



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 04:47 PM UTC

PDB ID : 8UU6 / pdb_00008uu6
EMDB ID : EMD-42561
Title : Cryo-EM structure of the ratcheted *Listeria innocua* 70S ribosome in complex with p/E-tRNA (structure II-A)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 3.30 Å(reported)
Based on initial model : 7NHN

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

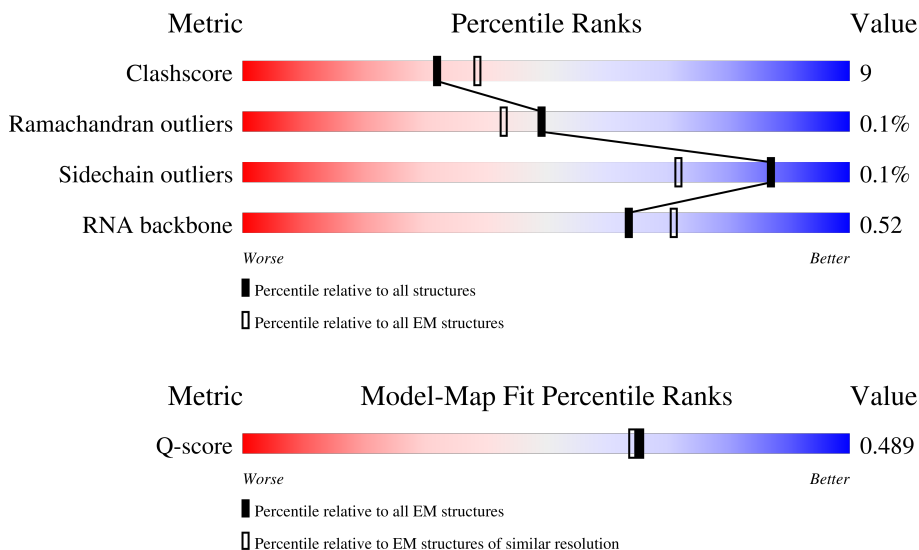
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1550	
2	b	249	
3	c	218	

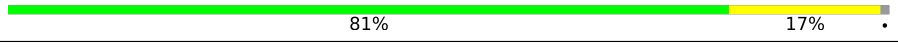
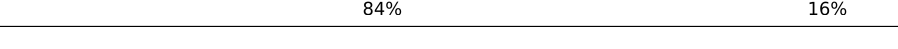
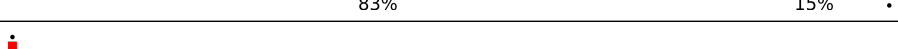
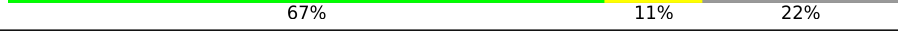
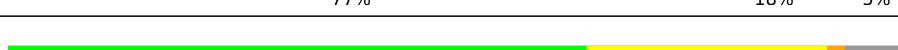
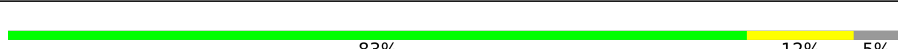
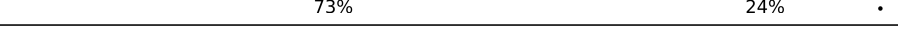
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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	167	
6	f	97	
7	g	156	
8	h	132	
9	i	130	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	90	
17	q	87	
18	r	79	
19	s	92	
20	t	84	
21	x	76	
22	w	21	
23	A	2932	
24	B	116	
25	C	277	
26	D	209	
27	E	207	
28	F	179	

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Mol	Chain	Length	Quality of chain
29	G	178	
30	L	145	
31	M	122	
32	N	146	
33	O	144	
34	P	135	
35	Q	119	
36	R	114	
37	S	119	
38	T	102	
39	U	118	
40	V	94	
41	W	103	
42	Y	96	
43	Z	62	
44	1	63	
45	2	59	
46	3	81	
47	4	57	
48	5	49	
49	6	44	
50	7	66	
51	8	37	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 136923 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	1516	Total	C	N	O	P	0	0
			32515	14504	5960	10535	1516		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	b	224	Total	C	N	O	0	0
			1228	757	236	235		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	203	Total	C	N	O	S	0	0
			1395	880	254	259	2		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	199	Total	C	N	O	S	0	0
			1429	893	269	266	1		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	156	Total	C	N	O	S	0	0
			1087	685	196	204	2		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	93	Total	C	N	O	S	0	0
			652	419	117	114	2		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	143	Total	C	N	O	S	0	0
			1015	634	191	186	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			929	597	159	171	2		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	125	Total	C	N	O	S	0	0
			920	578	183	158	1		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	97	Total	C	N	O	S	0	0
			714	449	129	135	1		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	114	Total	C	N	O	S	0	0
			681	415	131	133	2		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			935	584	184	166	1		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	114	Total	C	N	O	S	0	0
			780	483	157	139	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			463	295	89	74	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	87	Total	C	N	O	S	0	0
			635	393	124	116	2		

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			558	350	113	95			

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	64	Total	C	N	O	S	0	0
			449	288	84	75	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	81	Total	C	N	O	S	0	0
			502	314	100	87	1		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	81	Total	C	N	O	S	0	0
			493	298	95	100			

- Molecule 21 is a RNA chain called p/E Hybrid State Phenylalanine tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	x	74	Total	C	N	O	P	S	0	0
			1591	713	285	517	74	2		

- Molecule 22 is a RNA chain called F-Stop mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	6	Total	C	N	O	P		0	0
			126	57	22	41	6			

- Molecule 23 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	A	2904	Total	C	N	O	P		0	0
			62385	27841	11542	20098	2904			

- Molecule 24 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	B	114	Total	C	N	O	P		0	0
			2428	1082	428	804	114			

- Molecule 25 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	C	273	Total	C	N	O	S		0	0
			2059	1276	405	371	7			

- Molecule 26 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	D	206	Total	C	N	O	S		0	0
			1545	974	287	280	4			

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	E	205	Total	C	N	O			0	0
			1515	960	279	276				

- Molecule 28 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	167	Total	C	N	O	S	0	0
			1142	724	195	218	5		

- Molecule 29 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	160	Total	C	N	O	S	0	0
			1085	684	201	199	1		

- Molecule 30 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L	143	Total	C	N	O	S	0	0
			1084	689	201	191	3		

- Molecule 31 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	122	Total	C	N	O	S	0	0
			914	566	173	170	5		

- Molecule 32 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	N	145	Total	C	N	O	0	0
			1022	633	205	184		

- Molecule 33 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	O	134	Total	C	N	O	S	0	0
			1025	658	194	167	6		

- Molecule 34 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P	122	Total	C	N	O	S	0	0
			952	596	188	167	1		

- Molecule 35 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Q	112	Total	C	N	O	0	0
			701	431	139	131		

- Molecule 36 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	R	113	Total	C	N	O	S	0
			843	534	161	147	1	0

- Molecule 37 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	S	117	Total	C	N	O	S	0
			930	590	181	155	4	0

- Molecule 38 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	T	101	Total	C	N	O	S	0
			762	492	131	138	1	0

- Molecule 39 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	U	111	Total	C	N	O	0	0
			843	532	160	151		

- Molecule 40 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	V	92	Total	C	N	O	S	0
			724	460	122	140	2	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	W	102	Total	C	N	O	S	0
			735	464	135	133	3	0

- Molecule 42 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Y	75	Total	C	N	O	S	0	0
			549	338	106	104	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Z	59	Total	C	N	O	S	0	0
			439	271	90	76	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	59	Total	C	N	O	S	0	0
			467	286	92	88	1		

- Molecule 45 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	56	Total	C	N	O	S	0	0
			429	269	81	78	1		

- Molecule 46 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	3	76	Total	C	N	O	0	0
			529	332	92	105		

- Molecule 47 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	4	53	Total	C	N	O	S	0	0
			425	259	87	74	5		

- Molecule 48 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	48	Total	C	N	O	S	0	0
			380	233	75	68	4		

- Molecule 49 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	6	43	Total	C	N	O	S	0	0
			361	219	87	53	2		

- Molecule 50 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	7	64	Total	C	N	O	S	0	0
			512	316	112	79	5		

- Molecule 51 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	8	36	Total	C	N	O	S	0	0
			292	183	59	44	6		

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	a	18	Total	Mg	0
			18	18	
52	q	1	Total	Mg	0
			1	1	
52	A	78	Total	Mg	0
			78	78	
52	D	1	Total	Mg	0
			1	1	

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	n	1	Total	Zn	0
			1	1	
53	4	1	Total	Zn	0
			1	1	
53	5	1	Total	Zn	0
			1	1	
53	8	1	Total	Zn	0
			1	1	

- Molecule 54 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
54	O	1	Total	K	0
			1	1	

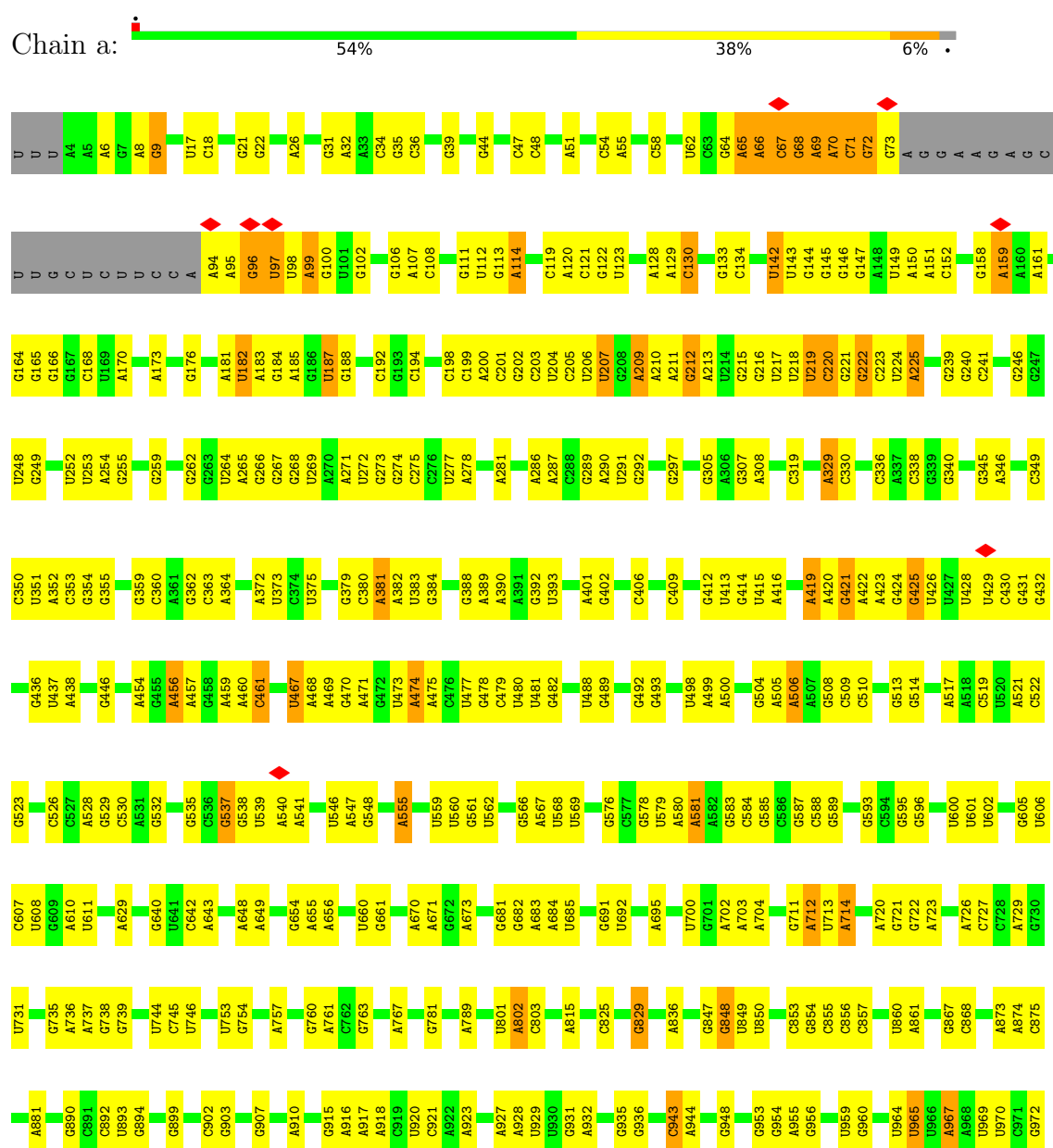
- Molecule 55 is water.

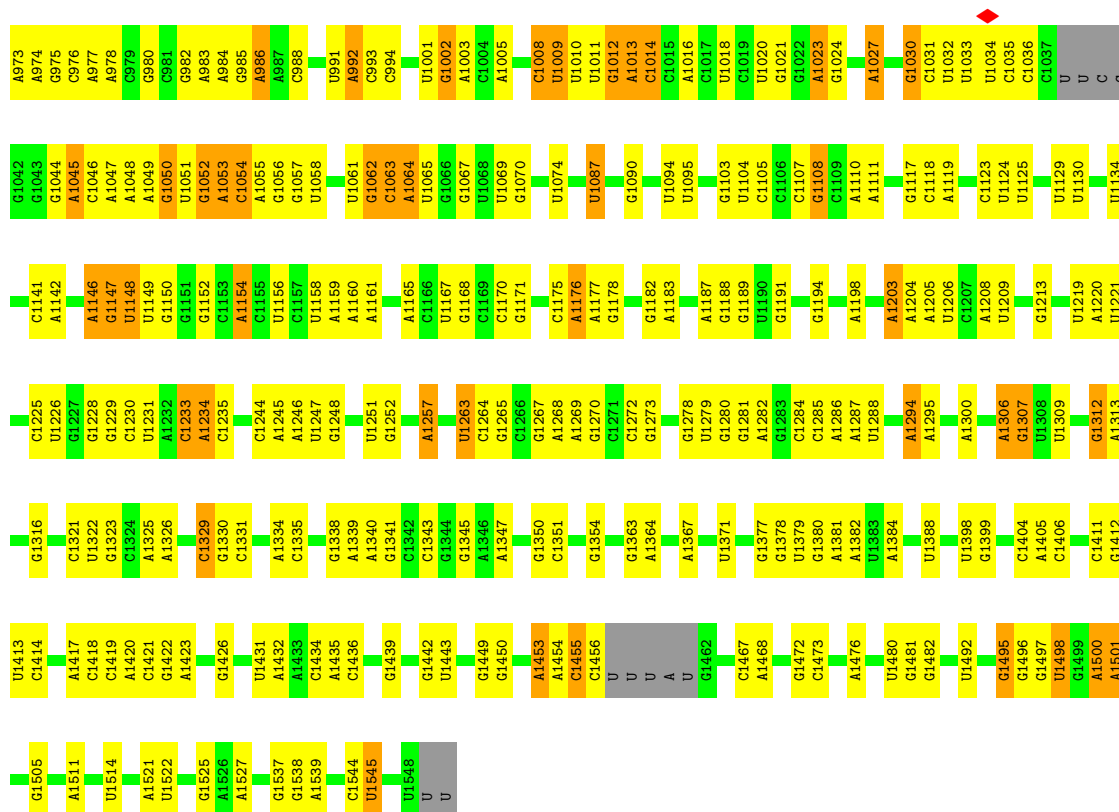
Mol	Chain	Residues	Atoms		AltConf
55	a	2	Total	O	0
			2	2	
55	A	3	Total	O	0
			3	3	

3 Residue-property plots

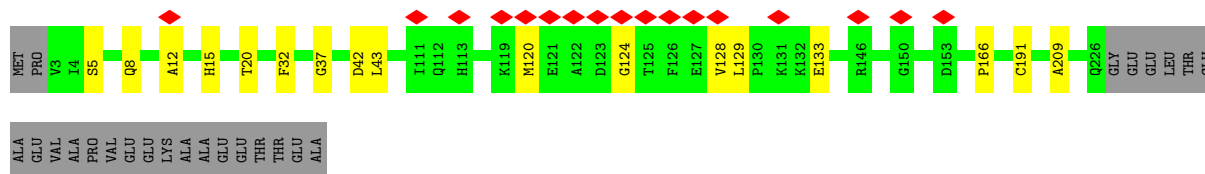
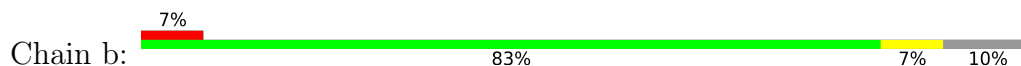
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA

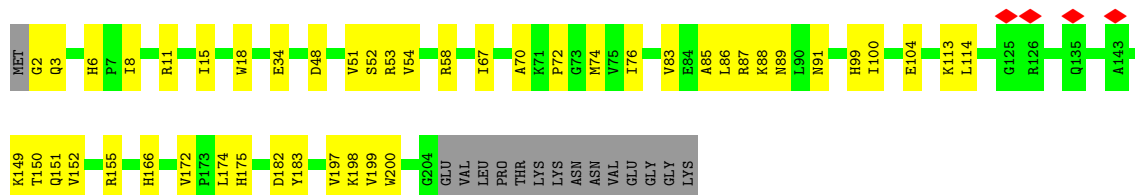




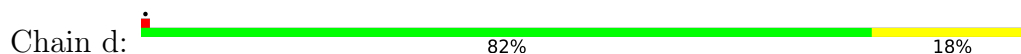
• Molecule 2: Small ribosomal subunit protein uS2

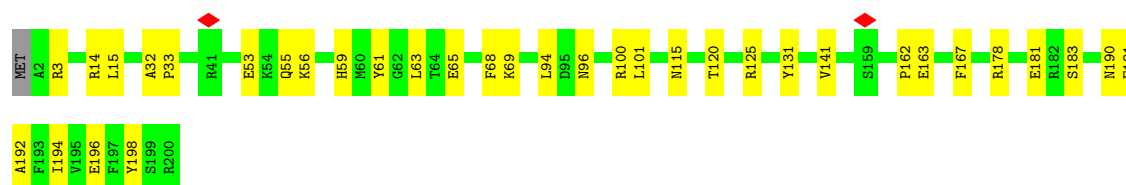


• Molecule 3: Small ribosomal subunit protein uS3

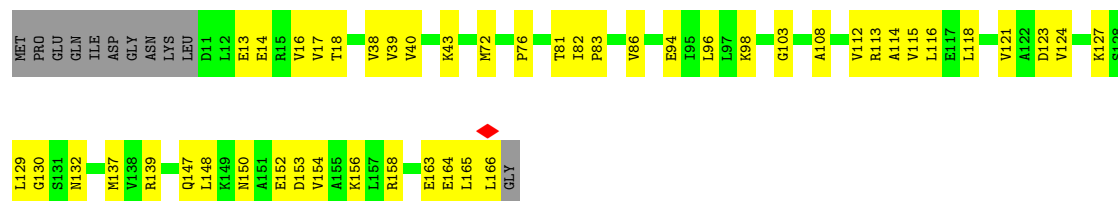


• Molecule 4: Small ribosomal subunit protein uS4

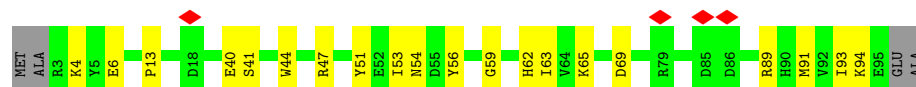
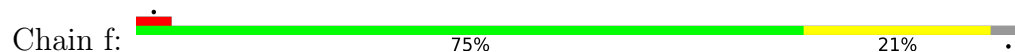




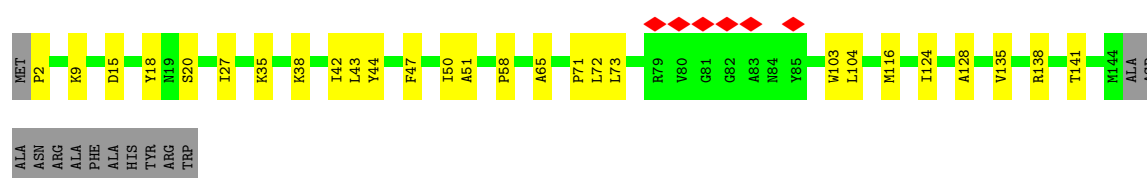
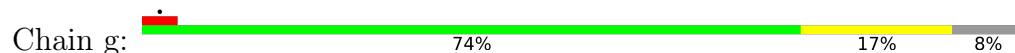
- Molecule 5: Small ribosomal subunit protein uS5



- Molecule 6: Small ribosomal subunit protein bS6



- Molecule 7: Small ribosomal subunit protein uS7



- Molecule 8: Small ribosomal subunit protein uS8



- Molecule 9: Small ribosomal subunit protein uS9

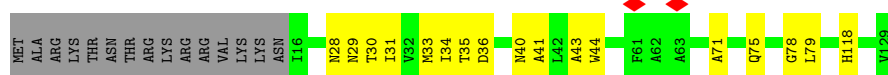
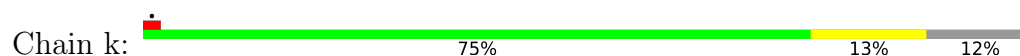




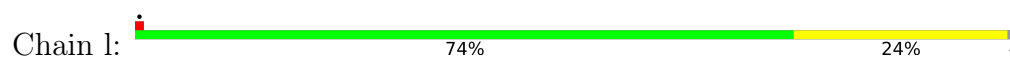
- Molecule 10: Small ribosomal subunit protein uS10



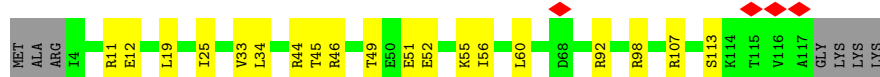
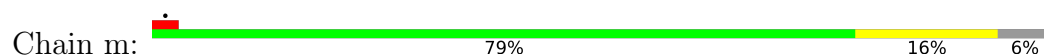
- Molecule 11: Small ribosomal subunit protein uS11



- Molecule 12: Small ribosomal subunit protein uS12



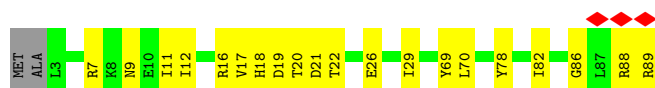
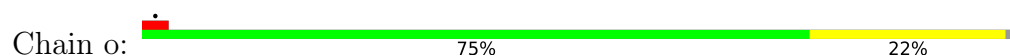
- Molecule 13: Small ribosomal subunit protein uS13



- Molecule 14: Small ribosomal subunit protein uS14

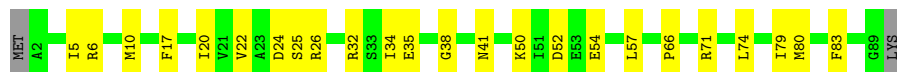


- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: Small ribosomal subunit protein bS16

Chain p:  71% 27% .



- Molecule 17: Small ribosomal subunit protein uS17

Chain q:  71% 21% 8%



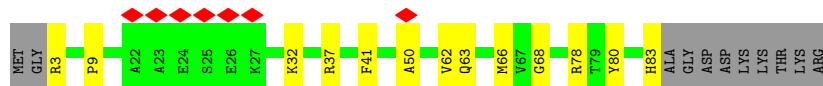
- Molecule 18: Small ribosomal subunit protein bS18

Chain r:  57% 23% 19%



- Molecule 19: Small ribosomal subunit protein uS19

Chain s:  8% 74% 14% 12%

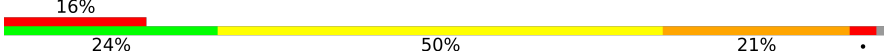


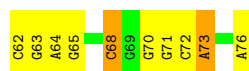
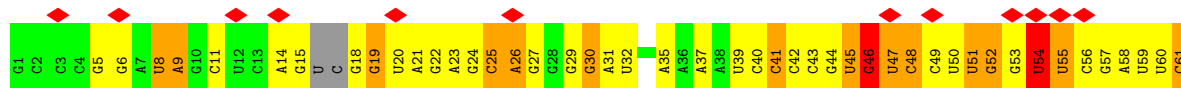
- Molecule 20: Small ribosomal subunit protein bS20

Chain t:  85% 12% .



- Molecule 21: p/E Hybrid State Phenylalanine tRNA

Chain x:  16% 24% 50% 21% . .

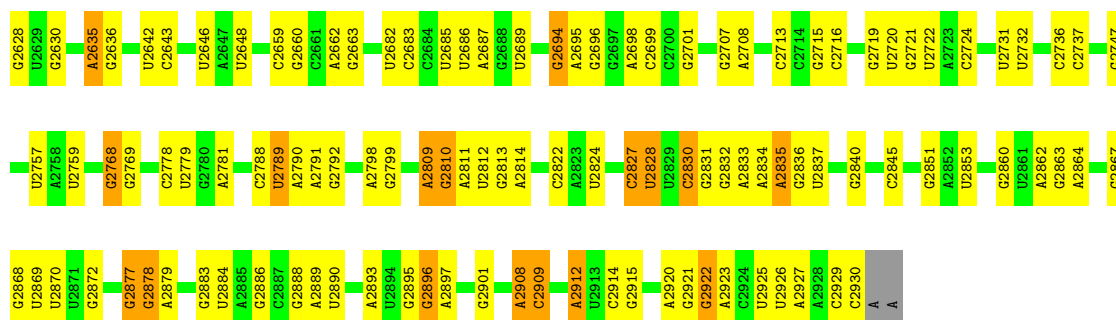


- Molecule 22: F-Stop mRNA

Chain w:  24% 5% 71%



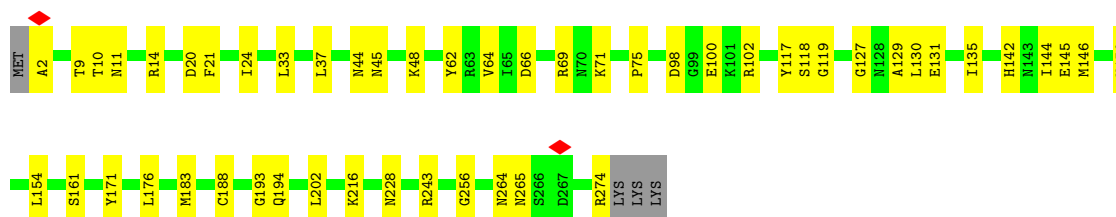
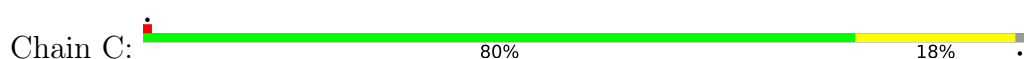
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C2488	G2364	U2278	G2199	C2138	A1807	G1696	U	A1520	A1429	G1320	C1264
C2489	C2365	G2279	U2200	G2139	G1809	G1697	C1592	U1525	A1430	G1205	G1206
C2490	C2366	A2280	G2201	C2140	G1810	G1698	C1593	U1526	A1431	A1321	
C2491	C2367	C2281	G2202	U2141	U1812	G1699	G1594	G1528	G1436	G1322	C1216
C2492	C2368	C2282	G2203	U2142	C1815	A1700	G1595	U1529	A1439	G1323	U
C2493	C2369	G2283	U2204	G2143	C1816	A1701	A1596	U1530	A1440	C	C
C2494	C2370	U2205	A2206	U2144	A1817	G1702	G1597	U1531	C1442	U	U
C2495	C2371	G2207	A2207	U2145	A1818	U1708	G1598	U1532	C1443	U	U
C2496	C2372	U2208	U2208	C2146	U1827	U1712	C1601	U1533	C1444	C	C
C2497	C2373	A2209	G2210	A2147	U1828	U1713	C1602	U1534	A1447	G	G
C2498	C2374	G2211	U2211	G2149	U1829	G1716	C1613	A1535	A1448	A	A
C2499	C2375	U2212	G2212	A2150	U1830	A1717	U1614	A1536	G1449	G1225	
C2500	C2376	U2213	U2213	U2151	U1831	C1719	A1618	A1537	A1450	G1226	
C2501	C2377	G2214	G2214	A2152	C1832	G1723	A1621	C1542	U1451	U1227	
C2502	C2378	U2215	G2215	G2153	A1834	A1726	A1622	C1543	U1452	G1230	
C2503	C2379	G2216	G2216	G1955	A1835	A1727	A1623	C1544	U1453	G1233	
C2504	C2380	U2217	U2217	U1956	A1836	A1728	A1624	C1545	U1454	U1234	
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C2522	C2398	A2235	A2235	A2004	G1890	A1773	G1659	U1571	U1385		
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C2525	C2401	G2238	G2238	U2025	G1893	G1776	A1665	U1574	U1396		
C2526	C2402	U2239	U2239	U2026	G1894	A1777	A1666	G1575	A1397		
C2527	C2403	G2240	G2240	C2027	G1895	G1778	A1667	G1576	A1398		
C2528	C2404	U2241	U2241	U2028	G1896	A1779	A1671	G1577	G1401		
C2529	C2405	G2242	G2242	U2029	U1897	G1780	G1677	A1578	G1402		
C2530	C2406	U2243	U2243	A2030	U1902	A1781	G1678	U1580	A1403		
C2531	C2407	A2244	A2244	A2031	G1903	G1782	G1679	A1581	G1404		
C2532	C2408	G2245	G2245	A2032	C1904	A1783	A1681	U1510	G1405		
C2533	C2409	U2246	U2246	A2033	G1905	G1784	A1682	G1511	C1406		
C2534	C2410	G2247	G2247	A2034	G1906	A1785	U1685	U1512	G1407		
C2535	C2411	U2248	U2248	U2035	G1907	G1786	C1686	G1513	G1309		
C2536	C2412	A2249	A2249	U2036	G1908	A1787	U1686	C1514	G1311		
C2537	C2413	G2250	G2250	U2037	G1909	G1788	A1687	G1515	C1315		
C2538	C2414	U2251	U2251	A2038	G1910	A1789	U1688	G1516	U1423		
C2539	C2415	G2252	G2252	U2039	G1911	G1790	A1689	G1517			
C2540	C2416	U2253	U2253	U2040	G1912	G1791					
C2541	C2417	A2254	A2254	U2041	G1913	G1792					
C2542	C2418	G2255	G2255	U2042	G1914	G1793					
C2543	C2419	U2256	U2256	A2043	G1915	G1794					
C2544	C2420	A2257	A2257	U2044	G1916	G1795					
C2545	C2421	G2258	G2258	U2045	G1917	G1796					
C2546	C2422	U2259	U2259	U2046	G1918	G1797					
C2547	C2423	A2260	A2260	U2047	G1919	G1798					
C2548	C2424	G2261	G2261	U2048	G1920	G1799					
C2549	C2425	U2262	U2262	U2049	G1921	G1800					
C2550	C2426	A2263	A2263	U2050	G1922	G1801					
C2551	C2427	G2264	G2264	U2051	G1923	G1802					
C2552	C2428	U2265	U2265	U2052	G1924	G1803					
C2553	C2429	A2266	A2266	U2053	G1925	G1804					
C2554	C2430	G2267	G2267	U2054	G1926	G1805					
C2555	C2431	U2268	U2268	U2055	G1927	G1806					
C2556	C2432	A2269	A2269	U2056	G1928	G1807					
C2557	C2433	G2270	G2270	U2057	G1929	G1808					
C2558	C2434	U2271	U2271	U2058	G1930	G1809					
C2559	C2435	A2272	A2272	U2059	G1931	G1810					
C2560	C2436	G2273	G2273	U2060	G1932	G1811					
C2561	C2437	U2274	U2274	U2061	G1933	G1812					
C2562	C2438	A2275	A2275	U2062	G1934	G1813					
C2563	C2439	G2276	G2276	U2063	G1935	G1814					
C2564	C2440	U2277	U2277	U2064	G1936	G1815					
C2565	C2441	A2278	A2278	U2065	G1937	G1816					
C2566	C2442	G2279	G2279	U2066	G1938	G1817					
C2567	C2443	U2280	U2280	U2067	G1939	G1818					
C2568	C2444	A2281	A2281	U2068	G1940	G1819					
C2569	C2445	G2282	G2282	U2069	G1941	G1820					
C2570	C2446	U2283	U2283	U2070	G1942	G1821					
C2571	C2447	A2284	A2284	U2071	G1943	G1822					
C2572	C2448	G2285	G2285	U2072	U1944	G1823					
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C2575	C2451	G2288	G2288	U2075	U1947	G1826					
C2576	C2452	U2289	U2289	U2076	U1948	G1827					
C2577	C2453	A2290	A2290	U2077	U1949	G1828					
C2578	C2454	G2291	G2291	U2078	U1950	G1829					
C2579	C2455	U2292	U2292	U2079	U1951	G1830					
C2580	C2456	A2293	A2293	U2080	U1952	G1831					
C2581	C2457	G2294	G2294	U2081	U1953	G1832					
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C2584	C2460	G2297	G2297	U2084	U1956	G1835					
C2585	C2461	U2298	U2298	U2085	U1957	G1836					
C2586	C2462	A2299	A2299	U2086	U1958	G1837					
C2587	C2463	G2300	G2300	U2087	G1959	G1838					
C2588	C2464	U2301	U2301	U2088	G1960	G1839					
C2589	C2465	A2302	A2302	U2089	G1961	G1840					
C2590	C2466	G2303	G2303	U2090	G1962	G1841					
C2591	C2467	U2304	U2304	U2091	G1963	G1842					
C2592	C2468	A2305	A2305	U2092	G1964	G1843					
C2593	C2469	G2306	G2306	U2093	G1965	G1844					
C2594	C2470	U2307	U2307	U2094	G1966	G1845					
C2595	C2471	A2308	A2308	U2095	G1967	G1846					
C2596	C2472	G2309	G2309	U2096	G1968	G1847					
C2597	C2473	U2310	U2310	U2097	G1969	G1848					
C2598	C2474	A2311	A2311	U2098	G1970	G1849					
C2599	C2475	G2312	G2312	U2099	G1971	G1850					
C2600	C2476	U2313	U2313	U2100	G1972	G1851					
C2601	C2477	A2314	A2314	U2101	U1973	G1852					
C2602	C2478	G2315	G2315	U2102	G1974	G1853					
C2603	C2479	U2316	U2316	U2103	G1975	G1854					
C2604	C2480	A2317	A2317	U2104	G1976	G1855					
C2605	C2481	G2318	G2318	U2105	G1977	G1856					
C2606	C2482	U2319	U2319	U2106	G1978	G1857					
C2607	C2483	A2320	A2320	U2107	G1979	G1858					
C2608	C2484	G2321	G2321	U2108	C2000	G1859					
C2609	C2485	U2322	U2322	U2109	A2003	G1860					
C2610	C2486	A2323	A2323	U2110	A2004	G1861					
C2611	C2487	G2324	G2324	U2111	G2005	G1862					
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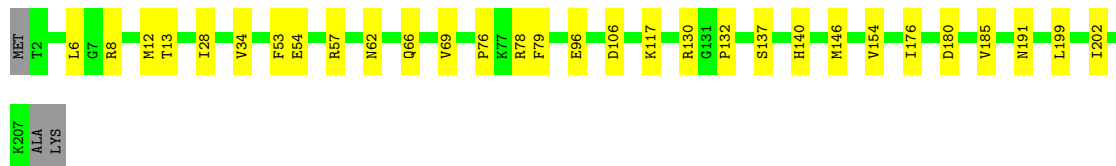
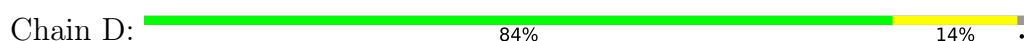
• Molecule 24: 5S Ribosomal RNA



