



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 12:04 PM UTC

PDB ID : 6WDD / pdb_00006wdd
EMDB ID : EMD-21632
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure V-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.20 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

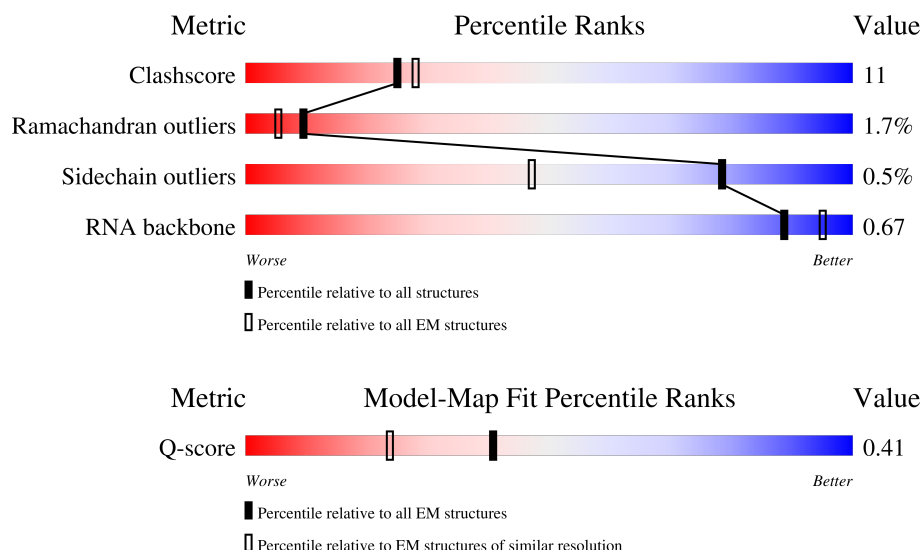
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



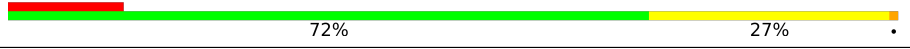
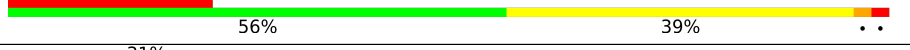
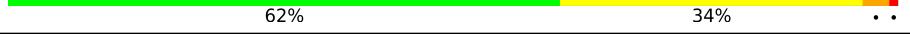
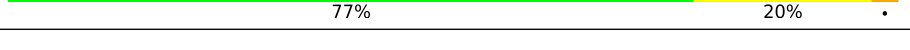
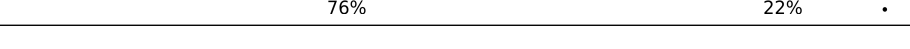
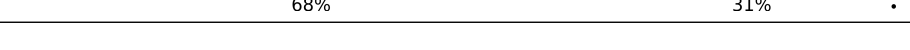
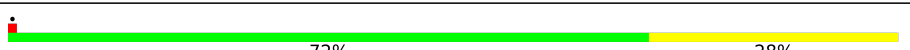
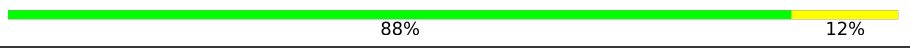
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	

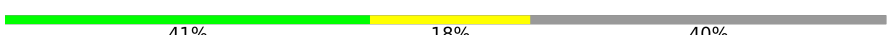
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	49% 46% 5%
55	5	77	53% 42% 5%
55	6	77	60% 36%
56	4	18	6% 67% 33%
57	7	76	62% 29% 9%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 150222 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		

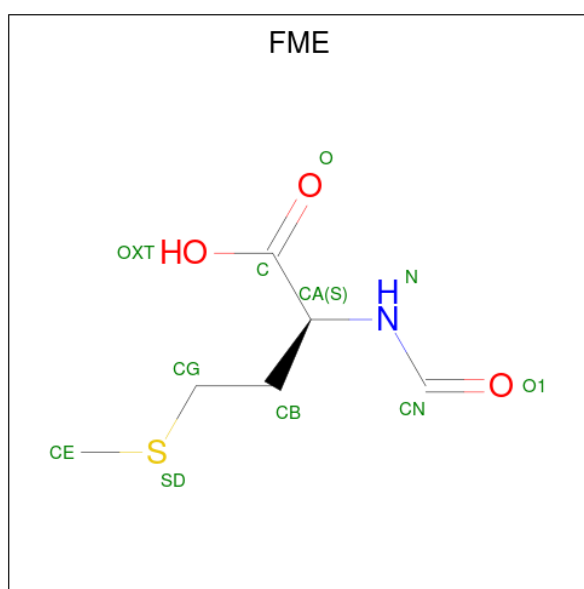
- Molecule 56 is a RNA chain called mRNA.

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

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

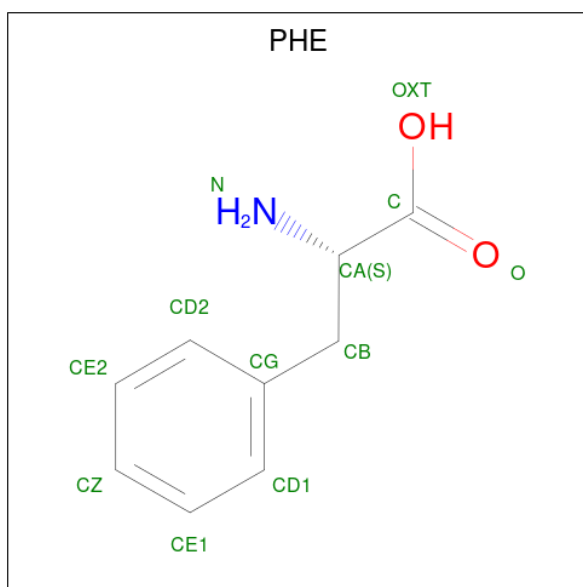
Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

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



Mol	Chain	Residues	Atoms					AltConf
58	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

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

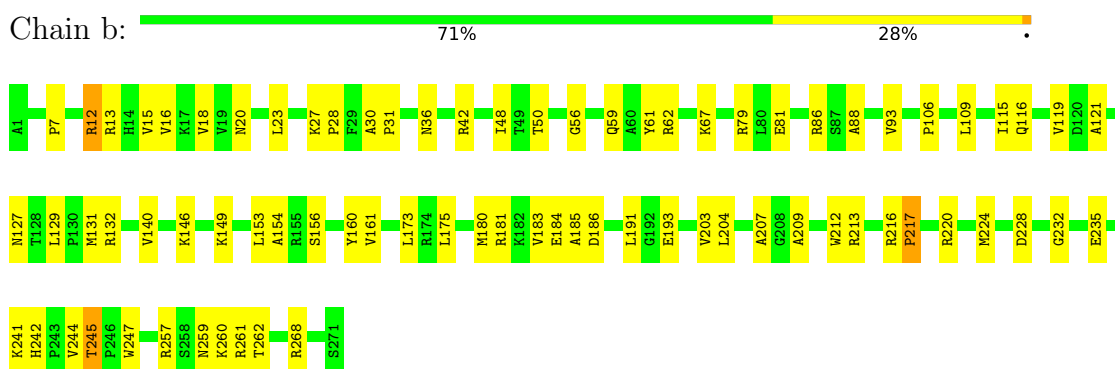


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
59	7	1	11	9	1	1	0

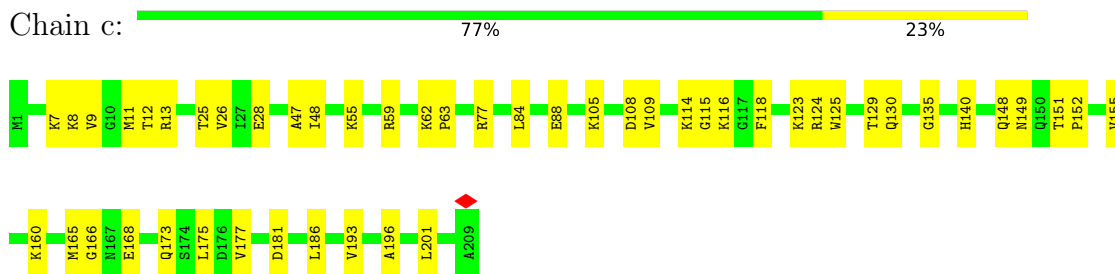
3 Residue-property plots [i](#)

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.

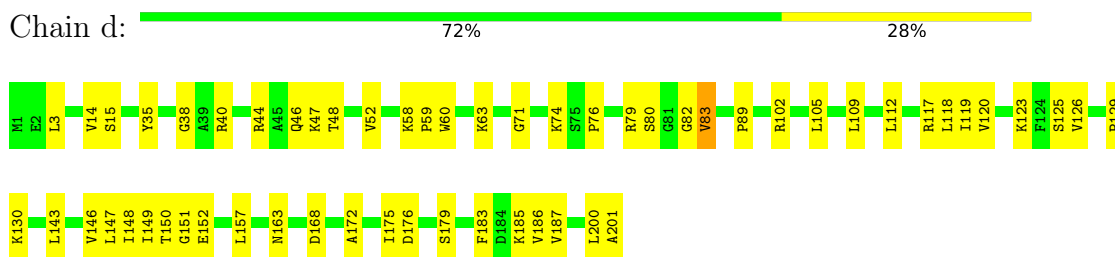
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

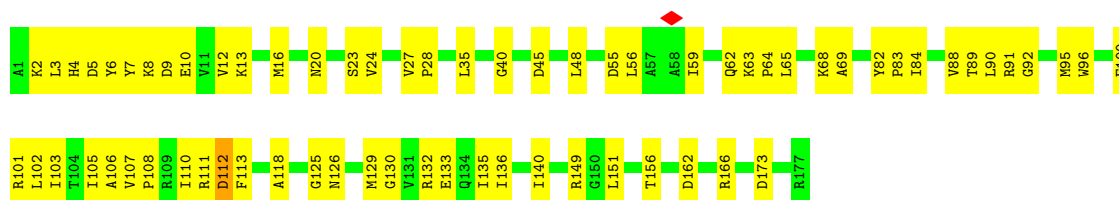


• Molecule 3: 50S ribosomal protein L4

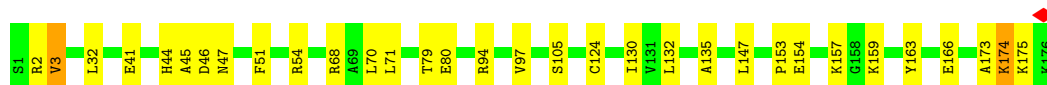
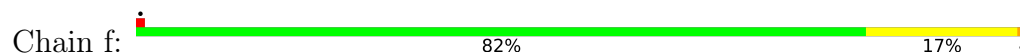


• Molecule 4: 50S ribosomal protein L5

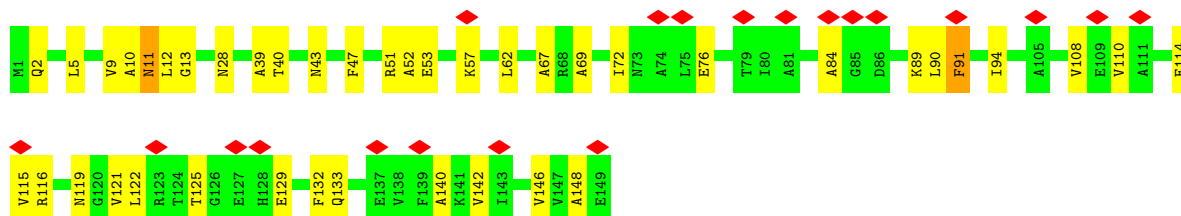
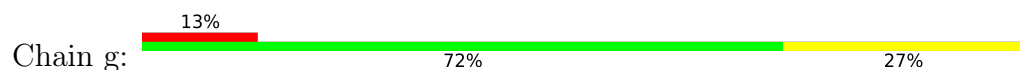




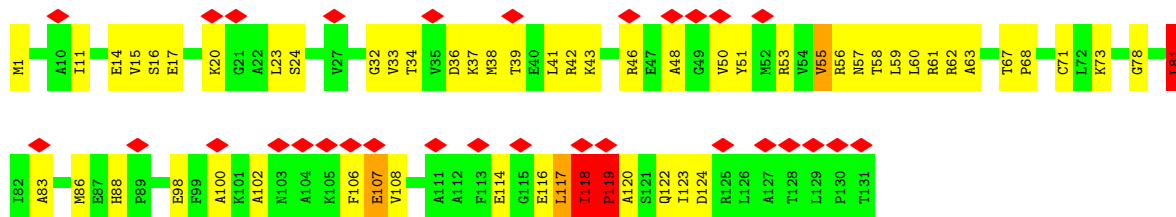
• Molecule 5: 50S ribosomal protein L6



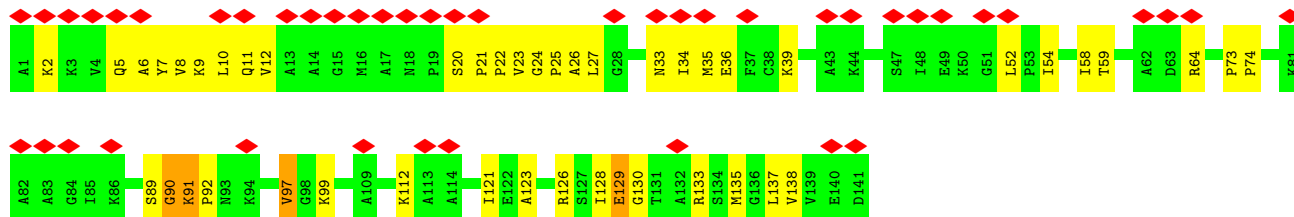
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

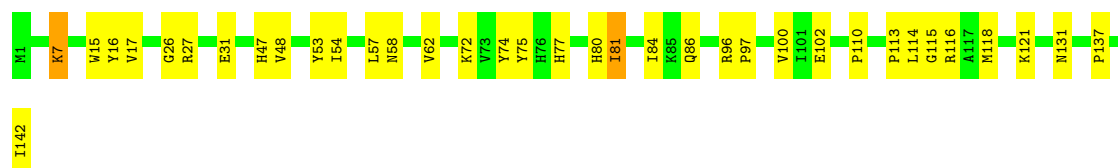


• Molecule 8: 50S ribosomal protein L11



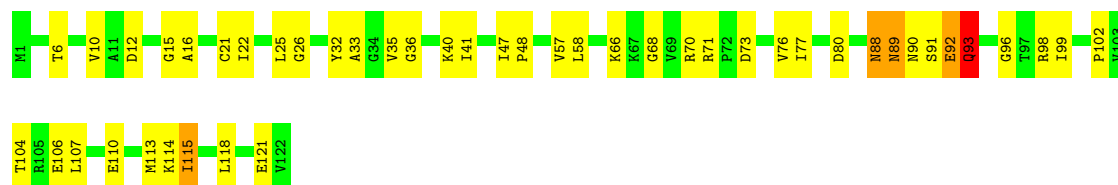
• Molecule 9: 50S ribosomal protein L13

Chain j:  75% 24% .



- Molecule 10: 50S ribosomal protein L14

Chain k:  62% 34% . .



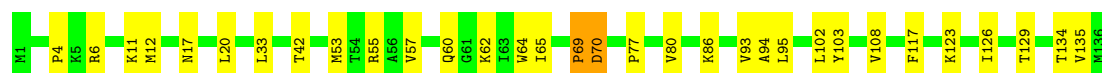
- Molecule 11: 50S ribosomal protein L15

Chain l:  77% 20% .



- Molecule 12: 50S ribosomal protein L16

Chain m:  76% 22% .



- Molecule 13: 50S ribosomal protein L17

Chain n:  68% 31% .



- Molecule 14: 50S ribosomal protein L18

Chain o:  68% 31% .





- Molecule 15: 50S ribosomal protein L19

Chain p: 74% 26%



- Molecule 16: 50S ribosomal protein L20

Chain q: 82% 18%



- Molecule 17: 50S ribosomal protein L21

Chain r: 75% 23%



- Molecule 18: 50S ribosomal protein L22

Chain s: 72% 28%



- Molecule 19: 50S ribosomal protein L23

Chain t: 72% 28%



- Molecule 20: 50S ribosomal protein L24

Chain u: 65% 34%

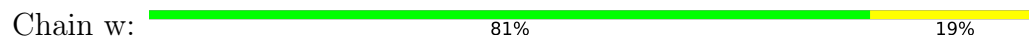


- Molecule 21: 50S ribosomal protein L25

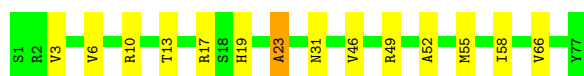
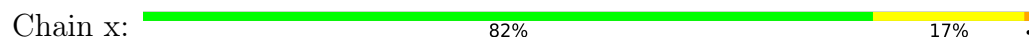
Chain v: 68% 29%



- Molecule 22: 50S ribosomal protein L27



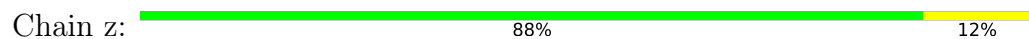
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29



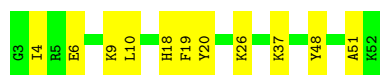
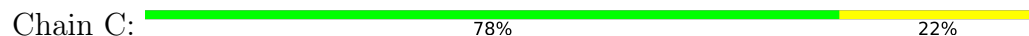
- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33

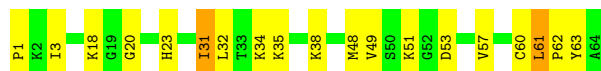


- Molecule 28: 50S ribosomal protein L34

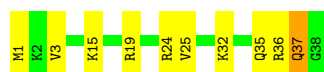




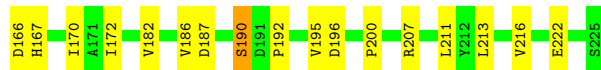
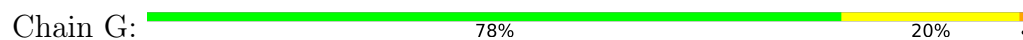
- Molecule 29: 50S ribosomal protein L35



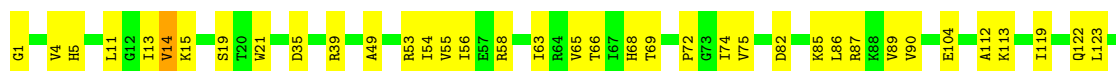
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 30S ribosomal protein S2



- Molecule 32: 30S ribosomal protein S3



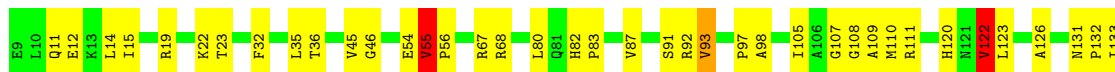
- Molecule 33: 30S ribosomal protein S4





• Molecule 34: 30S ribosomal protein S5

Chain J: 71% 26% ..



• Molecule 35: 30S ribosomal protein S6

Chain K: 53% 43% .



• Molecule 36: 30S ribosomal protein S7

Chain L: 75% 23% .



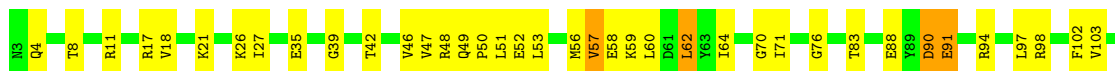
• Molecule 37: 30S ribosomal protein S8

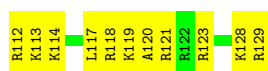
Chain M: 64% 36% .



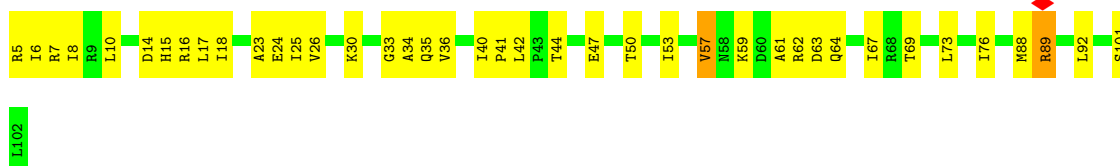
• Molecule 38: 30S ribosomal protein S9

Chain N: 61% 35% .

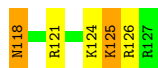
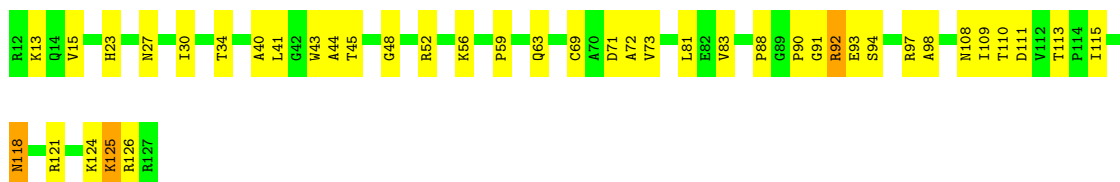




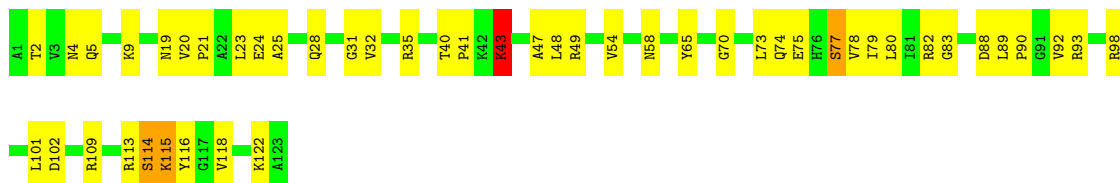
- Molecule 39: 30S ribosomal protein S10



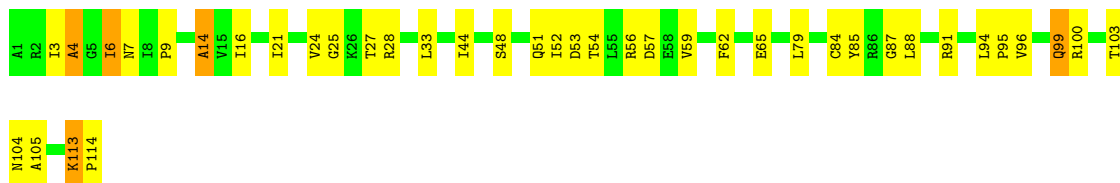
- Molecule 40: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S12

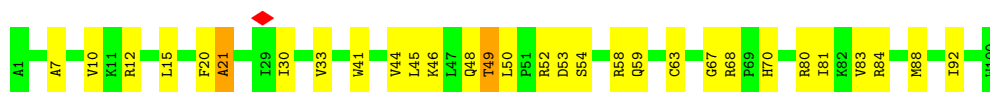


- Molecule 42: 30S ribosomal protein S13



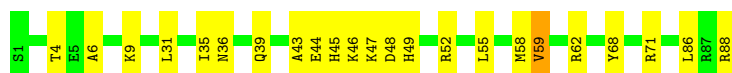
- Molecule 43: 30S ribosomal protein S14





- Molecule 44: 30S ribosomal protein S15

Chain T: 74% 25%



- Molecule 45: 30S ribosomal protein S16

Chain U: 61% 35%



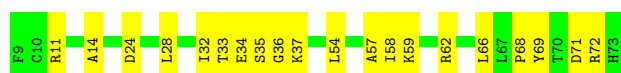
- Molecule 46: 30S ribosomal protein S17

Chain V: 59% 39%



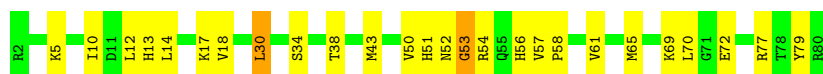
- Molecule 47: 30S ribosomal protein S18

Chain W: 69% 31%



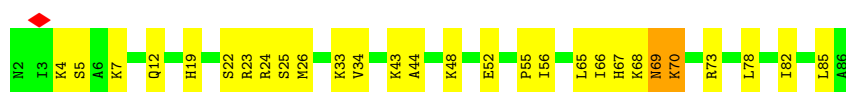
- Molecule 48: 30S ribosomal protein S19

Chain X: 67% 30%



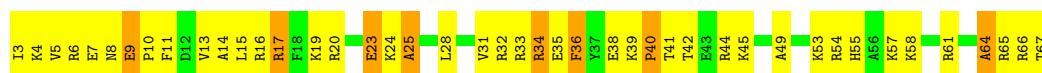
- Molecule 49: 30S ribosomal protein S20

Chain Y: 67% 31%

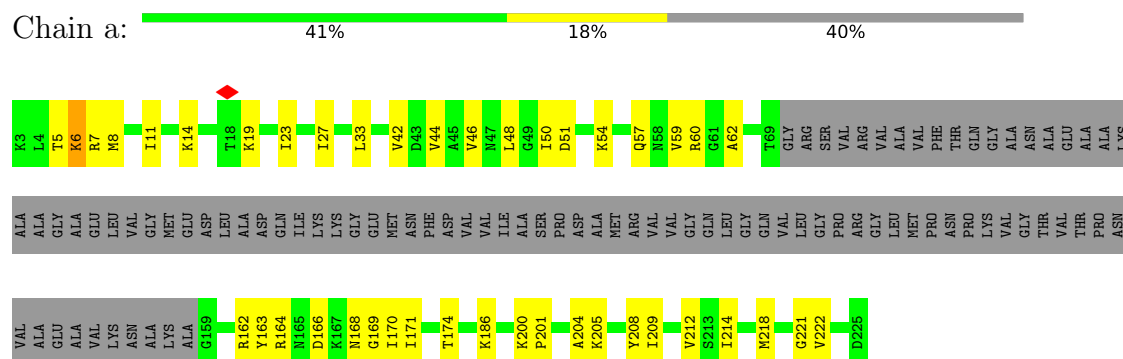


- Molecule 50: 30S ribosomal protein S21

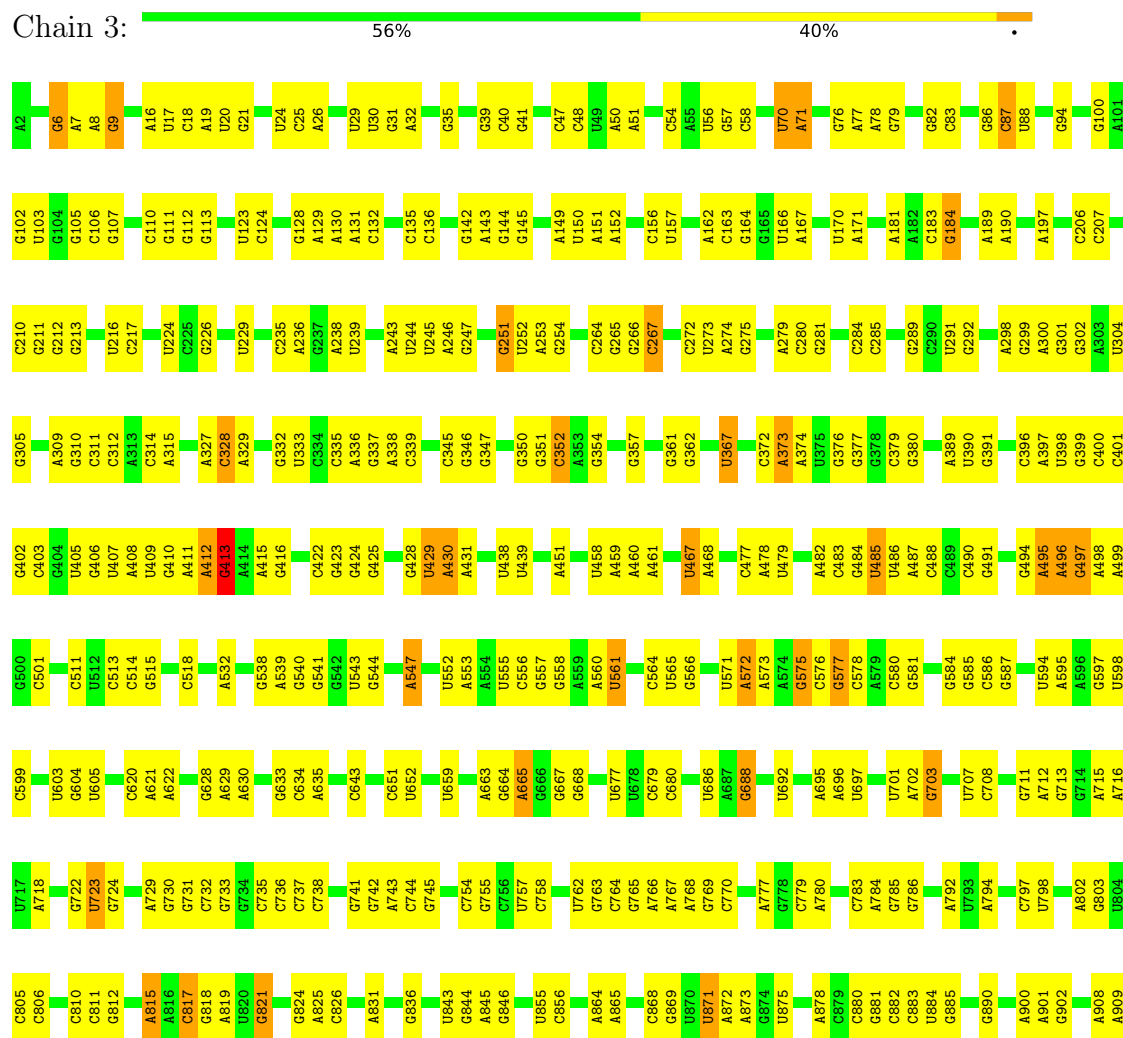
Chain Z: 32% 55% 12%

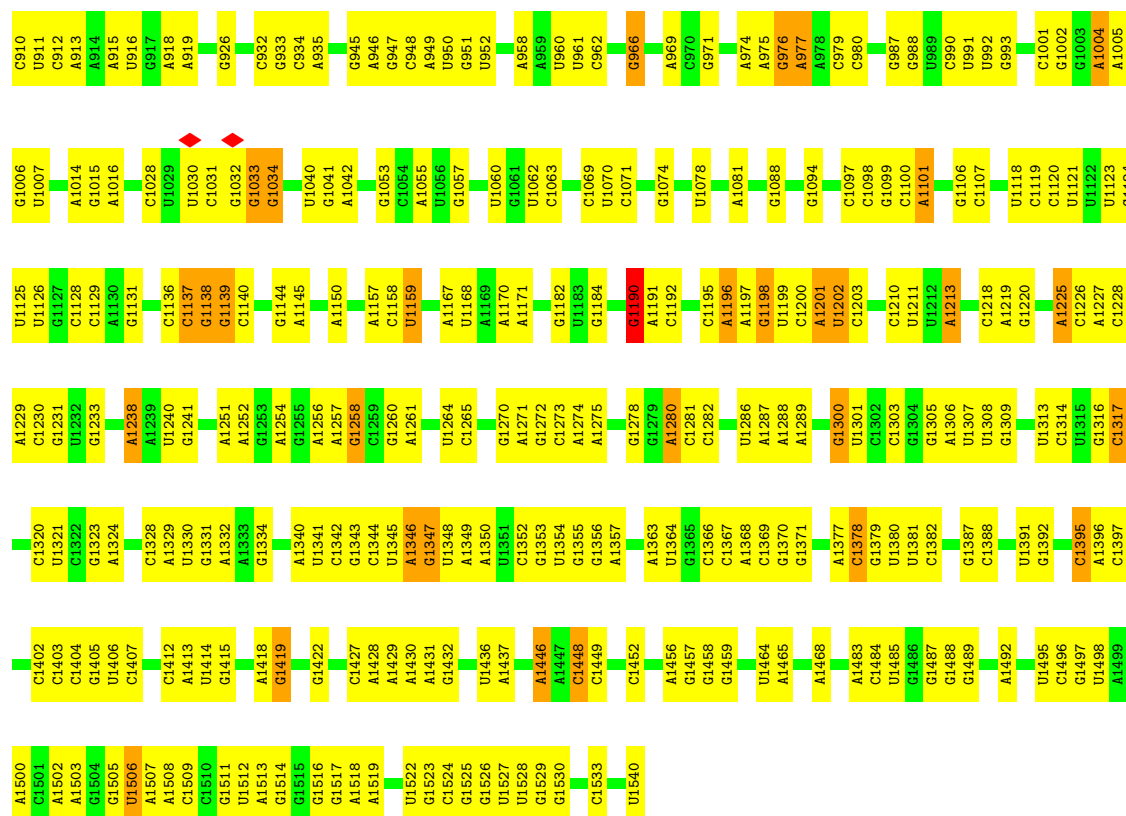


• Molecule 51: 50S ribosomal protein L1



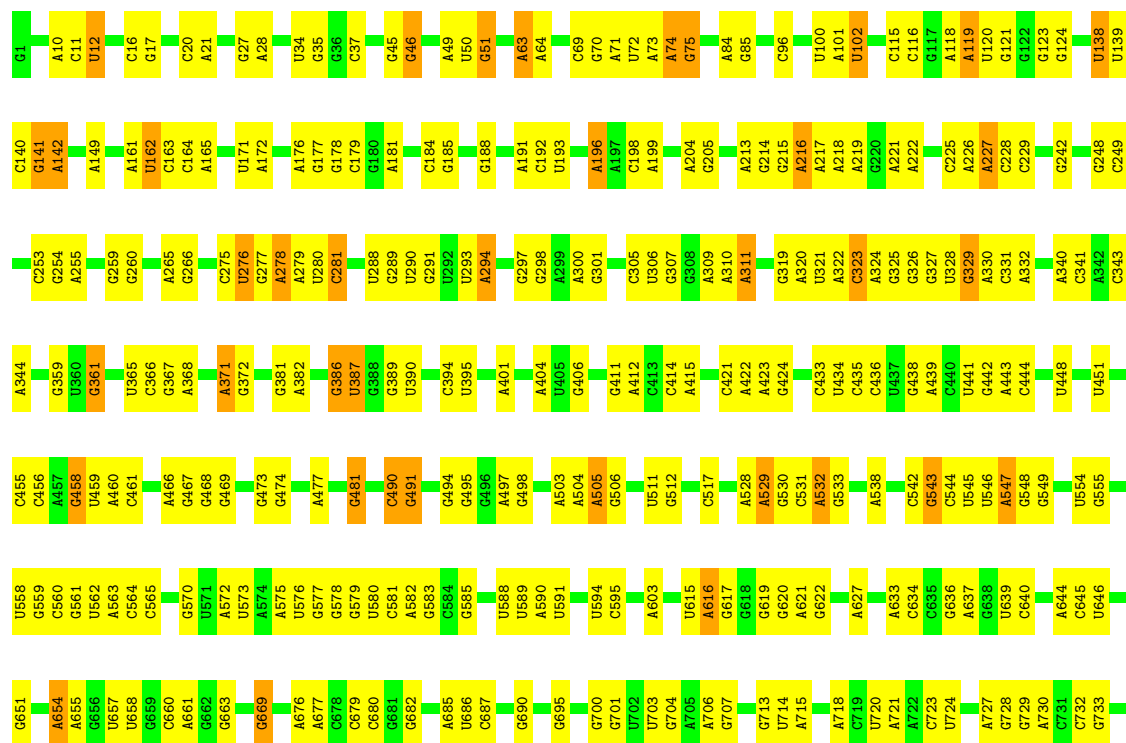
• Molecule 52: 16S ribosomal RNA



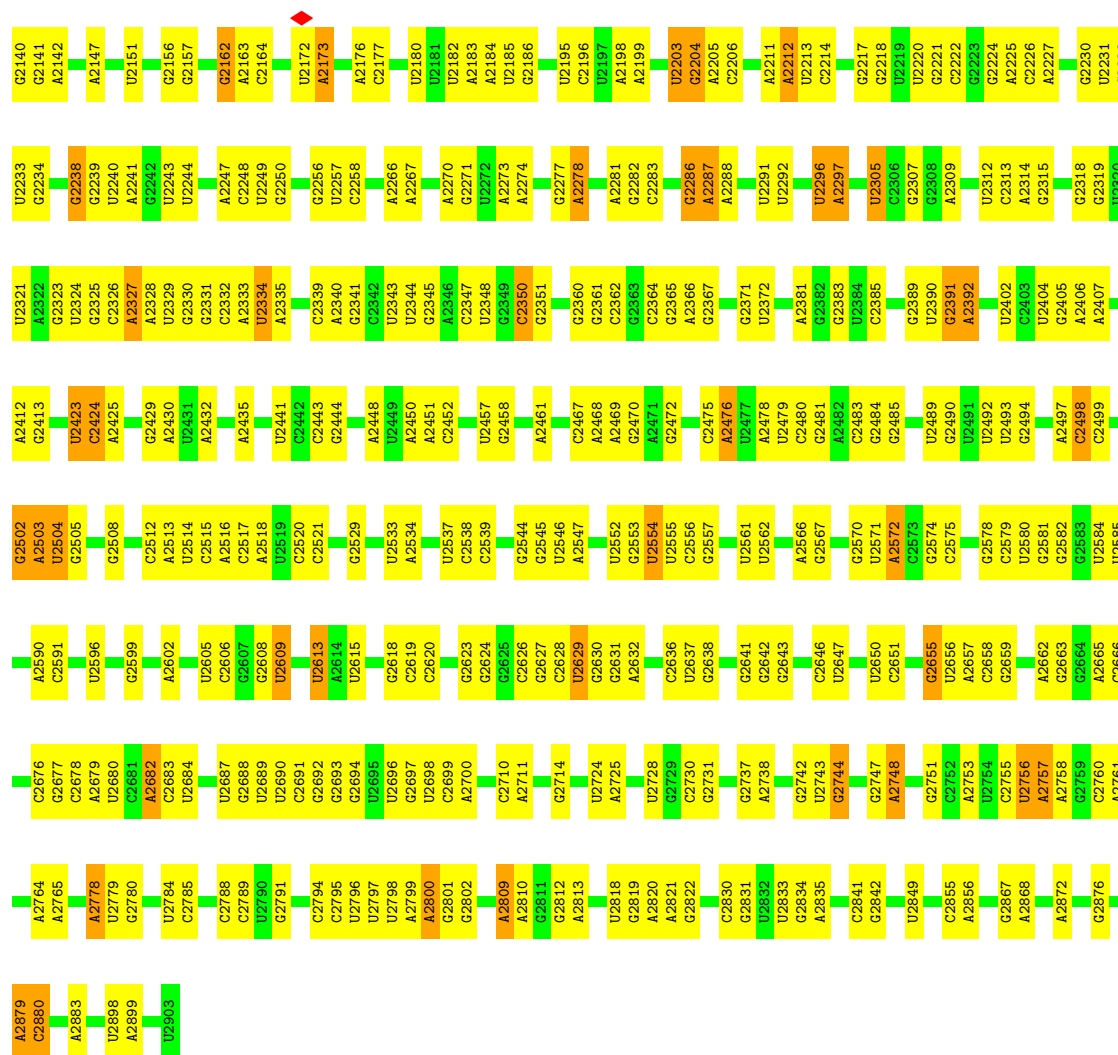


• Molecule 53: 23S ribosomal RNA

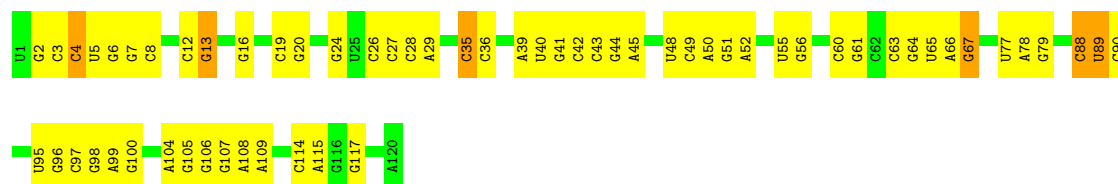
Chain 1: 57% 38% 5%



C2055	C2056	A2059	G2060	A2061	A2062	C2066	G2067	G2068	U2069	A2070	A2071	C2072	C2073	U2074	U2075	A2080	U2081	A2082	G2083	U2086	G2087	A2088	C2096	A2097	U2098	U2106	G2107	G2110	G2111	G2112	U2113	A2114	A2117	U2118	A2119	A2120	C2121	U2122	G2123	G2124	G2125	A2126	G2128	C2129	U2132	G2133	A2134	U2139			
U1963	G1964	C1965	A1966	C1967	G1968	A1969	G1970	C1971	G1972	U1979	G1980	U1991	G1992	U1993	C1997	A1998	C1999	G2000	C2001	U2007	C2008	A2009	G2010	U2011	A2012	U2013	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	C2036	G2040	U2041	A2042	C2043	C2044	C2045	U1955	U1956	C1957	C1958	G1959
A1877	A1885	A1889	A1890	G1891	C1892	C1893	A1900	A1901	C1902	G1903	G1904	C1905	G1906	G1907	C1908	C1909	G1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	A1918	A1919	C1920	G1921	G1922	U1923	C1924	C1925	G1929	G1930	U1931	A1932	G1933	C1934	U1935	A1936	A1937	A1938	U1943	U1944	C1947	G1948	U1955	U1956	C1957	C1958	G1959
A1785	A1786	C1790	A1791	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	G1807	A1808	A1809	A1810	G1811	U1812	G1814	A1815	C1816	G1817	U1818	G1824	U1825	G1826	U1827	G1828	A1829	C1833	U1834	C1837	C1838	G1839	G1846	A1847	U1856	G1857	A1858	U1859	A1860	G1861	G1862	G1863	A1871	A1872	G1873	C1874	G1875	A1876		
U1683	G1684	A1689	A1691	G1695	G1696	G1699	C1704	A1705	U1715	U1720	G1721	U1729	C1730	U1736	G1737	C1738	A1739	G1740	U1636	A1637	C1638	C1639	G1645	U1646	U1647	U1648	G1651	A1654	A1655	C1656	U1657	C1658	U1662	G1663	G1666	G1667	A1672	G1673	G1674	C1675	A1676	A1677	A1678	U1781	U1782	C1783	A1784				
G1568	A1569	A1570	A1571	G1581	G1587	C1592	A1593	U1594	C1595	U1599	C1600	A1603	C1607	A1608	A1609	C1611	A1616	U1636	A1637	C1638	C1639	G1645	U1646	U1647	U1648	G1651	A1654	A1655	C1656	U1657	C1658	U1662	G1663	G1666	G1667	A1672	G1673	G1674	C1675	A1676	A1677	A1678	U1781	U1782	C1783	A1784					
U1468	A1469	A1470	A1471	G1475	U1476	G1479	C1480	U1481	G1482	A1490	G1491	A1494	C1498	U1506	C1507	A1508	A1509	G1510	A1515	G1516	G1517	C1417	U1418	A1419	A1420	G1421	A1427	G1430	A1431	A1434	G1435	C1436	C1437	U1438	G1441	U1442	U1443	G1444	C1447	G1448	C1451	U1452	U1453	C1454	A1455	C1456	G1457				
C1363	G1364	A1365	A1366	G1368	G1369	C1370	G1371	A1373	A1378	U1379	G1380	A1383	A1384	A1385	C1386	U1394	G1401	U1402	U1415	G1416	C1417	G1418	A1419	A1420	G1421	A1427	G1430	A1431	A1434	G1435	C1436	C1437	U1438	G1441	U1442	U1443	G1444	C1447	G1448	C1451	U1452	U1453	C1454	A1455	C1456	G1457					
G1286	U1287	A1288	G1289	G1290	G1291	A1292	G1293	G1294	G1295	G1296	C1297	C1298	G1299	A1300	A1301	A1302	G1309	C1319	C1320	U1326	A1327	A1328	C1329	C1330	G1331	G1332	U1340	G1341	A1342	G1343	U1344	C1345	C1348	C1349	A1354	G1355	G1356	C1357	G1358	A1359	C1360	G1361	C1362								
U1132	A1133	A1134	C1135	G1138	C1139	U1141	A1142	A1143	G1149	C1150	A1151	C1152	C1153	G1157	C1161	G1162	U1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1190	G1191	U1199	C1200	G1206	G1210	G1211	G1212	A1213	G1236	A1237	G1238	G1250	C1251	A1252	A1253	G1256					
C1045	A1046	A1047	A1048	C1053	A1054	G1055	U1060	U1061	G1062	U1065	U1066	A1070	G1071	A1077	U1078	C1079	A1080	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	U1094	A1095	A1098	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	U1113	C1114	G1115	G1122	G1125	U1130	G1131			
G940	A941	G942	A943	C946	A947	C948	G949	G953	G954	U955	C961	G962	U967	C968	G969	U970	A972	A973	G974	A975	A983	A984	C985	C986	C987	A988	G989	A990	C995	A996	G997	A1001	G1002	U1012	C1013	U1019	A1020	A1021	G1022	U1023	G1026	A1027	A1028	U1033	A1040						
C737	G738	A739	A742	A743	U744	G745	U746	C747	G748	A751	A752	G759	G760	A761	G762	G763	A764	C765	U766	G767	U768	U769	G770	G771	G774	G775	G776	G780	A781	A782	A783	G784	G785	C786	C787	A788	G799	A800	G801	A802	G805	C806	U807	G808	C812	U813	C814	C817	G818	A819	

