



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 03:17 PM UTC

PDB ID : 8VSA / pdb_00008vsa
EMDB ID : EMD-43491
Title : Endogenous trans-translation complex with tmRNA*SmpB in the P site and alanyl-tRNA in the A site of E. coli 70S ribosome
Authors : Teran, D.; Zhang, Y.; Korostelev, A.A.
Deposited on : 2024-01-23
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

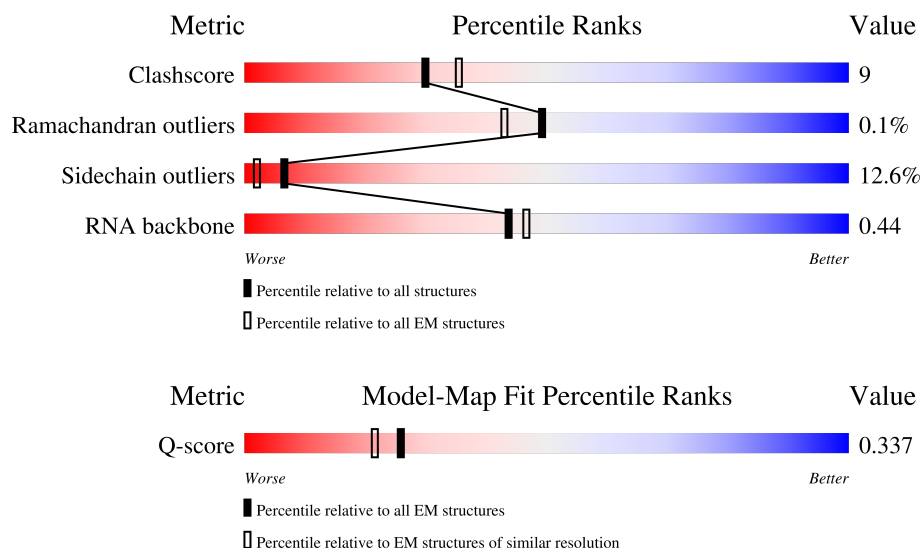
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

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



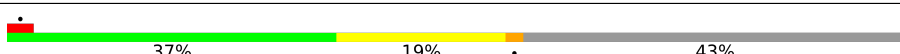
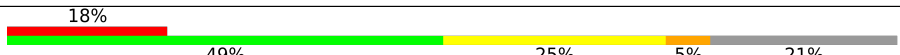
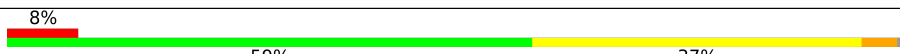
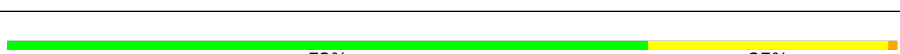
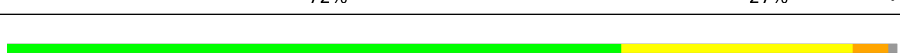
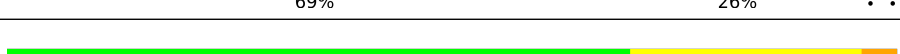
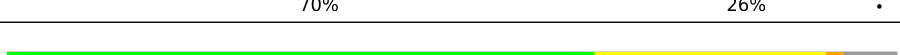
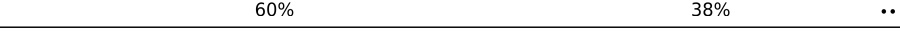
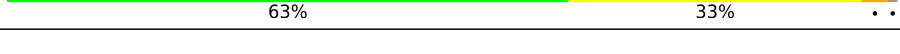
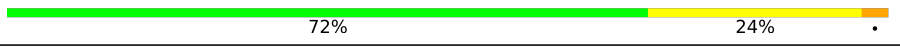
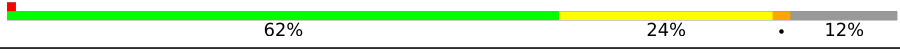
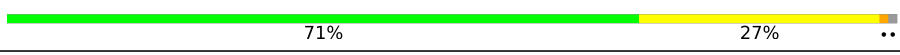
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	L02	273	
2	L03	209	
3	L04	201	

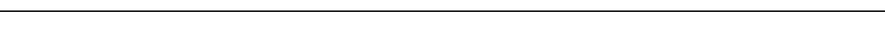
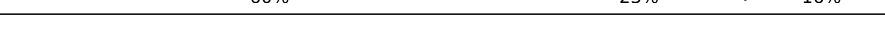
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Mol	Chain	Length	Quality of chain
4	L05	179	
5	L06	177	
6	L09	149	
7	L1	234	
8	L10	165	
9	L11	142	
10	L13	142	
11	L14	123	
12	L15	144	
13	L16	136	
14	L17	127	
15	L18	117	
16	L19	115	
17	L20	118	
18	L21	103	
19	L22	110	
20	L23	100	
21	L24	104	
22	L25	94	
23	L27	85	
24	L28	78	
25	L29	63	
26	L30	59	
27	L31	45	
28	L32	57	

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Mol	Chain	Length	Quality of chain
29	L33	55	
30	L34	46	
31	L35	65	
32	L36	38	
33	23S	2903	
34	5S	120	
35	TMRN	363	
36	16S	1539	
37	ATRN	76	
38	S02	241	
39	S03	233	
40	S04	206	
41	S05	167	
42	S06	135	
43	S07	179	
44	S08	130	
45	S09	130	
46	S10	103	
47	S11	129	
48	S12	124	
49	S13	118	
50	S14	101	
51	S15	89	
52	S16	82	
53	S17	84	

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Mol	Chain	Length	Quality of chain
54	S18	75	
55	S19	92	
56	S20	87	
57	S21	71	
58	SMPB	150	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 155832 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L02	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L03	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L04	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L05	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L06	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L1	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L15	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L18	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L20	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 18 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	L24	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	L25	94	Total	C	N	O	S	
			753	479	137	134	3	0

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L27	75	Total	C	N	O	S	
			575	356	116	102	1	0

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	L28	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	L29	63	Total	C	N	O	S	
			509	313	99	95	2	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L30	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 27 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	L31	45	Total	C	N	O	S	
			351	219	61	65	6	0

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L33	50	Total	C	N	O		0	0
			409	263	75	71			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 33 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	23S	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
23S	747	C	U	variant	GB 1036415628

- Molecule 34 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5S	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5S	120	A	U	conflict	GB 1370526515

- Molecule 35 is a RNA chain called TMRN.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	TMRN	363	Total	C	N	O	P	0	0
			7758	3465	1410	2520	363		

- Molecule 36 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	16S	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 37 is a RNA chain called A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ATRN	76	Total	C	N	O	P	0	0
			1621	722	289	534	76		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	S02	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S03	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 40 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S04	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S05	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S06	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S07	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S08	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 45 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S09	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S10	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S11	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S12	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S13	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S14	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 51 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S15	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 52 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S16	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S17	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S18	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S19	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S20	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 57 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S21	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

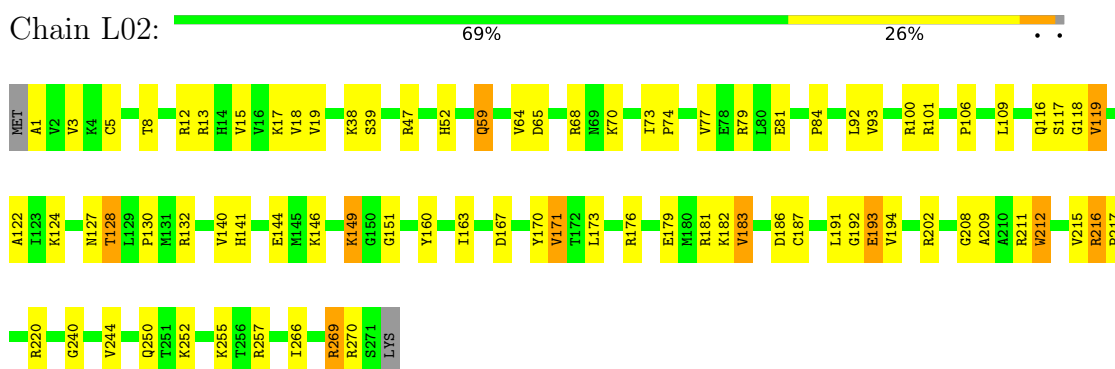
- Molecule 58 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SMPB	150	Total	C	N	O	S	0	0
			1209	763	226	216	4		

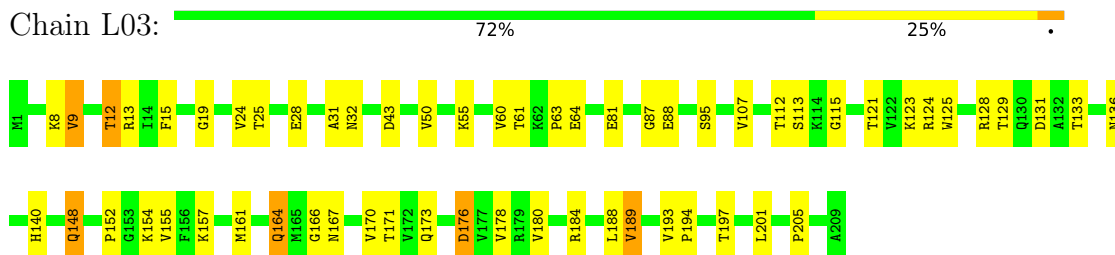
3 Residue-property plots

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

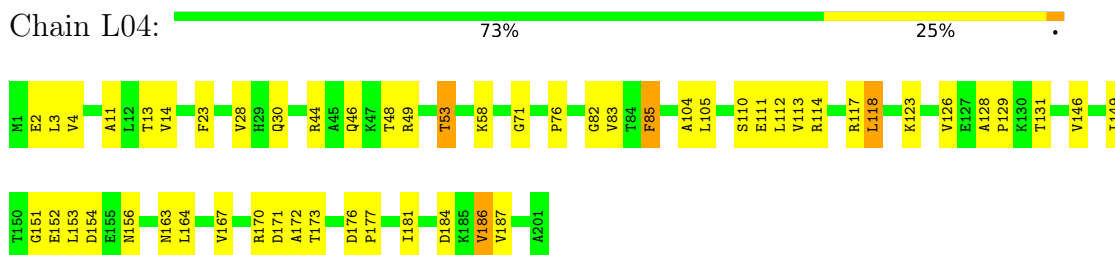
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

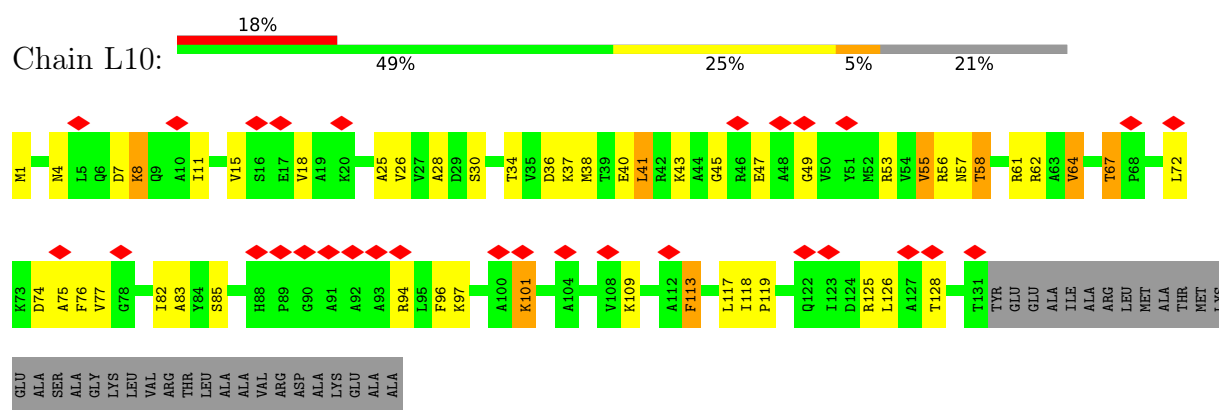


• Molecule 3: 50S ribosomal protein L4

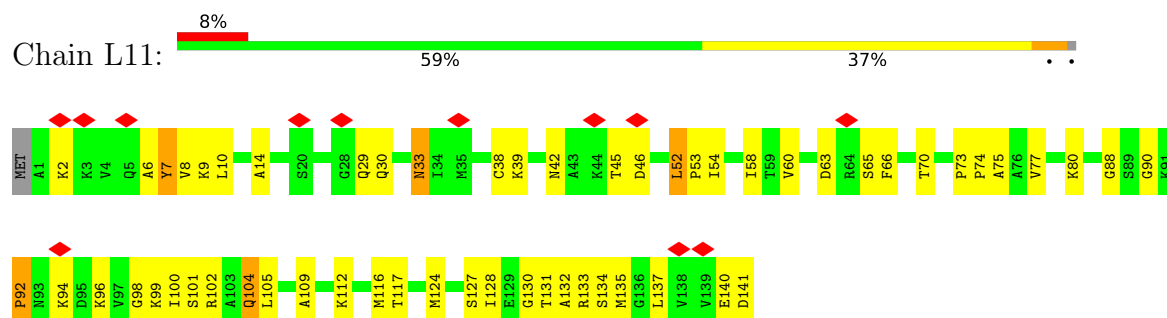


• Molecule 4: 50S ribosomal protein L5

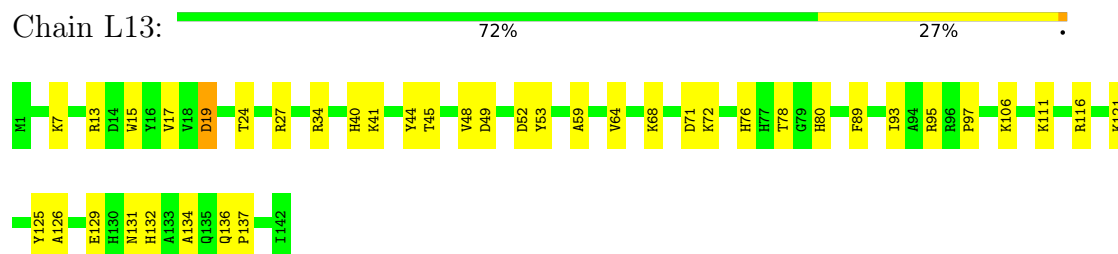




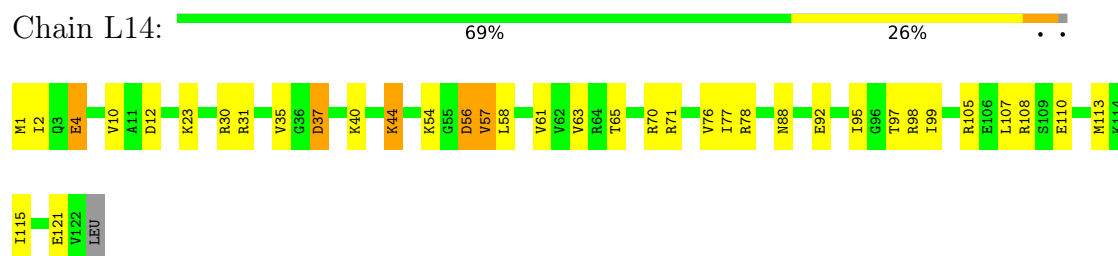
- Molecule 9: 50S ribosomal protein L11



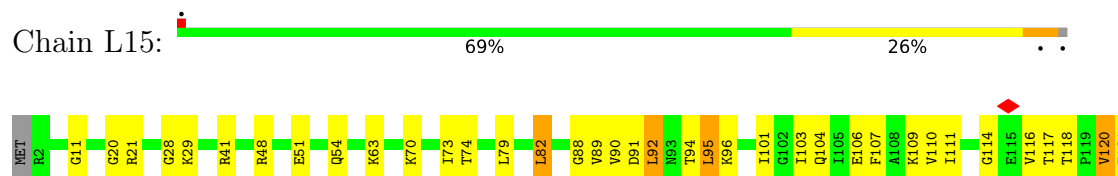
- Molecule 10: 50S ribosomal protein L13



- Molecule 11: 50S ribosomal protein L14



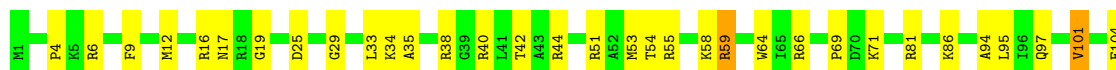
- Molecule 12: 50S ribosomal protein L15





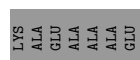
- Molecule 13: 50S ribosomal protein L16

Chain L16: 70% 26%



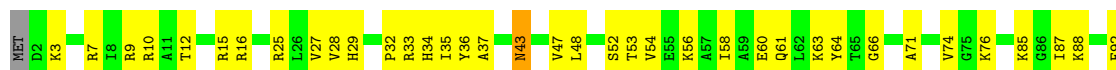
- Molecule 14: Large ribosomal subunit protein bL17

Chain L17: 66% 26% 6%



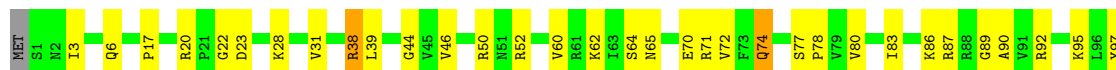
- Molecule 15: 50S ribosomal protein L18

Chain L18: 60% 38% 2%



- Molecule 16: 50S ribosomal protein L19

Chain L19: 63% 33% 4%

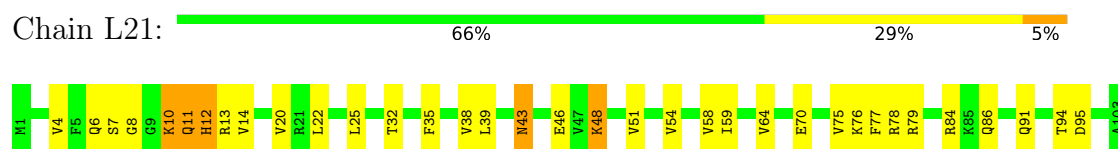


- Molecule 17: 50S ribosomal protein L20

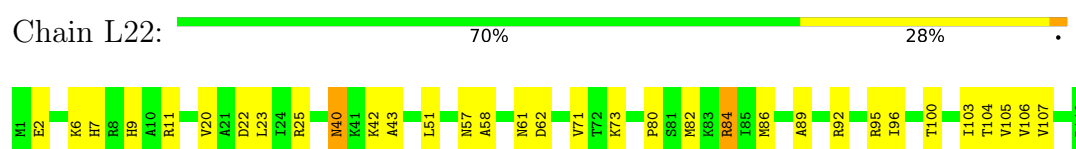
Chain L20: 71% 27% 2%



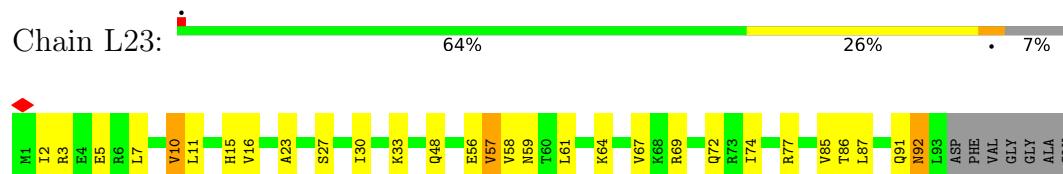
- Molecule 18: Ribosomal protein L21



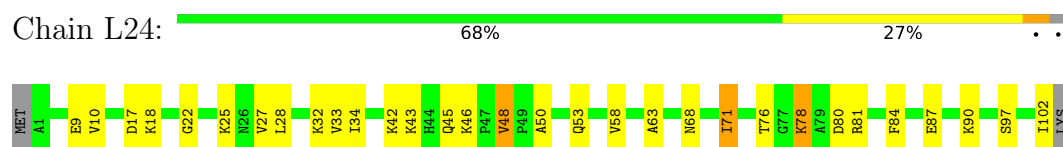
- Molecule 19: 50S ribosomal protein L22



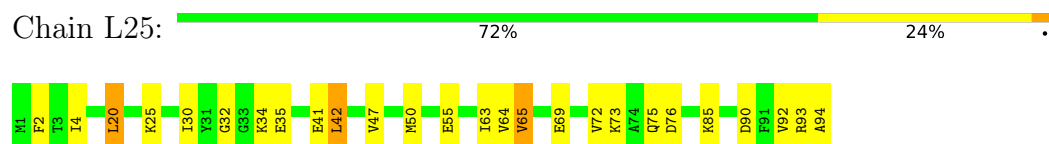
- Molecule 20: 50S ribosomal protein L23



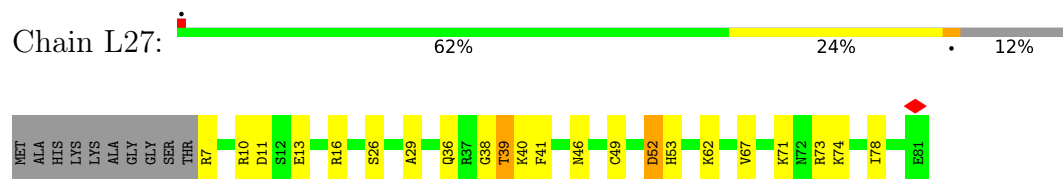
- Molecule 21: 50S ribosomal protein L24



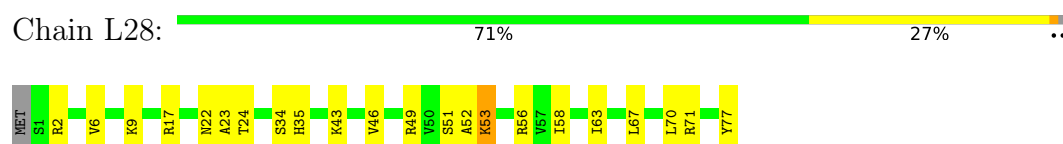
- Molecule 22: 50S ribosomal protein L25



- Molecule 23: 50S ribosomal protein L27



- Molecule 24: 50S ribosomal protein L28



• Molecule 25: 50S ribosomal protein L29

Chain L29:  70% 25% 5%

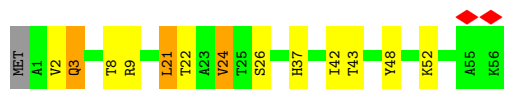
• Molecule 26: Large ribosomal subunit protein uL30

Chain L30:  64% 34% .

• Molecule 27: Large ribosomal subunit protein bL31

Chain L31:  53% 31% 16%

• Molecule 28: 50S ribosomal protein L32

Chain L32:  75% 18% 5% .

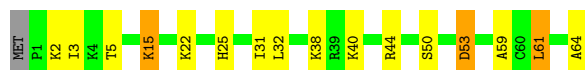
• Molecule 29: Large ribosomal subunit protein bL33

Chain L33:  58% 25% 7% 9%

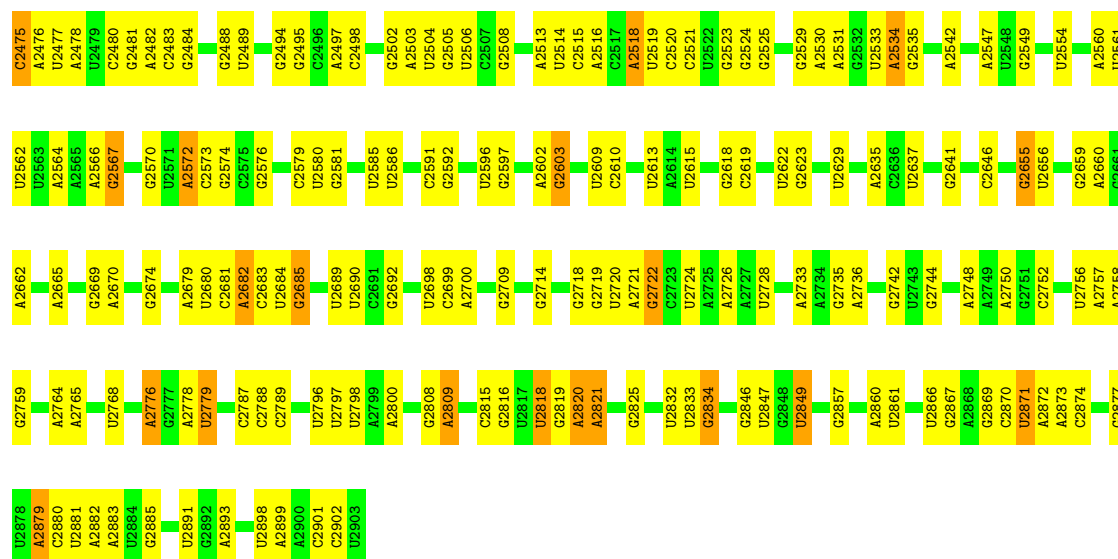
• Molecule 30: 50S ribosomal protein L34

Chain L34:  63% 33% .

• Molecule 31: 50S ribosomal protein L35

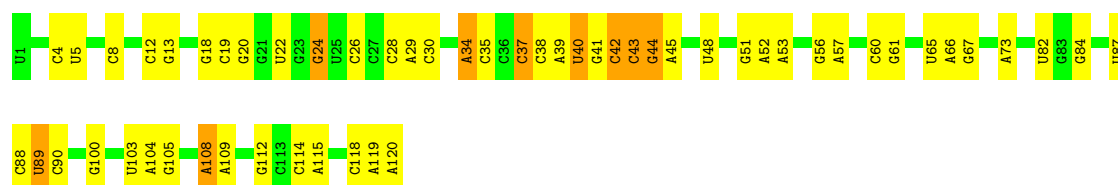
Chain L35:  74% 20% 5% .

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G2382	U1094	G1182	U1294	A1386	G1478	A1571	A1688	A1787	U1883	G1972	U2075	G2145	U2220	C2301	G2382
G2383	A1095	A1186	U1294	A1387	G1482	A1578	A1669	C1788	G1884	G1980	U2076	C2146	U2221	G2302	G2383
C2385	U1097	G1187	G1296	G1388	G1483	A1579	G1674	A1791	A1889	A1982	U2077	U2147	C2221	U2304	U2384
	A1098	U1188	G1297	A1392	G1488	A1580	G1675	U1796	A1890	U1982	C2078	U2148	G2223	C2305	C2385
G2391	U1101	A1189	C1297	A1393	G1489	A1581	A1676	U1797	G1891	G1983	U2079	G2150	A2225	G2306	G2391
A2392	C1102	G1190	U1299	A1394	A1490	U1584	A1677	U1798	G1898	U1991	G2083	U2151	A2226	G2307	A2392
U2393	C1103	U1199	G1300	A1395	G1491	G1587	A1678	G1799	U1899	G1992	C2084	U2152	C2226	A2309	U2393
C2394	C1104	U1205	A1302	G1401	G1492	G1588	U1679	G1800	A1900	U1993	U2086	U2155	U2234	C2310	C2394
G2396	U1105	G1206	A1305	U1402	U1497	U1589	U1688	G1799	A1901	C1996	G2087	G2156	G2235	U2312	C2396
G2397	G1106		C1306	U1403	U1497	U1590	U1689	A1801	A1902	C1997	A2088	G2157	G2236	C2313	G2397
			U1405	G1404	G1501	A1591	U1693	A1802	G1906	A1998		A2158	G2237	A2314	G2397
U2402	G1110		A1307	A1406	G1504	U1594	A1700	G1807	G1907	C1999	U2092	G2162	G2238	G2315	U2402
C2403	A1111	G1212	U1307	U1406	A1504	U1594	A1701	A1808	C1908	G2002	G2093	G2163	G2239	G2316	C2403
U2404	U1112	G1218	G1310	G1408	A1508	A1597	G1715	A1809	C1909	G2002	U2093	A2164	G2240	A2317	U2404
G2405	U1113		G1314	G1408	A1509	A1598	U1716	G1814	G1910	G2010	C2096	C2165	U2241	G2318	G2405
A2406	C1114	U1222	C1315	U1412	A1510	A1598	U1720	A1815	U1911	G2011	A2097	U2166	G2242	G2319	A2406
A2407	G1115	U1223	C1316	U1413	G1514	G1601	U1724	G1816	A1912	U2012	U2098	U2167	U2243	U2320	A2407
U2408	U1116	G1225	C1319	U1414	G1514	G1604	G1724	G1817	A1913	G2013	G2099	G2168	U2244	C2326	U2408
G2409		G1226	C1320	U1415	G1515	C1604	G1724	U1818	U1914	A2014	G2100	A2169	U2245	A2327	G2409
A2411	U1119	G1227	A1321	U1416	G1516	C1607	U1729	A1819	A1915	A2015	G2101	A2170	U2246	G2410	A2411
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U2419	G1122		U1231	U1419	G1516	A1608	G1731	A1820	A1917	A2017	G2103	C2172	U2248	G2330	U2419
C2420			U1234	U1420	G1522	A1609	G1732	A1821	C1920	A2018	C2104	A2173	U2249	G2331	C2420
U2423	A1126	U1234	U1330	U1421	U1523	A1610	G1733	G1825	G1921	C2021	G2107	C2174	U2250	C2332	U2423
G2424	A1127	G1235	G1331	G1421	G1524	A1611	G1734	G1826	G1922	U2022	G2108	C2175	U2251	A2333	G2424
A2425	G1131	G1236	G1332	A1427	G1525	C1612	U1735	G1827	U1923	C2023	G2110	C2176	U2252	U2334	A2425
	U1132	A1237	G1333	U1428	C1526	G1613	U1736	G1828	G1924	G2024	G2111	C2177	U2253	A2335	A2425
A2426	U1133		C1334	U1429	G1527	A1614	U1737	A1829	G1925	A2030	G2112	C2178	U2254	C2339	A2426
C2427	A1134	C1251	G1335	U1430	G1528	A1615	G1738	C1833	U1931	A2031	U2113	C2179	U2255	A2340	C2427
G2428	C1135	G1252	U1336	U1431	G1529	A1616	U1739	C1834	A1932	A2032	G2114	U2182	U2256	G2428	G2428
A2430	G1138	A1253	G1337	U1432	G1530	A1617	G1740	C1837	A1933	A2033	G2115	U2183	U2257	G2429	A2430
	G1139	U1254	U1338	U1433	G1531	A1618	A1744	G1842	A1934	A2034	G2116	A2184	U2258	C2342	A2430
C2443	G1140	G1256	C1345	U1434	G1532	A1619	G1754	C1843	A1935	A2035	G2117	U2185	U2259	U2343	C2443
U2447	U1141	G1257	U1352	U1435	G1533	A1620	G1755	C1844	A1936	U2039	G2118	U2186	U2260	U2344	U2447
G2444	A1142	G1259	G1356	U1436	G1534	A1621	U1756	U1851	A1937	U2040	G2119	U2187	U2261	G2345	G2444
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C2450	C1152		G1360	U1439	G1537	A1624	U1759	U1854	A1940	G2045	G2122	U2190	U2264	G2348	C2450
U2451	C1153		U1361	U1440	G1538	A1625	A1764	U1855	A1941	A2052	G2123	U2191	U2265	C2350	U2451
	G1154	A1265	A1365	U1441	G1539	A1626	G1765	U1856	A1942	G2053	G2124	U2192	U2266	G2351	G2444
U2457	A1155	A1268	G1368	U1442	G1540	A1627	U1766	U1857	A1943	G2054	G2125	U2193	U2267	A2352	G2445
	G1157		U1372	U1443	G1541	A1628	U1767	U1858	A1944	G2055	G2126	U2194	U2268	C2354	G2446
			G1373	U1444	G1542	A1629	U1768	U1859	A1945	G2056	G2127	U2195	U2269	U2355	G2447
C2473	C1170	G1271	U1374	U1445	G1543	A1630	U1769	U1860	A1946	A2057	U2131	U2196	U2270	G2365	U2449
U2474	G1171	U1272	U1375	U1446	G1544	A1631	U1770	U1861	A1947	G2058	U2132	U2197	U2271	A2369	U2450
	U1172	U1273	U1376	U1447	G1545	A1632	U1771	U1862	A1948	G2059	G2133	U2198	U2272	U2372	A2451
	U1174	A1275	U1377	U1448	G1546	A1633	U1772	U1863	A1949	G2060	U2134	U2199	U2273	U2373	U2457
A1175	U1175	G1278	A1378	U1449	G1547	A1634	U1773	U1864	A1950	A2061	G2135	U2200	U2274	G2374	A2469
U1176	U1176	G1279	A1379	U1450	G1548	A1635	U1774	U1865	A1951	G2062	U2136	U2201	U2275	C2375	U2472
G1177	G1177		G1380	U1451	G1549	A1636	U1775	U1866	A1952	G2063	G2137	U2202	U2276	G2376	G2473
C1178	C1178		A1383	U1452	A1549	A1637	U1776	U1867	A1953	G2064	U2138	U2203	U2277	U2474	U2474
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			U1411	U1481	A1549	A1666	U1805	U1896	A1982	G2093	G2167	U2232	U2306		
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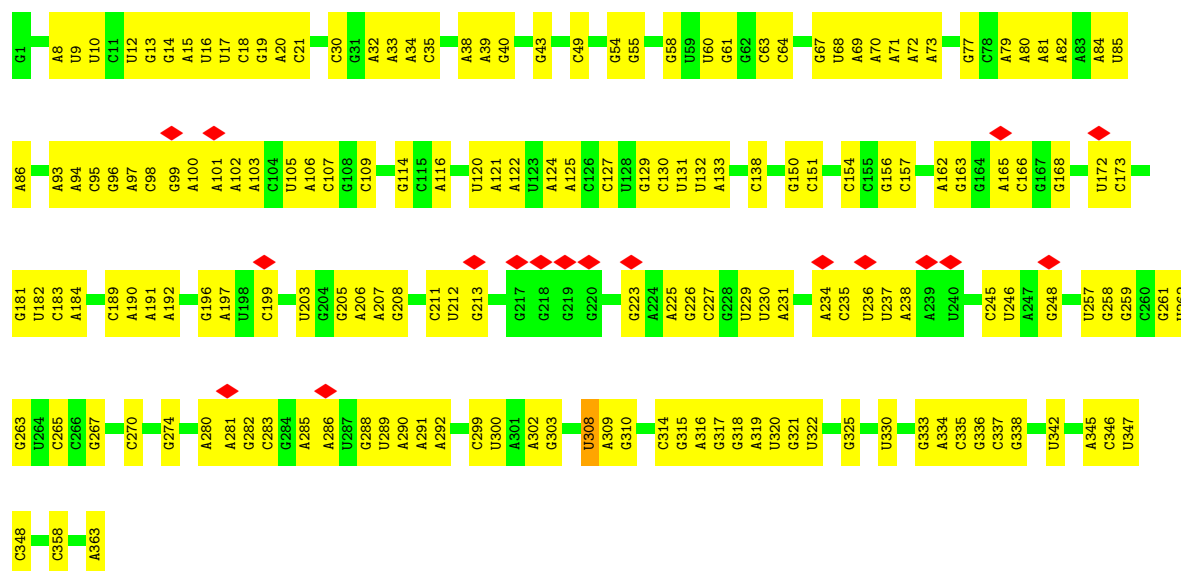
• Molecule 34: 5S ribosomal RNA

Chain 5S: 54% 38% 8%



• Molecule 35: TMRN

Chain TMRN: 5% 53% 47%



• Molecule 36: 16S ribosomal RNA

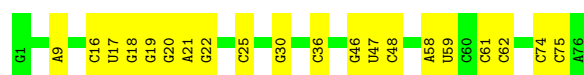
Chain 16S:  52% 41% 7%

C1226	A1145	G1053	A1145	A1146	A1147	A974	G881	A792	G703	C578	C501	G416	G347	G258	A179	U96	A2
A1227	C1146	C1054	A975	A976	A977	A978	U884	C796	U707	U589	G505	U421	G351	A262	A181	C99	A3
C1228	A1147	A1055	G976	G977	G978	G979	G885	C799	C708	C524	G506	C422	C352	A263	A182	C99	G6
A1229	A1151	G1064	A978	A979	A980	A981	G888	G799	U709	U593	C507	G423	A353	C264	C183	A101	A7
G1231	A1152	A1067	C979	C980	C981	C982	A889	U801	G710	C578	U508	G424	G354	G265	G184	G102	A8
U1232	C1158	A1077	C980	C981	C982	C983	A890	U802	G713	A596	A509	G425	C355	G266	U185	C106	G9
U1233	C1159	C1071	U981	U982	U983	U984	G890	G803	U716	G597	A510	U426	A356	C106	C186	G107	U13
U1234	G1160	U1072	A982	A983	A984	A985	A891	G803	A717	G604	U516	G428	U358	G275	G191	G22	G22
A1236	C1162	U1073	C984	C985	C986	C987	G892	C811	A718	U605	C517	U429	G359	G276	A192	G111	C23
C1237	A1163	G1077	G987	G988	G989	G990	A901	U813	C719	C612	C518	A430	G362	A279	C193	G112	U24
A1238	A1164	U1078	G987	G988	G989	G990	G902	A814	C720	G615	C519	A431	G362	G280	C194	G113	C23
A1239	U1165	C1079	U989	U990	U991	U992	G902	A815	U723	G618	C522	A432	G362	G281	C195	G114	U24
G1241	G1166	A1080	U989	U990	U991	U992	G902	A815	U723	G618	C522	A432	G362	G281	C195	G114	C32
C1249	A1167	G1084	C990	C991	C992	C993	A908	A816	G724	C618	A523	U433	U365	U287	G198	G115	A33
A1250	U1168	U1085	U991	U992	U993	U994	A909	A817	A728	C618	A523	U433	U365	U287	G198	G115	A33
A1251	A1169	U1086	U992	U993	U994	U995	C910	A818	U729	C618	A523	U433	U365	U287	G198	G115	A33
A1252	A1170	U1086	U993	U994	U995	U996	C911	A819	A729	C618	A523	U433	U365	U287	G198	G115	A33
G1253	U1173	G1089	A994	A995	A996	A997	C912	U820	A729	C618	A523	U433	U365	U287	G198	G115	A33
A1254	G1174	G1090	U997	U998	U999	U1000	C913	U821	G730	A621	G524	U437	U367	G289	G202	A119	C36
G1255	G1175	A1093	U997	U998	U999	U1000	C913	U821	G730	A621	G524	U437	U367	G289	G202	A119	C36
A1256	A1176	G1094	U997	U998	U999	U1000	C913	U821	G730	A621	G524	U437	U367	G289	G202	A119	C36
A1257	A1180	U1095	G1002	G1003	G1004	G1005	U920	G829	C737	C634	C530	G448	G376	G297	G203	U121	G38
G1258	C1181	C1096	G1003	G1004	G1005	G1006	U921	G830	C738	C634	C530	G448	G376	G297	G203	U121	G38
C1259	U1182	C1097	G1006	G1007	G1008	G1009	U922	G831	C739	A640	C531	G449	G377	A306	G212	G127	A51
A1261	U1183	U1099	G1007	G1008	G1009	G1010	U923	G832	U740	A641	C532	G450	G378	A309	G213	A129	C54
G1184	G1184	C1100	U1009	U1010	U1011	U1012	G925	G833	G741	A642	C533	G451	G379	G310	C214	A130	C54
A1269	A1190	A1101	U1010	U1011	U1012	U1013	G926	U834	G745	C643	C534	G452	G380	C310	C215	A131	A59
G1270	C1191	C1103	U1011	U1012	U1013	U1014	G927	U835	G746	C644	C535	G453	G381	C311	U216	C132	U62
A1271	C1192	G1104	U1012	U1013	U1014	U1015	C932	U836	A747	C645	C536	G454	G382	C312	U217	C133	U62
G1193	A1196	A1105	U1013	U1014	U1015	U1016	C933	U837	A748	C646	C537	G455	G383	C313	U218	C134	C63
A1274	A1197	G1106	U1014	U1015	U1016	U1017	C934	U838	A749	C647	C538	G456	G384	C314	U219	C135	G64
A1275	A1198	C1107	U1015	U1016	U1017	U1018	C935	U839	A750	C648	C539	G457	G385	C315	U220	C136	A65
G1278	A1199	U1108	U1016	U1017	U1018	U1019	G939	U840	C754	C649	C540	G458	G386	C316	C221	G145	U70
G1279	A1201	C1109	U1017	U1018	U1019	U1020	G940	U841	C755	C650	C541	G459	G387	C317	C222	G146	A71
A1280	U1202	A1110	U1018	U1019	U1020	U1021	G941	U842	C756	C651	C542	G460	G388	C318	C223	G147	A72
C1281	C1203	U1123	U1019	U1020	U1021	U1022	U950	U843	C757	C652	C543	G461	G389	C319	C224	G148	A73
C1282	A1204	G1124	U1020	U1021	U1022	U1023	G951	U844	C758	C653	C544	G462	G390	C320	C225	G149	A74
A1285	C1210	U1125	U1021	U1022	U1023	U1024	G952	U845	C759	C654	C545	G463	G391	C321	C226	G150	C72
A1287	U1211	U1126	U1022	U1023	U1024	U1025	G953	U846	C760	C655	C546	G464	G392	C322	C227	G151	A75
A1288	U1212	A1130	U1023	U1024	U1025	U1026	A958	U847	C761	C656	C547	G465	G393	C323	C228	G152	A76
U1291	A1213	G1131	U1024	U1025	U1026	U1027	A959	U848	C762	C657	C548	G466	G394	C324	C229	G153	G75
G1292	C1214	C1132	U1025	U1026	U1027	U1028	U960	U849	C763	C658	C549	G467	G395	C325	C230	G154	G76
C1216	G1215	C1133	U1026	U1027	U1028	U1029	U961	U850	C764	C659	C550	G468	G396	C326	C231	G155	A77
C1217	A1216	C1134	U1027	U1028	U1029	U1030	U962	U851	C765	C660	C551	G469	G397	C327	C232	G156	A78
C1218	C1217	C1135	U1028	U1029	U1030	U1031	U963	U852	C766	C661	C552	G470	G398	C328	C233	G157	A79
U1298	C1218	C1136	U1029	U1030	U1031	U1032	U964	U853	C767	C662	C553	G471	G399	C329	C234	G158	C80
A1299	G1221	C1137	U1030	U1031	U1032	U1033	U965	U854	C768	C663	C554	G472	G400	C330	C235	G159	A80
G1300	C1222	C1138	U1031	U1032	U1033	U1034	U966	U855	C769	C664	C555	G473	G401	C331	C236	G160	A81
U1301	C1223	C1139	U1032	U1033	U1034	U1035	U967	U856	C770	C665	C556	G474	G402	C332	C237	G161	A82
C1302	C1224	C1140	U1033	U1034	U1035	U1036	U968	U857	C771	C666	C557	G475	G403	C333	C238	G162	A83
A1303	G1225	C1141	U1034	U1035	U1036	U1037	U969	U858	C772	C667	C558	G476	G404	C334	C239	G163	C84
C1304	U1226	C1142	U1035	U1036	U1037	U1038	U970	U859	C773	C668	C559	G477	G405	C335	C240	G164	C85
A1305	A1227	C1143	U1036	U1037	U1038	U1039	U971	U860	C774	C669	C560	G478	G406	C336	C241	G165	C86
A1306	C1228	C1144	U1037	U1038	U1039	U1040	U972	U861	C775	C670	C561	G479	G407	C337	C242	G166	C87
A1307	C1229	C1145	U1038	U1039	U1040	U1041	U973	U862	C776	C671	C562	G480	G408	C338	C243	G167	C88
A1308	C1230	C1146	U1039	U1040	U1041	U1042	U974	U863	C777	C672	C563	G481	G409	C339	C244	G168	C89
A1309	C1231	C1147	U1040	U1041	U1042	U1043	U975	U864	C778	C673	C564	G482	G410	C340	C245	G169	C90
A1310	C1232	C1148	U1041	U1042	U1043	U1044	U976	U865	C779	C674	C565	G483	G411	C341	C246	G170	C91
A1311	C1233	C1149	U1042	U1043	U1044	U1045	U977	U866	C780	C675	C566	G484	G412	C342	C247	G171	C92
A1312	C1234	C1150	U1043	U1044	U1045	U1046	U978	U867	C781	C676	C567	G485	G413	C343	C248	G172	C93
A1313	C1235	C1151	U1044	U1045	U1046	U1047	U979	U868	C782	C677	C568	G486	G414	C344	C249	G173	C94
A1314	C1236	C1152	U1045	U1046	U1047	U1048	U980	U869	C783	C678	C569	G487	G415	C345	C250	G174	C95
A1315	C1237	C1153	U1046	U1047	U1048	U1049	U981	U870	C784	C679	C570	G488	G416	C346	C251	G175	C96
A1316	C1238	C1154	U1047	U1048	U1049	U1050	U982	U871	C785	C680	C571	G489	G417	C347	C252	G176	C97
A1317	C1239	C1155	U1048	U1049	U1050	U1051	U983	U872	C786	C681	C572	G490	G418	C348	C253	G177	C98
A1318	C1240	C1156	U1049	U1050	U1051	U1052	U984	U873	C787	C682	C573	G491	G419	C349	C254	G178	C99
A1319	C1241	C1157	U1050	U1051	U1052	U1053	U985	U874	C788	C683	C574	G492	G420	C350	C255	G179	C100
A1320	C1242	C1158	U1051	U1052	U1053	U1054	U986	U875	C789	C684	C575	G493	G421	C351	C256	G180	C101
A1321	C1243	C1159	U1052	U1053	U1054	U1055	U987	U876	C790	C685	C576	G494	G422	C352	C257	G181	C102
A1322	C1244	C1160	U1053	U1054	U1055	U1056	U988	U877	C791	C686	C577	G495	G423	C353	C258	G182	C103
A1323	C1245	C1161	U1054	U1055	U1056	U1057	U989	U878	C792	C687	C578	G496	G424	C354	C259	G183	C104
A1324	C1246	C1162	U1055	U1056	U1057	U1058	U990	U879	C793	C688	C579	G497	G425	C355	C260	G184	C105
A1325	C1247	C1163	U1056	U1057	U1058	U1059	U991	U880	C794	C689	C580	G498	G426	C356	C261	G185	C106
A1326	C1248	C1164	U1057	U1058	U1059	U1060	U992	U881	C795	C690	C581	G499	G427	C357	C262	G186	C107
A1327	C1249	C1165	U1058	U1059	U1060	U1061	U993	U882	C796	C691	C582	G500	G428	C358	C263	G187	C108
A1328	C1250	C1166	U1059	U1060	U1061	U1062	U994	U883	C797	C692	C583	G501	G429	C359	C264	G188	C109
A1329	C1251	C1167	U1060	U1061	U1062	U1063	U995	U884	C798	C693	C584	G502	G430	C360	C265	G189	C110
A1330	C1252	C1168	U1061	U1062	U1063	U1064	U996	U885	C799	C694	C585	G503	G431	C361	C266	G190	C111
A1331	C1253																



