



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 02:53 AM UTC

PDB ID : 8QPP / pdb_00008qpp
EMDB ID : EMD-18558
Title : Bacillus subtilis MutS2-collided disome complex (stalled 70S)
Authors : Park, E.; Mackens-Kiani, T.; Berhane, R.; Esser, H.; Erdenebat, C.; Burroughs, A.M.; Berninghausen, O.; Aravind, L.; Beckmann, R.; Green, R.; Buskirk, A.R.
Deposited on : 2023-10-02
Resolution : 3.40 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 : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

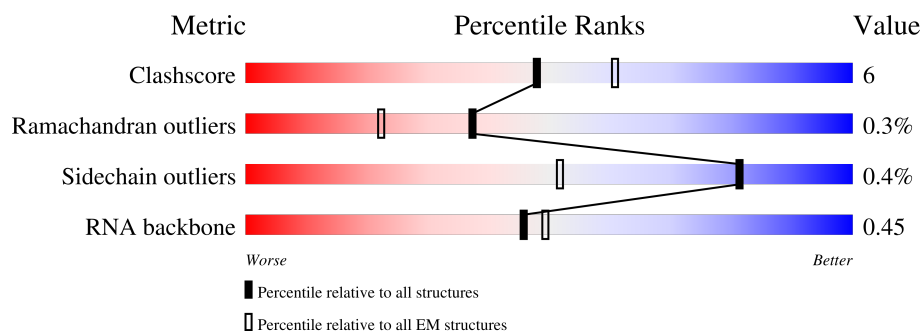
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



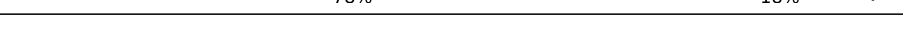
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	59	
2	1	48	
3	2	44	
4	3	66	
5	4	37	
6	6	64	
7	B	246	

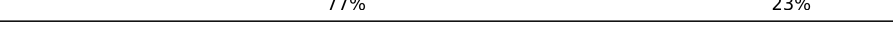
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Mol	Chain	Length	Quality of chain
8	C	218	
9	D	200	
10	E	166	
11	F	95	
12	G	156	
13	H	132	
14	I	130	
15	J	102	
16	K	131	
17	L	138	
18	M	121	
19	N	61	
20	O	89	
21	P	90	
22	Q	87	
23	R	79	
24	S	92	
25	T	88	
26	U	77	
27	V	33	
28	W	785	
29	Y	112	
30	Z	275	
31	a	207	
32	b	205	

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Mol	Chain	Length	Quality of chain
33	c	178	 70% 26% ..
34	d	175	 80% 20%
35	e	142	 75% 24% .
36	f	122	 75% 25%
37	i	146	 90% 10%
38	j	138	 78% 20% ..
39	k	119	 87% 13%
40	l	120	 82% 18%
41	m	115	 88% 12%
42	n	117	 82% 18%
43	o	101	 81% 19%
44	r	109	 81% 19%
45	s	93	 80% 17% .
46	t	101	 77% 23%
47	u	82	 84% 16%
48	v	58	 76% 24%
49	w	65	 66% 34%
50	x	58	 81% 19%
51	9	149	 60% 34% 6%
52	X	2928	 65% 27% 7% .
53	A	1533	 62% 30% 8%

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 237112 atoms, of which 94493 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 L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	54	Total	C	H	N	O	S	0	0
			872	262	446	86	71	7		

- Molecule 2 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	48	Total	C	H	N	O	S	0	0
			815	244	413	80	74	4		

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	44	Total	C	H	N	O	S	0	0
			778	222	410	89	55	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	64	Total	C	H	N	O	S	0	0
			1075	321	563	107	82	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	48	SER	ALA	conflict	UNP A0A063XFQ7

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	37	Total	C	H	N	O	S	0	0
			639	186	342	60	46	5		

- Molecule 6 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	6	63	Total	C	H	N	O	S	0	0
			990	312	491	91	91	5		

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	218	Total	C	H	N	O	S	0	0
			3588	1119	1831	309	323	6		

- Molecule 8 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C	206	Total	C	H	N	O	S	0	0
			3278	1011	1659	304	301	3		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	195	Total	C	H	N	O	S	0	0
			3174	991	1605	291	285	2		

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	164	Total	C	H	N	O	S	0	0
			2520	767	1301	225	225	2		

- Molecule 11 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	92	Total	C	H	N	O	S	0	0
			1502	476	747	132	146	1		

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	149	Total	C	H	N	O	S	0	0
			2417	740	1236	220	215	6		

- Molecule 13 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	H	131	Total	C	H	N	O	S	0	0
			2133	655	1096	191	188	3		

- Molecule 14 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	I	125	Total	C	H	N	O	S	0	0
			1972	599	1006	191	175	1		

- Molecule 15 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	J	95	Total	C	H	N	O	S	0	0
			1557	479	796	139	141	2		

- Molecule 16 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	K	114	Total	C	H	N	O	S	0	0
			1694	516	855	164	157	2		

- Molecule 17 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	L	136	Total	C	H	N	O	S	0	0
			2164	653	1112	211	186	2		

- Molecule 18 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	M	108	Total	C	H	N	O		0	0
			1794	534	926	176	158			

- Molecule 19 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	N	60	Total	C	H	N	O	S	0	0
			1030	317	532	98	78	5		

- Molecule 20 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	O	85	Total	C	H	N	O	S	0	0
			1446	436	736	144	129	1		

- Molecule 21 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	P	88	Total	C	H	N	O	S	0	0
			1417	441	722	128	124	2		

- Molecule 22 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	Q	84	Total	C	H	N	O	S	0	0
			1420	435	729	128	126	2		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	R	64	Total	C	H	N	O	S	0	0
			1074	332	556	96	88	2		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	S	78	Total	C	H	N	O	S	0	0
			1283	409	650	112	110	2		

- Molecule 25 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	T	83	Total	C	H	N	O	S	0	0
			1334	390	697	130	116	1		

- Molecule 26 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
26	U	77	Total	C	H	N	O	P	0	0
			2474	731	831	290	545	77		

- Molecule 27 is a RNA chain called mRNA (33-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
27	V	33	Total	C	H	N	O	P	0	0
			1063	315	359	130	226	33		

- Molecule 28 is a protein called Endonuclease MutS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	W	86	Total	C	H	N	O		0	0
			1335	411	673	124	127			

- Molecule 29 is a RNA chain called 5S rRNA (112-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Y	112	Total	C	H	N	O	P	0	0
			3605	1068	1213	435	778	111		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Z	272	Total	C	H	N	O	S	0	0
			4254	1296	2171	408	373	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	206	Total	C	H	N	O	S	0	0
			3209	985	1640	289	290	5		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	205	Total	C	H	N	O	S	0	0
			3211	980	1649	289	291	2		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	176	Total	C	H	N	O	S	0	0
			2835	882	1449	241	256	7		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	175	Total	C	H	N	O	S	0	0
			2734	835	1391	248	258	2		

- Molecule 35 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	142	Total	C	H	N	O	S	0	0
			2289	710	1165	206	203	5		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	122	Total	C	H	N	O	S	0	0
			1898	571	977	173	173	4		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	i	146	Total	C	H	N	O	S	0	0
			2214	671	1132	207	202	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	j	135	Total	C	H	N	O	S	0	0
			2221	690	1145	205	176	5		

- Molecule 39 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	k	119	Total	C	H	N	O	S	0	0
			1940	583	986	186	181	4		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	l	120	Total	C	H	N	O	S	0	0
			1860	564	947	176	172	1		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	m	115	Total	C	H	N	O	S	0	0
			1965	600	1020	185	159	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	n	117	Total	C	H	N	O	S	0	0
			1948	591	1007	189	157	4		

- Molecule 43 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	o	101	Total	C	H	N	O	S	0	0
			1616	501	829	139	147			

- Molecule 44 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	r	109	Total	C	H	N	O	S	0	0
			1745	525	902	164	151	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	s	90	Total	C	H	N	O	S	0	0
			1496	452	771	134	136	3		

- Molecule 46 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	t	101	Total	C	H	N	O	S	0	0
			1584	478	821	142	139	4		

- Molecule 47 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	u	82	Total	C	H	N	O	S	0	0
			1278	390	647	123	118			

- Molecule 48 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	v	58	Total	C	H	N	O	S	0	0
			935	275	490	92	76	2		

- Molecule 49 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	w	65	Total	C	H	N	O	S	0	0
			1099	328	568	102	99	2		

- Molecule 50 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	x	58	Total	C	H	N	O	S	0	0
			950	281	494	89	85	1		

- Molecule 51 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	9	149	Total	C	N	O	0	0
			733	435	149	149		

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	X	2887	Total	C	H	N	O	P	0	0
			93205	27661	31200	11460	19998	2886		

- Molecule 53 is a RNA chain called 16S rRNA (1533-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
53	A	1533	Total	C	H	N	O	P	0	0
			49450	14667	16559	6034	10657	1533		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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 L32

Chain 0:  73% 19% 8%

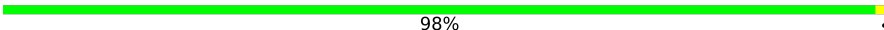


- Molecule 2: Large ribosomal subunit protein bL33

Chain 1:  71% 29%



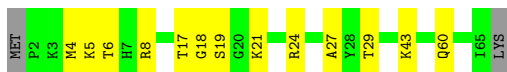
- Molecule 3: Large ribosomal subunit protein bL34

Chain 2:  98%



- Molecule 4: Large ribosomal subunit protein bL35

Chain 3:  77% 20%



- Molecule 5: 50S ribosomal protein L36

Chain 4:  54% 46%



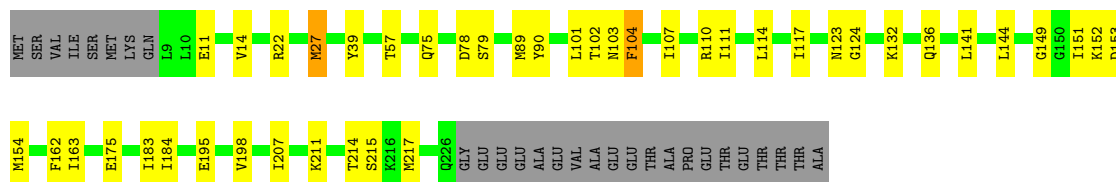
- Molecule 6: Large ribosomal subunit protein bL31

Chain 6:  83% 14%



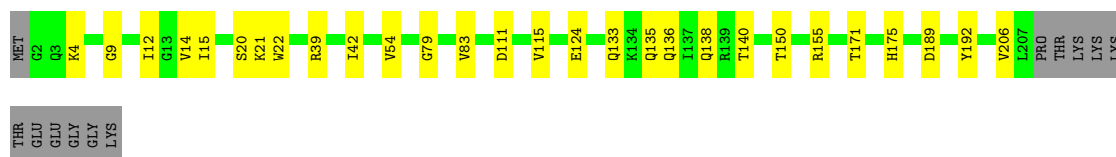
- Molecule 7: 30S ribosomal protein S2

Chain B: 71% 17% 11%



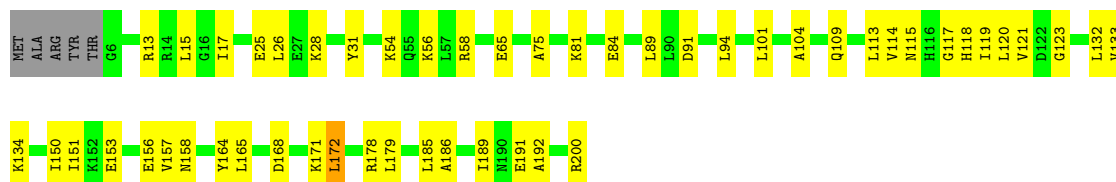
- Molecule 8: 30S ribosomal protein S3

Chain C: 82% 13% 6%



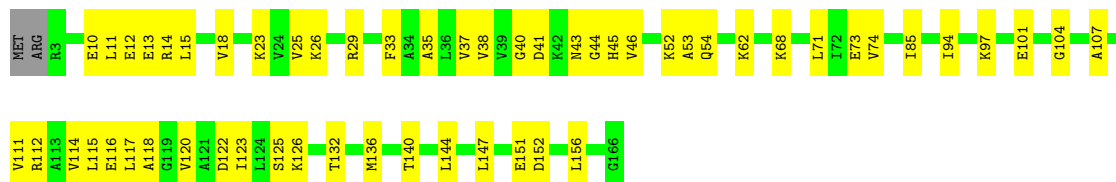
- Molecule 9: 30S ribosomal protein S4

Chain D: 72% 25% 3%



- Molecule 10: 30S ribosomal protein S5

Chain E: 66% 33% 1%

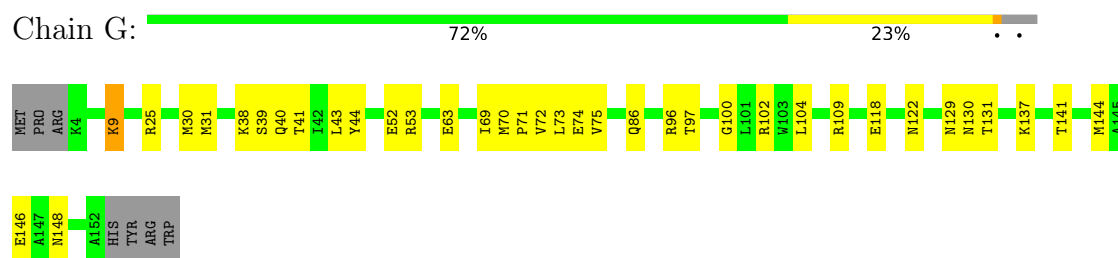


- Molecule 11: 30S ribosomal protein S6

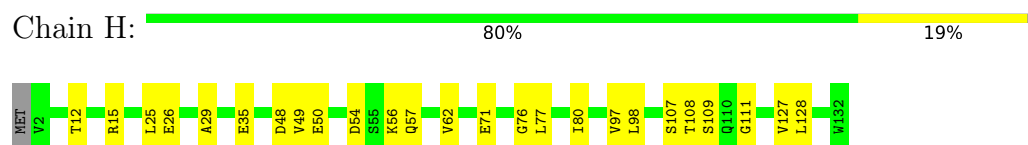
Chain F: 69% 27% 4%



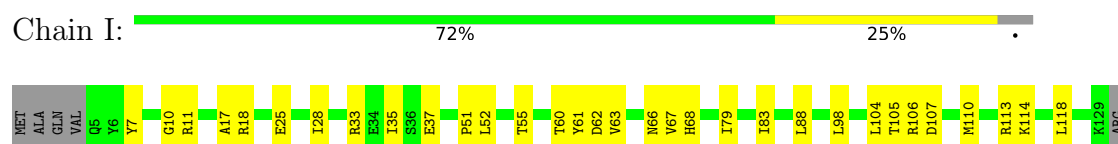
- Molecule 12: 30S ribosomal protein S7



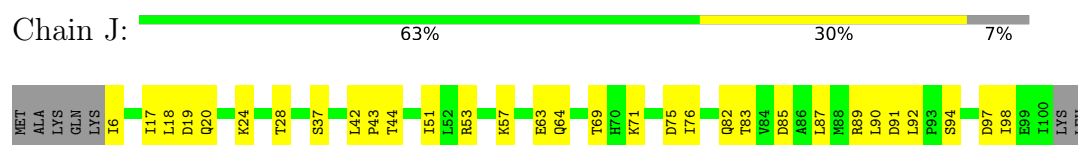
- Molecule 13: 30S ribosomal protein S8



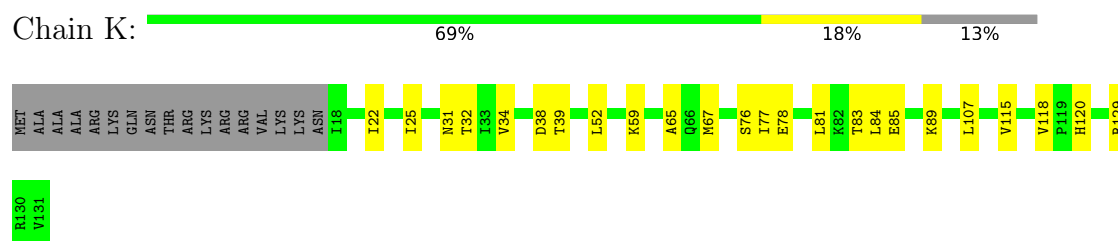
- Molecule 14: 30S ribosomal protein S9



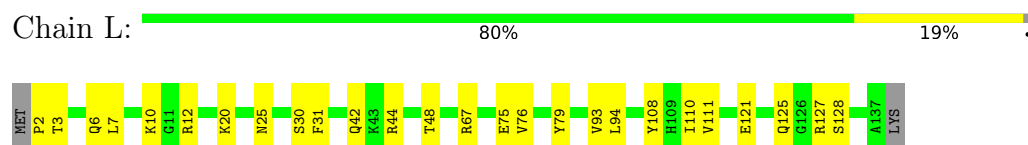
- Molecule 15: 30S ribosomal protein S10



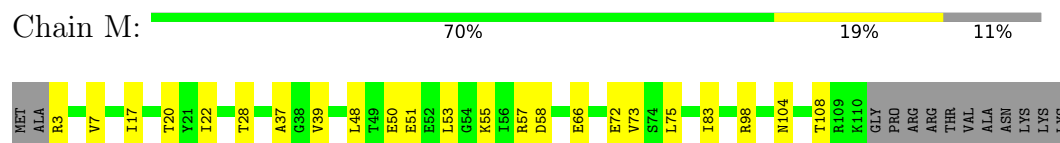
- Molecule 16: 30S ribosomal protein S11



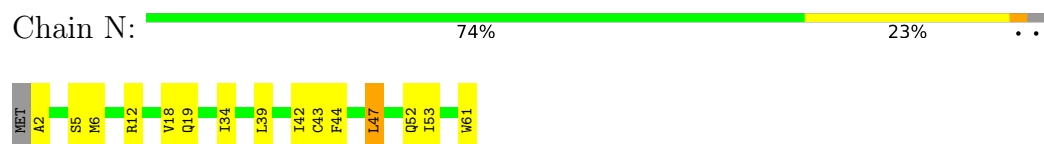
- Molecule 17: 30S ribosomal protein S12



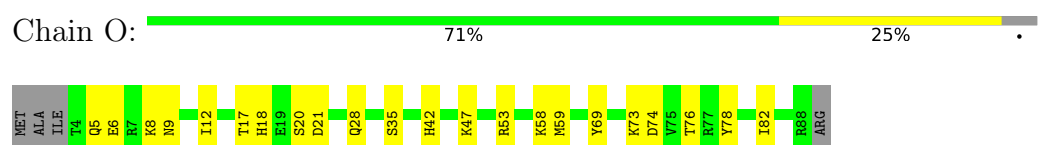
- Molecule 18: 30S ribosomal protein S13



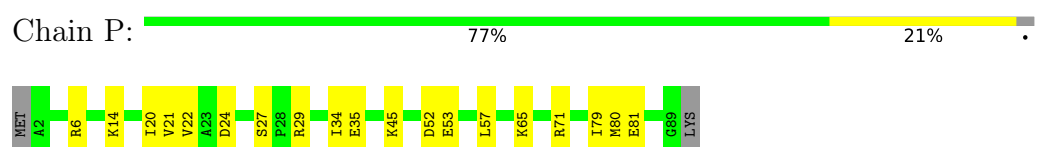
- Molecule 19: 30S ribosomal protein S14 type Z



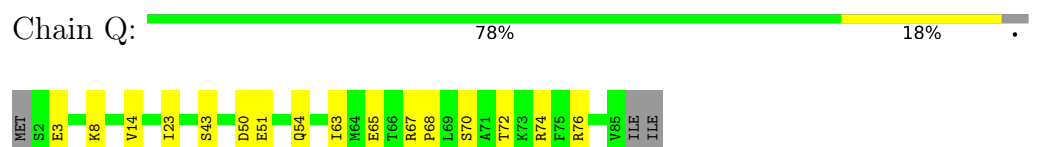
- Molecule 20: 30S ribosomal protein S15



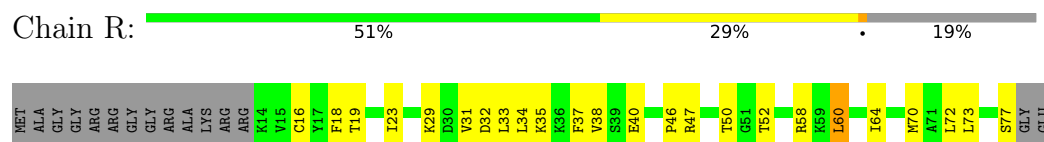
- Molecule 21: 30S ribosomal protein S16



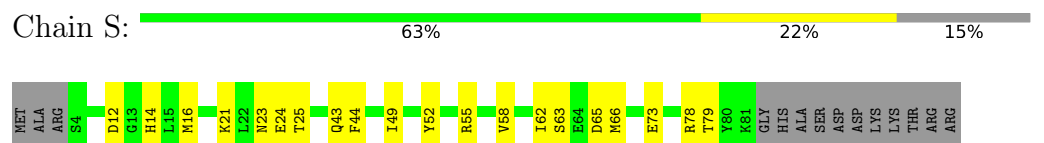
- Molecule 22: 30S ribosomal protein S17



- Molecule 23: 30S ribosomal protein S18

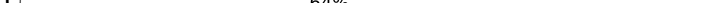


- Molecule 24: 30S ribosomal protein S19

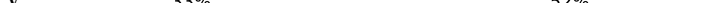


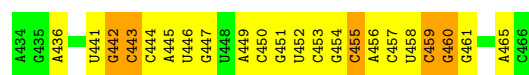
- Molecule 25: 30S ribosomal protein S20

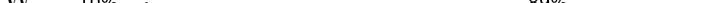


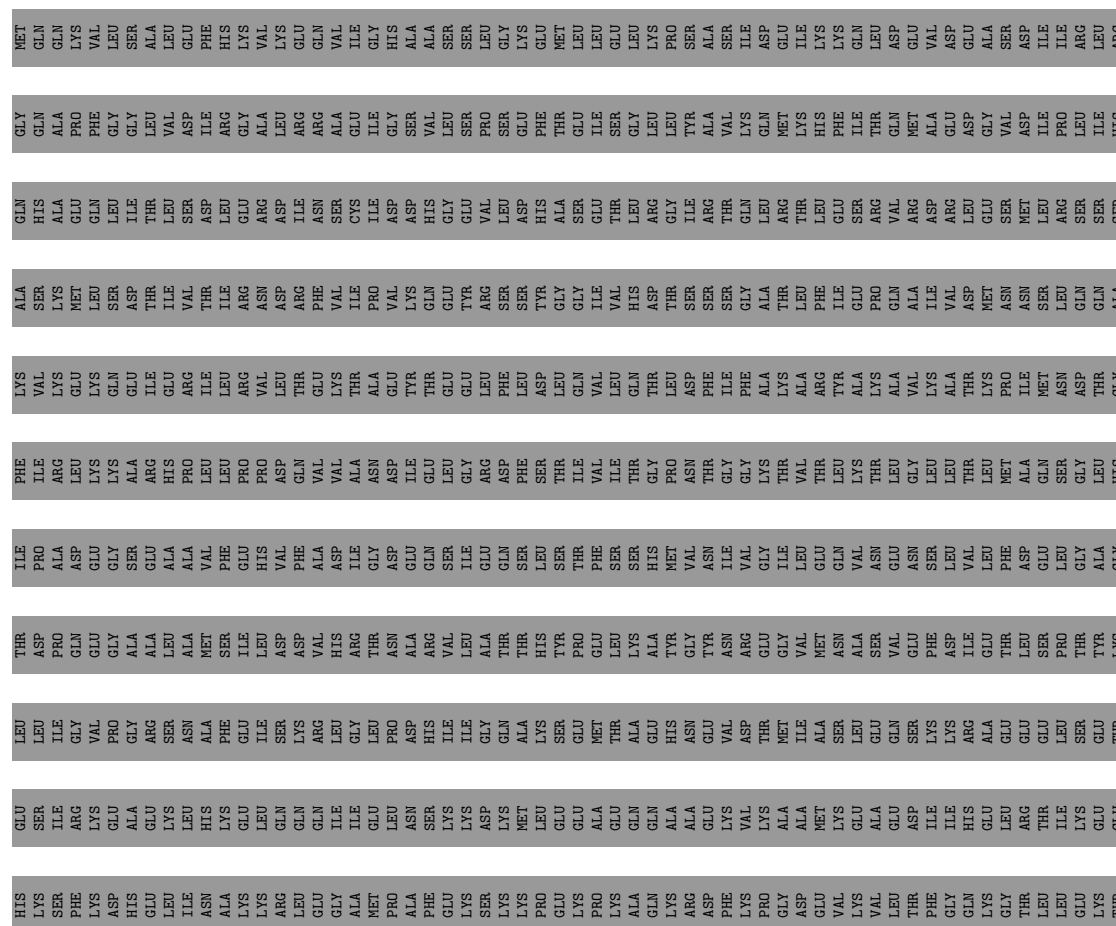
- Chain U:  64% 27% 9%

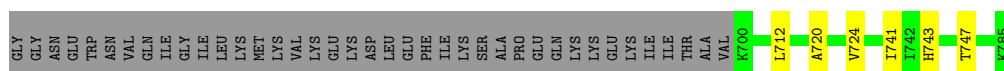


- Chain V:  33% 52% 15%



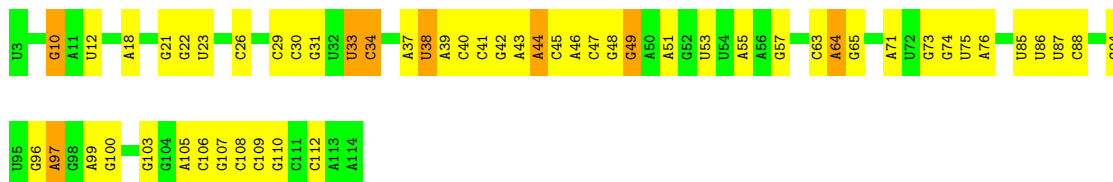
- Chain W:  10% 89%





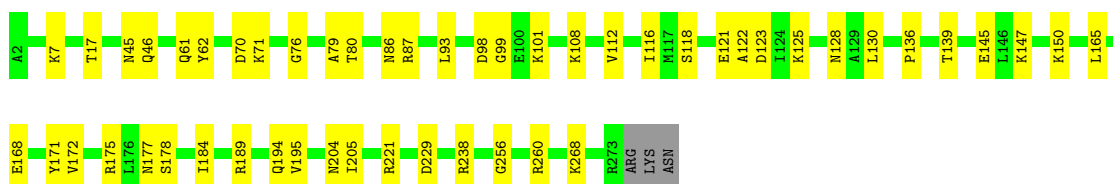
• Molecule 29: 5S rRNA (112-MER)