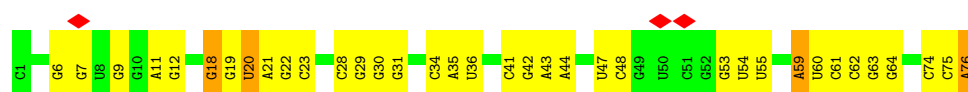


Chain 2: 49% 46% 5%



• Molecule 55: tRNA^{fMet}

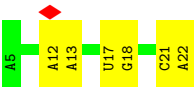
Chain 5: 53% 42% 5%



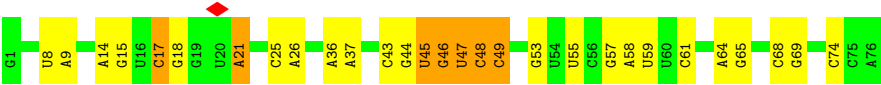
• Molecule 55: tRNA^{fMet}



• Molecule 56: mRNA



• Molecule 57: tRNAPhe



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32253	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	28.501	Depositor
Minimum map value	-14.672	Depositor
Average map value	0.119	Depositor
Map value standard deviation	1.117	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.30	0/2122	0.91	8/2852 (0.3%)
2	c	0.29	0/1586	0.82	0/2134
3	d	0.29	0/1571	0.81	0/2113
4	e	0.34	0/1435	0.82	0/1926
5	f	0.31	0/1343	0.84	2/1816 (0.1%)
6	g	0.32	0/1122	0.93	4/1515 (0.3%)
7	h	0.37	0/1002	1.08	9/1350 (0.7%)
8	i	0.38	0/1046	0.99	5/1410 (0.4%)
9	j	0.29	0/1152	0.90	5/1551 (0.3%)
10	k	0.28	0/948	0.95	7/1268 (0.6%)
11	l	0.30	0/1054	0.96	1/1403 (0.1%)
12	m	0.30	0/1093	0.85	1/1460 (0.1%)
13	n	0.30	0/974	0.93	5/1301 (0.4%)
14	o	0.30	0/902	0.90	3/1209 (0.2%)
15	p	0.30	0/929	0.80	1/1242 (0.1%)
16	q	0.29	0/960	0.88	3/1278 (0.2%)
17	r	0.31	0/829	0.80	0/1107
18	s	0.28	0/864	0.86	1/1156 (0.1%)
19	t	0.29	0/745	0.80	0/994
20	u	0.31	0/788	0.88	1/1051 (0.1%)
21	v	0.29	0/766	0.91	5/1025 (0.5%)
22	w	0.28	0/582	0.82	0/769
23	x	0.27	0/635	0.91	1/848 (0.1%)
24	y	0.27	0/510	0.83	0/677
25	z	0.30	0/453	0.77	0/605
26	B	0.28	0/450	0.78	1/599 (0.2%)
27	C	0.32	0/417	0.76	0/554
28	D	0.32	0/380	0.89	1/498 (0.2%)
29	E	0.32	0/513	0.98	2/676 (0.3%)
30	F	0.31	0/303	0.88	0/397
31	G	0.30	0/1788	0.87	8/2408 (0.3%)
32	H	0.31	0/1652	0.84	2/2225 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.31	0/1665	0.91	5/2227 (0.2%)
34	J	0.36	1/1170 (0.1%)	0.86	3/1573 (0.2%)
35	K	0.33	0/836	0.91	3/1128 (0.3%)
36	L	0.31	0/1196	0.92	2/1602 (0.1%)
37	M	0.31	0/989	0.93	4/1326 (0.3%)
38	N	0.30	0/1034	0.91	4/1375 (0.3%)
39	O	0.34	0/797	0.89	0/1077
40	P	0.32	0/886	0.98	2/1195 (0.2%)
41	Q	0.32	0/969	1.00	7/1300 (0.5%)
42	R	0.32	0/893	0.89	1/1193 (0.1%)
43	S	0.30	0/817	0.89	3/1088 (0.3%)
44	T	0.30	0/722	0.91	3/964 (0.3%)
45	U	0.33	0/659	0.91	3/884 (0.3%)
46	V	0.30	0/658	0.86	2/881 (0.2%)
47	W	0.31	0/545	0.91	1/731 (0.1%)
48	X	0.33	0/653	0.90	1/877 (0.1%)
49	Y	0.30	0/671	0.99	6/888 (0.7%)
50	Z	0.33	0/551	1.01	3/728 (0.4%)
51	a	0.33	0/1034	0.85	1/1387 (0.1%)
52	3	0.42	0/36963	0.48	3/57662 (0.0%)
53	1	0.40	0/69796	0.48	3/108888 (0.0%)
54	2	0.42	0/2872	0.48	0/4479
55	5	0.42	0/1832	0.46	0/2855
55	6	0.42	0/1832	0.48	0/2855
56	4	0.42	0/436	0.46	0/679
57	7	0.41	0/1809	0.46	0/2819
All	All	0.38	1/163199 (0.0%)	0.61	136/244078 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	J	55	VAL	CA-CB	5.58	1.57	1.54

All (136) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	61	LEU	CA-C-N	8.57	127.89	118.97
29	E	61	LEU	C-N-CA	8.57	127.89	118.97
37	M	67	GLY	N-CA-C	-8.47	102.01	113.37
43	S	49	THR	N-CA-C	-8.35	101.71	112.23
49	Y	5	SER	N-CA-C	-8.18	102.85	112.92
44	T	68	TYR	N-CA-C	-8.10	102.02	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	h	50	VAL	N-CA-C	7.66	118.25	110.82
6	g	10	ALA	N-CA-C	7.41	121.17	109.39
20	u	96	LYS	N-CA-C	-7.41	99.56	110.52
50	Z	58	LYS	N-CA-C	-7.32	103.01	112.23
41	Q	114	SER	N-CA-C	-7.25	103.07	110.97
8	i	91	LYS	CA-C-N	7.22	126.75	119.24
8	i	91	LYS	C-N-CA	7.22	126.75	119.24
49	Y	69	ASN	N-CA-C	-7.16	104.36	113.23
40	P	97	ARG	N-CA-C	-7.06	103.00	111.69
11	l	95	LEU	N-CA-C	-6.96	103.77	111.36
7	h	42	ARG	N-CA-C	-6.92	103.52	112.23
10	k	88	ASN	N-CA-C	6.90	120.27	110.68
33	I	165	GLU	N-CA-C	6.84	118.53	111.14
38	N	53	LEU	N-CA-C	-6.82	104.93	113.18
33	I	204	SER	N-CA-C	-6.81	103.94	111.36
21	v	80	HIS	N-CA-C	-6.80	101.49	109.93
45	U	78	VAL	N-CA-C	-6.68	103.21	112.50
31	G	45	THR	N-CA-C	6.64	118.17	111.07
7	h	55	VAL	N-CA-C	6.62	117.97	109.30
1	b	12	ARG	N-CA-C	-6.54	103.81	113.61
7	h	78	GLY	CA-C-N	6.50	127.96	119.84
7	h	78	GLY	C-N-CA	6.50	127.96	119.84
12	m	60	GLN	N-CA-C	6.49	118.39	110.41
53	l	1130	U	C2'-C3'-O3'	6.42	119.13	109.50
9	j	62	VAL	N-CA-C	-6.39	103.08	110.05
41	Q	43	LYS	N-CA-C	6.38	123.91	109.81
43	S	50	LEU	N-CA-C	-6.31	102.11	109.93
38	N	88	GLU	N-CA-C	-6.30	105.56	113.18
21	v	22	ALA	N-CA-C	-6.26	105.21	112.92
1	b	28	PRO	N-CA-C	6.25	120.27	111.33
46	V	16	MET	N-CA-C	6.24	120.17	111.56
7	h	119	PRO	N-CA-C	-6.24	105.87	114.98
5	f	3	VAL	N-CA-C	-6.21	106.75	112.96
9	j	96	ARG	CA-C-N	6.19	125.81	119.56
9	j	96	ARG	C-N-CA	6.19	125.81	119.56
50	Z	17	ARG	N-CA-C	-6.18	105.74	113.28
41	Q	74	GLN	N-CA-C	6.14	117.45	107.32
7	h	100	ALA	N-CA-C	-6.12	104.73	111.82
44	T	43	ALA	N-CA-C	-6.08	104.77	111.82
44	T	59	VAL	N-CA-C	-6.08	104.37	111.00
8	i	121	ILE	N-CA-C	6.06	116.80	110.62
14	o	20	GLU	N-CA-C	-6.06	104.59	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	K	68	GLN	N-CA-C	6.03	117.85	111.28
36	L	68	VAL	N-CA-C	-6.00	107.41	113.47
42	R	113	LYS	N-CA-C	6.00	123.07	109.81
41	Q	115	LYS	N-CA-C	-5.98	102.48	110.55
35	K	90	MET	N-CA-C	5.91	116.23	108.07
49	Y	7	LYS	N-CA-C	-5.89	106.10	113.28
6	g	115	VAL	N-CA-C	5.88	116.59	108.84
10	k	115	ILE	N-CA-C	5.84	116.58	110.62
45	U	33	ILE	N-CA-C	-5.75	104.92	110.72
34	J	152	VAL	N-CA-C	-5.74	107.17	113.43
16	q	3	VAL	N-CA-C	5.72	116.82	108.58
34	J	120	HIS	N-CA-C	-5.71	103.56	110.88
7	h	117	LEU	N-CA-C	5.70	118.85	109.85
51	a	6	LYS	N-CA-C	5.68	117.16	110.97
1	b	213	ARG	N-CA-C	-5.67	105.86	112.89
5	f	47	ASN	N-CA-C	-5.66	106.37	113.28
34	J	122	VAL	N-CA-C	5.62	121.02	109.34
16	q	50	ARG	N-CA-C	-5.60	106.49	113.55
10	k	32	TYR	N-CA-C	5.59	119.09	110.42
8	i	97	VAL	N-CA-C	5.59	118.03	111.05
38	N	62	LEU	N-CA-C	5.57	117.48	108.34
7	h	15	VAL	N-CA-C	-5.56	105.11	110.72
32	H	89	VAL	N-CA-C	5.55	116.28	110.62
52	3	1190	G	C2'-C3'-O3'	5.52	117.78	109.50
28	D	29	GLN	N-CA-C	-5.52	105.28	112.23
38	N	90	ASP	N-CA-C	5.49	122.50	110.80
43	S	21	ALA	N-CA-C	-5.49	105.17	113.51
47	W	69	TYR	N-CA-C	-5.49	105.22	111.14
41	Q	25	ALA	N-CA-C	5.47	119.25	111.92
23	x	23	ALA	N-CA-C	5.46	117.36	108.63
9	j	7	LYS	CA-C-N	5.42	126.62	119.84
9	j	7	LYS	C-N-CA	5.42	126.62	119.84
31	G	23	ASN	CA-C-N	5.41	125.12	119.82
31	G	23	ASN	C-N-CA	5.41	125.12	119.82
53	1	1020	A	C2'-C3'-O3'	5.40	117.60	109.50
13	n	67	PHE	N-CA-C	-5.38	106.85	113.41
21	v	21	ARG	N-CA-C	-5.37	106.69	113.18
45	U	17	TYR	N-CA-C	5.37	117.38	108.20
33	I	34	GLU	N-CA-C	5.34	122.17	110.80
31	G	167	HIS	N-CA-C	-5.33	106.77	113.28
31	G	144	GLU	N-CA-C	-5.33	105.51	112.23
36	L	142	ARG	N-CA-C	-5.32	106.77	113.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	q	70	GLN	N-CA-C	-5.31	106.30	112.89
52	3	1300	G	N9-C1'-C2'	5.31	119.96	112.00
1	b	27	LYS	CA-C-N	5.29	126.04	120.11
1	b	27	LYS	C-N-CA	5.29	126.04	120.11
46	V	68	LYS	N-CA-C	-5.28	105.64	111.71
49	Y	70	LYS	N-CA-C	-5.27	105.58	112.23
37	M	55	LYS	CA-C-N	5.27	125.57	119.93
37	M	55	LYS	C-N-CA	5.27	125.57	119.93
50	Z	55	HIS	N-CA-C	-5.25	106.72	113.23
41	Q	9	LYS	CA-C-N	5.25	126.40	119.84
41	Q	9	LYS	C-N-CA	5.25	126.40	119.84
14	o	41	ALA	CA-C-N	5.23	124.95	119.82
14	o	41	ALA	C-N-CA	5.23	124.95	119.82
33	I	146	GLU	N-CA-C	5.22	117.65	111.33
1	b	67	LYS	N-CA-C	5.22	116.97	111.28
33	I	77	GLU	N-CA-C	-5.22	105.67	111.36
21	v	48	MET	N-CA-C	-5.21	105.66	112.23
6	g	91	PHE	N-CA-C	-5.19	105.80	111.82
26	B	9	ARG	N-CA-C	-5.18	105.70	112.23
8	i	129	GLU	N-CA-C	-5.17	105.83	111.82
18	s	91	GLY	N-CA-C	5.16	121.98	115.42
31	G	190	SER	N-CA-C	5.16	117.47	110.35
37	M	28	SER	N-CA-C	5.15	116.75	110.41
13	n	48	VAL	N-CA-C	5.15	115.37	110.53
31	G	222	GLU	N-CA-C	-5.15	105.74	112.23
40	P	94	SER	N-CA-C	-5.14	106.96	113.43
31	G	111	LYS	N-CA-C	-5.14	105.86	111.82
10	k	107	LEU	N-CA-C	-5.13	106.87	113.23
10	k	33	ALA	N-CA-C	-5.13	102.19	110.14
13	n	53	THR	N-CA-C	-5.13	105.77	112.23
48	X	30	LEU	N-CA-C	5.12	117.59	109.96
13	n	71	ARG	N-CA-C	5.11	118.49	111.54
10	k	93	GLN	CA-C-N	5.11	125.11	119.90
10	k	93	GLN	C-N-CA	5.11	125.11	119.90
35	K	69	GLU	N-CA-C	5.10	116.64	111.14
13	n	79	LEU	N-CA-C	-5.09	102.22	110.32
6	g	67	ALA	N-CA-C	-5.09	105.81	111.36
53	1	1818	U	N1-C1'-C2'	5.08	119.62	112.00
52	3	413	G	N9-C1'-C2'	5.08	119.61	112.00
1	b	131	MET	N-CA-C	5.07	119.09	113.01
21	v	54	ALA	N-CA-C	5.07	116.80	111.28
1	b	245	THR	N-CA-C	-5.06	102.68	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	H	14	VAL	N-CA-C	5.04	116.35	112.12
49	Y	82	ILE	N-CA-C	5.03	115.80	110.72
49	Y	4	LYS	N-CA-C	-5.02	102.12	108.45
15	p	15	ASP	N-CA-C	5.01	117.69	108.58

