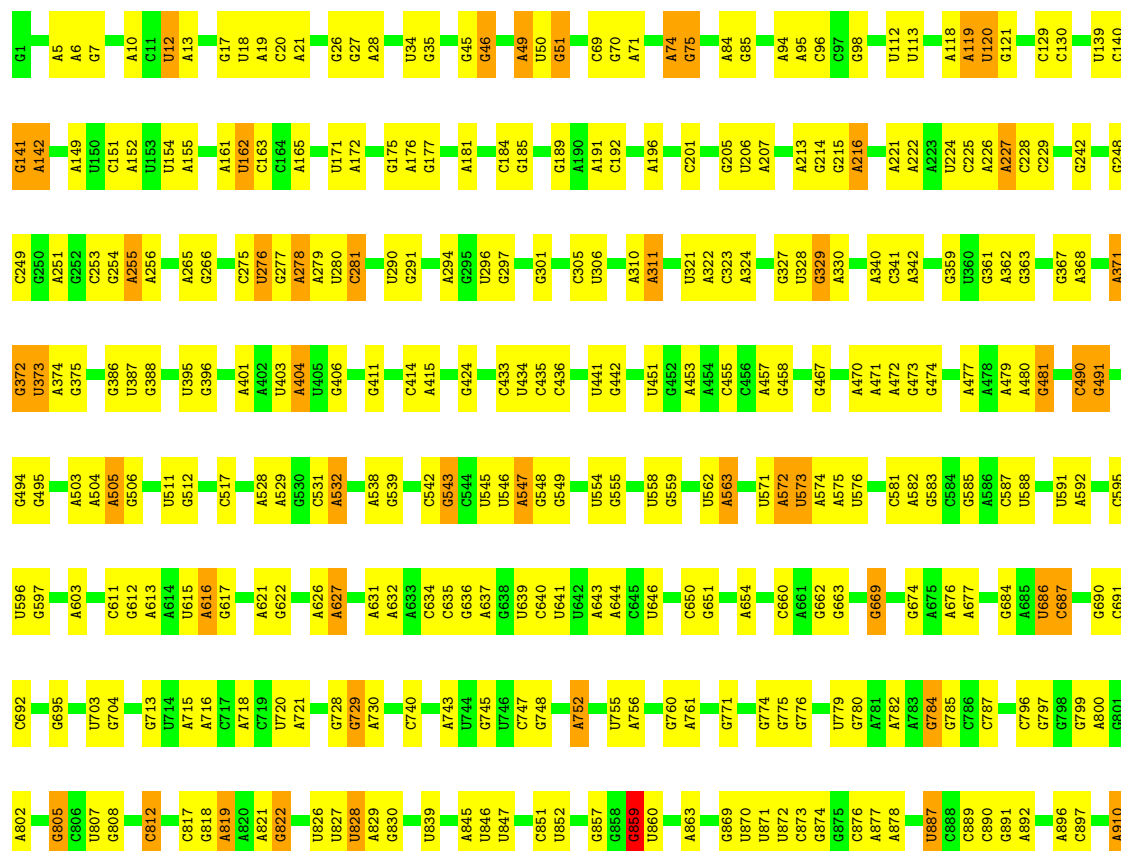
Chain 3: 



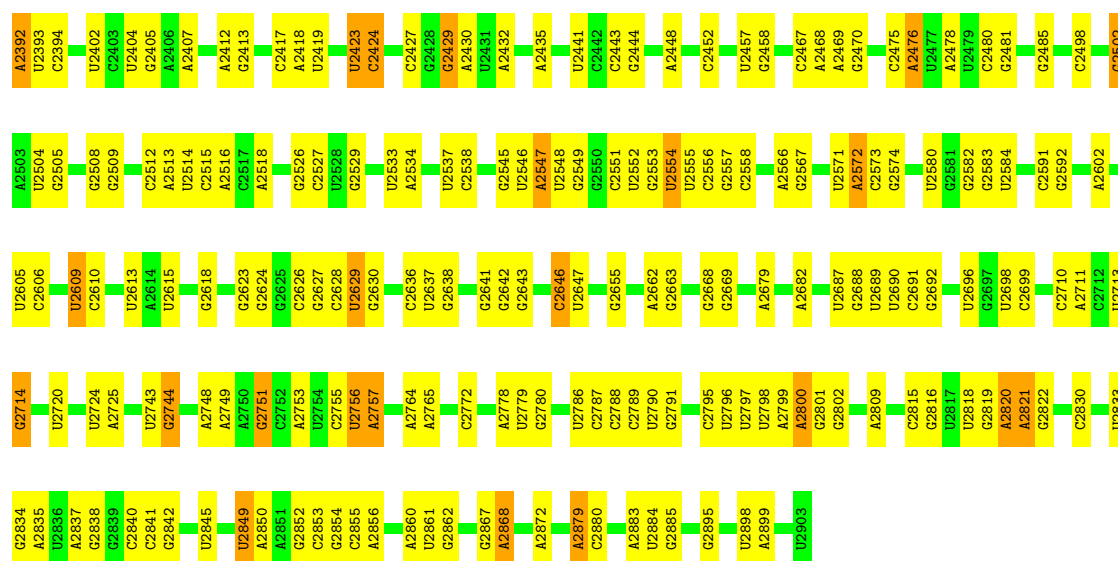


• Molecule 53: 23S ribosomal RNA

Chain 1: 62% 33% 5%

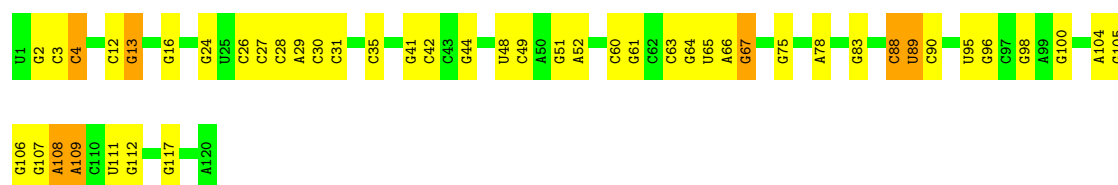


U2305	U2220	G2116	U2022	A1913	A1803	A1569	G1435	G1309	G1202	A1009	A911
G2308	G2221	U2118	C2024	C1914	G1807	G1581	C1436	G1310	C1104	A1010	A917
A2309	A2225	A2119	G2029	U1917	A1809	U1584	U1439	U1316	A1213	G1011	G924
C2313	U2229	G2120	A2030	A1919	A1810	C1585	U1440	G1317	G1216	C1013	A925
A2317	G2230	U2122	A2031	A1919	G1811	C1585	U1441	G1317	U1217	A1014	
G2318	G2239	G2123	G2032	G1929	G1816	C1592	G1441	A1321	G1218	U1015	U929
U2323	U2230	G2124	G2035	U1930	C1816	A1593	C1454	A1322	G1219	G1016	
G2324	G2234	A2126	C2036	A1931	A1819	A1600	C1461	U1326	G1220	U1019	U932
U2235	G2234	G2127	G2039	A1932	U1820	G1601	C1462	A1327	G1222	A1020	C935
U2236	G2237	U2128	U2039	A1936	G1826	U1715	C1463	A1328	G1223	A1021	A936
G2238	G2237	C2129	G2040	A1937	U1827	G1715	G1464	U1329	U1224	A1022	A937
U2329	U2238	U2132	A2042	A1938	G1828	U1720	U1468	C1330	G1225	U1023	G938
U2328	U2241	G2133	C2043	U1943	A1829	G1721	U1468	G1331	U1231	G1026	G940
G2330	G2242	U2139	C2044	U1944	C1830	U1729	G1475	G1332	G1232	A1027	G942
C2332	U2243	U2140	C2045	U1944	G1831	C1730	U1476	G1333	C1233	A1028	A941
U2333	U2244	G2141	G2048	C1947	G1837	C1732	G1482	A1336	U1234	A1029	
A2334	G2245	U2145	G2049	G1948	C1837	C1732	G1482	G1341	G1236	C1030	A943
A2335	A2247	C2145	C2055	U1955	G1846	U1736	A1490	G1344	G1250	U1033	C946
A2336	G2248	U2151	G2056	U1956	A1847	G1737	G1491	U1344	C1251	G1034	A947
G2337	G2250	U2155	A2060	C1957	A1848	G1738	C1498	C1345	G1252	U1035	C948
U2343	U2257	G2156	G2061	U1963	U1856	G1740	G1645	G1365	A1253	G1036	G949
G2344	G2258	C2156	A2062	G1964	G1857	G1740	G1646	U1366	G1254	A1039	C951
U2349	U2259	G2162	C2066	C1965	G1861	A1749	U1647	A1367	U1255		
C2350	G2260	A2163	G2067	A1966	G1861	G1749	U1648	G1368	C1138		
G2351	G2261	C2164	U2068	C1967	A1871	G1753	G1651	A1369	U1139		
A2352	U2265	U2172	G2069	A1970	A1872	A1757	G1652	C1370	C1139	C1045	U955
G2353	A2266	A2173	A2070	U1971	C1874	U1758	G1653	G1371	C1140	A1046	G956
	A2267		A2071	G1972	G1875		A1654		C1152	G1047	
A2358	A2268	U2180	C2072	G1983		C1764	A1664	U1378	C1153	C1053	C968
G2359	U2272	U2181	A2082	U1978	U1880	U1765	A1665	U1379	G1157	A1054	G969
G2360	A2273	U2182	G2083	G1980	C1881	G1766	G1659	G1381	C1161	A1057	U970
G2361	A2274	A2183			G1884	G1766	G1659	G1382	G1162	U1058	G971
A2366		A2184	U2086	G1983			A1664	A1383	G1059	A972	A973
G2367	G2277	U2189	G2087	G1983	A1889	U1774	A1665	C1386	C1167	U1060	G974
A2368	A2278	G2190	A2088	U1991	A1890	U1775	G1666	A1387	G1168	G1062	A975
G2369	G2279	A2191		G1992	C1891	G1776	A1669	U1394		U1066	
G2370	G2280	G2193	G2093	U1993	C1892	A1780	G1674	A1395	U1175		
G2371	G2281	C2196			C1893	U1781		C1398	A1176	A983	
U2372	G2282	U2197	C2096	C1996	G1894			C1398	G1177	A988	G989
	G2283	A2198		C1997		A1784		C1398	C1178	A1070	A990
A2376	A2284	A2199	C2104	A1998	A1899				G1179	G1071	
G2381	G2285	C2200	U2105	C1999	A1900	C1790	G1555	G1416	U1180		
A2381	G2286		U2106	A1999	A1901	A1791	G1564	A1419	C1297	U1077	C995
G2382	A2287	U2203	G2107	C2000	A1901	G1791	G1565	A1420	G1298	U1078	A996
G2383	A2288			C2001	G1906	U1796	G1566	G1685	G1299	A1079	
U2384			G2110	U2011	G1907	G1797	U1567	G1686	G1300	U1081	A1001
C2385	U2292	A2212	U2111	G2012	C1908	U1798	C1568	G1687	A1301	U1082	G1002
G2389	G2293	G2213	U2213	A2019	C1909	G1799	A1689	U1688	G1186	U1083	G1003
U2390	U2296	C2214	A2114	A2019	G1910	C1800	A1689	G1425	G1187	A1084	U1004
G2391	A2297	C2215	A2115	C2021	U1911	A1801	C1694	A1434	G1190	A1085	C1007
					A1912	A1802	G1568		A1307		A1008



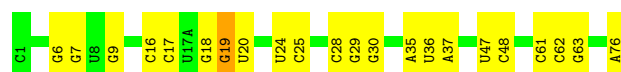
- Molecule 54: 5S ribosomal RNA

Chain 2: 61% 33% 6%



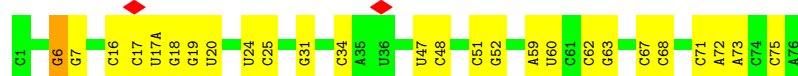
- Molecule 55: tRNA^{fMet}

Chain 5: 71% 27% .



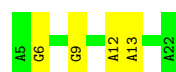
- Molecule 55: tRNA^{fMet}

Chain 6: 66% 32% .

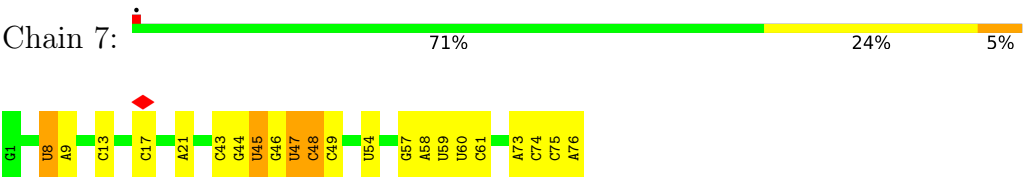


- Molecule 56: mRNA

Chain 4: 78% 22%



- Molecule 57: tRNA^{Phe}



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7369	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	20.349	Depositor
Minimum map value	-9.493	Depositor
Average map value	0.121	Depositor
Map value standard deviation	0.931	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	0.29	0/2122	0.97	7/2852 (0.2%)
2	c	0.29	0/1586	0.82	2/2134 (0.1%)
3	d	0.28	0/1571	0.90	3/2113 (0.1%)
4	e	0.31	0/1435	0.91	4/1926 (0.2%)
5	f	0.30	0/1343	0.86	4/1816 (0.2%)
6	g	0.34	0/1122	0.99	3/1515 (0.2%)
7	h	0.34	0/1002	1.01	8/1350 (0.6%)
8	i	0.35	0/1046	0.99	8/1410 (0.6%)
9	j	0.27	0/1152	0.82	4/1551 (0.3%)
10	k	0.28	0/948	0.97	3/1268 (0.2%)
11	l	0.30	0/1054	0.91	1/1403 (0.1%)
12	m	0.29	0/1093	0.89	3/1460 (0.2%)
13	n	0.31	0/974	0.91	2/1301 (0.2%)
14	o	0.29	0/902	0.89	5/1209 (0.4%)
15	p	0.29	0/929	0.83	2/1242 (0.2%)
16	q	0.29	0/960	0.86	1/1278 (0.1%)
17	r	0.30	0/829	0.90	2/1107 (0.2%)
18	s	0.27	0/864	0.85	0/1156
19	t	0.29	0/745	0.92	2/994 (0.2%)
20	u	0.29	0/788	0.89	2/1051 (0.2%)
21	v	0.28	0/766	0.86	2/1025 (0.2%)
22	w	0.30	0/582	0.83	0/769
23	x	0.29	0/635	0.78	0/848
24	y	0.28	0/510	0.78	1/677 (0.1%)
25	z	0.29	0/453	0.73	0/605
26	B	0.27	0/450	0.76	0/599
27	C	0.32	0/417	0.82	0/554
28	D	0.31	0/380	0.88	0/498
29	E	0.30	0/513	0.95	4/676 (0.6%)
30	F	0.35	0/303	0.90	2/397 (0.5%)
31	G	0.30	0/1788	0.90	3/2408 (0.1%)
32	H	0.30	0/1652	0.87	2/2225 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.93	6/2227 (0.3%)
34	J	0.33	0/1170	1.07	11/1573 (0.7%)
35	K	0.30	0/836	0.97	3/1128 (0.3%)
36	L	0.29	0/1196	0.90	3/1602 (0.2%)
37	M	0.30	0/989	0.95	3/1326 (0.2%)
38	N	0.29	0/1034	0.90	1/1375 (0.1%)
39	O	0.33	0/797	0.95	5/1077 (0.5%)
40	P	0.31	0/886	0.95	2/1195 (0.2%)
41	Q	0.31	0/969	1.03	5/1300 (0.4%)
42	R	0.30	0/893	0.87	0/1193
43	S	0.29	0/817	0.94	4/1088 (0.4%)
44	T	0.28	0/722	0.91	2/964 (0.2%)
45	U	0.32	0/659	0.97	4/884 (0.5%)
46	V	0.28	0/658	0.99	4/881 (0.5%)
47	W	0.30	0/545	0.88	2/731 (0.3%)
48	X	0.31	0/653	0.95	3/877 (0.3%)
49	Y	0.29	0/671	0.98	5/888 (0.6%)
50	Z	0.36	0/551	1.01	3/728 (0.4%)
51	a	0.33	0/1034	0.83	1/1387 (0.1%)
52	3	0.40	0/36963	0.50	2/57662 (0.0%)
53	1	0.39	0/69796	0.51	2/108888 (0.0%)
54	2	0.40	0/2872	0.51	0/4479
55	5	0.39	0/1832	0.48	0/2855
55	6	0.40	0/1832	0.51	0/2855
56	4	0.40	0/436	0.50	0/679
57	7	0.39	0/1809	0.48	0/2819
All	All	0.37	0/163199	0.64	151/244078 (0.1%)

There are no bond length outliers.

All (151) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	J	163	ILE	N-CA-C	10.98	120.96	110.42
3	d	73	ILE	N-CA-C	-9.62	103.77	113.10
17	r	50	GLY	N-CA-C	-7.93	102.62	112.77
36	L	16	LYS	N-CA-C	-7.76	105.78	114.62
34	J	55	VAL	N-CA-C	7.65	121.53	112.35
6	g	30	LEU	N-CA-C	7.60	119.20	111.07
7	h	117	LEU	N-CA-C	7.50	120.65	107.61
52	3	1201	A	C2'-C3'-O3'	7.47	120.71	109.50
8	i	24	GLY	CA-C-N	7.28	126.98	119.56
8	i	24	GLY	C-N-CA	7.28	126.98	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	f	47	ASN	N-CA-C	-7.15	103.86	112.59
43	S	39	ASP	N-CA-C	-7.02	104.19	112.89
29	E	63	TYR	N-CA-C	7.01	119.52	111.11
34	J	110	MET	N-CA-C	-6.97	104.24	112.89
1	b	66	PHE	N-CA-C	-6.75	105.18	113.41
39	O	21	ALA	N-CA-C	-6.62	103.89	112.23
6	g	6	LEU	N-CA-C	-6.57	106.21	114.56
31	G	222	GLU	N-CA-C	-6.57	103.95	112.23
1	b	265	PHE	N-CA-C	6.43	118.37	111.36
16	q	50	ARG	N-CA-C	-6.42	105.10	113.12
41	Q	43	LYS	N-CA-C	6.42	124.00	109.81
3	d	178	VAL	N-CA-C	6.42	117.17	110.62
9	j	119	PHE	N-CA-C	-6.37	105.54	113.38
8	i	127	SER	N-CA-C	-6.37	104.20	112.23
36	L	58	LEU	N-CA-C	6.36	118.22	111.28
46	V	68	LYS	N-CA-C	-6.33	104.38	111.28
14	o	68	LYS	N-CA-C	6.32	118.69	111.11
11	l	14	LYS	N-CA-C	-6.30	104.33	114.09
1	b	153	LEU	N-CA-C	6.27	119.76	110.48
19	t	56	GLU	N-CA-C	-6.27	104.07	111.03
49	Y	67	HIS	N-CA-C	6.24	119.36	110.68
5	f	139	VAL	N-CA-C	6.20	116.94	110.62
34	J	145	ASN	N-CA-C	-6.20	105.72	113.28
34	J	123	LEU	N-CA-C	-6.15	99.67	109.76
45	U	61	VAL	N-CA-C	-6.14	103.20	111.44
34	J	122	VAL	N-CA-C	6.13	122.09	109.34
15	p	16	VAL	N-CA-C	6.12	113.61	107.55
37	M	62	LEU	N-CA-C	6.09	117.74	110.19
41	Q	54	VAL	N-CA-C	6.08	117.53	108.46
7	h	94	ARG	N-CA-C	6.08	120.20	113.21
30	F	30	GLU	CA-C-N	6.06	125.95	119.28
30	F	30	GLU	C-N-CA	6.06	125.95	119.28
48	X	9	PHE	N-CA-C	6.04	118.56	110.35
39	O	40	ILE	CA-C-N	6.02	125.23	118.97
39	O	40	ILE	C-N-CA	6.02	125.23	118.97
47	W	69	TYR	N-CA-C	-6.02	104.65	112.23
52	3	1190	G	C2'-C3'-O3'	5.99	118.49	109.50
35	K	68	GLN	N-CA-C	5.95	119.64	112.38
8	i	130	GLY	N-CA-C	-5.95	105.39	113.37
50	Z	49	ALA	N-CA-C	-5.93	104.89	111.36
37	M	118	ALA	N-CA-C	-5.92	106.22	113.50
7	h	78	GLY	CA-C-N	5.89	127.21	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	h	78	GLY	C-N-CA	5.89	127.21	119.84
2	c	203	VAL	N-CA-C	5.89	116.42	108.17
32	H	34	SER	N-CA-C	-5.88	104.99	111.82
8	i	129	GLU	N-CA-C	-5.88	105.60	112.89
13	n	116	VAL	N-CA-C	5.88	121.57	109.34
37	M	127	TYR	N-CA-C	-5.86	101.53	110.14
12	m	118	LYS	N-CA-C	-5.85	104.26	111.40
49	Y	7	LYS	N-CA-C	-5.85	106.12	113.20
5	f	144	ALA	N-CA-C	-5.84	105.00	111.36
40	P	125	LYS	N-CA-C	5.83	123.21	110.80
33	I	166	LYS	CA-C-N	5.83	127.12	119.84
33	I	166	LYS	C-N-CA	5.83	127.12	119.84
46	V	63	CYS	N-CA-C	5.82	116.10	108.07
10	k	111	LYS	N-CA-C	-5.80	106.21	113.28
51	a	11	ILE	N-CA-C	5.77	115.90	110.30
33	I	199	ILE	N-CA-C	5.74	115.94	110.42
31	G	92	ASN	N-CA-C	5.65	120.70	113.18
33	I	94	GLU	N-CA-C	-5.65	106.39	113.28
40	P	69	CYS	N-CA-C	-5.64	106.44	113.38
45	U	76	LYS	N-CA-C	-5.64	105.12	112.23
48	X	40	PHE	CA-C-N	5.64	126.01	119.47
48	X	40	PHE	C-N-CA	5.64	126.01	119.47
29	E	61	LEU	CA-C-N	5.63	126.88	119.84
29	E	61	LEU	C-N-CA	5.63	126.88	119.84
43	S	84	ARG	N-CA-C	-5.61	105.17	112.23
8	i	91	LYS	CA-C-N	5.59	126.82	119.84
8	i	91	LYS	C-N-CA	5.59	126.82	119.84
41	Q	58	ASN	N-CA-C	-5.57	106.48	113.28
9	j	96	ARG	CA-C-N	5.56	125.17	119.56
9	j	96	ARG	C-N-CA	5.56	125.17	119.56
21	v	22	ALA	N-CA-C	-5.55	106.71	112.93
49	Y	68	LYS	N-CA-C	5.53	122.58	110.80
1	b	259	ASN	N-CA-C	-5.53	106.47	113.43
21	v	80	HIS	N-CA-C	-5.51	103.12	110.07
45	U	62	GLY	N-CA-C	-5.51	107.49	114.16
1	b	30	ALA	N-CA-C	5.50	121.97	109.81
20	u	96	LYS	N-CA-C	-5.50	102.62	110.59
41	Q	9	LYS	CA-C-N	5.49	126.26	120.11
41	Q	9	LYS	C-N-CA	5.49	126.26	120.11
20	u	75	ALA	N-CA-C	-5.48	107.85	114.75
15	p	68	GLY	N-CA-C	5.48	118.99	111.54
43	S	50	LEU	N-CA-C	-5.47	102.88	109.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	J	141	ASP	N-CA-C	-5.45	105.42	111.36
8	i	111	THR	N-CA-C	-5.43	105.44	111.36
29	E	38	LYS	N-CA-C	-5.43	105.52	111.82
9	j	121	LYS	N-CA-C	-5.43	106.50	113.23
53	l	859	G	N9-C1'-C2'	5.41	120.12	112.00
34	J	134	ASN	N-CA-C	5.40	117.17	111.28
43	S	40	ARG	N-CA-C	-5.39	105.57	111.82
45	U	78	VAL	N-CA-C	-5.38	105.75	113.07
49	Y	71	ALA	N-CA-C	-5.38	105.42	111.28
33	I	34	GLU	N-CA-C	5.37	122.24	110.80
32	H	41	TYR	N-CA-C	5.37	116.94	111.14
46	V	54	ILE	N-CA-C	5.34	115.28	107.37
50	Z	8	ASN	N-CA-C	5.34	122.17	110.80
24	y	28	LEU	N-CA-C	-5.33	106.28	112.89
4	e	6	TYR	N-CA-C	-5.33	105.64	111.82
35	K	15	SER	N-CA-C	-5.33	106.28	112.89
10	k	95	ILE	N-CA-C	-5.33	107.28	112.29
17	r	49	ILE	N-CA-C	5.32	114.96	106.88
31	G	93	HIS	N-CA-C	5.30	117.87	111.40
10	k	117	SER	N-CA-C	-5.29	106.34	112.89
13	n	68	ALA	N-CA-C	-5.29	105.63	111.71
35	K	64	VAL	N-CA-C	5.29	116.09	108.48
34	J	162	GLU	N-CA-C	5.28	117.46	111.02
7	h	119	PRO	N-CA-C	-5.27	101.61	112.47
14	o	56	LYS	N-CA-C	5.27	118.49	111.75
50	Z	45	LYS	N-CA-C	-5.27	106.36	112.89
2	c	152	PRO	N-CA-C	-5.25	106.37	113.40
36	L	4	ARG	N-CA-C	5.24	117.91	110.10
19	t	64	LYS	N-CA-C	5.24	117.29	110.53
14	o	41	ALA	CA-C-N	5.24	124.86	119.05
14	o	41	ALA	C-N-CA	5.24	124.86	119.05
33	I	33	ILE	N-CA-C	5.22	116.71	109.45
39	O	42	LEU	CA-C-N	5.22	125.21	119.89
39	O	42	LEU	C-N-CA	5.22	125.21	119.89
6	g	62	LEU	N-CA-C	-5.21	105.66	112.23
4	e	106	ALA	N-CA-C	5.20	116.64	110.97
49	Y	8	LYS	N-CA-C	-5.19	105.80	111.82
38	N	40	ARG	N-CA-C	-5.18	106.91	113.18
1	b	40	GLY	N-CA-C	-5.16	108.49	115.36
7	h	55	VAL	N-CA-C	5.15	115.73	109.30
34	J	87	VAL	N-CA-C	5.14	116.03	109.30
53	l	1020	A	C2'-C3'-O3'	5.12	117.18	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	e	107	VAL	CB-CA-C	-5.11	108.93	114.35
47	W	14	ALA	N-CA-C	-5.11	105.90	111.82
14	o	55	GLU	N-CA-C	-5.09	101.82	109.15
7	h	4	ASN	N-CA-C	5.09	119.76	111.37
3	d	146	VAL	N-CA-C	5.08	116.22	108.80
5	f	141	GLY	N-CA-C	-5.08	106.27	112.77
34	J	60	GLN	N-CA-C	-5.07	105.84	112.23
44	T	68	TYR	N-CA-C	-5.07	105.83	111.36
7	h	78	GLY	N-CA-C	5.07	122.68	112.34
46	V	32	ILE	CB-CA-C	-5.05	107.42	111.71
12	m	124	LEU	CA-C-N	5.04	124.65	119.56
12	m	124	LEU	C-N-CA	5.04	124.65	119.56
44	T	57	ARG	N-CA-C	-5.03	105.71	111.14
4	e	10	GLU	N-CA-C	5.03	117.53	111.40
1	b	223	ALA	N-CA-C	-5.00	107.17	114.12

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	67	0
2	c	1565	0	1616	42	0
3	d	1552	0	1619	37	0
4	e	1411	0	1447	42	0
5	f	1323	0	1374	24	0
6	g	1111	0	1148	30	0
7	h	989	0	1025	42	0
8	i	1032	0	1088	31	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	30	0
11	l	1045	0	1117	39	0
12	m	1074	0	1157	39	0
13	n	961	0	1000	35	0
14	o	892	0	923	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	p	917	0	965	24	0
16	q	947	0	1022	19	0
17	r	816	0	839	27	0
18	s	857	0	922	15	0
19	t	739	0	807	17	0
20	u	780	0	834	24	0
21	v	753	0	780	21	0
22	w	575	0	592	13	0
23	x	625	0	655	9	0
24	y	509	0	543	14	0
25	z	449	0	491	9	0
26	B	444	0	461	13	0
27	C	410	0	440	9	0
28	D	377	0	418	11	0
29	E	504	0	574	17	0
30	F	302	0	343	12	0
31	G	1757	0	1787	55	0
32	H	1625	0	1699	43	0
33	I	1643	0	1710	50	0
34	J	1157	0	1199	49	0
35	K	818	0	808	38	0
36	L	1182	0	1240	35	0
37	M	979	0	1034	33	0
38	N	1022	0	1070	40	0
39	O	787	0	828	26	0
40	P	870	0	878	27	0
41	Q	955	0	1019	31	0
42	R	884	0	944	28	0
43	S	805	0	847	29	0
44	T	714	0	737	13	0
45	U	649	0	666	26	0
46	V	649	0	691	22	0
47	W	536	0	552	11	0
48	X	638	0	665	26	0
49	Y	665	0	714	27	0
50	Z	545	0	579	38	0
51	a	1027	0	1092	40	0
52	3	33012	0	16618	411	0
53	1	62317	0	31346	747	0
54	2	2568	0	1303	43	0
55	5	1640	0	837	10	0
55	6	1640	0	837	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	4	388	0	197	2	0
57	7	1619	0	821	9	0
58	1	8	0	8	0	0
59	7	11	0	8	0	0
All	All	150220	0	101265	2328	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 9.