Chain Y: 52% 41% 7%



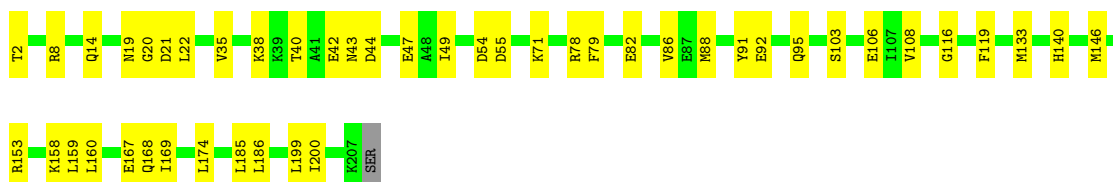
• Molecule 30: Large ribosomal subunit protein uL2

Chain Z: 80% 19%



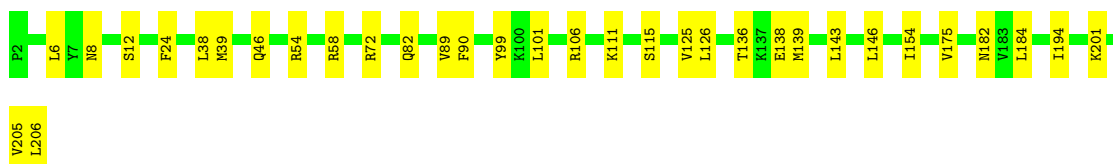
• Molecule 31: Large ribosomal subunit protein uL3

Chain a: 77% 22%



• Molecule 32: Large ribosomal subunit protein uL4

Chain b: 84% 16%



• Molecule 33: Large ribosomal subunit protein uL5

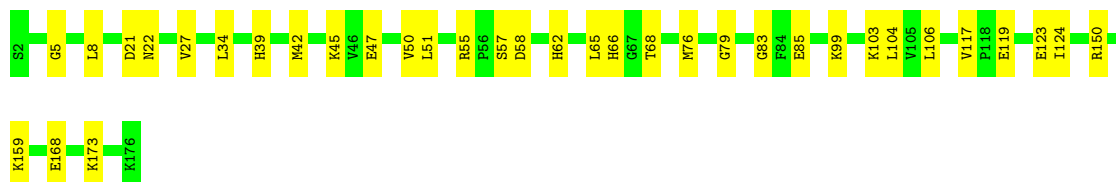
Chain c: 70% 26%





- Molecule 34: Large ribosomal subunit protein uL6

Chain d: 80% 20%



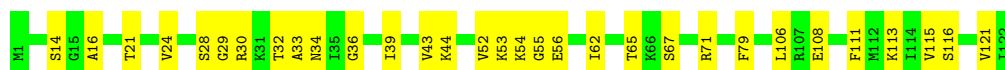
- Molecule 35: Large ribosomal subunit protein uL13

Chain e: 75% 24%



- Molecule 36: 50S ribosomal protein L14

Chain f: 75% 25%



- Molecule 37: 50S ribosomal protein L15

Chain i: 90% 10%



- Molecule 38: Large ribosomal subunit protein uL16

Chain j: 78% 20%

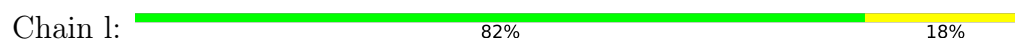


- Molecule 39: Large ribosomal subunit protein bL17

Chain k: 87% 13%



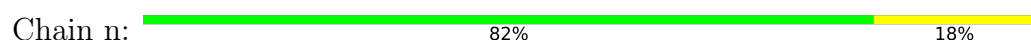
- Molecule 40: 50S ribosomal protein L18



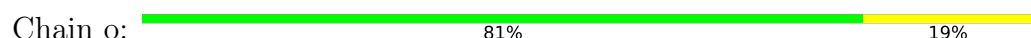
- Molecule 41: 50S ribosomal protein L19



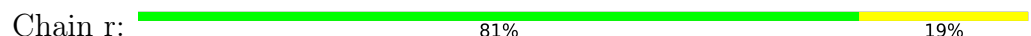
- Molecule 42: Large ribosomal subunit protein bL20



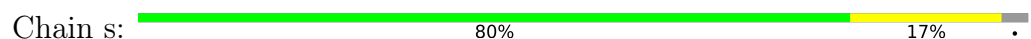
- Molecule 43: Large ribosomal subunit protein bL21



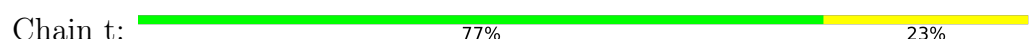
- Molecule 44: Large ribosomal subunit protein uL22

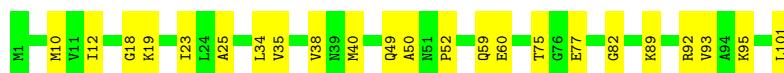


- Molecule 45: Large ribosomal subunit protein uL23

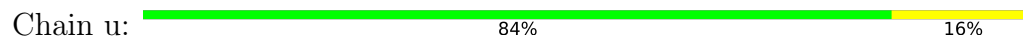


- Molecule 46: Large ribosomal subunit protein uL24

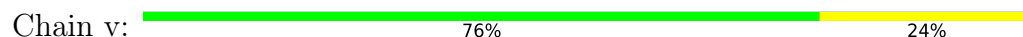




- Molecule 47: Large ribosomal subunit protein bL27



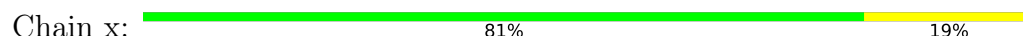
- Molecule 48: Large ribosomal subunit protein bL28



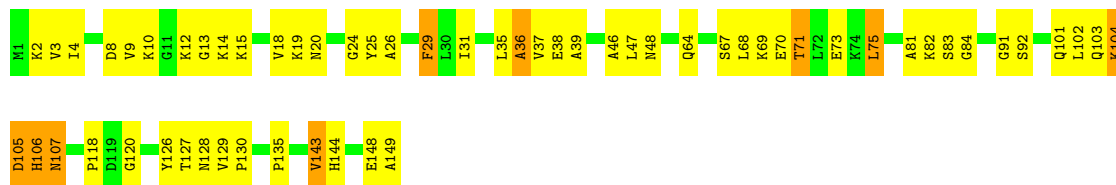
- Molecule 49: Large ribosomal subunit protein uL29



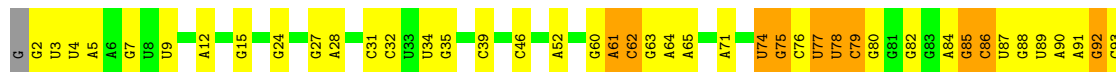
- Molecule 50: Large ribosomal subunit protein uL30



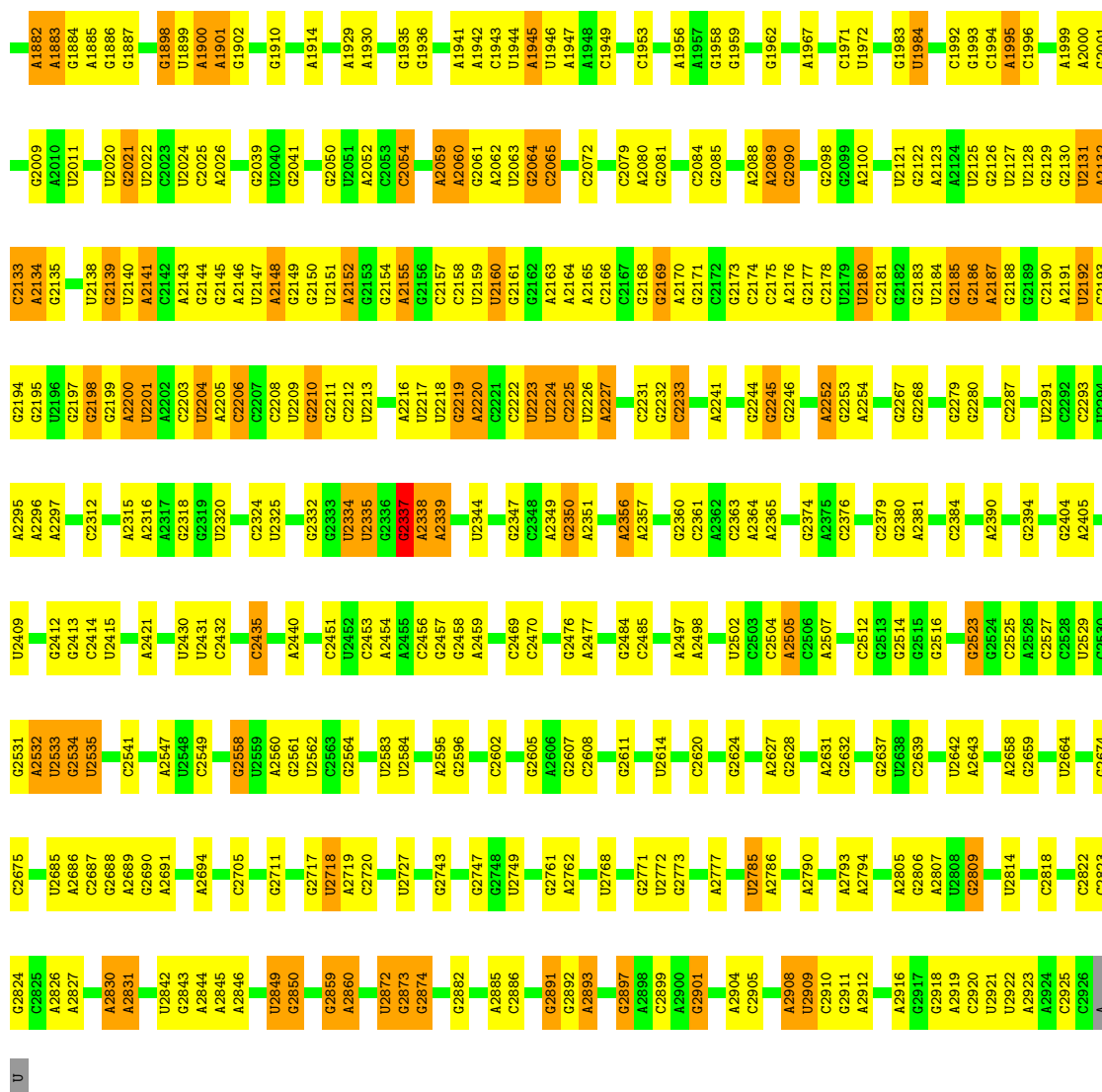
- Molecule 51: 50S ribosomal protein L9



- Molecule 52: 23S ribosomal RNA

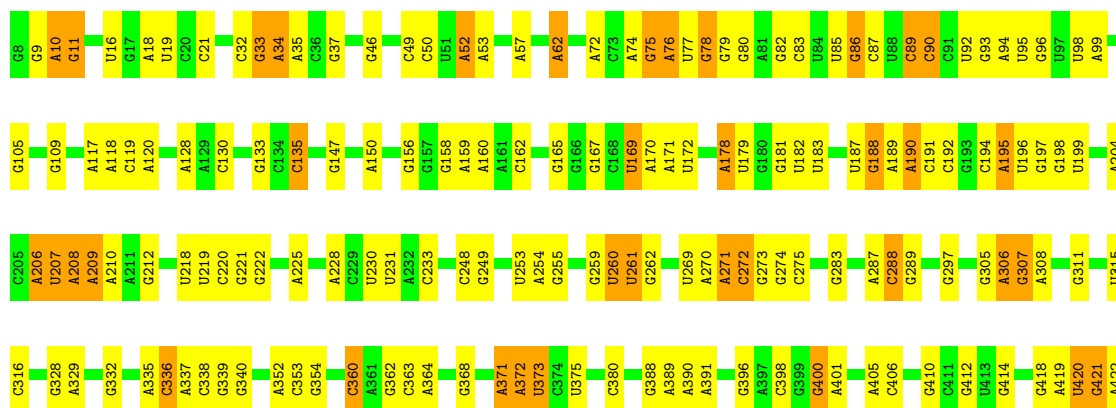


G1742	A1743	G1744	A1745	G1757	U1758	U1759	A1760	G1761	U1764	G1765	C1766	A1767	U1774	G1775	A1776	G1779	G1792	G1793	A1797	A1802	U1808	C1811	A1812	A1813	A1820	G1828	C1829	G1830	A1831	A1832	G1836	U1837	A1838	A1839	A1845	G1846	U1847	A1848	U1856	G1857	A1858	C1872	U1877							
A	G1589	A1592	C1598	U1599	G1600	U1601	C1602	U1605	A1617	A1618	U1626	G1630	A1631	G1632	G1633	C1645	A1653	A1654	A1655	C1683	C1693	G1694	A1695	G1696	A1697	A1698	A1699	U1704	G1710	G1711	G1712	A1713	G1715	U1716	G1717	G1718	G1719	G	A1727	G1732	U1733	A1734	U1738	U1739	C1741					
U1136	G1137	C1138	G1139	U1140	A1141	A1142	U1143	A1144	G1145	C1146	U1147	C1148	U1151	U1154	C1155	G1156	A1157	G1158	U1159	G1160	A1161	G1166	G1171	A1172	U1176	G1177	U1178	A1179	C1180	C1181	G1182	G1183	G1184	C1186	U1187	A1188	A1201	U1215	C1216	U	U	C	G1220	G1227	U1236	C1241	C1248			
C1256	G1402	G1403	A1404	A1405	A1406	G1410	U1411	A1417	U1418	A1423	A1424	C1425	A1426	G1427	U1433	A1434	U1435	U1436	C1437	A1442	C1449	C1450	U1451	C1452	A1453	C1454	G1455	U1456	U1457	U1458	U1459	G1460	A1461	G1462	U1465	U1466	G1467	G1471	G1472	A1473	C1474	A1477	A1480	A1483	U1484	A1485	U1489	A1490		
A1499	U1500	U1501	G1502	U1505	U1506	A1507	C1508	C1514	G1515	A1516	G1525	C1526	G1527	U1528	G1529	U1536	G1537	G1538	C1539	A1540	A1541	A1542	U1543	C1544	C1545	G1546	C1552	A1553	U	A1555	G1563	U1566	U1567	G1568	A1569	U1570	G1571	G1574	C1577	G	A	A	U	A	U					
A	G1589	A1592	C1598	U1599	G1600	U1601	C1602	U1605	A1617	A1618	U1626	G1630	A1631	G1632	G1633	C1645	A1653	A1654	A1655	C1683	C1693	G1694	A1695	G1696	A1697	A1698	A1699	U1704	G1710	G1711	G1712	A1713	G1715	U1716	G1717	G1718	G1719	G	A1727	G1732	U1733	A1734	U1738	U1739	C1741					
A94	A95	G96	U99	A224	A225	A226	G227	C228	A229	A230	A231	U232	G233	C234	U238	A244	G245	A246	A247	G251	C252	A258	U266	C267	A268	A275	C276	A279	G282	G283	C284	U285	U286	G287	C288	C289	U290	C291	U292	U293	G294	G295	G296	G297	U298	A302				
A307	C308	U309	C310	U	G	U	A	C	U	G	A	C	U	C	A	A	A	G	G328	A329	A330	C331	G332	U336	A337	G338	A342	G346	A345	G346	A353	A354	A355	A364	U365	A366	G367	U372	A373	A374	C375	A376	G377	C378	A389	A390	A391	C392	G396	U397
U398	C399	U	C	U	C	U	C	U	G406	A407	G408	C415	U416	G417	A418	G419	U420	A421	A428	A431	C432	G433	U434	G435	A436	A437	C441	C442	G446	G447	A448	A449	U450	C451	G452	G453	G458	A459	G471	U481	C482	C483	G489	A490	C491	A494	U495			
U498	C502	G503	A504	G510	U511	G512	A513	G528	C529	G540	G541	G542	A548	A549	G550	A551	G552	A553	U554	C555	C556	C563	G564	U567	C573	A574	A575	G576	U577	A578	G579	A584	U590	U591	A592	A593	C594	G595	G599	U606	G607	G617	A618	A619	U620					
G621	A630	G631	U632	A646	A647	G648	G649	G657	A658	A659	A661	A673	G674	C675	G682	A683	G684	G688	U691	G697	C698	A699	U700	G701	A702	U704	A717	C718	G719	C720	G729	U733	A740	A753	U761	A762	A763	C764	A765	A774	C777									
A790	U794	G795	U801	G804	G822	G823	G824	G825	U826	A829	A830	U831	G832	U837	A840	G852	C859	A866	A867	A868	C872	U873	U874	U875	U882	A904	G905	G906	G911	C912	A913	A917	G928	G929	A763	C930	C933	U934	A935	C936										
G939	U940	G941	U942	A943	A957	A958	C959	G963	A964	G973	C980	A987	G988	U1091	C990	A991	G992	A999	G1002	A1005	A1006	G1007	G1012	G1018	C1019	U1011	A1019	A1020	A1029	C1030	C1031	G1035	A1036	G1043	C1044	U1045	A1046	C1052	C1053	U1057	U1058	A1059	U1064	U1065						
G1068	U1069	G1070	U1071	A1072	A1073	A1074	G1076	U1079	G1080	U1081	G1085	U1086	U1087	U1090	U1091	A1092	G1093	A1100	G1101	A1103	U1104	G1105	U1106	U1107	G1109	C1110	U1111	U1112	A1113	G1114	A1115	U1117	C1118	A1119	G1120	C1121	A1123	C1124	C1125	A1126	U1127	U1128	U1129	A1130	U1131	A1132	G1133	A1134	G1135	
U1136	G1137	C1138	G1139	U1140	A1141	A1142	U1143	A1144	U1145	C1146	U1147	C1148	U1151	U1154	C1155	G1156	A1157	G1158	U1159	G1160	A1161	G1166	G1171	A1172	U1176	G1177	U1178	A1179	C1180	C1181	G1182	G1183	G1184	C1186	U1187	A1188	A1201	U1215	C1216	U	U	C	G1220	U1227	U1236	C1241	C1248			
C1256	G1402	G1403	A1404	A1405	A1406	G1410	U1411	A1417	U1418	A1423	A1424	C1425	A1426	G1427	U1433	A1434	U1435	U1436	C1437	A1442	C1449	C1450	U1451	C1452	A1453	C1454	G1455	U1456	U1457	U1458	U1459	G1460	A1461	G1462	U1465	U1466	G1467	G1471	G1472	A1473	C1474	A1477	A1480	A1483	U1484	A1485	U1489	A1490		
A1499	U1500	U1501	G1502	U1505	U1506	A1507	C1508	C1514	G1515	A1516	G1525	C1526	G1527	U1528	G1529	U1536	G1537	G1538	C1539	A1540	A1541	A1542	U1543	C1544	C1545	G1546	C1552	A1553	U	A1555	G1563	U1566	U1567	G1568	A1569	U1570	G1571	G1574	C1577	G	A	A	U	A	U					



• Molecule 53: 16S rRNA (1533-MER)