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	59	0
2	c	1565	0	1616	34	0
3	d	1552	0	1619	46	0
4	e	1411	0	1447	62	0
5	f	1323	0	1374	23	0
6	g	1111	0	1148	27	0
7	h	989	0	1025	58	0
8	i	1032	0	1088	43	0
9	j	1129	0	1162	25	0
10	k	939	0	1012	38	0
11	l	1045	0	1117	21	0
12	m	1074	0	1157	23	0
13	n	961	0	1000	23	0
14	o	892	0	923	29	0
15	p	917	0	965	25	0
16	q	947	0	1022	16	0
17	r	816	0	839	20	0
18	s	857	0	922	21	0
19	t	739	0	807	23	0
20	u	780	0	834	21	0
21	v	753	0	780	18	0
22	w	575	0	592	11	0
23	x	625	0	655	10	0
24	y	509	0	543	17	0
25	z	449	0	491	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	B	444	0	461	14	0
27	C	410	0	440	9	0
28	D	377	0	418	20	0
29	E	504	0	574	18	0
30	F	302	0	343	12	0
31	G	1757	0	1787	30	0
32	H	1625	0	1699	44	0
33	I	1643	0	1710	46	0
34	J	1157	0	1199	34	0
35	K	818	0	808	36	0
36	L	1182	0	1240	29	0
37	M	979	0	1034	32	0
38	N	1022	0	1070	41	0
39	O	787	0	828	27	0
40	P	870	0	878	31	0
41	Q	955	0	1019	35	0
42	R	884	0	944	46	0
43	S	805	0	847	26	0
44	T	714	0	737	18	0
45	U	649	0	666	31	0
46	V	649	0	691	26	0
47	W	536	0	552	17	0
48	X	638	0	665	17	0
49	Y	665	0	714	20	0
50	Z	545	0	579	41	0
51	a	1027	0	1092	30	0
52	3	33012	0	16618	556	0
53	1	62317	0	31346	904	0
54	2	2568	0	1303	59	0
55	5	1640	0	836	23	0
55	6	1640	0	837	22	0
56	4	388	0	196	5	0
57	7	1619	0	821	23	0
58	5	10	0	10	0	0
59	7	11	0	8	1	0
All	All	150222	0	101265	2648	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (2648) 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'	1.19	1.16
7:h:73:LYS:HE2	7:h:120:ALA:HA	1.36	1.06
53:1:2432:A:H1'	55:6:75:C:H5'	1.39	1.05
12:m:12:MET:HA	53:1:910:A:H62	1.22	1.02
36:L:4:ARG:H	36:L:4:ARG:HD2	1.21	1.02
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.40	1.01
30:F:32:LYS:HE3	53:1:2478:A:H5'	1.44	0.98
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.29	0.96
53:1:2277:G:H2'	53:1:2278:A:H5''	1.48	0.96
13:n:45:ARG:HD3	13:n:97:ILE:HD11	1.46	0.96
45:U:28:ARG:HH22	52:3:390:U:H4'	1.31	0.95
52:3:112:G:H21	52:3:354:G:H5'	1.29	0.93
33:I:195:ASN:HD22	33:I:198:LEU:HG	1.33	0.92
34:J:55:VAL:HG13	34:J:56:PRO:HD3	1.52	0.92
53:1:1053:C:H2'	53:1:1054:A:H5''	1.50	0.91
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.51	0.89
7:h:37:LYS:HE3	7:h:38:MET:HE2	1.54	0.89
12:m:20:LEU:HD13	21:v:81:PRO:HG2	1.53	0.89
42:R:25:GLY:H	52:3:1329:A:H5''	1.36	0.89
52:3:484:G:H4'	52:3:485:U:H5''	1.54	0.88
3:d:46:GLN:HB3	3:d:83:VAL:HG11	1.56	0.88
34:J:80:LEU:HD13	34:J:122:VAL:HG11	1.55	0.88
53:1:1133:A:H4'	53:1:1134:A:H5''	1.56	0.88
52:3:1306:A:H61	52:3:1331:G:H1'	1.40	0.87
45:U:28:ARG:NH2	52:3:390:U:H4'	1.89	0.87
17:r:49:ILE:HD12	17:r:52:PRO:HA	1.55	0.87
6:g:94:ILE:HD11	6:g:122:LEU:HD13	1.58	0.86
22:w:39:THR:H	53:1:2331:G:H4'	1.39	0.85
8:i:25:PRO:HB2	53:1:1095:A:H61	1.41	0.85
35:K:3:HIS:H	35:K:92:THR:HG22	1.40	0.85
13:n:2:ARG:O	13:n:2:ARG:HD3	1.77	0.85
41:Q:109:ARG:HB2	41:Q:118:VAL:HG21	1.60	0.84
52:3:327:A:O2'	52:3:328:C:H4'	1.78	0.84
33:I:33:ILE:H	33:I:33:ILE:HD12	1.41	0.84
53:1:1906:G:H2'	53:1:1907:G:H5''	1.60	0.84
53:1:2156:G:H2'	53:1:2157:G:H5'	1.59	0.83
7:h:23:LEU:HD21	7:h:118:ILE:HG13	1.60	0.83
23:x:17:ARG:HE	23:x:23:ALA:HB2	1.43	0.83
53:1:2048:G:H2'	53:1:2049:G:H5''	1.60	0.83
49:Y:67:HIS:O	49:Y:68:LYS:HG2	1.80	0.82
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.61	0.82
33:I:131:ILE:HD12	52:3:403:C:H5'	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:114:PRO:HG2	52:3:1228:C:H5''	1.63	0.81
53:1:1077:A:H2'	53:1:1078:U:H5'	1.61	0.81
19:t:10:VAL:HG13	19:t:11:LEU:HD12	1.63	0.81
54:2:3:C:H2'	54:2:4:C:H5''	1.60	0.81
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.60	0.81
53:1:1141:U:H4'	53:1:1142:A:O4'	1.79	0.81
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.10	0.81
53:1:329:G:O4'	53:1:477:A:H1'	1.81	0.81
39:O:53:ILE:HG22	43:S:84:ARG:HD2	1.60	0.80
53:1:1026:G:H2'	53:1:1027:A:H8	1.44	0.80
53:1:275:C:H2'	53:1:276:U:H4'	1.63	0.80
45:U:31:ARG:HG2	52:3:310:G:H5''	1.63	0.80
53:1:1020:A:H1'	53:1:1021:A:OP2	1.80	0.80
7:h:23:LEU:CD2	7:h:118:ILE:HG13	2.11	0.80
46:V:12:VAL:HB	46:V:21:VAL:HG13	1.63	0.79
13:n:65:LEU:HG	13:n:69:ARG:HH22	1.48	0.79
50:Z:8:ASN:HB3	50:Z:9:GLU:OE1	1.82	0.79
49:Y:55:PRO:HG2	49:Y:56:ILE:HD12	1.64	0.79
53:1:511:U:H2'	53:1:512:G:H5'	1.63	0.79
53:1:2682:A:H61	53:1:2728:U:H1'	1.47	0.78
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.66	0.78
32:H:39:ARG:HG3	32:H:54:ILE:HD11	1.66	0.78
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.47	0.78
7:h:61:ARG:HG3	53:1:1046:A:H4'	1.64	0.78
35:K:53:LYS:C	35:K:54:LEU:HD23	2.08	0.78
53:1:45:G:H5''	53:1:46:G:C5'	2.09	0.78
52:3:946:A:H2'	52:3:947:G:C8	2.18	0.77
38:N:59:LYS:HG2	38:N:60:LEU:HG	1.66	0.77
52:3:946:A:H2'	52:3:947:G:H8	1.49	0.77
38:N:71:ILE:H	38:N:71:ILE:HD12	1.50	0.77
4:e:63:LYS:O	54:2:42:C:H1'	1.84	0.77
40:P:43:TRP:HE1	52:3:686:U:H1'	1.48	0.76
52:3:151:A:H62	52:3:170:U:H3	1.31	0.76
55:5:76:A:HO2'	59:7:101:PHE:N	1.83	0.76
11:l:78:ARG:HE	11:l:113:ALA:HB1	1.48	0.76
36:L:4:ARG:HD2	36:L:4:ARG:N	1.96	0.76
7:h:73:LYS:HE3	7:h:117:LEU:HD23	1.68	0.76
7:h:117:LEU:O	7:h:118:ILE:HB	1.82	0.76
36:L:3:ARG:HH12	52:3:932:C:H5''	1.51	0.76
52:3:150:U:H3	52:3:171:A:H62	1.33	0.75
53:1:1019:U:H3	53:1:1142:A:H62	1.34	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:24:VAL:HG12	54:2:55:U:H4'	1.67	0.75
32:H:174:LEU:HD23	32:H:181:ILE:HD13	1.66	0.75
45:U:23:ASP:HB3	45:U:26:ASN:HD22	1.50	0.75
54:2:13:G:H21	54:2:16:G:H1'	1.50	0.75
5:f:3:VAL:HG21	53:1:2748:A:H5'	1.68	0.75
52:3:405:U:H3'	52:3:406:G:H5'	1.68	0.75
52:3:664:G:H22	52:3:741:G:H1	1.35	0.74
20:u:46:LYS:HD2	20:u:47:PRO:HD2	1.69	0.74
33:I:204:SER:HB2	52:3:8:A:H62	1.53	0.74
7:h:73:LYS:HE2	7:h:120:ALA:CA	2.16	0.74
51:a:42:VAL:HB	51:a:214:ILE:HD11	1.70	0.74
52:3:948:C:H2'	52:3:949:A:H8	1.53	0.74
53:1:1654:A:H2'	53:1:1655:A:H8	1.52	0.73
4:e:84:ILE:HG21	53:1:2312:U:H4'	1.68	0.73
53:1:2296:U:H5''	53:1:2297:A:OP1	1.87	0.73
21:v:20:LEU:HD11	21:v:27:PRO:HD3	1.69	0.73
53:1:1300:G:H4'	53:1:1301:A:H5''	1.68	0.73
52:3:29:U:O2'	52:3:30:U:H5'	1.89	0.73
53:1:1807:G:H2'	53:1:1808:A:H5'	1.71	0.73
34:J:45:VAL:HG22	34:J:46:GLY:H	1.54	0.72
44:T:71:ARG:NH2	52:3:754:C:H5'	2.04	0.72
53:1:2114:A:H61	53:1:2117:A:H62	1.37	0.72
52:3:1306:A:N6	52:3:1331:G:H1'	2.04	0.72
40:P:63:GLN:HG3	40:P:98:ALA:HB2	1.71	0.72
55:6:71:C:H2'	55:6:72:A:C8	2.25	0.72
13:n:2:ARG:HA	13:n:5:LYS:HD2	1.72	0.72
53:1:780:G:H2'	53:1:782:A:N7	2.04	0.72
49:Y:66:ILE:HG22	49:Y:68:LYS:H	1.54	0.72
53:1:2698:U:H2'	53:1:2699:C:C6	2.25	0.72
54:2:88:C:H5''	54:2:89:U:OP1	1.90	0.71
29:E:61:LEU:HD12	29:E:61:LEU:O	1.90	0.71
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.73	0.71
32:H:49:ALA:HA	32:H:74:ILE:HD11	1.71	0.71
6:g:11:ASN:HD22	6:g:12:LEU:HD22	1.55	0.71
38:N:119:LYS:HG3	52:3:1349:A:OP1	1.89	0.71
52:3:677:U:H3	52:3:713:G:H22	1.38	0.71
42:R:3:ILE:HG22	42:R:4:ALA:H	1.54	0.71
40:P:88:PRO:HD3	50:Z:28:LEU:HD21	1.73	0.70
8:i:2:LYS:HE3	8:i:5:GLN:HE22	1.54	0.70
11:l:77:ILE:HD11	11:l:101:ILE:HG23	1.72	0.70
38:N:57:VAL:HG12	38:N:58:GLU:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:64:ARG:HD2	52:3:264:C:H4'	1.73	0.70
53:1:974:G:H1'	53:1:975:A:C8	2.26	0.70
3:d:76:PRO:HA	3:d:82:GLY:CA	2.21	0.70
7:h:114:GLU:OE2	7:h:122:GLN:HB3	1.90	0.70
34:J:55:VAL:HG13	34:J:56:PRO:CD	2.21	0.70
47:W:11:ARG:HE	52:3:845:A:H4'	1.56	0.70
53:1:1906:G:C2'	53:1:1907:G:H5''	2.21	0.70
29:E:1:PRO:HG2	53:1:591:U:H1'	1.73	0.70
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.74	0.70
1:b:149:LYS:HD3	53:1:2204:G:H4'	1.73	0.69
53:1:1394:U:H4'	53:1:1603:A:H4'	1.72	0.69
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	1.74	0.69
45:U:28:ARG:HE	45:U:29:ASN:HD21	1.40	0.69
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.75	0.69
53:1:2537:U:H2'	53:1:2538:C:C6	2.27	0.69
52:3:352:C:H4'	52:3:354:G:OP1	1.92	0.69
53:1:2286:G:H5''	53:1:2287:A:OP1	1.91	0.69
17:r:65:ALA:HB3	17:r:95:ASP:HB2	1.73	0.69
52:3:1418:A:H3'	52:3:1419:G:H5''	1.73	0.69
52:3:1197:A:H2'	52:3:1198:G:H5''	1.72	0.69
8:i:9:LYS:O	8:i:10:LEU:HD22	1.93	0.69
38:N:128:LYS:HD3	38:N:129:ARG:HH12	1.57	0.69
52:3:769:G:H4'	52:3:1513:A:H4'	1.74	0.69
53:1:1300:G:H4'	53:1:1301:A:C5'	2.22	0.69
53:1:2128:G:H21	53:1:2173:A:H1'	1.57	0.69
24:y:2:LYS:HE3	53:1:102:U:H1'	1.75	0.69
10:k:35:VAL:HG21	10:k:106:GLU:HB2	1.75	0.68
39:O:92:LEU:HD23	39:O:92:LEU:H	1.58	0.68
53:1:2048:G:C2'	53:1:2049:G:H5''	2.22	0.68
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.74	0.68
53:1:1801:A:H5''	53:1:2203:U:H2'	1.75	0.68
7:h:71:CYS:HB3	7:h:117:LEU:HD11	1.73	0.68
11:l:93:ASN:O	11:l:94:THR:HG22	1.93	0.68
43:S:92:ILE:H	43:S:92:ILE:HD12	1.58	0.68
52:3:401:C:H2'	52:3:402:G:C8	2.29	0.68
53:1:2800:A:H3'	53:1:2801:G:H5'	1.73	0.68
54:2:3:C:C2'	54:2:4:C:H5''	2.24	0.68
20:u:33:VAL:HG13	20:u:66:VAL:HG22	1.76	0.68
52:3:112:G:N2	52:3:354:G:H5'	2.07	0.68
47:W:59:LYS:HD3	52:3:735:C:H5'	1.75	0.68
15:p:2:ASN:HD21	53:1:2876:G:H4'	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2156:G:C2'	53:1:2157:G:H5'	2.24	0.68
53:1:2818:U:H2'	53:1:2819:G:H8	1.59	0.68
10:k:10:VAL:HG11	10:k:16:ALA:HB3	1.76	0.68
6:g:122:LEU:HD11	6:g:146:VAL:HG21	1.76	0.67
30:F:36:ARG:HG2	30:F:37:GLN:H	1.58	0.67
4:e:35:LEU:HB3	4:e:88:VAL:HB	1.77	0.67
18:s:20:VAL:HG21	18:s:43:ALA:HB3	1.76	0.67
52:3:715:A:H2'	52:3:716:A:C8	2.29	0.67
52:3:715:A:H2'	52:3:716:A:H8	1.59	0.67
53:1:2277:G:C2'	53:1:2278:A:H5''	2.20	0.67
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.08	0.67
37:M:28:SER:HB3	37:M:56:PRO:HB2	1.77	0.67
42:R:113:LYS:HG3	42:R:114:PRO:HD3	1.75	0.67
52:3:962:C:H1'	52:3:1201:A:N6	2.09	0.67
10:k:40:LYS:HD2	10:k:57:VAL:HG22	1.77	0.67
11:l:101:ILE:HG13	11:l:102:GLY:H	1.60	0.67
28:D:26:ASN:CG	53:1:682:G:H5'	2.19	0.67
53:1:995:C:H6	53:1:995:C:H5'	1.60	0.67
53:1:1053:C:C2'	53:1:1054:A:H5''	2.22	0.67
52:3:1219:A:H2'	52:3:1220:G:C8	2.30	0.67
55:6:16:C:O2'	55:6:17:C:H5'	1.95	0.67
53:1:742:A:H2'	53:1:743:A:C8	2.30	0.67
53:1:1367:A:H2'	53:1:1368:G:H5'	1.75	0.67
14:o:31:THR:HG21	54:2:28:C:OP1	1.95	0.67
50:Z:49:ALA:O	50:Z:53:LYS:HG3	1.95	0.67
14:o:87:ILE:H	14:o:87:ILE:HD12	1.59	0.66
44:T:6:ALA:HA	44:T:9:LYS:HE2	1.77	0.66
52:3:346:G:C2'	52:3:347:G:H5'	2.25	0.66
53:1:1186:G:H2'	53:1:1187:G:O4'	1.94	0.66
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.75	0.66
44:T:52:ARG:HH11	53:1:715:A:H61	1.41	0.66
52:3:1379:G:O2'	52:3:1380:U:H5'	1.95	0.66
53:1:615:U:H5''	53:1:616:A:OP2	1.94	0.66
10:k:21:CYS:HA	10:k:41:ILE:HG22	1.77	0.66
51:a:174:THR:HB	53:1:2124:G:H4'	1.78	0.66
53:1:2243:U:H2'	53:1:2244:U:C6	2.29	0.66
53:1:1936:A:H2	53:1:1943:U:H3	1.44	0.66
7:h:33:VAL:HG12	7:h:34:THR:H	1.60	0.66
11:l:110:VAL:HB	11:l:127:VAL:HG13	1.78	0.66
28:D:10:LEU:HD23	53:1:770:G:H5''	1.78	0.66
52:3:701:U:H4'	52:3:703:G:H1'	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:m:12:MET:HA	53:1:910:A:N6	2.04	0.66
45:U:33:ILE:H	45:U:33:ILE:HD12	1.60	0.66
52:3:1219:A:H2'	52:3:1220:G:H8	1.59	0.66
2:c:151:THR:HB	2:c:152:PRO:HD3	1.77	0.66
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.78	0.66
32:H:152:VAL:HG12	32:H:197:VAL:HG22	1.78	0.66
50:Z:65:ARG:NE	52:3:1088:G:H4'	2.11	0.66
32:H:82:ASP:HA	32:H:85:LYS:HE3	1.77	0.65
40:P:126:ARG:HH22	52:3:692:U:H5''	1.61	0.65
52:3:70:U:H5''	52:3:71:A:OP1	1.97	0.65
1:b:116:GLN:HE21	1:b:121:ALA:HA	1.62	0.65
45:U:5:ARG:HB2	52:3:376:G:H5''	1.79	0.65
15:p:7:LEU:O	15:p:7:LEU:HD23	1.97	0.65
48:X:77:ARG:HH21	52:3:1225:A:H4'	1.62	0.65
53:1:2048:G:C3'	53:1:2049:G:H5''	2.27	0.65
53:1:2537:U:H2'	53:1:2538:C:H6	1.60	0.65
1:b:153:LEU:HD21	1:b:181:ARG:HH22	1.61	0.65
11:l:135:ILE:HB	11:l:142:ILE:HD11	1.79	0.65
14:o:29:HIS:HB3	14:o:36:TYR:HB2	1.79	0.65
52:3:695:A:H2'	52:3:696:A:C8	2.32	0.65
53:1:473:G:O2'	53:1:474:G:H5'	1.97	0.65
33:I:101:VAL:HG23	33:I:113:ALA:HB1	1.79	0.64
52:3:824:G:H2'	52:3:825:A:H8	1.63	0.64
53:1:1779:U:OP2	53:1:1784:A:N6	2.30	0.64
10:k:80:ASP:HB2	15:p:67:GLU:HB2	1.78	0.64
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.79	0.64
53:1:1991:U:H2'	53:1:1992:G:H5''	1.79	0.64
17:r:76:LYS:HB2	17:r:85:LYS:HB3	1.80	0.64
53:1:974:G:H8	53:1:990:A:H62	1.43	0.64
53:1:1300:G:C4'	53:1:1301:A:H5''	2.28	0.64
10:k:76:VAL:H	15:p:72:VAL:HG22	1.63	0.64
53:1:45:G:C5'	53:1:46:G:H5'	2.11	0.64
57:7:44:G:H2'	57:7:45:U:O4'	1.98	0.64
52:3:1139:G:H5''	52:3:1140:C:H5	1.62	0.64
53:1:2391:G:H4'	53:1:2392:A:OP1	1.97	0.64
17:r:35:PHE:HB2	17:r:59:ILE:HB	1.80	0.63
21:v:9:ARG:HG2	21:v:41:GLU:HB3	1.79	0.63
52:3:211:G:H2'	52:3:212:G:H5'	1.79	0.63
34:J:107:GLY:HA3	52:3:9:G:H5'	1.80	0.63
53:1:577:G:H2'	53:1:578:G:C8	2.33	0.63
33:I:120:LYS:HE2	33:I:130:ASN:HD21	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2086:U:H2'	53:1:2087:G:C8	2.33	0.63
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.81	0.63
53:1:184:C:H2'	53:1:185:G:H8	1.63	0.63
52:3:1280:A:O2'	52:3:1281:C:H5'	1.99	0.63
53:1:215:G:H4'	53:1:216:A:H4'	1.80	0.63
53:1:2432:A:H1'	55:6:75:C:C5'	2.22	0.63
3:d:105:LEU:HD13	3:d:175:ILE:HD11	1.81	0.63
16:q:5:ARG:NH1	53:1:585:G:N7	2.47	0.63
18:s:4:ILE:HG22	18:s:106:VAL:HG22	1.80	0.63
50:Z:17:ARG:HA	50:Z:20:ARG:HE	1.64	0.63
52:3:1513:A:H2'	52:3:1514:G:H8	1.63	0.63
53:1:310:A:C2'	53:1:311:A:H5''	2.28	0.63
39:O:15:HIS:O	39:O:18:ILE:HG22	1.99	0.63
42:R:16:ILE:H	42:R:16:ILE:HD12	1.62	0.63
53:1:1909:C:H2'	53:1:1910:G:H8	1.62	0.63
5:f:173:ALA:O	5:f:174:LYS:HG3	1.99	0.63
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.64	0.63
41:Q:41:PRO:HG3	41:Q:49:ARG:NE	2.14	0.63
43:S:48:GLN:HB2	48:X:12:LEU:HD23	1.81	0.63
49:Y:24:ARG:HG3	49:Y:65:LEU:HD21	1.81	0.63
52:3:390:U:H2'	52:3:391:G:H8	1.63	0.63
53:1:639:U:H2'	53:1:640:C:C6	2.34	0.63
53:1:742:A:H2'	53:1:743:A:H8	1.64	0.63
6:g:119:ASN:HD21	6:g:129:GLU:H	1.47	0.63
10:k:114:LYS:HE3	10:k:118:LEU:HD11	1.81	0.63
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.81	0.63
52:3:1352:C:H2'	52:3:1353:G:C8	2.33	0.63
52:3:304:U:O2'	52:3:305:G:H5'	1.98	0.62
28:D:24:THR:HG23	28:D:27:GLY:H	1.64	0.62
32:H:1:GLY:HA3	52:3:1060:U:H5	1.65	0.62
19:t:48:GLN:NE2	19:t:54:GLU:HA	2.15	0.62
28:D:34:ARG:HH21	28:D:39:ARG:HD2	1.64	0.62
35:K:36:ILE:HG13	35:K:64:VAL:HG12	1.80	0.62
52:3:163:C:H2'	52:3:164:G:O4'	1.99	0.62
52:3:401:C:H2'	52:3:402:G:H8	1.62	0.62
53:1:1077:A:C2'	53:1:1078:U:H5'	2.29	0.62
50:Z:16:ARG:HH21	50:Z:19:LYS:HG2	1.64	0.62
20:u:73:ASN:HD22	20:u:76:THR:HG22	1.64	0.62
28:D:12:ARG:NE	28:D:44:VAL:HG21	2.15	0.62
53:1:2533:U:H2'	53:1:2534:A:O4'	1.99	0.62
53:1:807:U:H2'	53:1:808:G:H8	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1344:U:H3'	53:1:1345:C:H5'	1.82	0.62
9:j:7:LYS:HG2	53:1:538:A:H4'	1.80	0.61
10:k:66:LYS:HD3	53:1:1666:G:OP1	2.00	0.61
36:L:4:ARG:H	36:L:4:ARG:CD	2.05	0.61
36:L:131:GLY:O	36:L:134:VAL:HG12	1.99	0.61
48:X:18:VAL:HG21	48:X:43:MET:HG2	1.82	0.61
53:1:546:U:H2'	53:1:547:A:H4'	1.82	0.61
53:1:2389:G:H5''	53:1:2390:U:O4'	1.99	0.61
7:h:43:LYS:HA	7:h:46:ARG:HE	1.64	0.61
10:k:98:ARG:HD3	52:3:339:C:OP2	2.00	0.61
41:Q:20:VAL:HG21	52:3:553:A:H5''	1.81	0.61
52:3:31:G:N2	52:3:47:C:H5''	2.14	0.61
7:h:24:SER:O	7:h:116:GLU:HB2	1.99	0.61
53:1:27:G:N2	53:1:512:G:H1'	2.16	0.61
14:o:94:ARG:HG2	14:o:97:PHE:O	1.99	0.61
32:H:171:ARG:HG3	52:3:1106:G:H5''	1.82	0.61
53:1:121:G:H4'	53:1:149:A:H5'	1.81	0.61
53:1:2286:G:H4'	53:1:2287:A:O5'	2.01	0.61
53:1:2327:A:H2'	53:1:2328:A:C8	2.36	0.61
4:e:84:ILE:HG21	53:1:2312:U:C5'	2.30	0.61
17:r:54:VAL:HG12	17:r:55:ASP:OD1	2.00	0.61
28:D:34:ARG:NH2	28:D:39:ARG:HD2	2.16	0.61
31:G:96:LEU:H	31:G:96:LEU:HD12	1.64	0.61
53:1:528:A:N1	53:1:2042:A:H2'	2.16	0.61
53:1:1360:G:H2'	53:1:1361:G:H5'	1.82	0.61
53:1:2281:A:O2'	53:1:2282:G:H5'	1.99	0.61
57:7:14:A:H2'	57:7:15:G:H5'	1.82	0.61
15:p:3:ILE:H	15:p:3:ILE:HD12	1.66	0.61
21:v:76:ASP:H	21:v:90:ASP:HB2	1.64	0.61
49:Y:23:ARG:O	49:Y:26:MET:HG3	2.01	0.61
53:1:1348:C:H2'	53:1:1349:C:H5'	1.82	0.61
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.64	0.61
7:h:73:LYS:HE3	7:h:117:LEU:CD2	2.31	0.61
26:B:54:ILE:HG23	26:B:56:LYS:H	1.65	0.61
53:1:619:G:H3'	53:1:620:G:H21	1.65	0.61
53:1:2799:A:H2'	53:1:2800:A:H5'	1.82	0.61
32:H:13:ILE:HG22	32:H:14:VAL:HG13	1.81	0.61
37:M:45:ILE:HD11	37:M:60:LEU:HB3	1.82	0.61
53:1:2238:G:H2'	53:1:2238:G:N3	2.15	0.61
21:v:42:LEU:H	21:v:42:LEU:HD23	1.66	0.61
21:v:49:ASN:OD1	53:1:1040:A:H4'	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1912:A:H62	53:1:1917:U:H3	1.47	0.61
27:C:4:ILE:H	27:C:4:ILE:HD12	1.66	0.61
51:a:23:ILE:HG22	51:a:186:LYS:HE2	1.83	0.61
53:1:310:A:O2'	53:1:311:A:H5''	2.00	0.61
3:d:151:GLY:HA2	3:d:172:ALA:HB2	1.82	0.60
12:m:102:LEU:HD11	12:m:126:ILE:HD11	1.82	0.60
36:L:91:ARG:NH1	52:3:1378:C:H1'	2.16	0.60
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.83	0.60
53:1:1111:A:H2'	53:1:1111:A:N3	2.16	0.60
53:1:1607:C:H5''	53:1:1608:A:H5'	1.82	0.60
55:5:75:C:H3'	55:5:76:A:H5''	1.82	0.60
52:3:951:G:O2'	52:3:952:U:H5'	2.00	0.60
52:3:1137:C:H4'	52:3:1138:G:N2	2.15	0.60
8:i:9:LYS:HE3	53:1:1061:U:OP2	2.01	0.60
18:s:6:LYS:HG3	53:1:494:G:H4'	1.84	0.60
43:S:80:ARG:O	43:S:83:VAL:HG12	2.01	0.60
53:1:2743:U:H2'	53:1:2744:G:H5''	1.83	0.60
33:I:37:PRO:HD2	33:I:41:GLY:HA3	1.83	0.60
37:M:12:ARG:NH2	52:3:826:C:H5'	2.17	0.60
40:P:30:ILE:HA	40:P:45:THR:HG22	1.83	0.60
41:Q:113:ARG:HD2	41:Q:118:VAL:O	2.01	0.60
43:S:12:ARG:HB3	43:S:59:GLN:HE22	1.67	0.60
52:3:1432:G:H1'	52:3:1468:A:N6	2.17	0.60
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.81	0.60
45:U:28:ARG:HH22	52:3:390:U:C4'	2.10	0.60
45:U:33:ILE:HG12	52:3:229:U:H5''	1.82	0.60
52:3:495:A:H4'	52:3:496:A:O5'	2.00	0.60
53:1:2134:A:N6	53:1:2157:G:H4'	2.16	0.60
1:b:12:ARG:HD3	53:1:728:G:H4'	1.82	0.60
3:d:47:LYS:O	3:d:83:VAL:HB	2.01	0.60
49:Y:56:ILE:HD12	49:Y:56:ILE:H	1.67	0.60
8:i:128:ILE:H	8:i:128:ILE:HD12	1.66	0.60
53:1:226:A:H2'	53:1:227:A:O4'	2.02	0.60
53:1:890:C:H2'	53:1:891:G:H5'	1.84	0.60
53:1:1666:G:C2'	53:1:1667:G:H5'	2.32	0.60
4:e:45:ASP:OD2	4:e:48:LEU:HB2	2.00	0.60
24:y:19:LEU:O	24:y:23:ARG:HB2	2.02	0.60
50:Z:23:GLU:C	50:Z:25:ALA:H	2.09	0.60
52:3:1497:G:O2'	52:3:1498:U:H5'	2.01	0.60
52:3:1513:A:H2'	52:3:1514:G:C8	2.36	0.60
53:1:2743:U:C3'	53:1:2744:G:H5''	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:5:LEU:HD22	6:g:13:GLY:HA3	1.83	0.60
8:i:12:VAL:HG12	53:1:1061:U:O2	2.01	0.60
52:3:864:A:H2'	52:3:865:A:C8	2.36	0.60
52:3:1342:C:H2'	52:3:1343:G:C8	2.37	0.60
53:1:69:C:O2'	53:1:70:G:H5'	2.02	0.60
55:5:18:G:H1	55:5:55:U:H6	1.49	0.60
4:e:84:ILE:CG2	53:1:2312:U:H4'	2.32	0.59
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.67	0.59
21:v:75:GLN:HB2	21:v:92:VAL:HG23	1.84	0.59
35:K:91:ARG:HG3	35:K:92:THR:H	1.66	0.59
36:L:70:PRO:HG3	36:L:98:LEU:HD23	1.84	0.59
36:L:110:ARG:HH22	36:L:121:ASN:HD22	1.47	0.59
47:W:11:ARG:HE	52:3:845:A:C4'	2.14	0.59
53:1:2029:G:O6	53:1:2032:G:H5''	2.02	0.59
7:h:71:CYS:HB3	7:h:117:LEU:CD1	2.30	0.59
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.84	0.59
4:e:91:ARG:NH2	54:2:45:A:H1'	2.16	0.59
31:G:166:ASP:HB2	31:G:190:SER:HA	1.84	0.59
38:N:51:LEU:HB3	38:N:56:MET:HB2	1.83	0.59
48:X:79:TYR:CZ	52:3:1226:C:H4'	2.37	0.59
52:3:17:U:H2'	52:3:18:C:C6	2.38	0.59
52:3:211:G:C2'	52:3:212:G:H5'	2.31	0.59
53:1:2282:G:H4'	53:1:2389:G:O2'	2.02	0.59
1:b:235:GLU:HG2	53:1:2599:G:C8	2.38	0.59
52:3:309:A:H2'	52:3:310:G:H8	1.67	0.59
52:3:1211:U:H4'	52:3:1213:A:N3	2.17	0.59
32:H:72:PRO:HG3	32:H:104:GLU:HG3	1.84	0.59
37:M:80:PRO:HG2	52:3:878:A:C5'	2.32	0.59
52:3:243:A:H4'	52:3:244:U:H3'	1.85	0.59
2:c:12:THR:HG22	2:c:13:ARG:H	1.67	0.59
15:p:92:ARG:HD3	53:1:1753:G:H5''	1.84	0.59
42:R:88:LEU:HD22	42:R:91:ARG:NH2	2.17	0.59
53:1:1810:A:H2'	53:1:1811:G:O4'	2.03	0.59
1:b:42:ARG:HH12	53:1:690:G:H21	1.51	0.59
29:E:31:ILE:O	29:E:31:ILE:HG13	2.03	0.59
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.17	0.59
53:1:1654:A:H2'	53:1:1655:A:C8	2.37	0.59
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.84	0.59
16:q:73:ILE:HD11	16:q:77:LYS:HB3	1.84	0.59
22:w:38:GLY:HA2	53:1:2330:G:H21	1.68	0.59
49:Y:34:VAL:HG11	49:Y:78:LEU:HD21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2220:U:H2'	53:1:2221:G:H8	1.66	0.59
19:t:73:ARG:HH12	53:1:456:C:H2'	1.68	0.58
39:O:6:ILE:H	39:O:6:ILE:HD12	1.68	0.58
53:1:438:G:H2'	53:1:439:A:C8	2.38	0.58
53:1:1190:G:H2'	53:1:1191:G:H8	1.68	0.58
53:1:1657:U:H2'	53:1:1658:C:H6	1.68	0.58
53:1:2799:A:C2'	53:1:2800:A:H5'	2.33	0.58
2:c:25:THR:HG21	2:c:193:VAL:HG22	1.84	0.58
43:S:80:ARG:HG3	43:S:81:ILE:HD12	1.85	0.58
52:3:314:C:O2'	52:3:315:A:H5'	2.02	0.58
53:1:49:A:H5'	53:1:51:G:O4'	2.03	0.58
53:1:1872:A:H2'	53:1:1873:G:O4'	2.03	0.58
53:1:2756:U:H4'	53:1:2757:A:OP1	2.04	0.58
28:D:34:ARG:HD3	53:1:467:G:OP2	2.03	0.58
55:5:6:G:O2'	55:5:7:G:H5'	2.03	0.58
2:c:55:LYS:HG3	2:c:77:ARG:HA	1.84	0.58
45:U:31:ARG:CG	52:3:310:G:H5''	2.31	0.58
52:3:1352:C:H2'	52:3:1353:G:H8	1.67	0.58
53:1:1319:C:O2'	53:1:1320:C:H5'	2.03	0.58
13:n:63:ARG:HD3	53:1:1454:C:O4'	2.02	0.58
52:3:731:G:O2'	52:3:732:C:H5'	2.04	0.58
54:2:3:C:C3'	54:2:4:C:H5''	2.34	0.58
24:y:12:GLU:O	24:y:15:ASN:OD1	2.22	0.58
33:I:131:ILE:HG22	33:I:133:SER:H	1.69	0.58
52:3:1218:C:H2'	52:3:1219:A:C8	2.39	0.58
8:i:64:ARG:HD2	8:i:64:ARG:O	2.04	0.58
31:G:165:ALA:HB1	31:G:172:ILE:HD11	1.84	0.58
31:G:182:VAL:HG13	31:G:195:VAL:HG13	1.84	0.58
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.86	0.58
51:a:54:LYS:HD2	51:a:57:GLN:CD	2.29	0.58
52:3:1527:U:O2'	52:3:1528:U:H5'	2.04	0.58
53:1:996:A:H2'	53:1:997:G:H8	1.68	0.58
35:K:47:LEU:H	35:K:47:LEU:HD12	1.69	0.58
38:N:91:GLU:HA	38:N:94:ARG:HB2	1.85	0.58
53:1:161:A:H3'	53:1:162:U:H5''	1.85	0.58
53:1:644:A:H2'	53:1:645:C:H5''	1.86	0.58
53:1:2329:U:H2'	53:1:2330:G:C8	2.39	0.58
53:1:2553:G:H3'	53:1:2554:U:H5''	1.86	0.58
53:1:2841:C:H2'	53:1:2842:G:H8	1.68	0.58
3:d:123:LYS:HE3	3:d:125:SER:HB2	1.84	0.57
52:3:1197:A:C2'	52:3:1198:G:H5''	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:859:G:HO2'	53:1:860:U:H6	1.48	0.57
53:1:2475:C:C2'	53:1:2476:A:H5'	2.34	0.57
52:3:206:C:H2'	52:3:207:C:O4'	2.04	0.57
52:3:513:C:H2'	52:3:514:C:H6	1.68	0.57
53:1:371:A:H61	53:1:401:A:H3'	1.69	0.57
53:1:543:G:H8	53:1:543:G:H5'	1.69	0.57
53:1:1539:U:H2'	53:1:1540:G:H8	1.69	0.57
53:1:2452:C:H42	53:1:2504:U:H3	1.52	0.57
55:6:3:C:H2'	55:6:4:G:H8	1.69	0.57
50:Z:39:LYS:HD3	50:Z:42:THR:HB	1.87	0.57
53:1:198:C:O2'	53:1:199:A:H5'	2.04	0.57
53:1:1565:C:O2'	53:1:1566:A:H2'	2.04	0.57
38:N:123:ARG:HB2	52:3:1343:G:H4'	1.86	0.57
31:G:20:ARG:HG2	52:3:831:A:H5'	1.85	0.57
34:J:14:LEU:HA	34:J:36:THR:HG22	1.84	0.57
41:Q:2:THR:HG21	41:Q:5:GLN:HG3	1.86	0.57
52:3:711:G:O2'	52:3:712:A:H5'	2.03	0.57
52:3:1397:C:H42	56:4:22:A:H2'	1.69	0.57
53:1:2163:A:H2'	53:1:2164:C:H5'	1.86	0.57
53:1:2475:C:H42	53:1:2529:G:H22	1.53	0.57
4:e:65:LEU:HD12	54:2:41:G:H21	1.68	0.57
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.86	0.57
24:y:1:MET:HB2	24:y:52:ARG:HH21	1.70	0.57
32:H:69:THR:HG21	32:H:75:VAL:HG21	1.86	0.57
40:P:83:VAL:HB	40:P:109:ILE:HA	1.86	0.57
52:3:514:C:H2'	52:3:515:G:H8	1.69	0.57
52:3:948:C:H2'	52:3:949:A:C8	2.36	0.57
53:1:542:C:H2'	53:1:543:G:H5'	1.87	0.57
53:1:2073:C:O2'	53:1:2074:U:H5'	2.04	0.57
3:d:58:LYS:HG2	3:d:71:GLY:HA2	1.86	0.57
5:f:97:VAL:HG23	5:f:124:CYS:SG	2.45	0.57
53:1:783:A:H2'	53:1:784:G:H5'	1.85	0.57
53:1:1105:U:H2'	53:1:1106:G:H5''	1.86	0.57
53:1:2233:U:H2'	53:1:2234:G:C8	2.39	0.57
7:h:106:PHE:O	7:h:107:GLU:HG2	2.05	0.57
45:U:20:VAL:HG22	45:U:21:VAL:H	1.69	0.57
46:V:13:SER:H	46:V:21:VAL:HG13	1.69	0.57
3:d:63:LYS:HD3	53:1:2443:C:OP1	2.05	0.57
22:w:73:ARG:HH22	53:1:2333:A:P	2.28	0.57
33:I:123:MET:HE2	33:I:145:ARG:HA	1.86	0.57
35:K:45:ARG:HH21	47:W:66:LEU:HD22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:20:VAL:HG22	45:U:21:VAL:N	2.20	0.57
52:3:70:U:H2'	52:3:94:G:O6	2.05	0.57
52:3:291:U:H2'	52:3:292:G:H8	1.69	0.57
53:1:503:A:H4'	53:1:505:A:H5''	1.86	0.57
53:1:2266:A:H4'	53:1:2267:A:N3	2.20	0.57
4:e:89:THR:HG22	4:e:91:ARG:HD2	1.86	0.57
41:Q:32:VAL:HA	41:Q:78:VAL:HG12	1.86	0.57
42:R:25:GLY:N	52:3:1329:A:H5''	2.14	0.57
53:1:386:G:H3'	53:1:387:U:H5''	1.87	0.57
10:k:102:PRO:HB3	10:k:121:GLU:HB2	1.86	0.56
52:3:423:G:H2'	52:3:424:G:H5'	1.87	0.56
53:1:1373:A:H5'	53:1:2212:A:H1'	1.87	0.56
53:1:1736:U:H2'	53:1:1737:G:O4'	2.05	0.56
53:1:2066:C:O2'	53:1:2067:G:H5'	2.04	0.56
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.05	0.56
39:O:41:PRO:HG3	52:3:1150:A:C2	2.40	0.56
52:3:757:U:H2'	52:3:758:C:O4'	2.05	0.56
52:3:1228:C:H2'	52:3:1229:A:H8	1.70	0.56
52:3:1273:C:H2'	52:3:1274:A:O4'	2.05	0.56
52:3:1368:A:O2'	52:3:1369:C:H5'	2.06	0.56
53:1:1373:A:C5'	53:1:2212:A:H1'	2.35	0.56
11:l:101:ILE:HB	11:l:105:ILE:HG13	1.87	0.56
23:x:6:VAL:HG11	23:x:58:ILE:HD11	1.87	0.56
33:I:131:ILE:HD12	52:3:403:C:C5'	2.34	0.56
38:N:71:ILE:HD11	52:3:1289:A:H61	1.71	0.56
39:O:6:ILE:HD12	39:O:6:ILE:N	2.20	0.56
39:O:50:THR:HG22	39:O:62:ARG:HD3	1.87	0.56
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.88	0.56
52:3:390:U:H2'	52:3:391:G:C8	2.41	0.56
53:1:310:A:H2'	53:1:311:A:H5''	1.86	0.56
53:1:644:A:H2'	53:1:645:C:C4'	2.35	0.56
52:3:1323:G:H2'	52:3:1324:A:C8	2.40	0.56
53:1:1415:U:H2'	53:1:1416:G:H4'	1.87	0.56
53:1:1417:C:H4'	53:1:1587:G:H21	1.69	0.56
53:1:2287:A:O2'	53:1:2288:A:H2'	2.05	0.56
53:1:2841:C:H2'	53:1:2842:G:C8	2.40	0.56
55:5:20:U:H2'	55:5:21:A:H5'	1.87	0.56
8:i:9:LYS:HD2	53:1:1061:U:H5''	1.86	0.56
41:Q:115:LYS:HG3	41:Q:116:TYR:CD2	2.41	0.56
43:S:81:ILE:HD12	43:S:81:ILE:H	1.70	0.56
53:1:532:A:H2'	53:1:532:A:N3	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:57:G:C2'	57:7:58:A:H5'	2.36	0.56
1:b:204:LEU:HB3	1:b:209:ALA:HB3	1.86	0.56
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.88	0.56
7:h:59:LEU:HB3	7:h:62:ARG:HB3	1.88	0.56
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.35	0.56
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.88	0.56
27:C:9:LYS:HD2	27:C:19:PHE:CD2	2.41	0.56
52:3:802:A:H2'	52:3:803:G:O4'	2.06	0.56
52:3:1342:C:H2'	52:3:1343:G:H8	1.70	0.56
53:1:278:A:H2'	53:1:278:A:N3	2.20	0.56
53:1:729:G:H4'	53:1:763:G:H5'	1.88	0.56
53:1:1386:C:H2'	53:1:1387:A:H8	1.71	0.56
53:1:1919:A:H2'	53:1:1920:C:H5'	1.87	0.56
53:1:2475:C:H2'	53:1:2476:A:H5'	1.86	0.56
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.87	0.56
13:n:60:VAL:HG22	53:1:1454:C:O2'	2.05	0.56
33:I:11:SER:HA	33:I:18:LEU:HD13	1.87	0.56
52:3:1413:A:O2'	52:3:1414:U:H5'	2.05	0.56
53:1:184:C:H2'	53:1:185:G:C8	2.40	0.56
53:1:2286:G:H4'	53:1:2287:A:O4'	2.05	0.56
1:b:129:LEU:N	1:b:129:LEU:HD23	2.21	0.56
7:h:61:ARG:HG3	53:1:1046:A:C4'	2.34	0.56
51:a:51:ASP:OD2	51:a:54:LYS:HG3	2.05	0.56
53:1:2183:A:H2'	53:1:2184:A:C8	2.41	0.56
4:e:135:ILE:HA	4:e:140:ILE:HD13	1.87	0.56
12:m:57:VAL:HG11	12:m:108:VAL:HG11	1.88	0.56
15:p:102:ARG:HG2	15:p:102:ARG:HH11	1.71	0.56
53:1:1827:U:O2'	53:1:1828:G:H5'	2.06	0.56
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.88	0.56
4:e:84:ILE:HG12	53:1:2312:U:H5'	1.87	0.56
15:p:105:LYS:O	15:p:108:ARG:HG2	2.06	0.56
28:D:34:ARG:HE	28:D:39:ARG:HD2	1.70	0.56
1:b:42:ARG:N	1:b:42:ARG:HD2	2.22	0.55
48:X:17:LYS:HB3	48:X:30:LEU:HD11	1.86	0.55
53:1:685:A:H5''	53:1:788:A:H62	1.71	0.55
53:1:1386:C:H2'	53:1:1387:A:C8	2.41	0.55
53:1:2629:U:O2'	53:1:2630:G:H5''	2.06	0.55
7:h:55:VAL:HA	53:1:1084:A:H5''	1.88	0.55
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.21	0.55
16:q:91:ARG:HG3	16:q:91:ARG:HH11	1.70	0.55
38:N:49:GLN:HA	38:N:52:GLU:OE2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:44:THR:HG23	39:O:69:THR:O	2.06	0.55
43:S:46:LYS:HD3	43:S:49:THR:HB	1.88	0.55
46:V:45:VAL:HG22	46:V:72:TRP:HB2	1.87	0.55
52:3:882:C:O2'	52:3:883:C:H5'	2.06	0.55
53:1:466:A:H2'	53:1:467:G:H5'	1.89	0.55
53:1:558:U:H2'	53:1:559:G:H8	1.71	0.55
53:1:1956:U:H2'	53:1:1957:C:H5'	1.88	0.55
53:1:2423:U:O2'	53:1:2425:A:H2'	2.06	0.55
53:1:2834:G:O2'	53:1:2835:A:H5'	2.06	0.55
4:e:101:ARG:HG3	4:e:105:ILE:HD11	1.88	0.55
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.39	0.55
35:K:33:GLU:OE2	35:K:35:LYS:HE2	2.06	0.55
40:P:23:HIS:HB3	40:P:30:ILE:HB	1.88	0.55
53:1:118:A:OP2	53:1:119:A:H5''	2.06	0.55
53:1:1657:U:H2'	53:1:1658:C:C6	2.41	0.55
53:1:2297:A:N1	53:1:2321:U:H5	2.04	0.55
22:w:46:ASN:HB2	22:w:78:ILE:HB	1.87	0.55
52:3:1033:G:C3'	52:3:1034:G:H5''	2.37	0.55
53:1:554:U:H2'	53:1:555:G:O4'	2.06	0.55
53:1:2480:C:H2'	53:1:2481:G:O4'	2.07	0.55
3:d:63:LYS:HD2	53:1:2444:G:OP2	2.07	0.55
6:g:116:ARG:HD2	6:g:133:GLN:HB3	1.89	0.55
7:h:56:ARG:NE	7:h:83:ALA:HB2	2.22	0.55
29:E:20:GLY:HA3	29:E:48:MET:HE1	1.89	0.55
29:E:57:VAL:HA	29:E:60:CYS:SG	2.46	0.55
52:3:410:G:H2'	52:3:429:U:C4	2.42	0.55
53:1:704:G:H1'	53:1:727:A:H61	1.70	0.55
53:1:2743:U:H3'	53:1:2744:G:H5''	1.89	0.55
52:3:102:G:H2'	52:3:103:U:C6	2.42	0.55
52:3:1158:C:H2'	52:3:1159:U:H4'	1.89	0.55
52:3:1346:A:O2'	52:3:1347:G:H4'	2.06	0.55
53:1:1662:U:H2'	53:1:1663:G:H8	1.71	0.55
53:1:1683:U:H2'	53:1:1684:G:C8	2.42	0.55
53:1:2798:U:H4'	53:1:2799:A:C4	2.42	0.55
11:l:19:LEU:HD12	11:l:19:LEU:N	2.20	0.55
47:W:35:SER:HA	47:W:71:ASP:HB2	1.89	0.55
52:3:70:U:H4'	52:3:71:A:H8	1.71	0.55
4:e:68:LYS:NZ	4:e:83:PRO:HD3	2.22	0.55
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.89	0.55
36:L:3:ARG:NH1	52:3:932:C:H5''	2.20	0.55
52:3:424:G:O2'	52:3:425:G:H5'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1005:A:H2'	52:3:1006:G:O4'	2.07	0.55
53:1:1421:G:H1'	53:1:1494:A:H61	1.71	0.55
53:1:2512:C:H2'	53:1:2513:A:O4'	2.07	0.55
4:e:110:ILE:HG13	4:e:136:ILE:HG21	1.89	0.55
28:D:34:ARG:NE	28:D:39:ARG:HD2	2.22	0.55
30:F:24:ARG:HH12	53:1:2742:G:P	2.29	0.55
41:Q:41:PRO:HG3	41:Q:49:ARG:CD	2.36	0.55
31:G:134:LEU:HG	31:G:138:ARG:HE	1.71	0.55
46:V:48:GLU:O	46:V:49:ASN:C	2.50	0.55
49:Y:56:ILE:HD12	49:Y:56:ILE:N	2.21	0.55
53:1:1690:A:H2'	53:1:1691:C:O4'	2.07	0.55
53:1:2329:U:H2'	53:1:2330:G:H8	1.72	0.55
4:e:62:GLN:OE1	54:2:43:C:H4'	2.07	0.54
29:E:18:LYS:HG3	53:1:651:G:H5'	1.89	0.54
40:P:15:VAL:HG21	40:P:41:LEU:HD21	1.87	0.54
42:R:114:PRO:HG2	52:3:1228:C:C5'	2.35	0.54
53:1:562:U:H2'	53:1:572:A:O4'	2.07	0.54
53:1:1833:C:H2'	53:1:1834:U:O4'	2.07	0.54
3:d:163:ASN:HB2	53:1:322:A:OP2	2.07	0.54
9:j:97:PRO:O	9:j:100:VAL:HG22	2.07	0.54
11:l:22:GLY:O	11:l:28:GLY:HA3	2.07	0.54
33:I:4:LEU:HD12	33:I:4:LEU:O	2.07	0.54
43:S:63:CYS:HB3	43:S:67:GLY:H	1.72	0.54
44:T:4:THR:HG23	52:3:659:U:H5''	1.90	0.54
52:3:265:G:H2'	52:3:267:C:H5	1.72	0.54
52:3:1271:A:H5'	52:3:1314:C:H5''	1.89	0.54
53:1:1846:G:H2'	53:1:1847:A:O4'	2.07	0.54
57:7:68:C:H2'	57:7:69:G:H8	1.72	0.54
1:b:242:HIS:O	1:b:244:VAL:HG13	2.07	0.54
42:R:9:PRO:HG2	42:R:44:ILE:HG13	1.89	0.54
52:3:357:G:OP1	52:3:367:U:H5''	2.08	0.54
52:3:580:C:H2'	52:3:581:G:O4'	2.08	0.54
53:1:1093:G:H21	53:1:1098:A:H62	1.55	0.54
44:T:71:ARG:HH22	52:3:754:C:H5'	1.71	0.54
52:3:1128:C:O2'	52:3:1129:C:H5'	2.06	0.54
53:1:279:A:H2'	53:1:280:U:H5'	1.89	0.54
53:1:438:G:H2'	53:1:439:A:H8	1.72	0.54
9:j:81:ILE:HD11	53:1:2514:U:H5'	1.88	0.54
32:H:155:ARG:HD2	52:3:1055:A:O2'	2.08	0.54
39:O:24:GLU:OE2	39:O:25:ILE:HG23	2.07	0.54
43:S:20:PHE:O	43:S:21:ALA:HB3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2638:G:H1'	53:1:2778:A:H61	1.71	0.54
53:1:2679:A:O2'	53:1:2680:U:H5'	2.08	0.54
34:J:131:ASN:HD22	52:3:19:A:P	2.30	0.54
37:M:6:ILE:HD11	37:M:31:LEU:HG	1.88	0.54
52:3:184:G:H4'	52:3:224:U:H4'	1.90	0.54
52:3:252:U:O2	52:3:252:U:H2'	2.07	0.54
10:k:10:VAL:HG21	10:k:16:ALA:O	2.08	0.54
40:P:44:ALA:HB3	40:P:69:CYS:HB2	1.89	0.54
42:R:3:ILE:H	42:R:7:ASN:HB3	1.72	0.54
52:3:1301:U:O2	52:3:1301:U:H2'	2.05	0.54
53:1:1930:G:H2'	53:1:1968:G:H1	1.73	0.54
10:k:35:VAL:HG13	10:k:36:GLY:H	1.73	0.54
48:X:50:VAL:HG11	48:X:70:LEU:HB3	1.90	0.54
52:3:1354:U:H2'	52:3:1355:G:H8	1.72	0.54
52:3:1414:U:H2'	52:3:1415:G:H8	1.73	0.54
52:3:1418:A:H3'	52:3:1419:G:C5'	2.36	0.54
53:1:828:U:H4'	53:1:831:G:N1	2.23	0.54
53:1:1105:U:C2'	53:1:1106:G:H5''	2.38	0.54
53:1:1268:A:H2'	53:1:1269:A:O4'	2.07	0.54
53:1:1278:C:H2'	53:1:1279:G:H8	1.72	0.54
4:e:23:SER:OG	54:2:56:G:H5'	2.07	0.54
24:y:24:GLU:HA	24:y:27:ASN:HB2	1.89	0.54
36:L:125:ASP:HA	36:L:128:GLU:OE2	2.08	0.54
52:3:346:G:H2'	52:3:347:G:H5'	1.90	0.54
52:3:908:A:H2'	52:3:909:A:H8	1.73	0.54
53:1:974:G:H5''	53:1:1186:G:H21	1.72	0.54
53:1:1645:G:H5''	53:1:1646:C:H5'	1.89	0.54
20:u:93:ARG:HB2	20:u:102:ILE:HD12	1.90	0.54
34:J:108:GLY:O	34:J:109:ALA:HB3	2.07	0.54
35:K:3:HIS:N	35:K:92:THR:HG22	2.17	0.54
3:d:76:PRO:HA	3:d:82:GLY:HA3	1.90	0.53
7:h:59:LEU:HD21	53:1:1047:G:C8	2.43	0.53
9:j:110:PRO:O	9:j:115:GLY:HA3	2.07	0.53
24:y:1:MET:HB2	24:y:52:ARG:NH2	2.23	0.53
52:3:966:G:N2	55:5:34:C:H5'	2.23	0.53
52:3:1251:A:O2'	52:3:1370:G:H5'	2.08	0.53
53:1:511:U:C2'	53:1:512:G:H5'	2.36	0.53
53:1:1856:U:H2'	53:1:1857:G:O4'	2.08	0.53
53:1:2180:U:H4'	55:6:17(A):U:O4'	2.08	0.53
14:o:87:ILE:HD12	14:o:87:ILE:N	2.22	0.53
19:t:4:GLU:HA	19:t:7:LEU:HD12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:139:THR:O	34:J:143:LEU:HD13	2.08	0.53
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.07	0.53
40:P:71:ASP:O	40:P:72:ALA:HB3	2.09	0.53
51:a:44:VAL:HG22	51:a:214:ILE:HD13	1.90	0.53
52:3:16:A:O2'	52:3:17:U:H5'	2.09	0.53
53:1:704:G:H1'	53:1:727:A:N6	2.24	0.53
53:1:2345:G:N3	53:1:2381:A:H2'	2.23	0.53
53:1:2552:U:C6	53:1:2554:U:H5'	2.44	0.53
6:g:114:GLU:HA	6:g:133:GLN:HE21	1.74	0.53
20:u:48:VAL:HG22	20:u:50:ALA:H	1.73	0.53
23:x:52:ALA:O	23:x:55:MET:HG2	2.08	0.53
28:D:12:ARG:HE	28:D:44:VAL:HG21	1.73	0.53
36:L:139:ASP:HA	36:L:142:ARG:HB2	1.90	0.53
42:R:28:ARG:HH21	42:R:62:PHE:HB2	1.74	0.53
42:R:56:ARG:O	42:R:59:VAL:HG12	2.08	0.53
53:1:293:U:H2'	53:1:294:A:H5''	1.90	0.53
53:1:962:G:H21	53:1:2250:G:H1	1.56	0.53
53:1:2051:A:H8	53:1:2051:A:OP2	1.91	0.53
9:j:72:LYS:HE3	9:j:74:TYR:CZ	2.43	0.53
16:q:107:ALA:HB1	17:r:48:LYS:HZ3	1.74	0.53
22:w:73:ARG:NH1	53:1:2332:C:H5''	2.22	0.53
25:z:13:ILE:HD12	53:1:989:G:C8	2.43	0.53
45:U:8:ARG:HD3	45:U:17:TYR:CE1	2.44	0.53
53:1:745:G:O2'	53:1:748:G:H1'	2.08	0.53
57:7:9:A:H1'	57:7:45:U:O2'	2.09	0.53
4:e:4:HIS:NE2	4:e:8:LYS:HE3	2.23	0.53
13:n:36:THR:HG22	53:1:1278:C:OP1	2.09	0.53
31:G:115:ASP:O	31:G:119:GLN:HG3	2.07	0.53
38:N:18:VAL:HA	38:N:64:ILE:HG23	1.89	0.53
52:3:407:U:H2'	52:3:408:A:C8	2.44	0.53
52:3:1088:G:H21	52:3:1167:A:H61	1.56	0.53
53:1:100:U:H4'	53:1:101:A:O4'	2.09	0.53
54:2:35:C:H2'	54:2:36:C:H5'	1.91	0.53
2:c:129:THR:HG23	2:c:140:HIS:O	2.08	0.53
8:i:24:GLY:O	8:i:27:LEU:HD23	2.08	0.53
19:t:50:LEU:HD13	24:y:26:PHE:CE2	2.43	0.53
37:M:17:GLN:HE21	37:M:71:VAL:HG22	1.74	0.53
44:T:47:LYS:O	44:T:49:HIS:N	2.41	0.53
45:U:33:ILE:HD12	45:U:33:ILE:N	2.24	0.53
53:1:953:G:H2'	53:1:954:G:H8	1.74	0.53
55:5:41:C:H2'	55:5:42:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:126:VAL:H	3:d:157:LEU:HD21	1.72	0.53
4:e:3:LEU:HA	4:e:6:TYR:HB3	1.90	0.53
4:e:126:ASN:ND2	4:e:156:THR:HG23	2.24	0.53
6:g:40:THR:OG1	6:g:43:ASN:ND2	2.42	0.53
22:w:36:GLN:OE1	22:w:40:LYS:N	2.41	0.53
31:G:66:ILE:HG13	31:G:159:ALA:HB3	1.90	0.53
52:3:598:U:H2'	52:3:599:C:C6	2.43	0.53
52:3:1251:A:H2'	52:3:1252:A:C8	2.44	0.53
53:1:381:G:O2'	53:1:382:A:H5'	2.09	0.53
53:1:1570:A:H2'	53:1:1571:A:C8	2.44	0.53
54:2:2:G:H2'	54:2:3:C:C6	2.44	0.53
1:b:224:MET:SD	53:1:782:A:C2	3.02	0.53
8:i:9:LYS:HE3	53:1:1061:U:P	2.48	0.53
8:i:23:VAL:HG13	8:i:26:ALA:HB3	1.91	0.53
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.91	0.53
52:3:792:A:H1'	52:3:794:A:N7	2.23	0.53
53:1:433:C:O2'	53:1:434:U:H5'	2.09	0.53
53:1:859:G:O2'	53:1:860:U:C6	2.61	0.53
53:1:2291:U:H2'	53:1:2292:U:C6	2.44	0.53
1:b:173:LEU:HD11	1:b:183:VAL:HG21	1.91	0.53
4:e:68:LYS:HZ3	4:e:83:PRO:HD3	1.73	0.53
7:h:17:GLU:HB3	7:h:86:MET:HG3	1.90	0.53
12:m:62:LYS:HD3	12:m:64:TRP:CZ2	2.43	0.53
33:I:159:GLU:OE2	33:I:160:LEU:HG	2.09	0.53
36:L:78:ARG:CZ	52:3:1382:C:H4'	2.37	0.53
38:N:113:LYS:HZ1	52:3:1367:C:P	2.32	0.53
53:1:1357:C:H2'	53:1:1358:G:O4'	2.09	0.53
53:1:2345:G:H5'	53:1:2347:C:H5'	1.91	0.53
32:H:150:VAL:HG23	32:H:199:VAL:HG22	1.89	0.53
37:M:80:PRO:HG2	52:3:878:A:H5'	1.91	0.53
49:Y:66:ILE:HG23	49:Y:70:LYS:HB3	1.90	0.53
52:3:26:A:N6	52:3:558:G:H1'	2.24	0.53
52:3:142:G:O2'	52:3:143:A:H5'	2.09	0.53
52:3:556:C:O2'	52:3:557:G:H5'	2.09	0.53
52:3:1070:U:H2'	52:3:1071:C:C6	2.44	0.53
53:1:644:A:H2'	53:1:645:C:C5'	2.39	0.53
53:1:786:C:O2'	53:1:787:C:H5'	2.08	0.53
53:1:2070:A:H2'	53:1:2071:A:O4'	2.09	0.53
54:2:51:G:H2'	54:2:52:A:O4'	2.09	0.53
1:b:154:ALA:HB2	1:b:161:VAL:HG23	1.91	0.52
7:h:55:VAL:HA	53:1:1084:A:H4'	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:48:GLY:HA3	22:w:58:LYS:HE3	1.90	0.52
45:U:1:MET:HB2	52:3:135:C:N3	2.24	0.52
52:3:78:A:H2'	52:3:79:G:O4'	2.09	0.52
52:3:291:U:H2'	52:3:292:G:C8	2.44	0.52
53:1:2658:C:H2'	53:1:2659:G:O4'	2.08	0.52
14:o:60:GLU:OE2	14:o:61:GLN:HG3	2.09	0.52
35:K:52:ASN:O	35:K:53:LYS:HB2	2.09	0.52
52:3:77:A:H2'	52:3:78:A:C8	2.43	0.52
52:3:779:C:H2'	52:3:780:A:O4'	2.09	0.52
53:1:1475:G:HO2'	53:1:1476:U:H6	1.56	0.52
53:1:2391:G:H2'	53:1:2424:C:H41	1.73	0.52
4:e:84:ILE:HG21	53:1:2312:U:C4'	2.38	0.52
8:i:20:SER:HB3	8:i:21:PRO:HD3	1.91	0.52
22:w:71:LYS:HG3	22:w:73:ARG:HG3	1.91	0.52
23:x:31:ASN:ND2	53:1:2230:G:N3	2.58	0.52
46:V:12:VAL:HG22	46:V:23:ALA:HB2	1.92	0.52
52:3:77:A:H2'	52:3:78:A:H8	1.75	0.52
53:1:225:C:H2'	53:1:226:A:O4'	2.10	0.52
53:1:807:U:H2'	53:1:808:G:C8	2.42	0.52
53:1:2502:G:H5'	53:1:2503:A:H5''	1.90	0.52
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.91	0.52
9:j:114:LEU:HG	9:j:118:MET:HE3	1.91	0.52
36:L:132:THR:HA	36:L:135:LYS:HD2	1.91	0.52
42:R:85:TYR:CE2	52:3:1321:U:H5''	2.45	0.52
52:3:1201:A:H4'	52:3:1203:C:OP2	2.09	0.52
53:1:171:U:H2'	53:1:172:A:C8	2.44	0.52
53:1:967:U:H2'	53:1:968:C:C6	2.44	0.52
53:1:2657:A:H1'	53:1:2665:A:N6	2.25	0.52
2:c:11:MET:O	53:1:2682:A:H5'	2.08	0.52
5:f:153:PRO:HA	5:f:159:LYS:O	2.10	0.52
14:o:33:ARG:NH2	54:2:27:C:OP2	2.42	0.52
19:t:73:ARG:HH22	53:1:456:C:H2'	1.74	0.52
37:M:28:SER:HB2	37:M:58:LEU:HB2	1.90	0.52
52:3:411:A:C4	52:3:413:G:H1'	2.44	0.52
52:3:1195:C:H5''	52:3:1196:A:OP2	2.09	0.52
53:1:213:A:H2'	53:1:214:G:C8	2.44	0.52
53:1:570:G:H2'	53:1:2030:A:N7	2.24	0.52
53:1:784:G:H5'	53:1:785:G:OP1	2.10	0.52
53:1:1509:A:H2'	53:1:1510:G:C8	2.44	0.52
53:1:1979:U:O2'	53:1:1980:G:H5'	2.09	0.52
8:i:89:SER:HA	8:i:135:MET:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:109:VAL:HG12	16:q:113:LYS:HE2	1.90	0.52
18:s:42:LYS:HE2	53:1:2011:U:OP1	2.09	0.52
52:3:123:U:H2'	52:3:124:C:C6	2.44	0.52
53:1:386:G:H3'	53:1:387:U:C5'	2.39	0.52
53:1:1965:C:H5''	53:1:1966:A:H2'	1.91	0.52
53:1:2443:C:O2'	53:1:2444:G:H5'	2.10	0.52
3:d:35:TYR:OH	3:d:176:ASP:OD2	2.28	0.52
7:h:102:ALA:HB1	7:h:107:GLU:HG3	1.92	0.52
9:j:84:ILE:HG23	9:j:84:ILE:O	2.10	0.52
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.90	0.52
34:J:97:PRO:HA	34:J:122:VAL:HG12	1.92	0.52
44:T:52:ARG:NH1	53:1:715:A:H61	2.05	0.52
53:1:1028:A:N6	53:1:1125:G:H2'	2.24	0.52
53:1:2141:G:H22	53:1:2151:U:H1'	1.75	0.52
36:L:69:ARG:HG3	36:L:95:ARG:HB3	1.92	0.52
41:Q:93:ARG:NH1	52:3:911:U:OP2	2.42	0.52
45:U:6:LEU:HD22	45:U:17:TYR:HB3	1.91	0.52
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.92	0.52
52:3:301:G:H2'	52:3:302:G:H8	1.73	0.52
52:3:540:G:H2'	52:3:541:G:H8	1.74	0.52
1:b:241:LYS:O	53:1:1902:C:H4'	2.10	0.52
3:d:163:ASN:OD1	53:1:323:C:H5''	2.09	0.52
15:p:20:ARG:HB3	15:p:21:PRO:HD2	1.92	0.52
24:y:6:LEU:HD12	24:y:60:LYS:HE2	1.91	0.52
34:J:107:GLY:HA2	52:3:8:A:H1'	1.92	0.52
41:Q:122:LYS:HD2	41:Q:122:LYS:N	2.24	0.52
51:a:221:GLY:N	53:1:2176:A:H5''	2.25	0.52
52:3:149:A:H1'	52:3:1446:A:H2	1.75	0.52
52:3:1004:A:H2'	52:3:1005:A:O4'	2.10	0.52
52:3:1430:A:H2'	52:3:1431:A:O4'	2.10	0.52
52:3:1525:G:H2'	52:3:1526:G:H8	1.74	0.52
53:1:1139:G:O2'	53:1:1140:C:H5'	2.09	0.52
53:1:1900:A:H1'	53:1:1970:A:H2'	1.92	0.52
53:1:2626:C:O2'	53:1:2627:G:H5'	2.09	0.52
55:5:11:A:H2'	55:5:12:G:O4'	2.10	0.52
57:7:46:G:O2'	57:7:48:C:H5'	2.10	0.52
14:o:49:VAL:HG21	14:o:82:ALA:HA	1.92	0.52
52:3:477:C:H2'	52:3:478:A:C8	2.45	0.52
52:3:1355:G:H2'	52:3:1356:G:H8	1.75	0.52
53:1:1213:A:N6	53:1:1236:G:H1'	2.25	0.52
53:1:1609:A:H1'	53:1:1616:A:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:95:U:H2'	54:2:96:G:H8	1.75	0.52
20:u:85:ARG:NH1	20:u:99:SER:OG	2.43	0.51
35:K:52:ASN:O	35:K:53:LYS:CB	2.59	0.51