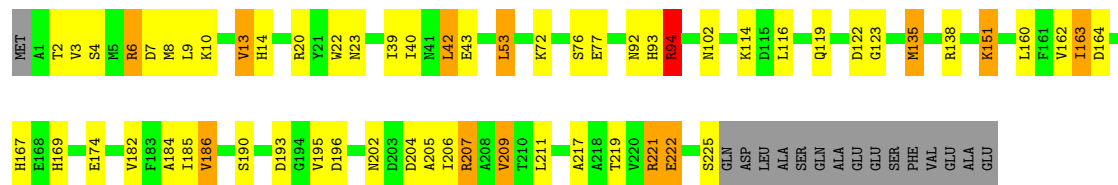
• Molecule 37: A-tRNA

Chain ATRN: 74% 26%



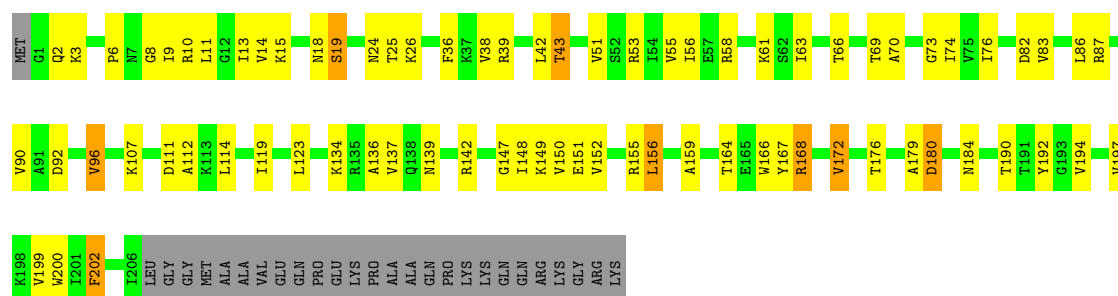
• Molecule 38: 30S ribosomal protein S2

Chain S02: 68% 20% 5% 7%



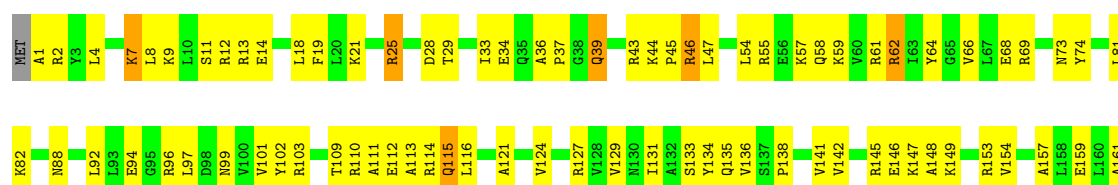
• Molecule 39: 30S ribosomal protein S3

Chain S03: 56% 29% 12%



• Molecule 40: 30S ribosomal protein S4

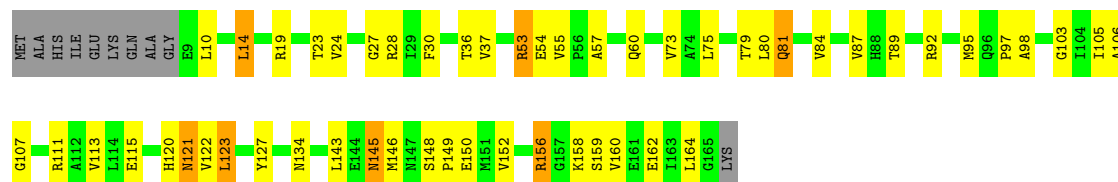
Chain S04: 54% 41%





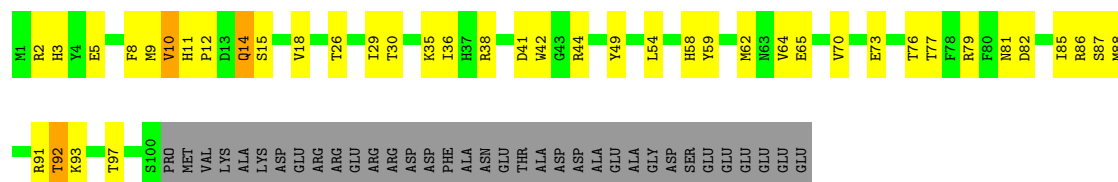
- Molecule 41: 30S ribosomal protein S5

Chain S05: 62% 28% 6%



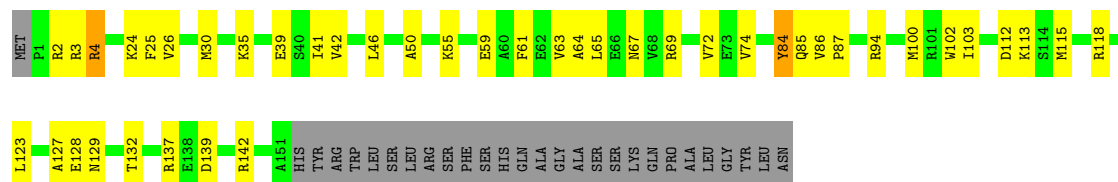
- Molecule 42: 30S ribosomal protein S6

Chain S06: 43% 29% 26%



- Molecule 43: 30S ribosomal protein S7

Chain S07: 60% 23% 16%



- Molecule 44: 30S ribosomal protein S8

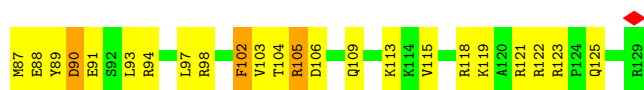
Chain S08: 68% 28% 2%



- Molecule 45: Small ribosomal subunit protein uS9

Chain S09: 54% 38% 5%

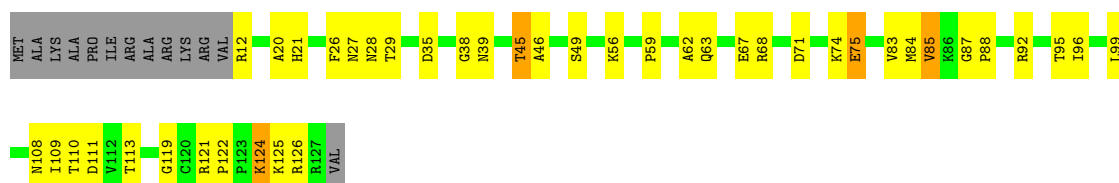




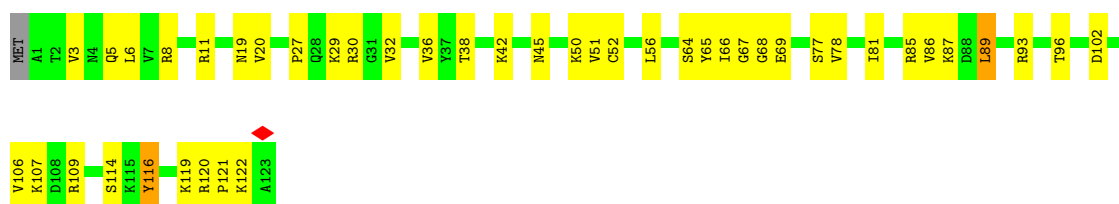
- Molecule 46: 30S ribosomal protein S10



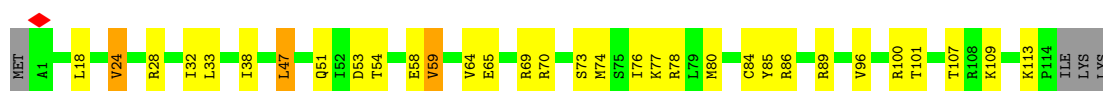
- Molecule 47: 30S ribosomal protein S11



- Molecule 48: 30S ribosomal protein S12

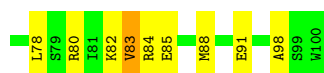


- Molecule 49: 30S ribosomal protein S13



- Molecule 50: Small ribosomal subunit protein uS14





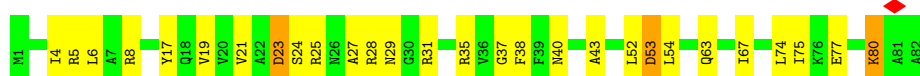
- Molecule 51: Small ribosomal subunit protein uS15

Chain S15: 75% 22% ..



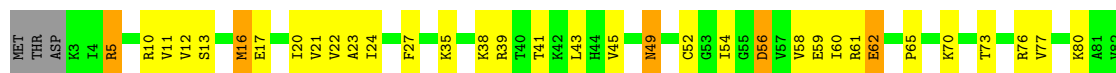
- Molecule 52: 30S ribosomal protein S16

Chain S16: 66% 30% .



- Molecule 53: Small ribosomal subunit protein uS17

Chain S17: 55% 35% 6% 5%



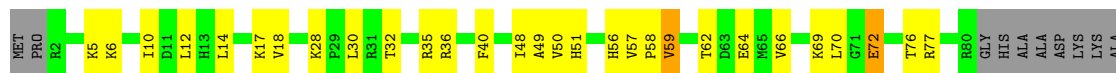
- Molecule 54: 30S ribosomal protein S18

Chain S18: 67% 16% 13%



- Molecule 55: 30S ribosomal protein S19

Chain S19: 54% 29% 14%

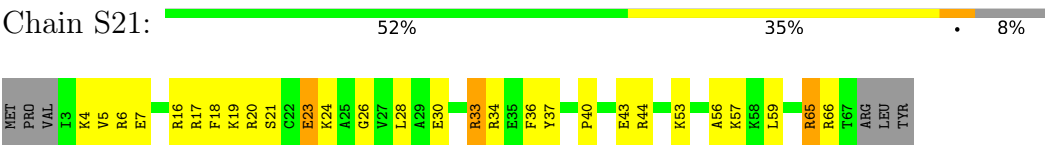


- Molecule 56: 30S ribosomal protein S20

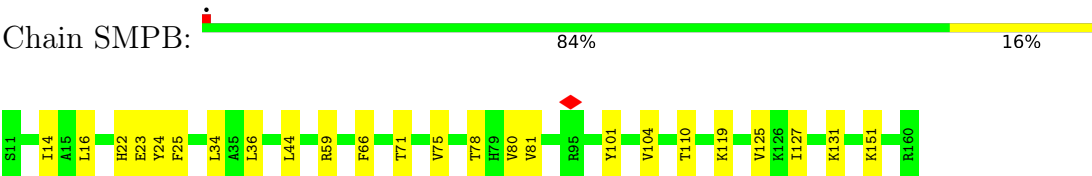
Chain S20: 71% 24% ..



● Molecule 57: 30S ribosomal protein S21



● Molecule 58: SsrA-binding protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5956	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.9	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1100	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.823	Depositor
Minimum map value	-10.783	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.735	Depositor
Recommended contour level	3	Depositor
Map size (Å)	487.2, 487.2, 487.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	Depositor

5 Model quality

5.1 Standard geometry

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	L02	0.23	0/2121	0.42	0/2852
2	L03	0.21	0/1586	0.40	0/2134
3	L04	0.18	0/1571	0.37	0/2113
4	L05	0.23	0/1434	0.50	0/1926
5	L06	0.16	0/1343	0.39	0/1816
6	L09	0.17	0/1122	0.41	0/1515
7	L1	0.16	0/1033	0.41	0/1387
8	L10	0.22	0/1001	0.57	2/1350 (0.1%)
9	L11	0.22	0/1046	0.47	0/1410
10	L13	0.20	0/1152	0.35	0/1551
11	L14	0.23	0/947	0.47	0/1268
12	L15	0.21	0/1054	0.47	0/1403
13	L16	0.22	0/1093	0.47	0/1460
14	L17	0.21	0/973	0.49	0/1301
15	L18	0.18	0/902	0.46	0/1209
16	L19	0.20	0/929	0.35	0/1242
17	L20	0.18	0/960	0.31	0/1278
18	L21	0.19	0/829	0.41	0/1107
19	L22	0.20	0/864	0.38	0/1156
20	L23	0.18	0/744	0.36	0/994
21	L24	0.19	0/787	0.46	0/1051
22	L25	0.19	0/766	0.37	0/1025
23	L27	0.20	0/582	0.34	0/769
24	L28	0.21	0/635	0.36	0/848
25	L29	0.16	0/510	0.41	0/677
26	L30	0.18	0/453	0.29	0/605
27	L31	0.31	0/358	0.75	1/480 (0.2%)
28	L32	0.20	0/450	0.46	0/599
29	L33	0.16	0/416	0.33	0/554
30	L34	0.20	0/380	0.35	0/498
31	L35	0.23	0/513	0.47	0/676
32	L36	0.20	0/303	0.38	0/397
33	23S	0.23	0/69796	0.34	0/108888
34	5S	0.22	0/2872	0.37	0/4479

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	TMRN	0.19	0/8681	0.39	1/13532 (0.0%)
36	16S	0.20	0/36963	0.32	0/57662
37	ATRN	0.22	0/1810	0.36	0/2820
38	S02	0.17	0/1787	0.41	2/2408 (0.1%)
39	S03	0.17	0/1651	0.35	0/2225
40	S04	0.18	0/1665	0.47	0/2227
41	S05	0.21	0/1169	0.53	2/1573 (0.1%)
42	S06	0.21	0/835	0.51	0/1128
43	S07	0.18	0/1195	0.41	0/1602
44	S08	0.18	0/989	0.39	0/1326
45	S09	0.18	0/1034	0.49	0/1375
46	S10	0.18	0/796	0.45	0/1077
47	S11	0.19	0/885	0.44	0/1195
48	S12	0.23	0/969	0.52	0/1300
49	S13	0.18	0/892	0.49	0/1193
50	S14	0.17	0/817	0.47	0/1088
51	S15	0.17	0/722	0.45	0/964
52	S16	0.17	0/659	0.39	0/884
53	S17	0.19	0/657	0.43	0/881
54	S18	0.17	0/544	0.40	0/731
55	S19	0.18	0/652	0.40	0/877
56	S20	0.16	0/671	0.37	0/888
57	S21	0.23	0/550	0.67	0/728
58	SMPB	0.21	0/1231	0.54	2/1655 (0.1%)
All	All	0.21	0/169349	0.37	10/253357 (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
4	L05	0	1
11	L14	0	1
27	L31	0	1
41	S05	0	2
All	All	0	5