Chain A: 62% 30% 8%



G1507	G1387	A1294	A1200	G1087	A1004	A899	A768	A649	A506	U429
U1508	G1388	A1295	C1201	U1088	G1005	G900	A769	A650	C510	C430
A1513	G1396	A1296	A1205	G1089	A1006	G908	G774	A651	G510	G431
G1514	U1306	A1206	A1206	G1091	U1012	G908	G778	G655	A518	G432
G1515	C1307	U1306	A1210	A1092	U1013	A911	A786	A659	A519	A433
U1516	A1308	C1307	U1211	U1093	A1014	G916	A790	C660	U434	U434
A1517	G1309	U1310	C1212	G1094	C1015	G916	A790	U662	C435	C435
A1523	U1311	U1310	A1213	U1096	U1018	A924	A796	G630	U437	U437
G1526	G1314	U1311	U1214	U1096	U1019	A924	A796	C531	A438	A438
A1529	G1315	C1315	G1215	G1104	C1020	A929	U797	G636	A439	A439
G1539	U1316	A1315	C1216	U1105	U1021	A929	U798	U643	A440	A440
G1540	C1317	U1316	C1217	C1106	A1022	G936	A799	U644	U443	U443
	G1318	C1317	C1218	A1111	G1023	G937	A799	U645	U444	U444
	U1324	U1318	C1219	G1113	A1024	G944	A801	U646	U446	U446
	G1325	G1318	U1220	G1114	G1025	A945	A802	U647	U447	U447
	G1326	U1324	U1221	G1115	A1028	G954	A803	A556	G455	G455
	G1327	G1325	U1222	G1116	G1029	G955	A804	A456	A456	A456
	G1328	U1326	A1223	G1117	G1030	G955	A805	A457	A457	A457
	C1329	C1326	U1224	G1118	A1031	G955	G812	G566	C461	C461
	U1330	C1327	C1225	C1119	G1032	G955	G812	G567	A462	A462
	C1331	C1328	C1226	G1120	G1033	G955	G812	G568	A463	A463
		C1329	C1227	G1121	U1034	G955	G812	A568	G464	G464
		C1330	C1228	G1122	C1035	G955	G812	U574	U465	U465
		C1331	C1229	G1123	C1036	G955	G812	U574	U466	U466
		C1332	C1230	G1124	U1039	G955	G812	U574	U467	U467
		C1333	C1231	G1125	U1040	G955	G812	U574	U468	U468
		C1334	C1232	G1126	C1041	G955	G812	U574	U469	U469
		C1335	C1233	G1127	C1042	G955	G812	U574	U470	U470
		C1336	C1234	G1128	G1043	G955	G812	U574	U471	U471
		C1337	C1235	G1129	U1046	G955	G812	U574	U472	U472
		C1338	C1236	G1130	C1047	G955	G812	U574	U473	U473
		C1339	C1237	G1131	A1048	G955	G812	U574	U474	U474
		C1340	C1238	G1132	U1053	G955	G812	U574	U475	U475
		C1341	C1239	G1133	A1054	G955	G812	U574	U476	U476
		C1342	C1240	G1134	C1055	G955	G812	U574	U477	U477
		C1343	C1241	G1135	A1056	G955	G812	U574	U478	U478
		C1344	C1242	G1136	G1057	G955	G812	U574	U479	U479
		C1345	C1243	G1137	U1058	G955	G812	U574	U480	U480
		C1346	C1244	G1138	U1059	G955	G812	U574	U481	U481
		C1347	C1245	G1139	G1060	G955	G812	U574	U482	U482
		C1348	C1246	G1140	U1061	G955	G812	U574	U483	U483
		C1349	C1247	G1141	G1062	G955	G812	U574	U484	U484
		C1350	C1248	G1142	C1063	G955	G812	U574	U485	U485
		C1351	C1249	G1143	C1064	G955	G812	U574	U486	U486
		C1352	C1250	G1144	A1065	G955	G812	U574	U487	U487
		C1353	C1251	G1145	U1066	G955	G812	U574	U488	U488
		C1354	C1252	G1146	G1067	G955	G812	U574	U489	U489
		C1355	C1253	G1147	U1068	G955	G812	U574	U490	U490
		C1356	C1254	G1148	G1069	G955	G812	U574	U491	U491
		C1357	C1255	G1149	U1070	G955	G812	U574	U492	U492
		C1358	C1256	G1150	C1071	G955	G812	U574	U493	U493
		C1359	C1257	G1151	U1072	G955	G812	U574	U494	U494
		C1360	C1258	G1152	G1073	G955	G812	U574	U495	U495
		C1361	C1259	G1153	U1074	G955	G812	U574	U496	U496
		C1362	C1260	G1154	G1075	G955	G812	U574	U497	U497
		C1363	C1261	G1155	A1076	G955	G812	U574	U498	U498
		C1364	C1262	G1156	C1077	G955	G812	U574	U499	U499
		C1365	C1263	G1157	U1078	G955	G812	U574	U500	U500
		C1366	C1264	G1158	G1079	G955	G812	U574	U501	U501
		C1367	C1265	G1159	U1080	G955	G812	U574	U502	U502
		C1368	C1266	G1160	G1081	G955	G812	U574	U503	U503
		C1369	C1267	G1161	U1082	G955	G812	U574	U504	U504
		C1370	C1268	G1162	G1083	G955	G812	U574	U505	U505
		C1371	C1269	G1163	U1084	G955	G812	U574	U506	U506
		C1372	C1270	G1164	G1085	G955	G812	U574	U507	U507
		C1373	C1271	G1165	U1086	G955	G812	U574	U508	U508
		C1374	C1272	G1166	G1087	G955	G812	U574	U509	U509
		C1375	C1273	G1167	U1088	G955	G812	U574	U510	U510
		C1376	C1274	G1168	G1089	G955	G812	U574	U511	U511
		C1377	C1275	G1169	U1090	G955	G812	U574	U512	U512
		C1378	C1276	G1170	G1091	G955	G812	U574	U513	U513
		C1379	C1277	G1171	U1092	G955	G812	U574	U514	U514
		C1380	C1278	G1172	G1093	G955	G812	U574	U515	U515
		C1381	C1279	G1173	U1094	G955	G812	U574	U516	U516
		C1382	C1280	G1174	G1095	G955	G812	U574	U517	U517
		C1383	C1281	G1175	U1096	G955	G812	U574	U518	U518
		C1384	C1282	G1176	G1097	G955	G812	U574	U519	U519
		C1385	C1283	G1177	U1098	G955	G812	U574	U520	U520
		C1386	C1284	G1178	G1099	G955	G812	U574	U521	U521
		C1387	C1285	G1179	U1100	G955	G812	U574	U522	U522
		C1388	C1286	G1180	G1101	G955	G812	U574	U523	U523
		C1389	C1287	G1181	U1102	G955	G812	U574	U524	U524
		C1390	C1288	G1182	G1103	G955	G812	U574	U525	U525
		C1391	C1289	G1183	U1104	G955	G812	U574	U526	U526
		C1392	C1290	G1184	G1105	G955	G812	U574	U527	U527
		C1393	C1291	G1185	U1106	G955	G812	U574	U528	U528
		C1394	C1292	G1186	G1107	G955	G812	U574	U529	U529
		C1395	C1293	G1187	U1108	G955	G812	U574	U530	U530
		C1396	C1294	G1188	G1109	G955	G812	U574	U531	U531
		C1397	C1295	G1189	U1110	G955	G812	U574	U532	U532
		C1398	C1296	G1190	G1111	G955	G812	U574	U533	U533
		C1399	C1297	G1191	U1112	G955	G812	U574	U534	U534
		C1400	C1298	G1192	G1113	G955	G812	U574	U535	U535
		C1401	C1299	G1193	U1114	G955	G812	U574	U536	U536
		C1402	C1300	G1194	G1115	G955	G812	U574	U537	U537
		C1403	C1301	G1195	U1116	G955	G812	U574	U538	U538
		C1404	C1302	G1196	G1117	G955	G812	U574	U539	U539
		C1405	C1303	G1197	U1118	G955	G812	U574	U540	U540
		C1406	C1304	G1198	G1119	G955	G812	U574	U541	U541
		C1407	C1305	G1199	U1120	G955	G812	U574	U542	U542
		C1408	C1306	G1200	G1121	G955	G812	U574	U543	U543
		C1409	C1307	G1201	U1122	G955	G812	U574	U544	U544
		C1410	C1308	G1202	G1123	G955	G812	U574	U545	U545
		C1411	C1309	G1203	U1124	G955	G812	U574	U546	U546
		C1412	C1310	G1204	G1125	G955	G812	U574	U547	U547
		C1413	C1311	G1205	U1126	G955	G812	U574	U548	U548
		C1414	C1312	G1206	G1127	G955	G812	U574	U549	U549
		C1415	C1313	G1207	U1128	G955	G812	U574	U550	U550
		C1416	C1314	G1208	G1129	G955	G812	U574	U551	U551
		C1417	C1315	G1209	U1130	G955	G812	U574	U552	U552
		C1418	C1316	G1210	G1131	G955	G812	U574	U553	U553
		C1419	C1317	G1211	U1132	G955	G812	U574	U554	U554
		C1420	C1318	G1212	G1133	G955	G812	U574	U555	U555
		C1421	C1319	G1213	U1134	G955	G812	U574	U556	U556
		C1422	C1320	G1214	G1135	G955	G812	U574	U557	U557
		C1423	C1321	G1215	U1136	G955	G812	U574	U558	U558
		C1424	C1322	G1216	G1137	G955	G812	U574	U559	U559
		C1425	C1323	G1217	U1138	G955	G812	U574	U560	U560
		C1426	C1324	G1218	G1139	G955	G812	U574	U561	U561
		C1427	C1325	G1219	U1140	G955	G812	U574	U562	U562
		C1428	C1326	G1220	G1141	G955	G812	U574	U563	U563
		C1429	C1327	G1221	U1142	G955	G812	U574	U564	U564
		C1430	C1328	G1222	G1143	G955	G812	U574	U565	U565
		C1431	C1329	G1223	U1144	G955	G812	U574	U566	U566
		C1432	C1330	G1224	G1145	G955	G812	U574	U567	U567
		C1433	C1331	G1225	U1146	G955	G812	U574	U568	U568
		C1434	C1332	G1226	G1147	G955	G812	U574	U569	U569
		C1435	C1333	G1227	U1148	G955	G812	U574	U570	U570
		C1436	C1334	G1228	G1149	G955	G812	U574	U571	U571
		C1437	C1335	G1229	U1150	G955	G812	U574	U572	U572
		C1438	C1336	G1230	G1151	G955	G812	U574	U573	U573
		C1439	C1337	G1231	U1152	G955	G812	U574	U574	U574
		C1440	C1338	G1232						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11740	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	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	0	0.21	0/433	0.51	0/574
2	1	0.22	0/407	0.51	0/540
3	2	0.18	0/371	0.45	0/483
4	3	0.18	0/519	0.44	0/680
5	4	0.21	0/300	0.54	0/393
6	6	0.20	0/509	0.49	0/678
7	B	0.25	0/1782	0.62	2/2392 (0.1%)
8	C	0.21	0/1641	0.50	0/2208
9	D	0.23	0/1599	0.56	0/2147
10	E	0.21	0/1231	0.51	0/1655
11	F	0.27	0/766	0.59	0/1031
12	G	0.29	0/1196	0.79	0/1604
13	H	0.24	0/1049	0.61	0/1407
14	I	0.25	0/979	0.57	0/1315
15	J	0.26	0/773	0.59	0/1044
16	K	0.24	0/853	0.56	0/1153
17	L	0.21	0/1069	0.52	0/1435
18	M	0.22	0/873	0.58	0/1166
19	N	0.24	0/508	0.63	0/672
20	O	0.24	0/718	0.57	0/960
21	P	0.25	0/708	0.57	0/950
22	Q	0.21	0/699	0.52	0/933
23	R	0.24	0/526	0.60	0/705
24	S	0.22	0/649	0.54	0/872
25	T	0.23	0/639	0.53	0/852
26	U	0.14	0/1834	0.29	0/2858
27	V	0.13	0/787	0.32	0/1224
28	W	0.15	0/670	0.29	0/894
29	Y	0.17	0/2675	0.35	0/4170
30	Z	0.20	0/2120	0.49	0/2845
31	a	0.19	0/1591	0.47	0/2132
32	b	0.21	0/1581	0.52	0/2132
33	c	0.33	0/1405	0.59	2/1887 (0.1%)
34	d	0.21	0/1361	0.48	0/1832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.21	0/1147	0.50	1/1542 (0.1%)
36	f	0.23	0/928	0.60	0/1245
37	i	0.21	0/1094	0.45	0/1457
38	j	0.23	0/1099	0.53	0/1468
39	k	0.21	0/961	0.54	0/1284
40	l	0.19	0/922	0.51	0/1236
41	m	0.20	0/958	0.52	0/1279
42	n	0.22	0/953	0.52	0/1266
43	o	0.22	0/798	0.53	0/1070
44	r	0.22	0/852	0.58	0/1146
45	s	0.23	0/731	0.55	0/974
46	t	0.25	0/773	0.64	1/1032 (0.1%)
47	u	0.20	0/639	0.45	0/847
48	v	0.22	0/449	0.52	0/596
49	w	0.25	0/532	0.66	0/707
50	x	0.20	0/458	0.51	0/613
51	9	0.77	1/732 (0.1%)	1.24	7/1016 (0.7%)
52	X	0.18	0/69451	0.33	3/108344 (0.0%)
53	A	0.16	0/36826	0.31	0/57450
All	All	0.19	1/155124 (0.0%)	0.40	16/232395 (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
33	c	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	9	104	LYS	N-CA	6.41	1.54	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	X	138	U	OP1-P-O3'	-27.15	26.55	108.00
51	9	69	LYS	N-CA-C	-11.56	98.76	111.36
46	t	52	PRO	CA-N-CD	-9.96	98.06	112.00
51	9	120	GLY	N-CA-C	-7.92	102.40	112.54
33	c	45	GLN	N-CA-C	-6.91	104.84	113.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	c	3	ARG	N-CA-C	-6.86	103.72	111.07
52	X	139	A	OP1-P-OP2	-6.82	99.13	119.60
51	9	105	ASP	N-CA-C	-6.46	103.69	113.89
51	9	25	TYR	N-CA-C	-6.38	104.59	112.38
51	9	10	LYS	CB-CA-C	-5.91	109.74	116.54
7	B	104	PHE	N-CA-C	-5.71	104.25	111.11
7	B	27	MET	CA-CB-CG	5.40	124.90	114.10
35	e	94	ARG	N-CA-C	-5.37	105.42	111.28
52	X	2337	G	C2'-C3'-O3'	5.23	117.34	109.50
51	9	106	HIS	N-CA-C	-5.15	108.75	114.62
51	9	91	GLY	N-CA-C	-5.13	106.57	112.83

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	c	43	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	446	445	8	0
2	1	402	413	413	10	0
3	2	368	410	410	1	0
4	3	512	563	561	10	0
5	4	297	342	342	13	0
6	6	499	491	491	7	0
7	B	1757	1831	1830	36	0
8	C	1619	1659	1658	17	0
9	D	1569	1605	1604	38	0
10	E	1219	1301	1300	44	0
11	F	755	747	746	20	0
12	G	1181	1236	1235	28	0
13	H	1037	1096	1095	20	0
14	I	966	1006	1005	30	0
15	J	761	796	795	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	K	839	855	854	21	0
17	L	1052	1112	1112	22	0
18	M	868	926	925	19	0
19	N	498	532	531	16	0
20	O	710	736	735	14	0
21	P	695	722	721	15	0
22	Q	691	729	728	12	0
23	R	518	556	555	18	0
24	S	633	650	649	16	0
25	T	637	697	696	16	0
26	U	1643	831	831	9	0
27	V	704	359	359	5	0
28	W	662	673	672	4	0
29	Y	2392	1213	1213	19	0
30	Z	2083	2171	2168	38	0
31	a	1569	1640	1637	32	0
32	b	1562	1649	1647	23	0
33	c	1386	1449	1446	35	0
34	d	1343	1391	1388	25	0
35	e	1124	1165	1162	31	0
36	f	921	977	977	21	0
37	i	1082	1132	1132	10	0
38	j	1076	1145	1145	27	0
39	k	954	986	983	12	0
40	l	913	947	947	16	0
41	m	945	1020	1020	11	0
42	n	941	1007	1005	14	0
43	o	787	829	826	13	0
44	r	843	902	899	17	0
45	s	725	771	770	14	0
46	t	763	821	821	15	0
47	u	631	647	644	11	0
48	v	445	490	487	11	0
49	w	531	568	568	19	0
50	x	456	494	491	8	0
51	9	733	0	348	48	0
52	X	62005	31200	31207	371	0
53	A	32891	16559	16559	234	0
All	All	142619	94493	94788	1357	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 6.