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.91	0.51
45:U:54:LEU:HA	45:U:57:ILE:HD12	1.93	0.51
52:3:1199:U:H2'	52:3:1200:C:H5'	1.92	0.51
52:3:1436:U:H2'	52:3:1437:A:C8	2.44	0.51
53:1:1827:U:C2'	53:1:1828:G:H5'	2.40	0.51
54:2:78:A:H62	54:2:98:G:H21	1.55	0.51
8:i:2:LYS:HE3	8:i:5:GLN:NE2	2.25	0.51
8:i:25:PRO:HB2	53:1:1095:A:N6	2.19	0.51
17:r:74:ILE:N	17:r:74:ILE:HD12	2.24	0.51
38:N:112:ARG:NH2	52:3:1368:A:OP1	2.40	0.51
38:N:117:LEU:HD12	38:N:117:LEU:N	2.26	0.51
53:1:859:G:O2'	53:1:860:U:H6	1.93	0.51
53:1:1447:C:H2'	53:1:1448:G:H8	1.74	0.51
53:1:1991:U:C2'	53:1:1992:G:H5''	2.40	0.51
53:1:2457:U:O2'	53:1:2458:G:H5'	2.10	0.51
53:1:2554:U:H2'	53:1:2555:U:C6	2.44	0.51
5:f:2:ARG:HH12	53:1:1113:U:H5'	1.75	0.51
32:H:156:LEU:HD12	32:H:156:LEU:O	2.10	0.51
34:J:54:GLU:HG2	34:J:56:PRO:HD2	1.92	0.51
41:Q:28:GLN:HB3	41:Q:80:LEU:HD11	1.93	0.51
45:U:8:ARG:CZ	45:U:15:PRO:HB3	2.40	0.51
47:W:28:LEU:HD23	47:W:58:ILE:HD13	1.92	0.51
52:3:162:A:H2'	52:3:163:C:O4'	2.10	0.51
52:3:1139:G:H5''	52:3:1140:C:C5	2.45	0.51
52:3:1355:G:H2'	52:3:1356:G:C8	2.45	0.51
55:6:12:G:H2'	55:6:13:C:C6	2.45	0.51
1:b:16:VAL:HB	1:b:203:VAL:HG22	1.92	0.51
2:c:48:ILE:HG23	2:c:84:LEU:HD11	1.93	0.51
4:e:55:ASP:OD2	4:e:149:ARG:NH2	2.41	0.51
7:h:55:VAL:HA	53:1:1084:A:C4'	2.40	0.51
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.92	0.51
16:q:21:LYS:HD3	53:1:20:C:OP1	2.10	0.51
52:3:784:A:H4'	53:1:1837:C:OP1	2.10	0.51
53:1:2360:G:H2'	53:1:2361:G:H5'	1.91	0.51
18:s:84:ARG:HB2	18:s:96:ILE:HG13	1.91	0.51
32:H:1:GLY:HA3	52:3:1060:U:C5	2.44	0.51
40:P:121:ARG:CZ	50:Z:35:GLU:HG2	2.41	0.51
50:Z:34:ARG:HH11	50:Z:34:ARG:HG3	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:20:U:H2'	52:3:21:G:O4'	2.11	0.51
53:1:414:C:H2'	53:1:415:A:C8	2.45	0.51
53:1:481:G:H1'	53:1:506:G:N2	2.26	0.51
53:1:2139:U:H2'	53:1:2140:G:C8	2.45	0.51
53:1:2743:U:C2'	53:1:2744:G:H5''	2.40	0.51
54:2:26:C:O2	54:2:117:G:H1'	2.10	0.51
6:g:108:VAL:HG12	6:g:110:VAL:HG13	1.92	0.51
7:h:53:ARG:HB3	53:1:1084:A:OP1	2.09	0.51
15:p:50:ARG:HH21	15:p:52:ARG:NH1	2.09	0.51
15:p:113:LEU:O	15:p:113:LEU:HD12	2.11	0.51
30:F:19:ARG:HD2	30:F:24:ARG:HD2	1.92	0.51
40:P:91:GLY:O	40:P:92:ARG:HG2	2.11	0.51
52:3:762:U:H2'	52:3:763:G:H8	1.75	0.51
53:1:2075:U:H4'	53:1:2596:U:O2	2.10	0.51
53:1:2760:C:O2'	53:1:2761:A:H5'	2.09	0.51
57:7:14:A:H61	57:7:21:A:H2	1.59	0.51
3:d:150:THR:HG22	3:d:152:GLU:H	1.75	0.51
52:3:142:G:H2'	52:3:143:A:O4'	2.11	0.51
52:3:273:U:H2'	52:3:274:A:H5'	1.92	0.51
52:3:311:C:H2'	52:3:312:C:C6	2.46	0.51
52:3:1506:U:O2'	52:3:1507:A:H5'	2.10	0.51
53:1:2508:G:H1	53:1:2580:U:H3	1.58	0.51
10:k:58:LEU:N	10:k:58:LEU:HD23	2.26	0.51
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.45	0.51
52:3:482:A:H2'	52:3:483:C:O4'	2.11	0.51
52:3:865:A:H5'	52:3:1078:U:O4	2.09	0.51
53:1:2126:A:H2'	53:1:2162:G:N2	2.26	0.51
53:1:2343:U:O2'	53:1:2344:U:H5'	2.11	0.51
53:1:2391:G:H2'	53:1:2424:C:N4	2.25	0.51
53:1:2467:C:H2'	53:1:2468:A:O4'	2.11	0.51
53:1:2623:G:H2'	53:1:2624:G:H8	1.76	0.51
53:1:2655:G:O2'	53:1:2656:U:H5	1.94	0.51
57:7:47:U:H3'	57:7:48:C:H5''	1.93	0.51
9:j:57:LEU:O	9:j:58:ASN:HB2	2.10	0.51
32:H:86:LEU:O	32:H:90:VAL:HG22	2.10	0.51
52:3:1436:U:H2'	52:3:1437:A:H8	1.76	0.51
53:1:1251:C:O2'	53:1:1252:G:H3'	2.11	0.51
53:1:1430:G:H2'	53:1:1431:A:O4'	2.11	0.51
53:1:1790:C:H2'	53:1:1791:A:C5	2.46	0.51
53:1:2339:C:H2'	53:1:2340:A:C8	2.46	0.51
53:1:2646:C:H2'	53:1:2647:U:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2788:C:H2'	53:1:2789:C:C6	2.45	0.51
1:b:59:GLN:HA	53:1:1568:G:H5'	1.93	0.51
1:b:119:VAL:HG21	6:g:91:PHE:O	2.11	0.51
1:b:216:ARG:HG3	1:b:217:PRO:HD2	1.93	0.51
12:m:55:ARG:HH22	57:7:53:G:C4'	2.24	0.51
23:x:58:ILE:HG12	23:x:66:VAL:HG21	1.92	0.51
32:H:56:ILE:HG22	32:H:63:ILE:HD11	1.93	0.51
32:H:129:PHE:CD2	32:H:156:LEU:HD22	2.46	0.51
37:M:12:ARG:CZ	52:3:826:C:H5'	2.41	0.51
40:P:91:GLY:O	40:P:93:GLU:N	2.36	0.51
41:Q:115:LYS:O	41:Q:116:TYR:HB2	2.10	0.51
43:S:41:TRP:O	43:S:45:LEU:HG	2.11	0.51
45:U:51:ARG:C	45:U:52:LEU:HD12	2.36	0.51
52:3:110:C:H2'	52:3:111:G:O4'	2.11	0.51
52:3:149:A:H1'	52:3:1446:A:C2	2.46	0.51
52:3:423:G:C2'	52:3:424:G:H5'	2.40	0.51
52:3:871:U:H5''	52:3:872:A:OP2	2.11	0.51
52:3:1202:U:H2'	52:3:1203:C:O4'	2.10	0.51
52:3:1346:A:H2'	52:3:1346:A:N3	2.26	0.51
53:1:191:A:H2'	53:1:192:C:C6	2.46	0.51
53:1:2747:G:O6	53:1:2755:C:H5''	2.11	0.51
4:e:10:GLU:HA	4:e:13:LYS:HZ2	1.76	0.50
7:h:58:THR:HA	7:h:63:ALA:HB3	1.92	0.50
15:p:74:GLN:HB2	15:p:77:SER:HB2	1.93	0.50
42:R:100:ARG:HG3	52:3:950:U:OP2	2.11	0.50
51:a:214:ILE:HG23	51:a:222:VAL:HG13	1.93	0.50
52:3:1404:C:H2'	52:3:1405:G:C8	2.46	0.50
53:1:941:A:H2'	53:1:942:G:O4'	2.11	0.50
1:b:140:VAL:HG12	1:b:191:LEU:HD23	1.92	0.50
6:g:110:VAL:HB	6:g:114:GLU:HG3	1.92	0.50
6:g:132:PHE:HB2	6:g:140:ALA:HB3	1.93	0.50
15:p:48:ALA:HB3	15:p:59:THR:OG1	2.11	0.50
17:r:53:PHE:O	17:r:54:VAL:C	2.54	0.50
44:T:88:ARG:HG3	53:1:714:U:H5	1.76	0.50
52:3:407:U:H2'	52:3:408:A:H8	1.75	0.50
52:3:1230:C:H2'	52:3:1231:G:H8	1.75	0.50
53:1:876:C:H2'	53:1:877:A:O4'	2.11	0.50
53:1:1892:C:H2'	53:1:1893:C:H6	1.76	0.50
15:p:50:ARG:NH2	15:p:52:ARG:HD2	2.25	0.50
24:y:41:HIS:CG	53:1:96:C:H4'	2.47	0.50
37:M:94:VAL:HB	37:M:99:GLY:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:88:MET:O	39:O:89:ARG:HG2	2.11	0.50
53:1:275:C:H3'	53:1:276:U:H5''	1.93	0.50
53:1:441:U:O2'	53:1:442:G:H5'	2.11	0.50
54:2:28:C:H2'	54:2:29:A:C8	2.46	0.50
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.46	0.50
16:q:23:TYR:CD1	53:1:533:G:H5'	2.46	0.50
24:y:56:LEU:HA	24:y:59:GLU:HG2	1.93	0.50
42:R:28:ARG:NH2	42:R:62:PHE:HB2	2.27	0.50
52:3:538:G:H2'	52:3:539:A:H8	1.76	0.50
52:3:667:G:H2'	52:3:668:G:H8	1.77	0.50
52:3:945:G:H21	52:3:1334:G:H4'	1.76	0.50
53:1:2687:U:H2'	53:1:2688:G:O4'	2.10	0.50
7:h:11:ILE:O	7:h:14:GLU:HG3	2.12	0.50
7:h:23:LEU:HD22	7:h:118:ILE:HG13	1.89	0.50
19:t:39:THR:HG1	53:1:1599:U:P	2.34	0.50
31:G:213:LEU:HA	31:G:216:VAL:HG22	1.92	0.50
33:I:7:LYS:HG2	52:3:430:A:OP2	2.10	0.50
40:P:34:THR:HG22	40:P:40:ALA:HA	1.93	0.50
43:S:68:ARG:HH12	43:S:70:HIS:HB2	1.77	0.50
49:Y:70:LYS:HA	49:Y:73:ARG:NH1	2.27	0.50
53:1:340:A:H2'	53:1:341:C:O4'	2.12	0.50
53:1:2328:A:H2'	53:1:2329:U:C6	2.46	0.50
55:5:53:G:H2'	55:5:54:U:C6	2.47	0.50
5:f:130:ILE:HD13	5:f:147:LEU:HD21	1.93	0.50
6:g:2:GLN:O	6:g:39:ALA:HB3	2.12	0.50
8:i:9:LYS:HG3	53:1:1070:A:H2	1.76	0.50
8:i:34:ILE:HG23	8:i:35:MET:HE2	1.94	0.50
26:B:32:THR:HG23	26:B:33:SER:H	1.76	0.50
34:J:80:LEU:HD13	34:J:122:VAL:CG1	2.36	0.50
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.92	0.50
39:O:14:ASP:HB3	39:O:17:LEU:HB3	1.93	0.50
41:Q:19:ASN:C	41:Q:21:PRO:HD3	2.36	0.50
43:S:80:ARG:CG	43:S:81:ILE:HD12	2.42	0.50
50:Z:65:ARG:CZ	52:3:1088:G:H4'	2.41	0.50
57:7:57:G:O2'	57:7:58:A:H5'	2.12	0.50
3:d:118:LEU:HA	3:d:186:VAL:HG23	1.94	0.50
4:e:133:GLU:HB3	4:e:135:ILE:HG22	1.93	0.50
5:f:32:LEU:HD11	5:f:135:ALA:O	2.12	0.50
14:o:76:LYS:O	14:o:80:GLU:HG3	2.11	0.50
27:C:4:ILE:HD12	27:C:4:ILE:N	2.27	0.50
40:P:124:LYS:O	50:Z:34:ARG:HD3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:56:U:H2'	52:3:57:G:C8	2.47	0.50
52:3:311:C:H2'	52:3:312:C:H6	1.77	0.50
53:1:2000:C:O2'	53:1:2001:C:H5'	2.12	0.50
53:1:2339:C:H2'	53:1:2340:A:H8	1.77	0.50
54:2:5:U:H2'	54:2:6:G:H8	1.77	0.50
4:e:3:LEU:HD23	4:e:100:GLU:HG2	1.93	0.50
29:E:34:LYS:HD2	53:1:2391:G:OP2	2.12	0.50
39:O:10:LEU:HD23	39:O:10:LEU:H	1.77	0.50
42:R:6:ILE:HG23	42:R:7:ASN:N	2.26	0.50
48:X:10:ILE:HG13	48:X:14:LEU:HD23	1.93	0.50
52:3:908:A:H2'	52:3:909:A:C8	2.47	0.50
53:1:1794:A:O2'	53:1:1795:C:H5'	2.12	0.50
53:1:2628:C:H3'	53:1:2629:U:H5'	1.94	0.50
31:G:42:LEU:HD12	31:G:42:LEU:H	1.77	0.50
34:J:15:ILE:HD12	34:J:15:ILE:N	2.27	0.50
38:N:121:ARG:HG3	52:3:1348:U:H4'	1.93	0.50
52:3:784:A:H2'	52:3:785:G:C8	2.47	0.50
52:3:880:C:H2'	52:3:881:G:H8	1.77	0.50
52:3:1097:C:H2'	52:3:1098:C:C6	2.47	0.50
53:1:37:C:H4'	53:1:451:U:OP1	2.12	0.50
53:1:473:G:C2'	53:1:474:G:H5'	2.42	0.50
53:1:948:C:H2'	53:1:949:G:C8	2.47	0.50
53:1:1434:A:H2'	53:1:1435:G:C8	2.47	0.50
53:1:1637:A:H5'	53:1:1760:C:O2'	2.12	0.50
53:1:1775:U:H2'	53:1:1776:G:H5'	1.94	0.50
53:1:1796:U:H2'	53:1:1797:G:C8	2.47	0.50
53:1:2350:C:H2'	53:1:2351:G:O4'	2.11	0.50
57:7:47:U:H3'	57:7:48:C:C5'	2.42	0.50
3:d:117:ARG:NH2	3:d:183:PHE:O	2.42	0.49
8:i:135:MET:HE1	53:1:1062:G:N3	2.27	0.49
10:k:15:GLY:O	10:k:47:ILE:HG12	2.12	0.49
14:o:7:ARG:HA	14:o:10:ARG:HE	1.77	0.49
18:s:72:THR:HG21	18:s:108:SER:HB3	1.93	0.49
37:M:8:ASP:HA	37:M:11:THR:HG22	1.94	0.49
52:3:868:C:H2'	52:3:869:G:O4'	2.12	0.49
53:1:575:A:O2'	53:1:576:U:H5'	2.11	0.49
53:1:669:G:H2'	53:1:669:G:N3	2.27	0.49
53:1:1079:C:H2'	53:1:1080:A:C8	2.46	0.49
53:1:1326:U:H2'	53:1:1327:A:H8	1.77	0.49
53:1:2676:C:H2'	53:1:2677:G:C8	2.47	0.49
7:h:61:ARG:NH1	53:1:1046:A:OP2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:81:ILE:HD11	53:1:2514:U:C5'	2.42	0.49
35:K:51:ILE:O	35:K:52:ASN:CG	2.55	0.49
38:N:119:LYS:HD2	52:3:1350:A:OP2	2.12	0.49
42:R:14:ALA:CB	42:R:33:LEU:HD21	2.42	0.49
53:1:676:A:H62	53:1:802:A:H61	1.60	0.49
53:1:1361:G:H2'	53:1:1362:C:C6	2.46	0.49
53:1:2097:A:H2'	53:1:2098:U:O4'	2.12	0.49
53:1:2185:U:H2'	53:1:2186:G:C8	2.47	0.49
1:b:79:ARG:HG3	1:b:81:GLU:OE2	2.13	0.49
3:d:44:ARG:HD2	53:1:444:C:OP2	2.12	0.49
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.94	0.49
7:h:122:GLN:CD	7:h:122:GLN:N	2.71	0.49
10:k:99:ILE:HD13	10:k:115:ILE:HG23	1.95	0.49
14:o:3:LYS:NZ	54:2:29:A:H5''	2.27	0.49
32:H:178:ARG:HD2	32:H:206:ILE:HG13	1.93	0.49
42:R:113:LYS:CG	42:R:114:PRO:HD3	2.40	0.49
52:3:328:C:H5'	52:3:329:A:H5'	1.93	0.49
52:3:1488:G:H2'	52:3:1489:G:H8	1.77	0.49
52:3:1516:G:H2'	52:3:1518:A:OP2	2.12	0.49
53:1:858:G:H5'	53:1:859:G:OP2	2.11	0.49
53:1:948:C:H2'	53:1:949:G:H8	1.77	0.49
53:1:1475:G:O2'	53:1:1476:U:H6	1.95	0.49
53:1:1683:U:H2'	53:1:1684:G:H8	1.76	0.49
53:1:1695:G:H2'	53:1:1696:G:O4'	2.13	0.49
54:2:3:C:H3'	54:2:4:C:H5''	1.95	0.49
55:6:6:G:O2'	55:6:7:G:H5'	2.12	0.49
57:7:9:A:N3	57:7:45:U:H2'	2.27	0.49
14:o:7:ARG:NH1	14:o:95:SER:O	2.45	0.49
18:s:31:GLN:HA	18:s:34:ASP:OD2	2.12	0.49
32:H:56:ILE:HD12	32:H:65:VAL:HG22	1.94	0.49
36:L:36:SER:HA	38:N:42:THR:HG21	1.95	0.49
41:Q:4:ASN:HD21	52:3:585:G:H4'	1.78	0.49
49:Y:44:ALA:O	49:Y:48:LYS:HG2	2.12	0.49
52:3:1256:A:H1'	52:3:1258:G:C4	2.47	0.49
53:1:141:G:H3'	53:1:142:A:O4'	2.13	0.49
53:1:1054:A:H2'	53:1:1055:G:C8	2.47	0.49
53:1:1138:G:H2'	53:1:1139:G:O4'	2.13	0.49
53:1:1360:G:H22	53:1:2214:C:H42	1.59	0.49
53:1:2361:G:O2'	53:1:2362:C:H5'	2.12	0.49
53:1:2579:C:O2'	53:1:2580:U:H5'	2.11	0.49
1:b:18:VAL:O	1:b:18:VAL:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:42:ARG:HH11	1:b:42:ARG:HG2	1.77	0.49
5:f:51:PHE:CE2	5:f:68:ARG:HA	2.48	0.49
15:p:102:ARG:NH2	53:1:1754:A:O2'	2.45	0.49
32:H:87:ARG:HD2	32:H:87:ARG:O	2.13	0.49
35:K:50:PRO:HG3	35:K:55:HIS:NE2	2.28	0.49
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.94	0.49
40:P:126:ARG:O	50:Z:34:ARG:NH2	2.44	0.49
52:3:514:C:H2'	52:3:515:G:C8	2.47	0.49
52:3:575:G:O2'	52:3:821:G:H5'	2.13	0.49
52:3:1033:G:H3'	52:3:1034:G:H5''	1.94	0.49
53:1:833:A:H2'	53:1:834:G:H8	1.77	0.49
53:1:2497:A:H8	53:1:2497:A:OP2	1.95	0.49
55:6:3:C:H2'	55:6:4:G:C8	2.46	0.49
7:h:55:VAL:HA	53:1:1084:A:C5'	2.43	0.49
8:i:52:LEU:O	8:i:54:ILE:HG13	2.13	0.49
8:i:97:VAL:HG23	8:i:137:LEU:HG	1.94	0.49
13:n:79:LEU:O	13:n:80:PHE:HB2	2.12	0.49
26:B:29:VAL:HG22	26:B:34:GLY:HA2	1.94	0.49
32:H:13:ILE:N	32:H:13:ILE:HD12	2.27	0.49
53:1:818:G:O2'	53:1:819:A:H5''	2.11	0.49
53:1:996:A:H2'	53:1:997:G:C8	2.48	0.49
33:I:77:GLU:O	33:I:81:LEU:HD13	2.13	0.49
35:K:10:VAL:HG12	35:K:58:HIS:HB3	1.94	0.49
51:a:59:VAL:C	51:a:60:ARG:HD2	2.37	0.49
52:3:1032:G:H3'	52:3:1032:G:N3	2.28	0.49
52:3:1288:A:O2'	52:3:1353:G:H5'	2.13	0.49
53:1:1048:A:H2	53:1:1112:G:H1'	1.77	0.49
53:1:1078:U:H5''	53:1:1079:C:H5''	1.93	0.49
53:1:2818:U:H2'	53:1:2819:G:C8	2.42	0.49
13:n:39:PRO:HG2	53:1:1651:G:H4'	1.94	0.49
27:C:6:GLU:OE1	27:C:26:LYS:HB2	2.13	0.49
32:H:39:ARG:NH1	32:H:54:ILE:HG13	2.27	0.49
35:K:81:ASN:HB3	35:K:84:VAL:HG12	1.95	0.49
41:Q:82:ARG:NH1	52:3:552:U:H5'	2.27	0.49
41:Q:114:SER:CB	52:3:35:G:H21	2.25	0.49
52:3:1001:C:H2'	52:3:1002:G:H8	1.77	0.49
53:1:819:A:C4	53:1:1189:A:C2	3.01	0.49
53:1:940:G:H2'	53:1:941:A:H5''	1.94	0.49
53:1:1786:A:H1'	53:1:1938:A:N6	2.27	0.49
53:1:2478:A:H2'	53:1:2479:U:O4'	2.13	0.49
3:d:59:PRO:HB2	3:d:60:TRP:CE3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:21:TRP:HB3	32:H:58:ARG:H	1.78	0.49
35:K:48:ALA:HB1	47:W:68:PRO:HG3	1.95	0.49
43:S:15:LEU:HG	43:S:54:SER:HB3	1.94	0.49
50:Z:61:ARG:HG2	50:Z:61:ARG:O	2.13	0.49
51:a:169:GLY:C	51:a:170:ILE:HD12	2.38	0.49
52:3:900:A:H2'	52:3:901:A:C8	2.48	0.49
52:3:990:C:H2'	52:3:991:U:O4'	2.12	0.49
53:1:1278:C:H2'	53:1:1279:G:C8	2.48	0.49
7:h:1:MET:HE1	53:1:1048:A:OP1	2.13	0.49
33:I:23:GLY:HA2	33:I:108:ALA:HB1	1.94	0.49
42:R:7:ASN:ND2	42:R:21:ILE:HD11	2.28	0.49
52:3:335:C:H2'	52:3:336:A:C8	2.48	0.49
53:1:331:C:O2'	53:1:332:A:H5'	2.13	0.49
53:1:2048:G:H3'	53:1:2049:G:H5''	1.95	0.49
53:1:2665:A:O2'	53:1:2666:C:H5'	2.12	0.49
54:2:106:G:H2'	54:2:107:G:O4'	2.13	0.49
55:6:50:U:H2'	55:6:51:C:C6	2.48	0.49
56:4:17:U:O2'	56:4:18:G:H5'	2.13	0.49
8:i:123:ALA:HA	8:i:126:ARG:NH1	2.28	0.48
34:J:22:LYS:HG3	52:3:1081:A:H5'	1.94	0.48
34:J:126:ALA:HB3	52:3:9:G:OP1	2.13	0.48
51:a:205:LYS:HB3	53:1:1860:G:O3'	2.13	0.48
52:3:1033:G:H2'	52:3:1034:G:H5''	1.95	0.48
52:3:1062:U:H2'	52:3:1063:C:C6	2.48	0.48
53:1:277:G:H1'	53:1:361:G:O6	2.13	0.48
53:1:468:G:H2'	53:1:469:G:O4'	2.13	0.48
53:1:1930:G:H2'	53:1:1968:G:N1	2.28	0.48
53:1:2013:A:H61	53:1:2613:U:H3	1.60	0.48
53:1:2313:C:H2'	53:1:2314:A:C8	2.48	0.48
1:b:62:ARG:HG3	1:b:62:ARG:NH1	2.27	0.48
22:w:25:GLU:OE1	53:1:923:G:H4'	2.14	0.48
32:H:112:ALA:HB3	32:H:184:ASN:HD22	1.78	0.48
52:3:1088:G:N2	52:3:1167:A:H61	2.10	0.48
52:3:1170:A:H2'	52:3:1171:A:O4'	2.11	0.48
52:3:1369:C:H2'	52:3:1370:G:C8	2.48	0.48
53:1:171:U:H2'	53:1:172:A:H8	1.77	0.48
53:1:752:A:O2'	53:1:1781:U:H5'	2.13	0.48
53:1:1666:G:O2'	53:1:1667:G:H5'	2.13	0.48
53:1:2314:A:H2'	53:1:2315:G:H8	1.78	0.48
14:o:33:ARG:HB2	54:2:52:A:N6	2.29	0.48
31:G:129:THR:HG22	31:G:132:GLU:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:49:ASP:O	33:I:52:VAL:HG22	2.13	0.48
35:K:6:ILE:HD13	35:K:74:LEU:HD11	1.94	0.48
35:K:50:PRO:HG3	35:K:55:HIS:CE1	2.49	0.48
42:R:27:THR:CG2	52:3:1328:C:H5''	2.42	0.48
50:Z:6:ARG:HB2	50:Z:6:ARG:HH11	1.79	0.48
52:3:166:U:H2'	52:3:167:A:C8	2.48	0.48
52:3:1483:A:H2'	52:3:1484:C:H5'	1.95	0.48
53:1:854:C:H2'	53:1:855:G:H8	1.78	0.48
53:1:1367:A:C2'	53:1:1368:G:H5'	2.42	0.48
53:1:1516:G:O2'	53:1:1517:G:H5'	2.13	0.48
8:i:7:TYR:HB3	8:i:59:THR:HA	1.95	0.48
15:p:2:ASN:ND2	53:1:2876:G:H4'	2.28	0.48
17:r:49:ILE:O	17:r:49:ILE:HG13	2.12	0.48
19:t:61:LEU:HD12	53:1:1340:U:H2'	1.96	0.48
21:v:7:GLU:HB2	21:v:41:GLU:OE2	2.14	0.48
30:F:25:VAL:HB	30:F:35:GLN:HG2	1.94	0.48
44:T:55:LEU:HA	44:T:58:MET:HE3	1.95	0.48
50:Z:41:THR:O	50:Z:45:LYS:HG2	2.13	0.48
52:3:1118:U:H2'	52:3:1119:C:C6	2.48	0.48
53:1:1354:A:H2'	53:1:1355:G:O4'	2.14	0.48
2:c:130:GLN:NE2	53:1:2578:G:H21	2.11	0.48
3:d:109:LEU:HD13	3:d:112:LEU:HD12	1.95	0.48
8:i:73:PRO:O	8:i:112:LYS:NZ	2.47	0.48
46:V:75:VAL:HG23	46:V:76:ARG:H	1.78	0.48
47:W:72:ARG:HH12	50:Z:4:LYS:HD3	1.78	0.48
52:3:70:U:H4'	52:3:71:A:C8	2.48	0.48
52:3:1391:U:H2'	52:3:1392:G:C8	2.49	0.48
53:1:818:G:C2'	53:1:819:A:H5''	2.43	0.48
53:1:2231:U:H2'	53:1:2232:C:C6	2.48	0.48
53:1:2461:A:H1'	53:1:2492:U:N3	2.29	0.48
10:k:35:VAL:HG23	10:k:104:THR:HG21	1.96	0.48
14:o:33:ARG:HD2	14:o:33:ARG:O	2.14	0.48
15:p:29:VAL:HG22	15:p:80:VAL:HG12	1.95	0.48
39:O:47:GLU:HG3	52:3:1254:A:OP1	2.13	0.48
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.95	0.48
52:3:212:G:H2'	52:3:213:G:H8	1.78	0.48
52:3:560:A:H5'	52:3:566:G:N2	2.29	0.48
53:1:16:C:O2'	53:1:17:G:H5'	2.14	0.48
53:1:580:U:H2'	53:1:581:C:C6	2.48	0.48
53:1:827:U:H4'	53:1:828:U:C5	2.48	0.48
53:1:1078:U:H4'	53:1:1079:C:H5''	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1443:U:H2'	53:1:1444:G:H8	1.77	0.48
53:1:1783:A:H5'	53:1:2608:G:H4'	1.95	0.48
53:1:2082:A:H2'	53:1:2083:G:O4'	2.14	0.48
1:b:207:ALA:HB2	53:1:1790:C:O2'	2.13	0.48
2:c:62:LYS:HB2	2:c:63:PRO:HD3	1.94	0.48
3:d:118:LEU:HD23	3:d:119:ILE:N	2.28	0.48
5:f:79:THR:HG23	5:f:80:GLU:HG3	1.94	0.48
11:l:55:MET:HE3	53:1:2392:A:C2	2.49	0.48
18:s:90:LYS:HA	53:1:751:A:O4'	2.14	0.48
32:H:11:LEU:HA	32:H:15:LYS:O	2.14	0.48
32:H:113:LYS:HE2	32:H:184:ASN:HB3	1.95	0.48
46:V:39:ARG:HA	52:3:280:C:O2	2.14	0.48
52:3:604:G:H2'	52:3:605:U:O4'	2.14	0.48
52:3:810:C:O2'	52:3:811:C:H5'	2.14	0.48
52:3:1432:G:H1'	52:3:1468:A:H61	1.78	0.48
52:3:1512:U:H2'	52:3:1513:A:C8	2.49	0.48
53:1:2106:U:H2'	53:1:2107:G:C8	2.49	0.48
53:1:2619:C:O2'	53:1:2620:C:H5'	2.14	0.48
53:1:2710:C:H2'	53:1:2711:A:C8	2.49	0.48
55:5:62:C:H2'	55:5:63:G:C8	2.49	0.48
2:c:155:VAL:HG21	53:1:2618:G:H21	1.79	0.48
3:d:129:PRO:HD2	3:d:130:LYS:HZ2	1.78	0.48
20:u:16:LYS:HG2	53:1:329:G:O6	2.14	0.48
21:v:72:VAL:HG12	21:v:73:LYS:H	1.78	0.48
29:E:38:LYS:NZ	53:1:2351:G:O6	2.47	0.48
35:K:92:THR:OG1	35:K:93:LYS:N	2.40	0.48
42:R:3:ILE:HG22	42:R:4:ALA:N	2.27	0.48
44:T:62:ARG:NH2	53:1:715:A:H4'	2.29	0.48
52:3:405:U:C3'	52:3:406:G:H5'	2.41	0.48
52:3:412:A:H62	52:3:431:A:H61	1.60	0.48
52:3:1230:C:H5'	55:5:30:G:H5''	1.94	0.48
53:1:215:G:C4'	53:1:216:A:H4'	2.44	0.48
53:1:953:G:O2'	53:1:954:G:H5'	2.14	0.48
53:1:1999:C:O2'	53:1:2000:C:H5'	2.13	0.48
4:e:96:TRP:O	4:e:100:GLU:HG3	2.12	0.48
7:h:33:VAL:HG12	7:h:34:THR:N	2.29	0.48
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.96	0.48
38:N:26:LYS:C	38:N:27:ILE:HD12	2.39	0.48
44:T:45:HIS:O	44:T:47:LYS:N	2.45	0.48
44:T:59:VAL:HG11	53:1:715:A:OP1	2.14	0.48
47:W:54:LEU:O	47:W:58:ILE:HG12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:82:G:H2'	52:3:83:C:H5'	1.94	0.48
52:3:1496:C:H2'	52:3:1497:G:O4'	2.14	0.48
53:1:1370:C:H2'	53:1:1371:G:O4'	2.14	0.48
53:1:2412:A:H2'	53:1:2413:G:O4'	2.13	0.48
55:6:72:A:H2'	55:6:73:A:O4'	2.13	0.48
1:b:20:ASN:HB3	1:b:23:LEU:HD13	1.95	0.48
34:J:108:GLY:C	34:J:110:MET:H	2.21	0.48
45:U:20:VAL:HG23	45:U:35:ARG:HB3	1.96	0.48
46:V:13:SER:H	46:V:21:VAL:CG1	2.27	0.48
51:a:7:ARG:HH21	51:a:7:ARG:HG3	1.79	0.48
52:3:245:U:O2'	52:3:246:A:H5'	2.13	0.48
52:3:594:U:H2'	52:3:595:A:O4'	2.14	0.48
52:3:701:U:C4'	52:3:703:G:H1'	2.44	0.48
52:3:869:G:H4'	52:3:872:A:C8	2.49	0.48
52:3:1228:C:H2'	52:3:1229:A:C8	2.48	0.48
52:3:1256:A:O2'	52:3:1257:A:H5''	2.14	0.48
53:1:1447:C:H2'	53:1:1448:G:C8	2.49	0.48
53:1:2636:C:H2'	53:1:2637:U:C6	2.49	0.48
2:c:7:LYS:HB3	2:c:28:GLU:OE2	2.15	0.47
7:h:114:GLU:O	7:h:123:ILE:HA	2.13	0.47
26:B:8:THR:CG2	53:1:2020:A:H5'	2.43	0.47
32:H:4:VAL:HB	52:3:1190:G:OP2	2.14	0.47
34:J:45:VAL:HG22	34:J:46:GLY:N	2.26	0.47
35:K:5:GLU:HA	35:K:63:ASN:HA	1.95	0.47
35:K:44:ARG:HA	35:K:58:HIS:HA	1.96	0.47
52:3:540:G:H2'	52:3:541:G:C8	2.49	0.47
52:3:1387:G:H2'	52:3:1388:C:C6	2.49	0.47
53:1:677:A:O2'	53:1:2071:A:H5'	2.14	0.47
53:1:2693:G:O2'	53:1:2694:G:H5'	2.14	0.47
3:d:40:ARG:HD2	53:1:443:A:C5	2.49	0.47
7:h:32:GLY:O	53:1:1055:G:H4'	2.14	0.47
8:i:9:LYS:C	8:i:10:LEU:HD22	2.40	0.47
10:k:92:GLU:O	10:k:93:GLN:C	2.58	0.47
39:O:50:THR:HG23	39:O:64:GLN:HG2	1.96	0.47
42:R:25:GLY:H	52:3:1329:A:C5'	2.18	0.47
46:V:5:ARG:NH1	52:3:128:G:H5'	2.28	0.47
52:3:603:U:H2'	52:3:604:G:C8	2.49	0.47
53:1:546:U:H2'	53:1:547:A:C4'	2.43	0.47
54:2:2:G:H2'	54:2:3:C:H6	1.79	0.47
20:u:60:LYS:HG2	20:u:61:GLU:H	1.79	0.47
21:v:21:ARG:HH12	54:2:77:U:H5''	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:23:GLY:HA3	52:3:409:U:OP1	2.15	0.47
33:I:74:TYR:OH	33:I:96:ARG:NH1	2.46	0.47
34:J:123:LEU:HD23	52:3:7:A:C8	2.49	0.47
36:L:2:ARG:HB3	52:3:933:G:OP2	2.14	0.47
40:P:27:ASN:O	40:P:56:LYS:HG2	2.13	0.47
46:V:29:LYS:HB2	46:V:36:PHE:CE1	2.49	0.47
50:Z:34:ARG:HG3	50:Z:34:ARG:NH1	2.29	0.47
52:3:629:A:H2'	52:3:630:A:O4'	2.15	0.47
53:1:1103:A:H2'	53:1:1103:A:N3	2.30	0.47
53:1:1662:U:H2'	53:1:1663:G:C8	2.47	0.47
53:1:2584:U:H2'	53:1:2585:U:H2'	1.97	0.47
53:1:2676:C:H2'	53:1:2677:G:H8	1.78	0.47
23:x:3:VAL:HG22	23:x:10:ARG:HB3	1.96	0.47
28:D:34:ARG:CZ	28:D:39:ARG:HD2	2.44	0.47
32:H:21:TRP:NE1	32:H:35:ASP:OD1	2.47	0.47
38:N:112:ARG:O	38:N:114:LYS:HD2	2.14	0.47
41:Q:89:LEU:HD12	41:Q:89:LEU:N	2.29	0.47
42:R:48:SER:O	42:R:52:ILE:HG13	2.15	0.47
45:U:4:ILE:HG12	45:U:21:VAL:HG22	1.96	0.47
47:W:28:LEU:HD21	47:W:57:ALA:HB1	1.97	0.47
52:3:539:A:H2'	52:3:540:G:C8	2.49	0.47
52:3:696:A:O2'	52:3:697:U:H5'	2.15	0.47
52:3:824:G:H2'	52:3:825:A:C8	2.47	0.47
53:1:322:A:H5'	53:1:340:A:H1'	1.97	0.47
53:1:807:U:O2'	53:1:808:G:H5'	2.14	0.47
53:1:851:C:H2'	53:1:852:U:C6	2.50	0.47
53:1:2163:A:H2'	53:1:2163:A:N3	2.28	0.47
2:c:115:GLY:HA3	53:1:2822:G:P	2.54	0.47
3:d:3:LEU:HB3	3:d:120:VAL:HG21	1.96	0.47
8:i:36:GLU:O	8:i:39:LYS:HG3	2.14	0.47
16:q:111:LYS:HD3	17:r:48:LYS:HD2	1.96	0.47
35:K:12:PRO:O	35:K:15:SER:OG	2.29	0.47
36:L:92:PRO:HA	36:L:95:ARG:HD2	1.94	0.47
52:3:1308:U:H2'	52:3:1309:G:H8	1.79	0.47
8:i:133:ARG:NH1	53:1:1079:C:H4'	2.29	0.47
9:j:113:PRO:HD2	53:1:558:U:P	2.55	0.47
13:n:55:ALA:HA	13:n:80:PHE:CE1	2.49	0.47
16:q:90:ASP:OD2	17:r:11:GLN:HB2	2.13	0.47
28:D:9:VAL:HG12	53:1:1309:G:OP1	2.13	0.47
33:I:24:VAL:HG22	52:3:409:U:H5''	1.96	0.47
33:I:104:MET:SD	33:I:170:LEU:HD22	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:14:ALA:HB3	42:R:33:LEU:HD21	1.96	0.47
46:V:12:VAL:HB	46:V:21:VAL:CG1	2.40	0.47
48:X:5:LYS:HB3	52:3:1313:U:OP2	2.15	0.47
52:3:273:U:C2'	52:3:274:A:H5'	2.44	0.47
52:3:490:C:H2'	52:3:491:G:H8	1.79	0.47
53:1:700:G:O2'	53:1:701:G:H5'	2.14	0.47
53:1:888:C:H2'	53:1:889:C:C6	2.50	0.47
53:1:890:C:C2'	53:1:891:G:H5'	2.44	0.47
53:1:1909:C:H2'	53:1:1910:G:C8	2.46	0.47
53:1:2366:A:H2'	53:1:2367:G:O4'	2.15	0.47
53:1:2450:A:OP1	53:1:2497:A:H2'	2.14	0.47
54:2:51:G:O2'	54:2:52:A:H5'	2.15	0.47
4:e:2:LYS:O	4:e:5:ASP:OD1	2.32	0.47
4:e:63:LYS:O	54:2:42:C:C1'	2.58	0.47
8:i:74:PRO:HG3	53:1:1060:U:OP1	2.14	0.47
10:k:25:LEU:HD22	53:1:2562:U:H4'	1.97	0.47
10:k:91:SER:O	10:k:92:GLU:C	2.57	0.47
19:t:73:ARG:HH12	53:1:456:C:C2'	2.28	0.47
29:E:23:HIS:HD2	29:E:49:VAL:HG22	1.79	0.47
31:G:26:MET:HE2	31:G:187:ASP:O	2.15	0.47
43:S:52:ARG:NE	52:3:1317:C:N3	2.63	0.47
44:T:44:GLU:O	44:T:45:HIS:HB2	2.15	0.47
51:a:218:MET:HE1	53:1:2128:G:H4'	1.95	0.47
52:3:1329:A:O2'	52:3:1330:U:H5'	2.15	0.47
53:1:281:C:N4	53:1:359:G:H1	2.13	0.47
53:1:394:C:H2'	53:1:395:U:O4'	2.14	0.47
53:1:458:G:O2'	53:1:459:U:H5	1.97	0.47
53:1:657:U:H2'	53:1:658:U:C6	2.49	0.47
53:1:713:G:H21	53:1:718:A:H62	1.62	0.47
53:1:732:C:H2'	53:1:733:G:O4'	2.14	0.47
53:1:1045:C:H5'	53:1:1046:A:H5''	1.96	0.47
53:1:1084:A:H2'	53:1:1105:U:O2'	2.15	0.47
53:1:1443:U:H2'	53:1:1444:G:C8	2.49	0.47
53:1:2520:C:O2'	53:1:2521:C:H5'	2.14	0.47
55:5:59:A:H2'	55:5:60:U:H5'	1.95	0.47
57:7:55:U:H2'	57:7:57:G:OP2	2.14	0.47
7:h:41:LEU:HD22	53:1:1083:U:OP1	2.15	0.47
7:h:67:THR:HB	7:h:68:PRO:HD3	1.97	0.47
13:n:103:ARG:HG2	13:n:105:GLY:H	1.80	0.47
35:K:42:TRP:HB2	35:K:59:TYR:HB2	1.96	0.47
37:M:80:PRO:HG2	52:3:878:A:H5''	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:27:THR:HG21	52:3:1328:C:OP1	2.14	0.47
47:W:71:ASP:HB3	50:Z:3:ILE:HG21	1.96	0.47
52:3:538:G:H2'	52:3:539:A:C8	2.49	0.47
52:3:634:C:H2'	52:3:635:A:C8	2.50	0.47
53:1:1421:G:H1'	53:1:1494:A:N6	2.29	0.47
53:1:1704:C:H2'	53:1:1705:A:C8	2.50	0.47
53:1:1744:A:H3'	53:1:1745:A:H8	1.79	0.47
53:1:2273:A:H2'	53:1:2274:A:C8	2.49	0.47
53:1:2554:U:H2'	53:1:2555:U:H6	1.79	0.47
1:b:257:ARG:NH1	53:1:1800:C:OP1	2.43	0.47
2:c:59:ARG:HH11	53:1:2830:C:H3'	1.79	0.47
10:k:6:THR:HG23	53:1:1666:G:H4'	1.97	0.47
17:r:64:VAL:HG13	17:r:65:ALA:N	2.29	0.47
30:F:24:ARG:NH1	53:1:2742:G:OP2	2.48	0.47
52:3:785:G:O2'	52:3:786:G:H5'	2.14	0.47
52:3:1456:A:H2'	52:3:1457:G:O4'	2.14	0.47
53:1:1199:U:H2'	53:1:1200:C:C6	2.50	0.47
53:1:1507:C:H2'	53:1:1508:A:O4'	2.14	0.47
53:1:2205:A:H2'	53:1:2206:C:C6	2.50	0.47
53:1:2248:C:C2'	53:1:2249:U:H5'	2.44	0.47
57:7:25:C:H2'	57:7:26:A:O4'	2.15	0.47
11:l:111:ILE:HD11	53:1:636:G:C6	2.50	0.47
19:t:61:LEU:N	19:t:61:LEU:HD23	2.30	0.47
52:3:1070:U:H2'	52:3:1071:C:H6	1.80	0.47
53:1:27:G:H22	53:1:512:G:H1'	1.79	0.47
53:1:703:U:H2'	53:1:704:G:O4'	2.14	0.47
53:1:825:A:H2'	53:1:826:U:O4'	2.15	0.47
53:1:2141:G:H2'	53:1:2142:A:H8	1.80	0.47
55:5:59:A:C2'	55:5:60:U:H5'	2.45	0.47
55:6:62:C:H2'	55:6:63:G:C8	2.49	0.47
10:k:99:ILE:CD1	10:k:115:ILE:HG23	2.44	0.46
10:k:110:GLU:HA	10:k:113:MET:HE3	1.96	0.46
16:q:91:ARG:HG3	16:q:91:ARG:NH1	2.30	0.46
34:J:23:THR:HG21	52:3:1396:A:H2	1.79	0.46
42:R:7:ASN:HD22	42:R:21:ILE:HD11	1.80	0.46
46:V:27:PHE:HB3	52:3:597:G:H4'	1.97	0.46
52:3:216:U:H2'	52:3:217:C:C6	2.50	0.46
52:3:1123:U:O2'	52:3:1124:G:H5'	2.14	0.46
52:3:1406:U:O2'	52:3:1407:C:H5'	2.15	0.46
53:1:799:G:H5''	53:1:800:A:H2'	1.97	0.46
53:1:1916:A:H2'	53:1:1917:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:124:ARG:HD3	2:c:125:TRP:NE1	2.29	0.46
18:s:86:MET:HE2	18:s:88:ARG:HD3	1.96	0.46
32:H:14:VAL:HG23	32:H:15:LYS:HG2	1.97	0.46
37:M:88:LYS:HE3	37:M:119:GLY:HA2	1.97	0.46
46:V:30:HIS:HB3	46:V:34:GLY:H	1.80	0.46
49:Y:43:LYS:HG2	49:Y:85:LEU:HG	1.97	0.46
51:a:170:ILE:HD12	51:a:170:ILE:N	2.30	0.46
52:3:235:C:H2'	52:3:236:A:C8	2.50	0.46
52:3:284:C:H2'	52:3:285:C:C6	2.49	0.46
52:3:1120:C:H2'	52:3:1121:U:C6	2.51	0.46
52:3:1316:G:H2'	52:3:1317:C:H5''	1.96	0.46
52:3:1397:C:N4	56:4:22:A:H2'	2.30	0.46
53:1:365:U:H2'	53:1:366:C:C6	2.50	0.46
53:1:973:A:O4'	53:1:1188:U:C6	2.68	0.46
53:1:1607:C:H4'	53:1:1608:A:O5'	2.15	0.46
53:1:2040:G:H2'	53:1:2041:U:O4'	2.15	0.46
53:1:2128:G:H1'	53:1:2173:A:N3	2.30	0.46
53:1:2313:C:H2'	53:1:2314:A:H8	1.80	0.46
53:1:2331:G:H2'	53:1:2332:C:C6	2.50	0.46
57:7:43:C:H2'	57:7:44:G:C8	2.51	0.46
3:d:14:VAL:HG22	3:d:15:SER:N	2.31	0.46
19:t:50:LEU:HD13	24:y:26:PHE:CZ	2.49	0.46
37:M:10:LEU:HD22	37:M:74:ILE:CD1	2.45	0.46
47:W:33:THR:HG22	47:W:37:LYS:H	1.80	0.46
48:X:51:HIS:HB2	48:X:56:HIS:CD2	2.51	0.46
52:3:376:G:H2'	52:3:377:G:H8	1.80	0.46
52:3:855:U:H2'	52:3:856:C:C6	2.51	0.46
53:1:974:G:N3	53:1:974:G:H2'	2.31	0.46
53:1:987:C:H2'	53:1:988:A:O4'	2.14	0.46
53:1:1678:A:H2'	53:1:1679:A:O4'	2.15	0.46
53:1:1796:U:H2'	53:1:1797:G:H8	1.80	0.46
53:1:2637:U:H2'	53:1:2638:G:O4'	2.16	0.46
54:2:5:U:H2'	54:2:6:G:C8	2.50	0.46
55:6:69:C:H2'	55:6:70:G:H8	1.79	0.46
3:d:143:LEU:HD13	3:d:146:VAL:HG11	1.97	0.46
12:m:77:PRO:O	12:m:80:VAL:HG22	2.14	0.46
30:F:1:MET:HB2	30:F:35:GLN:HA	1.98	0.46
33:I:100:VAL:O	33:I:104:MET:HG2	2.16	0.46
38:N:46:VAL:HA	38:N:49:GLN:HG3	1.96	0.46
39:O:6:ILE:HB	39:O:76:ILE:HB	1.97	0.46
42:R:105:ALA:HA	52:3:948:C:OP1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:634:C:H2'	52:3:635:A:H8	1.81	0.46
52:3:766:A:H2'	52:3:767:A:O4'	2.15	0.46
53:1:63:A:O2'	53:1:64:A:H5'	2.16	0.46
53:1:543:G:H2'	53:1:544:C:O4'	2.14	0.46
53:1:1040:A:H2	53:1:1115:G:H22	1.64	0.46
53:1:1045:C:P	53:1:1047:G:H5'	2.56	0.46
53:1:1295:C:H2'	53:1:1296:G:H8	1.80	0.46
53:1:2060:A:O4'	53:1:2502:G:H1'	2.15	0.46
6:g:62:LEU:HD23	6:g:62:LEU:O	2.15	0.46
27:C:18:HIS:HE1	27:C:20:TYR:CZ	2.34	0.46
27:C:37:LYS:HB2	27:C:48:TYR:CE2	2.50	0.46
31:G:207:ARG:O	31:G:211:LEU:HD23	2.16	0.46
35:K:53:LYS:O	35:K:54:LEU:HD23	2.16	0.46
37:M:87:ARG:H	37:M:90:GLU:HB3	1.81	0.46
39:O:30:LYS:HD3	39:O:36:VAL:H	1.80	0.46
39:O:67:ILE:HG13	39:O:67:ILE:O	2.15	0.46
40:P:124:LYS:HG3	40:P:125:LYS:N	2.30	0.46
41:Q:73:LEU:HD21	41:Q:79:ILE:HG21	1.98	0.46
52:3:335:C:H2'	52:3:336:A:H8	1.81	0.46
52:3:1210:C:H2'	52:3:1211:U:H5'	1.98	0.46
53:1:1958:C:O2'	53:1:1959:G:H5'	2.15	0.46
53:1:2834:G:H2'	53:1:2879:A:H61	1.79	0.46
54:2:48:U:H2'	54:2:49:C:C6	2.51	0.46
4:e:84:ILE:HG21	53:1:2312:U:H5''	1.97	0.46
5:f:44:HIS:O	5:f:46:ASP:N	2.48	0.46
6:g:76:GLU:O	6:g:142:VAL:HG13	2.16	0.46
26:B:14:MET:SD	53:1:2045:C:H5''	2.55	0.46
28:D:25:LYS:HG3	28:D:26:ASN:N	2.31	0.46
41:Q:114:SER:HB3	52:3:35:G:H21	1.79	0.46
45:U:70:ARG:NH2	52:3:451:A:OP2	2.49	0.46
52:3:695:A:H2'	52:3:696:A:H8	1.75	0.46
52:3:945:G:H2'	52:3:945:G:N3	2.29	0.46
52:3:1001:C:H2'	52:3:1002:G:C8	2.51	0.46
53:1:974:G:H1'	53:1:975:A:H8	1.76	0.46
53:1:1026:G:H2'	53:1:1027:A:C8	2.35	0.46
53:1:1179:G:N7	53:1:1180:U:H1'	2.30	0.46
53:1:1815:A:H8	53:1:1815:A:OP1	1.98	0.46
53:1:1817:G:C2	53:1:1818:U:H1'	2.50	0.46
53:1:2059:A:N6	53:1:2503:A:H2'	2.31	0.46
53:1:2217:G:O2'	53:1:2218:G:H5'	2.15	0.46
53:1:2556:C:H2'	53:1:2557:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2800:A:H3'	53:1:2801:G:C5'	2.42	0.46
5:f:154:GLU:HG2	5:f:159:LYS:HB2	1.96	0.46
13:n:10:LEU:HD13	13:n:40:LYS:HG2	1.98	0.46
29:E:51:LYS:HE3	53:1:937:C:OP2	2.16	0.46
39:O:23:ALA:O	39:O:26:VAL:HG12	2.16	0.46
50:Z:23:GLU:CD	50:Z:24:LYS:N	2.74	0.46
52:3:272:C:H2'	52:3:273:U:C6	2.50	0.46
52:3:373:A:H2'	52:3:374:A:H8	1.81	0.46
52:3:1144:G:O2'	52:3:1145:A:H5'	2.16	0.46
52:3:1225:A:H2'	52:3:1225:A:N3	2.30	0.46
52:3:1344:C:O2'	52:3:1345:U:H5'	2.16	0.46
53:1:1592:C:H2'	53:1:1593:A:H8	1.81	0.46
53:1:1857:G:H1'	53:1:1885:A:N6	2.31	0.46
53:1:1947:C:O2'	53:1:1948:G:H5'	2.16	0.46
53:1:2112:G:H2'	53:1:2113:U:H5'	1.97	0.46
1:b:261:ARG:HG3	1:b:262:THR:HG23	1.97	0.46
6:g:94:ILE:CD1	6:g:122:LEU:HD13	2.37	0.46
7:h:48:ALA:HB3	7:h:51:TYR:HE1	1.79	0.46
34:J:12:GLU:OE2	34:J:67:ARG:NH1	2.49	0.46
35:K:10:VAL:HG22	35:K:11:HIS:N	2.30	0.46
40:P:81:LEU:HD12	40:P:81:LEU:O	2.16	0.46
45:U:74:LEU:O	45:U:78:VAL:HG23	2.16	0.46
52:3:184:G:C4'	52:3:224:U:H4'	2.45	0.46
52:3:584:G:H2'	52:3:585:G:H8	1.81	0.46
52:3:664:G:N2	52:3:741:G:H1	2.07	0.46
52:3:1097:C:H2'	52:3:1098:C:H6	1.79	0.46
53:1:343:C:O2'	53:1:344:A:H5'	2.16	0.46
53:1:594:U:H2'	53:1:595:C:C6	2.51	0.46
53:1:1078:U:C5'	53:1:1079:C:H5'	2.46	0.46
53:1:1161:C:H2'	53:1:1162:G:H8	1.80	0.46
53:1:1609:A:H1'	53:1:1616:A:C1'	2.45	0.46
53:1:2220:U:H2'	53:1:2221:G:C8	2.48	0.46
54:2:63:C:H2'	54:2:64:G:C8	2.51	0.46
6:g:69:ALA:O	6:g:72:ILE:HG13	2.15	0.46
7:h:60:LEU:HD11	53:1:1047:G:O6	2.15	0.46
12:m:17:ASN:HB2	12:m:95:LEU:HD22	1.98	0.46
14:o:33:ARG:HH21	54:2:27:C:P	2.39	0.46
19:t:61:LEU:HD13	53:1:1341:G:H5'	1.97	0.46
32:H:122:GLN:O	32:H:127:VAL:HG12	2.15	0.46
38:N:47:VAL:HG23	38:N:48:ARG:HG3	1.96	0.46
42:R:104:ASN:HB3	42:R:105:ALA:H	1.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:33:VAL:O	43:S:33:VAL:HG22	2.16	0.46
50:Z:66:ARG:HD2	52:3:1099:G:H5'	1.97	0.46
52:3:376:G:O2'	52:3:377:G:H5'	2.16	0.46
52:3:487:A:H2'	52:3:488:C:O4'	2.15	0.46
52:3:560:A:H4'	52:3:561:U:H5'	1.98	0.46
52:3:730:G:H2'	52:3:731:G:H5'	1.98	0.46
53:1:192:C:H2'	53:1:193:U:H5'	1.97	0.46
53:1:466:A:C2'	53:1:467:G:H5'	2.46	0.46
53:1:720:U:H2'	53:1:721:A:H8	1.80	0.46
53:1:1213:A:H62	53:1:1236:G:H1'	1.79	0.46
53:1:1779:U:H5	53:1:1784:A:N7	2.14	0.46
53:1:1858:A:C2	53:1:1885:A:H1'	2.51	0.46
53:1:2364:C:H2'	53:1:2365:G:O4'	2.15	0.46
53:1:2553:G:H2'	53:1:2554:U:H4'	1.96	0.46
1:b:175:LEU:HD11	1:b:181:ARG:HH12	1.80	0.46
4:e:4:HIS:CD2	4:e:8:LYS:HE3	2.51	0.46
4:e:69:ALA:HB3	4:e:82:TYR:H	1.80	0.46
8:i:133:ARG:CZ	53:1:1079:C:H4'	2.46	0.46
21:v:26:PHE:HE2	21:v:89:ILE:HG13	1.80	0.46
32:H:171:ARG:HG2	52:3:1107:C:P	2.56	0.46
38:N:4:GLN:HE21	38:N:21:LYS:HD3	1.81	0.46
42:R:79:LEU:HD22	42:R:84:CYS:SG	2.56	0.46
52:3:1328:C:H2'	52:3:1329:A:H8	1.81	0.46
52:3:1366:C:H2'	52:3:1367:C:C6	2.50	0.46
53:1:84:A:H4'	53:1:85:G:O5'	2.16	0.46
53:1:389:G:C2'	53:1:390:U:H5'	2.46	0.46
53:1:616:A:H2'	53:1:617:G:O4'	2.16	0.46
53:1:1437:C:H2'	53:1:1438:U:C6	2.51	0.46
54:2:60:C:H2'	54:2:61:G:H8	1.80	0.46
1:b:62:ARG:NH2	53:1:1568:G:OP2	2.48	0.45
2:c:135:GLY:HA2	53:1:743:A:OP1	2.16	0.45
3:d:102:ARG:HH11	3:d:201:ALA:HB3	1.81	0.45
4:e:92:GLY:O	4:e:95:MET:HG3	2.16	0.45
27:C:20:TYR:OH	53:1:2348:U:H5'	2.16	0.45
37:M:14:ARG:HD2	52:3:875:U:O2'	2.16	0.45
52:3:29:U:C2'	52:3:30:U:H5'	2.46	0.45
53:1:307:G:N2	53:1:309:A:H3'	2.31	0.45
53:1:1023:U:O2'	53:1:1122:G:H5'	2.15	0.45
53:1:2055:C:H5'	53:1:2056:G:O5'	2.16	0.45
6:g:84:ALA:HA	6:g:91:PHE:H	1.81	0.45
7:h:56:ARG:HG3	53:1:1084:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:n:10:LEU:O	13:n:12:ARG:HG3	2.15	0.45
26:B:32:THR:HG23	26:B:33:SER:N	2.32	0.45
30:F:24:ARG:HG2	30:F:36:ARG:HG3	1.97	0.45
38:N:56:MET:O	38:N:57:VAL:C	2.60	0.45
52:3:513:C:H2'	52:3:514:C:C6	2.50	0.45
52:3:1256:A:H1'	52:3:1258:G:C5	2.52	0.45
52:3:1402:C:H2'	52:3:1403:C:O4'	2.16	0.45
52:3:1500:A:H5''	52:3:1508:A:H5''	1.98	0.45
53:1:331:C:H41	53:1:1210:G:N2	2.13	0.45
53:1:548:G:H2'	53:1:549:G:O4'	2.16	0.45
53:1:560:C:H2'	53:1:561:G:O4'	2.16	0.45
53:1:1086:A:H3'	53:1:1086:A:N3	2.31	0.45
53:1:1468:U:H2'	53:1:1522:A:N6	2.31	0.45
53:1:1549:A:H2'	53:1:1550:C:C6	2.51	0.45
53:1:1564:C:H2'	53:1:1565:C:O4'	2.15	0.45
53:1:2590:A:H2'	53:1:2591:C:C6	2.52	0.45
57:7:64:A:H2'	57:7:65:G:C8	2.52	0.45
1:b:86:ARG:HG3	1:b:88:ALA:H	1.81	0.45
6:g:28:ASN:HB3	53:1:2199:A:H5'	1.98	0.45
12:m:123:LYS:NZ	53:1:2483:C:N3	2.60	0.45
13:n:69:ARG:O	13:n:70:THR:OG1	2.27	0.45
23:x:19:HIS:HB3	53:1:2080:A:OP1	2.15	0.45
25:z:30:ARG:HD3	25:z:30:ARG:H	1.80	0.45
28:D:14:ARG:HD2	53:1:771:G:OP1	2.16	0.45
34:J:80:LEU:CD1	34:J:122:VAL:HG11	2.37	0.45
35:K:6:ILE:HG12	35:K:89:VAL:HG12	1.97	0.45
39:O:53:ILE:HD11	39:O:61:ALA:HB1	1.97	0.45
41:Q:31:GLY:HA3	41:Q:54:VAL:CG1	2.46	0.45
50:Z:44:ARG:NH1	52:3:722:G:OP2	2.50	0.45
52:3:373:A:O2'	52:3:374:A:H5'	2.17	0.45
53:1:621:A:H2'	53:1:622:G:H5'	1.97	0.45
53:1:1667:G:H22	53:1:1992:G:H5'	1.79	0.45
53:1:1889:A:H2'	53:1:1890:A:C8	2.51	0.45
53:1:2247:A:O2'	53:1:2248:C:H5'	2.16	0.45
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.16	0.45
3:d:14:VAL:HG22	3:d:15:SER:H	1.80	0.45
11:l:57:LEU:HD22	29:E:53:ASP:HB3	1.97	0.45
25:z:13:ILE:HD12	53:1:989:G:N7	2.31	0.45
29:E:23:HIS:CD2	29:E:49:VAL:HG22	2.51	0.45
38:N:119:LYS:O	38:N:120:ALA:HB3	2.17	0.45
46:V:56:ASP:N	46:V:56:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:a:5:THR:OG1	51:a:6:LYS:N	2.49	0.45
52:3:123:U:H2'	52:3:124:C:H6	1.80	0.45
52:3:166:U:H2'	52:3:167:A:H8	1.82	0.45
52:3:539:A:H2'	52:3:540:G:H8	1.81	0.45
52:3:543:U:O2'	52:3:544:G:H5'	2.17	0.45
52:3:1106:G:O2'	52:3:1107:C:H5'	2.16	0.45
53:1:1330:C:O2'	53:1:1331:G:H5'	2.17	0.45
53:1:2314:A:H2'	53:1:2315:G:C8	2.52	0.45
53:1:2489:U:O2'	53:1:2490:G:H5'	2.15	0.45
55:5:29:G:O2'	55:5:30:G:H5'	2.17	0.45
2:c:125:TRP:CG	2:c:160:LYS:HB3	2.51	0.45
3:d:176:ASP:O	3:d:179:SER:OG	2.34	0.45
4:e:118:ALA:HB1	4:e:166:ARG:HE	1.82	0.45
12:m:69:PRO:O	12:m:70:ASP:OD2	2.35	0.45
14:o:27:VAL:HA	14:o:93:ASP:HB3	1.98	0.45
16:q:107:ALA:HB1	17:r:48:LYS:NZ	2.32	0.45
45:U:52:LEU:HD22	45:U:78:VAL:HG21	1.98	0.45
51:a:48:LEU:HD11	51:a:171:ILE:HG22	1.98	0.45
52:3:765:G:C6	52:3:812:G:C4	3.05	0.45
52:3:1356:G:H2'	52:3:1357:A:C8	2.52	0.45
52:3:1497:G:C2'	52:3:1498:U:H5'	2.47	0.45
53:1:737:C:H2'	53:1:738:G:O4'	2.17	0.45
53:1:759:G:H2'	53:1:760:G:H8	1.82	0.45
53:1:1892:C:H2'	53:1:1893:C:C6	2.52	0.45
54:2:114:C:H2'	54:2:115:A:C8	2.52	0.45
1:b:184:GLU:HG3	1:b:186:ASP:H	1.80	0.45
2:c:59:ARG:NH1	53:1:2831:G:OP2	2.48	0.45
5:f:2:ARG:NH1	53:1:1113:U:H5'	2.32	0.45
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.45	0.45
9:j:77:HIS:HE1	9:j:80:HIS:O	1.99	0.45
10:k:35:VAL:HG13	10:k:36:GLY:N	2.32	0.45
33:I:187:ARG:HD2	33:I:190:LEU:HD21	1.99	0.45
41:Q:65:TYR:HB2	41:Q:92:VAL:HG11	1.97	0.45
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.98	0.45
52:3:82:G:H2'	52:3:83:C:O4'	2.17	0.45
52:3:918:A:H2'	52:3:919:A:O4'	2.17	0.45
53:1:1161:C:H2'	53:1:1162:G:C8	2.51	0.45
53:1:2048:G:H2'	53:1:2049:G:C5'	2.41	0.45
53:1:2128:G:H2'	53:1:2129:C:O4'	2.16	0.45
53:1:2484:G:O2'	53:1:2485:G:H5'	2.16	0.45
55:5:75:C:C3'	55:5:76:A:H5''	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:68:C:H2'	57:7:69:G:C8	2.51	0.45
4:e:7:TYR:O	4:e:12:VAL:HG23	2.17	0.45
17:r:80:ARG:NH2	53:1:572:A:OP2	2.50	0.45
35:K:3:HIS:H	35:K:92:THR:CG2	2.19	0.45
38:N:98:ARG:NH1	38:N:103:VAL:HG21	2.31	0.45
45:U:19:VAL:HG13	45:U:36:VAL:O	2.16	0.45
46:V:15:LYS:HE3	52:3:275:G:H5'	1.99	0.45
46:V:22:VAL:HG21	46:V:60:ILE:HD11	1.99	0.45
48:X:61:VAL:HA	48:X:65:MET:SD	2.56	0.45
49:Y:22:SER:OG	52:3:1459:G:H5'	2.17	0.45
50:Z:5:VAL:HG12	50:Z:19:LYS:NZ	2.31	0.45
50:Z:36:PHE:C	50:Z:38:GLU:H	2.25	0.45
52:3:737:C:H2'	52:3:738:C:C6	2.52	0.45
52:3:950:U:H2'	52:3:951:G:C8	2.52	0.45
52:3:1308:U:H2'	52:3:1309:G:C8	2.52	0.45
53:1:737:C:O2'	53:1:738:G:H5'	2.17	0.45
53:1:967:U:H2'	53:1:968:C:H6	1.81	0.45
53:1:2498:C:O2'	53:1:2499:C:H5'	2.17	0.45
54:2:60:C:H2'	54:2:61:G:C8	2.52	0.45
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.17	0.45
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.98	0.45
8:i:99:LYS:HE3	8:i:138:VAL:HB	1.99	0.45
21:v:21:ARG:HA	21:v:25:LYS:O	2.16	0.45
38:N:11:ARG:HG2	38:N:76:GLY:HA3	1.98	0.45
40:P:118:ASN:OD1	52:3:718:A:H5'	2.16	0.45
50:Z:23:GLU:O	50:Z:25:ALA:N	2.48	0.45
52:3:131:A:H2'	52:3:132:C:C6	2.52	0.45
52:3:399:G:H2'	52:3:400:C:C6	2.52	0.45
52:3:458:U:H2'	52:3:459:A:C8	2.52	0.45
52:3:762:U:H2'	52:3:763:G:C8	2.51	0.45
52:3:1138:G:H3'	52:3:1138:G:N3	2.32	0.45
52:3:1202:U:O2'	52:3:1203:C:H5'	2.16	0.45
52:3:1412:C:H2'	52:3:1413:A:C8	2.52	0.45
53:1:542:C:H2'	53:1:543:G:C5'	2.45	0.45
53:1:582:A:H2'	53:1:583:G:C8	2.52	0.45
53:1:1755:A:H2'	53:1:1756:G:H5'	1.99	0.45
53:1:1775:U:C2'	53:1:1776:G:H5'	2.47	0.45
53:1:2682:A:N6	53:1:2728:U:H1'	2.22	0.45
53:1:2830:C:O2'	53:1:2831:G:H5'	2.17	0.45
4:e:9:ASP:HB2	4:e:10:GLU:OE1	2.17	0.45
7:h:123:ILE:O	7:h:124:ASP:CG	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:15:TRP:HB3	9:j:137:PRO:HB3	1.98	0.45
10:k:88:ASN:O	10:k:90:ASN:N	2.50	0.45
13:n:12:ARG:O	13:n:17:ARG:NH2	2.50	0.45
29:E:3:ILE:HG21	29:E:62:PRO:HG2	1.99	0.45
32:H:55:VAL:HB	32:H:66:THR:HB	1.98	0.45
34:J:136:VAL:O	34:J:140:ILE:HG12	2.17	0.45
38:N:27:ILE:HG13	38:N:62:LEU:HD12	1.99	0.45
42:R:91:ARG:HD2	53:1:888:C:C2	2.52	0.45
47:W:11:ARG:HG3	47:W:14:ALA:HB3	1.99	0.45
47:W:36:GLY:O	47:W:62:ARG:NH2	2.49	0.45
48:X:52:ASN:OD1	48:X:53:GLY:N	2.48	0.45
51:a:62:ALA:HB2	51:a:162:ARG:HG3	1.99	0.45
52:3:6:G:O2'	52:3:298:A:H1'	2.16	0.45
52:3:56:U:H2'	52:3:57:G:H8	1.81	0.45
53:1:164:C:H2'	53:1:165:A:O4'	2.17	0.45
53:1:1020:A:C1'	53:1:1021:A:OP2	2.59	0.45
53:1:1720:U:H2'	53:1:1721:G:O4'	2.17	0.45
53:1:1838:C:H4'	53:1:1839:G:H8	1.81	0.45
55:5:30:G:O2'	55:5:31:G:H5'	2.17	0.45
55:5:63:G:H2'	55:5:64:G:H8	1.81	0.45
36:L:3:ARG:HG2	36:L:4:ARG:N	2.32	0.45
40:P:124:LYS:O	40:P:125:LYS:O	2.35	0.45
42:R:6:ILE:HG23	42:R:7:ASN:H	1.81	0.45
42:R:113:LYS:HG3	42:R:114:PRO:CD	2.46	0.45
52:3:422:C:H5'	52:3:423:G:N3	2.32	0.45
52:3:1405:G:O2'	52:3:1406:U:H5'	2.16	0.45
52:3:1524:C:H2'	52:3:1525:G:C8	2.52	0.45
53:1:327:G:H2'	53:1:328:U:O4'	2.17	0.45
53:1:460:A:H2'	53:1:461:C:O4'	2.17	0.45
53:1:2114:A:N6	53:1:2117:A:H62	2.10	0.45
53:1:2221:G:O2'	53:1:2222:C:H5'	2.17	0.45
53:1:2243:U:H2'	53:1:2244:U:H6	1.77	0.45
55:5:41:C:H2'	55:5:42:G:H8	1.82	0.45
2:c:8:LYS:HB2	2:c:201:LEU:HD11	1.99	0.44
16:q:30:VAL:HG13	53:1:580:U:O3'	2.16	0.44
16:q:40:LYS:HG2	16:q:44:TYR:CE2	2.52	0.44
29:E:51:LYS:HD2	53:1:937:C:OP1	2.17	0.44
32:H:196:GLY:HA3	52:3:1057:G:O3'	2.15	0.44
33:I:59:LYS:O	33:I:63:ILE:HG13	2.17	0.44
34:J:149:PRO:O	34:J:152:VAL:HG12	2.18	0.44
35:K:52:ASN:O	35:K:53:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:51:GLN:O	42:R:54:THR:OG1	2.34	0.44
52:3:291:U:O2'	52:3:292:G:H5'	2.16	0.44
52:3:483:C:H2'	52:3:484:G:C8	2.51	0.44
52:3:1099:G:H2'	52:3:1100:C:O4'	2.17	0.44
53:1:1904:G:H2'	53:1:1905:C:O4'	2.16	0.44
55:5:35:A:H2'	55:5:36:U:C6	2.53	0.44
4:e:40:GLY:HA2	4:e:84:ILE:CD1	2.48	0.44
7:h:34:THR:O	7:h:37:LYS:HG2	2.17	0.44
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.99	0.44
15:p:90:ALA:N	15:p:110:LYS:O	2.46	0.44
33:I:33:ILE:HG22	33:I:34:GLU:N	2.32	0.44
33:I:62:ARG:HD3	33:I:62:ARG:HA	1.77	0.44
34:J:68:ARG:NH2	52:3:1074:G:OP1	2.50	0.44
34:J:87:VAL:HA	34:J:91:SER:O	2.18	0.44
38:N:118:ARG:NH1	52:3:1233:G:H5'	2.33	0.44
41:Q:41:PRO:HG3	41:Q:49:ARG:HD3	1.99	0.44
41:Q:43:LYS:HD3	56:4:21:C:OP1	2.17	0.44
43:S:7:ALA:HA	43:S:10:VAL:HG12	2.00	0.44
49:Y:25:SER:OG	52:3:1458:G:H5''	2.17	0.44
52:3:499:A:C2	52:3:547:A:C4	3.05	0.44
52:3:1522:U:O2'	52:3:1523:G:H5'	2.16	0.44
53:1:2128:G:N2	53:1:2173:A:H1'	2.30	0.44