All (2328) 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)
53:1:45:G:H5''	53:1:46:G:H5'	1.23	1.11
36:L:78:ARG:HH22	52:3:1382:C:H5'	1.20	1.01
34:J:54:GLU:HG3	34:J:56:PRO:HD2	1.44	0.99
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.44	0.98
12:m:12:MET:HA	53:1:910:A:H62	1.33	0.92
23:x:58:ILE:HG23	23:x:63:ILE:HG22	1.50	0.91
39:O:57:VAL:HG22	39:O:58:ASN:H	1.37	0.90
36:L:91:ARG:HH21	52:3:1378:C:H4'	1.38	0.88
31:G:11:ALA:HB2	31:G:211:LEU:HD12	1.55	0.87
53:1:1906:G:H2'	53:1:1907:G:H5''	1.53	0.87
1:b:149:LYS:HD3	53:1:2204:G:H4'	1.57	0.87
4:e:107:VAL:HG23	4:e:108:PRO:HD3	1.56	0.87
53:1:2277:G:H2'	53:1:2278:A:H5''	1.57	0.87
42:R:7:ASN:HD22	42:R:21:ILE:HG13	1.37	0.87
53:1:1020:A:H1'	53:1:1021:A:OP2	1.75	0.86
33:I:9:LYS:HD3	52:3:428:G:H5''	1.56	0.86
53:1:2296:U:H5''	53:1:2297:A:OP1	1.75	0.85
33:I:10:LEU:HD13	33:I:62:ARG:HD2	1.58	0.85
8:i:12:VAL:HG22	8:i:13:ALA:H	1.42	0.84
3:d:149:ILE:HD12	3:d:175:ILE:HD11	1.60	0.84
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.60	0.83
20:u:11:ILE:HD11	20:u:79:ALA:HB2	1.61	0.82
50:Z:23:GLU:HG2	50:Z:24:LYS:H	1.44	0.82
52:3:1259:C:H3'	52:3:1260:G:H5''	1.61	0.82
53:1:2286:G:H5''	53:1:2287:A:OP1	1.80	0.81
52:3:405:U:H3'	52:3:406:G:H5'	1.62	0.81
2:c:151:THR:HB	2:c:152:PRO:HD3	1.62	0.81
52:3:484:G:H4'	52:3:485:U:H5''	1.62	0.81
9:j:3:THR:HG21	16:q:60:TRP:HE1	1.45	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:48:LEU:HB2	52:3:520:A:OP1	1.81	0.80
53:1:1053:C:H2'	53:1:1054:A:H5''	1.63	0.80
32:H:39:ARG:HG3	32:H:54:ILE:HD11	1.64	0.80
53:1:1645:G:H5''	53:1:1646:C:H5'	1.63	0.80
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.63	0.79
53:1:1077:A:H2'	53:1:1078:U:H5'	1.66	0.78
8:i:42:ASN:HA	8:i:45:THR:HG22	1.65	0.78
45:U:48:GLU:HG2	45:U:49:GLY:H	1.46	0.78
24:y:2:LYS:HZ1	24:y:6:LEU:HD22	1.49	0.77
33:I:120:LYS:HE3	52:3:439:U:H5''	1.65	0.77
54:2:3:C:H2'	54:2:4:C:H5''	1.67	0.77
38:N:57:VAL:HG23	38:N:58:GLU:H	1.50	0.77
49:Y:27:MET:HE2	49:Y:60:GLN:HG3	1.65	0.77
51:a:174:THR:HB	53:1:2124:G:H4'	1.68	0.76
52:3:769:G:H4'	52:3:1513:A:H4'	1.68	0.76
31:G:20:ARG:HE	52:3:831:A:H5''	1.50	0.75
53:1:1664:A:H61	53:1:1996:C:H42	1.33	0.75
48:X:18:VAL:HG11	48:X:43:MET:HE3	1.67	0.75
52:3:1301:U:O2	52:3:1301:U:H2'	1.86	0.75
41:Q:120:ARG:CZ	52:3:500:G:H5'	2.17	0.75
49:Y:25:SER:OG	52:3:1458:G:H5''	1.85	0.75
36:L:78:ARG:HH22	52:3:1382:C:C5'	1.98	0.75
44:T:71:ARG:HH22	52:3:754:C:H5'	1.52	0.75
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.66	0.75
1:b:180:MET:HB2	1:b:268:ARG:HB2	1.69	0.75
35:K:6:ILE:H	35:K:6:ILE:HD12	1.52	0.74
53:1:2834:G:H2'	53:1:2879:A:H61	1.51	0.74
1:b:94:LEU:HD21	53:1:1501:G:H4'	1.69	0.74
7:h:33:VAL:HG22	7:h:34:THR:H	1.51	0.74
37:M:35:ILE:HG13	37:M:102:VAL:HG11	1.69	0.74
37:M:125:ILE:HG22	37:M:126:CYS:SG	2.27	0.74
5:f:154:GLU:HG2	5:f:156:TYR:H	1.51	0.74
7:h:6:GLN:O	7:h:9:GLN:HG3	1.88	0.74
8:i:55:PRO:HG2	8:i:71:LYS:HB3	1.68	0.74
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.70	0.74
46:V:12:VAL:HG13	46:V:21:VAL:HG13	1.69	0.74
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.70	0.74
34:J:133:ILE:H	34:J:133:ILE:HD12	1.52	0.74
7:h:118:ILE:H	7:h:119:PRO:CD	2.00	0.74
39:O:40:ILE:HB	39:O:73:LEU:HB3	1.69	0.73
42:R:91:ARG:HH22	53:1:887:U:H5'	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1141:U:H4'	53:1:1142:A:O4'	1.88	0.73
1:b:144:GLU:HB2	1:b:187:CYS:HB3	1.70	0.73
53:1:2391:G:H4'	53:1:2392:A:OP1	1.87	0.73
53:1:329:G:O4'	53:1:477:A:H1'	1.88	0.73
52:3:1306:A:H61	52:3:1331:G:H1'	1.53	0.73
7:h:77:VAL:HG22	7:h:82:ILE:HG13	1.70	0.73
11:l:93:ASN:O	11:l:94:THR:HG22	1.88	0.73
41:Q:101:LEU:HD12	41:Q:101:LEU:H	1.53	0.73
31:G:34:ARG:HG2	31:G:39:ILE:HD11	1.70	0.72
2:c:155:VAL:HG21	53:1:2618:G:H21	1.54	0.72
3:d:108:ILE:HG13	3:d:109:LEU:HD12	1.70	0.72
34:J:22:LYS:HB3	34:J:29:ILE:HG23	1.70	0.72
29:E:3:ILE:H	29:E:3:ILE:HD12	1.53	0.72
41:Q:85:ARG:HH12	41:Q:87:LYS:HB2	1.53	0.72
53:1:807:U:H2'	53:1:808:G:H8	1.52	0.72
10:k:13:ASN:HD21	10:k:98:ARG:HB2	1.55	0.72
35:K:52:ASN:O	35:K:53:LYS:HG3	1.90	0.72
4:e:141:ASP:HB2	4:e:144:LYS:HD3	1.72	0.72
11:l:63:LYS:HE3	53:1:2394:C:H5''	1.72	0.72
18:s:82:MET:HB2	18:s:98:LYS:HB2	1.71	0.72
53:1:572:A:H61	53:1:2029:G:H21	1.36	0.72
2:c:81:GLU:OE1	53:1:2636:C:H4'	1.89	0.72
52:3:1033:G:H2'	52:3:1034:G:H5''	1.72	0.72
1:b:252:LYS:HD3	53:1:1901:A:H4'	1.72	0.72
9:j:96:ARG:HG3	9:j:99:ARG:HG2	1.72	0.72
53:1:676:A:H62	53:1:802:A:H61	1.38	0.72
46:V:18:LYS:HD3	52:3:255:G:H4'	1.70	0.72
40:P:126:ARG:NH2	52:3:692:U:H5''	2.04	0.71
3:d:63:LYS:HD2	53:1:2444:G:OP2	1.90	0.71
6:g:68:ARG:HH12	6:g:71:LYS:HB2	1.53	0.71
7:h:118:ILE:H	7:h:119:PRO:HD2	1.55	0.71
34:J:15:ILE:HD11	34:J:37:VAL:HG22	1.71	0.71
15:p:38:ARG:NE	52:3:345:C:H5'	2.06	0.71
52:3:1230:C:H5'	55:5:30:G:H5''	1.72	0.71
7:h:23:LEU:HD11	7:h:96:PHE:HB2	1.73	0.70
40:P:88:PRO:HD3	50:Z:28:LEU:HD21	1.72	0.70
48:X:28:LYS:HD3	48:X:29:PRO:HD2	1.74	0.70
32:H:21:TRP:HB3	32:H:58:ARG:H	1.55	0.70
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.71	0.70
15:p:24:THR:HG23	15:p:86:LYS:HB2	1.73	0.70
34:J:121:ASN:ND2	34:J:122:VAL:HG13	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:80:ARG:NH1	53:1:571:U:H2'	2.07	0.69
51:a:37:LYS:HB2	53:1:2127:G:H5'	1.73	0.69
4:e:32:LYS:HD3	4:e:91:ARG:NH2	2.07	0.69
4:e:40:GLY:HA2	4:e:84:ILE:HD11	1.74	0.69
33:I:103:ARG:HH12	33:I:110:ARG:HH21	1.40	0.69
53:1:821:A:H5''	53:1:822:G:H5''	1.74	0.69
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.73	0.69
36:L:91:ARG:NH2	52:3:1378:C:H4'	2.05	0.69
52:3:327:A:O2'	52:3:328:C:H4'	1.93	0.69
53:1:2427:C:H5''	53:1:2429:G:H5'	1.75	0.69
8:i:20:SER:OG	8:i:21:PRO:HD3	1.93	0.69
10:k:35:VAL:HG13	10:k:36:GLY:H	1.56	0.69
18:s:93:ALA:HB2	53:1:1614:A:N1	2.08	0.69
31:G:129:THR:HG22	31:G:130:LYS:H	1.57	0.69
6:g:4:ILE:HG23	6:g:37:VAL:HG23	1.75	0.69
10:k:104:THR:HG22	10:k:106:GLU:H	1.57	0.69
28:D:18:PHE:HB2	28:D:43:THR:HG21	1.73	0.69
45:U:18:GLN:HA	45:U:38:PHE:HA	1.75	0.69
50:Z:16:ARG:HD2	50:Z:19:LYS:HD3	1.73	0.69
53:1:1045:C:H5'	53:1:1046:A:H5''	1.74	0.69
53:1:1367:A:H2'	53:1:1368:G:H5'	1.74	0.69
2:c:142:VAL:HG22	2:c:143:PRO:HD2	1.75	0.69
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.74	0.69
5:f:173:ALA:O	5:f:174:LYS:HG3	1.93	0.69
53:1:2048:G:H3'	53:1:2049:G:H5''	1.75	0.69
32:H:139:ASN:HD22	32:H:142:ARG:HE	1.38	0.68
53:1:2452:C:H42	53:1:2504:U:H3	1.40	0.68
33:I:7:LYS:HG2	33:I:20:LEU:HB3	1.75	0.68
1:b:216:ARG:HG3	1:b:217:PRO:HD2	1.74	0.68
17:r:17:GLY:H	17:r:98:ILE:HG23	1.58	0.68
7:h:87:GLU:CD	7:h:93:ALA:HB3	2.18	0.68
31:G:56:LEU:HD23	31:G:59:ILE:HD11	1.76	0.68
48:X:28:LYS:HD3	48:X:29:PRO:CD	2.23	0.68
5:f:88:LEU:HD22	5:f:95:ALA:HB2	1.75	0.68
31:G:103:TRP:HE1	31:G:107:ARG:HH21	1.39	0.68
53:1:1906:G:C2'	53:1:1907:G:H5''	2.23	0.68
32:H:198:LYS:HE3	52:3:1058:G:OP1	1.93	0.68
11:l:90:VAL:HG13	11:l:95:LEU:HD11	1.76	0.68
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.75	0.68
45:U:54:LEU:H	45:U:54:LEU:HD12	1.59	0.68
12:m:13:HIS:HE1	53:1:2265:U:H4'	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:13:ARG:HH21	33:I:37:PRO:HB2	1.60	0.67
20:u:65:GLN:HB2	20:u:68:ASN:ND2	2.09	0.67
38:N:53:LEU:HD12	38:N:54:VAL:HG13	1.76	0.67
53:1:2277:G:C2'	53:1:2278:A:H5''	2.24	0.67
4:e:107:VAL:CG2	4:e:108:PRO:HD3	2.24	0.67
8:i:89:SER:HB2	8:i:92:PRO:HG3	1.77	0.67
38:N:46:VAL:HA	38:N:49:GLN:HG3	1.76	0.67
52:3:346:G:H2'	52:3:347:G:H5'	1.74	0.67
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.75	0.67
53:1:807:U:H2'	53:1:808:G:C8	2.29	0.67
2:c:9:VAL:HB	2:c:26:VAL:HG23	1.76	0.67
52:3:1137:C:H5'	52:3:1138:G:H5'	1.77	0.67
2:c:33:ARG:HD3	2:c:73:VAL:HB	1.75	0.67
29:E:61:LEU:HD12	29:E:61:LEU:O	1.95	0.67
36:L:78:ARG:NH2	52:3:1382:C:H5'	2.03	0.67
53:1:310:A:O2'	53:1:311:A:H5''	1.95	0.67
31:G:81:ASP:HA	31:G:84:LEU:HG	1.77	0.66
34:J:9:GLU:HG2	34:J:10:LEU:HD12	1.76	0.66
34:J:55:VAL:HG23	34:J:56:PRO:HD3	1.76	0.66
52:3:150:U:H3	52:3:171:A:H62	1.42	0.66
53:1:615:U:H5''	53:1:616:A:OP2	1.94	0.66
45:U:67:ILE:H	45:U:67:ILE:HD12	1.60	0.66
52:3:701:U:H4'	52:3:703:G:H1'	1.76	0.66
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.75	0.66
13:n:51:LEU:HD21	13:n:69:ARG:HD2	1.76	0.66
43:S:4:SER:OG	52:3:1216:A:H5''	1.95	0.66
53:1:2345:G:N3	53:1:2381:A:H2'	2.10	0.66
34:J:24:VAL:HG22	34:J:25:LYS:H	1.59	0.66
53:1:511:U:H2'	53:1:512:G:H5'	1.77	0.66
37:M:54:THR:HG23	37:M:55:LYS:HG3	1.77	0.66
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.77	0.66
13:n:22:ARG:HG3	13:n:70:THR:HA	1.77	0.66
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.77	0.66
52:3:1306:A:N6	52:3:1331:G:H1'	2.11	0.66
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.59	0.66
12:m:59:ARG:HG3	12:m:60:GLN:N	2.10	0.66
52:3:243:A:H4'	52:3:244:U:H3'	1.78	0.66
2:c:4:LEU:HD22	2:c:101:PHE:HE2	1.61	0.65
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.25	0.65
22:w:73:ARG:HH22	53:1:2333:A:P	2.20	0.65
52:3:1497:G:O2'	52:3:1498:U:H5'	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:161:A:H62	53:1:165:A:H61	1.42	0.65
53:1:1796:U:H2'	53:1:1797:G:H8	1.61	0.65
6:g:40:THR:HB	6:g:43:ASN:HD22	1.61	0.65
7:h:118:ILE:N	7:h:119:PRO:CD	2.60	0.65
29:E:2:LYS:HG3	53:1:242:G:N7	2.11	0.65
53:1:1300:G:H4'	53:1:1301:A:H5'	1.76	0.65
5:f:140:ILE:HA	5:f:143:VAL:HG22	1.78	0.65
36:L:70:PRO:HG3	36:L:98:LEU:HD23	1.77	0.65
11:l:105:ILE:HD12	11:l:105:ILE:H	1.61	0.65
36:L:68:VAL:HG23	36:L:99:ALA:HB1	1.79	0.65
53:1:2743:U:H2'	53:1:2744:G:H5''	1.78	0.65
40:P:125:LYS:HE3	52:3:797:C:OP1	1.97	0.65
53:1:713:G:H21	53:1:718:A:H62	1.44	0.65
2:c:170:VAL:HG11	53:1:2679:A:H5'	1.79	0.65
36:L:143:MET:HE1	55:6:31:G:H21	1.61	0.65
42:R:64:VAL:HG12	42:R:65:GLU:H	1.62	0.65
52:3:1197:A:H2'	52:3:1198:G:H5''	1.78	0.65
53:1:2287:A:O2'	53:1:2288:A:H2'	1.97	0.65
1:b:65:ASP:OD2	1:b:68:ARG:HD2	1.95	0.65
38:N:29:ILE:HG22	38:N:64:ILE:HB	1.77	0.65
45:U:75:ILE:O	45:U:78:VAL:HG12	1.97	0.65
47:W:59:LYS:HD3	52:3:734:G:O2'	1.96	0.65
54:2:3:C:C2'	54:2:4:C:H5''	2.26	0.64
53:1:2553:G:H3'	53:1:2554:U:H5''	1.78	0.64
2:c:14:ILE:HA	15:p:11:GLN:HE22	1.62	0.64
52:3:1404:C:H2'	52:3:1405:G:C8	2.32	0.64
53:1:2048:G:C3'	53:1:2049:G:H5''	2.28	0.64
50:Z:23:GLU:HG2	50:Z:24:LYS:N	2.12	0.64
52:3:1088:G:H21	52:3:1167:A:H61	1.46	0.64
52:3:1506:U:O2'	52:3:1507:A:H5'	1.97	0.64
53:1:2553:G:H1'	53:1:2582:G:H21	1.62	0.64
6:g:9:VAL:HB	6:g:13:GLY:HA3	1.80	0.64
36:L:78:ARG:HD2	36:L:81:GLY:O	1.98	0.64
13:n:53:THR:HG21	53:1:2840:C:H5''	1.78	0.64
18:s:66:ILE:H	18:s:66:ILE:HD12	1.63	0.64
40:P:111:ASP:OD1	40:P:113:THR:HG23	1.97	0.64
53:1:1186:G:H2'	53:1:1187:G:O4'	1.98	0.64
4:e:73:VAL:HG22	4:e:75:GLY:H	1.63	0.64
45:U:36:VAL:HG12	45:U:53:ASP:HB3	1.78	0.64
53:1:1807:G:H2'	53:1:1808:A:H5'	1.80	0.64
10:k:88:ASN:HB2	10:k:91:SER:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:44:THR:HG23	39:O:69:THR:O	1.98	0.63
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.80	0.63
52:3:1201:A:H1'	52:3:1202:U:OP2	1.98	0.63
53:1:1912:A:H62	53:1:1917:U:H3	1.45	0.63
47:W:37:LYS:HD2	52:3:719:C:H1'	1.81	0.63
49:Y:32:LYS:HD2	52:3:1439:G:OP1	1.98	0.63
12:m:53:MET:HE3	12:m:63:ILE:HG12	1.80	0.63
35:K:91:ARG:HG3	35:K:92:THR:H	1.64	0.63
52:3:77:A:H2'	52:3:78:A:H8	1.64	0.63
53:1:457:A:H61	53:1:470:A:H5''	1.64	0.63
45:U:5:ARG:HB2	52:3:376:G:H5''	1.81	0.63
51:a:212:VAL:HG13	51:a:224:VAL:HG23	1.80	0.63
1:b:264:LYS:HD3	1:b:264:LYS:C	2.23	0.63
32:H:69:THR:HG21	32:H:75:VAL:HG21	1.81	0.62
43:S:13:VAL:HG22	43:S:59:GLN:HE22	1.64	0.62
53:1:310:A:C2'	53:1:311:A:H5''	2.29	0.62
38:N:105:ARG:HE	52:3:1117:A:H4'	1.64	0.62
53:1:1394:U:H4'	53:1:1603:A:H4'	1.81	0.62
1:b:16:VAL:HB	1:b:203:VAL:HG22	1.81	0.62
53:1:2800:A:H3'	53:1:2801:G:H5'	1.81	0.62
34:J:148:SER:HB3	34:J:151:MET:HG2	1.81	0.62
11:l:101:ILE:HG13	11:l:102:GLY:H	1.65	0.62
13:n:79:LEU:HD23	13:n:83:LEU:HB3	1.82	0.62
53:1:215:G:H4'	53:1:216:A:H4'	1.81	0.62
53:1:821:A:H5''	53:1:822:G:C5'	2.28	0.62
53:1:371:A:H61	53:1:401:A:H3'	1.65	0.62
53:1:479:A:H4'	53:1:480:A:H5'	1.82	0.62
54:2:3:C:C3'	54:2:4:C:H5''	2.29	0.62
34:J:22:LYS:HZ2	52:3:921:U:H4'	1.65	0.62
31:G:69:VAL:HG23	31:G:91:VAL:HG13	1.82	0.62
29:E:2:LYS:HG3	53:1:242:G:C8	2.35	0.61
54:2:88:C:H5''	54:2:89:U:OP1	2.00	0.61
9:j:81:ILE:HD11	53:1:2514:U:H4'	1.81	0.61
50:Z:28:LEU:HA	50:Z:31:VAL:HG12	1.81	0.61
52:3:715:A:H2'	52:3:716:A:C8	2.35	0.61
1:b:153:LEU:HD23	1:b:175:LEU:HD21	1.81	0.61
8:i:126:ARG:HA	8:i:129:GLU:HB2	1.81	0.61
16:q:40:LYS:HE3	53:1:563:A:H4'	1.82	0.61
31:G:20:ARG:HH21	52:3:831:A:H4'	1.65	0.61
12:m:74:THR:HG21	12:m:86:LYS:HD2	1.82	0.61
43:S:88:MET:SD	43:S:89:ARG:HG3	2.40	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:87:PRO:HG3	36:L:148:LYS:HA	1.82	0.61
48:X:29:PRO:HB3	48:X:47:THR:O	2.00	0.61
53:1:290:U:H2'	53:1:291:G:H8	1.65	0.61
1:b:204:LEU:HB2	53:1:1791:A:O3'	2.00	0.61
29:E:18:LYS:HG3	53:1:651:G:H5'	1.82	0.61
42:R:7:ASN:ND2	42:R:21:ILE:HG13	2.13	0.61
51:a:177:LYS:NZ	53:1:2125:G:H5'	2.15	0.61
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.01	0.61
21:v:72:VAL:HG12	21:v:93:ARG:HA	1.82	0.61
53:1:760:G:H2'	53:1:761:A:O4'	2.01	0.61
10:k:22:ILE:HD11	10:k:40:LYS:HG3	1.83	0.61
31:G:165:ALA:HB1	31:G:172:ILE:HD11	1.83	0.61
53:1:441:U:O2'	53:1:442:G:H5'	1.99	0.61
57:7:44:G:H2'	57:7:45:U:O4'	1.99	0.61
8:i:89:SER:HB3	8:i:135:MET:HA	1.83	0.61
32:H:137:VAL:HG21	32:H:167:TYR:HD2	1.65	0.61
54:2:65:U:H3'	54:2:108:A:H61	1.66	0.61
8:i:13:ALA:HA	8:i:53:PRO:HA	1.83	0.61
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.82	0.60
53:1:1110:G:H2'	53:1:1111:A:H8	1.66	0.60
57:7:9:A:H1'	57:7:45:U:O2'	2.01	0.60
34:J:152:VAL:HA	34:J:155:LYS:HG2	1.83	0.60
53:1:189:G:H2'	53:1:205:G:H22	1.66	0.60
53:1:2646:C:H2'	53:1:2647:U:O4'	2.01	0.60
9:j:58:ASN:HA	9:j:126:ALA:O	2.00	0.60
15:p:113:LEU:O	15:p:113:LEU:HD12	2.01	0.60
26:B:8:THR:HG21	53:1:2020:A:H5'	1.83	0.60
5:f:26:LYS:HG2	5:f:31:GLU:HG3	1.82	0.60
35:K:92:THR:OG1	35:K:93:LYS:N	2.34	0.60
2:c:34:VAL:HG22	2:c:50:VAL:HG12	1.83	0.60
7:h:26:VAL:HG13	7:h:82:ILE:HG23	1.84	0.60
13:n:35:LYS:HE2	13:n:110:MET:HB3	1.84	0.60
24:y:41:HIS:CD2	53:1:96:C:H4'	2.36	0.60
48:X:5:LYS:HD2	52:3:1313:U:OP1	2.02	0.60
53:1:1476:U:H3	53:1:1515:A:H62	1.50	0.60
7:h:36:ASP:O	7:h:39:THR:HG22	2.01	0.60
40:P:56:LYS:NZ	52:3:691:G:O6	2.35	0.60
52:3:927:G:H21	52:3:1532:U:H5''	1.67	0.60
8:i:91:LYS:HB3	8:i:94:LYS:HB2	1.83	0.60
42:R:25:GLY:H	52:3:1329:A:H5''	1.66	0.60
49:Y:48:LYS:HA	49:Y:51:ASN:HD22	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:473:G:O2'	53:1:474:G:H5'	2.02	0.60
9:j:84:ILE:HG23	9:j:84:ILE:O	2.00	0.60
29:E:46:LYS:HD2	29:E:46:LYS:N	2.16	0.60
31:G:136:ARG:HA	31:G:139:GLU:HG2	1.83	0.60
37:M:80:PRO:HG2	52:3:878:A:H5''	1.83	0.60
44:T:71:ARG:NH2	52:3:754:C:H5'	2.17	0.60
4:e:37:MET:HE3	4:e:151:LEU:HB3	1.82	0.60
7:h:58:THR:HA	7:h:63:ALA:HB3	1.84	0.60
15:p:3:ILE:H	15:p:3:ILE:HD12	1.66	0.60
52:3:328:C:H5'	52:3:329:A:H5'	1.83	0.60
53:1:796:C:H2'	53:1:797:G:C8	2.37	0.60
1:b:216:ARG:NH2	53:1:691:C:H5'	2.17	0.59
9:j:72:LYS:HZ1	53:1:1139:G:P	2.25	0.59
40:P:34:THR:HG22	40:P:40:ALA:HA	1.83	0.59
11:l:55:MET:HE3	53:1:2392:A:C2	2.36	0.59
12:m:9:PHE:CZ	53:1:911:A:H2'	2.37	0.59
10:k:6:THR:HG23	53:1:1666:G:H4'	1.83	0.59
33:I:111:ALA:HB1	52:3:407:U:H5''	1.84	0.59
41:Q:85:ARG:NH1	41:Q:87:LYS:HB2	2.17	0.59
38:N:91:GLU:HA	38:N:94:ARG:HB3	1.83	0.59
33:I:184:LYS:HD3	33:I:185:PRO:HD2	1.85	0.59
52:3:1502:A:H8	52:3:1505:G:H22	1.51	0.59
53:1:669:G:H2'	53:1:669:G:N3	2.18	0.59
2:c:181:ASP:HB3	2:c:186:LEU:HB2	1.84	0.59
24:y:27:ASN:O	24:y:31:GLN:HG3	2.03	0.59
40:P:118:ASN:ND2	52:3:718:A:H5'	2.16	0.59
41:Q:113:ARG:HH22	52:3:37:U:H5'	1.67	0.59
32:H:49:ALA:HA	32:H:74:ILE:HD11	1.85	0.59
53:1:575:A:O2'	53:1:576:U:H5'	2.03	0.59
3:d:1:MET:HE3	3:d:2:GLU:H	1.66	0.59
7:h:33:VAL:HG13	7:h:35:VAL:H	1.66	0.59
1:b:63:ILE:H	1:b:63:ILE:HD12	1.66	0.58
22:w:38:GLY:HA2	53:1:2330:G:H21	1.68	0.58
45:U:1:MET:HB2	52:3:135:C:N3	2.18	0.58
50:Z:66:ARG:HH21	52:3:1099:G:H4'	1.67	0.58
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.85	0.58
53:1:305:C:H2'	53:1:306:U:C6	2.38	0.58
53:1:2533:U:H2'	53:1:2534:A:O4'	2.03	0.58
1:b:42:ARG:N	1:b:42:ARG:HD2	2.18	0.58
1:b:245:THR:HG23	1:b:247:TRP:H	1.68	0.58
4:e:56:LEU:HD23	4:e:59:ILE:HD12	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.86	0.58
25:z:45:GLY:HA3	53:1:852:U:H5'	1.86	0.58
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.85	0.58
52:3:505:G:H5'	52:3:534:U:H2'	1.84	0.58
54:2:13:G:H21	54:2:16:G:H1'	1.69	0.58
4:e:87:LYS:HD2	53:1:2313:C:H4'	1.84	0.58
11:l:38:GLN:HG2	53:1:805:G:H5''	1.86	0.58
36:L:58:LEU:H	36:L:58:LEU:HD12	1.69	0.58
53:1:546:U:H2'	53:1:547:A:H4'	1.84	0.58
50:Z:9:GLU:HB3	50:Z:10:PRO:HD3	1.84	0.58
53:1:1979:U:O2'	53:1:1980:G:H5'	2.04	0.58
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.68	0.58
4:e:88:VAL:HA	54:2:42:C:O2	2.03	0.58
55:5:6:G:O2'	55:5:7:G:H5'	2.03	0.58
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.86	0.58
10:k:36:GLY:HA2	10:k:62:VAL:O	2.04	0.58
41:Q:42:LYS:HG3	41:Q:44:PRO:HD2	1.85	0.58
44:T:71:ARG:O	44:T:71:ARG:HD2	2.04	0.58
53:1:395:U:H2'	53:1:396:G:H8	1.69	0.58
10:k:49:ARG:HH22	52:3:1423:G:H5'	1.69	0.58
17:r:68:ARG:HH11	17:r:90:ARG:HB2	1.69	0.57
36:L:113:LYS:HB2	36:L:117:LEU:HD23	1.85	0.57
44:T:21:THR:HG21	52:3:658:C:H1'	1.86	0.57
53:1:1509:A:H2'	53:1:1510:G:C8	2.38	0.57
20:u:6:ARG:O	20:u:24:VAL:HG23	2.04	0.57
33:I:18:LEU:HB2	33:I:20:LEU:HG	1.85	0.57
52:3:151:A:H62	52:3:170:U:H3	1.49	0.57
53:1:745:G:O2'	53:1:748:G:H1'	2.04	0.57
53:1:2093:G:N7	53:1:2225:A:H2'	2.19	0.57
11:l:62:PRO:HB2	29:E:29:ARG:HH11	1.70	0.57
12:m:29:GLY:HA2	12:m:106:ASP:HB2	1.86	0.57
41:Q:113:ARG:NH2	41:Q:120:ARG:HB2	2.19	0.57
45:U:57:ILE:O	45:U:61:VAL:HG23	2.04	0.57
12:m:41:LEU:HD23	12:m:96:ILE:HG13	1.86	0.57
18:s:1:MET:HE3	18:s:63:GLY:N	2.19	0.57
18:s:6:LYS:HG3	53:1:494:G:H4'	1.87	0.57
46:V:16:MET:HG3	46:V:19:SER:OG	2.04	0.57
53:1:275:C:H2'	53:1:276:U:H4'	1.86	0.57
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.86	0.57
13:n:28:LEU:HD22	13:n:44:LEU:HD21	1.87	0.57
37:M:21:LYS:HG2	37:M:22:ALA:H	1.67	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:97:ARG:HB2	42:R:99:GLN:HE22	1.69	0.57
52:3:346:G:C2'	52:3:347:G:H5'	2.35	0.57
53:1:542:C:H2'	53:1:543:G:H5'	1.87	0.57
1:b:35:LYS:HZ3	1:b:37:SER:HA	1.69	0.57
4:e:114:ARG:HG3	4:e:177:ARG:HD3	1.87	0.57
7:h:87:GLU:OE1	7:h:93:ALA:HB3	2.05	0.57
11:l:105:ILE:HD12	11:l:105:ILE:N	2.19	0.57
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.04	0.57
20:u:65:GLN:HB2	20:u:68:ASN:HD21	1.69	0.57
37:M:34:ALA:HA	37:M:37:ASN:ND2	2.20	0.57
45:U:51:ARG:C	45:U:52:LEU:HD12	2.29	0.57
52:3:494:G:O2'	52:3:496:A:H1'	2.05	0.57
53:1:2086:U:H2'	53:1:2087:G:C8	2.39	0.57
53:1:2329:U:H2'	53:1:2330:G:C8	2.38	0.57
9:j:88:THR:HG23	9:j:91:GLU:H	1.70	0.57
12:m:18:ARG:NH2	12:m:18:ARG:HB3	2.20	0.57
26:B:27:LEU:HG	26:B:36:LYS:HD2	1.87	0.57
37:M:9:MET:HG3	37:M:26:MET:SD	2.45	0.57
49:Y:34:VAL:HG11	49:Y:78:LEU:HD21	1.86	0.57
52:3:1346:A:H2'	52:3:1346:A:N3	2.19	0.57
53:1:2141:G:H22	53:1:2151:U:H1'	1.70	0.57
53:1:2417:C:H2'	53:1:2418:A:H8	1.70	0.57
4:e:92:GLY:O	4:e:95:MET:HG2	2.03	0.57
38:N:105:ARG:NE	52:3:1117:A:H4'	2.20	0.57
40:P:15:VAL:HG12	40:P:76:TYR:HB3	1.86	0.57
52:3:1432:G:H1'	52:3:1468:A:N6	2.19	0.57
12:m:9:PHE:HZ	53:1:911:A:H2'	1.69	0.57
13:n:64:ARG:HG3	53:1:1454:C:O2	2.03	0.57
41:Q:107:LYS:H	41:Q:107:LYS:HD2	1.70	0.57
54:2:3:C:H3'	54:2:4:C:H5''	1.85	0.57
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.85	0.57
48:X:35:ARG:HD2	48:X:51:HIS:O	2.04	0.57
53:1:503:A:H4'	53:1:505:A:H5''	1.86	0.57
6:g:55:GLU:O	6:g:58:LEU:HG	2.05	0.56
34:J:22:LYS:NZ	52:3:921:U:H4'	2.20	0.56
46:V:10:ARG:NE	46:V:57:VAL:HG22	2.20	0.56
53:1:1936:A:H2	53:1:1943:U:H3	1.53	0.56
53:1:2238:G:H2'	53:1:2238:G:N3	2.20	0.56
31:G:117:GLU:O	31:G:121:GLN:HG2	2.05	0.56
33:I:57:LYS:HD3	33:I:202:LEU:HD23	1.87	0.56
53:1:621:A:H2'	53:1:622:G:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:94:ARG:HD3	53:1:2376:A:N6	2.19	0.56
52:3:70:U:H5''	52:3:71:A:OP1	2.04	0.56
52:3:225:C:H2'	52:3:226:G:H5''	1.87	0.56
52:3:1200:C:H5''	52:3:1201:A:H3'	1.87	0.56
52:3:1316:G:H2'	52:3:1317:C:H5''	1.87	0.56
53:1:435:C:H2'	53:1:436:C:H5'	1.87	0.56
53:1:1893:C:H2'	53:1:1894:C:H5'	1.87	0.56
5:f:88:LEU:HG	5:f:161:VAL:HG12	1.88	0.56
10:k:48:PRO:HB2	10:k:49:ARG:HD2	1.87	0.56
33:I:3:TYR:C	33:I:4:LEU:HD23	2.30	0.56
48:X:77:ARG:HH21	52:3:1225:A:H4'	1.68	0.56
53:1:1105:U:H2'	53:1:1106:G:H5''	1.87	0.56
9:j:35:ARG:HA	9:j:40:HIS:CD2	2.41	0.56
10:k:13:ASN:ND2	10:k:98:ARG:HB2	2.19	0.56
15:p:59:THR:HG22	15:p:72:VAL:HG23	1.87	0.56
31:G:27:LYS:HB3	31:G:28:PRO:HD3	1.87	0.56
31:G:66:ILE:H	31:G:66:ILE:HD12	1.70	0.56
37:M:12:ARG:NH2	52:3:826:C:H5'	2.20	0.56
52:3:392:C:H2'	52:3:393:A:H8	1.70	0.56
53:1:306:U:H3	53:1:310:A:H62	1.54	0.56
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.88	0.56
3:d:184:ASP:OD1	3:d:185:LYS:HG2	2.06	0.56
14:o:29:HIS:HB3	14:o:36:TYR:HD2	1.70	0.56
19:t:12:ARG:HA	24:y:29:ARG:HE	1.70	0.56
38:N:117:LEU:HD12	38:N:117:LEU:N	2.21	0.56
48:X:45:GLY:H	48:X:61:VAL:HG23	1.71	0.56
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.86	0.56
52:3:29:U:O2'	52:3:30:U:H5'	2.06	0.56
11:l:110:VAL:HB	11:l:127:VAL:HG13	1.88	0.56
29:E:3:ILE:HD11	53:1:592:A:N3	2.21	0.56
33:I:23:GLY:HA3	52:3:409:U:OP1	2.06	0.56
34:J:84:VAL:HG23	34:J:145:ASN:HD22	1.71	0.56
35:K:46:GLN:HA	35:K:56:LYS:HG2	1.87	0.56
42:R:77:LYS:HA	42:R:80:MET:HE3	1.87	0.56
51:a:46:VAL:HG22	51:a:212:VAL:HG23	1.88	0.56
53:1:863:A:H4'	54:2:100:G:H21	1.70	0.56
53:1:2623:G:H2'	53:1:2624:G:H8	1.70	0.56
53:1:2698:U:H2'	53:1:2699:C:C6	2.41	0.56
2:c:21:SER:C	2:c:22:ILE:HD12	2.31	0.56
5:f:2:ARG:HD3	53:1:2751:G:C4	2.40	0.56
53:1:1827:U:H2'	53:1:1828:G:O4'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2837:A:H2'	53:1:2838:G:H8	1.70	0.56
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.88	0.55
19:t:56:GLU:OE2	19:t:88:LYS:HG2	2.07	0.55
19:t:64:LYS:N	19:t:64:LYS:HD2	2.21	0.55
43:S:80:ARG:O	43:S:83:VAL:HG12	2.06	0.55
52:3:1237:C:OP1	52:3:1238:A:H1'	2.06	0.55
53:1:528:A:N1	53:1:2042:A:H2'	2.21	0.55
17:r:74:ILE:N	17:r:74:ILE:HD12	2.20	0.55
18:s:14:ALA:O	18:s:18:ARG:HG3	2.05	0.55
32:H:67:ILE:H	32:H:67:ILE:HD12	1.71	0.55
52:3:948:C:H2'	52:3:949:A:H8	1.70	0.55
52:3:950:U:H2'	52:3:951:G:C8	2.41	0.55
53:1:2691:C:H2'	53:1:2692:G:C8	2.41	0.55
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.71	0.55
20:u:95:PHE:HD2	20:u:100:GLU:HB2	1.70	0.55
27:C:21:THR:HG21	53:1:2419:U:H4'	1.88	0.55
31:G:178:LEU:HD23	31:G:178:LEU:O	2.06	0.55
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.88	0.55
51:a:197:LYS:O	51:a:200:LYS:HG3	2.07	0.55
52:3:225:C:C3'	52:3:226:G:H5''	2.37	0.55
53:1:940:G:H2'	53:1:941:A:H5''	1.88	0.55
36:L:11:ILE:H	36:L:11:ILE:HD12	1.69	0.55
40:P:28:ASN:ND2	52:3:690:G:OP2	2.39	0.55
48:X:5:LYS:HE2	48:X:6:LYS:HE3	1.89	0.55
53:1:1133:A:H4'	53:1:1134:A:H5''	1.88	0.55
3:d:163:ASN:HB2	53:1:322:A:OP2	2.06	0.55
19:t:1:MET:HG3	19:t:3:ARG:H	1.71	0.55
19:t:10:VAL:HG11	19:t:42:GLU:HB3	1.88	0.55
32:H:162:ALA:CB	52:3:1056:U:H4'	2.37	0.55
45:U:13:LYS:HE3	52:3:392:C:H4'	1.88	0.55
53:1:2246:G:H2'	53:1:2247:A:C8	2.41	0.55
53:1:2350:C:H2'	53:1:2351:G:O4'	2.05	0.55
2:c:81:GLU:CD	53:1:2636:C:H4'	2.32	0.55
4:e:65:LEU:HD22	54:2:42:C:C4	2.41	0.55
33:I:150:LYS:HD3	33:I:177:MET:SD	2.47	0.55
35:K:79:ARG:HH22	52:3:671:G:H4'	1.71	0.55
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.07	0.55
53:1:1674:G:H21	53:1:1677:A:H61	1.55	0.55
53:1:2417:C:H2'	53:1:2418:A:C8	2.41	0.55
2:c:39:ASP:OD2	2:c:41:ALA:HB3	2.06	0.55
25:z:10:ARG:HG3	53:1:988:A:OP1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:27:CYS:H	30:F:34:LYS:HE3	1.70	0.55
35:K:6:ILE:HG13	35:K:89:VAL:HG12	1.88	0.55
49:Y:20:ASN:HB3	49:Y:24:ARG:HH21	1.71	0.55
50:Z:23:GLU:C	50:Z:25:ALA:H	2.14	0.55
51:a:14:LYS:HD3	51:a:32:GLU:HB3	1.88	0.55
53:1:863:A:H4'	54:2:100:G:N2	2.22	0.55
20:u:40:LEU:HD22	20:u:59:GLU:HG3	1.88	0.55
21:v:30:ILE:HG12	21:v:91:PHE:HB2	1.87	0.55
29:E:51:LYS:HD2	53:1:937:C:OP1	2.06	0.55
53:1:1251:C:O2'	53:1:1252:G:H3'	2.07	0.55
6:g:8:LYS:O	6:g:9:VAL:HB	2.07	0.55
10:k:109:SER:O	10:k:110:GLU:HG3	2.06	0.55
19:t:34:VAL:HG12	19:t:35:ALA:H	1.72	0.55
27:C:46:VAL:HG22	27:C:47:ILE:N	2.22	0.55
31:G:49:PHE:HD1	31:G:199:ILE:HD13	1.71	0.55
53:1:2853:C:H2'	53:1:2854:G:H8	1.71	0.55
7:h:118:ILE:N	7:h:119:PRO:HD2	2.20	0.55
12:m:75:GLU:HB3	12:m:90:GLU:CD	2.31	0.55
30:F:32:LYS:HE3	53:1:2478:A:H5'	1.89	0.55
52:3:352:C:H4'	52:3:354:G:OP1	2.07	0.55
53:1:2591:C:H2'	53:1:2592:G:C8	2.42	0.55
9:j:37:ARG:NH2	53:1:1007:C:OP1	2.38	0.54
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.89	0.54
29:E:22:LYS:HE2	53:1:650:C:H4'	1.89	0.54
35:K:3:HIS:HA	35:K:65:GLU:HA	1.89	0.54
49:Y:4:LYS:O	49:Y:7:LYS:HG3	2.07	0.54
50:Z:50:SER:O	50:Z:53:LYS:HG3	2.07	0.54
53:1:69:C:O2'	53:1:70:G:H5'	2.07	0.54
53:1:2326:C:O2'	53:1:2327:A:OP1	2.25	0.54
11:l:57:LEU:HA	11:l:60:ARG:HE	1.71	0.54
14:o:40:ILE:HG12	14:o:47:VAL:HG12	1.89	0.54
20:u:18:LYS:HE3	53:1:310:A:OP1	2.07	0.54
28:D:14:ARG:HD2	53:1:771:G:OP1	2.06	0.54
37:M:34:ALA:HA	37:M:37:ASN:HD22	1.71	0.54
52:3:757:U:H2'	52:3:758:C:O4'	2.07	0.54
53:1:2055:C:H5'	53:1:2056:G:O5'	2.07	0.54
1:b:18:VAL:O	1:b:18:VAL:HG13	2.07	0.54
18:s:31:GLN:HA	18:s:34:ASP:OD2	2.07	0.54
34:J:15:ILE:HD13	34:J:36:THR:HA	1.89	0.54
51:a:54:LYS:HD3	55:6:63:G:H5'	1.89	0.54
52:3:49:U:O2'	52:3:50:A:H2'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:644:A:H61	53:1:2349:G:H21	1.54	0.54
53:1:2039:U:H2'	53:1:2040:G:C8	2.41	0.54
53:1:2605:U:H2'	53:1:2606:C:C6	2.43	0.54
12:m:86:LYS:HE2	53:1:955:U:H5''	1.89	0.54
33:I:33:ILE:O	33:I:34:GLU:HG2	2.08	0.54
40:P:30:ILE:HG22	40:P:45:THR:HB	1.88	0.54
46:V:32:ILE:HD12	46:V:32:ILE:N	2.23	0.54
51:a:209:ILE:H	51:a:209:ILE:HD12	1.73	0.54
53:1:1796:U:H2'	53:1:1797:G:C8	2.41	0.54
1:b:116:GLN:HG3	1:b:121:ALA:HB2	1.89	0.54
31:G:66:ILE:HD12	31:G:66:ILE:N	2.23	0.54
31:G:138:ARG:O	31:G:142:LYS:HG2	2.08	0.54
50:Z:40:PRO:O	50:Z:44:ARG:HB2	2.07	0.54
53:1:2128:G:H21	53:1:2173:A:H1'	1.72	0.54
53:1:2257:U:O2'	53:1:2258:C:H5'	2.07	0.54
53:1:2591:C:H2'	53:1:2592:G:H8	1.71	0.54
1:b:216:ARG:HG3	1:b:217:PRO:CD	2.38	0.54
17:r:78:ARG:NH1	53:1:990:A:N1	2.55	0.54
20:u:43:LYS:HA	53:1:481:G:OP2	2.08	0.54
33:I:190:LEU:HD12	33:I:192:ALA:H	1.71	0.54
35:K:42:TRP:HB2	35:K:59:TYR:HB2	1.88	0.54
52:3:1540:U:O2	52:3:1540:U:H3'	2.08	0.54
53:1:191:A:H2'	53:1:192:C:C6	2.43	0.54
53:1:1111:A:H2'	53:1:1111:A:N3	2.23	0.54
15:p:24:THR:HG22	15:p:87:ARG:HB2	1.89	0.54
50:Z:35:GLU:O	50:Z:36:PHE:HB2	2.07	0.54
51:a:172:HIS:HB2	53:1:2123:G:H4'	1.90	0.54
52:3:372:C:N4	52:3:387:U:H2'	2.22	0.54
53:1:543:G:H5'	53:1:543:G:H8	1.72	0.54
53:1:828:U:H2'	53:1:829:A:C8	2.42	0.54
14:o:33:ARG:HB2	54:2:52:A:N6	2.23	0.54
33:I:169:TRP:CG	33:I:185:PRO:HG3	2.42	0.54
43:S:2:LYS:NZ	52:3:983:A:H5'	2.23	0.54
53:1:225:C:H2'	53:1:226:A:O4'	2.07	0.54
53:1:1697:G:H4'	53:1:1978:A:H5''	1.90	0.54
53:1:1736:U:H2'	53:1:1737:G:O4'	2.08	0.54
15:p:7:LEU:O	15:p:7:LEU:HD23	2.08	0.54
35:K:67:PRO:HG2	35:K:70:VAL:HG23	1.89	0.54
36:L:36:SER:HA	36:L:39:GLU:OE2	2.08	0.54
38:N:6:TYR:CZ	52:3:1147:C:H4'	2.43	0.54
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:802:A:H2'	52:3:803:G:O4'	2.08	0.54
54:2:51:G:H2'	54:2:52:A:O4'	2.08	0.54
12:m:34:LYS:O	12:m:129:THR:HG22	2.08	0.53
53:1:1874:C:H2'	53:1:1875:G:O4'	2.07	0.53
9:j:136:GLN:N	9:j:137:PRO:HD3	2.22	0.53
31:G:69:VAL:HG12	31:G:161:PHE:O	2.09	0.53
33:I:97:LEU:HD12	33:I:134:TYR:HB3	1.90	0.53
46:V:26:ARG:HH12	46:V:39:ARG:HD2	1.73	0.53
53:1:974:G:H1'	53:1:975:A:C8	2.42	0.53
53:1:2121:G:H2'	53:1:2122:U:O4'	2.08	0.53
55:6:17:C:H2'	55:6:17(A):U:H5	1.73	0.53
13:n:44:LEU:HD22	13:n:113:ILE:HD13	1.90	0.53
37:M:80:PRO:HG2	52:3:878:A:C5'	2.39	0.53
52:3:1139:G:H5''	52:3:1140:C:H5	1.73	0.53
53:1:1077:A:C2'	53:1:1078:U:H5'	2.36	0.53
53:1:2389:G:H5''	53:1:2390:U:O4'	2.09	0.53
42:R:7:ASN:OD1	42:R:9:PRO:HD3	2.08	0.53
51:a:205:LYS:HD2	53:1:1861:G:H5'	1.90	0.53
52:3:31:G:N2	52:3:47:C:H5''	2.23	0.53
52:3:211:G:H2'	52:3:212:G:H5'	1.89	0.53
52:3:410:G:H2'	52:3:429:U:C4	2.44	0.53
52:3:422:C:H5'	52:3:423:G:N3	2.24	0.53
52:3:1005:A:H2'	52:3:1006:G:O4'	2.08	0.53
53:1:226:A:H2'	53:1:227:A:O4'	2.09	0.53
53:1:1827:U:O2'	53:1:1828:G:H5'	2.08	0.53
53:1:2724:U:H2'	53:1:2725:A:C8	2.44	0.53
2:c:173:GLN:NE2	53:1:2772:C:H5'	2.23	0.53
6:g:31:VAL:CG1	6:g:32:PRO:HD3	2.39	0.53
39:O:57:VAL:HG22	39:O:58:ASN:N	2.16	0.53
52:3:1016:A:H4'	52:3:1218:C:H4'	1.91	0.53
52:3:1088:G:N2	52:3:1167:A:H61	2.06	0.53
53:1:49:A:H5'	53:1:51:G:O4'	2.08	0.53
53:1:1367:A:C2'	53:1:1368:G:H5'	2.39	0.53
53:1:1956:U:H2'	53:1:1957:C:H5'	1.90	0.53
53:1:2297:A:N6	53:1:2319:G:H1'	2.23	0.53
7:h:87:GLU:OE2	7:h:93:ALA:HB3	2.09	0.53
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.23	0.53
10:k:35:VAL:HG13	10:k:36:GLY:N	2.24	0.53
26:B:3:GLN:HA	53:1:2615:U:C2	2.44	0.53
36:L:55:LYS:HE3	36:L:59:GLU:OE2	2.09	0.53
38:N:49:GLN:N	38:N:50:PRO:HD2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:62:ALA:HB2	51:a:162:ARG:HD2	1.90	0.53
51:a:177:LYS:HZ1	53:1:2125:G:H5'	1.73	0.53
53:1:1053:C:C2'	53:1:1054:A:H5''	2.34	0.53
53:1:2066:C:O2'	53:1:2067:G:H5'	2.08	0.53
6:g:116:ARG:O	6:g:118:PRO:HD3	2.08	0.53
8:i:99:LYS:HG2	8:i:140:GLU:HG2	1.89	0.53
34:J:107:GLY:HA2	52:3:8:A:H1'	1.90	0.53
36:L:138:GLU:O	36:L:142:ARG:HD3	2.08	0.53
52:3:1137:C:H4'	52:3:1138:G:N2	2.24	0.53
53:1:414:C:H2'	53:1:415:A:C8	2.44	0.53
53:1:2343:U:H2'	53:1:2344:U:C6	2.44	0.53
5:f:41:GLU:HG3	5:f:54:ARG:HH21	1.73	0.53
7:h:33:VAL:HG22	7:h:34:THR:N	2.23	0.53
15:p:96:LEU:HB3	15:p:99:LEU:HD23	1.90	0.53
31:G:95:TRP:HH2	31:G:100:LEU:HD23	1.74	0.53
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.43	0.53
38:N:12:LYS:H	38:N:105:ARG:HH22	1.57	0.53
52:3:946:A:H2'	52:3:947:G:H8	1.74	0.53
3:d:61:ARG:HD2	3:d:63:LYS:O	2.09	0.53
12:m:59:ARG:HG3	12:m:60:GLN:H	1.73	0.53
30:F:36:ARG:O	30:F:37:GLN:HB2	2.08	0.53
31:G:45:THR:HG22	31:G:200:PRO:HB2	1.91	0.53
38:N:51:LEU:HD12	38:N:56:MET:HB3	1.91	0.53
42:R:105:ALA:HA	52:3:948:C:OP1	2.09	0.53
52:3:1464:U:H2'	52:3:1465:A:C8	2.44	0.53
3:d:102:ARG:O	3:d:106:LYS:HG3	2.07	0.53
8:i:12:VAL:HG22	8:i:13:ALA:N	2.17	0.53
9:j:99:ARG:NH1	53:1:2780:G:H1	2.07	0.53
31:G:78:ALA:HB1	31:G:213:LEU:HD21	1.91	0.53
36:L:16:LYS:HD2	36:L:17:PHE:CE1	2.44	0.53
49:Y:77:ASN:ND2	52:3:259:G:OP1	2.42	0.53
50:Z:40:PRO:HA	50:Z:44:ARG:HD3	1.91	0.53
52:3:945:G:H2'	52:3:945:G:N3	2.24	0.53
53:1:755:U:H2'	53:1:756:A:C8	2.44	0.53
53:1:2691:C:H2'	53:1:2692:G:H8	1.72	0.53
6:g:9:VAL:HG12	6:g:11:ASN:H	1.74	0.52
12:m:12:MET:HA	53:1:910:A:N6	2.15	0.52
25:z:40:THR:HG23	25:z:43:ILE:H	1.73	0.52
32:H:42:LEU:HD11	32:H:54:ILE:HD13	1.91	0.52
52:3:77:A:H2'	52:3:78:A:C8	2.45	0.52
53:1:968:C:H2'	53:1:969:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1810:A:H2'	53:1:1811:G:O4'	2.09	0.52
53:1:2162:G:H2'	53:1:2163:A:H8	1.74	0.52
53:1:2508:G:H1	53:1:2580:U:H3	1.57	0.52
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.91	0.52
5:f:37:ASN:ND2	5:f:39:ALA:HB3	2.24	0.52
10:k:10:VAL:HG12	10:k:12:ASP:H	1.74	0.52
41:Q:78:VAL:HG12	41:Q:102:ASP:OD2	2.09	0.52
52:3:692:U:H2'	52:3:694:A:OP2	2.09	0.52
20:u:94:PHE:HB2	20:u:100:GLU:O	2.10	0.52
33:I:186:GLU:HG3	33:I:188:SER:H	1.74	0.52
47:W:21:ASP:OD2	47:W:23:LYS:HG3	2.09	0.52
2:c:124:ARG:HD3	2:c:125:TRP:NE1	2.24	0.52
35:K:72:ASP:O	35:K:75:GLU:HG3	2.09	0.52
40:P:126:ARG:HH21	52:3:692:U:H5''	1.73	0.52
52:3:78:A:H2'	52:3:79:G:O4'	2.09	0.52
53:1:1049:C:H41	53:1:1110:G:H21	1.57	0.52
1:b:145:MET:HE1	1:b:181:ARG:NE	2.23	0.52
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.92	0.52
49:Y:77:ASN:HD22	52:3:259:G:P	2.31	0.52
52:3:1238:A:H2'	52:3:1239:A:H5'	1.91	0.52
53:1:290:U:H2'	53:1:291:G:C8	2.44	0.52
53:1:414:C:H2'	53:1:415:A:H8	1.74	0.52
53:1:1020:A:C1'	53:1:1021:A:OP2	2.52	0.52
53:1:1856:U:H2'	53:1:1857:G:O4'	2.09	0.52
53:1:2743:U:H2'	53:1:2744:G:C5'	2.39	0.52
5:f:24:THR:HG22	5:f:33:THR:HG22	1.92	0.52
12:m:20:LEU:HD22	21:v:81:PRO:HG2	1.91	0.52
28:D:16:HIS:HE1	53:1:684:G:H4'	1.75	0.52
40:P:93:GLU:HB2	50:Z:16:ARG:HH21	1.74	0.52
51:a:165:ASN:HD21	51:a:169:GLY:HA2	1.73	0.52
52:3:545:C:O2'	52:3:549:C:H5''	2.10	0.52
52:3:1170:A:H2'	52:3:1171:A:O4'	2.10	0.52
53:1:532:A:H2'	53:1:532:A:N3	2.25	0.52
53:1:796:C:H2'	53:1:797:G:H8	1.74	0.52
37:M:50:VAL:HA	37:M:58:LEU:HA	1.92	0.52
39:O:100:ILE:HD12	39:O:100:ILE:N	2.24	0.52
49:Y:23:ARG:NH2	52:3:176:C:H4'	2.25	0.52
53:1:581:C:H2'	53:1:582:A:H8	1.75	0.52
53:1:1846:G:H2'	53:1:1847:A:O4'	2.10	0.52
54:2:65:U:H3'	54:2:108:A:N6	2.25	0.52
52:3:392:C:H2'	52:3:393:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1256:A:H1'	52:3:1258:G:C4	2.45	0.52
53:1:112:U:H2'	53:1:113:U:H5'	1.91	0.52
53:1:189:G:H2'	53:1:205:G:N2	2.24	0.52
53:1:2215:C:H2'	53:1:2216:G:C8	2.45	0.52
10:k:49:ARG:HD2	10:k:49:ARG:N	2.25	0.52
17:r:49:ILE:HG22	17:r:54:VAL:H	1.73	0.52
21:v:30:ILE:HD11	21:v:63:ILE:HD12	1.92	0.52
22:w:17:LEU:H	22:w:17:LEU:HD12	1.74	0.52
34:J:24:VAL:HG22	34:J:25:LYS:N	2.24	0.52
52:3:1256:A:O2'	52:3:1257:A:H5''	2.10	0.52
52:3:1413:A:H2	52:3:1487:G:H22	1.57	0.52
53:1:962:G:H21	53:1:2250:G:H1	1.56	0.52
53:1:2286:G:H4'	53:1:2287:A:O4'	2.10	0.52
4:e:40:GLY:HA2	4:e:84:ILE:CD1	2.40	0.52
6:g:31:VAL:HG13	6:g:32:PRO:HD3	1.92	0.52
37:M:10:LEU:HD22	37:M:74:ILE:CD1	2.39	0.52
53:1:2163:A:H2'	53:1:2164:C:H5'	1.92	0.52
9:j:97:PRO:HG2	9:j:98:GLU:OE1	2.10	0.51
13:n:79:LEU:HD21	13:n:83:LEU:HD23	1.93	0.51
17:r:24:LYS:HA	17:r:94:THR:OG1	2.10	0.51
30:F:26:ILE:HA	30:F:34:LYS:HE3	1.93	0.51
38:N:94:ARG:HA	38:N:97:LEU:HB3	1.91	0.51
50:Z:49:ALA:HA	52:3:723:U:O4	2.10	0.51
51:a:6:LYS:HG3	51:a:7:ARG:H	1.75	0.51
52:3:948:C:H2'	52:3:949:A:C8	2.45	0.51
53:1:281:C:H42	53:1:359:G:H1	1.59	0.51
53:1:562:U:H2'	53:1:572:A:O4'	2.10	0.51
53:1:1801:A:H5''	53:1:2203:U:H2'	1.92	0.51
3:d:77:ILE:HG13	3:d:78:TRP:CD1	2.45	0.51
43:S:63:CYS:SG	43:S:78:LEU:HD12	2.50	0.51
1:b:141:HIS:CE1	1:b:190:THR:HB	2.44	0.51
2:c:142:VAL:CG2	2:c:143:PRO:HD2	2.40	0.51
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.93	0.51
52:3:245:U:O2'	52:3:246:A:H5'	2.10	0.51
53:1:175:G:H2'	53:1:176:A:C8	2.46	0.51
53:1:639:U:H2'	53:1:640:C:C6	2.45	0.51
57:7:43:C:H2'	57:7:44:G:C8	2.45	0.51
1:b:215:VAL:HG12	1:b:216:ARG:N	2.25	0.51
1:b:244:VAL:HG12	1:b:250:GLN:HA	1.93	0.51
2:c:115:GLY:HA2	2:c:166:GLY:HA3	1.92	0.51
31:G:20:ARG:HG2	52:3:831:A:OP1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:92:ARG:O	34:J:93:VAL:O	2.28	0.51
42:R:84:CYS:O	42:R:88:LEU:HD13	2.10	0.51
50:Z:41:THR:O	50:Z:45:LYS:HG2	2.10	0.51
52:3:70:U:H4'	52:3:71:A:H8	1.75	0.51
2:c:83:ARG:CZ	53:1:2637:U:H5''	2.40	0.51
13:n:2:ARG:HD3	53:1:2822:G:O6	2.11	0.51
16:q:48:ASP:HA	16:q:51:GLN:HB2	1.91	0.51
20:u:11:ILE:HG23	20:u:72:PHE:HB2	1.91	0.51
30:F:4:ARG:O	30:F:37:GLN:HB2	2.11	0.51
34:J:87:VAL:HA	34:J:91:SER:O	2.10	0.51
39:O:11:LYS:HB3	39:O:71:LEU:HD23	1.92	0.51
43:S:84:ARG:HH21	52:3:1059:C:H4'	1.76	0.51
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.76	0.51
52:3:56:U:H2'	52:3:57:G:C8	2.45	0.51
52:3:764:C:H2'	52:3:765:G:O4'	2.10	0.51
