



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 10:27 PM UTC

PDB ID : 8UU8 / pdb_00008uu8
EMDB ID : EMD-42571
Title : Cryo-EM structure of the *Listeria innocua* 70S ribosome (head-swiveled) in complex with HflXr and pe/E-tRNA (structure II-C)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 3.10 Å(reported)
Based on initial model : 7NHN

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

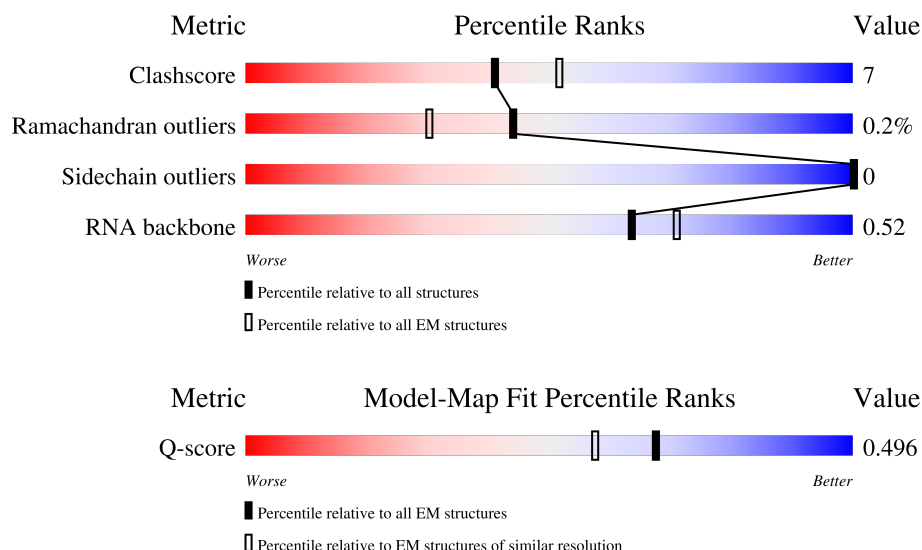
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



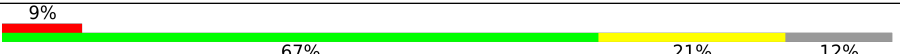
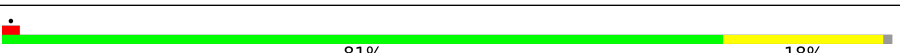
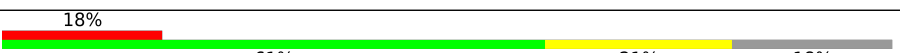
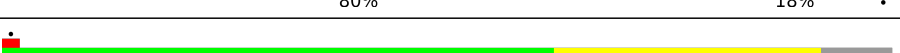
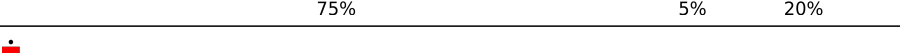
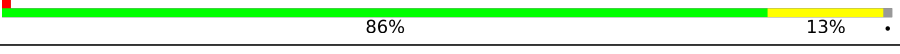
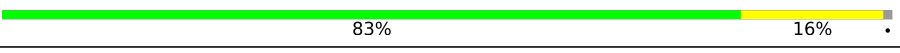
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	a	1550	5% 53% 35% 9% .
2	b	249	13% 65% 18% 16%
3	c	218	39% 90% . 6%

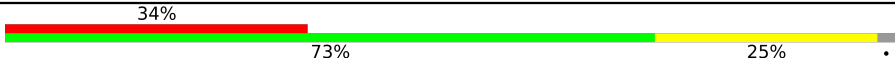
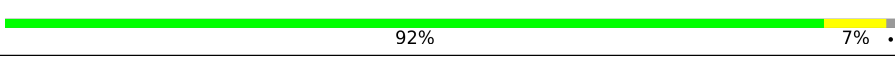
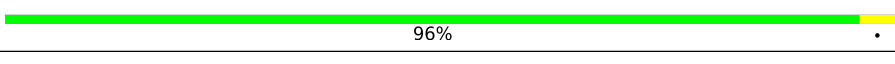
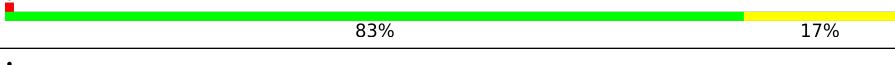
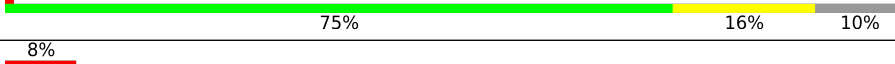
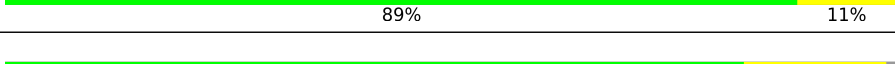
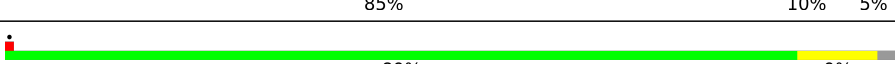
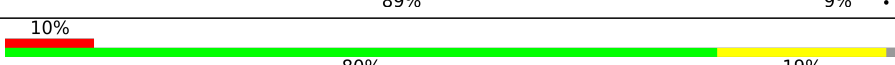
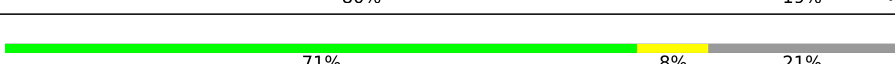
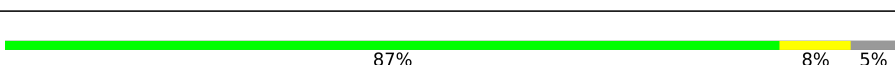
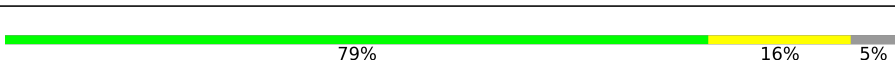
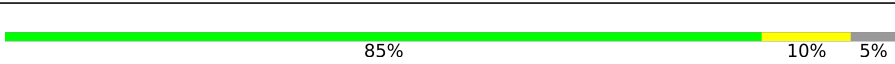
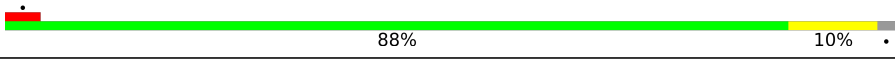
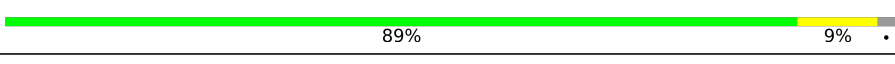
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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	167	
6	f	97	
7	g	156	
8	h	132	
9	i	130	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	90	
17	q	87	
18	r	79	
19	s	92	
20	t	84	
21	x	76	
22	w	21	
23	v	418	
24	A	2932	
25	B	116	
26	C	277	
27	D	209	
28	E	207	

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Mol	Chain	Length	Quality of chain
29	F	179	
30	G	178	
31	I	166	
32	H	141	
33	L	145	
34	M	122	
35	N	146	
36	O	144	
37	P	135	
38	Q	119	
39	R	114	
40	S	119	
41	T	102	
42	U	118	
43	V	94	
44	W	103	
45	Y	96	
46	Z	62	
47	1	63	
48	2	59	
49	3	81	
50	4	57	
51	5	49	
52	6	44	
53	7	66	

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Mol	Chain	Length	Quality of chain
54	8	37	78% 19%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 142031 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1516	Total	C	N	O	P	0	0
			32515	14504	5960	10535	1516		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	209	Total	C	N	O	S	0	0
			1396	888	249	255	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	c	204	Total	C	N	O	0	0
			1003	595	204	204		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	199	Total	C	N	O	S	0	0
			1562	978	289	293	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	152	Total	C	N	O	S	0	0
			1057	666	197	192	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	130	Total	C	N	O	S	0	0
			650	387	130	132	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1022	651	180	189	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	i	127	Total	C	N	O	0	0
			635	377	128	130		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	j	96	Total	C	N	O	0	0
			477	285	96	96		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	114	Total	C	N	O	S	0	0
			748	455	149	141	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			993	615	198	179	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	m	108	Total	C	N	O	0	0
			529	313	108	108		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	50	Total	C	N	O	S	0	0
			260	154	53	50	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	87	Total	C	N	O	S	0	0
			695	431	137	125	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	88	Total	C	N	O	S	0	0
			661	418	126	114	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			650	410	120	119	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	64	Total	C	N	O	S	0	0
			494	319	93	81	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	s	74	Total	C	N	O	0	0
			365	217	74	74		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	81	Total	C	N	O	S	0	0
			583	353	117	112	1		

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
22	w	9	Total	C	N	O	P		0	0
			190	86	34	61	9			

- Molecule 23 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	v	417	Total	C	N	O	S		0	0
			3282	2067	566	639	10			

- Molecule 24 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	A	2901	Total	C	N	O	P		0	0
			62318	27812	11528	20077	2901			

- Molecule 25 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	C	274	Total	C	N	O	S		0	0
			2084	1293	408	376	7			

- Molecule 27 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	D	206	Total	C	N	O	S		0	0
			1544	975	288	277	4			

- Molecule 28 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	E	205	Total	C	N	O	0	0
			1536	976	286	274		

- Molecule 29 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	175	Total	C	N	O	S	0	0
			1173	732	215	222	4		

- Molecule 30 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	G	171	Total	C	N	O	S	0	0
			1305	822	241	241	1		

- Molecule 31 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	I	129	Total	C	N	O	0	0
			636	378	129	129		

- Molecule 32 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	H	135	Total	C	N	O	0	0
			673	403	135	135		

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	143	Total	C	N	O	S	0	0
			1112	707	205	197	3		

- Molecule 34 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	122	Total	C	N	O	S	0	0
			893	554	170	165	4		

- Molecule 35 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	146	Total	C	N	O	S	0	0
			1071	662	209	199	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O	135	Total	C	N	O	S	0	0
			1062	679	203	174	6		

- Molecule 37 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	122	Total	C	N	O	S	0	0
			982	616	193	172	1		

- Molecule 38 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	119	Total	C	N	O	S	0	0
			884	545	172	166	1		

- Molecule 39 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	113	Total	C	N	O	S	0	0
			885	560	171	153	1		

- Molecule 40 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	118	Total	C	N	O	S	0	0
			949	602	187	156	4		

- Molecule 41 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T	101	Total	C	N	O	S	0	0
			774	502	134	137	1		

- Molecule 42 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	112	Total	C	N	O		
			850	537	159	154	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	92	Total	C	N	O	S	
			726	463	126	134	3	0

- Molecule 44 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	102	Total	C	N	O	S	
			760	482	140	135	3	0

- Molecule 45 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Y	76	Total	C	N	O	S	
			567	347	110	109	1	0

- Molecule 46 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Z	59	Total	C	N	O	S	
			444	274	92	76	2	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	1	60	Total	C	N	O	S	
			477	295	94	87	1	0

- Molecule 48 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	2	56	Total	C	N	O	S	
			433	272	82	78	1	0

- Molecule 49 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3	73	Total	C	N	O	S	0	0
			523	328	90	104	1		

- Molecule 50 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	4	53	Total	C	N	O	S	0	0
			417	256	86	70	5		

- Molecule 51 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	5	48	Total	C	N	O	S	0	0
			394	241	79	70	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	43	Total	C	N	O	S	0	0
			365	222	88	53	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	64	Total	C	N	O	S	0	0
			520	322	114	79	5		