1:b:160:TYR:HB3	1:b:193:GLU:CB	2.48	0.44
2:c:116:LYS:HB2	2:c:165:MET:HB3	1.99	0.44
3:d:129:PRO:O	53:1:321:U:H5'	2.18	0.44
18:s:4:ILE:HD12	18:s:6:LYS:HE3	2.00	0.44
27:C:9:LYS:O	27:C:51:ALA:HB3	2.17	0.44
29:E:63:TYR:CE2	53:1:242:G:H5''	2.52	0.44
33:I:190:LEU:HD12	33:I:192:ALA:H	1.83	0.44
44:T:86:LEU:N	44:T:86:LEU:HD23	2.32	0.44
49:Y:12:GLN:NE2	52:3:105:G:OP2	2.50	0.44
51:a:60:ARG:HG3	51:a:164:ARG:HG3	1.99	0.44
52:3:86:G:H4'	52:3:87:C:C5	2.52	0.44
52:3:413:G:N2	52:3:428:G:H1'	2.32	0.44
52:3:415:A:H2'	52:3:416:G:O4'	2.17	0.44
52:3:586:C:O2'	52:3:587:G:H5'	2.18	0.44
53:1:115:C:O2'	53:1:116:C:H5'	2.17	0.44
53:1:760:G:H2'	53:1:761:A:O4'	2.17	0.44
53:1:969:G:H2'	53:1:970:U:C6	2.51	0.44
53:1:1326:U:H2'	53:1:1327:A:C8	2.52	0.44
53:1:1672:A:C2	53:1:2582:G:H5'	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2270:A:H2'	53:1:2271:G:O4'	2.17	0.44
54:2:97:C:H2'	54:2:98:G:O4'	2.17	0.44
8:i:90:GLY:C	8:i:91:LYS:HD3	2.42	0.44
12:m:70:ASP:OD2	12:m:70:ASP:C	2.59	0.44
17:r:64:VAL:HG13	17:r:65:ALA:H	1.82	0.44
20:u:3:LYS:C	20:u:4:ILE:HD12	2.43	0.44
33:I:154:VAL:O	33:I:158:LEU:HD13	2.17	0.44
36:L:16:LYS:HE2	36:L:43:TYR:CZ	2.52	0.44
37:M:52:GLY:HA3	37:M:56:PRO:HA	1.98	0.44
38:N:49:GLN:N	38:N:50:PRO:HD2	2.32	0.44
39:O:14:ASP:OD1	39:O:16:ARG:HG2	2.17	0.44
52:3:129:A:H1'	52:3:130:A:C8	2.52	0.44
52:3:163:C:H2'	52:3:164:G:C4'	2.47	0.44
52:3:758:C:H4'	52:3:880:C:H4'	2.00	0.44
52:3:1125:U:H2'	52:3:1126:U:H2'	1.99	0.44
53:1:984:A:H5''	53:1:985:C:OP2	2.17	0.44
53:1:1561:C:H2'	53:1:1562:U:C6	2.52	0.44
53:1:2007:U:H2'	53:1:2008:C:H6	1.82	0.44
53:1:2074:U:H2'	53:1:2075:U:C6	2.53	0.44
1:b:245:THR:C	1:b:247:TRP:H	2.26	0.44
31:G:170:ILE:HD12	52:3:1101:A:C8	2.53	0.44
35:K:18:VAL:CG2	35:K:19:PRO:HD3	2.48	0.44
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.99	0.44
37:M:111:THR:HG23	37:M:114:ALA:H	1.83	0.44
39:O:44:THR:HG23	39:O:69:THR:C	2.42	0.44
39:O:59:LYS:HE2	39:O:62:ARG:HH22	1.82	0.44
49:Y:19:HIS:CE1	49:Y:23:ARG:HH11	2.35	0.44
52:3:82:G:N2	52:3:88:U:H1'	2.32	0.44
52:3:389:A:H2'	52:3:389:A:N3	2.33	0.44
52:3:744:C:H2'	52:3:745:G:H8	1.82	0.44
53:1:2238:G:N3	53:1:2238:G:C2'	2.80	0.44
53:1:2248:C:H2'	53:1:2249:U:H5'	1.98	0.44
53:1:2404:U:H2'	53:1:2405:G:O4'	2.17	0.44
53:1:2457:U:H3	53:1:2494:G:H1	1.66	0.44
53:1:2545:G:H2'	53:1:2546:U:O4'	2.17	0.44
53:1:2580:U:C2'	53:1:2581:G:H5'	2.47	0.44
54:2:95:U:H2'	54:2:96:G:C8	2.53	0.44
7:h:23:LEU:HD22	7:h:118:ILE:CG1	2.47	0.44
8:i:128:ILE:HD12	8:i:128:ILE:N	2.32	0.44
11:l:29:LYS:O	11:l:30:THR:OG1	2.23	0.44
14:o:67:ASN:ND2	14:o:69:ASP:OD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:30:ILE:HG23	19:t:85:VAL:HB	2.00	0.44
21:v:72:VAL:HG11	21:v:91:PHE:HB3	1.99	0.44
33:I:184:LYS:HA	33:I:185:PRO:HD3	1.87	0.44
37:M:50:VAL:HG22	37:M:50:VAL:O	2.17	0.44
44:T:31:LEU:O	44:T:35:ILE:HG13	2.17	0.44
44:T:36:ASN:HA	44:T:39:GLN:HG2	1.99	0.44
47:W:11:ARG:NE	52:3:845:A:H4'	2.30	0.44
52:3:135:C:H2'	52:3:136:C:H5'	2.00	0.44
53:1:995:C:H5'	53:1:995:C:C6	2.48	0.44
53:1:1053:C:C3'	53:1:1054:A:H5''	2.46	0.44
53:1:2737:G:H2'	53:1:2738:A:C8	2.53	0.44
3:d:129:PRO:HD2	3:d:130:LYS:NZ	2.33	0.44
4:e:110:ILE:HB	4:e:113:PHE:HB2	2.00	0.44
5:f:94:ARG:N	5:f:105:SER:OG	2.50	0.44
12:m:33:LEU:HD12	12:m:129:THR:O	2.17	0.44
12:m:55:ARG:NH2	57:7:53:G:H4'	2.32	0.44
14:o:71:ALA:O	14:o:74:VAL:HG12	2.18	0.44
27:C:10:LEU:N	27:C:20:TYR:O	2.50	0.44
30:F:15:LYS:NZ	53:1:2753:A:N3	2.55	0.44
31:G:186:VAL:HG23	31:G:190:SER:HB2	1.99	0.44
38:N:71:ILE:H	38:N:71:ILE:CD1	2.26	0.44
43:S:30:ILE:HG22	43:S:30:ILE:O	2.18	0.44
52:3:309:A:H2'	52:3:310:G:C8	2.49	0.44
52:3:765:G:H2'	52:3:812:G:N2	2.32	0.44
53:1:1108:U:H2'	53:1:1109:C:O4'	2.18	0.44
53:1:1636:U:H2'	53:1:1637:A:H8	1.82	0.44
53:1:2011:U:H2'	53:1:2012:G:O4'	2.17	0.44
53:1:2570:G:H2'	53:1:2571:U:O4'	2.18	0.44
54:2:28:C:H2'	54:2:29:A:H8	1.82	0.44
55:5:22:G:O2'	55:5:23:C:H5'	2.18	0.44
57:7:57:G:H2'	57:7:58:A:H5'	1.99	0.44
2:c:114:LYS:HE2	2:c:196:ALA:HB2	2.00	0.44
8:i:10:LEU:HB3	8:i:11:GLN:H	1.53	0.44
15:p:112:ARG:O	15:p:113:LEU:HG	2.17	0.44
20:u:6:ARG:N	53:1:85:G:OP1	2.50	0.44
35:K:9:MET:HE3	35:K:86:ARG:HB3	2.00	0.44
37:M:85:TYR:CD1	37:M:123:GLU:HB2	2.52	0.44
38:N:51:LEU:HD13	38:N:56:MET:HG3	1.99	0.44
43:S:45:LEU:O	48:X:12:LEU:HD21	2.17	0.44
52:3:151:A:H2'	52:3:152:A:O4'	2.18	0.44
52:3:594:U:O2'	52:3:595:A:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:665:A:O4'	52:3:733:G:H1'	2.17	0.44
52:3:1210:C:C2'	52:3:1211:U:H5'	2.47	0.44
52:3:1502:A:C8	52:3:1505:G:N2	2.86	0.44
53:1:297:G:H2'	53:1:298:G:O4'	2.18	0.44
53:1:971:G:H2'	53:1:972:A:O4'	2.18	0.44
53:1:1130:U:C2	53:1:2025:C:H5''	2.52	0.44
53:1:1874:C:H2'	53:1:1875:G:O4'	2.16	0.44
53:1:2544:G:H2'	53:1:2545:G:O4'	2.18	0.44
54:2:19:C:H2'	54:2:20:G:C8	2.53	0.44
54:2:104:A:H2'	54:2:105:G:O4'	2.18	0.44
2:c:47:ALA:HA	2:c:84:LEU:HG	2.00	0.44
3:d:38:GLY:HA3	53:1:615:U:O2	2.18	0.44
7:h:81:LEU:HA	53:1:1107:G:H4'	2.00	0.44
9:j:53:TYR:HA	9:j:121:LYS:HB3	1.99	0.44
9:j:102:GLU:CD	53:1:2780:G:H1	2.26	0.44
42:R:96:VAL:HG22	52:3:1308:U:OP1	2.18	0.44
44:T:71:ARG:NH2	52:3:754:C:OP1	2.51	0.44
52:3:769:G:H2'	52:3:770:C:H6	1.83	0.44
53:1:1739:A:H2'	53:1:1740:G:O4'	2.18	0.44
3:d:119:ILE:HB	3:d:187:VAL:HA	2.00	0.43
13:n:54:LEU:HD11	13:n:65:LEU:HD23	2.00	0.43
34:J:35:LEU:HD11	34:J:133:ILE:HB	1.99	0.43
38:N:128:LYS:HE3	55:5:34:C:OP2	2.18	0.43
50:Z:23:GLU:C	50:Z:25:ALA:N	2.76	0.43
52:3:31:G:H21	52:3:47:C:H5''	1.79	0.43
52:3:301:G:H2'	52:3:302:G:C8	2.53	0.43
53:1:214:G:O2'	53:1:215:G:H5'	2.18	0.43
53:1:371:A:N6	53:1:401:A:H3'	2.32	0.43
53:1:564:C:O2'	53:1:565:C:H5'	2.18	0.43
53:1:565:C:H4'	53:1:1253:A:N6	2.33	0.43
53:1:768:G:H22	53:1:1379:U:H1'	1.83	0.43
53:1:1054:A:H2'	53:1:1055:G:H8	1.83	0.43
53:1:1380:G:H1'	53:1:1569:A:H61	1.82	0.43
53:1:1922:G:H2'	53:1:1923:U:O4'	2.18	0.43
53:1:2724:U:H2'	53:1:2725:A:C8	2.53	0.43
53:1:2879:A:H1'	53:1:2880:C:C5	2.53	0.43
54:2:63:C:H2'	54:2:64:G:H8	1.82	0.43
5:f:70:LEU:HD11	53:1:2758:A:C2	2.53	0.43
11:l:93:ASN:HA	11:l:96:LYS:NZ	2.33	0.43
12:m:42:THR:HA	12:m:93:VAL:HG12	2.00	0.43
12:m:53:MET:HE1	12:m:103:TYR:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:14:ALA:O	14:o:18:LEU:HD23	2.18	0.43
15:p:59:THR:HG22	15:p:72:VAL:HG12	1.99	0.43
24:y:2:LYS:CE	53:1:102:U:H1'	2.46	0.43
28:D:26:ASN:OD1	53:1:682:G:H5'	2.17	0.43
29:E:32:LEU:HD23	29:E:35:LYS:HD2	2.00	0.43
33:I:33:ILE:H	33:I:33:ILE:CD1	2.16	0.43
35:K:91:ARG:HG3	35:K:92:THR:N	2.32	0.43
38:N:17:ARG:HH22	52:3:1129:C:H4'	1.82	0.43
44:T:88:ARG:HG3	53:1:714:U:C5	2.53	0.43
51:a:166:ASP:OD2	51:a:168:ASN:HB2	2.18	0.43
52:3:1346:A:C2'	52:3:1347:G:H4'	2.48	0.43
53:1:1434:A:H2'	53:1:1435:G:H8	1.83	0.43
53:1:1536:C:H4'	53:1:1537:G:C2	2.53	0.43
53:1:2297:A:N6	53:1:2319:G:H1'	2.32	0.43
54:2:66:A:H4'	54:2:67:G:N7	2.34	0.43
6:g:52:ALA:HB3	6:g:53:GLU:OE1	2.18	0.43
8:i:90:GLY:C	8:i:92:PRO:HD3	2.42	0.43
16:q:32:ARG:HG3	53:1:1252:G:N3	2.33	0.43
19:t:37:ASP:N	19:t:37:ASP:OD1	2.51	0.43
33:I:90:LEU:HD13	33:I:93:LEU:HD12	2.00	0.43
33:I:98:ASP:OD1	33:I:98:ASP:N	2.51	0.43
52:3:494:G:O2'	52:3:496:A:H1'	2.18	0.43
52:3:1040:U:H2'	52:3:1041:G:C8	2.53	0.43
52:3:1448:C:H2'	52:3:1449:C:C6	2.53	0.43
53:1:11:C:H2'	53:1:12:U:H5''	2.00	0.43
53:1:729:G:H4'	53:1:763:G:C5'	2.47	0.43
53:1:1111:A:O2'	53:1:1112:G:H4'	2.17	0.43
53:1:1300:G:H4'	53:1:1301:A:H5'	1.99	0.43
53:1:2371:G:O2'	53:1:2372:U:H5'	2.17	0.43
53:1:2472:G:H1'	53:1:2478:A:H61	1.84	0.43
53:1:2472:G:H1'	53:1:2478:A:N6	2.33	0.43
4:e:40:GLY:HA2	4:e:84:ILE:HD12	2.00	0.43
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.49	0.43
8:i:8:VAL:HG13	8:i:10:LEU:HD23	2.00	0.43
10:k:40:LYS:NZ	53:1:2561:U:O3'	2.41	0.43
28:D:34:ARG:HH21	28:D:39:ARG:CD	2.31	0.43
34:J:19:ARG:HB3	34:J:32:PHE:CE1	2.53	0.43
50:Z:49:ALA:HA	52:3:723:U:C4	2.53	0.43
50:Z:64:ALA:C	50:Z:66:ARG:H	2.26	0.43
53:1:654:A:H3'	53:1:654:A:N3	2.33	0.43
53:1:723:C:H2'	53:1:724:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:729:G:H2'	53:1:1775:U:H1'	1.99	0.43
53:1:974:G:C5'	53:1:1186:G:H21	2.30	0.43
53:1:1657:U:O2'	53:1:1658:C:H5'	2.19	0.43
53:1:2111:U:H5'	53:1:2112:G:OP2	2.19	0.43
53:1:2257:U:O2'	53:1:2258:C:H5'	2.19	0.43
54:2:65:U:H2'	54:2:66:A:H5'	2.00	0.43
55:6:47:U:H3'	55:6:48:C:C5'	2.48	0.43
1:b:132:ARG:HB3	1:b:185:ALA:HB1	2.00	0.43
9:j:131:ASN:OD1	9:j:131:ASN:N	2.51	0.43
20:u:100:GLU:HB3	20:u:101:THR:H	1.60	0.43
31:G:26:MET:O	31:G:30:ILE:HG12	2.18	0.43
43:S:41:TRP:O	43:S:44:VAL:HG22	2.18	0.43
52:3:130:A:O2'	52:3:264:C:H5'	2.19	0.43
52:3:815:A:H4'	52:3:817:C:C4	2.53	0.43
52:3:1395:C:H6	52:3:1395:C:H5'	1.84	0.43
53:1:1149:G:H2'	53:1:1150:C:C6	2.53	0.43
53:1:1299:G:O6	53:1:1639:C:H5''	2.19	0.43
53:1:1924:C:H2'	53:1:1925:C:C6	2.54	0.43
54:2:3:C:H3'	54:2:4:C:C5'	2.49	0.43
55:6:21:A:O2'	55:6:22:G:C8	2.72	0.43
2:c:105:LYS:O	2:c:177:VAL:HG12	2.19	0.43
4:e:59:ILE:O	4:e:101:ARG:NH1	2.51	0.43
12:m:53:MET:HE1	12:m:103:TYR:CB	2.48	0.43
19:t:40:LYS:HB3	19:t:58:VAL:HG13	2.00	0.43
19:t:67:VAL:HG23	19:t:67:VAL:O	2.18	0.43
33:I:70:GLN:O	33:I:73:ASN:OD1	2.37	0.43
45:U:1:MET:SD	45:U:24:SER:OG	2.76	0.43
52:3:411:A:N9	52:3:413:G:H1'	2.34	0.43
52:3:577:G:C2	52:3:578:C:C2	3.06	0.43
52:3:1227:A:H2'	52:3:1228:C:H5'	1.99	0.43
53:1:290:U:H2'	53:1:291:G:H8	1.83	0.43
53:1:1285:A:H2'	53:1:1286:A:H5'	2.00	0.43
53:1:2492:U:H2'	53:1:2493:U:C6	2.52	0.43
53:1:2623:G:H2'	53:1:2624:G:C8	2.54	0.43
55:6:69:C:H2'	55:6:70:G:C8	2.54	0.43
6:g:12:LEU:HD23	6:g:12:LEU:H	1.84	0.43
11:l:93:ASN:C	11:l:95:LEU:H	2.26	0.43
19:t:22:THR:HA	19:t:25:GLU:HG2	2.00	0.43
31:G:68:PHE:HA	31:G:161:PHE:HB3	1.99	0.43
35:K:66:ALA:HB1	35:K:70:VAL:HG11	2.00	0.43
41:Q:89:LEU:HA	41:Q:90:PRO:HD2	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:912:C:O2'	52:3:913:A:H5'	2.18	0.43
52:3:1238:A:N7	52:3:1303:C:H1'	2.33	0.43
52:3:1366:C:H2'	52:3:1367:C:H6	1.84	0.43
53:1:279:A:C2'	53:1:280:U:H5'	2.48	0.43
53:1:435:C:H2'	53:1:436:C:H5'	1.99	0.43
53:1:577:G:OP1	53:1:2502:G:H2'	2.18	0.43
53:1:765:C:O2'	53:1:766:U:H5'	2.18	0.43
53:1:817:C:H2'	53:1:818:G:O4'	2.19	0.43
53:1:1297:C:OP1	53:1:2710:C:H4'	2.19	0.43
53:1:2553:G:H2'	53:1:2554:U:C4'	2.48	0.43
1:b:156:SER:HB2	53:1:1818:U:H5'	2.01	0.43
1:b:209:ALA:HA	1:b:212:TRP:CE2	2.54	0.43
1:b:260:LYS:HB3	53:1:2227:A:H5''	2.00	0.43
9:j:16:TYR:HB2	9:j:54:ILE:HD13	2.01	0.43
14:o:29:HIS:CE1	54:2:7:G:H5'	2.53	0.43
14:o:33:ARG:O	14:o:34:HIS:HB2	2.17	0.43
18:s:34:ASP:HB2	26:B:27:LEU:HD12	1.99	0.43
52:3:405:U:O2	52:3:498:A:H2'	2.18	0.43
52:3:490:C:H2'	52:3:491:G:C8	2.54	0.43
52:3:552:U:H2'	52:3:553:A:C8	2.54	0.43
52:3:621:A:H2'	52:3:622:A:C8	2.54	0.43
52:3:628:G:H2'	52:3:629:A:C8	2.54	0.43
52:3:1340:A:O2'	52:3:1341:U:H5'	2.19	0.43
53:1:706:A:H2'	53:1:707:G:O4'	2.19	0.43
53:1:1295:C:H2'	53:1:1296:G:C8	2.54	0.43
53:1:1506:U:H2'	53:1:1507:C:C6	2.54	0.43
53:1:2028:U:H2'	53:1:2029:G:O4'	2.18	0.43
1:b:42:ARG:NH2	1:b:48:ILE:HD11	2.34	0.43
1:b:93:VAL:HG11	1:b:115:ILE:HD11	2.01	0.43
3:d:82:GLY:O	3:d:83:VAL:HB	2.18	0.43
3:d:147:LEU:HD12	3:d:168:ASP:O	2.19	0.43
6:g:125:THR:HG21	6:g:148:ALA:HB2	2.00	0.43
7:h:118:ILE:CG2	7:h:119:PRO:N	2.81	0.43
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.99	0.43
19:t:3:ARG:HG2	53:1:138:U:O4	2.18	0.43
31:G:20:ARG:HD2	31:G:20:ARG:O	2.19	0.43
32:H:119:ILE:O	32:H:123:LEU:HD23	2.19	0.43
32:H:133:MET:HE3	32:H:167:TYR:HB2	1.99	0.43
35:K:49:TYR:OH	35:K:86:ARG:NH1	2.52	0.43
38:N:128:LYS:HE3	38:N:129:ARG:HH22	1.83	0.43
42:R:91:ARG:HD2	53:1:888:C:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:6:ARG:CB	50:Z:6:ARG:NH1	2.82	0.43
52:3:76:G:H2'	52:3:77:A:O4'	2.19	0.43
52:3:422:C:H5'	52:3:423:G:C2	2.53	0.43
52:3:1488:G:H2'	52:3:1489:G:C8	2.53	0.43
53:1:1089:A:H2	53:1:1090:A:H62	1.67	0.43
55:6:62:C:H2'	55:6:63:G:H8	1.84	0.43
1:b:180:MET:HE3	1:b:268:ARG:HE	1.83	0.43
1:b:204:LEU:HB2	53:1:1791:A:H4'	2.01	0.43
4:e:125:GLY:HA2	4:e:162:ASP:HA	2.00	0.43
4:e:135:ILE:HA	4:e:140:ILE:HG21	2.00	0.43
5:f:154:GLU:OE2	5:f:157:LYS:HB2	2.19	0.43
10:k:41:ILE:HG13	10:k:58:LEU:O	2.19	0.43
14:o:40:ILE:HD13	54:2:8:C:O2'	2.19	0.43
18:s:71:VAL:HA	18:s:107:VAL:HG12	2.01	0.43
21:v:60:VAL:CG1	21:v:71:LYS:HB2	2.48	0.43
41:Q:70:GLY:O	41:Q:98:ARG:NH2	2.49	0.43
43:S:58:ARG:HD2	52:3:979:C:O2	2.18	0.43
46:V:16:MET:HG3	46:V:19:SER:OG	2.19	0.43
51:a:46:VAL:HG22	51:a:212:VAL:HG13	2.01	0.43
52:3:50:A:N6	52:3:361:G:H4'	2.34	0.43
52:3:113:G:H1'	52:3:354:G:H5''	2.01	0.43
52:3:361:G:H2'	52:3:362:G:O4'	2.19	0.43
52:3:467:U:H5'	52:3:468:A:OP2	2.19	0.43
52:3:1487:G:O2'	52:3:1488:G:H5'	2.19	0.43
53:1:580:U:H2'	53:1:581:C:H6	1.84	0.43
53:1:2184:A:O2'	53:1:2185:U:H5'	2.18	0.43
53:1:2475:C:H42	53:1:2529:G:N2	2.17	0.43
53:1:2699:C:H2'	53:1:2700:A:C8	2.54	0.43
11:l:17:LYS:HD3	53:1:663:G:H5''	2.01	0.42
31:G:128:LEU:HB3	31:G:132:GLU:HB2	2.01	0.42
39:O:7:ARG:HB2	39:O:101:SER:HB2	2.01	0.42
52:3:438:U:H2'	52:3:439:U:OP2	2.19	0.42
53:1:2364:C:O2'	53:1:2365:G:H5'	2.19	0.42
53:1:2469:A:H2'	53:1:2470:G:O4'	2.19	0.42
53:1:2812:G:H2'	53:1:2813:A:C8	2.54	0.42
1:b:50:THR:HG21	53:1:1814:G:H4'	2.00	0.42
5:f:2:ARG:HD3	53:1:2751:G:C5	2.53	0.42
15:p:55:HIS:HB3	53:1:2683:C:H5''	2.00	0.42
20:u:12:VAL:HA	20:u:69:VAL:HG12	2.00	0.42
37:M:86:LYS:HD2	37:M:90:GLU:HG2	2.01	0.42
43:S:81:ILE:HD12	43:S:81:ILE:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:911:U:H2'	52:3:912:C:C6	2.53	0.42
52:3:1330:U:H2'	52:3:1331:G:O4'	2.19	0.42
52:3:1391:U:H2'	52:3:1392:G:H8	1.84	0.42
53:1:942:G:H2'	53:1:943:A:O4'	2.19	0.42
53:1:1130:U:O2'	53:1:1131:G:OP1	2.29	0.42
53:1:1133:A:H4'	53:1:1134:A:C5'	2.38	0.42
53:1:1479:G:O2'	53:1:1480:C:H5'	2.20	0.42
53:1:1772:A:H2'	53:1:1773:A:H5'	2.02	0.42
53:1:2318:G:H2'	53:1:2319:G:O4'	2.19	0.42
53:1:2514:U:H2'	53:1:2515:C:C6	2.54	0.42
53:1:2678:C:O2'	53:1:2679:A:H5'	2.19	0.42
53:1:2795:C:H2'	53:1:2796:U:O4'	2.18	0.42
55:5:28:C:H2'	55:5:29:G:H8	1.84	0.42
4:e:35:LEU:HG	4:e:56:LEU:HG	2.00	0.42
7:h:57:ASN:HB3	7:h:62:ARG:HD3	2.02	0.42
10:k:22:ILE:HG12	10:k:40:LYS:O	2.19	0.42
19:t:39:THR:HG23	19:t:42:GLU:H	1.83	0.42
20:u:95:PHE:O	20:u:99:SER:HA	2.19	0.42
28:D:25:LYS:NZ	28:D:26:ASN:OD1	2.48	0.42
29:E:31:ILE:HD11	53:1:2391:G:C5'	2.44	0.42
36:L:67:ASN:HB3	36:L:129:ASN:HB3	2.00	0.42
36:L:91:ARG:H	36:L:91:ARG:HD3	1.83	0.42
37:M:90:GLU:HG2	37:M:90:GLU:O	2.20	0.42
40:P:71:ASP:C	40:P:73:VAL:H	2.26	0.42
51:a:50:ILE:HG23	51:a:57:GLN:HB3	2.00	0.42
52:3:82:G:C2'	52:3:83:C:H5'	2.49	0.42
52:3:253:A:H2'	52:3:254:G:C8	2.54	0.42
52:3:428:G:H4'	52:3:429:U:O5'	2.19	0.42
52:3:665:A:H1'	52:3:733:G:O4'	2.20	0.42
52:3:679:C:O2'	52:3:680:C:H5'	2.18	0.42
52:3:797:C:O2'	52:3:798:U:H5'	2.19	0.42
52:3:884:U:H4'	52:3:885:G:H5''	2.01	0.42
52:3:1306:A:H2'	52:3:1307:U:O4'	2.19	0.42
52:3:1484:C:H2'	52:3:1485:U:O4'	2.20	0.42
53:1:389:G:O2'	53:1:390:U:H5'	2.19	0.42
53:1:1372:U:O2'	53:1:1373:A:H5'	2.19	0.42
53:1:2631:G:O2'	53:1:2632:A:H5'	2.20	0.42
53:1:2682:A:H61	53:1:2728:U:C1'	2.25	0.42
3:d:52:VAL:O	3:d:74:LYS:HE3	2.19	0.42
4:e:151:LEU:N	4:e:151:LEU:HD23	2.34	0.42
21:v:38:LEU:HD22	21:v:40:ILE:CD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:w:79:GLU:O	22:w:81:GLU:HG2	2.19	0.42
25:z:40:THR:OG1	25:z:41:PRO:HD2	2.19	0.42
26:B:6:LYS:HA	26:B:7:PRO:HD3	1.90	0.42
26:B:37:HIS:ND1	26:B:38:LEU:O	2.48	0.42
31:G:129:THR:HG23	31:G:131:LYS:H	1.84	0.42
32:H:5:HIS:CG	43:S:88:MET:HB3	2.55	0.42
41:Q:47:ALA:C	41:Q:48:LEU:HD12	2.45	0.42
45:U:28:ARG:HE	45:U:29:ASN:ND2	2.12	0.42
48:X:13:HIS:CG	52:3:1014:A:H5'	2.54	0.42
48:X:54:ARG:HB3	52:3:958:A:C2	2.55	0.42
51:a:201:PRO:HG2	51:a:204:ALA:HB2	2.01	0.42
52:3:1202:U:H2'	52:3:1203:C:C5'	2.49	0.42
52:3:1305:G:H1'	52:3:1332:A:N6	2.34	0.42
53:1:2180:U:H4'	55:6:17(A):U:C4'	2.50	0.42
53:1:2641:G:O2'	53:1:2642:G:H5'	2.20	0.42
1:b:56:GLY:HA2	1:b:212:TRP:HA	2.02	0.42
4:e:13:LYS:O	4:e:16:MET:HG2	2.18	0.42
4:e:111:ARG:O	4:e:112:ASP:HB2	2.20	0.42
9:j:114:LEU:O	9:j:118:MET:HG2	2.20	0.42
14:o:32:PRO:HD2	54:2:29:A:OP2	2.20	0.42
14:o:80:GLU:O	14:o:83:LEU:HG	2.19	0.42
17:r:22:LEU:HD12	17:r:23:GLU:O	2.20	0.42
21:v:75:GLN:N	21:v:90:ASP:O	2.46	0.42
25:z:23:LEU:HD22	25:z:28:LEU:HD12	2.01	0.42
26:B:30:ASP:HB3	26:B:34:GLY:H	1.83	0.42
36:L:105:GLU:HA	36:L:108:ARG:HG2	2.01	0.42
38:N:18:VAL:HA	38:N:64:ILE:HD12	2.01	0.42
47:W:32:ILE:HD12	47:W:36:GLY:HA2	2.02	0.42
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.85	0.42
52:3:156:C:H2'	52:3:157:U:O4'	2.20	0.42
52:3:1015:G:O2'	52:3:1016:A:H5'	2.19	0.42
53:1:259:G:H2'	53:1:260:G:H8	1.84	0.42
53:1:579:G:H2'	53:1:580:U:C6	2.53	0.42
53:1:1548:A:H2'	53:1:1549:A:C8	2.54	0.42
53:1:1824:G:O2'	53:1:1825:U:H5'	2.19	0.42
53:1:1930:G:O2'	53:1:1931:U:C6	2.72	0.42
53:1:2256:G:H2'	53:1:2257:U:C6	2.54	0.42
53:1:2605:U:H2'	53:1:2606:C:C6	2.54	0.42
1:b:115:ILE:HA	1:b:127:ASN:HD21	1.83	0.42
5:f:173:ALA:O	5:f:175:LYS:N	2.51	0.42
6:g:90:LEU:H	6:g:90:LEU:HD12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:75:TYR:CD1	9:j:86:GLN:HB3	2.54	0.42
10:k:71:ARG:HB2	10:k:73:ASP:OD1	2.20	0.42
10:k:77:ILE:HG12	15:p:71:ARG:HG3	2.01	0.42
11:l:90:VAL:HG13	11:l:95:LEU:HD21	2.02	0.42
18:s:15:GLN:NE2	53:1:1266:G:C8	2.87	0.42
18:s:51:LEU:O	18:s:55:ILE:HG13	2.19	0.42
32:H:188:ALA:O	32:H:194:VAL:HA	2.20	0.42
41:Q:20:VAL:HG23	41:Q:20:VAL:O	2.19	0.42
52:3:663:A:H5'	52:3:836:G:OP1	2.19	0.42
52:3:779:C:O2'	52:3:780:A:H5'	2.19	0.42
52:3:815:A:H5''	52:3:817:C:N4	2.34	0.42
52:3:1137:C:H5'	52:3:1138:G:H5'	2.01	0.42
52:3:1498:U:C4	56:4:17:U:H5''	2.55	0.42
53:1:720:U:H2'	53:1:721:A:C8	2.54	0.42
53:1:2025:C:H2'	53:1:2026:U:C6	2.54	0.42
53:1:2121:G:H2'	53:1:2122:U:O4'	2.19	0.42
53:1:2176:A:H2'	53:1:2177:C:C6	2.55	0.42
53:1:2195:U:O2'	53:1:2196:C:H5'	2.20	0.42
53:1:2297:A:N1	53:1:2321:U:C5	2.87	0.42
53:1:2638:G:H1'	53:1:2778:A:N6	2.35	0.42
1:b:259:ASN:OD1	1:b:261:ARG:HG2	2.20	0.42
2:c:59:ARG:HG2	53:1:2830:C:OP1	2.19	0.42
4:e:129:MET:SD	4:e:129:MET:C	3.03	0.42
12:m:4:PRO:HG2	12:m:70:ASP:HA	2.01	0.42
13:n:43:GLU:OE2	13:n:46:ARG:NH2	2.53	0.42
18:s:53:SER:O	18:s:57:ASN:HB2	2.19	0.42
21:v:5:ASN:HA	21:v:64:VAL:HG23	2.02	0.42
35:K:68:GLN:O	35:K:71:ILE:HG22	2.20	0.42
38:N:27:ILE:HD12	38:N:27:ILE:N	2.34	0.42
39:O:59:LYS:CE	39:O:62:ARG:HH22	2.33	0.42
51:a:19:LYS:HD3	51:a:19:LYS:C	2.44	0.42
52:3:987:G:H2'	52:3:988:G:H8	1.83	0.42
53:1:74:A:H4'	53:1:75:G:O5'	2.18	0.42
53:1:481:G:H1'	53:1:506:G:H21	1.85	0.42
53:1:864:G:H2'	53:1:865:C:C6	2.55	0.42
53:1:1862:G:O2'	53:1:1863:G:H5'	2.19	0.42
53:1:2106:U:H2'	53:1:2107:G:H8	1.84	0.42
53:1:2114:A:H2'	53:1:2114:A:N3	2.34	0.42
53:1:2231:U:H2'	53:1:2232:C:H6	1.85	0.42
53:1:2696:U:H2'	53:1:2697:G:C8	2.54	0.42
1:b:7:PRO:HB3	1:b:13:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:149:ASN:O	2:c:152:PRO:HD2	2.19	0.42
10:k:12:ASP:HB2	10:k:96:GLY:HA3	2.00	0.42
20:u:32:LYS:HB3	20:u:63:ALA:HB1	2.02	0.42
34:J:132:PRO:O	34:J:136:VAL:HG23	2.19	0.42
35:K:6:ILE:CD1	35:K:74:LEU:HD11	2.50	0.42
36:L:3:ARG:HH22	52:3:932:C:C5'	2.32	0.42
37:M:113:ARG:O	37:M:117:GLN:HG2	2.20	0.42
41:Q:41:PRO:HB3	41:Q:88:ASP:HB3	2.01	0.42
45:U:51:ARG:O	45:U:52:LEU:HD12	2.20	0.42
52:3:243:A:C2	52:3:246:A:C8	3.08	0.42
52:3:1033:G:C2'	52:3:1034:G:H5''	2.50	0.42
52:3:1508:A:H2'	52:3:1509:C:O4'	2.20	0.42
52:3:1511:G:H2'	52:3:1512:U:O4'	2.20	0.42
53:1:940:G:C3'	53:1:941:A:H5''	2.50	0.42
53:1:973:A:H5'	53:1:1188:U:H1'	2.01	0.42
53:1:1112:G:O2'	53:1:1113:U:H5'	2.20	0.42
53:1:1599:U:H2'	53:1:1600:C:C6	2.55	0.42
53:1:1769:U:O2'	53:1:1770:G:H5'	2.20	0.42
53:1:2450:A:O2'	53:1:2451:A:H5'	2.20	0.42
53:1:2574:G:H2'	53:1:2575:C:O4'	2.20	0.42
54:2:78:A:H2'	54:2:79:G:O4'	2.19	0.42
2:c:181:ASP:HB3	2:c:186:LEU:HB2	2.01	0.42
7:h:36:ASP:O	7:h:39:THR:HG22	2.20	0.42
8:i:11:GLN:HE22	8:i:58:ILE:HD13	1.84	0.42
15:p:95:LYS:HB3	15:p:97:TYR:CE2	2.55	0.42
33:I:68:GLU:O	33:I:72:ARG:N	2.50	0.42
34:J:82:HIS:HB2	34:J:83:PRO:HD2	2.01	0.42
34:J:92:ARG:O	34:J:93:VAL:C	2.63	0.42
36:L:136:LYS:HA	36:L:136:LYS:HD2	1.90	0.42
42:R:95:PRO:HB2	42:R:99:GLN:HE21	1.85	0.42
42:R:103:THR:OG1	42:R:104:ASN:N	2.53	0.42
43:S:53:ASP:OD1	43:S:58:ARG:NH2	2.52	0.42
50:Z:54:ARG:HG2	50:Z:57:LYS:HE2	2.01	0.42
51:a:200:LYS:HD3	51:a:208:TYR:CD1	2.55	0.42
52:3:742:G:O2'	52:3:743:A:H5'	2.19	0.42
52:3:1202:U:C2'	52:3:1203:C:H5'	2.50	0.42
52:3:1354:U:H2'	52:3:1355:G:C8	2.54	0.42
53:1:28:A:O2'	53:1:583:G:H5'	2.20	0.42
53:1:72:U:O2'	53:1:73:A:H5'	2.20	0.42
53:1:639:U:H2'	53:1:640:C:H6	1.83	0.42
53:1:738:G:O2'	53:1:739:A:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1060:U:H4'	53:1:1061:U:H5'	2.02	0.42
1:b:12:ARG:HH11	1:b:15:VAL:HG11	1.85	0.42
2:c:108:ASP:OD2	2:c:173:GLN:HG2	2.20	0.42
3:d:79:ARG:HH21	53:1:448:U:C4'	2.32	0.42
4:e:65:LEU:CD1	54:2:41:G:H21	2.31	0.42
14:o:12:THR:OG1	53:1:2334:U:H4'	2.20	0.42
16:q:14:LYS:HB3	16:q:14:LYS:HE2	1.85	0.42
17:r:58:VAL:N	17:r:102:SER:OG	2.53	0.42
21:v:8:VAL:HG22	21:v:9:ARG:N	2.35	0.42
24:y:51:ALA:HA	53:1:72:U:O4'	2.20	0.42
40:P:115:ILE:O	40:P:115:ILE:HG13	2.20	0.42
41:Q:77:SER:HB2	41:Q:102:ASP:CB	2.50	0.42
41:Q:114:SER:OG	52:3:501:C:O3'	2.38	0.42
52:3:40:C:H2'	52:3:41:G:C8	2.54	0.42
52:3:423:G:H2'	52:3:424:G:C5'	2.50	0.42
52:3:1256:A:H4'	52:3:1258:G:O4'	2.19	0.42
52:3:1272:G:H2'	52:3:1273:C:O4'	2.20	0.42
52:3:1464:U:H2'	52:3:1465:A:C8	2.55	0.42
53:1:305:C:H2'	53:1:306:U:C6	2.55	0.42
53:1:1934:C:O2'	53:1:1935:G:H5'	2.20	0.42
1:b:42:ARG:O	53:1:1813:G:H4'	2.20	0.41
1:b:216:ARG:CG	1:b:217:PRO:HD2	2.50	0.41
2:c:9:VAL:HB	2:c:26:VAL:HB	2.01	0.41
10:k:92:GLU:CD	10:k:92:GLU:H	2.26	0.41
12:m:11:LYS:HD3	12:m:86:LYS:HB3	2.02	0.41
23:x:13:THR:HG21	53:1:188:G:H5'	2.02	0.41
30:F:3:VAL:HG21	53:1:2539:C:H5'	2.01	0.41
31:G:134:LEU:HA	31:G:137:THR:HG22	2.02	0.41
41:Q:83:GLY:O	52:3:552:U:H5''	2.19	0.41
42:R:27:THR:HG21	52:3:1328:C:H5''	2.01	0.41
42:R:54:THR:O	42:R:57:ASP:OD1	2.37	0.41
42:R:91:ARG:HD2	53:1:888:C:N3	2.35	0.41
46:V:28:VAL:HG22	46:V:29:LYS:N	2.35	0.41
51:a:7:ARG:HG2	51:a:8:MET:HE2	2.02	0.41
52:3:332:G:O2'	52:3:333:U:H5'	2.20	0.41
52:3:379:C:H2'	52:3:380:G:C8	2.55	0.41
53:1:217:A:H2'	53:1:218:A:O4'	2.19	0.41
53:1:528:A:C2	53:1:2042:A:H2'	2.55	0.41
53:1:2134:A:C6	53:1:2157:G:H4'	2.54	0.41
53:1:2163:A:C2'	53:1:2164:C:H5'	2.49	0.41
53:1:2655:G:O2'	53:1:2656:U:C5	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2730:C:H2'	53:1:2731:G:H8	1.85	0.41
3:d:79:ARG:O	3:d:80:SER:HB3	2.19	0.41
5:f:41:GLU:HB2	5:f:54:ARG:HE	1.86	0.41
7:h:123:ILE:O	7:h:123:ILE:HG23	2.20	0.41
8:i:23:VAL:HG12	8:i:26:ALA:HB3	2.02	0.41
10:k:58:LEU:HD23	10:k:58:LEU:H	1.83	0.41
30:F:36:ARG:O	30:F:37:GLN:O	2.38	0.41
38:N:94:ARG:HA	38:N:97:LEU:HB3	2.01	0.41
43:S:20:PHE:O	43:S:21:ALA:CB	2.68	0.41
50:Z:39:LYS:N	50:Z:40:PRO:CD	2.83	0.41
52:3:620:C:H2'	52:3:621:A:O4'	2.20	0.41
52:3:1495:U:O2'	52:3:1496:C:H5'	2.20	0.41
53:1:679:C:H2'	53:1:680:C:C6	2.55	0.41
53:1:1103:A:H2'	53:1:1104:C:OP1	2.19	0.41
53:1:1344:U:O2	53:1:1385:A:H5'	2.20	0.41
53:1:2087:G:H2'	53:1:2088:A:C8	2.55	0.41
53:1:2182:U:H2'	53:1:2183:A:C8	2.55	0.41
53:1:2642:G:H2'	53:1:2643:G:H8	1.85	0.41
53:1:2691:C:H2'	53:1:2692:G:C8	2.54	0.41
53:1:2801:G:H2'	53:1:2802:G:C8	2.56	0.41
2:c:109:VAL:HG23	2:c:175:LEU:HD12	2.03	0.41
4:e:45:ASP:OD1	4:e:45:ASP:N	2.54	0.41
8:i:8:VAL:HG22	8:i:9:LYS:N	2.35	0.41
10:k:57:VAL:O	10:k:57:VAL:HG13	2.20	0.41
10:k:92:GLU:O	10:k:93:GLN:O	2.37	0.41
14:o:52:SER:HB2	14:o:54:VAL:HG12	2.02	0.41
20:u:84:PHE:CE1	20:u:93:ARG:HG2	2.54	0.41
24:y:5:GLU:O	24:y:56:LEU:HD13	2.20	0.41
34:J:105:ILE:HA	34:J:111:ARG:HH22	1.85	0.41
50:Z:61:ARG:HG2	50:Z:61:ARG:HH11	1.85	0.41
52:3:350:G:O2'	52:3:351:G:H5'	2.20	0.41
52:3:603:U:H2'	52:3:604:G:H8	1.85	0.41
52:3:729:A:H2'	52:3:730:G:H8	1.85	0.41
52:3:901:A:H8	52:3:901:A:O5'	2.03	0.41
52:3:1270:G:H2'	52:3:1271:A:C8	2.56	0.41
53:1:367:G:H2'	53:1:368:A:O4'	2.20	0.41
53:1:2007:U:H2'	53:1:2008:C:C6	2.56	0.41
53:1:2516:A:O2'	53:1:2517:C:H5'	2.21	0.41
1:b:228:ASP:CG	53:1:780:G:H1	2.27	0.41
3:d:102:ARG:NH1	3:d:200:LEU:O	2.52	0.41
10:k:76:VAL:HG13	53:1:2684:U:H4'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:60:TRP:CZ2	16:q:92:LYS:HG3	2.55	0.41
19:t:40:LYS:HA	19:t:43:ILE:HG22	2.02	0.41
23:x:49:ARG:NH1	53:1:1364:G:OP2	2.43	0.41
31:G:151:LYS:NZ	31:G:152:ASP:OD2	2.52	0.41
32:H:126:ARG:HD2	32:H:126:ARG:N	2.36	0.41
33:I:131:ILE:HG23	52:3:403:C:C5'	2.51	0.41
33:I:138:PRO:HB3	33:I:183:ARG:HA	2.03	0.41
37:M:100:ILE:HG13	37:M:128:VAL:HB	2.01	0.41
40:P:48:GLY:HA2	52:3:688:G:H5'	2.02	0.41
43:S:84:ARG:NH1	43:S:88:MET:HE2	2.36	0.41
52:3:54:C:H2'	52:3:352:C:H41	1.85	0.41
52:3:251:G:H4'	52:3:252:U:O5'	2.20	0.41
52:3:552:U:H2'	52:3:553:A:H8	1.85	0.41
52:3:555:U:H2'	52:3:556:C:C6	2.55	0.41
52:3:779:C:C2'	52:3:780:A:H5'	2.50	0.41
52:3:974:A:H5'	52:3:976:G:OP1	2.20	0.41
53:1:300:A:H1'	53:1:319:G:H1'	2.01	0.41
53:1:558:U:H2'	53:1:559:G:C8	2.54	0.41
53:1:825:A:O2'	53:1:826:U:H5'	2.20	0.41
53:1:1071:G:OP1	53:1:1071:G:H3'	2.20	0.41
53:1:1451:C:H4'	53:1:1452:G:N9	2.35	0.41
53:1:1750:G:O2'	53:1:1751:U:H5'	2.21	0.41
53:1:2545:G:C2'	53:1:2546:U:H5'	2.50	0.41
53:1:2730:C:H2'	53:1:2731:G:C8	2.55	0.41
3:d:102:ARG:NH1	3:d:201:ALA:HB3	2.35	0.41
7:h:118:ILE:CG2	7:h:119:PRO:CD	2.93	0.41
11:l:13:LYS:NZ	53:1:660:C:O2'	2.53	0.41
18:s:74:ILE:HG23	18:s:74:ILE:O	2.20	0.41
41:Q:40:THR:HA	41:Q:41:PRO:HD3	1.86	0.41
41:Q:122:LYS:HD2	41:Q:122:LYS:H	1.83	0.41
42:R:94:LEU:HD13	52:3:1226:C:OP1	2.20	0.41
50:Z:31:VAL:O	50:Z:31:VAL:HG22	2.20	0.41
52:3:24:U:O2'	52:3:25:C:H5'	2.20	0.41
52:3:142:G:C2'	52:3:143:A:H5'	2.50	0.41
53:1:20:C:O2'	53:1:21:A:H5'	2.20	0.41
53:1:589:U:H2'	53:1:590:A:C8	2.56	0.41
53:1:752:A:H62	53:1:2609:U:H3	1.68	0.41
53:1:1999:C:H2'	53:1:2000:C:C6	2.55	0.41
53:1:2581:G:N3	53:1:2581:G:H2'	2.36	0.41
55:5:43:A:H2'	55:5:44:A:H8	1.85	0.41
3:d:123:LYS:HE3	3:d:125:SER:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:3:LEU:C	4:e:3:LEU:HD12	2.45	0.41
5:f:51:PHE:CZ	5:f:71:LEU:HD22	2.56	0.41
6:g:57:LYS:HD3	6:g:57:LYS:N	2.35	0.41
8:i:8:VAL:HG13	8:i:10:LEU:CD2	2.50	0.41
8:i:130:GLY:O	8:i:133:ARG:HG2	2.21	0.41
11:l:19:LEU:N	11:l:19:LEU:CD1	2.83	0.41
13:n:26:GLY:HA2	13:n:75:ILE:HG13	2.02	0.41
22:w:20:LYS:HD3	22:w:20:LYS:HA	1.86	0.41
28:D:34:ARG:HA	28:D:34:ARG:HD2	1.92	0.41
30:F:36:ARG:HD3	53:1:2742:G:OP1	2.21	0.41
31:G:96:LEU:O	31:G:99:MET:HG3	2.21	0.41
32:H:131:ARG:HA	32:H:134:LYS:NZ	2.35	0.41
32:H:188:ALA:HB3	32:H:195:ILE:HB	2.02	0.41
41:Q:23:LEU:HD22	41:Q:58:ASN:HB3	2.03	0.41
52:3:189:A:H2'	52:3:190:A:O4'	2.20	0.41
52:3:422:C:H4'	52:3:423:G:H5''	2.03	0.41
52:3:707:U:H2'	52:3:708:C:C6	2.55	0.41
52:3:783:C:O2'	52:3:784:A:H5'	2.20	0.41
52:3:909:A:H2'	52:3:910:C:O4'	2.21	0.41
52:3:977:A:H3'	52:3:977:A:N3	2.35	0.41
53:1:1528:A:H2'	53:1:1529:G:O4'	2.21	0.41
53:1:1565:C:O2'	53:1:1566:A:C8	2.74	0.41
53:1:2297:A:H62	53:1:2319:G:H1'	1.86	0.41
53:1:2333:A:H5''	53:1:2334:U:OP1	2.21	0.41
53:1:2784:U:H2'	53:1:2785:C:C6	2.56	0.41
53:1:2809:A:H2'	53:1:2810:A:C8	2.56	0.41
53:1:2855:C:H2'	53:1:2856:A:C8	2.55	0.41
55:6:36:U:H2'	55:6:37:A:O4'	2.20	0.41
55:6:70:G:O2'	55:6:71:C:H5'	2.20	0.41
57:7:17:C:O5'	57:7:18:G:H5''	2.20	0.41
1:b:42:ARG:HH21	1:b:48:ILE:HD11	1.86	0.41
3:d:148:ILE:HD13	3:d:187:VAL:CG1	2.51	0.41
4:e:27:VAL:HA	4:e:28:PRO:HD3	1.92	0.41
4:e:63:LYS:HG2	4:e:64:PRO:HD2	2.03	0.41
4:e:106:ALA:O	4:e:110:ILE:HD12	2.21	0.41
8:i:126:ARG:O	8:i:129:GLU:HB3	2.21	0.41
24:y:23:ARG:O	24:y:25:GLN:N	2.54	0.41
28:D:25:LYS:O	28:D:29:GLN:HG2	2.21	0.41
31:G:103:TRP:HE1	31:G:107:ARG:HH21	1.68	0.41
32:H:19:SER:HB3	32:H:21:TRP:HE1	1.86	0.41
33:I:112:GLU:HG3	52:3:407:U:O2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:165:GLU:HG2	33:I:167:PRO:HD3	2.02	0.41
40:P:52:ARG:HD2	40:P:52:ARG:HA	1.91	0.41
46:V:60:ILE:HD13	46:V:74:LEU:HD12	2.03	0.41
51:a:11:ILE:HA	51:a:14:LYS:NZ	2.36	0.41
52:3:460:A:H2'	52:3:461:A:C8	2.56	0.41
52:3:736:C:H2'	52:3:737:C:C6	2.55	0.41
52:3:915:A:C2'	52:3:916:U:H5'	2.51	0.41
52:3:1157:A:H4'	52:3:1158:C:O5'	2.21	0.41
53:1:371:A:H5''	53:1:423:A:C2	2.56	0.41
53:1:1092:C:H2'	53:1:1093:G:O4'	2.20	0.41
53:1:1182:G:H2'	53:1:1183:U:O4'	2.20	0.41
53:1:2071:A:H2'	53:1:2072:C:C6	2.56	0.41
54:2:99:A:C2	54:2:100:G:H1'	2.55	0.41
54:2:99:A:H2'	54:2:100:G:O4'	2.19	0.41
4:e:102:LEU:O	4:e:107:VAL:HG23	2.21	0.41
9:j:31:GLU:HG2	9:j:142:ILE:HG12	2.02	0.41
13:n:3:HIS:O	13:n:4:ARG:HB2	2.21	0.41
15:p:3:ILE:HD12	15:p:3:ILE:N	2.32	0.41
25:z:40:THR:HG23	25:z:43:ILE:H	1.86	0.41
31:G:196:ASP:OD2	31:G:196:ASP:N	2.54	0.41
34:J:110:MET:HG3	34:J:139:THR:HG21	2.02	0.41
35:K:11:HIS:CE1	35:K:54:LEU:HD11	2.55	0.41
46:V:30:HIS:HA	46:V:31:PRO:HD3	1.92	0.41
49:Y:67:HIS:C	49:Y:69:ASN:H	2.29	0.41
52:3:16:A:C2'	52:3:17:U:H5'	2.50	0.41
52:3:337:G:H2'	52:3:338:A:C8	2.55	0.41
52:3:438:U:C2'	52:3:439:U:OP2	2.69	0.41
52:3:767:A:O2'	52:3:768:A:H5'	2.20	0.41
52:3:950:U:H2'	52:3:951:G:H8	1.86	0.41
52:3:979:C:H2'	52:3:980:C:H5'	2.03	0.41
52:3:1006:G:O2'	52:3:1007:U:H5'	2.21	0.41
53:1:490:C:H4'	53:1:491:G:OP2	2.20	0.41
53:1:870:U:O2'	53:1:871:U:H5'	2.21	0.41
53:1:1675:C:H2'	53:1:1676:A:O4'	2.21	0.41
53:1:2224:G:H4'	53:1:2226:C:C2	2.55	0.41
53:1:2662:A:H2'	53:1:2663:G:O4'	2.20	0.41
2:c:88:GLU:N	2:c:88:GLU:OE1	2.54	0.41
4:e:135:ILE:HG13	4:e:135:ILE:O	2.20	0.41
6:g:121:VAL:O	6:g:121:VAL:HG12	2.20	0.41
7:h:119:PRO:CD	7:h:120:ALA:H	2.33	0.41
14:o:33:ARG:O	14:o:34:HIS:CB	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:p:1:SER:O	15:p:5:LYS:HB2	2.20	0.41
17:r:33:VAL:HG23	17:r:61:ALA:HB3	2.02	0.41
24:y:56:LEU:O	24:y:60:LYS:HB2	2.20	0.41
28:D:37:LYS:NZ	53:1:468:G:OP2	2.54	0.41
31:G:45:THR:HG22	31:G:200:PRO:HB2	2.02	0.41
31:G:122:ASP:OD1	31:G:124:THR:HG23	2.21	0.41
32:H:53:ARG:HG2	32:H:68:HIS:HB2	2.03	0.41
32:H:148:ILE:HG13	32:H:201:ILE:HG12	2.03	0.41
33:I:61:ARG:NH1	33:I:68:GLU:OE2	2.52	0.41
33:I:115:GLN:HE22	52:3:406:G:H1'	1.86	0.41
33:I:182:LYS:HB3	33:I:183:ARG:H	1.68	0.41
34:J:80:LEU:HD22	34:J:122:VAL:HG11	2.02	0.41
37:M:77:VAL:O	37:M:79:ARG:HG3	2.21	0.41
40:P:59:PRO:HD3	40:P:90:PRO:HB2	2.03	0.41
40:P:108:ASN:ND2	40:P:110:THR:OG1	2.54	0.41
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.86	0.41
46:V:18:LYS:HZ2	46:V:49:ASN:H	1.68	0.41
46:V:29:LYS:HB2	46:V:36:PHE:HE1	1.84	0.41
48:X:38:THR:HA	48:X:69:LYS:HA	2.01	0.41
50:Z:7:GLU:HG3	50:Z:15:LEU:HD12	2.02	0.41
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.50	0.41
50:Z:32:ARG:HG3	50:Z:33:ARG:HG3	2.03	0.41
51:a:209:ILE:O	51:a:209:ILE:HG13	2.21	0.41
52:3:57:G:H2'	52:3:58:C:C6	2.55	0.41
52:3:238:A:O2'	52:3:239:U:H5'	2.21	0.41
52:3:298:A:H2'	52:3:299:G:O4'	2.21	0.41
52:3:396:C:C3'	52:3:397:A:H5''	2.51	0.41
52:3:556:C:H2'	52:3:557:G:O4'	2.21	0.41
53:1:176:A:H3'	53:1:177:G:N2	2.36	0.41
53:1:178:G:O2'	53:1:179:C:H5'	2.21	0.41
53:1:319:G:H2'	53:1:320:A:O4'	2.20	0.41
53:1:325:G:H2'	53:1:326:G:H8	1.86	0.41
53:1:955:U:H3	53:1:962:G:H1	1.68	0.41
53:1:1001:A:H2'	53:1:1002:G:O4'	2.21	0.41
53:1:1188:U:O2'	53:1:1189:A:H5'	2.20	0.41
53:1:1343:G:N3	53:1:1343:G:H2'	2.35	0.41
53:1:1420:A:H5'	53:1:1421:G:OP2	2.21	0.41
53:1:1563:U:O2'	53:1:1564:C:H5'	2.21	0.41
53:1:1876:A:H2'	53:1:1877:A:O4'	2.21	0.41
53:1:1930:G:C2'	53:1:1931:U:OP2	2.69	0.41
53:1:2240:U:O2'	53:1:2241:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2699:C:H2'	53:1:2700:A:H8	1.85	0.41
54:2:35:C:C2'	54:2:36:C:H5'	2.50	0.41
57:7:46:G:HO2'	57:7:48:C:H5'	1.85	0.41
4:e:40:GLY:HA3	53:1:2307:G:O6	2.21	0.41
4:e:102:LEU:HA	4:e:106:ALA:HB3	2.03	0.41
5:f:132:LEU:HD23	5:f:132:LEU:H	1.86	0.41
7:h:16:SER:O	7:h:20:LYS:HG2	2.21	0.41
12:m:134:THR:OG1	12:m:135:VAL:N	2.54	0.41
14:o:30:ARG:HA	14:o:35:ILE:HD12	2.03	0.41
17:r:43:ASN:OD1	17:r:44:GLY:N	2.46	0.41
20:u:4:ILE:HD12	20:u:4:ILE:N	2.36	0.41
33:I:165:GLU:HG2	33:I:166:LYS:N	2.35	0.41
36:L:102:TRP:CH2	36:L:140:VAL:HG21	2.56	0.41
37:M:28:SER:OG	37:M:29:SER:N	2.54	0.41
40:P:111:ASP:OD1	40:P:113:THR:HG23	2.21	0.41
42:R:16:ILE:HD12	42:R:16:ILE:N	2.33	0.41
45:U:22:ALA:CB	45:U:32:PHE:HA	2.51	0.41
52:3:82:G:H2'	52:3:83:C:C5'	2.51	0.41
52:3:497:G:H2'	52:3:498:A:C8	2.56	0.41
52:3:651:C:H2'	52:3:652:U:C6	2.56	0.41
53:1:12:U:O2	53:1:2626:C:H4'	2.21	0.41
53:1:204:A:O3'	53:1:205:G:H4'	2.20	0.41
53:1:253:C:H2'	53:1:254:G:O4'	2.19	0.41
53:1:497:A:H2'	53:1:498:G:O4'	2.21	0.41
53:1:633:A:H2'	53:1:634:C:H5'	2.02	0.41
53:1:881:G:O2'	53:1:882:G:H5'	2.21	0.41
53:1:1077:A:C3'	53:1:1078:U:H5'	2.51	0.41
53:1:1592:C:H2'	53:1:1593:A:C8	2.56	0.41
53:1:1917:U:O2'	53:1:1918:A:H5'	2.21	0.41
53:1:2323:G:H2'	53:1:2324:U:O4'	2.21	0.41
53:1:2855:C:H2'	53:1:2856:A:H8	1.86	0.41
2:c:59:ARG:HG2	53:1:2830:C:P	2.62	0.40
3:d:149:ILE:O	3:d:149:ILE:HG23	2.21	0.40
9:j:116:ARG:NH2	53:1:529:A:OP2	2.51	0.40
17:r:1:MET:N	17:r:43:ASN:HA	2.36	0.40
23:x:46:VAL:HG23	23:x:46:VAL:O	2.21	0.40
37:M:30:LYS:NZ	52:3:643:C:OP1	2.53	0.40
39:O:8:ILE:HD12	39:O:8:ILE:N	2.37	0.40
42:R:21:ILE:HB	42:R:24:VAL:HG12	2.02	0.40
45:U:23:ASP:OD2	45:U:25:ARG:NH2	2.54	0.40
50:Z:67:THR:O	52:3:1167:A:C8	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:106:C:H2'	52:3:107:G:C8	2.56	0.40
52:3:398:U:H2'	52:3:399:G:H8	1.86	0.40
52:3:805:C:O2'	52:3:806:C:H5'	2.21	0.40
52:3:1328:C:H2'	52:3:1329:A:C8	2.57	0.40
53:1:861:A:H2'	53:1:862:G:O4'	2.21	0.40
53:1:1152:C:O2'	53:1:1153:C:H5'	2.21	0.40
53:1:1401:G:H2'	53:1:1402:U:C6	2.57	0.40
53:1:1817:G:N2	53:1:1818:U:H1'	2.36	0.40
53:1:2333:A:H5'	53:1:2335:A:H1'	2.04	0.40
54:2:88:C:C5'	54:2:89:U:OP1	2.65	0.40
55:6:13:C:O2'	55:6:14:A:H5'	2.21	0.40
7:h:33:VAL:HA	53:1:1055:G:H4'	2.02	0.40
7:h:43:LYS:HE3	7:h:98:GLU:HG3	2.03	0.40
14:o:61:GLN:C	14:o:62:LEU:HD22	2.47	0.40
18:s:57:ASN:OD1	53:1:495:G:H1'	2.22	0.40
19:t:56:GLU:CD	19:t:88:LYS:HG2	2.46	0.40
31:G:165:ALA:HB1	31:G:172:ILE:CD1	2.51	0.40
33:I:2:ARG:HD3	52:3:405:U:OP2	2.21	0.40
33:I:144:ILE:HB	33:I:149:LYS:NZ	2.36	0.40
36:L:90:VAL:CG2	36:L:94:ARG:HD3	2.52	0.40
37:M:112:ASP:O	37:M:116:ARG:HG3	2.20	0.40
45:U:55:ASP:OD1	45:U:56:ARG:N	2.55	0.40
46:V:45:VAL:HG11	46:V:60:ILE:HD12	2.02	0.40
46:V:58:VAL:HB	46:V:74:LEU:HD11	2.04	0.40
48:X:72:GLU:HG3	52:3:1320:C:H4'	2.03	0.40
49:Y:48:LYS:O	49:Y:52:GLU:HG3	2.21	0.40
52:3:346:G:O2'	52:3:347:G:H5'	2.21	0.40
52:3:763:G:H2'	52:3:764:C:C6	2.56	0.40
52:3:825:A:H2'	52:3:826:C:C6	2.55	0.40
52:3:1041:G:O2'	52:3:1042:A:H5'	2.21	0.40
52:3:1131:G:H22	52:3:1144:G:H4'	1.87	0.40
52:3:1264:U:H2'	52:3:1265:C:C6	2.56	0.40
52:3:1427:C:O2'	52:3:1428:A:H5'	2.20	0.40
53:1:196:A:H2'	53:1:196:A:N3	2.35	0.40
53:1:968:C:H2'	53:1:969:G:C8	2.57	0.40
53:1:1932:A:H2'	53:1:1933:G:O4'	2.22	0.40
53:1:2340:A:H2'	53:1:2341:G:H8	1.85	0.40
53:1:2698:U:H2'	53:1:2699:C:H6	1.78	0.40
54:2:40:U:H1'	54:2:43:C:C5	2.56	0.40
55:6:63:G:H2'	55:6:64:G:H8	1.85	0.40
2:c:166:GLY:C	2:c:168:GLU:H	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:103:ILE:HA	4:e:107:VAL:CG2	2.52	0.40
12:m:33:LEU:HB2	12:m:117:PHE:CD1	2.56	0.40
18:s:36:LEU:HA	18:s:39:THR:HG22	2.04	0.40
20:u:97:SER:O	20:u:98:ASN:HB3	2.22	0.40
26:B:3:GLN:HA	53:1:2615:U:N3	2.36	0.40
26:B:30:ASP:HB3	26:B:34:GLY:N	2.36	0.40
32:H:166:TRP:HZ3	32:H:168:ARG:HG2	1.86	0.40
40:P:43:TRP:NE1	52:3:686:U:H1'	2.27	0.40
40:P:121:ARG:NH2	50:Z:35:GLU:HG2	2.36	0.40
52:3:144:G:H2'	52:3:145:G:O4'	2.21	0.40
52:3:300:A:H1'	52:3:565:U:H3	1.87	0.40
52:3:597:G:H2'	52:3:598:U:H5'	2.03	0.40
52:3:1429:A:H2'	52:3:1430:A:H8	1.87	0.40
53:1:288:U:H2'	53:1:289:G:C8	2.56	0.40
53:1:813:U:H2'	53:1:814:C:C6	2.56	0.40
53:1:863:A:H2'	53:1:864:G:C8	2.56	0.40
53:1:1366:A:H2'	53:1:1367:A:O4'	2.21	0.40
53:1:1441:G:H2'	53:1:1442:U:C6	2.57	0.40
53:1:2650:U:H2'	53:1:2651:C:C6	2.56	0.40
54:2:42:C:H2'	54:2:43:C:O4'	2.20	0.40
54:2:49:C:H2'	54:2:50:A:C8	2.57	0.40
57:7:36:A:O2'	57:7:37:A:H5'	2.21	0.40
2:c:123:LYS:HE2	13:n:1:MET:HE1	2.03	0.40
3:d:48:THR:O	3:d:52:VAL:HG23	2.20	0.40
4:e:63:LYS:HB3	54:2:42:C:H4'	2.03	0.40
5:f:174:LYS:HD3	53:1:2529:G:H4'	2.04	0.40
7:h:20:LYS:HB2	7:h:88:HIS:CD2	2.56	0.40
10:k:98:ARG:HH11	52:3:339:C:H5	1.70	0.40
26:B:12:ARG:NH2	53:1:517:C:OP1	2.54	0.40
31:G:23:ASN:HA	31:G:24:PRO:HD3	1.89	0.40
33:I:44:LYS:HE3	33:I:44:LYS:HB3	1.95	0.40
33:I:134:TYR:HE1	52:3:620:C:H5'	1.86	0.40
36:L:32:ASP:OD1	52:3:1350:A:O2'	2.40	0.40
37:M:77:VAL:HG21	37:M:127:TYR:CD1	2.56	0.40
40:P:126:ARG:NH2	52:3:692:U:H5''	2.34	0.40
46:V:42:LYS:O	46:V:43:LEU:HD12	2.22	0.40
49:Y:33:LYS:HE3	49:Y:33:LYS:HB2	1.91	0.40
51:a:27:ILE:HD13	51:a:186:LYS:HE3	2.02	0.40
53:1:619:G:H3'	53:1:620:G:N2	2.35	0.40
53:1:2898:U:H2'	53:1:2899:A:C8	2.56	0.40
4:e:132:ARG:HH11	4:e:149:ARG:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:l:118:THR:O	11:l:120:VAL:N	2.55	0.40
12:m:65:ILE:HG12	12:m:103:TYR:HD1	1.87	0.40
18:s:3:THR:OG1	18:s:107:VAL:O	2.39	0.40
20:u:11:ILE:CG2	20:u:79:ALA:HB2	2.51	0.40
31:G:39:ILE:N	31:G:39:ILE:HD12	2.36	0.40
36:L:9:ARG:HH12	52:3:1377:A:H62	1.68	0.40
42:R:87:GLY:O	42:R:91:ARG:HG3	2.20	0.40
47:W:33:THR:OG1	47:W:34:GLU:N	2.53	0.40
50:Z:9:GLU:O	50:Z:11:PHE:CD1	2.75	0.40
51:a:14:LYS:HD2	51:a:33:LEU:HD23	2.03	0.40
52:3:571:U:H2'	52:3:572:A:H5''	2.04	0.40
52:3:1069:C:O2'	52:3:1192:C:H1'	2.21	0.40
53:1:123:G:O2'	53:1:124:G:H5'	2.21	0.40
53:1:216:A:H2'	53:1:217:A:O4'	2.21	0.40
53:1:660:C:H2'	53:1:661:A:C8	2.56	0.40
53:1:768:G:N2	53:1:1379:U:H1'	2.36	0.40
53:1:854:C:H2'	53:1:855:G:C8	2.56	0.40
53:1:863:A:H2'	53:1:864:G:H8	1.86	0.40
53:1:1469:A:H2'	53:1:1470:A:C8	2.56	0.40
53:1:1594:U:H2'	53:1:1595:C:C6	2.56	0.40
53:1:2492:U:O2'	53:1:2493:U:H5'	2.21	0.40
54:2:39:A:H2'	54:2:40:U:C6	2.57	0.40
57:7:8:U:H5'	57:7:49:C:OP2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	235 (87%)	33 (12%)	1 (0%)	30	62
2	c	207/209 (99%)	189 (91%)	17 (8%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	d	199/201 (99%)	180 (90%)	17 (8%)	2 (1%)	12	45
4	e	175/177 (99%)	156 (89%)	17 (10%)	2 (1%)	11	43
5	f	174/176 (99%)	160 (92%)	12 (7%)	2 (1%)	11	43
6	g	147/149 (99%)	126 (86%)	18 (12%)	3 (2%)	6	31
7	h	129/131 (98%)	95 (74%)	30 (23%)	4 (3%)	3	22
8	i	139/141 (99%)	124 (89%)	13 (9%)	2 (1%)	9	39
9	j	140/142 (99%)	133 (95%)	6 (4%)	1 (1%)	18	52
10	k	120/122 (98%)	98 (82%)	17 (14%)	5 (4%)	2	16
11	l	141/143 (99%)	119 (84%)	15 (11%)	7 (5%)	1	13
12	m	134/136 (98%)	113 (84%)	19 (14%)	2 (2%)	8	37
13	n	118/120 (98%)	106 (90%)	10 (8%)	2 (2%)	7	35
14	o	114/116 (98%)	106 (93%)	7 (6%)	1 (1%)	14	47
15	p	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
16	q	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
17	r	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	3	23
18	s	108/110 (98%)	95 (88%)	10 (9%)	3 (3%)	4	25
19	t	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
20	u	100/102 (98%)	84 (84%)	13 (13%)	3 (3%)	3	23
21	v	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
22	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	7	36
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
27	C	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
28	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
29	E	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	36
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	25
31	G	223/225 (99%)	202 (91%)	20 (9%)	1 (0%)	30	62
32	H	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
33	I	203/205 (99%)	184 (91%)	15 (7%)	4 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	J	155/157 (99%)	124 (80%)	27 (17%)	4 (3%)	4	26
35	K	98/100 (98%)	81 (83%)	12 (12%)	5 (5%)	1	13
36	L	149/151 (99%)	131 (88%)	17 (11%)	1 (1%)	18	52
37	M	127/129 (98%)	112 (88%)	13 (10%)	2 (2%)	7	36
38	N	125/127 (98%)	103 (82%)	18 (14%)	4 (3%)	3	21
39	O	96/98 (98%)	80 (83%)	11 (12%)	5 (5%)	1	12
40	P	114/116 (98%)	94 (82%)	17 (15%)	3 (3%)	4	26
41	Q	121/123 (98%)	94 (78%)	21 (17%)	6 (5%)	1	13
42	R	112/114 (98%)	98 (88%)	10 (9%)	4 (4%)	2	19
43	S	98/100 (98%)	76 (78%)	22 (22%)	0	100	100
44	T	86/88 (98%)	78 (91%)	6 (7%)	2 (2%)	5	29
45	U	80/82 (98%)	71 (89%)	8 (10%)	1 (1%)	9	40
46	V	78/80 (98%)	64 (82%)	12 (15%)	2 (3%)	4	26
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	36
48	X	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	4	26
49	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
50	Z	63/65 (97%)	47 (75%)	9 (14%)	7 (11%)	0	2
51	a	130/223 (58%)	124 (95%)	6 (5%)	0	100	100
All	All	5919/6112 (97%)	5192 (88%)	625 (11%)	102 (2%)	9	35

