



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 04:19 PM UTC

PDB ID : 5U9F / pdb_00005u9f
EMDB ID : EMD-8521
Title : 3.2 Å cryo-EM ArfA-RF2 ribosome rescue complex (Structure II)
Authors : Demo, G.; Svidritskiy, E.; Madireddy, R.; Diaz-Avalos, R.; Grant, T.; Grigorieff, N.; Sousa, D.; Korostelev, A.A.
Deposited on : 2016-12-16
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:

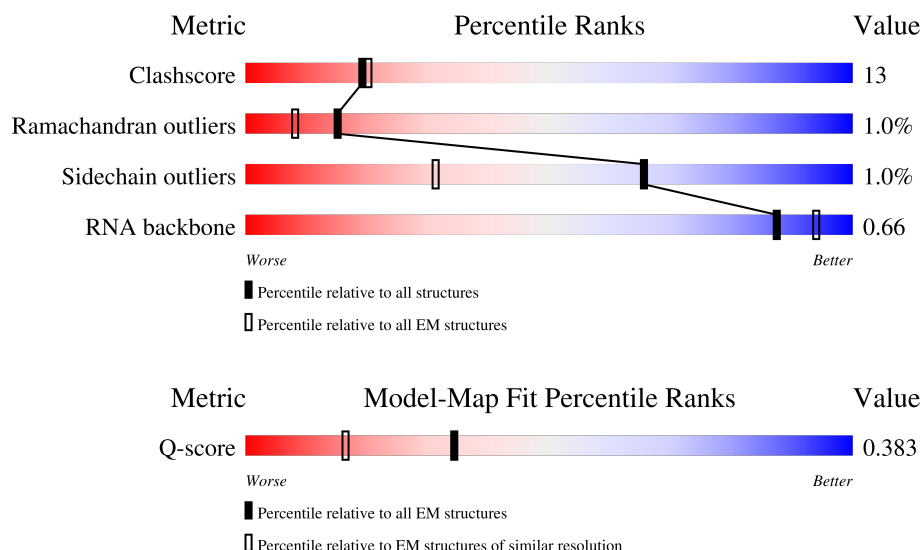
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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.



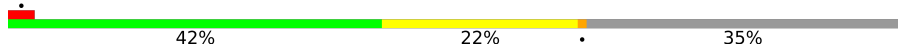
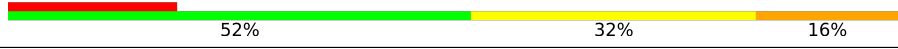
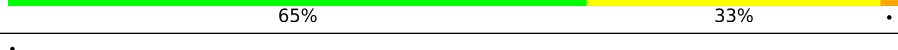
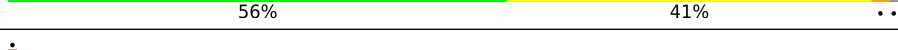
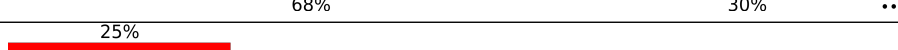
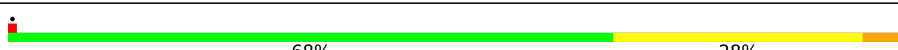
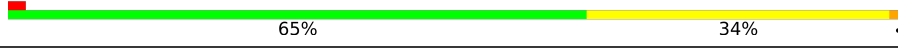
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	1539	
2	01	2903	
3	02	119	

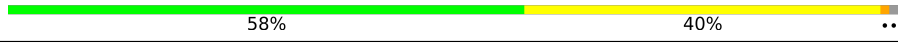
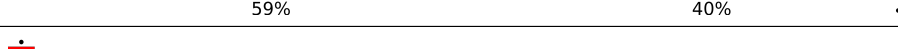
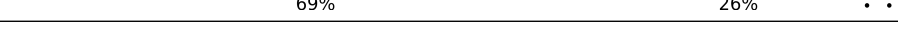
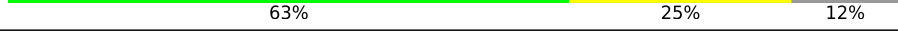
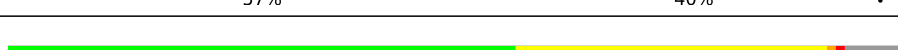
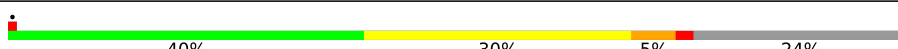
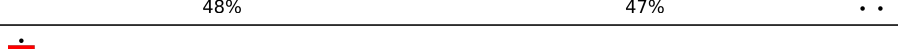
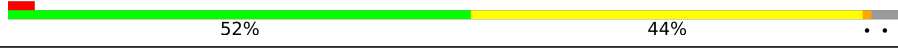
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Mol	Chain	Length	Quality of chain
4	Y	72	
5	W	77	
5	X	77	
6	03	234	
7	04	273	
8	05	209	
9	06	201	
10	07	179	
11	08	177	
12	09	149	
13	10	165	
14	11	142	
15	12	142	
16	13	123	
17	14	144	
18	15	136	
19	16	127	
20	17	117	
21	18	115	
22	19	118	
23	20	103	
24	21	110	
25	22	100	
26	23	104	
27	24	94	

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Mol	Chain	Length	Quality of chain
28	25	85	
29	26	78	
30	27	63	
31	28	59	
32	29	70	
33	30	57	
34	31	55	
35	32	46	
36	33	65	
37	34	38	
38	V	14	
39	Z	365	
40	B	241	
41	C	233	
42	D	206	
43	E	167	
44	F	131	
45	G	156	
46	H	130	
47	I	130	
48	J	103	
49	K	129	
50	L	124	
51	M	118	
52	N	101	

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Mol	Chain	Length	Quality of chain
53	O	89	
54	P	82	
55	Q	84	
56	R	75	
57	S	92	
58	T	87	
59	U	71	

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 152819 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 RNA chain called 16S ribosomal RNA.

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

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	01	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	1847	G	A	conflict	GB 2073407

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	02	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 4 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	47	Total	C	N	O	S	0	0
			377	233	78	65	1		

- Molecule 5 is a RNA chain called fMet-tRNA (P- and E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	77	Total	C	N	O	P	0	0
			1622	723	289	534	76		
5	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	03	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	04	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	07	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	16	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	22	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	23	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	29	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	31	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a RNA chain called truncated mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	14	Total	C	N	O	P	0	0
			306	138	64	91	13		

- Molecule 39 is a protein called Peptide chain release factor RF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	361	Total	C	N	O	S	0	0
			2844	1748	503	583	10		

- Molecule 40 is a protein called 30S ribosomal protein S2.

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

- Molecule 41 is a protein called 30S ribosomal protein S3.

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

- Molecule 42 is a protein called 30S ribosomal protein S4.

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

- Molecule 43 is a protein called 30S ribosomal protein S5.

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

- Molecule 44 is a protein called 30S ribosomal protein S6.

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

- Molecule 45 is a protein called 30S ribosomal protein S7.

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

- Molecule 46 is a protein called 30S ribosomal protein S8.

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

- Molecule 47 is a protein called 30S ribosomal protein S9.

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

- Molecule 48 is a protein called 30S ribosomal protein S10.

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

- Molecule 49 is a protein called 30S ribosomal protein S11.

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

- Molecule 50 is a protein called 30S ribosomal protein S12.

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

- Molecule 51 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	M	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 52 is a protein called 30S ribosomal protein S14.

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

- Molecule 53 is a protein called 30S ribosomal protein S15.

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

- Molecule 54 is a protein called 30S ribosomal protein S16.

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

- Molecule 55 is a protein called 30S ribosomal protein S17.

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

- Molecule 56 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	R	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 57 is a protein called 30S ribosomal protein S19.

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

- Molecule 58 is a protein called 30S ribosomal protein S20.

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

- Molecule 59 is a protein called 30S ribosomal protein S21.

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

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	A	118	Total	Mg	0
			118	118	
60	01	221	Total	Mg	0
			221	221	
60	02	6	Total	Mg	0
			6	6	
60	X	5	Total	Mg	0
			5	5	
60	17	1	Total	Mg	0
			1	1	
60	19	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
60	30	1	Total 1	Mg 1	0
60	31	1	Total 1	Mg 1	0
60	34	1	Total 1	Mg 1	0
60	V	1	Total 1	Mg 1	0
60	W	3	Total 3	Mg 3	0
60	I	1	Total 1	Mg 1	0

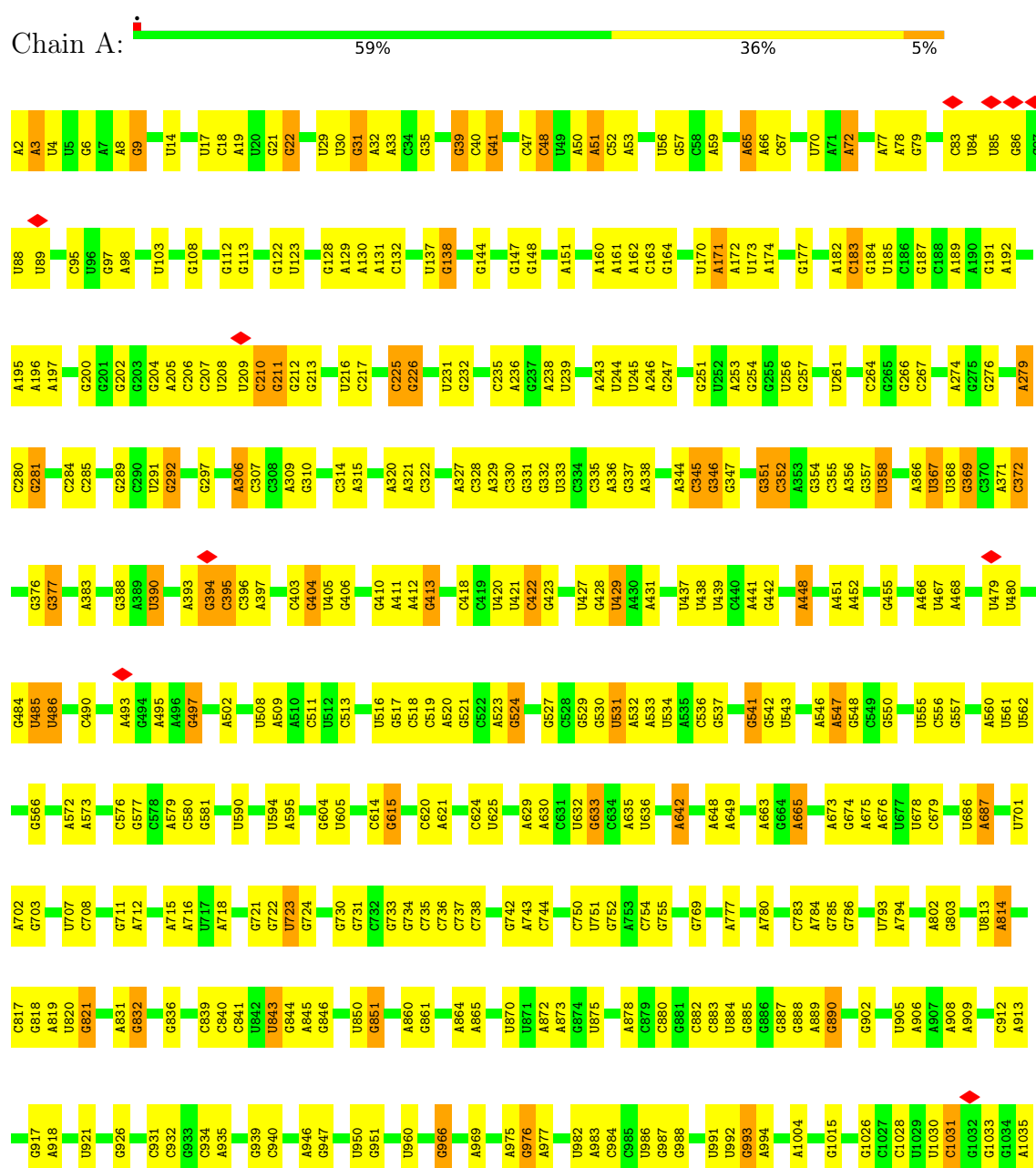
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

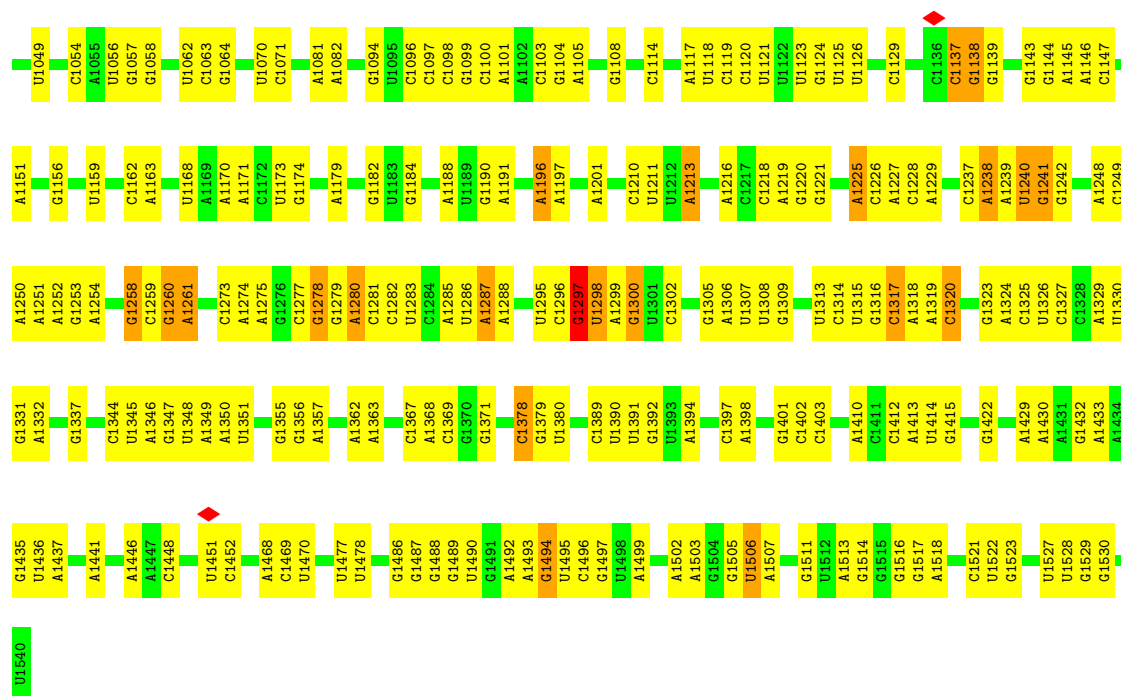
Mol	Chain	Residues	Atoms		AltConf
61	34	1	Total 1	Zn 1	0

3 Residue-property plots

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

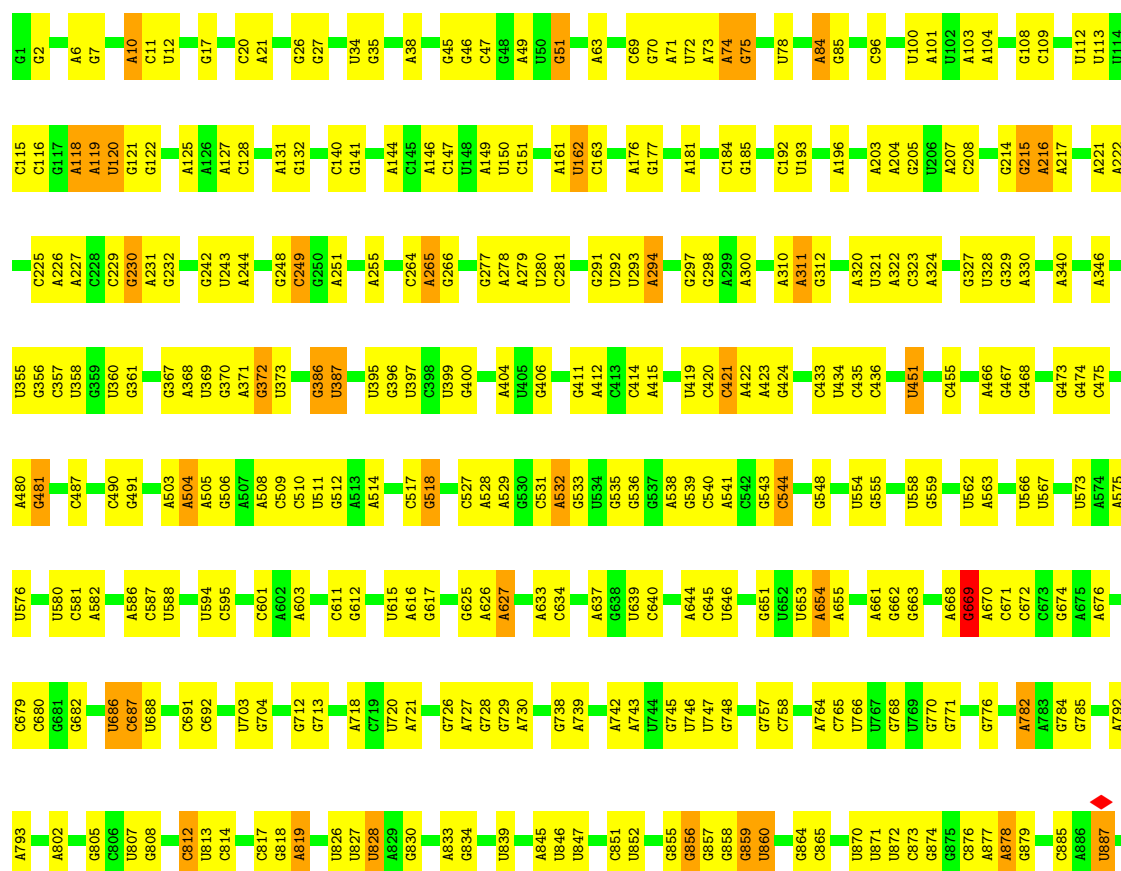
• Molecule 1: 16S ribosomal RNA



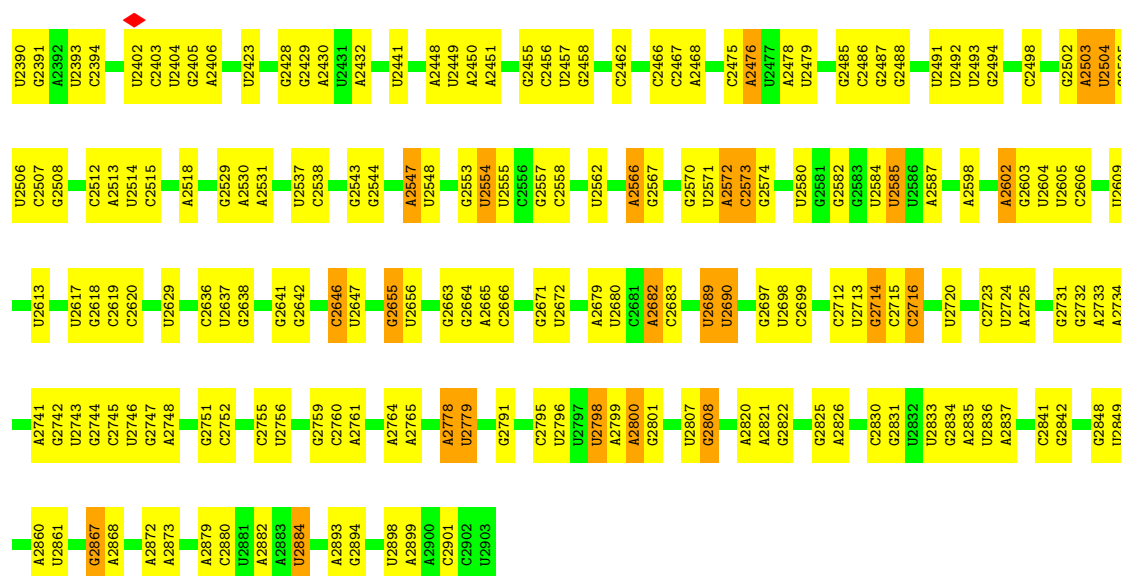


• Molecule 2: 23S ribosomal RNA

Chain 01: 62% 33% 5%

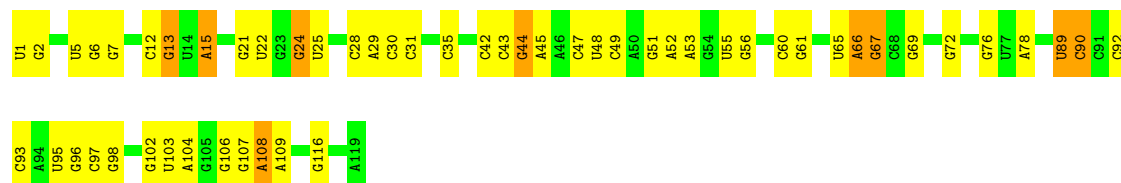


U2312	G2221	U2118	A2031	G1929	G1807	C1564	G1444	U1352	U1203	A1086	U1012	C890
C2313	C2222	A2119	G2032	G1930	A1808	C1565	C1447	A1353	A1204	G1087	C1013	C891
A2314	A2225	G2120	A2033	U1931	A1698	A1566	G1448	U1357	G1210	A1088	U1019	U894
G2315		G2121	U2034	A1932	G1699		G1449	C1357	C1212	C1092	A1020	U895
A2316		U2122	G2035	G1934	A1700	A1569	G1450	G1358	A1213	G1093	A1021	A896
G2317		G2123	C2036	G1935	A1701	A1571	C1451	A1359	U1295	U1094	G1022	C897
C2318		G2124		G1936	U1709	A1572	G1452	G1360		A1095		C898
G2319			U2039	A1937	G1710			G1361		A1096		A899
U2320		G2128	G2040	A1938		U1575	U1458					
U2321		U2131	C2043		G1715	U1576	G1459	A1365	A1230	U1027		U906
G2323		U2132		U1943	U1716		U1460	A1366	U1231	A1103		U907
U2324		G2133	G2048	U1944	G1826	G1592	A1461	A1367		C1104		
C2325		A2134	G2049		U1827	A1593	C1461	G1368		U1105		
G2326		A2135	C2050	U1955	G1728	U1594						
A2327		G2136	A2051		C1726		U1468					
C2328		U2137	G2052	U1963	C1728	G1601	U1475	A1373		G1106		
G2329		U2137	G2053	G1964	G1729	U1602	U1476	A1378		U1108		
C2330		G2140	A2054	C1965	C1730	G1730	U1476	U1379		A1111		
G2331		G2141	G2055	A1966	G1731	A1603				G1112		
C2332			G2056	G1967	U1736	C1606	C1480	A1383		U1113		
U2333		C2145	A2059	G1968	G1737	C1607	U1481	C1386		U1130		
G2334		A2146	G2060	A1969	G1738	A1808	G1482	A1387		G1131		
C2335		G2147	A2061	U1970	A1739		A1490			U1132		
A2336		G2148	A2062	G1971	G1740	C1611		U1394		A1133		
G2337				G1972						A1134		
C2338		G2156	C2065	G1973	A1744	A1616	U1497	C1398		A1046		
A2339		U2257	G2066	A1958	A1745		C1507			G1047		
G2340		C2258	C2067	G1869		C1637	A1508	C1288		G1055		
C2341		U2261	G2068	C1870	G1753	C1638	A1509	C1404		G1056		
A2342		U2166	U2069	A1754	A1754	C1639	G1510	U1405		G1057		
C2343			G2070	G1874	G1756	A1640	A1515	U1406		C1140		
G2344		A2170	A2071	C1875	A1757	A1641	G1516	U1409		U1141		
U2345		A2171	C2072	A1885	U1758	G1642				A1142		
C2346		U2172	A2073	G1890	U1759	G1645	G1521	U1415		G1149		
A2347		A2173	U2075	G1891	C1760	C1646	A1522	G1416		C1150		
G2348						U1647	U1523	C1417		G1062		
C2349		C2177	U2086	A1900	G1764	U1648	G1524	G1418		G1063		
U2350		A2183	G2087	A1901	A1773	G1649	A1528	A1419		U1151		
G2351		A2184	A2088	G1906	U1775	G1651	G1529	A1420		G1157		
C2352			C2089		G1776	A1652	G1530	G1421				
A2353		U2189	A2090	C1909	A1783	G1653	A1536	G1424		C1170		
G2354		G2190	C2091	G1910		U1657	G1537	G1425		G1171		
C2355		U2191		U1911	C1790	C1658	A1545	G1426		G1172		
U2356		G2192	A2094	A1912	A1791		G1546	A1427		U1173		
G2357		U2193	A2095	A1913	C1794	A1664	C1547	G1429		U1175		
A2358		U2195	U2104	C1914	A1794	A1665	G1548	G1432		U1176		
C2359		C2196	U2105	U1917	C1795	G1666	A1549	A1433		G1179		
G2360		U2197	U2106	A1918	U1796	G1667	C1550	A1434		U1180		
C2361		A2198	U2111	C1919	G1797	A1669	A1551	G1435		U1181		
U2362			U2112	C1920				G1436		U1182		
G2363		G2203	G2113	C1923	C1800	G1674		C1437		U1183		
A2364		U2204	U2114	A1801	A1801			U1438		G1186		
C2365		A2205	G2115	C1924	A1802	C1685		A1439		G1187		
G2366		A2212	G2116	A1928	A1803	G1687				G1190		
C2367		U2213	A2117									
U2368												
G2369												
A2370												
C2371												
U2372												
G2373												
A2374												
C2375												
U2376												
G2377												
A2378												
C2379												
U2380												
G2381												
A2382												
C2383												
U2384												
G2385												
A2386												
C2387												
U2388												
G2389												



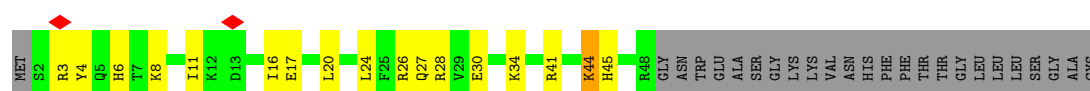
- Molecule 3: 5S ribosomal RNA

Chain 02: 55% 38% 8%



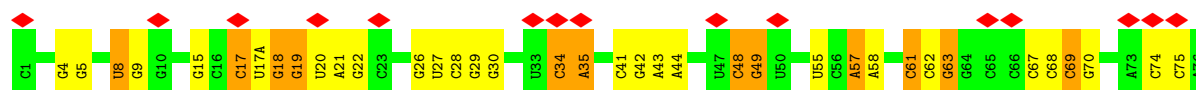
- Molecule 4: Alternative ribosome-rescue factor A

Chain Y: 42% 22% 35%



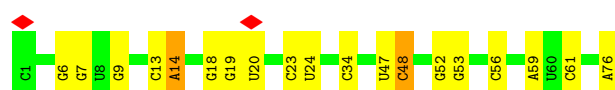
- Molecule 5: fMet-tRNA (P- and E-site)

Chain X: 19% 52% 32% 16%



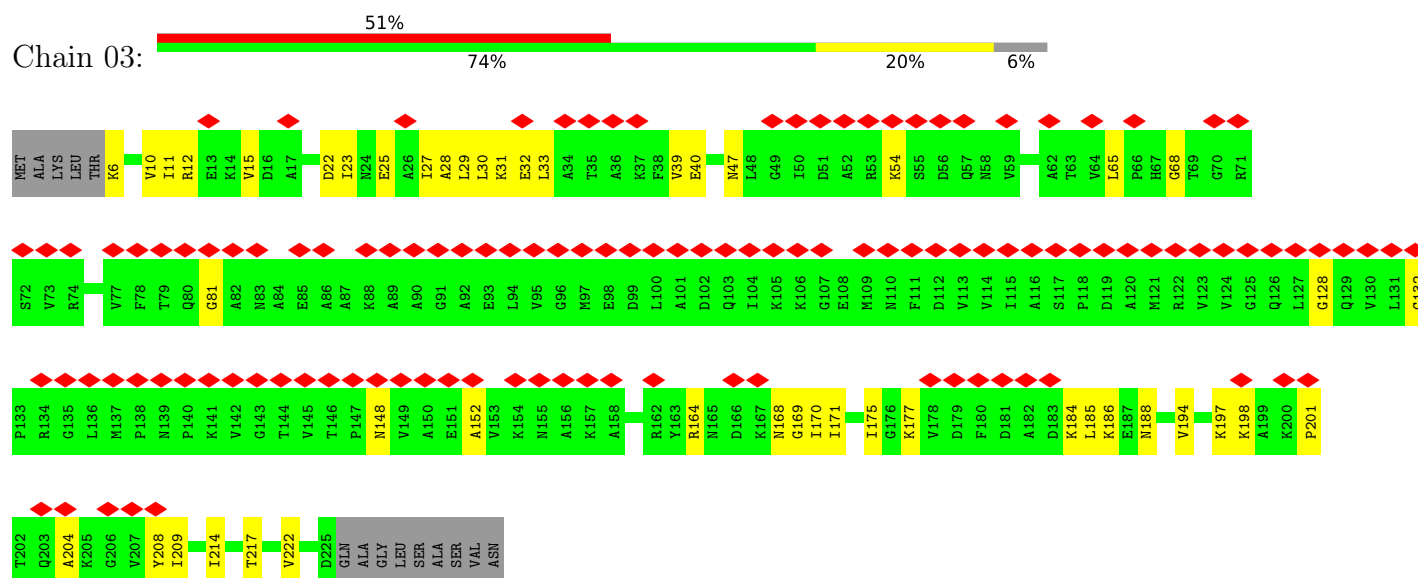
- Molecule 5: fMet-tRNA (P- and E-site)

Chain W: 75% 22%



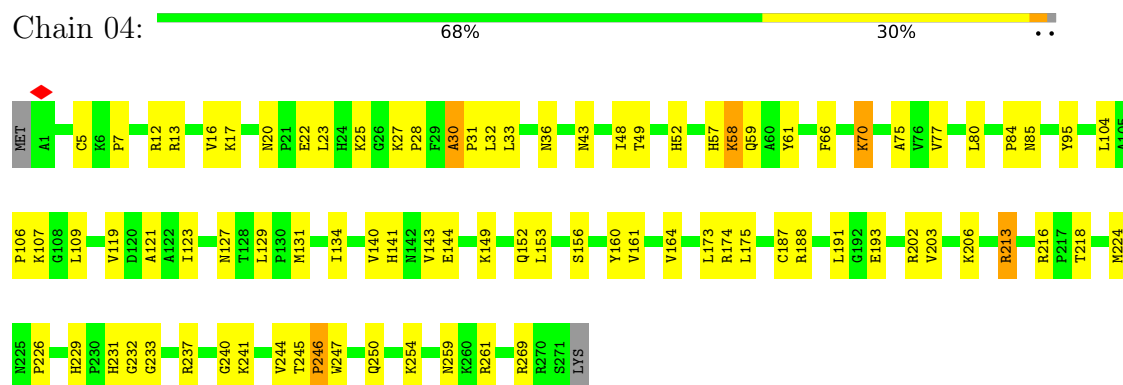
- Molecule 6: 50S ribosomal protein L1

Chain 03:



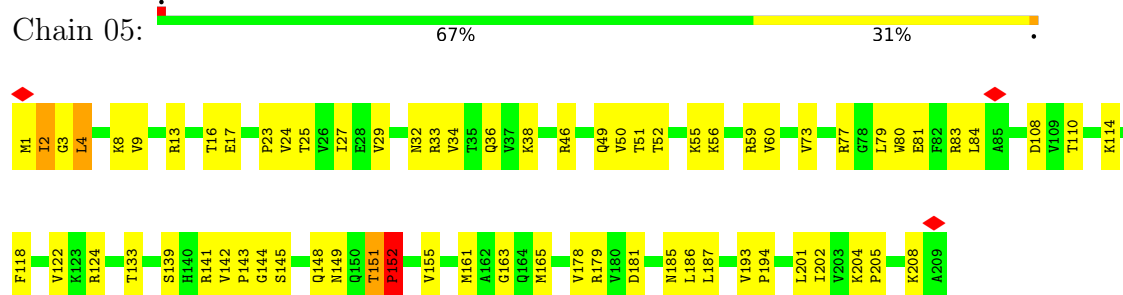
- Molecule 7: 50S ribosomal protein L2

Chain 04:



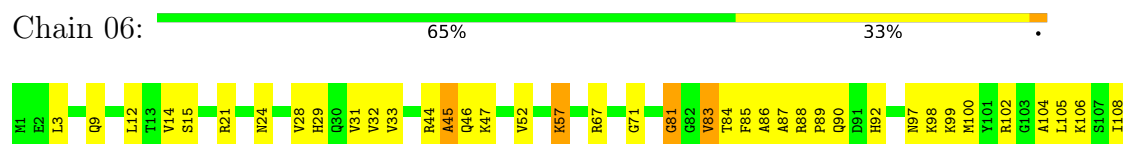
- Molecule 8: 50S ribosomal protein L3

Chain 05:



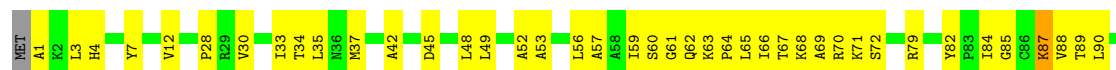
- Molecule 9: 50S ribosomal protein L4

Chain 06:





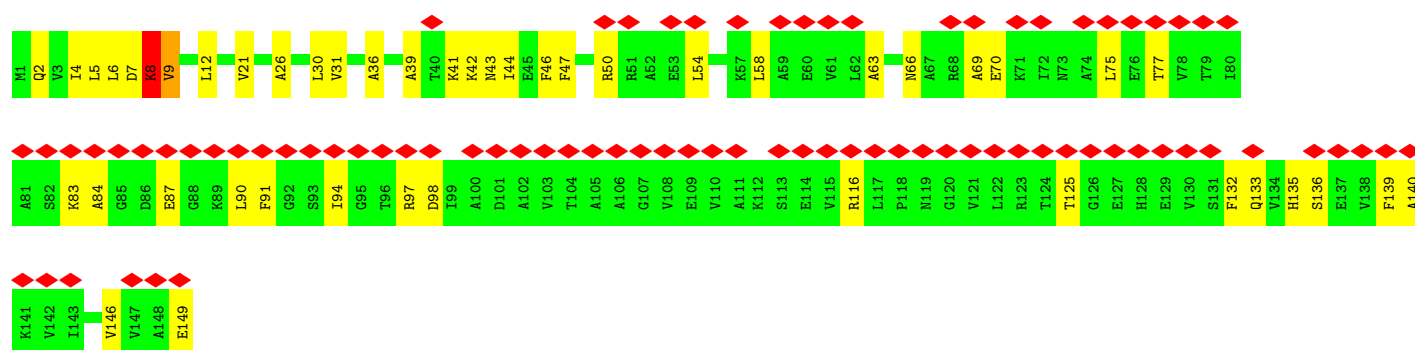
• Molecule 10: 50S ribosomal protein L5



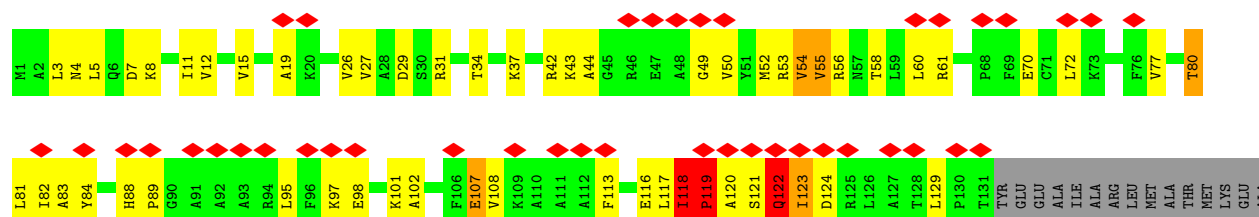
• Molecule 11: 50S ribosomal protein L6



• Molecule 12: 50S ribosomal protein L9

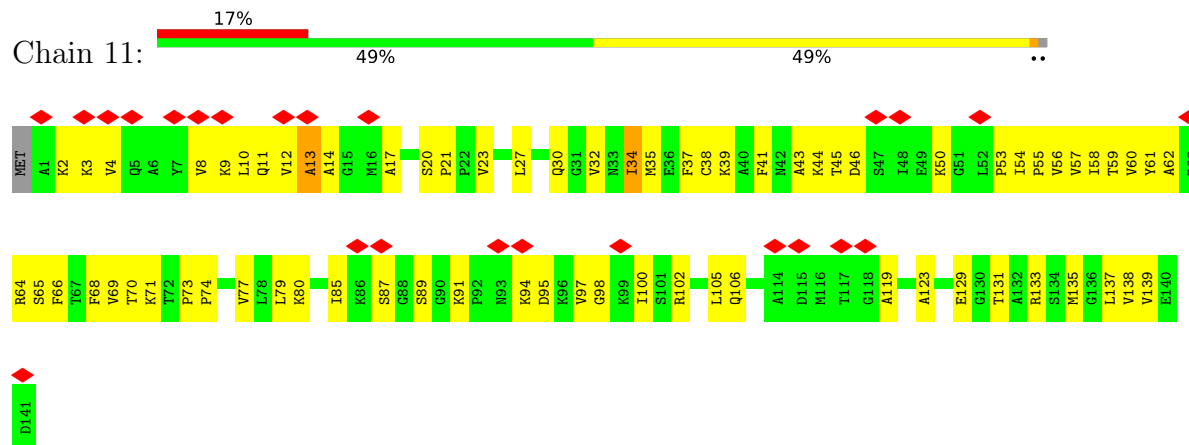


• Molecule 13: 50S ribosomal protein L10

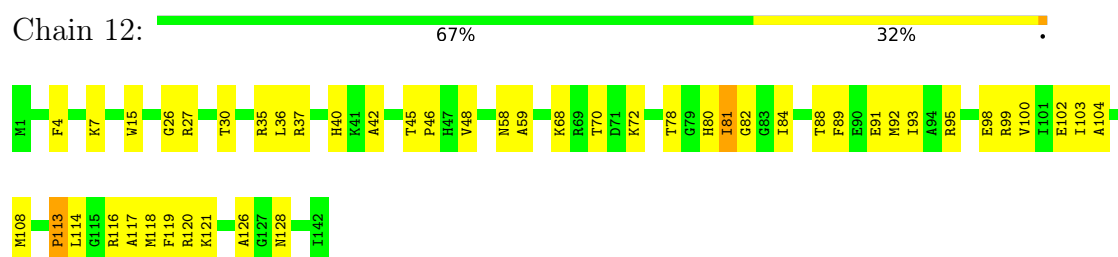


SER
ALA
GLY
LYS
LEU
VAL
ARG
THR
LEU
ALA
ALA
VAL
ARG
ASP
ALA
LYS
GLU
ALA
ALA

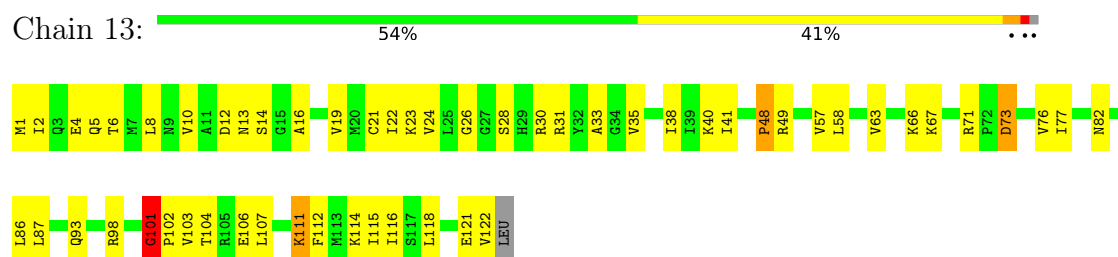
• Molecule 14: 50S ribosomal protein L11



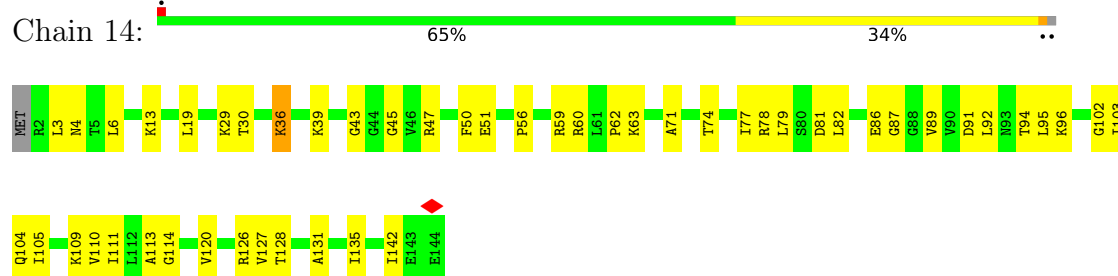
• Molecule 15: 50S ribosomal protein L13



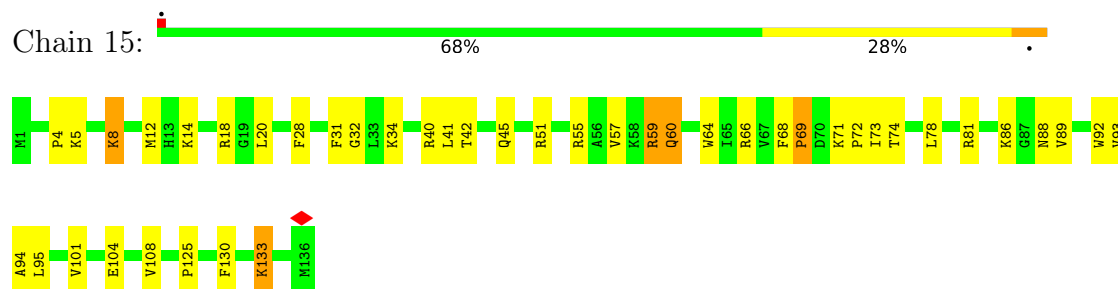
• Molecule 16: 50S ribosomal protein L14



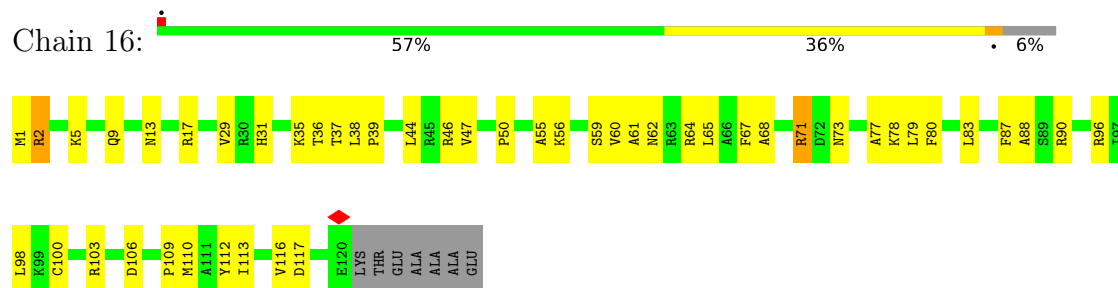
• Molecule 17: 50S ribosomal protein L15



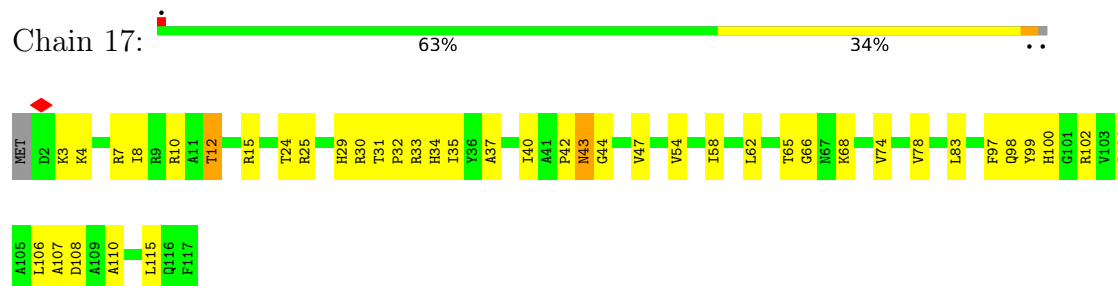
• Molecule 18: 50S ribosomal protein L16



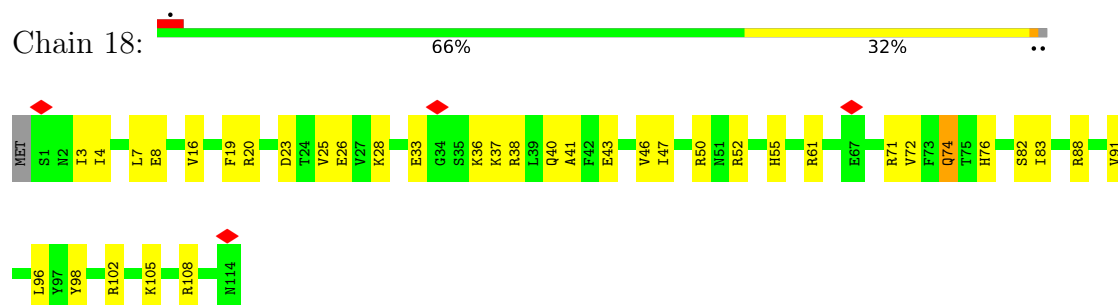
- Molecule 19: 50S ribosomal protein L17



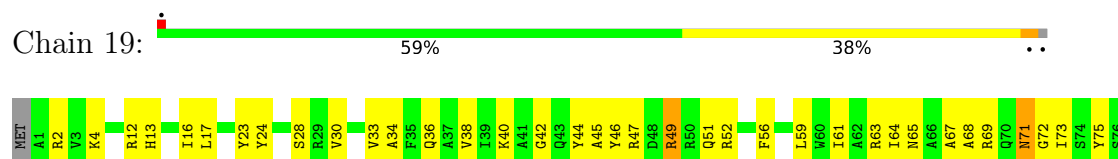
- Molecule 20: 50S ribosomal protein L18



- Molecule 21: 50S ribosomal protein L19

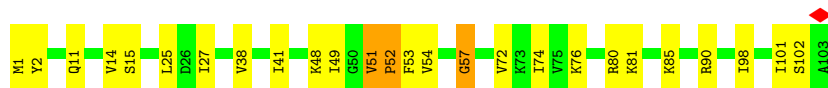
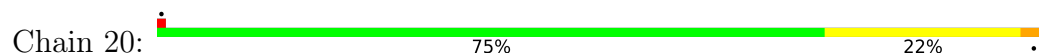


- Molecule 22: 50S ribosomal protein L20

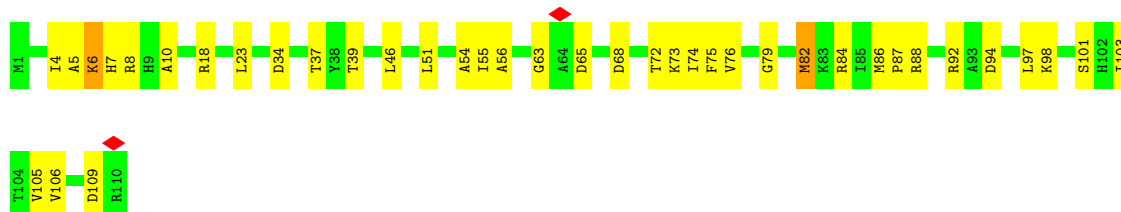




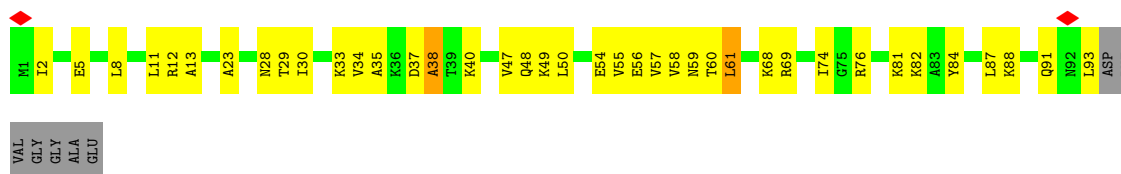
- Molecule 23: 50S ribosomal protein L21



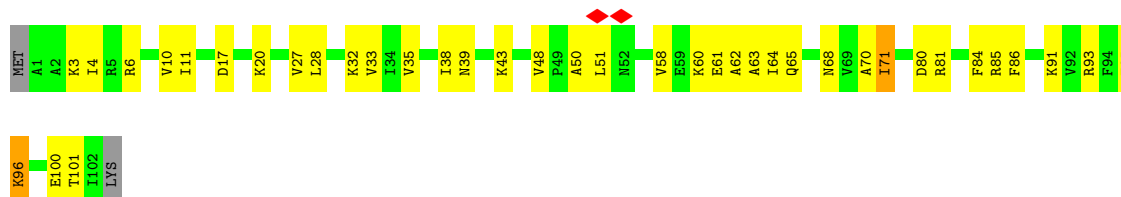
- Molecule 24: 50S ribosomal protein L22



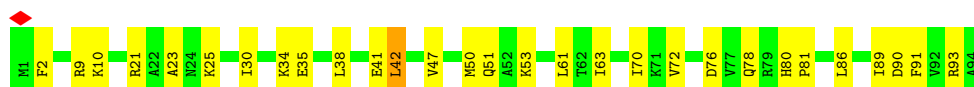
- Molecule 25: 50S ribosomal protein L23



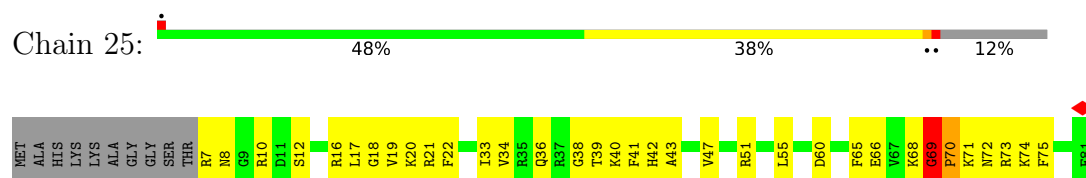
- Molecule 26: 50S ribosomal protein L24



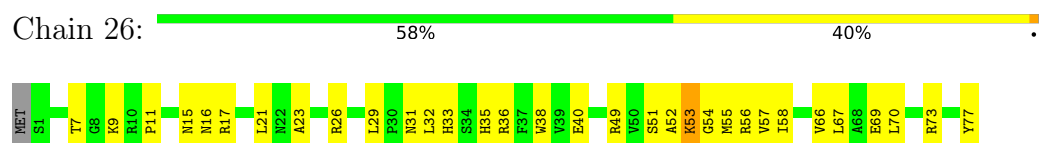
- Molecule 27: 50S ribosomal protein L25