53:1:45:G:C5'	53:1:46:G:H5'	2.16	0.51
53:1:278:A:H2'	53:1:278:A:N3	2.24	0.51
53:1:2514:U:H2'	53:1:2515:C:C6	2.45	0.51
11:l:32:GLY:HA2	53:1:1190:G:H5''	1.93	0.51
11:l:92:LEU:HD23	11:l:92:LEU:O	2.10	0.51
14:o:30:ARG:HA	14:o:35:ILE:HG22	1.93	0.51
32:H:55:VAL:HB	32:H:66:THR:HB	1.93	0.51
39:O:6:ILE:HA	39:O:102:LEU:HA	1.91	0.51
40:P:91:GLY:O	40:P:93:GLU:N	2.43	0.51
41:Q:47:ALA:HB1	52:3:520:A:OP2	2.10	0.51
52:3:211:G:C2'	52:3:212:G:H5'	2.41	0.51
53:1:395:U:H2'	53:1:396:G:C8	2.45	0.51
53:1:779:U:H2'	53:1:780:G:C8	2.45	0.51
53:1:2475:C:C2'	53:1:2476:A:H5'	2.40	0.51
13:n:69:ARG:O	13:n:70:THR:OG1	2.23	0.51
14:o:18:LEU:HD21	14:o:25:ARG:HB3	1.92	0.51
34:J:55:VAL:HG23	34:J:56:PRO:CD	2.40	0.51
52:3:1218:C:H2'	52:3:1219:A:C8	2.45	0.51
53:1:1837:C:H2'	53:1:1899:A:H61	1.76	0.51
13:n:45:ARG:HG2	13:n:95:THR:HG21	1.91	0.51
13:n:53:THR:HG21	53:1:2840:C:C5'	2.39	0.51
16:q:10:ARG:HH21	53:1:1216:G:H5''	1.75	0.51
18:s:77:ASP:OD2	18:s:77:ASP:N	2.43	0.51
51:a:5:THR:H	51:a:8:MET:CG	2.24	0.51
52:3:1128:C:O2'	52:3:1129:C:H5'	2.10	0.51
52:3:1478:U:H2'	52:3:1479:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.11	0.51
26:B:47:TYR:CE1	26:B:52:LYS:HD3	2.46	0.51
33:I:149:LYS:HG2	33:I:150:LYS:HG2	1.92	0.51
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.91	0.51
52:3:225:C:H3'	52:3:226:G:H5''	1.93	0.51
53:1:859:G:HO2'	53:1:860:U:H6	1.54	0.51
53:1:1045:C:H5'	53:1:1046:A:C5'	2.41	0.51
53:1:1138:G:H2'	53:1:1139:G:O4'	2.11	0.51
53:1:1306:C:H41	53:1:1606:C:H2'	1.76	0.51
53:1:2139:U:H2'	53:1:2140:G:C8	2.46	0.51
53:1:2183:A:H2'	53:1:2184:A:C8	2.45	0.51
1:b:94:LEU:HD13	1:b:100:ARG:HG2	1.92	0.51
7:h:54:VAL:O	53:1:1084:A:H5''	2.11	0.51
10:k:86:LEU:H	10:k:86:LEU:HD12	1.76	0.51
12:m:136:MET:HE2	21:v:57:TYR:HB3	1.93	0.51
14:o:31:THR:HG22	14:o:32:PRO:HD2	1.93	0.51
21:v:14:LYS:HE3	54:2:78:A:OP2	2.10	0.51
52:3:314:C:O2'	52:3:315:A:H5'	2.11	0.51
52:3:437:U:H2'	52:3:438:U:O4'	2.11	0.51
52:3:1517:G:H1'	53:1:1919:A:O2'	2.11	0.51
53:1:121:G:H4'	53:1:149:A:H5'	1.93	0.51
53:1:554:U:H2'	53:1:555:G:O4'	2.10	0.51
53:1:1045:C:P	53:1:1047:G:H5'	2.51	0.51
53:1:1071:G:OP1	53:1:1071:G:H3'	2.10	0.51
53:1:2086:U:H2'	53:1:2087:G:H8	1.75	0.51
53:1:2837:A:H2'	53:1:2838:G:C8	2.46	0.51
1:b:42:ARG:HH12	53:1:690:G:H21	1.57	0.50
3:d:71:GLY:N	53:1:674:G:H5''	2.26	0.50
17:r:71:LYS:NZ	53:1:1223:G:N7	2.59	0.50
33:I:143:SER:C	33:I:144:ILE:HD12	2.36	0.50
40:P:88:PRO:HA	40:P:92:ARG:HH11	1.76	0.50
44:T:62:ARG:HH22	53:1:715:A:H4'	1.75	0.50
53:1:310:A:H2'	53:1:311:A:H5''	1.92	0.50
53:1:2749:A:H62	53:1:2753:A:H61	1.57	0.50
4:e:107:VAL:HG23	4:e:108:PRO:CD	2.35	0.50
12:m:57:VAL:C	12:m:59:ARG:H	2.19	0.50
37:M:29:SER:OG	37:M:32:LYS:HG3	2.11	0.50
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.12	0.50
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.76	0.50
48:X:54:ARG:HG3	48:X:55:GLN:CD	2.35	0.50
52:3:86:G:H4'	52:3:87:C:C5	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:166:U:H2'	52:3:167:A:C8	2.46	0.50
52:3:1128:C:H4'	52:3:1148:U:O2	2.11	0.50
52:3:1280:A:O2'	52:3:1281:C:H5'	2.12	0.50
53:1:403:U:O3'	53:1:404:A:H4'	2.11	0.50
53:1:1019:U:H3	53:1:1142:A:H62	1.59	0.50
53:1:2743:U:C2'	53:1:2744:G:H5''	2.40	0.50
10:k:48:PRO:CG	52:3:1422:G:H5'	2.41	0.50
38:N:105:ARG:HD2	52:3:1117:A:H4'	1.93	0.50
53:1:2841:C:H2'	53:1:2842:G:C8	2.46	0.50
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.94	0.50
6:g:40:THR:O	6:g:44:ILE:HG13	2.11	0.50
7:h:117:LEU:HD23	7:h:117:LEU:C	2.37	0.50
52:3:868:C:H2'	52:3:869:G:O4'	2.12	0.50
53:1:558:U:H2'	53:1:559:G:H8	1.77	0.50
53:1:2713:U:H3'	53:1:2714:G:H5''	1.93	0.50
2:c:121:THR:HB	2:c:127:PHE:CD2	2.46	0.50
2:c:151:THR:HB	53:1:2571:U:O2'	2.11	0.50
33:I:96:ARG:NH2	33:I:98:ASP:OD2	2.45	0.50
43:S:8:ARG:HG2	43:S:12:ARG:NH1	2.26	0.50
49:Y:43:LYS:HB2	49:Y:86:ALA:HB2	1.93	0.50
52:3:563:A:H61	52:3:884:U:H3	1.60	0.50
52:3:763:G:H2'	52:3:764:C:C6	2.46	0.50
52:3:1287:A:H2	52:3:1353:G:H1'	1.77	0.50
53:1:2884:U:H2'	53:1:2885:G:C8	2.47	0.50
1:b:245:THR:C	1:b:247:TRP:H	2.19	0.50
9:j:81:ILE:HG23	9:j:82:GLY:N	2.27	0.50
20:u:4:ILE:HD12	20:u:4:ILE:N	2.27	0.50
52:3:70:U:H2'	52:3:94:G:O6	2.11	0.50
52:3:501:C:H2'	52:3:502:A:C8	2.46	0.50
34:J:108:GLY:O	34:J:109:ALA:HB3	2.11	0.50
34:J:129:SER:HB2	52:3:20:U:OP2	2.12	0.50
52:3:513:C:H2'	52:3:514:C:C6	2.47	0.50
52:3:1211:U:H4'	52:3:1213:A:N3	2.27	0.50
53:1:1213:A:N6	53:1:1236:G:H1'	2.27	0.50
17:r:68:ARG:HB3	17:r:90:ARG:HB3	1.94	0.50
32:H:130:ARG:O	32:H:134:LYS:HG2	2.12	0.50
53:1:876:C:H2'	53:1:877:A:O4'	2.12	0.50
53:1:2457:U:O2'	53:1:2458:G:H5'	2.12	0.50
12:m:77:PRO:O	12:m:80:VAL:HG12	2.12	0.50
13:n:63:ARG:HD3	53:1:1454:C:O4'	2.12	0.50
14:o:90:VAL:HG12	14:o:91:SER:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:105:LYS:HE3	15:p:108:ARG:CZ	2.42	0.50
32:H:80:GLY:O	32:H:84:GLU:HG3	2.12	0.50
52:3:428:G:H4'	52:3:429:U:O5'	2.11	0.50
53:1:1326:U:H2'	53:1:1327:A:H8	1.76	0.50
53:1:1420:A:H5'	53:1:1421:G:OP2	2.12	0.50
53:1:1999:C:H2'	53:1:2000:C:H6	1.77	0.50
53:1:2281:A:O2'	53:1:2282:G:H5'	2.12	0.50
29:E:15:LYS:HD2	29:E:19:GLY:HA2	1.93	0.49
39:O:6:ILE:HG23	39:O:8:ILE:HD11	1.94	0.49
43:S:84:ARG:O	43:S:88:MET:HG3	2.12	0.49
46:V:47:ASP:HB3	46:V:74:LEU:HB3	1.94	0.49
52:3:195:A:H2'	52:3:196:A:C8	2.47	0.49
52:3:1402:C:H2'	52:3:1403:C:O4'	2.12	0.49
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.93	0.49
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.27	0.49
11:l:62:PRO:HA	53:1:2393:U:O3'	2.12	0.49
12:m:74:THR:HG21	53:1:956:G:OP2	2.12	0.49
31:G:162:VAL:HB	31:G:184:ALA:HB2	1.93	0.49
45:U:74:LEU:HD23	45:U:77:GLU:OE2	2.12	0.49
47:W:40:PRO:HB2	47:W:42:ARG:HG2	1.93	0.49
52:3:70:U:H4'	52:3:71:A:C8	2.47	0.49
53:1:635:C:H2'	53:1:636:G:C8	2.47	0.49
3:d:47:LYS:HB3	3:d:51:GLU:HB2	1.94	0.49
8:i:126:ARG:HG3	53:1:1080:A:O2'	2.11	0.49
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.42	0.49
35:K:51:ILE:HG22	35:K:52:ASN:OD1	2.11	0.49
38:N:89:TYR:HB3	38:N:93:LEU:HD22	1.95	0.49
52:3:860:A:H2'	52:3:861:G:O4'	2.12	0.49
52:3:884:U:H4'	52:3:885:G:H5''	1.94	0.49
52:3:1138:G:H3'	52:3:1138:G:N3	2.27	0.49
53:1:968:C:H2'	53:1:969:G:C8	2.46	0.49
53:1:1083:U:H2'	53:1:1085:A:OP2	2.12	0.49
53:1:1686:C:H2'	53:1:1687:G:O4'	2.11	0.49
53:1:1880:U:H2'	53:1:1881:C:C6	2.48	0.49
53:1:1909:C:H2'	53:1:1910:G:H8	1.77	0.49
53:1:2834:G:H2'	53:1:2879:A:N6	2.25	0.49
9:j:3:THR:HG21	16:q:60:TRP:NE1	2.20	0.49
31:G:131:LYS:HD2	31:G:132:GLU:N	2.28	0.49
33:I:171:GLU:HB3	33:I:180:THR:HG23	1.93	0.49
38:N:71:ILE:HG23	38:N:72:SER:N	2.28	0.49
38:N:108:ARG:O	52:3:1347:G:H8	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:8:ARG:HG2	43:S:12:ARG:HH12	1.77	0.49
46:V:18:LYS:HG3	46:V:49:ASN:HA	1.93	0.49
53:1:596:U:H2'	53:1:597:G:H8	1.77	0.49
53:1:596:U:H2'	53:1:597:G:C8	2.48	0.49
53:1:1013:C:H2'	53:1:1014:A:H8	1.78	0.49
53:1:2345:G:H21	53:1:2381:A:H3'	1.78	0.49
55:6:16:C:O2'	55:6:17:C:H5'	2.13	0.49
9:j:81:ILE:HD11	53:1:2514:U:C4'	2.42	0.49
12:m:54:THR:HG21	57:7:54:U:H5''	1.95	0.49
27:C:36:LYS:HA	27:C:47:ILE:HA	1.92	0.49
34:J:133:ILE:O	34:J:136:VAL:HG12	2.13	0.49
40:P:71:ASP:O	40:P:72:ALA:HB3	2.12	0.49
42:R:97:ARG:HG3	52:3:1308:U:OP2	2.12	0.49
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.94	0.49
51:a:180:PHE:HB3	51:a:184:LYS:HD2	1.94	0.49
52:3:401:C:H2'	52:3:402:G:C8	2.47	0.49
52:3:946:A:H2'	52:3:947:G:C8	2.47	0.49
53:1:215:G:C4'	53:1:216:A:H4'	2.42	0.49
53:1:634:C:H2'	53:1:635:C:C6	2.47	0.49
53:1:1999:C:H2'	53:1:2000:C:C6	2.47	0.49
1:b:245:THR:OG1	1:b:246:PRO:HD2	2.12	0.49
10:k:35:VAL:HG21	10:k:106:GLU:HB3	1.93	0.49
31:G:221:ARG:HA	31:G:224:ARG:HB2	1.95	0.49
52:3:543:U:H2'	52:3:544:G:C8	2.47	0.49
54:2:66:A:H4'	54:2:67:G:N7	2.27	0.49
6:g:30:LEU:HB3	6:g:36:ALA:HB3	1.94	0.49
19:t:3:ARG:HG3	19:t:7:LEU:HD23	1.95	0.49
21:v:12:GLN:OE1	54:2:75:G:H5''	2.13	0.49
21:v:77:VAL:HG12	21:v:89:ILE:HG23	1.95	0.49
32:H:5:HIS:CD2	43:S:88:MET:HE2	2.48	0.49
34:J:152:VAL:HG12	34:J:155:LYS:HE2	1.94	0.49
35:K:51:ILE:C	35:K:53:LYS:H	2.21	0.49
40:P:73:VAL:HA	40:P:76:TYR:HD2	1.78	0.49
40:P:124:LYS:O	40:P:125:LYS:O	2.30	0.49
42:R:59:VAL:HG12	42:R:64:VAL:HG21	1.94	0.49
52:3:56:U:H2'	52:3:57:G:H8	1.77	0.49
1:b:216:ARG:CZ	53:1:691:C:H5'	2.42	0.49
10:k:87:LEU:HD22	10:k:92:GLU:O	2.13	0.49
19:t:13:ALA:HB1	24:y:33:ALA:HB1	1.93	0.49
21:v:42:LEU:HD12	21:v:47:VAL:HG11	1.95	0.49
32:H:9:ILE:HG23	32:H:10:ARG:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:74:VAL:HB	36:L:85:GLN:HB3	1.95	0.49
52:3:401:C:H2'	52:3:402:G:H8	1.77	0.49
53:1:296:U:H2'	53:1:297:G:C8	2.48	0.49
53:1:573:U:O2'	53:1:574:A:H3'	2.13	0.49
53:1:1013:C:H2'	53:1:1014:A:C8	2.48	0.49
7:h:119:PRO:CD	7:h:120:ALA:H	2.25	0.49
23:x:39:VAL:HG22	23:x:41:SER:H	1.78	0.49
32:H:137:VAL:HG13	32:H:148:ILE:HG23	1.94	0.49
35:K:36:ILE:HG23	35:K:64:VAL:HG22	1.94	0.49
38:N:34:LEU:HD23	38:N:34:LEU:O	2.13	0.49
42:R:79:LEU:HD22	42:R:84:CYS:SG	2.52	0.49
45:U:5:ARG:HD2	52:3:376:G:H4'	1.95	0.49
53:1:1658:C:H2'	53:1:1659:G:H8	1.78	0.49
53:1:2798:U:H4'	53:1:2799:A:C4	2.48	0.49
1:b:159:THR:HG21	53:1:1819:A:H5''	1.94	0.49
4:e:34:THR:HG22	4:e:89:THR:HG22	1.95	0.49
20:u:97:SER:O	20:u:98:ASN:HB3	2.13	0.49
29:E:1:PRO:N	53:1:591:U:H1'	2.28	0.49
31:G:173:LYS:O	31:G:177:ASN:ND2	2.45	0.49
35:K:9:MET:HE1	35:K:86:ARG:HD2	1.95	0.49
36:L:16:LYS:HD2	36:L:17:PHE:HE1	1.77	0.49
37:M:28:SER:HB2	37:M:56:PRO:HB2	1.95	0.49
37:M:77:VAL:HG23	37:M:126:CYS:HA	1.94	0.49
43:S:20:PHE:O	43:S:21:ALA:HB3	2.13	0.49
45:U:72:ALA:O	45:U:75:ILE:HG22	2.13	0.49
52:3:711:G:O2'	52:3:712:A:H5'	2.13	0.49
52:3:911:U:H2'	52:3:912:C:C6	2.47	0.49
52:3:1158:C:H2'	52:3:1159:U:H4'	1.95	0.49
53:1:1201:U:H2'	53:1:1202:G:H8	1.78	0.49
3:d:52:VAL:HG21	3:d:81:GLY:HA2	1.95	0.48
11:l:79:LEU:HD12	11:l:112:LEU:HD12	1.94	0.48
20:u:11:ILE:CD1	20:u:79:ALA:HB2	2.40	0.48
24:y:19:LEU:HA	24:y:22:LEU:HD12	1.95	0.48
28:D:34:ARG:NH1	53:1:467:G:OP2	2.46	0.48
45:U:22:ALA:HB2	45:U:32:PHE:HB3	1.95	0.48
53:1:471:A:H2'	53:1:472:A:O4'	2.13	0.48
53:1:1765:U:H2'	53:1:1766:G:H8	1.77	0.48
53:1:2629:U:O2'	53:1:2630:G:H5''	2.13	0.48
54:2:106:G:H2'	54:2:107:G:O4'	2.13	0.48
5:f:15:ASP:O	5:f:25:ILE:HG23	2.13	0.48
9:j:3:THR:HG23	53:1:995:C:O2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:18:VAL:HG23	38:N:64:ILE:HG13	1.95	0.48
52:3:477:C:H2'	52:3:478:A:C8	2.48	0.48
52:3:855:U:H2'	52:3:856:C:C6	2.48	0.48
52:3:1344:C:O2'	52:3:1345:U:H5'	2.13	0.48
53:1:611:C:H2'	53:1:612:G:O4'	2.13	0.48
53:1:817:C:O2'	53:1:839:U:H5''	2.14	0.48
53:1:1310:G:H3'	53:1:1311:G:C8	2.48	0.48
53:1:2743:U:C3'	53:1:2744:G:H5''	2.42	0.48
55:6:17:C:H2'	55:6:17(A):U:C5	2.48	0.48
7:h:37:LYS:HZ1	53:1:1057:A:H1'	1.78	0.48
25:z:29:ARG:NE	53:1:1183:U:H5''	2.29	0.48
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.48	0.48
32:H:39:ARG:NH1	32:H:54:ILE:HG13	2.29	0.48
39:O:57:VAL:HG13	39:O:58:ASN:ND2	2.28	0.48
51:a:183:ASP:O	51:a:187:GLU:HG3	2.13	0.48
52:3:82:G:H2'	52:3:83:C:O4'	2.13	0.48
52:3:381:C:H2'	52:3:382:A:O4'	2.13	0.48
53:1:362:A:H3'	53:1:363:G:H8	1.77	0.48
53:1:457:A:N6	53:1:470:A:H5''	2.28	0.48
53:1:1310:G:H3'	53:1:1311:G:H8	1.78	0.48
53:1:1790:C:H2'	53:1:1791:A:C5	2.47	0.48
54:2:26:C:O2	54:2:117:G:H1'	2.13	0.48
10:k:53:LYS:HD3	10:k:54:LYS:N	2.28	0.48
19:t:4:GLU:HA	19:t:7:LEU:HB2	1.96	0.48
20:u:95:PHE:O	20:u:99:SER:HA	2.14	0.48
32:H:155:ARG:HD3	32:H:192:TYR:O	2.13	0.48
46:V:5:ARG:NH2	52:3:636:U:H5'	2.28	0.48
52:3:1354:U:H2'	52:3:1355:G:H8	1.79	0.48
53:1:1326:U:H2'	53:1:1327:A:C8	2.48	0.48
53:1:1386:C:H2'	53:1:1387:A:C8	2.48	0.48
53:1:1773:A:C5	53:1:1829:A:H1'	2.49	0.48
53:1:2233:U:H2'	53:1:2234:G:H8	1.78	0.48
53:1:2818:U:H2'	53:1:2819:G:C8	2.47	0.48
3:d:45:ALA:HA	3:d:87:ALA:O	2.13	0.48
31:G:136:ARG:HA	31:G:139:GLU:CD	2.38	0.48
32:H:162:ALA:HB2	52:3:1056:U:H4'	1.95	0.48
53:1:479:A:H1'	53:1:481:G:H5''	1.94	0.48
53:1:2799:A:C2'	53:1:2800:A:H5'	2.44	0.48
53:1:2853:C:H2'	53:1:2854:G:C8	2.49	0.48
54:2:78:A:H62	54:2:98:G:H21	1.61	0.48
3:d:191:ASP:O	3:d:195:GLN:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:77:ILE:HD12	11:l:77:ILE:N	2.28	0.48
14:o:52:SER:HB2	14:o:55:GLU:HG3	1.96	0.48
32:H:119:ILE:O	32:H:123:LEU:HD23	2.13	0.48
34:J:40:ASP:OD2	34:J:42:ASN:HB2	2.13	0.48
37:M:46:GLU:HB2	37:M:63:LYS:HG2	1.96	0.48
38:N:78:ILE:O	38:N:82:ILE:HG13	2.14	0.48
42:R:23:GLY:O	52:3:1329:A:H4'	2.14	0.48
53:1:581:C:H2'	53:1:582:A:C8	2.49	0.48
53:1:2623:G:H2'	53:1:2624:G:C8	2.48	0.48
53:1:2849:U:H4'	53:1:2868:A:C2	2.49	0.48
55:6:72:A:H2'	55:6:73:A:O4'	2.14	0.48
3:d:52:VAL:O	3:d:74:LYS:HE3	2.13	0.48
15:p:38:ARG:HE	52:3:345:C:H5'	1.78	0.48
27:C:46:VAL:HG22	27:C:47:ILE:H	1.77	0.48
34:J:123:LEU:HD12	34:J:123:LEU:O	2.12	0.48
34:J:149:PRO:HA	34:J:152:VAL:HG22	1.95	0.48
36:L:48:THR:HG22	36:L:52:ARG:HD3	1.95	0.48
37:M:48:PHE:O	37:M:49:LYS:HD2	2.13	0.48
52:3:1305:G:H22	52:3:1331:G:H2'	1.77	0.48
53:1:1683:U:H2'	53:1:1684:G:C8	2.49	0.48
9:j:96:ARG:CG	9:j:99:ARG:HG2	2.43	0.48
19:t:33:LYS:HE3	19:t:80:TRP:CE3	2.49	0.48
33:I:96:ARG:O	33:I:100:VAL:HG23	2.13	0.48
42:R:9:PRO:HG2	42:R:44:ILE:HG13	1.96	0.48
50:Z:16:ARG:HG3	50:Z:20:ARG:HH21	1.79	0.48
52:3:770:C:H2'	52:3:771:G:H8	1.79	0.48
52:3:1527:U:O2'	52:3:1528:U:H5'	2.14	0.48
53:1:161:A:H3'	53:1:162:U:H5''	1.95	0.48
53:1:2432:A:H1'	55:6:75:C:H4'	1.96	0.48
1:b:86:ARG:HG3	1:b:86:ARG:HH11	1.79	0.48
16:q:7:VAL:HG23	16:q:8:ILE:HG23	1.95	0.48
17:r:38:VAL:HG23	17:r:54:VAL:HG23	1.96	0.48
18:s:86:MET:HB2	18:s:96:ILE:HG12	1.95	0.48
53:1:616:A:H2'	53:1:617:G:O4'	2.13	0.48
53:1:1889:A:H2'	53:1:1890:A:C8	2.48	0.48
53:1:2552:U:H2'	53:1:2554:U:H5''	1.96	0.48
53:1:2628:C:H3'	53:1:2629:U:H5'	1.94	0.48
24:y:5:GLU:HB3	24:y:13:GLU:OE2	2.14	0.48
24:y:32:ALA:HB2	24:y:37:LEU:HD23	1.95	0.48
36:L:110:ARG:HH12	36:L:121:ASN:HD22	1.62	0.48
44:T:36:ASN:HA	44:T:39:GLN:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2128:G:H1'	53:1:2173:A:N3	2.28	0.48
53:1:2273:A:H2'	53:1:2274:A:C8	2.49	0.48
2:c:124:ARG:HD3	2:c:125:TRP:HE1	1.78	0.47
4:e:55:ASP:O	4:e:59:ILE:HG13	2.14	0.47
5:f:102:ILE:HD11	5:f:116:LEU:HD11	1.96	0.47
6:g:1:MET:HB3	6:g:3:VAL:HG23	1.95	0.47
10:k:68:GLY:HA3	10:k:78:ARG:HG2	1.96	0.47
13:n:47:VAL:HG13	13:n:48:VAL:N	2.29	0.47
18:s:29:VAL:HG21	18:s:69:LEU:HD23	1.95	0.47
22:w:39:THR:HB	53:1:2331:G:O2'	2.14	0.47
26:B:12:ARG:NH2	53:1:517:C:OP1	2.46	0.47
48:X:35:ARG:HE	48:X:71:GLY:HA2	1.78	0.47
53:1:1105:U:C2'	53:1:1106:G:H5''	2.43	0.47
53:1:1664:A:H2'	53:1:1664:A:N3	2.29	0.47
3:d:94:GLN:HB2	53:1:660:C:OP1	2.14	0.47
3:d:158:PHE:HA	3:d:169:VAL:HG11	1.95	0.47
13:n:35:LYS:HD3	13:n:112:TYR:CE1	2.49	0.47
20:u:48:VAL:HG22	20:u:50:ALA:H	1.78	0.47
28:D:1:MET:HE2	53:1:1619:G:H21	1.79	0.47
31:G:138:ARG:HH12	52:3:1097:C:H5''	1.79	0.47
52:3:634:C:H2'	52:3:635:A:H8	1.79	0.47
52:3:1513:A:H2'	52:3:1514:G:C8	2.49	0.47
53:1:341:C:H2'	53:1:342:A:C8	2.49	0.47
53:1:1234:U:H2'	53:1:1235:G:O4'	2.14	0.47
1:b:227:VAL:HG11	53:1:784:G:C2	2.49	0.47
4:e:32:LYS:HD3	4:e:91:ARG:HH22	1.79	0.47
13:n:3:HIS:O	13:n:4:ARG:HB2	2.14	0.47
34:J:123:LEU:HD12	34:J:123:LEU:C	2.38	0.47
34:J:133:ILE:HD12	34:J:133:ILE:N	2.27	0.47
51:a:38:PHE:HB3	53:1:2127:G:O5'	2.15	0.47
52:3:701:U:C4'	52:3:703:G:H1'	2.44	0.47
53:1:490:C:O2'	53:1:491:G:OP2	2.32	0.47
53:1:955:U:H3	53:1:962:G:H1	1.60	0.47
54:2:28:C:H2'	54:2:29:A:C8	2.49	0.47
54:2:88:C:C5'	54:2:89:U:OP1	2.61	0.47
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.95	0.47
3:d:149:ILE:HG23	3:d:188:MET:HG3	1.97	0.47
3:d:190:ALA:O	3:d:193:VAL:HG12	2.14	0.47
7:h:34:THR:O	7:h:37:LYS:HB3	2.14	0.47
8:i:12:VAL:O	8:i:13:ALA:C	2.58	0.47
24:y:24:GLU:HB3	24:y:46:VAL:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:y:24:GLU:O	24:y:28:LEU:HB2	2.15	0.47
31:G:44:LYS:O	31:G:48:MET:HG2	2.14	0.47
33:I:124:VAL:HA	33:I:142:VAL:HA	1.96	0.47
40:P:126:ARG:O	50:Z:34:ARG:NH2	2.47	0.47
48:X:38:THR:HG22	48:X:69:LYS:HG2	1.95	0.47
52:3:499:A:H1'	52:3:500:G:C8	2.50	0.47
52:3:1516:G:H2'	52:3:1518:A:OP2	2.15	0.47
53:1:562:U:O4'	53:1:2036:C:H5'	2.14	0.47
53:1:687:C:H42	53:1:787:C:H4'	1.80	0.47
53:1:703:U:H2'	53:1:704:G:O4'	2.14	0.47
53:1:891:G:H2'	53:1:892:A:H8	1.79	0.47
53:1:2106:U:H2'	53:1:2107:G:C8	2.49	0.47
53:1:2277:G:C3'	53:1:2278:A:H5''	2.44	0.47
53:1:2537:U:H2'	53:1:2538:C:C6	2.48	0.47
1:b:158:GLY:HA3	53:1:1820:U:C4	2.50	0.47
6:g:121:VAL:HG22	6:g:121:VAL:O	2.14	0.47
22:w:39:THR:H	53:1:2331:G:H4'	1.79	0.47
31:G:136:ARG:HA	31:G:139:GLU:CG	2.44	0.47
35:K:79:ARG:NH2	52:3:671:G:O2'	2.47	0.47
39:O:11:LYS:HE2	39:O:71:LEU:HD21	1.96	0.47
41:Q:120:ARG:NE	52:3:500:G:H5'	2.30	0.47
45:U:54:LEU:H	45:U:54:LEU:CD1	2.27	0.47
51:a:50:ILE:HG23	51:a:57:GLN:HB3	1.95	0.47
52:3:184:G:H4'	52:3:224:U:H4'	1.94	0.47
52:3:225:C:C2'	52:3:226:G:H5''	2.44	0.47
53:1:213:A:H2'	53:1:214:G:C8	2.49	0.47
53:1:1775:U:H2'	53:1:1776:G:O4'	2.14	0.47
53:1:1906:G:C3'	53:1:1907:G:H5''	2.44	0.47
1:b:12:ARG:NH2	53:1:729:G:OP2	2.46	0.47
12:m:41:LEU:HD11	12:m:124:LEU:HD22	1.96	0.47
32:H:4:VAL:HG22	32:H:5:HIS:N	2.30	0.47
48:X:66:VAL:HG13	48:X:67:GLY:N	2.29	0.47
50:Z:33:ARG:NH1	50:Z:34:ARG:HB2	2.30	0.47
52:3:516:U:H3	52:3:533:A:H62	1.62	0.47
52:3:715:A:H2'	52:3:716:A:H8	1.77	0.47
52:3:1123:U:O2'	52:3:1124:G:H5'	2.15	0.47
52:3:1391:U:H2'	52:3:1392:G:C8	2.49	0.47
52:3:1510:C:H2'	52:3:1511:G:H8	1.78	0.47
53:1:1669:A:O3'	53:1:2549:G:H5'	2.15	0.47
53:1:2087:G:H2'	53:1:2088:A:H8	1.79	0.47
53:1:2155:U:H2'	53:1:2156:G:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2756:U:H4'	53:1:2757:A:OP1	2.12	0.47
2:c:101:PHE:HA	2:c:104:VAL:HG22	1.96	0.47
4:e:35:LEU:HB3	4:e:88:VAL:HB	1.96	0.47
6:g:8:LYS:O	6:g:13:GLY:HA3	2.14	0.47
15:p:52:ARG:HH21	53:1:2720:U:H5''	1.80	0.47
45:U:5:ARG:NH1	52:3:377:G:H5'	2.30	0.47
46:V:54:ILE:HD12	46:V:54:ILE:N	2.30	0.47
52:3:1504:G:OP1	52:3:1507:A:H4'	2.15	0.47
53:1:948:C:H2'	53:1:949:G:H8	1.80	0.47
53:1:2642:G:H2'	53:1:2643:G:H8	1.79	0.47
1:b:12:ARG:HD3	1:b:15:VAL:HG11	1.97	0.47
10:k:87:LEU:HD23	10:k:94:PRO:HB3	1.97	0.47
13:n:74:GLU:O	13:n:77:ALA:HB3	2.15	0.47
19:t:34:VAL:HG12	19:t:35:ALA:N	2.29	0.47
39:O:53:ILE:CD1	52:3:1060:U:H5''	2.45	0.47
43:S:26:LEU:HA	43:S:30:ILE:HD12	1.97	0.47
52:3:422:C:H4'	52:3:423:G:H5''	1.97	0.47
53:1:1219:U:H2'	53:1:1220:G:C8	2.49	0.47
53:1:1331:G:C2'	53:1:1332:G:H5''	2.44	0.47
53:1:2360:G:H2'	53:1:2361:G:H5'	1.97	0.47
54:2:95:U:H2'	54:2:96:G:C8	2.50	0.47
54:2:108:A:H5'	54:2:109:A:O5'	2.15	0.47
3:d:97:ASN:HB2	3:d:100:MET:HB2	1.97	0.47
8:i:23:VAL:CG2	8:i:26:ALA:HB3	2.44	0.47
13:n:23:ASN:HD21	53:1:1294:U:H1'	1.80	0.47
13:n:47:VAL:C	13:n:50:PRO:HD2	2.40	0.47
13:n:64:ARG:HH22	53:1:2852:G:H5'	1.80	0.47
31:G:48:MET:HA	31:G:51:GLU:HB3	1.97	0.47
32:H:5:HIS:CE1	32:H:7:ASN:HB3	2.49	0.47
32:H:13:ILE:HG22	32:H:14:VAL:HG13	1.96	0.47
35:K:3:HIS:N	35:K:92:THR:HG22	2.30	0.47
52:3:580:C:H2'	52:3:581:G:O4'	2.13	0.47
52:3:1033:G:C2'	52:3:1034:G:H5''	2.41	0.47
52:3:1346:A:H2'	52:3:1347:G:H4'	1.97	0.47
52:3:1412:C:H2'	52:3:1413:A:C8	2.49	0.47
53:1:631:A:H2'	53:1:632:A:O4'	2.15	0.47
53:1:1111:A:O2'	53:1:1112:G:H4'	2.15	0.47
53:1:2039:U:H2'	53:1:2040:G:H8	1.80	0.47
2:c:131:ASP:OD1	2:c:131:ASP:N	2.48	0.47
23:x:21:LEU:CD2	55:6:75:C:H41	2.28	0.47
37:M:9:MET:O	37:M:13:ILE:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:83:THR:O	39:O:87:LEU:HG	2.14	0.47
51:a:189:LEU:O	51:a:192:LEU:HG	2.15	0.47
53:1:1857:G:N2	53:1:1884:G:H2'	2.30	0.47
53:1:2111:U:H5'	53:1:2112:G:OP2	2.15	0.47
53:1:2515:C:H2'	53:1:2516:A:H8	1.79	0.47
2:c:173:GLN:HE21	53:1:2772:C:H5'	1.80	0.46
30:F:22:VAL:HG21	30:F:36:ARG:HH11	1.80	0.46
33:I:67:LEU:HD12	33:I:70:GLN:H	1.80	0.46
37:M:21:LYS:HG2	37:M:22:ALA:N	2.31	0.46
38:N:105:ARG:CD	52:3:1117:A:H4'	2.45	0.46
44:T:44:GLU:O	44:T:45:HIS:HB2	2.14	0.46
51:a:174:THR:HB	53:1:2124:G:C4'	2.40	0.46
52:3:825:A:H2'	52:3:826:C:C6	2.50	0.46
52:3:1434:A:H2'	52:3:1435:G:O4'	2.14	0.46
53:1:2104:C:H2'	53:1:2105:U:C6	2.50	0.46
53:1:2286:G:H4'	53:1:2287:A:O5'	2.15	0.46
53:1:2818:U:H2'	53:1:2819:G:H8	1.80	0.46
4:e:90:LEU:HD12	4:e:90:LEU:O	2.16	0.46
15:p:23:ASP:HB3	15:p:85:VAL:HG13	1.98	0.46
16:q:58:GLN:HB2	53:1:1009:A:O4'	2.16	0.46
22:w:17:LEU:HD12	22:w:17:LEU:N	2.30	0.46
31:G:160:LEU:HB3	31:G:182:VAL:HG12	1.98	0.46
37:M:86:LYS:HD2	37:M:90:GLU:HG2	1.96	0.46
51:a:4:LEU:HA	51:a:8:MET:SD	2.55	0.46
52:3:1499:A:O2'	52:3:1500:A:H5'	2.14	0.46
53:1:1298:C:H2'	53:1:1299:G:O4'	2.15	0.46
53:1:2126:A:H2'	53:1:2162:G:N2	2.31	0.46
1:b:68:ARG:NH1	1:b:128:THR:OG1	2.49	0.46
2:c:135:GLY:HA2	53:1:743:A:OP1	2.15	0.46
7:h:20:LYS:HE3	7:h:88:HIS:CE1	2.50	0.46
29:E:44:ARG:NH2	53:1:2349:G:OP1	2.47	0.46
31:G:153:MET:HE1	31:G:157:PRO:HB3	1.98	0.46
35:K:18:VAL:CG1	35:K:19:PRO:HD3	2.46	0.46
39:O:8:ILE:HD12	39:O:8:ILE:N	2.31	0.46
40:P:22:ILE:HG12	40:P:31:VAL:HG13	1.97	0.46
42:R:28:ARG:HH21	42:R:62:PHE:HB2	1.80	0.46
51:a:39:VAL:HG13	51:a:39:VAL:O	2.15	0.46
52:3:410:G:H2'	52:3:429:U:O4	2.15	0.46
53:1:511:U:C2'	53:1:512:G:H5'	2.45	0.46
53:1:917:A:H5''	53:1:2268:A:H61	1.79	0.46
57:7:9:A:N3	57:7:45:U:H2'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:98:ILE:HD11	17:r:101:ILE:HD11	1.98	0.46
20:u:11:ILE:HG22	20:u:21:ARG:HG2	1.97	0.46
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.30	0.46
22:w:67:VAL:HG22	22:w:67:VAL:O	2.15	0.46
53:1:2512:C:H2'	53:1:2513:A:O4'	2.14	0.46
1:b:81:GLU:HG2	1:b:82:TYR:N	2.31	0.46
2:c:29:VAL:HG23	2:c:98:VAL:HG21	1.97	0.46
11:l:33:ARG:HD2	53:1:587:C:H42	1.80	0.46
19:t:21:SER:O	19:t:24:MET:HB3	2.15	0.46
31:G:19:THR:HG22	31:G:38:HIS:CD2	2.51	0.46
31:G:94:ARG:HH21	52:3:1100:C:H3'	1.81	0.46
36:L:32:ASP:OD2	52:3:1351:U:H4'	2.16	0.46
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.97	0.46
46:V:67:SER:OG	46:V:68:LYS:N	2.48	0.46
49:Y:70:LYS:NZ	52:3:262:A:OP2	2.39	0.46
53:1:873:C:H2'	53:1:874:G:C8	2.51	0.46
53:1:2215:C:H2'	53:1:2216:G:H8	1.81	0.46
53:1:2266:A:H4'	53:1:2267:A:N3	2.31	0.46
53:1:2443:C:H2'	53:1:2444:G:C8	2.51	0.46
11:l:57:LEU:HB2	11:l:60:ARG:HH11	1.80	0.46
12:m:6:ARG:HG3	12:m:6:ARG:O	2.16	0.46
12:m:58:LYS:O	12:m:59:ARG:HB3	2.15	0.46
15:p:83:ILE:HD12	15:p:83:ILE:N	2.30	0.46
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.98	0.46
38:N:27:ILE:N	38:N:27:ILE:HD12	2.30	0.46
43:S:78:LEU:HD23	43:S:83:VAL:HA	1.97	0.46
52:3:12:U:H2'	52:3:13:U:H5''	1.98	0.46
52:3:337:G:H2'	52:3:338:A:C8	2.50	0.46
52:3:396:C:H2'	52:3:397:A:H5''	1.96	0.46
53:1:254:G:C2'	53:1:255:A:H5''	2.46	0.46
53:1:255:A:H2'	53:1:256:A:O4'	2.16	0.46
53:1:341:C:H2'	53:1:342:A:H8	1.80	0.46
53:1:910:A:H2'	53:1:911:A:C8	2.51	0.46
53:1:1507:C:H2'	53:1:1508:A:O4'	2.15	0.46
54:2:63:C:H2'	54:2:64:G:C8	2.51	0.46
54:2:104:A:H2'	54:2:105:G:O4'	2.15	0.46
55:6:71:C:H2'	55:6:72:A:C8	2.50	0.46
15:p:51:ASN:O	53:1:2845:U:H5''	2.16	0.46
19:t:68:LYS:HD2	53:1:1336:A:OP2	2.15	0.46
27:C:32:LYS:HB2	27:C:50:GLU:HB3	1.97	0.46
39:O:29:ALA:O	39:O:33:GLY:HA3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:71:HIS:HA	41:Q:98:ARG:HH12	1.80	0.46
49:Y:24:ARG:NH2	52:3:323:U:OP1	2.48	0.46
52:3:694:A:H2'	52:3:695:A:O4'	2.16	0.46
52:3:950:U:H2'	52:3:951:G:H8	1.78	0.46
52:3:1330:U:H2'	52:3:1331:G:O4'	2.16	0.46
53:1:1909:C:H2'	53:1:1910:G:C8	2.51	0.46
53:1:2141:G:N2	53:1:2151:U:H1'	2.30	0.46
53:1:2834:G:O2'	53:1:2835:A:H5'	2.15	0.46
55:5:36:U:H2'	55:5:37:A:H8	1.81	0.46
1:b:114:GLN:O	1:b:124:LYS:NZ	2.49	0.46
6:g:97:ARG:NH1	6:g:112:LYS:HZ1	2.14	0.46
11:l:19:LEU:HD23	11:l:27:LEU:HD13	1.98	0.46
18:s:17:VAL:HG13	18:s:76:VAL:HG11	1.98	0.46
27:C:29:LYS:HD3	53:1:2286:G:OP1	2.16	0.46
32:H:168:ARG:NH2	52:3:1106:G:H1'	2.30	0.46
35:K:96:VAL:HG22	35:K:98:GLU:HG2	1.97	0.46
49:Y:67:HIS:O	49:Y:69:ASN:N	2.36	0.46
52:3:770:C:H2'	52:3:771:G:C8	2.50	0.46
53:1:924:G:H2'	53:1:925:A:C8	2.50	0.46
53:1:948:C:H2'	53:1:949:G:C8	2.51	0.46
53:1:1695:G:H3'	53:1:1695:G:N3	2.31	0.46
53:1:1720:U:H2'	53:1:1721:G:O4'	2.15	0.46
53:1:1991:U:H2'	53:1:1992:G:H5'	1.97	0.46
53:1:2236:U:H2'	53:1:2237:G:O4'	2.16	0.46
53:1:2898:U:H2'	53:1:2899:A:C8	2.51	0.46
55:6:51:C:H2'	55:6:52:G:C8	2.51	0.46
1:b:164:VAL:HG13	52:3:712:A:H5''	1.98	0.46
4:e:55:ASP:OD2	4:e:149:ARG:NH2	2.48	0.46
6:g:4:ILE:CG2	6:g:37:VAL:HG23	2.43	0.46
8:i:11:GLN:OE1	8:i:58:ILE:HD11	2.16	0.46
11:l:96:LYS:HD2	11:l:103:ILE:HD12	1.97	0.46
13:n:32:GLU:CD	13:n:118:ARG:HG2	2.41	0.46
21:v:42:LEU:H	21:v:42:LEU:HD23	1.80	0.46
26:B:46:GLY:HA3	26:B:54:ILE:HB	1.98	0.46
33:I:80:ARG:HD2	33:I:80:ARG:O	2.16	0.46
38:N:129:ARG:HE	55:5:35:A:P	2.39	0.46
50:Z:54:ARG:O	50:Z:57:LYS:HG3	2.15	0.46
51:a:172:HIS:O	51:a:173:THR:HG23	2.15	0.46
52:3:494:G:H2'	52:3:496:A:H8	1.81	0.46
53:1:74:A:H4'	53:1:75:G:O5'	2.15	0.46
53:1:1380:G:H1'	53:1:1569:A:H61	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2055:C:H2'	53:1:2504:U:H5'	1.98	0.46
53:1:2105:U:H2'	53:1:2106:U:O4'	2.16	0.46
53:1:2475:C:H2'	53:1:2476:A:H5'	1.98	0.46
53:1:2526:G:H2'	53:1:2527:C:C6	2.51	0.46
5:f:163:TYR:O	5:f:166:GLU:HG2	2.16	0.46
8:i:33:ASN:HB2	8:i:36:GLU:HB3	1.98	0.46
14:o:31:THR:CG2	14:o:32:PRO:HD2	2.46	0.46
15:p:30:TRP:CE3	15:p:37:LYS:HG2	2.51	0.46
31:G:169:HIS:HA	31:G:172:ILE:HD12	1.97	0.46
32:H:196:GLY:H	52:3:1057:G:H4'	1.81	0.46
36:L:4:ARG:NE	36:L:6:ILE:HB	2.31	0.46
47:W:41:SER:HB3	47:W:51:GLN:NE2	2.31	0.46
49:Y:43:LYS:HB3	49:Y:85:LEU:HG	1.98	0.46
52:3:194:C:O2'	52:3:195:A:H5'	2.16	0.46
52:3:235:C:H2'	52:3:236:A:C8	2.51	0.46
52:3:297:G:H4'	52:3:557:G:H4'	1.98	0.46
52:3:682:G:H2'	52:3:683:G:H8	1.81	0.46
53:1:572:A:H61	53:1:2029:G:N2	2.10	0.46
53:1:1991:U:H2'	53:1:1992:G:C5'	2.46	0.46
53:1:2545:G:H2'	53:1:2546:U:O4'	2.16	0.46
1:b:63:ILE:HD12	1:b:63:ILE:N	2.31	0.45
1:b:242:HIS:O	1:b:244:VAL:HG13	2.16	0.45
9:j:78:THR:HG23	9:j:80:HIS:H	1.81	0.45
12:m:57:VAL:HB	12:m:60:GLN:HG2	1.98	0.45
22:w:65:PHE:CD2	53:1:857:G:H5'	2.51	0.45
30:F:36:ARG:O	30:F:37:GLN:CB	2.63	0.45
34:J:75:LEU:HD23	34:J:75:LEU:H	1.81	0.45
38:N:53:LEU:CD1	38:N:54:VAL:HG13	2.44	0.45
39:O:24:GLU:OE2	39:O:25:ILE:HG23	2.16	0.45
46:V:74:LEU:C	46:V:74:LEU:HD23	2.40	0.45
47:W:37:LYS:CD	52:3:719:C:H1'	2.46	0.45
49:Y:8:LYS:O	49:Y:11:ILE:HG22	2.16	0.45
52:3:300:A:H2'	52:3:301:G:O4'	2.17	0.45
52:3:350:G:H2'	52:3:351:G:C8	2.50	0.45
52:3:739:C:H2'	52:3:740:U:O4'	2.17	0.45
52:3:1004:A:H2'	52:3:1005:A:O4'	2.16	0.45
53:1:367:G:H2'	53:1:368:A:O4'	2.16	0.45
53:1:433:C:O2'	53:1:434:U:H5'	2.16	0.45
53:1:494:G:H2'	53:1:495:G:H8	1.81	0.45
53:1:1295:C:H2'	53:1:1296:G:H8	1.81	0.45
53:1:2197:U:H1'	53:1:2198:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.80	0.45
16:q:24:TYR:HE1	53:1:17:G:H4'	1.81	0.45
31:G:206:ILE:N	31:G:206:ILE:HD12	2.31	0.45
41:Q:85:ARG:HA	41:Q:93:ARG:HA	1.97	0.45
53:1:129:C:H2'	53:1:130:C:C6	2.51	0.45
53:1:2023:C:H2'	53:1:2024:G:H8	1.81	0.45
53:1:2029:G:O6	53:1:2032:G:H5''	2.16	0.45
54:2:63:C:H2'	54:2:64:G:H8	1.79	0.45
57:7:47:U:H3'	57:7:48:C:C5'	2.46	0.45
1:b:204:LEU:HB2	53:1:1791:A:H4'	1.98	0.45
13:n:54:LEU:HD22	13:n:69:ARG:HH22	1.81	0.45
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.81	0.45
29:E:37:THR:HA	29:E:40:LYS:HB2	1.99	0.45
31:G:67:LEU:HD22	31:G:157:PRO:HG3	1.96	0.45
31:G:146:SER:C	31:G:147:LEU:HD12	2.40	0.45
34:J:22:LYS:HB3	34:J:29:ILE:CG2	2.42	0.45
35:K:47:LEU:HD12	35:K:55:HIS:HA	1.96	0.45
39:O:17:LEU:HA	39:O:20:GLN:HE21	1.81	0.45
41:Q:85:ARG:HH12	41:Q:87:LYS:HE2	1.82	0.45
52:3:536:C:H2'	52:3:537:G:C8	2.52	0.45
52:3:760:G:H2'	52:3:761:G:H5'	1.98	0.45
53:1:2642:G:H2'	53:1:2643:G:C8	2.52	0.45
53:1:2815:C:H2'	53:1:2816:G:H8	1.80	0.45
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.97	0.45
5:f:126:THR:HG22	5:f:127:GLN:H	1.80	0.45
7:h:58:THR:HG21	7:h:82:ILE:HB	1.98	0.45
19:t:14:PRO:HA	19:t:32:LEU:HD13	1.98	0.45
26:B:9:ARG:HG3	26:B:12:ARG:NH2	2.30	0.45
34:J:35:LEU:HD23	34:J:36:THR:N	2.32	0.45
35:K:67:PRO:HG2	35:K:70:VAL:CG2	2.46	0.45
37:M:12:ARG:CZ	52:3:826:C:H5'	2.46	0.45
40:P:63:GLN:HG3	40:P:98:ALA:HB2	1.97	0.45
43:S:42:ASN:HA	43:S:45:LEU:HG	1.98	0.45
52:3:304:U:H2'	52:3:305:G:C8	2.52	0.45
53:1:18:U:H2'	53:1:19:A:C8	2.52	0.45
53:1:119:A:H4'	53:1:120:U:H5'	1.99	0.45
53:1:176:A:O2'	53:1:177:G:H5'	2.16	0.45
53:1:752:A:O2'	53:1:1781:U:H5'	2.17	0.45
54:2:30:C:H2'	54:2:31:C:O4'	2.15	0.45
55:5:36:U:H2'	55:5:37:A:C8	2.51	0.45
6:g:8:LYS:O	6:g:9:VAL:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:29:VAL:HG23	18:s:69:LEU:O	2.16	0.45
33:I:80:ARG:HG2	52:3:613:C:OP1	2.17	0.45
42:R:97:ARG:CB	42:R:99:GLN:HE22	2.28	0.45
52:3:34:C:H2'	52:3:35:G:C8	2.50	0.45
52:3:579:A:H2'	52:3:580:C:C6	2.50	0.45
52:3:1038:C:H2'	52:3:1039:G:H8	1.81	0.45
52:3:1395:C:O2'	52:3:1396:A:H5'	2.17	0.45
53:1:12:U:O2'	53:1:13:A:H5'	2.16	0.45
53:1:1331:G:H2'	53:1:1332:G:H5''	1.99	0.45
12:m:3:GLN:HE21	12:m:92:TRP:NE1	2.14	0.45
16:q:14:LYS:NZ	53:1:1217:U:H3'	2.31	0.45
29:E:1:PRO:H2	53:1:591:U:H1'	1.80	0.45
32:H:59:PRO:O	32:H:60:ALA:C	2.59	0.45
38:N:7:GLY:O	38:N:18:VAL:HG12	2.16	0.45
40:P:125:LYS:HG3	50:Z:33:ARG:HD2	1.98	0.45
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.82	0.45
52:3:865:A:H5'	52:3:1078:U:O4	2.17	0.45
52:3:1195:C:H5''	52:3:1196:A:OP2	2.17	0.45
53:1:1965:C:H5''	53:1:1966:A:H2'	1.97	0.45
53:1:2800:A:C2	53:1:2895:G:H1'	2.51	0.45
1:b:56:GLY:HA3	1:b:214:GLY:HA2	1.99	0.45
1:b:137:GLY:H	1:b:163:ILE:HG13	1.81	0.45
17:r:48:LYS:HG2	17:r:49:ILE:H	1.81	0.45
23:x:73:ARG:HB2	23:x:75:GLU:OE2	2.17	0.45
30:F:30:GLU:HA	30:F:31:PRO:HD3	1.77	0.45
31:G:46:VAL:N	31:G:47:PRO:HD2	2.31	0.45
33:I:131:ILE:HD12	33:I:131:ILE:N	2.32	0.45
36:L:62:GLU:O	36:L:66:GLU:HG2	2.17	0.45
41:Q:4:ASN:ND2	52:3:880:C:OP1	2.50	0.45
42:R:14:ALA:CB	42:R:33:LEU:HD11	2.47	0.45
49:Y:2:ASN:HB3	52:3:331:G:O3'	2.17	0.45
52:3:1354:U:H2'	52:3:1355:G:C8	2.50	0.45
53:1:873:C:H2'	53:1:874:G:H8	1.81	0.45
53:1:1437:C:H2'	53:1:1438:U:C6	2.52	0.45
53:1:1830:C:H2'	53:1:1831:G:H8	1.82	0.45
53:1:2292:U:H2'	53:1:2293:G:C8	2.52	0.45
1:b:86:ARG:HG3	1:b:86:ARG:NH1	2.30	0.45
6:g:121:VAL:C	6:g:122:LEU:HD12	2.41	0.45
9:j:81:ILE:CD1	53:1:2514:U:H5''	2.46	0.45
15:p:91:VAL:HG21	15:p:96:LEU:HD11	1.99	0.45
22:w:10:ARG:HD2	53:1:2280:G:O6	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:16:ASN:HB3	23:x:24:THR:HB	1.98	0.45
32:H:19:SER:HB2	43:S:91:GLU:O	2.17	0.45
32:H:128:MET:HB3	32:H:131:ARG:HB2	1.98	0.45
32:H:168:ARG:HD2	32:H:168:ARG:C	2.41	0.45
47:W:24:ASP:O	47:W:28:LEU:HD23	2.17	0.45
52:3:1497:G:C2'	52:3:1498:U:H5'	2.46	0.45
53:1:621:A:C2'	53:1:622:G:H5'	2.47	0.45
53:1:2819:G:H2'	53:1:2821:A:N7	2.32	0.45
2:c:55:LYS:HD2	2:c:77:ARG:HA	1.99	0.45
7:h:15:VAL:HA	7:h:18:VAL:HG12	1.99	0.45
11:l:17:LYS:HD3	53:1:663:G:H5''	1.98	0.45
13:n:8:ARG:HG3	13:n:8:ARG:HH21	1.81	0.45
34:J:36:THR:HG21	34:J:63:MET:CE	2.47	0.45
35:K:86:ARG:NH1	47:W:63:TYR:O	2.50	0.45
40:P:12:ARG:HG2	40:P:75:GLU:HB2	1.98	0.45
52:3:524:G:H2'	52:3:525:C:C6	2.52	0.45
52:3:1201:A:C1'	52:3:1202:U:OP2	2.65	0.45
53:1:214:G:O2'	53:1:215:G:H5'	2.16	0.45
53:1:2755:C:O2'	53:1:2756:U:H2'	2.17	0.45
2:c:9:VAL:HB	2:c:26:VAL:CG2	2.44	0.45
4:e:65:LEU:HD22	54:2:42:C:C5	2.51	0.45
23:x:6:VAL:HG23	23:x:50:VAL:HG12	1.98	0.45
49:Y:4:LYS:HE3	52:3:331:G:H2'	2.00	0.45
51:a:192:LEU:HA	51:a:195:ALA:HB3	1.98	0.45
52:3:24:U:H2'	52:3:25:C:C6	2.52	0.45
53:1:974:G:N3	53:1:974:G:H2'	2.32	0.45
54:2:60:C:H2'	54:2:61:G:H8	1.82	0.45
3:d:24:ASN:HD22	3:d:27:LEU:HB2	1.82	0.44
10:k:109:SER:C	10:k:110:GLU:HG3	2.42	0.44
13:n:56:LYS:NZ	13:n:88:ALA:HA	2.31	0.44
34:J:104:ILE:O	34:J:111:ARG:NH1	2.49	0.44
35:K:3:HIS:H	35:K:92:THR:HG22	1.82	0.44
52:3:634:C:H2'	52:3:635:A:C8	2.52	0.44
52:3:886:G:H2'	52:3:887:G:O4'	2.17	0.44
52:3:1273:C:H2'	52:3:1274:A:O4'	2.17	0.44
52:3:1513:A:H2'	52:3:1514:G:H8	1.81	0.44
53:1:69:C:H2'	53:1:70:G:C8	2.52	0.44
53:1:491:G:H2'	53:1:491:G:N3	2.32	0.44
53:1:1167:C:H2'	53:1:1168:G:H8	1.83	0.44
53:1:2557:G:H2'	53:1:2558:C:C6	2.50	0.44
8:i:83:ALA:HB2	8:i:100:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:23:ILE:HG23	17:r:82:HIS:CE1	2.52	0.44
12:m:57:VAL:O	12:m:58:LYS:HB2	2.16	0.44
15:p:109:ILE:N	15:p:109:ILE:HD12	2.32	0.44
18:s:66:ILE:HD12	18:s:66:ILE:N	2.32	0.44
37:M:104:SER:HB2	37:M:125:ILE:HD11	1.99	0.44
41:Q:11:ARG:HG3	52:3:563:A:OP2	2.17	0.44
44:T:55:LEU:O	44:T:59:VAL:HG23	2.16	0.44
50:Z:13:VAL:HG22	50:Z:15:LEU:HG	1.99	0.44
50:Z:58:LYS:O	50:Z:61:ARG:HG3	2.17	0.44
52:3:64:G:H4'	52:3:65:A:H3'	1.97	0.44
53:1:869:G:H2'	53:1:870:U:O4'	2.16	0.44
20:u:46:LYS:HB2	20:u:46:LYS:HE3	1.83	0.44
31:G:178:LEU:HB3	31:G:180:ILE:CD1	2.48	0.44
32:H:181:ILE:HD12	32:H:181:ILE:N	2.32	0.44
33:I:13:ARG:HE	33:I:37:PRO:HG2	1.82	0.44
36:L:102:TRP:CG	36:L:136:LYS:HD3	2.51	0.44
42:R:48:SER:OG	42:R:51:GLN:HG3	2.18	0.44
44:T:78:THR:HA	44:T:81:ILE:HG12	1.99	0.44
52:3:1436:U:H2'	52:3:1437:A:C8	2.53	0.44
52:3:1510:C:H2'	52:3:1511:G:C8	2.52	0.44
53:1:141:G:H3'	53:1:142:A:O4'	2.18	0.44
53:1:640:C:H2'	53:1:641:U:C6	2.53	0.44
53:1:1380:G:H2'	53:1:1381:G:H8	1.82	0.44
53:1:2114:A:H61	53:1:2117:A:H62	1.65	0.44
53:1:2467:C:H2'	53:1:2468:A:O4'	2.16	0.44
53:1:2469:A:H2'	53:1:2470:G:O4'	2.16	0.44
33:I:32:LYS:NZ	52:3:425:G:H5''	2.33	0.44
33:I:141:VAL:HG13	33:I:178:GLU:OE1	2.18	0.44
34:J:24:VAL:HG13	34:J:26:GLY:H	1.83	0.44
34:J:110:MET:O	34:J:113:VAL:HG12	2.17	0.44
40:P:30:ILE:HD11	52:3:706:A:H4'	1.99	0.44
40:P:88:PRO:HD3	50:Z:28:LEU:CD2	2.43	0.44
43:S:82:LYS:O	43:S:85:GLU:HB3	2.16	0.44
52:3:1299:A:H2'	52:3:1300:G:H4'	1.99	0.44
53:1:118:A:OP2	53:1:119:A:H5''	2.16	0.44
53:1:2267:A:H61	53:1:2272:U:H3	1.66	0.44
53:1:2366:A:H2'	53:1:2367:G:O4'	2.18	0.44
53:1:2368:C:H2'	53:1:2369:A:C8	2.52	0.44
6:g:42:LYS:HE3	6:g:46:PHE:CZ	2.52	0.44
29:E:62:PRO:HG2	29:E:63:TYR:H	1.81	0.44
31:G:140:LEU:C	31:G:140:LEU:HD23	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:71:ARG:O	32:H:75:VAL:HG23	2.18	0.44
52:3:543:U:H2'	52:3:544:G:H8	1.81	0.44
53:1:1179:G:N7	53:1:1180:U:H1'	2.33	0.44
53:1:2196:C:O2'	53:1:2197:U:H5'	2.17	0.44
53:1:2554:U:H2'	53:1:2555:U:C6	2.53	0.44
1:b:95:TYR:HB2	1:b:97:ASP:OD2	2.18	0.44
10:k:48:PRO:HG3	52:3:1422:G:C5'	2.48	0.44
11:l:20:GLY:O	11:l:21:ARG:NH2	2.43	0.44
12:m:11:LYS:HE2	12:m:86:LYS:HG2	1.99	0.44
14:o:107:ALA:O	14:o:111:ARG:HG3	2.18	0.44
17:r:74:ILE:HD12	17:r:74:ILE:H	1.80	0.44
17:r:88:GLY:HA3	53:1:1225:G:OP1	2.18	0.44
33:I:13:ARG:NH2	33:I:37:PRO:HB2	2.31	0.44
35:K:91:ARG:HG3	35:K:92:THR:N	2.31	0.44
42:R:100:ARG:HH21	42:R:102:LYS:HD3	1.81	0.44
53:1:940:G:C3'	53:1:941:A:H5''	2.48	0.44
53:1:995:C:H6	53:1:995:C:H5'	1.82	0.44
53:1:1028:A:N6	53:1:1125:G:H2'	2.32	0.44
53:1:1268:A:H2'	53:1:1269:A:O4'	2.18	0.44
53:1:2110:G:H5'	53:1:2118:U:O2'	2.18	0.44
53:1:2855:C:H2'	53:1:2856:A:H8	1.82	0.44
5:f:88:LEU:CD2	5:f:95:ALA:HB2	2.47	0.44
13:n:36:THR:OG1	13:n:37:THR:N	2.51	0.44
15:p:3:ILE:HD12	15:p:3:ILE:N	2.32	0.44
23:x:63:ILE:O	23:x:67:LEU:HD13	2.18	0.44
33:I:43:ARG:HH12	52:3:511:C:H4'	1.82	0.44
42:R:113:LYS:H	42:R:114:PRO:HD2	1.83	0.44
50:Z:20:ARG:HA	50:Z:24:LYS:HB2	2.00	0.44
52:3:678:U:H2'	52:3:679:C:C6	2.53	0.44
53:1:28:A:O2'	53:1:583:G:H5'	2.18	0.44
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.44
53:1:779:U:H2'	53:1:780:G:H8	1.83	0.44
53:1:1015:U:H2'	53:1:1016:G:C8	2.52	0.44
53:1:1161:C:H2'	53:1:1162:G:H8	1.83	0.44
53:1:2248:C:C2'	53:1:2249:U:H5'	2.48	0.44
11:l:141:LYS:HG2	11:l:142:ILE:N	2.32	0.44