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA
5	f	174	LYS
6	g	9	VAL
7	h	81	LEU
7	h	118	ILE
10	k	92	GLU
13	n	118	ARG
14	o	34	HIS
17	r	54	VAL
24	y	24	GLU
29	E	31	ILE
30	F	37	GLN

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Mol	Chain	Res	Type
33	I	34	GLU
34	J	93	VAL
34	J	122	VAL
35	K	53	LYS
35	K	54	LEU
37	M	47	ASP
38	N	57	VAL
38	N	90	ASP
40	P	92	ARG
40	P	125	LYS
42	R	4	ALA
44	T	46	LYS
50	Z	14	ALA
7	h	108	VAL
8	i	90	GLY
10	k	89	ASN
11	l	28	GLY
11	l	31	GLY
11	l	115	GLU
18	s	63	GLY
20	u	56	GLY
20	u	98	ASN
35	K	40	GLU
38	N	91	GLU
41	Q	24	GLU
41	Q	77	SER
42	R	14	ALA
44	T	48	ASP
46	V	17	GLU
46	V	49	ASN
48	X	34	SER
50	Z	25	ALA
4	e	20	ASN
11	l	15	ALA
11	l	29	LYS
12	m	69	PRO
18	s	11	ARG
33	I	152	SER
34	J	98	ALA
35	K	86	ARG
35	K	95	ALA
36	L	4	ARG