All (1357) 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)
51:9:3:VAL:HA	51:9:38:GLU:CA	1.75	1.16
51:9:3:VAL:CA	51:9:38:GLU:HA	1.83	1.09
51:9:3:VAL:HA	51:9:38:GLU:HA	1.05	1.04
51:9:2:LYS:HA	51:9:20:ASN:HA	1.39	1.03
19:N:47:LEU:HD13	19:N:53:ILE:HD11	1.41	1.02
35:e:109:MET:HE1	52:X:1184:G:H21	1.24	0.99
53:A:1061:G:N2	53:A:1216:C:O2	2.06	0.88
52:X:296:G:O2'	52:X:297:G:O4'	1.92	0.86
8:C:133:GLN:OE1	8:C:150:THR:OG1	1.92	0.86
53:A:1013:G:N2	53:A:1014:A:O2'	2.08	0.85
53:A:726:C:O2'	53:A:743:A:O4'	1.94	0.85
53:A:472:C:O2'	53:A:473:G:O4'	1.96	0.83
52:X:1451:U:O2'	52:X:1452:C:OP1	1.97	0.83
52:X:2338:A:O2'	52:X:2339:A:O4'	1.97	0.83
52:X:2223:U:O2'	52:X:2224:U:O5'	1.96	0.82
51:9:82:LYS:C	51:9:92:SER:CB	2.53	0.82
51:9:68:LEU:HA	51:9:71:THR:CB	2.09	0.81
12:G:72:VAL:HG23	12:G:73:LEU:HD12	1.62	0.81
52:X:1811:C:O2	52:X:2637:G:O2'	1.99	0.81
53:A:1219:C:O2'	53:A:1220:U:O4'	1.99	0.81
29:Y:48:G:O2'	29:Y:49:G:O5'	1.98	0.80
15:J:6:ILE:N	15:J:76:ILE:O	2.15	0.80
52:X:911:G:H21	52:X:913:A:H61	1.29	0.79
53:A:1001:U:O2'	53:A:1221:U:OP2	2.00	0.79
11:F:4:TYR:OH	53:A:747:U:OP1	1.99	0.79
53:A:1277:G:O2'	53:A:1278:A:O4'	1.99	0.79
30:Z:256:GLY:O	52:X:1872:C:O2'	1.99	0.79
19:N:12:ARG:NH2	53:A:1004:A:O2'	2.15	0.79
52:X:1808:U:OP2	52:X:1813:A:N6	2.15	0.79
52:X:2139:G:O6	52:X:2206:C:N4	2.15	0.78
14:I:7:TYR:HH	53:A:1156:C:HO2'	1.18	0.78
53:A:1213:A:O2'	53:A:1214:U:O5'	2.01	0.78
11:F:11:ARG:NH1	11:F:13:ASN:O	2.16	0.78
51:9:2:LYS:CA	51:9:20:ASN:HA	2.14	0.78
52:X:576:G:OP1	52:X:2050:G:O2'	2.01	0.78
34:d:45:LYS:NZ	34:d:47:GLU:OE1	2.16	0.78
53:A:390:A:O2'	53:A:391:A:O4'	1.99	0.78
33:c:68:THR:OG1	33:c:85:ILE:O	2.02	0.77
18:M:37:ALA:O	18:M:55:LYS:NZ	2.16	0.77
18:M:104:ASN:ND2	53:A:961:G:O6	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:38:ASP:OD1	16:K:39:THR:N	2.18	0.77
52:X:1359:G:N2	52:X:1359:G:OP2	2.17	0.77
52:X:2128:U:O2'	52:X:2219:G:N2	2.16	0.77
52:X:2688:G:N2	52:X:2691:A:OP2	2.16	0.77
53:A:109:G:O6	53:A:338:C:N4	2.18	0.77
10:E:62:LYS:NZ	53:A:1083:U:OP2	2.16	0.77
14:I:18:ARG:NH1	53:A:1156:C:O2	2.18	0.77
7:B:27:MET:SD	7:B:39:TYR:OH	2.42	0.77
46:t:59:GLN:OE1	46:t:59:GLN:N	2.17	0.77
30:Z:122:ALA:HB3	30:Z:130:LEU:HD21	1.66	0.77
52:X:1102:G:O2'	52:X:1103:A:OP1	2.01	0.77
53:A:1259:A:O2'	53:A:1296:A:N6	2.17	0.77
12:G:9:LYS:NZ	53:A:1384:A:OP1	2.17	0.76
51:9:4:ILE:HA	51:9:18:VAL:CB	2.15	0.76
53:A:305:G:N2	53:A:308:A:OP2	2.18	0.76
53:A:1057:G:N2	53:A:1220:U:O2	2.19	0.76
48:v:35:LYS:NZ	52:X:1402:C:OP1	2.18	0.76
35:e:66:THR:OG1	52:X:1187:U:OP2	2.02	0.76
52:X:1117:G:N2	52:X:1137:G:OP2	2.18	0.76
52:X:790:A:O2'	52:X:1704:U:OP1	2.04	0.75
52:X:2844:A:O2'	52:X:2846:A:N7	2.18	0.75
52:X:2212:C:O2'	52:X:2213:U:O4'	2.02	0.75
52:X:229:A:O2'	52:X:231:A:N1	2.19	0.75
9:D:31:TYR:OH	53:A:434:U:OP1	2.04	0.75
52:X:2605:G:O2'	52:X:2608:C:OP2	2.03	0.75
14:I:25:GLU:N	14:I:25:GLU:OE1	2.20	0.75
38:j:46:GLN:NE2	52:X:2514:G:OP1	2.20	0.75
49:w:44:ARG:NH1	52:X:61:A:OP1	2.20	0.75
52:X:2279:G:O2'	52:X:2525:C:OP1	2.05	0.75
2:1:21:LYS:NZ	2:1:26:ASN:O	2.20	0.75
45:s:59:TYR:OH	52:X:1379:U:OP2	2.04	0.74
37:i:54:GLN:OE1	52:X:872:C:O2'	2.04	0.74
38:j:26:GLU:N	38:j:26:GLU:OE1	2.20	0.74
52:X:2197:G:O6	52:X:2200:A:N6	2.20	0.74
52:X:2334:U:O2'	52:X:2335:U:O2	2.05	0.74
20:O:47:LYS:O	20:O:53:ARG:NH2	2.20	0.74
53:A:1024:A:O2'	53:A:1227:C:O2'	2.00	0.74
52:X:1820:A:N6	52:X:1857:G:O2'	2.20	0.74
52:X:275:A:O2'	52:X:415:C:O4'	2.06	0.74
9:D:94:LEU:HD11	9:D:114:VAL:HG21	1.70	0.74
10:E:41:ASP:OD1	10:E:43:ASN:N	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:42:HIS:HD1	53:A:748:C:HO2'	1.32	0.74
34:d:119:GLU:N	34:d:119:GLU:OE1	2.21	0.74
50:x:17:GLU:OE1	50:x:17:GLU:N	2.21	0.74
9:D:115:ASN:ND2	53:A:412:G:O5'	2.21	0.73
23:R:40:GLU:O	23:R:77:SER:OG	2.04	0.73
35:e:6:MET:N	35:e:6:MET:SD	2.62	0.73
53:A:182:U:OP1	53:A:208:A:N6	2.20	0.73
2:1:17:TYR:OH	52:X:2376:C:O2'	2.06	0.73
18:M:17:ILE:O	18:M:20:THR:OG1	2.06	0.73
53:A:472:C:O2'	53:A:473:G:O5'	2.04	0.73
14:I:105:THR:OG1	53:A:1189:A:OP1	2.06	0.73
53:A:1463:A:O2'	53:A:1464:G:OP1	2.07	0.73
10:E:14:ARG:NH2	10:E:116:GLU:OE1	2.21	0.73
24:S:78:ARG:NH2	53:A:1231:G:OP1	2.22	0.73
53:A:18:A:N3	53:A:1090:A:O2'	2.19	0.73
37:i:18:ARG:NH2	52:X:1290:G:N7	2.37	0.73
52:X:328:G:N2	52:X:399:C:O2'	2.21	0.73
40:l:32:ASN:OD1	40:l:33:VAL:N	2.22	0.73
30:Z:205:ILE:O	52:X:1820:A:O2'	2.01	0.73
52:X:284:C:O2	52:X:287:G:N2	2.21	0.73
52:X:1087:U:O2	52:X:1160:G:O6	2.06	0.73
1:0:30:CYS:SG	1:0:32:SER:OG	2.46	0.72
41:m:58:THR:OG1	41:m:74:PHE:O	2.07	0.72
52:X:1065:U:OP1	52:X:1081:U:O2'	2.06	0.72
36:f:53:LYS:N	36:f:56:GLU:OE2	2.22	0.72
43:o:63:GLU:N	43:o:63:GLU:OE2	2.22	0.72
52:X:1540:A:O2'	52:X:1541:A:O4'	2.05	0.72
14:I:52:LEU:HD11	14:I:83:ILE:HD11	1.71	0.72
49:w:40:THR:O	49:w:43:ILE:HG22	1.88	0.72
49:w:58:ARG:NH2	52:X:111:U:OP1	2.22	0.72
52:X:688:G:N2	52:X:691:U:OP2	2.20	0.72
13:H:50:GLU:OE1	13:H:50:GLU:N	2.23	0.72
24:S:16:MET:HE2	24:S:16:MET:HA	1.72	0.72
30:Z:150:LYS:NZ	52:X:2233:C:OP2	2.19	0.72
32:b:58:ARG:NH2	52:X:184:G:O6	2.23	0.72
52:X:309:U:O2'	52:X:310:C:O5'	2.08	0.72
52:X:911:G:N2	52:X:913:A:H61	1.88	0.72
23:R:32:ASP:OD1	23:R:33:LEU:N	2.23	0.72
52:X:1090:U:O2'	52:X:1157:A:N6	2.23	0.72
21:P:53:GLU:OE1	21:P:53:GLU:N	2.22	0.71
52:X:1465:A:O2'	52:X:1467:G:N7	2.17	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:L:20:LYS:NZ	17:L:20:LYS:O	2.24	0.71
17:L:127:ARG:NH2	53:A:510:C:OP1	2.23	0.71
39:k:78:ASP:OD1	39:k:79:ALA:N	2.23	0.71
52:X:867:A:N3	52:X:989:U:O2'	2.23	0.71
12:G:137:LYS:O	12:G:141:THR:HG23	1.89	0.71
9:D:132:LEU:O	9:D:134:LYS:NZ	2.23	0.71
17:L:79:TYR:OH	53:A:531:C:OP2	2.07	0.71
53:A:194:C:O2	53:A:195:A:N6	2.23	0.71
30:Z:145:GLU:OE1	30:Z:145:GLU:N	2.23	0.71
52:X:2882:G:N2	52:X:2885:A:OP2	2.24	0.71
10:E:125:SER:O	53:A:9:G:O2'	2.09	0.71
27:V:455:C:N4	28:W:712:LEU:O	2.23	0.71
52:X:1126:A:O2'	52:X:1127:U:OP2	2.08	0.71
27:V:465:A:OP1	53:A:1508:U:O2'	2.07	0.71
10:E:74:VAL:HG21	10:E:144:LEU:HD12	1.73	0.71
38:j:56:ARG:NH1	52:X:2498:A:O2'	2.23	0.71
52:X:1110:C:N4	52:X:1116:A:OP1	2.23	0.71
51:9:3:VAL:HA	51:9:39:ALA:N	2.05	0.70
1:0:35:GLU:OE1	1:0:35:GLU:N	2.24	0.70
53:A:335:A:O2'	53:A:336:C:O4'	2.09	0.70
52:X:353:A:N3	52:X:373:A:O2'	2.23	0.70
16:K:77:ILE:HD11	16:K:107:LEU:HD21	1.74	0.70
18:M:48:LEU:HD11	18:M:53:LEU:HD12	1.71	0.70
34:d:99:LYS:NZ	34:d:124:ILE:O	2.22	0.70
32:b:101:LEU:O	32:b:106:ARG:NH2	2.23	0.70
52:X:1474:C:O2'	52:X:1617:A:OP2	2.10	0.70
52:X:1542:A:O2'	52:X:1544:C:N4	2.24	0.70
52:X:1947:A:O2'	52:X:1949:C:N4	2.25	0.70
15:J:44:THR:OG1	15:J:69:THR:O	2.08	0.70
53:A:954:G:N2	53:A:1347:G:N7	2.39	0.70
11:F:42:ASP:OD1	11:F:43:TRP:N	2.25	0.70
10:E:54:GLN:N	10:E:54:GLN:OE1	2.24	0.69
18:M:51:GLU:N	18:M:51:GLU:OE1	2.24	0.69
51:9:31:ILE:HA	51:9:36:ALA:HB3	1.74	0.69
52:X:78:U:O2'	52:X:79:C:OP2	2.09	0.69
52:X:911:G:H21	52:X:913:A:N6	1.88	0.69
2:1:8:ALA:O	2:1:46:ARG:N	2.25	0.69
15:J:57:LYS:NZ	53:A:974:A:O2'	2.16	0.69
29:Y:33:U:O2'	29:Y:34:C:O4'	2.10	0.69
52:X:160:G:N2	52:X:168:A:OP2	2.24	0.69
9:D:178:ARG:NH1	9:D:179:LEU:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:1171:G:OP2	52:X:1172:A:O2'	2.08	0.69
13:H:107:SER:OG	53:A:651:A:N3	2.24	0.69
14:I:79:ILE:O	14:I:83:ILE:HG22	1.93	0.69
5:4:28:GLU:N	5:4:28:GLU:OE1	2.25	0.69
31:a:92:GLU:N	31:a:95:GLN:OE1	2.24	0.69
52:X:2219:G:O2'	52:X:2220:A:O4'	2.08	0.69
35:e:109:MET:HE1	52:X:1184:G:N2	2.05	0.69
48:v:3:ARG:NH1	52:X:1403:G:OP1	2.25	0.69
51:9:3:VAL:HA	51:9:39:ALA:H	1.58	0.69
52:X:1131:A:O2'	52:X:1132:A:O4'	2.08	0.69
52:X:2169:G:N1	52:X:2180:U:OP2	2.26	0.69
5:4:19:ARG:NH1	52:X:2785:U:OP2	2.26	0.69
52:X:31:C:O2'	52:X:1278:G:OP1	2.11	0.69
17:L:42:GLN:NE2	53:A:35:A:N3	2.40	0.69
30:Z:79:ALA:O	30:Z:80:THR:HG23	1.92	0.69
52:X:840:A:OP2	52:X:2100:A:O2'	2.12	0.68
53:A:1324:U:O2'	53:A:1369:A:N3	2.25	0.68
11:F:19:LYS:O	11:F:23:ILE:HD12	1.93	0.68
8:C:155:ARG:NE	8:C:192:TYR:O	2.23	0.68
38:j:43:THR:O	38:j:47:ILE:HD12	1.94	0.68
46:t:25:ALA:HB3	46:t:34:LEU:HB3	1.76	0.68
51:9:84:GLY:H	51:9:149:ALA:H	1.40	0.68
53:A:1275:G:O2'	53:A:1277:G:O6	2.10	0.68
16:K:59:LYS:NZ	53:A:700:G:O6	2.23	0.68
53:A:1023:G:O2'	53:A:1025:G:OP2	2.11	0.68
10:E:107:ALA:O	10:E:112:ARG:NH1	2.27	0.68
53:A:1460:U:O2'	53:A:1461:U:O4'	2.09	0.68
18:M:104:ASN:ND2	53:A:960:U:O4	2.27	0.68
45:s:89:GLU:N	45:s:89:GLU:OE1	2.27	0.68
49:w:47:ARG:NH1	52:X:74:U:OP1	2.27	0.68
49:w:51:ALA:O	49:w:55:THR:OG1	2.12	0.68
44:r:28:GLN:OE1	44:r:30:GLY:N	2.27	0.68
36:f:56:GLU:N	36:f:56:GLU:OE1	2.27	0.67
52:X:2873:G:O2'	52:X:2893:A:N6	2.27	0.67
13:H:97:VAL:HG22	13:H:98:LEU:CD2	2.24	0.67
26:U:15:G:N2	26:U:21:A:N3	2.42	0.67
53:A:455:G:O2'	53:A:456:A:OP1	2.09	0.67
20:O:8:LYS:O	20:O:12:ILE:HG22	1.94	0.67
30:Z:171:TYR:OH	52:X:2252:A:OP1	2.11	0.67
29:Y:63:C:O2'	29:Y:106:C:N4	2.27	0.67
32:b:82:GLN:OE1	32:b:82:GLN:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:I:51:PRO:O	14:I:55:THR:HG22	1.94	0.67
52:X:2219:G:O2'	52:X:2220:A:O5'	2.12	0.67
24:S:55:ARG:NH1	53:A:968:A:OP1	2.28	0.67
11:F:87:ARG:NH2	53:A:682:G:O3'	2.28	0.67
38:j:51:ARG:O	38:j:55:THR:HG22	1.95	0.67
52:X:1696:G:O2'	52:X:1697:A:OP2	2.13	0.67
34:d:39:HIS:HE1	34:d:65:LEU:HD13	1.60	0.67
52:X:458:G:OP2	52:X:2435:C:O2'	2.11	0.67
17:L:67:ARG:NH1	17:L:75:GLU:OE1	2.28	0.66
44:r:42:ALA:N	52:X:2039:G:OP1	2.29	0.66
30:Z:194:GLN:OE1	30:Z:195:VAL:N	2.27	0.66
43:o:36:GLU:N	43:o:36:GLU:OE2	2.27	0.66
7:B:101:LEU:N	7:B:175:GLU:OE2	2.29	0.66
7:B:149:GLY:O	7:B:152:LYS:NZ	2.28	0.66
31:a:38:LYS:NZ	31:a:88:MET:O	2.29	0.66
52:X:1460:G:O2'	52:X:1631:A:N6	2.27	0.66
52:X:1118:C:N4	52:X:1139:G:N7	2.44	0.66
52:X:1467:G:O2'	52:X:1540:A:N6	2.28	0.66
53:A:89:C:O2	53:A:90:C:N4	2.28	0.66
53:A:1217:C:N4	53:A:1218:C:N4	2.43	0.66
53:A:1217:C:C4	53:A:1218:C:N4	2.63	0.66
51:9:129:VAL:HA	51:9:143:VAL:HA	1.76	0.66
52:X:740:A:O2'	52:X:1392:A:N3	2.29	0.66
10:E:29:ARG:NH2	53:A:1406:C:OP2	2.29	0.66
43:o:89:ARG:NH1	52:X:1263:G:OP2	2.29	0.66
49:w:37:LEU:O	52:X:94:A:N6	2.28	0.66
52:X:65:A:O2'	52:X:503:C:N3	2.27	0.66
52:X:2560:A:H62	52:X:2691:A:H61	1.44	0.66
1:0:13:LYS:NZ	52:X:563:C:OP1	2.25	0.65
35:e:142:GLU:OE1	35:e:142:GLU:N	2.29	0.65
38:j:67:LYS:O	38:j:68:ILE:HD13	1.96	0.65
31:a:153:ARG:NH1	52:X:2054:C:OP1	2.29	0.65
51:9:3:VAL:HA	51:9:38:GLU:C	2.21	0.65
13:H:108:THR:OG1	13:H:111:GLY:O	2.13	0.65
53:A:728:C:O2'	53:A:729:C:OP1	2.13	0.65
33:c:121:SER:O	52:X:2332:G:O2'	2.14	0.65
47:u:23:ASP:OD1	47:u:24:SER:N	2.29	0.65
52:X:2060:A:N3	52:X:2484:G:O2'	2.30	0.65
5:4:33:LYS:NZ	52:X:2772:U:OP1	2.30	0.65
16:K:85:GLU:N	16:K:85:GLU:OE2	2.29	0.65
52:X:161:A:OP2	52:X:166:A:N6	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:2148:A:N6	52:X:2197:G:N7	2.44	0.65
9:D:150:ILE:HD12	9:D:151:ILE:N	2.11	0.65
42:n:13:ARG:NH2	52:X:1292:G:OP1	2.29	0.65
52:X:1882:A:O2'	52:X:1883:A:OP1	2.09	0.65
42:n:90:VAL:O	43:o:11:GLN:NE2	2.30	0.65
52:X:1030:G:OP1	52:X:1031:C:N4	2.30	0.65
53:A:1526:G:N1	53:A:1529:A:OP2	2.30	0.65
15:J:37:SER:OG	15:J:75:ASP:OD1	2.09	0.64
50:x:29:LYS:N	50:x:33:GLN:OE1	2.29	0.64
53:A:1015:C:O2'	53:A:1048:A:O2'	2.13	0.64
35:e:31:SER:OG	52:X:1058:U:O4	2.14	0.64
52:X:1945:A:O2'	52:X:1946:U:O4'	2.14	0.64
53:A:260:U:O2	53:A:283:G:N2	2.30	0.64
38:j:80:GLU:OE1	52:X:2523:G:O2'	2.13	0.64
30:Z:118:SER:O	30:Z:189:ARG:NH2	2.30	0.64
39:k:110:ASP:OD2	52:X:1694:G:O2'	2.07	0.64
4:3:5:LYS:NZ	52:X:256:C:OP2	2.30	0.64
18:M:98:ARG:NH2	53:A:1318:G:N7	2.45	0.64
38:j:128:LYS:NZ	52:X:1075:A:OP1	2.26	0.64
53:A:76:A:N6	53:A:78:G:O6	2.30	0.64
11:F:76:ASP:OD1	11:F:88:HIS:NE2	2.31	0.64
32:b:89:VAL:HG22	32:b:90:PHE:CD2	2.33	0.64
41:m:58:THR:HA	41:m:76:VAL:HG23	1.79	0.64
6:6:24:THR:OG1	33:c:101:ASP:OD2	2.13	0.64
12:G:71:PRO:O	12:G:96:ARG:NE	2.30	0.64
30:Z:98:ASP:OD1	30:Z:99:GLY:N	2.31	0.64
53:A:1275:G:N2	53:A:1278:A:OP2	2.30	0.64
47:u:79:ARG:NH2	47:u:81:GLY:O	2.31	0.64
51:9:82:LYS:CA	51:9:92:SER:CB	2.76	0.64
52:X:2:G:O2'	52:X:3:U:O4'	2.16	0.64
30:Z:121:GLU:N	30:Z:121:GLU:OE1	2.31	0.63
38:j:87:LYS:NZ	52:X:1002:G:OP2	2.31	0.63
53:A:1452:G:O6	53:A:1470:A:N6	2.31	0.63
30:Z:260:ARG:NE	52:X:1828:G:OP1	2.31	0.63
52:X:27:G:O2'	52:X:28:A:OP2	2.15	0.63
51:9:82:LYS:O	51:9:92:SER:CB	2.47	0.63
53:A:195:A:O2'	53:A:196:U:O4'	2.09	0.63
49:w:13:GLU:N	49:w:13:GLU:OE1	2.32	0.63
51:9:3:VAL:CB	51:9:38:GLU:HA	2.29	0.63
38:j:124:LYS:NZ	52:X:2512:C:N3	2.47	0.63
43:o:16:GLU:OE2	43:o:99:LYS:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:54:GLN:N	22:Q:54:GLN:OE1	2.31	0.63
43:o:35:PHE:O	43:o:57:THR:OG1	2.14	0.63
52:X:2192:U:O2'	52:X:2197:G:OP2	2.17	0.63
52:X:2287:C:O2'	52:X:2456:C:OP2	2.17	0.63
52:X:1380:U:OP1	52:X:1436:U:N3	2.32	0.63
53:A:405:A:N7	53:A:556:A:O2'	2.31	0.63
22:Q:72:THR:OG1	53:A:262:G:OP1	2.16	0.63
52:X:621:G:O2'	52:X:1294:A:OP1	2.16	0.62
52:X:1127:U:O2'	52:X:1129:U:OP2	2.07	0.62
22:Q:8:LYS:N	22:Q:65:GLU:OE2	2.30	0.62
34:d:150:ARG:NH1	34:d:168:GLU:OE2	2.32	0.62
42:n:8:THR:OG1	52:X:1256:C:OP1	2.15	0.62
52:X:164:U:O2'	52:X:165:C:OP1	2.11	0.62
53:A:1356:G:N2	53:A:1383:A:OP2	2.31	0.62
13:H:97:VAL:HG22	13:H:98:LEU:HD22	1.81	0.62
20:O:28:GLN:NE2	53:A:666:U:O4'	2.32	0.62
44:r:11:ARG:NH2	52:X:2041:G:OP1	2.31	0.62
47:u:83:ASP:OD1	47:u:84:ARG:N	2.32	0.62
4:3:8:ARG:NH2	52:X:247:A:OP2	2.32	0.62
8:C:136:GLN:NE2	8:C:140:THR:OG1	2.33	0.62
10:E:44:GLY:O	10:E:74:VAL:HG12	1.99	0.62
6:6:29:GLU:N	6:6:29:GLU:OE1	2.33	0.62
36:f:21:THR:HG22	36:f:39:ILE:HD13	1.82	0.62
53:A:19:U:O2'	53:A:1089:G:O2'	2.16	0.62
39:k:35:THR:HG21	52:X:1696:G:H3'	1.81	0.62
49:w:52:ARG:NE	52:X:77:U:OP1	2.32	0.62
52:X:139:A:O2'	52:X:1449:C:OP1	2.10	0.62
53:A:908:G:N2	53:A:911:A:OP2	2.31	0.62
24:S:12:ASP:OD2	24:S:14:HIS:NE2	2.32	0.62
48:v:18:ARG:NH1	52:X:428:A:OP1	2.33	0.62
51:9:83:SER:HA	51:9:149:ALA:CA	2.30	0.62
29:Y:47:C:N4	29:Y:48:G:O6	2.33	0.62
30:Z:123:ASP:O	30:Z:128:ASN:ND2	2.32	0.62
46:t:77:GLU:OE2	46:t:77:GLU:N	2.32	0.62
10:E:10:GLU:OE2	10:E:10:GLU:N	2.33	0.62
20:O:58:LYS:NZ	53:A:589:C:OP1	2.31	0.62
44:r:36:LEU:HD22	44:r:48:GLU:HB3	1.81	0.62
51:9:3:VAL:CA	51:9:39:ALA:H	2.12	0.62
10:E:151:GLU:N	10:E:151:GLU:OE1	2.33	0.61
33:c:119:LYS:O	33:c:167:ARG:NH1	2.32	0.61
53:A:1061:G:N1	53:A:1216:C:N3	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1231:G:O2'	53:A:1232:C:O4'	2.14	0.61
40:l:47:ASP:OD1	40:l:48:VAL:HG13	2.00	0.61
52:X:801:U:O2'	52:X:1312:A:N1	2.33	0.61
53:A:372:A:O2'	53:A:373:U:O5'	2.18	0.61
53:A:483:G:O2'	53:A:484:U:OP1	2.18	0.61
12:G:69:ILE:HG21	12:G:104:LEU:HD21	1.82	0.61
24:S:79:THR:OG1	53:A:967:U:O2'	2.16	0.61
11:F:5:GLU:OE1	11:F:5:GLU:N	2.34	0.61
52:X:1483:A:HO2'	52:X:1563:G:HO2'	1.48	0.61
33:c:38:MET:HE3	33:c:38:MET:HA	1.83	0.61
52:X:1462:G:O2'	52:X:1633:G:O2'	2.13	0.61
22:Q:3:GLU:OE2	22:Q:3:GLU:N	2.32	0.61
22:Q:14:VAL:HG13	22:Q:23:ILE:HD11	1.83	0.61
34:d:39:HIS:CE1	34:d:65:LEU:HD13	2.36	0.61
34:d:68:THR:HG21	52:X:2786:A:N1	2.15	0.61
52:X:1507:U:O2'	52:X:1508:C:OP2	2.16	0.61
52:X:2502:U:OP1	52:X:2558:G:N2	2.34	0.61
53:A:1093:U:O2'	53:A:1112:A:OP2	2.18	0.61
8:C:79:GLY:O	8:C:83:VAL:N	2.33	0.61
9:D:153:GLU:O	9:D:157:VAL:HG22	1.99	0.61
11:F:80:LYS:NZ	53:A:680:G:O3'	2.34	0.61
35:e:70:LEU:HD22	35:e:91:LEU:HD13	1.81	0.61
43:o:7:THR:OG1	43:o:8:GLY:N	2.31	0.61
44:r:36:LEU:HD21	44:r:44:SER:O	2.01	0.61
48:v:43:LYS:NZ	48:v:44:PRO:O	2.33	0.61
52:X:2874:G:O2'	52:X:2891:G:N2	2.34	0.61
25:T:9:LYS:O	25:T:13:THR:HG23	2.01	0.61
30:Z:147:LYS:NZ	52:X:2233:C:OP1	2.33	0.61
30:Z:70:ASP:OD1	30:Z:71:LYS:N	2.34	0.61
35:e:8:ASN:ND2	35:e:44:THR:OG1	2.33	0.61
53:A:206:A:O2'	53:A:207:U:OP1	2.18	0.61
12:G:144:MET:HE3	12:G:144:MET:HA	1.83	0.61
26:U:58:A:O2'	26:U:60:U:OP2	2.19	0.61
52:X:268:A:O2'	52:X:475:A:N6	2.34	0.61
10:E:46:VAL:O	10:E:71:LEU:HD12	2.01	0.60
31:a:167:GLU:N	31:a:167:GLU:OE1	2.33	0.60
7:B:89:MET:SD	7:B:89:MET:N	2.74	0.60
16:K:129:ARG:NH1	53:A:805:C:O3'	2.34	0.60
30:Z:221:ARG:NH1	52:X:1856:U:OP2	2.33	0.60
34:d:123:GLU:N	34:d:123:GLU:OE1	2.35	0.60
52:X:1029:A:O2'	52:X:1030:G:O5'	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:38:GLU:OE2	6:6:38:GLU:N	2.34	0.60
14:I:52:LEU:HD11	14:I:83:ILE:CD1	2.32	0.60
19:N:47:LEU:CD1	19:N:53:ILE:HD11	2.23	0.60
52:X:331:C:N4	52:X:332:G:O6	2.34	0.60
53:A:421:G:N2	53:A:436:G:O2'	2.33	0.60
39:k:95:GLN:N	39:k:95:GLN:OE1	2.35	0.60
53:A:959:A:O2'	53:A:981:G:O6	2.10	0.60
24:S:43:GLN:OE1	24:S:43:GLN:N	2.30	0.60
37:i:21:ARG:NH1	52:X:1290:G:OP2	2.34	0.60
26:U:43:G:O2'	26:U:44:A:O5'	2.19	0.60
35:e:136:GLN:OE1	35:e:136:GLN:N	2.34	0.60
47:u:64:ASP:OD1	47:u:66:THR:OG1	2.14	0.60
51:9:83:SER:HA	51:9:149:ALA:HA	1.84	0.60
52:X:1945:A:O2'	52:X:1946:U:O5'	2.19	0.60
10:E:40:GLY:HA3	10:E:117:LEU:HD21	1.84	0.60
30:Z:168:GLU:N	30:Z:168:GLU:OE1	2.35	0.60
52:X:1900:A:O2'	52:X:1901:A:O5'	2.18	0.60
52:X:2223:U:O2'	52:X:2224:U:O4'	2.20	0.60
52:X:2705:C:O2	52:X:2761:G:N2	2.29	0.60
25:T:35:VAL:HG12	25:T:50:ALA:HB1	1.84	0.60
44:r:83:LYS:O	44:r:84:ARG:NE	2.35	0.60
11:F:4:TYR:HD2	11:F:72:VAL:HG11	1.65	0.60
48:v:54:LEU:HD12	48:v:54:LEU:O	2.02	0.60
52:X:823:G:N2	52:X:823:G:OP1	2.35	0.60
53:A:52:A:O2'	53:A:368:G:N2	2.35	0.60
52:X:1713:A:O2'	52:X:1719:G:N7	2.30	0.59
16:K:78:GLU:N	16:K:78:GLU:OE1	2.35	0.59
32:b:139:MET:HE1	32:b:143:LEU:HD11	1.84	0.59
39:k:72:ASN:ND2	39:k:75:ASN:OD1	2.36	0.59
40:l:114:ARG:NH2	52:X:2405:A:N3	2.50	0.59
48:v:33:LEU:O	48:v:34:GLN:NE2	2.35	0.59
52:X:2131:U:O2'	52:X:2132:A:O4'	2.14	0.59
53:A:1447:G:OP2	53:A:1447:G:N2	2.36	0.59
23:R:18:PHE:CD1	23:R:23:ILE:HD11	2.38	0.59
10:E:40:GLY:CA	10:E:117:LEU:HD21	2.32	0.59
45:s:15:GLU:N	45:s:15:GLU:OE2	2.34	0.59
53:A:486:C:O2'	53:A:487:C:O5'	2.20	0.59
53:A:703:A:N6	53:A:796:A:O2'	2.35	0.59
1:0:37:LYS:NZ	1:0:38:LEU:O	2.32	0.59
15:J:53:ARG:NE	15:J:63:GLU:OE2	2.35	0.59
9:D:200:ARG:NH2	53:A:10:A:N1	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:133:MET:HE2	31:a:133:MET:HA	1.84	0.59
38:j:12:GLU:OE2	38:j:12:GLU:N	2.36	0.59
52:X:77:U:O2'	52:X:78:U:O5'	2.21	0.59
52:X:1713:A:N3	52:X:1715:C:N4	2.50	0.59
53:A:1460:U:O2'	53:A:1461:U:O5'	2.21	0.59
13:H:12:THR:HG21	53:A:886:A:H1'	1.85	0.59
4:3:6:THR:OG1	52:X:246:U:OP1	2.21	0.58
22:Q:68:PRO:O	53:A:272:C:O2'	2.19	0.58
29:Y:10:G:O4'	47:u:79:ARG:NH2	2.36	0.58
29:Y:33:U:O2'	29:Y:34:C:OP1	2.19	0.58
25:T:67:VAL:O	25:T:68:HIS:ND1	2.36	0.58
33:c:60:ILE:HD12	33:c:137:ILE:HD12	1.85	0.58
53:A:1078:G:OP1	53:A:1396:G:O2'	2.21	0.58
21:P:22:VAL:HG22	21:P:34:ILE:HD12	1.85	0.58
33:c:151:GLY:C	33:c:152:MET:HE2	2.28	0.58
31:a:146:MET:SD	52:X:2079:C:O2'	2.61	0.58
52:X:576:G:O2'	52:X:577:U:OP2	2.19	0.58
52:X:2685:U:O2	52:X:2694:A:N7	2.37	0.58
9:D:54:LYS:NZ	9:D:65:GLU:OE2	2.26	0.58
53:A:1383:A:O2'	53:A:1385:U:OP1	2.10	0.58
7:B:195:GLU:N	7:B:195:GLU:OE2	2.35	0.58
17:L:3:THR:HG22	17:L:7:LEU:CD2	2.34	0.58
53:A:686:U:O2	53:A:786:A:O2'	2.22	0.58
23:R:58:ARG:NE	53:A:673:G:OP1	2.35	0.58
42:n:81:HIS:O	42:n:85:LEU:HD12	2.02	0.58
12:G:118:GLU:O	12:G:122:ASN:ND2	2.37	0.58
30:Z:98:ASP:O	52:X:1546:G:N2	2.36	0.58
46:t:89:LYS:NZ	52:X:101:G:O6	2.37	0.58
31:a:82:GLU:OE1	52:X:2664:U:O2'	2.21	0.58
39:k:93:GLU:OE2	39:k:93:GLU:N	2.36	0.58
43:o:22:ILE:HD12	43:o:23:GLU:H	1.69	0.58
51:9:106:HIS:O	51:9:107:ASN:CB	2.52	0.58
52:X:441:C:O2'	52:X:442:C:O5'	2.13	0.58
53:A:986:G:N2	53:A:1368:C:O4'	2.37	0.58
24:S:52:TYR:OH	53:A:996:A:N3	2.31	0.57
27:V:455:C:OP1	28:W:747:THR:OG1	2.09	0.57
52:X:287:G:N3	52:X:288:C:N4	2.51	0.57
15:J:82:GLN:OE1	15:J:82:GLN:N	2.35	0.57
20:O:69:TYR:OH	20:O:73:LYS:NZ	2.37	0.57
35:e:109:MET:SD	52:X:1184:G:O2'	2.61	0.57
53:A:1187:G:N2	53:A:1190:G:OP2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:34:ILE:HD12	19:N:39:LEU:O	2.04	0.57
38:j:38:GLU:OE1	38:j:128:LYS:N	2.36	0.57
53:A:1039:U:O2'	53:A:1042:G:O6	2.13	0.57
14:I:60:THR:HG23	14:I:61:TYR:CD1	2.38	0.57
15:J:28:THR:HG23	15:J:87:LEU:CD1	2.34	0.57
52:X:1766:C:O2'	52:X:1767:A:OP1	2.22	0.57
52:X:2150:G:OP2	52:X:2201:U:N3	2.37	0.57
52:X:2849:U:OP2	52:X:2850:G:N2	2.36	0.57
31:a:119:PHE:O	52:X:1699:A:O2'	2.22	0.57
44:r:23:LEU:O	44:r:27:LYS:NZ	2.37	0.57
44:r:109:GLU:N	44:r:109:GLU:OE1	2.38	0.57
18:M:3:ARG:N	18:M:7:VAL:O	2.38	0.57
52:X:584:A:N6	52:X:599:G:O2'	2.36	0.57
52:X:2133:C:N4	52:X:2134:A:N6	2.53	0.57
52:X:2421:A:OP2	52:X:2451:C:N4	2.37	0.57
7:B:114:LEU:HD13	7:B:144:LEU:HD11	1.86	0.57
27:V:442:G:O2'	27:V:443:C:O5'	2.23	0.57
51:9:2:LYS:HA	51:9:20:ASN:CA	2.24	0.57
52:X:62:C:N3	52:X:92:G:N1	2.52	0.57
52:X:419:G:N2	52:X:448:A:OP2	2.37	0.57
52:X:2532:A:O2'	52:X:2534:G:OP2	2.23	0.57
10:E:13:GLU:OE1	10:E:13:GLU:N	2.38	0.57
13:H:12:THR:HG21	53:A:886:A:C1'	2.35	0.57
21:P:6:ARG:N	21:P:21:VAL:O	2.37	0.57
31:a:54:ASP:OD1	31:a:55:ASP:N	2.37	0.57
33:c:34:ILE:HD13	33:c:156:ILE:HG23	1.87	0.57
7:B:75:GLN:N	7:B:75:GLN:OE1	2.37	0.57
23:R:47:ARG:NH1	23:R:52:THR:O	2.37	0.57
25:T:43:GLU:OE2	25:T:47:ALA:N	2.38	0.57
30:Z:145:GLU:OE2	30:Z:189:ARG:N	2.38	0.57
9:D:118:HIS:O	9:D:119:ILE:HD13	2.04	0.57
10:E:152:ASP:OD1	10:E:152:ASP:N	2.37	0.57
52:X:1574:G:N1	52:X:1592:A:OP2	2.38	0.57
52:X:1695:A:HO2'	52:X:1696:G:P	2.28	0.56
8:C:124:GLU:OE2	8:C:189:ASP:N	2.37	0.56
15:J:43:PRO:O	15:J:71:LYS:NZ	2.39	0.56
25:T:76:LYS:NZ	53:A:183:U:O2	2.38	0.56
41:m:1:MET:N	52:X:2901:G:OP1	2.38	0.56
51:9:35:LEU:O	51:9:36:ALA:HB2	2.04	0.56
52:X:1836:G:N2	52:X:1839:A:OP2	2.38	0.56
52:X:2830:A:O2'	52:X:2831:A:OP2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1270:A:N6	53:A:1283:A:O2'	2.39	0.56
12:G:63:GLU:OE1	12:G:63:GLU:N	2.38	0.56
18:M:72:GLU:O	18:M:75:LEU:HD12	2.05	0.56
22:Q:50:ASP:OD1	22:Q:51:GLU:N	2.39	0.56
23:R:46:PRO:O	23:R:50:THR:HG22	2.05	0.56
32:b:54:ARG:NH1	52:X:720:C:OP1	2.34	0.56
52:X:1081:U:O2	52:X:1166:G:O6	2.23	0.56
52:X:2155:A:N6	52:X:2192:U:OP2	2.35	0.56
52:X:2909:U:O2'	52:X:2910:C:O4'	2.23	0.56
13:H:25:LEU:HD23	13:H:26:GLU:N	2.21	0.56
39:k:73:GLU:N	39:k:73:GLU:OE1	2.37	0.56
46:t:95:LYS:NZ	52:X:342:A:OP1	2.39	0.56
52:X:1838:A:O2'	52:X:1839:A:O4'	2.17	0.56
13:H:49:VAL:HG23	13:H:62:VAL:HG12	1.87	0.56
52:X:1757:G:O2'	52:X:1758:U:O3'	2.23	0.56
13:H:109:SER:OG	53:A:649:A:N3	2.38	0.56
27:V:459:C:O2'	27:V:460:G:OP2	2.19	0.56
29:Y:30:C:N4	29:Y:31:G:O6	2.39	0.56
34:d:55:ARG:NE	34:d:58:ASP:OD1	2.34	0.56
37:i:120:LYS:C	37:i:121:LEU:HD22	2.30	0.56
48:v:55:LYS:NZ	52:X:446:G:OP2	2.33	0.56
51:9:101:GLN:O	51:9:102:LEU:C	2.48	0.56
29:Y:44:A:O2'	29:Y:45:C:O4'	2.07	0.56
52:X:511:U:O2'	52:X:512:G:OP1	2.24	0.56
52:X:89:U:OP2	52:X:90:A:O2'	2.23	0.56
2:1:17:TYR:HH	52:X:2376:C:HO2'	1.47	0.56
7:B:102:THR:OG1	53:A:1084:G:O3'	2.23	0.56
10:E:46:VAL:HG11	10:E:118:ALA:HB2	1.88	0.56
19:N:52:GLN:C	19:N:53:ILE:HD12	2.31	0.56
20:O:74:ASP:CG	20:O:76:THR:HG1	2.14	0.56
24:S:73:GLU:N	24:S:73:GLU:OE1	2.38	0.56
34:d:57:SER:OG	34:d:62:HIS:ND1	2.37	0.56
52:X:84:A:O2'	52:X:85:G:OP2	2.20	0.56
53:A:1006:A:N1	53:A:1055:C:O2'	2.34	0.56
53:A:1220:U:O2'	53:A:1222:A:N6	2.38	0.56
32:b:154:ILE:HG23	32:b:175:VAL:HG22	1.88	0.55
52:X:39:C:O2'	52:X:659:A:N1	2.39	0.55
53:A:774:G:H1	53:A:821:G:HO2'	1.54	0.55
53:A:954:G:H21	53:A:1348:A:H62	1.53	0.55
9:D:58:ARG:NE	9:D:65:GLU:OE1	2.39	0.55
14:I:113:ARG:NH1	19:N:61:TRP:OXT	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:43:SER:OG	53:A:288:C:N3	2.32	0.55
31:a:103:SER:N	31:a:106:GLU:OE1	2.36	0.55
25:T:43:GLU:OE2	25:T:46:LYS:N	2.40	0.55
26:U:48:C:H42	26:U:59:G:H21	1.52	0.55
31:a:8:ARG:NH2	31:a:54:ASP:OD2	2.37	0.55
49:w:30:PHE:O	49:w:34:THR:HG22	2.07	0.55
53:A:468:C:N3	53:A:483:G:N2	2.54	0.55
21:P:53:GLU:HB2	21:P:79:ILE:HD13	1.89	0.55
25:T:49:THR:O	25:T:52:THR:OG1	2.22	0.55
52:X:441:C:HO2'	52:X:442:C:C5'	2.17	0.55
52:X:1176:U:O2'	52:X:1177:G:OP1	2.22	0.55
10:E:104:GLY:N	10:E:122:ASP:OD1	2.37	0.55
34:d:42:MET:HE3	34:d:65:LEU:HD11	1.88	0.55
52:X:1105:G:N1	52:X:1126:A:C6	2.75	0.55
52:X:1886:G:H8	52:X:1914:A:H62	1.54	0.55
33:c:34:ILE:HD11	33:c:154:ILE:CG2	2.36	0.55
7:B:153:ASP:C	7:B:154:MET:HE2	2.32	0.55
13:H:76:GLY:O	13:H:77:LEU:HD23	2.07	0.55
35:e:38:ARG:NH1	52:X:1053:C:OP1	2.38	0.55
52:X:1695:A:O2'	52:X:1696:G:O5'	2.25	0.55
52:X:2231:C:O2'	52:X:2233:C:OP1	2.25	0.55
36:f:16:ALA:HB2	36:f:52:VAL:HG21	1.89	0.55
46:t:82:GLY:N	46:t:93:VAL:O	2.40	0.55
45:s:77:ARG:NH1	52:X:1645:C:OP1	2.40	0.55
52:X:221:G:H22	52:X:238:U:H4'	1.72	0.55
23:R:19:THR:HG23	53:A:855:G:OP1	2.07	0.54
52:X:2064:G:H3'	52:X:2065:C:H5'	1.89	0.54
9:D:17:ILE:HD13	9:D:56:LYS:HD3	1.88	0.54
24:S:63:SER:OG	24:S:65:ASP:OD1	2.24	0.54
25:T:15:ASN:OD1	25:T:16:GLU:N	2.41	0.54
53:A:1316:U:O2'	53:A:1317:C:OP1	2.20	0.54
10:E:12:GLU:N	10:E:12:GLU:OE1	2.41	0.54
17:L:121:GLU:OE2	17:L:121:GLU:N	2.37	0.54
31:a:79:PHE:CD2	31:a:199:LEU:HD12	2.41	0.54
35:e:15:LYS:N	35:e:53:ASP:OD1	2.40	0.54
36:f:24:VAL:HG11	36:f:33:ALA:HB2	1.90	0.54
51:9:46:ALA:HB1	52:X:285:U:C2	2.43	0.54
30:Z:172:VAL:N	30:Z:184:ILE:O	2.39	0.54
47:u:58:ASN:ND2	47:u:89:VAL:O	2.41	0.54
5:4:23:VAL:HG22	5:4:36:GLN:NE2	2.22	0.54
32:b:138:GLU:N	32:b:138:GLU:OE1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:l:40:ILE:HD11	40:l:105:ARG:HE	1.71	0.54
43:o:68:ALA:O	43:o:89:ARG:NE	2.40	0.54
53:A:1217:C:N4	53:A:1218:C:H41	2.05	0.54
12:G:40:GLN:O	12:G:41:THR:HG23	2.07	0.54
53:A:86:G:O2'	53:A:87:C:O4'	2.21	0.54
26:U:55:U:O2'	26:U:57:G:N7	2.32	0.54
49:w:2:LYS:NZ	52:X:78:U:OP2	2.40	0.54
52:X:2785:U:HO2'	52:X:2786:A:P	2.31	0.54
53:A:1106:C:O2	53:A:1179:A:O2'	2.25	0.54
35:e:82:PRO:O	35:e:84:GLY:N	2.40	0.53
38:j:17:MET:HE1	38:j:40:SER:C	2.33	0.53
52:X:1683:C:O2	52:X:2727:U:O2'	2.26	0.53
52:X:2534:G:O2'	52:X:2535:U:O5'	2.20	0.53
53:A:986:G:O2'	53:A:987:A:OP2	2.21	0.53
53:A:1459:U:N3	53:A:1460:U:O2	2.41	0.53
33:c:34:ILE:HD13	33:c:156:ILE:CG2	2.37	0.53
53:A:1325:G:N1	53:A:1328:A:OP2	2.41	0.53
17:L:3:THR:HG22	17:L:7:LEU:HD23	1.90	0.53
31:a:19:ASN:OD1	31:a:20:GLY:N	2.40	0.53
33:c:38:MET:HE1	33:c:151:GLY:O	2.09	0.53
52:X:1012:G:O4'	52:X:2296:A:N6	2.41	0.53
52:X:2347:G:O2'	52:X:2350:G:O6	2.26	0.53
53:A:195:A:O2'	53:A:196:U:O5'	2.25	0.53
52:X:1501:U:O2'	52:X:1502:G:N7	2.42	0.53
9:D:104:ALA:HB1	9:D:109:GLN:HB3	1.89	0.53
34:d:159:LYS:NZ	52:X:2687:C:OP1	2.41	0.53
42:n:111:ASP:OD1	42:n:112:ALA:N	2.41	0.53
51:9:18:VAL:CB	51:9:39:ALA:HB2	2.38	0.53
53:A:937:G:O2'	53:A:1513:A:N1	2.40	0.53
16:K:76:SER:HB2	16:K:81:LEU:HD11	1.91	0.53
52:X:1711:G:O6	52:X:1712:G:N2	2.41	0.53
52:X:2244:G:HO2'	52:X:2245:G:P	2.32	0.53
52:X:2785:U:O2'	52:X:2786:A:O5'	2.16	0.53
53:A:1021:U:O2'	53:A:1022:A:O5'	2.24	0.53
9:D:91:ASP:OD2	9:D:164:TYR:OH	2.27	0.53
32:b:89:VAL:HG22	32:b:90:PHE:HD2	1.74	0.53
1:0:17:ARG:NH1	52:X:1306:G:OP2	2.41	0.53
7:B:90:TYR:CD1	7:B:154:MET:HE1	2.44	0.53
49:w:16:GLN:OE1	49:w:16:GLN:N	2.40	0.53
51:9:81:ALA:HB1	51:9:148:GLU:C	2.33	0.53
52:X:2561:G:O2'	52:X:2686:A:N1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:104:PHE:O	7:B:107:ILE:N	2.41	0.53
7:B:110:ARG:NH1	53:A:1114:G:O5'	2.41	0.53
17:L:2:PRO:O	17:L:6:GLN:NE2	2.42	0.53
29:Y:76:A:H62	29:Y:96:G:H21	1.56	0.53
10:E:126:LYS:NZ	53:A:11:G:OP2	2.24	0.53
52:X:2244:G:O2'	52:X:2245:G:O5'	2.26	0.53
1:0:35:GLU:OE2	1:0:45:ALA:HB3	2.08	0.52
12:G:72:VAL:HG23	12:G:73:LEU:CD1	2.36	0.52
24:S:49:ILE:CD1	24:S:62:ILE:HD11	2.38	0.52
9:D:25:GLU:C	9:D:26:LEU:HD22	2.33	0.52
10:E:115:LEU:HD12	10:E:120:VAL:HG21	1.90	0.52
20:O:6:GLU:OE1	20:O:6:GLU:N	2.40	0.52
49:w:48:LYS:NZ	52:X:75:G:O3'	2.42	0.52
53:A:1067:G:N1	53:A:1212:C:O2	2.43	0.52
22:Q:70:SER:O	22:Q:74:ARG:NH1	2.43	0.52
31:a:47:GLU:N	31:a:47:GLU:OE1	2.42	0.52
53:A:674:A:N7	53:A:733:G:O6	2.42	0.52
53:A:774:G:N2	53:A:822:U:OP2	2.42	0.52
7:B:90:TYR:CG	7:B:154:MET:HE1	2.45	0.52
38:j:111:GLU:OE2	38:j:115:ARG:NH2	2.42	0.52
53:A:332:G:N1	53:A:335:A:OP2	2.42	0.52
53:A:1369:A:O2'	53:A:1370:G:OP1	2.26	0.52
23:R:29:LYS:O	23:R:31:VAL:HG13	2.10	0.52
9:D:28:LYS:NZ	53:A:421:G:O6	2.36	0.52
17:L:94:LEU:O	17:L:111:VAL:HG12	2.10	0.52
35:e:73:LYS:HB3	35:e:90:ALA:HB2	1.92	0.52
46:t:92:ARG:O	46:t:101:LEU:N	2.40	0.52
52:X:2130:G:N7	52:X:2217:U:N3	2.56	0.52
25:T:70:ASN:ND2	53:A:271:A:O5'	2.43	0.52
30:Z:123:ASP:OD1	30:Z:123:ASP:N	2.43	0.52
33:c:125:ARG:NH2	52:X:2344:U:O2	2.43	0.52
52:X:291:C:O2'	52:X:292:U:O5'	2.24	0.52
53:A:1276:C:O2'	53:A:1277:G:OP1	2.27	0.52
7:B:14:VAL:HG12	7:B:14:VAL:O	2.09	0.52
47:u:84:ARG:NH1	52:X:2361:C:OP1	2.43	0.52
52:X:1087:U:O2	52:X:1160:G:C6	2.63	0.52
7:B:11:GLU:OE1	7:B:11:GLU:N	2.43	0.52
34:d:5:GLY:O	34:d:66:HIS:NE2	2.43	0.52
36:f:14:SER:O	36:f:52:VAL:HG22	2.10	0.52
38:j:47:ILE:HD12	38:j:47:ILE:H	1.75	0.52
39:k:72:ASN:O	39:k:76:ASN:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:2160:U:O2'	52:X:2186:G:N2	2.42	0.52
53:A:661:U:O4	53:A:761:G:O2'	2.20	0.52
2:1:9:CYS:SG	2:1:11:GLU:N	2.82	0.51
10:E:94:ILE:HD11	10:E:136:MET:HG3	1.92	0.51
13:H:26:GLU:N	13:H:26:GLU:OE1	2.43	0.51
52:X:1461:A:N6	52:X:1630:G:O2'	2.41	0.51
53:A:254:A:H62	53:A:289:G:N2	2.08	0.51
53:A:541:A:N6	53:A:1214:U:O2	2.43	0.51
53:A:598:U:H3	53:A:659:A:H62	1.58	0.51
11:F:9:ILE:HD13	11:F:87:ARG:HB2	1.93	0.51
12:G:74:GLU:N	12:G:74:GLU:OE1	2.43	0.51
15:J:97:ASP:OD1	15:J:98:ILE:N	2.43	0.51
45:s:5:ARG:NH2	49:w:23:GLU:OE2	2.42	0.51
49:w:28:LEU:HD21	49:w:42:ARG:CG	2.41	0.51
52:X:510:G:N2	52:X:513:A:OP2	2.38	0.51
44:r:57:ASN:O	44:r:64:MET:HE1	2.09	0.51
53:A:1001:U:O2'	53:A:1002:U:OP2	2.28	0.51
13:H:48:ASP:OD1	13:H:49:VAL:N	2.43	0.51
33:c:134:GLU:N	33:c:134:GLU:OE1	2.43	0.51
43:o:98:GLU:OE1	43:o:98:GLU:N	2.43	0.51
50:x:6:ILE:N	50:x:35:VAL:O	2.42	0.51
51:9:9:VAL:O	51:9:12:LYS:CB	2.58	0.51
52:X:32:C:N4	52:X:494:A:OP2	2.44	0.51
52:X:1074:A:OP2	52:X:1172:A:N6	2.41	0.51
52:X:1127:U:O2'	52:X:1128:U:O5'	2.29	0.51
7:B:78:ASP:OD1	7:B:79:SER:N	2.44	0.51
35:e:31:SER:HA	35:e:109:MET:HE2	1.92	0.51
36:f:28:SER:OG	36:f:29:GLY:N	2.40	0.51
42:n:27:SER:HB2	42:n:31:LEU:HD23	1.90	0.51
45:s:40:LYS:HG3	45:s:51:VAL:HG11	1.93	0.51
52:X:762:A:O2'	52:X:763:A:OP1	2.25	0.51
53:A:518:A:O2'	53:A:519:A:O4'	2.27	0.51
52:X:52:A:OP2	52:X:116:G:N1	2.42	0.51
53:A:1260:A:N6	53:A:1363:C:O2'	2.43	0.51
14:I:37:GLU:OE1	14:I:37:GLU:N	2.40	0.51
21:P:20:ILE:HD12	21:P:20:ILE:H	1.76	0.51
30:Z:79:ALA:HA	30:Z:112:VAL:HG23	1.92	0.51
40:l:66:GLU:N	40:l:66:GLU:OE1	2.44	0.51
51:9:8:ASP:HA	51:9:14:LYS:HA	1.91	0.51
52:X:342:A:N1	52:X:366:A:O2'	2.33	0.51
52:X:1156:G:O2'	52:X:1157:A:O5'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:328:G:HO2'	53:A:1444:G:HO2'	1.51	0.51
53:A:1369:A:HO2'	53:A:1370:G:P	2.32	0.51
12:G:102:ARG:NH1	53:A:949:G:O3'	2.40	0.51
13:H:54:ASP:OD1	13:H:56:LYS:N	2.42	0.51
36:f:115:VAL:HG13	36:f:121:VAL:HG11	1.92	0.51
37:i:110:LYS:NZ	52:X:682:G:N7	2.44	0.51
52:X:999:A:O2'	52:X:2295:A:OP2	2.29	0.51
15:J:28:THR:HG21	15:J:90:LEU:HD11	1.93	0.51
17:L:12:ARG:HD2	53:A:571:U:HI'	1.92	0.51
53:A:1063:G:N2	53:A:1068:G:O6	2.44	0.51
10:E:74:VAL:CG2	10:E:144:LEU:HD12	2.41	0.51
17:L:48:THR:N	17:L:67:ARG:O	2.44	0.51
38:j:6:ARG:NH1	52:X:917:A:OP1	2.44	0.51
52:X:2225:C:H2'	52:X:2226:U:C6	2.45	0.51