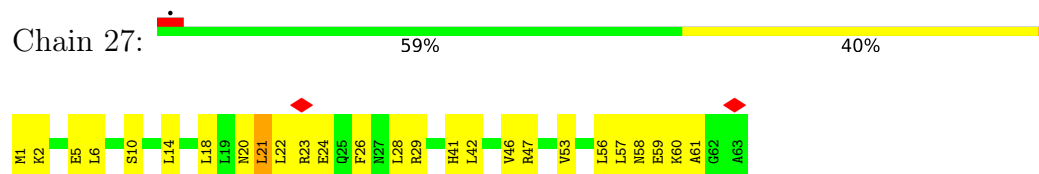
• Molecule 28: 50S ribosomal protein L27



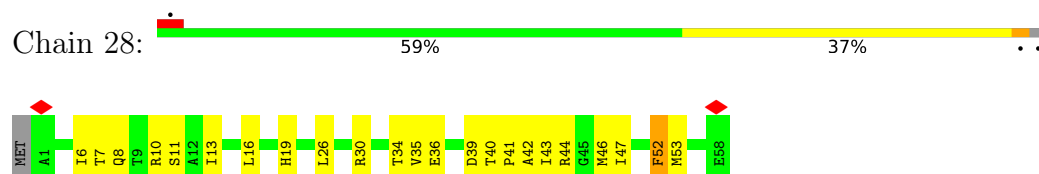
• Molecule 29: 50S ribosomal protein L28



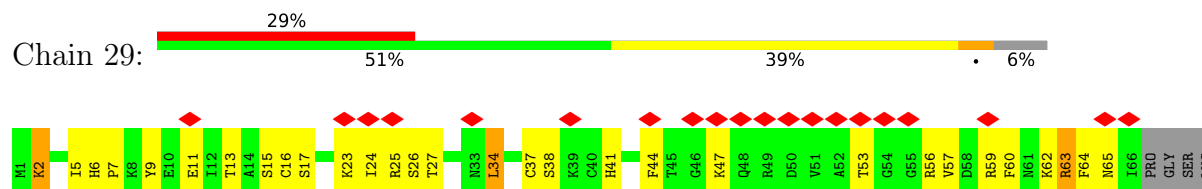
• Molecule 30: 50S ribosomal protein L29



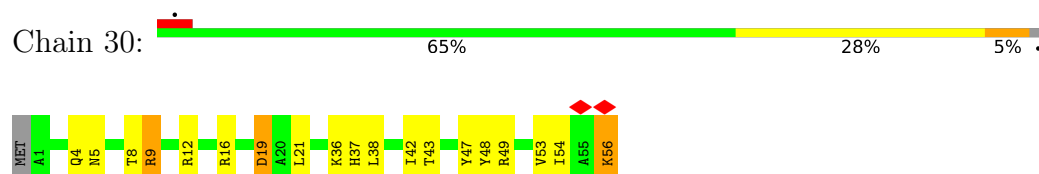
• Molecule 31: 50S ribosomal protein L30



• Molecule 32: 50S ribosomal protein L31



• Molecule 33: 50S ribosomal protein L32

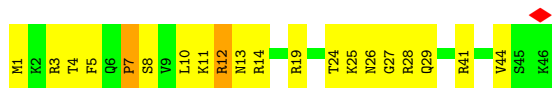


• Molecule 34: 50S ribosomal protein L33

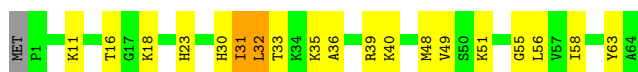




- Molecule 35: 50S ribosomal protein L34



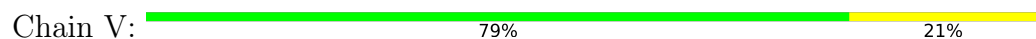
- Molecule 36: 50S ribosomal protein L35



- Molecule 37: 50S ribosomal protein L36



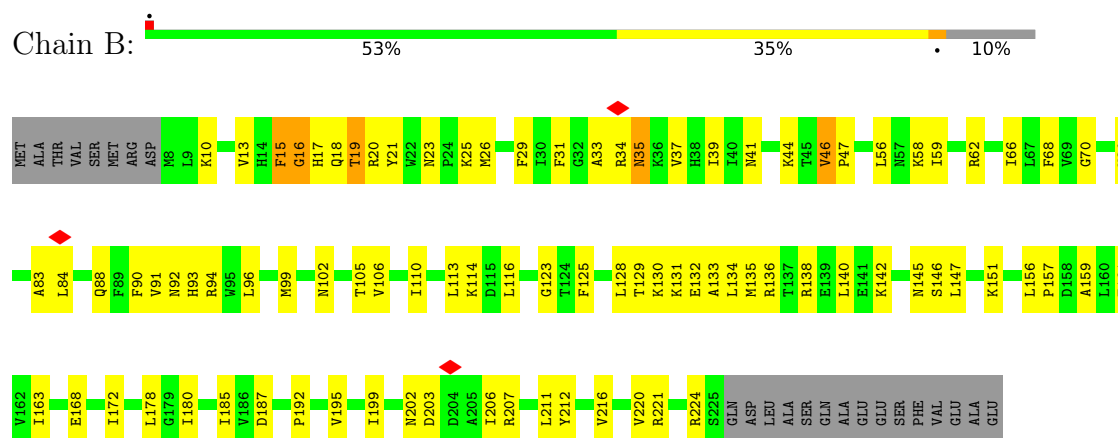
- Molecule 38: truncated mRNA



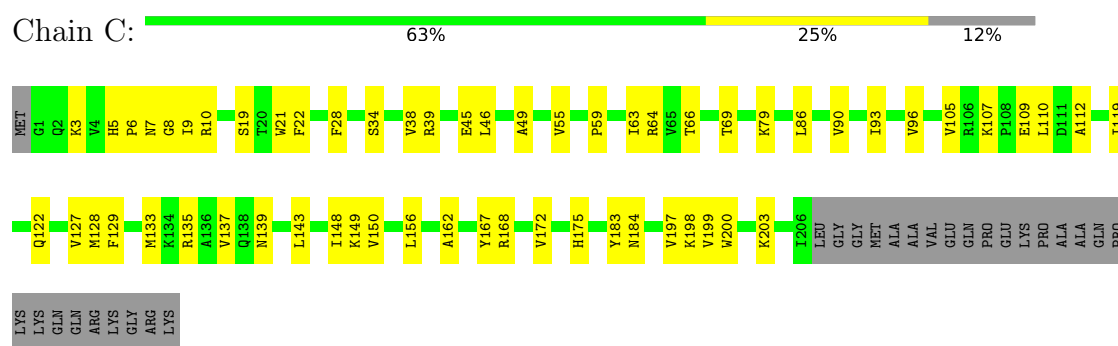
- Molecule 39: Peptide chain release factor RF2



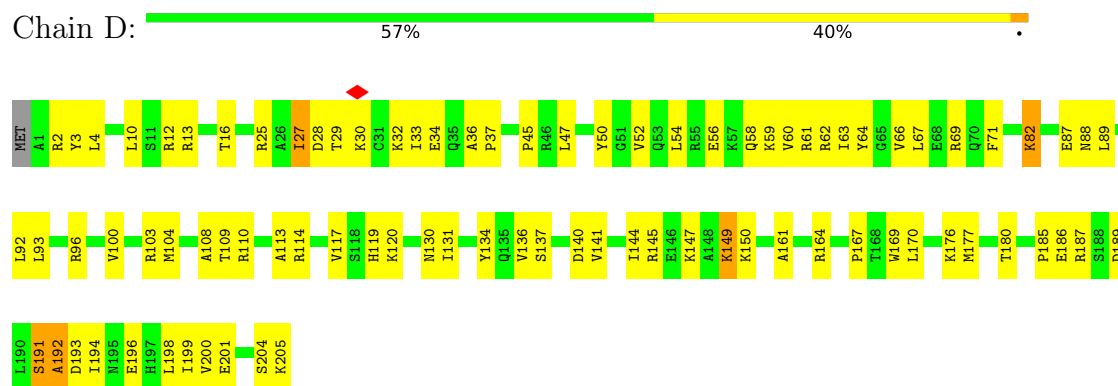
- Molecule 40: 30S ribosomal protein S2



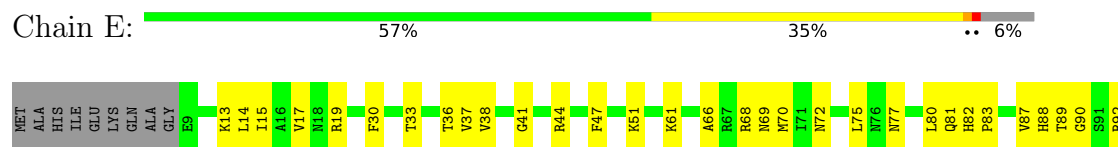
- Molecule 41: 30S ribosomal protein S3



- Molecule 42: 30S ribosomal protein S4

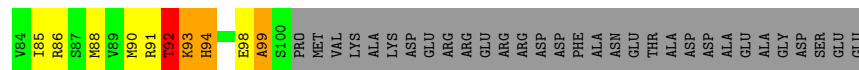


- Molecule 43: 30S ribosomal protein S5

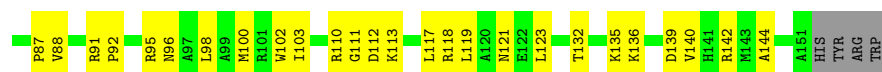




- Molecule 44: 30S ribosomal protein S6



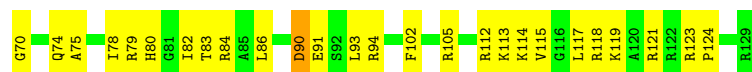
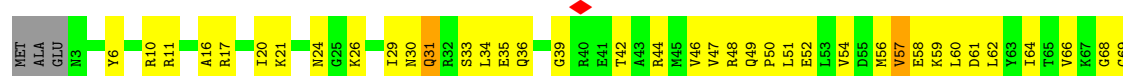
- Molecule 45: 30S ribosomal protein S7



- Molecule 46: 30S ribosomal protein S8

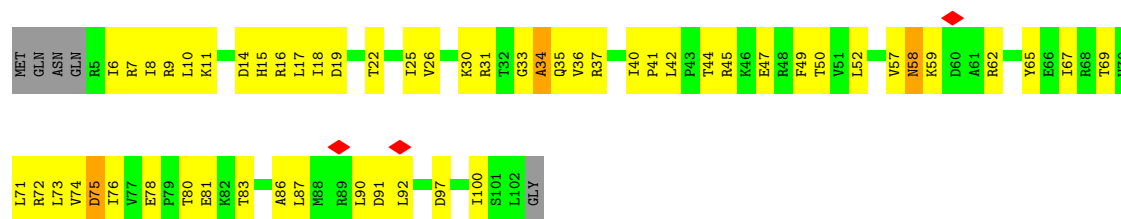


- Molecule 47: 30S ribosomal protein S9

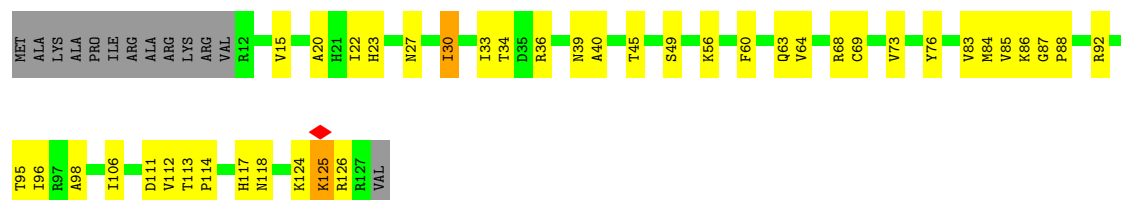


- Molecule 48: 30S ribosomal protein S10





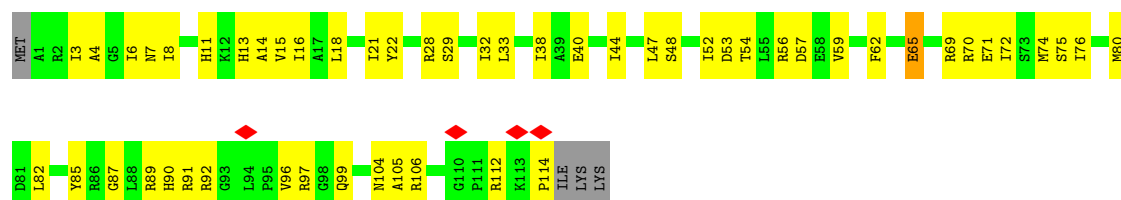
- Molecule 49: 30S ribosomal protein S11



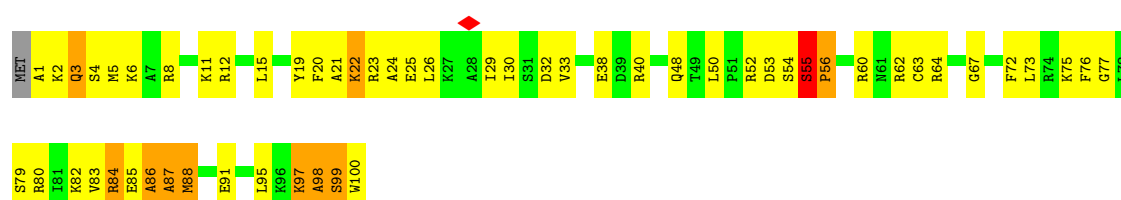
- Molecule 50: 30S ribosomal protein S12



- Molecule 51: 30S ribosomal protein S13



- Molecule 52: 30S ribosomal protein S14



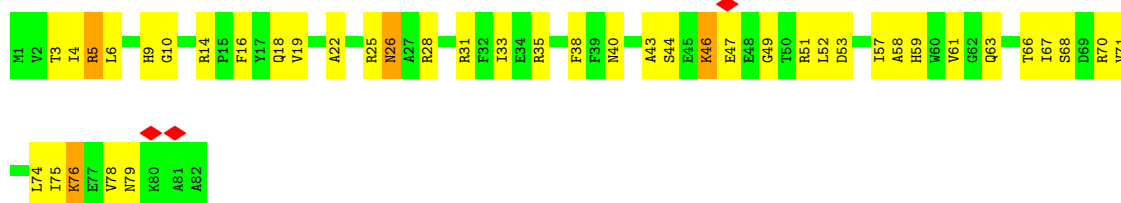
- Molecule 53: 30S ribosomal protein S15

Chain O:  69% 29% ..



- Molecule 54: 30S ribosomal protein S16

Chain P:  49% 46% 5%



- Molecule 55: 30S ribosomal protein S17

Chain Q:  50% 40% 5% 5%

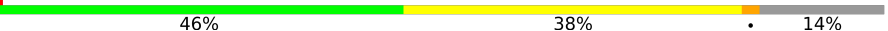


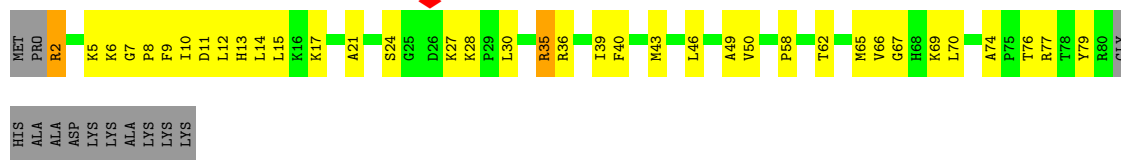
- Molecule 56: 30S ribosomal protein S18

Chain R:  56% 29% 13%



- Molecule 57: 30S ribosomal protein S19

Chain S:  46% 38% 14%

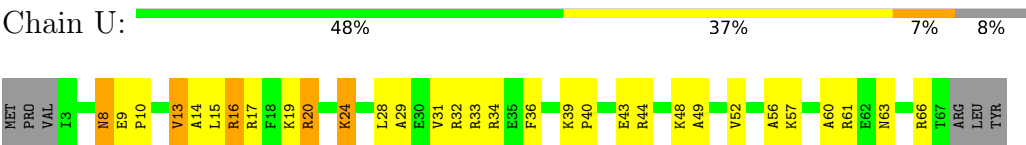


- Molecule 58: 30S ribosomal protein S20

Chain T:  66% 32% .



● Molecule 59: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96070	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 ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	29000	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	18.146	Depositor
Minimum map value	-6.484	Depositor
Average map value	-1.164	Depositor
Map value standard deviation	1.530	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.215, 1.215, 1.215	Depositor

5 Model quality

5.1 Standard geometry

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

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	A	0.39	0/36963	0.48	1/57662 (0.0%)
2	01	0.39	0/69797	0.48	3/108890 (0.0%)
3	02	0.40	0/2847	0.49	0/4440
4	Y	0.35	0/383	0.68	0/504
5	W	0.39	0/1832	0.45	0/2855
5	X	0.40	0/1811	0.54	0/2822
6	03	0.43	0/1361	0.96	3/1796 (0.2%)
7	04	0.41	0/2121	0.88	4/2852 (0.1%)
8	05	0.42	0/1586	0.85	4/2134 (0.2%)
9	06	0.39	0/1571	0.86	2/2113 (0.1%)
10	07	0.40	0/1434	0.86	1/1926 (0.1%)
11	08	0.38	0/1343	0.82	2/1816 (0.1%)
12	09	0.42	0/1122	0.99	8/1515 (0.5%)
13	10	0.53	0/1001	1.62	13/1350 (1.0%)
14	11	0.45	0/1046	0.93	3/1410 (0.2%)
15	12	0.41	0/1152	0.83	2/1551 (0.1%)
16	13	0.40	0/947	0.90	5/1268 (0.4%)
17	14	0.38	0/1054	0.87	1/1403 (0.1%)
18	15	0.40	0/1093	0.85	1/1460 (0.1%)
19	16	0.41	0/973	0.94	2/1301 (0.2%)
20	17	0.38	0/902	0.85	0/1209
21	18	0.38	0/929	0.82	2/1242 (0.2%)
22	19	0.37	0/960	0.79	1/1278 (0.1%)
23	20	0.37	0/829	0.83	3/1107 (0.3%)
24	21	0.40	0/864	0.90	3/1156 (0.3%)
25	22	0.40	0/744	0.89	1/994 (0.1%)
26	23	0.39	0/787	0.84	0/1051
27	24	0.35	0/766	0.78	0/1025
28	25	0.38	0/582	0.90	3/769 (0.4%)
29	26	0.37	0/635	0.79	1/848 (0.1%)
30	27	0.37	0/510	0.79	0/677
31	28	0.37	0/453	0.81	1/605 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	29	0.44	0/531	0.92	4/709 (0.6%)
33	30	0.38	0/450	0.80	1/599 (0.2%)
34	31	0.39	0/416	0.71	0/554
35	32	0.44	0/380	0.94	2/498 (0.4%)
36	33	0.37	0/513	0.91	1/676 (0.1%)
37	34	0.27	0/303	0.74	0/397
38	V	0.38	0/345	0.50	0/538
39	Z	0.36	0/2884	0.73	2/3884 (0.1%)
40	B	0.40	0/1735	0.92	4/2338 (0.2%)
41	C	0.40	0/1651	0.78	0/2225
42	D	0.39	0/1665	0.92	6/2227 (0.3%)
43	E	0.43	0/1169	1.03	7/1573 (0.4%)
44	F	0.45	0/835	1.07	7/1128 (0.6%)
45	G	0.38	0/1195	0.88	1/1602 (0.1%)
46	H	0.37	0/989	0.82	1/1326 (0.1%)
47	I	0.41	0/1034	0.99	2/1375 (0.1%)
48	J	0.43	0/796	0.94	2/1077 (0.2%)
49	K	0.41	0/885	0.88	1/1195 (0.1%)
50	L	0.44	0/969	1.00	8/1300 (0.6%)
51	M	0.39	0/892	0.93	1/1193 (0.1%)
52	N	0.54	0/817	1.16	9/1088 (0.8%)
53	O	0.37	0/722	0.84	1/964 (0.1%)
54	P	0.41	0/659	0.87	1/884 (0.1%)
55	Q	0.40	0/657	0.88	3/881 (0.3%)
56	R	0.36	0/544	0.85	2/731 (0.3%)
57	S	0.41	0/652	0.89	2/877 (0.2%)
58	T	0.40	0/671	0.93	1/888 (0.1%)
59	U	0.49	0/550	1.15	4/728 (0.5%)
All	All	0.39	0/165307	0.63	143/246484 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
52	N	0	1

There are no bond length outliers.

All (143) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	10	118	ILE	CA-C-N	27.00	153.59	119.84
13	10	118	ILE	C-N-CA	27.00	153.59	119.84
49	K	125	LYS	N-CA-C	11.94	129.21	110.70
13	10	118	ILE	C-N-CD	-10.81	80.67	125.00
13	10	54	VAL	N-CA-C	10.16	122.20	110.62
18	15	60	GLN	N-CA-C	9.80	122.97	110.33
36	33	33	THR	N-CA-C	-9.40	103.90	114.62
52	N	55	SER	N-CA-C	8.95	129.58	109.81
6	03	40	GLU	N-CA-C	8.81	121.22	110.91
48	J	35	GLN	N-CA-C	8.69	123.83	113.23
52	N	86	ALA	N-CA-C	-8.62	93.53	108.52
52	N	87	ALA	N-CA-C	8.07	127.99	110.80
58	T	7	LYS	N-CA-C	-8.01	103.51	113.28
44	F	54	LEU	N-CA-C	7.99	121.01	111.02
43	E	116	VAL	N-CA-C	-7.94	104.78	113.43
52	N	88	MET	N-CA-C	-7.73	103.82	113.18
52	N	84	ARG	N-CA-C	-7.73	103.86	113.28
7	04	30	ALA	N-CA-C	7.50	123.00	113.25
12	09	44	ILE	N-CA-C	-7.45	103.52	110.53
35	32	7	PRO	N-CA-C	7.39	122.42	111.03
50	L	115	LYS	N-CA-C	-7.34	99.41	110.28
24	21	6	LYS	N-CA-C	7.31	119.47	110.91
56	R	69	TYR	N-CA-C	-7.26	104.40	113.55
59	U	13	VAL	N-CA-C	-7.22	100.01	108.82
44	F	12	PRO	N-CA-C	7.07	127.03	112.47
16	13	48	PRO	N-CA-C	7.02	125.15	113.78
12	09	42	LYS	N-CA-C	-7.00	105.67	114.56
48	J	75	ASP	N-CA-C	6.92	119.01	110.91
40	B	16	GLY	N-CA-C	6.84	129.38	113.18
42	D	82	LYS	N-CA-C	6.81	119.10	110.24
31	28	52	PHE	N-CA-C	-6.79	106.19	114.75
19	16	68	ALA	N-CA-C	-6.72	103.88	111.07
43	E	41	GLY	N-CA-C	-6.63	106.08	115.43
13	10	107	GLU	N-CA-C	-6.62	98.44	108.96
13	10	108	VAL	N-CA-C	6.60	117.29	110.36
43	E	122	VAL	N-CA-C	6.54	122.94	109.34
50	L	88	ASP	N-CA-C	6.53	119.89	112.97
12	09	8	LYS	CA-C-N	6.52	133.70	121.97
12	09	8	LYS	C-N-CA	6.52	133.70	121.97
45	G	59	GLU	N-CA-C	-6.50	105.17	113.23
12	09	7	ASP	N-CA-C	-6.48	99.97	109.18
1	A	1297	G	C2'-C3'-O3'	6.48	119.22	109.50
44	F	93	LYS	N-CA-C	-6.48	97.00	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	06	81	GLY	N-CA-C	-6.46	104.54	112.68
55	Q	14	ASP	N-CA-C	6.46	121.07	111.96
14	11	80	LYS	N-CA-C	-6.45	105.57	113.50
13	10	119	PRO	CA-N-CD	-6.44	102.98	112.00
11	08	126	THR	N-CA-C	-6.43	100.45	110.42
55	Q	31	PRO	N-CA-C	6.37	121.87	114.03
14	11	62	ALA	N-CA-C	6.34	121.77	111.37
7	04	246	PRO	N-CA-C	-6.25	108.17	114.68
44	F	99	ALA	N-CA-C	6.24	119.70	111.28
8	05	152	PRO	N-CA-C	-6.21	99.69	112.47
23	20	52	PRO	N-CA-C	-6.20	99.70	112.47
17	14	36	LYS	N-CA-C	6.19	119.02	110.35
57	S	9	PHE	N-CA-C	6.19	119.63	109.72
46	H	47	ASP	N-CA-C	6.17	118.27	110.24
35	32	12	ARG	N-CA-C	-6.06	106.05	113.50
6	03	168	ASN	N-CA-C	-6.05	106.22	113.97
25	22	35	ALA	N-CA-C	6.05	119.09	110.68
13	10	116	GLU	N-CA-C	6.04	118.64	111.33
43	E	77	ASN	N-CA-C	6.02	119.93	112.47
52	N	56	PRO	N-CA-C	6.01	124.86	112.47
42	D	192	ALA	N-CA-C	6.00	123.58	110.80
11	08	12	ALA	N-CA-C	5.98	123.53	110.80
53	O	80	LEU	N-CA-C	5.98	117.59	111.14
42	D	149	LYS	N-CA-C	-5.97	102.09	110.50
13	10	119	PRO	N-CA-C	-5.93	100.24	112.47
16	13	35	VAL	N-CA-C	5.88	116.01	110.30
59	U	29	ALA	N-CA-C	-5.87	106.02	112.72
13	10	123	ILE	N-CA-C	5.85	121.51	109.34
7	04	213	ARG	N-CA-C	-5.80	106.82	114.31
42	D	108	ALA	N-CA-C	-5.78	105.06	111.36
13	10	55	VAL	N-CA-C	5.76	121.32	109.34
6	03	81	GLY	N-CA-C	5.75	121.81	111.34
52	N	24	ALA	N-CA-C	-5.74	105.61	113.30
50	L	43	LYS	N-CA-C	5.72	120.53	112.75
59	U	8	ASN	N-CA-C	5.71	122.96	110.80
32	29	65	ASN	N-CA-C	-5.70	106.32	113.28
7	04	237	ARG	N-CA-C	5.69	117.57	110.91
15	12	46	PRO	N-CA-C	5.68	121.23	113.84
39	Z	237	ALA	N-CA-C	-5.67	105.24	111.82
2	01	2177	C	N1-C1'-C2'	5.67	120.51	112.00
32	29	63	ARG	N-CA-C	-5.66	106.92	113.88
28	25	60	ASP	N-CA-C	5.66	118.85	110.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	E	158	LYS	N-CA-C	5.64	119.46	112.58
12	09	69	ALA	N-CA-C	-5.64	106.56	113.50
8	05	2	ILE	N-CA-C	5.63	121.05	109.34
28	25	69	GLY	CA-C-N	5.63	126.88	119.84
28	25	69	GLY	C-N-CA	5.63	126.88	119.84
15	12	113	PRO	N-CA-C	-5.63	106.20	113.57
50	L	113	ARG	N-CA-C	5.62	122.77	110.80
54	P	25	ARG	N-CA-C	-5.61	105.72	113.18
13	10	122	GLN	CA-C-N	5.59	132.04	121.97
13	10	122	GLN	C-N-CA	5.59	132.04	121.97
52	N	21	ALA	N-CA-C	-5.58	106.31	113.01
2	01	1020	A	C2'-C3'-O3'	5.57	117.86	109.50
44	F	94	HIS	N-CA-C	5.57	122.66	110.80
19	16	88	ALA	N-CA-C	5.55	117.19	111.03
16	13	101	GLY	CA-C-N	5.55	126.78	119.84
16	13	101	GLY	C-N-CA	5.55	126.78	119.84
44	F	92	THR	N-CA-C	5.51	122.54	110.80
51	M	11	HIS	N-CA-C	5.48	119.80	113.38
43	E	96	GLN	CA-C-N	5.47	126.68	119.84
43	E	96	GLN	C-N-CA	5.47	126.68	119.84
24	21	63	GLY	N-CA-C	-5.47	105.54	112.54
50	L	117	GLY	N-CA-C	5.46	122.34	114.10
47	I	50	PRO	N-CA-C	-5.43	106.63	114.18
56	R	71	ASP	N-CA-C	5.40	117.25	111.36
50	L	114	SER	N-CA-C	-5.39	104.95	112.45
52	N	32	ASP	N-CA-C	5.37	116.93	109.31
50	L	26	CYS	CA-C-N	5.35	126.53	119.84
50	L	26	CYS	C-N-CA	5.35	126.53	119.84
40	B	46	VAL	CB-CA-C	-5.34	108.62	113.70
8	05	151	THR	CA-C-N	-5.33	113.18	119.84
8	05	151	THR	C-N-CA	-5.33	113.18	119.84
23	20	51	VAL	N-CA-C	-5.30	97.43	108.88
12	09	87	GLU	N-CA-C	5.26	118.16	108.58
9	06	45	ALA	N-CA-C	5.26	122.00	110.80
40	B	206	ILE	N-CA-C	-5.26	107.64	111.90
29	26	11	PRO	N-CA-C	5.25	119.45	110.95
33	30	9	ARG	N-CA-C	-5.24	105.74	111.82
24	21	82	MET	N-CA-C	-5.24	103.11	110.50
21	18	20	ARG	N-CA-C	-5.24	103.07	110.29
55	Q	48	GLU	N-CA-C	-5.22	102.76	110.48
32	29	34	LEU	N-CA-C	5.21	117.56	109.60
47	I	90	ASP	N-CA-C	5.19	121.86	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	11	13	ALA	N-CA-C	5.17	121.81	110.80
12	09	50	ARG	N-CA-C	5.15	116.75	111.03
22	19	49	ARG	N-CA-C	-5.15	106.95	113.18
42	D	191	SER	N-CA-C	5.15	121.76	110.80
2	01	669	G	N9-C1'-C2'	5.12	119.68	112.00
59	U	20	ARG	N-CA-C	-5.11	105.83	111.71
40	B	157	PRO	N-CA-C	5.09	118.34	111.22
16	13	111	LYS	N-CA-C	-5.08	107.11	113.72
32	29	47	LYS	N-CA-C	-5.07	105.94	111.82
44	F	83	ALA	N-CA-C	-5.07	108.12	114.56
10	07	98	PHE	N-CA-C	-5.05	106.28	112.90
23	20	57	GLY	N-CA-C	5.04	122.56	115.30
39	Z	239	LEU	N-CA-C	5.04	116.80	110.91
57	S	35	ARG	N-CA-C	-5.02	106.74	112.92
21	18	74	GLN	N-CA-C	-5.02	101.92	109.15
42	D	52	VAL	N-CA-C	-5.01	106.79	111.45