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L10	117	LEU	CA-C-N	5.82	132.89	122.13
8	L10	117	LEU	C-N-CA	5.82	132.89	122.13
38	S02	93	HIS	CA-C-N	5.43	131.92	121.54
38	S02	93	HIS	C-N-CA	5.43	131.92	121.54
41	S05	121	ASN	CA-C-N	5.32	131.55	121.97
41	S05	121	ASN	C-N-CA	5.32	131.55	121.97
58	SMPB	80	VAL	CA-C-N	5.27	131.46	121.97
58	SMPB	80	VAL	C-N-CA	5.27	131.46	121.97
35	TMRN	308	U	P-O3'-C3'	5.15	127.93	120.20
27	L31	8	LYS	N-CA-C	5.14	121.76	110.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L05	61	GLY	Peptide
11	L14	92	GLU	Peptide
27	L31	1	MET	Peptide
41	S05	120	HIS	Peptide
41	S05	121	ASN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L02	2082	0	2157	56	0
2	L03	1565	0	1616	33	0
3	L04	1552	0	1619	28	0
4	L05	1410	0	1447	46	0
5	L06	1323	0	1374	32	0
6	L09	1111	0	1148	20	0
7	L1	1026	0	1092	25	0
8	L10	988	0	1025	26	0
9	L11	1032	0	1088	39	0
10	L13	1129	0	1162	25	0
11	L14	938	0	1012	23	0
12	L15	1045	0	1117	28	0
13	L16	1074	0	1157	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	L17	960	0	1000	25	0
15	L18	892	0	923	27	0
16	L19	917	0	965	35	0
17	L20	947	0	1022	24	0
18	L21	816	0	839	18	0
19	L22	857	0	922	19	0
20	L23	738	0	807	11	0
21	L24	779	0	834	15	0
22	L25	753	0	780	11	0
23	L27	575	0	592	16	0
24	L28	625	0	655	12	0
25	L29	509	0	543	12	0
26	L30	449	0	491	11	0
27	L31	351	0	350	17	0
28	L32	444	0	461	9	0
29	L33	409	0	440	10	0
30	L34	377	0	418	15	0
31	L35	504	0	574	14	0
32	L36	302	0	343	8	0
33	23S	62317	0	31346	690	0
34	5S	2568	0	1303	31	0
35	TMRN	7758	0	0	0	0
36	16S	33012	0	16618	460	0
37	ATRN	1621	0	0	0	0
38	S02	1756	0	1787	28	0
39	S03	1624	0	1699	39	0
40	S04	1643	0	1710	54	0
41	S05	1156	0	1199	24	0
42	S06	817	0	808	27	0
43	S07	1181	0	1240	20	0
44	S08	979	0	1034	25	0
45	S09	1022	0	1070	43	0
46	S10	786	0	828	33	0
47	S11	869	0	878	29	0
48	S12	955	0	1019	29	0
49	S13	883	0	944	17	0
50	S14	805	0	847	37	0
51	S15	714	0	737	10	0
52	S16	649	0	666	19	0
53	S17	648	0	691	22	0
54	S18	535	0	552	9	0
55	S19	637	0	665	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	S20	665	0	714	14	0
57	S21	544	0	579	22	0
58	SMPB	1209	0	0	0	0
All	All	155832	0	98907	2050	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 (2050) 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)
36:16S:978:A:N6	36:16S:1360:A:C2	2.19	1.10
33:23S:2104:C:N4	33:23S:2185:U:H3	1.51	1.06
36:16S:372:C:N4	36:16S:389:A:H62	1.53	1.05
36:16S:978:A:C2	36:16S:1316:G:N2	2.26	1.04
33:23S:1040:A:N6	33:23S:1115:G:H1	1.56	1.04
36:16S:978:A:N6	36:16S:1360:A:H2	1.53	1.03
33:23S:711:G:H1	33:23S:720:U:H3	1.01	1.01
33:23S:1072:C:H42	33:23S:1093:G:H22	0.99	0.98
36:16S:978:A:H2	36:16S:1316:G:H21	1.01	0.98
33:23S:2289:G:H1	33:23S:2343:U:H3	1.09	0.98
33:23S:1664:A:H61	33:23S:1996:C:H42	1.10	0.98
33:23S:1072:C:H42	33:23S:1093:G:N2	1.62	0.97
33:23S:1478:G:H1	33:23S:1513:U:H3	1.00	0.95
33:23S:307:G:H21	33:23S:330:A:H61	1.08	0.94
33:23S:1468:U:H3	33:23S:1524:G:H1	0.95	0.94
36:16S:372:C:H42	36:16S:389:A:H62	0.98	0.94
33:23S:2847:U:H3	33:23S:2869:G:H1	1.07	0.93
36:16S:978:A:H2	36:16S:1316:G:N2	1.65	0.93
33:23S:1664:A:H61	33:23S:1996:C:N4	1.67	0.92
33:23S:1415:U:H3	33:23S:1587:G:H1	0.95	0.89
36:16S:372:C:H42	36:16S:389:A:N6	1.72	0.88
36:16S:198:G:H1	36:16S:219:U:H3	1.19	0.88
33:23S:2457:U:H3	33:23S:2494:G:H1	0.90	0.87
36:16S:1009:U:H3	36:16S:1020:G:H1	0.90	0.87
33:23S:1907:G:H1	33:23S:1923:U:H3	1.19	0.87
33:23S:285:G:H1	33:23S:355:U:H3	1.20	0.87
36:16S:151:A:N6	36:16S:170:U:C2	2.44	0.85
33:23S:1408:G:H1	33:23S:1594:U:H3	1.21	0.85
36:16S:1006:G:H1	36:16S:1023:U:H3	0.87	0.85
36:16S:1319:A:H61	36:16S:1361:G:H21	1.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:1348:U:N3	36:16S:1374:A:C8	2.46	0.83
33:23S:1072:C:N4	33:23S:1093:G:H22	1.77	0.83
33:23S:307:G:H21	33:23S:330:A:N6	1.76	0.83
33:23S:2291:U:H3	33:23S:2341:G:H1	0.85	0.82
36:16S:605:U:H3	36:16S:633:G:H1	1.25	0.80
33:23S:196:A:H61	33:23S:831:G:H21	1.26	0.79
33:23S:1040:A:H61	33:23S:1115:G:H1	0.81	0.79
36:16S:1319:A:H61	36:16S:1361:G:N2	1.80	0.78
36:16S:944:G:H21	36:16S:1339:A:H62	1.30	0.78
33:23S:307:G:N2	33:23S:330:A:H61	1.81	0.78
33:23S:1664:A:N6	33:23S:1996:C:H42	1.82	0.77
36:16S:151:A:N6	36:16S:170:U:N3	2.33	0.77
36:16S:1348:U:C2	36:16S:1374:A:N7	2.53	0.76
19:L22:42:LYS:HB2	33:23S:2010:G:H5''	1.68	0.75
36:16S:927:G:H1	36:16S:1390:U:H3	1.33	0.75
33:23S:59:U:H3	33:23S:68:G:H1	1.35	0.74
33:23S:404:A:N6	33:23S:421:C:C4	2.55	0.74
33:23S:2104:C:H42	33:23S:2185:U:H3	0.76	0.73
33:23S:2508:G:H1	33:23S:2580:U:H3	1.37	0.72
33:23S:1072:C:N3	33:23S:1093:G:N1	2.35	0.72
33:23S:562:U:C4	33:23S:572:A:N7	2.58	0.71
57:S21:23:GLU:HB2	57:S21:26:GLY:H	1.55	0.71
42:S06:42:TRP:HB2	42:S06:59:TYR:HB2	1.71	0.71
33:23S:196:A:N6	33:23S:831:G:H21	1.90	0.70
36:16S:1160:G:H1	36:16S:1176:A:H61	1.37	0.70
7:L1:37:LYS:HB2	33:23S:2127:G:H5'	1.73	0.70
33:23S:2107:G:H1	33:23S:2182:U:H3	1.39	0.70
33:23S:408:G:H1	33:23S:419:U:H3	1.40	0.70
36:16S:1160:G:H1	36:16S:1176:A:N6	1.89	0.69
33:23S:881:G:H1	33:23S:895:U:H3	0.78	0.69
33:23S:2514:U:H3	33:23S:2570:G:H1	1.40	0.69
36:16S:978:A:N1	36:16S:1316:G:N3	2.41	0.69
36:16S:1130:A:N6	36:16S:1144:G:N3	2.40	0.69
38:S02:186:VAL:HG23	38:S02:190:SER:HB2	1.75	0.69
11:L14:56:ASP:N	11:L14:56:ASP:OD1	2.26	0.69
33:23S:999:U:O2	33:23S:1157:G:C2	2.47	0.68
36:16S:978:A:N1	36:16S:1316:G:C2	2.62	0.68
33:23S:2165:C:N4	33:23S:2170:A:N6	2.42	0.67
33:23S:1319:C:N4	33:23S:1320:C:N4	2.42	0.67
9:L11:14:ALA:HB3	9:L11:54:ILE:H	1.58	0.67
36:16S:672:U:H3	36:16S:734:G:H1	1.39	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L1:48:LEU:HD11	7:L1:171:ILE:HG22	1.77	0.67
33:23S:999:U:O2	33:23S:1157:G:N2	2.28	0.67
33:23S:15:G:H1	33:23S:525:U:H3	1.41	0.66
33:23S:196:A:H61	33:23S:831:G:N2	1.92	0.66
47:S11:20:ALA:HB3	47:S11:83:VAL:HA	1.77	0.66
12:L15:63:LYS:HE2	33:23S:2394:C:H5''	1.78	0.66
8:L10:58:THR:HG21	8:L10:82:ILE:H	1.59	0.66
33:23S:2117:A:N6	33:23S:2170:A:N1	2.43	0.66
40:S04:99:ASN:HA	40:S04:110:ARG:HH12	1.60	0.66
36:16S:1351:U:H3	36:16S:1371:G:H1	1.44	0.66
46:S10:88:MET:HG3	46:S10:89:ARG:HD3	1.77	0.66
36:16S:112:G:H21	36:16S:354:G:H5'	1.60	0.65
15:L18:7:ARG:HG3	15:L18:10:ARG:HH21	1.60	0.65
36:16S:991:U:O2	36:16S:1213:A:N7	2.29	0.65
30:L34:19:ARG:HG3	33:23S:126:A:H5'	1.79	0.65
47:S11:125:LYS:O	57:S21:34:ARG:NH2	2.29	0.65
43:S07:67:ASN:HB3	43:S07:129:ASN:HB3	1.78	0.65
45:S09:118:ARG:HB2	45:S09:122:ARG:HB3	1.78	0.65
9:L11:90:GLY:O	33:23S:1063:G:N2	2.28	0.65
13:L16:53:MET:HB2	13:L16:120:ALA:HB2	1.79	0.65
36:16S:151:A:N7	36:16S:170:U:O4	2.30	0.65
33:23S:2682:A:H61	33:23S:2728:U:H1'	1.61	0.65
36:16S:950:U:H3	36:16S:1231:G:H1	1.42	0.65
52:S16:53:ASP:N	52:S16:53:ASP:OD1	2.30	0.65
33:23S:1265:A:H61	33:23S:2013:A:H3'	1.62	0.65
34:5S:30:C:H1'	34:5S:57:A:H61	1.62	0.65
36:16S:888:G:H21	36:16S:909:A:H62	1.43	0.65
15:L18:33:ARG:NH1	34:5S:52:A:N7	2.44	0.64
33:23S:1936:A:H2	33:23S:1943:U:H3	1.44	0.64
46:S10:48:ARG:HG2	46:S10:66:GLU:HG2	1.79	0.64
36:16S:448:A:H62	36:16S:486:U:H3	1.46	0.64
36:16S:1319:A:N6	36:16S:1361:G:H21	1.94	0.64
36:16S:835:U:H3	36:16S:851:G:H1	1.45	0.64
10:L13:19:ASP:OD1	10:L13:19:ASP:N	2.31	0.64
36:16S:1237:C:O2'	36:16S:1300:G:N2	2.30	0.64
36:16S:674:G:OP1	42:S06:86:ARG:NH2	2.30	0.64
36:16S:1236:A:N6	36:16S:1337:G:C6	2.66	0.64
43:S07:3:ARG:HH11	43:S07:4:ARG:HH22	1.46	0.64
33:23S:1851:U:H3	33:23S:1891:G:H1	1.45	0.64
33:23S:1111:A:H2'	33:23S:1112:G:H4'	1.80	0.63
33:23S:1270:C:H5''	33:23S:1271:G:H5'	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:1348:U:O2	36:16S:1374:A:N7	2.31	0.63
45:S09:61:ASP:OD1	45:S09:61:ASP:N	2.31	0.63
11:L14:63:VAL:HG12	11:L14:107:LEU:HD21	1.80	0.63
33:23S:814:C:H1'	33:23S:1225:G:H21	1.61	0.63
47:S11:87:GLY:H	47:S11:113:THR:HG22	1.63	0.63
36:16S:372:C:N4	36:16S:389:A:N6	2.37	0.63
18:L21:35:PHE:HB2	18:L21:59:ILE:HB	1.80	0.63
33:23S:707:G:H1	33:23S:724:U:H3	1.44	0.63
36:16S:119:A:N7	36:16S:287:U:O2	2.32	0.63
15:L18:100:HIS:O	15:L18:104:GLN:NE2	2.32	0.63
33:23S:1319:C:C4	33:23S:1320:C:N4	2.67	0.62
43:S07:74:VAL:HA	43:S07:87:PRO:HA	1.80	0.62
36:16S:216:U:H4'	36:16S:464:U:H4'	1.81	0.62
17:L20:91:ARG:NH2	33:23S:1153:C:OP1	2.32	0.62
33:23S:2134:A:N7	33:23S:2156:G:N1	2.48	0.62
36:16S:54:C:OP1	36:16S:351:G:N2	2.32	0.62
1:L02:266:ILE:HG21	1:L02:269:ARG:HG2	1.80	0.62
7:L1:17:ALA:O	7:L1:20:GLN:NE2	2.32	0.62
23:L27:39:THR:H	33:23S:2331:G:H4'	1.65	0.62
40:S04:124:VAL:HG22	40:S04:142:VAL:HG23	1.82	0.62
42:S06:15:SER:OG	42:S06:44:ARG:NH1	2.33	0.62
22:L25:20:LEU:HB2	22:L25:25:LYS:HB2	1.80	0.62
25:L29:55:THR:HG23	33:23S:72:U:H3	1.65	0.62
36:16S:1064:G:O2'	36:16S:1190:G:N2	2.30	0.62
3:L04:76:PRO:HA	3:L04:82:GLY:HA2	1.81	0.62
14:L17:2:ARG:HG2	14:L17:5:LYS:HB2	1.82	0.62
33:23S:729:G:H2'	33:23S:1775:U:H1'	1.81	0.62
33:23S:2121:G:O6	33:23S:2176:A:N6	2.32	0.62
36:16S:391:G:H5''	52:S16:8:ARG:HH21	1.65	0.62
26:L30:5:LYS:HB2	26:L30:57:GLU:HB3	1.82	0.62
36:16S:380:G:N2	36:16S:383:A:OP2	2.32	0.62
36:16S:1160:G:N1	36:16S:1176:A:N6	2.44	0.62
41:S05:98:ALA:HB3	41:S05:122:VAL:HA	1.82	0.62
4:L05:62:GLN:N	27:L31:6:HIS:O	2.20	0.61
33:23S:1300:G:H4'	33:23S:1301:A:H5''	1.81	0.61
34:5S:34:A:N6	34:5S:44:G:O2'	2.33	0.61
36:16S:126:G:OP1	36:16S:633:G:N2	2.33	0.61
36:16S:1496:C:HO2'	36:16S:1517:G:H1	1.45	0.61
36:16S:76:G:H1	36:16S:93:U:H3	0.77	0.61
33:23S:2406:A:OP2	33:23S:2411:A:N6	2.33	0.61
36:16S:1236:A:N6	36:16S:1337:G:N1	2.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:L21:79:ARG:NH1	33:23S:563:A:OP2	2.33	0.61
33:23S:373:U:H2'	33:23S:374:A:H8	1.65	0.61
33:23S:668:A:H2'	33:23S:670:A:H62	1.64	0.61
42:S06:38:ARG:HD3	42:S06:97:THR:HA	1.82	0.61
36:16S:51:A:N7	36:16S:114:U:O2'	2.33	0.61
41:S05:80:LEU:HD22	41:S05:122:VAL:HG21	1.82	0.61
42:S06:10:VAL:HG12	42:S06:58:HIS:HB3	1.82	0.61
33:23S:2107:G:N1	33:23S:2182:U:N3	2.43	0.61
39:S03:58:ARG:HE	39:S03:96:VAL:HG21	1.65	0.61
32:L36:3:VAL:HG13	32:L36:36:ARG:HD3	1.81	0.61
33:23S:1044:C:O2'	33:23S:1111:A:N6	2.32	0.61
33:23S:1268:A:H62	33:23S:2012:G:H21	1.46	0.61
47:S11:71:ASP:HA	47:S11:74:LYS:HG2	1.82	0.61
36:16S:741:G:OP1	51:S15:34:GLN:NE2	2.34	0.61
2:L03:25:THR:HB	2:L03:189:VAL:HG23	1.82	0.61
33:23S:1438:U:H2'	33:23S:1439:A:H8	1.65	0.61
8:L10:57:ASN:HB3	8:L10:62:ARG:HG2	1.83	0.60
33:23S:238:C:O2'	33:23S:608:A:N3	2.34	0.60
33:23S:2881:U:H2'	33:23S:2882:A:H8	1.65	0.60
36:16S:891:U:H2'	36:16S:892:A:H8	1.65	0.60
33:23S:475:C:O2	33:23S:479:A:N6	2.34	0.60
33:23S:2396:G:H2'	33:23S:2397:G:H8	1.67	0.60
48:S12:38:THR:HG22	48:S12:50:LYS:HG3	1.83	0.60
33:23S:2489:U:O2'	33:23S:2518:A:N6	2.34	0.60
14:L17:30:ARG:NH1	14:L17:74:GLU:OE1	2.35	0.60
44:S08:10:LEU:HD22	44:S08:74:ILE:HD11	1.83	0.60
33:23S:1173:U:O2	33:23S:1176:U:N3	2.35	0.60
45:S09:94:ARG:HA	45:S09:97:LEU:HB2	1.82	0.60
1:L02:144:GLU:HB2	1:L02:187:CYS:HB3	1.83	0.60
1:L02:270:ARG:NH2	33:23S:1798:U:OP2	2.35	0.60
36:16S:974:A:H4'	36:16S:975:A:H3'	1.84	0.60
8:L10:25:ALA:HB3	8:L10:85:SER:HB2	1.84	0.60
30:L34:41:ARG:HA	30:L34:41:ARG:HH11	1.66	0.60
33:23S:2083:G:H1	33:23S:2236:U:H3	1.50	0.60
33:23S:1072:C:N4	33:23S:1098:A:OP2	2.35	0.60
42:S06:92:THR:OG1	42:S06:93:LYS:N	2.35	0.60
12:L15:110:VAL:O	12:L15:128:THR:OG1	2.20	0.60
33:23S:458:G:N2	33:23S:459:U:O4	2.35	0.60
9:L11:53:PRO:HD2	9:L11:77:VAL:HG11	1.83	0.59
36:16S:323:U:H3	36:16S:327:A:H62	1.49	0.59
36:16S:944:G:N2	36:16S:1339:A:H62	1.99	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L11:134:SER:O	33:23S:1062:G:N2	2.35	0.59
30:L34:37:LYS:NZ	33:23S:468:G:OP2	2.35	0.59
36:16S:1013:G:N2	36:16S:1016:A:OP2	2.36	0.59
33:23S:2530:A:O2'	33:23S:2534:A:N6	2.36	0.59
36:16S:263:A:OP1	56:S20:73:ARG:NH1	2.34	0.59
38:S02:206:ILE:HA	38:S02:209:VAL:HG12	1.85	0.59
42:S06:42:TRP:HZ2	54:S18:23:LYS:HE2	1.67	0.59
2:L03:31:ALA:HB1	2:L03:95:SER:HB3	1.84	0.59
5:L06:174:LYS:HD3	33:23S:2529:G:H4'	1.85	0.59
45:S09:18:VAL:HA	45:S09:64:ILE:HG23	1.84	0.59
15:L18:66:GLY:O	15:L18:102:ARG:NH1	2.36	0.59
33:23S:160:A:N3	33:23S:2208:C:O2'	2.34	0.59
36:16S:373:A:O2'	36:16S:451:A:N7	2.35	0.59
5:L06:96:ALA:HB3	5:L06:103:ASN:HB3	1.84	0.59
11:L14:31:ARG:NH1	33:23S:1996:C:OP1	2.36	0.59
33:23S:33:C:O2	33:23S:447:A:N6	2.35	0.59
33:23S:1478:G:N2	33:23S:1513:U:O2	2.31	0.59
36:16S:978:A:N7	36:16S:1360:A:N1	2.50	0.59
36:16S:1315:U:O2'	36:16S:1360:A:N3	2.33	0.59
48:S12:64:SER:OG	48:S12:65:TYR:N	2.36	0.59
23:L27:16:ARG:HG3	33:23S:2271:G:H5'	1.85	0.59
33:23S:1779:U:OP2	33:23S:1784:A:N6	2.33	0.59
36:16S:202:G:O2'	36:16S:468:A:N3	2.35	0.59
36:16S:1009:U:O2	36:16S:1020:G:N2	2.34	0.59
36:16S:1015:G:N3	36:16S:1218:C:O2'	2.35	0.59
54:S18:11:ARG:NH1	54:S18:11:ARG:O	2.35	0.59
5:L06:7:PRO:O	5:L06:68:ARG:NH2	2.36	0.59
33:23S:228:C:N3	33:23S:417:C:O2'	2.35	0.59
48:S12:50:LYS:HB3	48:S12:66:ILE:HD12	1.85	0.59
2:L03:176:ASP:OD1	2:L03:176:ASP:N	2.36	0.59
53:S17:56:ASP:OD1	53:S17:56:ASP:N	2.35	0.59
27:L31:2:LYS:HB2	34:5S:42:C:H3'	1.85	0.59
30:L34:10:LEU:HD23	33:23S:770:G:H5''	1.85	0.59
33:23S:2472:G:H3'	33:23S:2475:C:H42	1.68	0.59
39:S03:190:THR:HG23	39:S03:192:TYR:H	1.68	0.59
13:L16:25:ASP:OD1	13:L16:34:LYS:NZ	2.36	0.58
36:16S:516:U:O2'	36:16S:519:C:N3	2.34	0.58
43:S07:115:MET:HA	43:S07:118:ARG:HD2	1.85	0.58
22:L25:75:GLN:HE22	34:5S:104:A:H5'	1.68	0.58
33:23S:2345:G:H5'	33:23S:2347:C:H5'	1.84	0.58
36:16S:509:A:N3	36:16S:543:U:O2'	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:1256:A:H62	36:16S:1278:G:H5'	1.68	0.58
40:S04:74:TYR:OH	40:S04:96:ARG:NH1	2.35	0.58
48:S12:32:VAL:HA	48:S12:78:VAL:HG12	1.85	0.58
9:L11:102:ARG:HB2	9:L11:141:ASP:HA	1.85	0.58
36:16S:975:A:N1	46:S10:62:ARG:NH2	2.51	0.58
36:16S:1234:C:OP1	45:S09:118:ARG:NH2	2.36	0.58
49:S13:89:ARG:HB2	49:S13:96:VAL:HG12	1.85	0.58
4:L05:110:ILE:HG13	4:L05:136:ILE:HG21	1.85	0.58
36:16S:979:C:OP1	36:16S:1223:C:N4	2.36	0.58
55:S19:5:LYS:HE2	55:S19:6:LYS:HE3	1.84	0.58
4:L05:87:LYS:NZ	4:L05:89:THR:OG1	2.37	0.58
13:L16:44:ARG:NH1	33:23S:2484:G:OP1	2.37	0.58
33:23S:2155:U:OP1	33:23S:2157:G:N2	2.36	0.58
33:23S:2622:U:O2'	33:23S:2825:G:N7	2.36	0.58
36:16S:1221:G:OP1	55:S19:35:ARG:NH1	2.37	0.58
40:S04:94:GLU:O	40:S04:99:ASN:ND2	2.37	0.58
1:L02:59:GLN:NE2	1:L02:84:PRO:O	2.35	0.58
33:23S:2135:A:N6	33:23S:2156:G:O2'	2.37	0.58
36:16S:1305:G:H22	36:16S:1331:G:H2'	1.68	0.58
36:16S:1344:C:H4'	45:S09:121:ARG:HB3	1.84	0.58
46:S10:66:GLU:HB2	50:S14:98:ALA:HB2	1.86	0.58
19:L22:6:LYS:HA	19:L22:104:THR:HA	1.83	0.58
33:23S:2443:C:H2'	33:23S:2444:G:H8	1.68	0.58
43:S07:64:ALA:HA	43:S07:127:ALA:HA	1.86	0.58
14:L17:69:ARG:NH2	33:23S:2871:U:OP1	2.35	0.58
15:L18:37:ALA:HB2	15:L18:106:LEU:HD11	1.85	0.58
18:L21:76:LYS:NZ	33:23S:992:C:OP1	2.35	0.58
33:23S:1306:C:N4	33:23S:1607:C:OP2	2.35	0.58
36:16S:203:G:O2'	36:16S:465:A:N1	2.36	0.58
36:16S:1316:G:N1	36:16S:1319:A:OP2	2.37	0.58
11:L14:76:VAL:H	16:L19:72:VAL:HG22	1.69	0.58
57:S21:65:ARG:O	57:S21:65:ARG:NH1	2.37	0.58
18:L21:77:PHE:O	18:L21:78:ARG:NH1	2.37	0.57
27:L31:10:GLU:H	27:L31:27:THR:HA	1.69	0.57
33:23S:1352:U:O2	33:23S:1380:G:C2	2.56	0.57
36:16S:975:A:N1	36:16S:1366:C:O2'	2.36	0.57
36:16S:1029:U:O2	36:16S:1033:G:N2	2.36	0.57
40:S04:92:LEU:O	40:S04:135:GLN:NE2	2.37	0.57
36:16S:434:U:H2'	36:16S:435:A:H8	1.69	0.57
36:16S:796:C:O3'	47:S11:126:ARG:NH2	2.37	0.57
36:16S:1166:G:N1	36:16S:1169:A:OP2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:1226:C:OP2	49:S13:89:ARG:NH1	2.33	0.57
36:16S:1279:G:OP2	46:S10:11:LYS:NZ	2.37	0.57
39:S03:39:ARG:O	39:S03:43:THR:OG1	2.21	0.57
46:S10:7:ARG:HA	46:S10:75:ASP:HA	1.86	0.57
17:L20:5:ARG:NH1	33:23S:1251:C:OP2	2.37	0.57
40:S04:82:LYS:O	40:S04:88:ASN:ND2	2.37	0.57
16:L19:102:ARG:NH2	33:23S:1754:A:O2'	2.38	0.57
36:16S:1011:C:H2'	36:16S:1012:A:H8	1.69	0.57
1:L02:220:ARG:NH2	33:23S:1788:C:OP1	2.37	0.57
4:L05:27:VAL:O	4:L05:29:ARG:NH1	2.38	0.57
21:L24:68:ASN:OD1	33:23S:328:U:O2'	2.23	0.57
33:23S:45:G:H5''	33:23S:46:G:H5'	1.86	0.57
36:16S:1028:C:O2	36:16S:1033:G:N2	2.37	0.57
14:L17:106:ASP:N	14:L17:106:ASP:OD1	2.36	0.57
22:L25:32:GLY:O	22:L25:93:ARG:NH1	2.37	0.57
30:L34:42:LEU:HB3	33:23S:126:A:H61	1.69	0.57
33:23S:119:A:H4'	33:23S:120:U:H5'	1.86	0.57
36:16S:911:U:OP1	48:S12:93:ARG:NH1	2.38	0.57
45:S09:8:THR:OG1	45:S09:9:GLY:N	2.36	0.57
33:23S:881:G:N2	33:23S:895:U:O2	2.38	0.57
36:16S:1216:A:H5''	50:S14:4:SER:HB3	1.86	0.57
7:L1:172:HIS:NE2	33:23S:2122:U:O2	2.32	0.57
12:L15:122:VAL:HG12	12:L15:142:ILE:HA	1.87	0.57
33:23S:530:G:N2	33:23S:2034:U:O2'	2.37	0.57
33:23S:1032:A:N1	33:23S:1122:G:O6	2.38	0.57
36:16S:407:U:O2	40:S04:153:ARG:NH1	2.37	0.57
20:L23:69:ARG:NH2	33:23S:1334:G:OP1	2.38	0.57
36:16S:1320:C:N3	55:S19:35:ARG:NH1	2.52	0.57
16:L19:20:ARG:NH1	33:23S:2849:U:O4	2.38	0.57
20:L23:64:LYS:NZ	33:23S:1601:G:OP1	2.38	0.57
33:23S:1415:U:O2	33:23S:1587:G:N2	2.33	0.57
36:16S:180:U:O2	36:16S:195:A:N7	2.38	0.57
36:16S:1351:U:O4	45:S09:119:LYS:NZ	2.38	0.57
54:S18:24:ASP:OD1	54:S18:24:ASP:N	2.37	0.57
33:23S:2204:G:O6	33:23S:2220:U:O2	2.22	0.56
5:L06:104:LEU:HB2	5:L06:112:VAL:HB	1.86	0.56
7:L1:45:ALA:HB3	7:L1:213:SER:HB2	1.87	0.56
28:L32:9:ARG:NH2	33:23S:516:C:OP1	2.37	0.56
47:S11:85:VAL:HG11	57:S21:16:ARG:HH22	1.70	0.56
1:L02:122:ALA:O	1:L02:127:ASN:ND2	2.38	0.56
13:L16:25:ASP:O	13:L16:66:ARG:NH1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L16:81:ARG:NH1	33:23S:2251:G:OP1	2.38	0.56
16:L19:50:ARG:NH1	33:23S:2684:U:OP2	2.38	0.56
20:L23:10:VAL:HG13	20:L23:11:LEU:HD12	1.87	0.56
33:23S:1827:U:OP1	33:23S:1971:U:O2'	2.24	0.56
33:23S:2474:U:OP2	33:23S:2475:C:N4	2.33	0.56
36:16S:643:C:OP1	44:S08:30:LYS:NZ	2.38	0.56
4:L05:36:ASN:HA	4:L05:87:LYS:HA	1.86	0.56
8:L10:97:LYS:O	8:L10:101:LYS:N	2.36	0.56
9:L11:127:SER:OG	33:23S:1080:A:N3	2.39	0.56
13:L16:86:LYS:NZ	33:23S:956:G:OP2	2.39	0.56
15:L18:9:ARG:NH2	33:23S:2296:U:OP2	2.39	0.56
18:L21:91:GLN:NE2	33:23S:993:G:N3	2.52	0.56
22:L25:72:VAL:HA	22:L25:94:ALA:H	1.70	0.56
36:16S:151:A:OP2	36:16S:169:C:N4	2.33	0.56
36:16S:1222:G:H5''	55:S19:77:ARG:HH11	1.71	0.56
36:16S:1347:G:N7	45:S09:11:ARG:NH2	2.52	0.56
8:L10:28:ALA:HA	8:L10:56:ARG:HH22	1.70	0.56
10:L13:34:ARG:NH2	33:23S:1006:C:OP1	2.39	0.56
36:16S:401:C:O2'	36:16S:621:A:N3	2.38	0.56
28:L32:3:GLN:HE21	28:L32:3:GLN:H	1.53	0.56
30:L34:22:MET:O	30:L34:28:ARG:NH1	2.39	0.56
33:23S:793:A:N6	33:23S:2073:C:OP1	2.36	0.56
33:23S:885:C:H42	33:23S:891:G:H22	1.54	0.56
36:16S:390:U:O3'	52:S16:28:ARG:NH1	2.38	0.56
17:L20:50:ARG:NH1	33:23S:993:G:OP2	2.39	0.56
19:L22:61:ASN:OD1	33:23S:495:G:N2	2.36	0.56
22:L25:75:GLN:OE1	34:5S:103:U:O2'	2.23	0.56
33:23S:301:G:H5'	33:23S:317:G:H21	1.71	0.56
36:16S:112:G:H1	36:16S:315:A:H61	1.53	0.56
36:16S:227:G:O2'	52:S16:63:GLN:OE1	2.24	0.56
36:16S:338:A:N1	36:16S:351:G:O6	2.38	0.56
11:L14:108:ARG:HG3	11:L14:113:MET:HE1	1.88	0.56
15:L18:25:ARG:NH2	34:5S:8:C:O3'	2.39	0.56
33:23S:2447:G:N2	33:23S:2450:A:OP2	2.38	0.56
36:16S:1386:G:H2'	36:16S:1387:G:H8	1.70	0.56
39:S03:149:LYS:HA	39:S03:168:ARG:HA	1.88	0.56
4:L05:100:GLU:O	4:L05:104:THR:OG1	2.23	0.56
7:L1:184:LYS:O	7:L1:188:ASN:ND2	2.39	0.56
13:L16:40:ARG:NH2	33:23S:958:U:OP1	2.39	0.56
23:L27:36:GLN:OE1	23:L27:40:LYS:N	2.39	0.56
33:23S:1275:A:OP2	33:23S:1646:C:N4	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:37:U:OP1	48:S12:122:LYS:NZ	2.36	0.56
36:16S:671:G:O2'	42:S06:79:ARG:NH2	2.38	0.56
36:16S:971:G:HO2'	36:16S:1365:G:HO2'	1.54	0.56
38:S02:23:ASN:ND2	38:S02:190:SER:O	2.39	0.56
42:S06:12:PRO:O	42:S06:44:ARG:NH1	2.36	0.56
46:S10:40:ILE:HD12	46:S10:73:LEU:HB3	1.86	0.56
3:L04:129:PRO:HG3	3:L04:156:ASN:HB2	1.88	0.56
6:L09:3:VAL:HA	6:L09:39:ALA:HB2	1.87	0.56
8:L10:62:ARG:NH2	33:23S:1047:G:OP1	2.39	0.56
33:23S:353:C:H2'	33:23S:354:A:H8	1.71	0.56
36:16S:62:U:OP1	36:16S:385:C:O2'	2.23	0.56
36:16S:1376:U:H2'	36:16S:1377:A:H8	1.71	0.56
40:S04:101:VAL:HG23	40:S04:113:ALA:HB1	1.87	0.56
5:L06:6:ALA:O	5:L06:68:ARG:NE	2.36	0.55
33:23S:1315:C:O2'	33:23S:1392:A:N3	2.37	0.55
36:16S:148:G:O6	36:16S:174:A:N1	2.39	0.55
2:L03:194:PRO:HA	33:23S:2680:U:H5'	1.88	0.55
10:L13:44:TYR:O	17:L20:63:ARG:NE	2.38	0.55
15:L18:111:ARG:NH1	15:L18:117:PHE:OXT	2.39	0.55
33:23S:956:G:N2	33:23S:960:A:OP2	2.38	0.55
36:16S:94:G:N2	36:16S:96:U:O4	2.39	0.55
36:16S:708:C:OP1	47:S11:21:HIS:NE2	2.39	0.55
47:S11:92:ARG:NH2	47:S11:111:ASP:OD1	2.38	0.55
4:L05:139:GLU:HA	27:L31:28:VAL:HG13	1.87	0.55
9:L11:133:ARG:O	33:23S:1077:A:O2'	2.23	0.55
20:L23:87:LEU:HD13	20:L23:91:GLN:HG3	1.88	0.55
22:L25:76:ASP:HB2	22:L25:90:ASP:HB2	1.87	0.55
23:L27:26:SER:HB2	23:L27:62:LYS:HG2	1.88	0.55
33:23S:177:G:OP2	33:23S:177:G:N2	2.35	0.55
33:23S:284:U:H3	33:23S:356:G:H1	1.54	0.55
33:23S:2110:G:H1	33:23S:2179:C:H42	1.52	0.55
36:16S:779:C:O2'	47:S11:121:ARG:NH1	2.39	0.55
1:L02:52:HIS:HA	1:L02:216:ARG:HG2	1.88	0.55
11:L14:70:ARG:NH2	33:23S:2683:C:O2	2.39	0.55
33:23S:805:G:N2	33:23S:829:A:OP1	2.39	0.55
15:L18:43:ASN:OD1	15:L18:43:ASN:N	2.36	0.55
17:L20:107:ALA:O	18:L21:48:LYS:NZ	2.39	0.55
20:L23:92:ASN:OD1	20:L23:92:ASN:N	2.40	0.55
22:L25:42:LEU:HD12	22:L25:47:VAL:HG11	1.88	0.55
33:23S:2099:U:O2	33:23S:2190:G:O6	2.25	0.55
36:16S:413:G:N2	36:16S:428:G:O2'	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:490:C:OP1	40:S04:147:LYS:NZ	2.39	0.55
39:S03:155:ARG:NE	39:S03:159:ALA:O	2.38	0.55
8:L10:36:ASP:O	8:L10:40:GLU:N	2.36	0.55
33:23S:1077:A:N6	33:23S:1089:A:OP1	2.37	0.55
36:16S:280:C:O2'	53:S17:39:ARG:NH2	2.39	0.55
36:16S:812:G:H4'	36:16S:813:U:H5'	1.88	0.55
44:S08:11:THR:OG1	44:S08:15:ASN:ND2	2.39	0.55
45:S09:15:ALA:O	45:S09:67:LYS:NZ	2.39	0.55
9:L11:38:CYS:HA	9:L11:42:ASN:HB2	1.88	0.55
12:L15:51:GLU:OE2	12:L15:54:GLN:NE2	2.40	0.55
33:23S:1801:A:H5''	33:23S:2203:U:H2'	1.89	0.55
36:16S:202:G:H21	36:16S:466:A:H61	1.52	0.55
36:16S:321:A:N6	36:16S:328:C:O2'	2.39	0.55
45:S09:90:ASP:OD1	45:S09:90:ASP:N	2.35	0.55
57:S21:20:ARG:HA	57:S21:24:LYS:HB2	1.89	0.55
12:L15:109:LYS:HG2	12:L15:126:ARG:HB2	1.89	0.55
30:L34:39:ARG:NH2	33:23S:469:G:O6	2.40	0.55
33:23S:1826:G:O2'	33:23S:1971:U:OP2	2.25	0.55
36:16S:564:C:OP2	48:S12:11:ARG:NH2	2.40	0.55
36:16S:878:A:OP1	44:S08:79:ARG:NH1	2.37	0.55
36:16S:1343:G:H4'	45:S09:123:ARG:HB2	1.89	0.55
57:S21:40:PRO:HA	57:S21:43:GLU:HG2	1.89	0.55
33:23S:1072:C:O2	33:23S:1093:G:O6	2.25	0.55
36:16S:409:U:OP1	40:S04:21:LYS:NZ	2.40	0.55
36:16S:709:U:H2'	36:16S:710:G:H8	1.72	0.55
53:S17:24:ILE:HB	53:S17:41:THR:HB	1.87	0.55
4:L05:9:ASP:N	4:L05:9:ASP:OD1	2.39	0.55
14:L17:34:ILE:HG13	14:L17:113:ILE:HG23	1.89	0.55
33:23S:578:G:OP1	33:23S:1255:U:O2'	2.23	0.55
33:23S:619:G:H3'	33:23S:620:G:H21	1.72	0.55
33:23S:959:A:N3	33:23S:2457:U:O2'	2.39	0.55
36:16S:707:U:O2'	47:S11:38:GLY:O	2.25	0.55
36:16S:958:A:N6	55:S19:76:THR:O	2.40	0.55
53:S17:10:ARG:HH11	53:S17:11:VAL:H	1.53	0.55
3:L04:163:ASN:ND2	33:23S:320:A:N3	2.54	0.54
33:23S:2202:U:O2'	33:23S:2204:G:OP1	2.25	0.54
34:5S:118:C:H2'	34:5S:119:A:H8	1.72	0.54
36:16S:579:A:O2'	51:S15:53:ARG:NH2	2.40	0.54
36:16S:1359:C:OP2	50:S14:74:ARG:NH1	2.40	0.54
1:L02:79:ARG:NH1	1:L02:81:GLU:OE1	2.40	0.54
11:L14:44:LYS:NZ	33:23S:1952:A:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L17:3:HIS:O	33:23S:2722:G:O2'	2.24	0.54
18:L21:4:VAL:HB	18:L21:39:LEU:HB2	1.88	0.54
33:23S:2110:G:H5'	33:23S:2145:C:H41	1.71	0.54
36:16S:59:A:H3'	36:16S:331:G:H22	1.72	0.54
36:16S:410:G:H21	36:16S:432:A:H62	1.53	0.54
36:16S:1125:U:OP1	46:S10:37:ARG:NH1	2.40	0.54
36:16S:1414:U:H2'	36:16S:1415:G:H8	1.72	0.54
40:S04:187:ARG:NH1	40:S04:196:GLU:OE2	2.39	0.54
53:S17:49:ASN:OD1	53:S17:49:ASN:N	2.40	0.54
4:L05:92:GLY:O	4:L05:96:TRP:NE1	2.40	0.54
5:L06:37:ASN:ND2	33:23S:2758:A:O2'	2.40	0.54
13:L16:16:ARG:NH1	33:23S:954:G:OP2	2.38	0.54
21:L24:68:ASN:ND2	33:23S:329:G:OP2	2.40	0.54
33:23S:1054:A:H2'	33:23S:1055:G:H8	1.72	0.54
33:23S:1310:G:H1'	33:23S:1611:C:H5''	1.89	0.54
4:L05:25:MET:O	4:L05:29:ARG:NH2	2.40	0.54
4:L05:71:LYS:NZ	4:L05:72:SER:O	2.40	0.54
7:L1:181:ASP:H	7:L1:184:LYS:HD3	1.72	0.54
10:L13:106:LYS:O	10:L13:111:LYS:NZ	2.41	0.54
19:L22:40:ASN:N	19:L22:40:ASN:OD1	2.38	0.54
24:L28:9:LYS:HE3	24:L28:53:LYS:HB3	1.90	0.54
33:23S:789:A:N6	33:23S:1614:A:OP2	2.39	0.54
9:L11:124:MET:SD	9:L11:127:SER:OG	2.63	0.54
11:L14:30:ARG:HD2	33:23S:2674:G:H4'	1.89	0.54
33:23S:307:G:N1	33:23S:310:A:OP2	2.40	0.54
33:23S:1319:C:N4	33:23S:1320:C:H42	2.06	0.54
33:23S:2469:A:N6	33:23S:2481:G:O2'	2.40	0.54
39:S03:25:THR:HA	50:S14:75:LYS:HE3	1.90	0.54
40:S04:131:ILE:HG22	40:S04:133:SER:H	1.70	0.54
8:L10:61:ARG:HB3	33:23S:1046:A:H4'	1.89	0.54
12:L15:20:GLY:HA2	12:L15:28:GLY:HA2	1.90	0.54
12:L15:79:LEU:HD12	12:L15:114:GLY:H	1.73	0.54
14:L17:8:ARG:NH1	14:L17:43:GLU:OE1	2.39	0.54
33:23S:643:A:N1	33:23S:2369:A:O2'	2.35	0.54
34:5S:39:A:H2'	34:5S:40:U:C2	2.43	0.54
36:16S:549:C:OP1	40:S04:69:ARG:NH2	2.41	0.54
36:16S:1137:C:O2'	36:16S:1138:G:N2	2.41	0.54
40:S04:145:ARG:HH21	40:S04:148:ALA:HB2	1.70	0.54
50:S14:63:CYS:HG	50:S14:66:THR:HG1	1.55	0.54
2:L03:129:THR:OG1	2:L03:140:HIS:O	2.25	0.54
5:L06:21:GLN:NE2	5:L06:37:ASN:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L06:123:GLU:HG3	5:L06:125:PRO:HD3	1.90	0.54
9:L11:75:ALA:HB1	9:L11:128:ILE:HG23	1.90	0.54
10:L13:125:TYR:OH	10:L13:132:HIS:NE2	2.41	0.54
33:23S:881:G:N2	33:23S:897:C:O2	2.40	0.54
33:23S:1853:A:N3	33:23S:2233:U:O2'	2.38	0.54
33:23S:2297:A:N6	33:23S:2318:G:N2	2.56	0.54
36:16S:1432:G:N2	36:16S:1468:A:OP2	2.41	0.54
41:S05:145:ASN:ND2	44:S08:72:GLU:OE2	2.36	0.54
5:L06:19:ASN:HB3	5:L06:22:VAL:HB	1.90	0.54
30:L34:30:VAL:HG22	30:L34:33:ARG:HH22	1.72	0.54
33:23S:1054:A:H2'	33:23S:1055:G:C8	2.42	0.54
33:23S:1297:C:O2'	33:23S:1302:A:N1	2.36	0.54
33:23S:1945:G:N2	33:23S:1963:U:O4	2.41	0.54
45:S09:35:GLU:HA	45:S09:39:GLY:HA3	1.90	0.54
56:S20:41:GLY:O	56:S20:43:LYS:NZ	2.41	0.54
33:23S:959:A:N6	33:23S:2495:G:O2'	2.36	0.54
36:16S:1103:C:OP1	38:S02:94:ARG:NH2	2.41	0.54
36:16S:1414:U:O2	36:16S:1487:G:N2	2.41	0.54
50:S14:37:ASP:H	50:S14:40:ARG:HB2	1.72	0.54
9:L11:134:SER:OG	33:23S:1088:A:N6	2.40	0.54
15:L18:10:ARG:NH1	33:23S:2295:C:OP1	2.40	0.54
17:L20:51:GLN:HA	17:L20:54:ARG:HE	1.72	0.54
33:23S:863:A:O2'	34:5S:100:G:N3	2.39	0.54
33:23S:2474:U:O4	33:23S:2529:G:N2	2.41	0.54
36:16S:194:C:H5''	56:S20:59:ARG:HE	1.73	0.54
36:16S:1405:G:H21	36:16S:1518:A:H1'	1.73	0.54
5:L06:8:VAL:O	5:L06:49:LEU:N	2.39	0.53
23:L27:46:ASN:HB2	23:L27:78:ILE:HB	1.89	0.53
33:23S:1770:G:H1	33:23S:1982:U:H3	1.56	0.53
36:16S:618:C:N4	36:16S:621:A:OP2	2.35	0.53
36:16S:811:C:H4'	36:16S:901:A:H61	1.72	0.53
41:S05:106:ALA:O	41:S05:111:ARG:NH2	2.41	0.53
1:L02:13:ARG:HH12	33:23S:1693:U:H1'	1.72	0.53
16:L19:46:VAL:HG22	16:L19:60:VAL:HG22	1.91	0.53
17:L20:93:ILE:HD12	18:L21:13:ARG:HB2	1.89	0.53
19:L22:23:LEU:HD11	28:L32:21:LEU:HD12	1.90	0.53
33:23S:2750:A:O2'	33:23S:2752:C:N4	2.41	0.53
36:16S:371:A:H1'	36:16S:373:A:H62	1.72	0.53
36:16S:913:A:OP1	48:S12:42:LYS:NZ	2.41	0.53
40:S04:64:TYR:HB2	40:S04:66:VAL:HG23	1.90	0.53
45:S09:20:ILE:HG12	45:S09:60:LEU:HD22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S15:28:VAL:HG11	51:S15:66:LEU:HD21	1.90	0.53
52:S16:75:ILE:O	52:S16:80:LYS:NZ	2.39	0.53
3:L04:48:THR:OG1	3:L04:49:ARG:N	2.42	0.53
5:L06:126:THR:HG23	5:L06:129:GLU:HB2	1.91	0.53
9:L11:101:SER:HA	9:L11:140:GLU:HG3	1.91	0.53
14:L17:8:ARG:N	14:L17:43:GLU:OE2	2.42	0.53
15:L18:15:ARG:NH2	34:5S:8:C:OP1	2.42	0.53
16:L19:87:ARG:HE	16:L19:111:GLU:HB3	1.73	0.53
17:L20:29:ARG:NH1	33:23S:18:U:OP1	2.39	0.53
23:L27:29:ALA:O	33:23S:2353:G:O2'	2.25	0.53
31:L35:44:ARG:NH2	33:23S:2349:G:OP1	2.41	0.53
50:S14:45:LEU:HB3	55:S19:12:LEU:HD11	1.90	0.53
5:L06:21:GLN:OE1	5:L06:54:ARG:NH2	2.40	0.53
23:L27:13:GLU:OE2	23:L27:16:ARG:NH1	2.38	0.53
27:L31:26:SER:OG	27:L31:27:THR:N	2.40	0.53
33:23S:1860:G:H1	33:23S:1882:U:H3	1.56	0.53
33:23S:2075:U:OP2	33:23S:2238:G:O2'	2.27	0.53
33:23S:2857:G:N2	33:23S:2860:A:OP2	2.32	0.53
36:16S:37:U:H2'	36:16S:38:G:H8	1.73	0.53
36:16S:1016:A:O2'	36:16S:1217:C:O2'	2.25	0.53
39:S03:55:VAL:HB	39:S03:66:THR:HB	1.89	0.53
3:L04:154:ASP:OD1	3:L04:154:ASP:N	2.41	0.53
4:L05:60:SER:N	27:L31:7:PRO:O	2.41	0.53
36:16S:589:U:C2	36:16S:650:G:O6	2.62	0.53
36:16S:1317:C:H4'	50:S14:47:LEU:HD23	1.91	0.53
52:S16:35:ARG:NH2	52:S16:37:GLY:O	2.41	0.53
10:L13:116:ARG:NH2	33:23S:529:A:OP2	2.41	0.53
17:L20:89:ILE:HG12	18:L21:39:LEU:HD23	1.90	0.53
29:L33:32:LYS:HB2	29:L33:50:GLU:HB3	1.91	0.53
36:16S:345:C:O2	36:16S:346:G:N1	2.42	0.53
36:16S:880:C:H2'	36:16S:881:G:H8	1.73	0.53
36:16S:1071:C:O3'	41:S05:53:ARG:NH1	2.41	0.53
43:S07:46:LEU:O	43:S07:50:ALA:N	2.41	0.53
44:S08:46:GLU:O	44:S08:61:THR:OG1	2.25	0.53
49:S13:76:ILE:O	49:S13:80:MET:N	2.30	0.53
1:L02:171:VAL:HG23	1:L02:183:VAL:HG23	1.91	0.53
4:L05:141:ASP:OD1	4:L05:141:ASP:N	2.40	0.53
5:L06:94:ARG:HD2	5:L06:127:GLN:HB3	1.89	0.53
17:L20:3:VAL:HG22	33:23S:1199:U:H1'	1.91	0.53
31:L35:2:LYS:NZ	33:23S:242:G:OP2	2.38	0.53
31:L35:40:LYS:NZ	33:23S:2419:U:OP1	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:1073:A:HO2'	33:23S:2474:U:HO2'	1.57	0.53
33:23S:2127:G:H21	33:23S:2173:A:H1'	1.74	0.53
34:5S:37:C:N3	34:5S:48:U:O2'	2.38	0.53
36:16S:186:C:O2'	56:S20:75:LYS:O	2.27	0.53
36:16S:422:C:O2'	36:16S:423:G:N2	2.42	0.53
50:S14:54:SER:O	50:S14:54:SER:OG	2.26	0.53
27:L31:8:LYS:HD3	27:L31:9:TYR:H	1.72	0.53
32:L36:22:VAL:HB	32:L36:37:GLN:HB3	1.91	0.53
33:23S:285:G:O6	33:23S:354:A:N6	2.42	0.53
33:23S:306:U:H3	33:23S:310:A:H62	1.57	0.53
33:23S:527:C:N4	33:23S:2779:U:OP2	2.42	0.53
33:23S:935:C:H2'	33:23S:936:A:H8	1.74	0.53
33:23S:1992:G:N2	33:23S:1996:C:O2'	2.41	0.53
33:23S:2515:C:H2'	33:23S:2516:A:H8	1.74	0.53
33:23S:2637:U:O2	33:23S:2776:A:N7	2.42	0.53
36:16S:880:C:OP1	48:S12:8:ARG:NH2	2.40	0.53
45:S09:98:ARG:HG3	45:S09:103:VAL:HG21	1.90	0.53
57:S21:5:VAL:HG22	57:S21:7:GLU:H	1.74	0.53
4:L05:62:GLN:HA	27:L31:8:LYS:HE2	1.91	0.53
13:L16:17:ASN:OD1	13:L16:97:GLN:NE2	2.42	0.53
18:L21:43:ASN:OD1	18:L21:43:ASN:N	2.42	0.53
33:23S:1047:G:O2'	33:23S:1111:A:N6	2.37	0.53
33:23S:1769:U:O2	33:23S:1983:G:O6	2.27	0.53
34:5S:65:U:H3'	34:5S:108:A:H61	1.74	0.53
49:S13:59:VAL:HG22	49:S13:64:VAL:HG11	1.91	0.53
15:L18:7:ARG:NH1	15:L18:95:SER:O	2.40	0.53
33:23S:2117:A:N6	33:23S:2166:U:O4	2.42	0.53
36:16S:436:C:O2	40:S04:153:ARG:NH1	2.39	0.53
36:16S:1125:U:H2'	36:16S:1126:U:H2'	1.90	0.53
4:L05:87:LYS:HD2	33:23S:2313:C:H5''	1.91	0.52
9:L11:135:MET:HB3	9:L11:137:LEU:HD13	1.90	0.52
36:16S:198:G:O6	36:16S:219:U:O4	2.26	0.52
16:L19:89:GLY:O	16:L19:112:ARG:NH1	2.41	0.52
22:L25:72:VAL:HG12	22:L25:93:ARG:HA	1.91	0.52
33:23S:1427:A:N6	33:23S:1571:A:OP2	2.41	0.52
33:23S:1437:C:O2'	33:23S:1516:G:O2'	2.25	0.52
33:23S:2033:A:O2'	33:23S:2035:G:OP2	2.22	0.52
36:16S:33:A:H1'	48:S12:27:PRO:HG3	1.91	0.52
36:16S:923:A:N6	36:16S:1392:G:O6	2.42	0.52
1:L02:17:LYS:NZ	33:23S:1565:C:OP1	2.35	0.52
1:L02:208:GLY:O	1:L02:212:TRP:N	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L17:17:ARG:NH2	33:23S:2002:G:OP1	2.32	0.52
33:23S:1040:A:N1	33:23S:1115:G:N2	2.52	0.52
36:16S:1457:G:OP1	56:S20:33:LYS:NZ	2.42	0.52
57:S21:17:ARG:O	57:S21:21:SER:N	2.42	0.52
1:L02:252:LYS:NZ	33:23S:1825:U:O2	2.42	0.52
1:L02:255:LYS:NZ	33:23S:1844:C:O3'	2.42	0.52
14:L17:29:VAL:O	14:L17:78:LYS:NZ	2.38	0.52
17:L20:48:ASP:HA	17:L20:51:GLN:HB2	1.90	0.52
33:23S:1667:G:N1	33:23S:1992:G:OP2	2.31	0.52
48:S12:3:VAL:HG23	48:S12:6:LEU:HD12	1.91	0.52
15:L18:58:ILE:HA	15:L18:61:GLN:HE22	1.75	0.52
36:16S:127:G:O2'	53:S17:5:ARG:NH1	2.42	0.52
40:S04:13:ARG:HB2	40:S04:37:PRO:HB3	1.89	0.52
1:L02:13:ARG:NH1	33:23S:1693:U:O2	2.42	0.52
5:L06:79:THR:HG23	5:L06:80:GLU:HG3	1.91	0.52
6:L09:98:ASP:N	6:L09:98:ASP:OD1	2.42	0.52
11:L14:40:LYS:NZ	33:23S:2561:U:O3'	2.42	0.52
36:16S:738:C:OP1	42:S06:2:ARG:NH1	2.43	0.52
36:16S:1286:U:H2'	36:16S:1287:A:H4'	1.91	0.52
36:16S:1366:C:O2'	46:S10:62:ARG:NH2	2.43	0.52
47:S11:45:THR:OG1	47:S11:46:ALA:N	2.41	0.52
1:L02:257:ARG:NH1	33:23S:1800:C:OP1	2.41	0.52
17:L20:90:ASP:OD1	17:L20:90:ASP:N	2.42	0.52
33:23S:1181:U:H2'	33:23S:1182:G:H8	1.75	0.52
36:16S:197:A:N1	36:16S:220:G:O2'	2.39	0.52
36:16S:545:C:OP1	40:S04:61:ARG:NH1	2.43	0.52
36:16S:1356:G:H2'	36:16S:1357:A:H8	1.74	0.52
40:S04:14:GLU:OE2	40:S04:55:ARG:NH1	2.41	0.52
53:S17:59:GLU:HG3	53:S17:76:ARG:HG2	1.92	0.52
2:L03:115:GLY:HA2	2:L03:166:GLY:HA3	1.92	0.52
12:L15:63:LYS:NZ	33:23S:249:C:O2	2.43	0.52
23:L27:52:ASP:OD1	23:L27:52:ASP:N	2.42	0.52
33:23S:101:A:O2'	33:23S:103:A:OP1	2.24	0.52
33:23S:2685:G:H1	33:23S:2724:U:H3	1.56	0.52
33:23S:2847:U:O2	33:23S:2869:G:N2	2.37	0.52
36:16S:222:C:H2'	36:16S:223:A:C8	2.45	0.52
36:16S:935:A:O2'	36:16S:1383:C:O2	2.27	0.52
1:L02:140:VAL:HG12	1:L02:191:LEU:HA	1.91	0.52
12:L15:91:ASP:N	12:L15:91:ASP:OD1	2.41	0.52
33:23S:1356:G:H1	33:23S:1375:U:H3	1.57	0.52
33:23S:1907:G:N2	33:23S:1923:U:O2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:S08:112:ASP:OD2	44:S08:116:ARG:NH2	2.42	0.52
33:23S:1918:A:O2'	33:23S:1919:A:N7	2.43	0.52
33:23S:2291:U:O4	33:23S:2341:G:O6	2.28	0.52
33:23S:2374:C:N4	33:23S:2375:G:O6	2.43	0.52
46:S10:85:ASP:O	46:S10:89:ARG:NH1	2.42	0.52
47:S11:124:LYS:O	57:S21:34:ARG:NH2	2.40	0.52
13:L16:133:LYS:NZ	13:L16:134:THR:O	2.43	0.51
36:16S:222:C:H2'	36:16S:223:A:H8	1.75	0.51
36:16S:404:G:N7	40:S04:1:ALA:N	2.45	0.51
36:16S:417:G:O6	36:16S:426:U:O2	2.27	0.51
36:16S:657:U:O2	51:S15:21:THR:OG1	2.25	0.51
40:S04:44:LYS:NZ	40:S04:45:PRO:O	2.43	0.51
8:L10:53:ARG:HB3	8:L10:55:VAL:HG22	1.90	0.51
14:L17:2:ARG:NH1	33:23S:2820:A:OP2	2.43	0.51
33:23S:2165:C:N4	33:23S:2170:A:C6	2.78	0.51
36:16S:1151:A:O2'	46:S10:72:ARG:NH2	2.43	0.51
38:S02:114:LYS:NZ	38:S02:151:LYS:O	2.43	0.51
40:S04:73:ASN:OD1	40:S04:73:ASN:N	2.44	0.51
41:S05:14:LEU:HA	41:S05:36:THR:HA	1.92	0.51
41:S05:149:PRO:HA	41:S05:152:VAL:HB	1.91	0.51
49:S13:73:SER:O	49:S13:77:LYS:N	2.39	0.51
56:S20:4:LYS:HB3	56:S20:6:ALA:H	1.74	0.51
1:L02:65:ASP:OD2	1:L02:101:ARG:NH1	2.43	0.51
36:16S:123:U:OP1	36:16S:311:C:O2'	2.25	0.51
36:16S:1427:C:H2'	36:16S:1428:A:H8	1.76	0.51
43:S07:65:LEU:HD23	43:S07:69:ARG:HH21	1.75	0.51
2:L03:15:PHE:HB3	16:L19:78:PRO:HG3	1.92	0.51
33:23S:917:A:H5''	33:23S:2268:A:H61	1.74	0.51
33:23S:1429:G:H2'	33:23S:1430:G:H8	1.75	0.51
33:23S:2102:G:N2	33:23S:2187:U:O2	2.42	0.51
33:23S:2175:C:H2'	33:23S:2176:A:C8	2.46	0.51
33:23S:2531:A:H61	33:23S:2662:A:H61	1.58	0.51
36:16S:1425:U:H2'	36:16S:1426:G:H8	1.76	0.51
38:S02:163:ILE:HG23	38:S02:185:ILE:HB	1.92	0.51
13:L16:51:ARG:NH1	33:23S:2483:C:O2'	2.43	0.51
16:L19:50:ARG:NH2	33:23S:2683:C:OP1	2.36	0.51
16:L19:92:ARG:HD3	33:23S:1753:G:H5''	1.91	0.51
33:23S:788:A:OP1	33:23S:791:C:N4	2.40	0.51
33:23S:2258:C:O2'	33:23S:2427:C:OP2	2.26	0.51
34:5S:38:C:H2'	34:5S:39:A:C8	2.46	0.51
36:16S:1130:A:H4'	45:S09:4:GLN:HE22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:S02:76:SER:OG	38:S02:92:ASN:ND2	2.44	0.51
45:S09:50:PRO:HG3	45:S09:79:ARG:HA	1.91	0.51
9:L11:65:SER:OG	9:L11:66:PHE:N	2.43	0.51
18:L21:75:VAL:HG22	18:L21:86:GLN:HG2	1.92	0.51
26:L30:20:LYS:NZ	33:23S:969:G:OP1	2.41	0.51
33:23S:711:G:N2	33:23S:720:U:O2	2.41	0.51
33:23S:807:U:O2'	33:23S:2060:A:N1	2.43	0.51
38:S02:4:SER:OG	38:S02:6:ARG:NH1	2.43	0.51
40:S04:109:THR:H	40:S04:112:GLU:HB3	1.74	0.51
2:L03:155:VAL:HG21	33:23S:2618:G:H21	1.75	0.51
4:L05:22:ASN:OD1	4:L05:22:ASN:N	2.40	0.51
6:L09:73:ASN:ND2	6:L09:106:ALA:O	2.43	0.51
11:L14:70:ARG:HG2	11:L14:76:VAL:HG12	1.92	0.51
33:23S:1268:A:H62	33:23S:2012:G:N2	2.07	0.51
33:23S:1412:U:H2'	33:23S:1413:A:C8	2.46	0.51
36:16S:23:C:OP2	36:16S:561:U:N3	2.39	0.51
36:16S:362:G:N2	36:16S:365:U:OP2	2.38	0.51
36:16S:933:G:N7	43:S07:2:ARG:NH2	2.52	0.51
38:S02:72:LYS:HE2	38:S02:204:ASP:HA	1.93	0.51
1:L02:12:ARG:HD2	1:L02:15:VAL:HG11	1.93	0.51
1:L02:47:ARG:NH1	33:23S:1807:G:OP1	2.44	0.51
36:16S:257:G:H2'	36:16S:258:G:H8	1.76	0.51
36:16S:1285:A:N6	36:16S:1354:U:O2'	2.44	0.51
46:S10:28:THR:O	46:S10:32:THR:OG1	2.27	0.51
54:S18:21:ASP:OD2	54:S18:23:LYS:NZ	2.36	0.51
7:L1:20:GLN:OE1	7:L1:223:ALA:N	2.42	0.51
21:L24:76:THR:HG23	21:L24:78:LYS:H	1.75	0.51
24:L28:67:LEU:O	24:L28:77:TYR:OH	2.26	0.51
33:23S:1009:A:N3	33:23S:1153:C:O2'	2.43	0.51
36:16S:745:G:OP1	36:16S:851:G:O2'	2.28	0.51
36:16S:1028:C:N3	36:16S:1033:G:N1	2.48	0.51
40:S04:97:LEU:HB2	40:S04:134:TYR:HB3	1.92	0.51
50:S14:68:ARG:NH1	50:S14:70:HIS:O	2.44	0.51
54:S18:36:GLY:O	54:S18:62:ARG:NH2	2.43	0.51
12:L15:48:ARG:NH2	31:L35:59:ALA:O	2.43	0.51
15:L18:34:HIS:ND1	15:L18:53:THR:OG1	2.37	0.51
16:L19:52:ARG:NH2	33:23S:2720:U:OP1	2.44	0.51
33:23S:2655:G:N2	33:23S:2665:A:OP2	2.44	0.51
36:16S:979:C:N4	50:S14:57:SER:OG	2.41	0.51
36:16S:1147:C:O2	45:S09:17:ARG:NH1	2.44	0.51
40:S04:161:ALA:HA	40:S04:164:ARG:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S13:24:VAL:HG23	49:S13:28:ARG:HB3	1.93	0.51
53:S17:12:VAL:HB	53:S17:21:VAL:HG13	1.93	0.51
19:L22:7:HIS:N	19:L22:103:ILE:O	2.40	0.50
20:L23:30:ILE:HG22	20:L23:85:VAL:HB	1.93	0.50
36:16S:107:G:OP1	36:16S:325:A:N6	2.41	0.50
36:16S:434:U:H2'	36:16S:435:A:C8	2.46	0.50
36:16S:458:U:H2'	36:16S:459:A:C8	2.46	0.50
36:16S:589:U:O2	36:16S:650:G:O6	2.28	0.50
36:16S:1320:C:O2	55:S19:35:ARG:NH2	2.44	0.50
36:16S:1359:C:H5	50:S14:74:ARG:HH12	1.58	0.50
42:S06:77:THR:O	42:S06:81:ASN:N	2.39	0.50
49:S13:84:CYS:SG	49:S13:85:TYR:N	2.83	0.50
1:L02:100:ARG:NH2	33:23S:1501:G:OP1	2.41	0.50
10:L13:15:TRP:HB3	10:L13:137:PRO:HB3	1.93	0.50
33:23S:2572:A:H5''	33:23S:2574:G:H4'	1.94	0.50
36:16S:407:U:O2'	40:S04:112:GLU:OE1	2.29	0.50
36:16S:769:G:H4'	36:16S:1513:A:H4'	1.92	0.50
36:16S:1071:C:H2'	36:16S:1072:G:H8	1.76	0.50
53:S17:13:SER:OG	53:S17:16:MET:SD	2.69	0.50
1:L02:38:LYS:HB2	33:23S:692:C:H5''	1.93	0.50
13:L16:58:LYS:O	13:L16:59:ARG:NE	2.44	0.50
24:L28:17:ARG:HE	24:L28:23:ALA:HB2	1.76	0.50
33:23S:404:A:N6	33:23S:421:C:C5	2.80	0.50
33:23S:910:A:N3	33:23S:2264:C:O2'	2.39	0.50
33:23S:1716:U:H3	33:23S:1744:A:H62	1.56	0.50
33:23S:1724:G:O6	33:23S:1736:U:O2	2.29	0.50
33:23S:2100:G:H1	33:23S:2189:U:H3	1.59	0.50
41:S05:37:VAL:HG11	41:S05:113:VAL:HA	1.93	0.50
46:S10:42:LEU:HD12	46:S10:71:LEU:HB3	1.94	0.50
31:L35:38:LYS:NZ	33:23S:2351:G:O6	2.45	0.50
33:23S:1539:U:H2'	33:23S:1540:G:H8	1.76	0.50
36:16S:837:U:H2'	36:16S:838:G:H8	1.76	0.50
36:16S:884:U:H4'	36:16S:885:G:H5''	1.94	0.50
2:L03:8:LYS:HB2	2:L03:201:LEU:HD11	1.92	0.50
28:L32:24:VAL:HG22	28:L32:26:SER:H	1.76	0.50
33:23S:239:C:O2'	33:23S:622:G:O2'	2.26	0.50
33:23S:1085:A:H2'	33:23S:1086:A:C4	2.46	0.50
33:23S:1636:U:H2'	33:23S:1637:A:H8	1.76	0.50
36:16S:959:A:O2'	36:16S:984:C:O2'	2.27	0.50
40:S04:187:ARG:HD2	40:S04:190:LEU:HD11	1.92	0.50
53:S17:10:ARG:O	53:S17:23:ALA:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L04:113:VAL:HG22	3:L04:118:LEU:HD22	1.94	0.50
9:L11:102:ARG:H	9:L11:141:ASP:HA	1.76	0.50
17:L20:48:ASP:O	17:L20:52:ARG:N	2.41	0.50
33:23S:429:A:H2'	33:23S:430:A:C4	2.47	0.50
33:23S:2249:U:O2'	33:23S:2252:G:OP2	2.28	0.50
36:16S:376:G:H2'	36:16S:377:G:H8	1.76	0.50
36:16S:1232:U:H5''	45:S09:125:GLN:HB3	1.93	0.50
36:16S:1307:U:O4	36:16S:1331:G:N2	2.45	0.50
36:16S:1356:G:H2'	36:16S:1357:A:C8	2.46	0.50
39:S03:9:ILE:HG23	39:S03:10:ARG:HG3	1.93	0.50
44:S08:29:SER:H	44:S08:32:LYS:HB2	1.76	0.50
48:S12:120:ARG:NH1	48:S12:121:PRO:O	2.45	0.50
1:L02:93:VAL:O	1:L02:100:ARG:HA	2.12	0.50
2:L03:12:THR:O	2:L03:24:VAL:N	2.38	0.50
14:L17:98:LEU:O	14:L17:112:TYR:N	2.42	0.50
16:L19:17:PRO:HD2	16:L19:83:ILE:HD12	1.94	0.50
17:L20:53:LYS:HA	33:23S:995:C:H5''	1.94	0.50
18:L21:8:GLY:O	18:L21:10:LYS:NZ	2.44	0.50
19:L22:58:ALA:HA	19:L22:62:ASP:HB2	1.93	0.50
23:L27:38:GLY:O	23:L27:53:HIS:ND1	2.43	0.50
33:23S:863:A:O3'	34:5S:100:G:N2	2.39	0.50
33:23S:948:C:O2	33:23S:984:A:O2'	2.24	0.50
33:23S:1028:A:N6	33:23S:1126:A:OP1	2.41	0.50
33:23S:1796:U:H2'	33:23S:1797:G:H8	1.76	0.50
33:23S:2202:U:H3	33:23S:2221:G:H1	1.60	0.50
36:16S:952:U:H2'	36:16S:953:G:H8	1.76	0.50
36:16S:1269:A:N1	36:16S:1312:G:O2'	2.38	0.50
36:16S:1368:A:OP2	45:S09:113:LYS:NZ	2.43	0.50
39:S03:19:SER:OG	50:S14:91:GLU:O	2.28	0.50
40:S04:43:ARG:HH21	40:S04:46:ARG:HH12	1.60	0.50
42:S06:2:ARG:HG2	42:S06:91:ARG:HH22	1.77	0.50
44:S08:103:VAL:HB	44:S08:124:ILE:HG22	1.93	0.50
46:S10:36:VAL:HG13	46:S10:76:ILE:HA	1.94	0.50
10:L13:64:VAL:HB	10:L13:68:LYS:HE3	1.94	0.50
10:L13:134:ALA:O	33:23S:2898:U:O2'	2.28	0.50
14:L17:56:LYS:NZ	14:L17:88:ALA:O	2.42	0.50
24:L28:17:ARG:NH2	33:23S:201:C:OP1	2.44	0.50
33:23S:1068:G:N2	33:23S:1095:A:O2'	2.44	0.50
33:23S:2448:A:H3'	33:23S:2449:U:H2'	1.94	0.50
41:S05:148:SER:OG	41:S05:150:GLU:OE1	2.25	0.50
46:S10:84:VAL:O	46:S10:88:MET:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L10:56:ARG:HG2	8:L10:83:ALA:HB2	1.94	0.50
24:L28:56:ARG:NH1	33:23S:399:U:OP2	2.45	0.50
27:L31:27:THR:OG1	27:L31:27:THR:O	2.29	0.50
33:23S:1131:G:N2	33:23S:1132:U:O4	2.38	0.50
36:16S:64:G:H22	36:16S:101:A:H61	1.59	0.50
36:16S:76:G:N2	36:16S:93:U:O2	2.39	0.50
36:16S:264:C:O2'	53:S17:65:PRO:O	2.29	0.50
36:16S:768:A:N3	36:16S:1512:U:O2'	2.44	0.50
56:S20:55:PRO:O	56:S20:59:ARG:N	2.39	0.50
3:L04:110:SER:HB2	3:L04:114:ARG:HH12	1.77	0.49
6:L09:79:THR:HA	6:L09:145:ASN:HB3	1.94	0.49
7:L1:6:LYS:HA	7:L1:9:ARG:HE	1.76	0.49
9:L11:102:ARG:HH21	9:L11:105:LEU:HD13	1.77	0.49
33:23S:987:C:O2'	33:23S:1000:A:N3	2.42	0.49
33:23S:1969:A:O2'	33:23S:1972:G:N3	2.40	0.49
36:16S:522:C:OP2	48:S12:65:TYR:OH	2.30	0.49
36:16S:925:G:H1	36:16S:1391:U:H3	1.59	0.49
36:16S:927:G:N2	36:16S:1390:U:O2	2.38	0.49
36:16S:1162:C:H2'	36:16S:1163:A:H8	1.77	0.49
36:16S:1279:G:N7	46:S10:45:ARG:NH1	2.59	0.49
33:23S:1908:C:N3	33:23S:1909:C:C4	2.80	0.49
33:23S:1999:C:O3'	33:23S:2722:G:N2	2.45	0.49
36:16S:426:U:O2'	40:S04:39:GLN:OE1	2.30	0.49
36:16S:758:C:H4'	36:16S:880:C:H4'	1.94	0.49
42:S06:9:MET:HE3	42:S06:86:ARG:HB3	1.94	0.49
42:S06:36:ILE:HA	42:S06:64:VAL:HA	1.94	0.49
44:S08:103:VAL:HA	44:S08:124:ILE:HA	1.94	0.49
1:L02:244:VAL:HG12	1:L02:250:GLN:HA	1.95	0.49
4:L05:45:ASP:OD1	4:L05:45:ASP:N	2.44	0.49
4:L05:51:ASN:O	4:L05:55:ASP:N	2.42	0.49
10:L13:136:GLN:NE2	33:23S:2898:U:O2'	2.41	0.49
19:L22:9:HIS:O	19:L22:11:ARG:NH1	2.45	0.49
19:L22:86:MET:HB2	19:L22:96:ILE:HD13	1.93	0.49
33:23S:602:A:O2'	33:23S:604:G:O2'	2.28	0.49
33:23S:819:A:HO2'	33:23S:837:C:HO2'	1.60	0.49
36:16S:836:G:O6	36:16S:850:U:O2	2.30	0.49
43:S07:26:VAL:HG22	43:S07:42:VAL:HG11	1.93	0.49
13:L16:34:LYS:HA	13:L16:101:VAL:HA	1.94	0.49
14:L17:39:PRO:HG2	33:23S:1651:G:H4'	1.94	0.49
16:L19:22:GLY:N	16:L19:46:VAL:O	2.44	0.49
18:L21:25:LEU:HB2	18:L21:94:THR:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:L35:5:THR:HG22	31:L35:61:LEU:HA	1.94	0.49
31:L35:22:LYS:NZ	33:23S:631:A:OP2	2.40	0.49
32:L36:24:ARG:NH2	33:23S:2742:G:OP2	2.41	0.49
36:16S:963:G:H2'	36:16S:964:A:H8	1.77	0.49
49:S13:73:SER:HA	49:S13:76:ILE:HB	1.94	0.49
50:S14:36:SER:HA	50:S14:40:ARG:HD3	1.94	0.49
1:L02:119:VAL:HG13	1:L02:130:PRO:HG2	1.94	0.49
25:L29:6:LEU:HD13	25:L29:56:LEU:HD22	1.95	0.49
36:16S:250:A:N6	36:16S:275:G:O6	2.45	0.49
36:16S:593:U:H3	36:16S:646:G:H1	1.61	0.49
36:16S:993:G:O2'	36:16S:994:A:N7	2.41	0.49
2:L03:140:HIS:NE2	33:23S:1658:C:OP1	2.45	0.49
4:L05:35:LEU:HB3	4:L05:88:VAL:HB	1.95	0.49
9:L11:92:PRO:HD2	33:23S:1076:C:H1'	1.94	0.49
10:L13:72:LYS:HB3	10:L13:89:PHE:HB2	1.94	0.49
12:L15:88:GLY:O	12:L15:121:THR:N	2.45	0.49
16:L19:87:ARG:NH2	16:L19:109:ILE:O	2.46	0.49
16:L19:92:ARG:NH2	33:23S:2849:U:OP1	2.34	0.49
24:L28:35:HIS:NE2	33:23S:2199:A:O2'	2.44	0.49
29:L33:22:THR:OG1	29:L33:23:THR:N	2.46	0.49
33:23S:14:A:N1	33:23S:2044:C:O2'	2.40	0.49
33:23S:2233:U:H2'	33:23S:2234:G:H8	1.77	0.49
36:16S:310:G:H5''	52:S16:31:ARG:HB2	1.94	0.49
36:16S:478:A:C2	36:16S:479:U:O2	2.65	0.49
36:16S:765:G:N1	36:16S:812:G:O2'	2.37	0.49
7:L1:67:HIS:HB3	7:L1:184:LYS:HE3	1.94	0.49
9:L11:73:PRO:O	9:L11:112:LYS:NZ	2.38	0.49
26:L30:10:ARG:HB2	26:L30:53:MET:HB3	1.94	0.49
33:23S:1278:C:H2'	33:23S:1279:G:H8	1.77	0.49
36:16S:323:U:O4	36:16S:327:A:N7	2.46	0.49
46:S10:8:ILE:HB	46:S10:74:VAL:HB	1.94	0.49
48:S12:85:ARG:HH21	48:S12:87:LYS:HG3	1.77	0.49
13:L16:128:THR:OG1	13:L16:129:THR:N	2.46	0.49
23:L27:38:GLY:HA2	33:23S:2330:G:H21	1.77	0.49
33:23S:21:A:N6	33:23S:518:G:O6	2.46	0.49
36:16S:952:U:H5''	36:16S:964:A:H61	1.77	0.49
36:16S:1249:C:O2'	45:S09:69:GLY:O	2.31	0.49
40:S04:55:ARG:HA	40:S04:58:GLN:HB2	1.94	0.49
41:S05:79:THR:OG1	41:S05:80:LEU:N	2.44	0.49
43:S07:139:ASP:HA	43:S07:142:ARG:HD2	1.93	0.49
44:S08:49:LYS:HB2	44:S08:59:GLU:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L05:99:PHE:O	4:L05:103:ILE:N	2.37	0.49
10:L13:27:ARG:NH2	33:23S:1140:C:O2'	2.45	0.49
33:23S:106:C:H2'	33:23S:107:G:H8	1.77	0.49
33:23S:558:U:H2'	33:23S:559:G:H8	1.78	0.49
33:23S:1218:G:O6	33:23S:1231:U:O2	2.30	0.49
33:23S:2316:G:H2'	33:23S:2317:A:H8	1.77	0.49
36:16S:182:A:OP2	36:16S:193:C:N4	2.46	0.49
36:16S:1052:U:O2'	36:16S:1055:A:OP2	2.23	0.49
36:16S:1073:U:O2	38:S02:102:ASN:ND2	2.39	0.49
36:16S:1374:A:H1'	43:S07:30:MET:HE1	1.94	0.49
50:S14:10:VAL:HA	50:S14:13:VAL:HG12	1.95	0.49
3:L04:53:THR:O	3:L04:53:THR:OG1	2.25	0.49
4:L05:38:GLY:O	33:23S:2306:C:N4	2.46	0.49
5:L06:2:ARG:NH1	33:23S:1113:U:OP1	2.41	0.49
27:L31:1:MET:SD	34:5S:43:C:H2'	2.53	0.49
30:L34:34:ARG:NH2	33:23S:466:A:OP1	2.46	0.49
41:S05:89:THR:OG1	41:S05:134:ASN:OD1	2.30	0.49
42:S06:8:PHE:HB3	42:S06:87:SER:HB3	1.95	0.49
1:L02:117:SER:OG	1:L02:118:GLY:N	2.43	0.48
4:L05:146:ASP:N	4:L05:146:ASP:OD1	2.45	0.48
5:L06:163:TYR:HB2	5:L06:166:GLU:HB2	1.95	0.48
7:L1:37:LYS:HE2	33:23S:2127:G:H3'	1.95	0.48
9:L11:98:GLY:H	9:L11:137:LEU:HG	1.77	0.48
19:L22:80:PRO:O	19:L22:100:THR:OG1	2.24	0.48
20:L23:69:ARG:HB3	20:L23:74:ILE:HD13	1.95	0.48
21:L24:28:LEU:N	21:L24:32:LYS:O	2.43	0.48
29:L33:9:LYS:HB3	29:L33:51:ALA:HB3	1.93	0.48
33:23S:833:A:H2'	33:23S:834:G:C8	2.48	0.48
33:23S:1072:C:N4	33:23S:1093:G:N2	2.45	0.48
33:23S:1179:G:C2	33:23S:1180:U:H1'	2.47	0.48
33:23S:2289:G:O6	33:23S:2343:U:O4	2.31	0.48
36:16S:1496:C:O2	36:16S:1517:G:N2	2.41	0.48
46:S10:12:ALA:HB2	46:S10:96:VAL:HG13	1.94	0.48
5:L06:36:LEU:HD11	5:L06:71:LEU:HD11	1.94	0.48
9:L11:2:LYS:O	9:L11:7:TYR:OH	2.31	0.48
9:L11:131:THR:O	9:L11:135:MET:N	2.47	0.48
33:23S:1419:A:N6	33:23S:1421:G:N3	2.60	0.48
33:23S:2165:C:H42	33:23S:2170:A:N6	2.07	0.48
33:23S:2692:G:OP1	33:23S:2870:C:O2'	2.31	0.48
39:S03:8:GLY:HA2	39:S03:11:LEU:HG	1.95	0.48
52:S16:6:LEU:HB3	52:S16:17:TYR:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S16:40:ASN:HB3	52:S16:43:ALA:HB2	1.95	0.48
6:L09:33:GLN:O	6:L09:35:LYS:NZ	2.42	0.48
8:L10:119:PRO:HB3	8:L10:126:LEU:HD12	1.95	0.48
11:L14:121:GLU:OE1	16:L19:64:SER:OG	2.32	0.48
29:L33:24:LYS:HD2	29:L33:26:LYS:HG3	1.96	0.48
32:L36:2:LYS:NZ	32:L36:32:LYS:O	2.45	0.48
33:23S:511:U:H4'	33:23S:1235:G:H4'	1.95	0.48
33:23S:1509:A:H2'	33:23S:1510:G:C8	2.48	0.48
33:23S:2102:G:C2	33:23S:2187:U:O2	2.66	0.48
33:23S:2155:U:H3'	33:23S:2156:G:H8	1.79	0.48
36:16S:309:A:H2'	36:16S:310:G:H8	1.78	0.48
36:16S:1160:G:N2	36:16S:1176:A:N1	2.60	0.48
39:S03:42:LEU:HD11	39:S03:90:VAL:HG11	1.95	0.48
40:S04:58:GLN:O	40:S04:62:ARG:N	2.46	0.48
40:S04:59:LYS:HA	40:S04:62:ARG:HB2	1.94	0.48
57:S21:33:ARG:HE	57:S21:34:ARG:HG2	1.77	0.48
9:L11:109:ALA:HA	9:L11:112:LYS:HB2	1.96	0.48
23:L27:36:GLN:HE22	23:L27:41:PHE:H	1.62	0.48
23:L27:71:LYS:HG3	23:L27:73:ARG:HG3	1.95	0.48
31:L35:53:ASP:N	31:L35:53:ASP:OD1	2.46	0.48
33:23S:2297:A:N6	33:23S:2318:G:C2	2.81	0.48
36:16S:791:G:O6	36:16S:792:A:N6	2.46	0.48
39:S03:151:GLU:HA	39:S03:166:TRP:HA	1.94	0.48
40:S04:157:ALA:O	40:S04:164:ARG:NH2	2.46	0.48
45:S09:43:ALA:H	45:S09:44:ARG:HH21	1.62	0.48
7:L1:65:LEU:HD22	7:L1:188:ASN:HB3	1.96	0.48
18:L21:84:ARG:NH2	33:23S:813:U:OP1	2.46	0.48
33:23S:1508:A:O2'	33:23S:1509:A:O4'	2.31	0.48
33:23S:1800:C:N4	33:23S:1818:U:O2'	2.46	0.48
33:23S:2072:C:C4	33:23S:2073:C:N4	2.82	0.48
33:23S:2134:A:N6	33:23S:2157:G:O2'	2.46	0.48
33:23S:2581:G:OP2	33:23S:2581:G:N2	2.45	0.48
38:S02:217:ALA:O	38:S02:221:ARG:NH1	2.46	0.48
11:L14:30:ARG:NH2	11:L14:37:ASP:OD2	2.46	0.48
12:L15:95:LEU:HB2	12:L15:101:ILE:HG12	1.95	0.48
33:23S:741:U:H2'	33:23S:742:A:C8	2.48	0.48
33:23S:2521:C:O2'	33:23S:2564:A:N3	2.42	0.48
36:16S:456:A:H2'	36:16S:457:G:H8	1.79	0.48
36:16S:641:U:O2	36:16S:642:A:N6	2.40	0.48
36:16S:765:G:H1	36:16S:812:G:HO2'	1.58	0.48
36:16S:823:C:H2'	36:16S:824:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S07:41:ILE:HD13	43:S07:115:MET:HB2	1.95	0.48
50:S14:78:LEU:HD12	50:S14:83:VAL:HG23	1.94	0.48
3:L04:170:ARG:NH1	3:L04:176:ASP:OD2	2.45	0.48
16:L19:65:ASN:OD1	16:L19:65:ASN:N	2.43	0.48
29:L33:9:LYS:O	29:L33:51:ALA:N	2.45	0.48
33:23S:184:C:H2'	33:23S:185:G:C8	2.49	0.48
33:23S:1434:A:H2'	33:23S:1435:G:C8	2.48	0.48
33:23S:1908:C:N4	33:23S:1909:C:N4	2.62	0.48
33:23S:2818:U:H2'	33:23S:2819:G:H8	1.78	0.48
36:16S:403:C:H5'	40:S04:131:ILE:HG23	1.94	0.48
15:L18:94:ARG:NH2	33:23S:2294:G:OP1	2.46	0.48
17:L20:47:ARG:NH1	33:23S:560:C:O2'	2.47	0.48
22:L25:2:PHE:HD2	22:L25:50:MET:HB3	1.79	0.48
33:23S:285:G:N2	33:23S:355:U:O2	2.36	0.48
33:23S:288:U:H2'	33:23S:289:G:H8	1.78	0.48
33:23S:630:G:N2	33:23S:633:A:OP2	2.32	0.48
33:23S:2719:G:H4'	33:23S:2846:G:H4'	1.96	0.48
34:5S:66:A:OP2	34:5S:108:A:N6	2.44	0.48
36:16S:203:G:H1'	36:16S:465:A:H61	1.78	0.48
36:16S:299:G:N2	36:16S:565:U:O2	2.47	0.48
36:16S:544:G:OP1	40:S04:58:GLN:NE2	2.47	0.48
36:16S:923:A:O2'	36:16S:1399:C:OP2	2.28	0.48
36:16S:1077:G:N2	36:16S:1080:A:OP2	2.44	0.48
36:16S:1210:C:O2'	36:16S:1213:A:O2'	2.29	0.48
39:S03:147:GLY:O	39:S03:202:PHE:N	2.42	0.48
48:S12:29:LYS:O	48:S12:81:ILE:N	2.46	0.48
16:L19:28:LYS:HB3	16:L19:39:LEU:HD11	1.96	0.48
17:L20:57:ARG:NH1	33:23S:1154:G:OP2	2.47	0.48
30:L34:3:ARG:NE	33:23S:1613:G:OP1	2.42	0.48
33:23S:927:A:H2'	33:23S:928:A:C8	2.49	0.48
39:S03:112:ALA:HB3	39:S03:184:ASN:HD22	1.78	0.48
47:S11:12:ARG:HG3	47:S11:75:GLU:HB2	1.96	0.48
49:S13:32:ILE:HD12	49:S13:58:GLU:HB3	1.96	0.48
2:L03:148:GLN:HB2	2:L03:152:PRO:HG2	1.96	0.48
4:L05:135:ILE:HA	4:L05:140:ILE:HD13	1.96	0.48
5:L06:106:LEU:O	5:L06:151:ARG:NH2	2.37	0.48
10:L13:24:THR:HB	10:L13:27:ARG:HB2	1.95	0.48
33:23S:793:A:OP2	33:23S:2071:A:O2'	2.28	0.48
33:23S:1047:G:H2'	33:23S:1110:G:N1	2.29	0.48
33:23S:1088:A:H4'	33:23S:1089:A:H8	1.78	0.48
33:23S:1352:U:N3	33:23S:1380:G:N1	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:1408:G:N2	33:23S:1594:U:O2	2.38	0.48
33:23S:1469:A:H2'	33:23S:1470:A:C8	2.49	0.48
36:16S:1071:C:H2'	36:16S:1072:G:C8	2.49	0.48
48:S12:36:VAL:HG13	48:S12:52:CYS:HB3	1.96	0.48
49:S13:65:GLU:OE2	49:S13:69:ARG:NH2	2.47	0.48
1:L02:70:LYS:HB3	1:L02:73:ILE:HD12	1.96	0.47
1:L02:141:HIS:ND1	1:L02:192:GLY:O	2.47	0.47
2:L03:197:THR:O	33:23S:2820:A:N6	2.47	0.47
33:23S:276:U:O2'	33:23S:278:A:N6	2.43	0.47
33:23S:463:G:N2	33:23S:466:A:OP2	2.47	0.47
33:23S:1181:U:H2'	33:23S:1182:G:C8	2.49	0.47
33:23S:1833:C:O2'	33:23S:1969:A:N1	2.43	0.47
36:16S:195:A:O2'	36:16S:222:C:O2'	2.28	0.47
36:16S:689:C:OP1	47:S11:28:ASN:ND2	2.47	0.47
44:S08:8:ASP:OD2	44:S08:12:ARG:NE	2.45	0.47
15:L18:12:THR:O	15:L18:16:ARG:N	2.33	0.47
20:L23:23:ALA:HA	20:L23:27:SER:HB3	1.96	0.47
21:L24:81:ARG:HH12	33:23S:300:A:H3'	1.79	0.47
24:L28:51:SER:OG	24:L28:52:ALA:N	2.47	0.47
29:L33:22:THR:OG1	33:23S:2286:G:O6	2.29	0.47
36:16S:1093:A:O2'	36:16S:1095:U:OP1	2.28	0.47