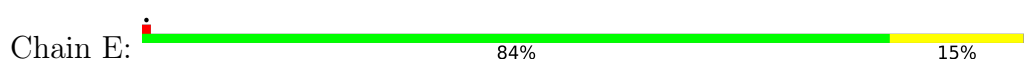
• Molecule 25: Large ribosomal subunit protein uL2



• Molecule 26: Large ribosomal subunit protein uL3

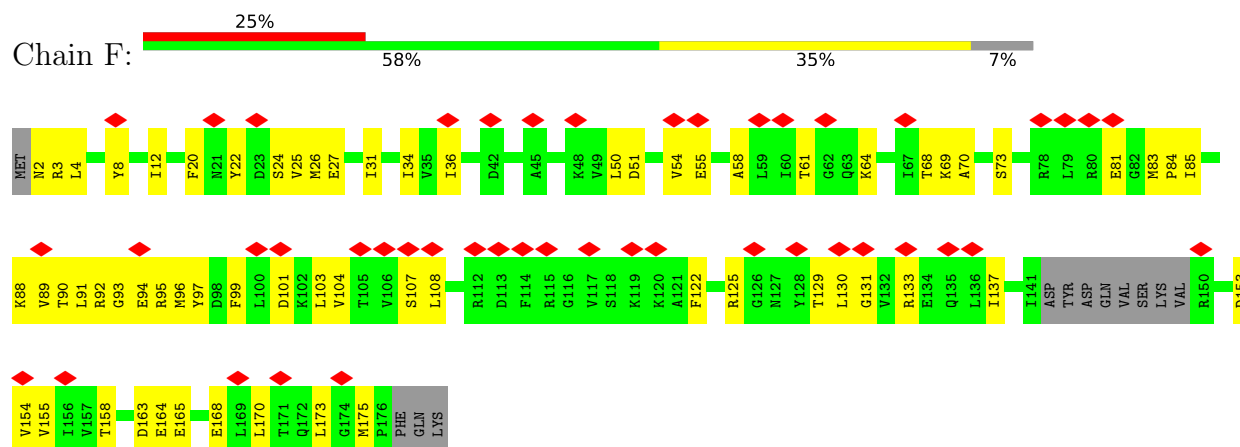


• Molecule 27: Large ribosomal subunit protein uL4

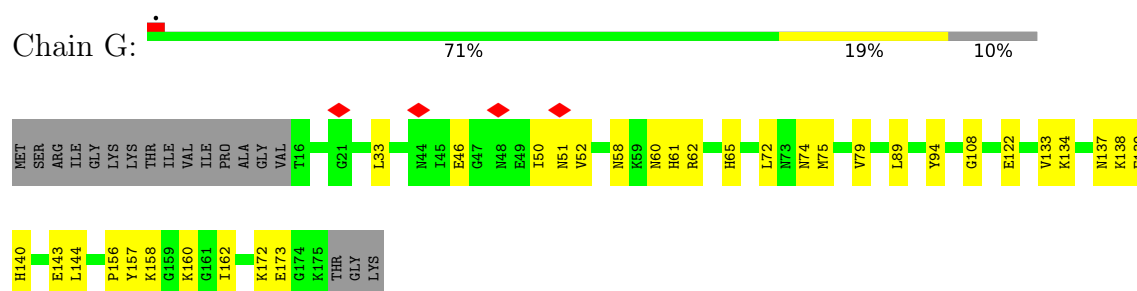


L206
ALA

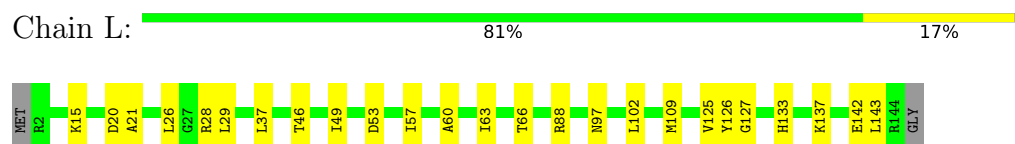
- Molecule 28: Large ribosomal subunit protein uL5



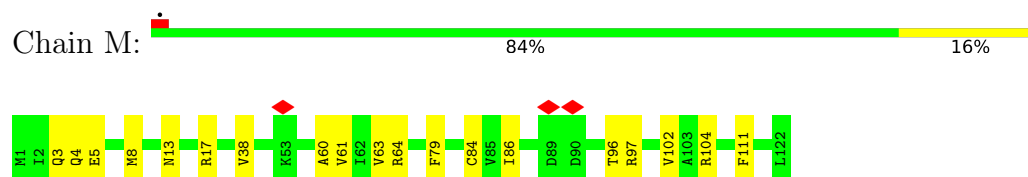
- Molecule 29: Large ribosomal subunit protein uL6



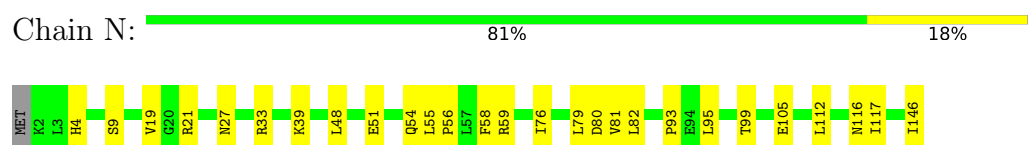
- Molecule 30: Large ribosomal subunit protein uL13



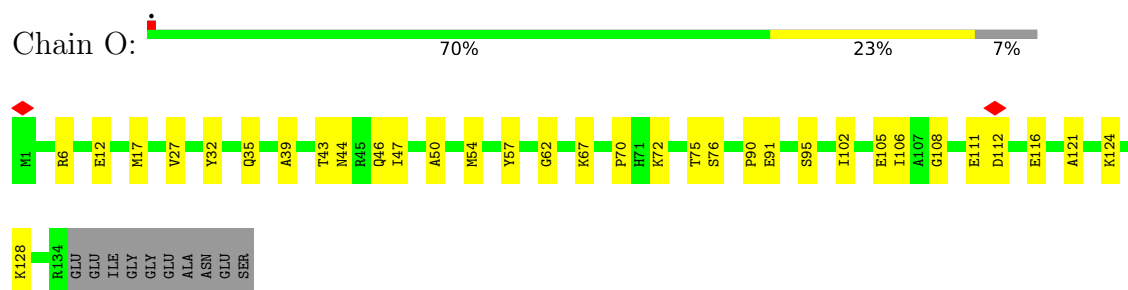
- Molecule 31: Large ribosomal subunit protein uL14



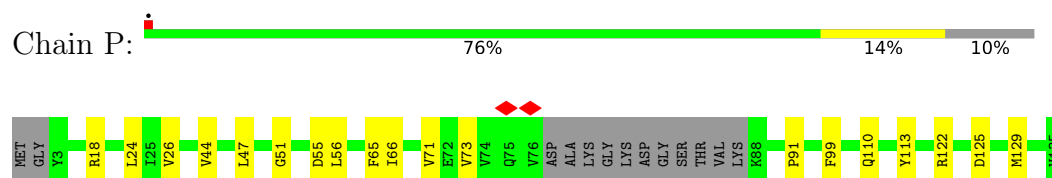
- Molecule 32: Large ribosomal subunit protein uL15



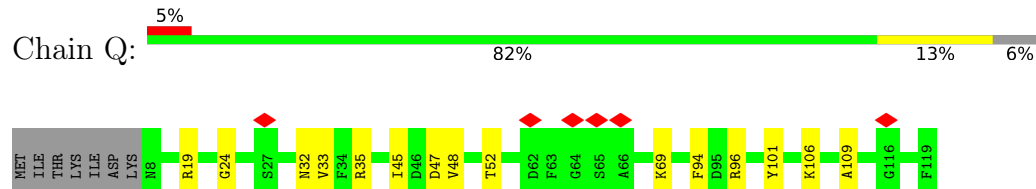
- Molecule 33: Large ribosomal subunit protein uL16



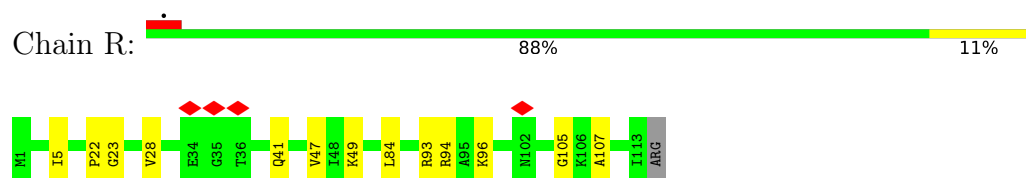
- Molecule 34: Large ribosomal subunit protein bL17



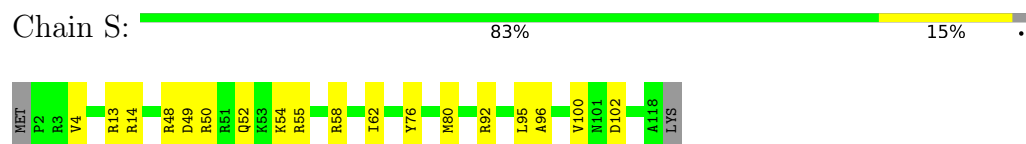
- Molecule 35: Large ribosomal subunit protein uL18



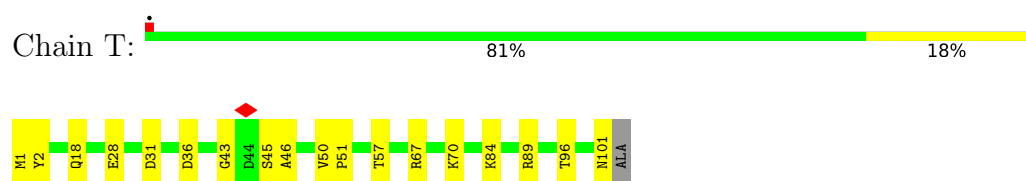
- Molecule 36: Large ribosomal subunit protein bL19



- Molecule 37: Large ribosomal subunit protein bL20



- Molecule 38: Large ribosomal subunit protein bL21



- Molecule 39: Large ribosomal subunit protein uL22

Chain U:  81% 14% 6%



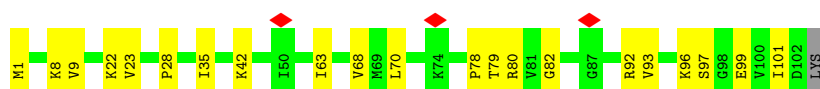
- Molecule 40: Large ribosomal subunit protein uL23

Chain V:  78% 20% .



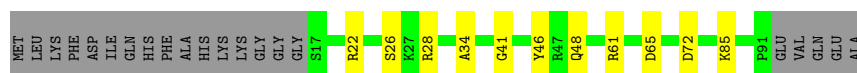
- Molecule 41: Large ribosomal subunit protein uL24

Chain W:  79% 20% .



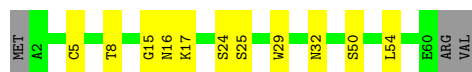
- Molecule 42: Large ribosomal subunit protein bL27

Chain Y:  67% 11% 22%



- Molecule 43: Large ribosomal subunit protein bL28

Chain Z:  77% 18% 5%



- Molecule 44: Large ribosomal subunit protein uL29

Chain 1:  65% 27% . 6%

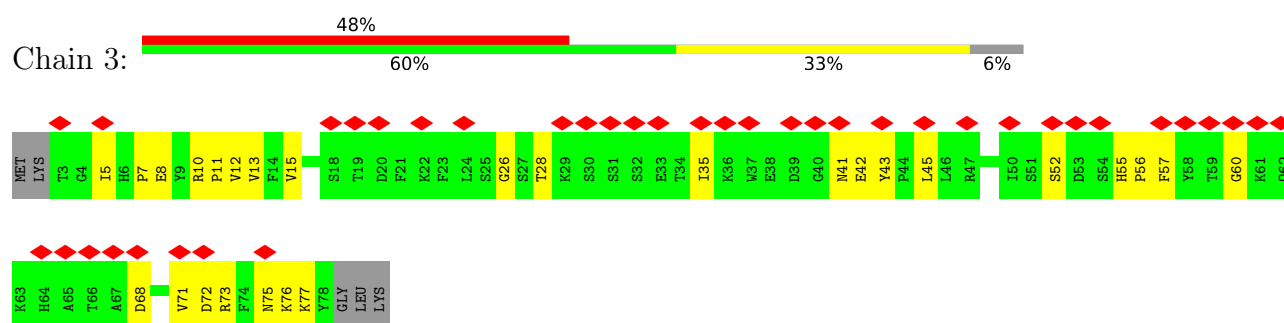


- Molecule 45: Large ribosomal subunit protein uL30

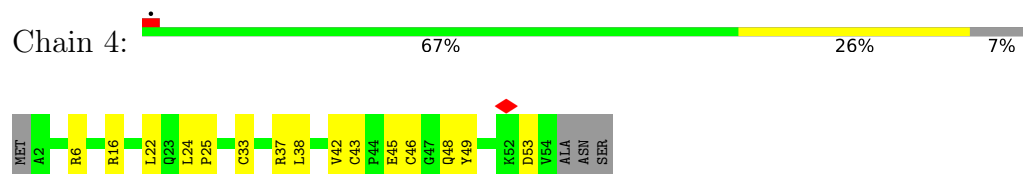
Chain 2:  83% 12% 5%



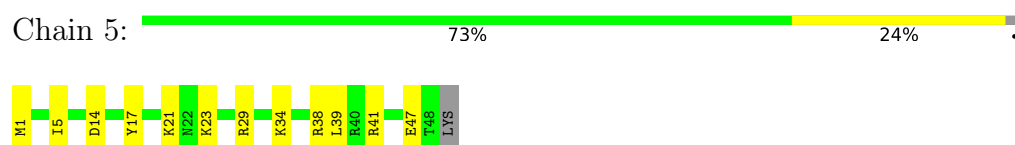
- Molecule 46: Large ribosomal subunit protein bL31B



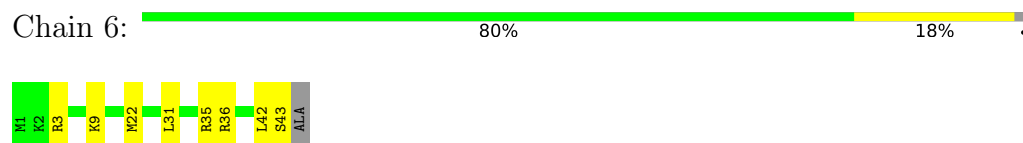
- Molecule 47: Large ribosomal subunit protein bL32



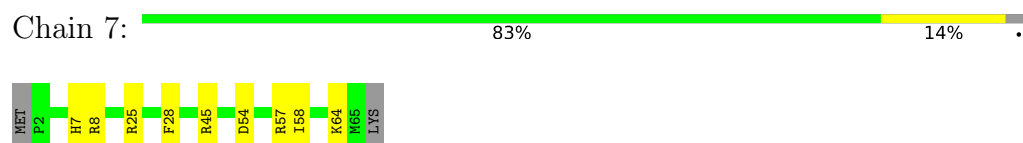
- Molecule 48: Large ribosomal subunit protein bL33



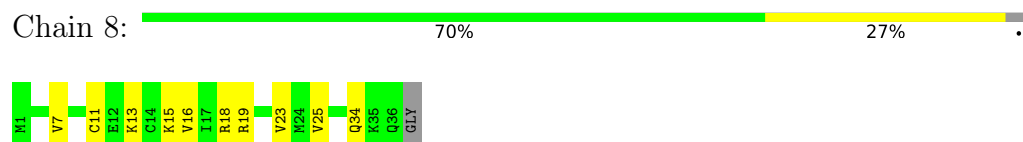
- Molecule 49: Large ribosomal subunit protein bL34



- Molecule 50: Large ribosomal subunit protein bL35



- Molecule 51: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15497	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	25.559	Depositor
Minimum map value	-12.278	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.072	Depositor
Recommended contour level	3.2	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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, 7MG, MIA, 5MU, K, PSU, 4SU

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	0.32	1/36403 (0.0%)	0.35	0/56778
2	b	0.15	0/1241	0.29	0/1721
3	c	0.32	0/1418	0.45	0/1939
4	d	0.25	0/1453	0.37	0/1976
5	e	0.27	0/1100	0.39	0/1496
6	f	0.21	0/663	0.34	0/904
7	g	0.28	0/1028	0.39	0/1396
8	h	0.30	0/942	0.37	0/1284
9	i	0.33	0/936	0.45	1/1267 (0.1%)
10	j	0.36	0/726	0.47	0/988
11	k	0.19	0/691	0.31	0/955
12	l	0.28	0/949	0.39	0/1290
13	m	0.30	0/786	0.37	0/1064
14	n	0.48	0/472	0.60	0/631
15	o	0.23	0/643	0.36	0/872
16	p	0.29	0/654	0.38	0/888
17	q	0.23	0/565	0.37	0/768
18	r	0.28	0/454	0.41	0/613
19	s	0.23	0/514	0.34	0/707
20	t	0.21	0/495	0.29	0/682
21	x	0.27	1/1605 (0.1%)	0.32	0/2497
22	w	0.19	0/140	0.26	0/215
23	A	0.31	0/69894	0.32	0/109035
24	B	0.19	0/2711	0.25	0/4224
25	C	0.32	0/2095	0.39	0/2821
26	D	0.32	0/1567	0.39	0/2111
27	E	0.30	0/1536	0.39	0/2082
28	F	0.18	0/1156	0.40	0/1579
29	G	0.19	0/1102	0.36	0/1508
30	L	0.29	0/1107	0.33	0/1495
31	M	0.28	0/921	0.34	0/1236
32	N	0.27	0/1032	0.33	0/1381

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	O	0.28	0/1047	0.36	0/1406
34	P	0.30	0/963	0.38	0/1294
35	Q	0.16	0/709	0.27	0/966
36	R	0.28	0/855	0.31	0/1158
37	S	0.32	0/943	0.37	0/1258
38	T	0.31	0/775	0.40	0/1045
39	U	0.30	0/853	0.35	0/1156
40	V	0.30	0/733	0.39	0/988
41	W	0.22	0/745	0.34	0/1005
42	Y	0.28	0/556	0.38	0/744
43	Z	0.29	0/444	0.43	0/593
44	1	0.25	0/468	0.38	0/628
45	2	0.30	0/432	0.38	0/581
46	3	0.18	0/542	0.41	0/743
47	4	0.29	0/433	0.41	0/577
48	5	0.23	0/384	0.29	0/518
49	6	0.32	0/364	0.35	0/475
50	7	0.30	0/519	0.41	0/677
51	8	0.28	0/295	0.44	0/387
All	All	0.30	2/149059 (0.0%)	0.34	1/224602 (0.0%)

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
14	n	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	8	4SU	O3'-P	7.27	1.63	1.56
1	a	95	A	C1'-N9	-5.45	1.39	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	i	53	VAL	N-CA-C	-5.37	107.59	112.96