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	N	86	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	33012	0	16618	474	0
2	01	62318	0	31345	789	0
3	02	2546	0	1292	50	0
4	Y	377	0	383	29	0
5	W	1640	0	837	11	0
5	X	1622	0	827	28	0
6	03	1353	0	1159	38	0
7	04	2082	0	2157	82	0
8	05	1565	0	1616	68	0
9	06	1552	0	1619	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	07	1410	0	1447	74	0
11	08	1323	0	1374	59	0
12	09	1111	0	1148	32	0
13	10	988	0	1025	51	0
14	11	1032	0	1088	59	0
15	12	1129	0	1162	48	0
16	13	938	0	1012	50	0
17	14	1045	0	1117	46	0
18	15	1074	0	1157	37	0
19	16	960	0	1000	48	0
20	17	892	0	923	40	0
21	18	917	0	965	41	0
22	19	947	0	1022	45	0
23	20	816	0	839	25	0
24	21	857	0	922	26	0
25	22	738	0	807	27	0
26	23	779	0	834	31	0
27	24	753	0	780	28	0
28	25	575	0	592	30	0
29	26	625	0	655	27	0
30	27	509	0	543	25	0
31	28	449	0	491	16	0
32	29	522	0	524	27	0
33	30	444	0	461	24	0
34	31	409	0	440	10	0
35	32	377	0	418	19	0
36	33	504	0	574	21	0
37	34	302	0	340	23	0
38	V	306	0	154	1	0
39	Z	2844	0	2739	120	0
40	B	1704	0	1732	79	0
41	C	1624	0	1699	52	0
42	D	1643	0	1710	85	0
43	E	1156	0	1199	59	0
44	F	817	0	808	37	0
45	G	1181	0	1240	48	0
46	H	979	0	1034	32	0
47	I	1022	0	1070	67	0
48	J	786	0	828	56	0
49	K	869	0	878	44	0
50	L	955	0	1019	41	0
51	M	883	0	944	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	N	805	0	847	64	0
53	O	714	0	737	22	0
54	P	649	0	666	39	0
55	Q	648	0	691	35	0
56	R	535	0	552	19	0
57	S	637	0	665	47	0
58	T	665	0	714	23	0
59	U	544	0	579	43	0
60	01	221	0	0	0	0
60	02	6	0	0	0	0
60	17	1	0	0	0	0
60	19	1	0	0	0	0
60	30	1	0	0	0	0
60	31	1	0	0	0	0
60	34	1	0	0	0	0
60	A	118	0	0	0	0
60	I	1	0	0	0	0
60	V	1	0	0	0	0
60	W	3	0	0	0	0
60	X	5	0	0	0	0
61	34	1	0	0	0	0
All	All	152819	0	104018	3245	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (3245) 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)
2:01:45:G:H5''	2:01:46:G:H5'	1.26	1.14
13:10:117:LEU:C	13:10:119:PRO:HD2	1.71	1.14
1:A:291:U:H2'	1:A:292:G:H5''	1.31	1.12
1:A:376:G:H2'	1:A:377:G:H5''	1.35	1.07
51:M:3:ILE:HG12	51:M:7:ASN:HB2	1.25	1.07
5:W:13:C:H2'	5:W:14:A:H5''	1.36	1.06
7:04:20:ASN:HD22	7:04:23:LEU:HG	1.18	1.05
37:34:23:ILE:H	37:34:23:ILE:HD12	1.18	1.03
2:01:517:C:H2'	2:01:518:G:H5''	1.38	1.01
54:P:5:ARG:HE	54:P:22:ALA:HB3	1.23	1.01
1:A:516:U:H5	1:A:533:A:H62	1.08	1.01
1:A:405:U:H3'	1:A:406:G:H5'	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:N:23:ARG:HH12	52:N:50:LEU:HD21	1.28	0.98
16:13:121:GLU:HG2	16:13:122:VAL:HG23	1.46	0.97
1:A:3:A:H5'	1:A:4:U:H5'	1.46	0.96
47:I:56:MET:HE1	47:I:60:LEU:H	1.29	0.95
1:A:403:C:H2'	1:A:404:G:H5''	1.46	0.94
1:A:170:U:H2'	1:A:171:A:H5''	1.47	0.93
14:11:57:VAL:HB	14:11:69:VAL:HB	1.50	0.93
14:11:55:PRO:HG2	14:11:71:LYS:HB3	1.50	0.92
42:D:27:ILE:HG13	42:D:29:THR:H	1.33	0.92
12:09:9:VAL:HB	12:09:12:LEU:O	1.69	0.92
2:01:1668:A:H4'	2:01:1669:A:H5'	1.50	0.92
39:Z:246:THR:HG22	39:Z:247:SER:H	1.35	0.91
2:01:543:G:H2'	2:01:544:C:H5''	1.50	0.91
1:A:291:U:C2'	1:A:292:G:H5''	2.01	0.91
2:01:2334:U:H5'	20:17:12:THR:HB	1.50	0.91
7:04:77:VAL:HG21	7:04:109:LEU:HD11	1.53	0.91
1:A:1259:C:H3'	1:A:1260:G:H5''	1.51	0.90
1:A:614:C:H2'	1:A:615:G:H5''	1.53	0.90
2:01:855:G:H2'	2:01:856:G:H5''	1.50	0.90
10:07:35:LEU:HD11	10:07:151:LEU:HD23	1.54	0.89
24:21:10:ALA:HB1	24:21:46:LEU:HD21	1.54	0.89
1:A:357:G:H2'	1:A:358:U:H5''	1.55	0.89
54:P:40:ASN:ND2	54:P:43:ALA:HB2	1.88	0.88
10:07:140:ILE:HG23	10:07:145:VAL:HG11	1.55	0.88
2:01:2457:U:H5	2:01:2494:G:H1	1.22	0.88
13:10:119:PRO:HG2	13:10:121:SER:H	1.38	0.88
2:01:2331:G:H4'	28:25:39:THR:H	1.39	0.88
44:F:85:ILE:HG22	44:F:86:ARG:HG2	1.56	0.87
4:Y:3:ARG:HG3	39:Z:316:ASP:HB2	1.56	0.87
16:13:49:ARG:HD3	16:13:49:ARG:H	1.39	0.87
4:Y:28:ARG:HB2	39:Z:215:THR:OG1	1.73	0.87
14:11:91:LYS:HB3	14:11:94:LYS:HB2	1.56	0.87
54:P:5:ARG:NE	54:P:22:ALA:HB3	1.90	0.86
1:A:376:G:C2'	1:A:377:G:H5''	2.05	0.86
13:10:118:ILE:N	13:10:119:PRO:HD2	1.83	0.85
1:A:1306:A:N6	1:A:1331:G:H1'	1.92	0.84
5:X:57:A:H2'	5:X:58:A:H5'	1.57	0.84
26:23:51:LEU:H	26:23:51:LEU:HD12	1.41	0.84
25:22:28:ASN:ND2	25:22:91:GLN:HB3	1.92	0.84
5:W:47:U:H4'	5:W:48:C:H5''	1.59	0.84
19:16:2:ARG:HA	19:16:5:LYS:HD2	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1807:G:H2'	2:01:1808:A:H5'	1.60	0.83
1:A:1030:U:H2'	1:A:1031:C:H5'	1.60	0.83
2:01:2848:G:O2'	2:01:2849:U:H5'	1.78	0.83
2:01:2720:U:H3	2:01:2873:A:H62	1.26	0.83
13:10:34:THR:HA	13:10:37:LYS:HE2	1.60	0.83
2:01:1020:A:H1'	2:01:1021:A:OP2	1.78	0.83
55:Q:46:HIS:HB2	55:Q:70:LYS:HZ3	1.43	0.83
2:01:674:G:H5''	9:06:71:GLY:H	1.40	0.83
37:34:36:ARG:HG2	37:34:37:GLN:H	1.44	0.83
54:P:40:ASN:HD22	54:P:43:ALA:HB2	1.43	0.83
27:24:42:LEU:HD12	27:24:47:VAL:HG21	1.60	0.83
52:N:97:LYS:HG3	52:N:98:ALA:H	1.44	0.83
1:A:40:C:H2'	1:A:41:G:H5''	1.57	0.82
52:N:8:ARG:HB3	52:N:12:ARG:HH12	1.44	0.82
22:19:59:LEU:HD21	22:19:63:ARG:HE	1.43	0.82
41:C:39:ARG:HH12	52:N:91:GLU:HG2	1.44	0.82
10:07:37:MET:HE1	10:07:52:ALA:HB1	1.62	0.82
7:04:25:LYS:H	7:04:25:LYS:HD3	1.43	0.81
8:05:46:ARG:HB2	8:05:84:LEU:HD12	1.60	0.81
35:32:1:MET:HB2	35:32:3:ARG:HH22	1.44	0.81
10:07:45:ASP:HB2	10:07:48:LEU:HD13	1.61	0.81
1:A:1124:G:H5''	48:J:37:ARG:HG3	1.63	0.81
2:01:955:U:H5	2:01:962:G:H1	1.27	0.81
47:I:54:VAL:HG11	47:I:93:LEU:HG	1.63	0.81
39:Z:270:ILE:HD11	39:Z:291:MET:HE1	1.62	0.81
1:A:850:U:H2'	1:A:851:G:H5''	1.61	0.80
2:01:1727:C:H2'	2:01:1728:C:H5'	1.61	0.80
5:W:13:C:C2'	5:W:14:A:H5''	2.12	0.80
18:15:42:THR:HG22	18:15:93:VAL:HG12	1.64	0.80
1:A:1410:A:H4'	4:Y:8:LYS:HA	1.62	0.80
1:A:357:G:C2'	1:A:358:U:H5''	2.11	0.80
49:K:23:HIS:HB3	49:K:30:ILE:HG23	1.64	0.80
55:Q:11:VAL:HG11	55:Q:20:ILE:HD11	1.64	0.80
56:R:11:ARG:HG3	56:R:14:ALA:HB3	1.64	0.80
40:B:56:LEU:HD21	40:B:216:VAL:HG13	1.64	0.79
16:13:1:MET:HE3	16:13:67:LYS:HD3	1.62	0.79
1:A:718:A:H5'	49:K:118:ASN:HB2	1.64	0.79
1:A:151:A:H62	1:A:170:U:H3	1.29	0.79
40:B:33:ALA:HB2	40:B:39:ILE:HG13	1.64	0.79
37:34:1:MET:HA	37:34:34:LYS:O	1.82	0.79
17:14:110:VAL:HB	17:14:127:VAL:HG12	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:G:H5''	54:P:5:ARG:HB2	1.63	0.79
15:12:117:ALA:HA	15:12:120:ARG:HE	1.46	0.79
7:04:16:VAL:HB	7:04:203:VAL:HG22	1.65	0.79
2:01:1716:U:H3	2:01:1744:A:H62	1.29	0.78
1:A:14:U:H5	4:Y:41:ARG:HE	1.30	0.78
2:01:2553:G:H3'	2:01:2554:U:H5''	1.65	0.78
9:06:112:LEU:HD13	9:06:186:VAL:HG21	1.65	0.78
18:15:60:GLN:HE21	18:15:108:VAL:HG12	1.48	0.78
40:B:91:VAL:HG21	40:B:99:MET:HE1	1.66	0.78
48:J:11:LYS:HB2	48:J:97:ASP:HB3	1.66	0.78
24:21:82:MET:HB2	24:21:98:LYS:HB2	1.64	0.78
18:15:64:TRP:HB2	18:15:104:GLU:HG3	1.64	0.78
1:A:484:G:H4'	1:A:485:U:H5'	1.64	0.78
10:07:114:ARG:HG3	51:M:70:ARG:HH22	1.48	0.78
2:01:475:C:H4'	2:01:510:C:H5'	1.66	0.78
2:01:74:A:H4'	2:01:75:G:H5''	1.64	0.77
2:01:517:C:C2'	2:01:518:G:H5''	2.12	0.77
2:01:2562:U:H1'	16:13:23:LYS:NZ	2.00	0.77
39:Z:248:GLY:HA3	39:Z:255:ASN:HD21	1.47	0.77
2:01:2807:U:H3'	2:01:2808:G:H5''	1.64	0.77
51:M:16:ILE:H	51:M:16:ILE:HD12	1.48	0.77
1:A:1432:G:H1'	1:A:1468:A:H62	1.49	0.77
1:A:170:U:C2'	1:A:171:A:H5''	2.14	0.77
14:11:4:VAL:HA	14:11:59:THR:HG21	1.67	0.77
1:A:1279:G:H5''	48:J:9:ARG:NH1	2.00	0.77
2:01:855:G:C2'	2:01:856:G:H5''	2.14	0.77
2:01:1081:U:H4'	14:11:123:ALA:HB1	1.64	0.76
1:A:276:G:H5''	55:Q:16:MET:HE1	1.67	0.76
1:A:403:C:C2'	1:A:404:G:H5''	2.14	0.76
13:10:117:LEU:O	13:10:119:PRO:HD2	1.84	0.76
26:23:81:ARG:HD2	26:23:96:LYS:HD2	1.65	0.76
46:H:6:ILE:HG12	46:H:31:LEU:HD23	1.66	0.76
48:J:57:VAL:HG22	48:J:58:ASN:H	1.50	0.76
51:M:3:ILE:HD11	51:M:21:ILE:HD11	1.66	0.76
1:A:1297:G:H1'	1:A:1298:U:OP2	1.86	0.76
42:D:27:ILE:HG13	42:D:28:ASP:H	1.50	0.76
54:P:46:LYS:H	54:P:46:LYS:HD2	1.50	0.76
6:03:39:VAL:HG22	6:03:177:LYS:HD3	1.66	0.76
2:01:1936:A:H2	2:01:1943:U:H3	1.32	0.76
1:A:845:A:H2'	56:R:9:PHE:HD2	1.50	0.76
2:01:1521:G:H3'	2:01:1522:A:H5''	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:10:88:HIS:HB2	13:10:89:PRO:HD3	1.68	0.76
44:F:91:ARG:HG2	44:F:92:THR:H	1.47	0.76
11:08:49:LEU:HD12	11:08:71:LEU:HD21	1.67	0.76
10:07:33:ILE:HB	10:07:90:LEU:HB2	1.67	0.75
42:D:104:MET:HE2	42:D:170:LEU:HD22	1.67	0.75
48:J:76:ILE:HG23	48:J:78:GLU:OE2	1.84	0.75
52:N:55:SER:HB3	52:N:56:PRO:HD3	1.69	0.75
1:A:420:U:H2'	1:A:422:C:O4'	1.87	0.75
14:11:34:ILE:HD12	14:11:35:MET:H	1.51	0.75
1:A:225:C:H2'	1:A:226:G:H5''	1.67	0.75
43:E:80:LEU:HD13	43:E:122:VAL:HG11	1.68	0.75
44:F:9:MET:HE3	44:F:86:ARG:HB2	1.68	0.75
8:05:13:ARG:HH22	21:18:74:GLN:NE2	1.85	0.75
14:11:74:PRO:HG2	14:11:77:VAL:HG22	1.67	0.74
18:15:4:PRO:HG3	18:15:68:PHE:HE2	1.52	0.74
32:29:59:ARG:HH21	32:29:62:LYS:HB3	1.52	0.74
2:01:17:G:H4'	22:19:24:TYR:HE1	1.51	0.74
2:01:543:G:C2'	2:01:544:C:H5''	2.16	0.74
43:E:88:HIS:NE2	43:E:137:ARG:HD2	2.02	0.74
59:U:15:LEU:HA	59:U:17:ARG:HH12	1.52	0.74
10:07:138:PRO:HG2	10:07:139:GLU:OE2	1.88	0.74
50:L:109:ARG:HB3	50:L:118:VAL:HG21	1.68	0.74
1:A:769:G:H4'	1:A:1513:A:H4'	1.69	0.74
2:01:906:U:H2'	2:01:907:G:H5''	1.70	0.74
40:B:99:MET:HA	40:B:106:VAL:HG21	1.68	0.74
59:U:36:PHE:CD1	59:U:39:LYS:HD2	2.23	0.74
3:02:66:A:H5''	3:02:67:G:OP1	1.88	0.74
1:A:1279:G:H5''	48:J:9:ARG:HH12	1.53	0.74
2:01:974:G:H1'	2:01:975:A:C8	2.23	0.73
2:01:1664:A:H61	2:01:1996:C:H42	1.33	0.73
20:17:25:ARG:HH12	20:17:44:GLY:HA2	1.53	0.73
59:U:16:ARG:HH21	59:U:19:LYS:HG2	1.52	0.73
50:L:54:VAL:HG21	50:L:81:ILE:HD11	1.69	0.73
16:13:104:THR:HG22	16:13:106:GLU:H	1.53	0.73
42:D:10:LEU:HD13	42:D:62:ARG:HD2	1.70	0.73
43:E:111:ARG:O	43:E:115:GLU:HG2	1.88	0.73
8:05:4:LEU:HD11	8:05:29:VAL:HG11	1.70	0.73
25:22:69:ARG:HG2	25:22:74:ILE:HG22	1.69	0.73
42:D:100:VAL:HG21	42:D:136:VAL:HG21	1.70	0.73
15:12:37:ARG:HA	15:12:118:MET:HE3	1.69	0.73
55:Q:46:HIS:HB2	55:Q:70:LYS:NZ	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:08:132:LEU:HD23	11:08:132:LEU:H	1.54	0.73
19:16:1:MET:O	19:16:2:ARG:HG3	1.89	0.73
55:Q:31:PRO:HG2	55:Q:32:ILE:HD12	1.71	0.73
9:06:88:ARG:HB3	9:06:89:PRO:HD2	1.69	0.73
48:J:52:LEU:HD21	48:J:59:LYS:HD3	1.70	0.73
2:01:2048:G:H2'	2:01:2049:G:H5''	1.71	0.72
47:I:11:ARG:HA	47:I:105:ARG:HH12	1.54	0.72
25:22:11:LEU:HD12	25:22:50:LEU:HD23	1.71	0.72
26:23:65:GLN:HB3	26:23:68:ASN:ND2	2.04	0.72
2:01:300:A:OP2	26:23:96:LYS:HD3	1.88	0.72
21:18:40:GLN:HG2	21:18:41:ALA:H	1.54	0.72
39:Z:117:ARG:HH22	39:Z:357:ILE:HG22	1.55	0.72
1:A:78:A:H2'	1:A:79:G:H5'	1.71	0.72
2:01:1140:C:H5'	15:12:26:GLY:HA3	1.72	0.72
2:01:1141:U:H4'	2:01:1142:A:O4'	1.88	0.72
2:01:713:G:H21	2:01:718:A:H62	1.35	0.72
37:34:18:LYS:HE2	37:34:21:GLY:HA2	1.71	0.72
40:B:163:ILE:HG23	40:B:185:ILE:HD11	1.69	0.72
52:N:23:ARG:NH1	52:N:50:LEU:HD21	2.05	0.72
2:01:1031:G:H5''	37:34:8:LYS:HE3	1.72	0.72
25:22:56:GLU:HG2	25:22:57:VAL:HG23	1.70	0.72
59:U:32:ARG:HG3	59:U:33:ARG:HG2	1.71	0.72
20:17:40:ILE:HG12	20:17:47:VAL:HG12	1.72	0.71
6:03:23:ILE:HD12	6:03:186:LYS:HG3	1.70	0.71
11:08:152:ARG:H	11:08:152:ARG:HD2	1.54	0.71
1:A:112:G:H21	1:A:354:G:H5'	1.55	0.71
9:06:149:ILE:HD13	9:06:188:MET:HE2	1.72	0.71
23:20:49:ILE:HD12	23:20:52:PRO:HA	1.71	0.71
48:J:8:ILE:HD13	48:J:76:ILE:HD13	1.71	0.71
1:A:614:C:C2'	1:A:615:G:H5''	2.19	0.71
41:C:107:LYS:HD2	41:C:110:LEU:HD22	1.72	0.71
8:05:51:THR:HB	8:05:79:LEU:HD23	1.70	0.71
48:J:19:ASP:HA	48:J:22:THR:HG22	1.73	0.71
1:A:1348:U:H4'	47:I:121:ARG:HD2	1.72	0.71
9:06:44:ARG:NH2	9:06:87:ALA:HB3	2.06	0.71
41:C:110:LEU:HD21	41:C:203:LYS:HD3	1.73	0.71
57:S:5:LYS:HG3	57:S:6:LYS:HD3	1.73	0.71
1:A:780:A:H5''	49:K:124:LYS:HE3	1.73	0.71
1:A:1330:U:H4'	51:M:22:TYR:CE1	2.26	0.71
2:01:1074:G:H2'	2:01:1075:C:H4'	1.73	0.71
1:A:9:G:H5'	43:E:107:GLY:HA3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:02:43:C:H4'	10:07:62:GLN:NE2	2.06	0.70
52:N:63:CYS:HB3	52:N:67:GLY:H	1.55	0.70
2:01:2508:G:H1	2:01:2580:U:H5	1.39	0.70
13:10:56:ARG:HD2	13:10:81:LEU:HB2	1.73	0.70
1:A:40:C:C2'	1:A:41:G:H5''	2.21	0.70
10:07:79:ARG:HG2	10:07:82:TYR:CE2	2.26	0.70
2:01:2356:U:O3'	28:25:16:ARG:HD3	1.92	0.70
36:33:32:LEU:HD23	36:33:35:LYS:HD2	1.73	0.70
2:01:12:U:O2	2:01:12:U:H2'	1.92	0.70
2:01:119:A:H4'	2:01:120:U:H5'	1.74	0.70
7:04:106:PRO:HD2	7:04:109:LEU:HD22	1.73	0.69
25:22:28:ASN:HD21	25:22:91:GLN:HB3	1.54	0.69
40:B:156:LEU:HD23	40:B:156:LEU:H	1.56	0.69
2:01:1059:G:H5'	14:11:71:LYS:HE3	1.75	0.69
7:04:59:GLN:HE21	7:04:84:PRO:HB2	1.57	0.69
12:09:75:LEU:HD23	12:09:75:LEU:H	1.58	0.69
42:D:149:LYS:NZ	42:D:177:MET:HE3	2.07	0.69
8:05:151:THR:OG1	8:05:152:PRO:HD3	1.93	0.69
49:K:88:PRO:HG3	59:U:28:LEU:HD13	1.75	0.69
1:A:1319:A:H5''	57:S:69:LYS:HE3	1.73	0.69
2:01:2054:A:H2'	33:30:4:GLN:HE21	1.58	0.69
13:10:8:LYS:HE2	13:10:8:LYS:HA	1.75	0.69
40:B:46:VAL:HB	40:B:47:PRO:HD3	1.75	0.69
7:04:121:ALA:HB1	7:04:127:ASN:HD22	1.57	0.69
16:13:13:ASN:HB2	16:13:98:ARG:HB2	1.74	0.69
33:30:8:THR:HG22	33:30:9:ARG:H	1.56	0.69
42:D:89:LEU:O	42:D:93:LEU:HD13	1.93	0.69
1:A:412:A:H3'	1:A:413:G:H5''	1.74	0.68
1:A:850:U:C2'	1:A:851:G:H5''	2.23	0.68
5:X:18:G:H2'	5:X:19:G:H4'	1.73	0.68
59:U:9:GLU:HB3	59:U:10:PRO:HD3	1.74	0.68
10:07:134:GLN:HG2	10:07:140:ILE:HG12	1.75	0.68
1:A:1100:C:OP2	40:B:94:ARG:HG2	1.94	0.68
10:07:142:TYR:HA	10:07:145:VAL:HG22	1.75	0.68
6:03:30:LEU:HD22	6:03:214:ILE:HD13	1.76	0.68
24:21:6:LYS:HE3	24:21:8:ARG:HD2	1.74	0.68
37:34:36:ARG:HD3	37:34:37:GLN:HG3	1.74	0.68
39:Z:238:ASP:HA	39:Z:266:ILE:HD12	1.76	0.68
32:29:34:LEU:HD23	32:29:34:LEU:H	1.57	0.68
1:A:1196:A:H1'	4:Y:34:LYS:HD3	1.75	0.68
44:F:11:HIS:CE1	44:F:83:ALA:HA	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:511:U:H2'	2:01:512:G:H5'	1.76	0.67
2:01:704:G:H1'	2:01:727:A:H61	1.58	0.67
1:A:1124:G:H4'	48:J:40:ILE:HD11	1.76	0.67
2:01:973:A:H5''	23:20:81:LYS:HD2	1.76	0.67
7:04:129:LEU:HD12	7:04:129:LEU:O	1.94	0.67
16:13:71:ARG:HD3	16:13:77:ILE:HD11	1.76	0.67
23:20:48:LYS:HG2	23:20:49:ILE:H	1.59	0.67
2:01:2715:C:H2'	2:01:2716:C:H5''	1.76	0.67
39:Z:117:ARG:HH12	39:Z:361:LEU:HD13	1.59	0.67
42:D:60:VAL:HG21	42:D:199:ILE:HD11	1.76	0.67
1:A:624:C:H4'	54:P:10:GLY:HA2	1.75	0.67
1:A:1432:G:H1'	1:A:1468:A:N6	2.08	0.67
11:08:17:LYS:HB2	11:08:17:LYS:HZ2	1.58	0.67
33:30:16:ARG:HA	33:30:19:ASP:CG	2.19	0.67
39:Z:52:ARG:HH12	39:Z:56:LEU:HD22	1.59	0.67
17:14:103:ILE:HD12	17:14:104:GLN:N	2.09	0.67
2:01:704:G:H1'	2:01:727:A:N6	2.09	0.67
5:X:29:G:H2'	5:X:30:G:O4'	1.94	0.67
14:11:87:SER:HB3	14:11:97:VAL:HG22	1.77	0.67
45:G:64:ALA:HA	45:G:67:ASN:HD22	1.58	0.67
47:I:57:VAL:HG23	47:I:58:GLU:H	1.59	0.67
21:18:36:LYS:HE2	21:18:36:LYS:HA	1.75	0.67
29:26:15:ASN:HD22	29:26:23:ALA:HB1	1.60	0.67
46:H:10:LEU:HD22	46:H:74:ILE:HD11	1.76	0.67
8:05:1:MET:HG3	8:05:205:PRO:HG2	1.77	0.67
31:28:26:LEU:HD11	31:28:46:MET:HB3	1.77	0.67
37:34:34:LYS:NZ	37:34:34:LYS:HB3	2.09	0.67
52:N:20:PHE:HE2	52:N:54:SER:HB3	1.60	0.66
11:08:70:LEU:O	11:08:70:LEU:HD23	1.95	0.66
13:10:11:ILE:O	13:10:15:VAL:HG23	1.96	0.66
37:34:36:ARG:HG2	37:34:37:GLN:N	2.11	0.66
47:I:48:ARG:HA	47:I:51:LEU:HD12	1.78	0.66
14:11:11:GLN:HB2	14:11:56:VAL:HG12	1.76	0.66
2:01:2177:C:O2	2:01:2177:C:H2'	1.93	0.66
7:04:70:LYS:HB2	7:04:70:LYS:NZ	2.10	0.66
11:08:44:HIS:HA	11:08:49:LEU:HD23	1.77	0.66
2:01:1142:A:H4'	15:12:27:ARG:NH2	2.10	0.66
24:21:4:ILE:HG22	24:21:106:VAL:HG22	1.76	0.66
2:01:161:A:H3'	2:01:162:U:H5''	1.77	0.66
2:01:2715:C:C3'	2:01:2716:C:H5''	2.26	0.66
16:13:112:PHE:HA	16:13:115:ILE:HD13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:O:61:GLN:O	53:O:65:LEU:HD23	1.96	0.66
1:A:225:C:C2'	1:A:226:G:H5''	2.25	0.66
2:01:2297:A:N6	2:01:2319:G:H1'	2.11	0.66
14:11:30:GLN:HB3	14:11:64:ARG:NH1	2.09	0.66
48:J:6:ILE:HG13	48:J:76:ILE:HB	1.78	0.66
53:O:24:THR:HG22	53:O:65:LEU:HD12	1.78	0.66
5:X:41:C:H2'	5:X:42:G:H8	1.60	0.66
5:X:62:C:H3'	5:X:63:G:H5''	1.77	0.66
40:B:15:PHE:H	40:B:15:PHE:HD1	1.43	0.66
57:S:66:VAL:HG23	57:S:67:GLY:N	2.11	0.66
39:Z:307:LYS:NZ	39:Z:307:LYS:HB2	2.11	0.66
2:01:1476:U:H3	2:01:1515:A:H62	1.43	0.65
25:22:13:ALA:HB3	25:22:33:LYS:HD3	1.77	0.65
47:I:46:VAL:HG21	47:I:75:ALA:HB1	1.78	0.65
52:N:82:LYS:HA	52:N:85:GLU:HB3	1.78	0.65
1:A:632:U:H3'	1:A:633:G:H5'	1.78	0.65
1:A:225:C:C3'	1:A:226:G:H5''	2.26	0.65
2:01:2267:A:H5''	2:01:2268:A:H5'	1.78	0.65
16:13:26:GLY:HA3	16:13:30:ARG:HH11	1.62	0.65
57:S:43:MET:O	57:S:46:LEU:HD13	1.96	0.65
2:01:45:G:C5'	2:01:46:G:H5'	2.16	0.65
13:10:44:ALA:HB2	13:10:52:MET:HE2	1.79	0.65
50:L:98:ARG:HB2	50:L:116:TYR:HA	1.78	0.65
1:A:9:G:H5'	43:E:107:GLY:CA	2.26	0.65
24:21:5:ALA:HB2	24:21:54:ALA:HB2	1.77	0.65
57:S:27:LYS:NZ	57:S:27:LYS:HB3	2.11	0.65
40:B:102:ASN:ND2	40:B:105:THR:HB	2.12	0.65
37:34:23:ILE:H	37:34:23:ILE:CD1	1.96	0.65
14:11:54:ILE:HG12	14:11:73:PRO:HG3	1.78	0.65
27:24:42:LEU:HD11	27:24:89:ILE:HD11	1.79	0.65
43:E:38:VAL:HG23	43:E:70:MET:HE3	1.78	0.65
50:L:29:LYS:NZ	50:L:58:ASN:HD21	1.95	0.65
2:01:2094:A:H2'	2:01:2095:A:H5''	1.79	0.65
50:L:86:VAL:HG23	50:L:87:LYS:H	1.62	0.65
14:11:85:ILE:HD12	14:11:85:ILE:O	1.96	0.65
2:01:517:C:H5''	33:30:12:ARG:HH12	1.62	0.64
2:01:2598:A:H5''	7:04:233:GLY:HA3	1.78	0.64
1:A:1026:G:H1	1:A:1035:A:H2	1.44	0.64
2:01:192:C:H2'	2:01:193:U:H5'	1.79	0.64
2:01:2048:G:C3'	2:01:2049:G:H5''	2.28	0.64
7:04:131:MET:HG2	7:04:134:ILE:HD12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:59:ILE:HD12	40:B:159:ALA:HB2	1.79	0.64
42:D:13:ARG:HD2	42:D:37:PRO:HB3	1.79	0.64
58:T:66:ILE:HG23	58:T:70:LYS:HD3	1.78	0.64
9:06:14:VAL:HG12	9:06:15:SER:H	1.61	0.64
59:U:33:ARG:HH12	59:U:34:ARG:NE	1.95	0.64
2:01:2094:A:C3'	2:01:2095:A:H5''	2.27	0.64
3:02:65:U:H3'	3:02:108:A:H61	1.62	0.64
6:03:22:ASP:H	6:03:25:GLU:HB2	1.62	0.64
11:08:32:LEU:HD23	11:08:33:THR:N	2.12	0.64
1:A:310:G:H5''	54:P:31:ARG:HB2	1.78	0.64
2:01:2641:G:H5''	15:12:78:THR:HB	1.80	0.64
13:10:118:ILE:N	13:10:119:PRO:CD	2.60	0.64
14:11:9:LYS:C	14:11:10:LEU:HD12	2.23	0.64
43:E:119:VAL:HG11	43:E:122:VAL:HG22	1.79	0.64
51:M:89:ARG:HB2	51:M:96:VAL:HG22	1.78	0.64
2:01:1753:G:OP1	21:18:92:ARG:HD2	1.98	0.64
5:W:48:C:H2'	5:W:59:A:H4'	1.79	0.64
59:U:33:ARG:HH22	59:U:34:ARG:HD3	1.63	0.64
12:09:12:LEU:HD11	12:09:21:VAL:HG12	1.79	0.64
15:12:104:ALA:O	15:12:108:MET:HE3	1.98	0.64
1:A:1228:C:H4'	51:M:114:PRO:HB3	1.79	0.64
2:01:2514:U:H5''	15:12:81:ILE:HD11	1.79	0.64
40:B:58:LYS:O	40:B:62:ARG:HG2	1.98	0.64
2:01:310:A:H2'	2:01:311:A:H5''	1.80	0.63
2:01:955:U:H5	2:01:962:G:N1	1.96	0.63
2:01:1142:A:H4'	15:12:27:ARG:HH22	1.63	0.63
16:13:76:VAL:H	21:18:72:VAL:HG22	1.63	0.63
20:17:37:ALA:HB2	20:17:106:LEU:HD11	1.78	0.63
7:04:245:THR:HB	7:04:246:PRO:HD2	1.80	0.63
35:32:25:LYS:HA	35:32:28:ARG:HH12	1.64	0.63
53:O:55:LEU:HA	53:O:58:MET:HE3	1.80	0.63
2:01:575:A:O2'	2:01:576:U:H5'	1.98	0.63
31:28:6:ILE:HD13	31:28:47:ILE:HD11	1.81	0.63
42:D:161:ALA:HA	42:D:164:ARG:HG3	1.80	0.63
56:R:25:ILE:HG21	56:R:66:LEU:HB3	1.80	0.63
5:X:34:C:H3'	5:X:35:A:H5''	1.79	0.63
13:10:27:VAL:HG21	13:10:107:GLU:OE2	1.98	0.63
40:B:131:LYS:O	40:B:135:MET:HG3	1.99	0.63
1:A:245:U:O2'	1:A:246:A:H5'	1.98	0.63
1:A:327:A:O2'	1:A:328:C:H4'	1.99	0.63
1:A:508:U:H4'	42:D:50:TYR:CD2	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:07:59:ILE:CD1	10:07:151:LEU:HD21	2.28	0.63
46:H:17:GLN:OE1	46:H:71:VAL:HB	1.98	0.63
2:01:1062:G:H2'	2:01:1063:G:H5''	1.81	0.63
2:01:1394:U:H4'	2:01:1603:A:H4'	1.79	0.63
2:01:1697:G:H4'	2:01:1978:A:H5''	1.79	0.63
2:01:2243:U:H2'	2:01:2244:U:C6	2.34	0.63
43:E:81:GLN:HG2	43:E:146:MET:HE3	1.81	0.63
1:A:355:C:H1'	1:A:388:G:H1'	1.79	0.63
16:13:73:ASP:O	21:18:74:GLN:HG3	1.97	0.63
41:C:79:LYS:HA	41:C:79:LYS:HE2	1.79	0.63
43:E:68:ARG:C	43:E:69:ASN:HD22	2.07	0.63
2:01:310:A:C2'	2:01:311:A:H5''	2.29	0.63
2:01:1801:A:H5''	2:01:2203:U:H2'	1.80	0.63
2:01:855:G:C3'	2:01:856:G:H5''	2.29	0.63
2:01:2720:U:H5''	21:18:52:ARG:HH21	1.63	0.63
19:16:2:ARG:O	19:16:2:ARG:HD3	1.99	0.63
30:27:42:LEU:O	30:27:46:VAL:HG23	1.99	0.63
39:Z:248:GLY:CA	39:Z:255:ASN:HD21	2.12	0.63
40:B:102:ASN:HD21	40:B:105:THR:HB	1.64	0.63
59:U:36:PHE:HB3	59:U:39:LYS:HB2	1.80	0.63
2:01:45:G:H5''	2:01:46:G:C5'	2.16	0.62
13:10:56:ARG:NH1	13:10:83:ALA:HB2	2.14	0.62
13:10:72:LEU:O	13:10:72:LEU:HD23	1.99	0.62
26:23:38:ILE:HG22	26:23:39:ASN:ND2	2.14	0.62
40:B:110:ILE:HG12	40:B:147:LEU:HD11	1.79	0.62
2:01:2799:A:H2'	2:01:2800:A:H5'	1.80	0.62
14:11:3:LYS:HG3	14:11:4:VAL:HG23	1.80	0.62
16:13:40:LYS:HD2	16:13:57:VAL:HG12	1.81	0.62
46:H:48:PHE:HB3	46:H:60:LEU:HD23	1.79	0.62
9:06:98:LYS:HB3	9:06:102:ARG:HH22	1.64	0.62
10:07:28:PRO:HB2	10:07:168:LEU:HD22	1.81	0.62
13:10:27:VAL:HG22	13:10:29:ASP:H	1.64	0.62
26:23:51:LEU:H	26:23:51:LEU:CD1	2.13	0.62
54:P:38:PHE:CE1	54:P:51:ARG:HB3	2.34	0.62
57:S:21:ALA:HB2	57:S:30:LEU:HD21	1.80	0.62
2:01:2035:G:H5'	2:01:2036:C:H5	1.64	0.62
3:02:43:C:H4'	10:07:62:GLN:HE22	1.64	0.62
9:06:90:GLN:HG3	9:06:92:HIS:CE1	2.34	0.62
25:22:37:ASP:CG	25:22:38:ALA:H	2.08	0.62
32:29:16:CYS:HB2	32:29:37:CYS:SG	2.39	0.62
1:A:1240:U:H4'	45:G:37:THR:CG2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1280:A:O2'	1:A:1281:C:H5'	1.99	0.62
2:01:704:G:H2'	2:01:726:G:H22	1.63	0.62
2:01:1068:G:H22	39:Z:54:GLN:HE21	1.46	0.62
5:X:74:C:H4'	5:X:75:C:H3'	1.81	0.62
7:04:259:ASN:OD1	7:04:261:ARG:HG2	2.00	0.62
14:11:34:ILE:HD12	14:11:35:MET:N	2.15	0.62
48:J:65:TYR:HB3	52:N:95:LEU:HD11	1.82	0.62
2:01:279:A:H2'	2:01:280:U:H5'	1.81	0.62
2:01:1012:U:H3	15:12:27:ARG:HG2	1.65	0.62
12:09:83:LYS:HA	12:09:149:GLU:HB2	1.82	0.62
42:D:27:ILE:HG13	42:D:29:THR:N	2.10	0.62
58:T:34:VAL:O	58:T:38:ILE:HG13	1.99	0.62
1:A:412:A:H3'	1:A:413:G:C5'	2.30	0.62
2:01:1818:U:O4	7:04:152:GLN:HG3	2.00	0.62
2:01:2334:U:C5'	20:17:12:THR:HB	2.25	0.62
10:07:114:ARG:HG3	51:M:70:ARG:NH2	2.15	0.62
1:A:850:U:C3'	1:A:851:G:H5''	2.30	0.61
50:L:109:ARG:HH21	50:L:112:ALA:HB3	1.65	0.61
40:B:70:GLY:HA3	40:B:163:ILE:HD12	1.83	0.61
1:A:1137:C:H4'	1:A:1138:G:N2	2.15	0.61
2:01:2145:C:H3'	2:01:2146:C:H5'	1.82	0.61
5:X:57:A:C2'	5:X:58:A:H5'	2.29	0.61
19:16:79:LEU:HD23	19:16:83:LEU:HD12	1.81	0.61
36:33:23:HIS:HD2	36:33:49:VAL:HG22	1.65	0.61
30:27:18:LEU:HB3	30:27:22:LEU:HD23	1.82	0.61
39:Z:103:LEU:HD23	39:Z:103:LEU:O	2.00	0.61
52:N:52:ARG:HH12	57:S:36:ARG:NH2	1.98	0.61
58:T:53:MET:HE3	58:T:57:VAL:HG21	1.82	0.61
2:01:1874:C:H2'	2:01:1875:G:O4'	2.00	0.61
19:16:90:ARG:HH12	19:16:116:VAL:CG1	2.13	0.61
51:M:85:TYR:O	51:M:89:ARG:HG2	2.00	0.61
59:U:32:ARG:NH1	59:U:33:ARG:HD3	2.15	0.61
1:A:730:G:H2'	1:A:731:G:H5'	1.81	0.61
2:01:558:U:P	15:12:113:PRO:HD2	2.40	0.61
9:06:172:ALA:HB3	9:06:195:GLN:OE1	2.00	0.61
26:23:95:PHE:HD2	26:23:100:GLU:HB2	1.65	0.61
52:N:5:MET:HB3	52:N:62:ARG:NH1	2.16	0.61
1:A:182:A:H2'	1:A:183:C:H5''	1.82	0.61
7:04:27:LYS:HB3	7:04:27:LYS:NZ	2.16	0.61
14:11:30:GLN:HB3	14:11:64:ARG:HH12	1.64	0.61
20:17:98:GLN:HE21	20:17:100:HIS:HB2	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:D:141:VAL:HG12	42:D:180:THR:HG22	1.83	0.61
45:G:112:ASP:C	45:G:113:LYS:HD2	2.26	0.61
54:P:71:VAL:O	54:P:74:LEU:HG	2.00	0.61
1:A:352:C:H4'	1:A:354:G:OP1	2.01	0.61
4:Y:30:GLU:OE1	39:Z:213:ARG:HD3	2.00	0.61
15:12:102:GLU:HG2	15:12:119:PHE:HZ	1.66	0.61
21:18:23:ASP:OD1	21:18:88:ARG:HA	2.00	0.61
53:O:81:ILE:HA	53:O:86:LEU:HD21	1.81	0.61
1:A:490:C:H5''	42:D:147:LYS:NZ	2.15	0.61
7:04:119:VAL:HB	12:09:91:PHE:CE1	2.35	0.61
39:Z:153:LEU:O	39:Z:153:LEU:HD23	2.01	0.61
2:01:1064:C:O2'	2:01:1065:U:H5'	2.01	0.61
2:01:1727:C:C2'	2:01:1728:C:H5'	2.31	0.60
2:01:2024:G:OP2	2:01:2034:U:H4'	2.02	0.60
10:07:71:LYS:HG3	10:07:72:SER:H	1.66	0.60
41:C:143:LEU:HD23	41:C:143:LEU:O	2.00	0.60
49:K:34:THR:HG22	49:K:40:ALA:HA	1.80	0.60
56:R:11:ARG:HD2	56:R:15:GLU:HG2	1.83	0.60
15:12:93:ILE:HD13	15:12:100:VAL:HG21	1.83	0.60
8:05:55:LYS:HD3	8:05:77:ARG:HA	1.83	0.60
39:Z:246:THR:HG22	39:Z:247:SER:N	2.11	0.60
22:19:13:HIS:O	22:19:17:LEU:HD13	2.01	0.60
43:E:113:VAL:HG11	43:E:136:VAL:HG13	1.84	0.60
2:01:2:G:H1	2:01:2901:C:H42	1.48	0.60
2:01:2048:G:C2'	2:01:2049:G:H5''	2.30	0.60
2:01:2313:C:H4'	10:07:87:LYS:HD3	1.83	0.60
10:07:121:PHE:HE1	10:07:127:TYR:HB2	1.66	0.60
23:20:76:LYS:HB2	23:20:85:LYS:HB2	1.82	0.60
39:Z:275:GLN:HA	39:Z:283:ASN:ND2	2.16	0.60
1:A:531:U:H5	39:Z:332:ARG:HH22	1.50	0.60
2:01:639:U:H2'	2:01:640:C:C6	2.37	0.60
8:05:2:ILE:HG13	8:05:3:GLY:H	1.67	0.60
12:09:133:GLN:HE21	12:09:139:PHE:HE1	1.49	0.60
8:05:34:VAL:HG22	8:05:50:VAL:HG12	1.84	0.60
37:34:11:CYS:O	37:34:14:CYS:HB2	2.01	0.60
2:01:668:A:H2'	2:01:670:A:H62	1.66	0.60
2:01:1726:C:H2'	2:01:1727:C:C6	2.37	0.60
2:01:2756:U:H3'	37:34:20:ASP:H	1.65	0.60
3:02:72:G:H21	3:02:104:A:H62	1.49	0.60
6:03:15:VAL:HG23	6:03:29:LEU:HD21	1.84	0.60
14:11:45:THR:HB	14:11:50:LYS:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:24:30:ILE:HB	27:24:38:LEU:HB3	1.83	0.60
32:29:9:TYR:OH	32:29:25:ARG:HB3	2.01	0.60
44:F:18:VAL:CG1	44:F:19:PRO:HD3	2.32	0.60
54:P:26:ASN:HD22	54:P:26:ASN:N	2.00	0.60
1:A:40:C:C3'	1:A:41:G:H5''	2.31	0.60
26:23:71:ILE:HD12	26:23:71:ILE:O	2.01	0.60
2:01:940:G:H2'	2:01:941:A:H5''	1.84	0.59
2:01:2105:U:H2'	2:01:2106:U:H5'	1.83	0.59
18:15:28:PHE:HB2	18:15:104:GLU:OE2	2.03	0.59
42:D:64:TYR:CD2	42:D:93:LEU:HD23	2.37	0.59
45:G:65:LEU:O	45:G:65:LEU:HD23	2.01	0.59
51:M:82:LEU:HD21	57:S:65:MET:HG2	1.84	0.59
1:A:279:A:H5'	1:A:281:G:H5'	1.84	0.59
1:A:405:U:C3'	1:A:406:G:H5'	2.27	0.59
1:A:784:A:H2'	1:A:785:G:C8	2.37	0.59
1:A:1221:G:H4'	57:S:76:THR:HG21	1.84	0.59
2:01:1651:G:H4'	19:16:39:PRO:HG2	1.82	0.59
7:04:144:GLU:HB2	7:04:187:CYS:HB3	1.84	0.59
7:04:241:LYS:HB2	7:04:241:LYS:NZ	2.17	0.59
17:14:135:ILE:HB	17:14:142:ILE:HD11	1.84	0.59
20:17:43:ASN:HD22	20:17:43:ASN:N	1.98	0.59
33:30:8:THR:HG22	33:30:9:ARG:N	2.17	0.59
43:E:82:HIS:HB2	43:E:83:PRO:HD2	1.84	0.59
2:01:674:G:H5''	9:06:71:GLY:N	2.15	0.59
19:16:55:ALA:HA	19:16:80:PHE:CE1	2.37	0.59
56:R:26:ALA:HA	56:R:29:LYS:HE2	1.84	0.59
4:Y:17:GLU:OE2	39:Z:133:GLN:HG2	2.03	0.59
57:S:35:ARG:HH12	57:S:74:ALA:HB3	1.66	0.59
2:01:559:G:H21	22:19:51:GLN:HG2	1.67	0.59
2:01:2636:C:H2'	2:01:2637:U:H6	1.67	0.59
10:07:98:PHE:HA	10:07:101:ARG:HG2	1.85	0.59
54:P:76:LYS:HB2	54:P:76:LYS:NZ	2.18	0.59
2:01:2573:C:O5'	39:Z:256:ARG:NH2	2.35	0.59
2:01:2715:C:C2'	2:01:2716:C:H5''	2.32	0.59
8:05:179:ARG:NH2	21:18:7:LEU:HD11	2.17	0.59
30:27:28:LEU:HD22	30:27:46:VAL:HG21	1.85	0.59
41:C:45:GLU:HG3	41:C:46:LEU:HD12	1.83	0.59
47:I:42:THR:HA	47:I:44:ARG:HH11	1.67	0.59
2:01:2572:A:H5'	2:01:2574:G:H4'	1.83	0.59
3:02:60:C:H2'	3:02:61:G:H8	1.67	0.59
26:23:96:LYS:HB2	26:23:96:LYS:NZ	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:116:LEU:HD21	40:B:136:ARG:NH2	2.17	0.59
1:A:59:A:H3'	1:A:331:G:H22	1.68	0.59
7:04:20:ASN:ND2	7:04:23:LEU:HG	2.03	0.59
11:08:12:ALA:O	11:08:14:VAL:N	2.36	0.59
17:14:78:ARG:HB2	17:14:81:ASP:OD2	2.01	0.59
43:E:104:ILE:HD11	43:E:114:LEU:HB3	1.85	0.59
55:Q:18:LYS:NZ	55:Q:18:LYS:HB2	2.18	0.59
1:A:1138:G:H3'	1:A:1138:G:N3	2.18	0.59
2:01:543:G:C3'	2:01:544:C:H5''	2.33	0.59
4:Y:11:ILE:HD12	39:Z:315:SER:HB3	1.85	0.59
7:04:202:ARG:HH21	7:04:213:ARG:NH2	2.01	0.59
47:I:56:MET:HE1	47:I:60:LEU:N	2.11	0.59
1:A:1162:C:H2'	1:A:1163:A:H8	1.68	0.58
2:01:704:G:H2'	2:01:726:G:N2	2.18	0.58
2:01:1181:U:H2'	2:01:1182:G:C8	2.38	0.58
2:01:2104:C:H2'	2:01:2105:U:C6	2.38	0.58
10:07:121:PHE:CE1	10:07:127:TYR:HB2	2.38	0.58
29:26:16:ASN:ND2	29:26:26:ARG:HB3	2.18	0.58
57:S:66:VAL:HG23	57:S:67:GLY:H	1.68	0.58
2:01:768:G:N2	2:01:1379:U:H1'	2.18	0.58
2:01:1062:G:C2'	2:01:1063:G:H5''	2.32	0.58
2:01:2204:G:H4'	7:04:149:LYS:HD3	1.84	0.58
24:21:86:MET:HE3	24:21:87:PRO:HD2	1.84	0.58
5:W:6:G:O2'	5:W:7:G:H5'	2.03	0.58
43:E:113:VAL:HG23	43:E:114:LEU:CD1	2.33	0.58
1:A:1124:G:H4'	48:J:40:ILE:CD1	2.33	0.58
2:01:1344:U:H3'	2:01:1345:C:H5'	1.84	0.58
3:02:44:G:H1'	3:02:47:C:N4	2.18	0.58
20:17:104:GLN:HG2	20:17:108:ASP:OD2	2.04	0.58
21:18:40:GLN:HG2	21:18:41:ALA:N	2.17	0.58
47:I:30:ASN:C	47:I:31:GLN:HE21	2.11	0.58
52:N:63:CYS:HB2	52:N:79:SER:OG	2.03	0.58
1:A:177:G:H5'	58:T:59:ARG:NH1	2.19	0.58
1:A:412:A:H62	1:A:431:A:H61	1.49	0.58
2:01:17:G:H4'	22:19:24:TYR:CE1	2.36	0.58
2:01:2134:A:H62	2:01:2156:G:H21	1.51	0.58
16:13:114:LYS:O	16:13:118:LEU:HD23	2.04	0.58
27:24:30:ILE:HD13	27:24:91:PHE:HB2	1.85	0.58
35:32:12:ARG:HG3	35:32:13:ASN:ND2	2.18	0.58
52:N:11:LYS:HA	52:N:11:LYS:HE2	1.85	0.58
52:N:84:ARG:HG2	52:N:84:ARG:HH11	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:U:13:VAL:HB	59:U:15:LEU:CD1	2.33	0.58
1:A:418:C:H5''	1:A:513:C:O2'	2.02	0.58
2:01:644:A:H2'	2:01:645:C:C4'	2.33	0.58
7:04:107:LYS:HE3	7:04:193:GLU:HB3	1.84	0.58
15:12:72:LYS:HB3	15:12:89:PHE:HB2	1.86	0.58
19:16:103:ARG:HG3	19:16:110:MET:SD	2.43	0.58
39:Z:325:SER:HB2	39:Z:334:LYS:HB3	1.86	0.58
1:A:1368:A:OP2	47:I:113:LYS:HB3	2.04	0.58
35:32:26:ASN:HA	35:32:29:GLN:HE21	1.68	0.58
47:I:34:LEU:HD11	47:I:47:VAL:HG21	1.86	0.58
2:01:1083:U:H2'	2:01:1085:A:OP2	2.03	0.58
1:A:396:C:H3'	1:A:397:A:H5''	1.86	0.58
1:A:1412:C:H2'	1:A:1413:A:C8	2.39	0.58
2:01:2715:C:H3'	2:01:2716:C:H5''	1.86	0.58
44:F:5:GLU:HB2	44:F:90:MET:HB2	1.86	0.58
4:Y:27:GLN:HB2	39:Z:137:GLY:HA2	1.84	0.58
12:09:84:ALA:HA	12:09:91:PHE:H	1.69	0.58
43:E:163:ILE:HD12	43:E:164:LEU:N	2.18	0.58
49:K:33:ILE:HG13	49:K:69:CYS:SG	2.43	0.58
1:A:1108:G:H5'	41:C:175:HIS:ND1	2.18	0.58
1:A:1295:U:H2'	1:A:1296:C:C6	2.39	0.58
2:01:517:C:H5''	33:30:12:ARG:HH22	1.67	0.58
2:01:1700:A:H2'	2:01:1701:A:H5'	1.84	0.58
2:01:2747:G:O6	2:01:2755:C:H5''	2.04	0.58
7:04:58:LYS:HB2	7:04:58:LYS:NZ	2.19	0.58
39:Z:266:ILE:HB	39:Z:267:PRO:HD3	1.84	0.58
47:I:16:ALA:HA	47:I:66:VAL:HA	1.86	0.58
1:A:369:G:H5'	1:A:369:G:H8	1.69	0.57
2:01:69:C:O2'	2:01:70:G:H5'	2.04	0.57
2:01:322:A:H5'	2:01:340:A:H1'	1.85	0.57
8:05:142:VAL:HG13	8:05:143:PRO:HD2	1.86	0.57
37:34:23:ILE:HD12	37:34:23:ILE:N	2.02	0.57
40:B:34:ARG:HD2	40:B:35:ASN:HD22	1.69	0.57
45:G:35:LYS:O	45:G:39:GLU:HG2	2.03	0.57
53:O:69:LEU:O	53:O:69:LEU:HD13	2.03	0.57
1:A:715:A:H2'	1:A:716:A:C8	2.40	0.57
1:A:845:A:H2'	56:R:9:PHE:CD2	2.34	0.57
1:A:878:A:H5''	46:H:80:PRO:HG2	1.85	0.57
1:A:1147:C:H4'	47:I:6:TYR:CE2	2.39	0.57
1:A:1307:U:H5''	51:M:99:GLN:HE22	1.69	0.57
2:01:1022:G:N7	15:12:68:LYS:HD3	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2508:G:N1	2:01:2580:U:H5	2.03	0.57
3:02:78:A:H62	3:02:98:G:H21	1.52	0.57
7:04:164:VAL:CG2	7:04:174:ARG:HB2	2.34	0.57
1:A:78:A:C2'	1:A:79:G:H5'	2.34	0.57
2:01:1076:C:H2'	2:01:1077:A:O4'	2.04	0.57
2:01:2799:A:C2'	2:01:2800:A:H5'	2.34	0.57
13:10:19:ALA:HA	13:10:70:GLU:OE1	2.04	0.57
15:12:81:ILE:HG23	15:12:82:GLY:H	1.69	0.57
16:13:49:ARG:H	16:13:49:ARG:CD	2.15	0.57
33:30:56:LYS:HB3	33:30:56:LYS:NZ	2.19	0.57
40:B:130:LYS:O	40:B:134:LEU:HD13	2.03	0.57
44:F:98:GLU:HG2	44:F:99:ALA:H	1.69	0.57
51:M:80:MET:HE3	51:M:90:HIS:HB3	1.86	0.57
1:A:1516:G:H2'	1:A:1518:A:OP2	2.04	0.57
2:01:686:U:H3'	2:01:687:C:H5'	1.85	0.57
12:09:9:VAL:HG11	12:09:12:LEU:HB3	1.87	0.57
23:20:27:ILE:HD12	23:20:27:ILE:N	2.19	0.57
1:A:1156:G:H21	1:A:1179:A:H61	1.53	0.57
1:A:1305:G:H1'	1:A:1332:A:N6	2.20	0.57
1:A:1506:U:O2'	1:A:1507:A:H5'	2.05	0.57
2:01:1914:C:H5	4:Y:11:ILE:HA	1.68	0.57
2:01:2432:A:O2'	5:X:75:C:H5'	2.05	0.57
45:G:42:VAL:O	45:G:46:LEU:HD13	2.04	0.57
51:M:82:LEU:HD11	57:S:65:MET:HG3	1.86	0.57
51:M:3:ILE:CD1	51:M:21:ILE:HD11	2.34	0.57
52:N:22:LYS:NZ	52:N:22:LYS:HB3	2.19	0.57
1:A:537:G:H5''	50:L:109:ARG:HH12	1.70	0.57
2:01:49:A:H5'	2:01:51:G:O4'	2.05	0.57
2:01:2848:G:H2'	2:01:2867:G:N2	2.19	0.57
3:02:52:A:H62	20:17:33:ARG:HB2	1.68	0.57
7:04:216:ARG:HG2	7:04:216:ARG:HH11	1.69	0.57
32:29:2:LYS:HB2	32:29:2:LYS:NZ	2.20	0.57
34:31:32:LYS:NZ	34:31:32:LYS:HB3	2.20	0.57
40:B:35:ASN:HD22	40:B:35:ASN:N	2.01	0.57
43:E:156:ARG:HH11	46:H:42:GLU:HB3	1.69	0.57
1:A:235:C:H1'	55:Q:62:GLU:OE2	2.04	0.57
1:A:884:U:H4'	1:A:885:G:H5''	1.86	0.57
6:03:65:LEU:HG	6:03:68:GLY:H	1.70	0.57
10:07:87:LYS:NZ	10:07:87:LYS:HB3	2.20	0.57
13:10:118:ILE:HG22	13:10:118:ILE:O	2.04	0.57
42:D:36:ALA:N	42:D:37:PRO:HD3	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:G:12:LEU:HD11	47:I:49:GLN:NE2	2.20	0.57
1:A:665:A:O4'	1:A:733:G:H1'	2.05	0.57
3:02:55:U:O2'	3:02:56:G:H5'	2.05	0.57
20:17:35:ILE:HD11	20:17:106:LEU:HD12	1.87	0.57
2:01:2636:C:H2'	2:01:2637:U:C6	2.40	0.57
7:04:123:ILE:HG23	7:04:191:LEU:HD13	1.87	0.57
22:19:90:ASP:H	23:20:11:GLN:HE22	1.53	0.57
33:30:54:ILE:HG23	33:30:56:LYS:H	1.70	0.57
1:A:521:G:H21	1:A:536:C:H5'	1.70	0.56
1:A:523:A:C2'	1:A:524:G:H5''	2.35	0.56
2:01:144:A:H5''	25:22:2:ILE:HD11	1.87	0.56
2:01:962:G:H21	2:01:2250:G:H1	1.53	0.56
2:01:2798:U:H4'	2:01:2799:A:C4	2.40	0.56
2:01:2836:U:H2'	2:01:2837:A:C8	2.39	0.56
30:27:20:ASN:HD22	30:27:20:ASN:N	2.02	0.56
41:C:5:HIS:HE1	41:C:7:ASN:HD22	1.53	0.56
1:A:108:G:N1	58:T:9:ARG:HG2	2.19	0.56
2:01:1827:U:H2'	2:01:1828:G:O4'	2.05	0.56
3:02:51:G:O2'	3:02:52:A:H5'	2.04	0.56
42:D:131:ILE:HG13	42:D:134:TYR:HB2	1.85	0.56
1:A:1118:U:H2'	1:A:1119:C:C6	2.39	0.56
2:01:74:A:H4'	2:01:75:G:C5'	2.32	0.56
2:01:1203:U:H5'	17:14:3:LEU:HD23	1.87	0.56
2:01:2094:A:C2'	2:01:2095:A:H5''	2.35	0.56
2:01:2504:U:H2'	2:01:2505:G:H5''	1.87	0.56
3:02:44:G:H1'	3:02:47:C:H42	1.70	0.56
7:04:160:TYR:HB3	7:04:193:GLU:HG3	1.88	0.56
9:06:29:HIS:O	9:06:33:VAL:HG23	2.05	0.56
11:08:89:VAL:HG11	11:08:162:ARG:HH11	1.70	0.56
17:14:79:LEU:H	17:14:113:ALA:HB3	1.70	0.56
17:14:103:ILE:CD1	17:14:104:GLN:HG3	2.35	0.56
32:29:13:THR:HA	32:29:23:LYS:HA	1.88	0.56
35:32:25:LYS:HA	35:32:28:ARG:NH1	2.19	0.56
39:Z:353:LEU:O	39:Z:357:ILE:HG12	2.04	0.56
43:E:14:LEU:HA	43:E:36:THR:HG22	1.87	0.56
44:F:91:ARG:CG	44:F:92:THR:H	2.16	0.56
48:J:10:LEU:HD12	48:J:10:LEU:N	2.21	0.56
48:J:57:VAL:HG22	48:J:58:ASN:N	2.18	0.56
2:01:1565:C:O2'	2:01:1566:A:H2'	2.05	0.56
2:01:2091:C:H4'	29:26:55:MET:HE1	1.86	0.56
7:04:36:ASN:HB2	7:04:61:TYR:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:142:VAL:HG12	8:05:144:GLY:H	1.69	0.56
13:10:80:THR:O	13:10:82:ILE:HG13	2.05	0.56
39:Z:263:ILE:HB	39:Z:272:THR:HB	1.87	0.56
2:01:1062:G:H21	14:11:135:MET:HE1	1.68	0.56
8:05:4:LEU:HD21	8:05:29:VAL:HG11	1.85	0.56
40:B:68:PHE:HD2	40:B:83:ALA:HB2	1.71	0.56
49:K:15:VAL:HG12	49:K:76:TYR:HB3	1.87	0.56
50:L:120:ARG:HG2	50:L:121:PRO:HD2	1.87	0.56
55:Q:18:LYS:HG2	55:Q:46:HIS:HE1	1.70	0.56
2:01:703:U:H2'	2:01:704:G:O4'	2.06	0.56
2:01:1181:U:H2'	2:01:1182:G:H8	1.70	0.56
20:17:24:THR:HG22	20:17:42:PRO:HD3	1.88	0.56
39:Z:322:GLN:CB	39:Z:336:LEU:HD21	2.36	0.56
41:C:63:ILE:HG22	41:C:96:VAL:HG23	1.87	0.56
1:A:841:C:O2'	1:A:843:U:H5''	2.04	0.56
2:01:1468:U:H2'	2:01:1522:A:N6	2.20	0.56
2:01:2655:G:O2'	2:01:2656:U:H5	1.88	0.56
4:Y:16:ILE:HD13	39:Z:197:GLY:N	2.21	0.56
7:04:25:LYS:H	7:04:25:LYS:CD	2.16	0.56
15:12:92:MET:HE2	15:12:99:ARG:HD3	1.86	0.56
39:Z:144:TRP:CE2	39:Z:201:LEU:HB2	2.41	0.56
44:F:29:ILE:HG22	44:F:34:GLY:HA3	1.87	0.56
47:I:61:ASP:C	47:I:62:LEU:HD12	2.30	0.56
51:M:53:ASP:OD1	51:M:54:THR:HG23	2.05	0.56
51:M:69:ARG:HA	51:M:72:ILE:HG12	1.88	0.56
2:01:264:C:C2'	2:01:265:A:H5''	2.35	0.56
2:01:1035:U:H2'	2:01:1036:G:H8	1.71	0.56
2:01:1046:A:C5'	2:01:1047:G:H5''	2.36	0.56
8:05:24:VAL:HG12	8:05:178:VAL:HG21	1.87	0.56
8:05:110:THR:HB	8:05:202:ILE:HB	1.87	0.56
9:06:90:GLN:HG3	9:06:92:HIS:HE1	1.70	0.56
11:08:45:ALA:N	11:08:48:THR:O	2.39	0.56
14:11:97:VAL:HB	14:11:137:LEU:HA	1.86	0.56
16:13:115:ILE:HD12	16:13:115:ILE:N	2.21	0.56
47:I:91:GLU:HA	47:I:94:ARG:HB3	1.87	0.56
57:S:62:THR:H	57:S:65:MET:HE3	1.71	0.56
1:A:530:G:H22	4:Y:28:ARG:HB3	1.70	0.56
1:A:614:C:C3'	1:A:615:G:H5''	2.36	0.56
1:A:1306:A:H61	1:A:1331:G:H1'	1.66	0.56
2:01:813:U:H2'	2:01:814:C:C6	2.41	0.56
2:01:1336:A:OP2	25:22:68:LYS:HD2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2164:C:H2'	2:01:2165:C:H5'	1.87	0.56
2:01:2584:U:H4'	39:Z:248:GLY:O	2.05	0.56
2:01:2884:U:C6	33:30:49:ARG:HG2	2.41	0.56
7:04:231:HIS:HA	7:04:241:LYS:HZ1	1.71	0.56
11:08:27:GLY:HA3	11:08:78:VAL:HB	1.87	0.56
16:13:21:CYS:HA	16:13:41:ILE:HG22	1.88	0.56
29:26:7:THR:OG1	29:26:9:LYS:HG3	2.06	0.56
39:Z:130:LEU:HB3	39:Z:181:ILE:HB	1.88	0.56
43:E:82:HIS:HD2	46:H:98:LEU:HD22	1.71	0.56
1:A:451:A:H4'	1:A:452:A:N3	2.21	0.56
1:A:1117:A:H4'	47:I:105:ARG:HE	1.69	0.56
2:01:1027:A:H2	2:01:2488:G:H4'	1.70	0.56
2:01:2066:C:O2'	2:01:2067:G:H5'	2.06	0.56
2:01:2297:A:H62	2:01:2319:G:H1'	1.70	0.56
9:06:123:LYS:HE2	9:06:125:SER:OG	2.06	0.56
21:18:50:ARG:NH1	21:18:52:ARG:HG3	2.21	0.56
23:20:80:ARG:HB2	23:20:80:ARG:NH1	2.21	0.56
27:24:10:LYS:HB3	27:24:10:LYS:NZ	2.21	0.56
42:D:186:GLU:HB2	42:D:189:ASP:HB2	1.87	0.56
1:A:723:U:O4	59:U:49:ALA:HA	2.05	0.55
5:X:69:C:H2'	5:X:70:G:H8	1.71	0.55
15:12:45:THR:HB	15:12:48:VAL:HG12	1.87	0.55
22:19:90:ASP:N	23:20:11:GLN:HE22	2.04	0.55
26:23:3:LYS:HB2	26:23:4:ILE:HD12	1.88	0.55
47:I:44:ARG:H	47:I:44:ARG:HD3	1.70	0.55
1:A:1251:A:H2'	1:A:1252:A:C8	2.41	0.55
2:01:1077:A:H2'	2:01:1078:U:O4'	2.06	0.55
2:01:1367:A:H2'	2:01:1368:G:H5'	1.86	0.55
2:01:2638:G:H1'	2:01:2778:A:H61	1.71	0.55
15:12:99:ARG:O	15:12:103:ILE:HG12	2.06	0.55
23:20:51:VAL:HG23	23:20:52:PRO:O	2.05	0.55
46:H:15:ASN:HD22	46:H:15:ASN:N	2.04	0.55
2:01:1186:G:H2'	2:01:1187:G:O4'	2.07	0.55
2:01:2297:A:N1	2:01:2321:U:C5	2.74	0.55
2:01:2514:U:H2'	2:01:2515:C:C6	2.41	0.55
12:09:94:ILE:HG23	12:09:98:ASP:HB2	1.88	0.55
14:11:2:LYS:HD2	14:11:61:TYR:HA	1.87	0.55
26:23:4:ILE:HD12	26:23:4:ILE:N	2.21	0.55
2:01:1063:G:C8	14:11:89:SER:HB3	2.42	0.55
2:01:1668:A:C4'	2:01:1669:A:H5'	2.31	0.55
5:X:41:C:H2'	5:X:42:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:36:GLN:HE21	8:05:38:LYS:HG2	1.70	0.55
27:24:51:GLN:HE22	27:24:86:LEU:HG	1.71	0.55
32:29:23:LYS:C	32:29:24:ILE:HD12	2.32	0.55
47:I:24:ASN:ND2	47:I:26:LYS:HG3	2.21	0.55
1:A:56:U:H2'	1:A:57:G:C8	2.41	0.55
1:A:882:C:O2'	1:A:883:C:H5'	2.06	0.55
1:A:1218:C:H2'	1:A:1219:A:C8	2.41	0.55
2:01:433:C:O2'	2:01:434:U:H5'	2.07	0.55
2:01:679:C:H2'	2:01:680:C:C6	2.41	0.55
2:01:851:C:H2'	2:01:852:U:C6	2.42	0.55
3:02:106:G:H2'	3:02:107:G:O4'	2.06	0.55
14:11:102:ARG:O	14:11:106:GLN:HG2	2.06	0.55
39:Z:155:TRP:CE2	39:Z:353:LEU:HD11	2.41	0.55
1:A:403:C:C3'	1:A:404:G:H5''	2.36	0.55
1:A:794:A:H4'	1:A:1521:C:O2'	2.06	0.55
2:01:1170:C:H2'	2:01:1171:G:C8	2.42	0.55
2:01:2618:G:H21	8:05:155:VAL:HG21	1.71	0.55
2:01:2720:U:H5''	21:18:52:ARG:NH2	2.22	0.55
10:07:62:GLN:HA	32:29:6:HIS:ND1	2.21	0.55
18:15:57:VAL:O	18:15:60:GLN:HG2	2.06	0.55
48:J:15:HIS:HA	48:J:18:ILE:HG22	1.87	0.55
50:L:49:ARG:HG3	50:L:89:LEU:HD21	1.89	0.55
52:N:20:PHE:HD2	52:N:55:SER:HB3	1.71	0.55
2:01:937:C:OP1	36:33:51:LYS:HD3	2.06	0.55
18:15:59:ARG:HH21	18:15:59:ARG:HG3	1.71	0.55
49:K:39:ASN:HD22	49:K:39:ASN:N	2.04	0.55
57:S:13:HIS:O	57:S:17:LYS:HG2	2.05	0.55
7:04:5:CYS:SG	7:04:17:LYS:HE2	2.47	0.55
12:09:8:LYS:O	12:09:9:VAL:HG23	2.06	0.55
19:16:38:LEU:HB2	19:16:39:PRO:HD3	1.89	0.55
27:24:21:ARG:NH1	27:24:21:ARG:HB2	2.22	0.55
42:D:187:ARG:HE	42:D:196:GLU:HG2	1.72	0.55
1:A:537:G:H5''	50:L:109:ARG:NH1	2.20	0.55
2:01:942:G:H2'	2:01:943:A:O4'	2.06	0.55
2:01:2071:A:H2'	2:01:2072:C:C6	2.41	0.55
3:02:12:C:H1'	3:02:15:A:C2	2.42	0.55
7:04:231:HIS:HA	7:04:241:LYS:NZ	2.22	0.55
8:05:9:VAL:HG11	21:18:3:ILE:HD11	1.88	0.55
10:07:28:PRO:HG2	10:07:168:LEU:HD13	1.89	0.55
42:D:12:ARG:HG2	42:D:37:PRO:HA	1.89	0.55
1:A:202:G:H21	1:A:466:A:H61	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2134:A:H62	2:01:2156:G:N2	2.05	0.55
2:01:2295:C:O2'	2:01:2296:U:H5'	2.07	0.55
2:01:2492:U:H4'	39:Z:258:GLU:OE1	2.07	0.55
11:08:23:ILE:HD12	11:08:23:ILE:N	2.23	0.55
13:10:56:ARG:HH11	13:10:83:ALA:HB2	1.72	0.55
41:C:133:MET:HE2	41:C:167:TYR:HB2	1.89	0.55
46:H:6:ILE:N	46:H:6:ILE:HD12	2.21	0.55
1:A:1026:G:N1	1:A:1035:A:H2	2.05	0.54
2:01:941:A:H2'	2:01:942:G:O4'	2.08	0.54
2:01:1251:C:O2'	2:01:1252:G:H3'	2.05	0.54
2:01:1529:G:H2'	2:01:1530:G:C4'	2.37	0.54
20:17:30:ARG:C	20:17:30:ARG:HD2	2.32	0.54
50:L:38:THR:HG22	50:L:50:LYS:HD3	1.89	0.54
58:T:41:GLY:HA2	58:T:85:LEU:HD11	1.88	0.54
2:01:1060:U:O4'	2:01:1062:G:H5'	2.06	0.54
8:05:4:LEU:HD21	8:05:29:VAL:CG1	2.37	0.54
9:06:166:LYS:N	9:06:166:LYS:HD2	2.22	0.54
18:15:32:GLY:HA2	18:15:104:GLU:HA	1.90	0.54
42:D:12:ARG:HD3	42:D:36:ALA:O	2.07	0.54
47:I:93:LEU:HD23	47:I:93:LEU:C	2.32	0.54
51:M:16:ILE:HD12	51:M:16:ILE:N	2.20	0.54
2:01:1645:G:H5''	2:01:1646:C:H5'	1.89	0.54
2:01:1783:A:N1	2:01:2587:A:H2'	2.22	0.54
2:01:2689:U:O2	2:01:2713:U:H5''	2.07	0.54
3:02:52:A:H62	20:17:33:ARG:CB	2.21	0.54
5:X:62:C:C3'	5:X:63:G:H5''	2.37	0.54
8:05:149:ASN:O	8:05:152:PRO:HD2	2.07	0.54
12:09:135:HIS:CD2	12:09:136:SER:H	2.25	0.54
14:11:39:LYS:O	14:11:43:ALA:N	2.40	0.54
19:16:56:LYS:HB2	19:16:56:LYS:NZ	2.23	0.54
21:18:105:LYS:O	21:18:108:ARG:NH2	2.40	0.54
27:24:51:GLN:HE22	27:24:86:LEU:CG	2.20	0.54
42:D:66:VAL:C	42:D:67:LEU:HD12	2.32	0.54
42:D:191:SER:OG	42:D:194:ILE:HD13	2.07	0.54
44:F:11:HIS:HE1	44:F:83:ALA:HA	1.70	0.54
58:T:20:ASN:HD22	58:T:20:ASN:N	2.06	0.54
2:01:20:C:H2'	2:01:21:A:H8	1.73	0.54
2:01:386:G:H3'	2:01:387:U:C5'	2.38	0.54
3:02:13:G:P	28:25:72:ASN:HD21	2.30	0.54
26:23:17:ASP:HB3	26:23:20:LYS:HB3	1.88	0.54
29:26:53:LYS:HB2	29:26:53:LYS:NZ	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:17:ARG:O	39:Z:21:LEU:HD13	2.08	0.54
52:N:48:GLN:OE1	57:S:11:ASP:HA	2.06	0.54
54:P:33:ILE:N	54:P:33:ILE:HD12	2.22	0.54
1:A:674:G:H21	49:K:117:HIS:HB2	1.72	0.54
1:A:711:G:O2'	1:A:712:A:H5'	2.08	0.54
1:A:1308:U:H2'	1:A:1309:G:H8	1.72	0.54
1:A:1351:U:O4	47:I:119:LYS:HE3	2.07	0.54
2:01:7:G:H4'	15:12:15:TRP:CH2	2.42	0.54
32:29:11:GLU:HG2	32:29:25:ARG:HG2	1.90	0.54
40:B:178:LEU:HD12	40:B:178:LEU:N	2.23	0.54
45:G:73:GLU:OE2	45:G:88:VAL:HG13	2.07	0.54
50:L:113:ARG:HB2	50:L:118:VAL:HB	1.88	0.54
1:A:530:G:N2	4:Y:28:ARG:HB3	2.22	0.54
1:A:1367:C:H4'	48:J:50:THR:HG21	1.88	0.54
43:E:19:ARG:HE	43:E:30:PHE:HB3	1.72	0.54
43:E:113:VAL:HG23	43:E:114:LEU:HD12	1.90	0.54
1:A:128:G:O2'	1:A:129:A:H5'	2.08	0.54
1:A:130:A:O2'	1:A:264:C:H5'	2.07	0.54
1:A:663:A:H5'	1:A:836:G:OP1	2.08	0.54
2:01:2898:U:H2'	2:01:2899:A:C8	2.42	0.54
7:04:32:LEU:O	7:04:33:LEU:HD12	2.06	0.54
13:10:50:VAL:HG12	13:10:50:VAL:O	2.08	0.54
19:16:98:LEU:HD21	33:30:53:VAL:HG21	1.88	0.54
44:F:51:ILE:HG21	44:F:85:ILE:HG21	1.88	0.54
45:G:74:VAL:HA	45:G:87:PRO:HA	1.88	0.54
1:A:35:G:H21	50:L:114:SER:HB2	1.72	0.54
1:A:376:G:C3'	1:A:377:G:H5''	2.37	0.54
1:A:533:A:O2'	1:A:534:U:H5''	2.07	0.54
1:A:1225:A:H4'	57:S:77:ARG:NH1	2.23	0.54
2:01:131:A:H2'	2:01:132:G:H8	1.73	0.54
2:01:455:C:O2	2:01:473:G:H5'	2.08	0.54
2:01:558:U:OP1	15:12:113:PRO:HD2	2.07	0.54
2:01:1669:A:H5''	16:13:5:GLN:HE21	1.72	0.54
2:01:2328:A:H2'	2:01:2329:U:C6	2.42	0.54
22:19:90:ASP:H	23:20:11:GLN:NE2	2.05	0.54
38:V:17:U:H2'	38:V:18:G:C8	2.43	0.54
48:J:8:ILE:O	48:J:74:VAL:HG12	2.07	0.54
48:J:10:LEU:HD21	48:J:25:ILE:HD12	1.89	0.54
49:K:126:ARG:HA	49:K:126:ARG:HE	1.73	0.54
5:X:8:U:H5'	5:X:49:G:H5'	1.89	0.54
7:04:43:ASN:HD22	7:04:49:THR:HG21	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:33:ARG:HG3	8:05:51:THR:HG23	1.90	0.54
16:13:49:ARG:HD3	16:13:49:ARG:N	2.14	0.54
43:E:38:VAL:HG22	43:E:66:ALA:HB1	1.90	0.54
44:F:4:TYR:CE2	44:F:71:ILE:HG13	2.42	0.54
49:K:126:ARG:N	59:U:33:ARG:HH21	2.06	0.54
2:01:96:C:H4'	30:27:41:HIS:CG	2.42	0.54
2:01:2554:U:H2'	2:01:2555:U:C6	2.43	0.54
2:01:2724:U:H2'	2:01:2725:A:C8	2.43	0.54
7:04:22:GLU:OE1	7:04:80:LEU:HD22	2.08	0.54
8:05:33:ARG:NH2	8:05:52:THR:HA	2.23	0.54
9:06:83:VAL:HB	9:06:86:ALA:HB2	1.88	0.54
13:10:8:LYS:O	13:10:12:VAL:HG23	2.07	0.54
39:Z:322:GLN:O	39:Z:336:LEU:HD11	2.08	0.54
40:B:56:LEU:HD12	40:B:59:ILE:HD11	1.90	0.54
43:E:133:ILE:HD12	43:E:133:ILE:N	2.22	0.54
45:G:24:LYS:O	45:G:28:ILE:HG13	2.08	0.54
50:L:86:VAL:HG23	50:L:87:LYS:N	2.23	0.54
1:A:427:U:H4'	1:A:541:G:H5'	1.90	0.53
1:A:495:A:H61	42:D:119:HIS:HE1	1.54	0.53
1:A:1379:G:O2'	1:A:1380:U:H5'	2.08	0.53
2:01:1373:A:H5'	2:01:2212:A:H1'	1.89	0.53
24:21:72:THR:HG22	24:21:73:LYS:HG3	1.90	0.53
24:21:88:ARG:HG3	24:21:94:ASP:OD2	2.08	0.53
32:29:53:THR:HG21	51:M:74:MET:HG3	1.90	0.53
37:34:34:LYS:HB3	37:34:34:LYS:HZ2	1.73	0.53
46:H:6:ILE:HD12	46:H:6:ILE:H	1.71	0.53
59:U:13:VAL:HB	59:U:15:LEU:HD12	1.90	0.53
1:A:1414:U:H2'	1:A:1415:G:H8	1.73	0.53
2:01:279:A:C2'	2:01:280:U:H5'	2.38	0.53
2:01:1838:C:H4'	2:01:1839:G:H5'	1.90	0.53
2:01:2074:U:H2'	2:01:2075:U:C6	2.43	0.53
5:X:68:C:H2'	5:X:69:C:O4'	2.07	0.53
18:15:133:LYS:NZ	18:15:133:LYS:HB3	2.22	0.53
23:20:14:VAL:HG11	23:20:98:ILE:CD1	2.39	0.53
29:26:54:GLY:O	29:26:58:ILE:HG13	2.09	0.53
2:01:1057:A:O2'	13:10:34:THR:HG23	2.08	0.53
2:01:2360:G:H2'	2:01:2361:G:H5'	1.89	0.53
5:W:47:U:H4'	5:W:48:C:C5'	2.35	0.53
39:Z:333:ILE:HD12	39:Z:333:ILE:N	2.24	0.53
1:A:1210:C:H2'	1:A:1211:U:H5'	1.90	0.53
1:A:1228:C:C5'	51:M:114:PRO:HB3	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1302:C:N4	51:M:13:HIS:HD2	2.06	0.53
1:A:1356:G:H2'	1:A:1357:A:C8	2.43	0.53
2:01:20:C:H2'	2:01:21:A:C8	2.43	0.53
2:01:1979:U:O2'	2:01:1980:G:H5'	2.09	0.53
9:06:102:ARG:O	9:06:106:LYS:HG3	2.09	0.53
10:07:37:MET:CE	10:07:52:ALA:HB1	2.37	0.53
10:07:59:ILE:HD12	10:07:151:LEU:HD21	1.89	0.53
24:21:18:ARG:HH21	24:21:76:VAL:HG23	1.73	0.53
40:B:113:LEU:HD23	40:B:147:LEU:HD22	1.90	0.53
45:G:11:ILE:C	45:G:11:ILE:HD12	2.34	0.53
57:S:39:ILE:HG23	57:S:43:MET:SD	2.48	0.53
1:A:195:A:H2'	1:A:196:A:C8	2.43	0.53
1:A:225:C:H3'	1:A:226:G:H5''	1.89	0.53
1:A:1313:U:OP2	57:S:5:LYS:HA	2.09	0.53
2:01:399:U:H2'	2:01:400:G:O4'	2.09	0.53
2:01:536:G:H4'	22:19:56:PHE:CZ	2.43	0.53
2:01:594:U:H2'	2:01:595:C:C6	2.44	0.53
2:01:1111:A:H3'	2:01:1111:A:N3	2.24	0.53
2:01:2136:G:H2'	2:01:2137:U:H5''	1.90	0.53
2:01:2177:C:C2	6:03:170:ILE:HG21	2.44	0.53
2:01:2286:G:H4'	2:01:2287:A:O4'	2.08	0.53
10:07:136:ILE:C	10:07:136:ILE:HD12	2.34	0.53
11:08:106:LEU:HB3	11:08:151:ARG:HD3	1.90	0.53
13:10:4:ASN:HA	13:10:7:ASP:HB2	1.90	0.53
42:D:191:SER:O	42:D:193:ASP:N	2.39	0.53
43:E:110:MET:O	43:E:114:LEU:HD13	2.08	0.53
51:M:106:ARG:NH1	51:M:112:ARG:HA	2.23	0.53
52:N:84:ARG:HG2	52:N:84:ARG:NH1	2.24	0.53
57:S:12:LEU:HD23	57:S:12:LEU:O	2.09	0.53
3:02:65:U:H3'	3:02:108:A:N6	2.23	0.53
7:04:7:PRO:HB2	7:04:13:ARG:NH1	2.23	0.53
7:04:140:VAL:O	7:04:161:VAL:N	2.40	0.53
14:11:97:VAL:HG12	14:11:98:GLY:N	2.23	0.53
16:13:41:ILE:HD11	16:13:86:LEU:CD2	2.39	0.53
19:16:98:LEU:HD11	33:30:48:TYR:CD2	2.42	0.53
22:19:23:TYR:HB2	22:19:28:SER:HB3	1.91	0.53
23:20:74:ILE:N	23:20:74:ILE:HD12	2.24	0.53
36:33:32:LEU:CD2	36:33:35:LYS:HD2	2.38	0.53
39:Z:307:LYS:O	39:Z:311:GLU:HG2	2.09	0.53
40:B:91:VAL:CG2	40:B:99:MET:HE1	2.36	0.53
42:D:103:ARG:HB2	42:D:170:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:F:81:ASN:OD1	44:F:83:ALA:HB3	2.09	0.53
47:I:115:VAL:HG21	48:J:62:ARG:CG	2.39	0.53
49:K:125:LYS:C	49:K:126:ARG:HG2	2.33	0.53
52:N:55:SER:CB	52:N:56:PRO:HD3	2.38	0.53
1:A:784:A:H2'	1:A:785:G:H8	1.73	0.53
2:01:2050:C:O2	8:05:161:MET:HE1	2.08	0.53
11:08:85:LYS:C	11:08:86:LEU:HD12	2.33	0.53
15:12:98:GLU:OE1	15:12:126:ALA:HB2	2.08	0.53
35:32:12:ARG:HH21	35:32:12:ARG:HB2	1.73	0.53
39:Z:322:GLN:HB2	39:Z:336:LEU:HD21	1.91	0.53
42:D:96:ARG:O	42:D:100:VAL:HG23	2.08	0.53
48:J:26:VAL:HG13	48:J:36:VAL:HG11	1.90	0.53
53:O:86:LEU:HD23	53:O:86:LEU:N	2.24	0.53
59:U:16:ARG:O	59:U:16:ARG:HD3	2.09	0.53
1:A:17:U:H2'	1:A:18:C:C6	2.43	0.53
2:01:1071:G:H1'	2:01:1089:A:C5	2.43	0.53
2:01:2529:G:H5''	2:01:2530:A:H5''	1.90	0.53
6:03:11:ILE:HD12	6:03:12:ARG:N	2.24	0.53
6:03:201:PRO:HG2	6:03:204:ALA:HB2	1.89	0.53
42:D:59:LYS:O	42:D:63:ILE:HG13	2.08	0.53
10:07:59:ILE:HD13	10:07:151:LEU:HD21	1.89	0.53
10:07:87:LYS:HB3	10:07:87:LYS:HZ3	1.73	0.53
16:13:86:LEU:C	16:13:87:LEU:HD12	2.34	0.53
26:23:51:LEU:HD12	26:23:51:LEU:N	2.20	0.53
43:E:98:ALA:HB2	43:E:123:LEU:HG	1.91	0.53
51:M:76:ILE:HG22	51:M:80:MET:SD	2.48	0.53
58:T:24:ARG:O	58:T:28:ARG:HG3	2.09	0.53
1:A:427:U:H2'	1:A:428:G:C8	2.44	0.53
2:01:2111:U:H2'	2:01:2112:G:H5'	1.91	0.53
2:01:2642:G:H5'	15:12:80:HIS:CD2	2.43	0.53
27:24:80:HIS:CD2	27:24:81:PRO:HD2	2.44	0.53
28:25:41:PHE:O	28:25:55:LEU:HD11	2.09	0.53
40:B:34:ARG:HD2	40:B:35:ASN:ND2	2.23	0.53
48:J:17:LEU:HD23	48:J:17:LEU:C	2.34	0.53
49:K:22:ILE:HB	49:K:85:VAL:HA	1.91	0.53
2:01:96:C:H4'	30:27:41:HIS:CD2	2.44	0.52
2:01:669:G:H2'	2:01:669:G:N3	2.24	0.52
2:01:995:C:H6	2:01:995:C:H5'	1.74	0.52
2:01:2800:A:H3'	2:01:2801:G:H5'	1.89	0.52
2:01:2834:G:H2'	2:01:2879:A:H61	1.74	0.52
5:X:4:G:H2'	5:X:5:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:26:G:N3	5:X:26:G:H2'	2.23	0.52
12:09:43:ASN:HA	12:09:46:PHE:HB2	1.90	0.52
36:33:30:HIS:ND1	36:33:31:ILE:HG13	2.24	0.52
39:Z:291:MET:CE	39:Z:295:LEU:HB2	2.39	0.52
43:E:13:LYS:HE2	43:E:115:GLU:OE2	2.09	0.52
47:I:24:ASN:HD22	47:I:26:LYS:HG3	1.75	0.52
49:K:86:LYS:HE3	49:K:114:PRO:CG	2.39	0.52
1:A:831:A:C3'	1:A:832:G:H5''	2.39	0.52
1:A:950:U:H2'	1:A:951:G:H8	1.75	0.52
1:A:988:G:H1'	1:A:1015:G:H22	1.73	0.52
1:A:1240:U:H4'	45:G:37:THR:HG21	1.89	0.52
2:01:112:U:H2'	2:01:113:U:H5'	1.91	0.52
2:01:1213:A:N6	2:01:1236:G:H1'	2.23	0.52
2:01:1243:C:H1'	17:14:4:ASN:O	2.10	0.52
2:01:2345:G:N3	2:01:2381:A:H2'	2.24	0.52
18:15:20:LEU:HD13	27:24:81:PRO:HG2	1.90	0.52
48:J:42:LEU:HB2	48:J:71:LEU:HB2	1.91	0.52
1:A:72:A:H61	1:A:98:A:H2	1.56	0.52
1:A:1367:C:H5''	47:I:115:VAL:HG23	1.91	0.52
2:01:917:A:H5''	2:01:2268:A:H61	1.74	0.52
2:01:1139:G:O2'	2:01:1140:C:H5'	2.09	0.52
2:01:1529:G:H3'	2:01:1530:G:H5''	1.92	0.52
2:01:2475:C:H2'	2:01:2476:A:H5'	1.90	0.52
6:03:208:TYR:CD2	6:03:209:ILE:HG23	2.45	0.52
26:23:86:PHE:CE1	26:23:91:LYS:HB3	2.43	0.52
29:26:38:TRP:HE1	29:26:40:GLU:HG2	1.74	0.52
32:29:57:VAL:HG22	57:S:66:VAL:HG11	1.92	0.52
39:Z:307:LYS:HB2	39:Z:307:LYS:HZ3	1.74	0.52
40:B:29:PHE:HA	40:B:44:LYS:HD3	1.91	0.52
48:J:7:ARG:C	48:J:8:ILE:HD12	2.34	0.52
51:M:29:SER:O	51:M:33:LEU:HD13	2.09	0.52
53:O:34:GLN:O	53:O:38:LEU:HD13	2.10	0.52
1:A:509:A:H1'	42:D:54:LEU:CD2	2.38	0.52
1:A:1259:C:H3'	1:A:1260:G:C5'	2.33	0.52
2:01:242:G:H5''	36:33:63:TYR:CE2	2.44	0.52