- Molecule 54 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	8	36	Total	C	N	O	S	0	0
			280	174	56	44	6		

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	a	151	Total	Mg	0
			151	151	
55	b	1	Total	Mg	0
			1	1	
55	c	1	Total	Mg	0
			1	1	

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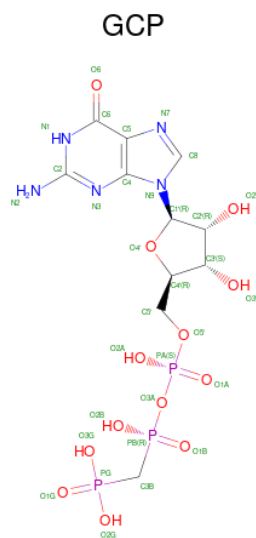
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Mol	Chain	Residues	Atoms		AltConf
55	g	1	Total 1	Mg 1	0
55	i	2	Total 2	Mg 2	0
55	m	1	Total 1	Mg 1	0
55	n	2	Total 2	Mg 2	0
55	o	1	Total 1	Mg 1	0
55	v	2	Total 2	Mg 2	0
55	A	249	Total 249	Mg 249	0
55	B	5	Total 5	Mg 5	0
55	C	1	Total 1	Mg 1	0
55	D	2	Total 2	Mg 2	0
55	M	1	Total 1	Mg 1	0
55	N	1	Total 1	Mg 1	0
55	S	1	Total 1	Mg 1	0
55	W	1	Total 1	Mg 1	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	n	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0
56	5	1	Total 1	Zn 1	0
56	8	1	Total 1	Zn 1	0

- Molecule 57 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
57	v	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms	AltConf
58	a	94	Total O 94 94	0
58	d	1	Total O 1 1	0
58	e	1	Total O 1 1	0
58	f	1	Total O 1 1	0
58	i	1	Total O 1 1	0
58	p	3	Total O 3 3	0
58	t	1	Total O 1 1	0
58	v	2	Total O 2 2	0
58	A	235	Total O 235 235	0
58	B	6	Total O 6 6	0
58	C	2	Total O 2 2	0

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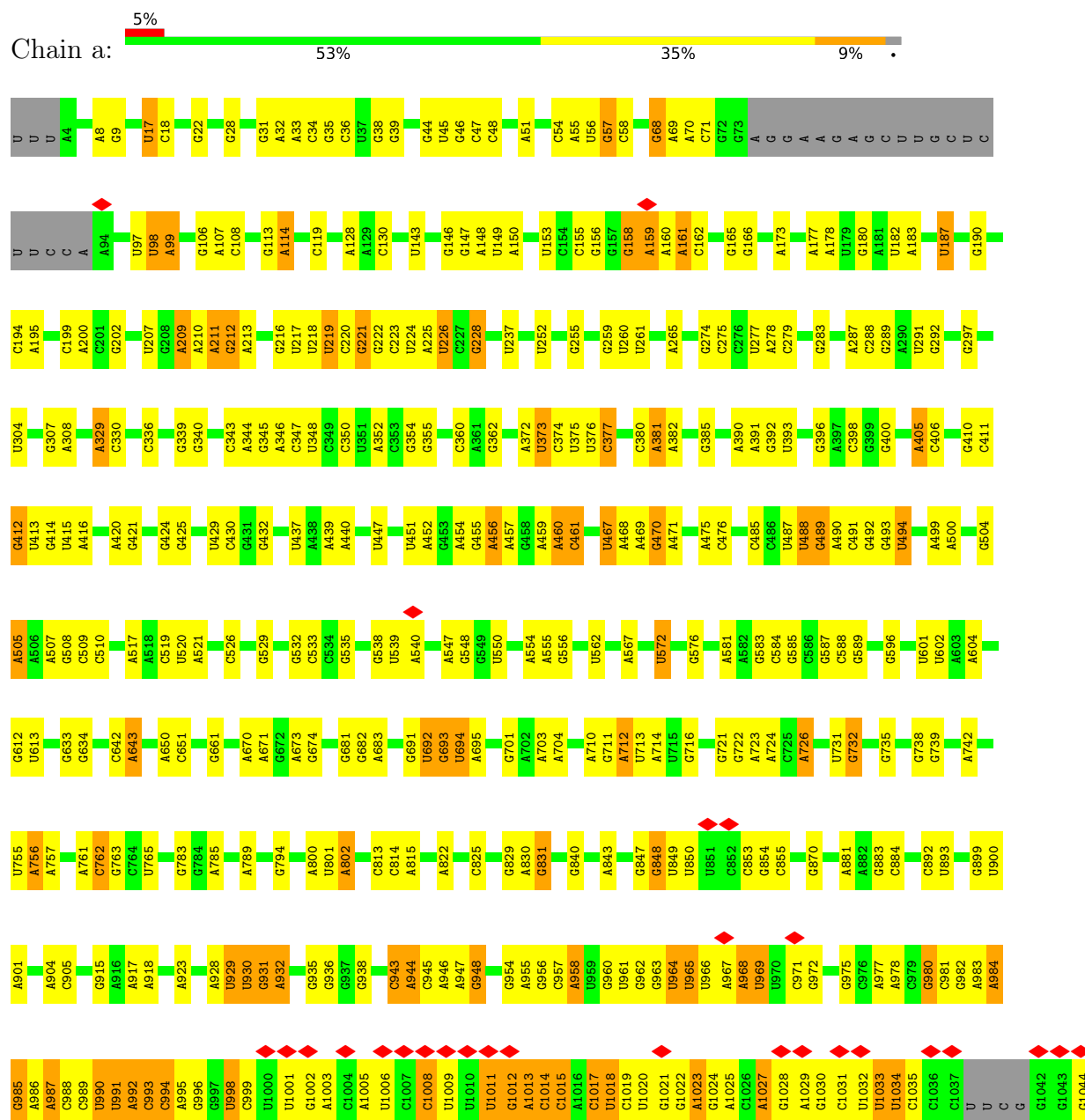
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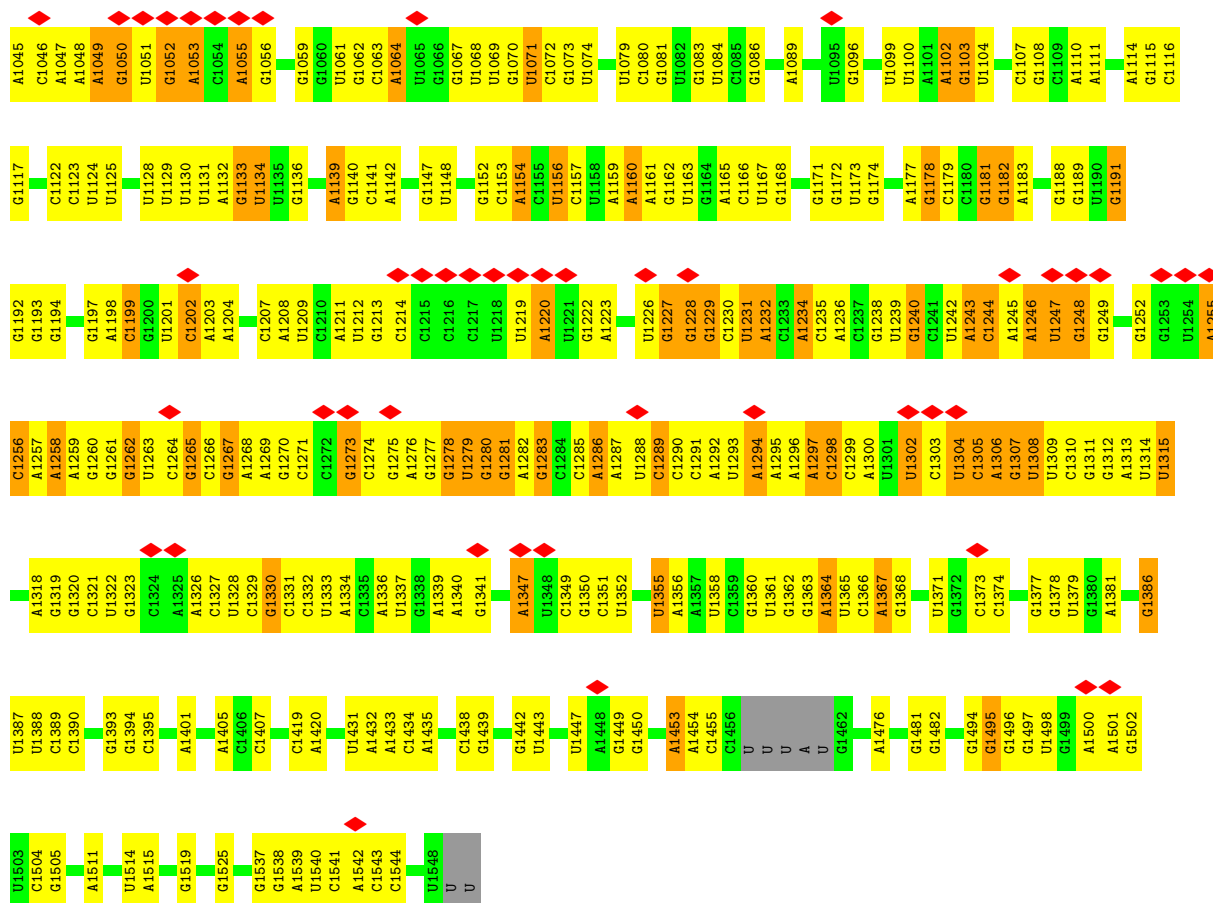
Mol	Chain	Residues	Atoms		AltConf
58	D	1	Total 1	O 1	0
58	N	5	Total 5	O 5	0
58	O	1	Total 1	O 1	0
58	P	1	Total 1	O 1	0
58	S	2	Total 2	O 2	0
58	T	1	Total 1	O 1	0
58	U	2	Total 2	O 2	0
58	V	1	Total 1	O 1	0
58	Z	2	Total 2	O 2	0
58	2	1	Total 1	O 1	0

3 Residue-property plots

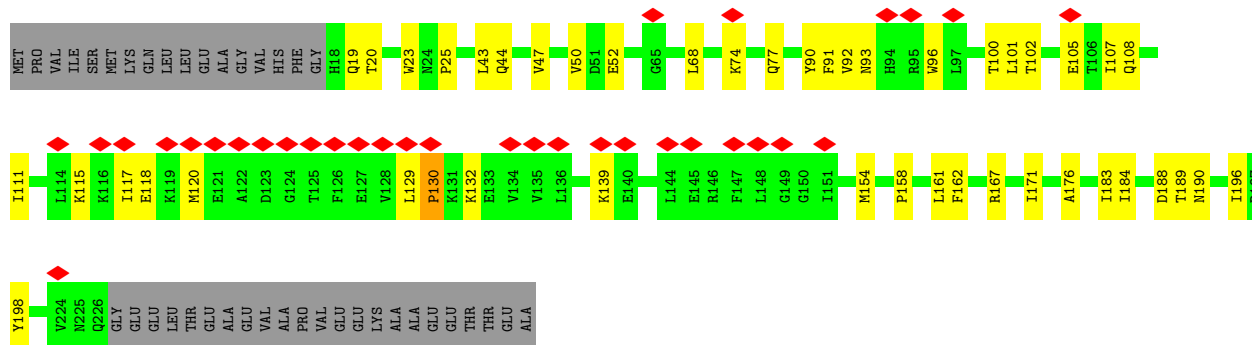
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S Ribosomal RNA