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	n	42	ILE	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	32515	0	16372	471	0
2	b	1228	0	715	9	0
3	c	1395	0	1246	31	0
4	d	1429	0	1287	27	0
5	e	1087	0	1094	30	0
6	f	652	0	560	18	0
7	g	1015	0	957	19	0
8	h	929	0	902	11	0
9	i	920	0	925	24	0
10	j	714	0	680	25	0
11	k	681	0	545	13	0
12	l	935	0	884	23	0
13	m	780	0	736	15	0
14	n	463	0	474	17	0
15	o	635	0	563	14	0
16	p	641	0	603	21	0
17	q	558	0	506	14	0
18	r	449	0	439	14	0
19	s	502	0	347	12	0
20	t	493	0	394	8	0
21	x	1591	0	819	47	0
22	w	126	0	65	0	0
23	A	62385	0	31368	738	0
24	B	2428	0	1229	25	0
25	C	2059	0	2082	38	0
26	D	1545	0	1587	21	0
27	E	1515	0	1554	26	0
28	F	1142	0	1039	50	0
29	G	1085	0	984	24	0
30	L	1084	0	1086	18	0
31	M	914	0	958	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	N	1022	0	1015	18	0
33	O	1025	0	1063	22	0
34	P	952	0	978	10	0
35	Q	701	0	545	12	0
36	R	843	0	848	11	0
37	S	930	0	983	15	0
38	T	762	0	780	14	0
39	U	843	0	895	12	0
40	V	724	0	724	11	0
41	W	735	0	755	14	0
42	Y	549	0	537	11	0
43	Z	439	0	452	6	0
44	1	467	0	470	15	0
45	2	429	0	468	6	0
46	3	529	0	427	27	0
47	4	425	0	423	11	0
48	5	380	0	377	6	0
49	6	361	0	406	7	0
50	7	512	0	549	8	0
51	8	292	0	334	8	0
52	A	78	0	0	0	0
52	D	1	0	0	0	0
52	a	18	0	0	0	0
52	q	1	0	0	0	0
53	4	1	0	0	0	0
53	5	1	0	0	0	0
53	8	1	0	0	0	0
53	n	1	0	0	0	0
54	O	1	0	0	0	0
55	A	3	0	0	2	0
55	a	2	0	0	0	0
All	All	136923	0	86029	1891	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1891) 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)
23:A:419:U:HO2'	23:A:420:A:H8	0.99	0.97
21:x:5:G:H1	21:x:68:C:H42	0.99	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:72:G:H1	1:a:94:A:H3'	1.33	0.94
23:A:1160:G:HO2'	23:A:1161:A:H8	1.10	0.93
1:a:991:U:H5''	14:n:6:MET:HE1	1.51	0.93
1:a:467:U:H3	1:a:482:G:H1	1.17	0.89
21:x:5:G:H1	21:x:68:C:N4	1.71	0.88
21:x:54:5MU:HN3	21:x:58:A:H62	1.19	0.88
23:A:1763:U:H3	23:A:1778:A:H62	1.16	0.87
34:P:47:LEU:HD21	34:P:66:ILE:HD11	1.56	0.87
1:a:1049:A:C6	1:a:1050:G:O6	2.28	0.86
28:F:2:ASN:N	28:F:97:TYR:HH	1.74	0.84
1:a:218:U:H2'	1:a:219:U:H2'	1.60	0.83
1:a:1363:G:H2'	1:a:1364:A:H8	1.44	0.83
1:a:1067:G:OP1	3:c:198:LYS:NZ	2.11	0.83
23:A:1763:U:H3	23:A:1778:A:N6	1.77	0.83
21:x:27:G:O6	21:x:43:C:N3	2.11	0.82
23:A:665:G:H4'	23:A:666:A:H5'	1.59	0.82
37:S:48:ARG:HD3	37:S:52:GLN:HE21	1.46	0.81
7:g:104:LEU:HD21	7:g:124:ILE:HD11	1.63	0.81
1:a:1146:A:N6	1:a:1148:U:O2'	2.14	0.80
23:A:1787:C:H5	36:R:94:ARG:HH21	1.25	0.79
23:A:2043:G:H5''	39:U:47:SER:HB3	1.64	0.79
1:a:217:U:H3	1:a:222:G:H1	1.28	0.79
1:a:1009:U:C2	1:a:1050:G:N1	2.50	0.79
23:A:2141:U:O2	23:A:2214:G:N2	2.16	0.79
34:P:55:ASP:OD1	34:P:56:LEU:N	2.16	0.79
23:A:1763:U:O4	23:A:1778:A:N7	2.16	0.79
1:a:602:U:N3	1:a:654:G:C6	2.50	0.79
5:e:17:VAL:HG12	5:e:18:THR:HG23	1.65	0.79
23:A:897:G:H21	45:2:46:MET:HE3	1.46	0.79
21:x:54:5MU:O4	21:x:58:A:N7	2.16	0.78
1:a:1480:U:OP1	31:M:17:ARG:NH2	2.17	0.78
23:A:2148:G:O2'	23:A:2199:G:N2	2.15	0.78
23:A:292:U:H2'	23:A:293:G:H8	1.50	0.77
1:a:149:U:H3	1:a:170:A:H62	1.32	0.77
23:A:1656:C:N4	23:A:1671:A:OP2	2.18	0.77
8:h:80:ILE:HG22	8:h:87:VAL:HG11	1.67	0.77
9:i:12:ARG:NH1	9:i:107:ASP:OD2	2.18	0.77
1:a:1009:U:N3	1:a:1050:G:N1	2.32	0.76
1:a:286:A:OP2	17:q:45:LYS:NZ	2.17	0.76
23:A:1111:U:N3	23:A:1120:G:N1	2.33	0.75
23:A:1075:A:H5''	33:O:128:LYS:HE2	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1453:G:H1	23:A:1642:U:H3	1.32	0.75
25:C:69:ARG:HE	25:C:129:ALA:HB2	1.51	0.75
1:a:459:A:N1	1:a:488:U:O2'	2.17	0.75
6:f:41:SER:HG	6:f:62:HIS:HE2	1.31	0.75
1:a:1087:U:H4'	5:e:139:ARG:HH12	1.52	0.74
4:d:15:LEU:HD21	4:d:56:LYS:HA	1.70	0.74
17:q:70:SER:HB3	17:q:73:LYS:HB2	1.70	0.74
23:A:2361:A:H2'	23:A:2362:A:C8	2.22	0.74
4:d:61:TYR:HE2	4:d:96:ASN:HD21	1.34	0.74
23:A:2339:U:H3'	23:A:2340:G:H2'	1.69	0.74
1:a:509:C:OP1	12:l:127:ARG:NH2	2.21	0.74
1:a:1294:A:H2'	1:a:1295:A:C8	2.23	0.73
7:g:35:LYS:HD2	7:g:38:LYS:HD3	1.69	0.73
28:F:91:LEU:HD23	28:F:95:ARG:HB3	1.69	0.73
6:f:93:ILE:HG13	18:r:65:ARG:HH22	1.54	0.73
23:A:2208:U:H2'	23:A:2209:A:H8	1.53	0.72
5:e:13:GLU:OE2	5:e:43:LYS:NZ	2.22	0.72
23:A:575:G:O2'	23:A:577:A:N7	2.22	0.72
2:b:5:SER:N	2:b:8:GLN:OE1	2.22	0.72
41:W:8:LYS:HE2	41:W:22:LYS:HE3	1.71	0.72
1:a:1481:G:H2'	1:a:1482:G:C8	2.25	0.72
23:A:1093:G:H21	23:A:1157:A:H62	1.38	0.72
23:A:917:U:OP1	33:O:6:ARG:NH2	2.23	0.71
23:A:1831:U:OP2	25:C:274:ARG:NH2	2.22	0.71
1:a:69:A:C8	1:a:97:U:H2'	2.24	0.71
1:a:602:U:N3	1:a:654:G:N1	2.38	0.71
1:a:1270:G:O6	1:a:1280:G:N2	2.24	0.71
31:M:13:ASN:HB2	31:M:97:ARG:HB2	1.71	0.71
23:A:2182:C:H2'	23:A:2183:A:C8	2.26	0.70
23:A:2192:G:H2'	23:A:2193:G:H8	1.55	0.70
1:a:269:U:OP2	20:t:73:ARG:NH2	2.24	0.70
41:W:1:MET:HE3	41:W:28:PRO:HA	1.74	0.70
1:a:1363:G:H2'	1:a:1364:A:C8	2.27	0.70
23:A:1354:G:OP2	49:6:9:LYS:NZ	2.22	0.70
1:a:1544:C:H2'	1:a:1545:U:H6	1.57	0.70
23:A:1132:A:O2'	23:A:1133:G:N7	2.24	0.70
23:A:2133:U:H3	23:A:2222:G:H1	1.37	0.70
23:A:905:G:OP2	42:Y:85:LYS:NZ	2.24	0.69
10:j:29:ALA:O	10:j:33:GLY:N	2.23	0.69
21:x:27:G:N1	21:x:43:C:O2	2.20	0.69
1:a:983:A:OP1	14:n:29:ARG:NH2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:x:19:G:O4'	21:x:57:G:N2	2.25	0.69
1:a:1165:A:N6	1:a:1187:A:N7	2.41	0.69
14:n:21:TYR:OH	14:n:23:ARG:NH1	2.26	0.69
23:A:1581:G:N1	23:A:1593:C:O2'	2.25	0.69
1:a:988:C:O2	14:n:19:GLN:NE2	2.26	0.69
23:A:2361:A:H2'	23:A:2362:A:H8	1.56	0.69
5:e:108:ALA:HB1	5:e:112:VAL:HG13	1.75	0.68
23:A:2788:C:O2'	23:A:2789:U:O2	2.12	0.68
24:B:7:A:OP1	35:Q:19:ARG:NH1	2.26	0.68
50:7:54:ASP:OD1	50:7:57:ARG:NH2	2.26	0.68
1:a:682:G:H2'	1:a:683:A:H8	1.57	0.68
1:a:1049:A:N1	1:a:1050:G:O6	2.26	0.68
1:a:187:U:O4	1:a:202:G:O6	2.10	0.68
1:a:681:G:H2'	1:a:682:G:C8	2.28	0.68
23:A:1129:G:N2	23:A:1132:A:OP2	2.24	0.68
23:A:2177:G:O2'	23:A:2180:A:N6	2.26	0.68
23:A:2338:A:OP2	28:F:133:ARG:NH2	2.26	0.68
24:B:13:G:OP2	24:B:67:G:N2	2.27	0.68
1:a:187:U:H3	1:a:202:G:H1	0.80	0.68
23:A:1315:C:H5''	23:A:1316:G:H5'	1.76	0.68
1:a:993:C:N3	1:a:1229:G:N2	2.40	0.68
1:a:71:C:N4	1:a:96:G:OP2	2.27	0.68
23:A:2713:C:H1'	26:D:191:ASN:HD22	1.58	0.68
1:a:522:C:H2'	1:a:523:G:H8	1.59	0.67
10:j:19:ASP:OD1	10:j:20:GLN:N	2.27	0.67
1:a:1014:C:HO2'	1:a:1047:A:HO2'	1.32	0.67
24:B:63:C:O2'	24:B:106:C:N4	2.27	0.67
48:5:14:ASP:OD1	48:5:38:ARG:NH2	2.26	0.67
2:b:12:ALA:HB1	2:b:209:ALA:HA	1.76	0.67
51:8:11:CYS:SG	51:8:13:LYS:HG2	2.35	0.67
41:W:9:VAL:HG13	41:W:68:VAL:HG13	1.76	0.67
1:a:1107:C:H2'	1:a:1108:G:C8	2.30	0.67
23:A:279:G:H2'	23:A:280:A:C8	2.30	0.67
1:a:1434:C:H2'	1:a:1435:A:H8	1.59	0.66
23:A:89:U:H5''	23:A:90:A:H2'	1.75	0.66
32:N:19:VAL:HG23	32:N:27:ASN:HB3	1.75	0.66
1:a:71:C:H3'	1:a:72:G:C8	2.29	0.66
3:c:183:TYR:HD1	3:c:200:TRP:HB3	1.60	0.66
42:Y:41:GLY:N	42:Y:72:ASP:OD1	2.27	0.66
23:A:1184:G:H21	30:L:109:MET:HE2	1.61	0.66
35:Q:45:ILE:HG12	35:Q:52:THR:HG22	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:879:C:O2'	50:7:57:ARG:NH1	2.28	0.66
24:B:46:A:OP1	35:Q:35:ARG:NH2	2.28	0.66
1:a:266:G:H2'	1:a:267:G:H8	1.60	0.66
1:a:1354:G:O6	9:i:12:ARG:NH2	2.28	0.66
1:a:1378:G:OP1	9:i:14:SER:OG	2.13	0.66
21:x:21:A:N6	21:x:48:C:OP2	2.28	0.66
24:B:101:U:H2'	24:B:102:A:H8	1.61	0.66
1:a:67:C:O2'	1:a:68:G:OP1	2.12	0.66
23:A:1530:G:H3'	23:A:1531:U:H5''	1.78	0.66
1:a:194:C:N4	17:q:5:ASN:O	2.29	0.66
1:a:424:G:H2'	1:a:425:G:H8	1.59	0.66
23:A:1248:A:H2'	23:A:1249:A:C8	2.31	0.66
23:A:274:A:H62	23:A:295:G:H21	1.45	0.65
1:a:305:G:N2	1:a:308:A:OP2	2.30	0.65
23:A:2192:G:H2'	23:A:2193:G:C8	2.31	0.65
26:D:132:PRO:O	26:D:137:SER:OG	2.12	0.65
23:A:2198:G:H2'	23:A:2199:G:C8	2.31	0.65
32:N:76:ILE:HG23	32:N:112:LEU:HD23	1.79	0.65
29:G:89:LEU:HD23	29:G:94:TYR:HB3	1.77	0.65
23:A:2182:C:H2'	23:A:2183:A:H8	1.61	0.65
23:A:2279:G:H2'	23:A:2280:A:H8	1.62	0.65
23:A:139:A:H2	23:A:1453:G:H1'	1.62	0.65
23:A:1159:U:N3	23:A:1160:G:N7	2.45	0.65
23:A:1199:C:OP1	37:S:92:ARG:NH2	2.29	0.65
13:m:44:ARG:HD3	13:m:46:ARG:HH22	1.63	0.64
21:x:64:A:H2'	21:x:65:G:H8	1.61	0.64
23:A:1531:U:O4	23:A:1561:G:O6	2.14	0.64
23:A:1569:U:H2'	23:A:1570:G:H8	1.63	0.64
23:A:1760:U:H5''	23:A:1761:A:H2'	1.78	0.64
25:C:71:LYS:NZ	25:C:98:ASP:OD2	2.26	0.64
27:E:9:GLN:HE21	27:E:129:LEU:HA	1.62	0.64
16:p:74:LEU:HB2	16:p:80:MET:HG2	1.79	0.64
1:a:147:G:O2'	1:a:1453:A:N3	2.29	0.64
12:l:62:LEU:O	12:l:64:LYS:NZ	2.30	0.64
1:a:1156:U:H1'	9:i:18:ARG:HH21	1.63	0.64
1:a:1481:G:H2'	1:a:1482:G:H8	1.61	0.64
23:A:1184:G:N2	30:L:109:MET:HE2	2.13	0.64
5:e:108:ALA:O	5:e:113:ARG:NH2	2.31	0.64
23:A:1876:C:O2'	25:C:256:GLY:O	2.16	0.64
1:a:746:U:OP2	6:f:94:LYS:NZ	2.30	0.64
23:A:759:G:H21	23:A:764:A:H2	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1105:G:OP2	23:A:1106:U:O2'	2.15	0.64
37:S:102:ASP:OD2	38:T:2:TYR:OH	2.15	0.64
23:A:1763:U:C2	23:A:1778:A:N6	2.66	0.64
23:A:2878:G:N7	23:A:2896:G:N2	2.46	0.64
1:a:508:G:H2'	1:a:509:C:C6	2.31	0.63
1:a:907:G:N2	1:a:910:A:OP2	2.31	0.63
2:b:129:LEU:O	2:b:133:GLU:N	2.29	0.63
1:a:499:A:H2'	1:a:500:A:H8	1.63	0.63
1:a:546:U:H2'	1:a:547:A:H8	1.63	0.63
25:C:144:ILE:HB	25:C:154:LEU:HB2	1.81	0.63
27:E:111:LYS:HE2	27:E:206:LEU:HD13	1.80	0.63
1:a:17:U:H2'	1:a:18:C:C6	2.34	0.63
23:A:2326:C:H5''	35:Q:96:ARG:HH12	1.63	0.63
23:A:2471:U:O3'	23:A:2472:A:H3'	1.99	0.63
23:A:1268:G:OP2	38:T:89:ARG:NH1	2.31	0.63
23:A:1456:A:H2'	23:A:1457:A:C8	2.34	0.63
23:A:2279:G:H2'	23:A:2280:A:C8	2.33	0.63
1:a:504:G:N2	1:a:506:A:OP2	2.31	0.63
24:B:47:C:H2'	24:B:48:G:H8	1.63	0.63
23:A:163:U:O2	23:A:166:A:N6	2.32	0.63
23:A:1106:U:N3	23:A:1134:A:N7	2.47	0.63
28:F:122:PHE:HD2	28:F:163:ASP:HB2	1.64	0.63
23:A:1540:G:O2'	25:C:100:GLU:OE2	2.12	0.63
10:j:25:ILE:HD11	10:j:74:ILE:HG13	1.79	0.63
23:A:1581:G:H1	23:A:1593:C:HO2'	1.41	0.63
28:F:68:THR:O	28:F:85:ILE:N	2.31	0.63
1:a:722:G:H2'	1:a:723:A:C8	2.34	0.62
46:3:13:VAL:HG13	46:3:43:TYR:HB2	1.81	0.62
29:G:50:ILE:HG23	29:G:52:VAL:HG22	1.80	0.62
1:a:1263:U:H5'	1:a:1265:G:H1'	1.81	0.62
23:A:865:A:OP2	23:A:1233:G:N2	2.29	0.62
23:A:1483:A:H2'	23:A:1484:A:C8	2.34	0.62
15:o:16:ARG:NH1	15:o:19:ASP:O	2.33	0.62
23:A:278:A:H2'	23:A:279:G:C8	2.35	0.62
1:a:412:G:O5'	4:d:115:ASN:ND2	2.33	0.62
1:a:392:G:H2'	1:a:393:U:C6	2.35	0.62
1:a:1231:U:O2'	1:a:1329:C:OP1	2.17	0.62
33:O:54:MET:HE2	33:O:106:ILE:HD11	1.82	0.62
3:c:87:ARG:O	3:c:91:ASN:ND2	2.32	0.62
23:A:1295:G:OP2	32:N:21:ARG:NH1	2.32	0.62
20:t:15:GLU:HA	20:t:18:ASN:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:258:A:H2'	23:A:259:A:H8	1.64	0.61
28:F:58:ALA:HB1	46:3:7:PRO:HG2	1.81	0.61
23:A:2324:U:H2'	23:A:2325:U:C6	2.34	0.61
23:A:2878:G:O2'	23:A:2895:G:N2	2.33	0.61
25:C:66:ASP:OD2	25:C:102:ARG:NH1	2.34	0.61
31:M:13:ASN:ND2	31:M:96:THR:OG1	2.33	0.61
21:x:54:5MU:HN3	21:x:58:A:N6	1.94	0.61
24:B:47:C:H2'	24:B:48:G:C8	2.36	0.61
6:f:93:ILE:HG13	18:r:65:ARG:NH2	2.15	0.61
23:A:2044:U:OP2	39:U:21:LYS:NZ	2.22	0.61
5:e:103:GLY:N	5:e:123:ASP:OD2	2.33	0.61
12:l:86:ASN:HD21	12:l:118:ALA:HB3	1.66	0.61
21:x:23:A:H2'	21:x:24:G:H8	1.64	0.61
23:A:1055:A:N3	23:A:1199:C:O2'	2.33	0.61
23:A:1093:G:N2	23:A:1156:G:O2'	2.31	0.61
14:n:41:ARG:HG3	14:n:42:ILE:HG23	1.83	0.61
23:A:228:A:O2'	23:A:231:A:N6	2.34	0.61
28:F:103:LEU:HA	28:F:107:SER:HB3	1.83	0.61
1:a:219:U:O2'	1:a:221:G:N1	2.34	0.61
1:a:307:G:H2'	1:a:308:A:C8	2.36	0.61
28:F:73:SER:N	28:F:81:GLU:OE2	2.34	0.61
46:3:11:PRO:HA	46:3:26:GLY:HA2	1.83	0.61
1:a:761:A:OP1	15:o:69:TYR:OH	2.19	0.61
23:A:2167:A:H2'	23:A:2168:G:H8	1.66	0.61
1:a:955:A:H2'	1:a:956:G:C8	2.36	0.61
1:a:1188:G:O2'	1:a:1189:G:N7	2.30	0.61
4:d:69:LYS:HE3	4:d:198:TYR:CD1	2.34	0.61
21:x:26:A:H61	21:x:45:U:H5	1.46	0.61
23:A:2408:G:N2	23:A:2411:A:OP2	2.28	0.61
1:a:72:G:N1	1:a:94:A:H3'	2.11	0.60
21:x:15:G:N2	21:x:59:U:O2	2.35	0.60
23:A:1268:G:N7	38:T:70:LYS:NZ	2.49	0.60
24:B:3:U:OP1	24:B:59:U:O2'	2.18	0.60
1:a:467:U:O2	1:a:482:G:N2	2.27	0.60
1:a:932:A:O2'	1:a:1406:C:OP2	2.17	0.60
3:c:34:GLU:OE2	3:c:58:ARG:NH1	2.34	0.60
23:A:906:G:N2	23:A:964:A:OP2	2.26	0.60
30:L:26:LEU:HD13	30:L:63:ILE:HG21	1.83	0.60
33:O:62:GLY:HA2	33:O:108:GLY:HA3	1.83	0.60
23:A:75:G:O3'	44:1:48:LYS:NZ	2.32	0.60
23:A:1253:C:O2'	23:A:1254:G:O5'	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:P:24:LEU:HD23	34:P:44:VAL:HG21	1.82	0.60
23:A:925:A:OP2	23:A:946:G:N2	2.33	0.60
1:a:967:A:N3	1:a:994:C:O2'	2.30	0.60
7:g:138:ARG:O	7:g:141:THR:OG1	2.19	0.60
21:x:23:A:H2'	21:x:24:G:C8	2.37	0.60
23:A:395:U:H2'	23:A:396:U:C6	2.36	0.60
23:A:2160:G:H2'	23:A:2161:C:C6	2.36	0.60
28:F:103:LEU:HG	28:F:108:LEU:HG	1.83	0.60
23:A:809:G:O2'	23:A:810:A:OP1	2.20	0.60
37:S:48:ARG:NH1	37:S:49:ASP:OD1	2.33	0.60
1:a:68:G:H5'	1:a:96:G:H1'	1.84	0.60
1:a:158:G:N2	1:a:161:A:OP2	2.35	0.60
1:a:409:C:O2'	1:a:629:A:N3	2.33	0.60
1:a:873:A:H2'	1:a:874:A:C8	2.37	0.60
1:a:1149:U:H2'	1:a:1150:G:H8	1.66	0.60
18:r:17:PHE:HE1	18:r:25:ILE:HD11	1.66	0.60
23:A:13:A:O2'	23:A:15:G:N7	2.33	0.60
21:x:53:G:C4	21:x:54:5MU:H72	2.37	0.59
34:P:122:ARG:NH2	34:P:125:ASP:OD2	2.34	0.59
1:a:70:A:H8	1:a:96:G:OP1	1.84	0.59
1:a:498:U:H2'	1:a:499:A:H8	1.66	0.59
1:a:1158:U:O4	1:a:1159:A:N6	2.35	0.59
23:A:1957:C:N3	23:A:1958:C:N4	2.49	0.59
27:E:75:GLN:OE1	27:E:83:TRP:NE1	2.33	0.59
4:d:53:GLU:HA	4:d:56:LYS:HD3	1.84	0.59
23:A:1763:U:OP2	23:A:1777:G:N1	2.35	0.59
23:A:2220:A:H2'	23:A:2221:U:O4'	2.01	0.59
23:A:2181:G:H2'	23:A:2182:C:C6	2.37	0.59
23:A:2424:G:O2'	23:A:2462:G:N2	2.35	0.59
23:A:363:A:N3	27:E:169:ASN:ND2	2.50	0.59
23:A:756:A:H2'	23:A:757:A:H8	1.67	0.59
23:A:1531:U:C4	23:A:1561:G:O6	2.56	0.59
36:R:49:LYS:HB2	36:R:96:LYS:HD2	1.83	0.59
4:d:69:LYS:HA	4:d:69:LYS:HE2	1.84	0.59
23:A:1482:G:H2'	23:A:1483:A:C8	2.36	0.59
40:V:2:ASP:OD1	40:V:3:ALA:N	2.35	0.59
4:d:100:ARG:HD3	4:d:162:PRO:HG2	1.84	0.59
23:A:1108:G:H2'	23:A:1109:G:H8	1.68	0.59
23:A:2339:U:H2'	23:A:2340:G:C8	2.38	0.59
25:C:161:SER:HB3	25:C:194:GLN:HG3	1.84	0.59
1:a:69:A:H5''	1:a:96:G:O5'	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1171:G:OP2	23:A:1172:A:O2'	2.16	0.59
24:B:110:G:H2'	24:B:111:C:C6	2.37	0.59
26:D:28:ILE:HD13	26:D:202:ILE:HD11	1.85	0.59
5:e:82:ILE:HB	5:e:148:LEU:HD21	1.85	0.59
9:i:19:VAL:HG13	9:i:65:VAL:HG12	1.84	0.59
23:A:1248:A:H2'	23:A:1249:A:H8	1.67	0.59
23:A:2141:U:H3	23:A:2214:G:H1	1.50	0.59
1:a:744:U:H2'	1:a:745:C:C6	2.38	0.58
23:A:2914:C:O2	47:4:37:ARG:NH2	2.36	0.58
1:a:345:G:H2'	1:a:346:A:H8	1.67	0.58
1:a:1225:C:H2'	1:a:1226:U:C6	2.37	0.58
4:d:181:GLU:O	4:d:183:SER:N	2.36	0.58
14:n:24:CYS:HB2	14:n:40:CYS:HB3	1.84	0.58
21:x:51:U:H2'	21:x:52:G:C8	2.38	0.58
23:A:1172:A:H4'	23:A:1173:A:H5'	1.86	0.58
23:A:1407:C:O2'	23:A:1842:A:N3	2.35	0.58
23:A:1531:U:N3	23:A:1561:G:N1	2.49	0.58
23:A:1598:G:OP2	23:A:1598:G:N2	2.27	0.58
23:A:2160:G:H2'	23:A:2161:C:H6	1.68	0.58
25:C:11:ASN:OD1	25:C:14:ARG:NH2	2.36	0.58
1:a:262:G:O6	1:a:281:A:N6	2.37	0.58
1:a:384:G:H5''	16:p:6:ARG:HB2	1.85	0.58
1:a:681:G:O3'	6:f:89:ARG:NH2	2.37	0.58
1:a:1149:U:H2'	1:a:1150:G:C8	2.39	0.58
3:c:151:GLN:HB3	3:c:166:HIS:HB3	1.83	0.58
1:a:1497:G:H2'	1:a:1498:U:C6	2.38	0.58
10:j:37:SER:OG	10:j:75:ASP:HB3	2.04	0.58
23:A:185:C:H2'	23:A:186:C:H5'	1.86	0.58
31:M:60:ALA:HB2	31:M:86:ILE:HD13	1.86	0.58
1:a:513:G:H2'	1:a:514:G:H8	1.69	0.58
23:A:258:A:H2'	23:A:259:A:C8	2.38	0.58
23:A:1253:C:O2'	23:A:1254:G:H8	1.85	0.58
23:A:1452:U:H2'	23:A:1453:G:H8	1.68	0.58
1:a:736:A:H2'	1:a:737:A:C8	2.39	0.58
23:A:140:G:H2'	23:A:141:U:H6	1.68	0.58
23:A:391:U:H2'	23:A:392:G:H8	1.68	0.58
23:A:2202:G:H2'	23:A:2203:G:C8	2.39	0.58
3:c:54:VAL:HG13	3:c:67:ILE:HG22	1.86	0.58
23:A:329:A:H2'	23:A:330:A:C8	2.38	0.58
23:A:509:G:N2	23:A:512:A:OP2	2.36	0.58
23:A:1594:G:O2'	23:A:1595:G:O4'	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:F:164:GLU:O	28:F:168:GLU:HG3	2.04	0.58
1:a:1048:A:H2'	1:a:1049:A:C8	2.39	0.58
23:A:10:A:N1	23:A:11:G:N2	2.52	0.58
3:c:152:VAL:HG22	3:c:197:VAL:HG12	1.86	0.57
21:x:5:G:N2	21:x:68:C:N3	2.43	0.57
23:A:343:G:OP2	41:W:80:ARG:NH2	2.36	0.57
1:a:62:U:OP1	1:a:393:U:O2'	2.22	0.57
1:a:129:A:O2'	1:a:130:C:O5'	2.21	0.57
1:a:1269:A:H61	1:a:1280:G:H1'	1.69	0.57
23:A:2125:G:H4'	23:A:2126:G:H5''	1.85	0.57
47:4:33:CYS:SG	47:4:45:GLU:HB2	2.45	0.57
23:A:220:G:H22	23:A:237:U:H4'	1.69	0.57
23:A:1950:U:H2'	23:A:1951:A:C8	2.40	0.57
1:a:224:U:H2'	1:a:225:A:H8	1.69	0.57
1:a:642:C:H2'	1:a:643:A:H8	1.69	0.57
1:a:1284:C:O2'	1:a:1286:A:N3	2.33	0.57
1:a:1442:G:H2'	1:a:1443:U:C6	2.40	0.57
23:A:89:U:H3'	23:A:90:A:H8	1.70	0.57
23:A:1090:U:O2'	23:A:1157:A:N1	2.30	0.57
23:A:1633:G:H2'	23:A:1634:A:O4'	2.04	0.57
26:D:69:VAL:HG11	26:D:76:PRO:HA	1.86	0.57
27:E:23:VAL:HA	27:E:111:LYS:HD2	1.84	0.57
1:a:753:U:H2'	1:a:754:G:H8	1.70	0.57
23:A:454:G:H2'	23:A:455:A:C8	2.40	0.57
48:5:1:MET:H3	48:5:23:LYS:H	1.53	0.57
1:a:744:U:H2'	1:a:745:C:H6	1.70	0.57
1:a:1152:G:N2	1:a:1154:A:H62	2.03	0.57
19:s:32:LYS:HA	19:s:50:ALA:HB3	1.85	0.57
25:C:2:ALA:N	25:C:20:ASP:OD1	2.38	0.57
1:a:508:G:H2'	1:a:509:C:H6	1.69	0.57
1:a:736:A:H2'	1:a:737:A:H8	1.69	0.57
23:A:750:G:O2'	23:A:772:G:N2	2.28	0.57
23:A:2291:C:O2'	23:A:2460:C:OP2	2.21	0.57
1:a:65:A:H4'	1:a:66:A:H5'	1.86	0.57
1:a:392:G:H2'	1:a:393:U:H6	1.70	0.57
1:a:547:A:H2'	1:a:548:G:C8	2.40	0.57
23:A:1771:A:OP2	23:A:1771:A:H8	1.88	0.57
25:C:69:ARG:NH2	25:C:127:GLY:O	2.37	0.57
17:q:15:VAL:HG21	17:q:26:VAL:HG13	1.87	0.56
23:A:454:G:H2'	23:A:455:A:H8	1.69	0.56
23:A:457:G:OP2	23:A:2439:C:O2'	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1680:G:N7	55:A:3101:HOH:O	2.32	0.56
24:B:48:G:OP2	35:Q:69:LYS:HE3	2.05	0.56
1:a:413:U:O4	4:d:3:ARG:NH1	2.38	0.56
1:a:583:G:O2'	1:a:829:G:OP2	2.18	0.56
1:a:602:U:C2	1:a:654:G:N1	2.73	0.56
1:a:1046:C:H2'	1:a:1047:A:H8	1.70	0.56
9:i:52:LEU:HD12	9:i:58:LEU:HD13	1.86	0.56
23:A:1716:G:O2'	23:A:2024:U:O4	2.18	0.56
23:A:2164:A:N6	23:A:2191:A:O2'	2.33	0.56
47:4:37:ARG:NH1	47:4:38:LEU:O	2.37	0.56
1:a:1124:U:H2'	1:a:1125:U:C6	2.40	0.56
41:W:82:GLY:N	41:W:93:VAL:O	2.32	0.56
46:3:15:VAL:HG22	46:3:45:LEU:HD22	1.86	0.56
46:3:76:LYS:HZ3	46:3:77:LYS:HE3	1.70	0.56
23:A:1065:U:OP1	23:A:1081:U:O2'	2.19	0.56
23:A:2156:A:H2'	23:A:2157:G:C8	2.41	0.56
23:A:2789:U:H5	23:A:2791:A:N7	2.03	0.56
29:G:46:GLU:OE2	29:G:51:ASN:N	2.37	0.56
35:Q:32:ASN:OD1	35:Q:33:VAL:N	2.38	0.56
1:a:566:G:OP2	1:a:567:A:O2'	2.24	0.56
1:a:955:A:H2'	1:a:956:G:H8	1.71	0.56
1:a:1047:A:H2'	1:a:1048:A:H8	1.70	0.56
1:a:1123:C:H1'	14:n:60:SER:OG	2.06	0.56
1:a:1398:U:H2'	1:a:1399:G:C8	2.41	0.56
13:m:92:ARG:HB3	13:m:92:ARG:NH1	2.20	0.56
25:C:264:ASN:OD1	25:C:265:ASN:N	2.39	0.56
33:O:70:PRO:HA	33:O:95:SER:HB3	1.87	0.56
1:a:17:U:H2'	1:a:18:C:H6	1.71	0.56
4:d:190:ASN:OD1	4:d:191:GLU:N	2.39	0.56
23:A:2107:U:H2'	23:A:2108:U:C6	2.40	0.56
24:B:110:G:H2'	24:B:111:C:H6	1.71	0.56
27:E:9:GLN:NE2	27:E:130:THR:H	2.04	0.56
41:W:97:SER:OG	41:W:99:GLU:OE1	2.17	0.56
1:a:389:A:C6	1:a:390:A:C2	2.94	0.56
23:A:579:U:H2'	23:A:580:U:C6	2.41	0.56
24:B:12:U:OP2	24:B:68:C:O2'	2.24	0.56
26:D:54:GLU:O	26:D:78:ARG:N	2.29	0.56
1:a:836:A:H62	1:a:867:G:H21	1.53	0.56
6:f:91:MET:HE1	6:f:93:ILE:HB	1.87	0.56
9:i:18:ARG:NH1	9:i:66:ASN:OD1	2.39	0.56
23:A:924:U:H2'	23:A:946:G:N2	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:N:33:ARG:NH1	32:N:39:LYS:O	2.39	0.56
1:a:217:U:O4	1:a:222:G:O6	2.24	0.55
1:a:714:A:H4'	11:k:31:ILE:HD11	1.88	0.55
1:a:1129:U:H2'	1:a:1130:U:C6	2.41	0.55
23:A:1370:U:HO2'	23:A:2043:G:HO2'	1.47	0.55
23:A:1483:A:H2'	23:A:1484:A:H8	1.71	0.55
23:A:2097:C:H2'	23:A:2098:C:C6	2.41	0.55
23:A:2181:G:H2'	23:A:2182:C:H6	1.70	0.55
46:3:76:LYS:NZ	46:3:77:LYS:HE3	2.21	0.55
23:A:878:G:H2'	23:A:879:C:C6	2.41	0.55
23:A:1309:G:OP1	47:4:16:ARG:NH2	2.35	0.55
23:A:2199:G:H2'	23:A:2200:U:C6	2.41	0.55
1:a:199:C:H2'	1:a:200:A:H8	1.70	0.55
1:a:221:G:OP2	1:a:221:G:N2	2.31	0.55
23:A:280:A:H2'	23:A:281:A:C8	2.41	0.55
23:A:1717:A:N3	23:A:1719:C:N4	2.55	0.55
23:A:2412:G:H2'	23:A:2413:U:C6	2.41	0.55
23:A:2845:C:O2	23:A:2912:A:O2'	2.25	0.55
1:a:474:A:H2'	1:a:475:A:C8	2.42	0.55
1:a:1049:A:H2'	1:a:1050:G:C8	2.41	0.55
13:m:11:ARG:O	13:m:45:THR:OG1	2.24	0.55
23:A:1592:A:H3'	23:A:1593:C:C6	2.42	0.55
23:A:2713:C:H1'	26:D:191:ASN:ND2	2.20	0.55
29:G:158:LYS:HD3	29:G:160:LYS:HD2	1.87	0.55
39:U:16:ARG:NH2	39:U:103:LYS:HD2	2.22	0.55
1:a:499:A:H2'	1:a:500:A:C8	2.42	0.55
1:a:222:G:H2'	1:a:223:C:C6	2.42	0.55
9:i:91:ALA:HB3	9:i:94:TYR:CE2	2.42	0.55
46:3:13:VAL:HG23	46:3:45:LEU:HD23	1.88	0.55
6:f:6:GLU:OE2	6:f:63:ILE:HG23	2.07	0.55
6:f:41:SER:OG	6:f:62:HIS:NE2	2.26	0.55
8:h:115:ASP:OD1	8:h:115:ASP:N	2.39	0.55
23:A:27:G:O2'	23:A:28:A:O5'	2.25	0.55
23:A:910:A:H2'	23:A:911:G:H8	1.71	0.55
23:A:1452:U:H2'	23:A:1453:G:C8	2.41	0.55
23:A:2158:G:H22	23:A:2205:U:H5'	1.72	0.55
1:a:874:A:H2'	1:a:875:C:C6	2.42	0.55
9:i:29:VAL:HB	9:i:64:LEU:HD23	1.88	0.55
21:x:51:U:H3	21:x:63:G:H1	0.74	0.55
23:A:292:U:H2'	23:A:293:G:C8	2.38	0.55
25:C:171:TYR:HB3	25:C:183:MET:HG2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:N:93:PRO:HG2	32:N:146:ILE:HD11	1.89	0.55
34:P:122:ARG:HD3	34:P:129:MET:HE2	1.88	0.55
1:a:781:G:H5''	25:C:202:LEU:HD13	1.89	0.54
21:x:51:U:O2	21:x:63:G:N2	2.24	0.54
23:A:221:A:N3	23:A:236:U:O2'	2.39	0.54
23:A:2362:A:H2'	23:A:2363:G:H8	1.72	0.54
1:a:1419:C:H2'	1:a:1420:A:C8	2.42	0.54
7:g:71:PRO:HG3	7:g:103:TRP:HZ3	1.73	0.54
10:j:59:LYS:O	10:j:62:ARG:NH1	2.40	0.54
17:q:70:SER:OG	17:q:71:ALA:N	2.39	0.54
23:A:925:A:C8	23:A:946:G:N2	2.75	0.54
23:A:2908:A:O2'	23:A:2909:C:OP2	2.23	0.54
36:R:93:ARG:O	36:R:94:ARG:NH1	2.41	0.54
40:V:17:THR:HA	40:V:20:LEU:HG	1.89	0.54
15:o:17:VAL:HG23	15:o:18:HIS:H	1.72	0.54
23:A:703:U:H2'	23:A:704:A:H8	1.70	0.54
12:l:27:GLY:O	12:l:36:THR:N	2.37	0.54
23:A:419:U:O2'	23:A:420:A:O5'	2.26	0.54
23:A:839:A:H61	25:C:228:ASN:HD22	1.55	0.54
3:c:48:ASP:HB3	3:c:74:MET:HE2	1.88	0.54
10:j:94:SER:OG	10:j:95:GLY:N	2.41	0.54
16:p:22:VAL:HG23	16:p:34:ILE:HB	1.90	0.54
23:A:1685:U:H2'	23:A:1686:C:C6	2.42	0.54
23:A:2109:U:OP2	23:A:2271:G:N2	2.35	0.54
23:A:2137:C:H2'	23:A:2138:C:H6	1.73	0.54
23:A:2840:G:H5''	26:D:62:ASN:HB2	1.90	0.54
1:a:262:G:O2'	17:q:20:ASP:O	2.25	0.54
23:A:66:C:H2'	23:A:67:A:H8	1.72	0.54
23:A:130:A:H2'	23:A:131:C:C6	2.42	0.54
23:A:712:G:H4'	32:N:48:LEU:HD21	1.90	0.54
23:A:1528:G:H2'	23:A:1529:U:H6	1.72	0.54
18:r:15:CYS:HB3	18:r:18:THR:HB	1.90	0.54
23:A:1812:U:OP2	23:A:1817:A:N6	2.40	0.54
23:A:2502:A:N6	23:A:2514:G:O2'	2.40	0.54
1:a:69:A:C8	1:a:96:G:H5'	2.43	0.54
1:a:1009:U:H2'	1:a:1010:U:C6	2.43	0.54
23:A:1957:C:H2'	23:A:1958:C:C6	2.42	0.54
1:a:1046:C:H2'	1:a:1047:A:C8	2.43	0.54
1:a:1047:A:H2'	1:a:1048:A:C8	2.42	0.54
23:A:1343:G:N1	23:A:1689:A:OP2	2.32	0.54
1:a:467:U:H2'	1:a:468:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1330:G:H2'	1:a:1331:C:C6	2.43	0.54
23:A:72:U:OP2	44:1:54:LYS:NZ	2.35	0.54
23:A:1528:G:H2'	23:A:1529:U:C6	2.43	0.54
1:a:559:U:H2'	1:a:560:U:H6	1.72	0.53
23:A:140:G:H2'	23:A:141:U:C6	2.44	0.53
1:a:528:A:H62	1:a:537:G:H21	1.56	0.53
21:x:51:U:O4	21:x:63:G:O6	2.25	0.53
23:A:1957:C:H2'	23:A:1958:C:C5	2.41	0.53
1:a:927:A:H2'	1:a:928:A:C8	2.44	0.53
14:n:60:SER:OG	14:n:61:TRP:N	2.41	0.53
25:C:37:LEU:HG	25:C:62:TYR:HB2	1.91	0.53
1:a:1247:U:C4	7:g:116:MET:HE1	2.43	0.53
10:j:17:ILE:HD12	10:j:20:GLN:HE22	1.73	0.53
15:o:70:LEU:HB3	15:o:78:TYR:HB2	1.91	0.53
23:A:687:G:N1	23:A:690:U:OP2	2.34	0.53
39:U:16:ARG:HD2	39:U:16:ARG:O	2.09	0.53
1:a:860:U:H2'	1:a:861:A:H8	1.72	0.53
1:a:1398:U:H2'	1:a:1399:G:H8	1.73	0.53
23:A:330:A:H2'	23:A:331:G:C8	2.43	0.53
23:A:2830:C:H3'	23:A:2831:G:C8	2.42	0.53
28:F:3:ARG:HG3	28:F:4:LEU:HD12	1.91	0.53
28:F:94:GLU:CD	28:F:97:TYR:HE1	2.17	0.53
1:a:972:G:C2	1:a:973:A:C8	2.97	0.53
1:a:1176:A:H2'	1:a:1177:A:C8	2.44	0.53
13:m:12:GLU:HA	13:m:46:ARG:HH11	1.72	0.53
23:A:305:C:H2'	23:A:306:A:H8	1.73	0.53
23:A:2107:U:H2'	23:A:2108:U:H6	1.73	0.53
23:A:2333:A:H2'	23:A:2334:A:H8	1.74	0.53
5:e:72:MET:HA	5:e:72:MET:HE2	1.89	0.53
23:A:284:U:H5''	23:A:285:U:C5	2.44	0.53
23:A:632:U:H2'	23:A:633:A:H8	1.72	0.53
23:A:2312:G:O6	42:Y:22:ARG:HD2	2.09	0.53
30:L:88:ARG:HH22	30:L:97:ASN:ND2	2.07	0.53
1:a:605:G:O2'	17:q:39:ARG:NH1	2.41	0.53
1:a:802:A:H2'	1:a:803:C:C6	2.43	0.53
1:a:1009:U:N3	1:a:1050:G:C6	2.77	0.53
10:j:20:GLN:O	10:j:24:LYS:N	2.39	0.53
23:A:341:A:N3	23:A:362:C:O2'	2.41	0.53
23:A:404:A:N6	23:A:405:G:O6	2.41	0.53
23:A:2689:U:O2	23:A:2698:A:N7	2.41	0.53
28:F:163:ASP:OD1	28:F:164:GLU:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:G:156:PRO:HG2	29:G:157:TYR:CD2	2.43	0.53
1:a:113:G:H4'	1:a:114:A:O5'	2.08	0.53
1:a:847:G:H2'	1:a:848:G:H8	1.73	0.53
1:a:1013:A:H5''	1:a:1033:U:H2'	1.91	0.53
23:A:394:C:H2'	23:A:395:U:C6	2.43	0.53
1:a:422:A:H2'	1:a:423:A:H8	1.73	0.53
1:a:530:C:H41	12:l:63:ARG:HH22	1.56	0.53
43:Z:16:ASN:OD1	43:Z:24:SER:OG	2.21	0.53
49:6:22:MET:HE2	49:6:31:LEU:HD12	1.90	0.53
1:a:1160:A:P	10:j:72:ARG:HH22	2.32	0.52
23:A:504:G:O2'	23:A:515:G:O6	2.27	0.52
23:A:1152:G:H2'	23:A:1153:G:C8	2.44	0.52
23:A:2389:U:H2'	23:A:2390:G:O4'	2.09	0.52
51:8:18:ARG:HG2	51:8:23:VAL:HG12	1.90	0.52
1:a:424:G:H2'	1:a:425:G:C8	2.43	0.52
1:a:1326:A:OP1	19:s:3:ARG:N	2.43	0.52
10:j:14:ASP:HB3	10:j:17:ILE:HG22	1.92	0.52
33:O:12:GLU:HG2	33:O:72:LYS:HG3	1.92	0.52
39:U:64:GLU:HB2	39:U:71:ILE:HD11	1.89	0.52
11:k:36:ASP:OD1	11:k:40:ASN:HB2	2.09	0.52
23:A:92:G:O2'	23:A:93:U:OP1	2.24	0.52
23:A:1044:U:P	37:S:92:ARG:HH12	2.32	0.52
23:A:1593:C:H2'	23:A:1594:G:C5	2.45	0.52
1:a:319:C:OP1	16:p:32:ARG:NH2	2.43	0.52
1:a:1316:G:OP2	13:m:98:ARG:NH1	2.42	0.52
23:A:2362:A:H2'	23:A:2363:G:C8	2.45	0.52
23:A:2694:G:OP2	23:A:2694:G:H8	1.93	0.52
28:F:22:TYR:OH	28:F:165:GLU:OE1	2.28	0.52
17:q:26:VAL:HG12	17:q:45:LYS:HB3	1.91	0.52
28:F:129:THR:HA	28:F:155:VAL:HA	1.92	0.52
33:O:112:ASP:O	33:O:116:GLU:HG2	2.08	0.52
1:a:26:A:H61	1:a:566:G:H1'	1.74	0.52
1:a:1044:G:H2'	1:a:1045:A:C8	2.45	0.52
5:e:94:GLU:H	5:e:130:GLY:HA3	1.74	0.52
23:A:281:A:H2'	23:A:282:G:H8	1.75	0.52
23:A:807:A:N7	55:A:3102:HOH:O	2.34	0.52
28:F:50:LEU:O	28:F:54:VAL:HG23	2.09	0.52
37:S:58:ARG:O	37:S:62:ILE:HG12	2.09	0.52
1:a:1321:C:H2'	1:a:1322:U:C6	2.45	0.52
3:c:182:ASP:O	3:c:200:TRP:HB2	2.10	0.52
23:A:625:G:H2'	23:A:626:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1384:U:OP2	40:V:58:TYR:OH	2.21	0.52
23:A:1569:U:H2'	23:A:1570:G:C8	2.44	0.52
48:5:5:ILE:HG21	48:5:21:LYS:HD3	1.92	0.52
1:a:184:G:H2'	1:a:185:A:H8	1.74	0.52
1:a:660:U:O4	1:a:760:G:O2'	2.18	0.52
1:a:729:A:OP2	18:r:46:ARG:NH1	2.43	0.52
1:a:993:C:C4	1:a:1229:G:N2	2.78	0.52
23:A:280:A:H2'	23:A:281:A:H8	1.74	0.52
23:A:1151:U:H2'	23:A:1152:G:C8	2.44	0.52
23:A:2217:U:H2'	23:A:2218:G:O4'	2.09	0.52
27:E:31:LYS:HG2	32:N:9:SER:HB2	1.91	0.52
42:Y:26:SER:O	42:Y:28:ARG:NH1	2.43	0.52
47:4:48:GLN:HG2	47:4:53:ASP:HA	1.91	0.52
1:a:537:G:O2'	1:a:541:A:N1	2.39	0.52
23:A:688:A:O2'	23:A:689:A:OP1	2.28	0.52
23:A:1430:C:H2'	23:A:1431:A:C8	2.45	0.52
33:O:67:LYS:NZ	33:O:105:GLU:OE2	2.22	0.52
48:5:17:TYR:HE2	48:5:34:LYS:HB3	1.73	0.52
1:a:602:U:C2	1:a:654:G:C2	2.98	0.52
1:a:1228:G:C6	1:a:1229:G:C2	2.98	0.52
23:A:245:U:OP2	50:7:8:ARG:NH1	2.42	0.52
23:A:2139:G:H2'	23:A:2140:C:C6	2.45	0.52
44:1:18:GLU:OE2	44:1:54:LYS:HE2	2.10	0.52
1:a:745:C:H2'	1:a:746:U:C6	2.45	0.51
1:a:1105:C:O2'	1:a:1177:A:O2'	2.23	0.51
15:o:9:ASN:HA	15:o:12:ILE:HG22	1.92	0.51
18:r:49:THR:HG23	18:r:51:THR:H	1.75	0.51
23:A:81:G:O6	23:A:82:G:N2	2.43	0.51
23:A:199:A:N6	23:A:2463:A:O2'	2.41	0.51
23:A:1812:U:H5	23:A:1817:A:N7	2.08	0.51
23:A:2170:C:H2'	23:A:2171:G:C8	2.45	0.51
29:G:122:GLU:N	29:G:134:LYS:O	2.40	0.51
1:a:35:G:H2'	1:a:36:C:H6	1.75	0.51
1:a:35:G:H2'	1:a:36:C:C6	2.45	0.51
1:a:589:G:N1	1:a:767:A:OP2	2.25	0.51
1:a:1246:A:H62	1:a:1306:A:H62	1.59	0.51
3:c:11:ARG:HB3	3:c:15:ILE:HG22	1.92	0.51
23:A:2159:A:O2'	23:A:2196:A:N3	2.44	0.51
23:A:2834:A:O2'	23:A:2835:A:H8	1.93	0.51
29:G:33:LEU:HD23	29:G:79:VAL:HG13	1.93	0.51
33:O:32:TYR:OH	33:O:111:GLU:OE1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1:10:SER:O	44:1:12:THR:N	2.43	0.51
46:3:41:ASN:HB3	46:3:43:TYR:CZ	2.45	0.51
1:a:111:G:H2'	1:a:112:U:C6	2.45	0.51
23:A:2463:A:N3	23:A:2463:A:H2'	2.26	0.51
36:R:22:PRO:HA	36:R:47:VAL:HG23	1.90	0.51
23:A:756:A:H2'	23:A:757:A:C8	2.46	0.51
23:A:1111:U:O4	23:A:1115:A:O2'	2.24	0.51
1:a:1350:G:H2'	1:a:1351:C:C6	2.46	0.51
4:d:163:GLU:OE1	4:d:178:ARG:NH2	2.41	0.51