2:01:864:G:O2'	2:01:865:C:H5'	2.10	0.52
2:01:2394:C:H5''	17:14:63:LYS:HD3	1.91	0.52
2:01:2836:U:H2'	2:01:2837:A:H8	1.73	0.52
5:X:27:U:H2'	5:X:28:C:C6	2.44	0.52
7:04:143:VAL:HB	7:04:153:LEU:HB2	1.92	0.52
7:04:226:PRO:HD3	7:04:233:GLY:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:17:4:LYS:O	20:17:8:ILE:HD13	2.09	0.52
21:18:26:GLU:HG2	21:18:43:GLU:HG2	1.92	0.52
32:29:60:PHE:O	32:29:64:PHE:N	2.36	0.52
37:34:30:GLU:C	37:34:32:LYS:H	2.17	0.52
51:M:14:ALA:HA	51:M:44:ILE:HD11	1.91	0.52
1:A:40:C:H2'	1:A:41:G:C5'	2.34	0.52
1:A:147:G:H2'	1:A:148:G:C8	2.45	0.52
1:A:191:G:H2'	1:A:192:A:C8	2.44	0.52
1:A:1422:G:H5'	16:13:48:PRO:HB3	1.92	0.52
1:A:1513:A:H2'	1:A:1514:G:C8	2.45	0.52
2:01:948:C:H2'	2:01:949:G:H8	1.74	0.52
15:12:120:ARG:HH21	15:12:120:ARG:HG2	1.74	0.52
25:22:61:LEU:HD23	25:22:82:LYS:HD2	1.91	0.52
44:F:18:VAL:HG13	44:F:19:PRO:HD3	1.91	0.52
49:K:60:PHE:O	49:K:64:VAL:HG23	2.10	0.52
55:Q:31:PRO:HG2	55:Q:32:ILE:CD1	2.38	0.52
1:A:335:C:H2'	1:A:336:A:C8	2.44	0.52
1:A:982:U:H4'	1:A:983:A:O4'	2.09	0.52
2:01:2094:A:H3'	2:01:2095:A:H5''	1.91	0.52
10:07:33:ILE:HG12	10:07:95:MET:HG3	1.92	0.52
11:08:163:TYR:HB2	11:08:166:GLU:HB2	1.92	0.52
30:27:24:GLU:O	30:27:28:LEU:HD13	2.10	0.52
43:E:47:PHE:HD1	43:E:47:PHE:H	1.56	0.52
51:M:106:ARG:NE	51:M:106:ARG:HA	2.25	0.52
51:M:106:ARG:HH11	51:M:112:ARG:HA	1.75	0.52
1:A:1261:A:H1'	1:A:1283:U:H5''	1.92	0.52
2:01:535:G:O2'	22:19:52:ARG:HG2	2.09	0.52
2:01:1319:C:O2'	2:01:1320:C:H5'	2.10	0.52
20:17:7:ARG:HD2	20:17:97:PHE:CZ	2.45	0.52
20:17:12:THR:HA	20:17:15:ARG:HB3	1.91	0.52
25:22:40:LYS:HE3	25:22:58:VAL:O	2.10	0.52
58:T:2:ASN:OD1	58:T:3:ILE:HG12	2.09	0.52
1:A:543:U:OP1	42:D:13:ARG:HG3	2.10	0.52
1:A:860:A:H2'	1:A:861:G:O4'	2.09	0.52
1:A:939:G:H2'	1:A:940:C:C6	2.45	0.52
2:01:320:A:H4'	2:01:322:A:N7	2.25	0.52
2:01:538:A:H5''	15:12:7:LYS:HE2	1.90	0.52
2:01:1357:C:H2'	2:01:1358:G:O4'	2.09	0.52
2:01:1709:U:H2'	2:01:1710:G:H8	1.75	0.52
11:08:70:LEU:O	11:08:74:MET:HG3	2.09	0.52
17:14:96:LYS:HE2	17:14:103:ILE:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:19:59:LEU:HD23	22:19:59:LEU:C	2.35	0.52
37:34:24:ARG:HG2	37:34:36:ARG:HA	1.91	0.52
39:Z:196:THR:CG2	39:Z:222:VAL:HG22	2.40	0.52
50:L:23:LEU:O	50:L:24:GLU:HB2	2.10	0.52
57:S:27:LYS:HB3	57:S:27:LYS:HZ2	1.75	0.52
2:01:885:C:H41	2:01:887:U:H1'	1.75	0.52
2:01:1300:G:H4'	2:01:1301:A:H5'	1.91	0.52
3:02:49:C:OP1	20:17:102:ARG:HG2	2.09	0.52
7:04:70:LYS:HB2	7:04:70:LYS:HZ3	1.73	0.52
7:04:85:ASN:HD22	7:04:85:ASN:N	2.06	0.52
9:06:156:ASN:HD22	9:06:156:ASN:N	2.07	0.52
11:08:104:LEU:HB2	11:08:112:VAL:HB	1.92	0.52
12:09:77:THR:O	12:09:77:THR:HG23	2.10	0.52
17:14:103:ILE:HD12	17:14:104:GLN:H	1.74	0.52
42:D:204:SER:HB3	43:E:105:ILE:HD12	1.92	0.52
51:M:33:LEU:HD23	51:M:40:GLU:HA	1.92	0.52
1:A:870:U:H4'	1:A:872:A:OP2	2.09	0.52
1:A:1219:A:OP1	52:N:52:ARG:HG2	2.10	0.52
1:A:1316:G:H2'	1:A:1317:C:H5''	1.91	0.52
6:03:184:LYS:O	6:03:188:ASN:N	2.43	0.52
19:16:116:VAL:HG12	19:16:117:ASP:N	2.24	0.52
28:25:42:HIS:CD2	28:25:73:ARG:HD3	2.44	0.52
31:28:7:THR:HG22	31:28:34:THR:HG23	1.92	0.52
39:Z:202:VAL:HB	39:Z:327:VAL:HA	1.92	0.52
1:A:131:A:H2'	1:A:132:C:C6	2.44	0.51
2:01:644:A:H2'	2:01:645:C:H4'	1.92	0.51
2:01:834:G:H1'	2:01:2358:A:N3	2.26	0.51
2:01:1930:G:N2	2:01:1968:G:H2'	2.25	0.51
6:03:169:GLY:C	6:03:170:ILE:HD12	2.36	0.51
14:11:14:ALA:H	14:11:53:PRO:HA	1.74	0.51
25:22:48:GLN:HE21	25:22:49:LYS:NZ	2.07	0.51
41:C:9:ILE:HG23	41:C:10:ARG:HG3	1.92	0.51
45:G:135:LYS:HG2	45:G:139:ASP:OD2	2.10	0.51
45:G:136:LYS:HA	45:G:139:ASP:HB2	1.92	0.51
49:K:27:ASN:O	49:K:56:LYS:HG3	2.09	0.51
50:L:29:LYS:O	50:L:80:LEU:HD12	2.11	0.51
59:U:20:ARG:HA	59:U:24:LYS:HB2	1.91	0.51
2:01:397:U:H5''	29:26:31:ASN:HB2	1.92	0.51
2:01:2305:U:H5''	10:07:130:GLY:HA3	1.91	0.51
2:01:2712:C:OP1	2:01:2714:G:H4'	2.10	0.51
42:D:58:GLN:O	42:D:62:ARG:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M:33:LEU:O	51:M:38:ILE:N	2.41	0.51
54:P:71:VAL:O	54:P:75:ILE:HG13	2.10	0.51
58:T:70:LYS:HA	58:T:73:ARG:NH1	2.25	0.51
1:A:1477:U:H2'	1:A:1478:U:C6	2.44	0.51
2:01:121:G:H4'	2:01:149:A:H5'	1.91	0.51
2:01:1151:A:H4'	22:19:80:ASN:OD1	2.10	0.51
2:01:1373:A:C5'	2:01:2212:A:H1'	2.40	0.51
2:01:1428:C:O2'	2:01:1429:G:H5'	2.11	0.51
2:01:1753:G:H5''	21:18:92:ARG:HD3	1.91	0.51
3:02:12:C:N3	28:25:70:PRO:HB3	2.25	0.51
15:12:37:ARG:HH21	15:12:118:MET:HE1	1.74	0.51
17:14:51:GLU:OE2	36:33:56:LEU:HD13	2.11	0.51
19:16:9:GLN:HA	19:16:17:ARG:HH21	1.74	0.51
40:B:96:LEU:O	40:B:99:MET:HG2	2.10	0.51
41:C:59:PRO:HG3	41:C:64:ARG:CZ	2.40	0.51
56:R:29:LYS:HA	56:R:32:ILE:HG12	1.92	0.51
1:A:736:C:H2'	1:A:737:C:C6	2.45	0.51
2:01:948:C:H2'	2:01:949:G:C8	2.45	0.51
2:01:2015:A:H5'	24:21:92:ARG:HH22	1.75	0.51
7:04:140:VAL:HG13	7:04:191:LEU:HA	1.92	0.51
13:10:97:LYS:HB2	13:10:129:LEU:HD11	1.92	0.51
13:10:119:PRO:HG2	13:10:120:ALA:N	2.24	0.51
19:16:47:VAL:C	19:16:50:PRO:HD2	2.35	0.51
30:27:24:GLU:HA	30:27:28:LEU:HD13	1.93	0.51
35:32:24:THR:HG23	35:32:27:GLY:H	1.76	0.51
41:C:156:LEU:HD12	41:C:156:LEU:H	1.74	0.51
42:D:137:SER:HB2	42:D:140:ASP:OD2	2.10	0.51
46:H:12:ARG:NH1	46:H:26:MET:HB3	2.26	0.51
51:M:28:ARG:O	51:M:32:ILE:HG12	2.10	0.51
52:N:23:ARG:HH11	52:N:50:LEU:HD11	1.75	0.51
53:O:31:LEU:O	53:O:35:ILE:HG12	2.10	0.51
2:01:2530:A:N6	11:08:155:PRO:HG3	2.26	0.51
3:02:7:G:H5'	20:17:29:HIS:CE1	2.46	0.51
12:09:4:ILE:HG13	12:09:39:ALA:HB2	1.93	0.51
13:10:122:GLN:O	13:10:124:ASP:N	2.43	0.51
15:12:84:ILE:HG23	15:12:84:ILE:O	2.11	0.51
39:Z:5:ASN:HD22	39:Z:6:PRO:CD	2.23	0.51
40:B:23:ASN:ND2	40:B:25:LYS:HB2	2.25	0.51
49:K:106:ILE:HD12	49:K:106:ILE:N	2.25	0.51
1:A:357:G:H2'	1:A:358:U:C5'	2.35	0.51
2:01:226:A:H2'	2:01:227:A:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2105:U:C2'	2:01:2106:U:H5'	2.41	0.51
7:04:48:ILE:O	7:04:48:ILE:HG23	2.09	0.51
19:16:83:LEU:HD22	19:16:87:PHE:HE2	1.76	0.51
22:19:59:LEU:HD21	22:19:63:ARG:NE	2.20	0.51
26:23:10:VAL:HG12	26:23:71:ILE:HA	1.93	0.51
31:28:52:PHE:CZ	31:28:53:MET:HE2	2.46	0.51
40:B:35:ASN:N	40:B:35:ASN:ND2	2.59	0.51
44:F:49:TYR:CE1	56:R:65:SER:HA	2.46	0.51
52:N:33:VAL:HG23	52:N:33:VAL:O	2.10	0.51
55:Q:18:LYS:HG2	55:Q:46:HIS:CE1	2.45	0.51
1:A:1238:A:C2	1:A:1241:G:H1'	2.46	0.51
3:02:12:C:N4	28:25:70:PRO:HB3	2.25	0.51
3:02:53:A:H2'	3:02:53:A:N3	2.26	0.51
18:15:42:THR:HA	18:15:93:VAL:HA	1.91	0.51
18:15:51:ARG:HB3	18:15:55:ARG:HH22	1.75	0.51
21:18:71:ARG:HH11	21:18:71:ARG:HG3	1.76	0.51
39:Z:117:ARG:HH21	39:Z:358:GLU:HA	1.76	0.51
49:K:36:ARG:NH1	49:K:36:ARG:HB3	2.25	0.51
50:L:41:PRO:HB3	50:L:88:ASP:OD2	2.10	0.51
1:A:108:G:H1	58:T:9:ARG:HG2	1.76	0.51
1:A:346:G:C2'	1:A:347:G:H5'	2.41	0.51
1:A:875:U:O2'	46:H:14:ARG:HD2	2.11	0.51
1:A:1259:C:C3'	1:A:1260:G:H5''	2.33	0.51
1:A:1308:U:H2'	1:A:1309:G:C8	2.46	0.51
3:02:12:C:C4	28:25:70:PRO:HB3	2.45	0.51
9:06:57:LYS:HB3	9:06:57:LYS:NZ	2.25	0.51
16:13:102:PRO:HB3	16:13:121:GLU:HB3	1.92	0.51
18:15:14:LYS:HE2	18:15:40:ARG:HH12	1.76	0.51
18:15:59:ARG:HG3	18:15:59:ARG:NH2	2.24	0.51
25:22:28:ASN:OD1	25:22:87:LEU:HB2	2.11	0.51
40:B:26:MET:HE2	40:B:187:ASP:O	2.10	0.51
40:B:178:LEU:HD22	40:B:180:ILE:HD11	1.92	0.51
41:C:22:PHE:CD2	48:J:97:ASP:HB2	2.44	0.51
42:D:25:ARG:HH12	42:D:30:LYS:NZ	2.08	0.51
52:N:52:ARG:NH1	57:S:36:ARG:HH22	2.08	0.51
1:A:356:A:H2'	1:A:357:G:O4'	2.11	0.51
1:A:560:A:H5'	1:A:566:G:N2	2.26	0.51
1:A:1103:C:O2	40:B:105:THR:HG21	2.11	0.51
1:A:1314:C:OP1	57:S:5:LYS:HD3	2.11	0.51
2:01:1755:A:H2'	2:01:1756:G:H5'	1.92	0.51
2:01:2317:A:H2'	2:01:2318:G:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:04:131:MET:CE	7:04:187:CYS:HB2	2.41	0.51
10:07:61:GLY:O	32:29:7:PRO:HD2	2.10	0.51
12:09:2:GLN:HG3	12:09:39:ALA:HB3	1.93	0.51
12:09:5:LEU:HD12	12:09:5:LEU:N	2.25	0.51
15:12:95:ARG:HG2	15:12:95:ARG:HH11	1.75	0.51
21:18:33:GLU:OE1	21:18:38:ARG:HD3	2.09	0.51
29:26:17:ARG:HH21	29:26:21:LEU:HB3	1.75	0.51
39:Z:74:LYS:HD2	39:Z:77:LEU:HD12	1.93	0.51
56:R:21:ASP:OD2	56:R:23:LYS:HB2	2.11	0.51
1:A:831:A:H3'	1:A:832:G:H5''	1.93	0.51
1:A:1287:A:H2'	1:A:1288:A:C8	2.46	0.51
1:A:1527:U:O2'	1:A:1528:U:H5'	2.10	0.51
2:01:2281:A:O2'	2:01:2282:G:H5'	2.11	0.51
2:01:2512:C:H2'	2:01:2513:A:O4'	2.11	0.51
5:X:4:G:H2'	5:X:5:G:H8	1.75	0.51
6:03:128:GLY:O	6:03:132:GLY:N	2.42	0.51
45:G:22:LEU:O	45:G:26:VAL:HG23	2.11	0.51
46:H:9:MET:HG3	46:H:26:MET:SD	2.51	0.51
1:A:56:U:H2'	1:A:57:G:H8	1.77	0.50
2:01:580:U:O3'	22:19:30:VAL:HG13	2.10	0.50
2:01:1061:U:O2	14:11:12:VAL:HG12	2.11	0.50
2:01:1856:U:C2'	2:01:1857:G:H5'	2.41	0.50
2:01:2177:C:O2	2:01:2177:C:C2'	2.59	0.50
23:20:2:TYR:H	23:20:2:TYR:HD1	1.60	0.50
36:33:16:THR:OG1	36:33:48:MET:HE1	2.10	0.50
42:D:2:ARG:O	42:D:4:LEU:HD13	2.11	0.50
1:A:8:A:C8	43:E:105:ILE:HG13	2.46	0.50
1:A:1371:G:O3'	47:I:70:GLY:HA3	2.11	0.50
2:01:226:A:H2'	2:01:227:A:C8	2.46	0.50
2:01:661:A:H5'	17:14:13:LYS:NZ	2.27	0.50
2:01:1856:U:H2'	2:01:1857:G:H5'	1.92	0.50
2:01:1900:A:H1'	2:01:1970:A:H2'	1.94	0.50
3:02:30:C:H2'	3:02:31:C:H5'	1.93	0.50
8:05:122:VAL:HG21	8:05:141:ARG:CG	2.41	0.50
16:13:2:ILE:O	16:13:33:ALA:N	2.43	0.50
17:14:39:LYS:HD2	17:14:45:GLY:HA2	1.92	0.50
29:26:77:TYR:HD1	29:26:77:TYR:H	1.59	0.50
40:B:17:HIS:HB3	40:B:37:VAL:HB	1.92	0.50
41:C:139:ASN:HD22	41:C:139:ASN:N	2.09	0.50
2:01:225:C:H2'	2:01:226:A:O4'	2.11	0.50
2:01:1079:C:H2'	2:01:1080:A:C8	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1094:U:H2'	2:01:1096:A:OP2	2.12	0.50
2:01:1424:G:H2'	2:01:1425:G:O4'	2.12	0.50
2:01:1669:A:O4'	16:13:5:GLN:HG3	2.11	0.50
2:01:2230:G:H2'	2:01:2231:U:C6	2.46	0.50
2:01:2383:G:O2'	2:01:2384:U:H5'	2.11	0.50
17:14:63:LYS:HE3	36:33:11:LYS:HD3	1.92	0.50
18:15:74:THR:HG21	18:15:86:LYS:HE2	1.94	0.50
27:24:76:ASP:HB2	27:24:90:ASP:OD2	2.10	0.50
32:29:9:TYR:OH	32:29:25:ARG:HD3	2.12	0.50
43:E:37:VAL:HG21	43:E:113:VAL:HG12	1.93	0.50
1:A:31:G:N1	1:A:48:C:H5''	2.27	0.50
1:A:50:A:H4'	1:A:51:A:H5'	1.93	0.50
2:01:533:G:H5'	22:19:23:TYR:CD1	2.47	0.50
2:01:2249:U:H3'	2:01:2250:G:H5'	1.94	0.50
2:01:2898:U:H2'	2:01:2899:A:H8	1.76	0.50
9:06:186:VAL:HG23	9:06:186:VAL:O	2.11	0.50
10:07:111:ARG:HG2	10:07:112:ASP:OD2	2.11	0.50
21:18:47:ILE:HG23	21:18:96:LEU:O	2.11	0.50
22:19:34:ALA:O	22:19:38:VAL:HG23	2.11	0.50
26:23:81:ARG:CD	26:23:96:LYS:HD2	2.37	0.50
27:24:80:HIS:HD2	27:24:81:PRO:HD2	1.75	0.50
28:25:36:GLN:HE21	28:25:40:LYS:HB3	1.77	0.50
29:26:31:ASN:ND2	29:26:33:HIS:HE1	2.09	0.50
47:I:31:GLN:NE2	47:I:31:GLN:N	2.59	0.50
47:I:82:ILE:O	47:I:86:LEU:HG	2.12	0.50
1:A:1344:C:O2'	1:A:1345:U:H5'	2.12	0.50
2:01:712:G:P	53:O:88:ARG:HH12	2.34	0.50
2:01:873:C:H2'	2:01:874:G:C8	2.46	0.50
2:01:898:C:H2'	2:01:899:A:O4'	2.12	0.50
2:01:1027:A:C2	2:01:2488:G:H4'	2.47	0.50
2:01:2529:G:H4'	11:08:174:LYS:CD	2.42	0.50
2:01:2723:C:OP1	8:05:114:LYS:HD2	2.12	0.50
6:03:30:LEU:HD12	6:03:33:LEU:HD12	1.92	0.50
7:04:123:ILE:HG23	7:04:191:LEU:CD1	2.41	0.50
35:32:19:ARG:HG2	35:32:19:ARG:HH21	1.77	0.50
40:B:23:ASN:HD21	40:B:25:LYS:HB2	1.76	0.50
46:H:8:ASP:O	46:H:12:ARG:HG2	2.12	0.50
46:H:104:SER:OG	46:H:125:ILE:HD11	2.11	0.50
1:A:1219:A:H2'	1:A:1220:G:H8	1.77	0.50
2:01:671:C:H2'	2:01:672:C:C6	2.47	0.50
2:01:771:G:OP1	35:32:14:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1079:C:H4'	14:11:133:ARG:HH21	1.76	0.50
2:01:2114:A:N3	2:01:2114:A:H2'	2.26	0.50
2:01:2584:U:H2'	2:01:2585:U:H5''	1.91	0.50
12:09:58:LEU:O	12:09:58:LEU:HD13	2.12	0.50
43:E:14:LEU:HD23	43:E:15:ILE:N	2.27	0.50
55:Q:20:ILE:HG22	55:Q:45:VAL:O	2.11	0.50
2:01:1666:G:H4'	16:13:6:THR:HG23	1.94	0.50
2:01:1727:C:H2'	2:01:1728:C:C5'	2.38	0.50
2:01:2636:C:H4'	8:05:81:GLU:CD	2.37	0.50
9:06:32:VAL:HG11	17:14:6:LEU:HD13	1.93	0.50
11:08:5:LYS:HB2	11:08:5:LYS:NZ	2.27	0.50
11:08:106:LEU:HB3	11:08:151:ARG:CD	2.42	0.50
40:B:26:MET:SD	40:B:192:PRO:HG3	2.52	0.50
51:M:71:GLU:O	51:M:75:SER:N	2.41	0.50
2:01:125:A:H4'	35:32:13:ASN:O	2.11	0.50
2:01:671:C:OP1	17:14:43:GLY:N	2.33	0.50
10:07:152:ASP:C	10:07:153:ILE:HD12	2.37	0.50
21:18:16:VAL:HG21	21:18:76:HIS:CE1	2.47	0.50
43:E:88:HIS:CD2	43:E:137:ARG:HD2	2.47	0.50
44:F:18:VAL:O	44:F:22:ILE:HG13	2.12	0.50
49:K:92:ARG:HH22	49:K:111:ASP:CG	2.19	0.50
53:O:54:GLY:O	53:O:58:MET:HG3	2.11	0.50
55:Q:13:SER:HB2	55:Q:21:VAL:HB	1.93	0.50
55:Q:24:ILE:HD11	55:Q:60:ILE:HD11	1.93	0.50
2:01:146:A:H2'	2:01:147:C:C6	2.47	0.50
2:01:528:A:H3'	15:12:116:ARG:NH2	2.27	0.50
2:01:1069:A:OP1	2:01:1070:A:H8	1.95	0.50
2:01:1965:C:H5''	2:01:1966:A:H2'	1.93	0.50
10:07:42:ALA:HB3	10:07:84:ILE:HD12	1.93	0.50
10:07:63:LYS:HD3	32:29:5:ILE:HB	1.94	0.50
13:10:44:ALA:O	13:10:49:GLY:N	2.45	0.50
13:10:56:ARG:HG2	13:10:82:ILE:C	2.37	0.50
19:16:67:PHE:O	19:16:71:ARG:HD2	2.12	0.50
39:Z:128:CYS:HB3	39:Z:189:TYR:HB2	1.94	0.50
41:C:55:VAL:CG1	41:C:66:THR:HB	2.42	0.50
43:E:51:LYS:H	43:E:61:LYS:HD3	1.77	0.50
44:F:64:VAL:HG22	44:F:65:GLU:N	2.26	0.50
54:P:68:SER:HB3	54:P:71:VAL:HG23	1.93	0.50
55:Q:22:VAL:HG22	55:Q:23:ALA:N	2.27	0.50
55:Q:67:SER:HB3	55:Q:70:LYS:HB3	1.94	0.50
2:01:676:A:H62	2:01:802:A:H61	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1571:A:H2'	2:01:1572:A:C8	2.47	0.49
2:01:2455:G:H2'	2:01:2456:C:C6	2.47	0.49
2:01:2636:C:H4'	8:05:81:GLU:OE2	2.12	0.49
6:03:194:VAL:O	6:03:198:LYS:N	2.43	0.49
12:09:5:LEU:C	12:09:6:LEU:HD12	2.37	0.49
16:13:38:ILE:HD11	16:13:112:PHE:HZ	1.77	0.49
18:15:31:PHE:HB3	18:15:130:PHE:CE1	2.47	0.49
42:D:170:LEU:HD12	42:D:170:LEU:O	2.11	0.49
54:P:3:THR:HA	54:P:66:THR:H	1.77	0.49
1:A:162:A:H2'	1:A:163:C:O4'	2.12	0.49
1:A:831:A:H5''	40:B:20:ARG:HE	1.77	0.49
1:A:1173:U:H2'	1:A:1174:G:H8	1.77	0.49
2:01:38:A:H4'	9:06:45:ALA:CB	2.43	0.49
2:01:1657:U:H2'	2:01:1658:C:C6	2.47	0.49
2:01:2086:U:H2'	2:01:2087:G:C8	2.46	0.49
7:04:25:LYS:HD3	7:04:25:LYS:N	2.20	0.49
11:08:152:ARG:H	11:08:152:ARG:CD	2.23	0.49
17:14:82:LEU:HB3	17:14:120:VAL:HG21	1.93	0.49
20:17:66:GLY:HA2	20:17:102:ARG:HH12	1.77	0.49
23:20:41:ILE:HD12	23:20:54:VAL:HG11	1.93	0.49
26:23:84:PHE:CE1	26:23:93:ARG:HG2	2.47	0.49
39:Z:148:LEU:HD21	39:Z:199:HIS:CD2	2.47	0.49
42:D:45:PRO:HG2	42:D:47:LEU:HD11	1.94	0.49
1:A:314:C:O2'	1:A:315:A:H5'	2.12	0.49
1:A:1401:G:H2'	1:A:1402:C:O4'	2.11	0.49
2:01:215:G:O3'	2:01:216:A:H4'	2.13	0.49
5:X:69:C:H2'	5:X:70:G:C8	2.48	0.49
22:19:65:ASN:O	22:19:69:ARG:HG3	2.12	0.49
30:27:6:LEU:HD11	30:27:59:GLU:OE2	2.12	0.49
36:33:30:HIS:O	36:33:32:LEU:HG	2.12	0.49
39:Z:234:ILE:O	39:Z:234:ILE:HG12	2.12	0.49
39:Z:337:ARG:HG2	39:Z:337:ARG:HH11	1.77	0.49
41:C:19:SER:HB3	41:C:21:TRP:HE1	1.76	0.49
55:Q:18:LYS:H	55:Q:50:ASN:HD21	1.59	0.49
57:S:49:ALA:HA	57:S:58:PRO:HA	1.93	0.49
1:A:346:G:H2'	1:A:347:G:H5'	1.94	0.49
1:A:427:U:H4'	1:A:541:G:C5'	2.42	0.49
1:A:1162:C:H2'	1:A:1163:A:C8	2.46	0.49
2:01:473:G:O2'	2:01:474:G:H5'	2.12	0.49
2:01:1570:A:H2'	2:01:1571:A:C8	2.47	0.49
2:01:2733:A:N1	8:05:208:LYS:HB2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2807:U:C3'	2:01:2808:G:H5''	2.39	0.49
3:02:90:C:H5'	18:15:18:ARG:HG2	1.94	0.49
9:06:130:LYS:HB2	9:06:133:LEU:HG	1.94	0.49
16:13:116:ILE:HD12	16:13:116:ILE:N	2.27	0.49
20:17:106:LEU:HD23	20:17:106:LEU:C	2.37	0.49
23:20:101:ILE:HG12	23:20:102:SER:N	2.26	0.49
37:34:18:LYS:HG2	37:34:21:GLY:HA2	1.93	0.49
44:F:67:PRO:HG2	44:F:70:VAL:HG23	1.93	0.49
49:K:86:LYS:HE3	49:K:114:PRO:HG2	1.95	0.49
54:P:58:ALA:HA	54:P:61:VAL:HG12	1.95	0.49
1:A:1329:A:O2'	1:A:1330:U:H5'	2.13	0.49
2:01:807:U:H2'	2:01:808:G:C8	2.48	0.49
2:01:2189:U:H2'	2:01:2190:G:H8	1.77	0.49
2:01:2619:C:O2'	2:01:2620:C:H5'	2.12	0.49
7:04:153:LEU:HD13	7:04:175:LEU:HD21	1.94	0.49
11:08:102:ILE:HD11	11:08:116:LEU:HD21	1.94	0.49
13:10:61:ARG:HD3	13:10:61:ARG:N	2.27	0.49
15:12:102:GLU:HG2	15:12:119:PHE:CZ	2.47	0.49
24:21:51:LEU:O	24:21:55:ILE:HG12	2.12	0.49
28:25:8:ASN:HA	28:25:10:ARG:NH1	2.27	0.49
45:G:110:ARG:NH1	45:G:121:ASN:HB3	2.27	0.49
2:01:414:C:H2'	2:01:415:A:C8	2.48	0.49
2:01:1434:A:H2'	2:01:1435:G:C8	2.48	0.49
2:01:2282:G:H4'	2:01:2389:G:O2'	2.12	0.49
7:04:75:ALA:HB2	7:04:95:TYR:CD1	2.47	0.49
8:05:77:ARG:NH2	8:05:80:TRP:HH2	2.11	0.49
14:11:8:VAL:HB	14:11:10:LEU:CD1	2.43	0.49
34:31:39:ASP:OD2	34:31:42:VAL:HG22	2.13	0.49
40:B:129:THR:HB	40:B:132:GLU:HB2	1.94	0.49
43:E:104:ILE:HG23	43:E:111:ARG:NH1	2.26	0.49
52:N:25:GLU:HA	52:N:29:ILE:HD12	1.94	0.49
55:Q:32:ILE:HD12	55:Q:32:ILE:N	2.26	0.49
1:A:390:U:H4'	54:P:28:ARG:NH1	2.27	0.49
1:A:1239:A:H61	1:A:1297:G:H5'	1.76	0.49
2:01:372:G:O2'	2:01:373:U:H5	1.94	0.49
2:01:1726:C:H2'	2:01:1727:C:H6	1.76	0.49
2:01:2298:A:H2'	2:01:2299:U:O4'	2.12	0.49
2:01:2345:G:OP2	34:31:37:LYS:HG2	2.12	0.49
2:01:2682:A:O2'	2:01:2683:C:H5'	2.12	0.49
9:06:145:ASP:HA	9:06:166:LYS:HB3	1.94	0.49
10:07:90:LEU:HB3	10:07:95:MET:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:09:54:LEU:HD23	12:09:54:LEU:C	2.37	0.49
14:11:23:VAL:O	14:11:23:VAL:HG12	2.12	0.49
17:14:91:ASP:H	17:14:94:THR:HG1	1.61	0.49
24:21:79:GLY:H	24:21:101:SER:HA	1.78	0.49
44:F:64:VAL:HG22	44:F:65:GLU:H	1.77	0.49
46:H:45:ILE:CD1	46:H:62:LEU:HA	2.43	0.49
51:M:6:ILE:HG13	51:M:6:ILE:O	2.12	0.49
1:A:1081:A:N7	43:E:51:LYS:NZ	2.61	0.49
2:01:1108:U:H5'	13:10:80:THR:HG22	1.94	0.49
2:01:1847:G:HO2'	2:01:1848:A:H8	1.59	0.49
2:01:2529:G:H4'	11:08:174:LYS:HG3	1.95	0.49
3:02:29:A:H2'	3:02:30:C:C6	2.47	0.49
32:29:63:ARG:HG2	57:S:8:PRO:HG2	1.94	0.49
33:30:37:HIS:ND1	33:30:38:LEU:O	2.42	0.49
40:B:94:ARG:HD2	40:B:94:ARG:N	2.28	0.49
47:I:46:VAL:HA	47:I:49:GLN:HG3	1.95	0.49
59:U:24:LYS:O	59:U:28:LEU:HD12	2.13	0.49
8:05:46:ARG:HG3	8:05:84:LEU:HB2	1.94	0.49
9:06:46:GLN:HB3	9:06:83:VAL:HG21	1.94	0.49
9:06:105:LEU:O	9:06:109:LEU:HD13	2.13	0.49
10:07:49:LEU:O	10:07:53:ALA:N	2.46	0.49
11:08:154:GLU:OE2	11:08:155:PRO:HD2	2.12	0.49
21:18:28:LYS:HG3	21:18:82:SER:HB3	1.95	0.49
22:19:46:TYR:HA	22:19:49:ARG:NH1	2.27	0.49
41:C:8:GLY:HA3	52:N:88:MET:HB3	1.95	0.49
47:I:115:VAL:HG21	48:J:62:ARG:HD3	1.95	0.49
49:K:88:PRO:CG	59:U:28:LEU:HD13	2.41	0.49
52:N:40:ARG:HH12	57:S:6:LYS:HG2	1.78	0.49
1:A:1227:A:H2'	1:A:1228:C:H5'	1.93	0.49
1:A:1513:A:H2'	1:A:1514:G:H8	1.78	0.49
2:01:651:G:H5'	36:33:18:LYS:HG3	1.95	0.49
2:01:1923:U:H2'	2:01:1924:C:C6	2.48	0.49
2:01:2404:U:H2'	2:01:2405:G:O4'	2.13	0.49
5:X:29:G:H2'	5:X:30:G:C4'	2.43	0.49
8:05:122:VAL:HG21	8:05:141:ARG:HG3	1.95	0.49
10:07:67:THR:N	10:07:85:GLY:O	2.43	0.49
14:11:8:VAL:HB	14:11:10:LEU:HD13	1.95	0.49
20:17:83:LEU:HD23	20:17:83:LEU:O	2.13	0.49
28:25:21:ARG:HG2	28:25:21:ARG:HH11	1.77	0.49
39:Z:246:THR:CG2	39:Z:247:SER:H	2.17	0.49
39:Z:361:LEU:O	39:Z:361:LEU:HD23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:96:LEU:HB2	40:B:99:MET:HB3	1.94	0.49
44:F:20:GLY:O	44:F:24:ARG:HG3	2.13	0.49
47:I:24:ASN:HD22	47:I:26:LYS:CD	2.26	0.49
1:A:137:U:H2'	1:A:138:G:C5'	2.42	0.48
1:A:1221:G:H5'	57:S:35:ARG:CD	2.42	0.48
2:01:320:A:N3	9:06:163:ASN:ND2	2.61	0.48
2:01:554:U:H2'	2:01:555:G:O4'	2.13	0.48
2:01:575:A:H2'	2:01:576:U:H6	1.78	0.48
2:01:1287:A:C2	2:01:1649:G:H4'	2.48	0.48
2:01:1753:G:H5''	21:18:92:ARG:CD	2.43	0.48
3:02:102:G:O2'	3:02:103:U:H5'	2.13	0.48
7:04:57:HIS:ND1	7:04:58:LYS:N	2.61	0.48
8:05:4:LEU:HD11	8:05:29:VAL:CG1	2.41	0.48
9:06:104:ALA:O	9:06:108:ILE:HG13	2.12	0.48
18:15:8:LYS:HB2	18:15:8:LYS:NZ	2.28	0.48
18:15:12:MET:O	18:15:86:LYS:NZ	2.46	0.48
25:22:54:GLU:HB3	25:22:88:LYS:HD2	1.94	0.48
27:24:35:GLU:OE1	27:24:93:ARG:HD3	2.13	0.48
27:24:70:ILE:HG21	27:24:93:ARG:HH12	1.77	0.48
43:E:81:GLN:HE21	43:E:81:GLN:HA	1.79	0.48
52:N:8:ARG:HB3	52:N:12:ARG:NH1	2.22	0.48
55:Q:16:MET:HB3	55:Q:19:SER:HB3	1.95	0.48
57:S:5:LYS:O	57:S:6:LYS:HD2	2.13	0.48
59:U:33:ARG:NH2	59:U:34:ARG:HD3	2.26	0.48
1:A:734:G:O2'	56:R:59:LYS:HD3	2.13	0.48
1:A:1147:C:H4'	47:I:6:TYR:HE2	1.78	0.48
2:01:586:A:H5'	9:06:84:THR:HG21	1.95	0.48
2:01:662:G:O2'	2:01:663:G:H5'	2.14	0.48
2:01:1107:G:H4'	13:10:81:LEU:N	2.28	0.48
2:01:1427:A:H4'	2:01:1428:C:O4'	2.12	0.48
2:01:1450:G:C2'	2:01:1451:C:H5'	2.43	0.48
2:01:2266:A:H4'	2:01:2267:A:N3	2.27	0.48
8:05:33:ARG:HD3	8:05:73:VAL:HB	1.95	0.48
9:06:29:HIS:HA	9:06:32:VAL:HG12	1.94	0.48
14:11:129:GLU:HG2	14:11:139:VAL:HG11	1.95	0.48
17:14:103:ILE:HD12	17:14:104:GLN:HG3	1.93	0.48
19:16:100:CYS:HA	33:30:42:ILE:HG12	1.94	0.48
29:26:52:ALA:HA	29:26:55:MET:HE3	1.94	0.48
40:B:163:ILE:O	40:B:185:ILE:HG13	2.12	0.48
40:B:187:ASP:OD2	40:B:203:ASP:OD2	2.32	0.48
49:K:106:ILE:HD12	49:K:106:ILE:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:O:68:TYR:HA	53:O:71:ARG:HE	1.78	0.48
1:A:2:A:H5''	42:D:82:LYS:HE2	1.94	0.48
1:A:337:G:H2'	1:A:338:A:C8	2.49	0.48
1:A:950:U:H2'	1:A:951:G:C8	2.47	0.48
1:A:1305:G:H22	1:A:1331:G:H2'	1.78	0.48
2:01:360:U:H2'	2:01:361:G:O4'	2.14	0.48
2:01:808:G:OP2	17:14:36:LYS:HE2	2.14	0.48
2:01:1058:U:H2'	2:01:1059:G:C8	2.47	0.48
2:01:1360:G:H2'	2:01:1361:G:H5'	1.95	0.48
2:01:2537:U:H2'	2:01:2538:C:C6	2.47	0.48
8:05:193:VAL:HG21	8:05:201:LEU:HD11	1.95	0.48
9:06:175:ILE:HD12	9:06:180:LEU:HD11	1.95	0.48
18:15:73:ILE:HG13	18:15:93:VAL:HG13	1.96	0.48
30:27:47:ARG:HH21	30:27:47:ARG:HG3	1.77	0.48
33:30:56:LYS:HB3	33:30:56:LYS:HZ3	1.77	0.48
47:I:48:ARG:O	47:I:52:GLU:HG2	2.13	0.48
47:I:79:ARG:HD3	47:I:102:PHE:HD1	1.78	0.48
47:I:93:LEU:HD23	47:I:93:LEU:O	2.13	0.48
1:A:297:G:H4'	1:A:557:G:H4'	1.95	0.48
1:A:555:U:H2'	1:A:556:C:C6	2.48	0.48
1:A:625:U:H5''	54:P:16:PHE:CD2	2.48	0.48
1:A:1147:C:H1'	47:I:17:ARG:NH2	2.28	0.48
2:01:562:U:O4'	2:01:2036:C:H5'	2.13	0.48
2:01:1084:A:H5'	13:10:54:VAL:HB	1.96	0.48
2:01:1802:A:H2'	2:01:1803:A:C8	2.48	0.48
2:01:1909:C:H2'	2:01:1910:G:H8	1.78	0.48
2:01:2249:U:O2'	2:01:2250:G:H5''	2.13	0.48
7:04:202:ARG:HH21	7:04:213:ARG:HH22	1.60	0.48
14:11:35:MET:HA	14:11:38:CYS:HB3	1.95	0.48
16:13:10:VAL:HG21	16:13:16:ALA:HB3	1.96	0.48
25:22:23:ALA:HB1	25:22:29:THR:HB	1.95	0.48
25:22:76:ARG:HG2	25:22:76:ARG:HH11	1.78	0.48
30:27:10:SER:O	30:27:14:LEU:N	2.45	0.48
42:D:167:PRO:HB3	42:D:169:TRP:CZ3	2.47	0.48
44:F:49:TYR:HE1	56:R:65:SER:HA	1.79	0.48
45:G:13:PRO:HG3	45:G:20:GLU:HG2	1.95	0.48
45:G:70:PRO:HD3	45:G:102:TRP:HZ3	1.78	0.48
47:I:56:MET:HE3	47:I:59:LYS:H	1.79	0.48
49:K:30:ILE:HA	49:K:45:THR:HG22	1.96	0.48
49:K:125:LYS:O	49:K:126:ARG:HG2	2.14	0.48
52:N:1:ALA:N	52:N:6:LYS:HE3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:O:70:LYS:HD3	53:O:77:TYR:CE2	2.49	0.48
54:P:78:VAL:O	54:P:78:VAL:HG22	2.13	0.48
56:R:54:LEU:O	56:R:58:ILE:HG13	2.13	0.48
59:U:57:LYS:HA	59:U:60:ALA:HB3	1.96	0.48
1:A:191:G:H2'	1:A:192:A:H8	1.78	0.48
1:A:521:G:H5'	50:L:68:GLY:O	2.13	0.48
1:A:1250:A:H4'	47:I:69:GLY:N	2.29	0.48
1:A:1435:G:H2'	1:A:1436:U:C6	2.48	0.48
2:01:467:G:O2'	2:01:468:G:H5'	2.12	0.48
2:01:2350:C:H2'	2:01:2351:G:O4'	2.13	0.48
11:08:132:LEU:H	11:08:132:LEU:CD2	2.24	0.48
52:N:23:ARG:HG2	52:N:50:LEU:HD11	1.95	0.48
58:T:27:MET:SD	58:T:66:ILE:HG13	2.53	0.48
1:A:1211:U:H4'	1:A:1213:A:N3	2.28	0.48
1:A:1318:A:H2'	1:A:1319:A:H5'	1.96	0.48
2:01:2297:A:N1	2:01:2321:U:H5	2.12	0.48
2:01:2457:U:H5	2:01:2494:G:N1	2.02	0.48
6:03:194:VAL:HA	6:03:197:LYS:HB3	1.95	0.48
19:16:59:SER:HB3	19:16:62:ASN:HD22	1.79	0.48
39:Z:293:ALA:O	39:Z:297:GLU:HG2	2.14	0.48
51:M:6:ILE:HB	51:M:8:ILE:HG23	1.95	0.48
51:M:54:THR:HA	51:M:57:ASP:OD2	2.14	0.48
54:P:70:ARG:HH11	54:P:70:ARG:HG3	1.79	0.48
2:01:757:G:H2'	2:01:758:C:H5'	1.96	0.48
2:01:1133:A:H4'	2:01:1134:A:H5''	1.94	0.48
2:01:2059:A:N6	2:01:2503:A:H2'	2.28	0.48
2:01:2087:G:H2'	2:01:2088:A:H8	1.78	0.48
2:01:2233:U:H2'	2:01:2234:G:C8	2.49	0.48
14:11:91:LYS:HE2	14:11:95:ASP:HB3	1.95	0.48
16:13:112:PHE:CA	16:13:115:ILE:HD13	2.43	0.48
26:23:48:VAL:HG22	26:23:50:ALA:H	1.78	0.48
27:24:34:LYS:HB2	27:24:35:GLU:OE2	2.14	0.48
33:30:16:ARG:HA	33:30:19:ASP:OD1	2.14	0.48
39:Z:148:LEU:HD21	39:Z:199:HIS:HD2	1.78	0.48
41:C:156:LEU:H	41:C:156:LEU:CD1	2.27	0.48
43:E:19:ARG:HE	43:E:30:PHE:CB	2.26	0.48
52:N:23:ARG:HD3	52:N:25:GLU:HG2	1.95	0.48
54:P:52:LEU:N	54:P:52:LEU:HD23	2.27	0.48
1:A:1030:U:C2'	1:A:1031:C:H5'	2.39	0.48
1:A:1297:G:C1'	1:A:1298:U:OP2	2.58	0.48
2:01:12:U:O2	2:01:12:U:C2'	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:297:G:H2'	2:01:298:G:H5'	1.95	0.48
2:01:1087:G:N2	2:01:1103:A:H1'	2.28	0.48
2:01:2389:G:H5''	2:01:2390:U:O4'	2.14	0.48
4:Y:20:LEU:HD22	39:Z:219:SER:OG	2.14	0.48
7:04:58:LYS:HB2	7:04:58:LYS:HZ2	1.79	0.48
9:06:3:LEU:HB2	9:06:12:LEU:HB2	1.94	0.48
9:06:97:ASN:HB2	9:06:100:MET:HG3	1.95	0.48
15:12:88:THR:HB	15:12:91:GLU:OE1	2.13	0.48
15:12:120:ARG:HG2	15:12:120:ARG:NH2	2.29	0.48
16:13:26:GLY:HA3	16:13:30:ARG:NH1	2.29	0.48
19:16:29:VAL:HG12	19:16:78:LYS:HG2	1.95	0.48
23:20:14:VAL:HG21	23:20:98:ILE:HD12	1.95	0.48
28:25:33:ILE:HG22	28:25:34:VAL:HG23	1.96	0.48
32:29:15:SER:O	32:29:34:LEU:HD23	2.14	0.48
39:Z:276:ASN:HD22	39:Z:276:ASN:N	2.10	0.48
44:F:47:LEU:HD21	44:F:57:ALA:HB3	1.94	0.48
45:G:66:GLU:HA	45:G:69:ARG:HG2	1.96	0.48
1:A:723:U:OP1	59:U:44:ARG:HG3	2.14	0.48
2:01:644:A:H2'	2:01:645:C:C5'	2.44	0.48
2:01:1386:C:H2'	2:01:1387:A:C8	2.49	0.48
2:01:1405:U:H2'	2:01:1406:U:C6	2.49	0.48
2:01:1432:G:H2'	2:01:1433:A:C8	2.49	0.48
2:01:2834:G:O2'	2:01:2835:A:H5'	2.14	0.48
29:26:32:LEU:HA	29:26:51:SER:HA	1.96	0.48
31:28:43:ILE:O	31:28:47:ILE:HG12	2.14	0.48
39:Z:73:MET:HA	39:Z:106:LEU:HD22	1.95	0.48
39:Z:134:ALA:HB2	39:Z:145:ALA:HB2	1.96	0.48
42:D:58:GLN:NE2	42:D:62:ARG:NE	2.62	0.48
52:N:20:PHE:HB2	52:N:55:SER:HB3	1.96	0.48
52:N:73:LEU:O	52:N:77:GLY:N	2.42	0.48
54:P:6:LEU:HD23	54:P:19:VAL:HA	1.95	0.48
59:U:31:VAL:O	59:U:31:VAL:HG22	2.14	0.48
1:A:451:A:H4'	1:A:452:A:C4	2.47	0.48
1:A:1173:U:H2'	1:A:1174:G:C8	2.49	0.48
1:A:1237:C:OP1	1:A:1238:A:H1'	2.13	0.48
1:A:1378:C:H3'	1:A:1378:C:OP2	2.14	0.48
8:05:36:GLN:NE2	8:05:38:LYS:HG2	2.29	0.48
10:07:140:ILE:HD12	10:07:140:ILE:N	2.29	0.48
20:17:106:LEU:HD23	20:17:106:LEU:O	2.14	0.48
31:28:41:PRO:HA	31:28:44:ARG:HB2	1.96	0.48
40:B:83:ALA:HB1	40:B:88:GLN:C	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:192:PRO:O	40:B:195:VAL:HG22	2.13	0.48
41:C:110:LEU:O	41:C:110:LEU:HD23	2.14	0.48
43:E:17:VAL:O	43:E:17:VAL:HG13	2.14	0.48
45:G:70:PRO:HG3	45:G:98:LEU:HD23	1.96	0.48
1:A:66:A:H4'	1:A:173:U:O4	2.14	0.47
1:A:678:U:H2'	1:A:679:C:C6	2.49	0.47
1:A:1144:G:H21	1:A:1146:A:H62	1.61	0.47
1:A:1221:G:H5'	57:S:35:ARG:HD3	1.95	0.47
2:01:115:C:O2'	2:01:116:C:H5'	2.13	0.47
2:01:2020:A:H62	33:30:5:ASN:ND2	2.12	0.47
2:01:2039:U:H2'	2:01:2040:G:C8	2.48	0.47
2:01:2822:G:O6	19:16:2:ARG:HD2	2.14	0.47
10:07:34:THR:HB	10:07:87:LYS:HD2	1.96	0.47
14:11:11:GLN:HB2	14:11:56:VAL:CG1	2.43	0.47
17:14:105:ILE:N	17:14:105:ILE:HD12	2.29	0.47
18:15:51:ARG:HB3	18:15:55:ARG:NH2	2.29	0.47
44:F:53:LYS:HB2	44:F:54:LEU:HD13	1.95	0.47
47:I:91:GLU:H	47:I:91:GLU:CD	2.21	0.47
48:J:7:ARG:HA	48:J:75:ASP:HA	1.96	0.47
49:K:63:GLN:OE1	49:K:98:ALA:HB2	2.13	0.47
49:K:86:LYS:HE3	49:K:114:PRO:CD	2.44	0.47
56:R:24:ASP:O	56:R:28:LEU:HD13	2.14	0.47
59:U:16:ARG:NH2	59:U:19:LYS:HG2	2.23	0.47
1:A:814:A:H5''	1:A:1511:G:H4'	1.95	0.47
2:01:279:A:H2'	2:01:280:U:C5'	2.44	0.47
2:01:871:U:H2'	2:01:872:U:C6	2.49	0.47
2:01:2830:C:O2'	2:01:2831:G:H5'	2.14	0.47
2:01:2860:A:H2'	2:01:2861:U:H5'	1.95	0.47
4:Y:4:TYR:HA	50:L:38:THR:OG1	2.13	0.47
13:10:81:LEU:N	13:10:81:LEU:HD23	2.29	0.47
13:10:113:PHE:H	13:10:113:PHE:HD1	1.62	0.47
14:11:61:TYR:N	14:11:65:SER:O	2.44	0.47
21:18:4:ILE:O	21:18:8:GLU:N	2.46	0.47
35:32:41:ARG:HG2	35:32:41:ARG:HH21	1.78	0.47
41:C:168:ARG:HG2	41:C:168:ARG:HH11	1.79	0.47
58:T:34:VAL:O	58:T:38:ILE:N	2.46	0.47
1:A:715:A:H2'	1:A:716:A:H8	1.79	0.47
1:A:1254:A:OP1	48:J:47:GLU:HG2	2.15	0.47
2:01:72:U:O2'	2:01:73:A:H5'	2.14	0.47
2:01:2183:A:H2'	2:01:2184:A:C8	2.50	0.47
2:01:2391:G:H5''	36:33:31:ILE:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:04:140:VAL:HG12	7:04:141:HIS:N	2.29	0.47
26:23:11:ILE:HG22	26:23:70:ALA:O	2.14	0.47
37:34:1:MET:HE3	37:34:34:LYS:NZ	2.29	0.47
40:B:211:LEU:HD23	40:B:211:LEU:C	2.38	0.47
44:F:52:ASN:O	44:F:53:LYS:HG2	2.14	0.47
47:I:33:SER:HB3	47:I:36:GLN:HG3	1.97	0.47
47:I:46:VAL:HA	47:I:49:GLN:CD	2.39	0.47
50:L:23:LEU:HB3	50:L:58:ASN:OD1	2.15	0.47
52:N:40:ARG:NH1	57:S:6:LYS:HG2	2.29	0.47
1:A:261:U:OP2	58:T:70:LYS:HE2	2.13	0.47
1:A:1099:G:H4'	59:U:66:ARG:HG3	1.96	0.47
1:A:1145:A:H2	1:A:1147:C:H41	1.61	0.47
1:A:1240:U:H5'	45:G:41:ILE:HD11	1.96	0.47
2:01:118:A:OP2	2:01:119:A:H5''	2.13	0.47
2:01:1468:U:H2'	2:01:1522:A:H61	1.80	0.47
2:01:1545:A:H2'	2:01:1546:G:H5'	1.96	0.47
2:01:1869:G:H3'	2:01:1870:C:C5'	2.44	0.47
2:01:2011:U:H2'	2:01:2012:G:O4'	2.14	0.47
2:01:2605:U:H2'	2:01:2606:C:C6	2.48	0.47
2:01:2698:U:H2'	2:01:2699:C:C6	2.49	0.47
3:02:92:C:H2'	3:02:93:C:C6	2.49	0.47
6:03:27:ILE:HG21	6:03:185:LEU:HB3	1.96	0.47
17:14:102:GLY:C	17:14:105:ILE:HD13	2.39	0.47
18:15:88:ASN:HD22	18:15:89:VAL:H	1.62	0.47
20:17:32:PRO:HG2	20:17:33:ARG:H	1.79	0.47
45:G:5:VAL:HG23	45:G:5:VAL:O	2.14	0.47
46:H:74:ILE:HG23	46:H:74:ILE:O	2.13	0.47
51:M:47:LEU:HD23	51:M:47:LEU:C	2.40	0.47
53:O:55:LEU:O	53:O:55:LEU:HD23	2.15	0.47
59:U:16:ARG:HG2	59:U:16:ARG:HH11	1.78	0.47
1:A:673:A:H2'	1:A:674:G:C8	2.49	0.47
1:A:1170:A:H2'	1:A:1171:A:H5'	1.96	0.47
1:A:1429:A:H2'	1:A:1430:A:H8	1.80	0.47
2:01:627:A:C5	17:14:111:ILE:HD12	2.49	0.47
2:01:906:U:H2'	2:01:907:G:C5'	2.41	0.47
2:01:1890:A:H2'	2:01:1891:G:O4'	2.14	0.47
2:01:2177:C:O2'	6:03:47:ASN:HB2	2.15	0.47
11:08:71:LEU:HD12	11:08:74:MET:HE3	1.97	0.47
17:14:86:GLU:HG2	17:14:87:GLY:H	1.80	0.47
18:15:88:ASN:ND2	18:15:89:VAL:H	2.11	0.47
39:Z:235:ASN:ND2	39:Z:237:ALA:HB3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:336:LEU:HD12	39:Z:336:LEU:C	2.39	0.47
40:B:128:LEU:N	40:B:128:LEU:HD23	2.29	0.47
50:L:98:ARG:HD2	50:L:103:CYS:SG	2.55	0.47
52:N:98:ALA:O	52:N:99:SER:HB2	2.14	0.47
2:01:100:U:H4'	2:01:101:A:O4'	2.14	0.47
2:01:1107:G:H4'	13:10:81:LEU:H	1.78	0.47
2:01:1991:U:H2'	2:01:1992:G:H5'	1.97	0.47
2:01:2345:G:H4'	2:01:2346:A:H3'	1.95	0.47
2:01:2641:G:H5''	15:12:78:THR:CB	2.44	0.47
16:13:58:LEU:HD11	16:13:86:LEU:HD22	1.95	0.47
42:D:61:ARG:HH21	42:D:67:LEU:HA	1.80	0.47
47:I:20:ILE:CG2	47:I:60:LEU:HD22	2.45	0.47
48:J:44:THR:HG23	48:J:69:THR:O	2.15	0.47
57:S:10:ILE:HD13	57:S:40:PHE:HE2	1.79	0.47
1:A:204:G:H2'	1:A:205:A:C8	2.50	0.47
1:A:351:G:H8	1:A:351:G:OP2	1.97	0.47
1:A:864:A:H5''	43:E:89:THR:HG23	1.96	0.47
1:A:1129:C:H4'	47:I:17:ARG:HH12	1.80	0.47
1:A:1219:A:H2'	1:A:1220:G:C8	2.49	0.47
1:A:1391:U:H2'	1:A:1392:G:C8	2.50	0.47
2:01:367:G:H2'	2:01:368:A:O4'	2.15	0.47
2:01:906:U:H2'	2:01:907:G:O4'	2.15	0.47
2:01:1031:G:H5''	37:34:8:LYS:CE	2.44	0.47
2:01:1083:U:O3'	13:10:53:ARG:HB3	2.14	0.47
2:01:1509:A:H2'	2:01:1510:G:C8	2.49	0.47
2:01:1529:G:C3'	2:01:1530:G:H5''	2.44	0.47
2:01:1535:A:H3'	2:01:1536:C:H5'	1.95	0.47
2:01:2048:G:H3'	2:01:2049:G:H5''	1.94	0.47
2:01:2191:A:H2'	2:01:2192:U:C6	2.50	0.47
2:01:2334:U:H5'	20:17:12:THR:CB	2.33	0.47
2:01:2475:C:C2'	2:01:2476:A:H5'	2.45	0.47
2:01:2507:C:H5''	39:Z:256:ARG:NH1	2.29	0.47
2:01:2641:G:H5''	15:12:78:THR:CG2	2.45	0.47
3:02:21:G:O2'	3:02:22:U:H5'	2.15	0.47
3:02:60:C:H2'	3:02:61:G:C8	2.47	0.47
3:02:116:G:H4'	20:17:54:VAL:O	2.14	0.47
6:03:22:ASP:N	6:03:25:GLU:HB2	2.28	0.47
7:04:66:PHE:HE1	7:04:104:LEU:HD11	1.78	0.47
10:07:153:ILE:HD12	10:07:153:ILE:N	2.30	0.47
11:08:125:PRO:HG2	11:08:126:THR:H	1.79	0.47
22:19:75:TYR:CZ	22:19:79:ILE:HG13	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C:137:VAL:HG21	41:C:167:TYR:CD2	2.50	0.47
42:D:58:GLN:NE2	42:D:62:ARG:HE	2.12	0.47
43:E:44:ARG:NH1	43:E:72:ASN:HB2	2.29	0.47
51:M:90:HIS:CE1	51:M:96:VAL:HG21	2.49	0.47
52:N:98:ALA:HB1	52:N:100:TRP:CZ3	2.49	0.47
54:P:43:ALA:HB1	54:P:46:LYS:HD3	1.97	0.47
59:U:39:LYS:N	59:U:40:PRO:CD	2.78	0.47
1:A:1144:G:H2'	1:A:1145:A:C8	2.49	0.47
2:01:682:G:H5'	35:32:26:ASN:CG	2.40	0.47
2:01:1736:U:H2'	2:01:1737:G:O4'	2.14	0.47
2:01:2122:U:H2'	2:01:2123:G:H5'	1.96	0.47
10:07:72:SER:O	5:W:56:C:H4'	2.15	0.47
13:10:27:VAL:HG22	13:10:29:ASP:N	2.30	0.47
21:18:19:PHE:HE2	21:18:46:VAL:HG21	1.80	0.47
48:J:9:ARG:C	48:J:10:LEU:HD12	2.40	0.47
50:L:52:CYS:SG	50:L:64:SER:HB3	2.54	0.47
52:N:3:GLN:HE22	52:N:6:LYS:NZ	2.13	0.47
53:O:55:LEU:HD23	53:O:59:VAL:HG23	1.96	0.47
1:A:122:G:O2'	1:A:123:U:H5'	2.15	0.47
1:A:396:C:C3'	1:A:397:A:H5''	2.44	0.47
1:A:839:C:H2'	1:A:840:C:C6	2.49	0.47
1:A:1323:G:H2'	1:A:1324:A:C8	2.50	0.47
2:01:140:C:H42	2:01:1409:U:H1'	1.79	0.47
2:01:814:C:H1'	2:01:1225:G:H21	1.79	0.47
2:01:919:U:H2'	2:01:920:A:O4'	2.15	0.47
2:01:2318:G:H2'	2:01:2319:G:O4'	2.15	0.47
2:01:2742:G:O2'	2:01:2743:U:H5'	2.15	0.47
6:03:39:VAL:CG2	6:03:177:LYS:HD3	2.40	0.47
8:05:108:ASP:N	8:05:204:LYS:O	2.48	0.47
20:17:66:GLY:HA2	20:17:102:ARG:NH1	2.30	0.47
25:22:59:ASN:HB2	25:22:84:TYR:HB2	1.97	0.47
35:32:8:SER:HB3	35:32:11:LYS:HB2	1.95	0.47
56:R:47:ARG:HD2	56:R:50:TYR:CD2	2.50	0.47
1:A:72:A:N6	1:A:98:A:H2	2.13	0.47
1:A:235:C:H2'	1:A:236:A:H8	1.80	0.47
2:01:419:U:H2'	2:01:420:C:C6	2.50	0.47
2:01:1258:U:H2'	2:01:1259:G:C8	2.50	0.47
2:01:1443:U:H2'	2:01:1444:G:C8	2.50	0.47
2:01:1447:C:H2'	2:01:1448:G:H8	1.79	0.47
2:01:1932:A:H2'	2:01:1933:G:O4'	2.15	0.47
2:01:2055:C:H5'	2:01:2056:G:O5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2261:C:C6	28:25:12:SER:HB3	2.50	0.47
2:01:2759:G:O2'	2:01:2760:C:H5'	2.15	0.47
2:01:2841:C:H2'	2:01:2842:G:H8	1.80	0.47
2:01:2849:U:H4'	2:01:2868:A:C2	2.50	0.47
5:W:48:C:H2'	5:W:59:A:C4'	2.45	0.47
39:Z:36:GLU:O	39:Z:40:GLU:HG2	2.14	0.47
47:I:54:VAL:HG11	47:I:93:LEU:CG	2.42	0.47
59:U:33:ARG:HH11	59:U:33:ARG:HG3	1.80	0.47
1:A:113:G:H1'	1:A:354:G:H5''	1.97	0.46
1:A:523:A:H2'	1:A:524:G:H5''	1.98	0.46
1:A:831:A:H2'	1:A:832:G:H5''	1.97	0.46
1:A:1064:G:H21	1:A:1190:G:H1'	1.79	0.46
2:01:481:G:H1'	2:01:506:G:N2	2.30	0.46
2:01:1637:A:H5'	2:01:1760:C:O2'	2.16	0.46
2:01:1824:G:O2'	2:01:1825:U:H5'	2.15	0.46
2:01:2882:A:H5'	19:16:96:ARG:HG3	1.97	0.46
8:05:13:ARG:NH1	21:18:55:HIS:HA	2.30	0.46
10:07:68:LYS:HB2	10:07:68:LYS:NZ	2.30	0.46
10:07:103:ILE:HD12	10:07:173:ASP:HB3	1.97	0.46
13:10:26:VAL:HB	13:10:82:ILE:CG2	2.45	0.46
17:14:29:LYS:O	17:14:30:THR:OG1	2.30	0.46
17:14:89:VAL:HG13	17:14:89:VAL:O	2.15	0.46
19:16:90:ARG:HH12	19:16:116:VAL:HG11	1.80	0.46
35:32:5:PHE:CZ	35:32:7:PRO:HB3	2.50	0.46
40:B:10:LYS:NZ	40:B:10:LYS:HB2	2.30	0.46
40:B:129:THR:O	40:B:133:ALA:N	2.46	0.46
41:C:172:VAL:HG23	41:C:172:VAL:O	2.15	0.46
42:D:149:LYS:HE2	42:D:177:MET:HG3	1.98	0.46
45:G:66:GLU:HA	45:G:69:ARG:NE	2.30	0.46
45:G:113:LYS:CB	45:G:117:LEU:HD13	2.44	0.46
51:M:53:ASP:OD1	51:M:54:THR:N	2.48	0.46
57:S:10:ILE:HD13	57:S:40:PHE:CE2	2.50	0.46
1:A:516:U:O4	1:A:533:A:N7	2.47	0.46
1:A:864:A:H2'	1:A:865:A:C8	2.50	0.46
1:A:1056:U:H4'	41:C:162:ALA:HB2	1.97	0.46
1:A:1522:U:H2'	1:A:1523:G:H8	1.79	0.46
2:01:176:A:O2'	2:01:177:G:H5'	2.15	0.46
2:01:532:A:H2'	2:01:532:A:N3	2.29	0.46
2:01:728:G:H4'	7:04:12:ARG:HD2	1.96	0.46
2:01:1020:A:C1'	2:01:1021:A:OP2	2.56	0.46
2:01:1268:A:H2'	2:01:1269:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2485:G:O2'	2:01:2486:C:H5'	2.15	0.46
7:04:52:HIS:CE1	7:04:218:THR:HA	2.50	0.46
10:07:35:LEU:HB3	10:07:88:VAL:HB	1.96	0.46
11:08:166:GLU:OE2	11:08:167:VAL:O	2.33	0.46
39:Z:167:GLU:HB2	39:Z:180:THR:HB	1.97	0.46
40:B:114:LYS:HA	40:B:151:LYS:HE3	1.98	0.46
41:C:129:PHE:CD2	41:C:156:LEU:HD23	2.50	0.46
42:D:56:GLU:HG2	42:D:198:LEU:HB2	1.97	0.46
42:D:109:THR:HG22	42:D:110:ARG:N	2.30	0.46
42:D:176:LYS:NZ	42:D:176:LYS:HB3	2.29	0.46
44:F:14:GLN:OE1	44:F:14:GLN:HA	2.14	0.46
46:H:5:PRO:HG2	46:H:6:ILE:HD12	1.96	0.46
54:P:33:ILE:HD12	54:P:33:ILE:H	1.79	0.46
1:A:966:G:N2	5:W:34:C:H5'	2.31	0.46
2:01:1709:U:H2'	2:01:1710:G:C8	2.50	0.46
2:01:1912:A:H62	2:01:1917:U:H5	1.56	0.46
2:01:2724:U:H2'	2:01:2725:A:H8	1.80	0.46
8:05:32:ASN:N	8:05:32:ASN:HD22	2.12	0.46
10:07:84:ILE:HG13	10:07:84:ILE:O	2.15	0.46
11:08:73:SER:OG	11:08:137:LYS:HB3	2.15	0.46
14:11:20:SER:HB3	14:11:21:PRO:HD3	1.95	0.46
16:13:4:GLU:OE2	16:13:24:VAL:HG23	2.16	0.46
26:23:39:ASN:HB2	26:23:62:ALA:HB3	1.97	0.46
26:23:43:LYS:N	26:23:58:VAL:O	2.46	0.46
46:H:50:VAL:HG22	46:H:50:VAL:O	2.15	0.46
49:K:88:PRO:HG3	59:U:28:LEU:CD1	2.45	0.46
1:A:839:C:H2'	1:A:840:C:H6	1.81	0.46
1:A:1412:C:H2'	1:A:1413:A:H8	1.80	0.46
2:01:1548:A:H2'	2:01:1549:A:C8	2.51	0.46
2:01:1807:G:C2'	2:01:1808:A:H5'	2.39	0.46
2:01:2257:U:O2'	2:01:2258:C:H5'	2.16	0.46
3:02:76:G:H21	27:24:78:GLN:HE22	1.63	0.46
11:08:71:LEU:O	11:08:75:VAL:HG23	2.15	0.46
13:10:102:ALA:HB3	13:10:107:GLU:OE1	2.14	0.46
21:18:25:VAL:HG22	21:18:26:GLU:N	2.30	0.46
26:23:35:VAL:HB	26:23:38:ILE:HG13	1.97	0.46
28:25:66:GLU:HG3	28:25:68:LYS:HG3	1.98	0.46
31:28:39:ASP:OD1	31:28:44:ARG:HD3	2.16	0.46
39:Z:128:CYS:HA	39:Z:224:PRO:HA	1.96	0.46
39:Z:200:ARG:HG3	39:Z:217:PHE:HE1	1.81	0.46
39:Z:361:LEU:HD23	39:Z:361:LEU:C	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:D:60:VAL:HG21	42:D:199:ILE:CD1	2.45	0.46
51:M:22:TYR:HB3	51:M:65:GLU:OE2	2.16	0.46
54:P:59:HIS:O	54:P:63:GLN:HG2	2.16	0.46
55:Q:21:VAL:HG22	55:Q:44:HIS:ND1	2.31	0.46
57:S:24:SER:HB2	57:S:27:LYS:HD2	1.96	0.46
1:A:1273:C:H2'	1:A:1274:A:O4'	2.15	0.46
1:A:1402:C:H2'	1:A:1403:C:O4'	2.14	0.46
2:01:291:G:O2'	2:01:292:U:H5'	2.15	0.46
2:01:1797:G:H4'	7:04:254:LYS:O	2.16	0.46
2:01:2019:A:H4'	22:19:33:VAL:HG21	1.97	0.46
2:01:2573:C:O2	2:01:2573:C:H2'	2.15	0.46
12:09:26:ALA:HA	12:09:30:LEU:HD12	1.98	0.46
16:13:12:ASP:OD2	16:13:14:SER:HB3	2.16	0.46
21:18:23:ASP:O	21:18:46:VAL:HG23	2.15	0.46
47:I:83:THR:HA	47:I:86:LEU:HD12	1.98	0.46
50:L:26:CYS:SG	50:L:29:LYS:HD3	2.56	0.46
1:A:529:G:H5'	1:A:530:G:OP2	2.16	0.46
2:01:46:G:H2'	2:01:47:C:C6	2.50	0.46
2:01:782:A:N1	7:04:224:MET:HE2	2.31	0.46
2:01:2022:U:O2'	2:01:2617:U:H5'	2.15	0.46
2:01:2291:U:H2'	2:01:2292:U:C6	2.50	0.46
5:X:8:U:H4'	5:X:48:C:H4'	1.97	0.46
14:11:44:LYS:HZ2	14:11:70:THR:HB	1.81	0.46
20:17:3:LYS:N	20:17:3:LYS:HD2	2.31	0.46
21:18:50:ARG:HH12	21:18:52:ARG:HG3	1.80	0.46
22:19:91:ARG:HH11	22:19:91:ARG:HG3	1.80	0.46
24:21:97:LEU:HD12	24:21:97:LEU:N	2.30	0.46
32:29:56:ARG:NH1	57:S:67:GLY:HA3	2.30	0.46
40:B:123:GLY:O	40:B:125:PHE:HD1	1.99	0.46
42:D:58:GLN:HE21	42:D:62:ARG:HE	1.62	0.46
42:D:103:ARG:CB	42:D:170:LEU:HD21	2.45	0.46
44:F:4:TYR:CD2	44:F:71:ILE:HG13	2.50	0.46
47:I:21:LYS:O	47:I:61:ASP:N	2.43	0.46
48:J:57:VAL:O	48:J:58:ASN:HB2	2.15	0.46
50:L:51:VAL:HG13	50:L:64:SER:O	2.15	0.46
1:A:137:U:C2'	1:A:138:G:H5''	2.46	0.46
1:A:170:U:C3'	1:A:171:A:H5''	2.46	0.46
1:A:238:A:O2'	1:A:239:U:H5'	2.16	0.46
1:A:335:C:H2'	1:A:336:A:H8	1.81	0.46
2:01:251:A:H5''	17:14:47:ARG:NH1	2.29	0.46
2:01:517:C:C3'	2:01:518:G:H5''	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1790:C:H2'	2:01:1791:A:C5	2.51	0.46
16:13:8:LEU:HB2	16:13:19:VAL:CG2	2.46	0.46
40:B:15:PHE:CD1	40:B:15:PHE:N	2.82	0.46
41:C:122:GLN:HB3	41:C:127:VAL:HG11	1.98	0.46
44:F:86:ARG:HH11	44:F:86:ARG:HG3	1.81	0.46
46:H:9:MET:O	46:H:13:ILE:HG13	2.16	0.46
48:J:26:VAL:O	48:J:30:LYS:HG3	2.16	0.46
52:N:52:ARG:NH1	57:S:36:ARG:NH2	2.62	0.46
59:U:13:VAL:HG12	59:U:14:ALA:H	1.80	0.46
1:A:345:C:H5'	21:18:38:ARG:HD2	1.97	0.46
1:A:517:G:H4'	1:A:519:C:C6	2.50	0.46
1:A:730:G:C2'	1:A:731:G:H5'	2.44	0.46
1:A:1054:C:N4	39:Z:212:ARG:HA	2.31	0.46
1:A:1058:G:OP1	41:C:198:LYS:HE3	2.15	0.46
2:01:807:U:H2'	2:01:808:G:H8	1.81	0.46
2:01:1131:G:C8	2:01:2025:C:H4'	2.51	0.46
2:01:1138:G:H2'	2:01:1139:G:O4'	2.16	0.46
6:03:27:ILE:HA	6:03:30:LEU:HB3	1.98	0.46
8:05:2:ILE:HG13	8:05:3:GLY:N	2.31	0.46
17:14:59:ARG:HH11	17:14:59:ARG:HG3	1.81	0.46
19:16:37:THR:HA	19:16:110:MET:HA	1.98	0.46
27:24:61:LEU:N	27:24:72:VAL:O	2.49	0.46
35:32:12:ARG:HB2	35:32:12:ARG:NH2	2.31	0.46
42:D:16:THR:HG21	42:D:59:LYS:HE3	1.98	0.46
42:D:170:LEU:HD12	42:D:170:LEU:C	2.41	0.46
52:N:73:LEU:HD12	52:N:83:VAL:HG11	1.96	0.46
53:O:81:ILE:HA	53:O:86:LEU:CD2	2.45	0.46
54:P:46:LYS:H	54:P:46:LYS:CD	2.26	0.46
55:Q:63:CYS:SG	55:Q:64:ARG:N	2.89	0.46
58:T:70:LYS:HG3	58:T:73:ARG:NH2	2.30	0.46
1:A:624:C:H2'	1:A:625:U:O4'	2.15	0.46
1:A:1326:U:O2'	1:A:1327:C:H5'	2.16	0.46
2:01:487:C:H4'	24:21:56:ALA:HB2	1.97	0.46
2:01:1639:C:O2'	2:01:1640:A:H5'	2.16	0.46
2:01:2880:C:O2'	19:16:90:ARG:HD3	2.16	0.46
3:02:12:C:H1'	3:02:15:A:N1	2.30	0.46
4:Y:11:ILE:HD12	39:Z:315:SER:CB	2.46	0.46
5:X:62:C:H4'	6:03:54:LYS:HE2	1.98	0.46
6:03:11:ILE:HD12	6:03:11:ILE:C	2.41	0.46
8:05:25:THR:HG21	8:05:193:VAL:HG22	1.98	0.46
8:05:118:PHE:CE1	8:05:163:GLY:HA2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:30:43:THR:HG23	33:30:47:TYR:O	2.16	0.46
37:34:2:LYS:HB2	37:34:2:LYS:NZ	2.31	0.46
39:Z:130:LEU:N	39:Z:181:ILE:O	2.39	0.46
39:Z:151:MET:HE1	39:Z:348:VAL:O	2.16	0.46
41:C:137:VAL:HG13	41:C:148:ILE:CG2	2.46	0.46
42:D:58:GLN:HE21	42:D:62:ARG:NE	2.14	0.46
42:D:187:ARG:HH21	42:D:196:GLU:HG3	1.80	0.46
45:G:119:LEU:O	45:G:123:LEU:HD13	2.15	0.46
46:H:86:LYS:HB3	46:H:90:GLU:HG3	1.97	0.46
49:K:68:ARG:HG3	49:K:68:ARG:HH11	1.80	0.46
51:M:16:ILE:H	51:M:16:ILE:CD1	2.24	0.46
55:Q:26:ARG:HG3	55:Q:26:ARG:HH11	1.81	0.46
59:U:60:ALA:O	59:U:63:ASN:ND2	2.48	0.46
1:A:8:A:N7	42:D:205:LYS:HB3	2.31	0.46
1:A:887:G:H2'	1:A:888:G:H5'	1.98	0.46
1:A:912:C:O2'	1:A:913:A:H5'	2.16	0.46
2:01:214:G:H2'	2:01:215:G:O4'	2.16	0.46
2:01:321:U:H5'	9:06:129:PRO:O	2.16	0.46
2:01:1149:G:H2'	2:01:1150:C:C6	2.50	0.46
2:01:2052:A:OP1	8:05:145:SER:HA	2.15	0.46
2:01:2312:U:OP1	10:07:69:ALA:HA	2.16	0.46
6:03:175:ILE:HD11	6:03:188:ASN:HB3	1.98	0.46
29:26:53:LYS:O	29:26:57:VAL:HG23	2.16	0.46
30:27:56:LEU:O	30:27:60:LYS:HG2	2.16	0.46
47:I:62:LEU:HD12	47:I:62:LEU:N	2.31	0.46
54:P:4:ILE:HD12	54:P:67:ILE:CD1	2.46	0.46
54:P:5:ARG:HD3	54:P:5:ARG:H	1.81	0.46
59:U:61:ARG:HD2	59:U:61:ARG:C	2.41	0.46
1:A:208:U:H2'	1:A:210:C:H1'	1.97	0.45
2:01:1420:A:H5'	2:01:1421:G:OP2	2.15	0.45
2:01:1759:A:C2	2:01:2697:G:H1'	2.51	0.45
2:01:2731:G:H2'	2:01:2732:G:C8	2.52	0.45
3:02:1:U:H2'	3:02:2:G:H8	1.82	0.45
7:04:43:ASN:HD22	7:04:49:THR:CG2	2.29	0.45
9:06:148:ILE:HG21	9:06:157:LEU:HD21	1.98	0.45
39:Z:324:ARG:HG2	39:Z:335:ASP:HA	1.98	0.45
43:E:15:ILE:N	43:E:15:ILE:HD12	2.30	0.45
48:J:86:ALA:O	48:J:90:LEU:HD12	2.16	0.45
1:A:332:G:O2'	1:A:333:U:H5'	2.16	0.45
1:A:993:G:H2'	1:A:993:G:N3	2.32	0.45
2:01:988:A:C8	31:28:13:ILE:HD12	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1417:C:H2'	2:01:1418:G:O4'	2.16	0.45
2:01:1928:A:H2'	2:01:1929:G:O4'	2.16	0.45
2:01:2004:G:H2'	2:01:2005:A:O4'	2.16	0.45
2:01:2241:A:H2'	2:01:2242:G:C8	2.51	0.45
2:01:2547:A:H2'	2:01:2548:U:C6	2.52	0.45
2:01:2680:U:H5'	8:05:194:PRO:HA	1.99	0.45
10:07:71:LYS:HG3	10:07:72:SER:N	2.31	0.45
20:17:8:ILE:HD12	20:17:8:ILE:N	2.31	0.45
33:30:12:ARG:HD2	33:30:16:ARG:NH2	2.31	0.45
39:Z:15:THR:HG22	39:Z:19:ASP:OD2	2.15	0.45
40:B:84:LEU:HB2	40:B:90:PHE:CE1	2.51	0.45
42:D:104:MET:CE	42:D:170:LEU:HB2	2.46	0.45
42:D:144:ILE:HG22	42:D:145:ARG:O	2.16	0.45
43:E:132:PRO:O	43:E:136:VAL:HG23	2.16	0.45
47:I:80:HIS:NE2	47:I:84:ARG:HD3	2.31	0.45
48:J:67:ILE:HG13	48:J:67:ILE:O	2.16	0.45
1:A:103:U:H5'	1:A:151:A:O2'	2.16	0.45
1:A:519:C:O2'	1:A:520:A:H5'	2.16	0.45
1:A:802:A:H2'	1:A:803:G:O4'	2.17	0.45
1:A:1422:G:C5'	16:13:48:PRO:HB3	2.46	0.45
1:A:1422:G:OP1	16:13:48:PRO:HA	2.16	0.45
2:01:742:A:H2'	2:01:743:A:C8	2.51	0.45
2:01:1019:U:H3	2:01:1142:A:H62	1.62	0.45
2:01:1112:G:H2'	2:01:1113:U:C6	2.51	0.45
10:07:66:ILE:HG13	10:07:66:ILE:O	2.17	0.45
10:07:103:ILE:HA	10:07:107:VAL:CG2	2.46	0.45
14:11:9:LYS:O	14:11:10:LEU:HD12	2.17	0.45
18:15:71:LYS:HG2	18:15:95:LEU:HD11	1.97	0.45
20:17:40:ILE:HG23	20:17:47:VAL:HG12	1.98	0.45
28:25:74:LYS:N	28:25:74:LYS:HD2	2.32	0.45
36:33:31:ILE:HG22	36:33:31:ILE:O	2.16	0.45
39:Z:200:ARG:HH11	39:Z:217:PHE:HE1	1.63	0.45
39:Z:322:GLN:HB3	39:Z:336:LEU:HD21	1.98	0.45
46:H:64:TYR:HD1	46:H:69:ALA:HA	1.81	0.45
1:A:59:A:H2'	1:A:59:A:N3	2.31	0.45
1:A:518:C:OP2	1:A:530:G:H4'	2.16	0.45
1:A:921:U:H5''	1:A:1082:A:H5'	1.98	0.45
2:01:435:C:H2'	2:01:436:C:H5'	1.98	0.45
2:01:633:A:H2'	2:01:634:C:H5'	1.98	0.45
2:01:812:C:O2'	2:01:813:U:H5'	2.16	0.45
2:01:1571:A:H2'	2:01:1572:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2270:A:H2'	2:01:2271:G:O4'	2.16	0.45
3:02:48:U:H2'	3:02:49:C:C6	2.51	0.45
8:05:33:ARG:CG	8:05:51:THR:HG23	2.46	0.45
13:10:43:LYS:HE3	13:10:98:GLU:HB2	1.97	0.45
14:11:56:VAL:HG22	14:11:57:VAL:N	2.31	0.45
14:11:100:ILE:H	14:11:139:VAL:HA	1.81	0.45
16:13:111:LYS:HE3	16:13:112:PHE:CE2	2.50	0.45
20:17:58:ILE:HG22	20:17:62:LEU:HG	1.98	0.45
26:23:85:ARG:NH1	26:23:101:THR:OG1	2.50	0.45
32:29:44:PHE:H	32:29:44:PHE:HD1	1.64	0.45
39:Z:5:ASN:HD22	39:Z:6:PRO:HD2	1.81	0.45
39:Z:270:ILE:CD1	39:Z:291:MET:HE1	2.41	0.45
40:B:136:ARG:O	40:B:140:LEU:N	2.50	0.45
40:B:216:VAL:O	40:B:220:VAL:HG23	2.17	0.45
42:D:32:LYS:HE2	42:D:34:GLU:HB3	1.98	0.45
42:D:33:ILE:HG13	42:D:33:ILE:O	2.17	0.45
48:J:40:ILE:HD12	48:J:75:ASP:OD2	2.16	0.45
51:M:18:LEU:HD12	51:M:33:LEU:HD11	1.98	0.45
51:M:56:ARG:HA	51:M:59:VAL:HG22	1.99	0.45
52:N:19:TYR:O	52:N:23:ARG:N	2.37	0.45
52:N:20:PHE:CD2	52:N:55:SER:HB3	2.51	0.45
54:P:53:ASP:O	54:P:57:ILE:HG13	2.16	0.45
57:S:28:LYS:NZ	57:S:28:LYS:HB3	2.31	0.45
58:T:43:LYS:HB3	58:T:86:ALA:HA	1.98	0.45
1:A:546:A:OP2	42:D:67:LEU:HB3	2.17	0.45
1:A:562:U:H1'	50:L:11:ARG:HG3	1.98	0.45
1:A:1125:U:O2'	1:A:1126:U:H5'	2.17	0.45
2:01:370:G:H2'	2:01:423:A:N7	2.31	0.45
2:01:451:U:H4'	9:06:47:LYS:HE3	1.98	0.45
2:01:1062:G:N2	14:11:135:MET:HE1	2.32	0.45
2:01:1083:U:O2'	2:01:1084:A:H5'	2.16	0.45
2:01:1450:G:H2'	2:01:1451:C:H5'	1.98	0.45
2:01:1515:A:H2'	2:01:1516:G:O4'	2.17	0.45
2:01:2177:C:O2	6:03:170:ILE:HG21	2.17	0.45
2:01:2741:A:H2'	2:01:2742:G:H5'	1.98	0.45
7:04:143:VAL:HG12	7:04:144:GLU:O	2.16	0.45
10:07:94:ARG:HD3	10:07:94:ARG:N	2.31	0.45
14:11:85:ILE:HD12	14:11:85:ILE:C	2.40	0.45
15:12:70:THR:HG22	15:12:70:THR:O	2.17	0.45
18:15:41:LEU:O	18:15:94:ALA:N	2.44	0.45
27:24:10:LYS:HB3	27:24:10:LYS:HZ2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:275:GLN:HA	39:Z:283:ASN:HD22	1.80	0.45
41:C:6:PRO:HG2	41:C:200:TRP:HE1	1.81	0.45
45:G:111:GLY:HA2	45:G:118:ARG:CZ	2.46	0.45
46:H:12:ARG:HH12	46:H:26:MET:HA	1.81	0.45
55:Q:78:VAL:HG23	55:Q:79:GLU:HG3	1.98	0.45
1:A:686:U:H2'	1:A:687:A:C8	2.52	0.45
1:A:1120:C:H2'	1:A:1121:U:C6	2.52	0.45
1:A:1277:C:H2'	1:A:1278:G:H5''	1.98	0.45
2:01:876:C:H2'	2:01:877:A:O4'	2.16	0.45
2:01:1909:C:H2'	2:01:1910:G:C8	2.51	0.45
6:03:6:LYS:O	6:03:10:VAL:HG23	2.16	0.45
11:08:17:LYS:HZ2	11:08:24:THR:HB	1.80	0.45
16:13:101:GLY:HA2	16:13:102:PRO:HD2	1.72	0.45
21:18:37:LYS:NZ	21:18:37:LYS:HB2	2.32	0.45
27:24:53:LYS:N	27:24:53:LYS:HD2	2.31	0.45
42:D:87:GLU:HG2	42:D:187:ARG:HD3	1.98	0.45
42:D:149:LYS:HZ1	42:D:177:MET:HE3	1.80	0.45
49:K:64:VAL:O	49:K:68:ARG:HG2	2.17	0.45
51:M:97:ARG:HH11	51:M:97:ARG:HG3	1.82	0.45
54:P:3:THR:HG23	54:P:5:ARG:HD2	1.98	0.45
1:A:531:U:OP1	39:Z:213:ARG:NH2	2.46	0.45
2:01:372:G:O2'	2:01:373:U:C5	2.69	0.45
2:01:922:C:H1'	28:25:22:PHE:CD2	2.52	0.45
2:01:1919:A:H2'	2:01:1920:C:H5'	1.98	0.45
2:01:2376:A:H2'	2:01:2377:A:O4'	2.17	0.45
2:01:2457:U:O2'	2:01:2458:G:H5'	2.17	0.45
10:07:7:TYR:O	10:07:12:VAL:HG23	2.17	0.45
11:08:71:LEU:HA	11:08:74:MET:CE	2.46	0.45
15:12:36:LEU:HD22	15:12:121:LYS:HB2	1.97	0.45
17:14:51:GLU:HG3	17:14:56:PRO:HA	1.99	0.45
18:15:69:PRO:HA	18:15:94:ALA:HB2	1.99	0.45
22:19:108:LEU:HD23	23:20:48:LYS:HD2	1.99	0.45
27:24:25:LYS:HE2	27:24:41:GLU:CD	2.40	0.45
39:Z:10:ARG:NH2	39:Z:13:ASP:OD2	2.50	0.45
42:D:167:PRO:HB3	42:D:169:TRP:CH2	2.52	0.45
49:K:113:THR:HG21	59:U:28:LEU:CD1	2.46	0.45
50:L:6:LEU:HB3	55:Q:33:TYR:CZ	2.51	0.45
52:N:20:PHE:CE2	52:N:54:SER:HB3	2.44	0.45
2:01:765:C:H2'	2:01:766:U:C6	2.52	0.45
2:01:792:A:H3'	2:01:793:A:H5'	1.98	0.45
2:01:873:C:H2'	2:01:874:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1103:A:H2'	2:01:1103:A:N3	2.32	0.45
2:01:1653:G:H3'	19:16:2:ARG:HG2	1.98	0.45
3:02:76:G:H5'	27:24:9:ARG:HH12	1.81	0.45
6:03:208:TYR:HD1	6:03:208:TYR:H	1.65	0.45
7:04:241:LYS:HB2	7:04:241:LYS:HZ2	1.81	0.45
8:05:179:ARG:HH21	21:18:7:LEU:HD11	1.79	0.45
16:13:107:LEU:N	16:13:107:LEU:HD12	2.32	0.45
19:16:59:SER:HB3	19:16:62:ASN:ND2	2.31	0.45
24:21:23:LEU:CD1	24:21:39:THR:HG21	2.46	0.45
29:26:49:ARG:HG2	29:26:49:ARG:HH11	1.82	0.45
29:26:67:LEU:HD12	29:26:70:LEU:HD12	1.99	0.45
39:Z:46:VAL:HG22	39:Z:53:ALA:HB2	1.98	0.45
40:B:212:TYR:O	40:B:216:VAL:HG23	2.17	0.45
44:F:17:GLN:HE21	44:F:17:GLN:HB3	1.55	0.45
47:I:114:LYS:O	47:I:117:LEU:HD13	2.17	0.45
54:P:44:SER:H	54:P:46:LYS:NZ	2.14	0.45
1:A:674:G:N2	49:K:117:HIS:HB2	2.31	0.45
2:01:264:C:O2'	2:01:265:A:H5''	2.17	0.45
2:01:1450:G:H21	2:01:1452:G:H1	1.65	0.45
2:01:2221:G:O2'	2:01:2222:C:H5'	2.17	0.45
2:01:2331:G:C4'	28:25:39:THR:H	2.20	0.45
3:02:43:C:H1'	10:07:89:THR:HB	1.99	0.45
4:Y:44:LYS:NZ	4:Y:44:LYS:HB3	2.31	0.45
17:14:47:ARG:HG3	17:14:50:PHE:HB2	1.99	0.45
41:C:127:VAL:HG22	41:C:128:MET:N	2.32	0.45
43:E:105:ILE:O	43:E:105:ILE:HG23	2.17	0.45
47:I:11:ARG:HH11	47:I:11:ARG:HG3	1.82	0.45
48:J:81:GLU:H	48:J:81:GLU:CD	2.24	0.45
53:O:55:LEU:HD23	53:O:55:LEU:C	2.42	0.45
55:Q:45:VAL:HG21	55:Q:60:ILE:HG21	1.99	0.45
55:Q:49:ASN:O	55:Q:51:GLU:N	2.50	0.45
57:S:14:LEU:HD21	57:S:43:MET:HE2	1.99	0.45
1:A:183:C:H5'	1:A:184:G:OP2	2.16	0.45
2:01:357:C:H2'	2:01:358:U:C6	2.52	0.45
2:01:833:A:H2'	2:01:834:G:H8	1.82	0.45
2:01:870:U:H5''	18:15:5:LYS:O	2.17	0.45
2:01:1092:C:H2'	2:01:1093:G:O4'	2.17	0.45
2:01:1480:C:H2'	2:01:1481:U:C6	2.52	0.45
2:01:2352:A:H2'	2:01:2353:G:H5'	1.98	0.45
3:02:13:G:H8	3:02:69:G:H21	1.65	0.45
3:02:30:C:C2'	3:02:31:C:H5'	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:03:30:LEU:HD22	6:03:214:ILE:CD1	2.46	0.45
10:07:57:ALA:HB2	10:07:64:PRO:HD3	1.99	0.45
11:08:14:VAL:HG13	11:08:27:GLY:HA2	1.98	0.45
12:09:116:ARG:HG3	12:09:133:GLN:OE1	2.16	0.45
22:19:38:VAL:O	22:19:42:GLY:N	2.50	0.45
27:24:51:GLN:NE2	27:24:86:LEU:HD11	2.32	0.45
36:33:30:HIS:C	36:33:32:LEU:H	2.25	0.45