12:m:3:GLN:HA	12:m:4:PRO:HD3	1.79	0.44
19:t:61:LEU:HB3	53:1:1341:G:H4'	2.00	0.44
32:H:80:GLY:O	32:H:83:VAL:HG22	2.18	0.44
33:I:144:ILE:HD12	33:I:144:ILE:N	2.32	0.44
34:J:76:ASN:O	34:J:79:THR:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:104:ILE:HD12	34:J:119:VAL:HG23	1.99	0.44
43:S:40:ARG:NH1	48:X:6:LYS:HD2	2.32	0.44
52:3:358:U:H2'	52:3:359:G:C8	2.52	0.44
52:3:600:A:H2'	52:3:601:G:C8	2.53	0.44
52:3:977:A:H3'	52:3:977:A:N3	2.33	0.44
52:3:1219:A:H2'	52:3:1220:G:C8	2.53	0.44
53:1:2583:G:H2'	53:1:2584:U:O4'	2.17	0.44
53:1:2637:U:H2'	53:1:2638:G:O4'	2.17	0.44
53:1:2786:U:O2'	53:1:2787:C:H5'	2.18	0.44
7:h:13:ALA:O	7:h:17:GLU:HG2	2.18	0.44
7:h:39:THR:HG23	7:h:40:GLU:CD	2.43	0.44
12:m:95:LEU:O	12:m:97:GLN:NE2	2.51	0.44
13:n:64:ARG:NH2	53:1:2852:G:H5'	2.33	0.44
28:D:43:THR:OG1	28:D:44:VAL:N	2.50	0.44
30:F:22:VAL:HG13	30:F:24:ARG:HG3	1.99	0.44
31:G:53:LEU:HD21	31:G:216:VAL:HG22	2.00	0.44
32:H:67:ILE:HD12	32:H:67:ILE:N	2.31	0.44
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.87	0.44
35:K:38:ARG:HD3	35:K:97:THR:HA	1.98	0.44
36:L:91:ARG:HH21	52:3:1378:C:C4'	2.20	0.44
41:Q:69:GLU:HG2	52:3:521:G:O5'	2.18	0.44
46:V:17:GLU:OE1	52:3:254:G:N2	2.51	0.44
47:W:47:ARG:HB3	47:W:50:TYR:HD2	1.83	0.44
48:X:16:LYS:HG3	48:X:17:LYS:N	2.33	0.44
48:X:19:GLU:O	48:X:23:GLU:HG2	2.18	0.44
48:X:54:ARG:HB3	52:3:958:A:C2	2.52	0.44
49:Y:75:LYS:HD2	52:3:186:C:O4'	2.18	0.44
50:Z:54:ARG:NE	56:4:6:G:OP1	2.50	0.44
52:3:244:U:O4	52:3:906:A:H1'	2.18	0.44
52:3:1015:G:O2'	52:3:1016:A:H5'	2.17	0.44
53:1:635:C:H2'	53:1:636:G:H8	1.82	0.44
54:2:2:G:H2'	54:2:3:C:C6	2.52	0.44
55:6:62:C:H2'	55:6:63:G:C8	2.53	0.44
55:6:67:C:O2'	55:6:68:C:H5'	2.17	0.44
1:b:175:LEU:HD13	53:1:1799:G:C5	2.52	0.43
7:h:41:LEU:HD13	53:1:1082:U:H2'	1.99	0.43
16:q:36:GLN:HE21	53:1:1252:G:H22	1.65	0.43
21:v:38:LEU:O	21:v:40:ILE:HD12	2.18	0.43
22:w:13:GLU:HG3	53:1:2261:C:OP2	2.18	0.43
48:X:28:LYS:HD3	48:X:29:PRO:HG2	2.00	0.43
51:a:49:GLY:CA	51:a:210:LYS:HE2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:34:C:H2'	52:3:35:G:H8	1.82	0.43
52:3:1017:U:H2'	52:3:1018:G:C8	2.53	0.43
53:1:572:A:N6	53:1:2029:G:H21	2.10	0.43
53:1:1035:U:H2'	53:1:1036:G:H8	1.83	0.43
53:1:1386:C:H2'	53:1:1387:A:H8	1.83	0.43
53:1:1890:A:H2'	53:1:1891:G:O4'	2.18	0.43
53:1:1892:C:H2'	53:1:1893:C:C6	2.53	0.43
53:1:1955:U:H2'	53:1:2551:C:O2'	2.18	0.43
53:1:2818:U:H4'	53:1:2837:A:H4'	1.99	0.43
57:7:57:G:H2'	57:7:58:A:H5'	2.00	0.43
3:d:76:PRO:HA	3:d:82:GLY:CA	2.42	0.43
7:h:61:ARG:O	53:1:1046:A:H4'	2.18	0.43
20:u:27:VAL:HG12	20:u:33:VAL:HG23	1.99	0.43
21:v:20:LEU:HD11	21:v:27:PRO:HD3	2.00	0.43
31:G:168:GLU:HG3	31:G:171:ALA:HB3	1.99	0.43
34:J:25:LYS:C	34:J:25:LYS:HD3	2.43	0.43
35:K:17:GLN:O	35:K:17:GLN:HG2	2.18	0.43
43:S:37:ASP:OD2	43:S:39:ASP:HB2	2.19	0.43
43:S:86:ALA:HB1	43:S:91:GLU:HB2	2.00	0.43
51:a:181:ASP:HB3	51:a:184:LYS:HB2	2.00	0.43
52:3:783:C:H2'	52:3:784:A:C8	2.53	0.43
52:3:820:U:H3'	52:3:821:G:C5'	2.48	0.43
52:3:1015:G:H2'	52:3:1016:A:O4'	2.18	0.43
53:1:84:A:H4'	53:1:85:G:O5'	2.19	0.43
53:1:277:G:H1'	53:1:361:G:O6	2.18	0.43
53:1:890:C:H2'	53:1:891:G:O4'	2.18	0.43
53:1:1127:A:H2'	53:1:1128:G:H5''	1.99	0.43
53:1:2093:G:H21	53:1:2198:A:N6	2.15	0.43
53:1:2114:A:H62	53:1:2119:A:H61	1.66	0.43
1:b:77:VAL:HA	1:b:93:VAL:HG12	1.99	0.43
5:f:53:PRO:HG3	5:f:61:TRP:CE2	2.53	0.43
6:g:114:GLU:HA	6:g:116:ARG:NH1	2.33	0.43
9:j:78:THR:HG21	53:1:2642:G:OP1	2.18	0.43
11:l:23:ILE:HG12	17:r:82:HIS:NE2	2.34	0.43
12:m:122:ALA:HB1	53:1:2467:C:H1'	2.01	0.43
13:n:39:PRO:HG2	53:1:1651:G:H4'	2.00	0.43
28:D:22:MET:HE3	28:D:28:ARG:HG2	2.00	0.43
34:J:15:ILE:HB	34:J:35:LEU:HD22	1.99	0.43
35:K:36:ILE:HD13	35:K:64:VAL:HG13	2.01	0.43
35:K:53:LYS:HB3	35:K:54:LEU:H	1.56	0.43
39:O:35:GLN:NE2	39:O:77:VAL:HG11	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:39:VAL:HG22	51:a:177:LYS:HD2	1.99	0.43
52:3:166:U:H2'	52:3:167:A:H8	1.84	0.43
52:3:1071:C:H2'	52:3:1072:G:H8	1.82	0.43
53:1:20:C:H2'	53:1:21:A:H8	1.83	0.43
53:1:154:U:H2'	53:1:155:A:C8	2.54	0.43
53:1:281:C:N4	53:1:359:G:H1	2.16	0.43
53:1:1023:U:O2'	53:1:1122:G:H5'	2.17	0.43
53:1:1600:C:H2'	53:1:1601:G:C8	2.53	0.43
53:1:2011:U:H2'	53:1:2012:G:O4'	2.18	0.43
53:1:2061:G:C5'	53:1:2502:G:H5'	2.48	0.43
53:1:2087:G:H2'	53:1:2088:A:C8	2.53	0.43
53:1:2190:G:H2'	53:1:2191:A:C8	2.54	0.43
53:1:2662:A:H2'	53:1:2663:G:O4'	2.19	0.43
4:e:140:ILE:N	4:e:140:ILE:HD12	2.34	0.43
7:h:56:ARG:HD2	53:1:1084:A:C4	2.53	0.43
11:l:119:PRO:HG3	11:l:138:ALA:O	2.18	0.43
16:q:96:ASP:OD2	17:r:13:ARG:NE	2.51	0.43
21:v:88:HIS:CD2	21:v:89:ILE:H	2.37	0.43
25:z:56:VAL:HG22	25:z:57:GLU:N	2.32	0.43
27:C:8:ILE:HD12	27:C:50:GLU:HG2	1.99	0.43
31:G:206:ILE:HD12	31:G:206:ILE:H	1.82	0.43
33:I:131:ILE:HG22	33:I:133:SER:H	1.83	0.43
37:M:5:PRO:HB2	37:M:32:LYS:NZ	2.32	0.43
41:Q:76:HIS:HB3	41:Q:77:SER:H	1.65	0.43
43:S:72:PHE:CZ	43:S:77:GLY:HA2	2.54	0.43
49:Y:65:LEU:O	49:Y:65:LEU:HD23	2.18	0.43
52:3:254:G:H2'	52:3:255:G:C8	2.54	0.43
52:3:317:U:H2'	52:3:318:G:C8	2.53	0.43
52:3:323:U:H2'	52:3:324:G:O4'	2.18	0.43
52:3:423:G:H2'	52:3:424:G:H5'	2.00	0.43
52:3:484:G:H4'	52:3:485:U:C5'	2.43	0.43
52:3:1277:C:H2'	52:3:1278:G:H5''	2.00	0.43
53:1:1463:C:H2'	53:1:1464:G:C8	2.54	0.43
53:1:1468:U:H2'	53:1:1522:A:H61	1.82	0.43
2:c:33:ARG:CZ	2:c:74:GLU:HB3	2.48	0.43
3:d:21:ARG:HH22	3:d:106:LYS:HZ3	1.67	0.43
11:l:27:LEU:O	11:l:31:GLY:HA2	2.19	0.43
13:n:13:ASN:ND2	13:n:15:SER:HB3	2.34	0.43
14:o:18:LEU:HD21	14:o:25:ARG:CB	2.49	0.43
21:v:64:VAL:HG22	21:v:69:GLU:HG2	2.01	0.43
26:B:42:ILE:HG22	26:B:48:TYR:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:109:GLU:HG3	32:H:139:ASN:HB3	2.01	0.43
34:J:14:LEU:C	34:J:15:ILE:HD12	2.43	0.43
39:O:90:LEU:O	39:O:90:LEU:HD23	2.19	0.43
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.18	0.43
52:3:358:U:H2'	52:3:359:G:H8	1.83	0.43
52:3:916:U:H2'	52:3:917:G:C8	2.53	0.43
53:1:490:C:O2'	53:1:491:G:P	2.77	0.43
53:1:494:G:H2'	53:1:495:G:C8	2.53	0.43
53:1:1001:A:H2'	53:1:1002:G:O4'	2.18	0.43
53:1:1694:C:H4'	53:1:1695:G:C2	2.53	0.43
53:1:1983:G:H4'	53:1:2606:C:H4'	2.01	0.43
53:1:2019:A:H2	53:1:2035:G:H22	1.66	0.43
53:1:2241:A:H2'	53:1:2242:G:C8	2.53	0.43
53:1:2515:C:H2'	53:1:2516:A:C8	2.53	0.43
53:1:2710:C:H2'	53:1:2711:A:C8	2.54	0.43
53:1:2860:A:H2'	53:1:2861:U:H5'	1.99	0.43
1:b:129:LEU:HD12	1:b:133:ASN:HD22	1.84	0.43
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.90	0.43
3:d:47:LYS:O	3:d:83:VAL:HB	2.18	0.43
4:e:39:VAL:HG12	4:e:149:ARG:HD2	2.00	0.43
4:e:131:VAL:HG12	4:e:133:GLU:H	1.84	0.43
5:f:5:LYS:O	5:f:7:PRO:HD3	2.18	0.43
26:B:37:HIS:HB3	26:B:43:THR:HG22	2.00	0.43
31:G:119:GLN:O	31:G:124:THR:HG22	2.19	0.43
34:J:33:THR:HA	34:J:51:LYS:HA	2.00	0.43
45:U:54:LEU:HD12	45:U:54:LEU:N	2.31	0.43
53:1:1004:U:H1'	53:1:1010:A:H2'	2.00	0.43
53:1:1704:C:H2'	53:1:1705:A:C8	2.53	0.43
53:1:1889:A:H2'	53:1:1890:A:H8	1.82	0.43
53:1:2246:G:H2'	53:1:2247:A:H8	1.80	0.43
53:1:2427:C:C5'	53:1:2429:G:H5'	2.46	0.43
53:1:2636:C:H2'	53:1:2637:U:C6	2.53	0.43
55:6:34:C:H2'	55:6:34:C:O2	2.19	0.43
4:e:7:TYR:OH	4:e:29:ARG:HB3	2.18	0.43
4:e:120:SER:HB2	4:e:127:TYR:CE1	2.54	0.43
5:f:134:GLY:HA3	5:f:140:ILE:HG21	1.99	0.43
26:B:47:TYR:CZ	26:B:52:LYS:HD3	2.53	0.43
32:H:156:LEU:HD11	32:H:163:ARG:HE	1.84	0.43
34:J:51:LYS:NZ	52:3:1081:A:OP2	2.46	0.43
41:Q:80:LEU:HD23	41:Q:97:VAL:HG21	2.01	0.43
42:R:7:ASN:ND2	42:R:20:SER:OG	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.54	0.43
45:U:12:LYS:O	45:U:13:LYS:HB2	2.19	0.43
50:Z:43:GLU:O	50:Z:47:ALA:N	2.51	0.43
52:3:45:G:H5''	52:3:307:C:O2'	2.19	0.43
52:3:603:U:H2'	52:3:604:G:C8	2.53	0.43
53:1:971:G:H2'	53:1:972:A:O4'	2.19	0.43
53:1:1182:G:H2'	53:1:1183:U:O4'	2.18	0.43
53:1:2220:U:H2'	53:1:2221:G:H8	1.84	0.43
53:1:2475:C:H42	53:1:2529:G:H22	1.66	0.43
53:1:2795:C:H2'	53:1:2796:U:O4'	2.17	0.43
55:6:59:A:H2'	55:6:60:U:H5'	2.00	0.43
2:c:51:THR:HB	2:c:79:LEU:HD23	1.99	0.43
5:f:104:LEU:HB2	5:f:112:VAL:HB	2.01	0.43
6:g:40:THR:HB	6:g:43:ASN:ND2	2.31	0.43
8:i:16:MET:N	8:i:16:MET:SD	2.92	0.43
8:i:110:GLN:O	8:i:113:ALA:HB3	2.19	0.43
10:k:35:VAL:HA	10:k:69:VAL:HG11	2.01	0.43
11:l:128:THR:HG22	53:1:636:G:OP2	2.19	0.43
13:n:56:LYS:HZ3	13:n:88:ALA:HA	1.83	0.43
14:o:75:GLY:O	14:o:78:VAL:HG12	2.19	0.43
28:D:1:MET:SD	28:D:3:ARG:NH1	2.91	0.43
33:I:82:LYS:HZ3	52:3:2:A:H4'	1.84	0.43
35:K:42:TRP:HE1	35:K:61:LEU:CD1	2.32	0.43
36:L:91:ARG:HG3	36:L:94:ARG:H	1.84	0.43
37:M:76:ARG:NH1	37:M:78:SER:O	2.51	0.43
41:Q:73:LEU:N	41:Q:73:LEU:HD22	2.33	0.43
48:X:35:ARG:NH2	48:X:74:ALA:HB3	2.33	0.43
51:a:48:LEU:HB3	51:a:50:ILE:HD13	2.00	0.43
52:3:137:U:H2'	52:3:138:G:H8	1.84	0.43
52:3:1404:C:H2'	52:3:1405:G:H8	1.81	0.43
53:1:5:A:H2'	53:1:6:A:C8	2.54	0.43
53:1:94:A:H2'	53:1:95:A:O4'	2.17	0.43
53:1:728:G:H3'	53:1:729:G:H5'	2.01	0.43
53:1:812:C:H5''	53:1:1250:G:O2'	2.19	0.43
53:1:1278:C:H2'	53:1:1279:G:H8	1.84	0.43
53:1:1286:A:H1'	53:1:1288:G:OP2	2.19	0.43
53:1:1930:G:O2'	53:1:1931:U:C5	2.71	0.43
53:1:2244:U:H2'	53:1:2245:U:O4'	2.19	0.43
4:e:19:PHE:HB2	4:e:21:TYR:CZ	2.53	0.43
4:e:62:GLN:HB3	4:e:94:ARG:HH21	1.84	0.43
6:g:42:LYS:HG3	6:g:46:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:94:ARG:HH12	7:h:131:THR:HA	1.82	0.43
16:q:96:ASP:O	16:q:99:VAL:HG12	2.18	0.43
20:u:11:ILE:HD11	20:u:79:ALA:CB	2.42	0.43
31:G:20:ARG:NE	52:3:831:A:H5''	2.25	0.43
32:H:114:LEU:O	32:H:117:ASP:OD1	2.36	0.43
43:S:20:PHE:C	43:S:22:LYS:H	2.26	0.43
46:V:19:SER:HB3	46:V:70:LYS:NZ	2.34	0.43
52:3:713:G:H2'	52:3:714:G:C8	2.54	0.43
52:3:1125:U:H2'	52:3:1126:U:H2'	2.00	0.43
53:1:1658:C:H2'	53:1:1659:G:C8	2.53	0.43
53:1:1802:A:H2'	53:1:1803:A:C8	2.53	0.43
1:b:229:HIS:CG	1:b:230:PRO:HD2	2.54	0.43
4:e:21:TYR:HB3	4:e:26:GLN:HB3	2.01	0.43
4:e:116:LEU:HD13	4:e:175:PRO:HD2	2.00	0.43
8:i:71:LYS:HE3	53:1:1059:G:H5'	2.01	0.43
12:m:86:LYS:HG3	12:m:87:GLY:N	2.34	0.43
22:w:73:ARG:NH2	53:1:2332:C:H5''	2.34	0.43
34:J:80:LEU:HD13	34:J:122:VAL:CG1	2.49	0.43
35:K:47:LEU:HG	35:K:56:LYS:H	1.84	0.43
38:N:34:LEU:HD23	38:N:34:LEU:C	2.44	0.43
38:N:99:LYS:NZ	52:3:1176:A:H5''	2.34	0.43
45:U:75:ILE:HG12	45:U:80:LYS:NZ	2.34	0.43
52:3:40:C:H2'	52:3:41:G:C8	2.53	0.43
52:3:432:A:H2'	52:3:433:G:O4'	2.19	0.43
52:3:668:G:H2'	52:3:669:G:C8	2.54	0.43
52:3:766:A:H2'	52:3:767:A:O4'	2.19	0.43
52:3:1070:U:H2'	52:3:1071:C:C6	2.54	0.43
53:1:755:U:H2'	53:1:756:A:H8	1.82	0.43
53:1:799:G:H5''	53:1:800:A:H2'	2.01	0.43
53:1:818:G:C2'	53:1:819:A:H5''	2.47	0.43
53:1:2404:U:H2'	53:1:2405:G:O4'	2.19	0.43
53:1:2668:G:H2'	53:1:2669:G:H8	1.84	0.43
53:1:2855:C:H2'	53:1:2856:A:C8	2.54	0.43
55:5:16:C:O2'	55:5:17:C:H5'	2.19	0.43
55:6:6:G:O2'	55:6:7:G:H5'	2.19	0.43
3:d:68:ALA:HA	53:1:1255:U:C6	2.54	0.42
8:i:59:THR:HG23	8:i:59:THR:O	2.19	0.42
8:i:98:GLY:H	8:i:137:LEU:HD23	1.84	0.42
9:j:11:VAL:HG13	9:j:11:VAL:O	2.18	0.42
11:l:105:ILE:H	11:l:105:ILE:CD1	2.29	0.42
13:n:79:LEU:O	13:n:80:PHE:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:24:LYS:HZ1	53:1:1163:G:P	2.42	0.42
17:r:38:VAL:HG21	17:r:41:ILE:HD11	2.00	0.42
31:G:216:VAL:HA	31:G:219:THR:HG22	2.01	0.42
39:O:6:ILE:HD11	39:O:100:ILE:HG23	2.01	0.42
43:S:57:SER:OG	52:3:1316:G:H4'	2.19	0.42
49:Y:22:SER:HA	52:3:1458:G:H4'	2.01	0.42
52:3:411:A:C4	52:3:413:G:H1'	2.54	0.42
52:3:1060:U:O2'	52:3:1061:G:H5'	2.19	0.42
52:3:1464:U:H2'	52:3:1465:A:H8	1.82	0.42
53:1:941:A:H2'	53:1:942:G:O4'	2.19	0.42
53:1:1739:A:H2'	53:1:1740:G:O4'	2.19	0.42
53:1:1748:C:H2'	53:1:1749:A:C8	2.53	0.42
53:1:1872:A:H2'	53:1:1873:G:O4'	2.19	0.42
53:1:2432:A:N3	55:6:75:C:H5'	2.33	0.42
53:1:2573:C:OP1	53:1:2574:G:H5''	2.19	0.42
54:2:30:C:C2'	54:2:31:C:H5'	2.49	0.42
1:b:222:THR:HG23	53:1:1826:G:OP1	2.18	0.42
3:d:129:PRO:O	53:1:321:U:H5'	2.19	0.42
5:f:3:VAL:O	5:f:68:ARG:HG3	2.19	0.42
10:k:77:ILE:HG23	10:k:77:ILE:O	2.19	0.42
17:r:38:VAL:HG23	17:r:54:VAL:CG2	2.49	0.42
23:x:36:ARG:HA	23:x:47:THR:HA	2.01	0.42
25:z:36:GLU:O	25:z:37:ARG:NH1	2.52	0.42
33:I:124:VAL:HG22	33:I:125:ASN:ND2	2.34	0.42
52:3:631:C:H5''	52:3:632:U:O4'	2.19	0.42
52:3:1202:U:H2'	52:3:1203:C:O4'	2.18	0.42
52:3:1496:C:H2'	52:3:1497:G:O4'	2.20	0.42
53:1:538:A:H2'	53:1:539:G:O4'	2.18	0.42
53:1:935:C:H2'	53:1:936:A:H8	1.84	0.42
53:1:1947:C:H2'	53:1:1948:G:C8	2.55	0.42
53:1:2800:A:H3'	53:1:2801:G:C5'	2.48	0.42
55:6:24:U:H2'	55:6:25:C:C6	2.53	0.42
16:q:25:GLY:O	16:q:29:ARG:NH1	2.53	0.42
38:N:57:VAL:HG23	38:N:58:GLU:N	2.27	0.42
43:S:100:TRP:HZ2	52:3:1368:A:H5''	1.84	0.42
45:U:5:ARG:HH12	52:3:377:G:H5'	1.84	0.42
50:Z:34:ARG:HG3	50:Z:36:PHE:CE2	2.54	0.42
52:3:130:A:O2'	52:3:264:C:H5'	2.19	0.42
52:3:1225:A:H2'	52:3:1225:A:N3	2.35	0.42
52:3:1369:C:H2'	52:3:1370:G:C8	2.54	0.42
53:1:1826:G:H2'	53:1:1827:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2180:U:H2'	53:1:2181:U:O4'	2.18	0.42
53:1:2609:U:H5'	53:1:2610:C:OP2	2.18	0.42
53:1:2789:C:H2'	53:1:2790:U:H5'	2.01	0.42
4:e:109:ARG:HH22	4:e:138:PRO:HG3	1.84	0.42
7:h:48:ALA:HB3	7:h:51:TYR:CE2	2.53	0.42
11:l:118:THR:HA	11:l:119:PRO:HD3	1.80	0.42
17:r:1:MET:N	17:r:43:ASN:HA	2.34	0.42
17:r:72:VAL:O	17:r:74:ILE:HD12	2.19	0.42
17:r:98:ILE:HD11	17:r:101:ILE:CD1	2.49	0.42
25:z:52:PHE:CD2	54:2:83:G:H4'	2.53	0.42
26:B:14:MET:HB3	53:1:2045:C:O3'	2.19	0.42
30:F:24:ARG:HH21	30:F:36:ARG:HD3	1.84	0.42
33:I:104:MET:HE3	33:I:170:LEU:HD13	2.01	0.42
41:Q:113:ARG:NH2	52:3:501:C:OP1	2.52	0.42
44:T:75:ALA:O	44:T:79:GLN:HG2	2.20	0.42
46:V:13:SER:HB3	46:V:21:VAL:CG1	2.48	0.42
47:W:25:ILE:HA	47:W:28:LEU:HB2	2.01	0.42
48:X:78:THR:OG1	48:X:79:TYR:N	2.52	0.42
49:Y:14:GLU:HA	49:Y:17:ARG:HG2	2.01	0.42
52:3:1405:G:O2'	52:3:1406:U:H5'	2.20	0.42
53:1:20:C:H2'	53:1:21:A:C8	2.55	0.42
53:1:677:A:O2'	53:1:2071:A:H5'	2.19	0.42
53:1:1424:G:H2'	53:1:1425:G:O4'	2.20	0.42
53:1:2412:A:H2'	53:1:2413:G:O4'	2.19	0.42
54:2:66:A:H4'	54:2:67:G:C8	2.54	0.42
1:b:66:PHE:HZ	1:b:86:ARG:HH21	1.66	0.42
3:d:85:PHE:HE2	53:1:587:C:H5'	1.84	0.42
5:f:94:ARG:HB2	5:f:105:SER:OG	2.20	0.42
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.42
8:i:58:ILE:HD12	8:i:58:ILE:N	2.34	0.42
10:k:92:GLU:O	10:k:93:GLN:C	2.63	0.42
14:o:33:ARG:HE	54:2:52:A:H62	1.67	0.42
21:v:36:ALA:HA	21:v:37:PRO:HD3	1.93	0.42
21:v:78:GLN:HB2	21:v:88:HIS:HB3	2.01	0.42
32:H:4:VAL:HG22	32:H:5:HIS:H	1.85	0.42
34:J:84:VAL:CG2	34:J:145:ASN:HD22	2.32	0.42
39:O:57:VAL:HG13	39:O:58:ASN:CG	2.44	0.42
39:O:65:TYR:HE1	43:S:97:LYS:HG2	1.83	0.42
41:Q:9:LYS:HA	41:Q:10:PRO:HD3	1.85	0.42
46:V:18:LYS:HG2	46:V:18:LYS:O	2.19	0.42
48:X:30:LEU:HB2	48:X:48:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:481:G:H1'	53:1:506:G:N2	2.34	0.42
53:1:662:G:H2'	53:1:663:G:H8	1.84	0.42
53:1:691:C:O2'	53:1:692:C:H5'	2.20	0.42
53:1:889:C:H2'	53:1:890:C:O4'	2.19	0.42
53:1:1130:U:O2'	53:1:1131:G:OP1	2.33	0.42
53:1:2112:G:H2'	53:1:2113:U:H5'	2.01	0.42
53:1:2122:U:O2'	53:1:2123:G:H5'	2.19	0.42
53:1:2743:U:H2'	53:1:2744:G:C4'	2.50	0.42
55:5:28:C:H2'	55:5:29:G:H8	1.84	0.42
1:b:261:ARG:HG3	1:b:262:THR:HG23	2.01	0.42
10:k:76:VAL:H	15:p:72:VAL:HG12	1.85	0.42
16:q:5:ARG:NH1	53:1:585:G:N7	2.64	0.42
36:L:72:VAL:HG12	36:L:89:GLU:HG3	2.01	0.42
36:L:102:TRP:CD2	36:L:136:LYS:HD3	2.55	0.42
44:T:55:LEU:HD21	53:1:715:A:C2	2.55	0.42
45:U:48:GLU:CG	45:U:49:GLY:H	2.25	0.42
51:a:194:VAL:O	51:a:198:LYS:HG2	2.19	0.42
52:3:668:G:H2'	52:3:669:G:H8	1.85	0.42
52:3:1094:G:N3	52:3:1094:G:H2'	2.35	0.42
53:1:1344:U:H3'	53:1:1345:C:H5'	2.01	0.42
53:1:1440:U:H2'	53:1:1441:G:C8	2.54	0.42
53:1:1536:C:H4'	53:1:1537:G:C2	2.55	0.42
53:1:2000:C:O2'	53:1:2001:C:H5'	2.19	0.42
54:2:88:C:C4'	54:2:89:U:OP1	2.67	0.42
6:g:69:ALA:HB3	6:g:134:VAL:HG21	2.01	0.42
7:h:27:VAL:O	7:h:83:ALA:HB3	2.20	0.42
7:h:66:GLY:HA2	7:h:69:PHE:HE2	1.83	0.42
16:q:24:TYR:CE1	53:1:17:G:H4'	2.55	0.42
24:y:2:LYS:HE2	24:y:6:LEU:HD13	2.01	0.42
32:H:61:LYS:O	32:H:61:LYS:HD3	2.19	0.42
33:I:63:ILE:O	33:I:110:ARG:NH1	2.52	0.42
35:K:66:ALA:HB1	35:K:67:PRO:HD2	2.01	0.42
38:N:45:MET:O	38:N:49:GLN:HG3	2.20	0.42
40:P:122:PRO:HB2	50:Z:33:ARG:HA	2.02	0.42
41:Q:110:LYS:HE3	52:3:538:G:O3'	2.19	0.42
45:U:33:ILE:N	45:U:33:ILE:HD12	2.35	0.42
48:X:28:LYS:HD3	48:X:29:PRO:CG	2.49	0.42
52:3:714:G:H2'	52:3:715:A:C8	2.54	0.42
52:3:1118:U:H2'	52:3:1119:C:C6	2.55	0.42
53:1:851:C:H2'	53:1:852:U:C6	2.55	0.42
53:1:1932:A:H2'	53:1:1933:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2443:C:H2'	53:1:2444:G:H8	1.83	0.42
53:1:2443:C:O2'	53:1:2444:G:H5'	2.20	0.42
3:d:147:LEU:HB3	3:d:186:VAL:HG23	2.01	0.42
7:h:1:MET:SD	7:h:1:MET:N	2.73	0.42
10:k:86:LEU:HD12	10:k:86:LEU:N	2.34	0.42
32:H:196:GLY:HA3	52:3:1057:G:O3'	2.20	0.42
39:O:8:ILE:HD12	39:O:8:ILE:H	1.84	0.42
41:Q:41:PRO:HG3	41:Q:49:ARG:HE	1.85	0.42
46:V:30:HIS:HA	46:V:31:PRO:HD3	1.87	0.42
49:Y:4:LYS:CE	52:3:331:G:H2'	2.50	0.42
52:3:20:U:H2'	52:3:21:G:O4'	2.20	0.42
52:3:396:C:C3'	52:3:397:A:H5''	2.50	0.42
53:1:1181:U:H2'	53:1:1182:G:C8	2.55	0.42
53:1:1378:A:H1'	53:1:1379:U:C5	2.54	0.42
53:1:1709:U:H2'	53:1:1710:G:C8	2.55	0.42
53:1:2480:C:H2'	53:1:2481:G:O4'	2.20	0.42
1:b:144:GLU:OE1	1:b:148:GLY:N	2.52	0.42
3:d:44:ARG:O	3:d:45:ALA:HB2	2.20	0.42
3:d:148:ILE:HB	3:d:169:VAL:HA	2.02	0.42
4:e:79:ARG:NH2	55:5:19:G:H22	2.18	0.42
12:m:21:ALA:HB2	12:m:97:GLN:HB2	2.01	0.42
14:o:34:HIS:NE2	54:2:27:C:OP1	2.52	0.42
17:r:49:ILE:HG22	17:r:54:VAL:N	2.34	0.42
33:I:184:LYS:HD3	33:I:185:PRO:CD	2.50	0.42
35:K:53:LYS:O	35:K:54:LEU:C	2.62	0.42
37:M:3:GLN:O	52:3:587:G:H4'	2.20	0.42
37:M:32:LYS:O	37:M:35:ILE:HG22	2.19	0.42
43:S:33:VAL:O	43:S:33:VAL:HG22	2.19	0.42
46:V:43:LEU:HD12	46:V:43:LEU:N	2.35	0.42
52:3:252:U:O2	52:3:252:U:H2'	2.19	0.42
52:3:1287:A:H2'	52:3:1288:A:C8	2.54	0.42
52:3:1366:C:H2'	52:3:1367:C:C6	2.55	0.42
53:1:942:G:H2'	53:1:943:A:O4'	2.19	0.42
53:1:2229:U:H2'	53:1:2230:G:H8	1.85	0.42
4:e:120:SER:HB2	4:e:127:TYR:HE1	1.85	0.42
6:g:8:LYS:HE3	6:g:8:LYS:HB3	1.89	0.42
7:h:67:THR:HB	7:h:68:PRO:HD3	2.02	0.42
11:l:93:ASN:C	11:l:95:LEU:H	2.27	0.42
11:l:127:VAL:HG12	11:l:128:THR:N	2.35	0.42
12:m:95:LEU:HD12	12:m:95:LEU:HA	1.95	0.42
14:o:11:ALA:O	14:o:15:ARG:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:31:THR:C	14:o:33:ARG:N	2.78	0.42
14:o:49:VAL:HG11	14:o:81:ARG:HG3	2.02	0.42
18:s:25:ARG:HE	18:s:74:ILE:HG23	1.85	0.42
21:v:40:ILE:HD12	21:v:40:ILE:N	2.35	0.42
24:y:42:LEU:HA	24:y:45:GLN:HG2	2.02	0.42
31:G:101:THR:O	52:3:1074:G:H4'	2.20	0.42
39:O:9:ARG:NH2	52:3:1279:G:P	2.93	0.42
40:P:124:LYS:HE2	52:3:1523:G:H5''	2.02	0.42
52:3:304:U:O2'	52:3:305:G:H5'	2.20	0.42
52:3:1114:C:H2'	52:3:1115:U:O4'	2.19	0.42
52:3:1115:U:O2'	52:3:1116:U:H5'	2.19	0.42
53:1:595:C:H2'	53:1:596:U:C6	2.55	0.42
53:1:1152:C:O2'	53:1:1153:C:H5'	2.19	0.42
53:1:1475:G:C2'	53:1:1476:U:OP2	2.68	0.42
53:1:1528:A:H2'	53:1:1529:G:O4'	2.20	0.42
53:1:1563:U:H2'	53:1:1564:C:C6	2.55	0.42
53:1:2122:U:H2'	53:1:2123:G:O4'	2.19	0.42
53:1:2317:A:H2'	53:1:2318:G:O4'	2.20	0.42
53:1:2801:G:H2'	53:1:2802:G:C8	2.54	0.42
53:1:2861:U:H2'	53:1:2862:G:C8	2.55	0.42
54:2:30:C:H2'	54:2:31:C:H5'	2.02	0.42
1:b:228:ASP:CG	53:1:780:G:H1	2.27	0.41
4:e:16:MET:SD	4:e:21:TYR:HB2	2.59	0.41
6:g:12:LEU:C	6:g:12:LEU:HD12	2.45	0.41
7:h:95:LEU:HD23	7:h:95:LEU:HA	1.81	0.41
14:o:30:ARG:HE	14:o:30:ARG:HB3	1.70	0.41
17:r:79:ARG:HH22	53:1:572:A:H5'	1.85	0.41
21:v:92:VAL:HG13	21:v:92:VAL:O	2.19	0.41
32:H:39:ARG:HH12	32:H:54:ILE:HG13	1.84	0.41
35:K:4:TYR:N	35:K:64:VAL:O	2.53	0.41
39:O:11:LYS:HB3	39:O:71:LEU:CD2	2.50	0.41
39:O:52:LEU:HB3	43:S:80:ARG:HD2	2.02	0.41
45:U:70:ARG:NH1	52:3:452:A:H1'	2.35	0.41
52:3:603:U:H2'	52:3:604:G:H8	1.84	0.41
52:3:1259:C:H3'	52:3:1260:G:C5'	2.42	0.41
52:3:1379:G:O2'	52:3:1380:U:H5'	2.20	0.41
53:1:374:A:H2'	53:1:375:G:O4'	2.19	0.41
53:1:937:C:H2'	53:1:938:G:C8	2.54	0.41
53:1:1029:A:H2'	53:1:1030:C:O4'	2.20	0.41
53:1:1105:U:H2'	53:1:1106:G:C5'	2.49	0.41
53:1:2082:A:H2'	53:1:2083:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2229:U:H2'	53:1:2230:G:C8	2.55	0.41
53:1:2273:A:H2'	53:1:2274:A:H8	1.86	0.41
1:b:69:ASN:HA	1:b:188:ARG:HH12	1.84	0.41
3:d:144:GLU:N	3:d:144:GLU:OE2	2.53	0.41
4:e:82:TYR:CD1	4:e:83:PRO:HD2	2.54	0.41
4:e:137:PHE:HB2	4:e:140:ILE:HD13	2.02	0.41
15:p:86:LYS:HA	15:p:86:LYS:HD3	1.93	0.41
20:u:24:VAL:HG12	20:u:35:VAL:HG22	2.02	0.41
35:K:47:LEU:HG	35:K:56:LYS:N	2.36	0.41
37:M:58:LEU:C	37:M:58:LEU:HD12	2.45	0.41
52:3:458:U:H2'	52:3:459:A:C8	2.56	0.41
52:3:505:G:OP2	52:3:535:A:H5'	2.20	0.41
52:3:1023:U:H2'	52:3:1024:G:C8	2.55	0.41
52:3:1032:G:H3'	52:3:1032:G:N3	2.34	0.41
52:3:1301:U:O2	52:3:1301:U:C2'	2.59	0.41
52:3:1372:U:H2'	52:3:1373:G:O4'	2.20	0.41
53:1:1295:C:H2'	53:1:1296:G:C8	2.54	0.41
53:1:2841:C:H2'	53:1:2842:G:H8	1.86	0.41
54:2:48:U:O2'	54:2:49:C:H5'	2.20	0.41
57:7:8:U:H5'	57:7:49:C:OP2	2.20	0.41
4:e:21:TYR:CD1	4:e:26:GLN:HG2	2.56	0.41
11:l:37:GLY:O	11:l:41:ARG:HG2	2.20	0.41
14:o:7:ARG:HA	14:o:10:ARG:HE	1.85	0.41
16:q:61:ILE:HG21	53:1:1010:A:H5'	2.02	0.41
38:N:48:ARG:O	38:N:52:GLU:HG2	2.19	0.41
41:Q:66:ILE:HD12	41:Q:66:ILE:N	2.35	0.41
52:3:73:C:H2'	52:3:74:A:C8	2.55	0.41
52:3:423:G:C2'	52:3:424:G:H5'	2.50	0.41
52:3:730:G:H2'	52:3:731:G:H5'	2.02	0.41
52:3:1197:A:C2'	52:3:1198:G:H5''	2.48	0.41
53:1:821:A:H5''	53:1:822:G:H5'	2.02	0.41
53:1:2199:A:H2'	53:1:2200:C:O4'	2.20	0.41
1:b:76:VAL:O	1:b:76:VAL:HG13	2.21	0.41
2:c:22:ILE:HD12	2:c:22:ILE:N	2.35	0.41
2:c:46:ARG:NH2	2:c:88:GLU:O	2.54	0.41
3:d:52:VAL:HG13	3:d:74:LYS:HE3	2.02	0.41
7:h:80:THR:O	7:h:81:LEU:C	2.64	0.41
7:h:122:GLN:HB3	7:h:123:ILE:H	1.71	0.41
8:i:99:LYS:HE2	8:i:140:GLU:HG2	2.03	0.41
13:n:3:HIS:CD2	53:1:2820:A:H4'	2.55	0.41
14:o:33:ARG:HE	54:2:52:A:N6	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:18:LYS:HE3	53:1:1219:U:OP2	2.19	0.41
25:z:29:ARG:CZ	53:1:1183:U:H5'	2.50	0.41
33:I:7:LYS:HG3	33:I:20:LEU:HD13	2.02	0.41
34:J:29:ILE:HG23	34:J:29:ILE:O	2.21	0.41
34:J:76:ASN:HB3	34:J:79:THR:HG23	2.02	0.41
34:J:105:ILE:O	34:J:105:ILE:HG22	2.20	0.41
41:Q:11:ARG:NH1	52:3:563:A:H2	2.18	0.41
42:R:113:LYS:N	42:R:114:PRO:HD2	2.35	0.41
52:3:537:G:H2'	52:3:538:G:C8	2.55	0.41
52:3:583:A:H2'	52:3:584:G:O4'	2.21	0.41
52:3:736:C:H2'	52:3:737:C:C6	2.56	0.41
53:1:327:G:H2'	53:1:328:U:O4'	2.20	0.41
53:1:1307:A:C2'	53:1:1308:A:H5'	2.50	0.41
53:1:1592:C:H2'	53:1:1593:A:C8	2.55	0.41
53:1:1601:G:C2'	53:1:1602:U:H5'	2.49	0.41
5:f:42:VAL:HG22	5:f:43:LYS:N	2.35	0.41
12:m:66:ARG:HG3	12:m:66:ARG:HH11	1.86	0.41
20:u:60:LYS:HG3	20:u:61:GLU:N	2.35	0.41
24:y:20:ASN:O	24:y:25:GLN:N	2.53	0.41
27:C:38:PHE:HB2	27:C:45:HIS:CE1	2.56	0.41
38:N:108:ARG:HB3	52:3:1347:G:O4'	2.21	0.41
39:O:47:GLU:HB2	39:O:67:ILE:HG13	2.03	0.41
51:a:162:ARG:HB3	51:a:162:ARG:NH2	2.35	0.41
52:3:628:G:H2'	52:3:629:A:O4'	2.20	0.41
53:1:184:C:H2'	53:1:185:G:C8	2.56	0.41
53:1:720:U:H2'	53:1:721:A:C8	2.56	0.41
53:1:2283:C:H2'	53:1:2284:A:O4'	2.19	0.41
53:1:2555:U:H2'	53:1:2556:C:H5'	2.02	0.41
1:b:67:LYS:HA	1:b:150:GLY:HA2	2.03	0.41
1:b:75:ALA:HA	1:b:95:TYR:HA	2.03	0.41
6:g:2:GLN:HE22	6:g:20:ASN:ND2	2.19	0.41
8:i:21:PRO:HD2	8:i:22:PRO:HD3	2.02	0.41
12:m:125:PRO:HB3	53:1:2485:G:O3'	2.21	0.41
19:t:33:LYS:HE3	19:t:80:TRP:CZ3	2.56	0.41
24:y:18:LEU:HG	24:y:22:LEU:HG	2.02	0.41
27:C:43:ARG:NH2	53:1:643:A:C4	2.89	0.41
30:F:27:CYS:N	30:F:34:LYS:HE3	2.35	0.41
31:G:140:LEU:O	31:G:144:GLU:HB2	2.21	0.41
31:G:212:TYR:O	31:G:216:VAL:HG23	2.21	0.41
41:Q:71:HIS:HB2	41:Q:73:LEU:HD23	2.03	0.41
45:U:60:TRP:HA	45:U:63:GLN:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:39:LYS:NZ	50:Z:42:THR:HG21	2.35	0.41
52:3:106:C:H2'	52:3:107:G:C8	2.56	0.41
52:3:119:A:H4'	52:3:120:A:C4	2.55	0.41
52:3:144:G:O2'	52:3:145:G:H5'	2.19	0.41
52:3:673:A:H2'	52:3:674:G:C8	2.56	0.41
53:1:453:A:H4'	53:1:472:A:N6	2.35	0.41
53:1:626:A:H3'	53:1:627:A:C5'	2.50	0.41
53:1:869:G:O2'	53:1:870:U:H5'	2.21	0.41
53:1:1231:U:H2'	53:1:1232:G:H8	1.86	0.41
53:1:1322:A:H61	53:1:1333:G:H21	1.68	0.41
18:s:74:ILE:HG23	18:s:74:ILE:O	2.20	0.41
29:E:29:ARG:HD3	29:E:29:ARG:HA	1.86	0.41
32:H:105:VAL:O	32:H:105:VAL:HG13	2.21	0.41
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.85	0.41
44:T:84:LEU:HD12	44:T:84:LEU:HA	1.90	0.41
46:V:45:VAL:HG21	46:V:60:ILE:HD12	2.03	0.41
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.82	0.41
51:a:174:THR:HB	53:1:2124:G:C5'	2.50	0.41
52:3:79:G:O2'	52:3:80:A:H5'	2.21	0.41
52:3:212:G:H2'	52:3:213:G:H8	1.85	0.41
52:3:955:U:H2'	52:3:956:U:O4'	2.20	0.41
53:1:151:C:H2'	53:1:152:A:H8	1.85	0.41
53:1:548:G:H2'	53:1:549:G:O4'	2.21	0.41
53:1:1758:U:C5	53:1:2696:U:H5'	2.56	0.41
53:1:2070:A:H2'	53:1:2071:A:O4'	2.20	0.41
53:1:2285:C:O2'	53:1:2287:A:H1'	2.20	0.41
2:c:186:LEU:HD23	2:c:188:LEU:HD21	2.03	0.41
28:D:11:LYS:HE2	53:1:686:U:H5''	2.03	0.41
42:R:25:GLY:N	52:3:1329:A:H5''	2.34	0.41
46:V:64:ARG:HA	46:V:65:PRO:HD3	1.89	0.41
50:Z:39:LYS:HA	50:Z:42:THR:HB	2.03	0.41
50:Z:46:ARG:HD2	50:Z:46:ARG:N	2.36	0.41
52:3:1038:C:H2'	52:3:1039:G:C8	2.55	0.41
53:1:1706:C:C2	53:1:1757:A:H5'	2.56	0.41
53:1:2048:G:H2'	53:1:2049:G:H5''	2.02	0.41
53:1:2220:U:H2'	53:1:2221:G:C8	2.55	0.41
1:b:3:VAL:HG12	1:b:17:LYS:O	2.21	0.41
1:b:47:ARG:NH2	53:1:774:G:OP1	2.53	0.41
4:e:68:LYS:HA	4:e:68:LYS:HD3	1.84	0.41
4:e:76:PHE:HE1	53:1:2308:G:C6	2.39	0.41
6:g:41:LYS:HA	6:g:44:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:66:GLY:HA2	7:h:69:PHE:CE2	2.55	0.41
8:i:49:GLU:OE1	8:i:52:LEU:HD13	2.20	0.41
11:l:22:GLY:O	11:l:28:GLY:HA3	2.21	0.41
11:l:63:LYS:HG2	53:1:2394:C:OP1	2.21	0.41
11:l:96:LYS:HG3	11:l:101:ILE:HD11	2.02	0.41
12:m:18:ARG:HB3	12:m:18:ARG:HH21	1.84	0.41
16:q:90:ASP:OD1	53:1:996:A:H4'	2.20	0.41
20:u:36:GLU:HA	20:u:61:GLU:HG2	2.02	0.41
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.87	0.41
31:G:100:LEU:HD11	31:G:157:PRO:HD2	2.02	0.41
33:I:150:LYS:HZ1	33:I:155:LYS:HA	1.86	0.41
35:K:51:ILE:O	35:K:52:ASN:HB2	2.21	0.41
36:L:41:ILE:HG23	36:L:116:ALA:HB2	2.02	0.41
37:M:95:MET:O	37:M:98:LEU:HG	2.20	0.41
38:N:38:PHE:HA	38:N:41:GLU:OE1	2.21	0.41
40:P:23:HIS:HB3	40:P:30:ILE:CG1	2.51	0.41
41:Q:15:VAL:O	41:Q:15:VAL:HG23	2.21	0.41
42:R:64:VAL:O	42:R:65:GLU:C	2.64	0.41
48:X:73:PHE:C	48:X:75:PRO:HD3	2.46	0.41
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.35	0.41
51:a:21:TYR:CD2	51:a:222:VAL:HG13	2.55	0.41
52:3:287:U:H2'	52:3:288:A:C8	2.56	0.41
52:3:483:C:H2'	52:3:484:G:C8	2.56	0.41
52:3:726:C:H2'	52:3:727:G:C8	2.56	0.41
52:3:824:G:H2'	52:3:825:A:H8	1.86	0.41
52:3:1071:C:H2'	52:3:1072:G:C8	2.55	0.41
52:3:1342:C:H2'	52:3:1343:G:C8	2.56	0.41
52:3:1345:U:H4'	52:3:1346:A:H8	1.85	0.41
53:1:296:U:H2'	53:1:297:G:H8	1.86	0.41
53:1:340:A:H2'	53:1:341:C:O4'	2.21	0.41
53:1:740:C:H5'	53:1:1784:A:H2'	2.03	0.41
53:1:1219:U:H2'	53:1:1220:G:H8	1.85	0.41
53:1:1316:U:H2'	53:1:1317:G:C8	2.56	0.41
53:1:1330:C:H2'	53:1:1331:G:C8	2.55	0.41
53:1:1435:G:H2'	53:1:1436:G:H8	1.86	0.41
53:1:1652:A:H2'	53:1:1653:G:O4'	2.21	0.41
53:1:1774:C:H4'	53:1:1979:U:O2	2.20	0.41
53:1:2070:A:O2'	53:1:2071:A:H5'	2.21	0.41
53:1:2115:G:H21	53:1:2119:A:N6	2.19	0.41
53:1:2358:A:H2'	53:1:2359:C:O4'	2.21	0.41
53:1:2371:G:O2'	53:1:2372:U:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2476:A:H2	53:1:2481:G:H1	1.68	0.41
57:7:59:U:H2'	57:7:60:U:H5'	2.03	0.41
4:e:148:VAL:HG22	4:e:148:VAL:O	2.21	0.41
12:m:41:LEU:CD1	12:m:124:LEU:HD22	2.51	0.41
15:p:56:SER:O	15:p:75:THR:HG22	2.20	0.41
33:I:30:LYS:HD2	52:3:411:A:H2'	2.02	0.41
36:L:56:SER:OG	36:L:59:GLU:HG2	2.20	0.41
37:M:128:VAL:HG13	37:M:128:VAL:O	2.21	0.41
38:N:22:PRO:HA	38:N:60:LEU:HD23	2.02	0.41
42:R:74:MET:SD	42:R:74:MET:C	3.04	0.41
47:W:12:PHE:CD2	47:W:12:PHE:N	2.89	0.41
50:Z:9:GLU:HB3	50:Z:10:PRO:CD	2.48	0.41
52:3:202:G:H2'	52:3:203:G:C8	2.56	0.41
52:3:312:C:H2'	52:3:313:A:C8	2.56	0.41
52:3:436:C:H2'	52:3:437:U:C6	2.56	0.41
53:1:26:G:O2'	53:1:27:G:H5'	2.20	0.41
53:1:279:A:H2'	53:1:280:U:H5'	2.03	0.41
53:1:826:U:H5''	53:1:2429:G:P	2.61	0.41
53:1:1078:U:H5''	53:1:1079:C:H5''	2.02	0.41
53:1:1542:U:H2'	53:1:1543:G:O4'	2.21	0.41
53:1:1956:U:C2'	53:1:1957:C:H5'	2.51	0.41
53:1:2329:U:H2'	53:1:2330:G:H8	1.83	0.41
53:1:2508:G:H2'	53:1:2509:G:H8	1.86	0.41
54:2:88:C:H3'	54:2:88:C:OP1	2.21	0.41
6:g:84:ALA:HA	6:g:91:PHE:H	1.85	0.40
9:j:78:THR:HB	53:1:2641:G:H5''	2.03	0.40
9:j:89:PHE:O	9:j:93:ILE:HG12	2.21	0.40
11:l:36:LYS:HD3	53:1:807:U:OP2	2.20	0.40
17:r:81:LYS:HE3	53:1:973:A:OP2	2.20	0.40
20:u:12:VAL:HG21	20:u:17:ASP:O	2.21	0.40
25:z:25:GLY:HA2	53:1:929:U:O2	2.21	0.40
31:G:59:ILE:HG22	31:G:62:ARG:HH21	1.86	0.40
33:I:33:ILE:C	33:I:34:GLU:HG2	2.45	0.40
34:J:23:THR:HG21	52:3:1396:A:H2	1.85	0.40
36:L:36:SER:HA	38:N:42:THR:HG21	2.03	0.40
37:M:76:ARG:HD2	37:M:126:CYS:SG	2.61	0.40
38:N:98:ARG:NH2	52:3:1180:A:OP2	2.54	0.40
42:R:54:THR:O	42:R:57:ASP:OD1	2.39	0.40
49:Y:23:ARG:HH21	52:3:176:C:H4'	1.86	0.40
52:3:492:C:H2'	52:3:493:A:C8	2.56	0.40
52:3:560:A:H4'	52:3:561:U:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1342:C:H2'	52:3:1343:G:H8	1.85	0.40
53:1:206:U:O2'	53:1:207:A:H5'	2.20	0.40
53:1:613:A:N3	53:1:613:A:H2'	2.37	0.40
53:1:871:U:H2'	53:1:872:U:C6	2.56	0.40
53:1:1423:G:H2'	53:1:1424:G:H8	1.86	0.40
53:1:1434:A:H2'	53:1:1435:G:C8	2.56	0.40
53:1:2333:A:H5'	53:1:2335:A:H1'	2.03	0.40
53:1:2626:C:O2'	53:1:2627:G:H5'	2.22	0.40
1:b:70:LYS:HD3	1:b:95:TYR:CE2	2.57	0.40
6:g:73:ASN:HB2	6:g:108:VAL:HG23	2.03	0.40
8:i:23:VAL:HG13	8:i:24:GLY:N	2.37	0.40
10:k:87:LEU:CD2	10:k:94:PRO:HB3	2.52	0.40
14:o:78:VAL:HG13	14:o:79:ALA:N	2.36	0.40
15:p:7:LEU:HD23	15:p:7:LEU:C	2.46	0.40
16:q:5:ARG:HD2	53:1:1250:G:H5''	2.03	0.40
23:x:48:LEU:HB3	23:x:50:VAL:HG13	2.02	0.40
28:D:30:VAL:O	28:D:34:ARG:HG2	2.22	0.40
30:F:1:MET:N	53:1:2526:G:N3	2.70	0.40
36:L:52:ARG:HH22	36:L:121:ASN:HA	1.85	0.40
41:Q:40:THR:HA	41:Q:41:PRO:HD3	1.86	0.40
50:Z:25:ALA:HB3	56:4:9:G:H5'	2.03	0.40
53:1:372:G:C2'	53:1:373:U:OP2	2.69	0.40
53:1:1368:G:H2'	53:1:1369:G:H8	1.86	0.40
53:1:2040:G:H2'	53:1:2041:U:O4'	2.21	0.40
53:1:2423:U:H5'	53:1:2424:C:C5'	2.51	0.40
53:1:2788:C:H2'	53:1:2789:C:C6	2.55	0.40
5:f:21:GLN:NE2	5:f:38:ASP:HA	2.36	0.40
8:i:7:TYR:HA	8:i:58:ILE:O	2.21	0.40
8:i:90:GLY:C	8:i:91:LYS:HD3	2.46	0.40
11:l:135:ILE:HB	11:l:142:ILE:HD11	2.03	0.40
19:t:63:VAL:O	19:t:63:VAL:HG13	2.21	0.40
21:v:14:LYS:HB2	54:2:98:G:H1	1.86	0.40
26:B:14:MET:SD	53:1:2045:C:H5''	2.62	0.40
28:D:27:GLY:O	28:D:30:VAL:HB	2.20	0.40
33:I:59:LYS:O	33:I:63:ILE:HG13	2.21	0.40
33:I:173:ASP:OD2	33:I:176:LYS:HG2	2.21	0.40
35:K:18:VAL:N	35:K:19:PRO:CD	2.85	0.40
46:V:48:GLU:O	46:V:49:ASN:C	2.63	0.40
50:Z:4:LYS:O	50:Z:4:LYS:HD2	2.21	0.40
50:Z:11:PHE:O	50:Z:13:VAL:HG12	2.22	0.40
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:6:A:H2'	53:1:7:G:C8	2.57	0.40
53:1:201:C:O2	53:1:251:A:H2	2.04	0.40
53:1:962:G:O2'	53:1:963:U:H5'	2.21	0.40
53:1:1130:U:O2'	53:1:1131:G:P	2.79	0.40
53:1:1370:C:H2'	53:1:1371:G:O4'	2.20	0.40
53:1:1930:G:O2'	53:1:1931:U:H5	2.04	0.40
53:1:2326:C:O2'	53:1:2327:A:P	2.80	0.40
2:c:152:PRO:HD3	53:1:2571:U:O2'	2.21	0.40
7:h:129:LEU:HA	7:h:130:PRO:HD3	1.89	0.40
32:H:168:ARG:HH22	52:3:1106:G:H1'	1.85	0.40
33:I:43:ARG:NH1	52:3:511:C:OP1	2.54	0.40
36:L:78:ARG:HD2	36:L:81:GLY:C	2.46	0.40
52:3:552:U:H2'	52:3:553:A:H8	1.85	0.40
52:3:1475:G:H4'	53:1:1689:A:H4'	2.04	0.40
53:1:253:C:H2'	53:1:254:G:O4'	2.20	0.40
53:1:479:A:C4'	53:1:480:A:H5'	2.49	0.40
53:1:950:G:H2'	53:1:951:C:C6	2.57	0.40
53:1:1060:U:H4'	53:1:1061:U:H5'	2.03	0.40
53:1:1566:A:O2'	53:1:1567:G:H5'	2.22	0.40
53:1:2687:U:H2'	53:1:2688:G:O4'	2.20	0.40
54:2:111:U:H2'	54:2:112:G:H8	1.87	0.40
55:5:62:C:H2'	55:5:63:G:C8	2.57	0.40
4:e:137:PHE:HA	4:e:138:PRO:HD3	1.94	0.40
9:j:113:PRO:HD2	53:1:558:U:P	2.61	0.40
12:m:59:ARG:HG3	12:m:59:ARG:HH21	1.87	0.40
17:r:22:LEU:HD12	17:r:23:GLU:O	2.21	0.40
22:w:28:LEU:HD12	53:1:2353:G:O3'	2.21	0.40
33:I:128:VAL:HG21	33:I:145:ARG:NH1	2.36	0.40
43:S:7:ALA:O	43:S:10:VAL:HG12	2.21	0.40
44:T:88:ARG:NH2	53:1:716:A:OP1	2.55	0.40
46:V:11:VAL:HG22	46:V:22:VAL:HG22	2.02	0.40
49:Y:4:LYS:NZ	52:3:331:G:H2'	2.36	0.40
50:Z:24:LYS:O	50:Z:24:LYS:HD3	2.21	0.40
50:Z:45:LYS:HE3	52:3:723:U:O4'	2.21	0.40
52:3:1162:C:H2'	52:3:1163:A:C8	2.57	0.40
52:3:1272:G:H2'	52:3:1273:C:O4'	2.21	0.40
53:1:151:C:H2'	53:1:152:A:C8	2.57	0.40
53:1:546:U:H2'	53:1:547:A:C4'	2.49	0.40
53:1:1039:A:H2	53:1:1116:G:H22	1.68	0.40
53:1:1277:G:H2'	53:1:1278:C:C6	2.57	0.40
53:1:2233:U:H2'	53:1:2234:G:C8	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2547:A:H2'	53:1:2548:U:C6	2.56	0.40
53:1:2799:A:H2'	53:1:2800:A:H5'	2.03	0.40
55:5:24:U:H2'	55:5:25:C:C6	2.56	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%)	236 (88%)	28 (10%)	5 (2%)	6	33
2	c	207/209 (99%)	181 (87%)	26 (13%)	0	100	100
3	d	199/201 (99%)	185 (93%)	13 (6%)	1 (0%)	24	56
4	e	175/177 (99%)	153 (87%)	21 (12%)	1 (1%)	21	52
5	f	174/176 (99%)	163 (94%)	9 (5%)	2 (1%)	11	42
6	g	147/149 (99%)	128 (87%)	17 (12%)	2 (1%)	9	37
7	h	129/131 (98%)	98 (76%)	25 (19%)	6 (5%)	2	18
8	i	139/141 (99%)	120 (86%)	15 (11%)	4 (3%)	3	26
9	j	140/142 (99%)	129 (92%)	10 (7%)	1 (1%)	18	50
10	k	120/122 (98%)	102 (85%)	15 (12%)	3 (2%)	4	29
11	l	141/143 (99%)	114 (81%)	22 (16%)	5 (4%)	3	24
12	m	134/136 (98%)	120 (90%)	11 (8%)	3 (2%)	5	31
13	n	118/120 (98%)	99 (84%)	16 (14%)	3 (2%)	4	29
14	o	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
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%)	88 (87%)	12 (12%)	1 (1%)	12	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	s	108/110 (98%)	98 (91%)	8 (7%)	2 (2%)	6	33
19	t	91/93 (98%)	84 (92%)	7 (8%)	0	100	100
20	u	100/102 (98%)	83 (83%)	13 (13%)	4 (4%)	2	21
21	v	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
22	w	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
23	x	75/77 (97%)	68 (91%)	3 (4%)	4 (5%)	1	16
24	y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
26	B	54/56 (96%)	51 (94%)	2 (4%)	1 (2%)	6	33
27	C	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	52 (84%)	8 (13%)	2 (3%)	3	25
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
31	G	223/225 (99%)	202 (91%)	21 (9%)	0	100	100
32	H	204/206 (99%)	183 (90%)	18 (9%)	3 (2%)	8	36
33	I	203/205 (99%)	177 (87%)	23 (11%)	3 (2%)	8	36
34	J	155/157 (99%)	131 (84%)	20 (13%)	4 (3%)	4	28
35	K	98/100 (98%)	83 (85%)	9 (9%)	6 (6%)	1	14
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	50
37	M	127/129 (98%)	113 (89%)	13 (10%)	1 (1%)	16	48
38	N	125/127 (98%)	100 (80%)	19 (15%)	6 (5%)	2	17
39	O	96/98 (98%)	79 (82%)	12 (12%)	5 (5%)	1	17
40	P	114/116 (98%)	93 (82%)	19 (17%)	2 (2%)	6	34
41	Q	121/123 (98%)	91 (75%)	24 (20%)	6 (5%)	1	17
42	R	112/114 (98%)	99 (88%)	8 (7%)	5 (4%)	2	18
43	S	98/100 (98%)	87 (89%)	9 (9%)	2 (2%)	6	32
44	T	86/88 (98%)	76 (88%)	9 (10%)	1 (1%)	10	40
45	U	80/82 (98%)	66 (82%)	12 (15%)	2 (2%)	4	29
46	V	78/80 (98%)	61 (78%)	15 (19%)	2 (3%)	4	28
47	W	63/65 (97%)	58 (92%)	3 (5%)	2 (3%)	3	25
48	X	77/79 (98%)	67 (87%)	9 (12%)	1 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Y	83/85 (98%)	80 (96%)	2 (2%)	1 (1%)	10	40
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	7
51	a	130/223 (58%)	124 (95%)	6 (5%)	0	100	100
All	All	5919/6112 (97%)	5178 (88%)	631 (11%)	110 (2%)	8	33