10:j:77:VAL:O	10:j:79:PRO:HD3	2.10	0.51
21:x:70:G:H2'	21:x:71:G:H8	1.75	0.51
23:A:910:A:H2'	23:A:911:G:C8	2.46	0.51
23:A:911:G:H2'	23:A:912:C:H6	1.75	0.51
23:A:1039:A:OP1	37:S:50:ARG:NH1	2.43	0.51
23:A:2682:U:H2'	23:A:2683:C:C6	2.45	0.51
28:F:104:VAL:HG12	28:F:108:LEU:HD12	1.93	0.51
1:a:345:G:H2'	1:a:346:A:C8	2.46	0.51
1:a:381:A:O2'	1:a:459:A:N7	2.43	0.51
1:a:1008:C:H1'	1:a:1052:G:H22	1.76	0.51
2:b:32:PHE:HE1	2:b:42:ASP:HA	1.76	0.51
23:A:684:U:H2'	23:A:685:C:C6	2.45	0.51
23:A:1763:U:O2'	23:A:1764:A:O5'	2.28	0.51
23:A:2208:U:H2'	23:A:2209:A:C8	2.41	0.51
26:D:8:ARG:NH1	26:D:54:GLU:OE1	2.42	0.51
12:l:66:ALA:HB2	12:l:80:ILE:HD11	1.92	0.51
23:A:911:G:H2'	23:A:912:C:C6	2.46	0.51
23:A:2461:G:N2	32:N:54:GLN:HE21	2.08	0.51
23:A:2789:U:OP2	51:8:19:ARG:NE	2.42	0.51
26:D:6:LEU:HD23	26:D:199:LEU:HD11	1.92	0.51
32:N:105:GLU:O	32:N:105:GLU:HG2	2.11	0.51
44:1:10:SER:N	44:1:13:GLU:OE2	2.35	0.51
1:a:381:A:C2	1:a:382:A:C8	2.99	0.51
1:a:602:U:O2	1:a:654:G:C2	2.64	0.51
23:A:1336:U:H2'	23:A:1337:U:C6	2.46	0.51
23:A:1699:A:O2'	23:A:1700:G:O5'	2.28	0.51
24:B:38:U:N3	24:B:42:G:OP2	2.36	0.51
26:D:13:THR:HG21	36:R:5:ILE:HG21	1.92	0.51
33:O:44:ASN:HA	33:O:47:ILE:HD12	1.93	0.51
50:7:54:ASP:O	50:7:58:ILE:HG12	2.11	0.51
23:A:2137:C:H2'	23:A:2138:C:C6	2.46	0.51
1:a:26:A:N6	1:a:566:G:H1'	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:76:ILE:HG22	3:c:83:VAL:HG21	1.93	0.51
23:A:282:G:H2'	23:A:283:C:H4'	1.93	0.51
23:A:891:U:O2'	23:A:893:A:OP1	2.29	0.51
23:A:1117:G:H2'	23:A:1118:C:C6	2.45	0.51
23:A:1596:A:H2'	23:A:1597:A:H8	1.75	0.51
35:Q:101:TYR:CE2	35:Q:106:LYS:HG3	2.46	0.51
1:a:106:G:N1	20:t:10:ARG:HG2	2.26	0.50
1:a:721:G:H2'	1:a:722:G:C8	2.46	0.50
4:d:15:LEU:HG	4:d:56:LYS:HG2	1.94	0.50
10:j:35:SER:HG	10:j:78:ASN:H	1.53	0.50
19:s:41:PHE:HA	46:3:73:ARG:NH1	2.25	0.50
23:A:1622:A:H2'	23:A:1623:A:C8	2.46	0.50
23:A:1941:C:H2'	23:A:1942:C:C6	2.46	0.50
23:A:2167:A:H2'	23:A:2168:G:C8	2.45	0.50
33:O:75:THR:HG22	33:O:90:PRO:HA	1.92	0.50
1:a:948:G:N3	1:a:1382:A:H2	2.09	0.50
16:p:74:LEU:HD22	16:p:79:ILE:HD11	1.91	0.50
23:A:1067:A:H62	23:A:1187:U:H3	1.59	0.50
23:A:1596:A:H2'	23:A:1597:A:C8	2.46	0.50
23:A:2167:A:H2	23:A:2192:G:O2'	1.94	0.50
23:A:2886:G:N2	23:A:2889:A:OP2	2.42	0.50
28:F:36:ILE:HD11	28:F:99:PHE:HE1	1.77	0.50
1:a:560:U:H2'	1:a:561:G:H8	1.76	0.50
1:a:1411:C:H2'	1:a:1412:G:C8	2.46	0.50
5:e:158:ARG:HH21	8:h:43:GLU:HB3	1.76	0.50
8:h:117:GLU:OE1	8:h:117:GLU:N	2.43	0.50
23:A:1201:A:H5''	37:S:55:ARG:HD3	1.94	0.50
23:A:2623:A:H2'	23:A:2624:C:H6	1.75	0.50
30:L:57:ILE:HB	30:L:125:VAL:HG23	1.93	0.50
1:a:684:A:H2'	1:a:685:U:C6	2.46	0.50
4:d:120:THR:HG22	4:d:125:ARG:HA	1.93	0.50
19:s:63:GLN:HG3	19:s:66:MET:HE3	1.92	0.50
23:A:2685:U:H2'	23:A:2686:U:C6	2.47	0.50
44:1:49:ALA:HA	44:1:52:ARG:HD2	1.94	0.50
1:a:1160:A:H2'	1:a:1161:A:H8	1.76	0.50
23:A:75:G:H22	23:A:110:A:H2	1.59	0.50
23:A:755:U:H2'	23:A:756:A:H8	1.76	0.50
23:A:2064:A:N3	23:A:2488:G:O2'	2.35	0.50
27:E:9:GLN:HA	27:E:142:PHE:HE1	1.77	0.50
27:E:42:ALA:O	27:E:45:ARG:HG2	2.11	0.50
41:W:92:ARG:O	41:W:101:ILE:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:199:C:H2'	1:a:200:A:C8	2.46	0.50
1:a:547:A:H2'	1:a:548:G:H8	1.75	0.50
23:A:10:A:C6	23:A:11:G:C2	3.00	0.50
23:A:1139:G:H21	23:A:1144:A:H62	1.59	0.50
23:A:1140:U:N3	23:A:1143:U:OP2	2.33	0.50
23:A:1829:U:H2'	23:A:1830:C:C6	2.47	0.50
1:a:943:C:O2'	1:a:1351:C:OP2	2.29	0.50
21:x:70:G:H2'	21:x:71:G:C8	2.47	0.50
23:A:1429:A:C6	23:A:1447:A:C5	3.00	0.50
23:A:1623:A:H2'	23:A:1624:A:C8	2.47	0.50
30:L:29:LEU:HD13	30:L:143:LEU:HD11	1.94	0.50
31:M:64:ARG:HB2	31:M:79:PHE:CD2	2.47	0.50
1:a:1044:G:H2'	1:a:1045:A:H8	1.75	0.50
15:o:26:GLU:HA	15:o:29:ILE:HG22	1.94	0.50
16:p:20:ILE:N	16:p:38:GLY:O	2.38	0.50
21:x:9:A:H2'	21:x:11:C:H41	1.77	0.50
23:A:1623:A:H2'	23:A:1624:A:H8	1.77	0.50
1:a:254:A:C2	1:a:290:A:C5	3.00	0.50
1:a:973:A:HO2'	10:j:57:LYS:HZ3	1.58	0.50
23:A:972:G:O3'	23:A:973:U:H2'	2.12	0.50
23:A:1532:G:HO2'	23:A:1533:A:H8	1.57	0.50
23:A:1551:U:H2'	23:A:1552:U:C6	2.47	0.50
23:A:1829:U:H2'	23:A:1830:C:H6	1.76	0.50
25:C:154:LEU:HD13	25:C:176:LEU:HD21	1.94	0.50
1:a:703:A:H2'	1:a:704:A:C8	2.47	0.49
1:a:1496:G:H2'	1:a:1497:G:C8	2.47	0.49
23:A:193:A:H2'	23:A:194:C:C6	2.47	0.49
23:A:2292:G:C8	23:A:2460:C:C4	3.00	0.49
39:U:14:THR:H	39:U:107:HIS:HD2	1.60	0.49
1:a:1434:C:H2'	1:a:1435:A:C8	2.42	0.49
19:s:68:GLY:HA2	46:3:73:ARG:NH2	2.27	0.49
23:A:314:C:H2'	23:A:315:G:O4'	2.12	0.49
23:A:422:G:H2'	23:A:423:A:H8	1.77	0.49
23:A:906:G:O2'	23:A:963:G:O6	2.22	0.49
23:A:1015:G:H2'	23:A:1016:U:C6	2.47	0.49
23:A:1136:U:H2'	23:A:1137:G:C8	2.46	0.49
23:A:2177:G:H21	23:A:2180:A:H2	1.60	0.49
23:A:2883:G:H2'	23:A:2884:U:C6	2.47	0.49
28:F:8:TYR:HA	28:F:12:ILE:HD12	1.94	0.49
31:M:4:GLN:HG2	31:M:5:GLU:HG2	1.92	0.49
1:a:546:U:H2'	1:a:547:A:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1639:U:H2'	23:A:1640:A:H8	1.76	0.49
28:F:4:LEU:HB2	28:F:97:TYR:CD2	2.48	0.49
1:a:72:G:H8	1:a:72:G:O5'	1.96	0.49
1:a:401:A:C2	1:a:402:G:C8	3.01	0.49
23:A:253:A:OP1	50:7:7:HIS:NE2	2.42	0.49
23:A:394:C:H2'	23:A:395:U:H6	1.76	0.49
23:A:879:C:H2'	23:A:880:U:C6	2.47	0.49
23:A:2138:C:H2'	23:A:2139:G:C8	2.47	0.49
23:A:2156:A:H2'	23:A:2157:G:H8	1.77	0.49
23:A:2791:A:H2'	23:A:2792:G:H5'	1.93	0.49
23:A:2927:A:H5'	30:L:137:LYS:HE3	1.94	0.49
5:e:39:VAL:HG21	5:e:115:VAL:HG12	1.93	0.49
15:o:88:ARG:HG2	15:o:89:ARG:H	1.76	0.49
21:x:63:G:H2'	21:x:64:A:C8	2.46	0.49
23:A:281:A:H2'	23:A:282:G:C8	2.47	0.49
23:A:1141:A:H2'	23:A:1142:A:C5	2.48	0.49
23:A:1296:A:OP1	37:S:13:ARG:NH1	2.45	0.49
27:E:200:GLU:N	27:E:200:GLU:OE2	2.45	0.49
48:5:39:LEU:HB3	48:5:41:ARG:NH1	2.28	0.49
1:a:929:U:HO2'	1:a:1090:G:HO2'	1.61	0.49
1:a:1281:G:O2'	1:a:1282:A:H8	1.96	0.49
23:A:460:C:H2'	23:A:461:A:C8	2.48	0.49
23:A:526:A:O2'	41:W:42:LYS:O	2.30	0.49
23:A:1106:U:H4'	23:A:1107:U:H2'	1.94	0.49
23:A:1325:G:H2'	23:A:1326:U:C6	2.48	0.49
44:1:38:GLU:OE1	44:1:38:GLU:N	2.46	0.49
1:a:150:A:C2	1:a:151:A:H1'	2.47	0.49
1:a:188:G:C6	1:a:202:G:C6	3.00	0.49
23:A:161:A:H2'	23:A:162:A:C8	2.48	0.49
23:A:1891:G:H1'	23:A:1917:A:N6	2.27	0.49
23:A:2830:C:H3'	23:A:2831:G:H8	1.77	0.49
25:C:145:GLU:HG3	25:C:188:CYS:HB3	1.94	0.49
28:F:122:PHE:HZ	28:F:170:LEU:HD21	1.76	0.49
33:O:50:ALA:O	33:O:54:MET:HB2	2.11	0.49
16:p:24:ASP:OD1	16:p:25:SER:N	2.46	0.49
16:p:71:ARG:NH1	16:p:80:MET:HG3	2.28	0.49
23:A:755:U:H2'	23:A:756:A:C8	2.47	0.49
23:A:1140:U:H2'	23:A:1142:A:N7	2.28	0.49
23:A:1277:G:C2	23:A:1278:G:C8	3.00	0.49
1:a:277:U:H2'	1:a:278:A:C8	2.48	0.49
1:a:890:G:OP2	12:l:9:ARG:NH2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:993:C:N4	1:a:1229:G:H22	2.11	0.49
1:a:1323:G:O2'	14:n:18:VAL:HG21	2.12	0.49
23:A:460:C:H2'	23:A:461:A:H8	1.78	0.49
23:A:1430:C:H2'	23:A:1431:A:H8	1.77	0.49
32:N:95:LEU:O	32:N:99:THR:OG1	2.30	0.49
46:3:55:HIS:CE1	46:3:57:PHE:HB3	2.48	0.49
1:a:593:G:H4'	12:l:5:ASN:ND2	2.28	0.49
1:a:1272:C:H2'	1:a:1273:G:H8	1.78	0.49
1:a:1345:G:N2	21:x:42:C:O4'	2.46	0.49
13:m:49:THR:HG23	13:m:52:GLU:H	1.77	0.49
23:A:171:G:H2'	23:A:172:U:C6	2.48	0.49
23:A:2333:A:H2'	23:A:2334:A:C8	2.48	0.49
1:a:509:C:O3'	12:l:128:SER:OG	2.29	0.48
1:a:1272:C:H2'	1:a:1273:G:C8	2.48	0.48
2:b:20:THR:N	2:b:37:GLY:O	2.46	0.48
12:l:3:THR:HG23	12:l:6:GLN:H	1.78	0.48
23:A:317:A:H2'	23:A:318:G:C8	2.47	0.48
23:A:864:G:N1	23:A:1234:U:OP2	2.32	0.48
29:G:133:VAL:HG11	29:G:144:LEU:HD22	1.94	0.48
1:a:684:A:H2'	1:a:685:U:H6	1.77	0.48
1:a:992:A:H5''	1:a:993:C:OP2	2.14	0.48
23:A:390:A:H2'	23:A:391:U:C6	2.48	0.48
23:A:703:U:H2'	23:A:704:A:C8	2.47	0.48
44:1:42:ARG:O	44:1:46:VAL:HG23	2.14	0.48
46:3:8:GLU:O	46:3:28:THR:OG1	2.18	0.48
1:a:142:U:H5'	1:a:143:U:H5'	1.95	0.48
1:a:559:U:H2'	1:a:560:U:C6	2.48	0.48
1:a:1064:A:C6	1:a:1213:G:C5	3.01	0.48
4:d:101:LEU:HD22	4:d:167:PHE:HB2	1.94	0.48
9:i:115:LYS:HG3	9:i:118:LEU:HD12	1.96	0.48
10:j:97:ASP:OD1	10:j:98:ILE:N	2.46	0.48
23:A:1152:G:H2'	23:A:1153:G:N9	2.28	0.48
23:A:2158:G:N2	23:A:2205:U:H5'	2.27	0.48
23:A:2225:C:H2'	23:A:2226:A:C8	2.48	0.48
23:A:2833:A:H2'	23:A:2834:A:C8	2.48	0.48
51:8:25:VAL:HG22	51:8:34:GLN:HB2	1.94	0.48
1:a:477:U:H2'	1:a:478:G:O4'	2.13	0.48
1:a:1230:C:OP2	19:s:78:ARG:NH2	2.46	0.48
21:x:22:G:H2'	21:x:23:A:H8	1.77	0.48
21:x:27:G:C6	21:x:43:C:N3	2.82	0.48
23:A:420:A:H2'	23:A:421:C:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:625:G:H2'	23:A:626:G:C8	2.48	0.48
23:A:1897:U:OP1	23:A:2443:G:O2'	2.31	0.48
32:N:51:GLU:OE2	32:N:56:PRO:HA	2.13	0.48
41:W:9:VAL:CG1	41:W:68:VAL:HG13	2.43	0.48
1:a:606:U:O4	1:a:607:C:N4	2.46	0.48
1:a:1129:U:H2'	1:a:1130:U:H6	1.77	0.48
1:a:1268:A:N6	1:a:1281:G:H1'	2.29	0.48
1:a:1454:A:OP1	1:a:1455:C:N4	2.35	0.48
23:A:2093:A:O2'	23:A:2094:G:OP2	2.30	0.48
34:P:18:ARG:HG2	34:P:65:PHE:CE2	2.49	0.48
41:W:35:ILE:HD12	41:W:63:ILE:HD11	1.95	0.48
46:3:10:ARG:NE	46:3:10:ARG:HA	2.29	0.48
1:a:745:C:H2'	1:a:746:U:H6	1.77	0.48
23:A:420:A:C2	23:A:421:C:H1'	2.48	0.48
23:A:1835:A:H2'	23:A:1836:A:C8	2.49	0.48
1:a:224:U:H2'	1:a:225:A:C8	2.48	0.48
1:a:700:U:H5	11:k:28:ASN:HD21	1.61	0.48
13:m:25:ILE:HD11	13:m:60:LEU:HD11	1.96	0.48
23:A:1552:U:H2'	23:A:1553:C:H6	1.79	0.48
23:A:1922:A:H1'	23:A:2120:G:H5'	1.96	0.48
23:A:2272:G:OP1	25:C:243:ARG:NH2	2.38	0.48
23:A:2324:U:H2'	23:A:2325:U:H6	1.79	0.48
23:A:2925:U:H2'	23:A:2926:U:C6	2.49	0.48
29:G:46:GLU:CD	29:G:50:ILE:HG13	2.39	0.48
29:G:52:VAL:HG23	29:G:65:HIS:HD2	1.78	0.48
42:Y:46:TYR:HE1	42:Y:48:GLN:HB3	1.78	0.48
5:e:116:LEU:HD13	5:e:124:VAL:HG11	1.96	0.48
23:A:277:A:C6	23:A:293:G:C6	3.02	0.48
23:A:1094:A:H1'	23:A:1158:G:H21	1.79	0.48
23:A:1155:C:H2'	23:A:1156:G:O4'	2.14	0.48
23:A:1297:G:OP2	37:S:14:ARG:NH2	2.43	0.48
27:E:101:LEU:H	27:E:101:LEU:HD23	1.78	0.48
28:F:24:SER:HB3	28:F:27:GLU:OE2	2.14	0.48
1:a:1268:A:C6	1:a:1282:A:C8	3.02	0.48
2:b:32:PHE:CE1	2:b:42:ASP:HA	2.49	0.48
5:e:86:VAL:HG21	5:e:147:GLN:HB2	1.95	0.48
10:j:39:PRO:HA	10:j:74:ILE:HD13	1.94	0.48
23:A:2:G:H2'	23:A:3:U:C6	2.49	0.48
23:A:66:C:H2'	23:A:67:A:C8	2.49	0.48
23:A:2720:U:H2'	23:A:2721:G:O4'	2.14	0.48
27:E:6:LEU:HB2	27:E:17:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:F:2:ASN:N	28:F:97:TYR:OH	2.43	0.48
30:L:20:ASP:OD1	30:L:21:ALA:N	2.46	0.48
31:M:104:ARG:HH12	36:R:41:GLN:HE22	1.62	0.48
49:6:43:SER:O	49:6:43:SER:OG	2.30	0.48
1:a:1244:C:O2'	1:a:1307:G:N2	2.37	0.48
19:s:9:PRO:HG3	46:3:77:LYS:HZ2	1.79	0.48
23:A:1327:G:N2	23:A:1330:A:OP2	2.46	0.48
23:A:2590:G:H2'	23:A:2591:C:C6	2.49	0.48
28:F:70:ALA:N	28:F:83:MET:O	2.45	0.48
28:F:104:VAL:HA	28:F:108:LEU:HD12	1.96	0.48
43:Z:15:GLY:HA3	43:Z:29:TRP:HZ3	1.79	0.48
1:a:1439:G:O2'	1:a:1476:A:N6	2.47	0.47
23:A:2926:U:H2'	23:A:2927:A:H8	1.79	0.47
29:G:74:ASN:HD21	29:G:138:LYS:HD3	1.78	0.47
1:a:65:A:C5	1:a:389:A:C6	3.02	0.47
1:a:1175:C:O2'	1:a:1176:A:O4'	2.32	0.47
1:a:1284:C:H2'	1:a:1285:C:H5''	1.95	0.47
1:a:1496:G:H2'	1:a:1497:G:H8	1.79	0.47
20:t:67:HIS:CD2	20:t:68:LYS:H	2.33	0.47
23:A:1117:G:N2	23:A:1135:G:O2'	2.42	0.47
23:A:1628:U:H2'	23:A:1629:C:C6	2.49	0.47
23:A:1639:U:H2'	23:A:1640:A:C8	2.49	0.47
23:A:2135:U:H2'	23:A:2136:A:H8	1.78	0.47
1:a:727:C:H1'	18:r:42:LYS:HD2	1.94	0.47
4:d:65:GLU:O	4:d:68:PHE:N	2.46	0.47
6:f:6:GLU:HG2	6:f:65:LYS:HD3	1.96	0.47
9:i:102:GLY:C	9:i:103:LEU:HD12	2.40	0.47
23:A:228:A:H2'	23:A:229:A:C8	2.49	0.47
23:A:391:U:H2'	23:A:392:G:C8	2.49	0.47
23:A:679:G:H2'	23:A:680:C:C6	2.49	0.47
23:A:746:G:O2'	23:A:1681:A:N3	2.43	0.47
23:A:789:A:O2'	23:A:1708:U:OP1	2.32	0.47
23:A:967:G:H21	23:A:2302:G:H8	1.61	0.47
23:A:2225:C:H2'	23:A:2226:A:H8	1.79	0.47
24:B:30:C:N4	24:B:31:G:O6	2.47	0.47
1:a:1009:U:C2	1:a:1050:G:C2	3.03	0.47
1:a:1205:A:H2'	1:a:1206:U:C6	2.49	0.47
16:p:10:MET:O	16:p:17:PHE:N	2.46	0.47
23:A:924:U:H2'	23:A:946:G:H22	1.80	0.47
23:A:1072:A:OP2	23:A:1180:C:O2'	2.32	0.47
23:A:1942:C:C2	23:A:1955:G:N2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2280:A:H2'	23:A:2281:C:H6	1.79	0.47
23:A:2425:A:H4'	50:7:28:PHE:CD1	2.49	0.47
1:a:99:A:N3	1:a:99:A:H5''	2.29	0.47
1:a:424:G:O2'	1:a:425:G:H5'	2.14	0.47
1:a:720:A:H2'	1:a:721:G:C8	2.49	0.47
1:a:1252:G:C6	1:a:1300:A:C6	3.02	0.47
1:a:1313:A:H61	1:a:1338:G:H1'	1.80	0.47
4:d:53:GLU:HA	4:d:56:LYS:CD	2.45	0.47
9:i:81:HIS:CE1	9:i:85:ARG:HE	2.32	0.47
23:A:1130:A:H2'	23:A:1131:A:C5	2.50	0.47
23:A:2070:A:H2'	23:A:2071:G:C8	2.49	0.47
23:A:2167:A:C2	23:A:2192:G:H1'	2.49	0.47
23:A:2334:A:H2'	23:A:2335:U:C6	2.50	0.47
23:A:2347:A:H2'	23:A:2348:U:C6	2.49	0.47
23:A:2412:G:H2'	23:A:2413:U:H6	1.78	0.47
23:A:2827:C:H3'	23:A:2828:U:H5''	1.97	0.47
1:a:853:C:H2'	1:a:854:G:O4'	2.15	0.47
1:a:1384:A:H2'	7:g:2:PRO:HD2	1.97	0.47
23:A:183:G:C5	49:6:36:ARG:HD3	2.49	0.47
23:A:909:G:H2'	23:A:910:A:O4'	2.15	0.47
23:A:1539:A:H2'	25:C:98:ASP:OD1	2.14	0.47
23:A:2863:G:H2'	23:A:2908:A:H61	1.80	0.47
31:M:61:VAL:HG21	31:M:111:PHE:CE1	2.50	0.47
47:4:37:ARG:HD3	47:4:43:CYS:HB3	1.97	0.47
1:a:206:U:H2'	1:a:207:U:C6	2.49	0.47
1:a:522:C:H2'	1:a:523:G:C8	2.46	0.47
3:c:51:VAL:HG21	3:c:67:ILE:HB	1.96	0.47
5:e:16:VAL:HG23	5:e:38:VAL:HG12	1.95	0.47
7:g:42:ILE:HG13	7:g:43:LEU:N	2.29	0.47
16:p:5:ILE:CD1	16:p:22:VAL:HG12	2.44	0.47
16:p:57:LEU:HA	16:p:57:LEU:HD23	1.76	0.47
21:x:47:U:C4	21:x:50:U:H5''	2.50	0.47
21:x:61:C:H2'	21:x:62:C:C6	2.50	0.47
23:A:290:C:H2'	23:A:291:U:C6	2.49	0.47
23:A:631:U:H2'	23:A:632:U:C6	2.50	0.47
23:A:637:U:H2'	23:A:638:U:C6	2.49	0.47
23:A:650:U:C5	23:A:665:G:C5	3.03	0.47
23:A:656:G:O2'	23:A:659:A:N6	2.39	0.47
23:A:735:A:H2'	23:A:736:C:C6	2.50	0.47
23:A:1726:A:H2'	23:A:1727:A:H8	1.80	0.47
27:E:9:GLN:HE22	27:E:130:THR:H	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:E:143:LEU:HD22	27:E:148:VAL:HG21	1.96	0.47
34:P:26:VAL:HG22	34:P:71:VAL:HG22	1.97	0.47
36:R:23:GLY:H	36:R:47:VAL:HG23	1.79	0.47
46:3:71:VAL:HG22	46:3:75:ASN:HD21	1.80	0.47
1:a:240:G:H2'	1:a:241:C:C6	2.50	0.47
1:a:498:U:H2'	1:a:499:A:C8	2.48	0.47
1:a:555:A:OP2	4:d:3:ARG:NH2	2.47	0.47
1:a:601:U:N3	1:a:602:U:O4	2.47	0.47
1:a:1295:A:H8	1:a:1295:A:O5'	1.96	0.47
4:d:14:ARG:HD3	4:d:33:PRO:HD2	1.96	0.47
23:A:1915:C:H2'	23:A:1916:G:O4'	2.15	0.47
23:A:2888:G:H2'	23:A:2889:A:C8	2.50	0.47
28:F:69:LYS:HA	28:F:84:PRO:HA	1.96	0.47
29:G:50:ILE:HG12	29:G:52:VAL:HG13	1.97	0.47
51:8:15:LYS:N	51:8:15:LYS:HD2	2.29	0.47
1:a:456:A:H2'	1:a:457:A:C8	2.50	0.47
1:a:470:G:H2'	1:a:471:A:C8	2.49	0.47
8:h:117:GLU:O	8:h:121:LYS:N	2.44	0.47
15:o:17:VAL:HG22	15:o:21:ASP:OD2	2.14	0.47
23:A:422:G:H2'	23:A:423:A:C8	2.50	0.47
23:A:1364:G:N2	23:A:1364:G:OP2	2.44	0.47
23:A:1576:G:H2'	23:A:1577:G:C8	2.49	0.47
33:O:35:GLN:HB2	33:O:102:ILE:HG12	1.97	0.47
1:a:986:A:O2'	1:a:988:C:OP2	2.29	0.47
12:l:42:GLN:HB3	12:l:94:LEU:HD11	1.96	0.47
16:p:80:MET:HE1	16:p:83:PHE:HD2	1.79	0.47
23:A:2778:C:C4	23:A:2779:U:C4	3.03	0.47
41:W:82:GLY:O	41:W:93:VAL:N	2.38	0.47
1:a:271:A:OP2	20:t:73:ARG:NH1	2.48	0.46
1:a:713:U:C4	1:a:714:A:C8	3.03	0.46
5:e:154:VAL:HG21	8:h:101:LEU:HD23	1.97	0.46
15:o:17:VAL:HG23	15:o:18:HIS:N	2.30	0.46
21:x:72:C:H2'	21:x:73:A:C8	2.50	0.46
23:A:1089:C:H2'	23:A:1090:U:C6	2.49	0.46
23:A:2350:C:H2'	23:A:2351:G:O4'	2.15	0.46
31:M:63:VAL:HG13	31:M:102:VAL:HG13	1.96	0.46
46:3:52:SER:HA	46:3:55:HIS:HB2	1.97	0.46
1:a:69:A:H2'	1:a:69:A:N3	2.31	0.46
1:a:521:A:H2'	1:a:522:C:C6	2.51	0.46
1:a:982:G:OP1	10:j:59:LYS:NZ	2.40	0.46
1:a:1063:C:O2	1:a:1203:A:N6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:f:13:PRO:HD3	6:f:59:GLY:HA2	1.97	0.46
6:f:44:TRP:HE3	6:f:47:ARG:HD2	1.81	0.46
15:o:7:ARG:NH2	15:o:11:ILE:HD11	2.30	0.46
18:r:73:PRO:HB2	18:r:76:ALA:H	1.81	0.46
23:A:1903:U:O2'	23:A:1904:C:O2	2.21	0.46
23:A:2140:C:H2'	23:A:2141:U:C6	2.49	0.46
23:A:2154:G:H5''	23:A:2203:G:H21	1.80	0.46
45:2:16:PRO:HD2	45:2:19:GLN:OE1	2.14	0.46
1:a:215:G:H1	1:a:224:U:H3	1.62	0.46
1:a:642:C:H2'	1:a:643:A:C8	2.50	0.46
1:a:735:G:N2	1:a:738:G:OP2	2.40	0.46
1:a:917:A:H2'	1:a:918:A:H8	1.81	0.46
1:a:1030:G:H2'	1:a:1031:C:C6	2.50	0.46
9:i:99:LYS:HA	9:i:104:LEU:HD13	1.97	0.46
23:A:597:U:H2'	23:A:598:G:O4'	2.15	0.46
23:A:1563:A:H2'	23:A:1564:U:O4'	2.16	0.46
23:A:1815:C:HO2'	23:A:1816:A:P	2.38	0.46
28:F:36:ILE:O	28:F:88:LYS:HA	2.15	0.46
28:F:90:THR:HG21	28:F:92:ARG:NH2	2.30	0.46
35:Q:24:GLY:O	35:Q:48:VAL:N	2.49	0.46
1:a:122:G:H2'	1:a:123:U:C6	2.51	0.46
4:d:192:ALA:O	4:d:196:GLU:HG2	2.16	0.46
21:x:24:G:O2'	21:x:25:C:OP1	2.28	0.46
23:A:873:U:O2'	23:A:2101:U:C2	2.68	0.46
23:A:925:A:H3'	23:A:926:G:C8	2.50	0.46
23:A:1110:C:N3	23:A:1121:C:N4	2.62	0.46
23:A:1727:A:H2'	23:A:1728:A:H8	1.79	0.46
23:A:1763:U:C4	23:A:1778:A:N7	2.82	0.46
23:A:1891:G:HO2'	23:A:1916:G:H22	1.64	0.46
23:A:2325:U:H2'	23:A:2326:C:H6	1.80	0.46
28:F:12:ILE:HD13	28:F:173:LEU:HD22	1.98	0.46
33:O:43:THR:N	33:O:46:GLN:OE1	2.47	0.46
1:a:1062:G:O2'	1:a:1206:U:H5	1.99	0.46
1:a:1182:G:H2'	1:a:1183:A:H8	1.80	0.46
10:j:35:SER:OG	10:j:78:ASN:N	2.39	0.46
17:q:64:SER:HB2	17:q:78:LEU:HD11	1.98	0.46
23:A:1108:G:H2'	23:A:1109:G:C8	2.50	0.46
23:A:1247:U:H2'	23:A:1248:A:H8	1.81	0.46
23:A:2190:G:OP2	23:A:2190:G:H8	1.98	0.46
46:3:13:VAL:HG13	46:3:43:TYR:HD2	1.80	0.46
1:a:1023:A:H2	1:a:1226:U:H1'	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1165:A:C2	1:a:1188:G:C4	3.04	0.46
4:d:55:GLN:O	4:d:59:HIS:HB2	2.16	0.46
9:i:71:GLY:O	9:i:75:GLN:NE2	2.48	0.46
10:j:36:VAL:HG13	10:j:76:ILE:HG13	1.96	0.46
11:k:78:GLY:O	11:k:79:LEU:HD23	2.14	0.46
23:A:1108:G:C2	23:A:1109:G:C5	3.04	0.46
23:A:1401:C:H2'	23:A:1402:G:O4'	2.16	0.46
23:A:2097:C:H2'	23:A:2098:C:H6	1.81	0.46
23:A:2187:G:H2'	23:A:2188:A:H8	1.80	0.46
40:V:23:LYS:HB3	40:V:82:VAL:HG12	1.97	0.46
1:a:421:G:H1'	1:a:436:G:N2	2.31	0.46
5:e:114:ALA:O	5:e:118:LEU:HD23	2.16	0.46
7:g:71:PRO:HG3	7:g:103:TRP:CZ3	2.50	0.46
10:j:80:THR:HG23	10:j:83:THR:H	1.81	0.46
23:A:330:A:H2'	23:A:331:G:H8	1.81	0.46
23:A:2166:G:O2'	23:A:2167:A:OP2	2.29	0.46
23:A:2520:G:H2'	23:A:2521:A:H8	1.80	0.46
23:A:2877:G:H21	23:A:2897:A:H62	1.63	0.46
27:E:74:ARG:O	27:E:75:GLN:NE2	2.48	0.46
29:G:140:HIS:HA	29:G:143:GLU:OE1	2.15	0.46
46:3:72:ASP:O	46:3:76:LYS:HG2	2.15	0.46
1:a:6:A:N3	5:e:98:LYS:NZ	2.64	0.46
1:a:218:U:N3	1:a:220:C:OP2	2.48	0.46
1:a:1414:C:O2'	23:A:1945:A:N1	2.43	0.46
23:A:174:A:H2'	23:A:175:G:H8	1.80	0.46
23:A:288:U:HO2'	23:A:289:U:C5'	2.28	0.46
23:A:329:A:H2'	23:A:330:A:H8	1.77	0.46
23:A:620:G:O2'	23:A:1299:A:OP1	2.34	0.46
23:A:2164:A:H62	23:A:2191:A:HO2'	1.61	0.46
51:8:11:CYS:SG	51:8:13:LYS:NZ	2.89	0.46
1:a:1170:C:H2'	1:a:1171:G:H8	1.81	0.46
3:c:172:VAL:HG12	3:c:174:LEU:HD22	1.98	0.46
7:g:135:VAL:HA	7:g:138:ARG:HG2	1.98	0.46
10:j:8:ILE:HD11	10:j:98:ILE:HG23	1.97	0.46
17:q:62:ARG:HD3	17:q:79:GLU:OE2	2.15	0.46
21:x:72:C:H2'	21:x:73:A:H8	1.81	0.46
23:A:943:A:H2'	23:A:944:C:H5''	1.98	0.46
23:A:1150:C:H2'	23:A:1151:U:C6	2.51	0.46
23:A:1187:U:H5''	30:L:66:THR:HG21	1.97	0.46
23:A:2189:G:H2'	23:A:2190:G:C8	2.51	0.46
23:A:2326:C:H2'	23:A:2327:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2345:U:H4'	28:F:85:ILE:O	2.14	0.46
49:6:22:MET:HE2	49:6:31:LEU:CD1	2.46	0.46
49:6:35:ARG:HG3	49:6:42:LEU:HD21	1.98	0.46
1:a:555:A:O5'	4:d:3:ARG:NH2	2.49	0.46
1:a:578:G:H2'	1:a:579:U:C6	2.51	0.46
1:a:588:C:H2'	1:a:589:G:O4'	2.16	0.46
4:d:141:VAL:O	4:d:141:VAL:HG12	2.16	0.46
10:j:59:LYS:HD3	10:j:62:ARG:HH22	1.81	0.46
12:l:115:LEU:HA	12:l:115:LEU:HD23	1.65	0.46
14:n:26:ARG:HB2	14:n:43:CYS:SG	2.56	0.46
23:A:5:A:H2'	23:A:6:A:C8	2.50	0.46
23:A:684:U:H2'	23:A:685:C:H6	1.81	0.46
23:A:1009:U:H2'	23:A:1010:C:C6	2.51	0.46
23:A:1552:U:H2'	23:A:1553:C:C6	2.51	0.46
23:A:1640:A:H2'	23:A:1641:G:C8	2.51	0.46
23:A:1727:A:C4	23:A:1728:A:C8	3.04	0.46
23:A:1874:U:C2	23:A:1875:G:C8	3.04	0.46
23:A:2052:U:OP2	47:4:6:ARG:NH2	2.45	0.46
23:A:2159:A:N6	23:A:2206:A:N7	2.64	0.46
45:2:57:LYS:HD2	45:2:57:LYS:C	2.41	0.46
1:a:504:G:H21	1:a:505:A:H3'	1.81	0.45
1:a:1251:U:N3	1:a:1252:G:N7	2.64	0.45
3:c:72:PRO:HG3	3:c:104:GLU:HG2	1.99	0.45
5:e:150:ASN:HB2	5:e:153:ASP:OD1	2.16	0.45
23:A:622:A:H2'	23:A:623:C:C6	2.51	0.45
23:A:1103:A:N6	23:A:1133:G:OP2	2.49	0.45
25:C:118:SER:HB2	25:C:129:ALA:HB3	1.98	0.45
26:D:34:VAL:HG22	26:D:96:GLU:HG2	1.98	0.45
29:G:137:ASN:HB2	29:G:139:GLU:OE1	2.15	0.45
43:Z:17:LYS:N	43:Z:25:SER:O	2.45	0.45
1:a:165:G:H2'	1:a:166:G:H8	1.81	0.45
1:a:212:G:H2'	1:a:213:A:H8	1.81	0.45
1:a:964:U:H2'	1:a:965:U:C6	2.51	0.45
5:e:14:GLU:HA	5:e:40:VAL:HA	1.99	0.45
17:q:48:ALA:O	17:q:73:LYS:NZ	2.48	0.45
23:A:156:A:H2'	23:A:157:C:C6	2.51	0.45
23:A:1108:G:C6	23:A:1123:A:N1	2.84	0.45
23:A:1226:G:H2'	23:A:1227:U:C6	2.51	0.45
23:A:1294:U:OP1	23:A:1294:U:H3'	2.16	0.45
23:A:1453:G:H2'	23:A:1454:C:C6	2.52	0.45
23:A:2269:U:H2'	23:A:2270:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:E:148:VAL:HG23	27:E:149:ASP:H	1.81	0.45
30:L:126:TYR:OH	30:L:133:HIS:NE2	2.45	0.45
32:N:58:PHE:CE2	32:N:59:ARG:HG3	2.52	0.45
37:S:95:LEU:HD23	37:S:95:LEU:HA	1.82	0.45
1:a:468:A:H2'	1:a:469:A:C8	2.50	0.45
1:a:468:A:H2'	1:a:469:A:H8	1.80	0.45
1:a:1023:A:C2	1:a:1226:U:H1'	2.51	0.45
1:a:1118:C:OP2	3:c:175:HIS:ND1	2.44	0.45
1:a:1160:A:H2'	1:a:1161:A:C8	2.51	0.45
1:a:1378:G:O3'	9:i:71:GLY:HA3	2.16	0.45
12:l:136:LYS:HA	12:l:136:LYS:HD3	1.72	0.45
21:x:18:G:O2'	21:x:57:G:N1	2.43	0.45
23:A:214:G:H2'	23:A:215:A:O4'	2.17	0.45
23:A:1677:G:H2'	23:A:1678:G:H8	1.81	0.45
23:A:1997:G:O2'	23:A:2000:C:OP2	2.20	0.45
23:A:2176:C:H2'	23:A:2177:G:O4'	2.15	0.45
24:B:30:C:H2'	24:B:31:G:C8	2.51	0.45
30:L:46:THR:HB	30:L:49:ILE:HG22	1.98	0.45
1:a:129:A:HO2'	1:a:130:C:P	2.40	0.45
1:a:581:A:N3	1:a:892:C:O2'	2.47	0.45
1:a:1194:G:H21	14:n:60:SER:CB	2.29	0.45
3:c:70:ALA:HB2	3:c:114:LEU:HD11	1.98	0.45
5:e:116:LEU:HD22	5:e:121:VAL:HG21	1.97	0.45
5:e:163:GLU:HG2	5:e:164:GLU:N	2.31	0.45
23:A:1095:C:C2	23:A:1096:A:C8	3.05	0.45
23:A:1108:G:OP1	23:A:1117:G:H5'	2.16	0.45
24:B:31:G:H2'	24:B:32:U:C6	2.51	0.45
26:D:66:GLN:HA	26:D:69:VAL:HG22	1.99	0.45
28:F:130:LEU:O	28:F:154:VAL:N	2.42	0.45
1:a:146:G:H2'	1:a:147:G:C8	2.52	0.45
1:a:682:G:H2'	1:a:683:A:C8	2.46	0.45
1:a:954:G:C2	1:a:955:A:C8	3.04	0.45
1:a:1146:A:N7	1:a:1148:U:H1'	2.32	0.45
1:a:1354:G:O2'	1:a:1380:G:O6	2.32	0.45
21:x:22:G:H2'	21:x:23:A:C8	2.51	0.45
21:x:40:C:H2'	21:x:41:C:C6	2.52	0.45
23:A:305:C:H2'	23:A:306:A:C8	2.50	0.45
23:A:1827:U:H2'	23:A:1828:C:C6	2.52	0.45
23:A:2163:G:O2'	23:A:2167:A:O4'	2.33	0.45
23:A:2340:G:H8	23:A:2340:G:OP1	2.00	0.45
23:A:2517:G:H1'	33:O:124:LYS:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2731:U:H2'	23:A:2732:U:C6	2.51	0.45
24:B:48:G:OP2	35:Q:69:LYS:HB2	2.15	0.45
9:i:21:LEU:HD22	9:i:63:VAL:HG12	1.97	0.45
9:i:52:LEU:CD1	9:i:58:LEU:HD13	2.46	0.45
17:q:22:THR:OG1	17:q:48:ALA:O	2.30	0.45
20:t:57:LEU:HD23	20:t:57:LEU:HA	1.80	0.45
23:A:137:U:N3	23:A:143:G:C6	2.85	0.45
23:A:410:G:H4'	23:A:411:A:H2	1.81	0.45
23:A:464:U:H2'	23:A:465:C:C6	2.52	0.45
23:A:2241:G:H2'	23:A:2242:C:C6	2.51	0.45
23:A:2259:C:C2	23:A:2260:A:C8	3.05	0.45
25:C:21:PHE:HB3	25:C:24:ILE:HG12	1.99	0.45
29:G:46:GLU:OE1	29:G:50:ILE:HG13	2.17	0.45
1:a:428:U:O2'	1:a:431:G:O6	2.30	0.45
1:a:1024:G:H1'	1:a:1225:C:O2'	2.16	0.45
18:r:17:PHE:CE1	18:r:25:ILE:HD11	2.50	0.45
23:A:139:A:C2	23:A:1453:G:H1'	2.46	0.45
23:A:272:A:OP2	23:A:296:G:N1	2.46	0.45
23:A:869:A:H2'	23:A:870:G:H8	1.82	0.45
23:A:1892:A:H2'	23:A:1893:G:O4'	2.17	0.45
23:A:1943:G:C6	23:A:1954:G:C6	3.04	0.45
23:A:2715:G:C2	23:A:2716:C:C6	3.05	0.45
27:E:131:PHE:O	27:E:162:ASN:ND2	2.33	0.45
1:a:509:C:H2'	1:a:510:C:C6	2.52	0.45
1:a:691:G:N2	11:k:40:ASN:HA	2.32	0.45
1:a:993:C:N4	1:a:1229:G:N2	2.64	0.45
1:a:1021:G:O6	1:a:1027:A:N6	2.50	0.45
3:c:18:TRP:CD1	14:n:54:PRO:HA	2.52	0.45
15:o:12:ILE:HD11	15:o:22:THR:HG22	1.99	0.45
23:A:24:G:H2'	23:A:25:U:C6	2.51	0.45
23:A:95:A:H4'	44:l:38:GLU:O	2.17	0.45
23:A:164:A:H2'	23:A:165:C:C6	2.51	0.45
23:A:1141:A:O2'	23:A:1142:A:O5'	2.30	0.45
23:A:1466:C:H2'	23:A:1467:C:H6	1.82	0.45
23:A:1531:U:N3	23:A:1561:G:C6	2.85	0.45
23:A:2215:G:H2'	23:A:2216:C:C6	2.51	0.45
28:F:34:ILE:HG13	28:F:155:VAL:O	2.17	0.45
1:a:329:A:H2'	1:a:330:C:C6	2.52	0.45
1:a:1053:A:N7	1:a:1054:C:H1'	2.31	0.45
3:c:183:TYR:CD1	3:c:200:TRP:HB3	2.48	0.45
11:k:34:ILE:HG22	11:k:43:ALA:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:B:58:C:H2'	24:B:59:U:C6	2.51	0.45
28:F:107:SER:OG	28:F:137:ILE:HG22	2.17	0.45
39:U:23:ARG:NH1	39:U:81:VAL:O	2.50	0.45
1:a:68:G:C5'	1:a:96:G:H1'	2.47	0.45
1:a:216:G:H2'	1:a:217:U:O4'	2.17	0.45
1:a:456:A:C8	1:a:457:A:C8	3.05	0.45
1:a:902:C:C2	1:a:903:G:C8	3.05	0.45
2:b:120:MET:HA	2:b:124:GLY:HA3	1.99	0.45
5:e:76:PRO:HG2	5:e:148:LEU:HG	1.98	0.45
23:A:1621:A:H2'	23:A:1622:A:C8	2.52	0.45
23:A:1851:U:O2'	25:C:154:LEU:O	2.35	0.45
23:A:2201:G:H2'	23:A:2203:G:OP2	2.16	0.45
23:A:2378:G:N3	23:A:2414:C:H2'	2.31	0.45
23:A:2699:C:N4	29:G:108:GLY:O	2.46	0.45
23:A:2768:G:C2	23:A:2769:G:C8	3.05	0.45
23:A:2860:G:OP1	26:D:57:ARG:NH2	2.50	0.45
25:C:130:LEU:HB2	25:C:135:ILE:HD11	1.99	0.45
28:F:34:ILE:CG2	28:F:91:LEU:HB2	2.47	0.45
38:T:50:VAL:HG13	38:T:50:VAL:O	2.16	0.45
1:a:69:A:H8	1:a:97:U:OP2	1.99	0.44
1:a:97:U:H3'	1:a:97:U:OP2	2.18	0.44
1:a:205:C:H2'	1:a:206:U:C6	2.52	0.44
1:a:849:U:H2'	1:a:850:U:O4'	2.17	0.44
1:a:1009:U:O2	1:a:1050:G:C2	2.71	0.44
1:a:1051:U:H2'	1:a:1052:G:C8	2.51	0.44
1:a:1334:A:H2'	1:a:1335:C:C6	2.52	0.44
1:a:1544:C:H2'	1:a:1545:U:C6	2.45	0.44
3:c:52:SER:OG	3:c:53:ARG:N	2.50	0.44
16:p:17:PHE:CE1	16:p:41:ASN:HB2	2.52	0.44
23:A:2140:C:H2'	23:A:2141:U:H6	1.82	0.44
23:A:2163:G:C2	23:A:2192:G:C6	3.05	0.44
23:A:2304:G:H5'	42:Y:28:ARG:HD3	1.98	0.44
23:A:2926:U:H2'	23:A:2927:A:C8	2.52	0.44
40:V:19:ILE:HG13	40:V:24:LYS:HB2	1.98	0.44
43:Z:5:CYS:HB3	43:Z:8:THR:O	2.17	0.44
1:a:21:G:H2'	1:a:22:G:C8	2.53	0.44
1:a:655:A:H2'	1:a:656:A:H8	1.83	0.44
1:a:1064:A:N3	3:c:155:ARG:NH1	2.65	0.44
1:a:1118:C:C2	1:a:1119:A:C8	3.04	0.44
4:d:69:LYS:HE3	4:d:198:TYR:CE1	2.52	0.44
13:m:44:ARG:HD3	13:m:46:ARG:NH2	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:52:GLU:HA	13:m:55:LYS:HB2	1.98	0.44
23:A:193:A:H2'	23:A:194:C:H6	1.82	0.44
23:A:1169:C:H2'	23:A:1170:C:C6	2.52	0.44
23:A:1276:U:N3	23:A:1277:G:N7	2.66	0.44
23:A:1551:U:H2'	23:A:1552:U:H6	1.82	0.44
23:A:1770:C:H2'	23:A:1771:A:C8	2.52	0.44
23:A:2190:G:HO2'	23:A:2191:A:H8	1.60	0.44
23:A:2353:A:N3	23:A:2353:A:H2'	2.32	0.44
23:A:2879:A:N7	23:A:2897:A:O2'	2.48	0.44
1:a:152:C:N3	1:a:168:C:N4	2.62	0.44
1:a:271:A:H2'	1:a:272:U:C6	2.52	0.44
1:a:1384:A:OP2	7:g:9:LYS:NZ	2.49	0.44
8:h:64:LEU:HD22	8:h:66:TYR:CZ	2.52	0.44
9:i:35:TRP:HH2	9:i:49:LYS:HZ1	1.64	0.44
9:i:52:LEU:HD13	9:i:58:LEU:HA	1.98	0.44
21:x:26:A:N6	21:x:45:U:H5	2.13	0.44
23:A:292:U:C2	23:A:293:G:C8	3.06	0.44
23:A:977:U:H2'	23:A:978:A:C8	2.52	0.44
23:A:1533:A:O2'	23:A:1534:G:OP1	2.30	0.44
23:A:1602:C:OP1	23:A:1768:U:O2'	2.31	0.44
23:A:2348:U:H2'	23:A:2349:U:C6	2.52	0.44
23:A:2624:C:H2'	23:A:2625:G:H8	1.81	0.44
23:A:2635:A:H2'	23:A:2635:A:N3	2.32	0.44
24:B:53:U:H1'	28:F:26:MET:HE1	1.99	0.44
26:D:146:MET:O	26:D:154:VAL:HG23	2.18	0.44
1:a:559:U:C2	1:a:560:U:C5	3.06	0.44
2:b:15:HIS:HA	2:b:43:LEU:HD11	1.99	0.44
23:A:136:U:H2'	23:A:137:U:C6	2.53	0.44
23:A:1129:G:N2	23:A:1131:A:O5'	2.50	0.44
23:A:2883:G:C6	23:A:2893:A:C6	3.06	0.44
29:G:60:ASN:OD1	29:G:61:HIS:N	2.50	0.44
33:O:17:MET:HE2	33:O:39:ALA:HB1	1.98	0.44
38:T:1:MET:HE2	38:T:1:MET:HB3	1.82	0.44
1:a:9:G:OP2	5:e:127:LYS:NZ	2.29	0.44
1:a:1230:C:P	19:s:78:ARG:HH21	2.40	0.44
1:a:1521:A:H2'	1:a:1522:U:C6	2.52	0.44
6:f:40:GLU:OE1	6:f:40:GLU:N	2.50	0.44
17:q:61:VAL:HG12	17:q:80:VAL:HA	1.99	0.44
23:A:658:A:N6	27:E:46:GLN:OE1	2.51	0.44
23:A:1103:A:OP2	23:A:1135:G:N2	2.38	0.44
23:A:1535:A:H2'	23:A:1536:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1763:U:H2'	23:A:1777:G:H22	1.82	0.44
23:A:2135:U:H2'	23:A:2136:A:C8	2.51	0.44
23:A:2168:G:H3'	23:A:2169:A:H8	1.82	0.44
23:A:2540:C:C2	23:A:2616:G:N2	2.86	0.44
23:A:2682:U:H2'	23:A:2683:C:H6	1.82	0.44
38:T:36:ASP:OD1	38:T:36:ASP:N	2.50	0.44
49:6:3:ARG:HD3	49:6:3:ARG:HA	1.67	0.44
1:a:1500:A:O2'	1:a:1501:A:O4'	2.30	0.44
4:d:94:LEU:HD22	4:d:131:TYR:HB3	2.00	0.44
9:i:50:GLN:N	9:i:51:PRO:HD2	2.33	0.44
12:l:25:ASN:O	12:l:26:LYS:HD3	2.18	0.44
23:A:27:G:O2'	23:A:28:A:H8	2.00	0.44
23:A:81:G:C2	23:A:105:C:C2	3.05	0.44
23:A:91:C:H2'	23:A:92:G:O4'	2.18	0.44