37:34:2:LYS:NZ	37:34:35:GLN:HE21	2.16	0.45
40:B:106:VAL:O	40:B:110:ILE:HG13	2.17	0.45
45:G:55:LYS:HD3	45:G:59:GLU:O	2.17	0.45
46:H:95:MET:SD	46:H:129:ALA:HB1	2.56	0.45
51:M:56:ARG:HA	51:M:59:VAL:CG2	2.47	0.45
51:M:92:ARG:HG2	51:M:92:ARG:HH11	1.82	0.45
53:O:7:THR:O	53:O:11:VAL:HG23	2.17	0.45
1:A:556:C:O2'	1:A:557:G:H5'	2.15	0.44
1:A:931:C:O2'	1:A:932:C:H5'	2.17	0.44
1:A:1433:A:OP1	21:18:105:LYS:HD3	2.17	0.44
2:01:1537:G:H3'	2:01:1537:G:N3	2.31	0.44
4:Y:6:HIS:HD2	4:Y:8:LYS:HG3	1.83	0.44
4:Y:44:LYS:HG2	4:Y:45:HIS:CE1	2.51	0.44
7:04:106:PRO:CD	7:04:109:LEU:HD22	2.45	0.44
8:05:9:VAL:HG12	21:18:4:ILE:HD11	1.98	0.44
22:19:45:ALA:O	22:19:49:ARG:HG3	2.17	0.44
33:30:19:ASP:OD1	33:30:19:ASP:N	2.50	0.44
37:34:36:ARG:CG	37:34:37:GLN:N	2.80	0.44
39:Z:332:ARG:C	39:Z:333:ILE:HD12	2.42	0.44
41:C:34:SER:O	41:C:38:VAL:HG23	2.16	0.44
43:E:136:VAL:O	43:E:140:ILE:HG12	2.17	0.44
45:G:25:PHE:HD1	45:G:100:MET:HG3	1.82	0.44
46:H:17:GLN:HA	46:H:64:TYR:OH	2.16	0.44
51:M:15:VAL:HG22	51:M:33:LEU:HD22	1.98	0.44
1:A:590:U:OP1	46:H:30:LYS:HG3	2.17	0.44
2:01:414:C:H2'	2:01:415:A:H8	1.82	0.44
2:01:770:G:H5''	35:32:10:LEU:HD23	2.00	0.44
2:01:1386:C:H2'	2:01:1387:A:H8	1.82	0.44
2:01:2029:G:O6	2:01:2032:G:H5''	2.16	0.44
2:01:2466:C:OP1	37:34:4:ARG:HB3	2.17	0.44
2:01:2553:G:C3'	2:01:2554:U:H5''	2.43	0.44
2:01:2570:G:H2'	2:01:2571:U:O4'	2.17	0.44
21:18:82:SER:O	21:18:83:ILE:HD13	2.17	0.44
27:24:63:ILE:HG23	27:24:70:ILE:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:8:ASN:HD22	39:Z:8:ASN:N	2.13	0.44
39:Z:245:ARG:HH11	39:Z:245:ARG:HG3	1.81	0.44
40:B:31:PHE:N	40:B:39:ILE:O	2.41	0.44
48:J:14:ASP:OD2	48:J:16:ARG:HB2	2.17	0.44
54:P:26:ASN:N	54:P:26:ASN:ND2	2.63	0.44
58:T:32:LYS:HA	58:T:35:TYR:HD2	1.81	0.44
1:A:137:U:H2'	1:A:138:G:H5'	1.99	0.44
1:A:845:A:O4'	56:R:11:ARG:HD3	2.18	0.44
1:A:908:A:H2'	1:A:909:A:C8	2.52	0.44
2:01:242:G:H5''	36:33:63:TYR:CD2	2.52	0.44
2:01:1028:A:H2'	2:01:1029:A:C8	2.52	0.44
2:01:1046:A:H5'	2:01:1047:G:H5''	1.97	0.44
2:01:1230:A:H2'	2:01:1231:U:O4'	2.17	0.44
2:01:1300:G:H4'	2:01:1301:A:C5'	2.48	0.44
2:01:1575:C:O2'	2:01:1576:U:H5'	2.17	0.44
2:01:2514:U:H5''	15:12:81:ILE:CD1	2.47	0.44
2:01:2573:C:O2	2:01:2573:C:C2'	2.65	0.44
22:19:71:ASN:HD22	22:19:71:ASN:HA	1.56	0.44
23:20:1:MET:HG3	23:20:15:SER:HB2	1.98	0.44
29:26:31:ASN:HD21	29:26:33:HIS:HE1	1.66	0.44
30:27:10:SER:O	30:27:14:LEU:HD13	2.16	0.44
32:29:59:ARG:NH2	32:29:62:LYS:HB3	2.25	0.44
36:33:30:HIS:O	36:33:32:LEU:N	2.50	0.44
36:33:36:ALA:O	36:33:40:LYS:HG3	2.17	0.44
39:Z:18:SER:O	39:Z:22:ARG:HG3	2.17	0.44
42:D:3:TYR:CD2	42:D:10:LEU:HD11	2.52	0.44
45:G:29:LEU:HD12	45:G:29:LEU:C	2.42	0.44
45:G:92:PRO:HA	45:G:95:ARG:HD2	1.99	0.44
47:I:29:ILE:HD11	47:I:66:VAL:HG12	1.99	0.44
50:L:70:GLY:O	50:L:98:ARG:NH2	2.49	0.44
53:O:47:LYS:N	53:O:47:LYS:HD2	2.33	0.44
54:P:26:ASN:OD1	54:P:31:ARG:HB3	2.17	0.44
55:Q:43:LEU:HD13	55:Q:72:TRP:CE2	2.52	0.44
1:A:256:U:H2'	1:A:257:G:C8	2.53	0.44
1:A:291:U:C3'	1:A:292:G:H5''	2.47	0.44
1:A:579:A:H2'	1:A:580:C:H6	1.82	0.44
1:A:1170:A:H2'	1:A:1171:A:O4'	2.17	0.44
2:01:738:G:O2'	2:01:739:A:H5'	2.17	0.44
2:01:906:U:C2'	2:01:907:G:H5''	2.42	0.44
2:01:974:G:H2'	2:01:974:G:N3	2.33	0.44
2:01:1818:U:H5'	7:04:156:SER:OG	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:06:189:THR:HG22	9:06:191:ASP:H	1.82	0.44
10:07:1:ALA:N	10:07:4:HIS:HB3	2.32	0.44
11:08:172:GLU:HG2	11:08:173:ALA:N	2.33	0.44
11:08:172:GLU:HG2	11:08:174:LYS:H	1.82	0.44
15:12:4:PHE:CD2	22:19:99:VAL:HG11	2.52	0.44
18:15:34:LYS:HD2	27:24:81:PRO:O	2.17	0.44
19:16:9:GLN:O	19:16:17:ARG:HD3	2.18	0.44
19:16:61:ALA:O	19:16:65:LEU:HD12	2.18	0.44
19:16:73:ASN:O	19:16:77:ALA:N	2.45	0.44
22:19:105:PHE:O	22:19:109:VAL:HG23	2.16	0.44
32:29:16:CYS:SG	32:29:17:SER:N	2.90	0.44
41:C:122:GLN:O	41:C:127:VAL:HG12	2.17	0.44
48:J:76:ILE:N	48:J:76:ILE:HD12	2.32	0.44
50:L:23:LEU:HD22	50:L:58:ASN:HB3	2.00	0.44
50:L:29:LYS:CE	50:L:58:ASN:HD21	2.30	0.44
1:A:579:A:H2'	1:A:580:C:C6	2.53	0.44
1:A:1114:C:H1'	52:N:99:SER:HB3	1.98	0.44
1:A:1413:A:H2	1:A:1487:G:H22	1.65	0.44
2:01:687:C:H5''	35:32:4:THR:O	2.16	0.44
2:01:940:G:C2'	2:01:941:A:H5''	2.47	0.44
2:01:940:G:C3'	2:01:941:A:H5''	2.47	0.44
2:01:1085:A:H5'	2:01:1105:U:O2'	2.18	0.44
2:01:2246:G:H2'	2:01:2247:A:C8	2.51	0.44
2:01:2841:C:H2'	2:01:2842:G:C8	2.53	0.44
11:08:123:GLU:HB2	11:08:131:VAL:O	2.18	0.44
13:10:31:ARG:HH11	13:10:31:ARG:HG3	1.82	0.44
16:13:1:MET:HG2	16:13:67:LYS:HD2	1.99	0.44
29:26:69:GLU:O	29:26:73:ARG:HG3	2.17	0.44
39:Z:144:TRP:CD1	39:Z:201:LEU:HD22	2.52	0.44
40:B:68:PHE:HD1	40:B:161:PHE:HB3	1.82	0.44
43:E:151:MET:HE3	43:E:154:ALA:HB3	1.99	0.44
43:E:158:LYS:N	43:E:158:LYS:HD2	2.32	0.44
44:F:18:VAL:HG21	44:F:58:HIS:CD2	2.53	0.44
47:I:60:LEU:HD12	47:I:60:LEU:O	2.18	0.44
51:M:76:ILE:O	51:M:80:MET:HG3	2.18	0.44
1:A:31:G:H5'	1:A:306:A:C2	2.53	0.44
1:A:1250:A:H5'	47:I:68:GLY:HA2	2.00	0.44
2:01:517:C:H5''	33:30:12:ARG:NH1	2.30	0.44
2:01:1021:A:H2'	2:01:1022:G:H4'	1.99	0.44
2:01:1111:A:H2'	2:01:1112:G:H4'	2.00	0.44
2:01:2055:C:H2'	2:01:2504:U:H5'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2140:G:O2'	2:01:2141:G:H5'	2.18	0.44
2:01:2331:G:H4'	28:25:39:THR:N	2.19	0.44
2:01:2603:G:O2'	2:01:2604:U:H5'	2.17	0.44
14:11:14:ALA:HA	14:11:41:PHE:CZ	2.53	0.44
16:13:63:VAL:HB	16:13:103:VAL:HG12	1.99	0.44
22:19:49:ARG:HH21	23:20:72:VAL:HG13	1.82	0.44
29:26:16:ASN:HD21	29:26:26:ARG:HB3	1.83	0.44
30:27:26:PHE:HD1	30:27:29:ARG:HH11	1.64	0.44
31:28:26:LEU:HD11	31:28:46:MET:CB	2.46	0.44
51:M:28:ARG:NH2	51:M:62:PHE:HB2	2.31	0.44
51:M:48:SER:O	51:M:52:ILE:HG13	2.18	0.44
52:N:97:LYS:CG	52:N:98:ALA:H	2.21	0.44
2:01:2243:U:H2'	2:01:2244:U:H6	1.81	0.44
2:01:2294:G:O2'	2:01:2295:C:H5'	2.17	0.44
5:X:19:G:H1'	5:X:57:A:N1	2.32	0.44
7:04:202:ARG:NH2	7:04:213:ARG:NH2	2.65	0.44
7:04:246:PRO:HG2	7:04:247:TRP:CE3	2.53	0.44
11:08:14:VAL:HG13	11:08:26:LYS:O	2.18	0.44
11:08:106:LEU:HB2	11:08:108:PHE:CE2	2.52	0.44
15:12:35:ARG:HA	15:12:40:HIS:HD2	1.82	0.44
16:13:38:ILE:HD11	16:13:112:PHE:CZ	2.53	0.44
22:19:12:ARG:HH21	22:19:12:ARG:HG3	1.83	0.44
22:19:16:ILE:HG23	22:19:38:VAL:HG21	1.99	0.44
22:19:61:ILE:HG23	22:19:75:TYR:CZ	2.52	0.44
39:Z:153:LEU:HD23	39:Z:153:LEU:C	2.43	0.44
40:B:13:VAL:HG21	40:B:207:ARG:HD3	1.99	0.44
40:B:138:ARG:HG2	40:B:138:ARG:HH11	1.81	0.44
41:C:119:ILE:HD11	41:C:197:VAL:HG11	2.00	0.44
45:G:68:VAL:HG21	45:G:103:ILE:HD11	1.98	0.44
1:A:279:A:H4'	1:A:281:G:C8	2.53	0.44
1:A:383:A:H4'	1:A:455:G:H5'	2.00	0.44
1:A:1064:G:N2	1:A:1190:G:H1'	2.33	0.44
1:A:1313:U:P	57:S:5:LYS:HA	2.57	0.44
1:A:1496:C:H2'	1:A:1497:G:O4'	2.18	0.44
2:01:581:C:H2'	2:01:582:A:C8	2.52	0.44
2:01:826:U:H2'	2:01:828:U:O4'	2.18	0.44
2:01:2322:A:H2'	2:01:2323:G:O4'	2.18	0.44
4:Y:20:LEU:HD21	39:Z:134:ALA:C	2.43	0.44
7:04:143:VAL:HG11	7:04:173:LEU:HD11	2.00	0.44
12:09:30:LEU:HB3	12:09:36:ALA:HB3	1.99	0.44
14:11:37:PHE:O	14:11:41:PHE:N	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:21:34:ASP:O	24:21:37:THR:OG1	2.36	0.44
25:22:8:LEU:CD1	30:27:21:LEU:HD12	2.48	0.44
30:27:53:VAL:O	30:27:57:LEU:HD13	2.17	0.44
39:Z:147:MET:HE1	39:Z:203:ARG:NH1	2.33	0.44
42:D:145:ARG:HG2	42:D:145:ARG:HH11	1.82	0.44
44:F:35:LYS:HB2	44:F:65:GLU:HB3	2.00	0.44
47:I:118:ARG:HH11	47:I:118:ARG:HG3	1.82	0.44
58:T:52:GLU:O	58:T:55:PRO:HD2	2.18	0.44
1:A:17:U:H2'	1:A:18:C:H6	1.83	0.44
1:A:366:A:H2	1:A:393:A:H61	1.66	0.44
1:A:394:G:H2'	1:A:395:C:H5''	1.98	0.44
1:A:1225:A:H5'	1:A:1226:C:OP2	2.18	0.44
1:A:1299:A:H2'	1:A:1300:G:H4'	2.00	0.44
2:01:27:G:N2	2:01:512:G:H1'	2.32	0.44
2:01:278:A:H2	2:01:279:A:N7	2.16	0.44
2:01:1057:A:H1'	13:10:37:LYS:NZ	2.33	0.44
2:01:1443:U:H2'	2:01:1444:G:H8	1.83	0.44
2:01:1447:C:H2'	2:01:1448:G:C8	2.52	0.44
2:01:1650:A:H4'	19:16:103:ARG:NH2	2.32	0.44
2:01:2266:A:H4'	2:01:2267:A:C2	2.52	0.44
2:01:2566:A:N1	16:13:28:SER:HB2	2.32	0.44
2:01:2755:C:O2'	2:01:2756:U:H2'	2.18	0.44
7:04:129:LEU:HD11	7:04:134:ILE:HG12	1.98	0.44
7:04:164:VAL:HG23	7:04:174:ARG:HB2	1.99	0.44
10:07:3:LEU:O	10:07:7:TYR:N	2.49	0.44
18:15:78:LEU:HD13	39:Z:281:HIS:ND1	2.33	0.44
32:29:38:SER:HA	32:29:41:HIS:HB2	1.99	0.44
43:E:75:LEU:O	43:E:75:LEU:HD12	2.18	0.44
44:F:7:VAL:HB	44:F:88:MET:HB3	2.00	0.44
44:F:18:VAL:HG12	44:F:19:PRO:HD3	2.00	0.44
48:J:91:ASP:CG	48:J:92:LEU:H	2.26	0.44
52:N:2:LYS:O	52:N:5:MET:N	2.45	0.44
1:A:88:U:H2'	1:A:89:U:C5	2.53	0.43
1:A:707:U:H2'	1:A:708:C:C6	2.53	0.43
1:A:813:U:H2'	1:A:814:A:H5''	2.00	0.43
1:A:1196:A:C4	4:Y:34:LYS:HB3	2.53	0.43
2:01:1437:C:H2'	2:01:1438:U:C6	2.53	0.43
2:01:2006:C:H5''	2:01:2048:G:H5''	2.00	0.43
2:01:2087:G:H2'	2:01:2088:A:C8	2.53	0.43
2:01:2364:C:H2'	2:01:2365:G:O4'	2.18	0.43
2:01:2391:G:C5'	36:33:31:ILE:HD12	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:27:ILE:HB	8:05:187:LEU:HB3	2.00	0.43
8:05:56:LYS:HB2	8:05:59:ARG:HB3	2.00	0.43
9:06:24:ASN:O	9:06:28:VAL:HG23	2.18	0.43
11:08:90:GLY:HA3	11:08:93:TYR:CE2	2.53	0.43
15:12:37:ARG:HG3	15:12:118:MET:HE1	1.99	0.43
17:14:92:LEU:O	17:14:96:LYS:HG2	2.18	0.43
19:16:90:ARG:HH12	19:16:116:VAL:HB	1.82	0.43
23:20:90:ARG:HG2	23:20:90:ARG:HH11	1.81	0.43
27:24:42:LEU:CD1	27:24:47:VAL:HG21	2.39	0.43
49:K:126:ARG:HB2	59:U:33:ARG:NH2	2.33	0.43
50:L:4:ASN:ND2	55:Q:35:LYS:NZ	2.66	0.43
50:L:58:ASN:N	50:L:58:ASN:ND2	2.66	0.43
59:U:13:VAL:HB	59:U:15:LEU:HD11	2.00	0.43
1:A:1062:U:H2'	1:A:1063:C:C6	2.53	0.43
1:A:1123:U:O2'	1:A:1124:G:H5'	2.18	0.43
1:A:1320:C:OP1	57:S:69:LYS:HE2	2.17	0.43
2:01:527:C:N3	2:01:2779:U:H2'	2.34	0.43
2:01:1038:G:H2'	2:01:1039:A:C8	2.54	0.43
2:01:1912:A:N6	2:01:1917:U:C5	2.76	0.43
7:04:131:MET:HE2	7:04:187:CYS:HB2	1.99	0.43
19:16:38:LEU:HD13	19:16:109:PRO:O	2.18	0.43
24:21:74:ILE:HD13	24:21:105:VAL:HG22	2.00	0.43
25:22:54:GLU:HB2	25:22:88:LYS:HB2	2.01	0.43
39:Z:138:GLY:O	39:Z:142:GLN:HG2	2.18	0.43
41:C:28:PHE:HE2	52:N:76:PHE:CD1	2.36	0.43
41:C:69:THR:O	41:C:105:VAL:HG23	2.18	0.43
44:F:44:ARG:HA	44:F:58:HIS:HA	1.99	0.43
2:01:729:G:C5	7:04:206:LYS:HB2	2.54	0.43
2:01:817:C:O2'	2:01:839:U:H5''	2.18	0.43
2:01:940:G:H2'	2:01:941:A:C5'	2.48	0.43
2:01:1794:A:H2'	2:01:1795:C:C6	2.53	0.43
2:01:2450:A:O2'	2:01:2451:A:H5'	2.18	0.43
3:02:49:C:H4'	20:17:68:LYS:HZ1	1.82	0.43
8:05:16:THR:HG22	8:05:17:GLU:N	2.32	0.43
8:05:181:ASP:HB2	8:05:186:LEU:HB2	2.01	0.43
11:08:10:VAL:HG12	11:08:47:ASN:O	2.18	0.43
14:11:46:ASP:HA	14:11:50:LYS:HD3	1.99	0.43
19:16:35:LYS:HE2	19:16:110:MET:SD	2.58	0.43
20:17:31:THR:HB	20:17:32:PRO:HD2	2.01	0.43
20:17:83:LEU:HD23	20:17:83:LEU:C	2.42	0.43
21:18:61:ARG:HG3	21:18:61:ARG:HH21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:18:96:LEU:HD22	21:18:98:TYR:HE1	1.84	0.43
22:19:2:ARG:HH22	22:19:4:LYS:HG2	1.83	0.43
39:Z:84:LEU:HD11	39:Z:96:PHE:HD1	1.83	0.43
39:Z:344:ASN:O	39:Z:348:VAL:HG23	2.18	0.43
42:D:201:GLU:CD	43:E:104:ILE:HG22	2.43	0.43
59:U:15:LEU:HA	59:U:17:ARG:NH1	2.28	0.43
1:A:546:A:OP1	42:D:69:ARG:HG2	2.18	0.43
1:A:1049:U:H5'	1:A:1201:A:P	2.59	0.43
1:A:1436:U:H2'	1:A:1437:A:H8	1.82	0.43
2:01:687:C:H2'	2:01:688:U:O4'	2.18	0.43
2:01:729:G:C6	7:04:206:LYS:HB2	2.54	0.43
2:01:1040:A:O2'	2:01:1041:G:H5'	2.18	0.43
2:01:1335:C:H2'	2:01:1336:A:C8	2.54	0.43
2:01:1775:U:H2'	2:01:1776:G:O4'	2.17	0.43
2:01:2345:G:H5'	2:01:2347:C:H5'	2.00	0.43
2:01:2348:U:H5'	34:31:20:TYR:OH	2.18	0.43
2:01:2741:A:C2'	2:01:2742:G:H5'	2.48	0.43
6:03:170:ILE:HD12	6:03:170:ILE:N	2.34	0.43
7:04:30:ALA:HB3	7:04:31:PRO:HD3	2.00	0.43
19:16:9:GLN:HA	19:16:17:ARG:NH2	2.33	0.43
24:21:84:ARG:HH21	24:21:84:ARG:HG2	1.82	0.43
26:23:60:LYS:HG3	26:23:61:GLU:N	2.33	0.43
32:29:6:HIS:HB3	32:29:7:PRO:HD2	2.00	0.43
39:Z:117:ARG:NH2	39:Z:357:ILE:HG22	2.29	0.43
41:C:150:VAL:HG22	41:C:199:VAL:HG23	2.00	0.43
43:E:119:VAL:CG1	43:E:122:VAL:HG22	2.48	0.43
47:I:78:ILE:O	47:I:82:ILE:HG13	2.19	0.43
53:O:2:LEU:HG	53:O:7:THR:OG1	2.18	0.43
1:A:52:C:H2'	1:A:53:A:H8	1.83	0.43
1:A:52:C:H2'	1:A:53:A:C8	2.53	0.43
1:A:502:A:O2'	1:A:550:G:H4'	2.18	0.43
1:A:722:G:H1	1:A:733:G:H1	1.67	0.43
1:A:750:C:H2'	1:A:751:U:C6	2.53	0.43
2:01:627:A:N7	17:14:111:ILE:HD12	2.33	0.43
2:01:996:A:H4'	22:19:90:ASP:OD2	2.18	0.43
2:01:1367:A:C2'	2:01:1368:G:H5'	2.48	0.43
2:01:1666:G:O2'	2:01:1667:G:H5'	2.19	0.43
2:01:2327:A:H2'	2:01:2328:A:C8	2.54	0.43
2:01:2741:A:H2'	2:01:2742:G:O4'	2.18	0.43
3:02:97:C:C2'	3:02:98:G:H5'	2.49	0.43
5:X:17:C:OP1	5:X:61:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:38:LYS:HE2	8:05:81:GLU:OE1	2.19	0.43
9:06:148:ILE:HD13	9:06:187:VAL:CG1	2.48	0.43
19:16:44:LEU:HD23	19:16:113:ILE:HD13	2.01	0.43
28:25:10:ARG:H	28:25:10:ARG:HD3	1.83	0.43
39:Z:144:TRP:CG	39:Z:201:LEU:HD22	2.53	0.43
48:J:49:PHE:CZ	52:N:75:LYS:HG2	2.54	0.43
49:K:33:ILE:HD12	49:K:73:VAL:HG11	1.98	0.43
52:N:23:ARG:NH1	52:N:50:LEU:HD11	2.34	0.43
52:N:26:LEU:O	52:N:30:ILE:HB	2.18	0.43
1:A:29:U:O2'	1:A:30:U:H5'	2.19	0.43
1:A:367:U:C2	1:A:393:A:C2	3.06	0.43
1:A:735:C:H5'	56:R:59:LYS:HD3	2.00	0.43
1:A:946:A:H2'	1:A:947:G:C8	2.54	0.43
1:A:983:A:H5'	1:A:984:C:OP2	2.18	0.43
2:01:184:C:H2'	2:01:185:G:C8	2.54	0.43
2:01:327:G:O2'	2:01:328:U:H5'	2.19	0.43
2:01:1666:G:C2'	2:01:1667:G:H5'	2.49	0.43
2:01:2025:C:H2'	2:01:2026:U:C6	2.53	0.43
7:04:28:PRO:HG2	7:04:33:LEU:HD21	2.00	0.43
7:04:85:ASN:N	7:04:85:ASN:ND2	2.66	0.43
8:05:38:LYS:NZ	8:05:49:GLN:HB2	2.33	0.43
9:06:187:VAL:HG13	9:06:187:VAL:O	2.19	0.43
9:06:188:MET:SD	9:06:193:VAL:HG22	2.58	0.43
10:07:97:GLU:CD	32:29:25:ARG:HD2	2.43	0.43
12:09:132:PHE:HB2	12:09:140:ALA:HB3	1.99	0.43
21:18:19:PHE:CE2	21:18:46:VAL:HG21	2.53	0.43
26:23:32:LYS:HB3	26:23:63:ALA:HB1	2.00	0.43
35:32:1:MET:HB2	35:32:3:ARG:NH2	2.24	0.43
39:Z:150:ARG:HA	39:Z:153:LEU:HB3	2.01	0.43
42:D:88:ASN:O	42:D:92:LEU:HG	2.18	0.43
48:J:100:ILE:O	48:J:100:ILE:HG13	2.18	0.43
52:N:80:ARG:HA	52:N:83:VAL:HG22	1.99	0.43
52:N:87:ALA:HB1	52:N:88:MET:H	1.51	0.43
59:U:52:VAL:O	59:U:56:ALA:N	2.43	0.43
1:A:371:A:H2'	1:A:372:C:O4'	2.18	0.43
1:A:448:A:H62	1:A:486:U:H3	1.67	0.43
1:A:1422:G:H5'	16:13:48:PRO:CG	2.49	0.43
1:A:1436:U:H2'	1:A:1437:A:C8	2.53	0.43
2:01:84:A:N7	2:01:101:A:H2	2.17	0.43
2:01:397:U:OP2	29:26:9:LYS:HD3	2.18	0.43
2:01:616:A:H2'	2:01:617:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:859:G:HO2'	2:01:860:U:H6	1.63	0.43
2:01:1210:G:P	2:01:1212:G:H5'	2.58	0.43
2:01:2665:A:O2'	2:01:2666:C:H5'	2.19	0.43
6:03:164:ARG:HG3	6:03:171:ILE:HD13	1.99	0.43
8:05:8:LYS:C	8:05:8:LYS:HD3	2.43	0.43
8:05:83:ARG:HG2	8:05:83:ARG:HH21	1.83	0.43
9:06:21:ARG:HG2	9:06:110:SER:OG	2.19	0.43
10:07:147:ARG:HB2	10:07:149:ARG:HG2	1.99	0.43
15:12:58:ASN:HD21	15:12:128:ASN:ND2	2.17	0.43
18:15:66:ARG:HG3	18:15:66:ARG:HH11	1.82	0.43
19:16:35:LYS:HB2	19:16:112:TYR:CE1	2.53	0.43
22:19:91:ARG:HG3	22:19:91:ARG:NH1	2.33	0.43
22:19:95:ALA:O	22:19:99:VAL:HG23	2.19	0.43
23:20:57:GLY:CA	23:20:102:SER:HB3	2.48	0.43
26:23:95:PHE:CD2	26:23:100:GLU:HB2	2.49	0.43
28:25:7:ARG:O	28:25:10:ARG:NH1	2.51	0.43
34:31:8:ILE:HD12	34:31:8:ILE:C	2.43	0.43
34:31:32:LYS:HZ3	34:31:50:GLU:HB3	1.82	0.43
39:Z:48:ASN:O	39:Z:48:ASN:ND2	2.52	0.43
39:Z:52:ARG:HG3	39:Z:52:ARG:HH11	1.83	0.43
39:Z:265:HIS:CD2	39:Z:267:PRO:HD2	2.53	0.43
42:D:194:ILE:N	42:D:194:ILE:HD12	2.33	0.43
50:L:68:GLY:HA3	50:L:98:ARG:NH1	2.34	0.43
55:Q:16:MET:HE3	55:Q:21:VAL:HG23	2.01	0.43
1:A:889:A:O3'	1:A:890:G:H4'	2.19	0.43
1:A:986:U:H2'	1:A:987:G:C8	2.53	0.43
2:01:395:U:H2'	2:01:396:G:C8	2.52	0.43
2:01:967:U:H2'	2:01:968:C:C6	2.54	0.43
2:01:1565:C:O2'	2:01:1566:A:C8	2.72	0.43
2:01:2183:A:H2'	2:01:2184:A:H8	1.84	0.43
2:01:2360:G:C2'	2:01:2361:G:H5'	2.48	0.43
2:01:2655:G:O2'	2:01:2656:U:C5	2.70	0.43
3:02:28:C:H2'	3:02:29:A:C8	2.53	0.43
8:05:77:ARG:HH21	8:05:77:ARG:HG3	1.83	0.43
11:08:42:VAL:HB	11:08:51:PHE:CD1	2.54	0.43
11:08:54:ARG:HH11	11:08:54:ARG:HG3	1.84	0.43
12:09:90:LEU:HD23	12:09:91:PHE:N	2.33	0.43
13:10:7:ASP:O	13:10:11:ILE:HG12	2.18	0.43
14:11:131:THR:O	14:11:135:MET:HG2	2.19	0.43
21:18:91:VAL:HG21	21:18:96:LEU:HD21	1.99	0.43
22:19:40:LYS:HG3	22:19:44:TYR:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:22:12:ARG:NH1	30:27:29:ARG:HH21	2.17	0.43
39:Z:103:LEU:HD23	39:Z:103:LEU:C	2.44	0.43
40:B:17:HIS:O	40:B:19:THR:N	2.44	0.43
41:C:6:PRO:HD2	41:C:183:TYR:CD2	2.53	0.43
45:G:91:ARG:O	45:G:95:ARG:HG3	2.18	0.43
46:H:45:ILE:HD12	46:H:62:LEU:HA	2.01	0.43
57:S:2:ARG:N	57:S:2:ARG:HD2	2.34	0.43
1:A:21:G:H2'	1:A:22:G:C8	2.54	0.43
1:A:410:G:H2'	1:A:429:U:C4	2.54	0.43
1:A:742:G:O2'	1:A:743:A:H5'	2.19	0.43
2:01:1528:A:H2'	2:01:1529:G:O4'	2.19	0.43
2:01:1545:A:C2'	2:01:1546:G:H5'	2.49	0.43
3:02:5:U:H2'	3:02:6:G:H8	1.84	0.43
4:Y:28:ARG:HH11	4:Y:28:ARG:HG3	1.83	0.43
9:06:153:LEU:HD23	9:06:153:LEU:C	2.44	0.43
13:10:43:LYS:NZ	13:10:95:LEU:HA	2.34	0.43
14:11:97:VAL:O	14:11:138:VAL:HG23	2.19	0.43
19:16:1:MET:C	19:16:2:ARG:HG3	2.43	0.43
19:16:60:VAL:O	19:16:64:ARG:HG2	2.19	0.43
39:Z:245:ARG:HG3	39:Z:245:ARG:NH1	2.34	0.43
42:D:71:PHE:HE1	42:D:93:LEU:HD21	1.83	0.43
50:L:4:ASN:HD22	55:Q:35:LYS:NZ	2.17	0.43
1:A:1097:C:H2'	1:A:1098:C:C6	2.54	0.43
1:A:1191:A:H5''	41:C:3:LYS:NZ	2.33	0.43
1:A:1241:G:H2'	1:A:1242:G:C8	2.54	0.43
2:01:6:A:H2'	2:01:7:G:C8	2.54	0.43
2:01:1934:C:H4'	2:01:1974:C:O3'	2.19	0.43
2:01:2164:C:C2'	2:01:2165:C:H5'	2.49	0.43
2:01:2531:A:H4'	11:08:156:TYR:CZ	2.53	0.43
4:Y:4:TYR:CZ	4:Y:24:LEU:HB2	2.54	0.43
7:04:134:ILE:HD13	7:04:140:VAL:HG21	1.99	0.43
9:06:31:VAL:HG21	9:06:104:ALA:HB2	2.01	0.43
10:07:97:GLU:O	10:07:101:ARG:HG2	2.19	0.43
15:12:114:LEU:HG	15:12:118:MET:SD	2.59	0.43
16:13:2:ILE:HD12	16:13:8:LEU:HD21	2.00	0.43
42:D:161:ALA:HA	42:D:164:ARG:HH11	1.84	0.43
46:H:21:LYS:O	46:H:62:LEU:HD12	2.19	0.43
48:J:33:GLY:O	48:J:34:ALA:HB2	2.19	0.43
52:N:85:GLU:C	52:N:87:ALA:N	2.77	0.43
54:P:76:LYS:HB2	54:P:76:LYS:HZ3	1.84	0.43
1:A:77:A:H2'	1:A:78:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:G:H2'	1:A:98:A:H5'	2.00	0.42
1:A:320:A:H2'	1:A:321:A:C8	2.54	0.42
1:A:368:U:H5'	1:A:369:G:H5''	2.01	0.42
1:A:676:A:H5''	49:K:114:PRO:HB3	2.01	0.42
1:A:820:U:H3'	1:A:821:G:C5'	2.49	0.42
1:A:880:C:OP2	50:L:4:ASN:HB3	2.19	0.42
1:A:1216:A:H5''	52:N:4:SER:OG	2.19	0.42
2:01:243:U:O2'	2:01:244:A:H5'	2.18	0.42
2:01:1404:C:O2'	2:01:1405:U:H5'	2.19	0.42
2:01:1522:A:H8	2:01:1522:A:OP1	2.02	0.42
2:01:1846:G:H2'	2:01:1847:G:C8	2.54	0.42
2:01:1858:A:H1'	2:01:1885:A:C2	2.53	0.42
2:01:2286:G:H4'	2:01:2287:A:C4	2.54	0.42
2:01:2641:G:H2'	2:01:2642:G:H8	1.84	0.42
2:01:2671:G:H2'	2:01:2672:U:C6	2.53	0.42
2:01:2834:G:H2'	2:01:2879:A:N6	2.32	0.42
4:Y:24:LEU:HA	50:L:40:THR:HG21	2.01	0.42
5:X:55:U:C4	5:X:57:A:H5''	2.54	0.42
6:03:175:ILE:HG12	6:03:188:ASN:OD1	2.19	0.42
9:06:14:VAL:HG12	9:06:15:SER:N	2.29	0.42
11:08:82:PHE:CE2	11:08:137:LYS:HB2	2.54	0.42
11:08:88:LEU:HD12	11:08:88:LEU:N	2.34	0.42
15:12:59:ALA:HB3	15:12:126:ALA:HA	2.01	0.42
17:14:79:LEU:HB3	17:14:114:GLY:H	1.84	0.42
25:22:93:LEU:HD23	25:22:93:LEU:C	2.44	0.42
39:Z:170:GLU:HA	39:Z:176:ILE:HA	2.01	0.42
40:B:168:GLU:O	40:B:172:ILE:HG13	2.18	0.42
45:G:11:ILE:HD11	45:G:20:GLU:HB3	2.01	0.42
45:G:96:ASN:O	45:G:100:MET:SD	2.77	0.42
45:G:132:THR:O	45:G:136:LYS:HG3	2.19	0.42
47:I:64:ILE:HD13	47:I:78:ILE:HG23	2.01	0.42
47:I:123:ARG:HG3	47:I:124:PRO:HD2	2.01	0.42
1:A:1143:G:O2'	1:A:1144:G:H5'	2.19	0.42
1:A:1151:A:H1'	48:J:41:PRO:HG3	2.00	0.42
2:01:127:A:H5''	2:01:128:C:O4'	2.20	0.42
2:01:150:U:H2'	2:01:151:C:C6	2.54	0.42
3:02:95:U:H2'	3:02:96:G:C8	2.55	0.42
6:03:27:ILE:O	6:03:31:LYS:N	2.52	0.42
6:03:28:ALA:O	6:03:32:GLU:HG2	2.18	0.42
8:05:139:SER:HA	8:05:142:VAL:CG2	2.49	0.42
12:09:97:ARG:HH11	12:09:97:ARG:HG3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:12:117:ALA:HA	15:12:120:ARG:NE	2.24	0.42
26:23:28:LEU:N	26:23:28:LEU:HD12	2.34	0.42
26:23:33:VAL:HG23	26:23:64:ILE:HG23	2.00	0.42
5:W:23:C:H2'	5:W:24:U:C6	2.53	0.42
42:D:27:ILE:HG13	42:D:28:ASP:N	2.27	0.42
43:E:44:ARG:HG2	43:E:44:ARG:HH11	1.83	0.42
45:G:9:ARG:HG3	45:G:9:ARG:HH11	1.84	0.42
45:G:142:ARG:HG2	45:G:142:ARG:HH11	1.84	0.42
51:M:72:ILE:O	51:M:76:ILE:HG13	2.19	0.42
54:P:18:GLN:NE2	54:P:35:ARG:HD2	2.34	0.42
55:Q:18:LYS:HD3	55:Q:48:GLU:OE2	2.19	0.42
1:A:163:C:H2'	1:A:164:G:C4'	2.50	0.42
1:A:917:G:H2'	1:A:918:A:C8	2.54	0.42
2:01:6:A:H2'	2:01:7:G:H8	1.84	0.42
2:01:249:C:H2'	2:01:2394:C:O2'	2.20	0.42
2:01:720:U:H2'	2:01:721:A:H8	1.84	0.42
2:01:859:G:O2'	2:01:860:U:C6	2.73	0.42
2:01:941:A:O2'	2:01:1190:G:H4'	2.19	0.42
2:01:1352:U:O2'	2:01:1353:A:H5'	2.19	0.42
2:01:2230:G:H5''	29:26:29:LEU:HD12	2.01	0.42
2:01:2646:C:H2'	2:01:2647:U:O4'	2.20	0.42
2:01:2679:A:O2'	2:01:2680:U:H5'	2.19	0.42
2:01:2825:G:H2'	2:01:2826:A:H5'	2.02	0.42
10:07:70:ARG:HG2	10:07:70:ARG:HH21	1.84	0.42
11:08:152:ARG:HD2	11:08:152:ARG:N	2.27	0.42
12:09:4:ILE:HG21	12:09:47:PHE:CD2	2.54	0.42
41:C:46:LEU:HB3	41:C:49:ALA:HB3	2.01	0.42
1:A:206:C:H2'	1:A:207:C:H5'	2.00	0.42
1:A:530:G:C6	4:Y:30:GLU:HA	2.55	0.42
1:A:1026:G:N1	1:A:1035:A:C2	2.77	0.42
1:A:1118:U:H2'	1:A:1119:C:H6	1.82	0.42
1:A:1170:A:C2'	1:A:1171:A:H5'	2.49	0.42
1:A:1522:U:H2'	1:A:1523:G:C8	2.54	0.42
2:01:184:C:H2'	2:01:185:G:H8	1.84	0.42
2:01:222:A:N6	2:01:232:G:H1'	2.34	0.42
2:01:386:G:H3'	2:01:387:U:H5''	2.01	0.42
2:01:566:U:H2'	2:01:567:U:O4'	2.19	0.42
2:01:1306:C:H41	2:01:1606:C:H2'	1.82	0.42
2:01:1651:G:H5'	19:16:39:PRO:HB2	2.00	0.42
2:01:2136:G:H2'	2:01:2137:U:C5'	2.49	0.42
2:01:2330:G:H21	28:25:38:GLY:HA2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2364:C:OP1	28:25:51:ARG:HD3	2.19	0.42
5:X:26:G:H1	5:X:44:A:H2	1.67	0.42
8:05:1:MET:CG	8:05:205:PRO:HG2	2.49	0.42
9:06:135:ALA:O	9:06:139:LYS:HG3	2.19	0.42
11:08:93:TYR:CD1	11:08:106:LEU:HA	2.55	0.42
23:20:38:VAL:HG11	23:20:57:GLY:HA3	2.01	0.42
28:25:66:GLU:O	28:25:75:PHE:N	2.50	0.42
29:26:58:ILE:HG12	29:26:66:VAL:HG21	2.02	0.42
39:Z:116:ARG:HH11	39:Z:116:ARG:HG3	1.84	0.42
39:Z:212:ARG:H	39:Z:212:ARG:HD3	1.84	0.42
40:B:68:PHE:CD2	40:B:83:ALA:HB2	2.54	0.42
41:C:135:ARG:HH11	41:C:135:ARG:HG3	1.84	0.42
45:G:55:LYS:HB2	45:G:60:ALA:HB2	2.02	0.42
48:J:83:THR:O	48:J:87:LEU:HG	2.19	0.42
51:M:18:LEU:HD12	51:M:33:LEU:CD1	2.49	0.42
51:M:104:ASN:HB3	51:M:105:ALA:H	1.65	0.42
57:S:15:LEU:O	57:S:15:LEU:HD23	2.19	0.42
1:A:547:A:H4'	1:A:548:G:O5'	2.20	0.42
1:A:629:A:H2'	1:A:630:A:O4'	2.19	0.42
2:01:420:C:O2'	2:01:421:C:H5'	2.20	0.42
2:01:878:A:H3'	2:01:879:G:H8	1.85	0.42
2:01:1458:U:H4'	2:01:1459:G:C4	2.54	0.42
2:01:1697:G:C4'	2:01:1978:A:H5''	2.49	0.42
2:01:1912:A:N7	2:01:1917:U:O4	2.52	0.42
2:01:2298:A:H62	2:01:2318:G:H21	1.67	0.42
10:07:110:ILE:HD13	10:07:136:ILE:HG21	2.00	0.42
12:09:70:GLU:OE1	12:09:140:ALA:HB2	2.20	0.42
14:11:105:LEU:HD22	14:11:139:VAL:HG21	2.02	0.42
17:14:77:ILE:HB	17:14:110:VAL:HG22	2.01	0.42
18:15:81:ARG:HG2	18:15:81:ARG:HH11	1.85	0.42
20:17:110:ALA:HB1	20:17:115:LEU:HD23	2.01	0.42
34:31:38:PHE:CZ	34:31:43:ARG:HA	2.54	0.42
39:Z:248:GLY:HA3	39:Z:255:ASN:ND2	2.24	0.42
44:F:38:ARG:HB2	44:F:63:ASN:HB2	2.02	0.42
47:I:66:VAL:HG21	47:I:74:GLN:HB3	2.02	0.42
55:Q:57:VAL:O	55:Q:78:VAL:HG22	2.19	0.42
57:S:5:LYS:C	57:S:6:LYS:HD2	2.44	0.42
1:A:976:G:N2	1:A:1362:A:H2'	2.35	0.42
1:A:1355:G:O2'	1:A:1356:G:H5'	2.19	0.42
1:A:1469:C:H2'	1:A:1470:U:H5'	2.01	0.42
2:01:368:A:H2'	2:01:369:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1079:C:H4'	14:11:133:ARG:NH2	2.35	0.42
2:01:2487:G:O2'	2:01:2488:G:H5'	2.20	0.42
7:04:224:MET:SD	7:04:229:HIS:HB2	2.60	0.42
8:05:4:LEU:HD21	8:05:29:VAL:CG2	2.50	0.42
10:07:102:LEU:O	10:07:107:VAL:HG23	2.19	0.42
12:09:4:ILE:C	12:09:5:LEU:HD12	2.44	0.42
16:13:104:THR:O	16:13:107:LEU:HD13	2.20	0.42
28:25:69:GLY:HA2	28:25:70:PRO:HD2	1.74	0.42
36:33:35:LYS:HB3	36:33:39:ARG:HD3	2.01	0.42
42:D:110:ARG:O	42:D:114:ARG:N	2.52	0.42
42:D:196:GLU:O	42:D:200:VAL:HG23	2.20	0.42
45:G:82:SER:HB3	45:G:84:TYR:CE1	2.55	0.42
45:G:140:VAL:O	45:G:144:ALA:N	2.52	0.42
47:I:24:ASN:HD22	47:I:26:LYS:CG	2.32	0.42
48:J:31:ARG:O	48:J:31:ARG:HD2	2.20	0.42
49:K:39:ASN:N	49:K:39:ASN:ND2	2.66	0.42
50:L:20:VAL:HB	50:L:94:TYR:CE1	2.55	0.42
52:N:20:PHE:HD2	52:N:56:PRO:HD3	1.84	0.42
1:A:88:U:H2'	1:A:89:U:C6	2.54	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.19	0.42
1:A:620:C:H4'	42:D:134:TYR:HE1	1.84	0.42
1:A:1096:C:H2'	1:A:1097:C:C6	2.55	0.42
1:A:1487:G:O2'	1:A:1488:G:H5'	2.19	0.42
2:01:10:A:H2'	2:01:11:C:H5'	2.02	0.42
2:01:85:G:N7	26:23:6:ARG:NH1	2.68	0.42
2:01:118:A:H2'	2:01:120:U:O4	2.20	0.42
2:01:1279:G:H4'	19:16:31:HIS:CD2	2.55	0.42
2:01:1335:C:H2'	2:01:1336:A:H8	1.85	0.42
2:01:1744:A:H2'	2:01:1745:A:O4'	2.19	0.42
2:01:1934:C:O2'	2:01:1935:G:H5'	2.20	0.42
2:01:2194:U:H2'	2:01:2195:U:C6	2.53	0.42
2:01:2467:C:H2'	2:01:2468:A:O4'	2.19	0.42
2:01:2682:A:C2	8:05:23:PRO:HB3	2.54	0.42
3:02:24:G:H4'	3:02:25:U:C5	2.55	0.42
8:05:142:VAL:CG1	8:05:143:PRO:HD2	2.48	0.42
14:11:79:LEU:HD12	14:11:79:LEU:N	2.35	0.42
17:14:92:LEU:HD13	17:14:95:LEU:HD12	2.02	0.42
19:16:13:ASN:O	19:16:17:ARG:HG3	2.19	0.42
20:17:99:TYR:HE1	20:17:107:ALA:HB3	1.84	0.42
23:20:25:LEU:HD12	23:20:25:LEU:O	2.20	0.42
39:Z:196:THR:HG23	39:Z:222:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:31:PHE:HB2	40:B:39:ILE:HB	2.01	0.42
40:B:156:LEU:HD23	40:B:156:LEU:N	2.29	0.42
43:E:163:ILE:HD12	43:E:163:ILE:C	2.45	0.42
49:K:86:LYS:HG3	49:K:114:PRO:HD3	2.02	0.42
1:A:65:A:O4'	1:A:200:G:H4'	2.19	0.42
1:A:185:U:H4'	58:T:68:LYS:HE3	2.02	0.42
1:A:723:U:OP1	59:U:48:LYS:HG3	2.19	0.42
2:01:293:U:H2'	2:01:294:A:H5''	2.01	0.42
2:01:720:U:H2'	2:01:721:A:C8	2.54	0.42
2:01:746:U:H1'	2:01:748:G:H21	1.84	0.42
2:01:2035:G:H5'	2:01:2036:C:C5	2.48	0.42
2:01:2355:G:O2'	28:25:20:LYS:HE3	2.20	0.42
2:01:2602:A:C6	39:Z:254:VAL:HG12	2.55	0.42
3:02:97:C:H2'	3:02:98:G:H5'	2.01	0.42
5:X:8:U:C4'	5:X:48:C:H4'	2.49	0.42
9:06:67:ARG:HG2	9:06:67:ARG:HH11	1.85	0.42
10:07:30:VAL:HG13	10:07:30:VAL:O	2.19	0.42
10:07:135:ILE:HG22	10:07:140:ILE:HG21	2.01	0.42
11:08:14:VAL:HG13	11:08:26:LYS:C	2.44	0.42
11:08:71:LEU:HA	11:08:74:MET:HE3	2.00	0.42
13:10:77:VAL:HB	13:10:84:TYR:OH	2.19	0.42
24:21:75:PHE:N	24:21:75:PHE:CD1	2.88	0.42
29:26:56:ARG:HG2	29:26:56:ARG:HH11	1.85	0.42
39:Z:10:ARG:HH21	39:Z:14:LEU:HD12	1.85	0.42
41:C:149:LYS:HG3	41:C:168:ARG:HB2	2.01	0.42
42:D:169:TRP:CG	42:D:185:PRO:HG3	2.54	0.42
44:F:46:GLN:HA	44:F:56:LYS:HA	2.02	0.42
50:L:53:ARG:HA	50:L:63:THR:HA	2.00	0.42
55:Q:80:LYS:HG3	55:Q:81:ALA:N	2.34	0.42
1:A:231:U:O2'	1:A:232:G:H5'	2.20	0.42
1:A:306:A:O2'	1:A:307:C:H5'	2.20	0.42
1:A:620:C:H4'	42:D:134:TYR:CE1	2.55	0.42
1:A:635:A:H2'	1:A:636:U:C6	2.55	0.42
1:A:642:A:N7	46:H:106:SER:HA	2.35	0.42
1:A:1315:U:H2'	1:A:1316:G:O4'	2.20	0.42
2:01:466:A:H2'	2:01:467:G:H5'	2.02	0.42
2:01:503:A:H4'	2:01:504:A:H5'	2.02	0.42
2:01:601:C:H4'	9:06:99:LYS:HE2	2.02	0.42
2:01:1550:C:H2'	2:01:1551:A:H8	1.84	0.42
2:01:1611:C:H5'	2:01:1611:C:H6	1.85	0.42
2:01:2294:G:OP1	20:17:10:ARG:HD3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2368:C:H2'	2:01:2369:A:H8	1.85	0.42
3:02:30:C:H2'	3:02:31:C:C5'	2.50	0.42
6:03:29:LEU:HD23	6:03:222:VAL:HG22	2.02	0.42
8:05:60:VAL:O	8:05:60:VAL:HG13	2.20	0.42
13:10:117:LEU:C	13:10:118:ILE:HG12	2.45	0.42
17:14:109:LYS:HG3	17:14:126:ARG:O	2.20	0.42
30:27:58:ASN:HA	30:27:61:ALA:HB3	2.01	0.42
31:28:35:VAL:HG22	31:28:36:GLU:N	2.35	0.42
42:D:201:GLU:OE1	43:E:104:ILE:HG22	2.20	0.42
44:F:18:VAL:HG13	44:F:19:PRO:CD	2.50	0.42
55:Q:30:HIS:HD2	55:Q:33:TYR:H	1.67	0.42
56:R:26:ALA:HA	56:R:29:LYS:CE	2.49	0.42
1:A:648:A:H2'	1:A:649:A:C8	2.55	0.42
1:A:675:A:H1'	49:K:117:HIS:CD2	2.55	0.42
1:A:783:C:H2'	1:A:784:A:H8	1.85	0.42
1:A:1325:C:O2'	1:A:1326:U:H5'	2.19	0.42
1:A:1369:C:OP2	47:I:112:ARG:HA	2.20	0.42
1:A:1489:G:H2'	1:A:1490:U:C6	2.55	0.42
1:A:1494:G:O2'	1:A:1495:U:H5'	2.19	0.42
2:01:535:G:O3'	22:19:52:ARG:HD3	2.19	0.42
2:01:833:A:H2'	2:01:834:G:C8	2.55	0.42
2:01:1601:G:C2'	2:01:1602:U:H5'	2.50	0.42
2:01:1641:A:H2'	2:01:1642:G:O4'	2.20	0.42
2:01:1810:A:H2'	2:01:1811:G:O4'	2.19	0.42
2:01:1826:G:H2'	2:01:1827:U:O4'	2.20	0.42
2:01:2124:G:H21	6:03:217:THR:HG22	1.85	0.42
6:03:148:ASN:O	6:03:152:ALA:N	2.51	0.42
13:10:60:LEU:C	13:10:61:ARG:HD3	2.45	0.42
19:16:98:LEU:HD11	33:30:48:TYR:CE2	2.55	0.42
20:17:74:VAL:O	20:17:78:VAL:HG13	2.20	0.42
22:19:47:ARG:HG2	22:19:47:ARG:HH21	1.84	0.42
22:19:64:ILE:HD11	22:19:94:LEU:HB2	2.01	0.42
24:21:7:HIS:N	24:21:103:ILE:O	2.53	0.42
28:25:19:VAL:HG13	28:25:34:VAL:HG22	2.02	0.42
28:25:69:GLY:O	28:25:71:LYS:N	2.52	0.42
29:26:53:LYS:HB2	29:26:53:LYS:HZ2	1.84	0.42
41:C:143:LEU:HD23	41:C:143:LEU:C	2.45	0.42
42:D:131:ILE:HD11	42:D:134:TYR:HD1	1.85	0.42
45:G:65:LEU:HD23	45:G:65:LEU:C	2.45	0.42
47:I:30:ASN:C	47:I:31:GLN:NE2	2.77	0.42
47:I:35:GLU:HA	47:I:39:GLY:HA3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J:50:THR:HG22	48:J:62:ARG:NE	2.35	0.42
54:P:40:ASN:N	54:P:49:GLY:O	2.53	0.42
57:S:30:LEU:HD12	57:S:30:LEU:N	2.35	0.42
1:A:508:U:H4'	42:D:50:TYR:HD2	1.80	0.41
1:A:1228:C:H2'	1:A:1229:A:H8	1.84	0.41
2:01:1450:G:O2'	2:01:1451:C:H5'	2.20	0.41
2:01:1665:A:H5''	16:13:66:LYS:HG3	2.01	0.41
2:01:1739:A:H2'	2:01:1740:G:O4'	2.20	0.41
2:01:1858:A:C2	2:01:1885:A:H1'	2.54	0.41
2:01:1935:G:H1'	2:01:1964:G:N2	2.35	0.41
2:01:2039:U:H2'	2:01:2040:G:H8	1.83	0.41
2:01:2366:A:H2'	2:01:2367:G:O4'	2.18	0.41
2:01:2493:U:H5''	39:Z:257:THR:HG23	2.01	0.41
10:07:107:VAL:HB	10:07:108:PRO:HD3	2.01	0.41
11:08:32:LEU:HD23	11:08:32:LEU:C	2.45	0.41
17:14:71:ALA:O	17:14:74:THR:HG22	2.20	0.41
20:17:43:ASN:N	20:17:43:ASN:ND2	2.61	0.41
25:22:34:VAL:HG22	25:22:81:LYS:O	2.19	0.41
34:31:19:PHE:CD1	34:31:19:PHE:N	2.88	0.41
36:33:55:GLY:HA2	36:33:58:ILE:HG22	2.01	0.41
40:B:185:ILE:HA	40:B:199:ILE:HB	2.01	0.41
41:C:69:THR:O	41:C:105:VAL:N	2.49	0.41
53:O:62:ARG:O	53:O:66:LEU:HG	2.20	0.41
1:A:78:A:C3'	1:A:79:G:H5'	2.49	0.41
1:A:594:U:O2'	1:A:595:A:H5'	2.20	0.41
1:A:843:U:H3'	1:A:844:G:H5''	2.01	0.41
2:01:782:A:C6	7:04:224:MET:HE2	2.54	0.41
2:01:2478:A:H2'	2:01:2479:U:O4'	2.19	0.41
2:01:2747:G:H5''	11:08:69:ALA:HB1	2.02	0.41
4:Y:26:ARG:HH22	50:L:43:LYS:HA	1.86	0.41
8:05:51:THR:HB	8:05:79:LEU:CD2	2.46	0.41
8:05:124:ARG:HA	8:05:165:MET:CE	2.49	0.41
10:07:113:PHE:CE2	10:07:175:PRO:HB2	2.54	0.41
10:07:166:ARG:HG3	10:07:166:ARG:HH11	1.84	0.41
12:09:26:ALA:O	12:09:31:VAL:HG23	2.19	0.41
14:11:87:SER:CB	14:11:97:VAL:HG22	2.45	0.41
15:12:42:ALA:HB2	22:19:67:ALA:HB2	2.02	0.41
19:16:90:ARG:NH1	19:16:116:VAL:HG11	2.34	0.41
31:28:8:GLN:NE2	31:28:30:ARG:C	2.78	0.41
32:29:2:LYS:HG2	32:29:2:LYS:O	2.20	0.41
43:E:33:THR:HG22	43:E:51:LYS:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J:69:THR:O	48:J:71:LEU:HD12	2.20	0.41
49:K:112:VAL:HG23	49:K:112:VAL:O	2.20	0.41
51:M:70:ARG:HA	51:M:70:ARG:HD3	1.83	0.41
51:M:106:ARG:HA	51:M:106:ARG:HE	1.84	0.41
53:O:56:LEU:C	53:O:56:LEU:HD23	2.46	0.41
54:P:14:ARG:HG2	54:P:14:ARG:HH11	1.84	0.41
57:S:10:ILE:HG21	57:S:40:PHE:HE2	1.85	0.41
59:U:32:ARG:HH12	59:U:33:ARG:HD3	1.85	0.41
1:A:9:G:H5'	43:E:107:GLY:HA2	1.99	0.41
1:A:212:G:O2'	1:A:213:G:H5'	2.19	0.41
1:A:721:G:H4'	1:A:722:G:O4'	2.20	0.41
1:A:785:G:O2'	1:A:786:G:H5'	2.20	0.41
1:A:1248:A:O2'	1:A:1249:C:H5'	2.19	0.41
2:01:277:G:H3'	2:01:277:G:N3	2.36	0.41
2:01:958:U:H2'	3:02:89:U:H1'	2.01	0.41
2:01:2746:U:H5''	11:08:137:LYS:HE3	2.01	0.41
2:01:2795:C:H2'	2:01:2796:U:O4'	2.20	0.41
4:Y:3:ARG:HG3	39:Z:316:ASP:CB	2.40	0.41
4:Y:27:GLN:NE2	39:Z:137:GLY:O	2.53	0.41
5:X:18:G:H3'	5:X:19:G:H5''	2.01	0.41
9:06:52:VAL:HG11	9:06:81:GLY:HA2	2.01	0.41
13:10:119:PRO:HG2	13:10:121:SER:N	2.20	0.41
17:14:92:LEU:HD22	17:14:92:LEU:N	2.35	0.41
19:16:46:ARG:HG2	19:16:46:ARG:O	2.19	0.41
25:22:47:VAL:HB	25:22:55:VAL:HG21	2.03	0.41
40:B:16:GLY:H	40:B:202:ASN:HB2	1.84	0.41
40:B:142:LYS:HA	40:B:145:ASN:HD21	1.84	0.41
41:C:90:VAL:HA	41:C:93:ILE:HG22	2.03	0.41
42:D:113:ALA:O	42:D:117:VAL:HG23	2.20	0.41
46:H:103:VAL:HG23	46:H:105:THR:HG23	2.02	0.41
50:L:86:VAL:CG2	50:L:87:LYS:H	2.26	0.41
52:N:20:PHE:HD1	52:N:23:ARG:HB3	1.85	0.41
1:A:39:G:H2'	1:A:40:C:C6	2.56	0.41
1:A:112:G:N2	1:A:354:G:H5'	2.29	0.41
1:A:1252:A:O2'	1:A:1253:G:H5'	2.19	0.41
1:A:1258:G:H2'	1:A:1259:C:C6	2.56	0.41
2:01:399:U:OP1	2:01:2090:A:H5''	2.21	0.41
2:01:511:U:C2'	2:01:512:G:H5'	2.45	0.41
2:01:538:A:H2'	2:01:539:G:O4'	2.19	0.41
2:01:857:G:H2'	2:01:858:G:O4'	2.21	0.41
2:01:1666:G:H5''	16:13:82:ASN:HD21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2557:G:H2'	2:01:2558:C:C6	2.55	0.41
7:04:269:ARG:HH11	7:04:269:ARG:HG3	1.86	0.41
8:05:4:LEU:HD21	8:05:29:VAL:HG21	2.02	0.41
18:15:41:LEU:HD23	18:15:42:THR:N	2.35	0.41
39:Z:323:ILE:CD1	39:Z:337:ARG:HD2	2.50	0.41
40:B:41:ASN:OD1	40:B:44:LYS:HG3	2.20	0.41
41:C:156:LEU:HD12	41:C:156:LEU:N	2.35	0.41
43:E:89:THR:O	43:E:89:THR:HG22	2.20	0.41
44:F:88:MET:HB2	56:R:64:LEU:HD21	2.02	0.41
45:G:39:GLU:HG3	47:I:42:THR:HG21	2.02	0.41
47:I:83:THR:HG21	47:I:102:PHE:HB3	2.02	0.41
48:J:80:THR:HB	48:J:83:THR:OG1	2.19	0.41
49:K:20:ALA:HA	49:K:33:ILE:HA	2.02	0.41
51:M:87:GLY:O	51:M:91:ARG:HG3	2.19	0.41
55:Q:18:LYS:HB2	55:Q:18:LYS:HZ2	1.84	0.41
1:A:67:C:H4'	1:A:172:A:H4'	2.02	0.41
1:A:211:G:H2'	1:A:212:G:H5'	2.02	0.41
1:A:243:A:H4'	1:A:244:U:H3'	2.03	0.41
2:01:78:U:OP2	30:27:2:LYS:HD2	2.20	0.41
2:01:2065:C:H1'	2:01:2449:U:H3	1.86	0.41
2:01:2229:U:H2'	2:01:2230:G:H8	1.85	0.41
3:02:42:C:O4'	10:07:65:LEU:HB2	2.21	0.41
4:Y:16:ILE:HD13	39:Z:197:GLY:HA2	2.02	0.41
9:06:44:ARG:HH21	9:06:87:ALA:HB3	1.81	0.41
10:07:60:SER:HB3	10:07:90:LEU:HD21	2.02	0.41
10:07:133:GLU:HG3	10:07:135:ILE:HG12	2.02	0.41
11:08:90:GLY:HA3	11:08:93:TYR:CD2	2.55	0.41
28:25:17:LEU:HB3	28:25:18:GLY:H	1.77	0.41
30:27:20:ASN:N	30:27:20:ASN:ND2	2.67	0.41
31:28:16:LEU:HB2	31:28:19:HIS:ND1	2.34	0.41
39:Z:87:ALA:HB2	39:Z:95:THR:HG22	2.03	0.41
45:G:30:MET:SD	45:G:31:VAL:N	2.94	0.41
46:H:45:ILE:HG13	46:H:46:GLU:N	2.34	0.41
48:J:57:VAL:CG2	48:J:58:ASN:H	2.25	0.41
52:N:63:CYS:HA	52:N:72:PHE:HE1	1.86	0.41
57:S:66:VAL:CG2	57:S:67:GLY:N	2.80	0.41
1:A:309:A:H2'	1:A:310:G:H8	1.84	0.41
1:A:337:G:H2'	1:A:338:A:H8	1.86	0.41
1:A:751:U:H2'	1:A:752:G:H5'	2.03	0.41
1:A:1054:C:H42	39:Z:212:ARG:HA	1.86	0.41
1:A:1228:C:H2'	1:A:1229:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:203:A:H5''	2:01:204:A:H2'	2.03	0.41
2:01:1685:C:H2'	2:01:1686:C:C6	2.56	0.41
2:01:2197:U:O2'	2:01:2198:A:H5''	2.20	0.41
6:03:208:TYR:CE2	6:03:209:ILE:HG23	2.56	0.41
7:04:216:ARG:HG2	7:04:216:ARG:NH1	2.35	0.41
7:04:244:VAL:HG12	7:04:250:GLN:HA	2.02	0.41
12:09:63:ALA:HA	12:09:66:ASN:ND2	2.36	0.41
14:11:14:ALA:HA	14:11:41:PHE:HZ	1.85	0.41
15:12:35:ARG:HG2	15:12:40:HIS:CD2	2.55	0.41
15:12:98:GLU:OE1	15:12:98:GLU:N	2.54	0.41
16:13:22:ILE:HD11	16:13:40:LYS:HG3	2.03	0.41
18:15:72:PRO:HG3	18:15:92:TRP:CZ3	2.55	0.41
22:19:68:ALA:O	22:19:72:GLY:N	2.53	0.41
24:21:23:LEU:HD11	33:30:21:LEU:HD23	2.02	0.41
27:24:2:PHE:HB3	27:24:50:MET:SD	2.61	0.41
27:24:23:ALA:O	27:24:25:LYS:HG3	2.20	0.41
37:34:30:GLU:O	37:34:32:LYS:N	2.51	0.41
5:W:52:G:O2'	5:W:53:G:H5'	2.21	0.41
39:Z:97:ASN:ND2	39:Z:97:ASN:O	2.53	0.41
39:Z:328:LEU:HD12	39:Z:328:LEU:N	2.35	0.41
40:B:66:ILE:HA	40:B:159:ALA:HB3	2.01	0.41
40:B:80:LYS:HG2	40:B:90:PHE:CE2	2.55	0.41
40:B:145:ASN:OD1	40:B:146:SER:N	2.54	0.41
47:I:10:ARG:O	47:I:105:ARG:NH2	2.51	0.41
52:N:60:ARG:HA	52:N:60:ARG:HD2	1.89	0.41
59:U:40:PRO:HA	59:U:43:GLU:HB3	2.03	0.41
1:A:187:G:H2'	1:A:189:A:OP2	2.20	0.41
1:A:284:C:H2'	1:A:285:C:C6	2.56	0.41
1:A:321:A:O2'	1:A:322:C:H5'	2.20	0.41
1:A:438:U:HO2'	1:A:439:U:H5	1.67	0.41
1:A:441:A:H1'	1:A:497:G:N2	2.36	0.41
1:A:1057:G:H2'	1:A:1058:G:O4'	2.21	0.41
1:A:1251:A:H2'	1:A:1252:A:H8	1.81	0.41
2:01:192:C:C2'	2:01:193:U:H5'	2.47	0.41
2:01:204:A:O3'	2:01:205:G:H4'	2.21	0.41
2:01:1341:G:H4'	25:22:60:THR:O	2.20	0.41
2:01:1521:G:C3'	2:01:1522:A:H5''	2.44	0.41
2:01:1564:C:H2'	2:01:1565:C:O4'	2.20	0.41
2:01:1686:C:H2'	2:01:1687:G:O4'	2.21	0.41
2:01:1993:U:H4'	8:05:133:THR:HG22	2.03	0.41
10:07:59:ILE:HG22	10:07:98:PHE:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:09:125:THR:HA	12:09:146:VAL:HB	2.02	0.41
14:11:27:LEU:HB2	14:11:32:VAL:HB	2.03	0.41
29:26:9:LYS:HE3	29:26:53:LYS:HB3	2.03	0.41
34:31:32:LYS:HB3	34:31:32:LYS:HZ2	1.84	0.41
40:B:19:THR:HG21	40:B:21:TYR:CZ	2.55	0.41
40:B:224:ARG:HH21	40:B:224:ARG:HG3	1.85	0.41
42:D:120:LYS:HG2	42:D:130:ASN:OD1	2.21	0.41
45:G:117:LEU:HD23	45:G:117:LEU:C	2.46	0.41
1:A:216:U:H2'	1:A:217:C:C6	2.56	0.41
1:A:743:A:O2'	1:A:744:C:H5'	2.21	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.21	0.41
2:01:216:A:H2'	2:01:217:A:O4'	2.20	0.41
2:01:653:U:H3'	2:01:654:A:H5''	2.02	0.41
2:01:1179:G:C5	2:01:1180:U:H1'	2.56	0.41
2:01:1592:C:H2'	2:01:1593:A:C8	2.56	0.41
2:01:2314:A:H2'	2:01:2315:G:C8	2.56	0.41
2:01:2462:C:H1'	2:01:2491:U:O4	2.21	0.41
2:01:2505:G:O2'	2:01:2506:U:H5'	2.20	0.41
2:01:2531:A:H4'	11:08:156:TYR:CE2	2.55	0.41
6:03:65:LEU:HD23	6:03:65:LEU:N	2.36	0.41
8:05:29:VAL:O	8:05:185:ASN:HB3	2.19	0.41
12:09:75:LEU:H	12:09:75:LEU:CD2	2.30	0.41
14:11:58:ILE:HD13	14:11:68:PHE:HA	2.03	0.41
18:15:71:LYS:HB3	18:15:93:VAL:O	2.21	0.41
22:19:73:ILE:HD11	22:19:77:LYS:CB	2.50	0.41
31:28:6:ILE:CD1	31:28:47:ILE:HD11	2.50	0.41
31:28:10:ARG:HG2	31:28:10:ARG:HH21	1.86	0.41
31:28:11:SER:OG	31:28:13:ILE:HG13	2.21	0.41
39:Z:10:ARG:HG2	39:Z:103:LEU:HD11	2.01	0.41
40:B:16:GLY:C	40:B:17:HIS:ND1	2.79	0.41
42:D:36:ALA:N	42:D:37:PRO:CD	2.83	0.41
42:D:120:LYS:O	42:D:145:ARG:HD3	2.21	0.41
43:E:159:SER:HB2	43:E:162:GLU:HB3	2.03	0.41
48:J:17:LEU:HD23	48:J:17:LEU:O	2.21	0.41
48:J:52:LEU:HB2	52:N:80:ARG:HD2	2.02	0.41
52:N:15:LEU:HD13	52:N:53:ASP:HB2	2.03	0.41
52:N:64:ARG:HH11	52:N:64:ARG:HG2	1.86	0.41
58:T:53:MET:O	58:T:57:VAL:HG23	2.21	0.41
1:A:19:A:OP1	43:E:90:GLY:HA3	2.21	0.41
1:A:642:A:C2	46:H:104:SER:HB3	2.56	0.41
1:A:737:C:H2'	1:A:738:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:754:C:O2	1:A:754:C:H3'	2.21	0.41
1:A:1188:A:O2'	52:N:97:LYS:HD2	2.21	0.41
1:A:1379:G:O6	45:G:1:PRO:HD2	2.20	0.41
2:01:103:A:H2'	2:01:104:A:O4'	2.21	0.41
2:01:144:A:C5'	25:22:2:ILE:HD11	2.51	0.41
2:01:230:G:O2'	2:01:231:A:H5'	2.21	0.41
2:01:625:G:O2'	2:01:626:A:H5'	2.21	0.41
2:01:894:U:H2'	2:01:895:U:H5'	2.03	0.41
2:01:1005:C:O2'	15:12:30:THR:HG21	2.21	0.41
2:01:1055:G:H2'	2:01:1056:G:O4'	2.21	0.41
2:01:2065:C:H2'	2:01:2066:C:C6	2.56	0.41
2:01:2204:G:H2'	2:01:2205:A:H8	1.86	0.41
2:01:2292:U:H2'	2:01:2293:G:H8	1.86	0.41
2:01:2663:G:H2'	2:01:2664:G:O4'	2.21	0.41
2:01:2760:C:O2'	2:01:2761:A:H5'	2.21	0.41
7:04:27:LYS:HB3	7:04:27:LYS:HZ2	1.83	0.41
9:06:99:LYS:HG2	9:06:102:ARG:NH1	2.36	0.41
13:10:42:ARG:HD2	13:10:42:ARG:C	2.46	0.41
13:10:97:LYS:O	13:10:101:LYS:HG2	2.20	0.41
14:11:102:ARG:HH11	14:11:102:ARG:HG3	1.86	0.41
15:12:58:ASN:OD1	15:12:128:ASN:HA	2.21	0.41
17:14:109:LYS:HE2	17:14:128:THR:HG22	2.03	0.41
19:16:106:ASP:OD1	19:16:106:ASP:N	2.54	0.41
20:17:99:TYR:CZ	20:17:104:GLN:HG3	2.56	0.41
21:18:102:ARG:HH11	21:18:102:ARG:HG3	1.86	0.41
24:21:34:ASP:OD1	33:30:36:LYS:HD2	2.20	0.41
30:27:22:LEU:CD1	30:27:23:ARG:HG2	2.51	0.41
30:27:28:LEU:HD12	30:27:28:LEU:N	2.36	0.41
39:Z:196:THR:HG22	39:Z:222:VAL:HG22	2.03	0.41
41:C:86:LEU:O	41:C:90:VAL:HG23	2.20	0.41
41:C:112:ALA:HB3	41:C:184:ASN:HD22	1.85	0.41
43:E:87:VAL:HG21	43:E:92:ARG:HH11	1.86	0.41
43:E:156:ARG:NH2	43:E:163:ILE:HG22	2.36	0.41
45:G:25:PHE:O	45:G:29:LEU:HG	2.21	0.41
48:J:49:PHE:HZ	52:N:75:LYS:HG2	1.85	0.41
49:K:22:ILE:HG21	49:K:95:THR:HG21	2.03	0.41
58:T:74:HIS:O	58:T:78:LEU:HD13	2.21	0.41
59:U:19:LYS:HD2	59:U:19:LYS:N	2.36	0.41
1:A:235:C:H2'	1:A:236:A:C8	2.55	0.41
1:A:405:U:H3'	1:A:406:G:C5'	2.32	0.41
1:A:1345:U:H5''	47:I:121:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:45:G:H2'	2:01:215:G:C5	2.56	0.41
2:01:355:U:H2'	2:01:356:G:H8	1.86	0.41
2:01:540:C:H2'	2:01:541:A:C8	2.56	0.41
2:01:558:U:H2'	2:01:559:G:H8	1.86	0.41
2:01:857:G:H5'	28:25:65:PHE:CG	2.56	0.41
2:01:1317:G:H2'	2:01:1318:U:O4'	2.21	0.41
2:01:1529:G:H2'	2:01:1530:G:C5'	2.50	0.41
2:01:1664:A:H61	2:01:1996:C:N4	2.10	0.41
2:01:2061:G:OP1	2:01:2061:G:H4'	2.20	0.41
2:01:2115:G:H2'	2:01:2117:A:OP2	2.20	0.41
2:01:2428:G:H21	17:14:60:ARG:CZ	2.34	0.41
2:01:2751:G:O2'	2:01:2752:C:H5'	2.20	0.41
9:06:88:ARG:HB3	9:06:89:PRO:CD	2.46	0.41
13:10:3:LEU:CD1	13:10:5:LEU:H	2.34	0.41
14:11:60:VAL:HG22	14:11:66:PHE:HB3	2.02	0.41
16:13:31:ARG:HG3	16:13:31:ARG:HH11	1.86	0.41
23:20:38:VAL:HG13	23:20:54:VAL:HB	2.03	0.41
26:23:80:ASP:OD2	26:23:96:LYS:N	2.54	0.41
39:Z:189:TYR:CG	39:Z:224:PRO:HG3	2.56	0.41
41:C:109:GLU:HB2	41:C:143:LEU:HD12	2.02	0.41
47:I:31:GLN:HE21	47:I:31:GLN:N	2.18	0.41
49:K:84:MET:HE2	49:K:112:VAL:HG11	2.02	0.41
53:O:69:LEU:HD13	53:O:69:LEU:C	2.46	0.41
59:U:17:ARG:HH11	59:U:17:ARG:HG2	1.86	0.41
1:A:750:C:H2'	1:A:751:U:H6	1.86	0.40
1:A:1349:A:H2'	1:A:1350:A:O4'	2.21	0.40
2:01:121:G:H2'	2:01:122:G:H8	1.85	0.40
2:01:140:C:H42	2:01:1409:U:C1'	2.34	0.40
2:01:207:A:H2'	2:01:208:C:O4'	2.20	0.40
2:01:611:C:H2'	2:01:612:G:O4'	2.21	0.40
2:01:1086:A:H3'	2:01:1086:A:N3	2.36	0.40
2:01:2282:G:H5''	2:01:2283:C:O4'	2.21	0.40
2:01:2286:G:H21	2:01:2287:A:N6	2.20	0.40
2:01:2849:U:H3	2:01:2867:G:H5''	1.86	0.40
11:08:17:LYS:HZ2	11:08:17:LYS:CB	2.30	0.40
11:08:88:LEU:HD22	11:08:95:ALA:HB2	2.02	0.40
17:14:131:ALA:O	17:14:135:ILE:HG13	2.21	0.40
23:20:38:VAL:CG1	23:20:54:VAL:HB	2.50	0.40
24:21:74:ILE:O	24:21:74:ILE:HG23	2.21	0.40
24:21:86:MET:HE3	24:21:87:PRO:CD	2.48	0.40
25:22:30:ILE:HD11	25:22:87:LEU:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:27:47:ARG:HG3	30:27:47:ARG:NH2	2.36	0.40
31:28:40:THR:HG22	31:28:42:ALA:H	1.86	0.40
39:Z:140:GLU:OE1	39:Z:206:PRO:HD2	2.21	0.40
40:B:80:LYS:HE3	40:B:92:ASN:HD21	1.86	0.40
45:G:58:LEU:HD12	45:G:58:LEU:N	2.35	0.40
48:J:8:ILE:HB	48:J:74:VAL:CG1	2.51	0.40
48:J:40:ILE:N	48:J:73:LEU:O	2.40	0.40
48:J:72:ARG:HG2	48:J:72:ARG:HH11	1.86	0.40
49:K:49:SER:HA	49:K:68:ARG:NH1	2.36	0.40
49:K:83:VAL:HG11	49:K:96:ILE:CG2	2.51	0.40
1:A:3:A:C5'	1:A:4:U:H5'	2.33	0.40
1:A:604:G:H2'	1:A:605:U:O4'	2.20	0.40
1:A:1226:C:H4'	57:S:79:TYR:CZ	2.56	0.40
2:01:26:G:H1'	2:01:514:A:N6	2.37	0.40
2:01:251:A:H5''	17:14:47:ARG:HH11	1.84	0.40
2:01:639:U:H2'	2:01:640:C:H6	1.85	0.40
2:01:691:C:O2'	2:01:692:C:H5'	2.21	0.40
2:01:745:G:O2'	2:01:748:G:H1'	2.20	0.40
2:01:1082:U:H5''	14:11:119:ALA:HB3	2.03	0.40
2:01:2529:G:H5''	2:01:2530:A:C5'	2.50	0.40
2:01:2690:U:O2'	2:01:2872:A:H1'	2.21	0.40
18:15:45:GLN:OE1	18:15:125:PRO:HD3	2.21	0.40
19:16:56:LYS:HB2	19:16:56:LYS:HZ2	1.86	0.40
24:21:84:ARG:HG2	24:21:84:ARG:NH2	2.36	0.40
26:23:71:ILE:H	26:23:71:ILE:HG13	1.66	0.40
29:26:67:LEU:HA	29:26:70:LEU:HD12	2.03	0.40
42:D:149:LYS:O	42:D:150:LYS:HG2	2.21	0.40
45:G:39:GLU:O	45:G:43:TYR:CD2	2.75	0.40
48:J:45:ARG:HG2	48:J:47:GLU:HG3	2.03	0.40
1:A:254:G:H21	55:Q:17:GLU:CD	2.30	0.40
1:A:542:G:O2'	1:A:543:U:H5'	2.21	0.40
1:A:905:U:H2'	1:A:906:A:H5'	2.03	0.40
1:A:1070:U:O2'	1:A:1071:C:H5'	2.20	0.40
1:A:1104:G:O2'	1:A:1105:A:H5'	2.21	0.40
1:A:1253:G:H2'	1:A:1254:A:C8	2.56	0.40
1:A:1389:C:H2'	1:A:1390:U:C6	2.56	0.40
2:01:321:U:H5''	9:06:131:THR:HG23	2.01	0.40
2:01:679:C:H2'	2:01:680:C:H6	1.86	0.40
2:01:1593:A:H2'	2:01:1594:U:O4'	2.20	0.40
2:01:2131:U:H5'	2:01:2132:U:H5''	2.03	0.40
2:01:2393:U:H5''	17:14:62:PRO:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2543:G:H2'	2:01:2544:G:C8	2.55	0.40
3:02:28:C:H2'	3:02:29:A:H8	1.87	0.40
7:04:80:LEU:HD12	7:04:80:LEU:N	2.36	0.40
8:05:33:ARG:HH22	8:05:52:THR:HA	1.86	0.40
9:06:98:LYS:HB3	9:06:102:ARG:NH2	2.32	0.40
11:08:139:VAL:O	11:08:143:VAL:HG23	2.21	0.40
14:11:17:ALA:HA	14:11:41:PHE:HE2	1.86	0.40
18:15:4:PRO:HD2	18:15:92:TRP:CZ3	2.56	0.40
20:17:62:LEU:HD13	20:17:65:THR:HG22	2.03	0.40
25:22:2:ILE:HG22	25:22:5:GLU:OE1	2.21	0.40
30:27:18:LEU:O	30:27:22:LEU:HG	2.21	0.40
32:29:26:SER:OG	32:29:27:THR:N	2.54	0.40
33:30:38:LEU:HD12	33:30:38:LEU:N	2.37	0.40
39:Z:84:LEU:HA	39:Z:87:ALA:HB3	2.02	0.40
41:C:28:PHE:HE2	52:N:76:PHE:HD1	1.68	0.40
41:C:39:ARG:HH11	41:C:39:ARG:HG3	1.86	0.40
1:A:580:C:H2'	1:A:581:G:O4'	2.21	0.40
1:A:813:U:H2'	1:A:814:A:C5'	2.51	0.40
2:01:1182:G:H2'	2:01:1183:U:O4'	2.22	0.40
2:01:1415:U:H2'	2:01:1416:G:H4'	2.04	0.40
2:01:1796:U:H2'	2:01:1797:G:H8	1.85	0.40
2:01:2035:G:C5'	2:01:2036:C:H5	2.33	0.40
2:01:2292:U:H2'	2:01:2293:G:C8	2.57	0.40
2:01:2304:G:H5'	10:07:120:SER:OG	2.22	0.40
8:05:13:ARG:HH22	21:18:74:GLN:HE21	1.63	0.40
9:06:121:VAL:O	9:06:190:ALA:N	2.54	0.40
10:07:33:ILE:O	10:07:90:LEU:N	2.41	0.40
11:08:82:PHE:CB	11:08:140:ILE:HD13	2.51	0.40
17:14:19:LEU:HD12	17:14:19:LEU:N	2.35	0.40
17:14:63:LYS:HE3	36:33:11:LYS:CD	2.51	0.40
19:16:36:THR:OG1	19:16:37:THR:N	2.55	0.40
22:19:68:ALA:HB1	22:19:73:ILE:HG23	2.03	0.40
24:21:65:ASP:OD2	24:21:68:ASP:HB2	2.22	0.40
28:25:43:ALA:HB1	28:25:47:VAL:HG23	2.04	0.40
29:26:35:HIS:ND1	29:26:36:ARG:N	2.69	0.40
40:B:93:HIS:NE2	40:B:145:ASN:HB2	2.36	0.40
40:B:221:ARG:HH11	40:B:221:ARG:HG3	1.86	0.40
41:C:137:VAL:HG21	41:C:167:TYR:HD2	1.85	0.40
43:E:110:MET:SD	43:E:126:ALA:HB2	2.61	0.40
49:K:88:PRO:CD	59:U:28:LEU:HD13	2.52	0.40
50:L:82:ARG:HG2	50:L:82:ARG:HH11	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:R:70:THR:OG1	56:R:71:ASP:N	2.49	0.40
59:U:33:ARG:HG3	59:U:33:ARG:NH1	2.37	0.40
1:A:208:U:H4'	1:A:212:G:N1	2.37	0.40
1:A:261:U:H5	58:T:73:ARG:NE	2.20	0.40
1:A:625:U:OP1	54:P:9:HIS:HB3	2.21	0.40
1:A:1282:C:H2'	1:A:1283:U:C6	2.56	0.40
1:A:1441:A:H3'	1:A:1441:A:N3	2.36	0.40
1:A:1502:A:C8	1:A:1505:G:N2	2.90	0.40
2:01:108:G:H2'	2:01:109:C:O4'	2.21	0.40
2:01:587:C:H5'	9:06:85:PHE:CE2	2.57	0.40
2:01:818:G:C2'	2:01:819:A:H5''	2.52	0.40
2:01:1130:U:O2'	2:01:1131:G:OP1	2.32	0.40
2:01:1252:G:H22	22:19:36:GLN:NE2	2.20	0.40
2:01:1438:U:O2'	2:01:1439:A:H5'	2.21	0.40
2:01:1507:C:H2'	2:01:1508:A:O4'	2.22	0.40
2:01:1522:A:H1'	2:01:1524:G:C5	2.57	0.40
2:01:2733:A:O2'	2:01:2734:A:H5'	2.22	0.40
2:01:2744:G:O2'	2:01:2745:C:H5'	2.22	0.40
7:04:188:ARG:HG2	7:04:188:ARG:NH1	2.37	0.40
9:06:46:GLN:HB2	9:06:86:ALA:HB1	2.02	0.40
10:07:37:MET:HB3	10:07:56:LEU:HD11	2.04	0.40
18:15:34:LYS:HA	18:15:101:VAL:HA	2.03	0.40
21:18:47:ILE:HD11	21:18:61:ARG:CB	2.52	0.40
27:24:63:ILE:CG2	27:24:70:ILE:HB	2.52	0.40
30:27:1:MET:O	30:27:5:GLU:HG2	2.21	0.40
32:29:59:ARG:HH21	32:29:62:LYS:CB	2.26	0.40
34:31:8:ILE:HB	34:31:50:GLU:OE2	2.21	0.40
35:32:26:ASN:HA	35:32:29:GLN:NE2	2.35	0.40
40:B:161:PHE:HZ	40:B:212:TYR:HB3	1.86	0.40
41:C:5:HIS:HB2	52:N:88:MET:SD	2.62	0.40
42:D:104:MET:HE1	42:D:170:LEU:HB2	2.04	0.40
43:E:132:PRO:HA	43:E:135:VAL:HG22	2.04	0.40
50:L:58:ASN:N	50:L:58:ASN:HD22	2.20	0.40
57:S:50:VAL:HG11	57:S:70:LEU:HB3	2.02	0.40
58:T:59:ARG:O	58:T:63:LYS:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Y	45/72 (62%)	40 (89%)	5 (11%)	0	100	100
6	03	218/234 (93%)	195 (89%)	23 (11%)	0	100	100
7	04	269/273 (98%)	242 (90%)	25 (9%)	2 (1%)	18	52
8	05	207/209 (99%)	189 (91%)	17 (8%)	1 (0%)	24	59
9	06	199/201 (99%)	180 (90%)	17 (8%)	2 (1%)	12	45
10	07	175/179 (98%)	155 (89%)	20 (11%)	0	100	100
11	08	174/177 (98%)	154 (88%)	17 (10%)	3 (2%)	7	35
12	09	147/149 (99%)	131 (89%)	13 (9%)	3 (2%)	6	31
13	10	129/165 (78%)	95 (74%)	28 (22%)	6 (5%)	2	14
14	11	139/142 (98%)	120 (86%)	18 (13%)	1 (1%)	18	52
15	12	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
16	13	120/123 (98%)	100 (83%)	18 (15%)	2 (2%)	7	35
17	14	141/144 (98%)	128 (91%)	13 (9%)	0	100	100
18	15	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	8	37
19	16	118/127 (93%)	106 (90%)	11 (9%)	1 (1%)	16	50
20	17	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	14	47
21	18	112/115 (97%)	98 (88%)	14 (12%)	0	100	100
22	19	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
23	20	101/103 (98%)	84 (83%)	16 (16%)	1 (1%)	12	45
24	21	108/110 (98%)	97 (90%)	11 (10%)	0	100	100
25	22	91/100 (91%)	77 (85%)	13 (14%)	1 (1%)	11	43
26	23	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
27	24	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
28	25	73/85 (86%)	60 (82%)	11 (15%)	2 (3%)	4	25
29	26	75/78 (96%)	69 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	27	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
31	28	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
32	29	64/70 (91%)	55 (86%)	9 (14%)	0	100	100
33	30	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
34	31	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
35	32	44/46 (96%)	38 (86%)	5 (11%)	1 (2%)	5	29
36	33	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	3	21
37	34	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
39	Z	359/365 (98%)	332 (92%)	26 (7%)	1 (0%)	36	68
40	B	216/241 (90%)	188 (87%)	26 (12%)	2 (1%)	14	47
41	C	204/233 (88%)	189 (93%)	15 (7%)	0	100	100
42	D	203/206 (98%)	177 (87%)	25 (12%)	1 (0%)	24	59
43	E	155/167 (93%)	125 (81%)	29 (19%)	1 (1%)	21	56
44	F	98/131 (75%)	77 (79%)	16 (16%)	5 (5%)	1	13
45	G	149/156 (96%)	134 (90%)	14 (9%)	1 (1%)	18	52
46	H	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
47	I	125/130 (96%)	101 (81%)	22 (18%)	2 (2%)	7	36
48	J	96/103 (93%)	85 (88%)	9 (9%)	2 (2%)	5	31
49	K	114/129 (88%)	102 (90%)	11 (10%)	1 (1%)	14	47
50	L	121/124 (98%)	92 (76%)	23 (19%)	6 (5%)	1	13
51	M	112/118 (95%)	94 (84%)	16 (14%)	2 (2%)	6	34
52	N	98/101 (97%)	79 (81%)	13 (13%)	6 (6%)	1	9
53	O	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
54	P	80/82 (98%)	65 (81%)	13 (16%)	2 (2%)	4	27
55	Q	78/84 (93%)	63 (81%)	14 (18%)	1 (1%)	9	40
56	R	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
57	S	77/92 (84%)	69 (90%)	7 (9%)	1 (1%)	9	40
58	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
59	U	63/71 (89%)	44 (70%)	17 (27%)	2 (3%)	3	21
All	All	6468/6864 (94%)	5705 (88%)	696 (11%)	67 (1%)	15	45