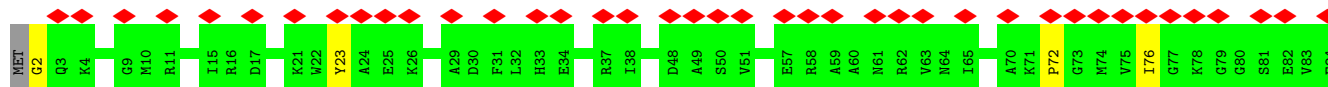
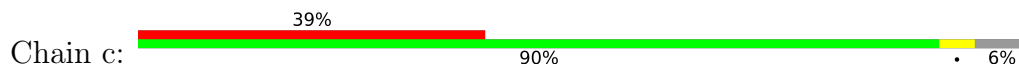


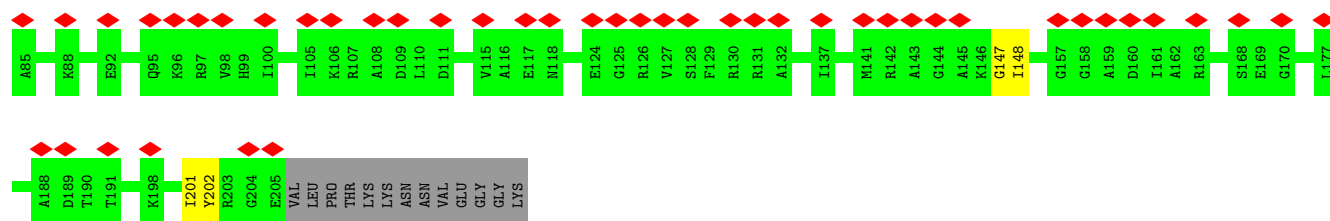


• Molecule 2: Small ribosomal subunit protein uS2

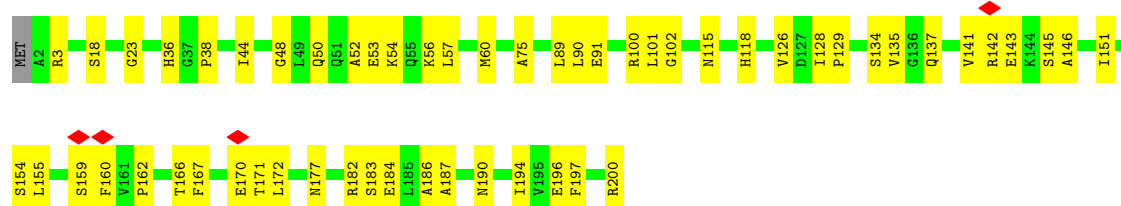


• Molecule 3: Small ribosomal subunit protein uS3

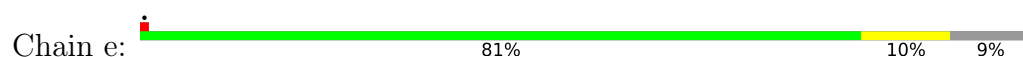




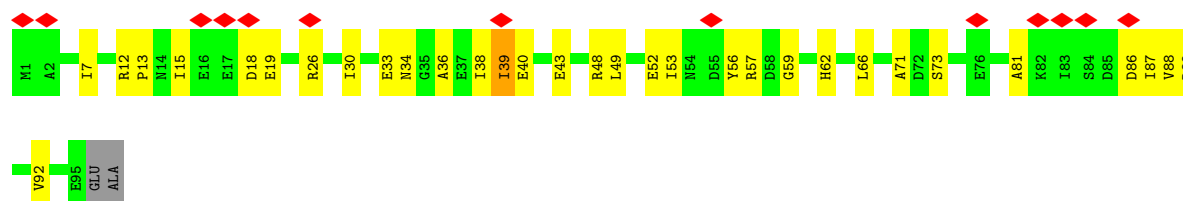
- Molecule 4: Small ribosomal subunit protein uS4



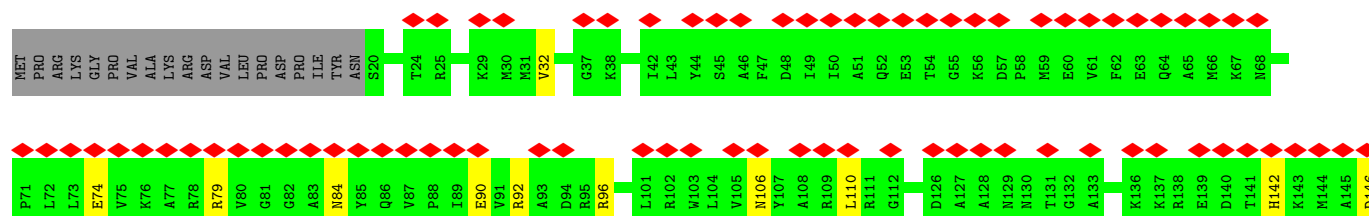
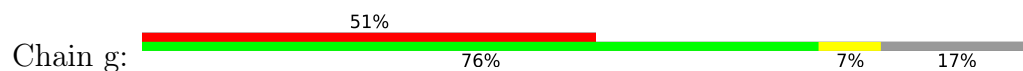
- Molecule 5: Small ribosomal subunit protein uS5

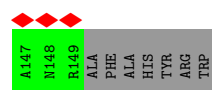


- Molecule 6: Small ribosomal subunit protein bS6



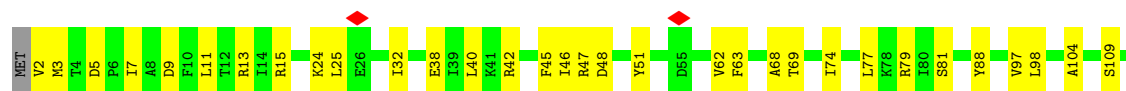
- Molecule 7: Small ribosomal subunit protein uS7





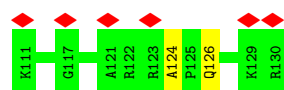
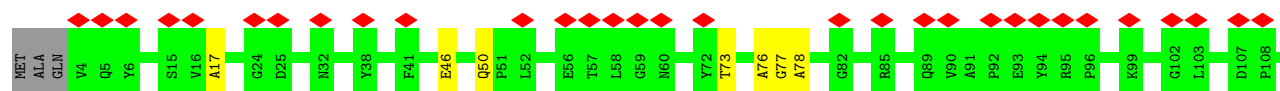
- Molecule 8: Small ribosomal subunit protein uS8

Chain h: 72% 27%



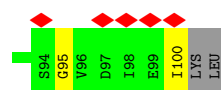
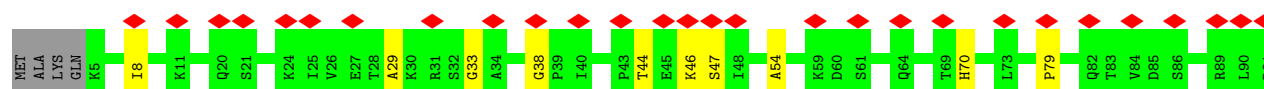
- Molecule 9: Small ribosomal subunit protein uS9

Chain i: 28% 91% 7%



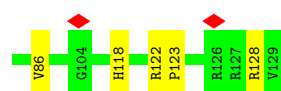
- Molecule 10: Small ribosomal subunit protein uS10

Chain j: 32% 82% 12% 6%



- Molecule 11: Small ribosomal subunit protein uS11

Chain k: 9% 67% 21% 12%

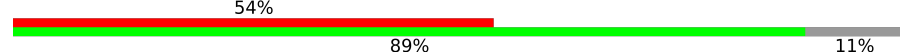


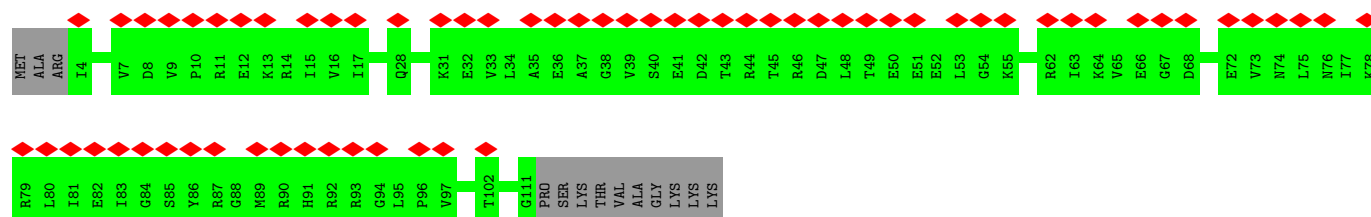
- Molecule 12: Small ribosomal subunit protein uS12

Chain l: 



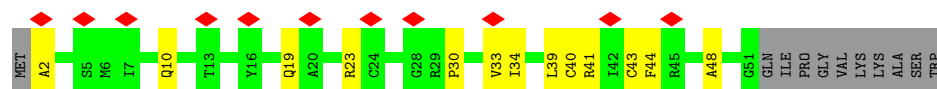
- Molecule 13: Small ribosomal subunit protein uS13

Chain m: 



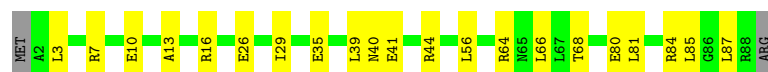
- Molecule 14: Small ribosomal subunit protein uS14

Chain n: 



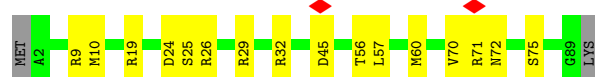
- Molecule 15: Small ribosomal subunit protein uS15

Chain o: 



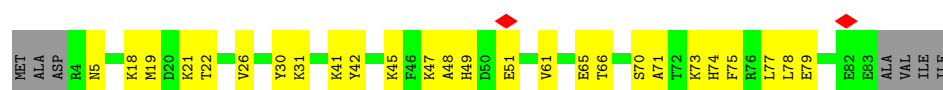
- Molecule 16: Small ribosomal subunit protein bS16

Chain p: 



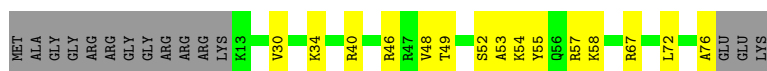
- Molecule 17: Small ribosomal subunit protein uS17

Chain q: 

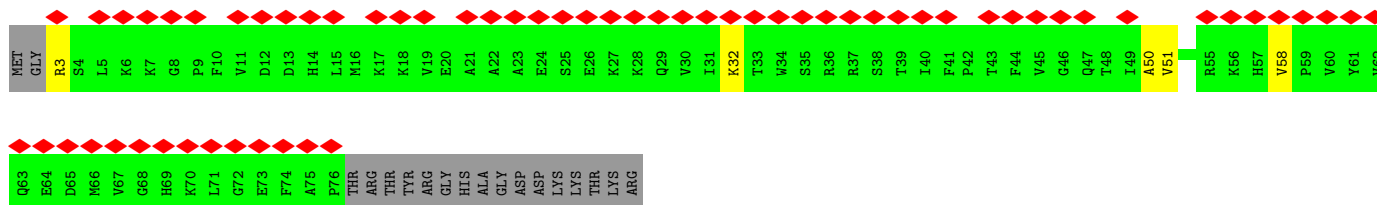
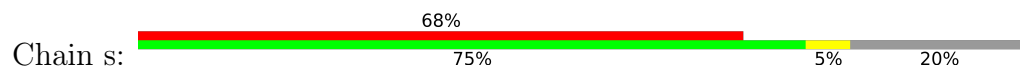