36:16S:1301:U:OP2	36:16S:1303:C:N4	2.46	0.47
42:S06:35:LYS:HB2	42:S06:65:GLU:HB3	1.96	0.47
45:S09:37:TYR:HD2	45:S09:38:PHE:HD2	1.62	0.47
57:S21:18:PHE:HA	57:S21:21:SER:HB3	1.95	0.47
1:L02:176:ARG:HH21	33:23S:1820:U:H5	1.62	0.47
4:L05:51:ASN:HA	4:L05:54:ALA:HB3	1.96	0.47
4:L05:90:LEU:HD22	4:L05:95:MET:HB3	1.96	0.47
33:23S:49:A:N7	33:23S:120:U:N3	2.62	0.47
33:23S:83:A:O2'	33:23S:103:A:N6	2.47	0.47
33:23S:1449:G:H2'	33:23S:1450:G:H8	1.79	0.47
33:23S:1667:G:O2'	33:23S:1991:U:O4	2.29	0.47
33:23S:1952:A:N3	33:23S:2560:A:O2'	2.34	0.47
36:16S:102:G:O2'	36:16S:151:A:N3	2.41	0.47
36:16S:781:A:O2'	36:16S:1522:U:O2	2.31	0.47
45:S09:79:ARG:HD2	45:S09:102:PHE:HD1	1.79	0.47
48:S12:67:GLY:H	48:S12:96:THR:HG22	1.79	0.47
4:L05:122:ASP:HB3	33:23S:2315:G:H1'	1.97	0.47
7:L1:43:ASP:N	7:L1:215:SER:O	2.44	0.47
15:L18:29:HIS:HB3	15:L18:36:TYR:HB2	1.96	0.47
17:L20:64:ILE:O	17:L20:68:ALA:N	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:L27:67:VAL:HG22	23:L27:74:LYS:HG3	1.96	0.47
33:23S:212:G:H2'	33:23S:213:A:C8	2.49	0.47
33:23S:299:A:N3	33:23S:319:G:O2'	2.40	0.47
33:23S:606:U:O2	33:23S:622:G:O6	2.32	0.47
33:23S:632:A:N6	33:23S:641:U:OP1	2.46	0.47
33:23S:1962:C:O2'	33:23S:1964:G:OP2	2.28	0.47
36:16S:71:A:N1	36:16S:99:C:O2'	2.46	0.47
36:16S:501:C:O3'	48:S12:114:SER:OG	2.30	0.47
36:16S:952:U:H2'	36:16S:953:G:C8	2.49	0.47
36:16S:980:C:O3'	50:S14:12:ARG:NH1	2.41	0.47
36:16S:1002:G:H2'	36:16S:1003:G:C8	2.49	0.47
46:S10:82:LYS:HA	46:S10:85:ASP:HB3	1.96	0.47
11:L14:78:ARG:NH2	16:L19:70:GLU:OE2	2.43	0.47
13:L16:6:ARG:NH1	33:23S:870:U:OP1	2.42	0.47
25:L29:24:GLU:HA	25:L29:27:ASN:HB2	1.96	0.47
33:23S:1105:U:H2'	33:23S:1106:G:H8	1.79	0.47
33:23S:1589:U:O4	33:23S:1590:A:N6	2.48	0.47
43:S07:123:LEU:O	43:S07:127:ALA:N	2.48	0.47
45:S09:27:ILE:HG21	45:S09:34:LEU:HB3	1.97	0.47
5:L06:25:ILE:HG22	5:L06:78:VAL:HG21	1.96	0.47
7:L1:67:HIS:HB2	7:L1:188:ASN:HD21	1.78	0.47
26:L30:48:ASN:HA	26:L30:51:SER:HB3	1.97	0.47
33:23S:145:C:H2'	33:23S:146:A:H8	1.80	0.47
36:16S:321:A:OP2	36:16S:328:C:N4	2.47	0.47
36:16S:427:U:O2'	36:16S:541:G:OP1	2.32	0.47
36:16S:490:C:N4	36:16S:491:G:O6	2.48	0.47
36:16S:666:G:O6	36:16S:740:U:O2	2.31	0.47
36:16S:1270:G:H2'	36:16S:1271:A:H8	1.79	0.47
36:16S:1513:A:H2'	36:16S:1514:G:H8	1.79	0.47
39:S03:6:PRO:HG2	39:S03:200:TRP:HE1	1.80	0.47
41:S05:81:GLN:HE21	41:S05:148:SER:HA	1.80	0.47
47:S11:49:SER:HB3	47:S11:68:ARG:HG3	1.97	0.47
47:S11:83:VAL:HG11	47:S11:96:ILE:HG22	1.95	0.47
47:S11:88:PRO:HD3	57:S21:28:LEU:HD11	1.97	0.47
48:S12:5:GLN:HG2	48:S12:8:ARG:HH12	1.80	0.47
57:S21:30:GLU:OE2	57:S21:44:ARG:NH2	2.48	0.47
3:L04:117:ARG:NH1	3:L04:184:ASP:OD1	2.48	0.47
3:L04:153:LEU:HD13	3:L04:171:ASP:HB3	1.97	0.47
8:L10:30:SER:O	33:23S:1054:A:O2'	2.29	0.47
17:L20:71:ASN:HB3	17:L20:109:VAL:HG11	1.96	0.47
21:L24:45:GLN:NE2	21:L24:46:LYS:O	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L29:12:GLU:O	25:L29:15:ASN:ND2	2.47	0.47
33:23S:13:A:O2'	33:23S:15:G:N7	2.39	0.47
33:23S:224:U:O4	33:23S:419:U:O2'	2.33	0.47
33:23S:954:G:O2'	33:23S:2274:A:N1	2.43	0.47
33:23S:1060:U:H1'	33:23S:1062:G:H5'	1.96	0.47
33:23S:1173:U:H2'	33:23S:1174:U:H4'	1.96	0.47
33:23S:1278:C:H2'	33:23S:1279:G:C8	2.50	0.47
33:23S:1283:G:N1	33:23S:1286:A:OP2	2.47	0.47
33:23S:1306:C:H2'	33:23S:1307:A:H8	1.79	0.47
36:16S:265:G:O2'	36:16S:267:C:OP1	2.32	0.47
36:16S:1031:C:H4'	36:16S:1033:G:H1'	1.95	0.47
36:16S:1350:A:N7	45:S09:119:LYS:NZ	2.63	0.47
36:16S:1357:A:H61	36:16S:1365:G:H1	1.62	0.47
39:S03:119:ILE:HG21	39:S03:197:VAL:HG11	1.97	0.47
48:S12:51:VAL:HG12	48:S12:65:TYR:HA	1.97	0.47
50:S14:59:GLN:O	50:S14:60:ARG:NH1	2.46	0.47
52:S16:4:ILE:HG12	52:S16:21:VAL:HG13	1.96	0.47
1:L02:146:LYS:HB2	1:L02:149:LYS:HB2	1.97	0.47
2:L03:194:PRO:HG3	33:23S:2679:A:H4'	1.97	0.47
3:L04:151:GLY:HA2	3:L04:172:ALA:HB2	1.96	0.47
33:23S:404:A:C6	33:23S:421:C:C4	3.03	0.47
33:23S:1720:U:O2	33:23S:1740:G:O6	2.32	0.47
33:23S:1980:G:O2'	33:23S:1982:U:OP2	2.33	0.47
33:23S:2087:G:H2'	33:23S:2088:A:H8	1.80	0.47
36:16S:875:U:O2'	44:S08:14:ARG:NH1	2.48	0.47
36:16S:893:C:N4	36:16S:894:G:O6	2.48	0.47
5:L06:42:VAL:HB	5:L06:51:PHE:HA	1.97	0.47
9:L11:100:ILE:HG23	9:L11:104:GLN:HB2	1.96	0.47
9:L11:132:ALA:HA	9:L11:135:MET:HB2	1.97	0.47
17:L20:4:LYS:NZ	33:23S:447:A:OP1	2.36	0.47
33:23S:62:U:O2'	33:23S:63:A:N7	2.47	0.47
33:23S:220:G:O2'	33:23S:233:A:N3	2.38	0.47
33:23S:1105:U:H2'	33:23S:1106:G:C8	2.50	0.47
33:23S:1133:A:H4'	33:23S:1134:A:H5''	1.97	0.47
36:16S:834:U:H3	36:16S:852:G:H1	1.62	0.47
38:S02:222:GLU:O	38:S02:225:SER:OG	2.30	0.47
55:S19:48:ILE:O	55:S19:59:VAL:N	2.39	0.47
55:S19:69:LYS:N	55:S19:72:GLU:OE1	2.48	0.47
1:L02:132:ARG:NH1	1:L02:186:ASP:OD1	2.48	0.47
33:23S:407:G:H2'	33:23S:408:G:H8	1.80	0.47
33:23S:1945:G:O6	33:23S:1960:A:N6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:36:C:OP1	48:S12:119:LYS:NZ	2.45	0.47
36:16S:333:U:OP1	56:S20:2:ASN:N	2.49	0.47
36:16S:422:C:H4'	36:16S:423:G:C2	2.50	0.47
36:16S:521:G:H4'	48:S12:69:GLU:HG2	1.97	0.47
40:S04:9:LYS:HA	40:S04:12:ARG:HE	1.80	0.47
47:S11:35:ASP:OD1	47:S11:39:ASN:N	2.48	0.47
50:S14:84:ARG:NE	50:S14:85:GLU:OE1	2.43	0.47
7:L1:8:MET:HA	7:L1:11:ILE:HB	1.98	0.46
7:L1:172:HIS:HB2	33:23S:2123:G:H4'	1.97	0.46
10:L13:17:VAL:HG23	10:L13:137:PRO:HB2	1.96	0.46
11:L14:99:ILE:HD13	11:L14:115:ILE:HG23	1.97	0.46
22:L25:73:LYS:O	22:L25:92:VAL:N	2.47	0.46
33:23S:1057:A:N7	33:23S:1086:A:H2'	2.30	0.46
33:23S:1073:A:O2'	33:23S:2474:U:O2'	2.30	0.46
40:S04:8:LEU:HD12	40:S04:11:SER:HB3	1.96	0.46
50:S14:29:ILE:HA	50:S14:32:ASP:HB2	1.96	0.46
2:L03:55:LYS:HD3	2:L03:60:VAL:HB	1.98	0.46
5:L06:8:VAL:HB	5:L06:49:LEU:HB2	1.98	0.46
29:L33:8:ILE:HG21	29:L33:24:LYS:HE3	1.97	0.46
33:23S:311:A:HO2'	33:23S:331:C:HO2'	1.63	0.46
33:23S:404:A:C6	33:23S:421:C:N3	2.83	0.46
33:23S:512:G:OP1	33:23S:1234:U:O2'	2.33	0.46
36:16S:411:A:OP1	40:S04:25:ARG:NH2	2.35	0.46
36:16S:981:U:OP1	50:S14:8:ARG:NH1	2.44	0.46
33:23S:767:U:H2'	33:23S:768:G:H8	1.79	0.46
33:23S:1378:A:O2'	33:23S:1380:G:OP2	2.33	0.46
33:23S:1715:G:N2	33:23S:1716:U:O4	2.49	0.46
33:23S:2217:G:H2'	33:23S:2218:G:C8	2.50	0.46
36:16S:195:A:H2'	36:16S:196:A:C4	2.50	0.46
36:16S:888:G:N2	36:16S:909:A:H62	2.10	0.46
46:S10:82:LYS:O	46:S10:86:ALA:N	2.43	0.46
52:S16:37:GLY:HA2	52:S16:52:LEU:HA	1.96	0.46
6:L09:132:PHE:HE2	6:L09:142:VAL:HB	1.80	0.46
8:L10:34:THR:O	33:23S:1057:A:O2'	2.33	0.46
13:L16:69:PRO:HA	13:L16:94:ALA:HB2	1.97	0.46
24:L28:34:SER:HA	24:L28:49:ARG:HA	1.97	0.46
33:23S:319:G:H1	33:23S:323:C:H41	1.63	0.46
33:23S:539:G:O6	33:23S:555:G:N2	2.48	0.46
33:23S:1579:A:H2'	33:23S:1580:A:C8	2.51	0.46
33:23S:2457:U:O2	33:23S:2494:G:N2	2.45	0.46
33:23S:2515:C:H2'	33:23S:2516:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:640:A:H1'	44:S08:106:SER:HB3	1.97	0.46
36:16S:716:A:H1'	47:S11:119:GLY:HA2	1.96	0.46
36:16S:1329:A:H5''	49:S13:24:VAL:HA	1.98	0.46
42:S06:11:HIS:HB3	42:S06:14:GLN:HB2	1.97	0.46
3:L04:112:LEU:HD13	3:L04:186:VAL:HG21	1.98	0.46
4:L05:34:THR:HG21	33:23S:2314:A:H4'	1.97	0.46
4:L05:157:THR:OG1	4:L05:158:THR:N	2.49	0.46
12:L15:88:GLY:HA2	12:L15:120:VAL:HG12	1.98	0.46
15:L18:48:LEU:O	15:L18:85:LYS:NZ	2.47	0.46
33:23S:581:C:H2'	33:23S:582:A:C8	2.51	0.46
33:23S:1127:A:N7	33:23S:2488:G:O2'	2.48	0.46
33:23S:1590:A:H2'	33:23S:1591:A:C8	2.51	0.46
33:23S:1909:C:H2'	33:23S:1910:G:H8	1.81	0.46
33:23S:2576:G:O2'	33:23S:2579:C:OP2	2.26	0.46
36:16S:9:G:H5'	41:S05:107:GLY:HA3	1.97	0.46
36:16S:166:U:H2'	36:16S:167:A:C8	2.50	0.46
36:16S:297:G:N2	36:16S:300:A:OP2	2.46	0.46
36:16S:597:G:N2	44:S08:85:TYR:OH	2.48	0.46
43:S07:35:LYS:O	43:S07:39:GLU:N	2.49	0.46
44:S08:105:THR:OG1	44:S08:110:MET:SD	2.68	0.46
4:L05:8:LYS:HB2	4:L05:8:LYS:HE3	1.80	0.46
8:L10:64:VAL:HG13	8:L10:75:ALA:HA	1.98	0.46
9:L11:80:LYS:HE3	9:L11:88:GLY:HA2	1.98	0.46
9:L11:130:GLY:HA2	9:L11:133:ARG:HG2	1.97	0.46
13:L16:29:GLY:N	13:L16:104:GLU:OE1	2.46	0.46
33:23S:20:C:H2'	33:23S:21:A:H8	1.81	0.46
33:23S:353:C:H2'	33:23S:354:A:C8	2.49	0.46
33:23S:573:U:O2'	33:23S:575:A:OP1	2.31	0.46
33:23S:1019:U:H3	33:23S:1142:A:H62	1.62	0.46
33:23S:2523:G:H2'	33:23S:2524:G:H8	1.80	0.46
34:5S:38:C:H2'	34:5S:39:A:H8	1.80	0.46
36:16S:535:A:OP1	36:16S:536:C:N4	2.44	0.46
53:S17:61:ARG:HG3	53:S17:73:THR:HB	1.98	0.46
8:L10:62:ARG:HH21	33:23S:1046:A:H2'	1.81	0.46
33:23S:818:G:N1	33:23S:1188:U:OP2	2.32	0.46
33:23S:1447:C:O2'	33:23S:1544:A:N3	2.40	0.46
33:23S:2297:A:H62	33:23S:2318:G:N2	2.14	0.46
34:5S:24:G:O2'	34:5S:56:G:N7	2.44	0.46
36:16S:81:A:N1	36:16S:87:C:N4	2.64	0.46
36:16S:145:G:N2	36:16S:178:C:N3	2.64	0.46
36:16S:750:C:O2'	51:S15:20:ASP:OD1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:S03:10:ARG:HB2	39:S03:15:LYS:HG2	1.98	0.46
2:L03:63:PRO:HG3	33:23S:2787:C:H1'	1.98	0.46
4:L05:43:ILE:HD12	4:L05:77:LYS:HB3	1.96	0.46
12:L15:21:ARG:NH1	33:23S:587:C:OP2	2.45	0.46
14:L17:11:ASN:OD1	33:23S:1652:A:N6	2.40	0.46
18:L21:7:SER:HB3	18:L21:12:HIS:HE1	1.80	0.46
33:23S:530:G:H21	33:23S:2034:U:HO2'	1.63	0.46
33:23S:1079:C:N4	33:23S:1088:A:O4'	2.49	0.46
36:16S:766:A:H61	36:16S:1511:G:H1'	1.81	0.46
36:16S:1166:G:O2'	36:16S:1169:A:N6	2.49	0.46
36:16S:1496:C:O2'	36:16S:1517:G:N1	2.44	0.46
36:16S:1525:G:H2'	36:16S:1526:G:H8	1.81	0.46
38:S02:42:LEU:H	38:S02:42:LEU:HG	1.46	0.46
1:L02:144:GLU:HA	1:L02:151:GLY:HA2	1.97	0.46
33:23S:220:G:N2	33:23S:428:A:OP2	2.46	0.46
33:23S:664:G:O2'	33:23S:940:G:OP1	2.32	0.46
36:16S:497:G:H2'	36:16S:498:A:C8	2.51	0.46
52:S16:23:ASP:OD1	52:S16:25:ARG:NE	2.42	0.46
33:23S:639:U:H2'	33:23S:640:C:C6	2.51	0.46
33:23S:948:C:H2'	33:23S:949:G:H8	1.81	0.46
33:23S:958:U:O2	34:5S:89:U:O2'	2.30	0.46
33:23S:1491:G:H2'	33:23S:1492:G:C8	2.51	0.46
33:23S:1604:C:O2'	33:23S:1610:A:N1	2.46	0.46
33:23S:2692:G:H1'	33:23S:2847:U:H1'	1.97	0.46
36:16S:34:C:H2'	36:16S:35:G:C8	2.51	0.46
36:16S:542:G:OP1	40:S04:9:LYS:NZ	2.44	0.46
36:16S:1009:U:O4	36:16S:1020:G:O6	2.34	0.46
38:S02:116:LEU:HA	38:S02:119:GLN:HB2	1.98	0.46
40:S04:81:LEU:HD23	40:S04:88:ASN:HB3	1.97	0.46
45:S09:27:ILE:HG21	45:S09:34:LEU:HD23	1.97	0.46
51:S15:9:LYS:HE3	51:S15:9:LYS:HB2	1.80	0.46
56:S20:75:LYS:O	56:S20:79:THR:OG1	2.26	0.46
1:L02:181:ARG:NH2	33:23S:1800:C:OP2	2.50	0.45
8:L10:43:LYS:O	8:L10:47:GLU:N	2.49	0.45
9:L11:131:THR:HA	33:23S:1088:A:H61	1.81	0.45
11:L14:63:VAL:HA	11:L14:107:LEU:HD11	1.97	0.45
19:L22:89:ALA:O	19:L22:92:ARG:NH1	2.49	0.45
33:23S:228:C:H42	33:23S:417:C:H1'	1.81	0.45
33:23S:598:U:H2'	33:23S:599:A:C8	2.51	0.45
33:23S:1041:G:H2'	33:23S:1042:G:H8	1.80	0.45
33:23S:1688:U:O2'	33:23S:1700:A:N7	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:1791:A:N6	33:23S:1828:G:O2'	2.40	0.45
33:23S:2039:U:H2'	33:23S:2040:G:C8	2.52	0.45
54:S18:35:SER:HB3	57:S21:18:PHE:HE2	1.80	0.45
1:L02:39:SER:OG	33:23S:1814:G:OP1	2.28	0.45
11:L14:4:GLU:OE2	11:L14:23:LYS:NZ	2.37	0.45
12:L15:73:ILE:O	12:L15:106:GLU:N	2.48	0.45
30:L34:34:ARG:HB3	30:L34:42:LEU:HD12	1.98	0.45
33:23S:2208:C:H2'	33:23S:2209:G:C8	2.51	0.45
33:23S:2220:U:H2'	33:23S:2221:G:C8	2.50	0.45
33:23S:2329:U:H2'	33:23S:2330:G:H8	1.80	0.45
33:23S:2533:U:OP1	33:23S:2665:A:O2'	2.28	0.45
36:16S:64:G:H5''	36:16S:65:A:H3'	1.98	0.45
36:16S:769:G:OP2	36:16S:803:G:O2'	2.31	0.45
36:16S:1354:U:H2'	36:16S:1355:G:H8	1.82	0.45
38:S02:122:ASP:OD1	38:S02:123:GLY:N	2.49	0.45
1:L02:92:LEU:HD11	1:L02:100:ARG:HB3	1.97	0.45
9:L11:52:LEU:HD22	9:L11:73:PRO:HG3	1.98	0.45
10:L13:78:THR:HB	33:23S:2641:G:H5''	1.98	0.45
12:L15:82:LEU:HD12	12:L15:90:VAL:HG21	1.99	0.45
14:L17:2:ARG:NH2	33:23S:2820:A:OP1	2.49	0.45
22:L25:63:ILE:HG22	22:L25:65:VAL:HG22	1.98	0.45
33:23S:1668:A:H61	33:23S:1676:A:H61	1.65	0.45
33:23S:2241:A:H2'	33:23S:2242:G:C8	2.51	0.45
36:16S:1255:G:O2'	36:16S:1258:G:N3	2.42	0.45
36:16S:1317:C:O2	55:S19:36:ARG:NH2	2.38	0.45
44:S08:42:GLU:HG3	44:S08:100:ILE:HG21	1.98	0.45
46:S10:45:ARG:O	46:S10:69:THR:OG1	2.34	0.45
1:L02:74:PRO:HA	1:L02:116:GLN:HB3	1.97	0.45
6:L09:47:PHE:HA	6:L09:51:ARG:HB2	1.98	0.45
33:23S:2052:A:H2'	33:23S:2053:G:H8	1.81	0.45
33:23S:2243:U:H2'	33:23S:2244:U:H6	1.81	0.45
36:16S:252:U:O4	36:16S:253:A:N6	2.43	0.45
36:16S:691:G:N7	47:S11:27:ASN:ND2	2.64	0.45
36:16S:1123:U:O2'	46:S10:39:PRO:O	2.33	0.45
36:16S:1354:U:H2'	36:16S:1355:G:C8	2.52	0.45
36:16S:1412:C:H2'	36:16S:1413:A:C8	2.52	0.45
36:16S:1481:U:H2'	36:16S:1482:G:H8	1.82	0.45
1:L02:47:ARG:HH21	33:23S:774:G:H5''	1.82	0.45
1:L02:208:GLY:HA2	1:L02:211:ARG:HB2	1.99	0.45
2:L03:13:ARG:NH2	16:L19:74:GLN:OE1	2.43	0.45
3:L04:112:LEU:HD21	3:L04:117:ARG:HH21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:489:G:N2	33:23S:1321:A:OP1	2.48	0.45
33:23S:2165:C:N4	33:23S:2170:A:H62	2.13	0.45
36:16S:300:A:O2'	36:16S:564:C:N3	2.46	0.45
36:16S:358:U:H2'	36:16S:359:G:H8	1.81	0.45
36:16S:831:A:H5'	38:S02:20:ARG:HG3	1.99	0.45
43:S07:30:MET:HE3	43:S07:30:MET:HB3	1.77	0.45
49:S13:70:ARG:O	49:S13:74:MET:N	2.46	0.45
2:L03:19:GLY:HA2	16:L19:78:PRO:HG2	1.99	0.45
3:L04:131:THR:HG23	33:23S:321:U:H5''	1.99	0.45
6:L09:131:SER:HA	6:L09:141:LYS:HG2	1.99	0.45
9:L11:29:GLN:OE1	33:23S:1096:A:N6	2.36	0.45
33:23S:349:U:H2'	33:23S:350:G:H8	1.82	0.45
33:23S:370:G:O2'	33:23S:424:G:OP1	2.34	0.45
33:23S:675:A:N7	33:23S:803:U:O2	2.50	0.45
33:23S:1386:C:O2'	33:23S:1469:A:O2'	2.35	0.45
33:23S:1908:C:C4	33:23S:1909:C:N4	2.84	0.45
36:16S:110:C:O2'	52:S16:25:ARG:O	2.26	0.45
36:16S:376:G:H5''	52:S16:5:ARG:HB2	1.98	0.45
36:16S:450:G:H5''	36:16S:451:A:H5''	1.97	0.45
36:16S:1137:C:H4'	36:16S:1138:G:C2	2.52	0.45
1:L02:160:TYR:HB3	1:L02:193:GLU:HB3	1.98	0.45
8:L10:55:VAL:HA	33:23S:1084:A:H4'	1.99	0.45
12:L15:79:LEU:HD13	12:L15:116:VAL:HB	1.99	0.45
33:23S:302:C:H2'	33:23S:303:G:C8	2.52	0.45
33:23S:414:C:H1'	33:23S:1864:U:H1'	1.98	0.45
33:23S:675:A:N3	33:23S:2443:C:O2'	2.47	0.45
33:23S:2085:U:O2	33:23S:2234:G:O6	2.34	0.45
33:23S:2163:A:OP1	33:23S:2171:A:N6	2.50	0.45
33:23S:2291:U:O2'	33:23S:2374:C:O2	2.31	0.45
33:23S:2292:U:H2'	33:23S:2293:G:H8	1.81	0.45
36:16S:106:C:H2'	36:16S:107:G:H8	1.82	0.45
41:S05:57:ALA:O	41:S05:60:GLN:NE2	2.50	0.45
41:S05:57:ALA:HA	41:S05:60:GLN:HE21	1.81	0.45
44:S08:48:PHE:HB2	44:S08:58:LEU:HD11	1.98	0.45
45:S09:14:SER:OG	45:S09:73:GLY:O	2.33	0.45
45:S09:91:GLU:HA	45:S09:94:ARG:HB2	1.99	0.45
50:S14:26:LEU:HD11	50:S14:46:LYS:HG2	1.99	0.45
50:S14:30:ILE:HG22	50:S14:40:ARG:HA	1.98	0.45
3:L04:123:LYS:HD2	3:L04:123:LYS:HA	1.75	0.45
13:L16:71:LYS:HE3	13:L16:95:LEU:HD11	1.99	0.45
15:L18:32:PRO:O	15:L18:64:TYR:OH	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L18:52:SER:HB2	15:L18:54:VAL:HG12	1.99	0.45
33:23S:1027:A:H2	33:23S:2488:G:H5''	1.82	0.45
33:23S:1491:G:H2'	33:23S:1492:G:H8	1.82	0.45
33:23S:2680:U:H2'	33:23S:2681:C:H6	1.82	0.45
36:16S:3:A:O2'	36:16S:612:C:O2'	2.29	0.45
36:16S:403:C:H2'	36:16S:404:G:H8	1.81	0.45
36:16S:1032:G:N2	36:16S:1033:G:O2'	2.49	0.45
36:16S:1130:A:O2'	45:S09:4:GLN:OE1	2.28	0.45
36:16S:1193:G:N7	39:S03:2:GLN:NE2	2.62	0.45
1:L02:5:CYS:SG	1:L02:12:ARG:NH1	2.89	0.45
4:L05:126:ASN:HB3	4:L05:156:THR:HA	1.98	0.45
7:L1:54:LYS:HD3	7:L1:203:GLN:HG2	1.98	0.45
9:L11:9:LYS:HE3	33:23S:1061:U:H5''	1.98	0.45
15:L18:12:THR:HA	15:L18:15:ARG:HB2	1.99	0.45
16:L19:38:ARG:NE	36:16S:345:C:OP2	2.41	0.45
26:L30:9:THR:OG1	26:L30:53:MET:O	2.30	0.45
32:L36:9:LYS:HG2	32:L36:14:CYS:HB2	1.98	0.45
33:23S:323:C:O2'	33:23S:1205:A:N1	2.44	0.45
36:16S:151:A:N6	36:16S:170:U:H3	2.11	0.45
36:16S:908:A:H2'	36:16S:909:A:C8	2.51	0.45
36:16S:1162:C:H2'	36:16S:1163:A:C8	2.52	0.45
38:S02:202:ASN:OD1	38:S02:205:ALA:N	2.39	0.45
6:L09:72:ILE:H	6:L09:108:VAL:HG22	1.82	0.45
33:23S:26:G:H1'	33:23S:515:A:H61	1.82	0.45
33:23S:1401:G:H21	33:23S:1469:A:H2	1.65	0.45
33:23S:1677:A:H2'	33:23S:1678:A:C8	2.52	0.45
33:23S:2788:C:O2'	33:23S:2809:A:N3	2.40	0.45
36:16S:128:G:O2'	53:S17:62:GLU:OE2	2.29	0.45
36:16S:149:A:H61	36:16S:172:A:H62	1.65	0.45
36:16S:152:A:OP2	36:16S:153:C:N4	2.43	0.45
36:16S:169:C:H2'	36:16S:170:U:H6	1.82	0.45
36:16S:212:G:H2'	36:16S:213:G:H8	1.82	0.45
36:16S:376:G:H2'	36:16S:377:G:C8	2.51	0.45
36:16S:1504:G:OP2	36:16S:1507:A:O2'	2.33	0.45
36:16S:1530:G:H2'	36:16S:1531:A:C8	2.52	0.45
39:S03:137:VAL:HA	39:S03:148:ILE:HD13	1.97	0.45
39:S03:176:THR:HG22	39:S03:179:ALA:H	1.82	0.45
43:S07:61:PHE:HZ	43:S07:100:MET:HG2	1.82	0.45
47:S11:59:PRO:O	47:S11:63:GLN:N	2.50	0.45
47:S11:122:PRO:HB2	57:S21:33:ARG:HA	1.99	0.45
21:L24:34:ILE:HG12	21:L24:63:ALA:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:L30:4:ILE:N	26:L30:37:ARG:O	2.44	0.44
29:L33:5:ARG:HH12	33:23S:2285:C:H3'	1.82	0.44
33:23S:784:G:O6	33:23S:2072:C:O2'	2.34	0.44
33:23S:1102:C:H2'	33:23S:1103:A:H8	1.80	0.44
33:23S:1889:A:N3	33:23S:2086:U:O2'	2.42	0.44
33:23S:2119:A:N1	33:23S:2169:A:N6	2.65	0.44
33:23S:2266:A:N6	33:23S:2273:A:OP2	2.46	0.44
36:16S:1458:G:H2'	36:16S:1459:G:H8	1.82	0.44
38:S02:14:HIS:HB2	38:S02:40:ILE:H	1.82	0.44
43:S07:67:ASN:O	43:S07:137:ARG:NE	2.43	0.44
44:S08:6:ILE:HD13	44:S08:32:LYS:HD3	1.99	0.44
4:L05:73:VAL:H	4:L05:78:ILE:HG22	1.81	0.44
6:L09:40:THR:OG1	6:L09:43:ASN:OD1	2.31	0.44
11:L14:12:ASP:OD1	11:L14:12:ASP:N	2.51	0.44
11:L14:40:LYS:HD2	11:L14:57:VAL:HG23	1.98	0.44
33:23S:500:G:N1	33:23S:503:A:OP2	2.50	0.44
33:23S:1013:C:H2'	33:23S:1014:A:C8	2.52	0.44
33:23S:1047:G:N2	33:23S:1111:A:OP2	2.51	0.44
33:23S:2789:C:H3'	33:23S:2893:A:H62	1.83	0.44
36:16S:528:C:H41	48:S12:45:ASN:HD21	1.64	0.44
44:S08:76:ARG:NH2	44:S08:78:SER:O	2.51	0.44
50:S14:23:ARG:HE	50:S14:26:LEU:HD22	1.82	0.44
1:L02:68:ARG:HG3	1:L02:128:THR:HG21	1.99	0.44
2:L03:32:ASN:HB3	2:L03:50:VAL:HB	2.00	0.44
4:L05:29:ARG:H	4:L05:158:THR:HG1	1.65	0.44
4:L05:112:ASP:N	4:L05:112:ASP:OD1	2.50	0.44
24:L28:2:ARG:NH1	33:23S:1365:A:OP1	2.43	0.44
33:23S:1853:A:N7	33:23S:1889:A:N6	2.65	0.44
33:23S:2602:A:H5''	33:23S:2603:G:H5''	1.98	0.44
36:16S:1233:G:H21	36:16S:1364:U:H3	1.65	0.44
38:S02:6:ARG:NH1	38:S02:7:ASP:OD1	2.46	0.44
45:S09:86:LEU:HB3	45:S09:89:TYR:HB2	2.00	0.44
5:L06:158:GLY:O	5:L06:162:ARG:NH2	2.50	0.44
16:L19:89:GLY:HA2	16:L19:111:GLU:HA	1.99	0.44
24:L28:22:ASN:OD1	33:23S:2079:U:O2'	2.33	0.44
25:L29:13:GLU:O	25:L29:16:THR:OG1	2.34	0.44
33:23S:86:G:O2'	33:23S:104:A:O2'	2.23	0.44
33:23S:1079:C:H2'	33:23S:1080:A:C8	2.53	0.44
33:23S:2327:A:H2'	33:23S:2328:A:C8	2.51	0.44
36:16S:1238:A:N7	36:16S:1299:A:N6	2.65	0.44
39:S03:24:ASN:OD1	39:S03:24:ASN:N	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:S03:83:VAL:HA	39:S03:86:LEU:HD12	2.00	0.44
10:L13:40:HIS:CE1	10:L13:41:LYS:HG3	2.53	0.44
24:L28:6:VAL:HA	24:L28:70:LEU:HD21	1.98	0.44
27:L31:23:LYS:HE2	27:L31:23:LYS:HB2	1.87	0.44
33:23S:1631:G:N2	33:23S:1634:A:OP2	2.44	0.44
33:23S:2735:G:H2'	33:23S:2736:A:H8	1.82	0.44
36:16S:718:A:OP1	36:16S:720:C:N4	2.51	0.44
39:S03:152:VAL:HG12	39:S03:197:VAL:HG22	2.00	0.44
45:S09:11:ARG:HD3	45:S09:106:ASP:HB3	2.00	0.44
45:S09:14:SER:HB3	45:S09:69:GLY:HA3	1.99	0.44
5:L06:106:LEU:HD12	5:L06:112:VAL:HG21	2.00	0.44
14:L17:79:LEU:HD23	14:L17:83:LEU:HB2	1.99	0.44
16:L19:77:SER:HB3	16:L19:80:VAL:HG22	2.00	0.44
19:L22:22:ASP:OD1	19:L22:25:ARG:NH1	2.50	0.44
19:L22:73:LYS:HB2	19:L22:106:VAL:HB	2.00	0.44
23:L27:10:ARG:O	33:23S:2278:A:N6	2.51	0.44
33:23S:1223:G:N2	33:23S:1226:A:OP2	2.47	0.44
34:5S:22:U:O2	34:5S:61:G:N2	2.42	0.44
36:16S:254:G:O2'	53:S17:17:GLU:O	2.33	0.44
36:16S:401:C:H2'	36:16S:402:G:H8	1.82	0.44
36:16S:1006:G:N2	36:16S:1023:U:O2	2.46	0.44
36:16S:1376:U:H2'	36:16S:1377:A:C8	2.53	0.44
51:S15:29:ALA:HA	51:S15:84:LEU:HD21	1.99	0.44
4:L05:95:MET:HE2	4:L05:95:MET:HB2	1.85	0.44
6:L09:28:ASN:ND2	33:23S:2092:U:OP2	2.42	0.44
10:L13:93:ILE:HA	10:L13:97:PRO:HB3	2.00	0.44
19:L22:51:LEU:HD13	19:L22:105:VAL:HG11	1.99	0.44
33:23S:145:C:H2'	33:23S:146:A:C8	2.53	0.44
33:23S:532:A:N1	33:23S:2020:A:H1'	2.32	0.44
33:23S:2133:G:O6	33:23S:2157:G:N1	2.51	0.44
36:16S:776:G:N2	36:16S:802:A:OP2	2.45	0.44
36:16S:832:G:H1	36:16S:854:U:H3	1.65	0.44
39:S03:73:GLY:HA2	39:S03:76:ILE:HG22	2.00	0.44
49:S13:53:ASP:N	49:S13:53:ASP:OD1	2.48	0.44
1:L02:211:ARG:HD3	1:L02:217:PRO:HD3	1.99	0.44
14:L17:1:MET:HE2	14:L17:1:MET:HB3	1.83	0.44
15:L18:63:LYS:NZ	34:5S:52:A:OP2	2.50	0.44
33:23S:298:G:O2'	33:23S:322:A:N1	2.47	0.44
33:23S:660:C:H2'	33:23S:661:A:H8	1.83	0.44
33:23S:1920:C:H2'	33:23S:1921:G:H8	1.82	0.44
33:23S:2300:C:C4	33:23S:2301:C:N4	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:2451:A:OP1	33:23S:2497:A:N6	2.51	0.44
36:16S:430:A:OP2	40:S04:7:LYS:NZ	2.35	0.44
36:16S:1251:A:H2'	36:16S:1252:A:O4'	2.18	0.44
36:16S:1317:C:N3	50:S14:52:ARG:NE	2.65	0.44
36:16S:1481:U:H2'	36:16S:1482:G:C8	2.52	0.44
47:S11:28:ASN:HB2	47:S11:56:LYS:HE3	1.99	0.44
47:S11:111:ASP:HB2	57:S21:19:LYS:HE2	2.00	0.44
3:L04:126:VAL:HG12	3:L04:128:ALA:H	1.83	0.44
5:L06:138:GLN:OE1	33:23S:2759:G:N2	2.48	0.44
7:L1:164:ARG:HH22	33:23S:2122:U:H4'	1.83	0.44
8:L10:67:THR:HG22	8:L10:72:LEU:HA	2.00	0.44
9:L11:46:ASP:OD1	9:L11:46:ASP:N	2.50	0.44
12:L15:74:THR:HB	12:L15:107:PHE:HB2	2.00	0.44
24:L28:6:VAL:HG11	24:L28:58:ILE:HD11	1.99	0.44
29:L33:36:LYS:HD3	29:L33:45:HIS:HB3	2.00	0.44
32:L36:9:LYS:HG3	32:L36:16:ILE:HD11	1.98	0.44
33:23S:171:U:H2'	33:23S:172:A:H8	1.83	0.44
33:23S:1039:A:H2	33:23S:1116:G:H22	1.64	0.44
33:23S:1387:A:H2'	33:23S:1388:G:H8	1.83	0.44
33:23S:1539:U:H2'	33:23S:1540:G:C8	2.53	0.44
41:S05:98:ALA:HB2	41:S05:123:LEU:HD12	1.99	0.44
46:S10:54:SER:O	50:S14:80:ARG:NH1	2.48	0.44
48:S12:77:SER:HB2	48:S12:102:ASP:HB3	1.99	0.44
56:S20:71:ALA:O	56:S20:75:LYS:N	2.44	0.44
4:L05:99:PHE:HD1	4:L05:99:PHE:HA	1.71	0.43
6:L09:42:LYS:O	6:L09:46:PHE:N	2.50	0.43
8:L10:37:LYS:HB2	8:L10:41:LEU:HB2	1.98	0.43
15:L18:9:ARG:O	15:L18:12:THR:OG1	2.34	0.43
33:23S:155:A:H2'	33:23S:156:A:C8	2.53	0.43
33:23S:184:C:H2'	33:23S:185:G:H8	1.82	0.43
33:23S:1527:G:N1	33:23S:1544:A:OP2	2.41	0.43
33:23S:1629:U:O2'	33:23S:2698:U:OP1	2.35	0.43
36:16S:453:G:O6	36:16S:479:U:N3	2.51	0.43
36:16S:1038:C:H2'	36:16S:1039:G:C8	2.52	0.43
36:16S:1513:A:H2'	36:16S:1514:G:C8	2.53	0.43
39:S03:8:GLY:HA3	50:S14:88:MET:HE3	1.98	0.43
39:S03:55:VAL:N	39:S03:66:THR:O	2.47	0.43
40:S04:44:LYS:HE3	40:S04:44:LYS:HB3	1.82	0.43
43:S07:84:TYR:HD1	43:S07:84:TYR:HA	1.71	0.43
54:S18:50:TYR:HA	54:S18:53:GLN:HB2	1.99	0.43
55:S19:17:LYS:HB3	55:S19:30:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L02:1:ALA:N	1:L02:19:VAL:O	2.40	0.43
5:L06:23:ILE:HG13	5:L06:36:LEU:HD22	2.00	0.43
6:L09:51:ARG:O	6:L09:56:ALA:N	2.51	0.43
10:L13:76:HIS:NE2	33:23S:2641:G:OP1	2.41	0.43
25:L29:60:LYS:HE3	25:L29:60:LYS:HB3	1.75	0.43
36:16S:728:A:H2'	36:16S:729:A:C8	2.53	0.43
36:16S:1367:C:H5''	45:S09:115:VAL:HG13	2.00	0.43
38:S02:13:VAL:O	38:S02:202:ASN:N	2.51	0.43
2:L03:171:THR:HG22	2:L03:173:GLN:HG2	1.99	0.43
10:L13:7:LYS:HG2	33:23S:538:A:H4'	1.99	0.43
33:23S:349:U:H2'	33:23S:350:G:C8	2.53	0.43
33:23S:859:G:N2	33:23S:917:A:OP2	2.31	0.43
33:23S:2669:G:H2'	33:23S:2670:A:C8	2.54	0.43
53:S17:10:ARG:NH1	53:S17:11:VAL:H	2.15	0.43
55:S19:49:ALA:HA	55:S19:58:PRO:HA	1.99	0.43
2:L03:157:LYS:NZ	33:23S:2619:C:OP1	2.41	0.43
6:L09:29:PHE:HB2	33:23S:2198:A:N3	2.34	0.43
30:L34:31:LEU:O	30:L34:35:ARG:NH1	2.52	0.43
33:23S:589:U:H2'	33:23S:590:A:C8	2.54	0.43
33:23S:820:A:N3	33:23S:943:A:O2'	2.47	0.43
33:23S:1296:G:OP1	33:23S:2709:G:O2'	2.32	0.43
33:23S:1548:A:H2'	33:23S:1549:A:C8	2.54	0.43
33:23S:1853:A:H2'	33:23S:1854:A:C8	2.54	0.43
33:23S:2834:G:H2'	33:23S:2879:A:N6	2.34	0.43
36:16S:34:C:H2'	36:16S:35:G:H8	1.84	0.43
36:16S:426:U:H5''	40:S04:36:ALA:HB1	2.01	0.43
39:S03:139:ASN:OD1	39:S03:142:ARG:NE	2.49	0.43
39:S03:150:VAL:HG23	39:S03:199:VAL:HG13	2.00	0.43
40:S04:102:TYR:HD2	40:S04:103:ARG:HD3	1.84	0.43
18:L21:6:GLN:HA	18:L21:11:GLN:HG3	2.00	0.43
20:L23:77:ARG:NE	33:23S:63:A:O2'	2.50	0.43
21:L24:25:LYS:N	21:L24:34:ILE:O	2.51	0.43
25:L29:28:LEU:HB3	25:L29:37:LEU:HD22	1.98	0.43
27:L31:8:LYS:O	27:L31:27:THR:OG1	2.36	0.43
28:L32:9:ARG:H	28:L32:9:ARG:HG3	1.52	0.43
33:23S:910:A:H2'	33:23S:911:A:C8	2.54	0.43
33:23S:1429:G:H2'	33:23S:1430:G:C8	2.53	0.43
33:23S:2111:U:O4	33:23S:2144:G:O2'	2.35	0.43
34:5S:19:C:H2'	34:5S:20:G:H8	1.82	0.43
36:16S:218:U:H2'	36:16S:219:U:C6	2.54	0.43
36:16S:701:U:H5''	36:16S:703:G:H1'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:16S:767:A:O2'	36:16S:1524:C:O2	2.36	0.43
39:S03:136:ALA:HA	39:S03:139:ASN:HB2	2.01	0.43
45:S09:39:GLY:HA2	45:S09:44:ARG:HB3	2.00	0.43
2:L03:167:ASN:ND2	33:23S:2821:A:O3'	2.40	0.43
4:L05:129:MET:HA	33:23S:2304:G:H4'	2.00	0.43
5:L06:24:THR:HG22	5:L06:33:THR:HG23	1.99	0.43
8:L10:8:LYS:HA	8:L10:11:ILE:HB	1.99	0.43
13:L16:64:TRP:HB2	13:L16:104:GLU:HB2	2.00	0.43
19:L22:57:ASN:OD1	19:L22:61:ASN:ND2	2.51	0.43
30:L34:28:ARG:HA	30:L34:31:LEU:HB2	2.00	0.43
33:23S:177:G:H3'	33:23S:178:G:H8	1.83	0.43
36:16S:107:G:O6	56:S20:9:ARG:NH1	2.48	0.43
36:16S:111:G:O6	36:16S:330:C:N4	2.51	0.43
36:16S:517:G:N2	36:16S:533:A:OP2	2.51	0.43
39:S03:61:LYS:HD3	39:S03:61:LYS:HA	1.86	0.43
49:S13:78:ARG:NH2	55:S19:64:GLU:O	2.52	0.43
53:S17:52:CYS:HA	53:S17:80:LYS:HZ1	1.83	0.43
1:L02:77:VAL:HG21	1:L02:109:LEU:HD21	2.01	0.43
2:L03:124:ARG:NH1	2:L03:164:GLN:O	2.52	0.43
8:L10:101:LYS:HE3	8:L10:101:LYS:HB3	1.91	0.43
9:L11:116:MET:HG2	33:23S:1059:G:H4'	1.99	0.43
9:L11:117:THR:HG22	9:L11:124:MET:HE2	2.01	0.43
19:L22:82:MET:HB3	19:L22:84:ARG:NH1	2.33	0.43
33:23S:5:A:H2'	33:23S:6:A:C8	2.53	0.43
33:23S:221:A:N1	33:23S:265:A:O2'	2.50	0.43
33:23S:796:C:H2'	33:23S:797:G:C8	2.54	0.43
33:23S:2408:U:H2'	33:23S:2409:G:C8	2.54	0.43
36:16S:335:C:H2'	36:16S:336:A:H8	1.84	0.43
36:16S:1101:A:N6	38:S02:174:GLU:OE2	2.52	0.43
36:16S:1152:A:H5'	46:S10:15:HIS:CE1	2.53	0.43
39:S03:149:LYS:HB2	39:S03:172:VAL:HG11	2.00	0.43
39:S03:149:LYS:HB3	39:S03:200:TRP:HB2	2.01	0.43
39:S03:156:LEU:H	39:S03:156:LEU:HG	1.66	0.43
41:S05:87:VAL:HA	41:S05:92:ARG:HA	2.00	0.43
41:S05:146:MET:HB3	41:S05:146:MET:HE2	1.72	0.43
48:S12:56:LEU:HD23	48:S12:56:LEU:HA	1.92	0.43
52:S16:4:ILE:HD12	52:S16:67:ILE:HG12	1.99	0.43
4:L05:132:ARG:HH22	33:23S:2306:C:H1'	1.84	0.43
5:L06:17:LYS:HB3	5:L06:17:LYS:HE3	1.85	0.43
5:L06:32:LEU:HD11	5:L06:136:ASP:HB2	2.01	0.43
10:L13:59:ALA:HB3	10:L13:126:ALA:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L18:60:GLU:H	15:L18:60:GLU:HG3	1.69	0.43
25:L29:13:GLU:H	25:L29:13:GLU:HG2	1.62	0.43
33:23S:546:U:C4	33:23S:547:A:H1'	2.54	0.43
33:23S:1336:A:H2'	33:23S:1337:G:C8	2.54	0.43
33:23S:2372:U:H2'	33:23S:2373:G:H8	1.84	0.43
33:23S:2699:C:H2'	33:23S:2700:A:H8	1.82	0.43
36:16S:106:C:H2'	36:16S:107:G:C8	2.54	0.43
36:16S:991:U:O4	36:16S:1212:U:O2'	2.33	0.43
41:S05:84:VAL:HG12	41:S05:95:MET:HB2	2.01	0.43
10:L13:45:THR:HB	10:L13:48:VAL:HB	2.01	0.43
14:L17:96:ARG:HH21	33:23S:2881:U:H5''	1.84	0.43
17:L20:96:ASP:OD2	18:L21:13:ARG:NE	2.51	0.43
29:L33:5:ARG:HH21	29:L33:25:ASN:H	1.66	0.43
31:L35:15:LYS:NZ	31:L35:64:ALA:OXT	2.52	0.43
33:23S:964:C:O2'	33:23S:2273:A:N3	2.45	0.43
33:23S:2881:U:H2'	33:23S:2882:A:C8	2.51	0.43
45:S09:18:VAL:HA	45:S09:64:ILE:HD12	1.99	0.43
56:S20:27:MET:H	56:S20:27:MET:HG3	1.63	0.43
57:S21:53:LYS:HA	57:S21:56:ALA:HB3	2.01	0.43
1:L02:84:PRO:HG3	33:23S:1567:G:H3'	2.01	0.43
4:L05:139:GLU:HG3	27:L31:28:VAL:HG22	2.01	0.43
8:L10:4:ASN:HA	8:L10:7:ASP:HB2	2.01	0.43
9:L11:96:LYS:HB2	9:L11:99:LYS:HE3	2.00	0.43
16:L19:90:ALA:HB2	16:L19:112:ARG:HA	2.00	0.43
19:L22:84:ARG:NH2	33:23S:1322:A:O3'	2.51	0.43
21:L24:80:ASP:OD2	21:L24:97:SER:OG	2.34	0.43
26:L30:43:ILE:HD13	26:L30:43:ILE:HA	1.94	0.43
33:23S:171:U:H2'	33:23S:172:A:C8	2.54	0.43
33:23S:459:U:H2'	33:23S:460:A:H8	1.84	0.43
33:23S:2112:G:H5'	33:23S:2113:U:C5	2.54	0.43
36:16S:202:G:H2'	36:16S:203:G:H8	1.83	0.43
36:16S:255:G:OP1	53:S17:70:LYS:NZ	2.38	0.43
36:16S:1351:U:O2	36:16S:1371:G:N2	2.41	0.43
42:S06:3:HIS:HB2	42:S06:92:THR:HA	2.00	0.43
42:S06:29:ILE:HD12	42:S06:36:ILE:HB	2.01	0.43
48:S12:109:ARG:HD2	48:S12:109:ARG:HA	1.84	0.43
9:L11:6:ALA:HA	9:L11:30:GLN:HB3	2.01	0.42
12:L15:29:LYS:HE3	33:23S:566:U:H5''	2.01	0.42
12:L15:128:THR:O	12:L15:132:ARG:N	2.51	0.42
16:L19:44:GLY:HA3	16:L19:62:LYS:HB2	2.00	0.42
33:23S:135:U:H2'	33:23S:136:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:552:U:H2'	33:23S:553:G:C8	2.54	0.42
33:23S:946:C:H2'	33:23S:947:A:H8	1.83	0.42
33:23S:999:U:N3	33:23S:1157:G:N1	2.67	0.42
33:23S:1299:G:N1	33:23S:1640:A:OP2	2.45	0.42
33:23S:2699:C:H2'	33:23S:2700:A:C8	2.54	0.42
36:16S:415:A:N7	36:16S:428:G:O6	2.52	0.42
36:16S:932:C:H2'	36:16S:933:G:C8	2.54	0.42
36:16S:951:G:N3	36:16S:970:C:O2'	2.45	0.42
39:S03:111:ASP:HB3	39:S03:114:LEU:HG	2.00	0.42
42:S06:73:GLU:O	42:S06:76:THR:OG1	2.37	0.42
46:S10:54:SER:OG	46:S10:57:VAL:O	2.26	0.42
53:S17:35:LYS:HE2	53:S17:35:LYS:HB3	1.92	0.42
1:L02:59:GLN:HA	33:23S:1568:G:H5'	1.99	0.42
2:L03:154:LYS:NZ	33:23S:2024:G:O3'	2.50	0.42
7:L1:217:THR:O	33:23S:2124:G:N2	2.52	0.42
9:L11:7:TYR:HD2	9:L11:60:VAL:H	1.67	0.42
9:L11:33:ASN:OD1	9:L11:33:ASN:N	2.53	0.42
11:L14:105:ARG:HA	11:L14:105:ARG:HD3	1.89	0.42
16:L19:95:LYS:HB3	16:L19:97:TYR:HD2	1.83	0.42
17:L20:23:TYR:HB2	17:L20:28:SER:HB2	2.02	0.42
33:23S:290:U:H2'	33:23S:291:G:C8	2.54	0.42
33:23S:546:U:H2'	33:23S:547:A:H4'	2.01	0.42
33:23S:1013:C:H2'	33:23S:1014:A:H8	1.83	0.42
33:23S:2165:C:C4	33:23S:2170:A:N6	2.86	0.42
36:16S:737:C:H2'	36:16S:738:C:C6	2.55	0.42
36:16S:1096:C:O2	36:16S:1170:A:O2'	2.36	0.42
36:16S:1287:A:H2	36:16S:1353:G:H1'	1.84	0.42
42:S06:88:MET:HB2	54:S18:63:TYR:HE2	1.84	0.42
57:S21:53:LYS:O	57:S21:57:LYS:N	2.46	0.42
14:L17:64:ARG:O	14:L17:68:ALA:N	2.45	0.42
17:L20:52:ARG:NH1	33:23S:536:G:OP1	2.52	0.42
33:23S:195:A:N6	33:23S:198:C:OP2	2.53	0.42
33:23S:1222:U:O2	33:23S:1227:G:O6	2.36	0.42
33:23S:1796:U:H2'	33:23S:1797:G:C8	2.54	0.42
36:16S:363:A:OP2	48:S12:30:ARG:NH2	2.53	0.42
36:16S:709:U:H2'	36:16S:710:G:C8	2.51	0.42
36:16S:1180:A:OP2	45:S09:98:ARG:NH2	2.44	0.42
36:16S:1192:C:OP2	39:S03:3:LYS:NZ	2.38	0.42
41:S05:79:THR:OG1	41:S05:97:PRO:O	2.37	0.42
53:S17:45:VAL:HG21	53:S17:60:ILE:HD12	2.00	0.42
1:L02:255:LYS:HD3	1:L02:269:ARG:HH22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L06:43:LYS:HB2	5:L06:43:LYS:HE2	1.84	0.42
6:L09:104:THR:HG22	6:L09:109:GLU:HA	2.01	0.42
11:L14:71:ARG:HH22	11:L14:105:ARG:HB3	1.83	0.42
16:L19:64:SER:OG	16:L19:65:ASN:OD1	2.35	0.42
33:23S:186:G:H2'	33:23S:187:G:H8	1.85	0.42
33:23S:941:A:O2'	33:23S:1190:G:O3'	2.37	0.42
33:23S:1842:G:H1	33:23S:1898:U:H3	1.67	0.42
34:5S:60:C:H2'	34:5S:61:G:C8	2.54	0.42
36:16S:1249:C:N4	36:16S:1288:A:OP2	2.52	0.42
36:16S:1405:G:N3	36:16S:1518:A:O2'	2.38	0.42
38:S02:8:MET:HB3	38:S02:13:VAL:HG11	2.01	0.42
50:S14:62:ARG:HG2	50:S14:69:PRO:HA	2.02	0.42
3:L04:28:VAL:HG12	3:L04:104:ALA:HB1	2.01	0.42
6:L09:82:SER:N	6:L09:147:VAL:O	2.53	0.42
8:L10:45:GLY:HA2	8:L10:49:GLY:HA2	2.00	0.42
9:L11:9:LYS:NZ	33:23S:1071:G:OP2	2.45	0.42
11:L14:77:ILE:HG23	16:L19:71:ARG:HB2	2.02	0.42
13:L16:12:MET:HE3	13:L16:12:MET:HB2	1.88	0.42
28:L32:48:TYR:OH	33:23S:2883:A:OP1	2.34	0.42
34:5S:22:U:H3	34:5S:61:G:H1	1.68	0.42
34:5S:114:C:H2'	34:5S:115:A:C8	2.54	0.42
36:16S:166:U:H2'	36:16S:167:A:H8	1.84	0.42
36:16S:352:C:O2	36:16S:355:C:N4	2.49	0.42
36:16S:385:C:H2'	36:16S:386:C:C6	2.54	0.42
36:16S:1099:G:H5'	57:S21:66:ARG:HH11	1.85	0.42
36:16S:1345:U:OP1	45:S09:121:ARG:NH1	2.52	0.42
39:S03:15:LYS:HZ2	39:S03:180:ASP:HA	1.85	0.42
40:S04:116:LEU:HG	40:S04:121:ALA:HB3	2.01	0.42
45:S09:54:VAL:HG11	45:S09:93:LEU:HD21	2.02	0.42
50:S14:6:LYS:HA	50:S14:6:LYS:HD2	1.87	0.42
50:S14:11:LYS:HE3	50:S14:11:LYS:HB2	1.87	0.42
55:S19:51:HIS:HB2	55:S19:56:HIS:CE1	2.54	0.42
3:L04:71:GLY:N	33:23S:674:G:H5''	2.34	0.42
4:L05:57:ALA:HA	27:L31:7:PRO:HB3	2.01	0.42
7:L1:219:GLY:O	33:23S:2175:C:O2'	2.38	0.42
10:L13:95:ARG:NH2	33:23S:2768:U:O2'	2.52	0.42
11:L14:1:MET:HE3	11:L14:1:MET:HB2	1.83	0.42
12:L15:48:ARG:HH12	31:L35:3:ILE:HG22	1.85	0.42
13:L16:35:ALA:HA	13:L16:128:THR:HB	2.01	0.42
13:L16:118:LYS:HE3	13:L16:118:LYS:HB3	1.91	0.42
15:L18:92:PHE:HB2	15:L18:117:PHE:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:L27:7:ARG:HA	23:L27:7:ARG:HD3	1.86	0.42
28:L32:42:ILE:HG22	28:L32:48:TYR:HB2	2.01	0.42
33:23S:452:G:N2	33:23S:457:A:O2'	2.52	0.42
33:23S:657:U:H2'	33:23S:658:U:C6	2.54	0.42
38:S02:10:LYS:O	38:S02:207:ARG:NH1	2.53	0.42
42:S06:41:ASP:OD1	42:S06:42:TRP:N	2.52	0.42
42:S06:82:ASP:N	42:S06:82:ASP:OD1	2.53	0.42
47:S11:124:LYS:C	57:S21:34:ARG:HH21	2.26	0.42
50:S14:30:ILE:H	50:S14:30:ILE:HG12	1.71	0.42
2:L03:161:MET:SD	33:23S:2619:C:O2'	2.74	0.42
14:L17:10:LEU:HD13	14:L17:40:LYS:HG2	2.02	0.42
26:L30:23:LEU:HD11	26:L30:53:MET:HE1	2.00	0.42
31:L35:32:LEU:N	33:23S:2420:C:OP2	2.42	0.42
33:23S:576:U:H2'	33:23S:577:G:C8	2.54	0.42
33:23S:1837:C:H2'	33:23S:1899:A:H61	1.84	0.42
33:23S:2104:C:N4	33:23S:2185:U:N3	2.31	0.42
33:23S:2136:G:N2	33:23S:2155:U:O4	2.51	0.42
33:23S:2292:U:H2'	33:23S:2293:G:C8	2.54	0.42
34:5S:118:C:H2'	34:5S:119:A:C8	2.52	0.42
36:16S:1250:A:N3	36:16S:1370:G:O2'	2.47	0.42
36:16S:1393:U:HO2'	36:16S:1501:C:HO2'	1.60	0.42
36:16S:1404:C:O2	36:16S:1519:A:O2'	2.30	0.42
40:S04:138:PRO:HB3	40:S04:183:ARG:HA	2.02	0.42
40:S04:197:HIS:CE1	41:S05:103:GLY:HA3	2.54	0.42
48:S12:68:GLY:HA2	48:S12:116:TYR:CZ	2.54	0.42
50:S14:61:ASN:OD1	50:S14:61:ASN:N	2.51	0.42
1:L02:77:VAL:HA	1:L02:93:VAL:HG12	2.01	0.42
6:L09:43:ASN:O	6:L09:47:PHE:N	2.51	0.42
14:L17:73:ASN:HB3	33:23S:1453:A:N7	2.35	0.42
17:L20:93:ILE:HG23	18:L21:13:ARG:HB2	2.02	0.42
30:L34:5:PHE:O	33:23S:1612:C:O2'	2.37	0.42
33:23S:858:G:O2'	33:23S:859:G:OP1	2.34	0.42
33:23S:1028:A:H2'	33:23S:1029:A:C8	2.55	0.42
33:23S:1258:U:H2'	33:23S:1259:G:C8	2.55	0.42
33:23S:2076:U:H3	33:23S:2596:U:H1'	1.85	0.42
33:23S:2286:G:H4'	33:23S:2287:A:O4'	2.20	0.42
33:23S:2818:U:H2'	33:23S:2819:G:C8	2.53	0.42
36:16S:77:A:H2'	36:16S:78:A:C8	2.54	0.42
36:16S:832:G:N2	36:16S:854:U:O2	2.43	0.42
36:16S:1105:A:H2'	36:16S:1106:G:H8	1.84	0.42
36:16S:1530:G:H2'	36:16S:1531:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S06:35:LYS:HA	42:S06:35:LYS:HD3	1.80	0.42
45:S09:26:LYS:HG2	45:S09:61:ASP:HB3	2.02	0.42
50:S14:1:ALA:N	50:S14:3:GLN:OE1	2.43	0.42
53:S17:58:VAL:HG12	53:S17:77:VAL:HG22	2.02	0.42
2:L03:81:GLU:OE1	33:23S:2635:A:O2'	2.37	0.42
12:L15:11:GLY:O	33:23S:597:G:O2'	2.31	0.42
15:L18:87:ILE:O	15:L18:88:LYS:NZ	2.48	0.42
16:L19:108:ARG:NH2	36:16S:1464:U:OP2	2.46	0.42
33:23S:59:U:O2	33:23S:68:G:N2	2.41	0.42
33:23S:729:G:N2	33:23S:1774:C:C2	2.78	0.42
33:23S:1434:A:H2'	33:23S:1435:G:H8	1.84	0.42
36:16S:501:C:H2'	36:16S:502:A:C8	2.54	0.42
36:16S:1018:G:H2'	36:16S:1019:A:C8	2.55	0.42
40:S04:62:ARG:HA	40:S04:62:ARG:HD3	1.87	0.42
44:S08:76:ARG:NH1	44:S08:125:ILE:HG23	2.35	0.42
45:S09:83:THR:HG21	45:S09:102:PHE:HB2	2.01	0.42
56:S20:44:ALA:O	56:S20:48:LYS:NZ	2.38	0.42
2:L03:184:ARG:HH22	16:L19:6:GLN:HB2	1.85	0.42
7:L1:42:VAL:HA	7:L1:216:THR:HA	2.02	0.42
33:23S:523:C:H2'	33:23S:524:G:H8	1.84	0.42
33:23S:548:G:C5	33:23S:549:G:H1'	2.55	0.42
33:23S:848:C:H2'	33:23S:849:A:C8	2.55	0.42
33:23S:1387:A:H2'	33:23S:1388:G:C8	2.55	0.42
33:23S:1769:U:H2'	33:23S:1770:G:H8	1.85	0.42
33:23S:2139:U:H2'	33:23S:2140:G:H8	1.85	0.42
36:16S:801:U:H2'	36:16S:802:A:C8	2.55	0.42
36:16S:1064:G:OP2	36:16S:1385:G:O2'	2.35	0.42
44:S08:65:PHE:CD2	44:S08:66:GLN:HG2	2.54	0.42
47:S11:29:THR:HG21	47:S11:62:ALA:HB2	2.02	0.42
2:L03:125:TRP:NE1	2:L03:161:MET:O	2.46	0.41
21:L24:9:GLU:OE2	21:L24:22:GLY:N	2.48	0.41
25:L29:24:GLU:HG2	25:L29:46:VAL:HG11	2.01	0.41
33:23S:311:A:O2'	33:23S:331:C:O2'	2.31	0.41
33:23S:1057:A:C8	33:23S:1086:A:H2'	2.55	0.41
33:23S:2815:C:H2'	33:23S:2816:G:H8	1.85	0.41
36:16S:137:U:H2'	36:16S:138:G:C8	2.55	0.41
36:16S:1143:G:H2'	36:16S:1144:G:C8	2.55	0.41
39:S03:39:ARG:NE	50:S14:91:GLU:OE1	2.52	0.41
40:S04:161:ALA:HB1	40:S04:166:LYS:HE3	2.02	0.41
46:S10:6:ILE:O	46:S10:76:ILE:N	2.53	0.41
49:S13:51:GLN:O	49:S13:54:THR:OG1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:S15:22:GLY:O	51:S15:27:GLN:NE2	2.51	0.41
52:S16:6:LEU:HD13	52:S16:17:TYR:CG	2.55	0.41
4:L05:57:ALA:O	27:L31:8:LYS:N	2.52	0.41
6:L09:51:ARG:HA	6:L09:55:GLU:HB2	2.01	0.41
21:L24:43:LYS:NZ	33:23S:480:A:OP2	2.40	0.41
36:16S:24:U:O3'	36:16S:524:G:O2'	2.38	0.41
36:16S:977:A:O2'	36:16S:1223:C:N4	2.54	0.41
39:S03:56:ILE:HG23	39:S03:63:ILE:HD11	2.01	0.41
41:S05:92:ARG:HH21	41:S05:127:TYR:HB3	1.86	0.41
46:S10:25:ILE:O	46:S10:28:THR:OG1	2.34	0.41
52:S16:5:ARG:NH2	52:S16:27:ALA:O	2.53	0.41
2:L03:61:THR:N	2:L03:64:GLU:OE1	2.39	0.41
3:L04:30:GLN:OE1	33:23S:659:G:N2	2.48	0.41
4:L05:125:GLY:HA2	4:L05:162:ASP:HA	2.01	0.41
5:L06:9:VAL:HA	5:L06:48:THR:HA	2.01	0.41
6:L09:86:ASP:OD1	6:L09:86:ASP:N	2.51	0.41
7:L1:46:VAL:HB	7:L1:171:ILE:HG23	2.02	0.41
28:L32:37:HIS:HB3	28:L32:43:THR:HG22	2.03	0.41
33:23S:2141:G:H2'	33:23S:2142:A:C8	2.55	0.41
33:23S:2516:A:N6	33:23S:2567:G:O6	2.53	0.41
36:16S:632:U:H5''	36:16S:633:G:C8	2.55	0.41
36:16S:1319:A:H5''	55:S19:69:LYS:HE3	2.02	0.41
41:S05:24:VAL:N	41:S05:27:GLY:O	2.53	0.41
46:S10:7:ARG:HB3	46:S10:73:LEU:HD21	2.03	0.41
47:S11:95:THR:O	47:S11:99:LEU:N	2.53	0.41
2:L03:87:GLY:N	2:L03:88:GLU:OE1	2.54	0.41
4:L05:62:GLN:HG3	27:L31:4:ASP:HA	2.01	0.41
5:L06:165:ASP:OD1	5:L06:165:ASP:N	2.53	0.41
12:L15:41:ARG:NH2	33:23S:807:U:OP2	2.51	0.41
14:L17:100:CYS:H	14:L17:111:ALA:HA	1.84	0.41
16:L19:23:ASP:OD1	16:L19:89:GLY:N	2.52	0.41
33:23S:80:G:H4'	33:23S:346:A:H1'	2.03	0.41
33:23S:318:C:H2'	33:23S:319:G:H8	1.85	0.41
33:23S:1407:G:H2'	33:23S:1408:G:H8	1.85	0.41
33:23S:1827:U:H5'	33:23S:1971:U:H4'	2.02	0.41
36:16S:202:G:H2'	36:16S:203:G:C8	2.56	0.41
36:16S:262:A:H4'	56:S20:69:ASN:HB2	2.01	0.41
36:16S:578:C:O2'	36:16S:728:A:N3	2.48	0.41
36:16S:634:C:H2'	36:16S:635:A:C8	2.56	0.41
36:16S:991:U:C2	36:16S:1213:A:N7	2.88	0.41
38:S02:184:ALA:HB2	38:S02:195:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:S06:26:THR:O	42:S06:30:THR:OG1	2.31	0.41
44:S08:26:MET:O	44:S08:58:LEU:N	2.53	0.41
1:L02:106:PRO:HD2	1:L02:109:LEU:HD22	2.03	0.41
3:L04:44:ARG:HH21	3:L04:46:GLN:HE22	1.69	0.41
7:L1:65:LEU:HD21	7:L1:192:LEU:HD13	2.02	0.41
10:L13:13:ARG:NH1	10:L13:53:TYR:OH	2.54	0.41
19:L22:20:VAL:HG21	19:L22:43:ALA:HB3	2.02	0.41
30:L34:19:ARG:HH21	33:23S:124:G:H3'	1.86	0.41
32:L36:4:ARG:NH1	33:23S:2477:U:O2	2.35	0.41
33:23S:121:G:H2'	33:23S:122:G:H8	1.85	0.41
33:23S:558:U:H2'	33:23S:559:G:C8	2.55	0.41
33:23S:1372:U:O2'	33:23S:2212:A:O2'	2.35	0.41
33:23S:1674:G:N2	33:23S:1991:U:O2	2.54	0.41
33:23S:2721:A:H3'	33:23S:2722:G:H8	1.85	0.41
34:5S:5:U:OP1	34:5S:61:G:O2'	2.33	0.41
36:16S:257:G:H2'	36:16S:258:G:C8	2.54	0.41
36:16S:401:C:H2'	36:16S:402:G:C8	2.54	0.41
36:16S:553:A:H2'	36:16S:554:A:H8	1.85	0.41
36:16S:662:U:H2'	36:16S:663:A:C8	2.54	0.41
38:S02:72:LYS:O	38:S02:76:SER:N	2.52	0.41
38:S02:164:ASP:HB3	38:S02:167:HIS:HB3	2.02	0.41
48:S12:86:VAL:HG21	48:S12:89:LEU:HD12	2.03	0.41
57:S21:16:ARG:H	57:S21:16:ARG:HG2	1.52	0.41
2:L03:178:VAL:N	2:L03:188:LEU:O	2.53	0.41
3:L04:4:VAL:HA	3:L04:11:ALA:HA	2.02	0.41
3:L04:58:LYS:NZ	33:23S:675:A:OP1	2.38	0.41
20:L23:57:VAL:H	20:L23:86:THR:HG1	1.60	0.41
21:L24:10:VAL:HA	21:L24:71:ILE:HA	2.02	0.41
31:L35:50:SER:OG	31:L35:53:ASP:OD1	2.35	0.41
32:L36:22:VAL:HG23	32:L36:24:ARG:HG3	2.03	0.41
33:23S:175:G:H2'	33:23S:176:A:C8	2.56	0.41
33:23S:523:C:H2'	33:23S:524:G:C8	2.55	0.41
33:23S:1071:G:O2'	33:23S:1088:A:O3'	2.38	0.41
33:23S:1135:C:N4	33:23S:1138:G:OP2	2.44	0.41
33:23S:1960:A:O2'	36:16S:1484:C:O2'	2.35	0.41
34:5S:65:U:H3'	34:5S:108:A:N6	2.34	0.41
36:16S:129:A:H61	36:16S:232:G:H1	1.68	0.41
36:16S:385:C:N3	36:16S:386:C:C4	2.89	0.41
36:16S:1203:C:H2'	36:16S:1204:A:H8	1.86	0.41
36:16S:1427:C:H2'	36:16S:1428:A:C8	2.55	0.41
39:S03:69:THR:OG1	39:S03:70:ALA:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:S04:111:ALA:O	40:S04:115:GLN:N	2.54	0.41
45:S09:105:ARG:NH2	45:S09:109:GLN:OE1	2.44	0.41
1:L02:106:PRO:HG2	1:L02:109:LEU:HB2	2.02	0.41
1:L02:240:GLY:HA3	33:23S:2597:G:H5'	2.03	0.41
2:L03:107:VAL:HA	2:L03:205:PRO:HA	2.02	0.41
3:L04:23:PHE:HB2	3:L04:111:GLU:HB2	2.03	0.41
4:L05:53:ALA:HB1	4:L05:64:PRO:HB2	2.03	0.41
12:L15:95:LEU:HD12	12:L15:101:ILE:HD13	2.02	0.41
33:23S:278:A:O2'	33:23S:279:A:O4'	2.35	0.41
36:16S:184:G:O6	36:16S:192:A:N6	2.53	0.41
36:16S:456:A:H2'	36:16S:457:G:C8	2.55	0.41
36:16S:505:G:H2'	36:16S:506:G:C8	2.56	0.41
36:16S:920:U:H2'	36:16S:921:U:C6	2.56	0.41
36:16S:1018:G:H2'	36:16S:1019:A:H8	1.85	0.41
36:16S:1173:U:H2'	36:16S:1174:G:C8	2.55	0.41
43:S07:113:LYS:HA	43:S07:113:LYS:HD3	1.96	0.41
44:S08:110:MET:HE2	44:S08:110:MET:HB3	1.98	0.41
46:S10:52:LEU:HD11	46:S10:59:LYS:HA	2.02	0.41
51:S15:47:LYS:HA	51:S15:47:LYS:HD3	1.91	0.41
55:S19:14:LEU:HD13	55:S19:32:THR:HG21	2.01	0.41
12:L15:92:LEU:O	12:L15:96:LYS:NZ	2.52	0.41
26:L30:11:SER:HB3	26:L30:13:ILE:HG12	2.01	0.41
33:23S:1061:U:H4'	33:23S:1070:A:H1'	2.03	0.41
36:16S:254:G:H2'	36:16S:255:G:H8	1.86	0.41
36:16S:322:C:N4	36:16S:329:A:N7	2.69	0.41
36:16S:1250:A:H2'	36:16S:1251:A:C4	2.56	0.41
40:S04:146:GLU:HA	40:S04:149:LYS:HB2	2.02	0.41
46:S10:30:LYS:HD2	46:S10:31:ARG:HH12	1.85	0.41
47:S11:108:ASN:OD1	47:S11:110:THR:OG1	2.37	0.41
49:S13:38:ILE:HG12	49:S13:47:LEU:HD22	2.03	0.41
53:S17:80:LYS:HE3	53:S17:80:LYS:HB3	1.95	0.41
1:L02:170:TYR:HD2	1:L02:182:LYS:HB3	1.86	0.41
3:L04:146:VAL:HG22	3:L04:167:VAL:HG22	2.03	0.41
6:L09:117:LEU:HD13	6:L09:121:VAL:HG13	2.03	0.41
7:L1:5:THR:HG23	7:L1:8:MET:HB2	2.02	0.41
11:L14:97:THR:OG1	11:L14:98:ARG:N	2.54	0.41
14:L17:55:ALA:HA	14:L17:80:PHE:CE1	2.55	0.41
15:L18:35:ILE:HG21	15:L18:71:ALA:HA	2.02	0.41
21:L24:90:LYS:HE2	21:L24:90:LYS:HB3	1.86	0.41
23:L27:11:ASP:OD1	33:23S:2263:C:N4	2.37	0.41
25:L29:9:LYS:HB3	25:L29:12:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:L29:14:LEU:HD23	25:L29:14:LEU:HA	1.87	0.41
27:L31:22:MET:HE2	27:L31:22:MET:HB2	1.98	0.41
33:23S:181:A:H2'	33:23S:182:A:C8	2.55	0.41
33:23S:282:A:H2'	33:23S:283:G:C8	2.56	0.41
33:23S:284:U:O2	33:23S:356:G:N2	2.42	0.41
33:23S:302:C:H2'	33:23S:303:G:H8	1.86	0.41
33:23S:552:U:H2'	33:23S:553:G:H8	1.85	0.41
33:23S:633:A:O2'	33:23S:2404:U:OP1	2.31	0.41
33:23S:871:U:H2'	33:23S:872:U:C6	2.55	0.41
33:23S:897:C:H2'	33:23S:898:C:H6	1.86	0.41
33:23S:1152:C:H2'	33:23S:1153:C:C6	2.56	0.41
33:23S:1171:G:N2	33:23S:1179:G:N7	2.69	0.41
33:23S:1597:A:H5''	33:23S:1598:A:H5'	2.03	0.41
33:23S:1865:U:O2'	33:23S:1875:G:N2	2.54	0.41
33:23S:2329:U:H2'	33:23S:2330:G:C8	2.55	0.41
33:23S:2591:C:H2'	33:23S:2592:G:C8	2.56	0.41
33:23S:2898:U:H2'	33:23S:2899:A:C8	2.56	0.41
36:16S:169:C:H2'	36:16S:170:U:C6	2.56	0.41
36:16S:193:C:H2'	36:16S:194:C:C6	2.56	0.41
36:16S:385:C:C4	36:16S:386:C:N4	2.89	0.41
36:16S:754:C:OP1	51:S15:71:ARG:NH2	2.36	0.41
36:16S:766:A:OP2	36:16S:812:G:N2	2.52	0.41
36:16S:783:C:H2'	36:16S:784:A:C8	2.56	0.41
36:16S:1280:A:N3	46:S10:43:PRO:HG3	2.36	0.41
36:16S:1291:U:H2'	36:16S:1292:G:C8	2.56	0.41
36:16S:1310:G:OP2	49:S13:86:ARG:NH2	2.54	0.41
36:16S:1363:A:H2'	36:16S:1365:G:C8	2.56	0.41
40:S04:196:GLU:H	40:S04:196:GLU:HG2	1.56	0.41
42:S06:49:TYR:OH	54:S18:62:ARG:O	2.32	0.41
45:S09:6:TYR:HE1	45:S09:17:ARG:HA	1.85	0.41
47:S11:75:GLU:H	47:S11:75:GLU:HG2	1.60	0.41
2:L03:9:VAL:HG11	16:L19:3:ILE:HD12	2.03	0.41
8:L10:74:ASP:HA	8:L10:77:VAL:HB	2.02	0.41
10:L13:49:ASP:OD1	10:L13:121:LYS:NZ	2.48	0.41
13:L16:34:LYS:HE2	13:L16:101:VAL:HG22	2.03	0.41
16:L19:64:SER:OG	16:L19:65:ASN:N	2.54	0.41
21:L24:48:VAL:HG22	21:L24:50:ALA:H	1.86	0.41
26:L30:51:SER:HA	26:L30:54:VAL:HG22	2.02	0.41
28:L32:8:THR:OG1	33:23S:2021:C:OP1	2.33	0.41
31:L35:32:LEU:O	31:L35:40:LYS:NZ	2.40	0.41
33:23S:201:C:O2'	33:23S:251:A:N1	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:23S:272:A:H2'	33:23S:273:G:C8	2.56	0.41
33:23S:861:A:H62	33:23S:916:G:H21	1.69	0.41
33:23S:968:C:H2'	33:23S:969:G:H8	1.86	0.41
36:16S:227:G:N2	52:S16:63:GLN:O	2.35	0.41
36:16S:994:A:O2'	50:S14:11:LYS:NZ	2.54	0.41
36:16S:1237:C:OP1	36:16S:1303:C:O2'	2.35	0.41
38:S02:53:LEU:HB3	38:S02:219:THR:HG21	2.03	0.41
46:S10:44:THR:HG22	46:S10:46:LYS:HG3	2.03	0.41
1:L02:163:ILE:HG12	1:L02:173:LEU:HD22	2.03	0.40
1:L02:209:ALA:HA	1:L02:212:TRP:NE1	2.37	0.40
3:L04:171:ASP:OD2	3:L04:173:THR:OG1	2.35	0.40
7:L1:10:VAL:HA	7:L1:13:GLU:HB2	2.02	0.40
8:L10:113:PHE:HD2	8:L10:125:ARG:HD2	1.85	0.40
9:L11:74:PRO:HG2	9:L11:77:VAL:HG12	2.03	0.40
33:23S:413:C:H2'	33:23S:414:C:C6	2.56	0.40
33:23S:1010:A:N3	33:23S:1153:C:H1'	2.36	0.40
36:16S:73:C:H41	36:16S:94:G:H1	1.69	0.40
36:16S:76:G:O6	36:16S:93:U:O4	2.39	0.40
36:16S:149:A:H1'	36:16S:1446:A:H2	1.86	0.40
36:16S:177:G:OP2	36:16S:177:G:N2	2.51	0.40
36:16S:212:G:H2'	36:16S:213:G:C8	2.56	0.40
36:16S:861:G:O2'	36:16S:874:G:O2'	2.29	0.40
36:16S:959:A:N6	55:S19:77:ARG:HG2	2.35	0.40
36:16S:1163:A:H2'	36:16S:1164:G:H8	1.85	0.40
42:S06:62:MET:HB3	42:S06:64:VAL:HG13	2.03	0.40
46:S10:52:LEU:HB3	50:S14:80:ARG:HH11	1.85	0.40
1:L02:13:ARG:HH22	33:23S:1693:U:HO2'	1.57	0.40
1:L02:179:GLU:HG3	1:L02:269:ARG:HA	2.03	0.40
4:L05:115:GLY:HA3	4:L05:177:ARG:HB2	2.03	0.40
4:L05:168:LEU:HD22	4:L05:168:LEU:HA	1.91	0.40
8:L10:37:LYS:HG3	8:L10:38:MET:HE2	2.03	0.40
31:L35:38:LYS:NZ	33:23S:2365:G:O6	2.53	0.40
33:23S:306:U:H3	33:23S:310:A:N6	2.18	0.40
33:23S:948:C:H2'	33:23S:949:G:C8	2.56	0.40
33:23S:1667:G:H22	33:23S:1992:G:H5'	1.87	0.40
33:23S:2519:U:O4'	33:23S:2542:A:N6	2.55	0.40
34:5S:18:G:O6	34:5S:65:U:O2	2.38	0.40
34:5S:28:C:H2'	34:5S:29:A:C8	2.56	0.40
36:16S:182:A:N1	36:16S:223:A:O2'	2.53	0.40
36:16S:1141:C:H2'	36:16S:1142:G:H8	1.86	0.40
57:S21:4:LYS:HE2	57:S21:4:LYS:HB3	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L04:85:PHE:CG	33:23S:588:U:H1'	2.56	0.40
5:L06:117:PRO:HD2	5:L06:120:ILE:HG13	2.03	0.40
12:L15:70:LYS:HE2	12:L15:70:LYS:HB2	1.92	0.40
13:L16:119:LEU:HD22	13:L16:119:LEU:HA	1.97	0.40
26:L30:42:ALA:O	33:23S:851:C:O2'	2.34	0.40
33:23S:247:G:OP2	33:23S:249:C:N4	2.49	0.40
33:23S:1629:U:H1'	33:23S:2698:U:H5''	2.03	0.40
33:23S:2099:U:H2'	33:23S:2100:G:C8	2.56	0.40
36:16S:70:U:H1'	36:16S:71:A:N7	2.36	0.40
36:16S:235:C:H2'	36:16S:236:A:C8	2.56	0.40
36:16S:1140:C:H2'	36:16S:1141:C:C6	2.56	0.40
36:16S:1151:A:H2'	36:16S:1152:A:C8	2.56	0.40
36:16S:1270:G:H2'	36:16S:1271:A:C8	2.55	0.40
36:16S:1512:U:H3	36:16S:1523:G:H1	1.69	0.40
41:S05:152:VAL:O	41:S05:156:ARG:N	2.54	0.40
44:S08:87:ARG:H	44:S08:90:GLU:HB3	1.85	0.40
10:L13:71:ASP:OD1	10:L13:71:ASP:N	2.51	0.40
12:L15:110:VAL:HG11	12:L15:135:ILE:HD11	2.04	0.40
12:L15:117:THR:HG23	12:L15:118:THR:HG23	2.03	0.40
14:L17:90:ARG:HD3	14:L17:90:ARG:HA	1.92	0.40
17:L20:13:HIS:ND1	33:23S:582:A:OP1	2.42	0.40
19:L22:71:VAL:HA	19:L22:107:VAL:HG12	2.03	0.40
21:L24:18:LYS:H	21:L24:18:LYS:HG2	1.55	0.40
33:23S:143:C:H2'	33:23S:144:A:H8	1.86	0.40
33:23S:414:C:H2'	33:23S:415:A:C8	2.57	0.40
33:23S:570:G:N7	33:23S:2030:A:N6	2.69	0.40
33:23S:1384:A:N3	33:23S:1405:U:H1'	2.36	0.40
33:23S:1864:U:OP1	33:23S:2410:G:O2'	2.35	0.40
33:23S:2345:G:N3	33:23S:2381:A:H2'	2.37	0.40
36:16S:830:G:H2'	36:16S:831:A:H8	1.87	0.40
36:16S:1175:G:H2'	36:16S:1176:A:H8	1.87	0.40
36:16S:1291:U:H2'	36:16S:1292:G:H8	1.87	0.40
38:S02:135:MET:HA	38:S02:138:ARG:HH21	1.86	0.40
40:S04:47:LEU:HD12	40:S04:47:LEU:HA	1.94	0.40
40:S04:54:LEU:O	40:S04:58:GLN:N	2.50	0.40
43:S07:55:LYS:HB3	43:S07:59:GLU:HG3	2.02	0.40
50:S14:9:GLU:OE1	50:S14:62:ARG:NH2	2.54	0.40
52:S16:29:ASN:OD1	52:S16:29:ASN:N	2.54	0.40
55:S19:57:VAL:HA	55:S19:58:PRO:HD3	1.95	0.40
3:L04:105:LEU:HD21	3:L04:177:PRO:HG3	2.04	0.40
13:L16:19:GLY:O	13:L16:38:ARG:NH2	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L19:28:LYS:HD3	16:L19:39:LEU:HD21	2.03	0.40
20:L23:11:LEU:HB2	25:L29:26:PHE:HZ	1.86	0.40
33:23S:648:G:H2'	33:23S:649:G:H8	1.86	0.40
33:23S:848:C:H2'	33:23S:849:A:H8	1.87	0.40
33:23S:2075:U:O2'	33:23S:2596:U:O2	2.37	0.40
33:23S:2204:G:C6	33:23S:2220:U:O2	2.75	0.40
33:23S:2443:C:H2'	33:23S:2444:G:C8	2.52	0.40
36:16S:64:G:H22	36:16S:101:A:N6	2.19	0.40
36:16S:116:A:N1	36:16S:313:A:O2'	2.45	0.40
36:16S:356:A:N3	36:16S:368:U:O2'	2.39	0.40
53:S17:38:LYS:HB2	53:S17:38:LYS:HE3	1.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L02	269/273 (98%)	243 (90%)	26 (10%)	0	100	100
2	L03	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
3	L04	199/201 (99%)	187 (94%)	11 (6%)	1 (0%)	24	56
4	L05	175/179 (98%)	152 (87%)	23 (13%)	0	100	100
5	L06	174/177 (98%)	162 (93%)	12 (7%)	0	100	100
6	L09	147/149 (99%)	129 (88%)	17 (12%)	1 (1%)	18	50
7	L1	130/234 (56%)	117 (90%)	13 (10%)	0	100	100
8	L10	129/165 (78%)	100 (78%)	28 (22%)	1 (1%)	16	48
9	L11	139/142 (98%)	118 (85%)	21 (15%)	0	100	100
10	L13	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
11	L14	120/123 (98%)	106 (88%)	14 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L15	141/144 (98%)	125 (89%)	16 (11%)	0	100	100
13	L16	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
14	L17	118/127 (93%)	106 (90%)	12 (10%)	0	100	100
15	L18	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
16	L19	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
17	L20	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
18	L21	101/103 (98%)	89 (88%)	11 (11%)	1 (1%)	12	43
19	L22	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
20	L23	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
21	L24	100/104 (96%)	84 (84%)	16 (16%)	0	100	100
22	L25	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	L27	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
24	L28	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
25	L29	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
26	L30	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
27	L31	43/45 (96%)	35 (81%)	8 (19%)	0	100	100
28	L32	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
29	L33	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
30	L34	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
31	L35	62/65 (95%)	55 (89%)	6 (10%)	1 (2%)	7	35
32	L36	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
38	S02	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	60
39	S03	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
40	S04	203/206 (98%)	180 (89%)	23 (11%)	0	100	100
41	S05	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
42	S06	98/135 (73%)	81 (83%)	17 (17%)	0	100	100
43	S07	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
44	S08	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
45	S09	125/130 (96%)	107 (86%)	18 (14%)	0	100	100
46	S10	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
47	S11	114/129 (88%)	98 (86%)	16 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	S12	121/124 (98%)	100 (83%)	21 (17%)	0	100	100
49	S13	112/118 (95%)	101 (90%)	11 (10%)	0	100	100
50	S14	98/101 (97%)	88 (90%)	10 (10%)	0	100	100
51	S15	86/89 (97%)	73 (85%)	12 (14%)	1 (1%)	10	40
52	S16	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
53	S17	78/84 (93%)	65 (83%)	13 (17%)	0	100	100
54	S18	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
55	S19	77/92 (84%)	70 (91%)	7 (9%)	0	100	100
56	S20	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
57	S21	63/71 (89%)	42 (67%)	21 (33%)	0	100	100
58	SMPB	148/150 (99%)	124 (84%)	23 (16%)	1 (1%)	18	50
All	All	6110/6579 (93%)	5513 (90%)	589 (10%)	8 (0%)	49	78