23:A:1191:C:H2'	23:A:1192:A:H8	1.83	0.44
23:A:1833:C:H5'	25:C:146:MET:HE1	1.99	0.44
23:A:2337:G:N2	28:F:153:ASP:OD1	2.51	0.44
24:B:25:A:H2'	24:B:26:C:O4'	2.18	0.44
37:S:50:ARG:O	37:S:54:LYS:NZ	2.51	0.44
1:a:267:G:H2'	1:a:268:G:H8	1.82	0.44
1:a:467:U:H2'	1:a:468:A:H8	1.81	0.44
9:i:44:LEU:H	9:i:44:LEU:HD23	1.83	0.44
14:n:61:TRP:HA	14:n:61:TRP:CE3	2.51	0.44
21:x:8:4SU:S4	21:x:14:A:N7	2.91	0.44
21:x:9:A:H4'	21:x:46:7MG:H5''	1.99	0.44
23:A:5:A:H2'	23:A:6:A:H8	1.83	0.44
23:A:130:A:H2'	23:A:131:C:H6	1.81	0.44
23:A:525:A:H1'	23:A:526:A:H5''	2.00	0.44
23:A:731:A:H5'	23:A:820:A:N6	2.33	0.44
23:A:1110:C:N4	23:A:1121:C:H42	2.15	0.44
23:A:1193:U:C2	23:A:1194:A:C8	3.05	0.44
23:A:1576:G:H2'	23:A:1577:G:H8	1.81	0.44
23:A:2098:C:H2'	23:A:2099:C:H6	1.82	0.44
23:A:2104:A:H2'	23:A:2105:G:H8	1.82	0.44
23:A:2182:C:C2	23:A:2183:A:N7	2.86	0.44
23:A:2736:C:H2'	23:A:2737:C:H6	1.82	0.44
24:B:11:A:O2'	24:B:13:G:OP2	2.34	0.44
24:B:37:A:H8	24:B:37:A:OP2	2.01	0.44
25:C:9:THR:HG22	25:C:10:THR:HG23	2.00	0.44
27:E:121:GLU:HA	27:E:121:GLU:OE2	2.18	0.44
31:M:8:MET:HE3	31:M:84:CYS:SG	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:O:43:THR:HG22	33:O:46:GLN:OE1	2.18	0.44
41:W:79:THR:HG22	41:W:96:LYS:HD3	1.99	0.44
46:3:12:VAL:HA	46:3:43:TYR:HB3	2.00	0.44
1:a:121:C:OP1	1:a:319:C:O2'	2.36	0.44
1:a:469:A:H2'	1:a:470:G:H8	1.83	0.44
1:a:560:U:C2	1:a:561:G:C8	3.06	0.44
1:a:1008:C:H1'	1:a:1052:G:N2	2.33	0.44
1:a:1148:U:C2	1:a:1149:U:C5	3.06	0.44
1:a:1246:A:H62	1:a:1306:A:N6	2.14	0.44
1:a:1306:A:H2'	1:a:1306:A:N3	2.32	0.44
3:c:85:ALA:O	3:c:89:ASN:N	2.44	0.44
3:c:151:GLN:CB	3:c:166:HIS:HB3	2.45	0.44
16:p:17:PHE:HD1	16:p:41:ASN:HD22	1.66	0.44
23:A:78:U:H2'	23:A:79:U:C6	2.52	0.44
23:A:137:U:C2	23:A:143:G:N1	2.85	0.44
23:A:200:C:H5'	23:A:2277:U:OP1	2.18	0.44
23:A:899:C:H2'	23:A:900:A:H8	1.83	0.44
23:A:1035:G:OP1	45:2:31:THR:OG1	2.29	0.44
23:A:1137:G:H2'	23:A:1138:C:C6	2.53	0.44
23:A:1634:A:H5'	23:A:1635:A:OP1	2.18	0.44
23:A:1956:U:H2'	23:A:1957:C:C6	2.52	0.44
23:A:2139:G:H2'	23:A:2140:C:H6	1.82	0.44
23:A:2275:G:H2'	23:A:2276:U:O4'	2.18	0.44
40:V:39:LYS:O	40:V:43:GLU:HG3	2.18	0.44
42:Y:46:TYR:CE1	42:Y:48:GLN:HB3	2.52	0.44
1:a:991:U:H5'	1:a:992:A:C8	2.53	0.44
1:a:1225:C:H2'	1:a:1226:U:H6	1.79	0.44
1:a:1269:A:N6	1:a:1280:G:H1'	2.33	0.44
15:o:82:ILE:O	15:o:86:GLY:N	2.49	0.44
23:A:1105:G:H3'	23:A:1106:U:H2'	2.00	0.44
23:A:1956:U:H2'	23:A:1957:C:C5	2.53	0.44
23:A:2255:G:H2'	23:A:2256:A:C8	2.52	0.44
23:A:2320:A:N7	23:A:2322:G:C8	2.85	0.44
23:A:2587:U:H2'	23:A:2588:U:C6	2.53	0.44
23:A:2883:G:H2'	23:A:2884:U:H6	1.83	0.44
38:T:18:GLN:O	38:T:96:THR:HA	2.18	0.44
38:T:57:THR:OG1	38:T:101:ASN:OD1	2.31	0.44
1:a:122:G:C4	1:a:246:G:N2	2.86	0.43
1:a:547:A:C2	1:a:548:G:C5	3.06	0.43
1:a:561:G:H2'	1:a:562:U:H6	1.83	0.43
1:a:781:G:C6	1:a:815:A:N6	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1049:A:N1	1:a:1050:G:C6	2.86	0.43
1:a:1230:C:H5''	1:a:1231:U:H5''	2.00	0.43
1:a:1339:A:C2	1:a:1340:A:C4	3.06	0.43
16:p:17:PHE:HE1	16:p:41:ASN:HB2	1.82	0.43
21:x:54:5MU:C4	21:x:58:A:N7	2.85	0.43
23:A:612:U:O2'	23:A:1029:A:N1	2.50	0.43
23:A:2142:U:H2'	23:A:2143:G:C8	2.53	0.43
23:A:2226:A:H2'	23:A:2227:U:C6	2.52	0.43
23:A:2869:U:H2'	23:A:2870:U:C6	2.53	0.43
26:D:106:ASP:O	26:D:176:ILE:HG22	2.18	0.43
28:F:61:THR:HG21	28:F:89:VAL:HG11	2.00	0.43
50:7:25:ARG:NH2	50:7:45:ARG:O	2.51	0.43
1:a:446:G:N2	1:a:504:G:N7	2.62	0.43
6:f:13:PRO:HD2	6:f:56:TYR:CD2	2.53	0.43
11:k:33:MET:SD	11:k:44:TRP:HB3	2.58	0.43
12:l:80:ILE:HG13	12:l:110:ILE:HD12	1.99	0.43
23:A:579:U:H2'	23:A:580:U:H6	1.81	0.43
23:A:1094:A:H1'	23:A:1158:G:N2	2.32	0.43
23:A:1162:C:H2'	23:A:1163:C:C6	2.53	0.43
23:A:1205:U:C2	23:A:1206:G:C8	3.06	0.43
23:A:1453:G:O6	23:A:1642:U:O4	2.36	0.43
23:A:1555:U:H2'	23:A:1556:G:H5''	2.00	0.43
23:A:1760:U:H3'	23:A:1761:A:H8	1.83	0.43
39:U:24:ILE:HG13	47:4:22:LEU:HD22	2.00	0.43
1:a:112:U:O2'	1:a:113:G:H5'	2.18	0.43
1:a:745:C:C2	1:a:746:U:C5	3.06	0.43
1:a:1160:A:OP1	10:j:72:ARG:NH1	2.50	0.43
1:a:1381:A:N6	1:a:1382:A:N6	2.66	0.43
3:c:86:LEU:HA	3:c:89:ASN:HB3	1.99	0.43
4:d:191:GLU:HA	4:d:194:ILE:HD13	2.01	0.43
5:e:81:THR:HG23	5:e:123:ASP:O	2.18	0.43
5:e:132:ASN:HA	5:e:137:MET:HE3	1.98	0.43
7:g:42:ILE:HD12	7:g:116:MET:HE3	2.00	0.43
13:m:49:THR:C	13:m:51:GLU:H	2.25	0.43
19:s:80:TYR:OH	19:s:83:HIS:HB2	2.18	0.43
23:A:294:G:H2'	23:A:295:G:H8	1.83	0.43
23:A:947:A:H2'	23:A:948:A:O4'	2.18	0.43
23:A:1245:U:H1'	37:S:4:VAL:HG22	1.99	0.43
23:A:1601:C:H2'	23:A:1602:C:H6	1.83	0.43
23:A:2111:C:H2'	23:A:2112:U:C6	2.52	0.43
23:A:2662:A:C6	23:A:2923:A:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:F:51:ASP:O	28:F:55:GLU:OE1	2.35	0.43
30:L:63:ILE:HG13	30:L:102:LEU:HD21	1.99	0.43
31:M:104:ARG:NH1	36:R:41:GLN:HE22	2.16	0.43
39:U:14:THR:H	39:U:107:HIS:CD2	2.36	0.43
1:a:72:G:N2	1:a:94:A:C4	2.86	0.43
1:a:892:C:O2'	1:a:893:U:H5'	2.18	0.43
1:a:993:C:H42	1:a:1229:G:H22	1.65	0.43
17:q:11:THR:HG22	17:q:62:ARG:HG2	2.00	0.43
23:A:365:A:OP2	27:E:169:ASN:HB2	2.17	0.43
23:A:899:C:H2'	23:A:900:A:C8	2.54	0.43
23:A:925:A:H3'	23:A:926:G:H8	1.84	0.43
23:A:1094:A:N7	23:A:1157:A:C6	2.87	0.43
23:A:1137:G:H2'	23:A:1138:C:H6	1.83	0.43
23:A:1880:A:H2	23:A:1881:A:H62	1.65	0.43
23:A:2152:A:N6	23:A:2203:G:N7	2.67	0.43
23:A:2302:G:C4	23:A:2303:A:C8	3.06	0.43
31:M:38:VAL:HG22	31:M:61:VAL:HG22	2.01	0.43
43:Z:54:LEU:HD23	43:Z:54:LEU:O	2.18	0.43
1:a:108:C:O2'	16:p:26:ARG:O	2.36	0.43
1:a:133:G:H2'	1:a:134:C:O4'	2.19	0.43
1:a:205:C:H2'	1:a:206:U:H6	1.84	0.43
1:a:329:A:H2'	1:a:330:C:H6	1.84	0.43
1:a:1012:G:H2'	1:a:1012:G:N3	2.33	0.43
1:a:1030:G:C6	1:a:1031:C:N4	2.87	0.43
1:a:1069:U:H2'	1:a:1070:G:H8	1.84	0.43
1:a:1175:C:O2'	1:a:1176:A:O5'	2.37	0.43
1:a:1257:A:C6	1:a:1294:A:C5	3.06	0.43
12:l:10:LYS:HA	12:l:11:PRO:HD3	1.89	0.43
18:r:69:MET:HE3	18:r:69:MET:HB3	1.94	0.43
23:A:10:A:N6	23:A:2662:A:C5	2.86	0.43
23:A:294:G:H2'	23:A:295:G:C8	2.54	0.43
23:A:769:C:H2'	23:A:770:U:H6	1.83	0.43
23:A:1111:U:O4	23:A:1120:G:O6	2.37	0.43
23:A:1339:C:C2	23:A:1340:A:C8	3.07	0.43
25:C:44:ASN:N	25:C:48:LYS:O	2.45	0.43
26:D:12:MET:HE3	26:D:12:MET:HB2	1.76	0.43
27:E:182:SER:HB2	27:E:185:GLU:HG2	2.00	0.43
28:F:125:ARG:NH1	28:F:158:THR:O	2.52	0.43
29:G:72:LEU:HD13	29:G:75:MET:HE3	2.00	0.43
29:G:137:ASN:ND2	29:G:140:HIS:HD2	2.17	0.43
35:Q:94:PHE:CZ	35:Q:109:ALA:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:l:13:GLU:H	44:l:13:GLU:CD	2.27	0.43
1:a:271:A:H2'	1:a:272:U:C5	2.54	0.43
1:a:1278:G:C6	1:a:1279:U:C4	3.07	0.43
12:l:87:LEU:HD11	12:l:117:THR:HG22	2.00	0.43
23:A:81:G:C6	23:A:82:G:C2	3.06	0.43
23:A:629:A:H5'	27:E:89:VAL:HG21	2.01	0.43
23:A:1476:G:C6	23:A:1477:A:C6	3.06	0.43
23:A:1532:G:O2'	23:A:1533:A:H5''	2.18	0.43
23:A:2516:C:N3	33:O:124:LYS:HE3	2.32	0.43
23:A:2694:G:H2'	23:A:2695:A:O4'	2.19	0.43
28:F:173:LEU:O	28:F:175:MET:HE2	2.18	0.43
38:T:45:SER:OG	38:T:46:ALA:N	2.52	0.43
47:4:42:VAL:HG22	47:4:49:TYR:HB2	2.00	0.43
1:a:601:U:N3	1:a:602:U:C4	2.86	0.43
1:a:1020:U:H2'	1:a:1021:G:C8	2.54	0.43
3:c:150:THR:HG22	3:c:199:VAL:HG13	2.00	0.43
6:f:6:GLU:HB3	6:f:93:ILE:CG2	2.49	0.43
9:i:44:LEU:O	9:i:47:VAL:HG12	2.19	0.43
13:m:107:ARG:HD2	13:m:113:SER:HB2	2.01	0.43
23:A:941:U:H2'	23:A:942:U:C6	2.54	0.43
23:A:977:U:H2'	23:A:978:A:H8	1.84	0.43
23:A:1763:U:N3	23:A:1778:A:N6	2.36	0.43
23:A:2104:A:H2'	23:A:2105:G:C8	2.53	0.43
23:A:2325:U:H2'	23:A:2326:C:C6	2.53	0.43
23:A:2374:G:H2'	23:A:2375:C:C6	2.54	0.43
23:A:2547:U:H2'	23:A:2548:C:C6	2.54	0.43
23:A:2930:C:O5'	23:A:2930:C:H6	2.02	0.43
25:C:142:HIS:ND1	25:C:193:GLY:O	2.51	0.43
25:C:216:LYS:HE3	25:C:216:LYS:HB2	1.61	0.43
28:F:20:PHE:HE2	28:F:168:GLU:OE1	2.02	0.43
28:F:31:ILE:HD13	28:F:158:THR:HG22	2.00	0.43
30:L:142:GLU:OE1	30:L:142:GLU:N	2.51	0.43
1:a:691:G:H21	11:k:40:ASN:ND2	2.17	0.43
1:a:860:U:H2'	1:a:861:A:C8	2.53	0.43
1:a:1061:U:O2'	1:a:1064:A:OP2	2.36	0.43
6:f:4:LYS:HD2	6:f:4:LYS:HA	1.74	0.43
8:h:108:THR:OG1	8:h:109:SER:N	2.51	0.43
23:A:2:G:H2'	23:A:3:U:H6	1.83	0.43
23:A:27:G:HO2'	23:A:28:A:P	2.41	0.43
23:A:1169:C:H2'	23:A:1170:C:H6	1.83	0.43
23:A:1497:G:C4	23:A:1515:G:N2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2146:C:H2'	23:A:2147:A:O4'	2.19	0.43
23:A:2719:G:H2'	23:A:2720:U:C6	2.54	0.43
27:E:192:LEU:HD12	27:E:192:LEU:HA	1.85	0.43
38:T:28:GLU:N	38:T:31:ASP:OD1	2.52	0.43
1:a:415:U:H2'	1:a:416:A:H8	1.83	0.43
1:a:546:U:OP1	12:l:124:GLY:N	2.49	0.43
1:a:959:U:H2'	1:a:960:G:C8	2.53	0.43
12:l:5:ASN:HA	12:l:8:VAL:HG12	2.00	0.43
21:x:26:A:N6	21:x:45:U:C5	2.87	0.43
23:A:1663:A:C6	39:U:92:PRO:HB3	2.53	0.43
23:A:2158:G:N1	23:A:2205:U:OP1	2.52	0.43
25:C:33:LEU:HB3	25:C:64:VAL:HG12	1.99	0.43
26:D:13:THR:HG21	36:R:5:ILE:CG2	2.49	0.43
40:V:55:VAL:HG21	40:V:76:ARG:HH21	1.84	0.43
1:a:726:A:C8	11:k:118:HIS:CG	3.07	0.43
1:a:1056:G:OP1	14:n:4:LYS:NZ	2.50	0.43
1:a:1334:A:H2'	1:a:1335:C:H6	1.84	0.43
1:a:1431:U:H2'	1:a:1432:A:C8	2.54	0.43
7:g:18:TYR:O	7:g:20:SER:N	2.52	0.43
23:A:1035:G:OP2	45:2:11:SER:OG	2.33	0.43
33:O:57:TYR:CE2	33:O:116:GLU:HB2	2.54	0.43
1:a:1147:G:H4'	1:a:1148:U:O5'	2.19	0.42
1:a:1412:G:H2'	1:a:1413:U:H6	1.84	0.42
5:e:96:LEU:HD23	5:e:129:LEU:HD11	2.00	0.42
21:x:64:A:H2'	21:x:65:G:C8	2.49	0.42
23:A:339:U:H2'	23:A:340:G:O4'	2.18	0.42
23:A:475:A:H2'	23:A:476:A:C8	2.54	0.42
23:A:674:C:O2	23:A:684:U:O2'	2.36	0.42
23:A:1513:G:H2'	23:A:1514:C:C6	2.54	0.42
32:N:55:LEU:HA	32:N:55:LEU:HD12	1.81	0.42
32:N:116:ASN:OD1	32:N:117:ILE:N	2.52	0.42
41:W:23:VAL:HG12	41:W:35:ILE:HG12	2.00	0.42
44:1:53:MET:O	44:1:57:VAL:HG23	2.18	0.42
51:8:16:VAL:HG22	51:8:25:VAL:HG12	2.00	0.42
1:a:221:G:H21	1:a:221:G:P	2.41	0.42
1:a:262:G:C6	1:a:281:A:C6	3.06	0.42
1:a:382:A:C6	1:a:383:U:C4	3.07	0.42
1:a:916:A:H2'	1:a:917:A:O4'	2.18	0.42
1:a:1014:C:O2'	1:a:1047:A:O2'	2.11	0.42
10:j:8:ILE:O	10:j:73:LEU:HD12	2.19	0.42
15:o:19:ASP:OD1	15:o:20:THR:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1090:U:O2'	23:A:1091:U:H5''	2.19	0.42
23:A:1834:A:OP2	25:C:150:LYS:NZ	2.52	0.42
23:A:1902:U:O2'	23:A:1905:G:O6	2.34	0.42
23:A:2623:A:H2'	23:A:2624:C:C6	2.52	0.42
30:L:60:ALA:HB3	30:L:127:GLY:HA2	2.01	0.42
39:U:15:VAL:HG11	39:U:51:ILE:HG21	2.01	0.42
44:1:11:THR:HB	44:1:60:ARG:HH11	1.83	0.42
1:a:847:G:H2'	1:a:848:G:C8	2.54	0.42
23:A:345:G:H2'	23:A:346:G:H8	1.84	0.42
23:A:1172:A:H4'	23:A:1173:A:C5'	2.49	0.42
23:A:1578:G:H1	23:A:1595:G:H2'	1.84	0.42
23:A:1627:C:H2'	23:A:1628:U:C6	2.54	0.42
23:A:2198:G:H2'	23:A:2199:G:H8	1.80	0.42
29:G:58:ASN:C	29:G:62:ARG:HE	2.27	0.42
46:3:71:VAL:O	46:3:75:ASN:ND2	2.53	0.42
1:a:222:G:H2'	1:a:223:C:H6	1.82	0.42
1:a:363:C:C4	1:a:364:A:N7	2.88	0.42
1:a:521:A:H2'	1:a:522:C:H6	1.85	0.42
1:a:712:A:N3	1:a:712:A:H2'	2.34	0.42
1:a:1307:G:C2	1:a:1341:G:C6	3.07	0.42
1:a:1418:C:H2'	1:a:1419:C:C6	2.55	0.42
1:a:1420:A:N1	1:a:1495:G:O6	2.53	0.42
1:a:1467:C:H2'	1:a:1468:A:H8	1.85	0.42
5:e:164:GLU:N	5:e:164:GLU:OE1	2.42	0.42
23:A:301:A:H2'	23:A:302:G:C8	2.55	0.42
23:A:348:C:H2'	23:A:349:U:C6	2.55	0.42
23:A:1277:G:N3	23:A:1278:G:C8	2.88	0.42
38:T:50:VAL:HA	38:T:51:PRO:HA	1.84	0.42
1:a:568:U:H4'	1:a:569:U:H5''	2.01	0.42
1:a:836:A:H62	1:a:867:G:N2	2.16	0.42
1:a:1233:C:H4'	1:a:1234:A:OP1	2.20	0.42
3:c:6:HIS:CE1	3:c:8:ILE:HB	2.54	0.42
10:j:80:THR:HG23	10:j:83:THR:N	2.35	0.42
23:A:196:G:H2'	23:A:197:A:O4'	2.20	0.42
23:A:1249:A:N3	32:N:4:HIS:HB3	2.35	0.42
23:A:1332:U:H5	23:A:1370:U:H3	1.67	0.42
23:A:1397:A:H2'	23:A:1398:A:H8	1.84	0.42
23:A:1544:A:H2'	23:A:1545:A:C8	2.54	0.42
23:A:2304:G:OP1	42:Y:26:SER:HB3	2.19	0.42
23:A:2810:G:OP2	23:A:2814:A:O2'	2.28	0.42
23:A:2851:G:O2'	23:A:2853:U:OP2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2867:G:C4	23:A:2868:G:C8	3.08	0.42
26:D:53:PHE:HB3	26:D:79:PHE:HB2	2.01	0.42
34:P:110:GLN:O	34:P:113:TYR:OH	2.34	0.42
3:c:88:LYS:HA	3:c:91:ASN:HD22	1.84	0.42
21:x:50:U:N3	21:x:65:G:C6	2.88	0.42
23:A:30:G:H2'	23:A:31:C:H6	1.85	0.42
23:A:995:U:N3	23:A:996:G:N7	2.68	0.42
23:A:1225:G:H2'	23:A:1226:G:H8	1.84	0.42
23:A:2276:U:H2'	23:A:2277:U:C6	2.55	0.42
23:A:2587:U:H2'	23:A:2588:U:H6	1.85	0.42
28:F:101:ASP:HA	28:F:104:VAL:HG22	2.00	0.42
45:2:5:GLU:HB3	45:2:57:LYS:HE3	2.00	0.42
47:4:24:LEU:HD12	47:4:25:PRO:HD2	2.02	0.42
1:a:692:U:O2'	11:k:41:ALA:O	2.35	0.42
1:a:991:U:H4'	1:a:992:A:O5'	2.19	0.42
1:a:1020:U:H2'	1:a:1021:G:H8	1.84	0.42
5:e:83:PRO:HD2	5:e:148:LEU:HG	2.01	0.42
7:g:51:ALA:HB2	7:g:58:PRO:HG3	2.02	0.42
23:A:445:G:H2'	23:A:446:G:O4'	2.19	0.42
23:A:566:U:H2'	23:A:567:G:C8	2.55	0.42
23:A:1453:G:H2'	23:A:1454:C:H6	1.84	0.42
23:A:1518:C:H2'	23:A:1573:A:N6	2.35	0.42
23:A:1896:C:H2'	23:A:1897:U:H6	1.84	0.42
23:A:2149:G:H5''	23:A:2150:A:C8	2.54	0.42
32:N:82:LEU:HD23	32:N:82:LEU:HA	1.83	0.42
46:3:13:VAL:O	46:3:45:LEU:HA	2.19	0.42
1:a:856:C:H2'	1:a:857:C:H6	1.85	0.42
1:a:1417:A:H2'	1:a:1418:C:C6	2.55	0.42
1:a:1421:C:H2'	1:a:1422:G:H8	1.85	0.42
13:m:19:LEU:HD11	13:m:34:LEU:HD21	2.02	0.42
15:o:12:ILE:HG12	15:o:16:ARG:HD3	2.01	0.42
21:x:54:5MU:H2'	21:x:55:PSU:O4'	2.20	0.42
23:A:632:U:H2'	23:A:633:A:C8	2.52	0.42
23:A:2028:U:O2	31:M:3:GLN:NE2	2.53	0.42
23:A:2213:U:N3	23:A:2214:G:N7	2.68	0.42
23:A:2520:G:H2'	23:A:2521:A:C8	2.55	0.42
23:A:2659:C:H2'	23:A:2660:G:H8	1.85	0.42
29:G:172:LYS:HG2	29:G:173:GLU:H	1.84	0.42
1:a:221:G:C5	1:a:222:G:H1'	2.55	0.42
1:a:272:U:H2'	1:a:273:G:O4'	2.19	0.42
1:a:1165:A:H62	1:a:1187:A:H62	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1472:G:H2'	1:a:1473:C:H6	1.85	0.42
3:c:52:SER:HA	3:c:113:LYS:HG2	2.01	0.42
5:e:165:LEU:C	5:e:166:LEU:HD22	2.44	0.42
12:l:7:LEU:HA	12:l:7:LEU:HD12	1.84	0.42
19:s:9:PRO:HG2	19:s:41:PHE:CE1	2.54	0.42
23:A:65:A:H2'	23:A:66:C:H6	1.84	0.42
23:A:390:A:H2'	23:A:391:U:H6	1.85	0.42
23:A:412:U:H2'	23:A:413:C:H6	1.85	0.42
28:F:93:GLY:N	28:F:96:MET:SD	2.92	0.42
33:O:54:MET:HG3	33:O:121:ALA:HB2	2.01	0.42
35:Q:24:GLY:HA3	35:Q:47:ASP:H	1.84	0.42
42:Y:48:GLN:NE2	42:Y:65:ASP:HB3	2.34	0.42
1:a:184:G:H2'	1:a:185:A:C8	2.53	0.42
1:a:481:U:H2'	1:a:482:G:H8	1.84	0.42
1:a:610:A:C6	1:a:611:U:C4	3.07	0.42
1:a:1325:A:H1'	19:s:37:ARG:NH1	2.35	0.42
7:g:65:ALA:HB2	7:g:128:ALA:HB2	2.01	0.42
16:p:52:ASP:C	16:p:54:GLU:H	2.27	0.42
23:A:412:U:H2'	23:A:413:C:C6	2.55	0.42
23:A:1891:G:H1'	23:A:1917:A:H61	1.85	0.42
23:A:2037:G:C5	23:A:2038:A:C8	3.07	0.42
23:A:2057:C:H2'	23:A:2058:C:C6	2.55	0.42
23:A:2226:A:H2'	23:A:2227:U:H6	1.85	0.42
23:A:2338:A:H3'	23:A:2338:A:N3	2.35	0.42
24:B:46:A:H2'	24:B:47:C:C6	2.55	0.42
32:N:79:LEU:HD23	32:N:79:LEU:HA	1.80	0.42
36:R:28:VAL:HG22	36:R:84:LEU:HD11	2.02	0.42
40:V:90:GLN:O	40:V:91:PHE:HB2	2.20	0.42
44:l:9:LEU:HD22	44:l:13:GLU:HG3	2.02	0.42
50:7:64:LYS:HA	50:7:64:LYS:HD2	1.80	0.42
1:a:600:U:H2'	1:a:601:U:C6	2.55	0.41
16:p:38:GLY:HA3	16:p:50:LYS:O	2.20	0.41
20:t:8:ILE:O	20:t:11:VAL:HG12	2.20	0.41
23:A:61:A:C6	23:A:94:A:C2	3.08	0.41
23:A:156:A:C6	23:A:173:G:C6	3.08	0.41
23:A:174:A:H2'	23:A:175:G:C8	2.55	0.41
23:A:1130:A:H2'	23:A:1131:A:C4	2.55	0.41
23:A:1243:G:H2'	23:A:1244:U:H6	1.85	0.41
23:A:1336:U:H2'	23:A:1337:U:H6	1.82	0.41
23:A:1535:A:H2'	23:A:1536:A:H8	1.84	0.41
23:A:2158:G:H2'	23:A:2159:A:N7	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2323:G:H2'	23:A:2324:U:C6	2.54	0.41
23:A:2354:G:H5''	23:A:2355:A:O5'	2.20	0.41
23:A:2707:G:H2'	23:A:2708:A:C8	2.54	0.41
42:Y:61:ARG:NE	42:Y:65:ASP:OD1	2.51	0.41
46:3:13:VAL:HG13	46:3:43:TYR:CD2	2.55	0.41
47:4:46:CYS:O	47:4:48:GLN:HG3	2.19	0.41
1:a:219:U:H1'	1:a:220:C:H2'	2.00	0.41
1:a:648:A:H2'	1:a:649:A:C8	2.55	0.41
1:a:1257:A:C2	1:a:1294:A:C6	3.08	0.41
1:a:1378:G:C6	1:a:1379:U:C4	3.09	0.41
9:i:112:GLU:HG2	9:i:113:ARG:H	1.84	0.41
20:t:3:ASN:OD1	20:t:3:ASN:N	2.53	0.41
23:A:144:G:H2'	23:A:145:A:H8	1.85	0.41
23:A:861:U:OP2	38:T:84:LYS:NZ	2.54	0.41
23:A:1129:G:N2	23:A:1131:A:H3'	2.36	0.41
23:A:1404:G:N7	23:A:1405:G:C8	2.88	0.41
23:A:1442:C:C2	23:A:1443:C:C5	3.08	0.41
23:A:2057:C:H2'	23:A:2058:C:H6	1.84	0.41
23:A:2255:G:H2'	23:A:2256:A:H8	1.85	0.41
28:F:130:LEU:N	28:F:154:VAL:O	2.29	0.41
33:O:27:VAL:HG23	33:O:105:GLU:OE1	2.19	0.41
44:1:46:VAL:O	44:1:50:ILE:HG13	2.21	0.41
51:8:7:VAL:HG22	51:8:34:GLN:HB3	2.01	0.41
1:a:221:G:C6	1:a:222:G:H1'	2.55	0.41
1:a:1198:A:OP2	3:c:2:GLY:HA3	2.20	0.41
13:m:52:GLU:O	13:m:56:ILE:N	2.51	0.41
23:A:309:C:H2'	23:A:310:U:C6	2.55	0.41
23:A:310:U:H2'	23:A:311:A:O4'	2.21	0.41
23:A:1322:A:H2'	23:A:1323:G:H8	1.85	0.41
23:A:2686:U:OP2	23:A:2687:A:O2'	2.24	0.41
25:C:119:GLY:O	25:C:130:LEU:HD23	2.20	0.41
33:O:76:SER:HB3	33:O:91:GLU:CD	2.45	0.41
40:V:14:GLU:H	40:V:14:GLU:CD	2.28	0.41
44:1:52:ARG:O	44:1:56:ILE:HG12	2.20	0.41
1:a:388:G:N2	1:a:390:A:H8	2.18	0.41
1:a:1064:A:O5'	1:a:1064:A:H8	2.03	0.41
6:f:51:TYR:CE1	18:r:70:ALA:HA	2.56	0.41
6:f:53:ILE:HG13	6:f:54:ASN:N	2.34	0.41
6:f:69:ASP:OD1	6:f:69:ASP:N	2.54	0.41
16:p:5:ILE:HB	16:p:66:PRO:HA	2.00	0.41
21:x:53:G:C2	21:x:62:C:C2	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:842:U:H2'	23:A:843:U:C6	2.55	0.41
23:A:1095:C:H2'	23:A:1096:A:H8	1.85	0.41
23:A:1524:G:H2'	23:A:1525:U:C6	2.55	0.41
23:A:2080:C:H2'	23:A:2081:G:H8	1.86	0.41
23:A:2266:A:H2'	23:A:2267:G:H8	1.85	0.41
46:3:56:PRO:HA	46:3:60:GLY:O	2.20	0.41
1:a:264:U:H2'	1:a:265:A:C8	2.55	0.41
1:a:593:G:H4'	12:l:5:ASN:HD21	1.85	0.41
7:g:15:ASP:OD2	7:g:44:TYR:OH	2.35	0.41
11:k:35:THR:OG1	11:k:40:ASN:O	2.17	0.41
18:r:71:LEU:C	18:r:72:LEU:HD12	2.45	0.41
23:A:422:G:C2	23:A:423:A:C5	3.08	0.41
23:A:1405:G:H2'	23:A:1406:C:C6	2.55	0.41
23:A:1845:G:H1'	25:C:45:ASN:HB2	2.02	0.41
26:D:130:ARG:HB3	26:D:140:HIS:O	2.20	0.41
30:L:142:GLU:H	30:L:142:GLU:CD	2.28	0.41
48:5:29:ARG:HA	48:5:47:GLU:OE2	2.20	0.41
1:a:159:A:OP1	1:a:159:A:C8	2.74	0.41
1:a:287:A:H5'	1:a:289:G:O4'	2.21	0.41
1:a:504:G:N2	1:a:505:A:H3'	2.35	0.41
1:a:528:A:H62	1:a:537:G:N2	2.17	0.41
1:a:899:G:O2'	1:a:915:G:O6	2.31	0.41
3:c:3:GLN:OE1	3:c:3:GLN:N	2.53	0.41
7:g:47:PHE:HA	7:g:50:ILE:HG22	2.01	0.41
23:A:265:A:H2'	23:A:266:G:O4'	2.20	0.41
23:A:2338:A:OP2	28:F:131:GLY:HA3	2.20	0.41
23:A:2809:A:H4'	23:A:2810:G:O5'	2.20	0.41
27:E:148:VAL:HG23	27:E:149:ASP:N	2.35	0.41
28:F:8:TYR:HA	28:F:12:ILE:HB	2.03	0.41
30:L:37:LEU:HD23	30:L:37:LEU:HA	1.87	0.41
46:3:35:ILE:HD13	46:3:45:LEU:HB2	2.02	0.41
1:a:58:C:O2	1:a:58:C:H2'	2.20	0.41
1:a:223:C:H2'	1:a:224:U:O4'	2.20	0.41
1:a:388:G:C2	1:a:392:G:C6	3.09	0.41
1:a:607:C:H2'	1:a:608:U:C6	2.56	0.41
1:a:723:A:H8	1:a:723:A:O5'	2.04	0.41
7:g:27:ILE:CD1	7:g:43:LEU:HD13	2.50	0.41
14:n:45:ARG:NH1	14:n:49:TYR:OH	2.54	0.41
23:A:10:A:C6	23:A:11:G:N1	2.88	0.41
23:A:921:G:O6	23:A:951:C:N4	2.53	0.41
23:A:1276:U:C2	23:A:1277:G:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1763:U:H2'	23:A:1777:G:N2	2.35	0.41
23:A:2189:G:O2'	23:A:2190:G:H5'	2.20	0.41
23:A:2280:A:H2'	23:A:2281:C:C6	2.56	0.41
23:A:2520:G:C2	23:A:2521:A:C5	3.08	0.41
25:C:75:PRO:HB3	25:C:117:TYR:CE1	2.55	0.41
25:C:131:GLU:O	25:C:135:ILE:HG12	2.21	0.41
1:a:145:G:C2	1:a:176:G:N7	2.89	0.41
1:a:460:A:H2'	1:a:461:C:H4'	2.03	0.41
1:a:1194:G:H21	14:n:60:SER:HB2	1.86	0.41
1:a:1228:G:C6	1:a:1229:G:N2	2.89	0.41
1:a:1422:G:H2'	1:a:1423:A:H8	1.86	0.41
1:a:1544:C:H4'	1:a:1545:U:OP1	2.21	0.41
7:g:72:LEU:O	7:g:73:LEU:HD23	2.20	0.41
21:x:22:G:C2	21:x:23:A:C5	3.09	0.41
23:A:89:U:H3'	23:A:90:A:C8	2.52	0.41
23:A:288:U:O2'	23:A:289:U:O5'	2.34	0.41
23:A:1268:G:OP1	38:T:67:ARG:NH1	2.54	0.41
23:A:1613:C:H2'	23:A:1614:U:C6	2.55	0.41
23:A:1773:G:H2'	23:A:1774:C:H6	1.86	0.41
23:A:1874:U:N3	23:A:1875:G:N7	2.69	0.41
23:A:2101:U:H3	23:A:2463:A:H62	1.69	0.41
23:A:2175:G:N1	23:A:2183:A:C6	2.88	0.41
23:A:2179:U:H4'	23:A:2180:A:H5''	2.01	0.41
25:C:44:ASN:CG	25:C:45:ASN:H	2.28	0.41
29:G:89:LEU:HG	29:G:162:ILE:HD13	2.03	0.41
41:W:70:LEU:O	41:W:78:PRO:HA	2.21	0.41
1:a:34:C:H2'	1:a:35:G:H8	1.85	0.41
1:a:111:G:H2'	1:a:112:U:H6	1.85	0.41
1:a:204:U:H2'	1:a:205:C:C6	2.55	0.41
1:a:379:G:H21	1:a:381:A:N6	2.19	0.41
1:a:1002:G:O2'	1:a:1003:A:N7	2.54	0.41
3:c:99:HIS:CD2	3:c:100:ILE:H	2.39	0.41
4:d:63:LEU:HD23	4:d:63:LEU:H	1.86	0.41
8:h:20:VAL:O	8:h:20:VAL:HG22	2.21	0.41
11:k:29:ASN:OD1	11:k:30:THR:N	2.50	0.41
11:k:71:ALA:O	11:k:75:GLN:HG2	2.21	0.41
16:p:74:LEU:HB3	16:p:79:ILE:HG13	2.03	0.41
18:r:13:LYS:HB3	18:r:14:VAL:H	1.66	0.41
23:A:116:G:OP2	23:A:118:A:O2'	2.29	0.41
23:A:157:C:H2'	23:A:158:G:H8	1.86	0.41
23:A:704:A:H2'	23:A:705:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:920:G:C6	23:A:921:G:N7	2.89	0.41
23:A:999:A:C2	23:A:1000:G:C8	3.09	0.41
23:A:1131:A:N7	23:A:1132:A:C6	2.89	0.41
23:A:1145:G:H2'	23:A:1146:C:H6	1.86	0.41
23:A:1451:G:H2'	23:A:1452:U:C6	2.55	0.41
23:A:1621:A:C6	23:A:1622:A:C6	3.09	0.41
23:A:1640:A:H2'	23:A:1641:G:H8	1.84	0.41
23:A:2169:A:H2'	23:A:2170:C:C6	2.56	0.41
23:A:2687:A:H8	23:A:2687:A:OP1	2.03	0.41
23:A:2757:U:OP1	26:D:117:LYS:HE2	2.21	0.41
23:A:2922:G:H2'	23:A:2922:G:N3	2.35	0.41
25:C:37:LEU:CG	25:C:62:TYR:HB2	2.50	0.41
25:C:75:PRO:HB3	25:C:117:TYR:HE1	1.86	0.41
27:E:111:LYS:HE3	27:E:111:LYS:HB2	1.73	0.41
30:L:15:LYS:O	30:L:53:ASP:HB3	2.20	0.41
36:R:105:GLY:C	36:R:107:ALA:H	2.29	0.41
37:S:76:TYR:CZ	37:S:80:MET:HG3	2.55	0.41
43:Z:32:ASN:O	43:Z:50:SER:HA	2.20	0.41
46:3:68:ASP:O	46:3:71:VAL:HG12	2.21	0.41
1:a:181:A:O2'	1:a:182:U:P	2.79	0.41
1:a:479:C:C2	1:a:480:U:C5	3.09	0.41
1:a:920:U:H2'	1:a:921:C:C6	2.56	0.41
1:a:1278:G:C5	1:a:1279:U:C4	3.09	0.41
8:h:81:SER:HA	8:h:87:VAL:HG12	2.02	0.41
12:l:20:THR:O	12:l:107:ARG:NH2	2.34	0.41
14:n:25:GLU:H	14:n:25:GLU:HG2	1.59	0.41
21:x:8:4SU:H4'	21:x:48:C:H4'	2.02	0.41
21:x:30:G:C4	21:x:31:A:C8	3.09	0.41
23:A:82:G:N2	23:A:104:C:H42	2.19	0.41
23:A:278:A:H2'	23:A:279:G:H8	1.86	0.41
23:A:464:U:H2'	23:A:465:C:H6	1.86	0.41
23:A:1774:C:H2'	23:A:1775:C:C6	2.56	0.41
23:A:1958:C:O5'	23:A:1958:C:H6	2.03	0.41
23:A:2203:G:OP2	23:A:2203:G:H8	2.04	0.41
23:A:2548:C:H2'	23:A:2549:G:H8	1.86	0.41
23:A:2564:A:C4	23:A:2565:G:C8	3.09	0.41
34:P:51:GLY:HA2	34:P:99:PHE:CE1	2.55	0.41
34:P:73:VAL:HA	34:P:91:PRO:HA	2.03	0.41
46:3:42:GLU:H	46:3:42:GLU:CD	2.28	0.41
1:a:203:C:H2'	1:a:204:U:C6	2.56	0.40
1:a:291:U:C2	1:a:292:G:C8	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:953:G:N1	1:a:1345:G:OP2	2.47	0.40
8:h:98:LEU:HD21	8:h:132:TRP:HE3	1.86	0.40
13:m:33:VAL:HG12	13:m:34:LEU:HD23	2.02	0.40
16:p:22:VAL:HG22	16:p:35:GLU:O	2.20	0.40
23:A:1449:C:H2'	23:A:1450:A:H8	1.86	0.40
23:A:2107:U:O2'	23:A:2630:G:O2'	2.32	0.40
23:A:2181:G:H8	23:A:2181:G:OP2	2.03	0.40
23:A:2188:A:H2'	23:A:2189:G:O4'	2.22	0.40
23:A:2580:U:H2'	23:A:2581:G:H8	1.86	0.40
23:A:2627:C:N4	23:A:2628:G:O6	2.54	0.40
23:A:2685:U:H3	23:A:2701:G:H1	1.67	0.40
23:A:2908:A:O2'	23:A:2909:C:P	2.79	0.40
23:A:2921:G:OP2	23:A:2921:G:H8	2.03	0.40
24:B:92:C:H2'	24:B:93:U:C6	2.56	0.40
28:F:34:ILE:HG22	28:F:91:LEU:O	2.22	0.40
37:S:96:ALA:O	37:S:100:VAL:HG23	2.20	0.40
38:T:43:GLY:C	38:T:45:SER:H	2.30	0.40
39:U:73:ASN:OD1	39:U:114:GLU:HG3	2.21	0.40
40:V:23:LYS:NZ	40:V:88:GLU:OE1	2.54	0.40
1:a:198:C:H2'	1:a:199:C:H6	1.86	0.40
1:a:1182:G:H2'	1:a:1183:A:C8	2.56	0.40
1:a:1500:A:O2'	1:a:1501:A:O5'	2.37	0.40
2:b:166:PRO:HG2	2:b:191:CYS:CB	2.51	0.40
19:s:62:VAL:HA	19:s:66:MET:SD	2.61	0.40
23:A:408:U:H2'	23:A:409:G:C8	2.56	0.40
23:A:680:C:H2'	23:A:681:G:O4'	2.21	0.40
23:A:870:G:H2'	23:A:871:C:C6	2.56	0.40
23:A:1253:C:O2'	23:A:1254:G:C8	2.72	0.40
23:A:1579:A:N6	23:A:1595:G:H1'	2.37	0.40
1:a:129:A:H1'	1:a:271:A:O2'	2.21	0.40
1:a:181:A:O2'	1:a:182:U:OP1	2.39	0.40
1:a:388:G:N1	1:a:392:G:O6	2.55	0.40
1:a:419:A:H61	1:a:438:A:H62	1.68	0.40
1:a:1257:A:C6	1:a:1294:A:C4	3.09	0.40
3:c:149:LYS:NZ	3:c:200:TRP:CZ2	2.83	0.40
5:e:152:GLU:O	5:e:156:LYS:HG2	2.21	0.40
9:i:68:HIS:O	9:i:68:HIS:ND1	2.55	0.40
10:j:20:GLN:HA	10:j:23:GLU:HB3	2.03	0.40
23:A:293:G:C2	23:A:294:G:C8	3.10	0.40
23:A:383:A:H2'	23:A:384:G:O4'	2.22	0.40
23:A:926:G:C6	23:A:946:G:C2	3.08	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1070:G:C6	23:A:1071:G:C6	3.10	0.40
23:A:1100:A:N6	23:A:1152:G:O6	2.54	0.40
23:A:1321:A:H2'	23:A:1322:A:C8	2.56	0.40
23:A:1461:U:H1'	23:A:1635:A:C5	2.56	0.40
23:A:1774:C:H2'	23:A:1775:C:H6	1.87	0.40
23:A:2266:A:H2'	23:A:2267:G:C8	2.56	0.40
24:B:30:C:C2	24:B:49:G:C2	3.09	0.40
28:F:64:LYS:HE2	46:3:5:ILE:O	2.21	0.40
32:N:80:ASP:OD1	32:N:81:VAL:N	2.54	0.40
40:V:62:LEU:HD13	40:V:71:TYR:CZ	2.56	0.40
1:a:209:A:H2'	1:a:210:A:C8	2.57	0.40
1:a:425:G:H2'	1:a:426:U:H6	1.86	0.40
1:a:640:G:C6	1:a:642:C:C4	3.10	0.40
1:a:1252:G:O6	1:a:1300:A:N6	2.54	0.40
18:r:63:ILE:HG22	18:r:67:ARG:HG3	2.04	0.40
23:A:788:C:H2'	23:A:789:A:H8	1.85	0.40
23:A:969:C:O2'	42:Y:34:ALA:HB2	2.20	0.40
23:A:1187:U:OP1	30:L:28:ARG:NH1	2.53	0.40
23:A:2173:G:C6	23:A:2185:A:C6	3.09	0.40
26:D:180:ASP:HB3	26:D:185:VAL:HG22	2.02	0.40
27:E:151:LYS:O	27:E:190:ASP:HB3	2.22	0.40
28:F:24:SER:OG	28:F:25:VAL:N	2.53	0.40
29:G:58:ASN:H	29:G:61:HIS:HB2	1.86	0.40
29:G:137:ASN:OD1	29:G:137:ASN:N	2.54	0.40
1:a:200:A:H2'	1:a:201:C:C6	2.55	0.40
1:a:670:A:H2'	1:a:671:A:C8	2.56	0.40
1:a:1057:G:H5'	1:a:1058:U:OP1	2.21	0.40
1:a:1312:G:H22	1:a:1338:G:H2'	1.86	0.40
1:a:1322:U:O2'	1:a:1367:A:N3	2.39	0.40
4:d:14:ARG:HH11	4:d:32:ALA:HB1	1.87	0.40
7:g:50:ILE:HD12	7:g:50:ILE:HA	1.95	0.40
12:l:43:LYS:O	12:l:95:ILE:HG22	2.21	0.40
13:m:49:THR:HG23	13:m:51:GLU:H	1.86	0.40
23:A:92:G:H2'	23:A:93:U:C6	2.57	0.40
23:A:759:G:H2'	23:A:760:U:C6	2.56	0.40
23:A:1827:U:H2'	23:A:1828:C:H6	1.86	0.40
23:A:1987:G:O2'	23:A:1989:U:O4	2.35	0.40
23:A:2061:U:H2'	23:A:2062:G:C8	2.57	0.40
23:A:2130:G:H2'	23:A:2131:U:C6	2.56	0.40
23:A:2223:A:H2'	23:A:2224:C:C6	2.56	0.40
23:A:2319:A:H4'	23:A:2320:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2326:C:H5''	35:Q:96:ARG:NH1	2.32	0.40
23:A:2382:G:C6	23:A:2402:A:C6	3.10	0.40
23:A:2778:C:H2'	23:A:2779:U:C6	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/249 (89%)	202 (91%)	19 (9%)	1 (0%)	24	55
3	c	201/218 (92%)	179 (89%)	22 (11%)	0	100	100
4	d	197/200 (98%)	178 (90%)	19 (10%)	0	100	100
5	e	154/167 (92%)	138 (90%)	16 (10%)	0	100	100
6	f	91/97 (94%)	84 (92%)	7 (8%)	0	100	100
7	g	141/156 (90%)	136 (96%)	5 (4%)	0	100	100
8	h	129/132 (98%)	122 (95%)	7 (5%)	0	100	100
9	i	123/130 (95%)	114 (93%)	9 (7%)	0	100	100
10	j	95/102 (93%)	88 (93%)	7 (7%)	0	100	100
11	k	112/129 (87%)	106 (95%)	6 (5%)	0	100	100
12	l	133/137 (97%)	119 (90%)	14 (10%)	0	100	100
13	m	112/121 (93%)	103 (92%)	9 (8%)	0	100	100
14	n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
15	o	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
16	p	86/90 (96%)	81 (94%)	5 (6%)	0	100	100
17	q	78/87 (90%)	71 (91%)	7 (9%)	0	100	100
18	r	62/79 (78%)	56 (90%)	5 (8%)	1 (2%)	7	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	s	79/92 (86%)	69 (87%)	10 (13%)	0	100	100
20	t	79/84 (94%)	76 (96%)	3 (4%)	0	100	100
25	C	271/277 (98%)	257 (95%)	14 (5%)	0	100	100
26	D	204/209 (98%)	193 (95%)	11 (5%)	0	100	100
27	E	203/207 (98%)	193 (95%)	10 (5%)	0	100	100
28	F	163/179 (91%)	151 (93%)	12 (7%)	0	100	100
29	G	158/178 (89%)	149 (94%)	9 (6%)	0	100	100
30	L	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
31	M	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
32	N	143/146 (98%)	131 (92%)	12 (8%)	0	100	100
33	O	132/144 (92%)	127 (96%)	5 (4%)	0	100	100
34	P	118/135 (87%)	108 (92%)	10 (8%)	0	100	100
35	Q	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
36	R	111/114 (97%)	106 (96%)	5 (4%)	0	100	100
37	S	115/119 (97%)	111 (96%)	4 (4%)	0	100	100
38	T	99/102 (97%)	94 (95%)	5 (5%)	0	100	100
39	U	109/118 (92%)	106 (97%)	3 (3%)	0	100	100
40	V	90/94 (96%)	83 (92%)	7 (8%)	0	100	100
41	W	100/103 (97%)	90 (90%)	10 (10%)	0	100	100
42	Y	73/96 (76%)	65 (89%)	8 (11%)	0	100	100
43	Z	57/62 (92%)	49 (86%)	8 (14%)	0	100	100
44	1	57/63 (90%)	54 (95%)	2 (4%)	1 (2%)	6	29
45	2	54/59 (92%)	52 (96%)	2 (4%)	0	100	100
46	3	74/81 (91%)	58 (78%)	16 (22%)	0	100	100
47	4	51/57 (90%)	46 (90%)	5 (10%)	0	100	100
48	5	46/49 (94%)	41 (89%)	5 (11%)	0	100	100
49	6	41/44 (93%)	40 (98%)	1 (2%)	0	100	100
50	7	62/66 (94%)	56 (90%)	6 (10%)	0	100	100
51	8	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
All	All	5173/5545 (93%)	4802 (93%)	368 (7%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	128	VAL
18	r	14	VAL
44	1	11	THR