- Molecule 18: Small ribosomal subunit protein bS18

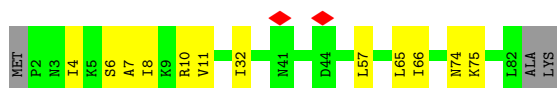
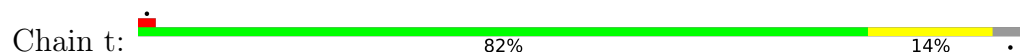
Chain r: 



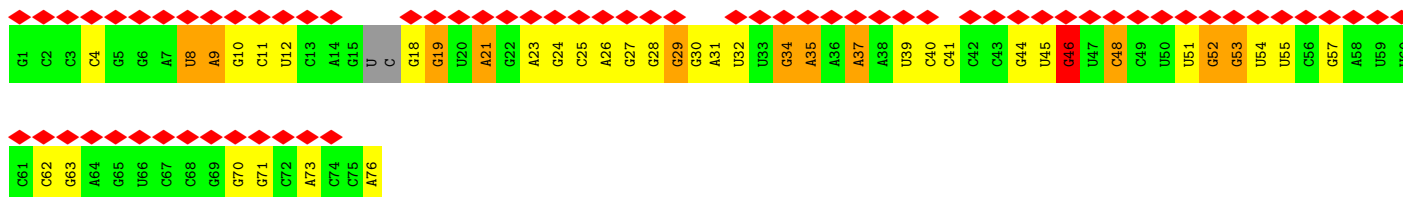
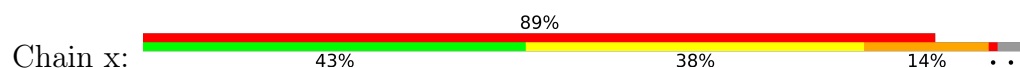
- Molecule 19: Small ribosomal subunit protein uS19



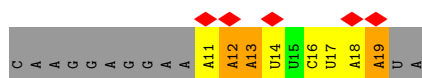
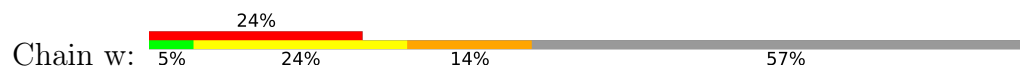
- Molecule 20: Small ribosomal subunit protein bS20



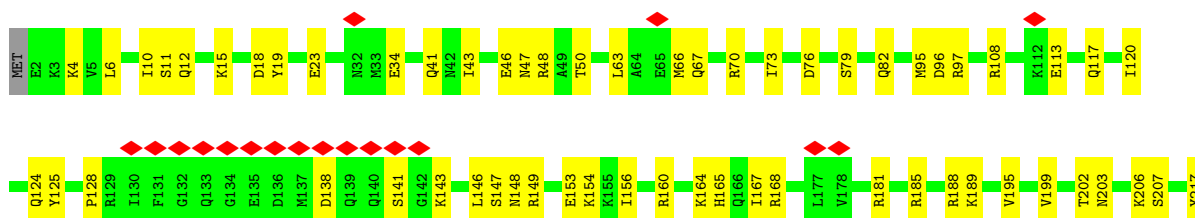
- Molecule 21: pe/E Hybrid State Phenylalanine tRNA