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	L10	118	ILE
31	L35	31	ILE
58	SMPB	81	VAL
38	S02	94	ARG
3	L04	83	VAL
18	L21	54	VAL
51	S15	46	LYS
6	L09	9	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L02	216/218 (99%)	197 (91%)	19 (9%)	9	33
2	L03	164/164 (100%)	145 (88%)	19 (12%)	5	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	L04	165/165 (100%)	152 (92%)	13 (8%)	11	37
4	L05	148/150 (99%)	121 (82%)	27 (18%)	2	11
5	L06	137/138 (99%)	118 (86%)	19 (14%)	3	19
6	L09	114/114 (100%)	101 (89%)	13 (11%)	5	24
7	L1	110/181 (61%)	90 (82%)	20 (18%)	2	11
8	L10	100/123 (81%)	83 (83%)	17 (17%)	2	13
9	L11	109/110 (99%)	96 (88%)	13 (12%)	5	23
10	L13	116/116 (100%)	111 (96%)	5 (4%)	26	50
11	L14	103/104 (99%)	88 (85%)	15 (15%)	3	17
12	L15	102/103 (99%)	91 (89%)	11 (11%)	6	27
13	L16	109/109 (100%)	96 (88%)	13 (12%)	5	23
14	L17	100/103 (97%)	95 (95%)	5 (5%)	22	48
15	L18	86/87 (99%)	77 (90%)	9 (10%)	6	28
16	L19	99/100 (99%)	91 (92%)	8 (8%)	11	36
17	L20	89/90 (99%)	81 (91%)	8 (9%)	9	33
18	L21	84/84 (100%)	68 (81%)	16 (19%)	1	10
19	L22	93/93 (100%)	89 (96%)	4 (4%)	26	50
20	L23	80/84 (95%)	63 (79%)	17 (21%)	1	7
21	L24	83/85 (98%)	71 (86%)	12 (14%)	3	17
22	L25	78/78 (100%)	66 (85%)	12 (15%)	2	16
23	L27	57/63 (90%)	54 (95%)	3 (5%)	20	46
24	L28	67/68 (98%)	61 (91%)	6 (9%)	9	33
25	L29	55/55 (100%)	49 (89%)	6 (11%)	6	26
26	L30	48/49 (98%)	44 (92%)	4 (8%)	10	35
27	L31	42/42 (100%)	29 (69%)	13 (31%)	0	2
28	L32	47/48 (98%)	41 (87%)	6 (13%)	4	21
29	L33	45/49 (92%)	36 (80%)	9 (20%)	1	9
30	L34	38/38 (100%)	34 (90%)	4 (10%)	6	28
31	L35	51/52 (98%)	47 (92%)	4 (8%)	11	37
32	L36	34/34 (100%)	30 (88%)	4 (12%)	5	23
38	S02	186/199 (94%)	159 (86%)	27 (14%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	S03	170/190 (90%)	144 (85%)	26 (15%)	3	16
40	S04	172/173 (99%)	139 (81%)	33 (19%)	1	9
41	S05	119/126 (94%)	96 (81%)	23 (19%)	1	9
42	S06	87/116 (75%)	79 (91%)	8 (9%)	8	32
43	S07	124/147 (84%)	110 (89%)	14 (11%)	5	25
44	S08	104/105 (99%)	96 (92%)	8 (8%)	12	38
45	S09	105/107 (98%)	91 (87%)	14 (13%)	4	20
46	S10	86/90 (96%)	76 (88%)	10 (12%)	5	24
47	S11	89/99 (90%)	81 (91%)	8 (9%)	9	33
48	S12	103/104 (99%)	97 (94%)	6 (6%)	18	45
49	S13	92/96 (96%)	82 (89%)	10 (11%)	6	26
50	S14	83/84 (99%)	68 (82%)	15 (18%)	2	12
51	S15	76/77 (99%)	68 (90%)	8 (10%)	6	28
52	S16	65/65 (100%)	56 (86%)	9 (14%)	3	19
53	S17	74/78 (95%)	64 (86%)	10 (14%)	4	20
54	S18	56/65 (86%)	48 (86%)	8 (14%)	3	18
55	S19	70/79 (89%)	60 (86%)	10 (14%)	3	18
56	S20	65/66 (98%)	57 (88%)	8 (12%)	4	22
57	S21	55/61 (90%)	48 (87%)	7 (13%)	4	21
58	SMPB	125/125 (100%)	103 (82%)	22 (18%)	2	12
All	All	5075/5349 (95%)	4437 (87%)	638 (13%)	6	21