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	
2	b	31/214 (14%)	31 (100%)	0	100	100
3	c	112/177 (63%)	112 (100%)	0	100	100
4	d	124/170 (73%)	124 (100%)	0	100	100
5	e	108/131 (82%)	108 (100%)	0	100	100
6	f	49/85 (58%)	49 (100%)	0	100	100
7	g	90/130 (69%)	90 (100%)	0	100	100
8	h	86/110 (78%)	86 (100%)	0	100	100
9	i	85/102 (83%)	85 (100%)	0	100	100
10	j	71/93 (76%)	71 (100%)	0	100	100
11	k	44/100 (44%)	44 (100%)	0	100	100
12	l	83/118 (70%)	83 (100%)	0	100	100
13	m	64/102 (63%)	64 (100%)	0	100	100
14	n	46/52 (88%)	44 (96%)	2 (4%)	26	54
15	o	54/81 (67%)	54 (100%)	0	100	100
16	p	60/80 (75%)	60 (100%)	0	100	100
17	q	45/78 (58%)	45 (100%)	0	100	100
18	r	39/67 (58%)	39 (100%)	0	100	100
19	s	24/78 (31%)	24 (100%)	0	100	100
20	t	31/66 (47%)	31 (100%)	0	100	100
25	C	209/225 (93%)	209 (100%)	0	100	100
26	D	159/171 (93%)	159 (100%)	0	100	100
27	E	156/174 (90%)	156 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	F	100/155 (64%)	100 (100%)	0	100	100
29	G	90/147 (61%)	90 (100%)	0	100	100
30	L	109/121 (90%)	109 (100%)	0	100	100
31	M	98/101 (97%)	98 (100%)	0	100	100
32	N	93/115 (81%)	93 (100%)	0	100	100
33	O	98/113 (87%)	98 (100%)	0	100	100
34	P	94/111 (85%)	94 (100%)	0	100	100
35	Q	40/97 (41%)	40 (100%)	0	100	100
36	R	83/99 (84%)	83 (100%)	0	100	100
37	S	92/97 (95%)	92 (100%)	0	100	100
38	T	76/82 (93%)	76 (100%)	0	100	100
39	U	89/97 (92%)	89 (100%)	0	100	100
40	V	76/84 (90%)	76 (100%)	0	100	100
41	W	76/88 (86%)	76 (100%)	0	100	100
42	Y	54/76 (71%)	54 (100%)	0	100	100
43	Z	44/53 (83%)	44 (100%)	0	100	100
44	1	47/55 (86%)	47 (100%)	0	100	100
45	2	49/52 (94%)	49 (100%)	0	100	100
46	3	45/73 (62%)	45 (100%)	0	100	100
47	4	47/50 (94%)	47 (100%)	0	100	100
48	5	41/48 (85%)	41 (100%)	0	100	100
49	6	38/39 (97%)	38 (100%)	0	100	100
50	7	52/56 (93%)	52 (100%)	0	100	100
51	8	35/35 (100%)	35 (100%)	0	100	100
All	All	3436/4648 (74%)	3434 (100%)	2 (0%)	87	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	n	25	GLU
14	n	38	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
3	c	91	ASN
3	c	99	HIS
3	c	166	HIS
5	e	46	HIS
5	e	150	ASN
7	g	40	GLN
8	h	18	ASN
9	i	81	HIS
10	j	20	GLN
11	k	28	ASN
11	k	40	ASN
12	l	5	ASN
12	l	86	ASN
12	l	109	HIS
16	p	62	ASN
16	p	72	ASN
17	q	74	HIS
19	s	83	HIS
25	C	15	HIS
25	C	53	HIS
25	C	86	ASN
25	C	153	GLN
26	D	32	GLN
26	D	120	GLN
26	D	168	GLN
26	D	173	ASN
27	E	9	GLN
27	E	40	GLN
27	E	145	ASN
27	E	171	GLN
29	G	65	HIS
29	G	140	HIS
29	G	147	ASN
30	L	78	HIS
30	L	80	GLN
30	L	97	ASN
30	L	118	GLN
31	M	13	ASN
32	N	27	ASN
32	N	78	ASN
36	R	12	GLN
36	R	41	GLN
36	R	102	ASN