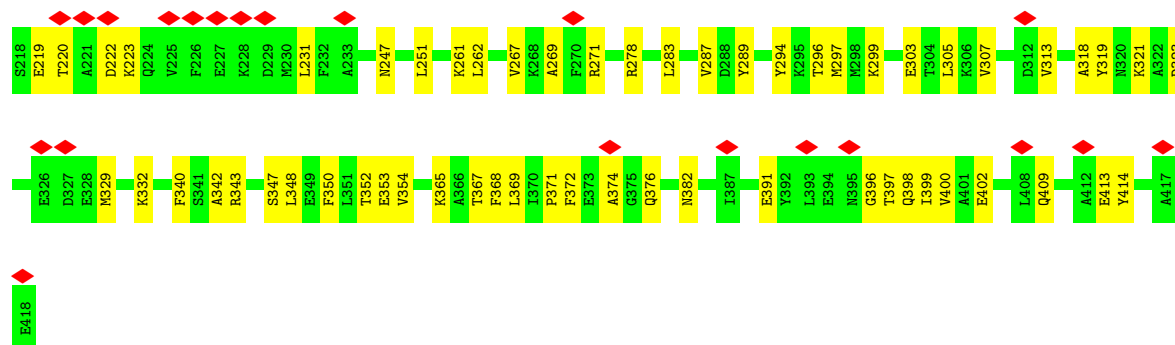


- Molecule 22: F-Stop mRNA



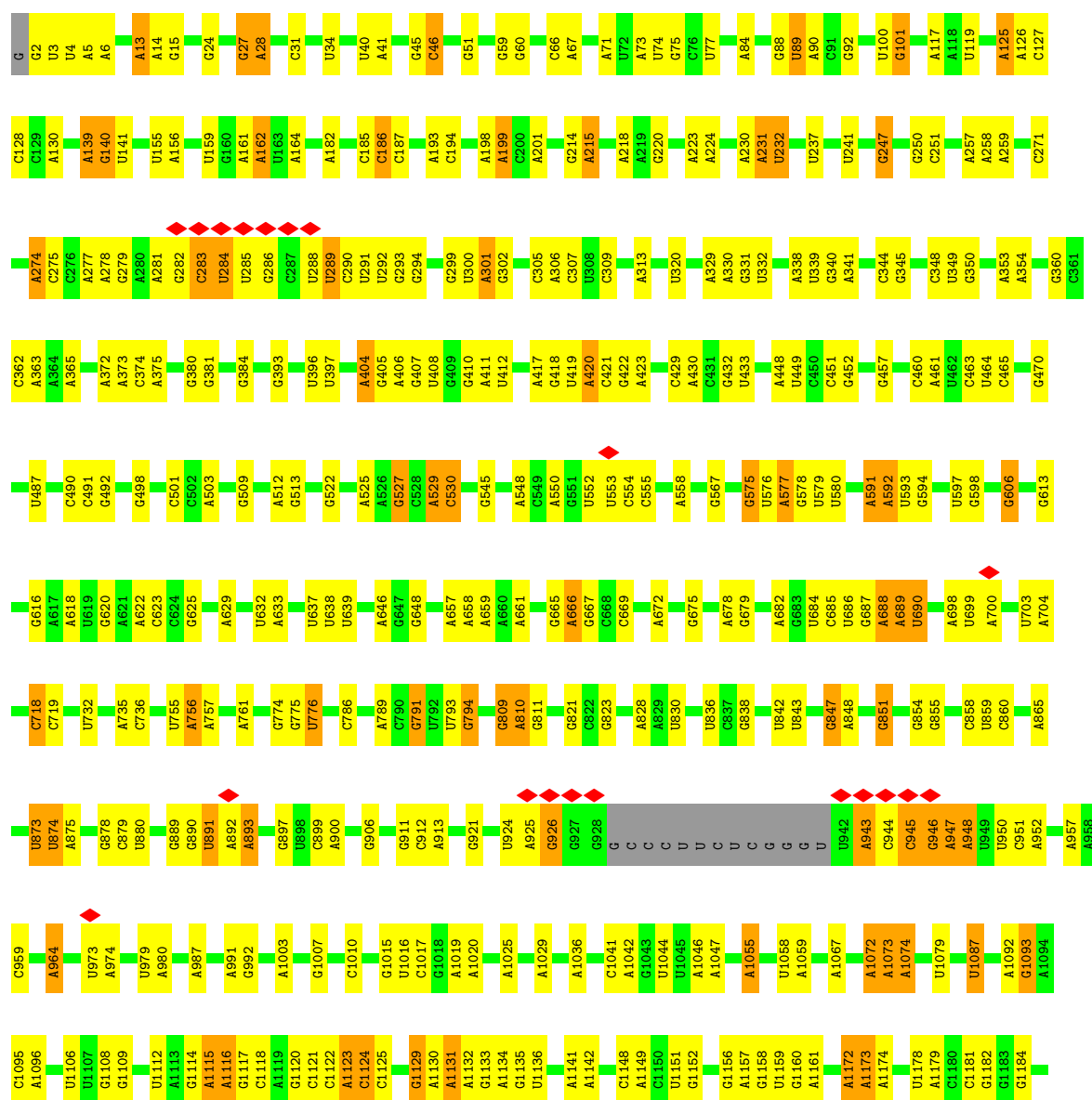
- Molecule 23: GTPase HflX



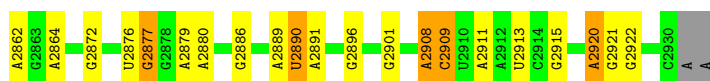


• Molecule 24: 23S Ribosomal RNA

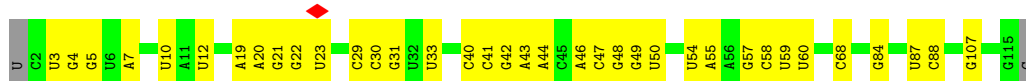
Chain A: 66% 27% 6%



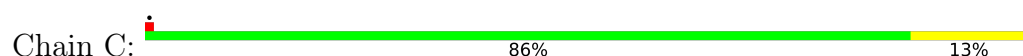
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A1310	G1311	G1316	A1317	A1318	A1319	G1320	U1336	U1337	A1344	A1345	U1357	C1358	G1364	A1365	C1369	U1373	U1384	U1385	C1394	C1395	U1396	A1397	A1398	G1404	G1405	A1409	A1422	U1423	A1429	C1430	A1431	G1432	A1433	U1434	A1435	A1439	A1447	U1452	G1453	A1456	A1457																	
U1462	U1463	A1464	A1465	C1466	C1467	A1468	A1469	U1470	G1471	C1478	G1482	A1483	A1484	A1487	U1488	G1497	A1503	U1504	G1505	A1509	U1510	G1511	C1517	C1518	A1519	G1528	U1529	G1530	U1531	G1532	A1533	G1534	A1535	A1536	A1539	C1542	A1543	A1544	A1545	U1546	U1555	G1556	C1557	G1558	A1559	A1560	G1561	C1562										
A1563	U1564	G1565	A1566	U1569	G1570	U1571	G1572	U1573	U1574	G1578	A1579	A1580	G1581	A	A	U	U	A	G	U1591	A1592	C1593	G1594	G1595	A1596	A1597	G1598	U1608	A1618	A1621	A1622	A1623	A1624	U1630	A1634	A1635	G1636	G1637	G1638	U1639	A1640	C1656	A1657	A1658	A1659	A1671												
A1683	A1684	U1685	C1686	G1694	A1695	G1696	C1697	U1698	A1699	G1700	A1701	G1702	A1703	A1704	U1708	U1712	G1716	G1723	C1724	A1727	A1728	U1729	G1730	A1731	C1732	A1749	A1761	U1762	U1763	A1764	C1770	A1771	A1772	G1773	C1774	C1775	A1778	A1779	A1780	G1781	A1782	G1783	C1784	G1785	G1786	C1787	A1793	U1794										
A1795	G1796	G1797	A1806	G1809	U1812	C1815	A1816	A1817	A1818	A1819	A1822	C1823	A1824	U1829	C1830	U1831	G1832	C1833	A1834	A1835	A1836	A1842	C1849	G1850	U1851	A1852	A1862	G1879	A1880	A1881	A1886	A1887	G1888	A1889	G1890	A1899	U1903	C1904	G1905	G1906	C1907	G1915	A1918															
A1922	A1923	G1939	C1947	U1948	U1949	U1950	G1962	G1963	C1967	G1968	A1969	U1973	U1988	C1996	G1997	C1998	A1999	C2000	A2003	A2004	G2005	U2024	G2025	U2026	A2030	G2043	A2048	U2052	A2053	G2054	U2055	A2056	C2057	C2058	U2059	A2063	A2064	G2065	A2066	G2072	C2076	C2088																
G2089	A2093	G2094	A2095	C2096	C2097	C2098	U2101	G2102	G2103	A2104	G2105	C2106	U2107	U2108	U2109	U2112	G2113	C2114	A2115	G2120	A2121	G2125	A2126	A2127	U2131	U2132	U2133	G2134	U2135	A2136	C2137	C2138	G2139	C2140	U2141	U2142	G2143	U2144	A2145	C2146	A2147	G2148	G2149	A2150	U2151	A2152	G2153	G2154	U2155	A2156	G2157	G2158	A2159					
C2162	G2163	A2164	A2165	C2166	A2167	C2168	A2169	C2170	G2171	U2172	G2173	U2174	G2175	C2176	G2177	C2178	U2179	A2180	G2181	C2182	A2183	U2184	A2185	C2186	G2187	A2188	G2189	G2190	A2191	G2192	G2193	C2194	A2195	A2196	U2197	G2198	G2199	U2200	C2201	G2202	G2203	A2204	U2205	A2206	C2207	U2208	A2209	C2210	C2211	C2212	U2213	G2214	G2215	C2216	U2217	G2218	U2219	A2220
U2221	G2222	A2223	C2224	C2225	A2226	U2227	U2230	A2231	G2236	C2237	A2245	G2250	A2258	A2266	U2276	U2277	U2278	G2279	A2280	G2292	U2295	A2299	A2306	G2312	C2316	C2317	C2318	A2319	A2320	A2321	G2322	G2323	U2324	U2325	C2326	C2327	G2328	U2329	A2333	A2334	A2338	A2339	G2446	C2455														
U2339	G2340	G2341	A2344	U2345	C2346	A2347	U2348	C2349	C2350	C2351	C2352	A2353	G2354	A2355	G2358	U2359	A2360	A2361	A2362	G2363	C2367	A2368	G2378	A2379	C2380	C2383	U2389	G2390	A2391	A2394	G2398	G2412	U2413	C2414	G2415	G2416	G2417	C2418	G2424	U2435	C2436	C2437	G2438	C2439	G2446	C2455												
U2456	C2457	A2458	A2459	C2460	G2461	G2462	A2463	U2471	A2472	C2473	C2474	A2481	G2488	A2492	C2498	C2499	C2500	A2501	A2502	U2506	C2507	C2508	A2509	C2510	A2511	G2514	G2519	G2520	A2521	G2522	U2524	G2535	A2536	U2537	G2538	G2546	U2547	C2548	G2549	C2550	A2551	G2562	G2568	C2569	U2570	C2571												
G2576	G2577	U2587	G2590	C2591	A2599	G2600	U2618	A2623	C2624	G2625	G2628	A2631	A2635	C2643	U2646	A2647	U2648	G2658	C2659	G2663	U2668	U2669	U2670	G2671	C2679	G2688	C2691	G2692	A2693	G2694	A2695	G2696	G2697	G2715	G2719	U2720	G2721	U2722	A2723	C2724																		
U2731	U2732	C2743	G2747	U2759	C2766	A2767	G2768	A2775	U2778	U2779	G2780	A2781	C2785	A2786	U2787	C2788	U2789	A2790	G2791	G2792	A2797	G2798	U2799	C2802	A2809	G2810	U2811	U2812	G2813	C2822	U2826	C2827	U2828	U2829	C2830	G2831	G2832	A2833	A2834	A2835	U2842	G2843	G2860	U2861														



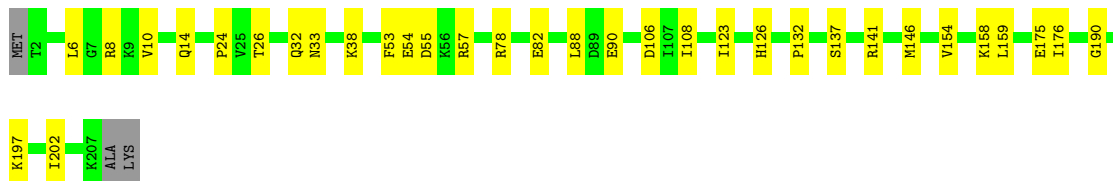
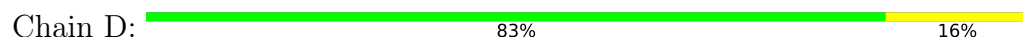
• Molecule 25: 5S Ribosomal RNA



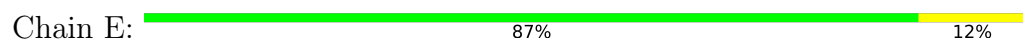
• Molecule 26: Large ribosomal subunit protein uL2



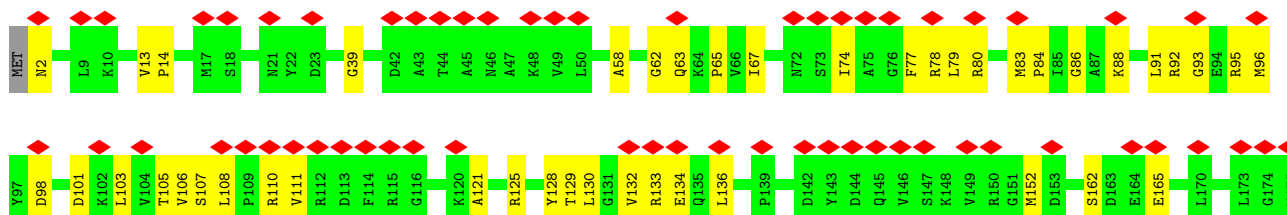
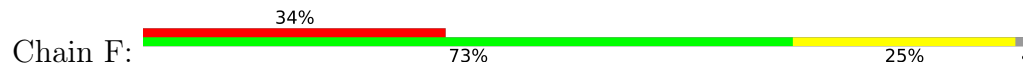
• Molecule 27: Large ribosomal subunit protein uL3



• Molecule 28: Large ribosomal subunit protein uL4



• Molecule 29: Large ribosomal subunit protein uL5

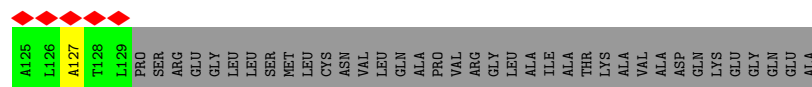
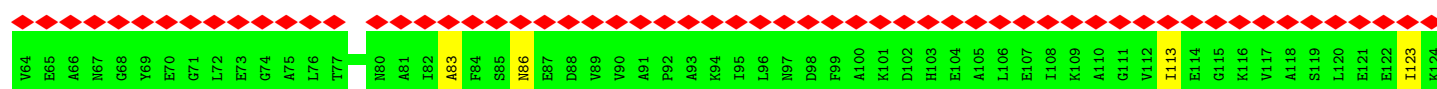
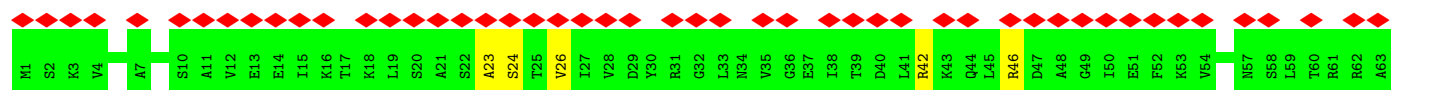




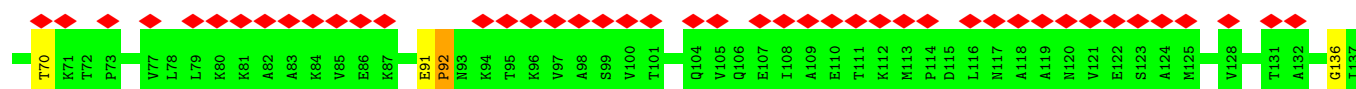
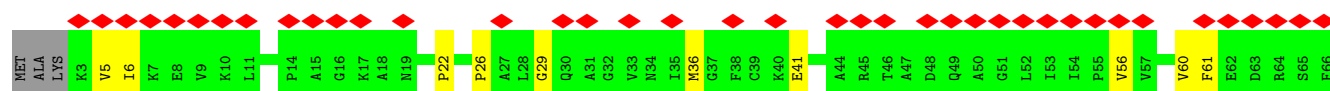
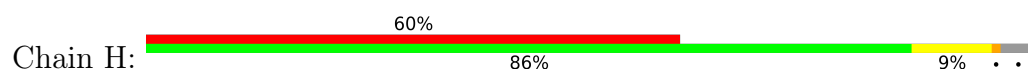
- Molecule 30: Large ribosomal subunit protein uL6



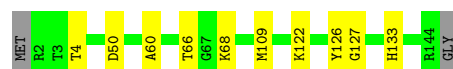
- Molecule 31: Large ribosomal subunit protein uL10



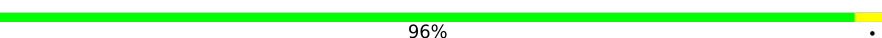
- Molecule 32: Large ribosomal subunit protein uL11



- Molecule 33: Large ribosomal subunit protein uL13



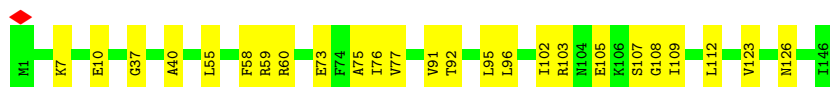
- Molecule 34: Large ribosomal subunit protein uL14

Chain M:  96%



- Molecule 35: Large ribosomal subunit protein uL15

Chain N:  83% 17%



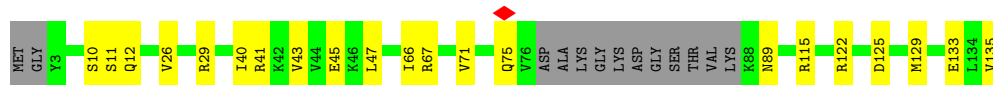
- Molecule 36: Large ribosomal subunit protein uL16

Chain O:  86% 8% 6%



- Molecule 37: Large ribosomal subunit protein bL17

Chain P:  75% 16% 10%



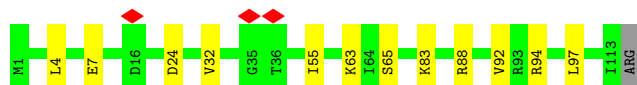
- Molecule 38: Large ribosomal subunit protein uL18

Chain Q:  8% 79% 21%



- Molecule 39: Large ribosomal subunit protein bL19

Chain R:  89% 11%

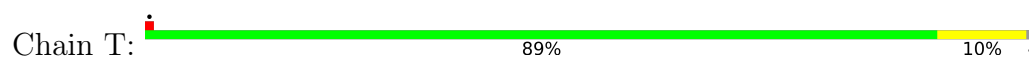


- Molecule 40: Large ribosomal subunit protein bL20

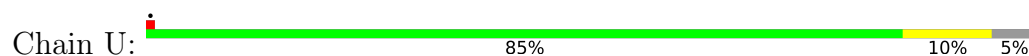
Chain S:  83% 16%



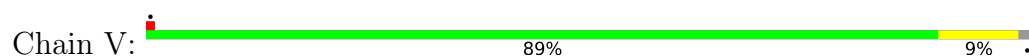
- Molecule 41: Large ribosomal subunit protein bL21



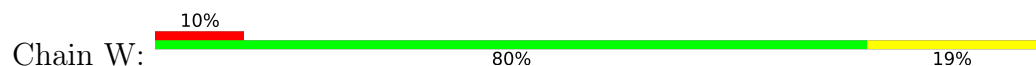
- Molecule 42: Large ribosomal subunit protein uL22