18:M:39:VAL:HG12	18:M:39:VAL:O	2.11	0.50
44:r:9:THR:O	44:r:9:THR:OG1	2.20	0.50
14:I:18:ARG:NE	14:I:66:ASN:OD1	2.44	0.50
14:I:67:VAL:O	14:I:68:HIS:ND1	2.32	0.50
16:K:22:ILE:HD11	16:K:39:THR:HA	1.93	0.50
30:Z:17:THR:OG1	30:Z:204:ASN:N	2.42	0.50
4:3:4:MET:HE1	4:3:60:GLN:HG3	1.93	0.50
9:D:15:LEU:HD12	9:D:56:LYS:HG3	1.93	0.50
17:L:25:ASN:OD1	17:L:25:ASN:N	2.42	0.50
24:S:23:ASN:OD1	24:S:24:GLU:N	2.45	0.50
38:j:105:GLU:C	38:j:106:ILE:HD13	2.36	0.50
46:t:40:MET:HE3	46:t:40:MET:HA	1.93	0.50
12:G:70:MET:HE1	12:G:97:THR:HA	1.93	0.50
34:d:27:VAL:HB	34:d:76:MET:HE1	1.92	0.50
52:X:822:G:OP1	52:X:824:G:O2'	2.27	0.50
9:D:171:LYS:O	9:D:172:LEU:HD23	2.12	0.50
15:J:19:ASP:OD1	15:J:19:ASP:N	2.43	0.50
21:P:52:ASP:OD1	21:P:53:GLU:N	2.44	0.50
26:U:18:G:O2'	26:U:57:G:N2	2.45	0.50
45:s:25:LYS:NZ	52:X:1437:C:O3'	2.40	0.50
29:Y:40:C:O2'	33:c:63:GLN:OE1	2.29	0.50
10:E:152:ASP:O	10:E:156:LEU:HD23	2.11	0.50
52:X:1139:G:N2	52:X:1146:C:O2	2.45	0.50
52:X:2823:C:N4	52:X:2826:A:OP1	2.44	0.50
53:A:1018:U:O4	53:A:1033:G:N2	2.45	0.50
53:A:1046:G:O2'	53:A:1047:C:O4'	2.29	0.50
19:N:19:GLN:N	19:N:19:GLN:OE1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:S:16:MET:HE1	24:S:44:PHE:CZ	2.47	0.50
53:A:954:G:H21	53:A:1348:A:N6	2.09	0.50
12:G:75:VAL:HG21	12:G:86:GLN:HB3	1.94	0.50
18:M:108:THR:HG21	53:A:1316:U:O4'	2.11	0.50
19:N:42:ILE:HG23	19:N:43:CYS:H	1.77	0.50
51:9:84:GLY:N	51:9:149:ALA:H	2.08	0.50
52:X:2497:A:O2'	52:X:2498:A:O5'	2.29	0.50
25:T:35:VAL:HG12	25:T:50:ALA:CB	2.42	0.49
52:X:1115:A:N7	52:X:1119:A:N6	2.59	0.49
52:X:1898:G:N2	52:X:1901:A:OP2	2.41	0.49
14:I:60:THR:HG23	14:I:61:TYR:HD1	1.76	0.49
21:P:45:LYS:HE3	21:P:45:LYS:HA	1.93	0.49
52:X:1994:C:OP1	52:X:1995:A:O2'	2.28	0.49
10:E:97:LYS:O	10:E:123:ILE:HD12	2.12	0.49
31:a:38:LYS:NZ	31:a:91:TYR:O	2.37	0.49
42:n:66:ASN:ND2	52:X:1057:G:OP2	2.44	0.49
44:r:36:LEU:HA	44:r:39:THR:HG22	1.93	0.49
51:9:2:LYS:HA	51:9:19:LYS:O	2.12	0.49
53:A:388:G:N2	53:A:391:A:OP2	2.44	0.49
9:D:113:LEU:O	9:D:117:GLY:N	2.44	0.49
24:S:21:LYS:O	24:S:25:THR:HG22	2.12	0.49
51:9:8:ASP:HA	51:9:13:GLY:O	2.12	0.49
52:X:1945:A:HO2'	52:X:1946:U:C4'	2.25	0.49
2:l:19:SER:OG	2:l:20:LYS:N	2.46	0.49
9:D:113:LEU:HG	9:D:119:ILE:HD11	1.94	0.49
34:d:8:LEU:HD21	34:d:50:VAL:HG22	1.94	0.49
35:e:121:LYS:NZ	52:X:2809:G:OP2	2.45	0.49
36:f:106:LEU:HD22	36:f:111:PHE:HD2	1.76	0.49
53:A:306:A:O2'	53:A:307:G:OP1	2.30	0.49
22:Q:51:GLU:N	22:Q:51:GLU:OE2	2.46	0.49
46:t:23:ILE:HD11	46:t:35:VAL:HG22	1.95	0.49
9:D:15:LEU:HD12	9:D:56:LYS:CG	2.43	0.49
10:E:132:THR:OG1	53:A:21:C:OP2	2.29	0.49
20:O:35:SER:OG	20:O:59:MET:SD	2.64	0.49
29:Y:37:A:O2'	29:Y:38:U:O4'	2.25	0.49
46:t:49:GLN:OE1	46:t:50:ALA:N	2.46	0.49
52:X:2534:G:HO2'	52:X:2535:U:P	2.35	0.49
53:A:1330:U:OP2	53:A:1331:C:O2'	2.28	0.49
7:B:163:ILE:CD1	7:B:183:ILE:HD11	2.42	0.49
41:m:102:GLU:N	41:m:102:GLU:OE1	2.46	0.49
52:X:2141:A:N7	52:X:2198:G:N2	2.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:23:LYS:HE3	2:1:23:LYS:HA	1.94	0.49
10:E:38:VAL:HG21	10:E:114:VAL:HG22	1.95	0.49
13:H:80:ILE:HD11	13:H:127:VAL:HG22	1.95	0.49
36:f:34:ASN:O	36:f:62:ILE:HD11	2.12	0.49
36:f:34:ASN:C	36:f:62:ILE:HD11	2.37	0.49
52:X:160:G:N2	52:X:167:U:O2	2.46	0.49
52:X:2089:A:O2'	52:X:2090:G:OP2	2.27	0.49
53:A:603:U:C2	53:A:655:G:N1	2.81	0.49
5:4:35:LYS:NZ	52:X:2771:G:OP1	2.44	0.49
6:6:40:HIS:O	6:6:44:THR:HG23	2.13	0.49
9:D:84:GLU:N	9:D:84:GLU:OE1	2.46	0.49
31:a:43:ASN:OD1	31:a:44:ASP:N	2.46	0.49
33:c:143:TYR:O	33:c:146:VAL:HG12	2.12	0.49
10:E:46:VAL:HG12	10:E:117:LEU:HD23	1.94	0.48
10:E:85:ILE:HG21	10:E:147:LEU:HD11	1.95	0.48
34:d:103:LYS:HG3	34:d:117:VAL:HG22	1.95	0.48
46:t:40:MET:HE1	46:t:60:GLU:OE1	2.13	0.48
49:w:5:GLU:OE2	49:w:5:GLU:N	2.37	0.48
52:X:309:U:O2'	52:X:407:A:N1	2.39	0.48
52:X:2497:A:O5'	52:X:2505:A:N6	2.46	0.48
16:K:25:ILE:CG2	16:K:34:VAL:HG23	2.42	0.48
16:K:83:THR:C	16:K:84:LEU:HD22	2.38	0.48
16:K:118:VAL:HG13	16:K:118:VAL:O	2.13	0.48
31:a:35:VAL:HG22	31:a:49:ILE:HD12	1.96	0.48
47:u:24:SER:OG	52:X:2291:U:OP2	2.30	0.48
52:X:292:U:O2'	52:X:293:U:O4'	2.31	0.48
52:X:1945:A:HO2'	52:X:1946:U:C5'	2.26	0.48
53:A:1087:G:N2	53:A:1090:A:OP2	2.40	0.48
6:6:16:CYS:SG	6:6:17:ALA:N	2.87	0.48
15:J:24:LYS:O	15:J:28:THR:HG22	2.13	0.48
32:b:38:LEU:HD11	52:X:1285:G:H4'	1.94	0.48
34:d:34:LEU:HD22	34:d:76:MET:HE3	1.96	0.48
38:j:91:GLU:OE2	38:j:91:GLU:N	2.46	0.48
40:l:1:MET:HE2	40:l:2:ILE:O	2.12	0.48
53:A:587:C:O2'	53:A:737:A:N3	2.44	0.48
14:I:88:LEU:HD21	14:I:98:LEU:HD23	1.95	0.48
31:a:199:LEU:HD23	31:a:200:ILE:N	2.28	0.48
42:n:26:GLY:O	42:n:29:HIS:ND1	2.47	0.48
51:9:24:GLY:C	51:9:26:ALA:N	2.67	0.48
52:X:1125:C:H41	52:X:1134:A:H5''	1.79	0.48
53:A:1247:A:OP1	53:A:1344:C:O2'	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:10:THR:OG1	2:1:46:ARG:NH2	2.46	0.48
16:K:89:LYS:NZ	53:A:716:U:OP1	2.36	0.48
25:T:45:ASP:OD1	25:T:46:LYS:N	2.46	0.48
30:Z:123:ASP:OD2	30:Z:125:LYS:NZ	2.46	0.48
33:c:69:ARG:HH21	33:c:70:ALA:HB3	1.78	0.48
33:c:161:ASN:N	33:c:165:GLU:OE2	2.42	0.48
36:f:44:LYS:O	36:f:54:LYS:NZ	2.44	0.48
41:m:21:ARG:NH2	52:X:2874:G:O6	2.43	0.48
51:9:64:GLN:HA	51:9:67:SER:CB	2.44	0.48
53:A:1276:C:HO2'	53:A:1277:G:P	2.37	0.48
14:I:33:ARG:NH2	14:I:37:GLU:OE2	2.46	0.48
17:L:3:THR:O	17:L:7:LEU:HD23	2.13	0.48
34:d:51:LEU:HD12	34:d:51:LEU:O	2.13	0.48
9:D:185:LEU:HD23	9:D:186:ALA:HB2	1.96	0.48
9:D:191:GLU:OE1	9:D:192:ALA:N	2.46	0.48
32:b:182:ASN:ND2	52:X:661:A:N3	2.61	0.48
51:9:3:VAL:CA	51:9:38:GLU:CA	2.62	0.48
52:X:774:A:OP1	52:X:1477:A:O2'	2.29	0.48
52:X:2337:G:O2'	52:X:2338:A:N3	2.46	0.48
38:j:54:MET:HE3	38:j:54:MET:HA	1.96	0.48
39:k:104:LEU:HD11	39:k:116:ILE:HG12	1.96	0.48
44:r:78:GLU:O	52:X:24:G:O2'	2.26	0.48
52:X:164:U:HO2'	52:X:165:C:P	2.31	0.48
52:X:1070:G:OP2	52:X:1071:G:O2'	2.27	0.48
7:B:57:THR:HG21	7:B:217:MET:SD	2.54	0.48
7:B:211:LYS:O	7:B:215:SER:OG	2.22	0.48
9:D:101:LEU:HD23	9:D:165:LEU:HD13	1.96	0.48
12:G:146:GLU:OE2	12:G:146:GLU:N	2.46	0.48
15:J:91:ASP:O	15:J:92:LEU:HD22	2.14	0.48
29:Y:29:C:O2'	29:Y:51:A:N1	2.37	0.48
52:X:1567:U:O2'	52:X:1568:G:OP1	2.31	0.48
5:4:12:GLU:OE2	5:4:12:GLU:N	2.38	0.48
9:D:17:ILE:HD13	9:D:56:LYS:CD	2.43	0.48
14:I:114:LYS:NZ	14:I:118:LEU:O	2.46	0.48
31:a:71:LYS:NZ	52:X:2814:U:O3'	2.46	0.48
46:t:10:MET:HE3	46:t:18:GLY:CA	2.43	0.48
52:X:2356:A:H2'	52:X:2357:A:C8	2.48	0.48
4:3:24:ARG:NH1	52:X:2390:A:OP1	2.45	0.47
26:U:31:C:HO2'	53:A:1349:A:HO2'	1.59	0.47
52:X:868:A:H61	52:X:1018:G:C2'	2.27	0.47
52:X:1064:U:O2'	52:X:1166:G:N2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:1598:C:OP1	52:X:1764:U:O2'	2.21	0.47
4:3:18:GLY:O	4:3:19:SER:OG	2.29	0.47
19:N:39:LEU:HD21	19:N:47:LEU:HD11	1.95	0.47
21:P:57:LEU:HD13	21:P:79:ILE:HD11	1.95	0.47
51:9:148:GLU:O	51:9:149:ALA:C	2.55	0.47
7:B:75:GLN:CG	7:B:207:ILE:HG22	2.44	0.47
7:B:184:ILE:HD12	7:B:198:VAL:HB	1.96	0.47
18:M:72:GLU:OE1	18:M:73:VAL:N	2.47	0.47
31:a:168:GLN:O	31:a:169:ILE:HD13	2.14	0.47
32:b:24:PHE:O	32:b:115:SER:OG	2.31	0.47
44:r:41:ARG:NH1	52:X:2039:G:OP2	2.47	0.47
53:A:372:A:HO2'	53:A:373:U:C5'	2.26	0.47
23:R:60:LEU:O	23:R:64:ILE:HD12	2.14	0.47
24:S:49:ILE:HD13	24:S:62:ILE:HD11	1.96	0.47
52:X:684:G:N1	52:X:697:G:O6	2.48	0.47
8:C:4:LYS:NZ	53:A:1201:C:OP2	2.47	0.47
10:E:23:LYS:NZ	53:A:1092:A:OP1	2.39	0.47
23:R:37:PHE:HD2	23:R:60:LEU:HD11	1.79	0.47
31:a:2:THR:HG23	31:a:86:VAL:HG12	1.96	0.47
40:l:43:GLN:OE1	40:l:52:THR:HG21	2.15	0.47
44:r:28:GLN:HA	44:r:70:VAL:HG23	1.97	0.47
51:9:31:ILE:HA	51:9:36:ALA:CB	2.43	0.47
53:A:437:U:O2'	53:A:438:A:OP2	2.24	0.47
53:A:900:G:O2'	53:A:916:G:O6	2.17	0.47
12:G:102:ARG:NH2	53:A:949:G:O3'	2.48	0.47
18:M:28:THR:HG21	53:A:1337:C:O5'	2.14	0.47
26:U:9:A:O2'	26:U:10:G:N7	2.47	0.47
47:u:85:LYS:NZ	52:X:904:A:OP1	2.47	0.47
53:A:1135:U:O2'	53:A:1136:U:O5'	2.27	0.47
7:B:151:ILE:O	7:B:151:ILE:HG22	2.15	0.47
12:G:129:ASN:OD1	12:G:130:ASN:N	2.48	0.47
14:I:10:GLY:N	14:I:17:ALA:O	2.45	0.47
16:K:31:ASN:ND2	53:A:699:G:OP2	2.47	0.47
17:L:93:VAL:HG21	17:L:110:ILE:HD12	1.96	0.47
29:Y:97:A:H61	29:Y:99:A:N6	2.12	0.47
32:b:46:GLN:NE2	52:X:489:G:O4'	2.47	0.47
52:X:646:A:O2'	52:X:648:G:O2'	2.29	0.47
52:X:1007:G:H22	52:X:2059:A:P	2.38	0.47
52:X:2717:G:N1	52:X:2749:U:OP2	2.39	0.47
52:X:2909:U:O2'	52:X:2910:C:O5'	2.31	0.47
7:B:123:ASN:OD1	7:B:124:GLY:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:11:LEU:HD22	10:E:68:LYS:HD2	1.96	0.47
52:X:101:G:HO2'	52:X:102:A:P	2.38	0.47
52:X:1474:C:N4	52:X:1618:A:OP2	2.41	0.47
53:A:75:G:N1	53:A:93:G:OP2	2.44	0.47
53:A:778:G:H4'	53:A:1523:A:H4'	1.96	0.47
31:a:133:MET:HE1	31:a:140:HIS:HB3	1.96	0.47
40:l:22:LEU:HD12	40:l:23:SER:N	2.29	0.47
49:w:34:THR:HG23	49:w:36:GLN:OE1	2.15	0.47
52:X:673:A:O4'	52:X:683:A:N6	2.47	0.47
53:A:1213:A:HO2'	53:A:1214:U:P	2.32	0.47
8:C:14:VAL:O	8:C:15:ILE:HD13	2.15	0.47
8:C:175:HIS:ND1	53:A:1119:C:OP2	2.48	0.47
31:a:199:LEU:O	31:a:200:ILE:HD13	2.15	0.47
33:c:42:ASP:O	33:c:43:ALA:C	2.56	0.47
37:i:76:VAL:HG13	37:i:112:LEU:HD23	1.97	0.47
52:X:282:G:O2'	52:X:283:G:OP2	2.26	0.47
52:X:939:G:O2'	52:X:940:G:O4'	2.32	0.47
7:B:103:ASN:ND2	53:A:1084:G:O4'	2.41	0.46
8:C:21:LYS:O	15:J:94:SER:OG	2.30	0.46
12:G:30:MET:HE2	12:G:31:MET:H	1.79	0.46
14:I:88:LEU:CD2	14:I:98:LEU:HD23	2.45	0.46
30:Z:62:TYR:OH	52:X:1846:G:OP1	2.30	0.46
36:f:108:GLU:OE2	36:f:108:GLU:N	2.39	0.46
37:i:6:LEU:O	52:X:1283:U:O2'	2.31	0.46
5:4:17:ILE:HG21	5:4:26:ILE:HG12	1.97	0.46
30:Z:86:ASN:O	30:Z:87:ARG:NE	2.48	0.46
32:b:125:VAL:HA	32:b:194:ILE:HG23	1.98	0.46
33:c:36:ILE:HG21	33:c:57:LEU:HD11	1.97	0.46
38:j:38:GLU:N	38:j:38:GLU:OE2	2.48	0.46
52:X:2529:U:O2'	52:X:2533:U:OP1	2.24	0.46
53:A:1288:A:O2'	53:A:1291:C:N4	2.48	0.46
7:B:163:ILE:HD11	7:B:183:ILE:HD11	1.97	0.46
10:E:111:VAL:O	10:E:115:LEU:HD23	2.15	0.46
11:F:89:ILE:HG13	23:R:70:MET:HE3	1.97	0.46
16:K:81:LEU:HD12	16:K:81:LEU:O	2.15	0.46
32:b:6:LEU:HA	32:b:125:VAL:HG13	1.98	0.46
33:c:42:ASP:OD2	33:c:44:VAL:HG23	2.14	0.46
52:X:1712:G:N2	52:X:2021:G:OP2	2.48	0.46
53:A:1499:G:O2'	53:A:1500:U:OP1	2.28	0.46
9:D:156:GLU:OE2	9:D:157:VAL:HG13	2.15	0.46
11:F:9:ILE:HG23	11:F:59:PHE:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:H:97:VAL:HG22	13:H:98:LEU:HD23	1.97	0.46
52:X:1105:G:N1	52:X:1126:A:N1	2.63	0.46
2:1:15:ARG:NH2	2:1:39:ASP:OD2	2.45	0.46
10:E:45:HIS:NE2	10:E:73:GLU:OE2	2.48	0.46
18:M:50:GLU:OE1	18:M:50:GLU:N	2.40	0.46
21:P:14:LYS:NZ	53:A:400:G:O3'	2.47	0.46
47:u:47:ARG:NH1	52:X:2384:C:O2'	2.48	0.46
53:A:86:G:O2'	53:A:87:C:O5'	2.33	0.46
9:D:75:ALA:HB2	9:D:89:LEU:HD12	1.97	0.46
20:O:17:THR:N	20:O:21:ASP:OD2	2.47	0.46
29:Y:47:C:OP2	40:l:105:ARG:NH1	2.48	0.46
29:Y:55:A:C2	33:c:26:MET:HE1	2.51	0.46
30:Z:7:LYS:NZ	52:X:753:A:OP1	2.28	0.46
34:d:85:GLU:N	34:d:85:GLU:OE1	2.48	0.46
35:e:66:THR:HG21	52:X:1187:U:OP1	2.15	0.46
42:n:86:SER:N	42:n:116:GLN:OE1	2.49	0.46
52:X:2320:U:OP1	52:X:2409:U:O2'	2.34	0.46
52:X:2922:U:O4	52:X:2923:A:N6	2.48	0.46
30:Z:229:ASP:OD1	30:Z:229:ASP:N	2.44	0.46
32:b:8:ASN:N	32:b:12:SER:O	2.46	0.46
53:A:798:U:O2'	53:A:800:G:N7	2.45	0.46
33:c:112:ARG:NH2	33:c:134:GLU:OE2	2.48	0.46
52:X:1734:A:OP2	52:X:1743:A:N6	2.48	0.46
5:4:17:ILE:HD12	5:4:18:ARG:H	1.81	0.46
10:E:25:VAL:HG22	10:E:26:LYS:H	1.80	0.46
21:P:22:VAL:HG12	21:P:35:GLU:O	2.16	0.46
33:c:13:ALA:HB3	33:c:14:PRO:HD3	1.97	0.46
40:l:97:ARG:NE	40:l:100:TYR:O	2.45	0.46
41:m:13:LEU:HD12	41:m:14:ARG:O	2.16	0.46
52:X:1130:A:N3	52:X:1151:U:O2'	2.46	0.46
5:4:16:VAL:HG22	5:4:25:VAL:HG12	1.98	0.46
8:C:15:ILE:CG2	8:C:206:VAL:HG21	2.45	0.46
9:D:157:VAL:O	9:D:157:VAL:HG23	2.16	0.46
13:H:29:ALA:HB3	13:H:57:GLN:O	2.15	0.46
17:L:76:VAL:HG21	17:L:108:TYR:CE2	2.50	0.46
18:M:66:GLU:OE2	18:M:66:GLU:N	2.48	0.46
35:e:19:VAL:HG21	35:e:143:LEU:HD21	1.97	0.45
38:j:12:GLU:HA	52:X:957:A:H62	1.81	0.45
51:9:103:GLN:O	51:9:105:ASP:N	2.50	0.45
52:X:116:G:OP2	52:X:118:A:O2'	2.21	0.45
53:A:363:C:O2'	53:A:396:G:N3	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:728:C:HO2'	53:A:729:C:P	2.35	0.45
7:B:163:ILE:HG13	7:B:183:ILE:HD11	1.97	0.45
53:A:260:U:O2'	53:A:261:U:O5'	2.32	0.45
53:A:994:C:N3	53:A:1231:G:N2	2.64	0.45
4:3:17:THR:HG22	4:3:21:LYS:O	2.16	0.45
10:E:11:LEU:HD22	10:E:68:LYS:CD	2.46	0.45
21:P:71:ARG:NH2	53:A:481:C:O3'	2.50	0.45
35:e:30:SER:HA	35:e:33:VAL:HG12	1.98	0.45
52:X:1380:U:P	52:X:1433:U:HO2'	2.38	0.45
53:A:682:G:H2'	53:A:683:G:C8	2.51	0.45
33:c:34:ILE:HD12	33:c:155:VAL:O	2.16	0.45
45:s:40:LYS:CG	45:s:51:VAL:HG11	2.46	0.45
52:X:1006:A:HO2'	52:X:2485:C:HO2'	1.64	0.45
53:A:1472:C:O3'	53:A:1473:C:H4'	2.17	0.45
19:N:6:MET:HE3	19:N:6:MET:H	1.81	0.45
20:O:20:SER:O	20:O:20:SER:OG	2.33	0.45
40:l:8:ASN:O	40:l:12:LEU:HD23	2.16	0.45
5:4:20:LYS:O	5:4:22:LYS:NZ	2.50	0.45
9:D:120:LEU:HD13	9:D:123:GLY:O	2.16	0.45
10:E:18:VAL:HG12	10:E:35:ALA:HB2	1.98	0.45
12:G:69:ILE:HG21	12:G:104:LEU:CD2	2.46	0.45
14:I:88:LEU:HD21	14:I:104:LEU:HD21	1.97	0.45
19:N:18:VAL:HG13	53:A:1369:A:H62	1.82	0.45
25:T:64:THR:O	25:T:64:THR:OG1	2.35	0.45
30:Z:108:LYS:N	30:Z:194:GLN:O	2.37	0.45
35:e:12:ILE:N	35:e:12:ILE:HD12	2.32	0.45
51:9:47:LEU:O	51:9:48:ASN:C	2.60	0.45
51:9:101:GLN:C	51:9:103:GLN:N	2.74	0.45
8:C:135:GLN:O	8:C:138:GLN:NE2	2.50	0.45
16:K:120:HIS:CD2	53:A:683:G:H21	2.35	0.45
40:l:55:SER:O	40:l:84:ARG:NH1	2.50	0.45
52:X:906:G:O2'	52:X:963:G:O6	2.33	0.45
53:A:1153:G:N2	53:A:1155:A:H62	2.15	0.45
12:G:25:ARG:HE	12:G:30:MET:HB2	1.82	0.45
29:Y:34:C:N4	29:Y:47:C:O2'	2.46	0.45
31:a:54:ASP:O	31:a:78:ARG:N	2.38	0.45
11:F:67:SER:OG	11:F:68:ASP:N	2.50	0.45
31:a:158:LYS:NZ	52:X:2541:C:O2'	2.50	0.45
33:c:55:GLU:OE1	33:c:55:GLU:N	2.39	0.45
35:e:59:ASN:OD1	35:e:129:SER:OG	2.32	0.45
50:x:15:ARG:HD2	50:x:53:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:2:ALA:N	53:A:1059:U:OP1	2.50	0.44
29:Y:40:C:N4	29:Y:41:C:H41	2.14	0.44
35:e:50:ASP:OD1	35:e:122:LYS:NZ	2.49	0.44
37:i:71:ARG:HG3	37:i:73:GLU:HG2	1.99	0.44
41:m:78:THR:HG23	41:m:81:ILE:HG22	2.00	0.44
44:r:36:LEU:C	44:r:36:LEU:HD23	2.41	0.44
53:A:1211:U:O2'	53:A:1212:C:OP1	2.29	0.44
15:J:83:THR:O	15:J:87:LEU:HD23	2.17	0.44
16:K:77:ILE:HD11	16:K:107:LEU:CD2	2.46	0.44
17:L:125:GLN:NE2	53:A:547:U:OP2	2.51	0.44
29:Y:64:A:H61	29:Y:105:A:H2'	1.82	0.44
30:Z:76:GLY:O	30:Z:116:ILE:N	2.50	0.44
52:X:1516:A:OP2	52:X:1569:A:N6	2.48	0.44
52:X:2225:C:H2'	52:X:2226:U:N1	2.32	0.44
53:A:306:A:HO2'	53:A:307:G:P	2.40	0.44
7:B:154:MET:HE2	7:B:154:MET:N	2.32	0.44
12:G:43:LEU:O	12:G:44:TYR:HB2	2.17	0.44
15:J:42:LEU:HD12	15:J:43:PRO:CD	2.46	0.44
14:I:35:ILE:HD12	14:I:35:ILE:H	1.82	0.44
15:J:85:ASP:O	15:J:89:ARG:NH2	2.50	0.44
23:R:34:LEU:O	23:R:38:VAL:HG12	2.18	0.44
30:Z:268:LYS:NZ	52:X:2253:G:OP1	2.37	0.44
33:c:3:ARG:HD2	33:c:3:ARG:C	2.42	0.44
52:X:762:A:HO2'	52:X:763:A:P	2.41	0.44
52:X:2152:A:H61	52:X:2204:U:C1'	2.31	0.44
53:A:774:G:N2	53:A:821:G:HO2'	2.15	0.44
16:K:115:VAL:O	16:K:115:VAL:HG13	2.17	0.44
18:M:83:ILE:HD11	24:S:66:MET:HG3	1.99	0.44
32:b:126:LEU:HD22	32:b:146:LEU:HD21	2.00	0.44
43:o:70:LYS:NZ	52:X:1265:A:OP1	2.37	0.44
52:X:435:G:O6	52:X:437:A:O2'	2.33	0.44
52:X:2360:G:O2'	52:X:2365:A:N1	2.46	0.44
5:4:25:VAL:HG22	5:4:34:GLN:HG2	2.00	0.44
7:B:162:PHE:CE2	7:B:214:THR:HG22	2.52	0.44
14:I:11:ARG:HB2	14:I:106:ARG:HE	1.81	0.44
36:f:30:ARG:NH2	36:f:32:THR:O	2.50	0.44
42:n:99:ALA:O	42:n:102:ASP:C	2.61	0.44
48:v:45:LYS:NZ	48:v:46:LYS:O	2.50	0.44
51:9:82:LYS:HA	51:9:92:SER:CB	2.46	0.44
52:X:1836:G:O2'	52:X:1838:A:N6	2.31	0.44
34:d:173:LYS:NZ	52:X:2558:G:OP2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:1727:A:OP2	52:X:1744:G:N2	2.44	0.44
52:X:1983:G:O2'	52:X:1984:U:OP2	2.31	0.44
52:X:2624:G:N2	52:X:2627:A:OP2	2.43	0.44
53:A:209:A:O4'	53:A:230:U:O2'	2.36	0.44
14:I:28:ILE:HG23	14:I:63:VAL:HG22	2.00	0.44
17:L:30:SER:OG	17:L:31:PHE:N	2.51	0.44
20:O:5:GLN:NE2	20:O:9:ASN:OD1	2.51	0.44
26:U:43:G:HO2'	26:U:44:A:C5'	2.31	0.44
44:r:64:MET:SD	44:r:64:MET:N	2.91	0.44
50:x:5:GLU:OE1	50:x:5:GLU:N	2.47	0.44
52:X:1322:G:N2	52:X:1325:A:OP2	2.50	0.44
52:X:2225:C:H2'	52:X:2226:U:C2	2.53	0.44
53:A:1028:A:H2'	53:A:1029:G:O4'	2.18	0.44
4:3:43:LYS:NZ	52:X:2394:G:O6	2.51	0.44
9:D:121:VAL:HG11	9:D:133:VAL:HG22	1.99	0.44
10:E:46:VAL:C	10:E:71:LEU:HD12	2.43	0.44
12:G:52:GLU:OE2	12:G:53:ARG:N	2.50	0.44
31:a:116:GLY:N	52:X:2846:A:OP1	2.45	0.44
41:m:44:GLU:OE2	41:m:45:GLY:N	2.51	0.44
51:9:4:ILE:O	51:9:36:ALA:HA	2.18	0.44
52:X:441:C:HO2'	52:X:442:C:P	2.36	0.44
52:X:2324:C:O2'	52:X:2325:U:O5'	2.32	0.44
53:A:198:G:O2'	53:A:199:U:O5'	2.36	0.44
6:6:21:GLU:OE2	6:6:22:PHE:N	2.51	0.43
10:E:18:VAL:HG12	10:E:35:ALA:CB	2.48	0.43
14:I:88:LEU:CD2	14:I:104:LEU:HD21	2.48	0.43
15:J:42:LEU:HD12	15:J:43:PRO:HD2	1.99	0.43
32:b:111:LYS:HE3	32:b:206:LEU:HD12	1.99	0.43
53:A:420:U:O2'	53:A:421:G:O5'	2.36	0.43
17:L:128:SER:O	53:A:37:G:O2'	2.22	0.43
23:R:16:CYS:HB3	23:R:19:THR:HG22	1.99	0.43
30:Z:61:GLN:NE2	52:X:1617:A:O3'	2.48	0.43
36:f:79:PHE:CD2	41:m:70:VAL:HG12	2.53	0.43
7:B:151:ILE:C	7:B:154:MET:HE3	2.43	0.43
8:C:20:SER:OG	8:C:22:TRP:NE1	2.51	0.43
12:G:38:LYS:O	12:G:39:SER:OG	2.32	0.43
18:M:7:VAL:CG2	18:M:22:ILE:HG22	2.48	0.43
19:N:44:PHE:O	19:N:47:LEU:HD12	2.18	0.43
25:T:17:ARG:NH1	53:A:332:G:OP1	2.51	0.43
33:c:105:SER:OG	33:c:106:VAL:HG13	2.18	0.43
52:X:657:G:O2'	52:X:661:A:N6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:658:A:H62	52:X:660:G:N2	2.15	0.43
52:X:2080:A:N6	52:X:2643:A:O2'	2.50	0.43
52:X:2164:A:OP1	52:X:2185:G:N2	2.44	0.43
8:C:111:ASP:O	8:C:115:VAL:HG23	2.19	0.43
30:Z:136:PRO:HG2	30:Z:139:THR:HG21	2.00	0.43
34:d:8:LEU:HD11	34:d:50:VAL:HG13	2.00	0.43
34:d:22:ASN:OD1	34:d:22:ASN:O	2.37	0.43
50:x:11:SER:OG	52:X:1035:G:OP2	2.34	0.43
52:X:2210:G:N2	52:X:2211:G:N7	2.62	0.43
2:1:9:CYS:SG	2:1:10:THR:N	2.92	0.43
31:a:159:LEU:C	31:a:160:LEU:HD22	2.44	0.43
48:v:18:ARG:NH2	52:X:204:C:OP1	2.51	0.43
51:9:14:LYS:O	51:9:15:LYS:C	2.61	0.43
53:A:977:C:OP2	53:A:978:A:O2'	2.19	0.43
7:B:117:ILE:CG2	7:B:141:LEU:HD21	2.49	0.43
10:E:15:LEU:HD11	10:E:18:VAL:HG13	2.00	0.43
30:Z:93:LEU:HD11	30:Z:101:LYS:HB3	2.00	0.43
46:t:10:MET:HE3	46:t:18:GLY:HA3	2.01	0.43
49:w:14:ILE:O	49:w:18:VAL:HG23	2.19	0.43
51:9:128:ASN:O	51:9:144:HIS:N	2.51	0.43
52:X:1456:A:O2'	52:X:1457:U:O4'	2.35	0.43
53:A:1427:A:N6	53:A:1492:G:O2'	2.51	0.43
11:F:93:GLU:OE2	11:F:94:GLU:N	2.52	0.43
12:G:148:ASN:N	12:G:148:ASN:OD1	2.51	0.43
15:J:17:ILE:O	15:J:20:GLN:NE2	2.52	0.43
17:L:44:ARG:NE	53:A:371:A:OP2	2.46	0.43
52:X:2747:G:O2'	52:X:2872:U:OP1	2.34	0.43
53:A:150:A:N7	53:A:169:U:O4	2.51	0.43
53:A:190:A:O2'	53:A:191:C:O4'	2.21	0.43
53:A:943:G:N2	53:A:945:A:O4'	2.51	0.43
19:N:5:SER:OG	53:A:1226:C:OP1	2.26	0.43
31:a:14:GLN:HB2	31:a:22:LEU:HD11	2.00	0.43
52:X:511:U:HO2'	52:X:512:G:P	2.40	0.43
12:G:9:LYS:HD2	53:A:1355:A:H62	1.84	0.43
16:K:52:LEU:HD13	16:K:67:MET:CG	2.49	0.43
16:K:77:ILE:CD1	16:K:107:LEU:HD11	2.49	0.43
31:a:40:THR:OG1	31:a:42:GLU:OE1	2.35	0.43
52:X:286:U:C4'	52:X:287:G:H21	2.31	0.43
25:T:20:HIS:O	25:T:23:THR:OG1	2.35	0.43
34:d:79:GLY:O	34:d:83:GLY:N	2.49	0.43
35:e:91:LEU:HD12	35:e:94:ARG:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:l:59:LEU:HD12	40:l:59:LEU:O	2.18	0.43
23:R:37:PHE:CD2	23:R:60:LEU:HD11	2.54	0.42
31:a:19:ASN:ND2	31:a:21:ASP:OD2	2.52	0.42
37:i:69:ILE:HG23	37:i:70:ASN:N	2.33	0.42
38:j:106:ILE:HG12	38:j:118:LEU:HD21	2.01	0.42
39:k:38:LYS:NZ	52:X:2842:U:OP1	2.50	0.42
52:X:2187:A:O2'	52:X:2188:G:N7	2.51	0.42
9:D:121:VAL:CG1	9:D:133:VAL:HG22	2.49	0.42
35:e:92:GLU:C	35:e:93:MET:SD	3.02	0.42
45:s:5:ARG:NH1	49:w:23:GLU:OE1	2.53	0.42
52:X:957:A:N3	52:X:2293:C:O2'	2.45	0.42
52:X:1485:A:H2	52:X:1600:G:H21	1.66	0.42
52:X:2169:G:N7	52:X:2178:C:N4	2.67	0.42
53:A:187:U:H2'	53:A:188:G:C1'	2.49	0.42
53:A:594:G:O2'	53:A:889:C:OP1	2.37	0.42
7:B:75:GLN:HG3	7:B:207:ILE:HG22	2.02	0.42
10:E:15:LEU:HA	10:E:37:VAL:HG23	2.01	0.42
21:P:29:ARG:NH1	53:A:398:C:O2'	2.48	0.42
28:W:741:ILE:HG22	28:W:743:HIS:CE1	2.54	0.42
33:c:123:ASP:OD1	33:c:124:GLY:N	2.52	0.42
36:f:43:VAL:HG11	36:f:53:LYS:O	2.19	0.42
36:f:43:VAL:HG13	36:f:55:GLY:H	1.84	0.42
40:l:47:ASP:OD1	40:l:48:VAL:N	2.52	0.42
47:u:58:ASN:HB3	47:u:71:ILE:HG22	2.00	0.42
52:X:761:U:O2'	52:X:763:A:N7	2.30	0.42
52:X:1398:A:OP2	52:X:1410:G:N2	2.49	0.42
53:A:1365:G:H2'	53:A:1366:A:C8	2.53	0.42
1:0:15:LEU:O	1:0:18:THR:HG22	2.20	0.42
7:B:114:LEU:HD22	7:B:144:LEU:HD11	2.01	0.42
9:D:113:LEU:HD12	9:D:117:GLY:HA3	2.01	0.42
22:Q:63:ILE:HD13	22:Q:76:ARG:O	2.19	0.42
33:c:40:VAL:O	33:c:42:ASP:N	2.52	0.42
33:c:117:VAL:HG12	33:c:118:SER:H	1.84	0.42
37:i:92:THR:O	37:i:96:LEU:HD23	2.19	0.42
40:l:22:LEU:O	40:l:23:SER:OG	2.36	0.42
43:o:12:ILE:HD12	43:o:20:VAL:HG11	2.01	0.42
43:o:58:VAL:HG22	43:o:100:ILE:HD12	2.00	0.42
52:X:1885:A:H3'	52:X:1886:G:H21	1.85	0.42
52:X:1886:G:O2'	52:X:1887:G:O5'	2.26	0.42
52:X:1936:G:O6	52:X:1953:C:N4	2.51	0.42
7:B:183:ILE:O	7:B:184:ILE:HD13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:39:ARG:NH1	8:C:54:VAL:O	2.53	0.42
11:F:42:ASP:OD1	11:F:44:GLY:N	2.52	0.42
13:H:71:GLU:OE1	13:H:71:GLU:N	2.49	0.42
17:L:6:GLN:HG3	17:L:10:LYS:HD2	2.01	0.42
22:Q:67:ARG:NH1	53:A:272:C:O2'	2.52	0.42
52:X:1732:G:O2'	52:X:1733:U:O4'	2.29	0.42
52:X:1766:C:HO2'	52:X:1767:A:P	2.41	0.42
53:A:389:A:N6	53:A:390:A:N1	2.67	0.42
53:A:851:U:H3	53:A:854:C:H41	1.68	0.42
53:A:987:A:N6	53:A:1233:U:O5'	2.52	0.42
5:4:4:ARG:NH1	5:4:6:SER:O	2.53	0.42
7:B:132:LYS:O	7:B:136:GLN:HG2	2.20	0.42
13:H:12:THR:HG22	13:H:15:ARG:NH1	2.35	0.42
30:Z:45:ASN:OD1	30:Z:46:GLN:N	2.52	0.42
52:X:64:A:H61	52:X:90:A:H61	1.67	0.42
52:X:1035:G:O2'	52:X:1036:A:O5'	2.35	0.42
52:X:1525:G:HO2'	52:X:1526:G:P	2.41	0.42
9:D:13:ARG:NH1	53:A:435:C:OP1	2.48	0.42
10:E:33:PHE:N	10:E:53:ALA:O	2.49	0.42
14:I:106:ARG:NH1	14:I:107:ASP:O	2.53	0.42
18:M:3:ARG:O	18:M:57:ARG:NH1	2.52	0.42
52:X:2009:G:O2'	52:X:2011:U:OP2	2.31	0.42
53:A:899:A:O2'	53:A:900:G:OP2	2.31	0.42
11:F:9:ILE:HD12	11:F:9:ILE:N	2.35	0.42
14:I:62:ASP:OD1	14:I:62:ASP:N	2.46	0.42
34:d:21:ASP:OD1	34:d:21:ASP:N	2.53	0.42
46:t:12:ILE:HG23	52:X:345:A:H1'	2.01	0.42
9:D:81:LYS:NZ	10:E:101:GLU:OE1	2.33	0.42
20:O:78:TYR:O	20:O:82:ILE:HG22	2.20	0.42
30:Z:238:ARG:NH1	52:X:2620:C:OP1	2.53	0.42
35:e:16:TRP:C	35:e:17:LEU:HD12	2.44	0.42
35:e:26:LEU:O	35:e:30:SER:OG	2.21	0.42
42:n:81:HIS:CE1	42:n:85:LEU:HD11	2.55	0.42
53:A:410:G:H5'	53:A:629:C:H41	1.84	0.42
53:A:1441:G:O2'	53:A:1442:A:OP2	2.33	0.42
3:2:34:ARG:NH1	52:X:513:A:OP1	2.53	0.42
17:L:93:VAL:CG2	17:L:110:ILE:HG23	2.50	0.42
21:P:65:LYS:NZ	53:A:135:C:O3'	2.53	0.42
23:R:73:LEU:HD12	23:R:73:LEU:N	2.34	0.42
28:W:720:ALA:O	28:W:724:VAL:HG23	2.20	0.42
32:b:39:MET:HE2	32:b:101:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:j:8:LYS:NZ	52:X:959:C:OP1	2.46	0.42
38:j:34:ILE:HB	38:j:118:LEU:HD12	2.02	0.42
41:m:81:ILE:HG23	41:m:81:ILE:O	2.20	0.42
52:X:75:G:H22	52:X:110:A:H2	1.67	0.42
52:X:432:C:O2'	52:X:435:G:N2	2.52	0.42
52:X:2125:U:H2'	52:X:2126:G:O4'	2.20	0.42
5:4:25:VAL:C	5:4:26:ILE:HD13	2.45	0.41
9:D:186:ALA:HB1	9:D:189:ILE:O	2.19	0.41
21:P:24:ASP:OD1	21:P:27:SER:N	2.45	0.41
24:S:58:VAL:HG13	24:S:58:VAL:O	2.20	0.41
25:T:52:THR:HG22	53:A:206:A:H1'	2.01	0.41
42:n:91:ASN:OD1	42:n:92:ARG:N	2.53	0.41
46:t:19:LYS:HD3	46:t:38:VAL:HG12	2.02	0.41
53:A:590:G:N1	53:A:768:A:OP2	2.47	0.41
14:I:106:ARG:HH22	14:I:110:MET:HE2	1.85	0.41
23:R:72:LEU:C	23:R:73:LEU:HD12	2.45	0.41
36:f:65:THR:OG1	36:f:67:SER:O	2.38	0.41
38:j:67:LYS:O	38:j:68:ILE:CD1	2.67	0.41
42:n:17:VAL:HG23	42:n:39:VAL:HG21	2.02	0.41
50:x:6:ILE:HD13	50:x:56:VAL:HG23	2.02	0.41
51:9:29:PHE:CB	52:X:2227:A:C5	3.03	0.41
52:X:1929:A:O2'	52:X:1930:A:OP1	2.32	0.41
53:A:62:A:N1	53:A:105:G:O2'	2.39	0.41
53:A:178:A:H62	53:A:210:A:H62	1.67	0.41
1:0:27:MET:HE2	1:0:27:MET:H	1.85	0.41
11:F:9:ILE:HD12	11:F:87:ARG:O	2.19	0.41
12:G:131:THR:O	12:G:131:THR:OG1	2.34	0.41
25:T:74:ARG:NH1	53:A:271:A:OP1	2.53	0.41
31:a:185:LEU:C	31:a:186:LEU:HD22	2.45	0.41
35:e:16:TRP:HE3	35:e:56:ILE:HD11	1.85	0.41
45:s:62:LYS:O	45:s:73:THR:OG1	2.29	0.41
52:X:1105:G:C6	52:X:1126:A:N1	2.88	0.41
52:X:1742:G:OP2	52:X:1743:A:O2'	2.32	0.41
52:X:2138:U:OP1	52:X:2178:C:O2'	2.38	0.41
30:Z:177:ASN:O	30:Z:178:SER:OG	2.33	0.41
35:e:58:ILE:HG23	35:e:129:SER:HA	2.02	0.41
36:f:36:GLY:HA2	36:f:106:LEU:HD23	2.03	0.41
45:s:54:VAL:HG22	45:s:81:VAL:HG12	2.03	0.41
48:v:38:ILE:O	48:v:45:LYS:N	2.51	0.41
53:A:456:A:H2'	53:A:457:A:O4'	2.20	0.41
29:Y:26:C:O2	29:Y:57:G:N2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:60:ILE:HD12	33:c:137:ILE:CD1	2.49	0.41
38:j:105:GLU:N	38:j:105:GLU:OE1	2.53	0.41
52:X:1109:G:O2'	52:X:1122:C:N4	2.53	0.41
53:A:33:G:O2'	53:A:34:A:O5'	2.28	0.41
53:A:62:A:OP1	53:A:339:G:N1	2.48	0.41
9:D:113:LEU:CG	9:D:119:ILE:HD11	2.51	0.41
31:a:108:VAL:O	31:a:174:LEU:N	2.51	0.41
32:b:136:THR:HG21	52:X:364:A:H2'	2.02	0.41
33:c:108:LEU:O	33:c:111:VAL:HG23	2.20	0.41
52:X:481:U:O2	52:X:482:C:N4	2.43	0.41
53:A:78:G:H2'	53:A:79:G:O4'	2.20	0.41
8:C:15:ILE:HG21	8:C:206:VAL:HG21	2.02	0.41
10:E:140:THR:O	10:E:144:LEU:HD23	2.21	0.41
19:N:42:ILE:HG23	19:N:43:CYS:N	2.35	0.41
33:c:7:LYS:HE2	33:c:12:ILE:HD11	2.03	0.41
33:c:168:GLU:O	33:c:171:THR:OG1	2.24	0.41
36:f:113:LYS:O	36:f:116:SER:OG	2.35	0.41
39:k:74:GLU:OE1	39:k:74:GLU:N	2.39	0.41
48:v:6:VAL:HG11	48:v:47:VAL:HG21	2.03	0.41
52:X:1845:A:O2'	52:X:1846:G:OP2	2.35	0.41
4:3:27:ALA:O	4:3:29:THR:HG23	2.20	0.41
11:F:69:ALA:O	11:F:73:GLN:NE2	2.53	0.41
35:e:92:GLU:HG3	35:e:93:MET:N	2.35	0.41
35:e:92:GLU:HB3	35:e:93:MET:SD	2.61	0.41
38:j:37:LEU:HD12	38:j:38:GLU:OE2	2.20	0.41
45:s:27:THR:HG22	45:s:80:ILE:HD13	2.02	0.41
9:D:168:ASP:O	9:D:172:LEU:N	2.54	0.41
14:I:106:ARG:NH2	14:I:110:MET:HE2	2.35	0.41
15:J:28:THR:HG21	15:J:90:LEU:CD1	2.50	0.41
19:N:52:GLN:N	19:N:52:GLN:OE1	2.54	0.41
23:R:64:ILE:HD12	23:R:64:ILE:H	1.85	0.41
30:Z:165:LEU:HD11	30:Z:175:ARG:HB2	2.03	0.41
34:d:104:LEU:HD21	34:d:106:LEU:CD2	2.51	0.41
44:r:50:VAL:HG11	44:r:103:ILE:HG21	2.02	0.41
52:X:1733:U:O2'	52:X:1745:A:N7	2.46	0.41
53:A:170:A:O2'	53:A:171:A:O4'	2.27	0.41
53:A:1441:G:HO2'	53:A:1442:A:P	2.43	0.41
7:B:111:ILE:HD11	7:B:114:LEU:HD23	2.03	0.41
13:H:49:VAL:CG2	13:H:62:VAL:HG12	2.51	0.41
16:K:32:THR:HG21	16:K:65:ALA:HB1	2.03	0.41
16:K:77:ILE:HD11	16:K:107:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:80:MET:SD	21:P:81:GLU:N	2.94	0.41
32:b:39:MET:HE1	32:b:99:TYR:C	2.46	0.41
36:f:71:ARG:HG3	36:f:71:ARG:HH11	1.86	0.41
52:X:376:A:O2'	52:X:378:C:OP2	2.30	0.41
52:X:2859:G:O2'	52:X:2860:A:OP2	2.28	0.41
53:A:57:A:OP2	53:A:360:C:N4	2.54	0.41
53:A:159:A:H2'	53:A:160:A:O4'	2.21	0.41
6:6:25:GLY:O	33:c:102:LYS:NZ	2.49	0.40
12:G:100:GLY:O	12:G:104:LEU:HD23	2.21	0.40
52:X:649:G:N3	52:X:704:U:O2'	2.54	0.40
7:B:22:ARG:O	7:B:22:ARG:NH1	2.49	0.40
8:C:9:GLY:HA2	8:C:12:ILE:HD12	2.03	0.40
8:C:42:ILE:HD11	8:C:54:VAL:HG11	2.03	0.40
11:F:86:ILE:HD12	11:F:86:ILE:N	2.36	0.40
12:G:109:ARG:NH2	53:A:1249:U:O4	2.54	0.40
20:O:18:HIS:N	20:O:21:ASP:OD2	2.49	0.40
23:R:31:VAL:O	23:R:35:LYS:NZ	2.34	0.40
32:b:72:ARG:NH2	52:X:1297:C:OP1	2.54	0.40
35:e:109:MET:HE3	52:X:1052:C:H1'	2.03	0.40
39:k:66:ILE:HD11	39:k:80:LEU:HD22	2.03	0.40
42:n:58:ARG:NH1	52:X:1043:G:OP2	2.50	0.40
45:s:12:VAL:C	45:s:13:ILE:HD13	2.45	0.40
52:X:2718:U:OP2	52:X:2897:G:N2	2.52	0.40
53:A:16:U:N3	53:A:19:U:OP2	2.43	0.40
10:E:52:LYS:NZ	53:A:1091:G:OP2	2.42	0.40
40:l:92:ASP:N	40:l:92:ASP:OD1	2.53	0.40
49:w:48:LYS:NZ	52:X:75:G:O2'	2.52	0.40
50:x:22:THR:HG22	52:X:897:G:O2'	2.21	0.40
52:X:266:U:O2'	52:X:476:A:N3	2.53	0.40
52:X:992:G:O6	52:X:1018:G:N2	2.54	0.40
53:A:372:A:H4'	53:A:373:U:OP1	2.20	0.40
11:F:75:PHE:CD1	11:F:75:PHE:C	3.00	0.40
14:I:110:MET:HE1	53:A:1127:G:O5'	2.21	0.40
45:s:62:LYS:N	45:s:73:THR:OG1	2.55	0.40
51:9:70:GLU:O	51:9:71:THR:C	2.64	0.40
52:X:85:G:O2'	52:X:86:C:OP2	2.29	0.40
52:X:2859:G:H21	52:X:2908:A:H62	1.69	0.40
4:3:17:THR:OG1	52:X:675:C:OP1	2.36	0.40
14:I:67:VAL:C	14:I:68:HIS:HD1	2.24	0.40
15:J:64:GLN:HA	15:J:64:GLN:OE1	2.22	0.40
18:M:58:ASP:OD1	18:M:58:ASP:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:201:LYS:O	32:b:205:VAL:HG23	2.21	0.40
41:m:36:ASN:OD1	41:m:36:ASN:O	2.39	0.40
51:9:3:VAL:O	51:9:18:VAL:HA	2.22	0.40
51:9:73:GLU:C	51:9:75:LEU:H	2.29	0.40
52:X:1105:G:O6	52:X:1126:A:N6	2.55	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	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
2	1	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
3	2	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
4	3	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	61/64 (95%)	52 (85%)	9 (15%)	0	100	100
7	B	216/246 (88%)	199 (92%)	17 (8%)	0	100	100
8	C	204/218 (94%)	189 (93%)	15 (7%)	0	100	100
9	D	193/200 (96%)	171 (89%)	22 (11%)	0	100	100
10	E	162/166 (98%)	148 (91%)	14 (9%)	0	100	100
11	F	90/95 (95%)	84 (93%)	6 (7%)	0	100	100
12	G	147/156 (94%)	126 (86%)	21 (14%)	0	100	100
13	H	129/132 (98%)	119 (92%)	10 (8%)	0	100	100
14	I	123/130 (95%)	113 (92%)	10 (8%)	0	100	100
15	J	93/102 (91%)	87 (94%)	6 (6%)	0	100	100
16	K	112/131 (86%)	107 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	L	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
18	M	106/121 (88%)	95 (90%)	11 (10%)	0	100	100
19	N	58/61 (95%)	48 (83%)	10 (17%)	0	100	100
20	O	83/89 (93%)	75 (90%)	8 (10%)	0	100	100
21	P	86/90 (96%)	80 (93%)	6 (7%)	0	100	100
22	Q	82/87 (94%)	79 (96%)	3 (4%)	0	100	100
23	R	62/79 (78%)	57 (92%)	5 (8%)	0	100	100
24	S	76/92 (83%)	67 (88%)	9 (12%)	0	100	100
25	T	81/88 (92%)	78 (96%)	3 (4%)	0	100	100
28	W	84/785 (11%)	78 (93%)	6 (7%)	0	100	100
30	Z	270/275 (98%)	253 (94%)	17 (6%)	0	100	100
31	a	204/207 (99%)	190 (93%)	14 (7%)	0	100	100
32	b	203/205 (99%)	186 (92%)	17 (8%)	0	100	100
33	c	174/178 (98%)	160 (92%)	13 (8%)	1 (1%)	21	50
34	d	173/175 (99%)	154 (89%)	19 (11%)	0	100	100
35	e	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
36	f	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
37	i	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
38	j	133/138 (96%)	123 (92%)	10 (8%)	0	100	100
39	k	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
40	l	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
41	m	113/115 (98%)	106 (94%)	7 (6%)	0	100	100
42	n	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
43	o	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
44	r	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
45	s	88/93 (95%)	81 (92%)	7 (8%)	0	100	100
46	t	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
47	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
48	v	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
49	w	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
50	x	56/58 (97%)	52 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	9	147/149 (99%)	107 (73%)	27 (18%)	13 (9%)	0	3
All	All	5438/6399 (85%)	4977 (92%)	447 (8%)	14 (0%)	37	65