All (110) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
6	g	9	VAL
7	h	78	GLY
7	h	81	LEU
7	h	108	VAL
7	h	118	ILE
10	k	110	GLU
17	r	54	VAL
30	F	37	GLN
32	H	60	ALA
33	I	34	GLU
34	J	93	VAL
34	J	122	VAL
35	K	54	LEU
38	N	57	VAL
38	N	90	ASP
39	O	37	ARG
40	P	92	ARG
40	P	125	LYS
41	Q	24	GLU
42	R	4	ALA
42	R	14	ALA
46	V	49	ASN
49	Y	68	LYS
50	Z	8	ASN
50	Z	64	ALA
5	f	174	LYS
6	g	120	GLY
8	i	6	ALA
11	l	28	GLY
12	m	59	ARG
12	m	60	GLN
12	m	69	PRO

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Mol	Chain	Res	Type
13	n	117	ASP
26	B	25	THR
29	E	31	ILE
32	H	156	LEU
33	I	4	LEU
35	K	39	LEU
35	K	99	ALA
38	N	91	GLU
41	Q	88	ASP
42	R	7	ASN
42	R	65	GLU
44	T	46	LYS
45	U	47	GLU
45	U	79	ASN
50	Z	25	ALA
50	Z	34	ARG
1	b	260	LYS
5	f	45	ALA
7	h	119	PRO
8	i	13	ALA
10	k	35	VAL
13	n	118	ARG
18	s	3	THR
20	u	51	LEU
20	u	97	SER
23	x	18	SER
23	x	25	LYS
35	K	53	LYS
35	K	86	ARG
35	K	95	ALA
37	M	47	ASP
38	N	100	ALA
38	N	125	GLN
39	O	35	GLN
39	O	42	LEU
41	Q	27	PRO
41	Q	77	SER
43	S	3	GLN
47	W	17	VAL
4	e	176	PHE
7	h	58	THR
8	i	11	GLN