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	06	83	VAL
11	08	12	ALA
12	09	9	VAL
13	10	55	VAL
13	10	119	PRO
13	10	123	ILE
36	33	31	ILE
42	D	192	ALA
43	E	122	VAL
44	F	92	THR
44	F	94	HIS
47	I	57	VAL
47	I	90	ASP
48	J	58	ASN
50	L	101	LEU
51	M	4	ALA
51	M	65	GLU
59	U	8	ASN
59	U	24	LYS
7	04	232	GLY
9	06	9	GLN
11	08	13	GLY
13	10	80	THR
13	10	122	GLN
14	11	13	ALA
20	17	34	HIS
28	25	70	PRO
39	Z	137	GLY
40	B	18	GLN
48	J	34	ALA
50	L	119	LYS
52	N	38	GLU
54	P	47	GLU
7	04	240	GLY
12	09	8	LYS
16	13	101	GLY
36	33	32	LEU
40	B	19	THR
45	G	56	SER
50	L	23	LEU
52	N	3	GLN
52	N	97	LYS
52	N	99	SER

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Mol	Chain	Res	Type
55	Q	50	ASN
18	15	59	ARG
23	20	53	PHE
25	22	38	ALA
44	F	93	LYS
50	L	86	VAL
54	P	79	ASN
12	09	41	LYS
13	10	118	ILE
19	16	71	ARG
44	F	40	GLU
44	F	53	LYS
49	K	87	GLY
57	S	7	GLY
8	05	152	PRO
16	13	93	GLN
18	15	69	PRO
50	L	87	LYS
50	L	113	ARG
52	N	98	ALA
28	25	69	GLY
35	32	44	VAL
11	08	11	PRO
52	N	55	SER