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Mol	Chain	Res	Type
37	S	52	GLN
39	U	107	HIS
40	V	54	ASN
40	V	90	GLN
41	W	67	ASN
42	Y	58	ASN
43	Z	20	HIS
43	Z	23	ASN
45	2	17	GLN
46	3	75	ASN
47	4	23	GLN
50	7	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550 (97%)	261 (17%)	0
21	x	72/76 (94%)	25 (34%)	0
22	w	5/21 (23%)	1 (20%)	0
23	A	2900/2932 (98%)	507 (17%)	31 (1%)
24	B	113/116 (97%)	13 (11%)	0
All	All	4602/4695 (98%)	807 (17%)	31 (0%)

All (807) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	A
1	a	9	G
1	a	31	G
1	a	32	A
1	a	39	G
1	a	44	G
1	a	47	C
1	a	48	C
1	a	51	A
1	a	54	C
1	a	55	A
1	a	64	G
1	a	65	A
1	a	66	A
1	a	67	C

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Mol	Chain	Res	Type
1	a	68	G
1	a	69	A
1	a	70	A
1	a	71	C
1	a	72	G
1	a	73	G
1	a	96	G
1	a	97	U
1	a	98	U
1	a	99	A
1	a	100	G
1	a	102	G
1	a	107	A
1	a	114	A
1	a	119	C
1	a	120	A
1	a	128	A
1	a	130	C
1	a	142	U
1	a	144	G
1	a	159	A
1	a	164	G
1	a	173	A
1	a	182	U
1	a	183	A
1	a	187	U
1	a	192	C
1	a	207	U
1	a	209	A
1	a	211	A
1	a	212	G
1	a	219	U
1	a	220	C
1	a	222	G
1	a	225	A
1	a	239	G
1	a	248	U
1	a	249	G
1	a	252	U
1	a	253	U
1	a	255	G
1	a	259	G

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Mol	Chain	Res	Type
1	a	274	G
1	a	275	C
1	a	297	G
1	a	329	A
1	a	336	C
1	a	338	C
1	a	340	G
1	a	349	C
1	a	350	C
1	a	351	U
1	a	352	A
1	a	353	C
1	a	354	G
1	a	355	G
1	a	359	G
1	a	360	C
1	a	362	G
1	a	372	A
1	a	373	U
1	a	375	U
1	a	380	C
1	a	381	A
1	a	406	C
1	a	414	G
1	a	419	A
1	a	420	A
1	a	421	G
1	a	425	G
1	a	429	U
1	a	430	C
1	a	432	G
1	a	437	U
1	a	454	A
1	a	456	A
1	a	461	C
1	a	467	U
1	a	473	U
1	a	474	A
1	a	489	G
1	a	492	G
1	a	493	G
1	a	506	A

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Mol	Chain	Res	Type
1	a	517	A
1	a	519	C
1	a	526	C
1	a	529	G
1	a	532	G
1	a	535	G
1	a	537	G
1	a	538	G
1	a	539	U
1	a	540	A
1	a	555	A
1	a	576	G
1	a	580	A
1	a	581	A
1	a	584	C
1	a	585	G
1	a	587	G
1	a	595	G
1	a	596	G
1	a	661	G
1	a	673	A
1	a	695	A
1	a	702	A
1	a	711	G
1	a	712	A
1	a	714	A
1	a	731	U
1	a	739	G
1	a	757	A
1	a	763	G
1	a	789	A
1	a	801	U
1	a	802	A
1	a	825	C
1	a	829	G
1	a	848	G
1	a	855	C
1	a	868	C
1	a	881	A
1	a	894	G
1	a	923	A
1	a	931	G

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Mol	Chain	Res	Type
1	a	935	G
1	a	936	G
1	a	943	C
1	a	944	A
1	a	965	U
1	a	967	A
1	a	969	U
1	a	970	U
1	a	974	A
1	a	975	G
1	a	976	C
1	a	977	A
1	a	978	A
1	a	980	G
1	a	984	A
1	a	985	G
1	a	986	A
1	a	992	A
1	a	1001	U
1	a	1002	G
1	a	1005	A
1	a	1008	C
1	a	1009	U
1	a	1011	U
1	a	1012	G
1	a	1013	A
1	a	1014	C
1	a	1016	A
1	a	1018	U
1	a	1023	A
1	a	1027	A
1	a	1030	G
1	a	1032	U
1	a	1034	U
1	a	1035	C
1	a	1036	C
1	a	1045	A
1	a	1050	G
1	a	1052	G
1	a	1053	A
1	a	1054	C
1	a	1055	A

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Mol	Chain	Res	Type
1	a	1062	G
1	a	1063	C
1	a	1064	A
1	a	1065	U
1	a	1074	U
1	a	1087	U
1	a	1094	U
1	a	1095	U
1	a	1103	G
1	a	1104	U
1	a	1108	G
1	a	1110	A
1	a	1111	A
1	a	1117	G
1	a	1134	U
1	a	1141	C
1	a	1142	A
1	a	1146	A
1	a	1147	G
1	a	1148	U
1	a	1154	A
1	a	1167	U
1	a	1168	G
1	a	1176	A
1	a	1178	G
1	a	1191	G
1	a	1203	A
1	a	1204	A
1	a	1208	A
1	a	1209	U
1	a	1219	U
1	a	1220	A
1	a	1221	U
1	a	1233	C
1	a	1234	A
1	a	1235	C
1	a	1245	A
1	a	1248	G
1	a	1257	A
1	a	1263	U
1	a	1264	C
1	a	1267	G

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Mol	Chain	Res	Type
1	a	1287	A
1	a	1288	U
1	a	1294	A
1	a	1306	A
1	a	1307	G
1	a	1309	U
1	a	1312	G
1	a	1329	C
1	a	1343	C
1	a	1347	A
1	a	1371	U
1	a	1377	G
1	a	1388	U
1	a	1404	C
1	a	1405	A
1	a	1426	G
1	a	1436	C
1	a	1449	G
1	a	1450	G
1	a	1453	A
1	a	1455	C
1	a	1456	C
1	a	1492	U
1	a	1495	G
1	a	1498	U
1	a	1500	A
1	a	1501	A
1	a	1505	G
1	a	1511	A
1	a	1514	U
1	a	1525	G
1	a	1527	A
1	a	1537	G
1	a	1538	G
1	a	1539	A
1	a	1545	U
21	x	6	G
21	x	9	A
21	x	19	G
21	x	20	U
21	x	25	C
21	x	26	A

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Mol	Chain	Res	Type
21	x	29	G
21	x	30	G
21	x	35	A
21	x	41	C
21	x	44	G
21	x	45	U
21	x	46	7MG
21	x	47	U
21	x	48	C
21	x	49	C
21	x	51	U
21	x	52	G
21	x	54	5MU
21	x	56	C
21	x	60	U
21	x	61	C
21	x	68	C
21	x	73	A
21	x	76	A
22	w	13	A
23	A	10	A
23	A	13	A
23	A	14	A
23	A	15	G
23	A	28	A
23	A	34	U
23	A	45	G
23	A	46	C
23	A	49	A
23	A	51	G
23	A	60	G
23	A	71	A
23	A	74	U
23	A	75	G
23	A	89	U
23	A	91	C
23	A	93	U
23	A	96	G
23	A	99	U
23	A	100	U
23	A	101	G
23	A	117	A

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Mol	Chain	Res	Type
23	A	119	U
23	A	125	A
23	A	126	A
23	A	140	G
23	A	150	A
23	A	159	U
23	A	164	A
23	A	166	A
23	A	167	U
23	A	175	G
23	A	182	A
23	A	186	C
23	A	187	C
23	A	198	A
23	A	199	A
23	A	200	C
23	A	201	A
23	A	215	A
23	A	218	A
23	A	223	A
23	A	224	A
23	A	230	A
23	A	231	A
23	A	232	U
23	A	241	U
23	A	247	G
23	A	250	G
23	A	251	C
23	A	257	A
23	A	274	A
23	A	280	A
23	A	282	G
23	A	283	C
23	A	285	U
23	A	287	C
23	A	289	U
23	A	290	C
23	A	295	G
23	A	296	G
23	A	300	U
23	A	301	A
23	A	307	C

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Mol	Chain	Res	Type
23	A	308	U
23	A	309	C
23	A	313	A
23	A	320	U
23	A	323	A
23	A	345	G
23	A	354	A
23	A	372	A
23	A	373	A
23	A	374	C
23	A	388	A
23	A	396	U
23	A	404	A
23	A	406	A
23	A	410	G
23	A	411	A
23	A	412	U
23	A	417	A
23	A	418	G
23	A	420	A
23	A	432	G
23	A	433	U
23	A	434	G
23	A	449	U
23	A	452	G
23	A	457	G
23	A	458	A
23	A	470	G
23	A	481	C
23	A	490	C
23	A	501	C
23	A	503	A
23	A	526	A
23	A	527	G
23	A	536	A
23	A	550	A
23	A	552	U
23	A	553	U
23	A	554	C
23	A	555	C
23	A	567	G
23	A	575	G

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Mol	Chain	Res	Type
23	A	576	U
23	A	577	A
23	A	578	G
23	A	591	A
23	A	592	A
23	A	593	U
23	A	594	G
23	A	606	G
23	A	616	G
23	A	618	A
23	A	629	A
23	A	646	A
23	A	657	A
23	A	658	A
23	A	659	A
23	A	666	A
23	A	667	G
23	A	672	A
23	A	679	G
23	A	682	A
23	A	689	A
23	A	690	U
23	A	698	A
23	A	699	U
23	A	700	A
23	A	718	C
23	A	732	U
23	A	747	G
23	A	763	U
23	A	776	U
23	A	793	U
23	A	794	G
23	A	810	A
23	A	811	G
23	A	821	G
23	A	828	A
23	A	829	A
23	A	830	U
23	A	839	A
23	A	851	G
23	A	858	C
23	A	865	A

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Mol	Chain	Res	Type
23	A	873	U
23	A	874	U
23	A	890	G
23	A	891	U
23	A	892	A
23	A	893	A
23	A	913	A
23	A	931	C
23	A	941	U
23	A	943	A
23	A	944	C
23	A	957	A
23	A	959	C
23	A	964	A
23	A	970	A
23	A	973	U
23	A	974	A
23	A	979	U
23	A	980	A
23	A	987	A
23	A	991	A
23	A	992	G
23	A	1007	G
23	A	1020	A
23	A	1025	A
23	A	1029	A
23	A	1035	G
23	A	1042	A
23	A	1051	C
23	A	1058	U
23	A	1059	A
23	A	1068	G
23	A	1069	U
23	A	1072	A
23	A	1073	A
23	A	1079	U
23	A	1091	U
23	A	1092	A
23	A	1093	G
23	A	1094	A
23	A	1100	A
23	A	1105	G

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Mol	Chain	Res	Type
23	A	1106	U
23	A	1107	U
23	A	1112	U
23	A	1115	A
23	A	1116	A
23	A	1117	G
23	A	1119	A
23	A	1129	G
23	A	1133	G
23	A	1134	A
23	A	1142	A
23	A	1143	U
23	A	1154	U
23	A	1155	C
23	A	1157	A
23	A	1158	G
23	A	1161	A
23	A	1173	A
23	A	1174	A
23	A	1179	A
23	A	1181	C
23	A	1182	G
23	A	1185	G
23	A	1187	U
23	A	1188	A
23	A	1189	A
23	A	1203	A
23	A	1226	G
23	A	1230	G
23	A	1249	A
23	A	1250	G
23	A	1254	G
23	A	1265	A
23	A	1283	G
23	A	1298	A
23	A	1301	G
23	A	1311	G
23	A	1317	A
23	A	1320	G
23	A	1344	A
23	A	1345	A
23	A	1346	U

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Mol	Chain	Res	Type
23	A	1357	U
23	A	1369	C
23	A	1373	U
23	A	1382	G
23	A	1385	U
23	A	1394	C
23	A	1396	U
23	A	1409	A
23	A	1423	U
23	A	1428	A
23	A	1429	A
23	A	1430	C
23	A	1436	G
23	A	1439	A
23	A	1447	A
23	A	1455	U
23	A	1457	A
23	A	1462	U
23	A	1463	U
23	A	1464	A
23	A	1465	A
23	A	1469	A
23	A	1478	C
23	A	1489	A
23	A	1493	A
23	A	1494	A
23	A	1505	G
23	A	1509	A
23	A	1510	U
23	A	1511	G
23	A	1519	A
23	A	1528	G
23	A	1529	U
23	A	1530	G
23	A	1531	U
23	A	1532	G
23	A	1533	A
23	A	1534	G
23	A	1536	A
23	A	1539	A
23	A	1542	C
23	A	1543	A

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Mol	Chain	Res	Type
23	A	1546	U
23	A	1556	G
23	A	1557	C
23	A	1558	G
23	A	1560	A
23	A	1570	G
23	A	1571	U
23	A	1573	A
23	A	1574	U
23	A	1575	G
23	A	1580	A
23	A	1581	G
23	A	1594	G
23	A	1596	A
23	A	1618	A
23	A	1621	A
23	A	1630	U
23	A	1638	G
23	A	1656	C
23	A	1657	A
23	A	1659	A
23	A	1665	A
23	A	1695	A
23	A	1696	G
23	A	1697	C
23	A	1700	G
23	A	1701	A
23	A	1702	G
23	A	1712	U
23	A	1723	G
23	A	1743	C
23	A	1747	A
23	A	1748	G
23	A	1749	A
23	A	1761	A
23	A	1762	U
23	A	1764	A
23	A	1771	A
23	A	1772	A
23	A	1773	G
23	A	1780	A
23	A	1781	G

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Mol	Chain	Res	Type
23	A	1782	A
23	A	1783	G
23	A	1786	G
23	A	1789	G
23	A	1796	G
23	A	1797	G
23	A	1806	A
23	A	1809	G
23	A	1815	C
23	A	1833	C
23	A	1834	A
23	A	1849	C
23	A	1862	A
23	A	1886	A
23	A	1887	A
23	A	1890	G
23	A	1891	G
23	A	1892	A
23	A	1895	G
23	A	1903	U
23	A	1906	G
23	A	1939	G
23	A	1945	A
23	A	1946	A
23	A	1947	C
23	A	1948	U
23	A	1952	A
23	A	1954	G
23	A	1963	G
23	A	1969	A
23	A	1971	A
23	A	1973	U
23	A	1988	U
23	A	1996	C
23	A	2000	C
23	A	2003	A
23	A	2004	A
23	A	2005	G
23	A	2024	U
23	A	2026	U
23	A	2029	C
23	A	2030	A

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Mol	Chain	Res	Type
23	A	2056	A
23	A	2064	A
23	A	2065	G
23	A	2066	A
23	A	2067	U
23	A	2072	G
23	A	2076	C
23	A	2088	C
23	A	2089	G
23	A	2093	A
23	A	2094	G
23	A	2095	A
23	A	2102	G
23	A	2126	G
23	A	2127	A
23	A	2128	A
23	A	2133	U
23	A	2143	G
23	A	2144	U
23	A	2145	A
23	A	2149	G
23	A	2150	A
23	A	2151	U
23	A	2159	A
23	A	2165	A
23	A	2166	G
23	A	2167	A
23	A	2173	G
23	A	2190	G
23	A	2191	A
23	A	2192	G
23	A	2193	G
23	A	2198	G
23	A	2202	G
23	A	2203	G
23	A	2205	U
23	A	2206	A
23	A	2221	U
23	A	2223	A
23	A	2231	A
23	A	2232	A
23	A	2236	G

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Mol	Chain	Res	Type
23	A	2237	C
23	A	2244	A
23	A	2245	A
23	A	2256	A
23	A	2258	A
23	A	2271	G
23	A	2272	G
23	A	2299	A
23	A	2312	G
23	A	2316	C
23	A	2319	A
23	A	2320	A
23	A	2321	A
23	A	2329	U
23	A	2337	G
23	A	2338	A
23	A	2339	U
23	A	2341	G
23	A	2342	A
23	A	2343	A
23	A	2344	A
23	A	2353	A
23	A	2354	G
23	A	2355	A
23	A	2358	G
23	A	2360	A
23	A	2364	G
23	A	2367	C
23	A	2378	G
23	A	2380	C
23	A	2383	C
23	A	2391	A
23	A	2394	A
23	A	2412	G
23	A	2416	G
23	A	2418	C
23	A	2421	A
23	A	2435	U
23	A	2439	C
23	A	2455	C
23	A	2458	A
23	A	2462	G

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Mol	Chain	Res	Type
23	A	2463	A
23	A	2473	C
23	A	2474	C
23	A	2481	A
23	A	2485	C
23	A	2498	C
23	A	2507	C
23	A	2509	A
23	A	2535	G
23	A	2536	A
23	A	2537	U
23	A	2538	G
23	A	2540	C
23	A	2551	A
23	A	2587	U
23	A	2599	A
23	A	2600	G
23	A	2605	A
23	A	2606	C
23	A	2607	G
23	A	2635	A
23	A	2636	G
23	A	2642	U
23	A	2643	C
23	A	2646	U
23	A	2648	U
23	A	2663	G
23	A	2694	G
23	A	2696	G
23	A	2722	U
23	A	2724	C
23	A	2747	G
23	A	2759	U
23	A	2768	G
23	A	2781	A
23	A	2790	A
23	A	2798	A
23	A	2799	G
23	A	2810	G
23	A	2811	A
23	A	2812	U
23	A	2813	G

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Mol	Chain	Res	Type
23	A	2822	C
23	A	2824	U
23	A	2827	C
23	A	2828	U
23	A	2830	C
23	A	2832	G
23	A	2835	A
23	A	2836	G
23	A	2837	U
23	A	2862	A
23	A	2864	A
23	A	2872	G
23	A	2877	G
23	A	2878	G
23	A	2890	U
23	A	2896	G
23	A	2901	G
23	A	2909	C
23	A	2912	A
23	A	2915	G
23	A	2920	A
23	A	2922	G
23	A	2929	C
24	B	10	U
24	B	23	U
24	B	27	A
24	B	33	U
24	B	37	A
24	B	40	C
24	B	51	A
24	B	54	U
24	B	55	A
24	B	87	U
24	B	88	C
24	B	107	G
24	B	109	U

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	27	G
23	A	88	G

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Mol	Chain	Res	Type
23	A	92	G
23	A	96	G
23	A	139	A
23	A	286	G
23	A	371	U
23	A	525	A
23	A	553	U
23	A	688	A
23	A	756	A
23	A	809	G
23	A	847	G
23	A	854	G
23	A	979	U
23	A	1017	C
23	A	1172	A
23	A	1248	A
23	A	1249	A
23	A	1497	G
23	A	1528	G
23	A	1532	G
23	A	1533	A
23	A	1569	U
23	A	1595	G
23	A	1886	A
23	A	2320	A
23	A	2472	A
23	A	2789	U
23	A	2809	A
23	A	2908	A

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	5MU	x	54	21	19,22,23	1.32	4 (21%)	27,32,35	2.34	10 (37%)
21	PSU	x	39	21	18,21,22	1.34	2 (11%)	21,30,33	2.13	4 (19%)
21	7MG	x	46	21	23,26,27	1.29	3 (13%)	27,39,42	2.74	7 (25%)
21	4SU	x	8	21	18,21,22	1.90	4 (22%)	25,30,33	2.42	5 (20%)
21	MIA	x	37	21	28,31,32	2.32	6 (21%)	38,44,47	2.78	14 (36%)
21	PSU	x	55	21	18,21,22	1.37	2 (11%)	21,30,33	2.03	5 (23%)
21	PSU	x	32	21	18,21,22	1.38	3 (16%)	21,30,33	2.02	4 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	5MU	x	54	21	-	0/7/25/26	0/2/2/2
21	PSU	x	39	21	-	1/7/25/26	0/2/2/2
21	7MG	x	46	21	-	4/7/37/38	0/3/3/3
21	4SU	x	8	21	-	2/7/25/26	0/2/2/2
21	MIA	x	37	21	-	3/15/33/34	0/3/3/3
21	PSU	x	55	21	-	2/7/25/26	0/2/2/2
21	PSU	x	32	21	-	0/7/25/26	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	37	MIA	C2-S10	-7.12	1.69	1.75
21	x	37	MIA	C13-C14	6.78	1.52	1.32
21	x	8	4SU	C4-S4	-5.27	1.59	1.68
21	x	37	MIA	C5-C4	4.55	1.47	1.39
21	x	55	PSU	C6-C5	3.40	1.39	1.35
21	x	8	4SU	C4-N3	-3.39	1.34	1.37
21	x	46	7MG	C5-C4	3.20	1.47	1.37
21	x	8	4SU	C5-C4	-3.13	1.38	1.42
21	x	39	PSU	C6-C5	3.10	1.38	1.35
21	x	32	PSU	C6-C5	3.03	1.38	1.35
21	x	46	7MG	C4-N9	-2.79	1.34	1.37
21	x	54	5MU	C6-N1	-2.72	1.33	1.38
21	x	37	MIA	C5-C6	2.70	1.48	1.41
21	x	54	5MU	C4-N3	-2.61	1.34	1.38
21	x	32	PSU	C4-N3	-2.58	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	46	7MG	C6-N1	-2.58	1.34	1.38
21	x	55	PSU	C4-N3	-2.51	1.34	1.38
21	x	39	PSU	C4-N3	-2.50	1.34	1.38
21	x	37	MIA	C5-N7	-2.36	1.34	1.39
21	x	37	MIA	C8-N7	2.28	1.36	1.31
21	x	54	5MU	C2-N1	2.21	1.41	1.38
21	x	8	4SU	C2-N3	-2.13	1.34	1.38
21	x	54	5MU	C6-C5	2.13	1.38	1.34
21	x	32	PSU	C2-N1	-2.06	1.34	1.36

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	x	46	7MG	N9-C4-N3	9.52	139.41	125.46
21	x	37	MIA	C12-C13-C14	-8.37	111.98	127.01
21	x	37	MIA	C5-C4-N3	-8.22	118.52	127.18
21	x	8	4SU	C4-N3-C2	-7.18	120.43	127.31
21	x	39	PSU	N1-C2-N3	6.44	121.96	115.17
21	x	8	4SU	C5-C4-N3	6.34	120.64	114.75
21	x	37	MIA	N3-C4-N9	6.26	134.93	126.99
21	x	55	PSU	N1-C2-N3	6.25	121.76	115.17
21	x	32	PSU	N1-C2-N3	6.18	121.69	115.17
21	x	46	7MG	C5-C4-N3	-5.61	117.59	128.13
21	x	54	5MU	C4-N3-C2	-5.60	120.00	127.34
21	x	46	7MG	N9-C8-N7	-5.34	95.80	103.37
21	x	54	5MU	N3-C2-N1	5.25	121.72	114.89
21	x	8	4SU	C5-C4-S4	-4.87	118.74	124.31
21	x	54	5MU	O4-C4-C5	-4.71	119.53	124.92
21	x	46	7MG	C2-N3-C4	4.57	120.18	112.30
21	x	39	PSU	C4-N3-C2	-4.54	120.11	126.37
21	x	32	PSU	O2-C2-N1	-4.13	118.53	122.79
21	x	37	MIA	C16-C14-C13	-4.07	110.44	122.66
21	x	55	PSU	C4-N3-C2	-3.99	120.87	126.37
21	x	8	4SU	N3-C2-N1	3.91	119.98	114.89
21	x	54	5MU	C5-C4-N3	3.90	118.71	115.32
21	x	54	5MU	C5-C6-N1	-3.82	119.16	123.31
21	x	37	MIA	C15-C14-C13	-3.77	111.33	122.66
21	x	32	PSU	C4-N3-C2	-3.72	121.25	126.37
21	x	37	MIA	C11-S10-C2	-3.69	99.48	102.25
21	x	55	PSU	O2-C2-N1	-3.65	119.02	122.79
21	x	39	PSU	O2-C2-N1	-3.59	119.08	122.79
21	x	37	MIA	C4-C5-N7	-3.53	106.55	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	x	37	MIA	C2-N3-C4	3.37	121.13	112.29
21	x	54	5MU	O2-C2-N1	-3.23	118.59	122.80
21	x	37	MIA	C6-C5-N7	3.10	135.81	132.43
21	x	46	7MG	C5-C6-N1	3.01	116.25	110.94
21	x	46	7MG	C5-C4-N9	-2.62	102.98	106.33
21	x	37	MIA	C5-N7-C8	2.47	107.33	103.45
21	x	37	MIA	C4-N9-C8	2.31	108.16	105.74
21	x	54	5MU	C5M-C5-C6	-2.30	119.74	122.85
21	x	55	PSU	O4'-C1'-C2'	2.25	108.26	105.15
21	x	32	PSU	O4'-C1'-C2'	2.24	108.25	105.15
21	x	8	4SU	C1'-N1-C2	2.24	121.61	117.59
21	x	54	5MU	C1'-N1-C2	2.23	121.61	117.59
21	x	37	MIA	C2-N1-C6	2.19	121.70	117.54
21	x	37	MIA	N3-C2-N1	-2.18	123.02	127.00
21	x	54	5MU	C6-C5-C4	2.13	119.78	118.02
21	x	39	PSU	C6-C5-C4	-2.11	116.75	118.17
21	x	46	7MG	O6-C6-C5	-2.10	122.45	127.62
21	x	54	5MU	C1'-N1-C6	-2.09	117.70	121.15
21	x	37	MIA	N6-C6-N1	2.07	121.11	118.33
21	x	55	PSU	C5-C6-N1	-2.02	119.34	122.14

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	x	37	MIA	C12-C13-C14-C15
21	x	8	4SU	O4'-C4'-C5'-O5'
21	x	46	7MG	O4'-C1'-N9-C8
21	x	46	7MG	O4'-C1'-N9-C4
21	x	8	4SU	C3'-C4'-C5'-O5'
21	x	37	MIA	C5-C6-N6-C12
21	x	55	PSU	O4'-C1'-C5-C4
21	x	46	7MG	O4'-C4'-C5'-O5'
21	x	39	PSU	O4'-C4'-C5'-O5'
21	x	37	MIA	N1-C6-N6-C12
21	x	55	PSU	O4'-C1'-C5-C6
21	x	46	7MG	C4'-C5'-O5'-P

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	x	54	5MU	6	0
21	x	46	7MG	1	0
21	x	8	4SU	2	0
21	x	55	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 103 ligands modelled in this entry, 103 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.