- Molecule 43: Large ribosomal subunit protein uL23



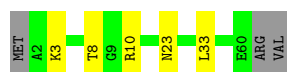
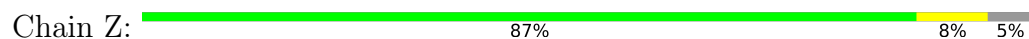
- Molecule 44: Large ribosomal subunit protein uL24



- Molecule 45: Large ribosomal subunit protein bL27



- Molecule 46: Large ribosomal subunit protein bL28



- Molecule 47: Large ribosomal subunit protein uL29

Chain 1:  79% 16% 5%



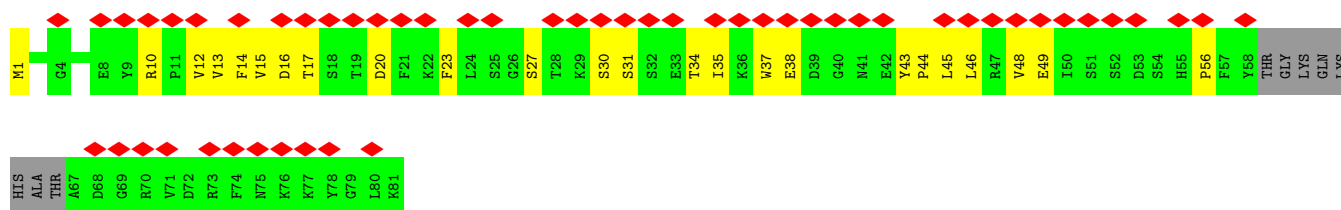
- Molecule 48: Large ribosomal subunit protein uL30

Chain 2:  85% 10% 5%



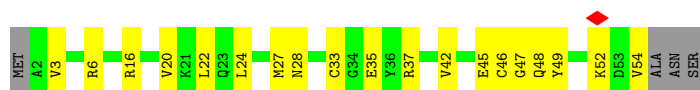
- Molecule 49: Large ribosomal subunit protein bL31B

Chain 3:  65% 60% 30% 10%



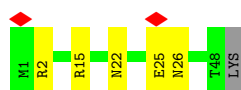
- Molecule 50: Large ribosomal subunit protein bL32

Chain 4:  60% 33% 7%



- Molecule 51: Large ribosomal subunit protein bL33

Chain 5:  88% 10%



- Molecule 52: Large ribosomal subunit protein bL34

Chain 6:  89% 9%

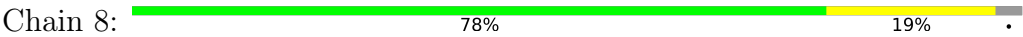


- Molecule 53: Large ribosomal subunit protein bL35

Chain 7:  83% 14%



- Molecule 54: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	55099	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	34.334	Depositor
Minimum map value	-17.982	Depositor
Average map value	0.002	Depositor
Map value standard deviation	1.124	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, GCP, 5MU, MIA, ZN, PSU, MG, 4SU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.26	0/36403	0.35	1/56778 (0.0%)
2	b	0.19	0/1419	0.42	1/1945 (0.1%)
3	c	0.15	0/1002	0.32	0/1391
4	d	0.23	0/1590	0.37	0/2142
5	e	0.25	0/1069	0.41	0/1451
6	f	0.20	0/797	0.48	0/1068
7	g	0.15	0/649	0.37	0/901
8	h	0.29	0/1035	0.45	0/1392
9	i	0.18	0/636	0.37	0/878
10	j	0.18	0/476	0.41	0/663
11	k	0.18	0/760	0.36	0/1031
12	l	0.25	0/1009	0.43	0/1365
13	m	0.15	0/528	0.32	0/731
14	n	0.25	0/259	0.56	0/357
15	o	0.23	0/705	0.53	0/949
16	p	0.24	0/674	0.47	0/909
17	q	0.23	0/659	0.40	0/882
18	r	0.27	0/502	0.46	0/673
19	s	0.13	0/364	0.30	0/505
20	t	0.23	0/586	0.44	0/788
21	x	0.23	0/1605	0.30	0/2497
22	w	0.15	0/212	0.30	0/327
23	v	0.20	0/3324	0.40	0/4483
24	A	0.24	0/69819	0.30	0/108917
25	B	0.15	0/2711	0.21	0/4224
26	C	0.24	0/2120	0.31	0/2848
27	D	0.25	0/1566	0.36	0/2108
28	E	0.22	0/1557	0.34	0/2103
29	F	0.13	0/1186	0.38	0/1615
30	G	0.16	0/1327	0.30	0/1793
31	I	0.07	0/635	0.19	0/882
32	H	0.12	0/676	0.32	0/942

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L	0.23	0/1135	0.28	0/1526
34	M	0.22	0/900	0.29	0/1212
35	N	0.22	0/1082	0.31	0/1446
36	O	0.21	0/1084	0.29	0/1450
37	P	0.24	0/993	0.31	0/1328
38	Q	0.13	0/893	0.27	0/1201
39	R	0.22	0/897	0.31	0/1206
40	S	0.25	0/962	0.28	0/1280
41	T	0.25	0/787	0.32	0/1057
42	U	0.24	0/860	0.29	0/1165
43	V	0.21	0/735	0.28	0/988
44	W	0.18	0/770	0.33	0/1032
45	Y	0.23	0/574	0.37	0/766
46	Z	0.22	0/449	0.33	0/597
47	1	0.16	0/478	0.25	0/640
48	2	0.22	0/436	0.28	0/585
49	3	0.13	0/532	0.36	0/720
50	4	0.34	0/425	0.49	0/567
51	5	0.17	0/398	0.26	0/534
52	6	0.27	0/368	0.28	0/479
53	7	0.25	0/527	0.41	0/685
54	8	0.24	0/283	0.27	0/375
All	All	0.24	0/153428	0.33	2/230377 (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
12	l	0	1
16	p	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	130	PRO	CA-N-CD	-8.04	100.75	112.00
1	a	756	A	C2'-C3'-O3'	7.94	121.41	109.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	l	57	LYS	Peptide
16	p	45	ASP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32515	0	16372	462	0
2	b	1396	0	1188	30	0
3	c	1003	0	487	5	0
4	d	1562	0	1543	38	0
5	e	1057	0	1082	11	0
6	f	785	0	774	21	0
7	g	650	0	328	6	0
8	h	1022	0	1078	26	0
9	i	635	0	321	7	0
10	j	477	0	203	9	0
11	k	748	0	658	20	0
12	l	993	0	995	16	0
13	m	529	0	239	0	0
14	n	260	0	140	9	0
15	o	695	0	684	13	0
16	p	661	0	638	10	0
17	q	650	0	676	15	0
18	r	494	0	502	10	0
19	s	365	0	163	3	0
20	t	583	0	578	7	0
21	x	1591	0	818	26	0
22	w	190	0	97	6	0
23	v	3282	0	3294	88	0
24	A	62318	0	31333	496	0
25	B	2428	0	1229	20	0
26	C	2084	0	2133	23	0
27	D	1544	0	1591	21	0
28	E	1536	0	1617	18	0
29	F	1173	0	1020	30	0
30	G	1305	0	1347	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	I	636	0	321	5	0
32	H	673	0	350	8	0
33	L	1112	0	1142	7	0
34	M	893	0	919	3	0
35	N	1071	0	1084	16	0
36	O	1062	0	1121	6	0
37	P	982	0	1043	16	0
38	Q	884	0	880	18	0
39	R	885	0	933	10	0
40	S	949	0	1018	16	0
41	T	774	0	812	6	0
42	U	850	0	901	11	0
43	V	726	0	743	5	0
44	W	760	0	818	14	0
45	Y	567	0	559	6	0
46	Z	444	0	465	3	0
47	1	477	0	492	7	0
48	2	433	0	479	5	0
49	3	523	0	454	18	0
50	4	417	0	412	16	0
51	5	394	0	403	4	0
52	6	365	0	417	3	0
53	7	520	0	571	8	0
54	8	280	0	301	5	0
55	A	249	0	0	0	0
55	B	5	0	0	0	0
55	C	1	0	0	0	0
55	D	2	0	0	0	0
55	M	1	0	0	0	0
55	N	1	0	0	0	0
55	S	1	0	0	0	0
55	W	1	0	0	0	0
55	a	151	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	g	1	0	0	0	0
55	i	2	0	0	0	0
55	m	1	0	0	0	0
55	n	2	0	0	0	0
55	o	1	0	0	0	0
55	v	2	0	0	0	0
56	4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	5	1	0	0	0	0
56	8	1	0	0	0	0
56	n	1	0	0	0	0
57	v	32	0	14	3	0
58	2	1	0	0	1	0
58	A	235	0	0	4	0
58	B	6	0	0	0	0
58	C	2	0	0	0	0
58	D	1	0	0	0	0
58	N	5	0	0	0	0
58	O	1	0	0	0	0
58	P	1	0	0	0	0
58	S	2	0	0	1	0
58	T	1	0	0	0	0
58	U	2	0	0	1	0
58	V	1	0	0	0	0
58	Z	2	0	0	0	0
58	a	94	0	0	1	0
58	d	1	0	0	0	0
58	e	1	0	0	0	0
58	f	1	0	0	0	0
58	i	1	0	0	0	0
58	p	3	0	0	1	0
58	t	1	0	0	0	0
58	v	2	0	0	1	0
All	All	142031	0	89780	1545	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 7.