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	
4	Y	38/59 (64%)	37 (97%)	1 (3%)	40	69
6	03	106/181 (59%)	106 (100%)	0	100	100
7	04	216/218 (99%)	214 (99%)	2 (1%)	70	81
8	05	164/164 (100%)	162 (99%)	2 (1%)	63	79
9	06	165/165 (100%)	164 (99%)	1 (1%)	78	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	07	148/150 (99%)	146 (99%)	2 (1%)	59	77
11	08	137/138 (99%)	135 (98%)	2 (2%)	57	76
12	09	114/114 (100%)	114 (100%)	0	100	100
13	10	100/123 (81%)	99 (99%)	1 (1%)	68	80
14	11	109/110 (99%)	108 (99%)	1 (1%)	70	81
15	12	116/116 (100%)	115 (99%)	1 (1%)	70	81
16	13	103/104 (99%)	102 (99%)	1 (1%)	68	80
17	14	102/103 (99%)	102 (100%)	0	100	100
18	15	109/109 (100%)	107 (98%)	2 (2%)	51	74
19	16	100/104 (96%)	99 (99%)	1 (1%)	68	80
20	17	86/87 (99%)	84 (98%)	2 (2%)	44	70
21	18	99/100 (99%)	99 (100%)	0	100	100
22	19	89/90 (99%)	88 (99%)	1 (1%)	65	79
23	20	84/84 (100%)	84 (100%)	0	100	100
24	21	93/93 (100%)	92 (99%)	1 (1%)	65	79
25	22	80/84 (95%)	79 (99%)	1 (1%)	61	78
26	23	83/85 (98%)	80 (96%)	3 (4%)	31	63
27	24	78/78 (100%)	77 (99%)	1 (1%)	61	78
28	25	57/63 (90%)	57 (100%)	0	100	100
29	26	67/68 (98%)	66 (98%)	1 (2%)	57	76
30	27	55/55 (100%)	54 (98%)	1 (2%)	51	74
31	28	48/49 (98%)	48 (100%)	0	100	100
32	29	59/62 (95%)	58 (98%)	1 (2%)	53	75
33	30	47/48 (98%)	45 (96%)	2 (4%)	26	59
34	31	45/49 (92%)	45 (100%)	0	100	100
35	32	38/38 (100%)	38 (100%)	0	100	100
36	33	51/52 (98%)	51 (100%)	0	100	100
37	34	34/34 (100%)	32 (94%)	2 (6%)	18	50
39	Z	303/311 (97%)	300 (99%)	3 (1%)	68	80
40	B	180/199 (90%)	178 (99%)	2 (1%)	65	79
41	C	170/190 (90%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	D	172/173 (99%)	171 (99%)	1 (1%)	78	84
43	E	119/126 (94%)	118 (99%)	1 (1%)	73	82
44	F	87/112 (78%)	85 (98%)	2 (2%)	44	70
45	G	124/129 (96%)	124 (100%)	0	100	100
46	H	104/105 (99%)	104 (100%)	0	100	100
47	I	105/107 (98%)	104 (99%)	1 (1%)	68	80
48	J	86/90 (96%)	86 (100%)	0	100	100
49	K	89/99 (90%)	88 (99%)	1 (1%)	65	79
50	L	103/104 (99%)	102 (99%)	1 (1%)	68	80
51	M	92/96 (96%)	92 (100%)	0	100	100
52	N	83/84 (99%)	82 (99%)	1 (1%)	63	79
53	O	76/77 (99%)	75 (99%)	1 (1%)	61	78
54	P	65/65 (100%)	61 (94%)	4 (6%)	16	49
55	Q	74/78 (95%)	73 (99%)	1 (1%)	59	77
56	R	56/65 (86%)	56 (100%)	0	100	100
57	S	70/79 (89%)	69 (99%)	1 (1%)	59	77
58	T	65/66 (98%)	65 (100%)	0	100	100
59	U	55/61 (90%)	54 (98%)	1 (2%)	51	74
All	All	5298/5593 (95%)	5244 (99%)	54 (1%)	65	80