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Mol	Chain	Res	Type
8	i	22	PRO
11	l	29	LYS
32	H	109	GLU
41	Q	91	GLY
46	V	17	GLU
47	W	13	THR
48	X	4	LEU
50	Z	36	PHE
1	b	236	GLY
1	b	253	GLY
11	l	85	VAL
11	l	87	GLY
13	n	116	VAL
20	u	56	GLY
20	u	98	ASN
23	x	17	ARG
34	J	11	GLN
36	L	80	GLY
38	N	102	PHE
39	O	47	GLU
41	Q	56	LEU
43	S	34	ASN
9	j	81	ILE
18	s	63	GLY
23	x	6	VAL
42	R	5	GLY
50	Z	26	GLY
1	b	240	GLY
1	b	246	PRO
10	k	101	GLY
11	l	16	GLY
29	E	62	PRO
34	J	105	ILE
39	O	33	GLY
33	I	6	PRO

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	74
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	74
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	62
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	78 (98%)	2 (2%)	42	61
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	67
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	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	H	170/170 (100%)	170 (100%)	0	100	100
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	119 (100%)	0	100	100
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	76
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	90 (98%)	2 (2%)	45	63
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%)	64 (98%)	1 (2%)	57	68
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4908/4972 (99%)	4888 (100%)	20 (0%)	81	81