All (638) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L02	3	VAL
1	L02	8	THR
1	L02	18	VAL
1	L02	59	GLN
1	L02	64	VAL
1	L02	119	VAL
1	L02	124	LYS
1	L02	128	THR
1	L02	149	LYS
1	L02	167	ASP

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Mol	Chain	Res	Type
1	L02	171	VAL
1	L02	183	VAL
1	L02	193	GLU
1	L02	194	VAL
1	L02	202	ARG
1	L02	212	TRP
1	L02	215	VAL
1	L02	216	ARG
1	L02	269	ARG
2	L03	9	VAL
2	L03	12	THR
2	L03	28	GLU
2	L03	43	ASP
2	L03	112	THR
2	L03	113	SER
2	L03	121	THR
2	L03	123	LYS
2	L03	128	ARG
2	L03	131	ASP
2	L03	133	THR
2	L03	136	ASN
2	L03	148	GLN
2	L03	164	GLN
2	L03	170	VAL
2	L03	176	ASP
2	L03	180	VAL
2	L03	189	VAL
2	L03	193	VAL
3	L04	2	GLU
3	L04	3	LEU
3	L04	13	THR
3	L04	14	VAL
3	L04	53	THR
3	L04	85	PHE
3	L04	118	LEU
3	L04	149	ILE
3	L04	152	GLU
3	L04	164	LEU
3	L04	181	ILE
3	L04	186	VAL
3	L04	187	VAL
4	L05	9	ASP

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Mol	Chain	Res	Type
4	L05	27	VAL
4	L05	29	ARG
4	L05	30	VAL
4	L05	31	GLU
4	L05	34	THR
4	L05	35	LEU
4	L05	39	VAL
4	L05	55	ASP
4	L05	79	ARG
4	L05	82	TYR
4	L05	89	THR
4	L05	97	GLU
4	L05	99	PHE
4	L05	109	ARG
4	L05	110	ILE
4	L05	112	ASP
4	L05	119	LYS
4	L05	129	MET
4	L05	133	GLU
4	L05	139	GLU
4	L05	140	ILE
4	L05	142	TYR
4	L05	155	ILE
4	L05	157	THR
4	L05	168	LEU
4	L05	174	PHE
5	L06	9	VAL
5	L06	10	VAL
5	L06	29	ASN
5	L06	32	LEU
5	L06	48	THR
5	L06	50	THR
5	L06	57	TYR
5	L06	72	ASN
5	L06	83	THR
5	L06	89	VAL
5	L06	113	ASP
5	L06	115	GLN
5	L06	116	LEU
5	L06	126	THR
5	L06	138	GLN
5	L06	147	LEU

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Mol	Chain	Res	Type
5	L06	151	ARG
5	L06	159	LYS
5	L06	174	LYS
6	L09	17	ASP
6	L09	58	LEU
6	L09	83	LYS
6	L09	86	ASP
6	L09	89	LYS
6	L09	91	PHE
6	L09	98	ASP
6	L09	101	ASP
6	L09	121	VAL
6	L09	124	THR
6	L09	125	THR
6	L09	130	VAL
6	L09	133	GLN
7	L1	4	LEU
7	L1	5	THR
7	L1	18	THR
7	L1	23	ILE
7	L1	24	ASN
7	L1	30	LEU
7	L1	42	VAL
7	L1	44	VAL
7	L1	50	ILE
7	L1	59	VAL
7	L1	64	VAL
7	L1	69	THR
7	L1	163	TYR
7	L1	170	ILE
7	L1	192	LEU
7	L1	194	VAL
7	L1	207	VAL
7	L1	209	ILE
7	L1	217	THR
7	L1	222	VAL
8	L10	1	MET
8	L10	8	LYS
8	L10	15	VAL
8	L10	18	VAL
8	L10	26	VAL
8	L10	41	LEU

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Mol	Chain	Res	Type
8	L10	55	VAL
8	L10	58	THR
8	L10	64	VAL
8	L10	67	THR
8	L10	76	PHE
8	L10	94	ARG
8	L10	96	PHE
8	L10	101	LYS
8	L10	109	LYS
8	L10	113	PHE
8	L10	128	THR
9	L11	7	TYR
9	L11	8	VAL
9	L11	10	LEU
9	L11	33	ASN
9	L11	39	LYS
9	L11	45	THR
9	L11	52	LEU
9	L11	58	ILE
9	L11	63	ASP
9	L11	70	THR
9	L11	92	PRO
9	L11	94	LYS
9	L11	104	GLN
10	L13	19	ASP
10	L13	52	ASP
10	L13	80	HIS
10	L13	129	GLU
10	L13	131	ASN
11	L14	2	ILE
11	L14	4	GLU
11	L14	10	VAL
11	L14	35	VAL
11	L14	37	ASP
11	L14	44	LYS
11	L14	54	LYS
11	L14	56	ASP
11	L14	57	VAL
11	L14	58	LEU
11	L14	61	VAL
11	L14	65	THR
11	L14	88	ASN

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Mol	Chain	Res	Type
11	L14	95	ILE
11	L14	110	GLU
12	L15	82	LEU
12	L15	89	VAL
12	L15	92	LEU
12	L15	94	THR
12	L15	95	LEU
12	L15	103	ILE
12	L15	104	GLN
12	L15	111	ILE
12	L15	120	VAL
12	L15	122	VAL
12	L15	128	THR
13	L16	4	PRO
13	L16	9	PHE
13	L16	33	LEU
13	L16	42	THR
13	L16	54	THR
13	L16	55	ARG
13	L16	59	ARG
13	L16	101	VAL
13	L16	119	LEU
13	L16	128	THR
13	L16	129	THR
13	L16	132	THR
13	L16	134	THR
14	L17	2	ARG
14	L17	31	HIS
14	L17	106	ASP
14	L17	113	ILE
14	L17	116	VAL
15	L18	3	LYS
15	L18	27	VAL
15	L18	28	VAL
15	L18	43	ASN
15	L18	47	VAL
15	L18	56	LYS
15	L18	74	VAL
15	L18	76	LYS
15	L18	112	GLU
16	L19	31	VAL
16	L19	38	ARG