All (1545) 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)
24:A:419:U:HO2'	24:A:420:A:H8	1.00	0.97
1:a:68:G:H1	1:a:99:A:N6	1.62	0.96
1:a:693:G:H21	1:a:714:A:H61	1.14	0.95
1:a:1270:G:H1	1:a:1279:U:H3	1.11	0.94
1:a:1173:U:H3	1:a:1178:G:H1	1.09	0.94
1:a:963:G:H21	1:a:1234:A:H62	1.16	0.94
1:a:849:U:H3	1:a:854:G:H1	1.09	0.93
24:A:1087:U:H3	24:A:1160:G:H1	0.94	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1531:U:H3	24:A:1561:G:H1	0.92	0.91
1:a:1061:U:H3	1:a:1213:G:H1	0.96	0.90
24:A:1129:G:N2	24:A:1132:A:OP2	2.07	0.88
24:A:2134:G:H1	24:A:2221:U:H3	1.22	0.87
24:A:665:G:H4'	24:A:666:A:H5'	1.57	0.87
1:a:1268:A:H8	1:a:1281:G:H21	1.23	0.86
21:x:51:U:H3	21:x:63:G:H1	0.88	0.85
1:a:992:A:HO2'	14:n:2:ALA:N	1.76	0.83
1:a:218:U:H2'	1:a:219:U:H2'	1.60	0.83
30:G:7:LYS:O	30:G:51:ASN:ND2	2.12	0.83
1:a:955:A:H2'	1:a:956:G:H8	1.43	0.82
1:a:68:G:H1	1:a:99:A:H61	0.83	0.82
1:a:1259:A:H2'	1:a:1260:G:C8	2.14	0.82
44:W:69:MET:HE3	44:W:78:PRO:HB2	1.60	0.82
1:a:1048:A:H2'	1:a:1049:A:H8	1.46	0.81
2:b:188:ASP:OD1	2:b:189:THR:N	2.14	0.80
19:s:32:LYS:HA	19:s:50:ALA:HB3	1.63	0.80
24:A:1297:G:H1	40:S:37:GLN:HE21	1.28	0.80
29:F:106:VAL:HG12	29:F:110:ARG:HH12	1.44	0.80
1:a:987:A:C2	1:a:1323:G:N2	2.51	0.79
25:B:48:G:H5''	38:Q:68:SER:HB3	1.64	0.79
1:a:1168:G:H1	1:a:1183:A:N6	1.82	0.78
24:A:1116:A:N1	24:A:1142:A:O2'	2.15	0.78
29:F:80:ARG:HB3	29:F:83:MET:HE1	1.66	0.78
23:v:372:PHE:HB2	23:v:396:GLY:HA2	1.64	0.78
1:a:1362:G:H2'	1:a:1363:G:H8	1.49	0.77
1:a:1271:C:N3	1:a:1279:U:O4	2.17	0.77
24:A:2424:G:O2'	24:A:2462:G:N2	2.17	0.77
23:v:143:LYS:NZ	24:A:2635:A:OP1	2.18	0.77
21:x:34:G:O6	22:w:16:C:N3	2.18	0.76
1:a:1267:G:N2	1:a:1282:A:OP2	2.19	0.76
1:a:964:U:H2'	1:a:965:U:C2	2.20	0.75
16:p:24:ASP:O	16:p:26:ARG:N	2.20	0.75
24:A:606:G:H21	40:S:37:GLN:HE22	1.35	0.74
1:a:68:G:N2	1:a:99:A:N1	2.30	0.74
23:v:323:ASP:OD2	23:v:343:ARG:NH2	2.20	0.74
18:r:46:ARG:HH12	18:r:53:ALA:HA	1.49	0.74
1:a:237:U:O2'	16:p:24:ASP:OD2	2.05	0.74
1:a:1257:A:N1	1:a:1361:U:O2'	2.19	0.74
1:a:1061:U:O4	1:a:1213:G:O6	2.06	0.74
25:B:3:U:OP1	25:B:59:U:O2'	2.06	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:11:SER:OG	24:A:1950:U:OP1	2.06	0.73
1:a:411:C:O2'	1:a:412:G:O5'	2.06	0.73
36:O:54:MET:HE1	36:O:104:PHE:HB3	1.69	0.73
1:a:554:A:HO2'	1:a:556:G:HO2'	1.31	0.73
24:A:2915:G:H1'	50:4:28:ASN:HD21	1.53	0.73
4:d:170:GLU:HG2	4:d:171:THR:HG23	1.71	0.72
24:A:1579:A:N6	24:A:1595:G:O2'	2.21	0.72
1:a:987:A:H61	1:a:1323:G:H1'	1.55	0.72
1:a:963:G:H21	1:a:1234:A:N6	1.85	0.72
1:a:1008:C:N3	1:a:1051:U:O4	2.23	0.72
1:a:1168:G:H1	1:a:1183:A:H61	1.38	0.72
35:N:55:LEU:O	35:N:60:ARG:NH1	2.23	0.72
15:o:41:GLU:HG3	15:o:44:ARG:HH21	1.55	0.72
24:A:2781:A:H62	24:A:2787:U:H3	1.38	0.72
24:A:791:G:HO2'	24:A:794:G:HO2'	1.35	0.71
1:a:987:A:H2	1:a:1323:G:H21	1.34	0.71
24:A:84:A:N6	24:A:101:G:O2'	2.24	0.71
2:b:100:THR:HA	2:b:107:ILE:HG13	1.73	0.71
24:A:625:G:N7	58:A:3306:HOH:O	2.24	0.71
1:a:1259:A:H2'	1:a:1260:G:H8	1.55	0.70
24:A:2361:A:H2'	24:A:2362:A:C8	2.26	0.70
1:a:153:U:H3	1:a:166:G:H1	1.37	0.70
9:i:73:THR:HA	9:i:76:ALA:HB3	1.72	0.70
1:a:682:G:H2'	1:a:683:A:H8	1.54	0.70
1:a:987:A:H2	1:a:1323:G:N2	1.89	0.70
1:a:943:C:O2'	1:a:1351:C:OP2	2.09	0.70
1:a:701:G:N2	21:x:37:MIA:S10	2.65	0.70
8:h:47:ARG:HG2	8:h:48:ASP:H	1.55	0.70
4:d:50:GLN:HB3	4:d:197:PHE:HB2	1.74	0.70
4:d:134:SER:HB3	4:d:137:GLN:HE21	1.57	0.70
24:A:1248:A:H2'	24:A:1249:A:C8	2.26	0.70
29:F:103:LEU:HA	29:F:107:SER:HB3	1.74	0.69
27:D:38:LYS:HE3	27:D:88:LEU:HD22	1.73	0.69
18:r:46:ARG:NH1	18:r:53:ALA:HA	2.07	0.69
14:n:33:VAL:HA	14:n:40:CYS:HA	1.74	0.69
1:a:1349:C:H2'	1:a:1350:G:H8	1.58	0.69
1:a:1362:G:H2'	1:a:1363:G:C8	2.27	0.69
8:h:25:LEU:HB2	8:h:62:VAL:HG12	1.75	0.69
1:a:955:A:H2'	1:a:956:G:C8	2.26	0.68
44:W:9:VAL:HG13	44:W:68:VAL:HG13	1.74	0.68
24:A:1832:G:N7	26:C:178:SER:OG	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1598:G:OP2	24:A:1598:G:N2	2.26	0.68
1:a:424:G:H2'	1:a:425:G:H8	1.59	0.68
24:A:1452:U:H2'	24:A:1453:G:H8	1.58	0.68
45:Y:61:ARG:NH2	45:Y:65:ASP:OD1	2.20	0.68
24:A:350:G:N1	24:A:353:A:OP2	2.26	0.68
24:A:2112:U:O2'	46:Z:23:ASN:ND2	2.27	0.68
24:A:1531:U:O4	24:A:1561:G:O6	2.12	0.68
1:a:917:A:H2'	1:a:918:A:H8	1.58	0.68
23:v:124:GLN:HG3	23:v:167:ILE:HD11	1.76	0.68
1:a:1132:A:H4'	10:j:38:GLY:HA3	1.75	0.68
27:D:123:ILE:HD11	27:D:141:ARG:CZ	2.23	0.67
1:a:1355:U:H2'	1:a:1356:A:H8	1.58	0.67
2:b:108:GLN:HA	2:b:111:ILE:HG12	1.76	0.67
24:A:2135:U:H2'	24:A:2136:A:H8	1.57	0.67
26:C:248:SER:OG	26:C:251:GLY:O	2.12	0.67
24:A:897:G:H21	48:2:46:MET:HE3	1.58	0.67
1:a:1333:U:H2'	1:a:1334:A:H8	1.58	0.67
24:A:2188:A:H2'	24:A:2189:G:H8	1.58	0.67
40:S:43:TYR:HB3	41:T:74:TYR:HB3	1.77	0.67
6:f:36:ALA:HB1	6:f:66:LEU:HD11	1.75	0.67
23:v:149:ARG:NH2	24:A:2538:G:OP2	2.27	0.67
23:v:195:VAL:HG12	23:v:251:LEU:HB2	1.76	0.67
21:x:34:G:N1	22:w:16:C:O2	2.22	0.67
1:a:1276:A:N3	1:a:1320:G:O2'	2.27	0.67
23:v:289:TYR:HB2	23:v:319:TYR:HB3	1.76	0.67
37:P:75:GLN:NE2	37:P:89:ASN:OD1	2.28	0.67
47:1:42:ARG:NH1	47:1:45:GLU:OE2	2.27	0.67
24:A:220:G:H22	24:A:237:U:H4'	1.59	0.67
23:v:206:LYS:NZ	57:v:503:GCP:O1G	2.28	0.66
37:P:26:VAL:HG13	37:P:71:VAL:HG23	1.77	0.66
24:A:2312:G:N7	45:Y:22:ARG:NH1	2.43	0.66
38:Q:25:THR:HG23	38:Q:28:ARG:H	1.61	0.66
1:a:1270:G:O6	1:a:1279:U:O4	2.13	0.66
14:n:41:ARG:O	14:n:43:CYS:N	2.28	0.66
47:1:11:THR:OG1	47:1:60:ARG:NH1	2.28	0.66
1:a:1199:C:OP1	3:c:2:GLY:N	2.28	0.66
23:v:271:ARG:O	23:v:278:ARG:NH2	2.29	0.66
24:A:1055:A:N3	24:A:1199:C:O2'	2.29	0.66
50:4:46:CYS:SG	50:4:48:GLN:HG3	2.35	0.66
4:d:118:HIS:ND1	4:d:145:SER:OG	2.29	0.65
20:t:65:LEU:HD12	20:t:66:ILE:HG23	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:44:A:H5''	38:Q:7:LYS:HE2	1.78	0.65
1:a:1268:A:H2'	1:a:1269:A:O4'	1.96	0.65
37:P:29:ARG:HG3	37:P:133:GLU:HG2	1.78	0.65
54:8:2:LYS:HE3	54:8:10:MET:HE1	1.79	0.65
38:Q:30:ARG:NH1	38:Q:47:ASP:OD2	2.30	0.65
24:A:847:G:OP2	58:A:3301:HOH:O	2.14	0.65
24:A:2149:G:H2'	24:A:2150:A:N7	2.11	0.65
1:a:1048:A:H2'	1:a:1049:A:C8	2.29	0.65
28:E:75:GLN:NE2	28:E:83:TRP:HE1	1.94	0.65
11:k:35:THR:HG22	11:k:41:ALA:HA	1.79	0.65
1:a:1177:A:OP1	2:b:139:LYS:NZ	2.29	0.64
49:3:16:ASP:HB3	49:3:20:ASP:H	1.63	0.64
1:a:1246:A:H4'	1:a:1247:U:H5''	1.78	0.64
1:a:1277:G:H2'	1:a:1278:G:H8	1.61	0.64
24:A:2221:U:H3'	24:A:2222:G:H8	1.63	0.64
24:A:2346:C:O3'	29:F:88:LYS:NZ	2.30	0.64
49:3:14:PHE:N	49:3:23:PHE:O	2.30	0.64
1:a:963:G:N2	1:a:1234:A:H62	1.92	0.64
1:a:1244:C:OP1	1:a:1310:C:O2'	2.15	0.64
24:A:1199:C:OP1	40:S:92:ARG:NH2	2.31	0.64
24:A:1151:U:H2'	24:A:1152:G:H8	1.63	0.64
24:A:1824:A:C2	24:A:1862:A:H4'	2.31	0.64
25:B:5:G:H21	38:Q:43:GLN:HE22	1.44	0.64
23:v:220:THR:HG21	24:A:2507:C:H4'	1.80	0.64