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	c	9	VAL
7	h	76	PHE
9	j	141	ASP
10	k	47	ILE
11	l	94	THR
14	o	53	THR
14	o	65	THR
15	p	83	ILE
18	s	39	THR
19	t	7	LEU

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Mol	Chain	Res	Type
19	t	34	VAL
22	w	17	LEU
31	G	187	ASP
35	K	55	HIS
36	L	65	LEU
37	M	126	CYS
39	O	27	GLU
42	R	18	LEU
42	R	64	VAL
45	U	36	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (119) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	127	ASN
1	b	133	ASN
1	b	141	HIS
1	b	199	HIS
1	b	231	HIS
1	b	242	HIS
1	b	250	GLN
2	c	42	ASN
2	c	49	GLN
2	c	150	GLN
2	c	164	GLN
2	c	173	GLN
2	c	185	ASN
3	d	30	GLN
3	d	41	GLN
3	d	97	ASN
3	d	115	GLN
3	d	165	HIS
3	d	195	GLN
4	e	51	ASN
4	e	80	GLN
5	f	37	ASN
5	f	72	ASN
5	f	138	GLN
6	g	20	ASN
6	g	33	GLN
6	g	43	ASN

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Mol	Chain	Res	Type
6	g	145	ASN
7	h	103	ASN
8	i	104	GLN
9	j	40	HIS
9	j	58	ASN
9	j	76	HIS
9	j	135	GLN
10	k	3	GLN
11	l	54	GLN
12	m	3	GLN
12	m	13	HIS
13	n	3	HIS
13	n	23	ASN
13	n	81	ASN
14	o	61	GLN
14	o	100	HIS
14	o	104	GLN
15	p	11	GLN
15	p	76	HIS
16	q	36	GLN
18	s	7	HIS
18	s	9	HIS
19	t	59	ASN
19	t	70	HIS
20	u	45	GLN
20	u	73	ASN
21	v	5	ASN
21	v	24	ASN
21	v	49	ASN
21	v	78	GLN
21	v	88	HIS
22	w	8	ASN
23	x	15	ASN
23	x	22	ASN
23	x	33	HIS
24	y	15	ASN
25	z	8	GLN
26	B	5	ASN
27	C	25	ASN
27	C	44	GLN
28	D	16	HIS
31	G	38	HIS

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Mol	Chain	Res	Type
31	G	41	ASN
31	G	50	ASN
31	G	167	HIS
31	G	176	ASN
31	G	177	ASN
32	H	5	HIS
32	H	31	ASN
32	H	139	ASN
33	I	53	GLN
33	I	58	GLN
33	I	125	ASN
33	I	139	ASN
33	I	151	GLN
33	I	197	HIS
34	J	42	ASN
34	J	69	ASN
34	J	76	ASN
34	J	81	GLN
34	J	131	ASN
34	J	145	ASN
36	L	67	ASN
37	M	37	ASN
38	N	4	GLN
39	O	20	GLN
39	O	35	GLN
39	O	58	ASN
40	P	14	GLN
40	P	37	GLN
40	P	118	ASN
41	Q	4	ASN
41	Q	45	ASN
41	Q	111	GLN
42	R	7	ASN
43	S	3	GLN
43	S	42	ASN
43	S	59	GLN
43	S	70	HIS
44	T	27	GLN
45	U	26	ASN
45	U	29	ASN
46	V	30	HIS
49	Y	47	GLN

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Mol	Chain	Res	Type
49	Y	51	ASN
49	Y	81	GLN
51	a	24	ASN
51	a	57	GLN
51	a	58	ASN
51	a	168	ASN
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	136 (8%)	2 (0%)
53	1	2902/2903 (99%)	333 (11%)	11 (0%)
54	2	119/120 (99%)	12 (10%)	1 (0%)
55	5	76/77 (98%)	8 (10%)	0
55	6	76/77 (98%)	6 (7%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	13 (17%)	0
All	All	4803/4810 (99%)	510 (10%)	14 (0%)

All (510) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	85	U
52	3	87	C
52	3	95	C
52	3	100	G
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U

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Mol	Chain	Res	Type
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	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
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
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	723	U
52	3	724	G
52	3	755	G

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Mol	Chain	Res	Type
52	3	777	A
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	842	U
52	3	843	U
52	3	844	G
52	3	846	G
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	1031	C
52	3	1033	G
52	3	1034	G
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

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Mol	Chain	Res	Type
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1241	G
52	3	1253	G
52	3	1258	G
52	3	1260	G
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	1320	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1381	U
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	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

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Mol	Chain	Res	Type
53	1	71	A
53	1	74	A
53	1	75	G
53	1	98	G
53	1	119	A
53	1	120	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	221	A
53	1	222	A
53	1	224	U
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
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	324	A
53	1	329	G
53	1	330	A
53	1	371	A
53	1	372	G
53	1	373	U
53	1	386	G
53	1	387	U
53	1	388	G
53	1	404	A

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Mol	Chain	Res	Type
53	1	406	G
53	1	411	G
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	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	547	A
53	1	563	A
53	1	572	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
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	729	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	775	G
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

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Mol	Chain	Res	Type
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	859	G
53	1	878	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	975	A
53	1	983	A
53	1	995	C
53	1	996	A
53	1	1009	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
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	1060	U
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	1104	C

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Mol	Chain	Res	Type
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	1175	A
53	1	1177	G
53	1	1180	U
53	1	1212	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	1289	C
53	1	1301	A
53	1	1302	A
53	1	1321	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1333	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1398	C
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G

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Mol	Chain	Res	Type
53	1	1498	C
53	1	1515	A
53	1	1524	G
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	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1654	A
53	1	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1732	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
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	1848	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1914	C

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Mol	Chain	Res	Type
53	1	1929	G
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	1992	G
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
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2145	C
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2189	U

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Mol	Chain	Res	Type
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2212	A
53	1	2213	U
53	1	2225	A
53	1	2259	U
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	2337	G
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2407	A
53	1	2423	U
53	1	2424	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2502	G
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	2609	U

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Mol	Chain	Res	Type
53	1	2613	U
53	1	2629	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	2751	G
53	1	2757	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	2800	A
53	1	2809	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2850	A
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2879	A
53	1	2880	C
53	1	2883	A
54	2	4	C
54	2	12	C
54	2	13	G
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	90	C
54	2	108	A

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Mol	Chain	Res	Type
54	2	109	A
55	5	9	G
55	5	18	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	61	C
55	5	76	A
55	6	6	G
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
56	4	12	A
56	4	13	A
57	7	8	U
57	7	13	C
57	7	17	C
57	7	21	A
57	7	45	U
57	7	46	G
57	7	47	U
57	7	48	C
57	7	61	C
57	7	73	A
57	7	74	C
57	7	75	C
57	7	76	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	1190	G
52	3	1201	A
53	1	227	A
53	1	372	G
53	1	490	C
53	1	1020	A
53	1	1130	U
53	1	1475	G

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Mol	Chain	Res	Type
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
53	1	2756	U
54	2	88	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	FME	1	3001	59	6,7,10	0.60	0	2,7,11	0.20	0
59	PHE	7	101	57,58	10,11,12	0.68	0	8,13,15	0.35	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FME	1	3001	59	-	0/5/6/11	-
59	PHE	7	101	57,58	-	3/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	7	101	PHE	O-C-CA-CB
59	7	101	PHE	CA-CB-CG-CD1
59	7	101	PHE	CA-CB-CG-CD2

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.

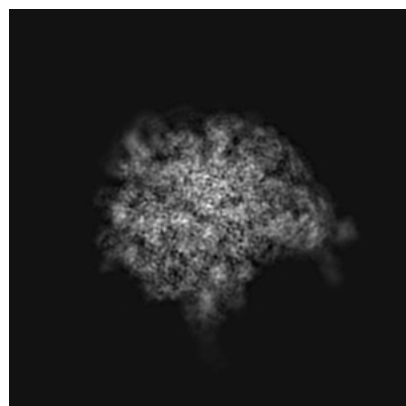
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21640. These allow visual inspection of the internal detail of the map and identification of artifacts.

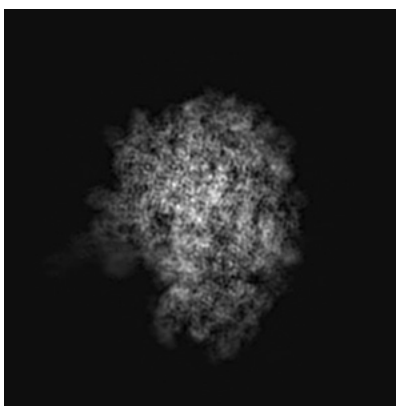
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

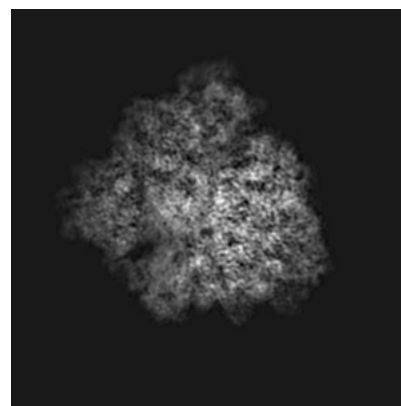
6.1.1 Primary map



X

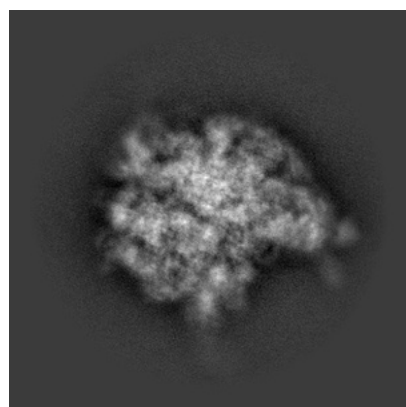


Y

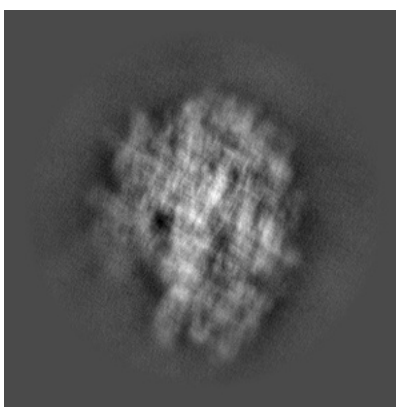


Z

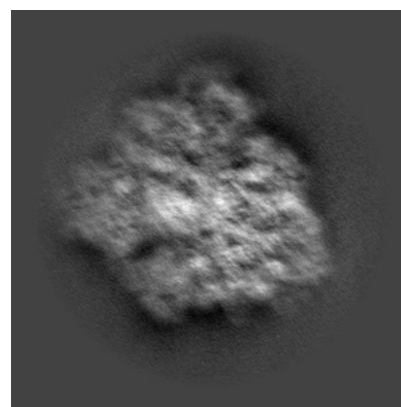
6.1.2 Raw map



X



Y

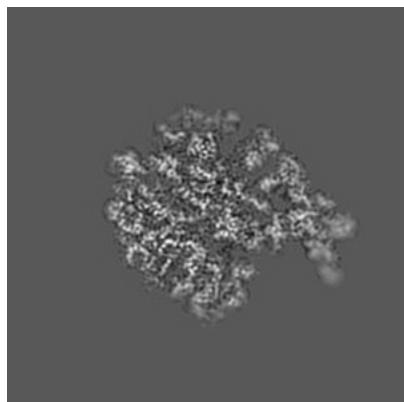


Z

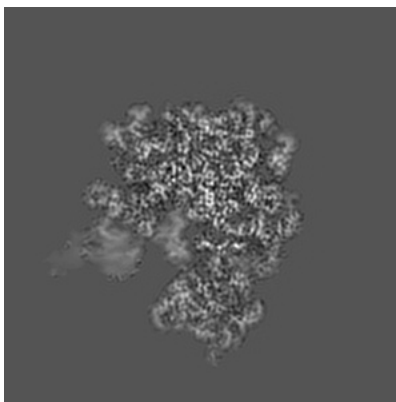
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

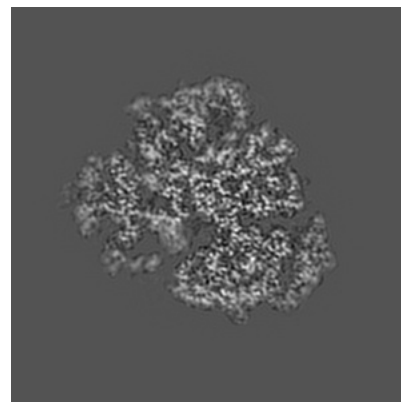
6.2.1 Primary map



X Index: 144

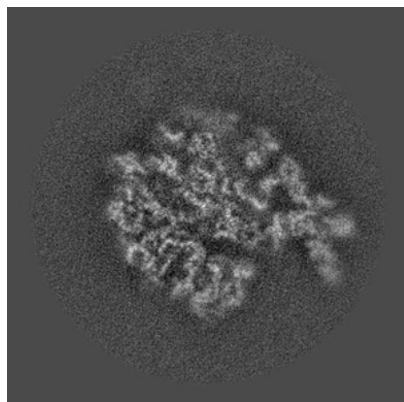


Y Index: 144

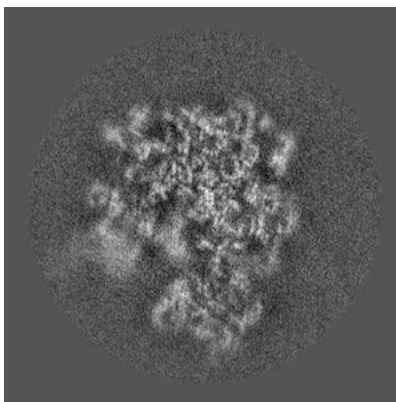


Z Index: 144

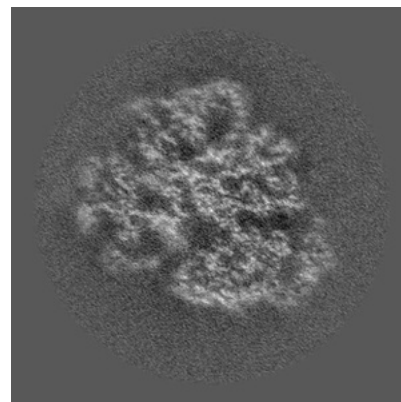
6.2.2 Raw map



X Index: 144



Y Index: 144

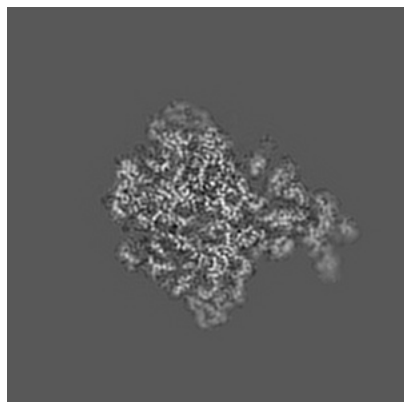


Z Index: 144

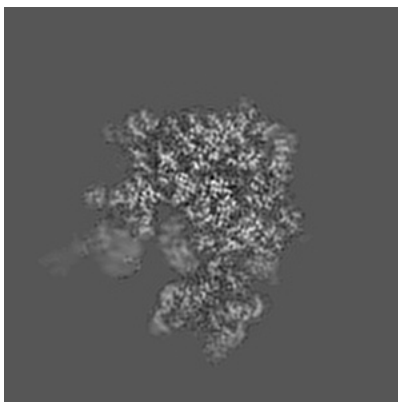
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

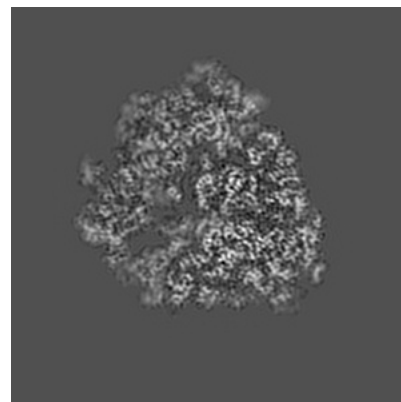
6.3.1 Primary map



X Index: 150

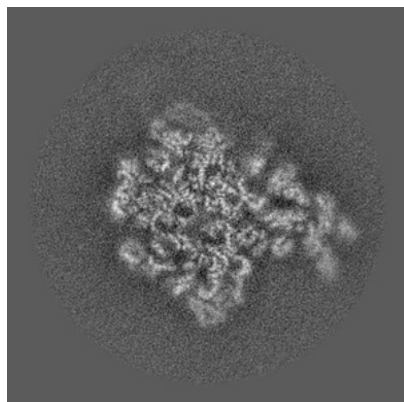


Y Index: 148

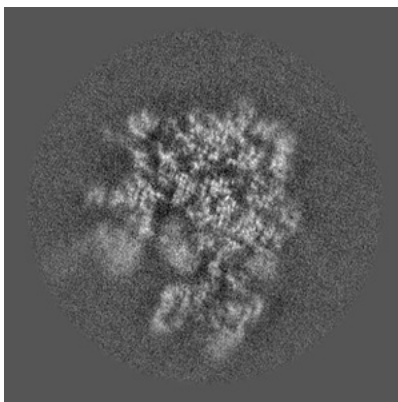


Z Index: 135

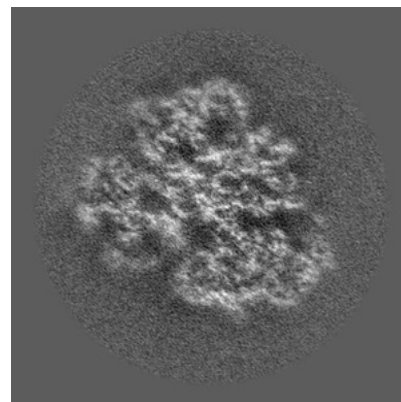
6.3.2 Raw map



X Index: 150



Y Index: 148

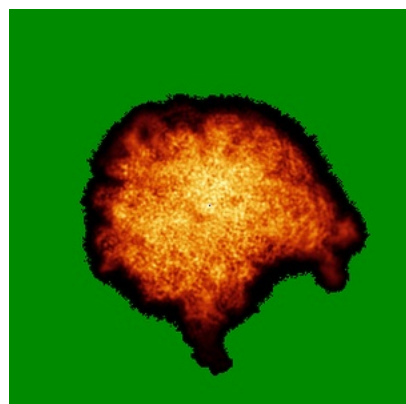


Z Index: 145

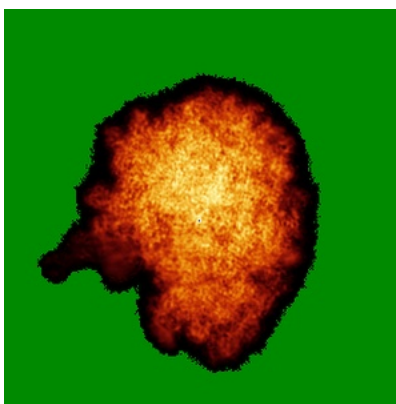
The images above show the largest variance slices of the map in three orthogonal directions.