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
51	9	37	VAL
51	9	107	ASN
51	9	130	PRO
51	9	135	PRO
51	9	104	LYS
51	9	126	TYR
51	9	127	THR
51	9	29	PHE
51	9	71	THR
51	9	118	PRO
51	9	143	VAL
51	9	36	ALA
51	9	75	LEU
33	c	41	GLY

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	0	48/53 (91%)	48 (100%)	0	100	100
2	1	46/46 (100%)	45 (98%)	1 (2%)	45	63
3	2	39/39 (100%)	39 (100%)	0	100	100
4	3	54/57 (95%)	54 (100%)	0	100	100
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	53/53 (100%)	52 (98%)	1 (2%)	50	66
7	B	189/212 (89%)	189 (100%)	0	100	100
8	C	168/178 (94%)	167 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	D	169/173 (98%)	167 (99%)	2 (1%)	63	72
10	E	128/130 (98%)	128 (100%)	0	100	100
11	F	81/84 (96%)	80 (99%)	1 (1%)	63	72
12	G	125/132 (95%)	124 (99%)	1 (1%)	73	77
13	H	111/112 (99%)	109 (98%)	2 (2%)	51	67
14	I	98/102 (96%)	98 (100%)	0	100	100
15	J	86/92 (94%)	84 (98%)	2 (2%)	44	63
16	K	86/100 (86%)	86 (100%)	0	100	100
17	L	114/116 (98%)	114 (100%)	0	100	100
18	M	94/104 (90%)	94 (100%)	0	100	100
19	N	53/54 (98%)	52 (98%)	1 (2%)	50	66
20	O	80/83 (96%)	80 (100%)	0	100	100
21	P	74/76 (97%)	74 (100%)	0	100	100
22	Q	77/80 (96%)	77 (100%)	0	100	100
23	R	56/64 (88%)	55 (98%)	1 (2%)	51	67
24	S	70/81 (86%)	70 (100%)	0	100	100
25	T	66/70 (94%)	65 (98%)	1 (2%)	57	69
28	W	69/673 (10%)	69 (100%)	0	100	100
30	Z	220/223 (99%)	220 (100%)	0	100	100
31	a	167/168 (99%)	167 (100%)	0	100	100
32	b	169/169 (100%)	168 (99%)	1 (1%)	78	80
33	c	151/153 (99%)	148 (98%)	3 (2%)	48	65
34	d	148/148 (100%)	148 (100%)	0	100	100
35	e	120/120 (100%)	120 (100%)	0	100	100
36	f	101/101 (100%)	101 (100%)	0	100	100
37	i	110/110 (100%)	110 (100%)	0	100	100
38	j	109/111 (98%)	108 (99%)	1 (1%)	70	76
39	k	99/99 (100%)	99 (100%)	0	100	100
40	l	93/93 (100%)	93 (100%)	0	100	100
41	m	100/100 (100%)	100 (100%)	0	100	100
42	n	96/96 (100%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	o	83/83 (100%)	83 (100%)	0	100	100
44	r	90/90 (100%)	90 (100%)	0	100	100
45	s	81/84 (96%)	81 (100%)	0	100	100
46	t	85/85 (100%)	84 (99%)	1 (1%)	63	72
47	u	64/64 (100%)	64 (100%)	0	100	100
48	v	47/47 (100%)	47 (100%)	0	100	100
49	w	56/56 (100%)	56 (100%)	0	100	100
50	x	52/52 (100%)	52 (100%)	0	100	100
All	All	4510/5251 (86%)	4490 (100%)	20 (0%)	81	83