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Mol	Chain	Res	Type
38	N	8	THR
39	O	33	GLY
39	O	35	GLN
40	P	13	LYS
41	Q	43	LYS
45	U	79	ASN
50	Z	23	GLU
50	Z	34	ARG
50	Z	36	PHE
2	c	118	PHE
7	h	107	GLU
33	I	28	ASP
39	O	34	ALA
39	O	42	LEU
41	Q	101	LEU
42	R	65	GLU
48	X	53	GLY
50	Z	9	GLU
4	e	173	ASP
6	g	11	ASN
8	i	6	ALA
10	k	26	GLY
11	l	85	VAL
12	m	6	ARG
13	n	14	SER
17	r	16	GLU
33	I	47	LEU
34	J	11	GLN
41	Q	35	ARG
41	Q	75	GLU
42	R	6	ILE
50	Z	64	ALA
6	g	89	LYS
10	k	93	GLN
20	u	54	PRO
21	v	81	PRO
47	W	24	ASP
3	d	89	PRO
10	k	68	GLY
3	d	83	VAL
11	l	56	PRO
39	O	57	VAL

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Mol	Chain	Res	Type
17	r	44	GLY
9	j	81	ILE
18	s	80	PRO
31	G	192	PRO
37	M	102	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	215 (100%)	1 (0%)	81	85
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	77
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%)	97 (97%)	3 (3%)	36	66
8	i	109/109 (100%)	108 (99%)	1 (1%)	70	81
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	80
11	l	102/102 (100%)	101 (99%)	1 (1%)	68	80
12	m	109/109 (100%)	108 (99%)	1 (1%)	70	81
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	79
15	p	99/99 (100%)	99 (100%)	0	100	100
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%)	93 (100%)	0	100	100
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	78
20	u	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	v	78/78 (100%)	77 (99%)	1 (1%)	61	78
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	84
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	84
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	82
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	79
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	80
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	83 (96%)	3 (4%)	32	64
40	P	89/89 (100%)	88 (99%)	1 (1%)	65	79
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	79
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	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%)	54 (98%)	1 (2%)	51	74
51	a	110/174 (63%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	4908/4972 (99%)	4884 (100%)	24 (0%)	78	85

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	217	PRO
4	e	90	LEU
4	e	112	ASP
7	h	81	LEU
7	h	118	ILE
7	h	119	PRO
8	i	33	ASN
10	k	89	ASN
11	l	94	THR
12	m	70	ASP
14	o	34	HIS
19	t	2	ILE
21	v	72	VAL
32	H	156	LEU
33	I	31	CYS
34	J	55	VAL
35	K	88	MET
37	M	103	VAL
39	O	57	VAL
39	O	63	ASP
39	O	89	ARG
40	P	118	ASN
42	R	99	GLN
50	Z	40	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (112) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	36	ASN
1	b	44	ASN
1	b	45	ASN
1	b	52	HIS
1	b	69	ASN
1	b	89	ASN
1	b	116	GLN
1	b	127	ASN

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Mol	Chain	Res	Type
1	b	199	HIS
1	b	225	ASN
2	c	49	GLN
2	c	130	GLN
3	d	24	ASN
3	d	41	GLN
3	d	97	ASN
4	e	20	ASN
4	e	36	ASN
4	e	80	GLN
5	f	63	GLN
5	f	100	ASN
5	f	110	HIS
6	g	2	GLN
6	g	11	ASN
6	g	33	GLN
6	g	43	ASN
6	g	119	ASN
6	g	133	GLN
6	g	135	HIS
6	g	145	ASN
7	h	4	ASN
7	h	88	HIS
7	h	122	GLN
8	i	5	GLN
8	i	11	GLN
9	j	58	ASN
9	j	80	HIS
9	j	86	GLN
9	j	135	GLN
10	k	5	GLN
10	k	13	ASN
11	l	54	GLN
11	l	93	ASN
12	m	22	GLN
13	n	13	ASN
13	n	31	HIS
13	n	62	ASN
13	n	73	ASN
14	o	61	GLN
14	o	100	HIS
15	p	2	ASN

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Mol	Chain	Res	Type
15	p	6	GLN
15	p	11	GLN
16	q	71	ASN
17	r	82	HIS
19	t	15	HIS
19	t	28	ASN
19	t	59	ASN
20	u	73	ASN
21	v	24	ASN
21	v	44	HIS
22	w	8	ASN
22	w	42	HIS
22	w	53	HIS
24	y	39	GLN
24	y	58	ASN
26	B	18	HIS
27	C	18	HIS
28	D	13	ASN
30	F	37	GLN
31	G	17	HIS
31	G	18	GLN
31	G	38	HIS
31	G	176	ASN
31	G	202	ASN
32	H	31	ASN
32	H	99	GLN
32	H	139	ASN
32	H	184	ASN
33	I	40	HIS
33	I	53	GLN
33	I	130	ASN
33	I	195	ASN
33	I	197	HIS
34	J	77	ASN
34	J	81	GLN
34	J	131	ASN
34	J	134	ASN
35	K	11	HIS
35	K	14	GLN
35	K	37	HIS
36	L	67	ASN
36	L	129	ASN

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Mol	Chain	Res	Type
37	M	17	GLN
37	M	66	GLN
39	O	56	HIS
39	O	58	ASN
40	P	108	ASN
41	Q	4	ASN
41	Q	111	GLN
43	S	48	GLN
43	S	59	GLN
43	S	70	HIS
44	T	34	GLN
45	U	26	ASN
45	U	63	GLN
46	V	44	HIS
47	W	18	GLN
48	X	55	GLN
48	X	56	HIS
49	Y	12	GLN
49	Y	69	ASN
51	a	188	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	141 (9%)	4 (0%)
53	1	2902/2903 (99%)	332 (11%)	14 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	10 (13%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	2 (11%)	0
57	7	75/76 (98%)	10 (13%)	0
All	All	4803/4810 (99%)	513 (10%)	19 (0%)

All (513) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
52	3	51	A
52	3	71	A
52	3	87	C
52	3	100	G
52	3	181	A
52	3	183	C
52	3	184	G
52	3	197	A
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	279	A
52	3	281	G
52	3	289	G
52	3	328	C
52	3	345	C
52	3	352	C
52	3	367	U
52	3	372	C
52	3	373	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	430	A
52	3	467	U
52	3	479	U
52	3	485	U
52	3	486	U
52	3	496	A
52	3	497	G
52	3	511	C
52	3	518	C
52	3	532	A
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A
52	3	575	G

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Mol	Chain	Res	Type
52	3	576	C
52	3	577	G
52	3	633	G
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
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	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	873	A
52	3	890	G
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	971	G
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G

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Mol	Chain	Res	Type
52	3	1053	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
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1261	A
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1378	C
52	3	1381	U
52	3	1395	C
52	3	1419	G
52	3	1446	A
52	3	1448	C

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Mol	Chain	Res	Type
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1519	A
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	50	U
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	102	U
53	1	119	A
53	1	120	U
53	1	138	U
53	1	139	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A
53	1	216	A
53	1	219	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A

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Mol	Chain	Res	Type
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	361	G
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	412	A
53	1	422	A
53	1	424	G
53	1	455	C
53	1	458	G
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	545	U
53	1	547	A
53	1	563	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A

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Mol	Chain	Res	Type
53	1	637	A
53	1	646	U
53	1	654	A
53	1	655	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	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
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	858	G
53	1	859	G
53	1	860	U
53	1	878	A
53	1	885	C
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	983	A

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Mol	Chain	Res	Type
53	1	995	C
53	1	996	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	1090	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1175	A
53	1	1177	G
53	1	1180	U
53	1	1206	G
53	1	1212	G
53	1	1238	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A

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Mol	Chain	Res	Type
53	1	1275	A
53	1	1289	C
53	1	1301	A
53	1	1302	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1427	A
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1581	G
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C

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Mol	Chain	Res	Type
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1781	U
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1914	C
53	1	1929	G
53	1	1930	G
53	1	1931	U
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	1971	U
53	1	1972	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

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Mol	Chain	Res	Type
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	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2212	A
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2239	G
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	A
53	1	2407	A
53	1	2423	U
53	1	2424	C

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Mol	Chain	Res	Type
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	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2609	U
53	1	2613	U
53	1	2629	U
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	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
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

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Mol	Chain	Res	Type
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	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
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	59	A
55	5	61	C
55	5	74	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
55	6	61	C
56	4	12	A
56	4	13	A
57	7	17	C
57	7	21	A
57	7	45	U
57	7	46	G
57	7	47	U
57	7	48	C

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Mol	Chain	Res	Type
57	7	49	C
57	7	59	U
57	7	61	C
57	7	74	C

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	70	U
52	3	429	U
52	3	495	A
52	3	1190	G
53	1	227	A
53	1	421	C
53	1	490	C
53	1	774	G
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	1930	G
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	PHE	7	101	57	10,11,12	1.22	1 (10%)	8,13,15	0.64	0
58	FME	5	101	55	8,9,10	0.63	0	8,9,11	0.95	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	PHE	7	101	57	-	0/5/6/8	0/1/1/1
58	FME	5	101	55	-	2/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	7	101	PHE	CB-CG	-2.82	1.44	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	5	101	FME	O1-CN-N-CA
58	5	101	FME	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	7	101	PHE	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

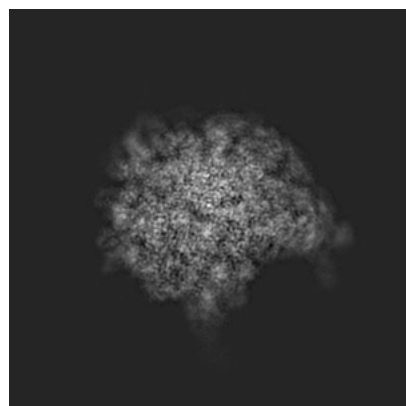
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21632. These allow visual inspection of the internal detail of the map and identification of artifacts.