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Mol	Chain	Res	Type
16	L19	74	GLN
16	L19	86	LYS
16	L19	101	GLU
16	L19	108	ARG
16	L19	110	LYS
16	L19	114	ASN
17	L20	8	ILE
17	L20	14	LYS
17	L20	36	GLN
17	L20	40	LYS
17	L20	57	ARG
17	L20	70	GLN
17	L20	94	LEU
17	L20	102	LYS
18	L21	10	LYS
18	L21	11	GLN
18	L21	12	HIS
18	L21	14	VAL
18	L21	20	VAL
18	L21	22	LEU
18	L21	32	THR
18	L21	38	VAL
18	L21	43	ASN
18	L21	46	GLU
18	L21	48	LYS
18	L21	51	VAL
18	L21	58	VAL
18	L21	64	VAL
18	L21	70	GLU
18	L21	95	ASP
19	L22	2	GLU
19	L22	40	ASN
19	L22	84	ARG
19	L22	95	ARG
20	L23	2	ILE
20	L23	3	ARG
20	L23	5	GLU
20	L23	7	LEU
20	L23	10	VAL
20	L23	15	HIS
20	L23	16	VAL
20	L23	33	LYS

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Mol	Chain	Res	Type
20	L23	48	GLN
20	L23	56	GLU
20	L23	57	VAL
20	L23	58	VAL
20	L23	59	ASN
20	L23	61	LEU
20	L23	67	VAL
20	L23	72	GLN
20	L23	92	ASN
21	L24	17	ASP
21	L24	27	VAL
21	L24	33	VAL
21	L24	42	LYS
21	L24	48	VAL
21	L24	53	GLN
21	L24	58	VAL
21	L24	71	ILE
21	L24	78	LYS
21	L24	84	PHE
21	L24	87	GLU
21	L24	102	ILE
22	L25	4	ILE
22	L25	20	LEU
22	L25	30	ILE
22	L25	34	LYS
22	L25	35	GLU
22	L25	41	GLU
22	L25	42	LEU
22	L25	55	GLU
22	L25	64	VAL
22	L25	65	VAL
22	L25	69	GLU
22	L25	85	LYS
23	L27	39	THR
23	L27	49	CYS
23	L27	52	ASP
24	L28	24	THR
24	L28	43	LYS
24	L28	46	VAL
24	L28	53	LYS
24	L28	63	ILE
24	L28	71	ARG

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Mol	Chain	Res	Type
25	L29	13	GLU
25	L29	15	ASN
25	L29	22	LEU
25	L29	25	GLN
25	L29	45	GLN
25	L29	55	THR
26	L30	24	LEU
26	L30	30	ARG
26	L30	40	THR
26	L30	56	VAL
27	L31	4	ASP
27	L31	5	ILE
27	L31	6	HIS
27	L31	11	GLU
27	L31	12	ILE
27	L31	16	CYS
27	L31	23	LYS
27	L31	25	ARG
27	L31	26	SER
27	L31	27	THR
27	L31	30	HIS
27	L31	44	PHE
27	L31	45	THR
28	L32	2	VAL
28	L32	3	GLN
28	L32	21	LEU
28	L32	22	THR
28	L32	24	VAL
28	L32	52	LYS
29	L33	5	ARG
29	L33	11	VAL
29	L33	16	THR
29	L33	18	HIS
29	L33	19	PHE
29	L33	22	THR
29	L33	29	LYS
29	L33	32	LYS
29	L33	45	HIS
30	L34	3	ARG
30	L34	9	VAL
30	L34	24	THR
30	L34	41	ARG

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Mol	Chain	Res	Type
31	L35	15	LYS
31	L35	25	HIS
31	L35	53	ASP
31	L35	61	LEU
32	L36	12	ARG
32	L36	18	LYS
32	L36	30	GLU
32	L36	36	ARG
38	S02	2	THR
38	S02	3	VAL
38	S02	6	ARG
38	S02	9	LEU
38	S02	13	VAL
38	S02	22	TRP
38	S02	39	ILE
38	S02	42	LEU
38	S02	43	GLU
38	S02	53	LEU
38	S02	77	GLU
38	S02	94	ARG
38	S02	135	MET
38	S02	151	LYS
38	S02	160	LEU
38	S02	162	VAL
38	S02	163	ILE
38	S02	169	HIS
38	S02	182	VAL
38	S02	186	VAL
38	S02	193	ASP
38	S02	196	ASP
38	S02	207	ARG
38	S02	209	VAL
38	S02	211	LEU
38	S02	221	ARG
38	S02	222	GLU
39	S03	13	ILE
39	S03	14	VAL
39	S03	18	ASN
39	S03	19	SER
39	S03	26	LYS
39	S03	36	PHE
39	S03	38	VAL

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Mol	Chain	Res	Type
39	S03	43	THR
39	S03	51	VAL
39	S03	53	ARG
39	S03	74	ILE
39	S03	82	ASP
39	S03	87	ARG
39	S03	92	ASP
39	S03	96	VAL
39	S03	107	LYS
39	S03	123	LEU
39	S03	134	LYS
39	S03	156	LEU
39	S03	164	THR
39	S03	167	TYR
39	S03	168	ARG
39	S03	172	VAL
39	S03	180	ASP
39	S03	194	VAL
39	S03	202	PHE
40	S04	2	ARG
40	S04	4	LEU
40	S04	7	LYS
40	S04	18	LEU
40	S04	19	PHE
40	S04	25	ARG
40	S04	28	ASP
40	S04	29	THR
40	S04	33	ILE
40	S04	34	GLU
40	S04	39	GLN
40	S04	46	ARG
40	S04	57	LYS
40	S04	62	ARG
40	S04	68	GLU
40	S04	114	ARG
40	S04	115	GLN
40	S04	127	ARG
40	S04	129	VAL
40	S04	136	VAL
40	S04	141	VAL
40	S04	154	VAL
40	S04	159	GLU

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Mol	Chain	Res	Type
40	S04	165	GLU
40	S04	171	GLU
40	S04	172	VAL
40	S04	177	MET
40	S04	183	ARG
40	S04	189	ASP
40	S04	190	LEU
40	S04	193	ASP
40	S04	194	ILE
40	S04	196	GLU
41	S05	10	LEU
41	S05	14	LEU
41	S05	19	ARG
41	S05	23	THR
41	S05	28	ARG
41	S05	30	PHE
41	S05	53	ARG
41	S05	54	GLU
41	S05	55	VAL
41	S05	73	VAL
41	S05	75	LEU
41	S05	81	GLN
41	S05	105	ILE
41	S05	115	GLU
41	S05	123	LEU
41	S05	143	LEU
41	S05	145	ASN
41	S05	156	ARG
41	S05	158	LYS
41	S05	159	SER
41	S05	160	VAL
41	S05	162	GLU
41	S05	164	LEU
42	S06	5	GLU
42	S06	10	VAL
42	S06	14	GLN
42	S06	18	VAL
42	S06	54	LEU
42	S06	70	VAL
42	S06	85	ILE
42	S06	92	THR
43	S07	4	ARG

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Mol	Chain	Res	Type
43	S07	24	LYS
43	S07	25	PHE
43	S07	63	VAL
43	S07	72	VAL
43	S07	84	TYR
43	S07	85	GLN
43	S07	86	VAL
43	S07	94	ARG
43	S07	102	TRP
43	S07	103	ILE
43	S07	112	ASP
43	S07	128	GLU
43	S07	132	THR
44	S08	8	ASP
44	S08	32	LYS
44	S08	39	LEU
44	S08	45	ILE
44	S08	60	LEU
44	S08	70	VAL
44	S08	74	ILE
44	S08	103	VAL
45	S09	31	GLN
45	S09	41	GLU
45	S09	42	THR
45	S09	44	ARG
45	S09	46	VAL
45	S09	60	LEU
45	S09	61	ASP
45	S09	67	LYS
45	S09	87	MET
45	S09	88	GLU
45	S09	90	ASP
45	S09	102	PHE
45	S09	104	THR
45	S09	105	ARG
46	S10	10	LEU
46	S10	15	HIS
46	S10	24	GLU
46	S10	42	LEU
46	S10	57	VAL
46	S10	73	LEU
46	S10	84	VAL

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Mol	Chain	Res	Type
46	S10	85	ASP
46	S10	89	ARG
46	S10	90	LEU
47	S11	26	PHE
47	S11	45	THR
47	S11	67	GLU
47	S11	75	GLU
47	S11	84	MET
47	S11	85	VAL
47	S11	109	ILE
47	S11	124	LYS
48	S12	19	ASN
48	S12	20	VAL
48	S12	89	LEU
48	S12	106	VAL
48	S12	107	LYS
48	S12	116	TYR
49	S13	18	LEU
49	S13	24	VAL
49	S13	33	LEU
49	S13	47	LEU
49	S13	59	VAL
49	S13	100	ARG
49	S13	101	THR
49	S13	107	THR
49	S13	109	LYS
49	S13	113	LYS
50	S14	20	PHE
50	S14	25	GLU
50	S14	30	ILE
50	S14	32	ASP
50	S14	48	GLN
50	S14	52	ARG
50	S14	53	ASP
50	S14	55	SER
50	S14	60	ARG
50	S14	61	ASN
50	S14	63	CYS
50	S14	65	GLN
50	S14	73	LEU
50	S14	82	LYS
50	S14	83	VAL

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Mol	Chain	Res	Type
51	S15	4	THR
51	S15	5	GLU
51	S15	23	SER
51	S15	39	GLN
51	S15	46	LYS
51	S15	56	LEU
51	S15	65	LEU
51	S15	87	ARG
52	S16	19	VAL
52	S16	23	ASP
52	S16	24	SER
52	S16	38	PHE
52	S16	53	ASP
52	S16	54	LEU
52	S16	74	LEU
52	S16	77	GLU
52	S16	80	LYS
53	S17	5	ARG
53	S17	16	MET
53	S17	20	ILE
53	S17	22	VAL
53	S17	27	PHE
53	S17	43	LEU
53	S17	49	ASN
53	S17	54	ILE
53	S17	56	ASP
53	S17	62	GLU
54	S18	9	PHE
54	S18	11	ARG
54	S18	12	PHE
54	S18	17	VAL
54	S18	23	LYS
54	S18	24	ASP
54	S18	30	ASN
54	S18	43	ILE
55	S19	10	ILE
55	S19	18	VAL
55	S19	28	LYS
55	S19	40	PHE
55	S19	50	VAL
55	S19	59	VAL
55	S19	62	THR

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Mol	Chain	Res	Type
55	S19	66	VAL
55	S19	70	LEU
55	S19	72	GLU
56	S20	17	ARG
56	S20	18	LYS
56	S20	27	MET
56	S20	29	THR
56	S20	32	LYS
56	S20	33	LYS
56	S20	50	PHE
56	S20	78	LEU
57	S21	6	ARG
57	S21	23	GLU
57	S21	33	ARG
57	S21	36	PHE
57	S21	37	TYR
57	S21	59	LEU
57	S21	65	ARG
58	SMPB	14	ILE
58	SMPB	16	LEU
58	SMPB	22	HIS
58	SMPB	23	GLU
58	SMPB	24	TYR
58	SMPB	25	PHE
58	SMPB	34	LEU
58	SMPB	36	LEU
58	SMPB	44	LEU
58	SMPB	59	ARG
58	SMPB	66	PHE
58	SMPB	71	THR
58	SMPB	75	VAL
58	SMPB	78	THR
58	SMPB	101	TYR
58	SMPB	104	VAL
58	SMPB	110	THR
58	SMPB	119	LYS
58	SMPB	125	VAL
58	SMPB	127	ILE
58	SMPB	131	LYS
58	SMPB	151	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
7	L1	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	23S	2902/2903 (99%)	618 (21%)	14 (0%)
34	5S	119/120 (99%)	29 (24%)	1 (0%)
35	TMRN	362/363 (99%)	168 (46%)	13 (3%)
36	16S	1538/1539 (99%)	321 (20%)	5 (0%)
37	ATRN	75/76 (98%)	20 (26%)	1 (1%)
All	All	4996/5001 (99%)	1156 (23%)	34 (0%)

All (1156) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
33	23S	10	A
33	23S	12	U
33	23S	15	G
33	23S	23	G
33	23S	34	U
33	23S	35	G
33	23S	39	G
33	23S	46	G
33	23S	50	U
33	23S	51	G
33	23S	55	G
33	23S	61	C
33	23S	63	A
33	23S	71	A
33	23S	74	A
33	23S	75	G
33	23S	80	G
33	23S	82	U
33	23S	84	A
33	23S	87	U
33	23S	91	A
33	23S	96	C
33	23S	100	U
33	23S	102	U
33	23S	103	A
33	23S	110	G
33	23S	114	U

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Mol	Chain	Res	Type
33	23S	118	A
33	23S	119	A
33	23S	120	U
33	23S	123	G
33	23S	125	A
33	23S	128	C
33	23S	135	U
33	23S	136	G
33	23S	137	U
33	23S	139	U
33	23S	140	C
33	23S	141	G
33	23S	162	U
33	23S	163	C
33	23S	166	U
33	23S	181	A
33	23S	196	A
33	23S	199	A
33	23S	204	A
33	23S	205	G
33	23S	216	A
33	23S	219	A
33	23S	220	G
33	23S	222	A
33	23S	228	C
33	23S	229	C
33	23S	243	U
33	23S	248	G
33	23S	255	A
33	23S	265	A
33	23S	266	G
33	23S	271	G
33	23S	276	U
33	23S	277	G
33	23S	278	A
33	23S	281	C
33	23S	285	G
33	23S	294	A
33	23S	299	A
33	23S	301	G
33	23S	311	A
33	23S	316	C

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Mol	Chain	Res	Type
33	23S	322	A
33	23S	323	C
33	23S	329	G
33	23S	330	A
33	23S	334	C
33	23S	353	C
33	23S	361	G
33	23S	367	G
33	23S	371	A
33	23S	372	G
33	23S	373	U
33	23S	386	G
33	23S	387	U
33	23S	396	G
33	23S	403	U
33	23S	404	A
33	23S	406	G
33	23S	411	G
33	23S	412	A
33	23S	422	A
33	23S	424	G
33	23S	448	U
33	23S	451	U
33	23S	456	C
33	23S	457	A
33	23S	458	G
33	23S	459	U
33	23S	467	G
33	23S	473	G
33	23S	479	A
33	23S	481	G
33	23S	483	A
33	23S	490	C
33	23S	491	G
33	23S	504	A
33	23S	505	A
33	23S	508	A
33	23S	509	C
33	23S	517	C
33	23S	518	G
33	23S	528	A
33	23S	530	G

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Mol	Chain	Res	Type
33	23S	532	A
33	23S	542	C
33	23S	543	G
33	23S	544	C
33	23S	545	U
33	23S	547	A
33	23S	549	G
33	23S	555	G
33	23S	562	U
33	23S	563	A
33	23S	573	U
33	23S	575	A
33	23S	592	A
33	23S	602	A
33	23S	603	A
33	23S	613	A
33	23S	614	A
33	23S	616	A
33	23S	622	G
33	23S	627	A
33	23S	637	A
33	23S	645	C
33	23S	646	U
33	23S	647	G
33	23S	651	G
33	23S	654	A
33	23S	655	A
33	23S	656	G
33	23S	664	G
33	23S	669	G
33	23S	676	A
33	23S	678	C
33	23S	685	A
33	23S	686	U
33	23S	695	G
33	23S	696	G
33	23S	714	U
33	23S	717	C
33	23S	730	A
33	23S	734	A
33	23S	738	G
33	23S	747	C

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Mol	Chain	Res	Type
33	23S	752	A
33	23S	764	A
33	23S	774	G
33	23S	776	G
33	23S	782	A
33	23S	784	G
33	23S	785	G
33	23S	789	A
33	23S	792	A
33	23S	800	A
33	23S	805	G
33	23S	806	C
33	23S	811	U
33	23S	812	C
33	23S	819	A
33	23S	827	U
33	23S	828	U
33	23S	830	G
33	23S	844	A
33	23S	845	A
33	23S	846	U
33	23S	847	U
33	23S	856	G
33	23S	859	G
33	23S	860	U
33	23S	866	A
33	23S	869	G
33	23S	878	A
33	23S	886	A
33	23S	887	U
33	23S	890	C
33	23S	891	G
33	23S	896	A
33	23S	897	C
33	23S	902	C
33	23S	910	A
33	23S	914	G
33	23S	915	C
33	23S	919	U
33	23S	941	A
33	23S	945	A
33	23S	946	C

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Mol	Chain	Res	Type
33	23S	953	G
33	23S	957	C
33	23S	959	A
33	23S	961	C
33	23S	973	A
33	23S	974	G
33	23S	983	A
33	23S	985	C
33	23S	989	G
33	23S	995	C
33	23S	996	A
33	23S	1005	C
33	23S	1009	A
33	23S	1012	U
33	23S	1013	C
33	23S	1020	A
33	23S	1021	A
33	23S	1022	G
33	23S	1023	U
33	23S	1026	G
33	23S	1028	A
33	23S	1033	U
33	23S	1040	A
33	23S	1045	C
33	23S	1046	A
33	23S	1047	G
33	23S	1051	G
33	23S	1054	A
33	23S	1058	U
33	23S	1061	U
33	23S	1062	G
33	23S	1063	G
33	23S	1065	U
33	23S	1066	U
33	23S	1068	G
33	23S	1069	A
33	23S	1070	A
33	23S	1071	G
33	23S	1073	A
33	23S	1074	G
33	23S	1075	C
33	23S	1076	C

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Mol	Chain	Res	Type
33	23S	1078	U
33	23S	1080	A
33	23S	1081	U
33	23S	1082	U
33	23S	1083	U
33	23S	1084	A
33	23S	1085	A
33	23S	1088	A
33	23S	1090	A
33	23S	1095	A
33	23S	1096	A
33	23S	1098	A
33	23S	1101	U
33	23S	1103	A
33	23S	1104	C
33	23S	1111	A
33	23S	1119	U
33	23S	1126	A
33	23S	1132	U
33	23S	1133	A
33	23S	1135	C
33	23S	1139	G
33	23S	1142	A
33	23S	1151	A
33	23S	1156	A
33	23S	1170	C
33	23S	1172	C
33	23S	1174	U
33	23S	1175	A
33	23S	1177	G
33	23S	1178	C
33	23S	1180	U
33	23S	1186	G
33	23S	1206	G
33	23S	1212	G
33	23S	1227	G
33	23S	1237	A
33	23S	1252	G
33	23S	1253	A
33	23S	1255	U
33	23S	1256	G
33	23S	1262	A

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Mol	Chain	Res	Type
33	23S	1271	G
33	23S	1272	A
33	23S	1273	U
33	23S	1294	U
33	23S	1300	G
33	23S	1301	A
33	23S	1302	A
33	23S	1305	C
33	23S	1306	C
33	23S	1314	C
33	23S	1321	A
33	23S	1329	U
33	23S	1330	C
33	23S	1332	G
33	23S	1344	U
33	23S	1345	C
33	23S	1360	G
33	23S	1365	A
33	23S	1368	G
33	23S	1374	G
33	23S	1378	A
33	23S	1379	U
33	23S	1383	A
33	23S	1386	C
33	23S	1394	U
33	23S	1395	A
33	23S	1403	A
33	23S	1412	U
33	23S	1414	C
33	23S	1416	G
33	23S	1419	A
33	23S	1420	A
33	23S	1427	A
33	23S	1428	C
33	23S	1433	A
33	23S	1451	C
33	23S	1453	A
33	23S	1458	U
33	23S	1461	C
33	23S	1468	U
33	23S	1475	G
33	23S	1482	G

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Mol	Chain	Res	Type
33	23S	1483	G
33	23S	1488	C
33	23S	1490	A
33	23S	1491	G
33	23S	1497	U
33	23S	1504	A
33	23S	1509	A
33	23S	1515	A
33	23S	1522	A
33	23S	1524	G
33	23S	1525	A
33	23S	1529	G
33	23S	1530	G
33	23S	1534	U
33	23S	1535	A
33	23S	1536	C
33	23S	1537	G
33	23S	1554	U
33	23S	1559	U
33	23S	1560	G
33	23S	1566	A
33	23S	1569	A
33	23S	1578	U
33	23S	1581	G
33	23S	1584	U
33	23S	1588	G
33	23S	1607	C
33	23S	1608	A
33	23S	1611	C
33	23S	1613	G
33	23S	1616	A
33	23S	1646	C
33	23S	1647	U
33	23S	1648	U
33	23S	1649	G
33	23S	1660	G
33	23S	1668	A
33	23S	1669	A
33	23S	1674	G
33	23S	1676	A
33	23S	1677	A
33	23S	1715	G

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Mol	Chain	Res	Type
33	23S	1729	U
33	23S	1730	C
33	23S	1732	C
33	23S	1733	G
33	23S	1735	A
33	23S	1738	G
33	23S	1758	U
33	23S	1759	A
33	23S	1764	C
33	23S	1773	A
33	23S	1780	A
33	23S	1782	U
33	23S	1784	A
33	23S	1785	A
33	23S	1786	A
33	23S	1787	A
33	23S	1791	A
33	23S	1800	C
33	23S	1801	A
33	23S	1802	A
33	23S	1808	A
33	23S	1809	A
33	23S	1815	A
33	23S	1816	C
33	23S	1820	U
33	23S	1829	A
33	23S	1847	A
33	23S	1857	G
33	23S	1866	A
33	23S	1870	C
33	23S	1871	A
33	23S	1884	G
33	23S	1901	A
33	23S	1906	G
33	23S	1907	G
33	23S	1912	A
33	23S	1915	U
33	23S	1918	A
33	23S	1919	A
33	23S	1929	G
33	23S	1930	G
33	23S	1931	U

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Mol	Chain	Res	Type
33	23S	1933	G
33	23S	1937	A
33	23S	1938	A
33	23S	1944	U
33	23S	1955	U
33	23S	1960	A
33	23S	1966	A
33	23S	1967	C
33	23S	1970	A
33	23S	1971	U
33	23S	1972	G
33	23S	1981	A
33	23S	1982	U
33	23S	1991	U
33	23S	1993	U
33	23S	1997	C
33	23S	2015	A
33	23S	2020	A
33	23S	2022	U
33	23S	2023	C
33	23S	2030	A
33	23S	2031	A
33	23S	2032	G
33	23S	2033	A
33	23S	2034	U
33	23S	2043	C
33	23S	2052	A
33	23S	2055	C
33	23S	2056	G
33	23S	2060	A
33	23S	2061	G
33	23S	2062	A
33	23S	2063	C
33	23S	2069	G
33	23S	2077	A
33	23S	2093	G
33	23S	2096	C
33	23S	2098	U
33	23S	2100	G
33	23S	2107	G
33	23S	2110	G
33	23S	2112	G

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Mol	Chain	Res	Type
33	23S	2113	U
33	23S	2114	A
33	23S	2115	G
33	23S	2116	G
33	23S	2118	U
33	23S	2119	A
33	23S	2125	G
33	23S	2126	A
33	23S	2131	U
33	23S	2132	U
33	23S	2133	G
33	23S	2139	U
33	23S	2144	G
33	23S	2145	C
33	23S	2147	A
33	23S	2149	U
33	23S	2151	U
33	23S	2152	G
33	23S	2157	G
33	23S	2158	A
33	23S	2162	G
33	23S	2163	A
33	23S	2164	C
33	23S	2166	U
33	23S	2167	U
33	23S	2170	A
33	23S	2171	A
33	23S	2172	U
33	23S	2173	A
33	23S	2178	C
33	23S	2182	U
33	23S	2184	A
33	23S	2189	U
33	23S	2190	G
33	23S	2197	U
33	23S	2198	A
33	23S	2203	U
33	23S	2204	G
33	23S	2211	A
33	23S	2212	A
33	23S	2223	G
33	23S	2225	A

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Mol	Chain	Res	Type
33	23S	2226	C
33	23S	2238	G
33	23S	2239	G
33	23S	2250	G
33	23S	2278	A
33	23S	2279	G
33	23S	2283	C
33	23S	2287	A
33	23S	2288	A
33	23S	2295	C
33	23S	2297	A
33	23S	2305	U
33	23S	2308	G
33	23S	2309	A
33	23S	2311	A
33	23S	2312	U
33	23S	2320	U
33	23S	2327	A
33	23S	2333	A
33	23S	2334	U
33	23S	2335	A
33	23S	2339	C
33	23S	2345	G
33	23S	2350	C
33	23S	2354	C
33	23S	2379	G
33	23S	2383	G
33	23S	2385	C
33	23S	2392	A
33	23S	2402	U
33	23S	2403	C
33	23S	2406	A
33	23S	2410	G
33	23S	2423	U
33	23S	2424	C
33	23S	2425	A
33	23S	2428	G
33	23S	2429	G
33	23S	2430	A
33	23S	2435	A
33	23S	2439	A
33	23S	2441	U

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Mol	Chain	Res	Type
33	23S	2445	G
33	23S	2447	G
33	23S	2448	A
33	23S	2449	U
33	23S	2475	C
33	23S	2476	A
33	23S	2478	A
33	23S	2480	C
33	23S	2482	A
33	23S	2498	C
33	23S	2502	G
33	23S	2503	A
33	23S	2504	U
33	23S	2505	G
33	23S	2506	U
33	23S	2513	A
33	23S	2518	A
33	23S	2520	C
33	23S	2525	G
33	23S	2534	A
33	23S	2535	G
33	23S	2547	A
33	23S	2549	G
33	23S	2554	U
33	23S	2562	U
33	23S	2566	A
33	23S	2567	G
33	23S	2572	A
33	23S	2573	C
33	23S	2585	U
33	23S	2586	U
33	23S	2603	G
33	23S	2609	U
33	23S	2610	C
33	23S	2613	U
33	23S	2615	U
33	23S	2623	G
33	23S	2629	U
33	23S	2646	C
33	23S	2655	G
33	23S	2656	U
33	23S	2659	G

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Mol	Chain	Res	Type
33	23S	2660	A
33	23S	2682	A
33	23S	2685	G
33	23S	2689	U
33	23S	2690	U
33	23S	2714	G
33	23S	2718	G
33	23S	2722	G
33	23S	2726	A
33	23S	2733	A
33	23S	2744	G
33	23S	2748	A
33	23S	2757	A
33	23S	2764	A
33	23S	2765	A
33	23S	2776	A
33	23S	2778	A
33	23S	2779	U
33	23S	2796	U
33	23S	2797	U
33	23S	2798	U
33	23S	2800	A
33	23S	2808	G
33	23S	2809	A
33	23S	2818	U
33	23S	2820	A
33	23S	2821	A
33	23S	2832	U
33	23S	2833	U
33	23S	2834	G
33	23S	2849	U
33	23S	2861	U
33	23S	2866	U
33	23S	2867	G
33	23S	2871	U
33	23S	2872	A
33	23S	2873	A
33	23S	2874	C
33	23S	2877	G
33	23S	2879	A
33	23S	2880	C
33	23S	2885	G

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Mol	Chain	Res	Type
33	23S	2891	U
33	23S	2901	C
33	23S	2902	C
34	5S	4	C
34	5S	12	C
34	5S	13	G
34	5S	24	G
34	5S	26	C
34	5S	34	A
34	5S	35	C
34	5S	37	C
34	5S	40	U
34	5S	41	G
34	5S	42	C
34	5S	43	C
34	5S	44	G
34	5S	45	A
34	5S	51	G
34	5S	53	A
34	5S	67	G
34	5S	73	A
34	5S	82	U
34	5S	84	G
34	5S	87	U
34	5S	88	C
34	5S	89	U
34	5S	90	C
34	5S	105	G
34	5S	108	A
34	5S	109	A
34	5S	112	G
34	5S	120	A
35	TMRN	8	A
35	TMRN	9	U
35	TMRN	10	U
35	TMRN	12	U
35	TMRN	13	G
35	TMRN	14	G
35	TMRN	15	A
35	TMRN	16	U
35	TMRN	17	U
35	TMRN	18	C

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Mol	Chain	Res	Type
35	TMRN	19	G
35	TMRN	20	A
35	TMRN	21	C
35	TMRN	30	C
35	TMRN	32	A
35	TMRN	33	A
35	TMRN	34	A
35	TMRN	35	C
35	TMRN	39	A
35	TMRN	40	G
35	TMRN	43	G
35	TMRN	49	C
35	TMRN	54	G
35	TMRN	55	G
35	TMRN	58	G
35	TMRN	61	G
35	TMRN	63	C
35	TMRN	64	C
35	TMRN	67	G
35	TMRN	68	U
35	TMRN	69	A
35	TMRN	70	A
35	TMRN	71	A
35	TMRN	72	A
35	TMRN	73	A
35	TMRN	77	G
35	TMRN	79	A
35	TMRN	80	A
35	TMRN	81	A
35	TMRN	82	A
35	TMRN	84	A
35	TMRN	85	U
35	TMRN	86	A
35	TMRN	94	A
35	TMRN	95	C
35	TMRN	96	G
35	TMRN	97	A
35	TMRN	98	C
35	TMRN	99	G
35	TMRN	100	A
35	TMRN	101	A
35	TMRN	102	A

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Mol	Chain	Res	Type
35	TMRN	103	A
35	TMRN	105	U
35	TMRN	106	A
35	TMRN	107	C
35	TMRN	109	C
35	TMRN	114	G
35	TMRN	116	A
35	TMRN	120	U
35	TMRN	121	A
35	TMRN	122	A
35	TMRN	124	A
35	TMRN	125	A
35	TMRN	127	C
35	TMRN	129	G
35	TMRN	130	C
35	TMRN	131	U
35	TMRN	132	U
35	TMRN	133	A
35	TMRN	138	C
35	TMRN	150	G
35	TMRN	151	C
35	TMRN	154	C
35	TMRN	156	G
35	TMRN	157	C
35	TMRN	162	A
35	TMRN	163	G
35	TMRN	165	A
35	TMRN	166	C
35	TMRN	168	G
35	TMRN	172	U
35	TMRN	173	C
35	TMRN	181	G
35	TMRN	182	U
35	TMRN	183	C
35	TMRN	184	A
35	TMRN	189	C
35	TMRN	190	A
35	TMRN	191	A
35	TMRN	192	A
35	TMRN	196	G
35	TMRN	197	A
35	TMRN	199	C

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Mol	Chain	Res	Type
35	TMRN	203	U
35	TMRN	205	G
35	TMRN	206	A
35	TMRN	207	A
35	TMRN	208	G
35	TMRN	211	C
35	TMRN	212	U
35	TMRN	213	G
35	TMRN	223	G
35	TMRN	225	A
35	TMRN	226	G
35	TMRN	227	C
35	TMRN	229	U
35	TMRN	230	U
35	TMRN	231	A
35	TMRN	234	A
35	TMRN	235	C
35	TMRN	236	U
35	TMRN	237	U
35	TMRN	238	A
35	TMRN	245	C
35	TMRN	246	U
35	TMRN	248	G
35	TMRN	257	U
35	TMRN	258	G
35	TMRN	259	G
35	TMRN	261	G
35	TMRN	262	U
35	TMRN	263	G
35	TMRN	265	C
35	TMRN	267	G
35	TMRN	270	C
35	TMRN	274	G
35	TMRN	280	A
35	TMRN	281	A
35	TMRN	282	G
35	TMRN	283	C
35	TMRN	285	A
35	TMRN	286	A
35	TMRN	288	G
35	TMRN	289	U
35	TMRN	290	A

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Mol	Chain	Res	Type
35	TMRN	291	A
35	TMRN	292	A
35	TMRN	299	C
35	TMRN	300	U
35	TMRN	302	A
35	TMRN	303	G
35	TMRN	308	U
35	TMRN	309	A
35	TMRN	310	G
35	TMRN	315	G
35	TMRN	316	A
35	TMRN	317	G
35	TMRN	318	G
35	TMRN	319	A
35	TMRN	320	U
35	TMRN	321	G
35	TMRN	322	U
35	TMRN	325	G
35	TMRN	330	U
35	TMRN	333	G
35	TMRN	334	A
35	TMRN	335	C
35	TMRN	336	G
35	TMRN	337	C
35	TMRN	338	G
35	TMRN	342	U
35	TMRN	345	A
35	TMRN	346	C
35	TMRN	347	U
35	TMRN	348	C
35	TMRN	358	C
35	TMRN	363	A
36	16S	6	G
36	16S	7	A
36	16S	8	A
36	16S	9	G
36	16S	13	U
36	16S	22	G
36	16S	32	A
36	16S	39	G
36	16S	47	C
36	16S	48	C

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Mol	Chain	Res	Type
36	16S	71	A
36	16S	75	G
36	16S	79	G
36	16S	81	A
36	16S	82	G
36	16S	83	C
36	16S	87	C
36	16S	88	U
36	16S	90	C
36	16S	94	G
36	16S	99	C
36	16S	100	G
36	16S	121	U
36	16S	122	G
36	16S	130	A
36	16S	132	C
36	16S	149	A
36	16S	153	C
36	16S	161	A
36	16S	162	A
36	16S	163	C
36	16S	174	A
36	16S	181	A
36	16S	183	C
36	16S	184	G
36	16S	191	G
36	16S	204	G
36	16S	208	U
36	16S	209	U
36	16S	211	G
36	16S	212	G
36	16S	214	C
36	16S	215	C
36	16S	223	A
36	16S	240	G
36	16S	245	U
36	16S	247	G
36	16S	250	A
36	16S	251	G
36	16S	266	G
36	16S	267	C
36	16S	275	G

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Mol	Chain	Res	Type
36	16S	276	G
36	16S	279	A
36	16S	281	G
36	16S	289	G
36	16S	301	G
36	16S	306	A
36	16S	315	A
36	16S	316	C
36	16S	327	A
36	16S	328	C
36	16S	329	A
36	16S	343	U
36	16S	344	A
36	16S	345	C
36	16S	346	G
36	16S	347	G
36	16S	348	G
36	16S	351	G
36	16S	352	C
36	16S	363	A
36	16S	367	U
36	16S	368	U
36	16S	372	C
36	16S	373	A
36	16S	379	C
36	16S	385	C
36	16S	388	G
36	16S	390	U
36	16S	392	C
36	16S	397	A
36	16S	398	U
36	16S	406	G
36	16S	411	A
36	16S	412	A
36	16S	413	G
36	16S	417	G
36	16S	421	U
36	16S	422	C
36	16S	424	G
36	16S	428	G
36	16S	430	A
36	16S	438	U

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Mol	Chain	Res	Type
36	16S	453	G
36	16S	455	G
36	16S	462	G
36	16S	465	A
36	16S	467	U
36	16S	468	A
36	16S	479	U
36	16S	484	G
36	16S	486	U
36	16S	493	A
36	16S	494	G
36	16S	496	A
36	16S	497	G
36	16S	508	U
36	16S	509	A
36	16S	510	A
36	16S	511	C
36	16S	521	G
36	16S	524	G
36	16S	528	C
36	16S	530	G
36	16S	531	U
36	16S	532	A
36	16S	533	A
36	16S	534	U
36	16S	547	A
36	16S	548	G
36	16S	559	A
36	16S	561	U
36	16S	562	U
36	16S	564	C
36	16S	570	G
36	16S	572	A
36	16S	573	A
36	16S	575	G
36	16S	576	C
36	16S	577	G
36	16S	579	A
36	16S	596	A
36	16S	604	G
36	16S	615	G
36	16S	639	G

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Mol	Chain	Res	Type
36	16S	642	A
36	16S	652	U
36	16S	661	G
36	16S	665	A
36	16S	666	G
36	16S	682	G
36	16S	702	A
36	16S	703	G
36	16S	713	G
36	16S	723	U
36	16S	724	G
36	16S	731	G
36	16S	747	A
36	16S	748	G
36	16S	755	G
36	16S	777	A
36	16S	799	G
36	16S	812	G
36	16S	815	A
36	16S	817	C
36	16S	818	G
36	16S	819	A
36	16S	821	G
36	16S	829	G
36	16S	832	G
36	16S	836	G
36	16S	842	U
36	16S	843	U
36	16S	844	G
36	16S	846	G
36	16S	871	U
36	16S	872	A
36	16S	876	C
36	16S	884	U
36	16S	889	A
36	16S	890	G
36	16S	891	U
36	16S	902	G
36	16S	914	A
36	16S	926	G
36	16S	933	G
36	16S	934	C

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Mol	Chain	Res	Type
36	16S	935	A
36	16S	939	G
36	16S	960	U
36	16S	961	U
36	16S	966	G
36	16S	969	A
36	16S	971	G
36	16S	975	A
36	16S	976	G
36	16S	977	A
36	16S	983	A
36	16S	984	C
36	16S	987	G
36	16S	989	U
36	16S	991	U
36	16S	992	U
36	16S	993	G
36	16S	994	A
36	16S	997	U
36	16S	1004	A
36	16S	1011	C
36	16S	1016	A
36	16S	1017	U
36	16S	1020	G
36	16S	1023	U
36	16S	1026	G
36	16S	1028	C
36	16S	1031	C
36	16S	1033	G
36	16S	1050	G
36	16S	1053	G
36	16S	1067	A
36	16S	1078	U
36	16S	1084	G
36	16S	1085	U
36	16S	1086	U
36	16S	1089	G
36	16S	1094	G
36	16S	1098	C
36	16S	1101	A
36	16S	1108	G
36	16S	1110	A

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Mol	Chain	Res	Type
36	16S	1124	G
36	16S	1125	U
36	16S	1130	A
36	16S	1131	G
36	16S	1132	C
36	16S	1136	C
36	16S	1137	C
36	16S	1138	G
36	16S	1139	G
36	16S	1140	C
36	16S	1145	A
36	16S	1158	C
36	16S	1159	U
36	16S	1160	G
36	16S	1165	U
36	16S	1168	U
36	16S	1169	A
36	16S	1182	G
36	16S	1184	G
36	16S	1191	A
36	16S	1193	G
36	16S	1196	A
36	16S	1197	A
36	16S	1201	A
36	16S	1212	U
36	16S	1215	G
36	16S	1225	A
36	16S	1226	C
36	16S	1227	A
36	16S	1228	C
36	16S	1229	A
36	16S	1238	A
36	16S	1240	U
36	16S	1241	G
36	16S	1249	C
36	16S	1253	G
36	16S	1256	A
36	16S	1258	G
36	16S	1260	G
36	16S	1261	A
36	16S	1274	A
36	16S	1275	A

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Mol	Chain	Res	Type
36	16S	1278	G
36	16S	1279	G
36	16S	1280	A
36	16S	1281	C
36	16S	1282	C
36	16S	1287	A
36	16S	1297	G
36	16S	1300	G
36	16S	1304	G
36	16S	1305	G
36	16S	1310	G
36	16S	1316	G
36	16S	1317	C
36	16S	1318	A
36	16S	1320	C
36	16S	1325	C
36	16S	1336	C
36	16S	1337	G
36	16S	1338	G
36	16S	1346	A
36	16S	1347	G
36	16S	1348	U
36	16S	1363	A
36	16S	1364	U
36	16S	1370	G
36	16S	1379	G
36	16S	1395	C
36	16S	1397	C
36	16S	1398	A
36	16S	1402	C
36	16S	1429	A
36	16S	1442	G
36	16S	1446	A
36	16S	1447	A
36	16S	1448	C
36	16S	1451	U
36	16S	1452	C
36	16S	1453	G
36	16S	1455	G
36	16S	1457	G
36	16S	1461	G
36	16S	1475	G

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Mol	Chain	Res	Type
36	16S	1487	G
36	16S	1492	A
36	16S	1494	G
36	16S	1499	A
36	16S	1502	A
36	16S	1503	A
36	16S	1506	U
36	16S	1507	A
36	16S	1517	G
36	16S	1519	A
36	16S	1529	G
36	16S	1530	G
36	16S	1533	C
36	16S	1534	A
36	16S	1538	C
36	16S	1539	C
36	16S	1540	U
37	ATRN	9	A
37	ATRN	16	C
37	ATRN	17	U
37	ATRN	18	G
37	ATRN	19	G
37	ATRN	20	G
37	ATRN	21	A
37	ATRN	22	G
37	ATRN	25	C
37	ATRN	30	G
37	ATRN	36	C
37	ATRN	46	G
37	ATRN	47	U
37	ATRN	48	C
37	ATRN	58	A
37	ATRN	59	U
37	ATRN	61	C
37	ATRN	62	C
37	ATRN	74	C
37	ATRN	75	C

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	23S	372	G

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Mol	Chain	Res	Type
33	23S	421	C
33	23S	458	G
33	23S	490	C
33	23S	858	G
33	23S	859	G
33	23S	1020	A
33	23S	1865	U
33	23S	1930	G
33	23S	2286	G
33	23S	2326	C
33	23S	2391	G
33	23S	2655	G
33	23S	2756	U
34	5S	42	C
35	TMRN	17	U
35	TMRN	38	A
35	TMRN	60	U
35	TMRN	93	A
35	TMRN	130	C
35	TMRN	212	U
35	TMRN	229	U
35	TMRN	261	G
35	TMRN	290	A
35	TMRN	308	U
35	TMRN	314	C
35	TMRN	334	A
35	TMRN	337	C
36	16S	70	U
36	16S	890	G
36	16S	982	U
36	16S	1190	G
36	16S	1347	G
37	ATRN	16	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

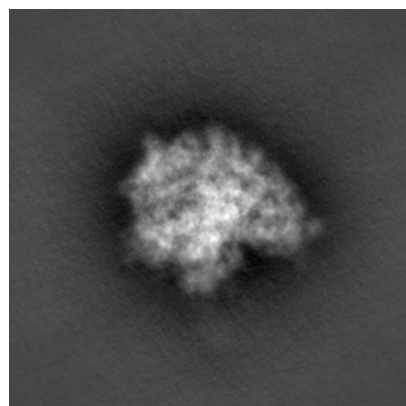
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43491. These allow visual inspection of the internal detail of the map and identification of artifacts.