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

Mol	Chain	Res	Type
2	1	28	ASP
6	6	22	PHE
8	C	171	THR
9	D	158	ASN
9	D	172	LEU
11	F	30	LEU
12	G	9	LYS
13	H	35	GLU
13	H	128	LEU
15	J	18	LEU
15	J	51	ILE
19	N	47	LEU
23	R	60	LEU
25	T	83	VAL
32	b	184	LEU
33	c	42	ASP
33	c	45	GLN
33	c	101	ASP
38	j	68	ILE
46	t	75	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	40	GLN

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Mol	Chain	Res	Type
8	C	113	GLN
8	C	122	GLN
8	C	136	GLN
9	D	82	HIS
9	D	96	ASN
9	D	159	ASN
10	E	93	ASN
11	F	13	ASN
11	F	33	ASN
14	I	38	HIS
20	O	5	GLN
20	O	18	HIS
30	Z	143	ASN
31	a	50	GLN
34	d	22	ASN
35	e	8	ASN
35	e	78	HIS
35	e	80	GLN
37	i	35	HIS
38	j	13	HIS
39	k	61	GLN
39	k	72	ASN
40	l	43	GLN
42	n	101	ASN
43	o	50	ASN
48	v	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	U	76/77 (98%)	21 (27%)	0
27	V	32/33 (96%)	21 (65%)	0
29	Y	111/112 (99%)	35 (31%)	3 (2%)
52	X	2881/2928 (98%)	685 (23%)	36 (1%)
53	A	1532/1533 (99%)	384 (25%)	20 (1%)
All	All	4632/4683 (98%)	1146 (24%)	59 (1%)