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

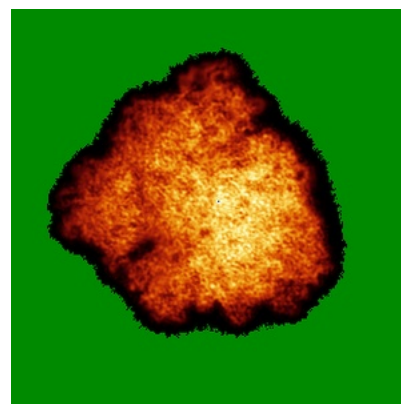
6.4.1 Primary map



X

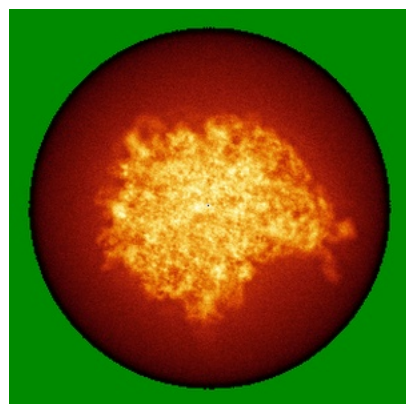


Y

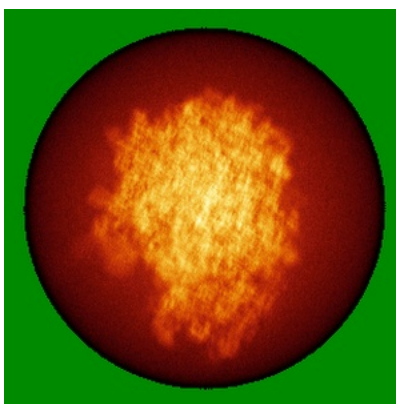


Z

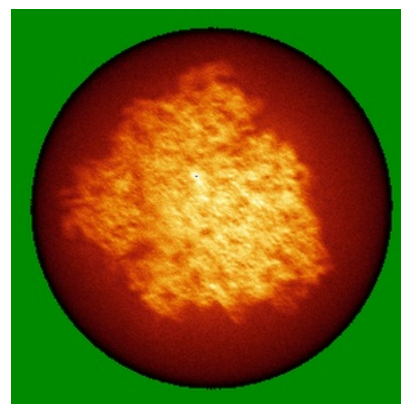
6.4.2 Raw map



X



Y

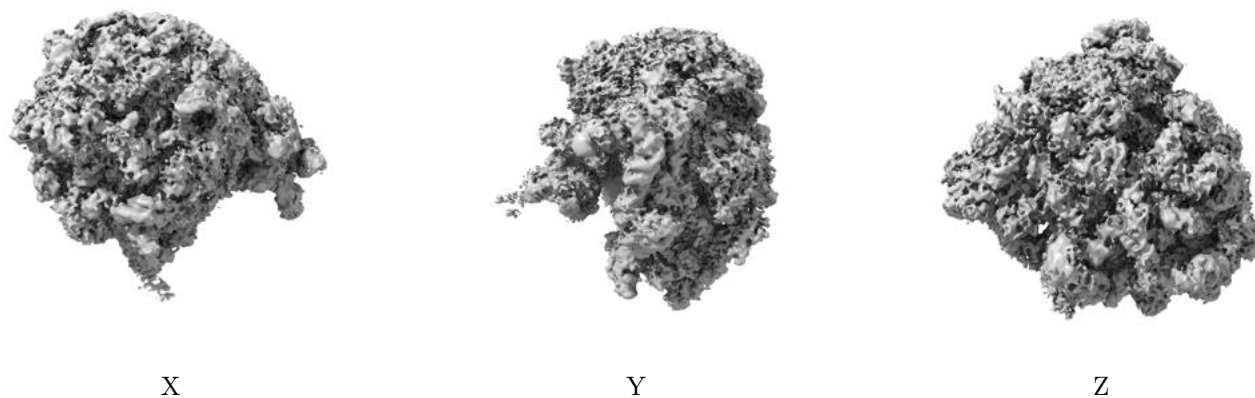


Z

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.

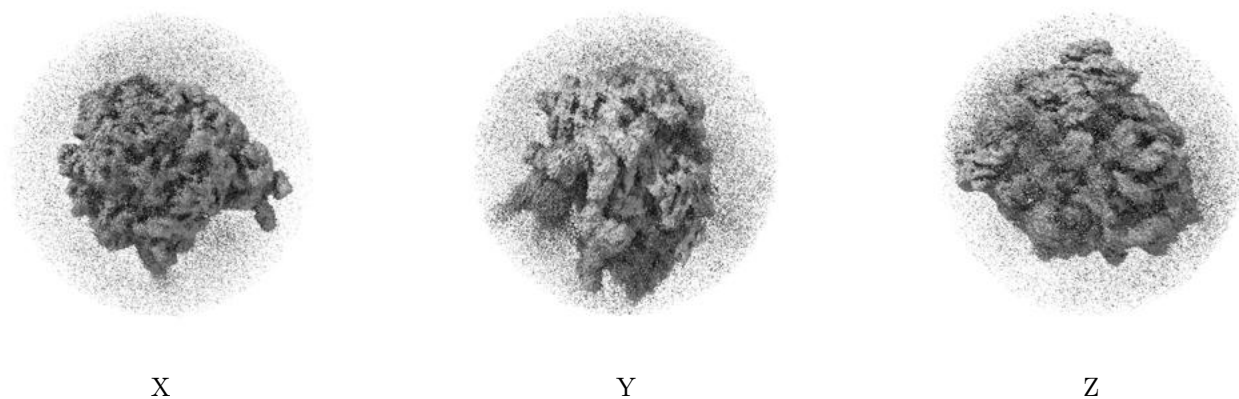
6.5 Orthogonal surface views [i](#)

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.

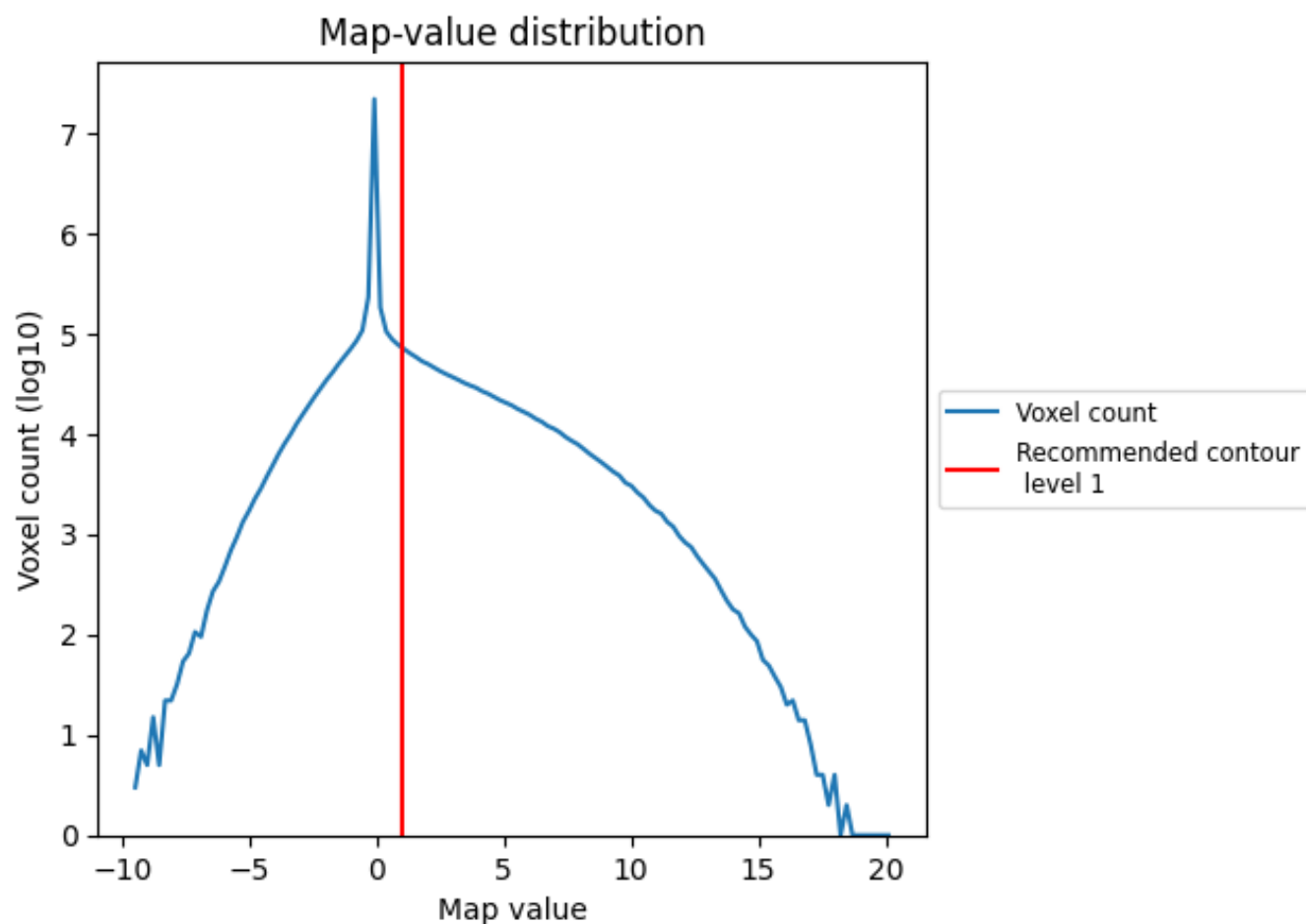
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

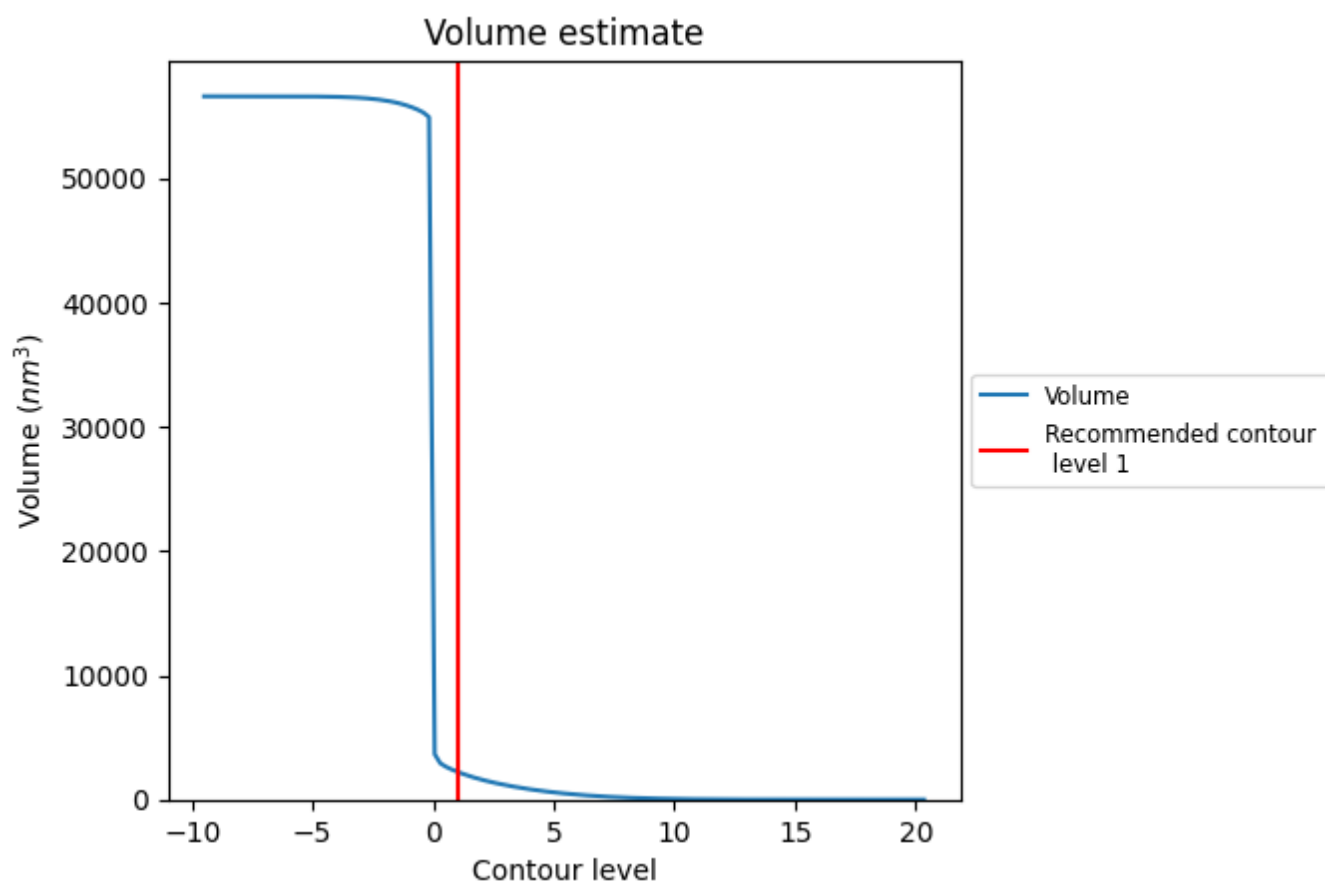
This section contains the results of statistical analysis of the map.

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.

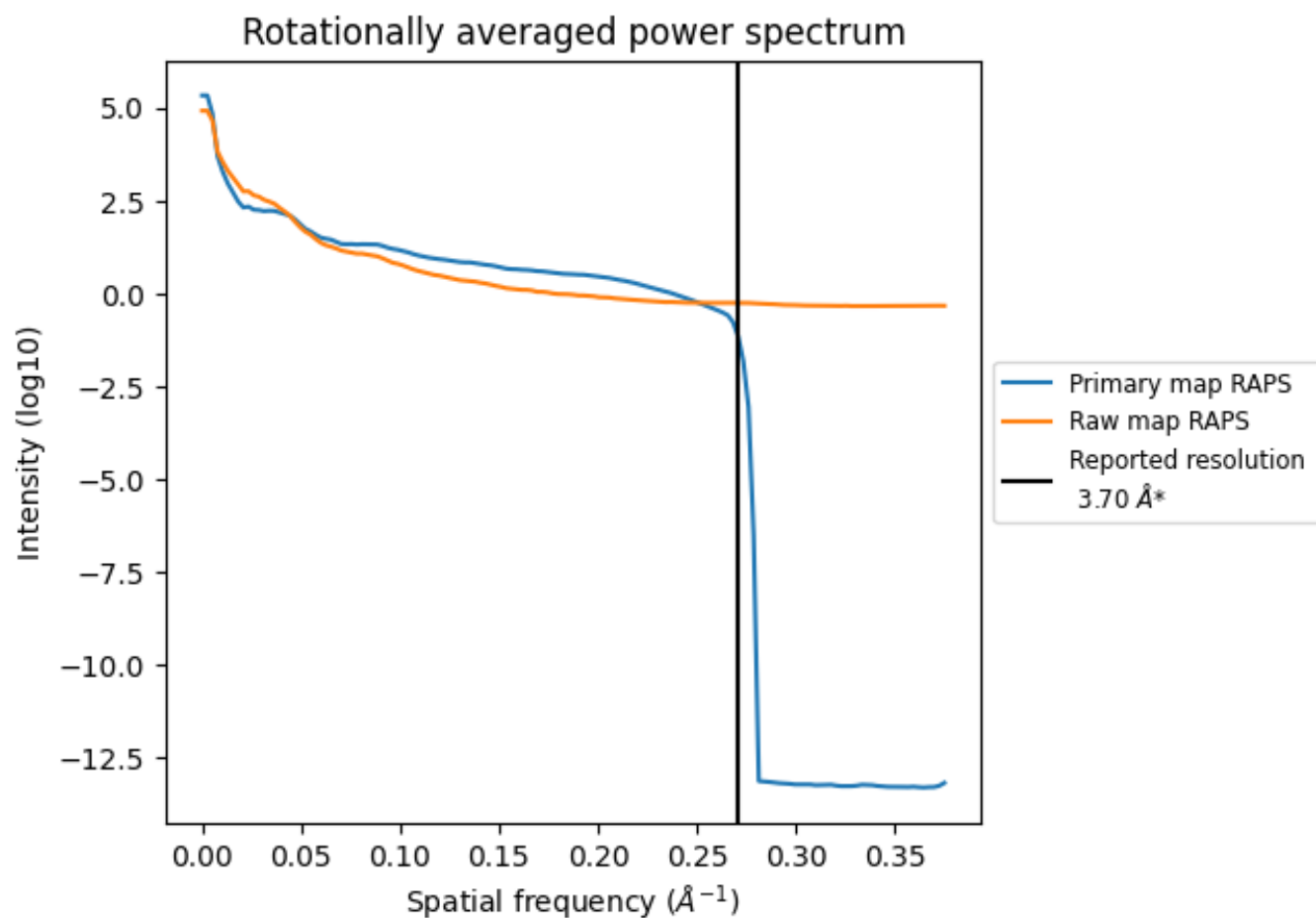
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2237 nm^3 ; this corresponds to an approximate mass of 2021 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 ⓘ

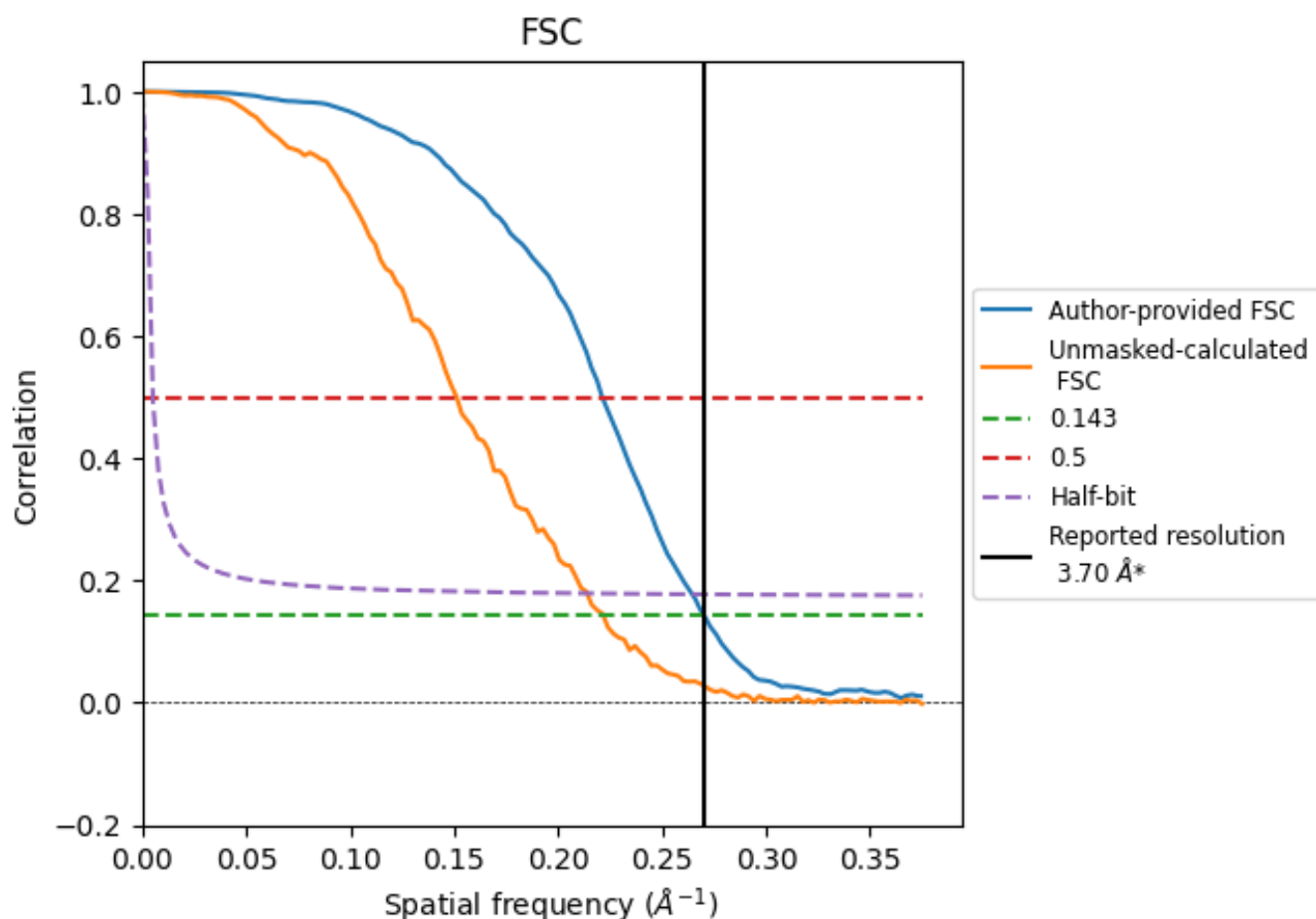


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

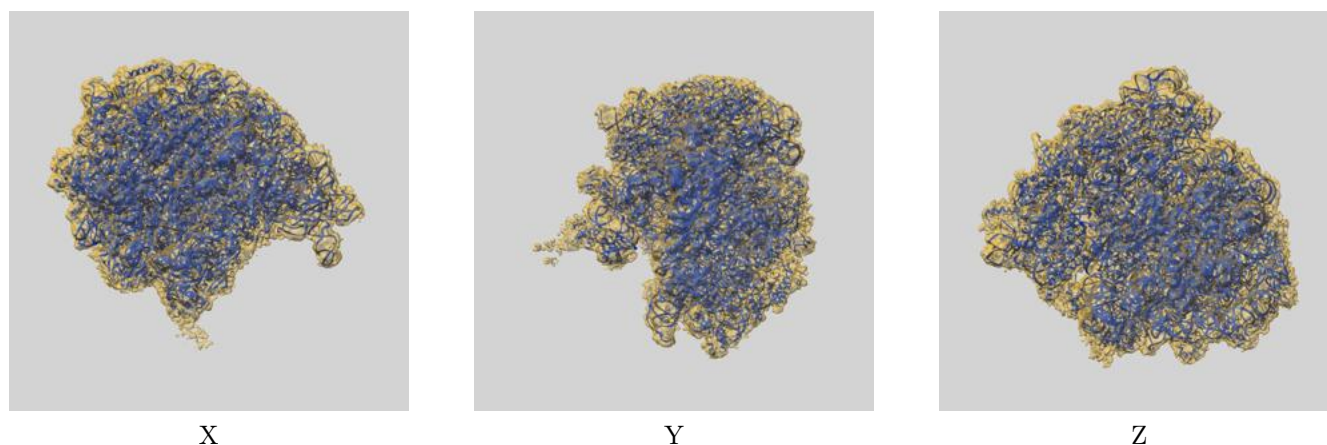
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.52	3.78
Unmasked-calculated*	4.51	6.61	4.67

*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 4.51 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21640 and PDB model 6WDL. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



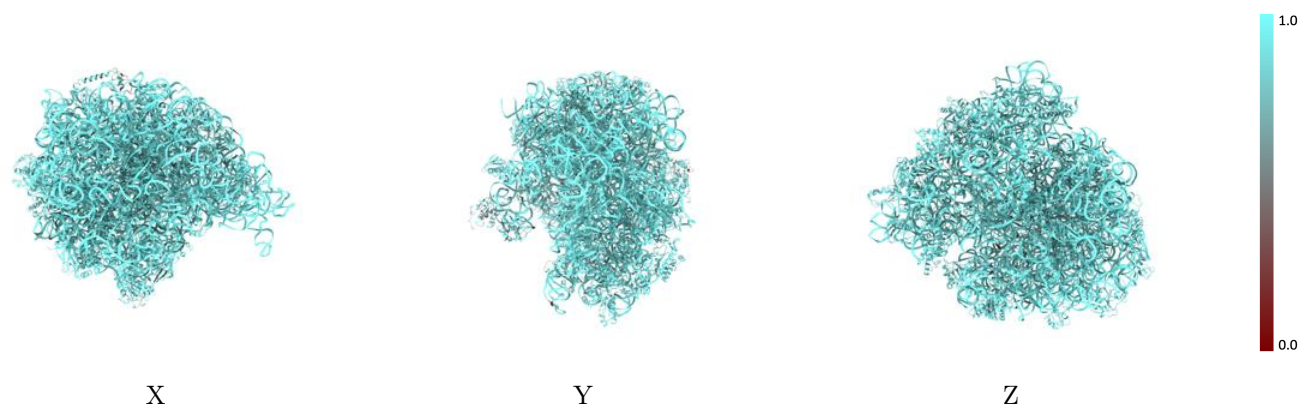
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



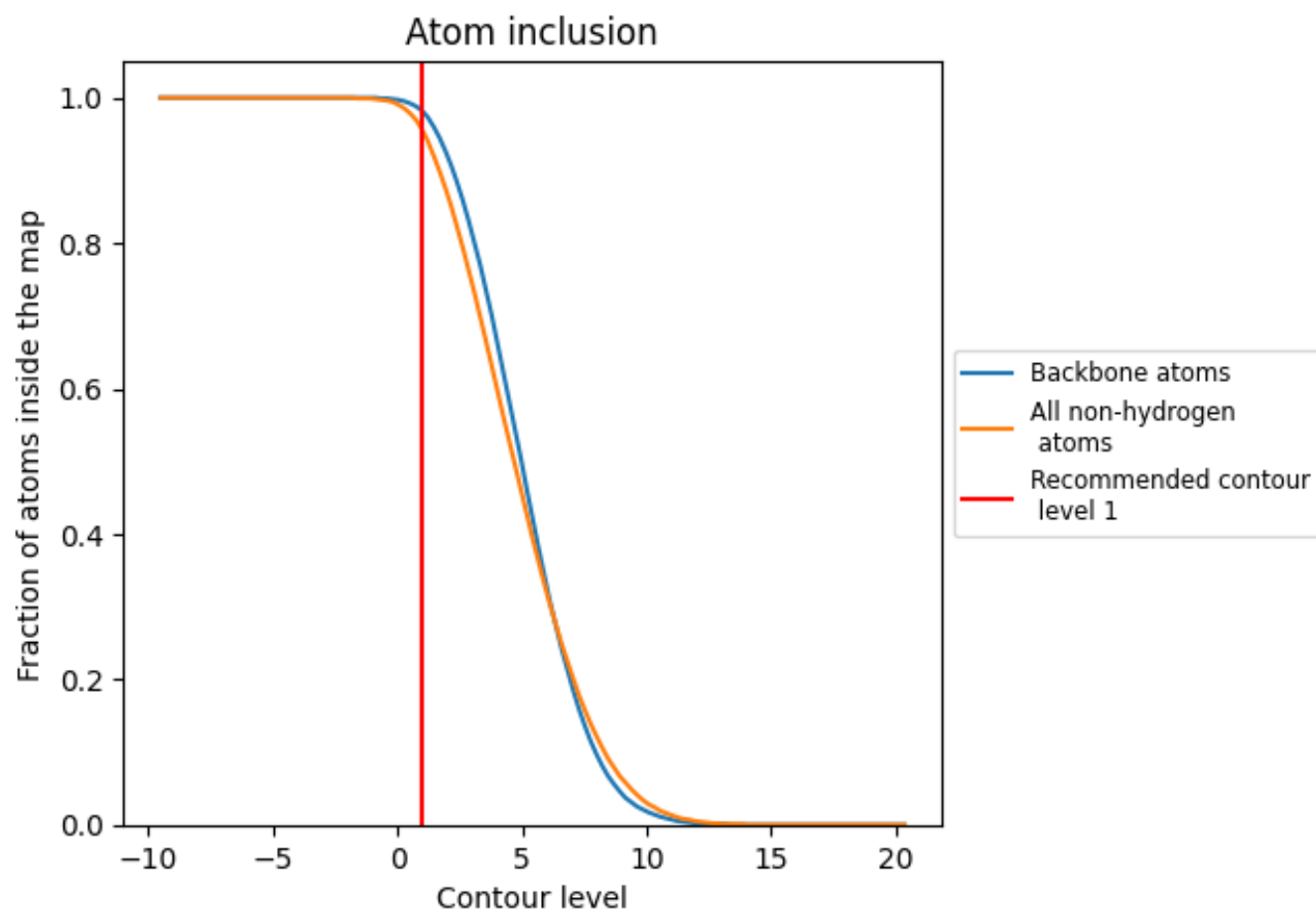
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (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	 0.9560	 0.3480
1	 0.9780	 0.3620
2	 0.9820	 0.3340
3	 0.9750	 0.3330
4	 0.8690	 0.2310
5	 0.9580	 0.2750
6	 0.8350	 0.1260
7	 0.9100	 0.1960
B	 0.9420	 0.4080
C	 0.8900	 0.3680
D	 0.9410	 0.4340
E	 0.9470	 0.4510
F	 0.8120	 0.3780
G	 0.8930	 0.3180
H	 0.9180	 0.3740
I	 0.8210	 0.2640
J	 0.9110	 0.3880
K	 0.9560	 0.3490
L	 0.9350	 0.3190
M	 0.9260	 0.3960
N	 0.9170	 0.3230
O	 0.8700	 0.3240
P	 0.9480	 0.3810
Q	 0.9490	 0.3770
R	 0.9430	 0.3180
S	 0.8990	 0.3650
T	 0.9550	 0.3800
U	 0.8980	 0.3290
V	 0.9450	 0.3730
W	 0.9160	 0.3810
X	 0.9600	 0.3270
Y	 0.9290	 0.3330
Z	 0.8880	 0.3090
a	 0.8740	 0.1620
b	 0.9490	 0.4350



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Chain	Atom inclusion	Q-score
c	 0.9400	 0.4200
d	 0.9380	 0.3820
e	 0.9480	 0.3130
f	 0.9530	 0.3320
g	 0.8330	 0.2700
h	 0.7230	 0.1520
i	 0.7960	 0.1050
j	 0.9470	 0.4270
k	 0.9380	 0.4240
l	 0.9360	 0.4090
m	 0.9220	 0.4160
n	 0.9420	 0.4170
o	 0.9470	 0.3670
p	 0.9440	 0.4010
q	 0.9350	 0.4130
r	 0.9590	 0.4110
s	 0.9160	 0.4210
t	 0.9220	 0.4100
u	 0.9310	 0.3750
v	 0.9570	 0.3990
w	 0.9280	 0.4320
x	 0.9480	 0.4080
y	 0.9210	 0.3300
z	 0.9430	 0.4150