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Y	44	LYS
7	04	58	LYS
7	04	70	LYS
8	05	4	LEU
8	05	148	GLN
9	06	57	LYS
10	07	87	LYS
10	07	94	ARG
11	08	9	VAL
11	08	17	LYS
13	10	58	THR
14	11	34	ILE
15	12	81	ILE

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Mol	Chain	Res	Type
16	13	73	ASP
18	15	8	LYS
18	15	133	LYS
19	16	2	ARG
20	17	12	THR
20	17	43	ASN
22	19	71	ASN
24	21	109	ASP
25	22	61	LEU
26	23	27	VAL
26	23	71	ILE
26	23	96	LYS
27	24	42	LEU
29	26	53	LYS
30	27	21	LEU
32	29	2	LYS
33	30	19	ASP
33	30	56	LYS
37	34	2	LYS
37	34	23	ILE
39	Z	212	ARG
39	Z	245	ARG
39	Z	307	LYS
40	B	15	PHE
40	B	35	ASN
42	D	27	ILE
43	E	156	ARG
44	F	17	GLN
44	F	54	LEU
47	I	31	GLN
49	K	30	ILE
50	L	27	PRO
52	N	22	LYS
53	O	86	LEU
54	P	5	ARG
54	P	26	ASN
54	P	46	LYS
54	P	76	LYS
55	Q	18	LYS
57	S	2	ARG
59	U	16	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (161)

such sidechains are listed below:

Mol	Chain	Res	Type
4	Y	5	GLN
4	Y	27	GLN
6	03	168	ASN
7	04	20	ASN
7	04	36	ASN
7	04	44	ASN
7	04	52	HIS
7	04	59	GLN
7	04	69	ASN
7	04	89	ASN
7	04	116	GLN
7	04	127	ASN
7	04	133	ASN
7	04	142	ASN
7	04	199	HIS
8	05	36	GLN
8	05	42	ASN
8	05	167	ASN
9	06	90	GLN
9	06	92	HIS
9	06	156	ASN
10	07	20	ASN
10	07	22	ASN
10	07	26	GLN
11	08	47	ASN
11	08	63	GLN
11	08	127	GLN
12	09	11	ASN
12	09	135	HIS
13	10	57	ASN
13	10	122	GLN
14	11	33	ASN
14	11	42	ASN
14	11	93	ASN
15	12	40	HIS
15	12	86	GLN
15	12	128	ASN
15	12	131	ASN
16	13	29	HIS
16	13	82	ASN
16	13	89	ASN
17	14	38	GLN

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Mol	Chain	Res	Type
17	14	54	GLN
17	14	99	ASN
18	15	17	ASN
18	15	60	GLN
18	15	88	ASN
19	16	62	ASN
20	17	29	HIS
20	17	43	ASN
20	17	98	GLN
21	18	2	ASN
21	18	6	GLN
21	18	51	ASN
21	18	74	GLN
21	18	76	HIS
22	19	19	GLN
22	19	36	GLN
22	19	80	ASN
23	20	11	GLN
23	20	87	GLN
24	21	57	ASN
25	22	48	GLN
25	22	59	ASN
26	23	39	ASN
27	24	24	ASN
27	24	51	GLN
27	24	78	GLN
27	24	80	HIS
28	25	42	HIS
28	25	46	ASN
28	25	72	ASN
29	26	15	ASN
29	26	16	ASN
29	26	31	ASN
30	27	20	ASN
30	27	27	ASN
30	27	41	HIS
32	29	41	HIS
33	30	5	ASN
33	30	40	HIS
34	31	18	HIS
34	31	25	ASN
35	32	13	ASN

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Mol	Chain	Res	Type
35	32	26	ASN
35	32	29	GLN
36	33	23	HIS
37	34	35	GLN
39	Z	5	ASN
39	Z	8	ASN
39	Z	38	ASN
39	Z	48	ASN
39	Z	54	GLN
39	Z	97	ASN
39	Z	133	GLN
39	Z	214	HIS
39	Z	235	ASN
39	Z	255	ASN
39	Z	276	ASN
39	Z	280	GLN
39	Z	283	ASN
39	Z	286	GLN
39	Z	301	GLN
39	Z	304	ASN
40	B	23	ASN
40	B	35	ASN
40	B	41	ASN
40	B	50	ASN
40	B	102	ASN
40	B	119	GLN
40	B	167	HIS
40	B	177	ASN
41	C	7	ASN
41	C	18	ASN
41	C	24	ASN
41	C	138	GLN
41	C	139	ASN
41	C	184	ASN
42	D	58	GLN
42	D	84	ASN
42	D	119	HIS
42	D	151	GLN
43	E	60	GLN
43	E	69	ASN
43	E	81	GLN
43	E	131	ASN

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Mol	Chain	Res	Type
43	E	134	ASN
43	E	145	ASN
44	F	17	GLN
44	F	37	HIS
44	F	68	GLN
45	G	27	ASN
45	G	67	ASN
45	G	121	ASN
46	H	15	ASN
46	H	37	ASN
47	I	24	ASN
47	I	31	GLN
48	J	56	HIS
48	J	58	ASN
48	J	64	GLN
49	K	39	ASN
50	L	4	ASN
50	L	28	GLN
50	L	58	ASN
50	L	72	ASN
51	M	7	ASN
51	M	99	GLN
52	N	3	GLN
52	N	59	GLN
52	N	61	ASN
53	O	19	ASN
53	O	36	ASN
54	P	26	ASN
54	P	40	ASN
55	Q	30	HIS
55	Q	46	HIS
55	Q	49	ASN
55	Q	50	ASN
58	T	12	GLN
58	T	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	182 (11%)	1 (0%)
2	01	2902/2903 (99%)	320 (11%)	6 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	02	118/119 (99%)	11 (9%)	1 (0%)
38	V	13/14 (92%)	1 (7%)	0
5	W	76/77 (98%)	8 (10%)	0
5	X	76/77 (98%)	20 (26%)	1 (1%)
All	All	4723/4729 (99%)	542 (11%)	9 (0%)

All (542) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	6	G
1	A	9	G
1	A	22	G
1	A	31	G
1	A	32	A
1	A	33	A
1	A	39	G
1	A	41	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	65	A
1	A	70	U
1	A	72	A
1	A	83	C
1	A	84	U
1	A	85	U
1	A	86	G
1	A	95	C
1	A	138	G
1	A	144	G
1	A	171	A
1	A	174	A
1	A	183	C
1	A	197	A
1	A	209	U
1	A	210	C
1	A	211	G
1	A	225	C
1	A	226	G
1	A	247	G
1	A	251	G

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Mol	Chain	Res	Type
1	A	253	A
1	A	266	G
1	A	267	C
1	A	274	A
1	A	279	A
1	A	280	C
1	A	281	G
1	A	289	G
1	A	292	G
1	A	306	A
1	A	329	A
1	A	330	C
1	A	344	A
1	A	345	C
1	A	346	G
1	A	351	G
1	A	352	C
1	A	358	U
1	A	367	U
1	A	369	G
1	A	372	C
1	A	377	G
1	A	390	U
1	A	394	G
1	A	395	C
1	A	404	G
1	A	411	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	429	U
1	A	437	U
1	A	442	G
1	A	448	A
1	A	467	U
1	A	468	A
1	A	479	U
1	A	480	U
1	A	485	U
1	A	486	U
1	A	493	A

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Mol	Chain	Res	Type
1	A	497	G
1	A	511	C
1	A	524	G
1	A	527	G
1	A	531	U
1	A	532	A
1	A	541	G
1	A	547	A
1	A	561	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	615	G
1	A	621	A
1	A	633	G
1	A	642	A
1	A	665	A
1	A	687	A
1	A	701	U
1	A	702	A
1	A	703	G
1	A	723	U
1	A	724	G
1	A	755	G
1	A	777	A
1	A	793	U
1	A	814	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	832	G
1	A	843	U
1	A	846	G
1	A	851	G
1	A	873	A
1	A	890	G
1	A	902	G
1	A	926	G
1	A	934	C
1	A	935	A

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Mol	Chain	Res	Type
1	A	960	U
1	A	966	G
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1028	C
1	A	1031	C
1	A	1033	G
1	A	1094	G
1	A	1101	A
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1159	U
1	A	1168	U
1	A	1182	G
1	A	1184	G
1	A	1196	A
1	A	1197	A
1	A	1213	A
1	A	1225	A
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1258	G
1	A	1260	G
1	A	1261	A
1	A	1275	A
1	A	1278	G
1	A	1280	A
1	A	1285	A
1	A	1286	U
1	A	1287	A
1	A	1297	G
1	A	1298	U
1	A	1300	G

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Mol	Chain	Res	Type
1	A	1317	C
1	A	1320	C
1	A	1337	G
1	A	1346	A
1	A	1347	G
1	A	1363	A
1	A	1378	C
1	A	1394	A
1	A	1397	C
1	A	1398	A
1	A	1446	A
1	A	1448	C
1	A	1451	U
1	A	1452	C
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1499	A
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
2	01	10	A
2	01	34	U
2	01	35	G
2	01	51	G
2	01	63	A
2	01	71	A
2	01	74	A
2	01	75	G
2	01	84	A
2	01	118	A
2	01	119	A
2	01	120	U
2	01	141	G
2	01	162	U
2	01	163	C
2	01	181	A
2	01	196	A
2	01	215	G
2	01	216	A

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Mol	Chain	Res	Type
2	01	221	A
2	01	229	C
2	01	230	G
2	01	248	G
2	01	249	C
2	01	255	A
2	01	265	A
2	01	266	G
2	01	281	C
2	01	294	A
2	01	311	A
2	01	312	G
2	01	323	C
2	01	324	A
2	01	329	G
2	01	330	A
2	01	346	A
2	01	371	A
2	01	372	G
2	01	386	G
2	01	387	U
2	01	404	A
2	01	406	G
2	01	411	G
2	01	412	A
2	01	422	A
2	01	424	G
2	01	451	U
2	01	480	A
2	01	481	G
2	01	490	C
2	01	491	G
2	01	504	A
2	01	505	A
2	01	508	A
2	01	509	C
2	01	518	G
2	01	529	A
2	01	531	C
2	01	532	A
2	01	544	C
2	01	548	G

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Mol	Chain	Res	Type
2	01	563	A
2	01	573	U
2	01	588	U
2	01	603	A
2	01	615	U
2	01	627	A
2	01	637	A
2	01	646	U
2	01	654	A
2	01	655	A
2	01	669	G
2	01	686	U
2	01	687	C
2	01	730	A
2	01	747	U
2	01	764	A
2	01	776	G
2	01	782	A
2	01	784	G
2	01	785	G
2	01	805	G
2	01	812	C
2	01	819	A
2	01	827	U
2	01	828	U
2	01	830	G
2	01	845	A
2	01	846	U
2	01	847	U
2	01	856	G
2	01	860	U
2	01	878	A
2	01	887	U
2	01	891	G
2	01	896	A
2	01	897	C
2	01	907	G
2	01	910	A
2	01	915	C
2	01	932	U
2	01	941	A
2	01	946	C

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Mol	Chain	Res	Type
2	01	961	C
2	01	974	G
2	01	975	A
2	01	983	A
2	01	995	C
2	01	996	A
2	01	1012	U
2	01	1013	C
2	01	1021	A
2	01	1022	G
2	01	1026	G
2	01	1033	U
2	01	1046	A
2	01	1047	G
2	01	1059	G
2	01	1062	G
2	01	1063	G
2	01	1064	C
2	01	1065	U
2	01	1066	U
2	01	1067	A
2	01	1070	A
2	01	1071	G
2	01	1072	C
2	01	1073	A
2	01	1074	G
2	01	1075	C
2	01	1076	C
2	01	1079	C
2	01	1084	A
2	01	1088	A
2	01	1094	U
2	01	1095	A
2	01	1104	C
2	01	1111	A
2	01	1131	G
2	01	1132	U
2	01	1135	C
2	01	1157	G
2	01	1173	U
2	01	1175	A
2	01	1176	U

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Mol	Chain	Res	Type
2	01	1180	U
2	01	1204	A
2	01	1212	G
2	01	1250	G
2	01	1251	C
2	01	1253	A
2	01	1256	G
2	01	1271	G
2	01	1272	A
2	01	1275	A
2	01	1289	C
2	01	1301	A
2	01	1332	G
2	01	1345	C
2	01	1365	A
2	01	1378	A
2	01	1379	U
2	01	1383	A
2	01	1398	C
2	01	1416	G
2	01	1420	A
2	01	1428	C
2	01	1461	C
2	01	1475	G
2	01	1482	G
2	01	1490	A
2	01	1497	U
2	01	1515	A
2	01	1522	A
2	01	1524	G
2	01	1530	G
2	01	1535	A
2	01	1536	C
2	01	1537	G
2	01	1555	G
2	01	1560	G
2	01	1569	A
2	01	1608	A
2	01	1611	C
2	01	1616	A
2	01	1647	U
2	01	1648	U

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Mol	Chain	Res	Type
2	01	1674	G
2	01	1699	G
2	01	1715	G
2	01	1729	U
2	01	1730	C
2	01	1731	G
2	01	1738	G
2	01	1758	U
2	01	1764	C
2	01	1773	A
2	01	1800	C
2	01	1801	A
2	01	1808	A
2	01	1816	C
2	01	1829	A
2	01	1901	A
2	01	1906	G
2	01	1914	C
2	01	1929	G
2	01	1930	G
2	01	1937	A
2	01	1938	A
2	01	1944	U
2	01	1955	U
2	01	1963	U
2	01	1967	C
2	01	1970	A
2	01	1971	U
2	01	1972	G
2	01	1991	U
2	01	1992	G
2	01	1993	U
2	01	1997	C
2	01	2022	U
2	01	2023	C
2	01	2030	A
2	01	2031	A
2	01	2036	C
2	01	2043	C
2	01	2049	G
2	01	2052	A
2	01	2055	C

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Mol	Chain	Res	Type
2	01	2056	G
2	01	2060	A
2	01	2061	G
2	01	2062	A
2	01	2069	G
2	01	2072	C
2	01	2095	A
2	01	2111	U
2	01	2112	G
2	01	2115	G
2	01	2118	U
2	01	2119	A
2	01	2120	G
2	01	2128	G
2	01	2132	U
2	01	2133	G
2	01	2137	U
2	01	2146	C
2	01	2148	G
2	01	2166	U
2	01	2170	A
2	01	2172	U
2	01	2173	A
2	01	2198	A
2	01	2204	G
2	01	2213	U
2	01	2225	A
2	01	2238	G
2	01	2239	G
2	01	2250	G
2	01	2283	C
2	01	2287	A
2	01	2297	A
2	01	2305	U
2	01	2309	A
2	01	2325	G
2	01	2327	A
2	01	2333	A
2	01	2334	U
2	01	2383	G
2	01	2385	C
2	01	2388	A

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Mol	Chain	Res	Type
2	01	2402	U
2	01	2403	C
2	01	2406	A
2	01	2423	U
2	01	2429	G
2	01	2430	A
2	01	2441	U
2	01	2448	A
2	01	2476	A
2	01	2498	C
2	01	2502	G
2	01	2503	A
2	01	2504	U
2	01	2518	A
2	01	2547	A
2	01	2554	U
2	01	2566	A
2	01	2567	G
2	01	2572	A
2	01	2573	C
2	01	2582	G
2	01	2585	U
2	01	2602	A
2	01	2609	U
2	01	2613	U
2	01	2629	U
2	01	2646	C
2	01	2655	G
2	01	2682	A
2	01	2689	U
2	01	2690	U
2	01	2714	G
2	01	2716	C
2	01	2748	A
2	01	2764	A
2	01	2765	A
2	01	2778	A
2	01	2779	U
2	01	2791	G
2	01	2798	U
2	01	2800	A
2	01	2808	G

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Mol	Chain	Res	Type
2	01	2820	A
2	01	2821	A
2	01	2833	U
2	01	2867	G
2	01	2884	U
2	01	2893	A
2	01	2894	G
3	02	13	G
3	02	15	A
3	02	24	G
3	02	35	C
3	02	44	G
3	02	45	A
3	02	67	G
3	02	89	U
3	02	90	C
3	02	108	A
3	02	109	A
5	X	8	U
5	X	9	G
5	X	15	G
5	X	17	C
5	X	17(A)	U
5	X	18	G
5	X	19	G
5	X	20	U
5	X	21	A
5	X	22	G
5	X	34	C
5	X	35	A
5	X	43	A
5	X	48	C
5	X	49	G
5	X	57	A
5	X	61	C
5	X	63	G
5	X	67	C
5	X	69	C
38	V	12	A
5	W	9	G
5	W	14	A
5	W	18	G

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Mol	Chain	Res	Type
5	W	19	G
5	W	20	U
5	W	48	C
5	W	61	C
5	W	76	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1297	G
2	01	421	C
2	01	859	G
2	01	1020	A
2	01	1130	U
2	01	2296	U
2	01	2326	C
3	02	66	A
5	X	17(A)	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 361 ligands modelled in this entry, 361 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

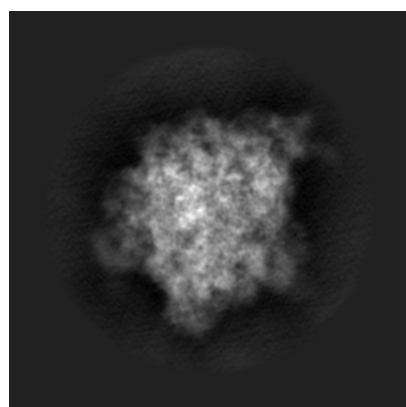
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8521. These allow visual inspection of the internal detail of the map and identification of artifacts.

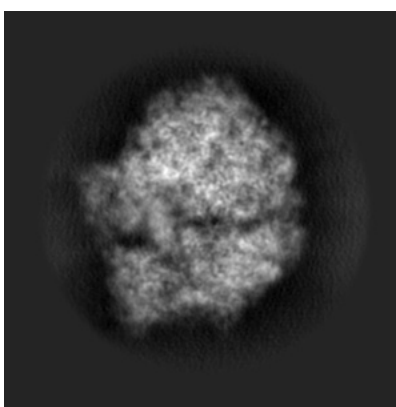
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

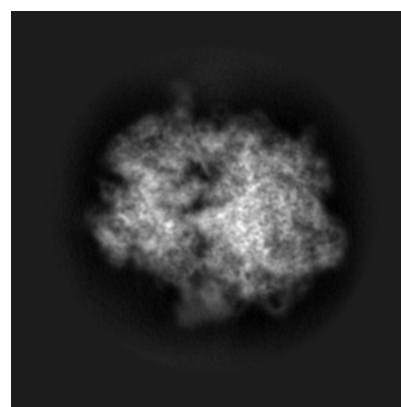
6.1.1 Primary map



X



Y

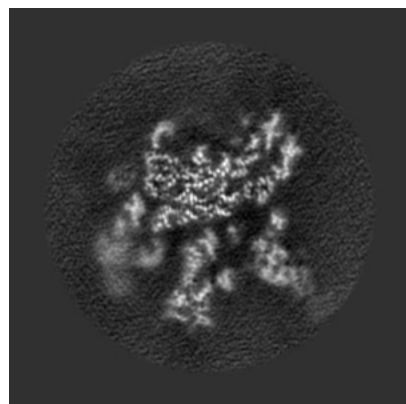


Z

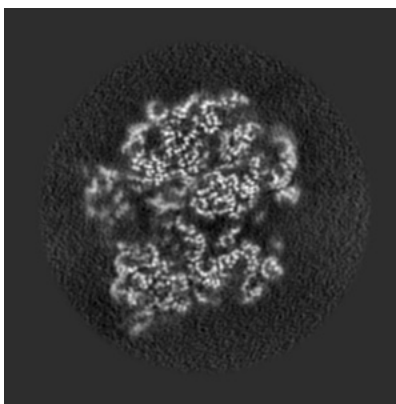
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

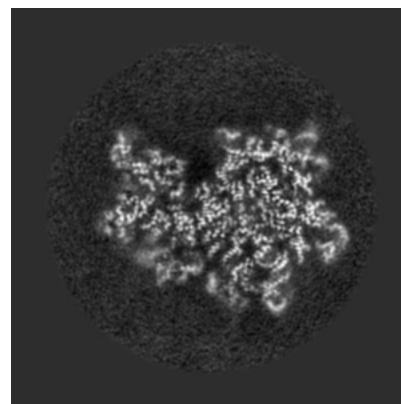
6.2.1 Primary map



X Index: 160



Y Index: 160

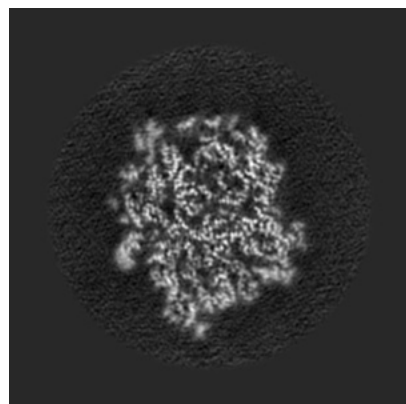


Z Index: 160

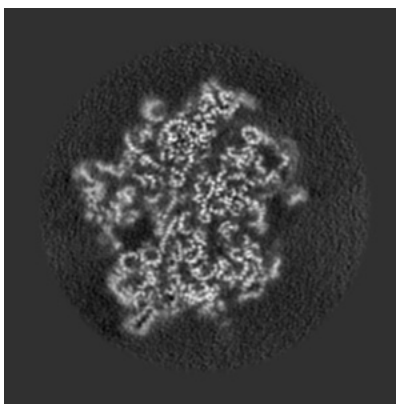
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

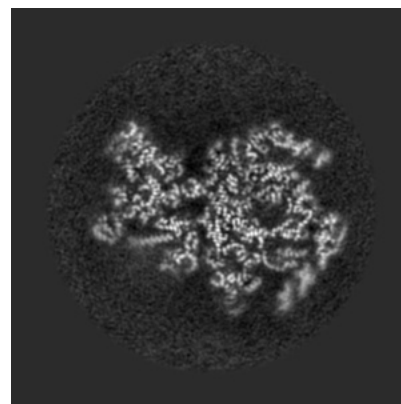
6.3.1 Primary map



X Index: 188



Y Index: 154

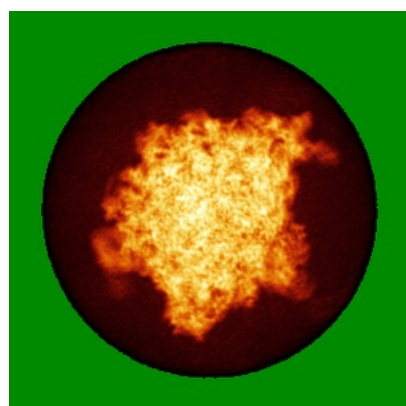


Z Index: 170

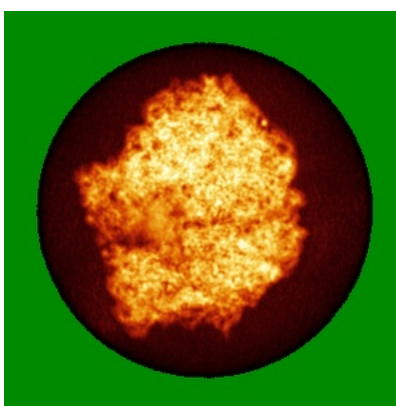
The images above show the largest variance slices of the map in three orthogonal directions.

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

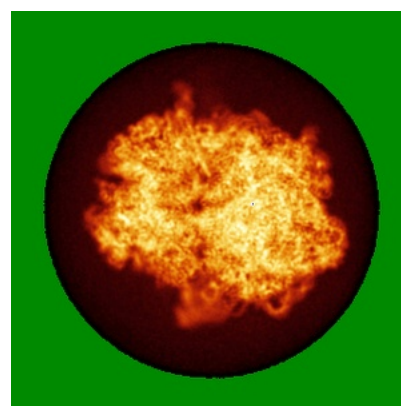
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

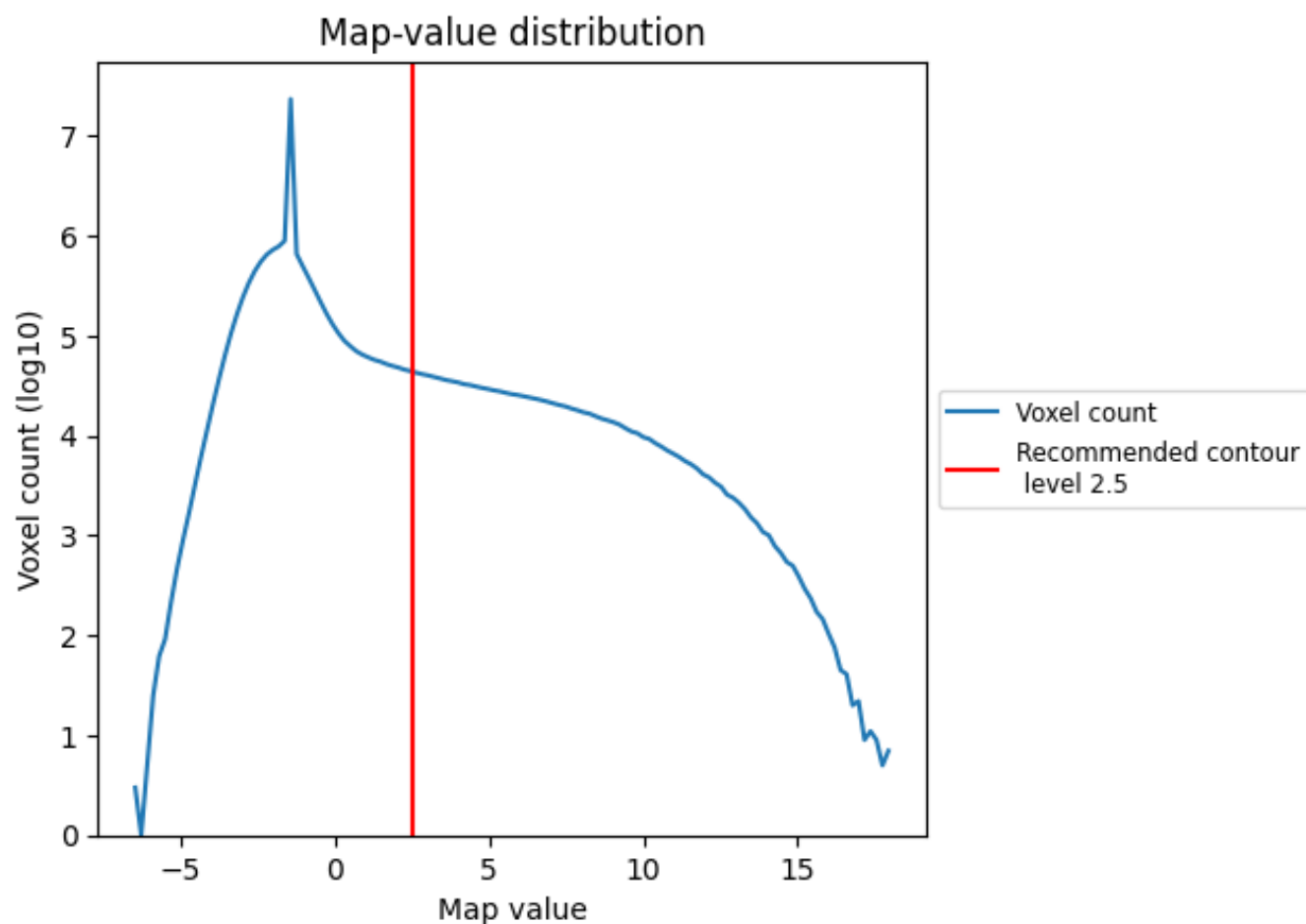
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

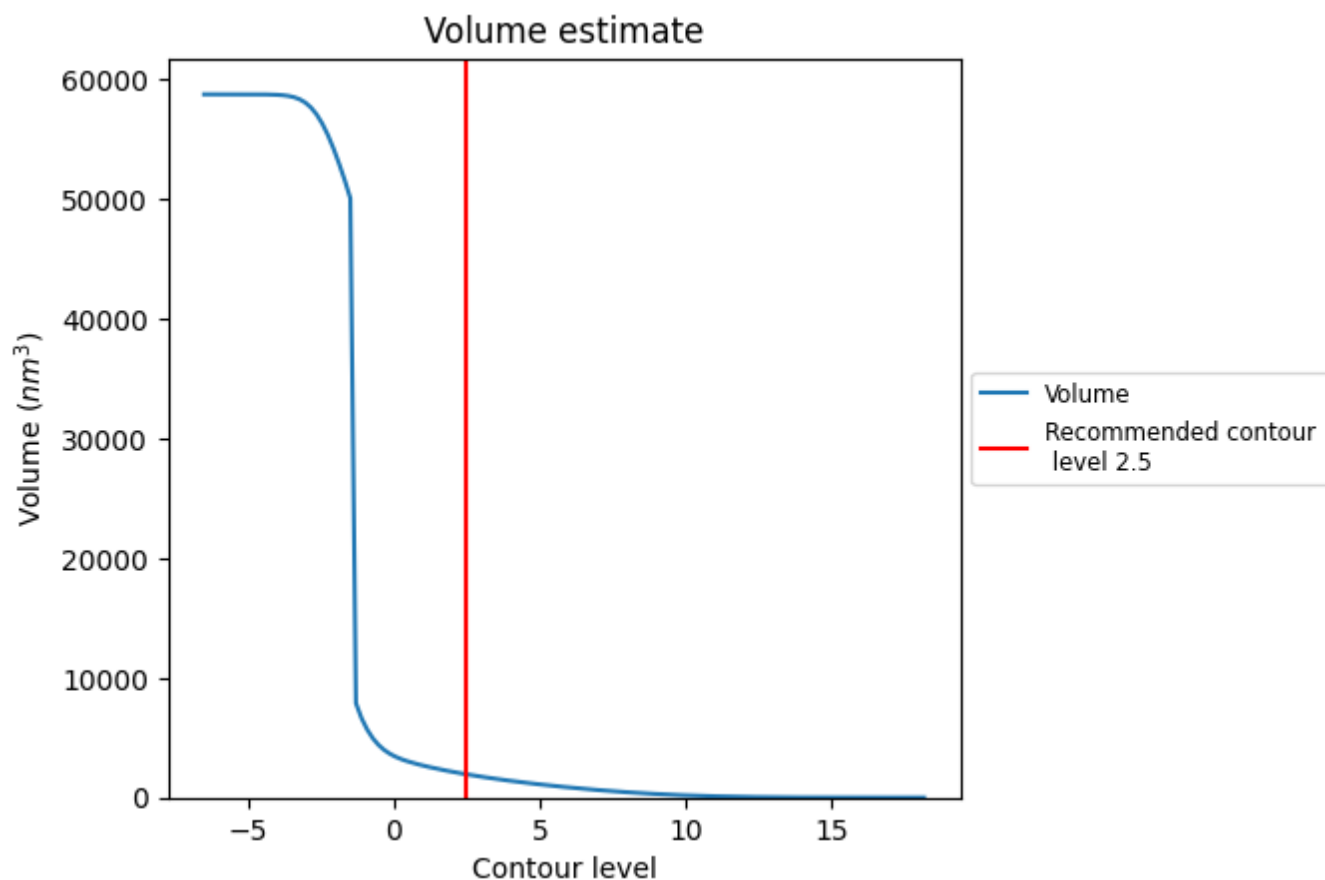
This section contains the results of statistical analysis of the map.

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.

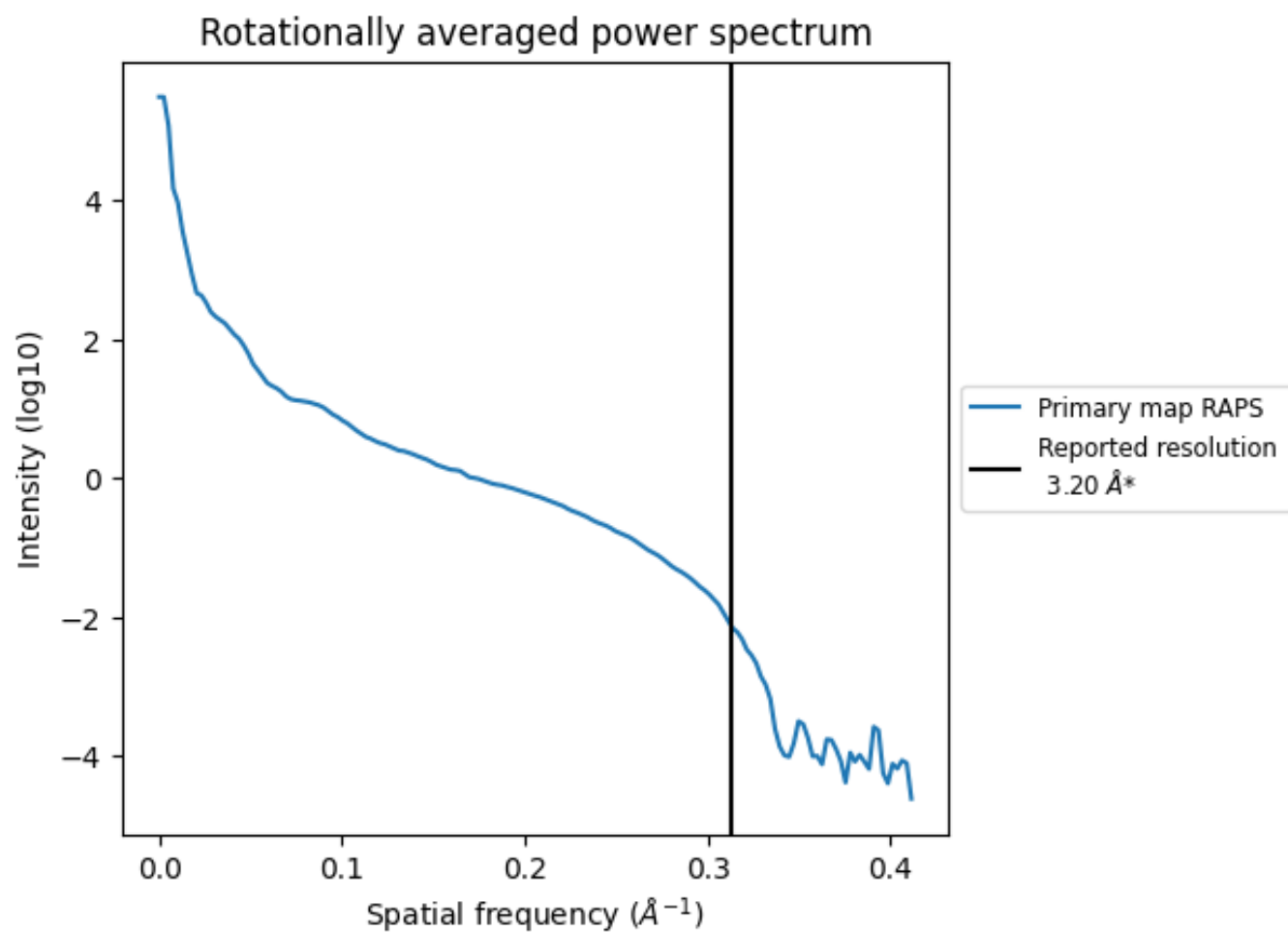
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1941 nm³; this corresponds to an approximate mass of 1753 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

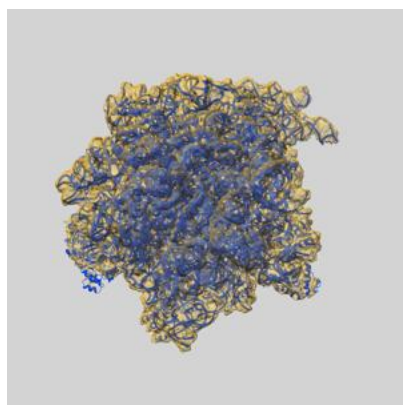
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

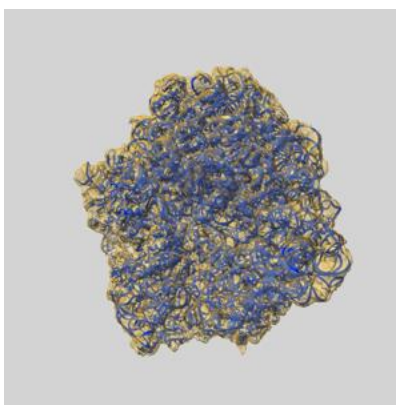
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8521 and PDB model 5U9F. Per-residue inclusion information can be found in section [3](#) on page [16](#).

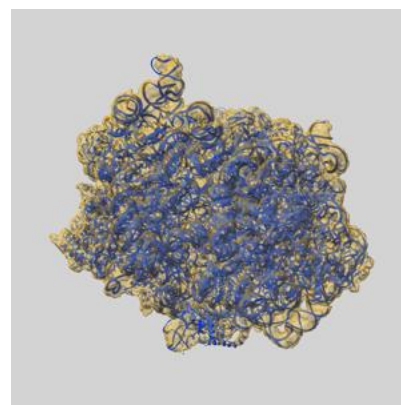
9.1 Map-model overlay [i](#)



X



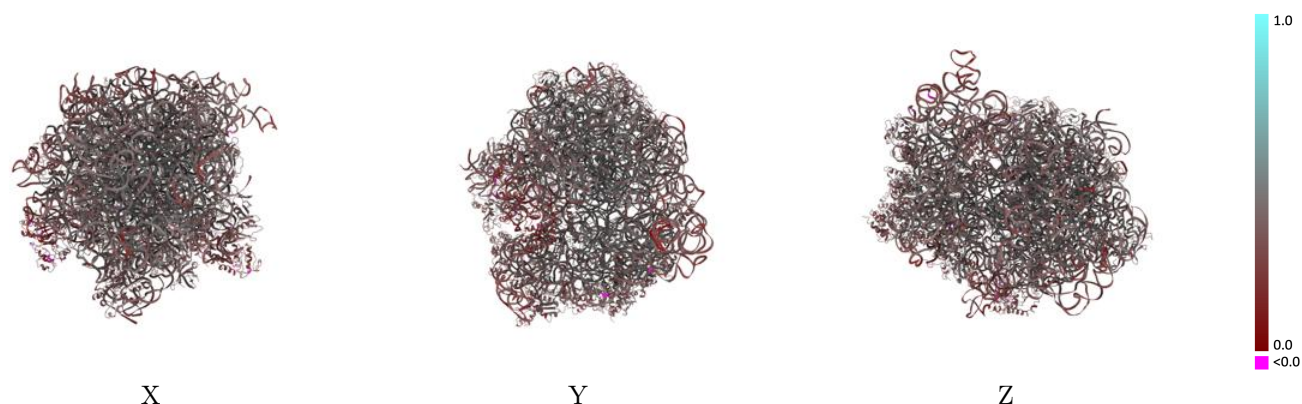
Y



Z

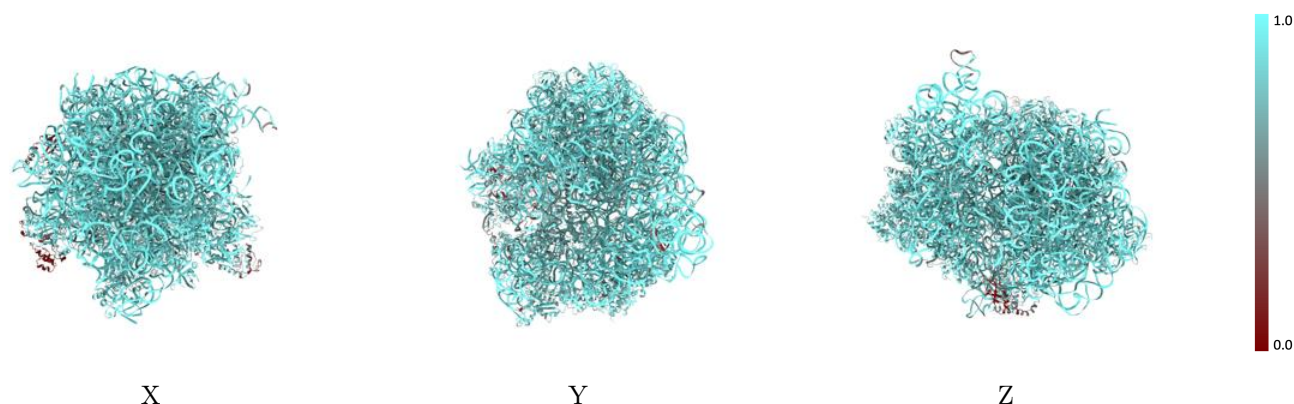
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



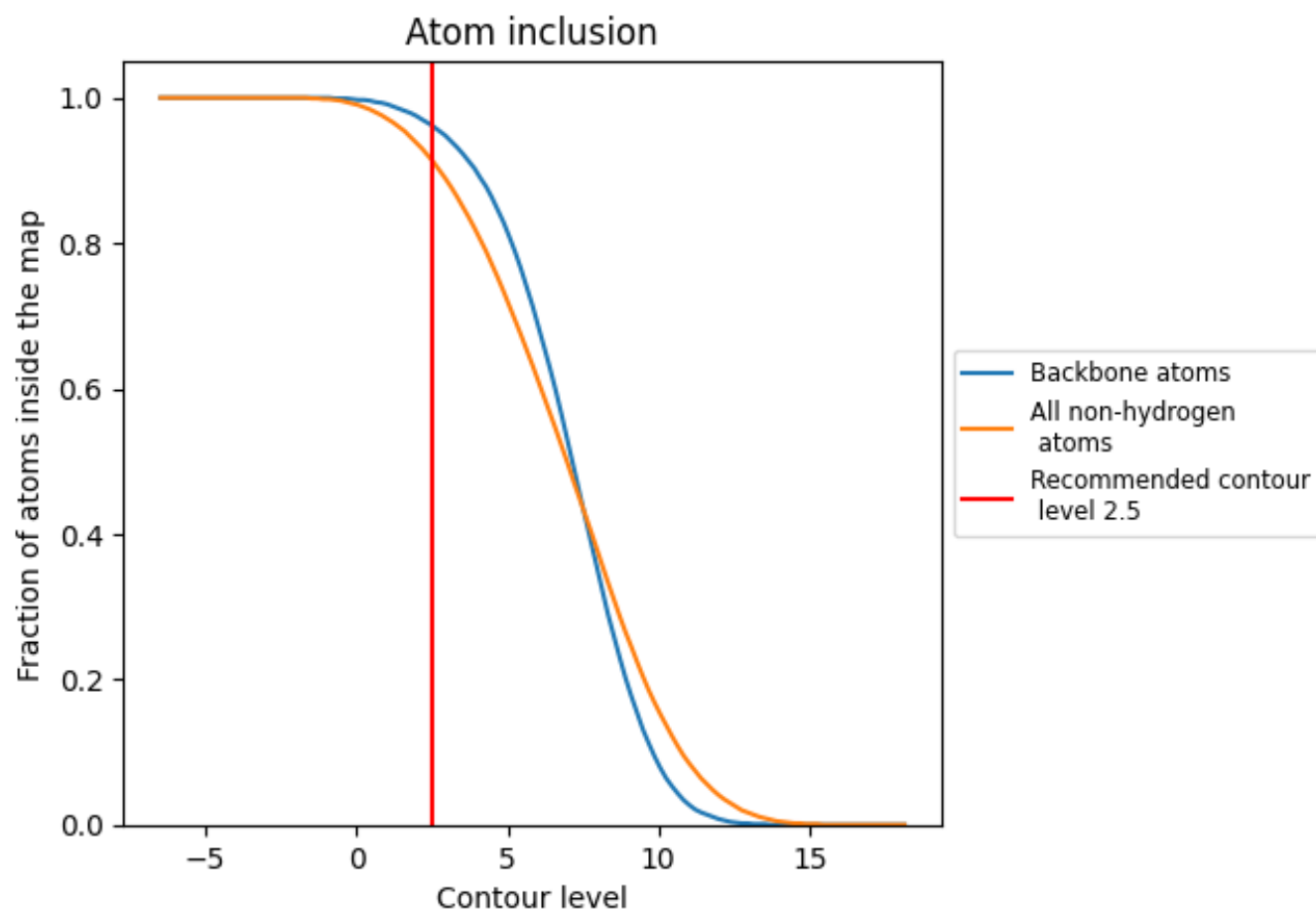
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.3830
01	 0.9760	 0.4040
02	 0.9790	 0.3530
03	 0.4600	 0.1980
04	 0.8360	 0.4350
05	 0.8650	 0.4250
06	 0.8650	 0.4000
07	 0.8590	 0.3230
08	 0.8480	 0.3650
09	 0.3690	 0.3050
10	 0.5420	 0.2120
11	 0.6920	 0.2380
12	 0.8750	 0.4120
13	 0.8030	 0.4230
14	 0.8820	 0.4140
15	 0.8110	 0.4120
16	 0.8930	 0.3900
17	 0.8900	 0.3420
18	 0.8240	 0.4010
19	 0.8770	 0.4080
20	 0.8760	 0.4140
21	 0.8340	 0.4090
22	 0.8010	 0.3790
23	 0.8400	 0.3800
24	 0.8820	 0.3800
25	 0.8940	 0.4230
26	 0.8370	 0.4040
27	 0.8150	 0.3030
28	 0.8440	 0.4040
29	 0.5380	 0.2840
30	 0.8530	 0.4020
31	 0.7980	 0.4010
32	 0.8620	 0.4280
33	 0.8860	 0.4290
34	 0.7790	 0.3680



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Chain	Atom inclusion	Q-score
A	 0.9730	 0.3860
B	 0.8110	 0.3300
C	 0.8190	 0.3740
D	 0.8430	 0.3600
E	 0.8700	 0.4010
F	 0.8130	 0.3530
G	 0.8090	 0.3290
H	 0.8650	 0.3960
I	 0.8570	 0.3340
J	 0.8270	 0.3250
K	 0.8580	 0.3870
L	 0.8280	 0.4250
M	 0.8070	 0.3170
N	 0.8550	 0.3310
O	 0.8730	 0.3590
P	 0.8840	 0.4020
Q	 0.8450	 0.3770
R	 0.8310	 0.3680
S	 0.8570	 0.3540
T	 0.8390	 0.3360
U	 0.7450	 0.2650
V	 0.8730	 0.3070
W	 0.9350	 0.3850
X	 0.6450	 0.2180
Y	 0.7570	 0.3830
Z	 0.6680	 0.3170