All (1146) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	U	2	G

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Mol	Chain	Res	Type
26	U	6	G
26	U	8	U
26	U	16	U
26	U	17	U
26	U	17(A)	G
26	U	18	G
26	U	20	U
26	U	24	A
26	U	42	G
26	U	46	G
26	U	47	U
26	U	48	C
26	U	55	U
26	U	56	C
26	U	57	G
26	U	58	A
26	U	59	G
26	U	60	U
26	U	68	G
26	U	76	A
27	V	436	A
27	V	441	U
27	V	442	G
27	V	443	C
27	V	444	C
27	V	445	A
27	V	446	U
27	V	447	G
27	V	449	A
27	V	450	C
27	V	451	G
27	V	452	U
27	V	453	C
27	V	454	G
27	V	455	C
27	V	456	A
27	V	457	C
27	V	458	U
27	V	459	C
27	V	460	G
27	V	461	G
29	Y	10	G

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Mol	Chain	Res	Type
29	Y	12	U
29	Y	18	A
29	Y	21	G
29	Y	22	G
29	Y	23	U
29	Y	33	U
29	Y	34	C
29	Y	38	U
29	Y	39	A
29	Y	42	G
29	Y	43	A
29	Y	44	A
29	Y	46	A
29	Y	49	G
29	Y	53	U
29	Y	64	A
29	Y	65	G
29	Y	71	A
29	Y	73	G
29	Y	74	G
29	Y	75	U
29	Y	85	U
29	Y	86	U
29	Y	87	U
29	Y	88	C
29	Y	94	G
29	Y	97	A
29	Y	100	G
29	Y	103	G
29	Y	107	G
29	Y	108	C
29	Y	109	C
29	Y	110	G
29	Y	112	C
52	X	4	U
52	X	5	A
52	X	7	G
52	X	9	U
52	X	12	A
52	X	15	G
52	X	34	U
52	X	35	G

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Mol	Chain	Res	Type
52	X	46	C
52	X	60	G
52	X	61	A
52	X	62	C
52	X	63	G
52	X	71	A
52	X	74	U
52	X	75	G
52	X	76	C
52	X	77	U
52	X	78	U
52	X	79	C
52	X	80	G
52	X	82	G
52	X	85	G
52	X	86	C
52	X	87	U
52	X	88	G
52	X	91	A
52	X	92	G
52	X	93	C
52	X	94	A
52	X	95	A
52	X	96	G
52	X	99	U
52	X	100	U
52	X	101	G
52	X	102	A
52	X	117	A
52	X	119	U
52	X	125	A
52	X	126	A
52	X	127	C
52	X	130	A
52	X	140	A
52	X	150	A
52	X	161	A
52	X	162	A
52	X	164	U
52	X	165	C
52	X	168	A
52	X	176	A

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Mol	Chain	Res	Type
52	X	177	G
52	X	178	A
52	X	179	A
52	X	182	C
52	X	183	A
52	X	184	G
52	X	189	G
52	X	199	A
52	X	200	A
52	X	202	A
52	X	216	A
52	X	218	G
52	X	219	A
52	X	221	G
52	X	224	A
52	X	225	A
52	X	226	A
52	X	227	G
52	X	230	A
52	X	231	A
52	X	232	U
52	X	233	G
52	X	234	C
52	X	244	A
52	X	251	G
52	X	252	C
52	X	253	G
52	X	258	A
52	X	275	A
52	X	276	C
52	X	279	A
52	X	282	G
52	X	284	C
52	X	285	U
52	X	286	U
52	X	287	G
52	X	288	C
52	X	289	C
52	X	291	C
52	X	292	U
52	X	294	G
52	X	295	G

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Mol	Chain	Res	Type
52	X	296	G
52	X	298	U
52	X	302	A
52	X	307	A
52	X	308	C
52	X	310	C
52	X	329	A
52	X	330	A
52	X	332	G
52	X	336	U
52	X	337	A
52	X	338	G
52	X	345	A
52	X	346	G
52	X	355	A
52	X	367	G
52	X	372	U
52	X	373	A
52	X	374	A
52	X	377	G
52	X	389	A
52	X	390	A
52	X	392	C
52	X	396	G
52	X	397	U
52	X	399	C
52	X	407	A
52	X	408	G
52	X	417	G
52	X	418	A
52	X	419	G
52	X	421	A
52	X	431	A
52	X	433	G
52	X	434	U
52	X	442	C
52	X	448	A
52	X	450	U
52	X	451	C
52	X	453	G
52	X	458	G
52	X	459	A

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Mol	Chain	Res	Type
52	X	471	G
52	X	476	A
52	X	483	C
52	X	491	C
52	X	495	U
52	X	498	U
52	X	502	C
52	X	504	A
52	X	512	G
52	X	528	G
52	X	529	C
52	X	540	G
52	X	542	G
52	X	548	A
52	X	550	G
52	X	551	A
52	X	552	G
52	X	554	U
52	X	555	C
52	X	556	C
52	X	564	G
52	X	567	U
52	X	573	C
52	X	575	A
52	X	576	G
52	X	577	U
52	X	578	A
52	X	579	G
52	X	590	U
52	X	592	A
52	X	593	A
52	X	594	C
52	X	595	G
52	X	606	U
52	X	607	G
52	X	617	G
52	X	619	A
52	X	630	A
52	X	632	U
52	X	646	A
52	X	647	A
52	X	658	A

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Mol	Chain	Res	Type
52	X	660	G
52	X	673	A
52	X	683	A
52	X	691	U
52	X	697	G
52	X	698	C
52	X	699	A
52	X	700	U
52	X	701	G
52	X	702	A
52	X	717	A
52	X	719	C
52	X	729	G
52	X	733	U
52	X	762	A
52	X	763	A
52	X	765	A
52	X	777	C
52	X	794	U
52	X	795	G
52	X	804	G
52	X	822	G
52	X	823	G
52	X	824	G
52	X	826	U
52	X	829	A
52	X	831	U
52	X	832	G
52	X	837	U
52	X	852	G
52	X	859	C
52	X	866	A
52	X	874	U
52	X	875	U
52	X	892	U
52	X	906	G
52	X	913	A
52	X	928	G
52	X	929	G
52	X	930	C
52	X	933	C
52	X	934	U

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Mol	Chain	Res	Type
52	X	936	C
52	X	940	G
52	X	941	U
52	X	943	A
52	X	957	A
52	X	959	C
52	X	964	A
52	X	973	G
52	X	980	C
52	X	987	A
52	X	991	A
52	X	992	G
52	X	999	A
52	X	1005	A
52	X	1007	G
52	X	1018	G
52	X	1019	A
52	X	1020	A
52	X	1030	G
52	X	1031	C
52	X	1036	A
52	X	1046	A
52	X	1058	U
52	X	1059	A
52	X	1068	G
52	X	1069	U
52	X	1072	A
52	X	1073	A
52	X	1076	G
52	X	1079	U
52	X	1085	G
52	X	1090	U
52	X	1091	U
52	X	1092	A
52	X	1093	G
52	X	1100	A
52	X	1102	G
52	X	1103	A
52	X	1107	U
52	X	1108	G
52	X	1109	G
52	X	1111	U

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Mol	Chain	Res	Type
52	X	1113	A
52	X	1116	A
52	X	1118	C
52	X	1119	A
52	X	1121	C
52	X	1122	C
52	X	1123	A
52	X	1124	C
52	X	1125	C
52	X	1126	A
52	X	1127	U
52	X	1128	U
52	X	1130	A
52	X	1131	A
52	X	1133	G
52	X	1134	A
52	X	1135	G
52	X	1136	U
52	X	1137	G
52	X	1138	C
52	X	1139	G
52	X	1140	U
52	X	1141	A
52	X	1142	A
52	X	1143	U
52	X	1144	A
52	X	1145	G
52	X	1147	U
52	X	1148	C
52	X	1154	U
52	X	1157	A
52	X	1158	G
52	X	1159	U
52	X	1160	G
52	X	1161	A
52	X	1177	G
52	X	1178	U
52	X	1179	A
52	X	1180	C
52	X	1181	C
52	X	1182	G
52	X	1183	G

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Mol	Chain	Res	Type
52	X	1185	G
52	X	1188	A
52	X	1201	A
52	X	1215	U
52	X	1216	C
52	X	1227	G
52	X	1236	G
52	X	1241	C
52	X	1248	C
52	X	1260	A
52	X	1265	A
52	X	1277	A
52	X	1278	G
52	X	1293	A
52	X	1295	U
52	X	1296	G
52	X	1311	G
52	X	1312	A
52	X	1315	G
52	X	1339	A
52	X	1340	A
52	X	1353	C
52	X	1364	C
52	X	1368	U
52	X	1369	C
52	X	1371	G
52	X	1388	A
52	X	1389	C
52	X	1391	U
52	X	1402	C
52	X	1404	A
52	X	1406	A
52	X	1417	A
52	X	1418	U
52	X	1423	A
52	X	1425	C
52	X	1426	A
52	X	1427	G
52	X	1434	A
52	X	1435	U
52	X	1442	A
52	X	1449	C

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Mol	Chain	Res	Type
52	X	1450	C
52	X	1452	C
52	X	1453	A
52	X	1455	C
52	X	1458	U
52	X	1460	G
52	X	1461	A
52	X	1465	A
52	X	1466	U
52	X	1471	G
52	X	1473	A
52	X	1474	C
52	X	1480	A
52	X	1489	U
52	X	1490	A
52	X	1499	A
52	X	1500	U
52	X	1505	U
52	X	1506	A
52	X	1507	U
52	X	1508	C
52	X	1514	C
52	X	1516	A
52	X	1525	G
52	X	1526	G
52	X	1528	U
52	X	1529	G
52	X	1536	A
52	X	1537	G
52	X	1539	C
52	X	1540	A
52	X	1543	U
52	X	1544	C
52	X	1552	C
52	X	1553	A
52	X	1566	G
52	X	1568	G
52	X	1569	A
52	X	1570	U
52	X	1571	G
52	X	1601	A
52	X	1602	U

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Mol	Chain	Res	Type
52	X	1617	A
52	X	1626	U
52	X	1632	G
52	X	1653	A
52	X	1655	A
52	X	1693	C
52	X	1696	G
52	X	1697	A
52	X	1710	A
52	X	1713	A
52	X	1717	C
52	X	1719	G
52	X	1732	G
52	X	1738	U
52	X	1739	C
52	X	1741	G
52	X	1745	A
52	X	1757	G
52	X	1758	U
52	X	1759	U
52	X	1760	A
52	X	1761	G
52	X	1765	G
52	X	1767	A
52	X	1774	A
52	X	1776	A
52	X	1779	G
52	X	1792	G
52	X	1793	G
52	X	1797	A
52	X	1802	A
52	X	1811	C
52	X	1820	A
52	X	1828	G
52	X	1829	C
52	X	1830	G
52	X	1831	A
52	X	1832	A
52	X	1837	U
52	X	1845	A
52	X	1848	A
52	X	1858	A

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Mol	Chain	Res	Type
52	X	1877	A
52	X	1882	A
52	X	1883	A
52	X	1884	G
52	X	1898	G
52	X	1899	U
52	X	1900	A
52	X	1901	A
52	X	1902	G
52	X	1910	G
52	X	1935	G
52	X	1941	A
52	X	1942	A
52	X	1943	C
52	X	1944	U
52	X	1945	A
52	X	1956	A
52	X	1958	G
52	X	1959	G
52	X	1962	G
52	X	1967	A
52	X	1971	C
52	X	1972	U
52	X	1984	U
52	X	1992	C
52	X	1993	G
52	X	1995	A
52	X	1996	C
52	X	1999	A
52	X	2000	A
52	X	2001	G
52	X	2020	U
52	X	2021	G
52	X	2022	U
52	X	2024	U
52	X	2025	C
52	X	2026	A
52	X	2052	A
52	X	2054	C
52	X	2059	A
52	X	2060	A
52	X	2061	G

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Mol	Chain	Res	Type
52	X	2062	A
52	X	2063	U
52	X	2064	G
52	X	2065	C
52	X	2072	C
52	X	2081	G
52	X	2084	C
52	X	2085	G
52	X	2088	A
52	X	2089	A
52	X	2090	G
52	X	2098	G
52	X	2121	U
52	X	2122	G
52	X	2123	A
52	X	2127	U
52	X	2129	G
52	X	2131	U
52	X	2132	A
52	X	2133	C
52	X	2134	A
52	X	2135	G
52	X	2139	G
52	X	2140	U
52	X	2141	A
52	X	2143	A
52	X	2144	G
52	X	2145	G
52	X	2146	A
52	X	2147	U
52	X	2148	A
52	X	2149	G
52	X	2151	U
52	X	2152	A
52	X	2154	G
52	X	2155	A
52	X	2157	C
52	X	2158	C
52	X	2159	U
52	X	2160	U
52	X	2161	G
52	X	2163	A

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Mol	Chain	Res	Type
52	X	2165	A
52	X	2166	C
52	X	2168	G
52	X	2169	G
52	X	2170	A
52	X	2171	G
52	X	2173	G
52	X	2174	C
52	X	2175	C
52	X	2176	A
52	X	2177	G
52	X	2181	C
52	X	2183	G
52	X	2184	U
52	X	2185	G
52	X	2186	G
52	X	2187	A
52	X	2190	C
52	X	2191	A
52	X	2193	C
52	X	2194	G
52	X	2195	G
52	X	2198	G
52	X	2199	G
52	X	2200	A
52	X	2201	U
52	X	2203	C
52	X	2204	U
52	X	2205	A
52	X	2206	C
52	X	2208	C
52	X	2209	U
52	X	2210	G
52	X	2216	A
52	X	2218	U
52	X	2219	G
52	X	2220	A
52	X	2222	C
52	X	2223	U
52	X	2224	U
52	X	2225	C
52	X	2227	A

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Mol	Chain	Res	Type
52	X	2232	G
52	X	2233	C
52	X	2241	A
52	X	2245	G
52	X	2246	G
52	X	2252	A
52	X	2254	A
52	X	2267	G
52	X	2268	G
52	X	2280	G
52	X	2297	A
52	X	2312	C
52	X	2315	A
52	X	2316	A
52	X	2318	G
52	X	2334	U
52	X	2335	U
52	X	2337	G
52	X	2338	A
52	X	2339	A
52	X	2349	A
52	X	2350	G
52	X	2351	A
52	X	2356	A
52	X	2363	C
52	X	2364	A
52	X	2374	G
52	X	2379	C
52	X	2381	A
52	X	2404	G
52	X	2412	G
52	X	2414	C
52	X	2415	U
52	X	2430	U
52	X	2431	U
52	X	2432	C
52	X	2435	C
52	X	2440	A
52	X	2453	C
52	X	2454	A
52	X	2457	G
52	X	2458	G

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Mol	Chain	Res	Type
52	X	2459	A
52	X	2469	C
52	X	2470	C
52	X	2476	G
52	X	2477	A
52	X	2504	C
52	X	2505	A
52	X	2507	A
52	X	2516	G
52	X	2523	G
52	X	2527	C
52	X	2531	G
52	X	2532	A
52	X	2533	U
52	X	2534	G
52	X	2535	U
52	X	2547	A
52	X	2549	C
52	X	2558	G
52	X	2562	U
52	X	2564	G
52	X	2583	U
52	X	2584	U
52	X	2595	A
52	X	2596	G
52	X	2602	C
52	X	2607	G
52	X	2611	G
52	X	2614	U
52	X	2628	G
52	X	2631	A
52	X	2632	G
52	X	2639	C
52	X	2642	U
52	X	2658	A
52	X	2659	G
52	X	2674	G
52	X	2675	C
52	X	2689	A
52	X	2690	G
52	X	2711	G
52	X	2718	U

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Mol	Chain	Res	Type
52	X	2719	A
52	X	2720	C
52	X	2743	G
52	X	2762	A
52	X	2768	U
52	X	2773	G
52	X	2777	A
52	X	2785	U
52	X	2790	A
52	X	2793	A
52	X	2794	A
52	X	2806	G
52	X	2807	A
52	X	2809	G
52	X	2818	C
52	X	2822	C
52	X	2824	G
52	X	2827	A
52	X	2830	A
52	X	2831	A
52	X	2843	G
52	X	2845	A
52	X	2849	U
52	X	2850	G
52	X	2859	G
52	X	2860	A
52	X	2872	U
52	X	2873	G
52	X	2874	G
52	X	2886	C
52	X	2891	G
52	X	2892	G
52	X	2893	A
52	X	2897	G
52	X	2899	C
52	X	2901	G
52	X	2905	C
52	X	2908	A
52	X	2909	U
52	X	2911	G
52	X	2912	A
52	X	2916	A

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Mol	Chain	Res	Type
52	X	2918	G
52	X	2919	A
52	X	2920	C
52	X	2921	U
52	X	2925	C
53	A	10	A
53	A	11	G
53	A	32	C
53	A	33	G
53	A	34	A
53	A	46	G
53	A	49	C
53	A	50	C
53	A	52	A
53	A	53	A
53	A	62	A
53	A	72	A
53	A	74	A
53	A	75	G
53	A	76	A
53	A	77	U
53	A	78	G
53	A	80	G
53	A	82	G
53	A	83	C
53	A	85	U
53	A	86	G
53	A	89	C
53	A	90	C
53	A	92	U
53	A	94	A
53	A	95	U
53	A	96	G
53	A	98	U
53	A	99	A
53	A	117	A
53	A	118	A
53	A	119	C
53	A	120	A
53	A	128	A
53	A	130	C
53	A	133	G

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Mol	Chain	Res	Type
53	A	135	C
53	A	147	G
53	A	156	G
53	A	158	G
53	A	162	C
53	A	165	G
53	A	167	G
53	A	169	U
53	A	172	U
53	A	178	A
53	A	179	U
53	A	181	G
53	A	188	G
53	A	189	A
53	A	190	A
53	A	192	C
53	A	195	A
53	A	197	G
53	A	204	A
53	A	206	A
53	A	207	U
53	A	208	A
53	A	209	A
53	A	212	G
53	A	218	U
53	A	219	U
53	A	220	C
53	A	221	G
53	A	222	G
53	A	225	A
53	A	228	A
53	A	231	U
53	A	233	C
53	A	248	C
53	A	249	G
53	A	253	U
53	A	255	G
53	A	259	G
53	A	260	U
53	A	261	U
53	A	269	U
53	A	270	A

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Mol	Chain	Res	Type
53	A	271	A
53	A	272	C
53	A	273	G
53	A	274	G
53	A	275	C
53	A	287	A
53	A	288	C
53	A	297	G
53	A	307	G
53	A	311	G
53	A	316	C
53	A	329	A
53	A	336	C
53	A	337	A
53	A	340	G
53	A	352	A
53	A	353	C
53	A	354	G
53	A	360	C
53	A	362	G
53	A	364	A
53	A	371	A
53	A	373	U
53	A	375	U
53	A	380	C
53	A	400	G
53	A	401	A
53	A	406	C
53	A	414	G
53	A	418	G
53	A	419	A
53	A	420	U
53	A	421	G
53	A	422	A
53	A	429	U
53	A	430	C
53	A	432	G
53	A	437	U
53	A	440	A
53	A	443	U
53	A	445	U
53	A	446	G

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Mol	Chain	Res	Type
53	A	447	U
53	A	456	A
53	A	461	C
53	A	462	A
53	A	463	A
53	A	464	G
53	A	465	U
53	A	472	C
53	A	473	G
53	A	475	A
53	A	476	U
53	A	477	A
53	A	478	G
53	A	481	C
53	A	483	G
53	A	484	U
53	A	485	A
53	A	488	U
53	A	493	G
53	A	494	G
53	A	497	C
53	A	500	A
53	A	502	C
53	A	503	C
53	A	505	G
53	A	506	A
53	A	518	A
53	A	520	C
53	A	527	C
53	A	530	G
53	A	536	G
53	A	540	U
53	A	541	A
53	A	556	A
53	A	566	G
53	A	568	A
53	A	571	U
53	A	573	U
53	A	574	U
53	A	580	U
53	A	581	A
53	A	582	A

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Mol	Chain	Res	Type
53	A	585	G
53	A	586	G
53	A	590	G
53	A	597	G
53	A	603	U
53	A	605	A
53	A	628	U
53	A	630	A
53	A	631	A
53	A	641	G
53	A	642	U
53	A	643	C
53	A	659	A
53	A	662	U
53	A	674	A
53	A	695	U
53	A	696	A
53	A	697	G
53	A	703	A
53	A	704	A
53	A	720	G
53	A	728	C
53	A	729	C
53	A	732	U
53	A	740	G
53	A	742	G
53	A	757	A
53	A	764	G
53	A	790	A
53	A	802	U
53	A	803	A
53	A	812	G
53	A	823	A
53	A	824	A
53	A	826	C
53	A	829	U
53	A	830	G
53	A	837	A
53	A	841	G
53	A	845	G
53	A	849	G
53	A	850	U

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Mol	Chain	Res	Type
53	A	851	U
53	A	853	C
53	A	856	C
53	A	861	U
53	A	874	A
53	A	875	A
53	A	882	A
53	A	886	A
53	A	924	A
53	A	929	A
53	A	936	G
53	A	944	C
53	A	945	A
53	A	954	G
53	A	955	G
53	A	967	U
53	A	968	A
53	A	970	U
53	A	971	U
53	A	972	C
53	A	976	G
53	A	977	C
53	A	978	A
53	A	979	A
53	A	981	G
53	A	985	A
53	A	986	G
53	A	987	A
53	A	993	A
53	A	999	U
53	A	1002	U
53	A	1003	G
53	A	1006	A
53	A	1012	U
53	A	1013	G
53	A	1014	A
53	A	1015	C
53	A	1018	U
53	A	1019	C
53	A	1020	C
53	A	1021	U
53	A	1022	A

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Mol	Chain	Res	Type
53	A	1023	G
53	A	1024	A
53	A	1028	A
53	A	1030	G
53	A	1031	A
53	A	1033	G
53	A	1034	U
53	A	1035	C
53	A	1036	C
53	A	1039	U
53	A	1041	C
53	A	1043	G
53	A	1048	A
53	A	1053	G
53	A	1059	U
53	A	1060	G
53	A	1063	G
53	A	1065	A
53	A	1088	U
53	A	1089	G
53	A	1095	U
53	A	1096	U
53	A	1104	G
53	A	1105	U
53	A	1111	A
53	A	1118	G
53	A	1134	G
53	A	1135	U
53	A	1137	G
53	A	1145	U
53	A	1146	C
53	A	1148	G
53	A	1152	G
53	A	1153	G
53	A	1165	G
53	A	1168	U
53	A	1169	G
53	A	1176	A
53	A	1177	C
53	A	1180	A
53	A	1186	G
53	A	1187	G

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Mol	Chain	Res	Type
53	A	1188	A
53	A	1193	G
53	A	1200	A
53	A	1205	A
53	A	1206	A
53	A	1210	A
53	A	1211	U
53	A	1212	C
53	A	1214	U
53	A	1215	G
53	A	1216	C
53	A	1218	C
53	A	1220	U
53	A	1221	U
53	A	1222	A
53	A	1223	U
53	A	1224	G
53	A	1234	A
53	A	1236	A
53	A	1247	A
53	A	1248	A
53	A	1249	U
53	A	1250	G
53	A	1265	C
53	A	1267	G
53	A	1269	G
53	A	1277	G
53	A	1283	A
53	A	1284	A
53	A	1287	C
53	A	1289	A
53	A	1290	U
53	A	1294	A
53	A	1295	C
53	A	1296	A
53	A	1306	U
53	A	1308	A
53	A	1309	G
53	A	1311	U
53	A	1314	G
53	A	1317	C
53	A	1329	C

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Mol	Chain	Res	Type
53	A	1337	C
53	A	1339	U
53	A	1340	G
53	A	1345	U
53	A	1355	A
53	A	1356	G
53	A	1362	G
53	A	1369	A
53	A	1370	G
53	A	1372	A
53	A	1373	U
53	A	1380	G
53	A	1383	A
53	A	1384	A
53	A	1385	U
53	A	1386	A
53	A	1387	C
53	A	1388	G
53	A	1407	A
53	A	1410	G
53	A	1414	G
53	A	1428	G
53	A	1435	A
53	A	1445	U
53	A	1446	C
53	A	1447	G
53	A	1448	G
53	A	1449	U
53	A	1451	A
53	A	1453	G
53	A	1454	U
53	A	1455	A
53	A	1460	U
53	A	1461	U
53	A	1462	U
53	A	1463	A
53	A	1464	G
53	A	1465	G
53	A	1466	A
53	A	1468	C
53	A	1473	C
53	A	1474	G

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Mol	Chain	Res	Type
53	A	1477	G
53	A	1500	U
53	A	1503	A
53	A	1504	G
53	A	1507	G
53	A	1513	A
53	A	1515	G
53	A	1516	U
53	A	1517	A
53	A	1539	G
53	A	1540	G

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	Y	21	G
29	Y	33	U
29	Y	38	U
52	X	101	G
52	X	164	U
52	X	252	C
52	X	407	A
52	X	441	C
52	X	450	U
52	X	511	U
52	X	528	G
52	X	549	A
52	X	762	A
52	X	1035	G
52	X	1045	U
52	X	1156	G
52	X	1176	U
52	X	1451	U
52	X	1507	U
52	X	1525	G
52	X	1567	U
52	X	1712	G
52	X	1766	C
52	X	1882	A
52	X	1900	A
52	X	2131	U
52	X	2133	C

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Mol	Chain	Res	Type
52	X	2180	U
52	X	2192	U
52	X	2219	G
52	X	2223	U
52	X	2334	U
52	X	2337	G
52	X	2380	G
52	X	2413	G
52	X	2469	C
52	X	2534	G
52	X	2805	A
52	X	2904	A
53	A	206	A
53	A	306	A
53	A	315	U
53	A	372	A
53	A	455	G
53	A	483	G
53	A	642	U
53	A	728	C
53	A	848	G
53	A	855	G
53	A	1022	A
53	A	1088	U
53	A	1147	A
53	A	1211	U
53	A	1276	C
53	A	1316	U
53	A	1369	A
53	A	1460	U
53	A	1463	A
53	A	1499	G

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-18558. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.