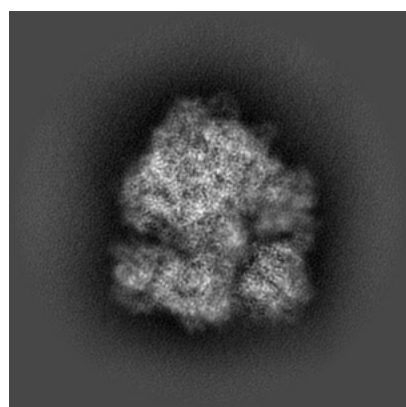
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42561. These allow visual inspection of the internal detail of the map and identification of artifacts.

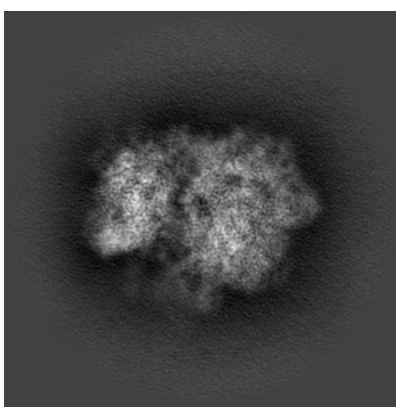
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

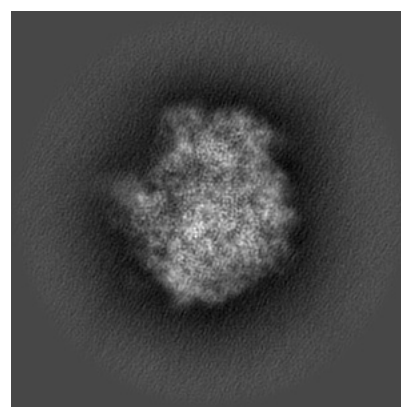
6.1.1 Primary map



X



Y

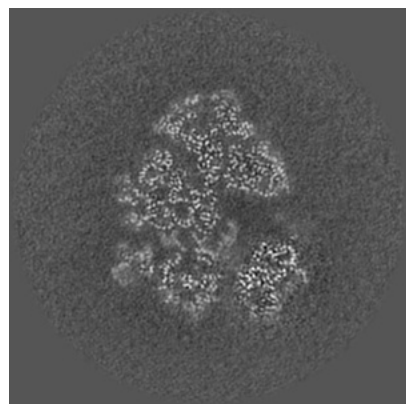


Z

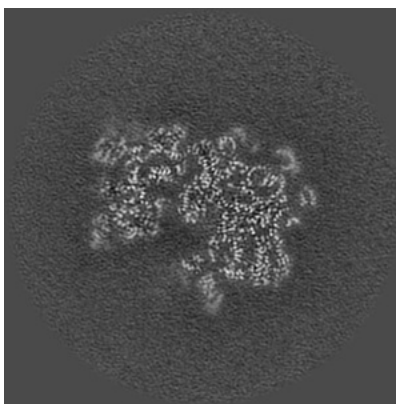
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

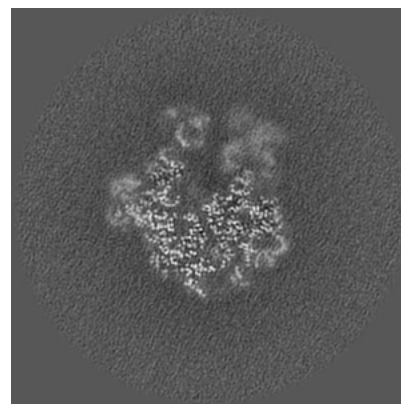
6.2.1 Primary map



X Index: 256



Y Index: 256

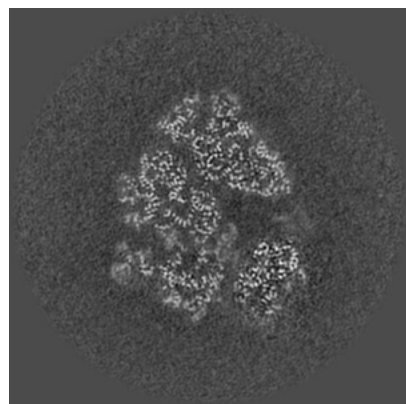


Z Index: 256

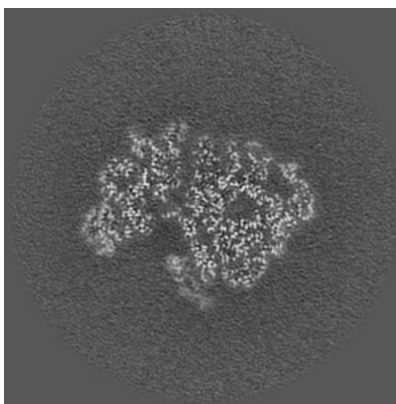
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

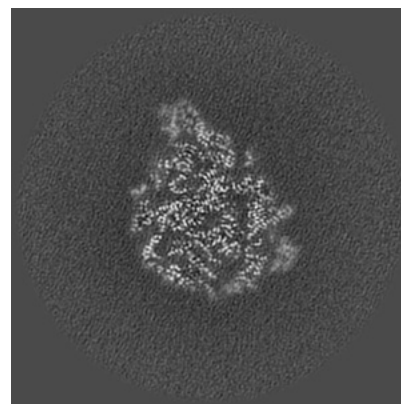
6.3.1 Primary map



X Index: 254



Y Index: 234

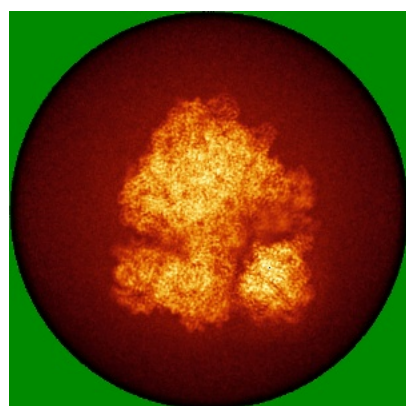


Z Index: 296

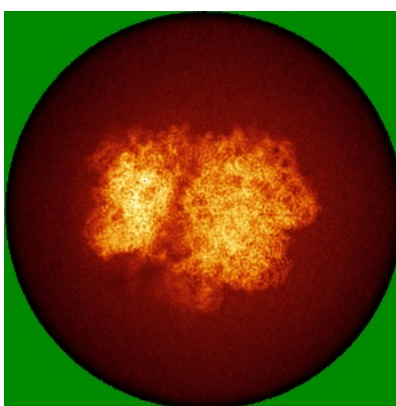
The images above show the largest variance slices of the map in three orthogonal directions.

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

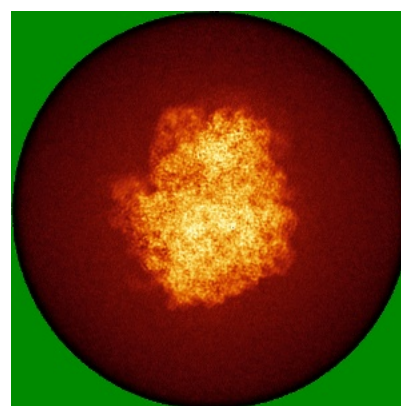
6.4.1 Primary map



X



Y

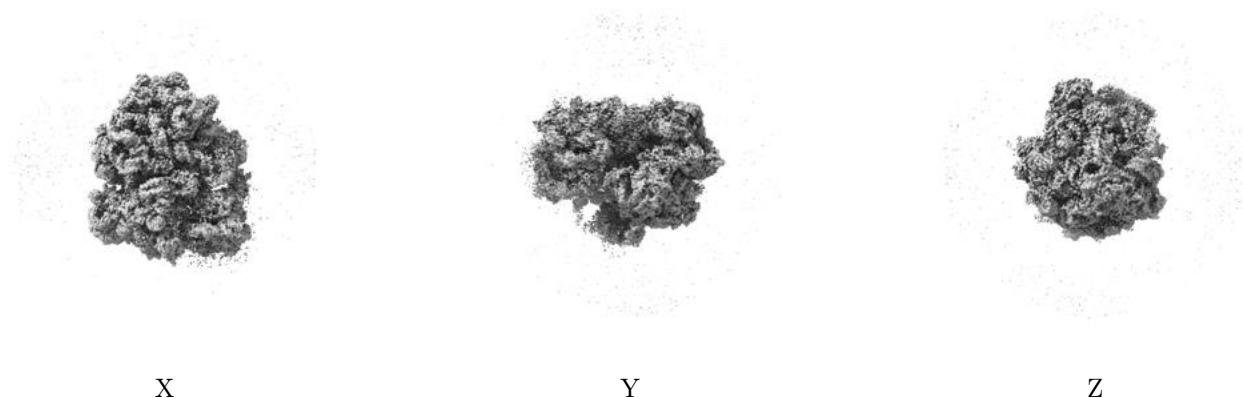


Z

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 3.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

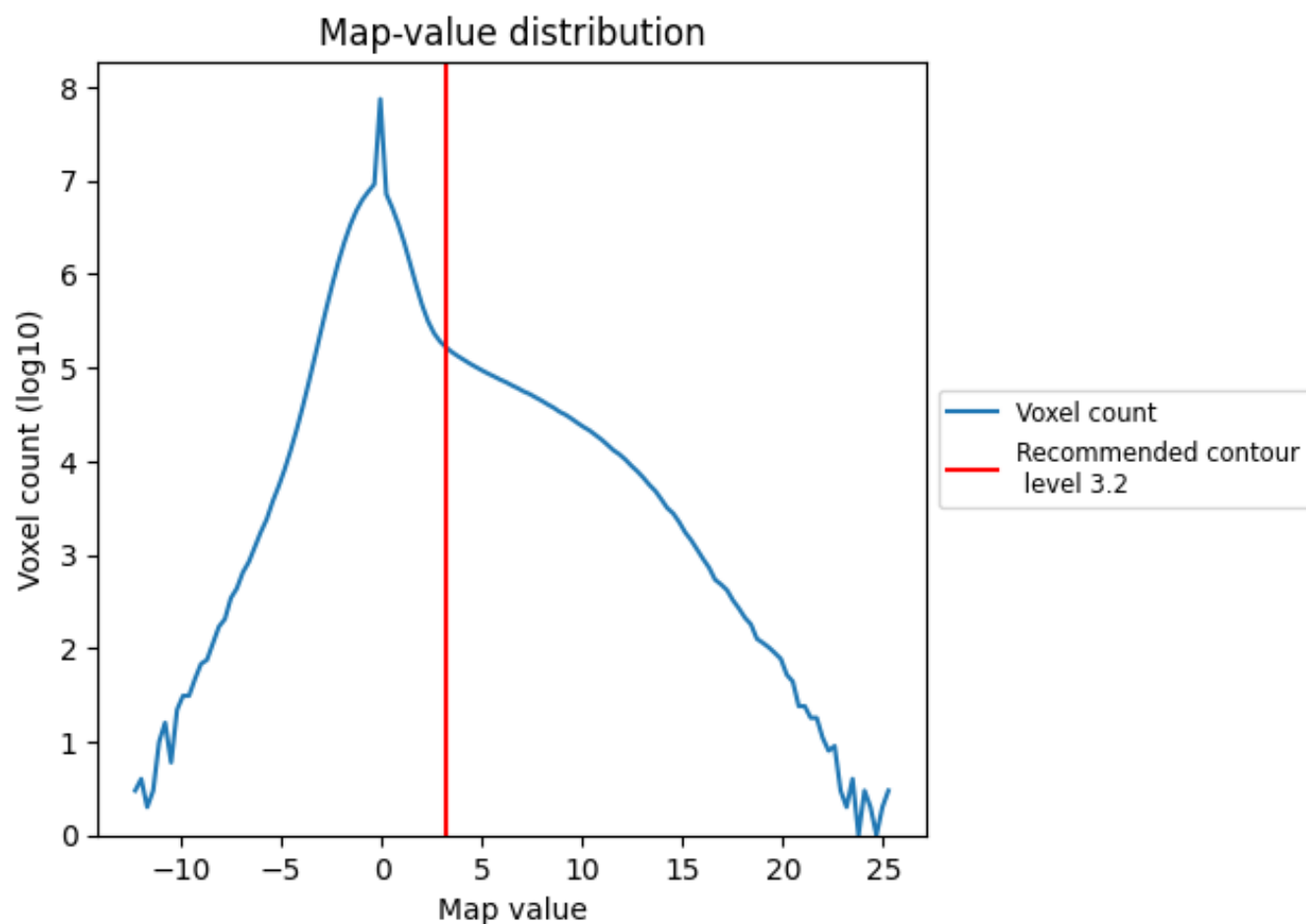
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

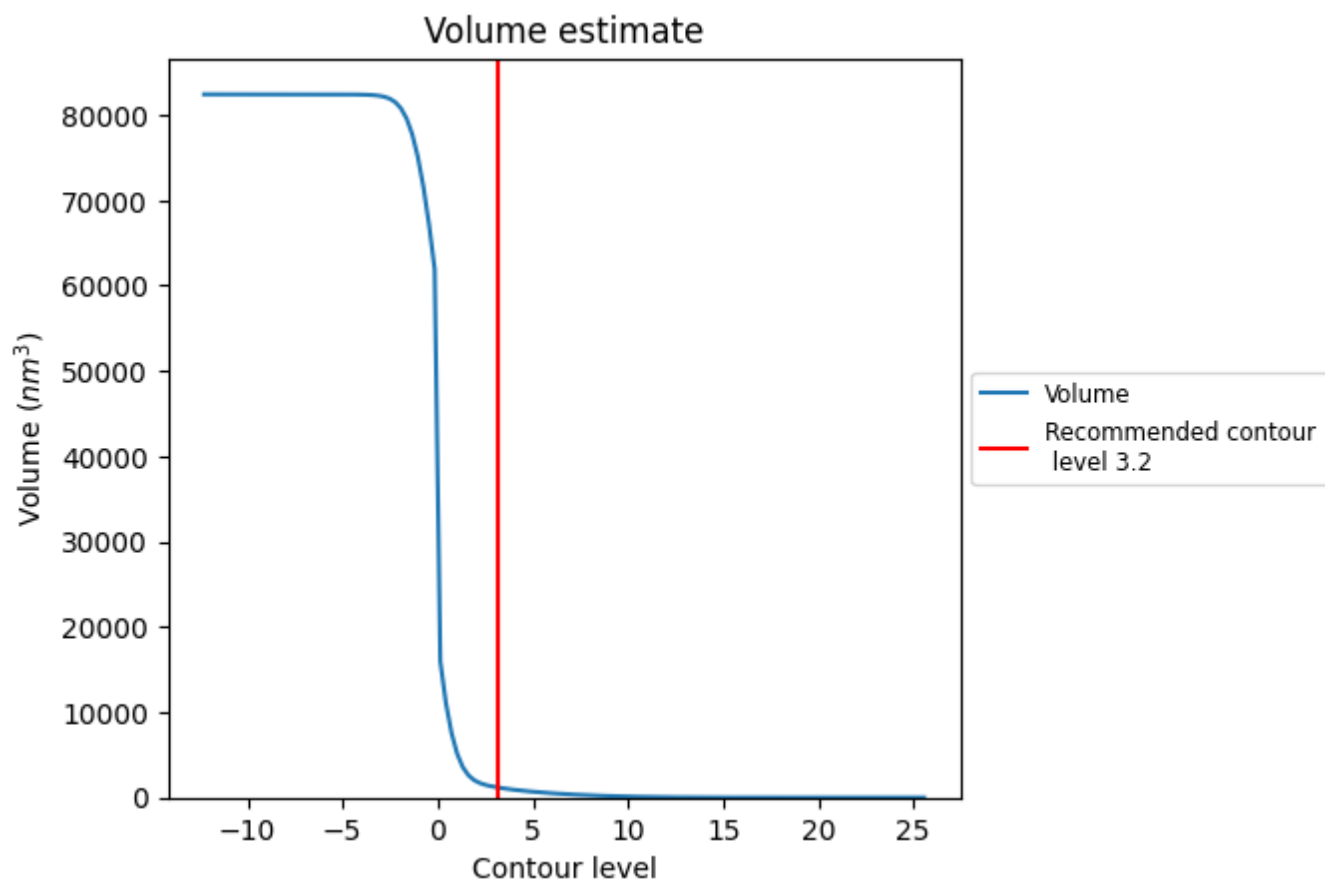
This section contains the results of statistical analysis of the map.

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.

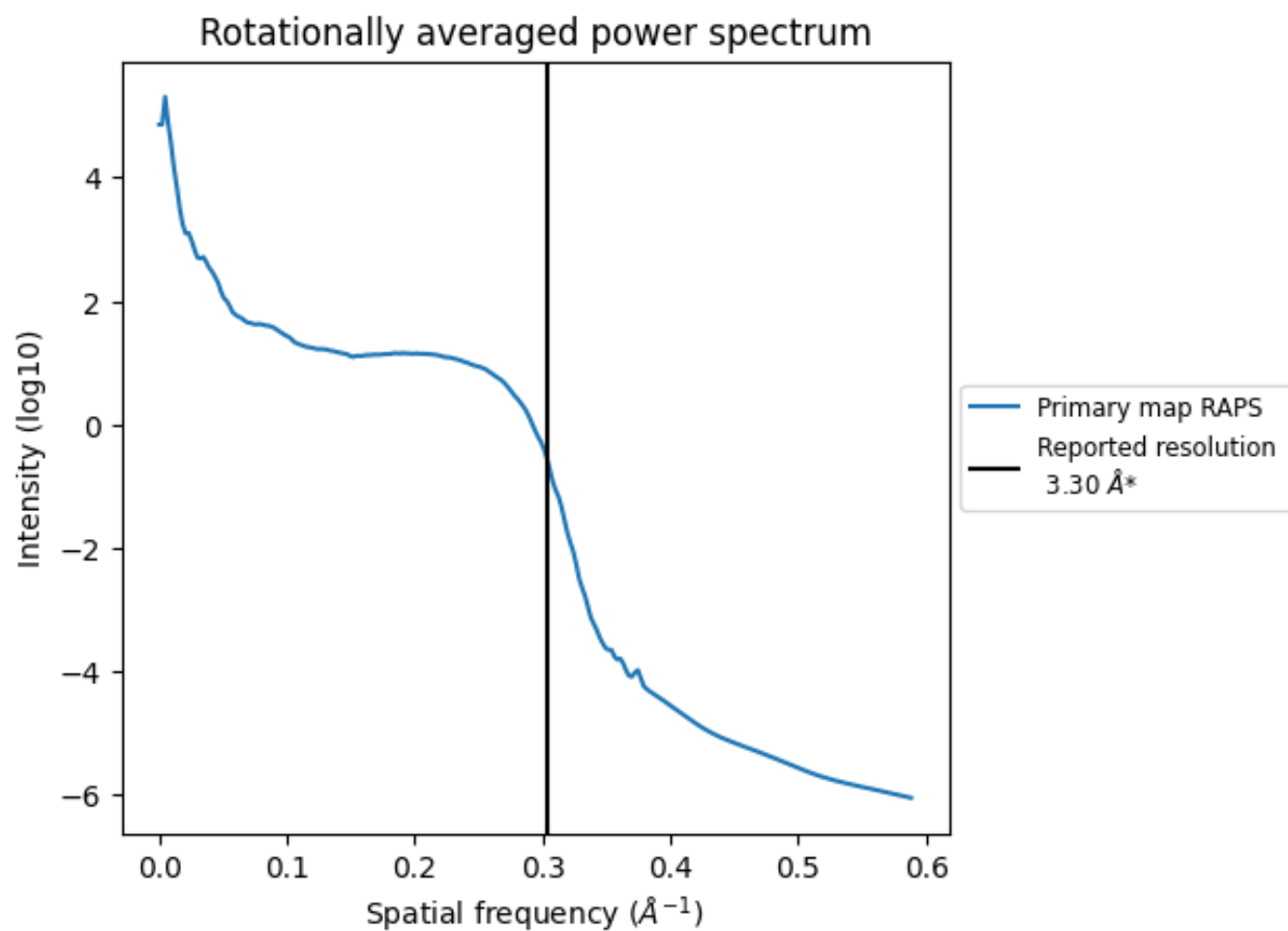
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1168 nm³; this corresponds to an approximate mass of 1055 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



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

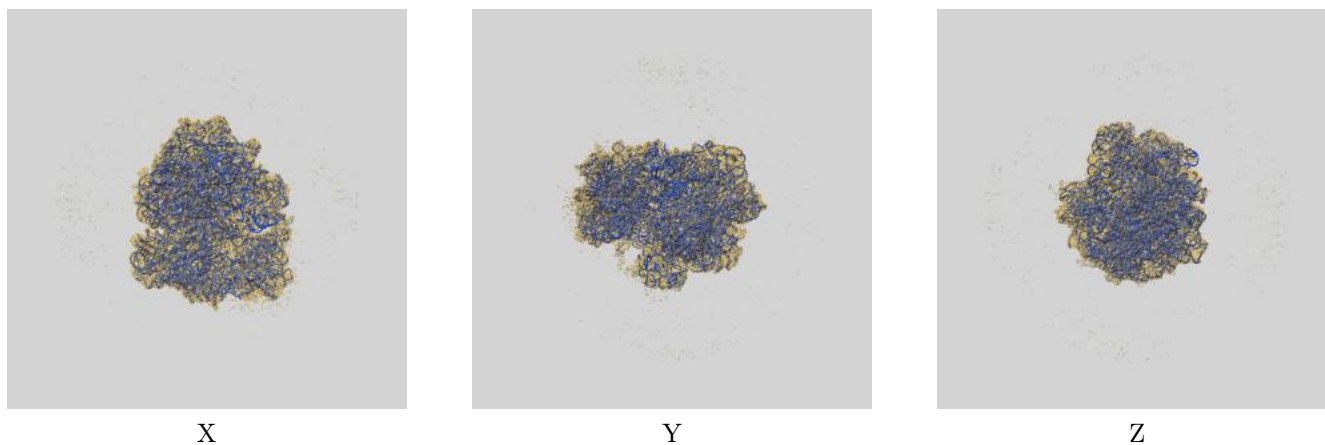
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

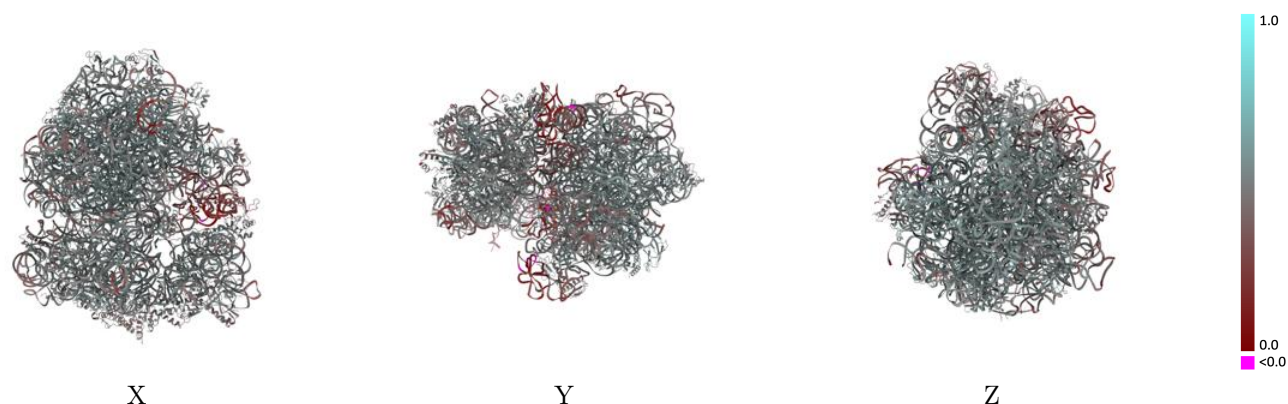
This section contains information regarding the fit between EMDB map EMD-42561 and PDB model 8UU6. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



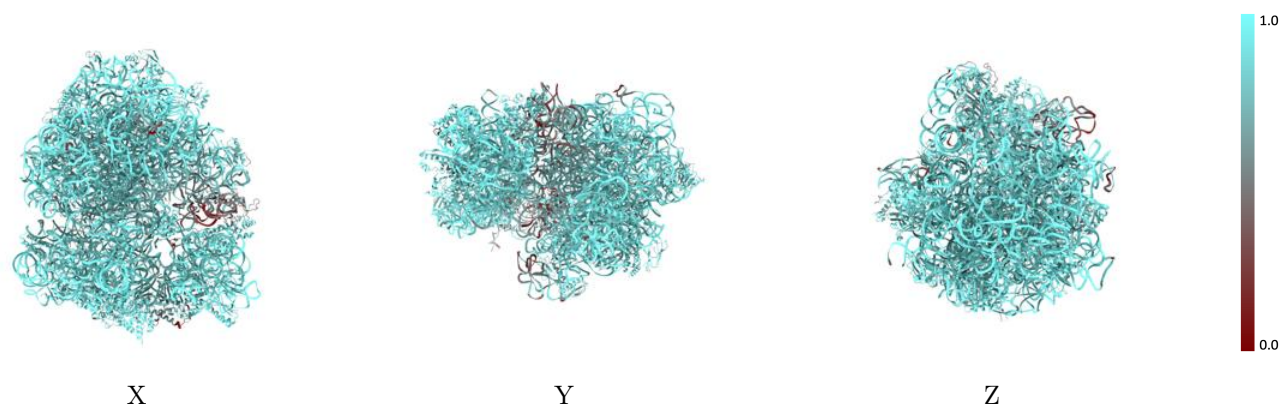
The images above show the 3D surface view of the map at the recommended contour level 3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



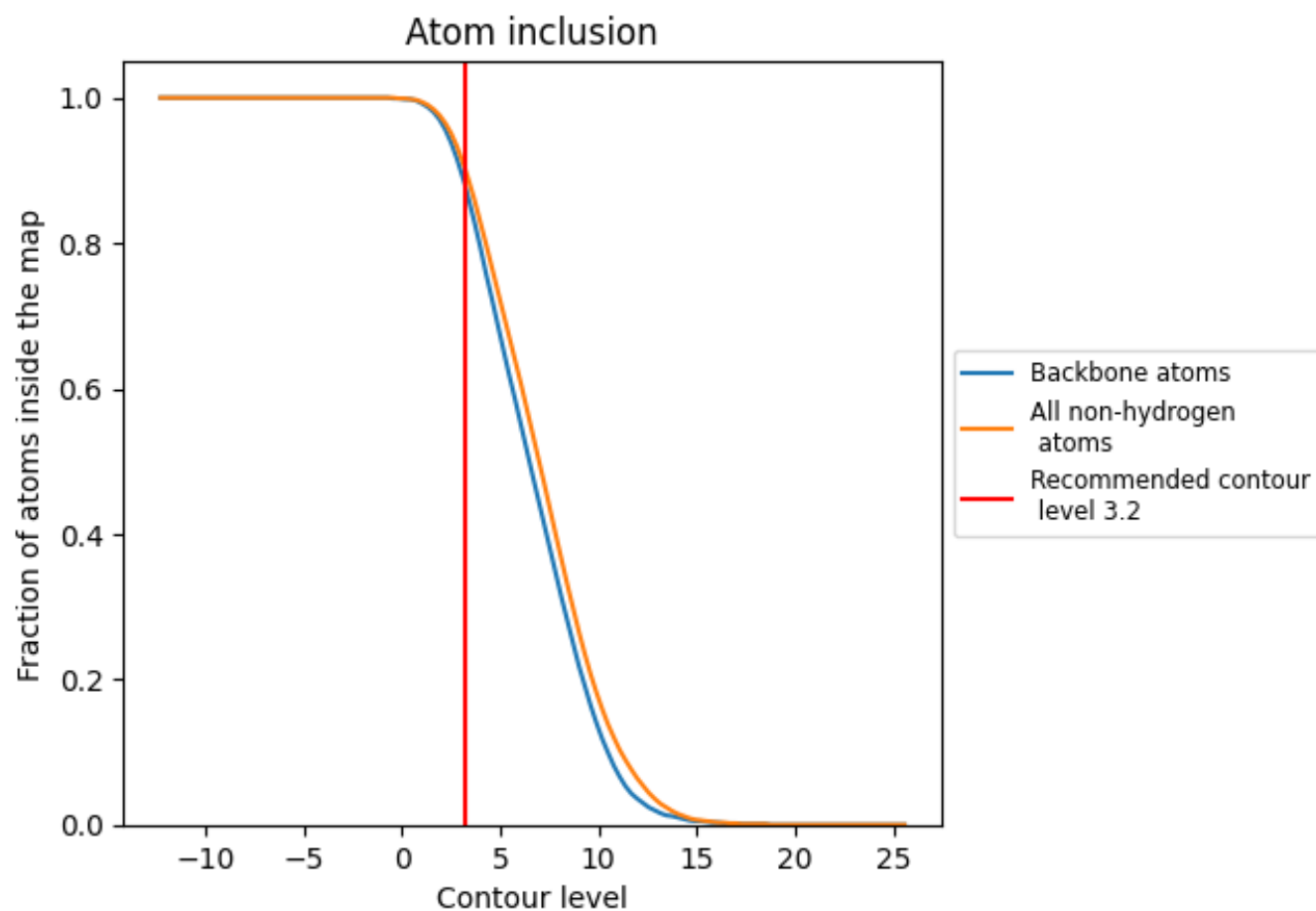
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 90% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9030	 0.4890
1	 0.8740	 0.4880
2	 0.8650	 0.5280
3	 0.4180	 0.3130
4	 0.8540	 0.5110
5	 0.8500	 0.5350
6	 0.8990	 0.5620
7	 0.9190	 0.5670
8	 0.8220	 0.5480
A	 0.9230	 0.4900
B	 0.9350	 0.4280
C	 0.8570	 0.5560
D	 0.8820	 0.5520
E	 0.8670	 0.5280
F	 0.5630	 0.3370
G	 0.8240	 0.4470
L	 0.9150	 0.5550
M	 0.7640	 0.5390
N	 0.8800	 0.5330
O	 0.8500	 0.5280
P	 0.8810	 0.5350
Q	 0.8440	 0.4580
R	 0.8500	 0.5430
S	 0.9050	 0.5490
T	 0.9020	 0.5490
U	 0.8780	 0.5470
V	 0.8390	 0.5230
W	 0.8370	 0.5090
Y	 0.8930	 0.5530
Z	 0.8880	 0.5500
a	 0.9330	 0.4730
b	 0.8320	 0.4720
c	 0.8820	 0.5100
d	 0.8990	 0.4840
e	 0.8560	 0.5140



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Chain	Atom inclusion	Q-score
f	 0.8610	 0.4800
g	 0.8880	 0.4840
h	 0.9190	 0.5170
i	 0.9560	 0.5090
j	 0.9230	 0.4930
k	 0.8670	 0.4890
l	 0.8810	 0.5290
m	 0.8900	 0.4940
n	 0.9580	 0.5400
o	 0.8230	 0.5070
p	 0.9200	 0.5090
q	 0.9150	 0.5070
r	 0.9180	 0.5100
s	 0.7900	 0.5220
t	 0.9080	 0.4810
w	 0.8250	 0.4920
x	 0.6190	 0.3410