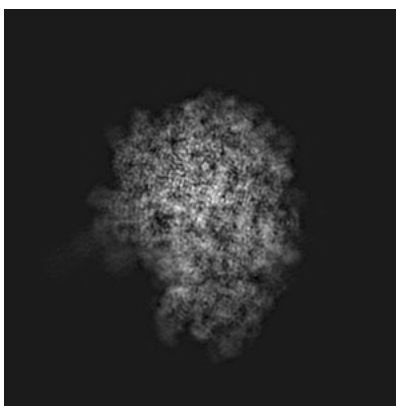
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

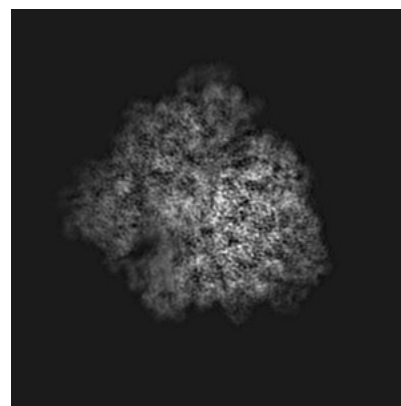
6.1.1 Primary map



X

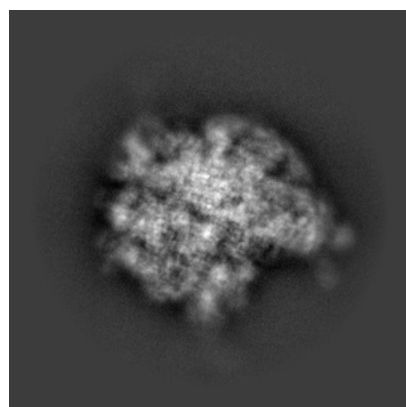


Y

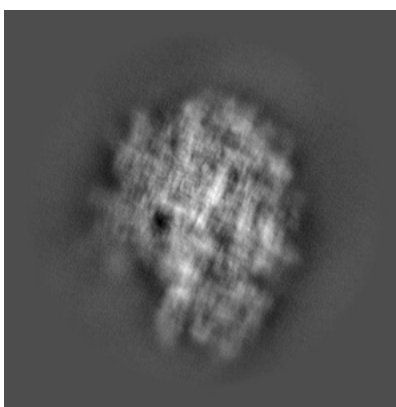


Z

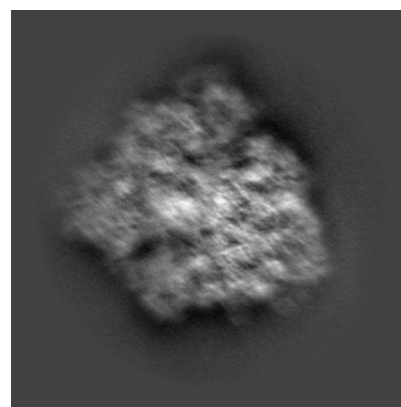
6.1.2 Raw map



X



Y

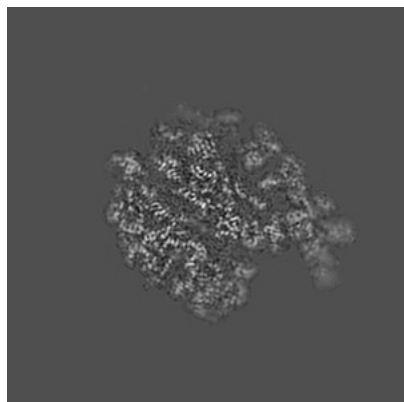


Z

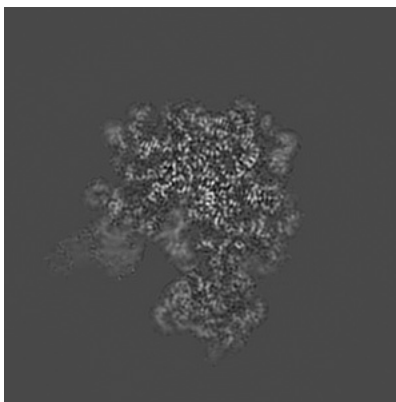
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

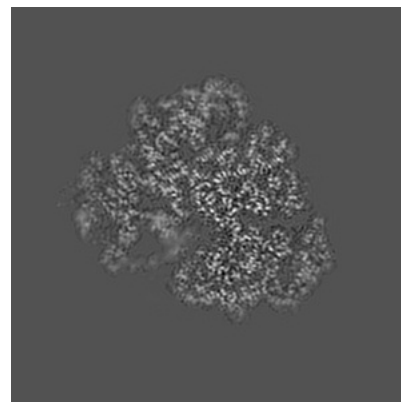
6.2.1 Primary map



X Index: 144

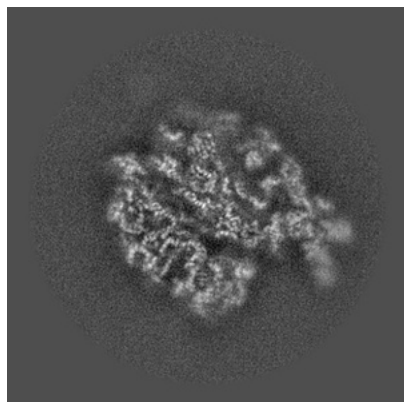


Y Index: 144

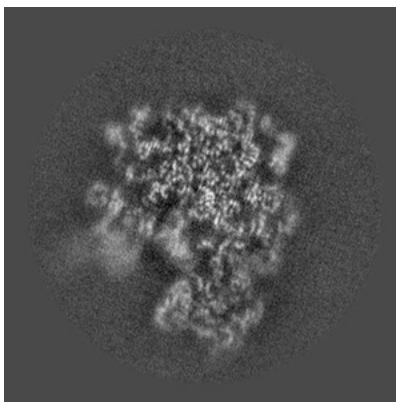


Z Index: 144

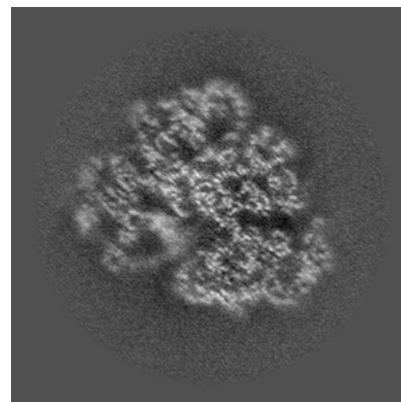
6.2.2 Raw map



X Index: 144



Y Index: 144

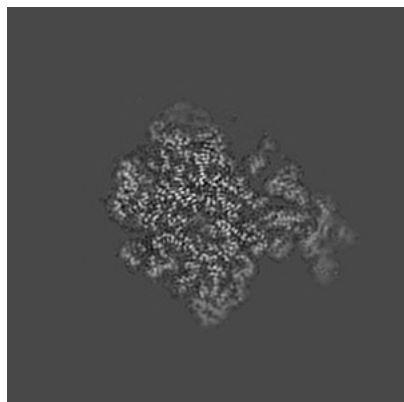


Z Index: 144

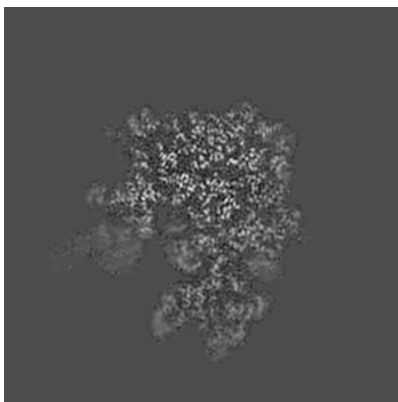
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

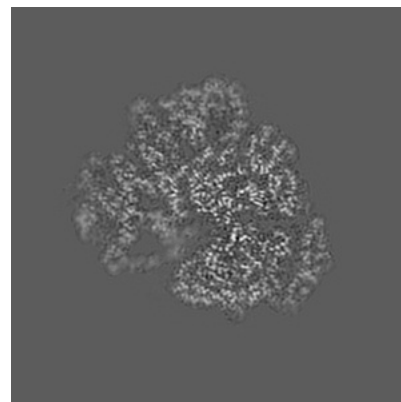
6.3.1 Primary map



X Index: 149

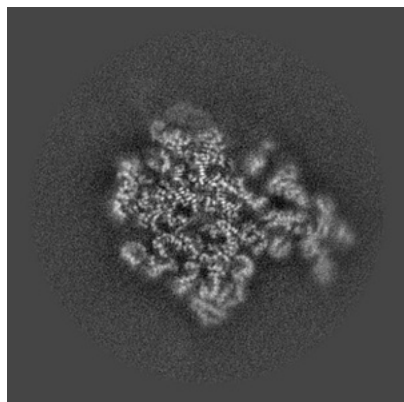


Y Index: 149

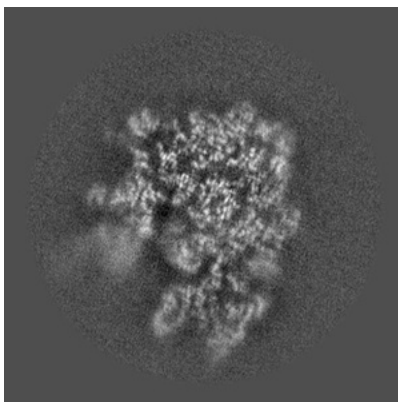


Z Index: 143

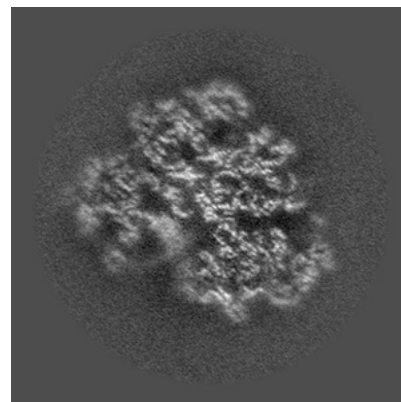
6.3.2 Raw map



X Index: 149



Y Index: 149

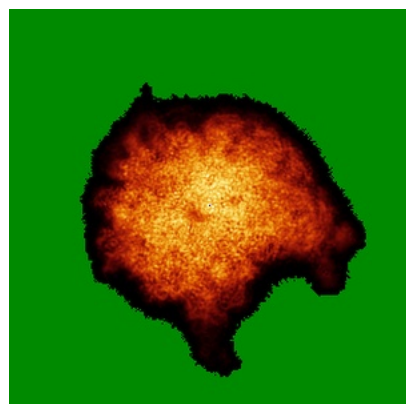


Z Index: 146

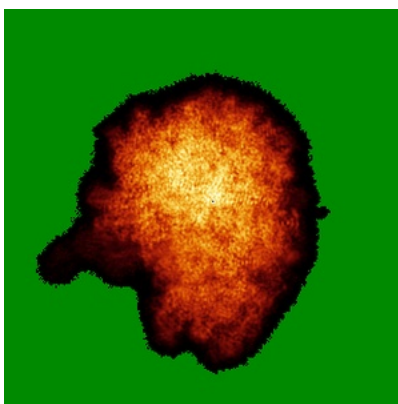
The images above show the largest variance slices of the map in three orthogonal directions.

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

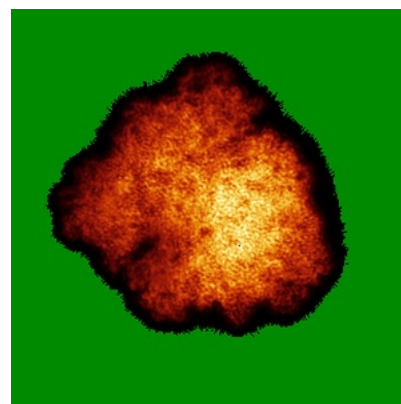
6.4.1 Primary map



X

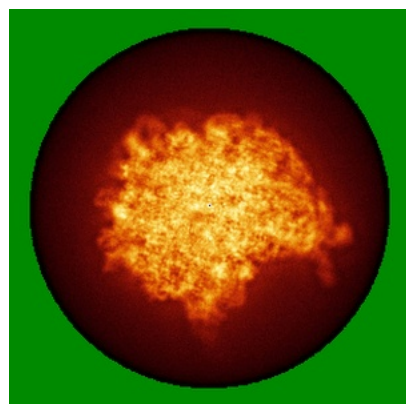


Y

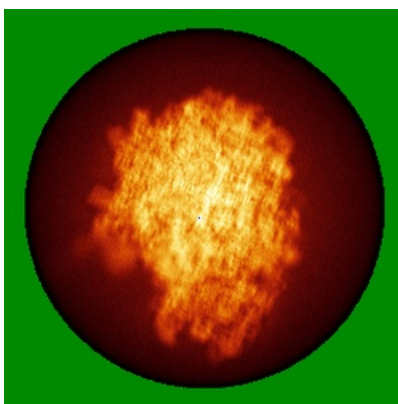


Z

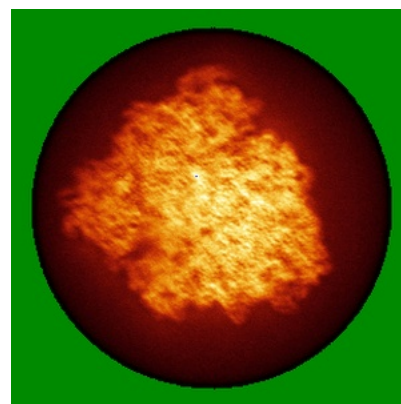
6.4.2 Raw map



X



Y

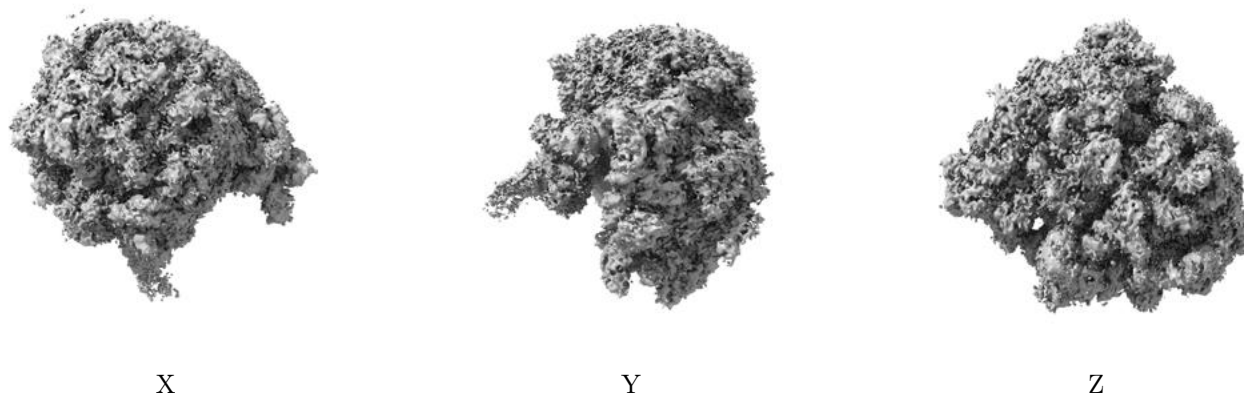


Z

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.

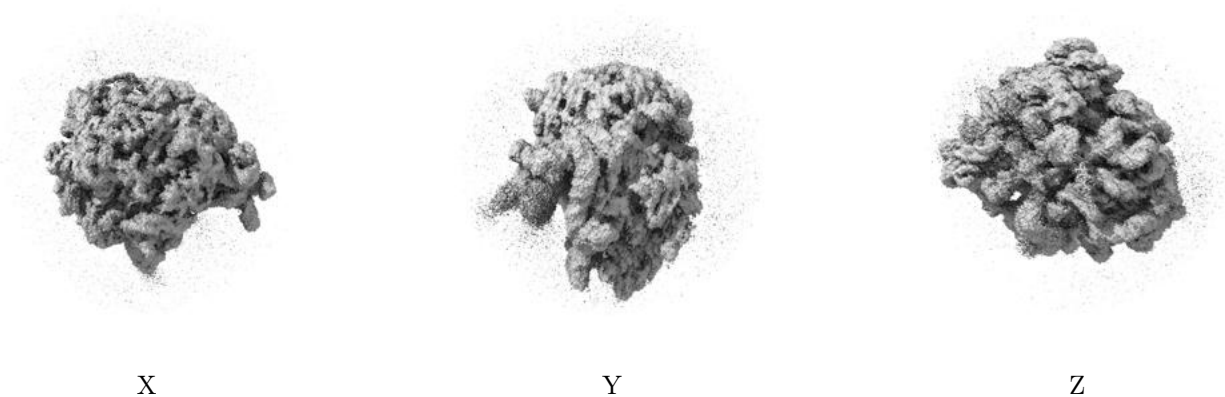
6.5 Orthogonal surface views [i](#)

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.

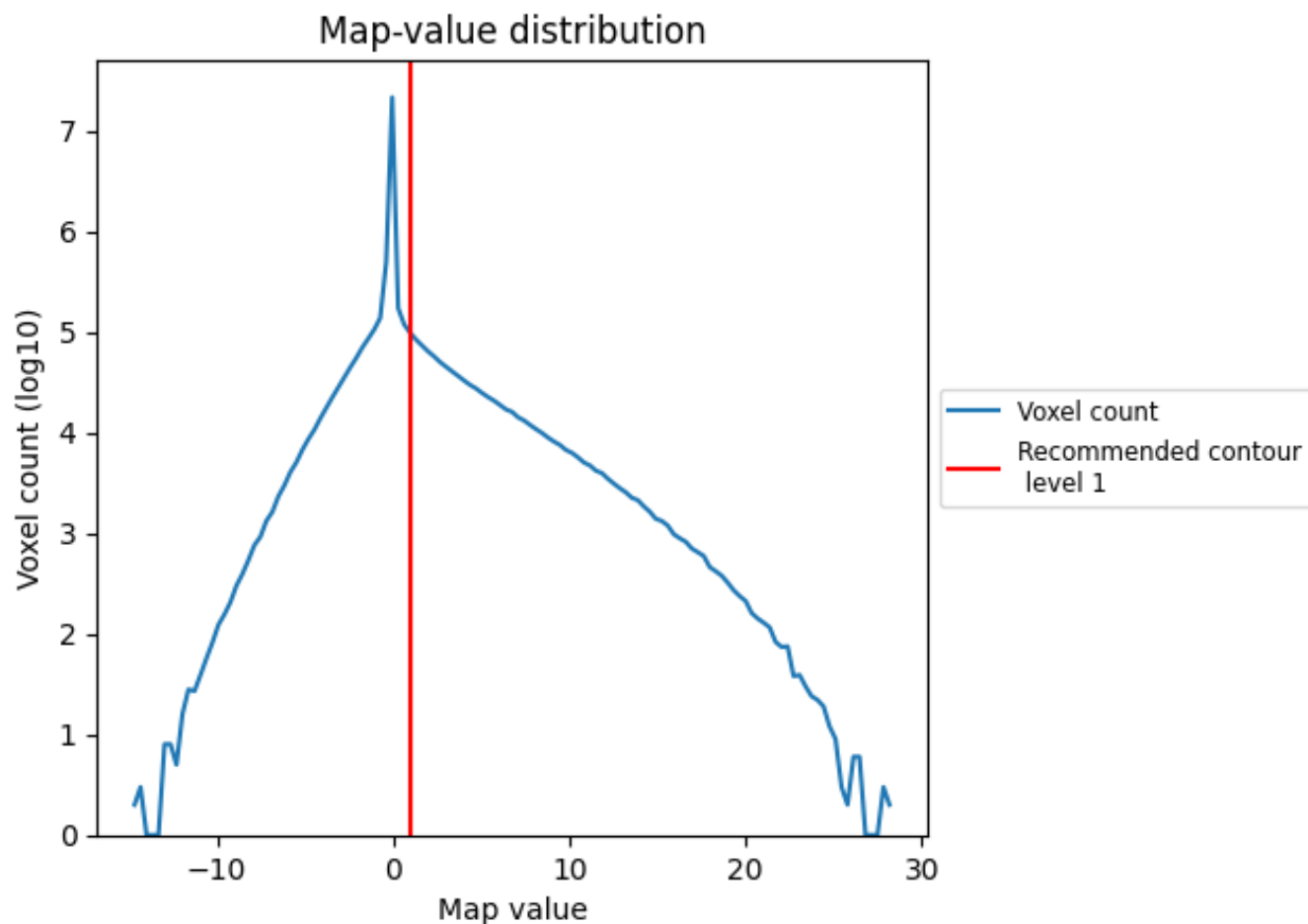
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

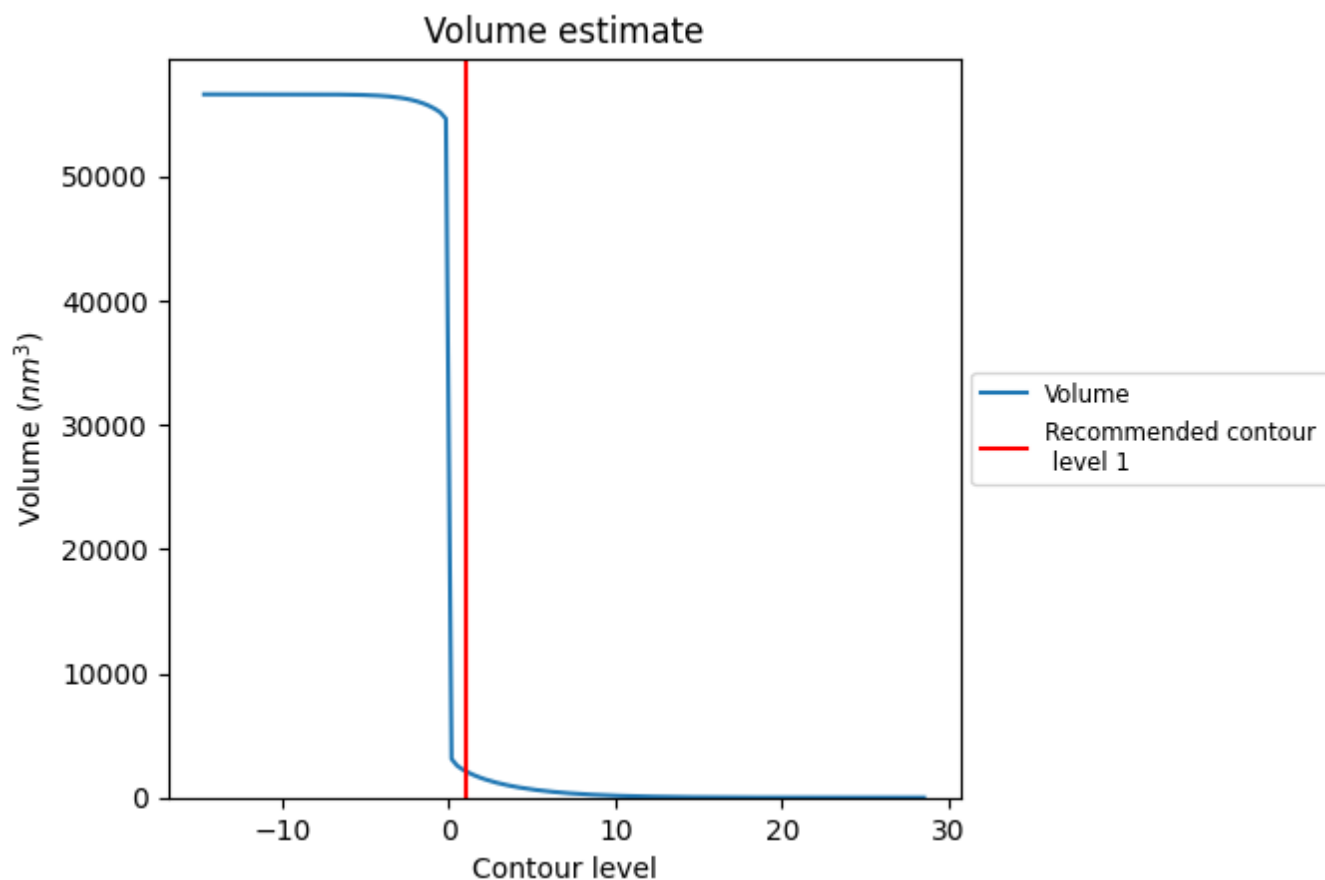
This section contains the results of statistical analysis of the map.

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.

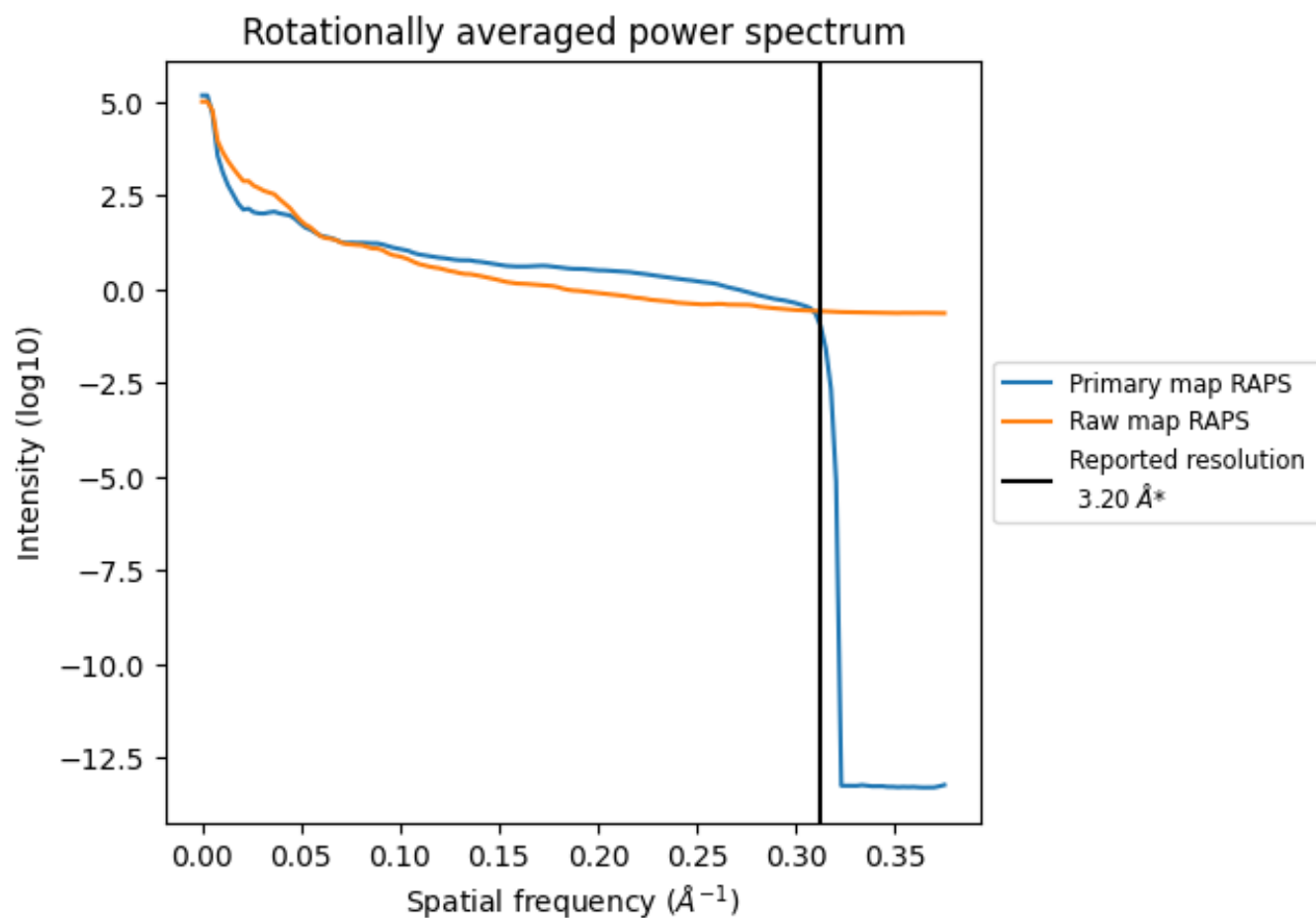
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2140 nm³; this corresponds to an approximate mass of 1933 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 ⓘ

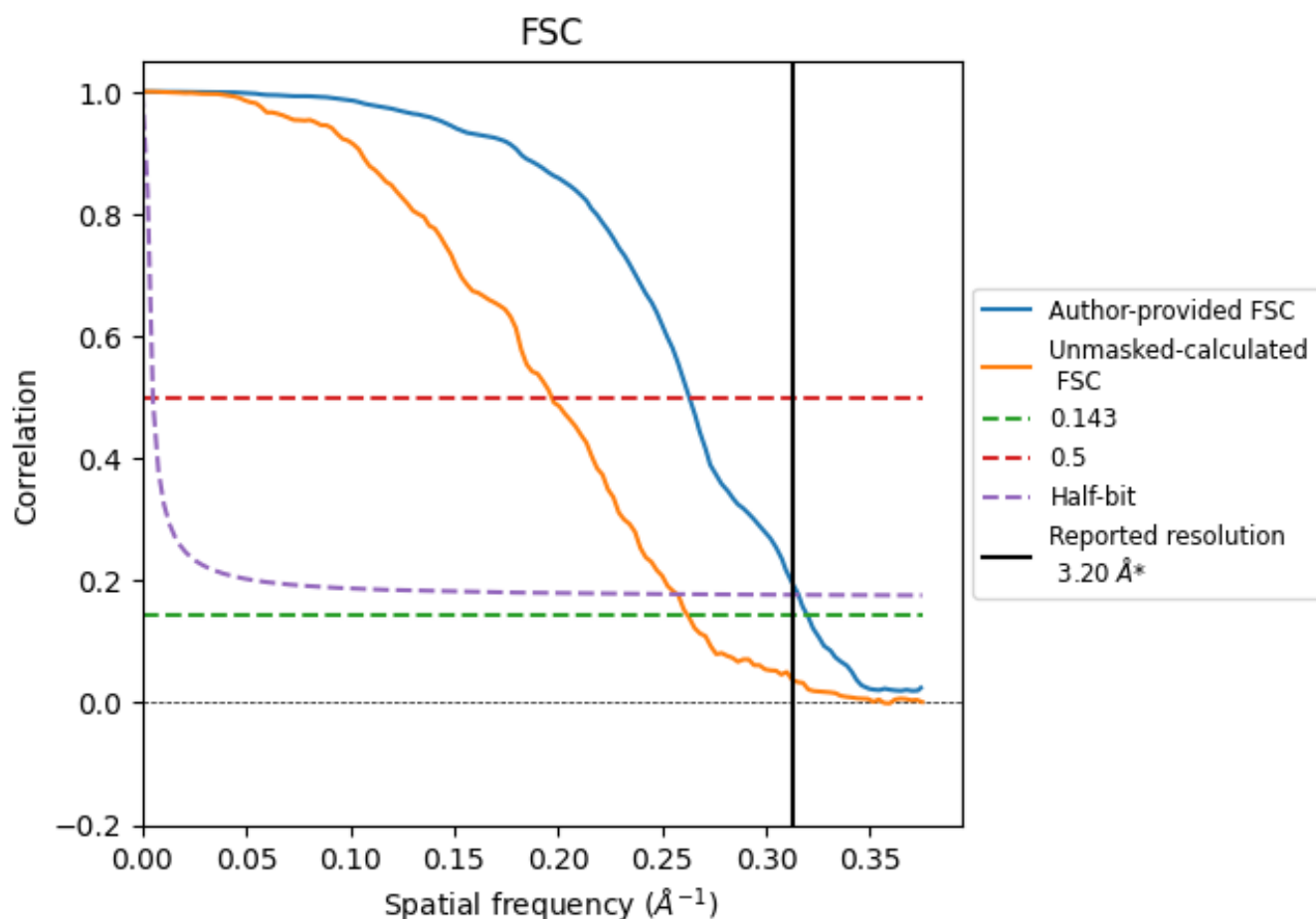


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

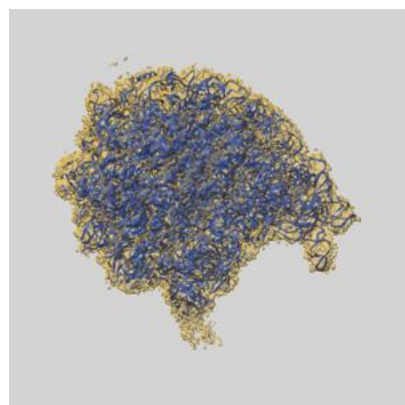
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.13	3.80	3.17
Unmasked-calculated*	3.81	5.08	3.89

*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 3.81 differs from the reported value 3.2 by more than 10 %

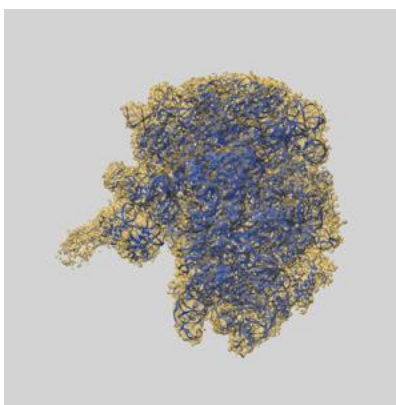
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21632 and PDB model 6WDD. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

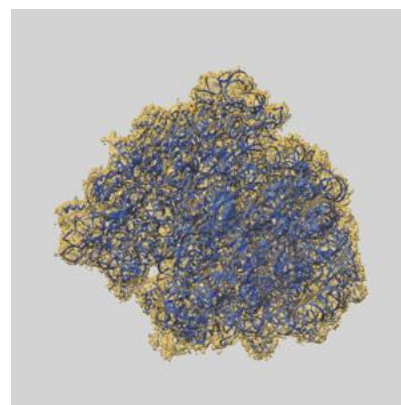
9.1 Map-model overlay [i](#)



X



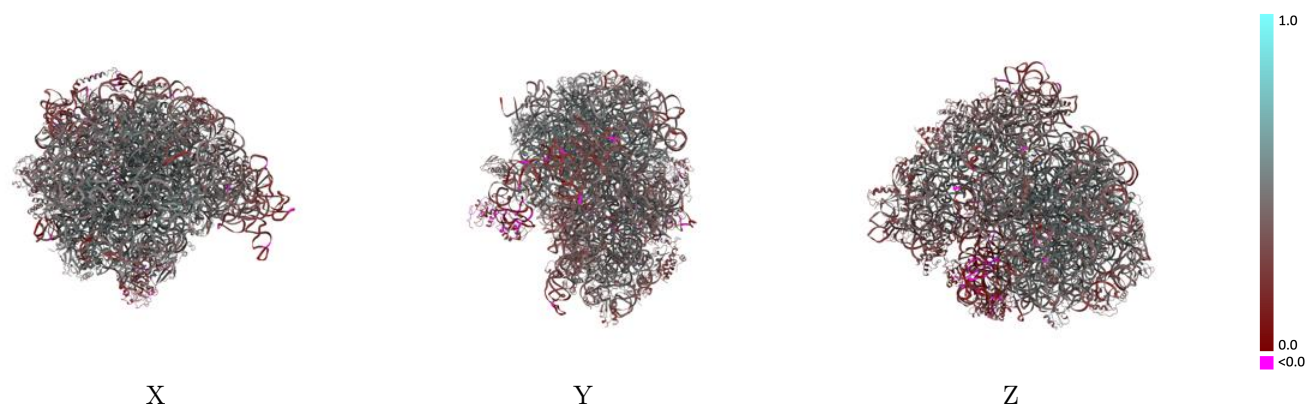
Y



Z

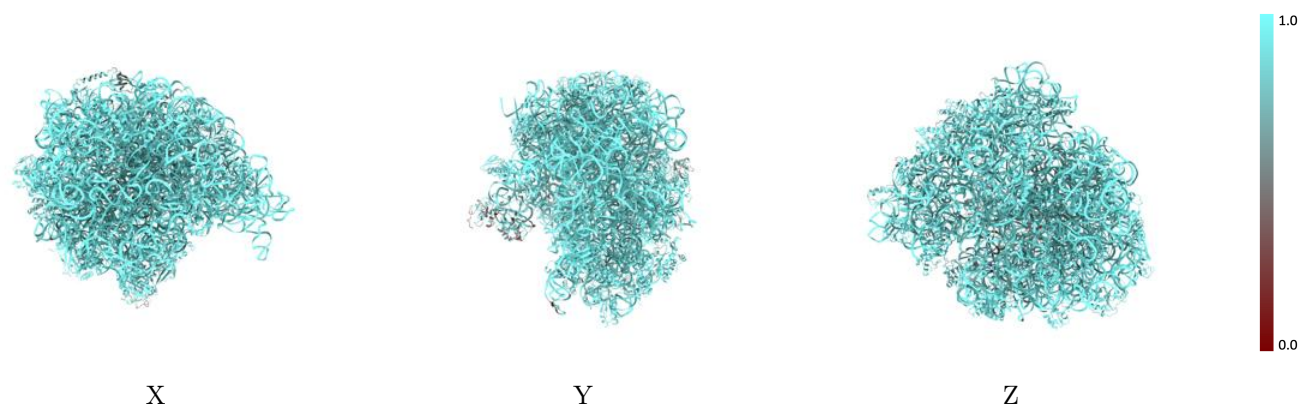
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



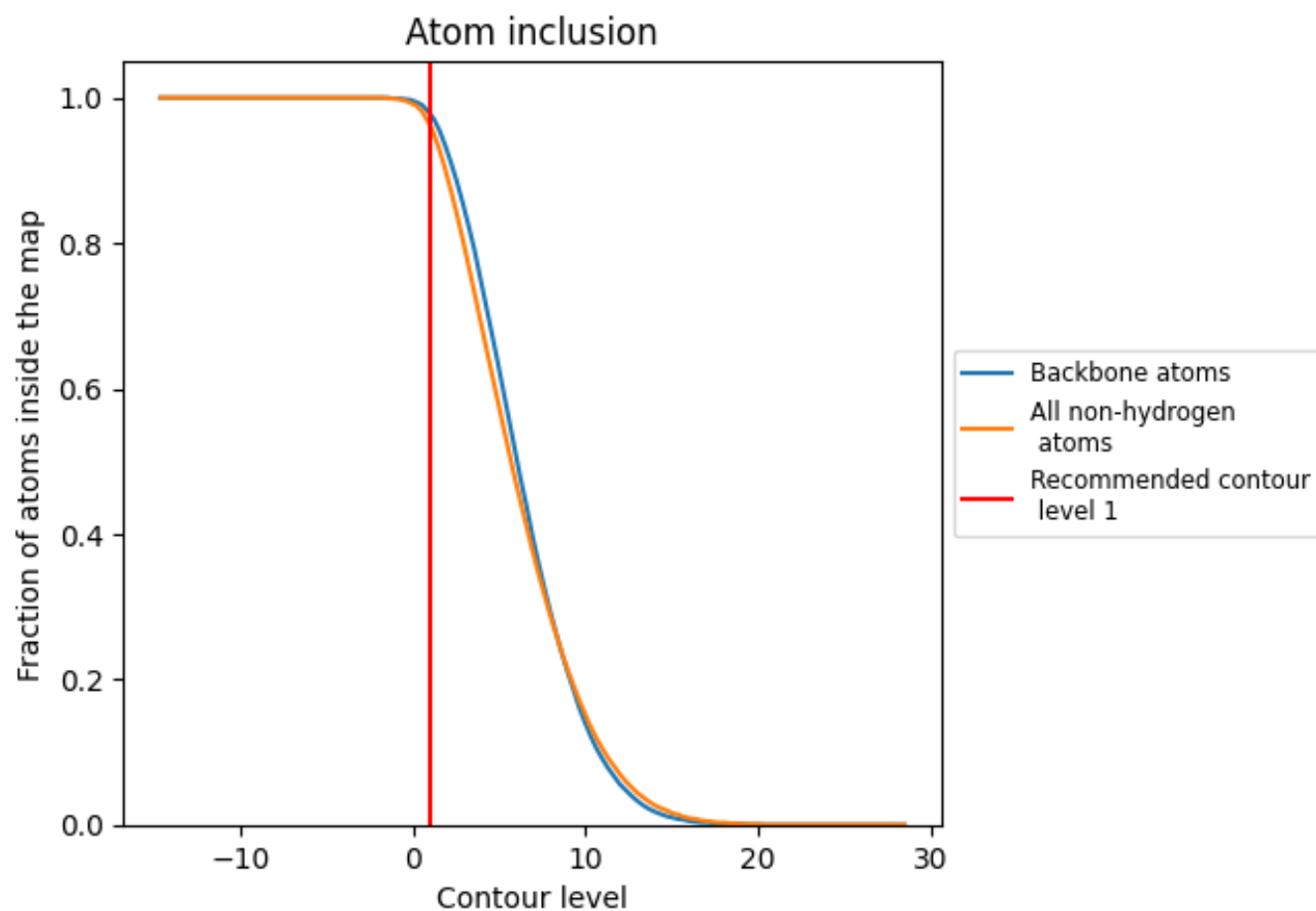
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9610	 0.4100
1	 0.9820	 0.4400
2	 0.9830	 0.3580
3	 0.9780	 0.3940
4	 0.9230	 0.3160
5	 0.8470	 0.2010
6	 0.8510	 0.1520
7	 0.9360	 0.2670
B	 0.9580	 0.4890
C	 0.8980	 0.4300
D	 0.9580	 0.5150
E	 0.9590	 0.5090
F	 0.9010	 0.4580
G	 0.9050	 0.3700
H	 0.9350	 0.4320
I	 0.9180	 0.3740
J	 0.9440	 0.4360
K	 0.9590	 0.4070
L	 0.9420	 0.3480
M	 0.9490	 0.4310
N	 0.9420	 0.3840
O	 0.8780	 0.3620
P	 0.9590	 0.4170
Q	 0.9520	 0.4730
R	 0.9460	 0.3280
S	 0.9170	 0.3920
T	 0.9680	 0.4170
U	 0.9030	 0.3780
V	 0.9590	 0.4190
W	 0.9280	 0.3950
X	 0.9570	 0.3460
Y	 0.9400	 0.3790
Z	 0.8650	 0.3220
a	 0.8970	 0.1760
b	 0.9700	 0.5070



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Chain	Atom inclusion	Q-score
c	 0.9630	 0.4940
d	 0.9500	 0.4390
e	 0.9210	 0.2490
f	 0.9650	 0.3780
g	 0.7640	 0.2830
h	 0.6460	 0.1480
i	 0.6350	 0.1380
j	 0.9630	 0.4930
k	 0.9650	 0.4840
l	 0.9510	 0.4650
m	 0.9440	 0.4790
n	 0.9660	 0.4960
o	 0.9570	 0.3980
p	 0.9580	 0.4730
q	 0.9640	 0.4970
r	 0.9640	 0.4650
s	 0.9460	 0.4920
t	 0.9470	 0.4630
u	 0.9440	 0.4160
v	 0.9620	 0.4420
w	 0.9640	 0.4880
x	 0.9800	 0.4940
y	 0.9400	 0.3980
z	 0.9680	 0.4740