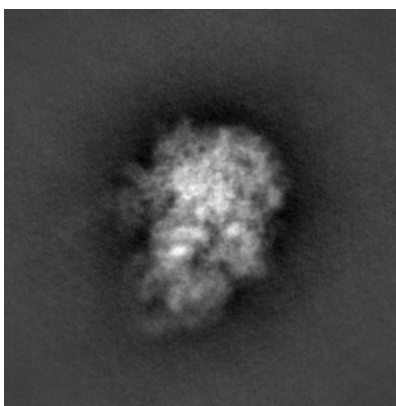
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

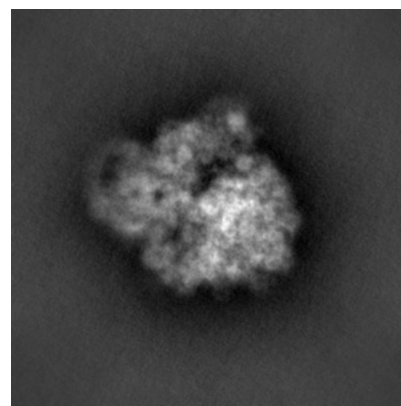
6.1.1 Primary map



X

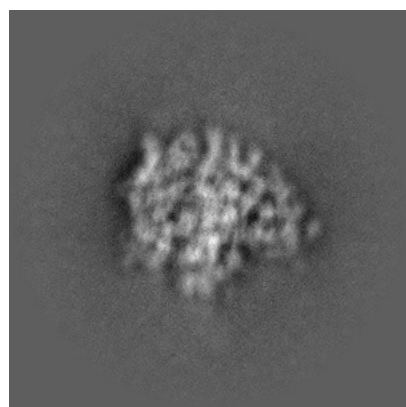


Y

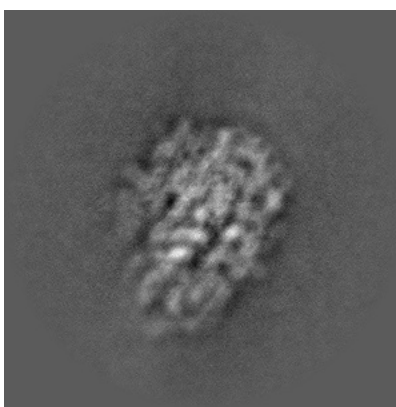


Z

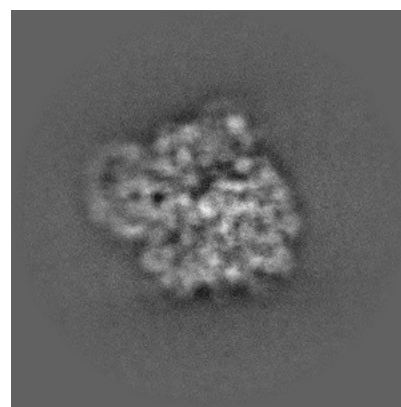
6.1.2 Raw map



X



Y

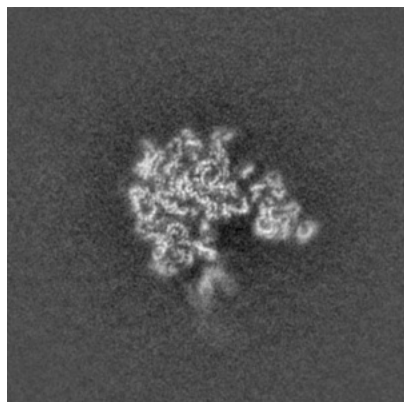


Z

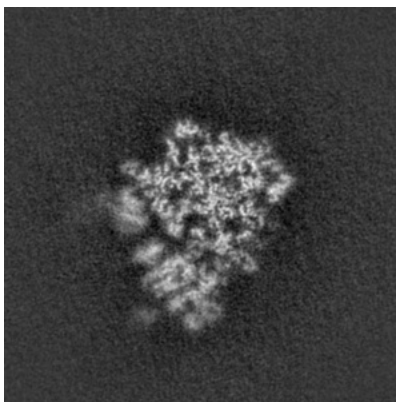
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

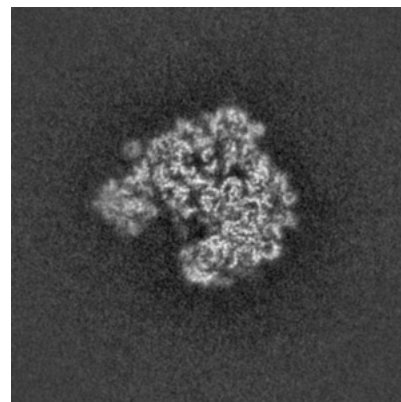
6.2.1 Primary map



X Index: 280

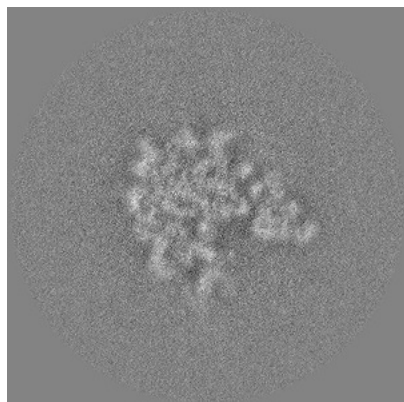


Y Index: 280

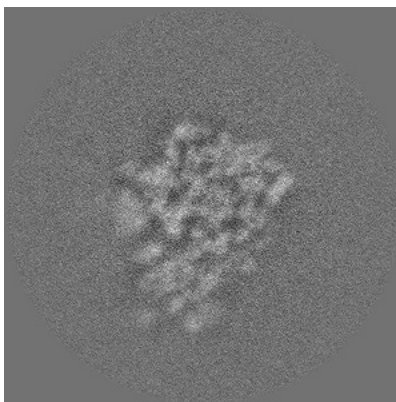


Z Index: 280

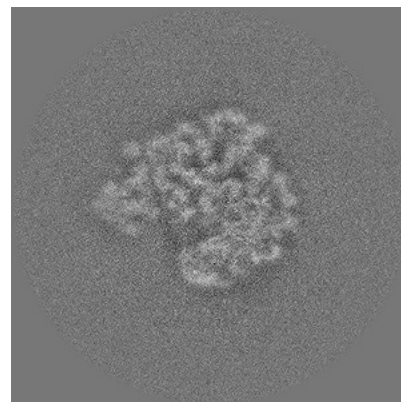
6.2.2 Raw map



X Index: 280



Y Index: 280

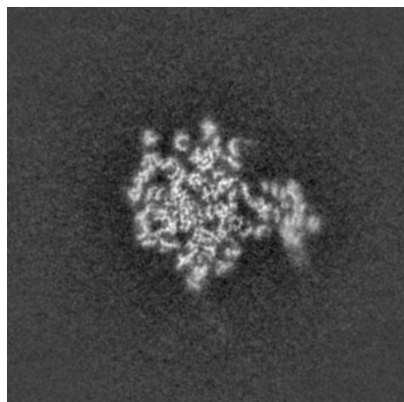


Z Index: 280

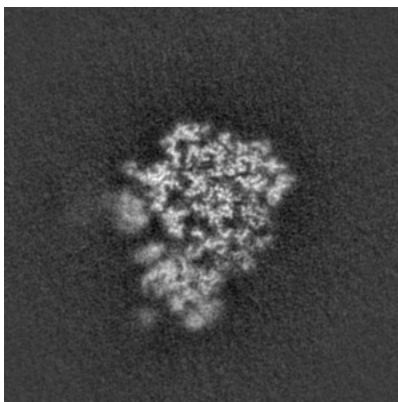
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

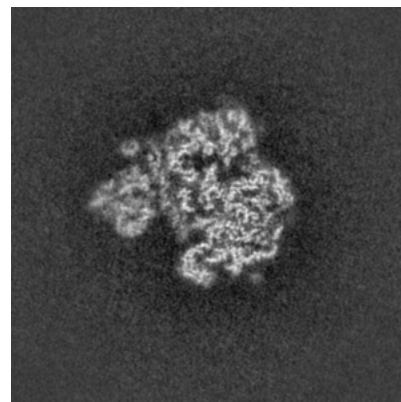
6.3.1 Primary map



X Index: 310

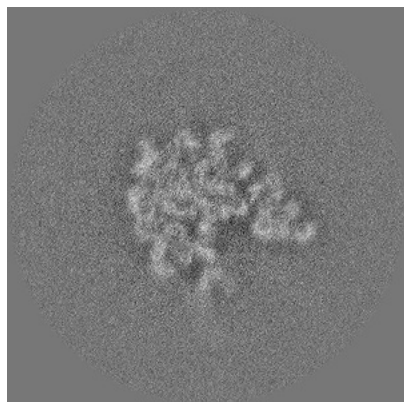


Y Index: 284

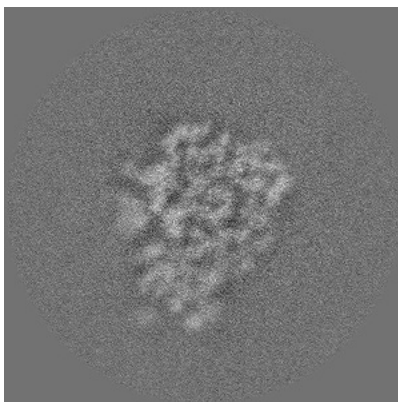


Z Index: 273

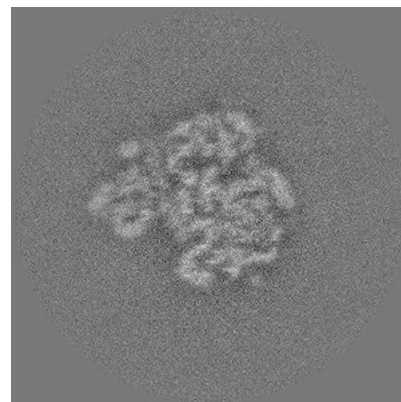
6.3.2 Raw map



X Index: 279



Y Index: 283

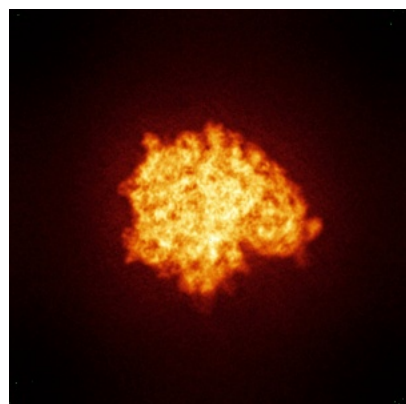


Z Index: 271

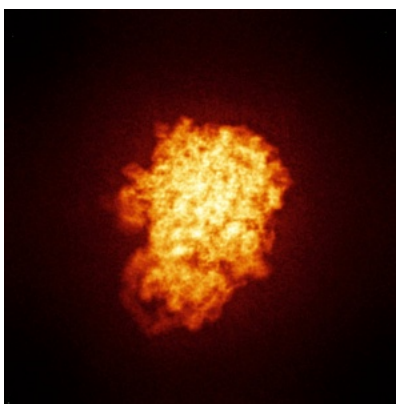
The images above show the largest variance slices of the map in three orthogonal directions.

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

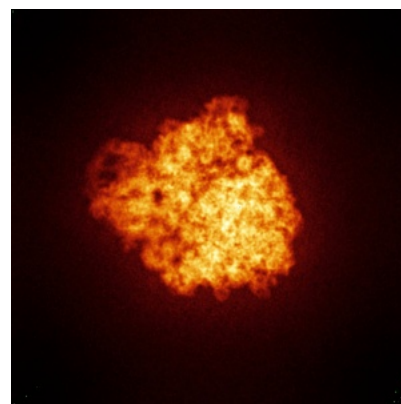
6.4.1 Primary map



X

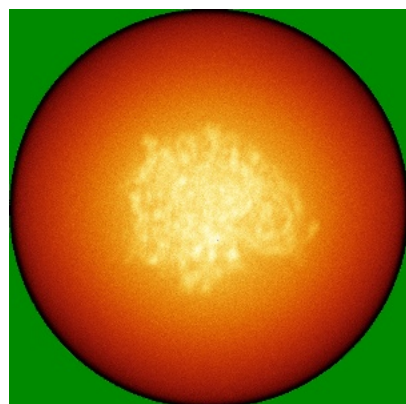


Y

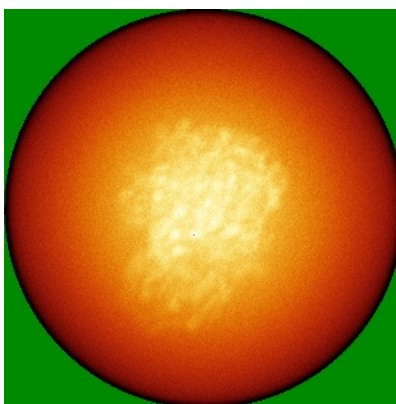


Z

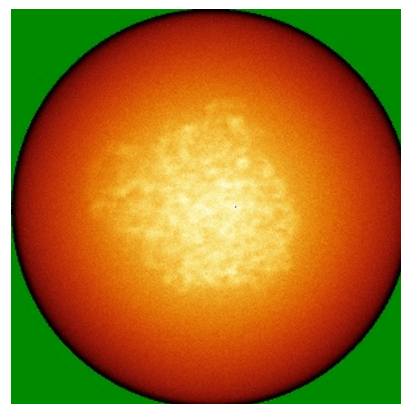
6.4.2 Raw map



X



Y

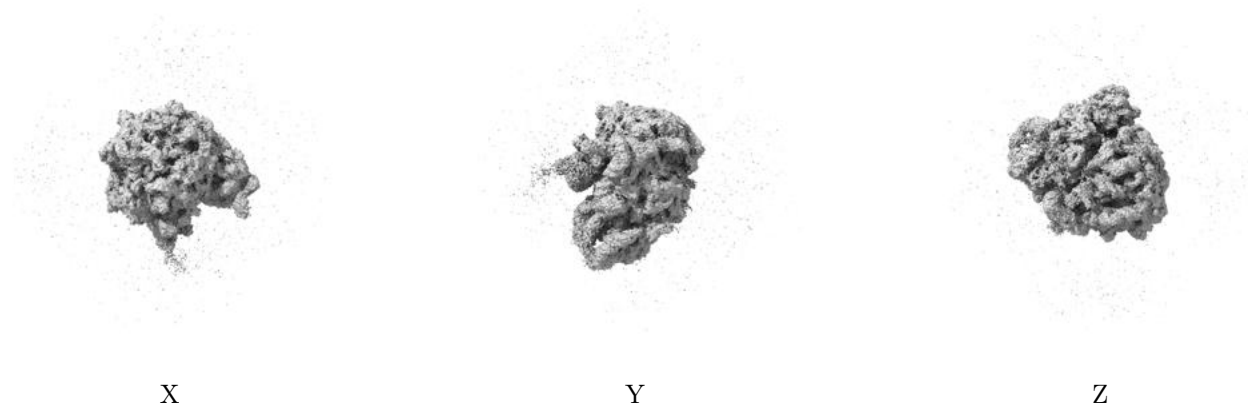


Z

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

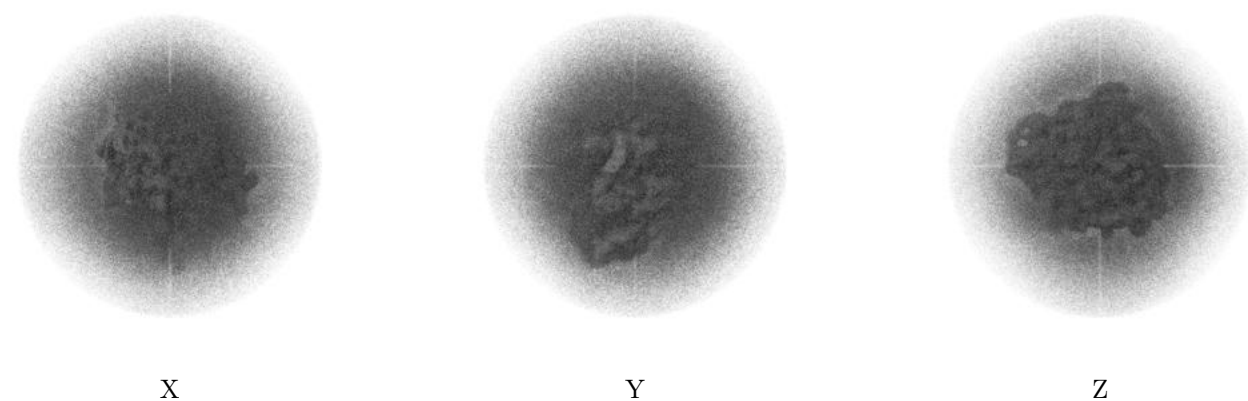
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

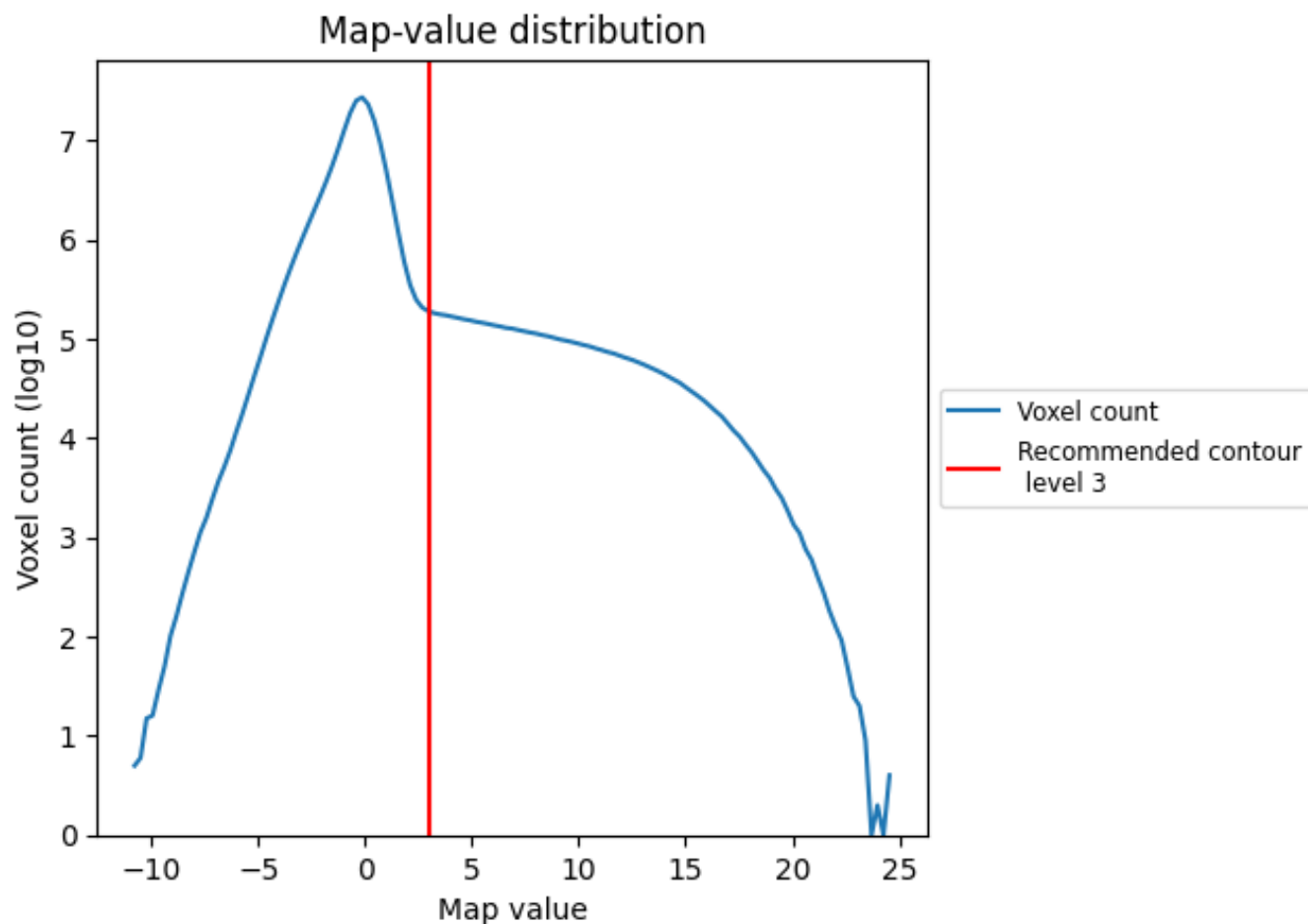
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

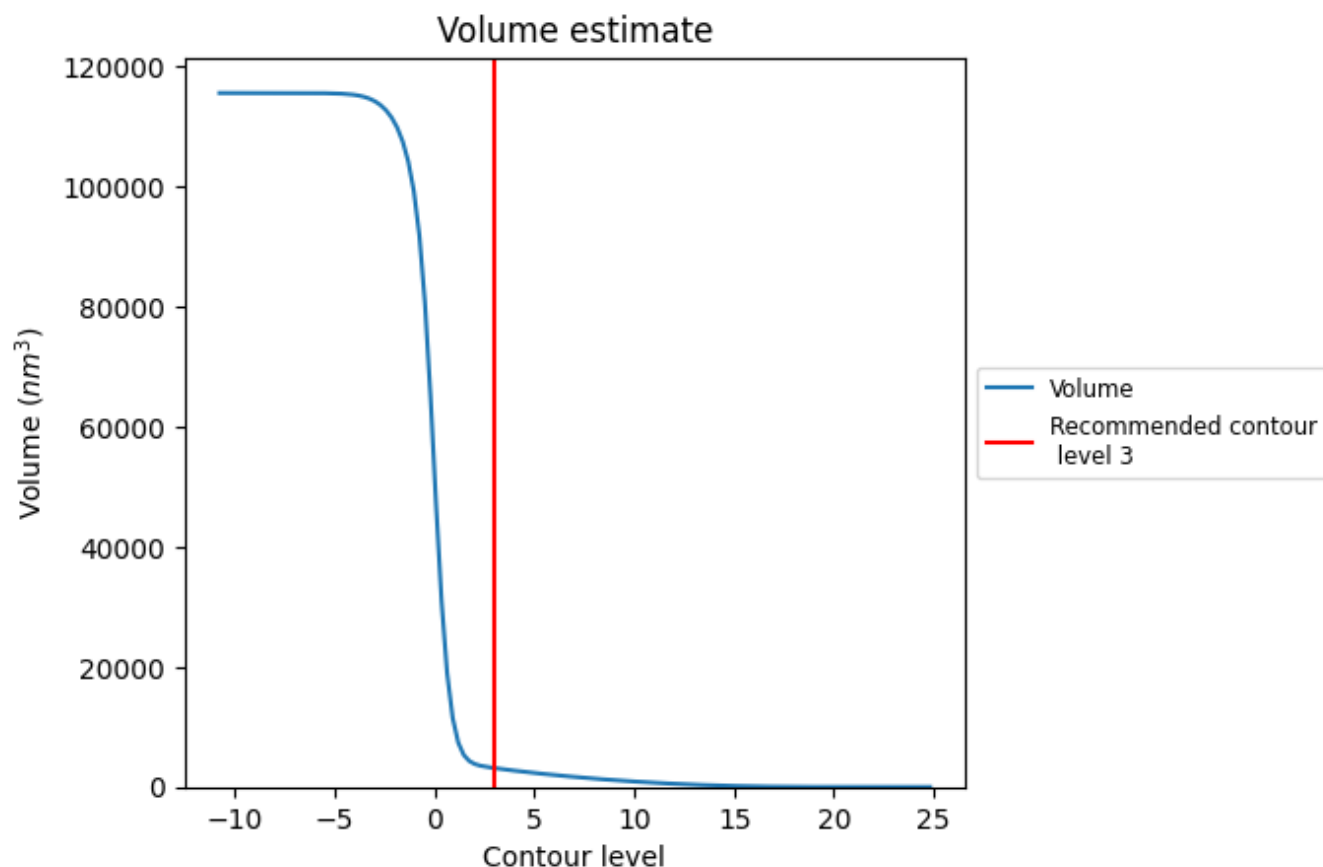
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

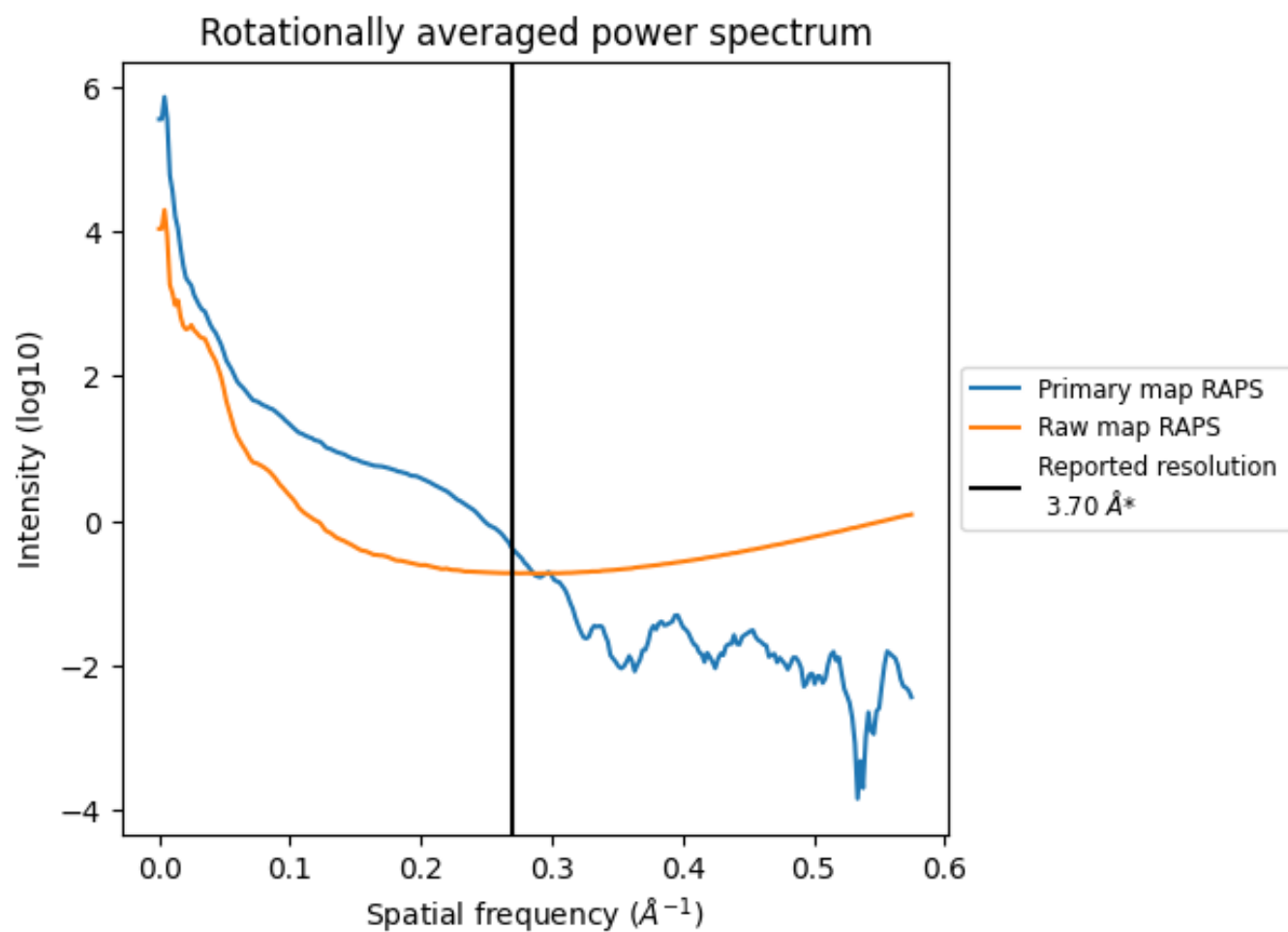
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3143 nm³; this corresponds to an approximate mass of 2839 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

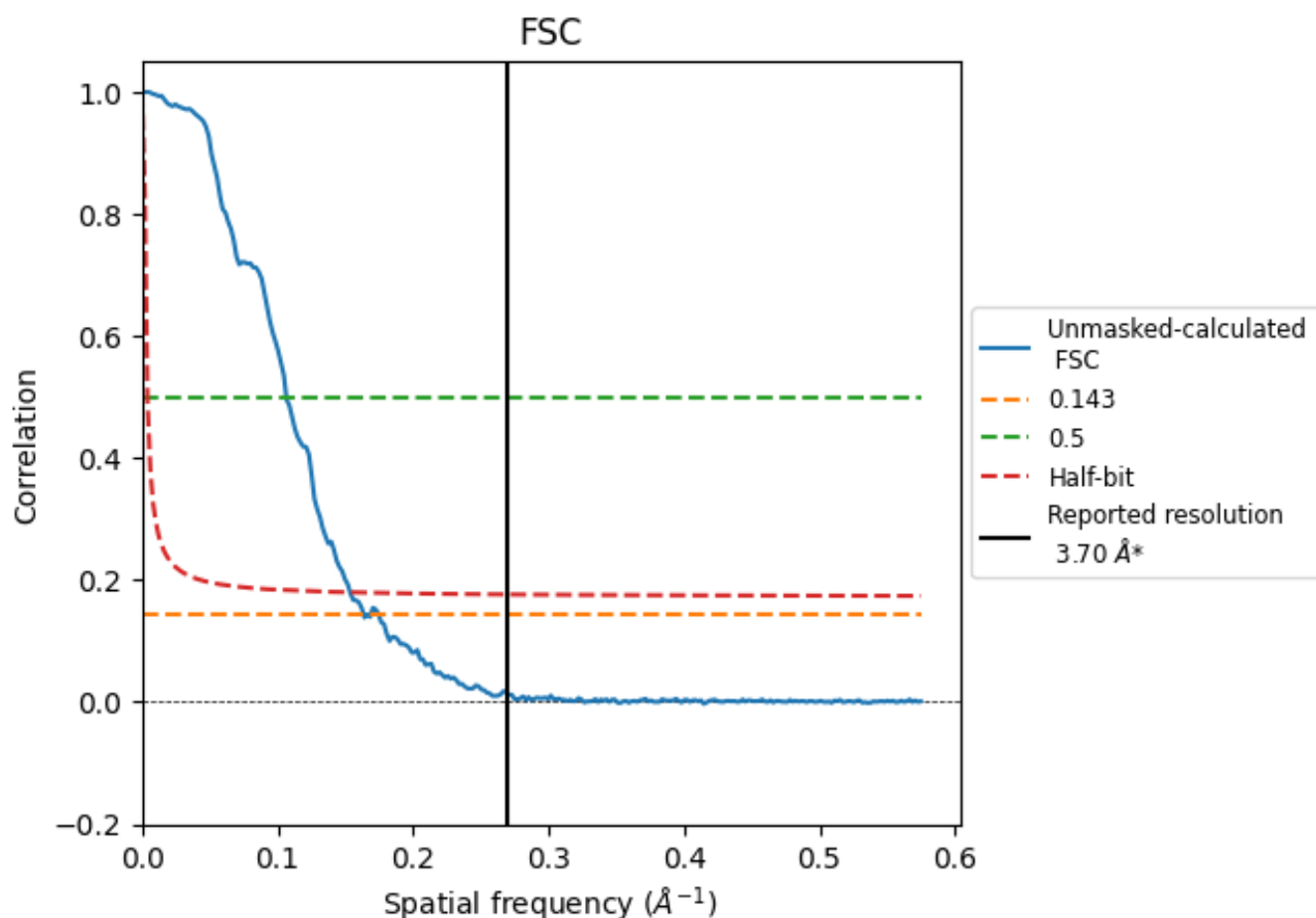


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

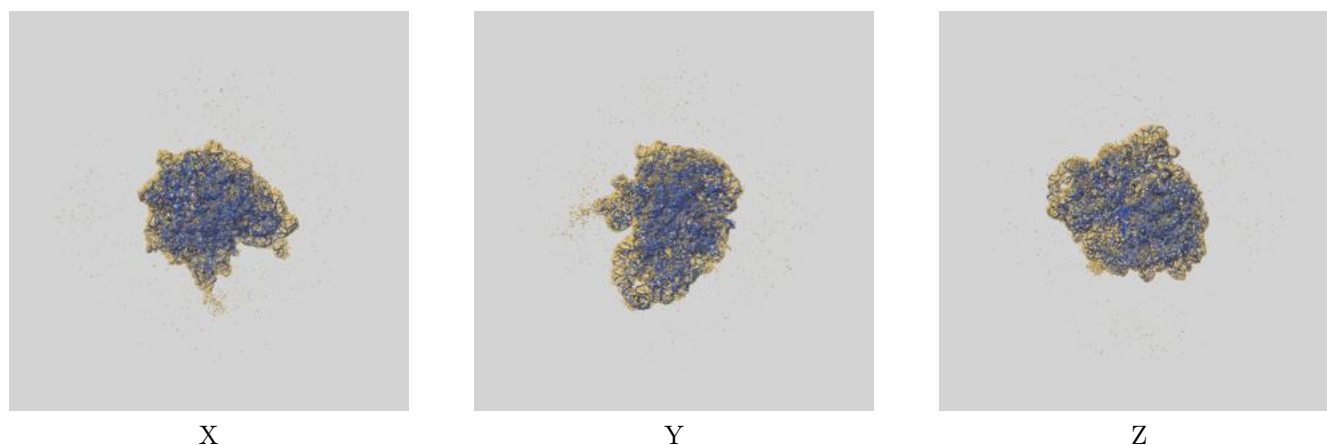
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.12	9.39	6.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.12 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43491 and PDB model 8VSA. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



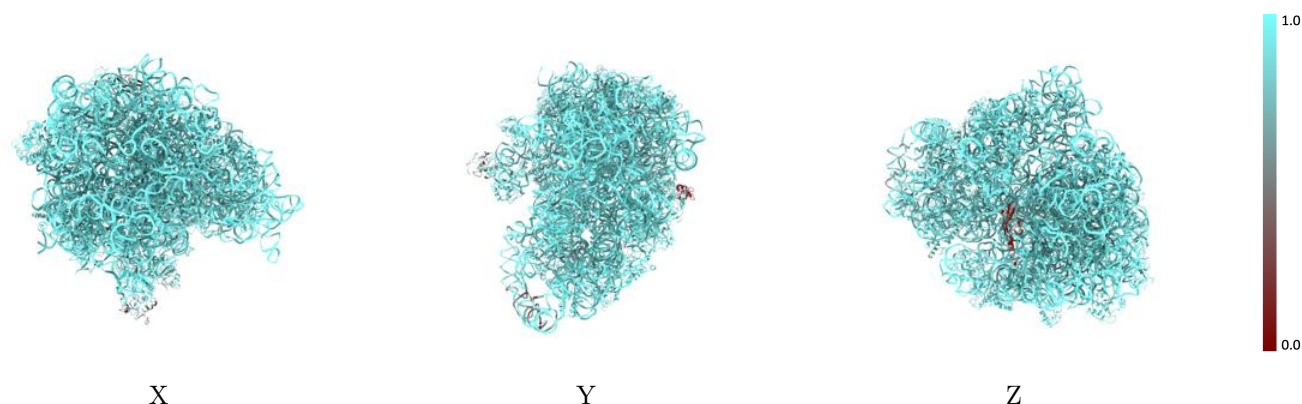
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



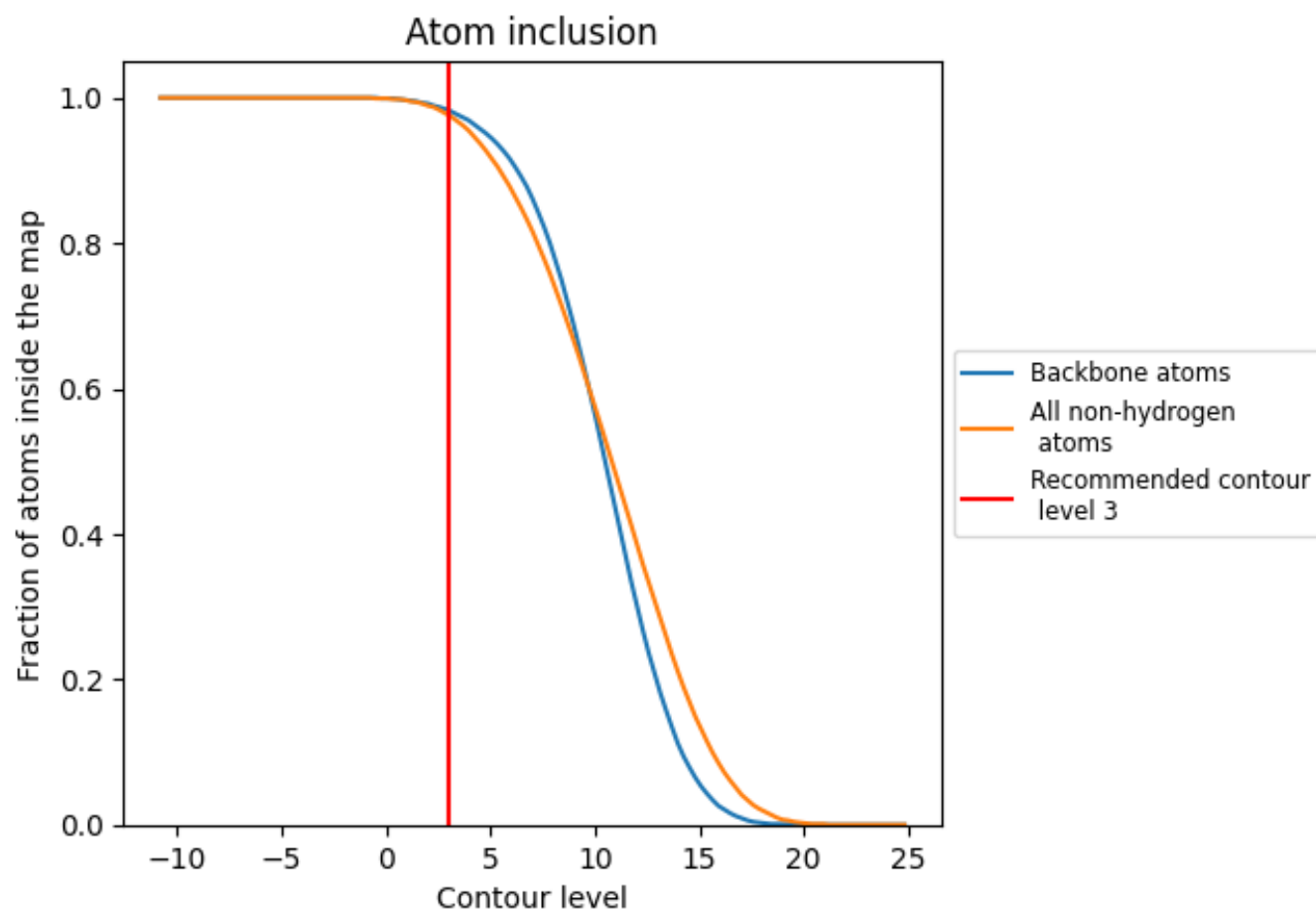
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3).

9.4 Atom inclusion [i](#)



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

Chain	Atom inclusion	Q-score
All	 0.9760	 0.3370
16S	 0.9980	 0.3320
23S	 0.9980	 0.3620
5S	 0.9980	 0.3300
ATRN	 0.9940	 0.3320
L02	 0.9710	 0.3920
L03	 0.9700	 0.3820
L04	 0.9680	 0.3500
L05	 0.9770	 0.2830
L06	 0.9710	 0.3240
L09	 0.4100	 0.2890
L1	 0.8880	 0.2150
L10	 0.7050	 0.1920
L11	 0.8460	 0.1940
L13	 0.9770	 0.3650
L14	 0.9310	 0.3940
L15	 0.9700	 0.3610
L16	 0.9600	 0.3710
L17	 0.9860	 0.3570
L18	 0.9940	 0.3270
L19	 0.9490	 0.3740
L20	 0.9750	 0.3470
L21	 0.9800	 0.3670
L22	 0.9430	 0.3630
L23	 0.9570	 0.3590
L24	 0.9640	 0.3390
L25	 0.9730	 0.3490
L27	 0.9710	 0.3670
L28	 0.9630	 0.3520
L29	 0.9640	 0.3020
L30	 0.9540	 0.3510
L31	 0.9680	 0.2220
L32	 0.9440	 0.3740
L33	 0.9800	 0.3490
L34	 0.9800	 0.3680



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Chain	Atom inclusion	Q-score
L35	 0.9880	 0.3820
L36	 0.9930	 0.3920
S02	 0.9310	 0.3190
S03	 0.9590	 0.3150
S04	 0.9740	 0.2870
S05	 0.9700	 0.3560
S06	 0.9370	 0.3290
S07	 0.9390	 0.2910
S08	 0.9600	 0.3370
S09	 0.9780	 0.2780
S10	 0.9440	 0.3130
S11	 0.9810	 0.3520
S12	 0.9350	 0.3450
S13	 0.9680	 0.2790
S14	 0.9790	 0.2980
S15	 0.9750	 0.3180
S16	 0.9860	 0.3290
S17	 0.9730	 0.3180
S18	 0.9770	 0.3310
S19	 0.9920	 0.3040
S20	 0.9740	 0.2690
S21	 0.9280	 0.3050
SMPB	 0.9220	 0.3130
TMRN	 0.9060	 0.2300