23:v:181:ARG:HE	23:v:185:ARG:HH22	1.45	0.64
48:2:3:LYS:N	58:2:101:HOH:O	2.30	0.64
24:A:1248:A:H2'	24:A:1249:A:H8	1.62	0.64
7:g:74:GLU:H	7:g:90:GLU:HA	1.63	0.64
23:v:348:LEU:O	23:v:352:THR:HG23	1.98	0.64
1:a:38:G:H22	1:a:405:A:H5'	1.62	0.63
1:a:1349:C:H2'	1:a:1350:G:C8	2.32	0.63
1:a:1277:G:H2'	1:a:1278:G:C8	2.33	0.63
1:a:1013:A:N7	1:a:1034:U:C4	2.66	0.63
24:A:2789:U:O2'	24:A:2790:A:OP2	2.15	0.63
42:U:16:ARG:HH21	42:U:103:LYS:HD2	1.64	0.63
1:a:460:A:O2'	1:a:461:C:O5'	2.15	0.63
4:d:143:GLU:HA	4:d:146:ALA:HB2	1.80	0.63
24:A:2361:A:H2'	24:A:2362:A:H8	1.63	0.63
2:b:101:LEU:HD11	2:b:158:PRO:HD2	1.81	0.62
44:W:6:GLY:H	44:W:23:VAL:HG23	1.63	0.62
50:4:52:LYS:HZ2	50:4:54:VAL:HG12	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:28:G:O2'	1:a:304:U:OP1	2.14	0.62
1:a:681:G:H2'	1:a:682:G:C8	2.34	0.62
1:a:1259:A:N1	1:a:1292:A:N6	2.48	0.62
23:v:146:LEU:HD23	24:A:2618:U:H1'	1.82	0.62
1:a:277:U:H2'	1:a:278:A:H8	1.63	0.62
1:a:1047:A:H2'	1:a:1048:A:C8	2.33	0.62
24:A:509:G:N2	24:A:512:A:OP2	2.24	0.62
1:a:158:G:N2	1:a:161:A:OP2	2.19	0.62
1:a:1347:A:HO2'	21:x:31:A:HO2'	1.44	0.62
23:v:185:ARG:HD3	23:v:189:LYS:HE2	1.80	0.62
1:a:345:G:H2'	1:a:346:A:H8	1.64	0.62
1:a:1071:U:H2'	1:a:1072:C:C6	2.34	0.62
24:A:125:A:H5''	52:6:19:ARG:HG3	1.82	0.62
1:a:1283:G:N3	1:a:1289:C:O2'	2.28	0.62
22:w:11:A:H2'	22:w:12:A:H4'	1.82	0.62
23:v:12:GLN:NE2	23:v:76:ASP:OD2	2.33	0.62
24:A:1656:C:N4	24:A:1671:A:OP2	2.25	0.62
1:a:850:U:O2'	1:a:853:C:N4	2.33	0.61
24:A:1253:C:O2'	24:A:1254:G:H8	1.82	0.61
1:a:966:U:O2	1:a:969:U:N3	2.33	0.61
8:h:98:LEU:HD11	8:h:132:TRP:HD1	1.64	0.61
23:v:156:ILE:O	23:v:160:ARG:HG3	2.00	0.61
24:A:2911:A:OP1	37:P:115:ARG:NH1	2.32	0.61
8:h:38:GLU:OE2	8:h:51:TYR:OH	2.16	0.61
37:P:47:LEU:HD21	37:P:66:ILE:HD11	1.82	0.61
1:a:1256:C:O2'	1:a:1294:A:N6	2.31	0.61
23:v:23:GLU:OE2	23:v:97:ARG:NH2	2.33	0.61
24:A:2692:G:O2'	30:G:175:LYS:NZ	2.33	0.61
38:Q:11:ARG:NH1	38:Q:97:GLY:O	2.33	0.61
40:S:50:ARG:O	40:S:54:LYS:NZ	2.32	0.61
24:A:251:C:O2	53:7:12:LYS:NZ	2.34	0.61
24:A:2338:A:O2'	29:F:133:ARG:NH1	2.32	0.61
24:A:2196:A:OP1	24:A:2204:A:O2'	2.18	0.61
24:A:2318:C:OP2	51:5:2:ARG:NH2	2.33	0.61
4:d:100:ARG:HD2	4:d:162:PRO:HG2	1.81	0.61
24:A:2164:A:H5'	24:A:2165:A:H2'	1.81	0.60
24:A:1890:G:H21	24:A:1918:A:H62	1.48	0.60
23:v:371:PRO:HG2	23:v:374:ALA:HB3	1.84	0.60
24:A:1464:A:N7	24:A:1634:A:N6	2.49	0.60
1:a:212:G:H2'	1:a:213:A:H8	1.67	0.60
1:a:1323:G:N1	1:a:1326:A:OP2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1442:G:H2'	1:a:1443:U:C6	2.37	0.60
9:i:73:THR:O	9:i:77:GLY:N	2.31	0.60
1:a:1168:G:N2	1:a:1183:A:N1	2.49	0.60
16:p:10:MET:HE2	16:p:19:ARG:HG3	1.83	0.60
24:A:2860:G:OP1	27:D:57:ARG:NH2	2.35	0.60
23:v:217:TYR:HE2	23:v:352:THR:HG21	1.67	0.60
27:D:6:LEU:H	27:D:33:ASN:HD21	1.50	0.60
1:a:187:U:H3	1:a:202:G:H1	1.49	0.60
12:l:53:MET:HE3	12:l:103:LEU:HD22	1.84	0.60
1:a:1481:G:H2'	1:a:1482:G:C8	2.37	0.59
24:A:2694:G:OP2	24:A:2694:G:H8	1.85	0.59
24:A:1591:U:H2'	24:A:1592:A:C8	2.37	0.59
1:a:1262:G:N2	1:a:1289:C:O2	2.35	0.59
1:a:1307:G:H4'	1:a:1308:U:H5''	1.83	0.59
24:A:1309:G:OP1	50:4:16:ARG:NH2	2.26	0.59
1:a:1310:C:H2'	1:a:1311:G:C8	2.38	0.59
24:A:1591:U:H2'	24:A:1592:A:H8	1.66	0.59
11:k:22:HIS:HB2	11:k:33:MET:HB3	1.85	0.59
1:a:992:A:OP2	1:a:1228:G:H2'	2.02	0.59
24:A:2159:A:N6	24:A:2205:U:OP2	2.35	0.59
1:a:947:A:H2'	1:a:948:G:C8	2.38	0.59
24:A:28:A:H2	40:S:11:ARG:HH12	1.48	0.59
24:A:2324:U:H2'	24:A:2325:U:C6	2.37	0.59
49:3:10:ARG:NH1	49:3:27:SER:O	2.36	0.59
30:G:109:TYR:HE2	30:G:152:ARG:HH11	1.51	0.59
24:A:2471:U:O3'	24:A:2472:A:H3'	2.02	0.59
1:a:1407:C:O3'	22:w:19:A:N6	2.34	0.59
4:d:118:HIS:HD1	4:d:145:SER:HG	1.49	0.59
15:o:29:ILE:HG13	15:o:66:LEU:HD11	1.85	0.59
24:A:339:U:OP1	44:W:90:LYS:NZ	2.30	0.59
24:A:1532:G:N2	24:A:1557:C:O4'	2.36	0.59
1:a:345:G:H2'	1:a:346:A:C8	2.38	0.58
1:a:470:G:H2'	1:a:471:A:C8	2.38	0.58
24:A:2223:A:H2'	24:A:2224:C:H6	1.68	0.58
29:F:77:PHE:O	29:F:78:ARG:HD3	2.02	0.58
1:a:1313:A:C2	1:a:1339:A:C4	2.91	0.58
21:x:19:G:O4'	21:x:57:G:N2	2.35	0.58
26:C:69:ARG:HE	26:C:129:ALA:HB2	1.68	0.58
29:F:91:LEU:HD12	29:F:95:ARG:HB3	1.83	0.58
1:a:146:G:H2'	1:a:147:G:C8	2.38	0.58
24:A:1253:C:O2'	24:A:1254:G:O5'	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:G:96:ALA:HB2	30:G:105:LEU:HD23	1.84	0.58
12:l:79:TYR:HB2	12:l:106:VAL:HG11	1.86	0.58
21:x:9:A:N7	21:x:46:G7M:N2	2.52	0.58
36:O:65:TRP:HB2	36:O:105:GLU:HB2	1.85	0.58
1:a:1295:A:H2'	1:a:1296:A:H8	1.68	0.58
17:q:49:HIS:HB2	17:q:73:LYS:HD3	1.86	0.58
26:C:37:LEU:HG	26:C:62:TYR:HB2	1.85	0.58
24:A:1268:G:OP1	41:T:67:ARG:NH1	2.37	0.58
1:a:547:A:H2'	1:a:548:G:H8	1.69	0.58
23:v:223:LYS:NZ	24:A:2507:C:OP2	2.31	0.58
24:A:1087:U:O4	24:A:1160:G:O6	2.22	0.58
24:A:2141:U:H3	24:A:2214:G:H22	1.50	0.58
32:H:6:ILE:H	32:H:61:PHE:HA	1.69	0.58
1:a:508:G:H2'	1:a:509:C:C6	2.39	0.58
25:B:12:U:OP2	25:B:68:C:O2'	2.22	0.58
26:C:118:SER:HB2	26:C:129:ALA:HB3	1.86	0.58
21:x:51:U:O2	21:x:63:G:N2	2.29	0.57
51:5:22:ASN:HB3	51:5:25:GLU:HB2	1.86	0.57
3:c:72:PRO:O	3:c:76:ILE:N	2.36	0.57
24:A:1253:C:HO2'	24:A:1254:G:H8	1.48	0.57
1:a:468:A:H2'	1:a:469:A:H8	1.70	0.57
1:a:1048:A:C6	1:a:1049:A:N6	2.73	0.57
7:g:79:ARG:HA	7:g:84:ASN:HA	1.87	0.57
8:h:2:VAL:HG22	8:h:3:MET:H	1.69	0.57
1:a:682:G:H2'	1:a:683:A:C8	2.38	0.57
23:v:321:LYS:HG2	57:v:503:GCP:C6	2.35	0.57
1:a:1330:G:H2'	1:a:1331:C:C6	2.39	0.57
15:o:26:GLU:HG3	15:o:81:LEU:HD22	1.85	0.57
24:A:185:C:H2'	24:A:186:C:H5'	1.87	0.57
1:a:1259:A:H5''	10:j:46:LYS:O	2.04	0.57
4:d:142:ARG:O	4:d:143:GLU:HG3	2.05	0.57
5:e:158:ARG:NH1	5:e:161:THR:OG1	2.38	0.57
21:x:9:A:H1'	21:x:45:U:C6	2.40	0.57
24:A:1539:A:H2'	26:C:98:ASP:OD2	2.04	0.57
24:A:2135:U:H2'	24:A:2136:A:C8	2.38	0.57
1:a:1246:A:H62	1:a:1305:C:H41	1.51	0.57
1:a:1268:A:P	1:a:1281:G:H22	2.28	0.57
24:A:2140:C:H2'	24:A:2141:U:C6	2.40	0.57
1:a:219:U:O2'	1:a:221:G:N2	2.36	0.57
1:a:1191:G:C2	1:a:1192:G:C8	2.93	0.57
23:v:63:LEU:O	23:v:67:GLN:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:U:64:GLU:HG2	42:U:71:ILE:HD11	1.86	0.57
1:a:947:A:H2'	1:a:948:G:H8	1.68	0.57
24:A:675:G:OP1	53:7:23:LYS:NZ	2.38	0.57
31:I:23:ALA:H	31:I:86:ASN:HA	1.68	0.57
42:U:40:ILE:HA	50:4:27:MET:HE1	1.87	0.56
16:p:71:ARG:O	16:p:75:SER:N	2.34	0.56
24:A:2043:G:H5''	42:U:47:SER:HB2	1.86	0.56
1:a:211:A:N1	1:a:228:G:O2'	2.38	0.56
1:a:962:G:O6	1:a:1236:A:N6	2.38	0.56
24:A:89:U:H5''	24:A:90:A:H2'	1.87	0.56
24:A:1452:U:H2'	24:A:1453:G:C8	2.38	0.56
24:A:1639:U:H2'	24:A:1640:A:H8	1.70	0.56
1:a:212:G:H2'	1:a:213:A:C8	2.40	0.56
1:a:765:U:OP1	1:a:830:A:O2'	2.23	0.56
1:a:1050:G:H2'	1:a:1051:U:C6	2.41	0.56
1:a:1313:A:C5	1:a:1314:U:N3	2.74	0.56
24:A:2134:G:N1	24:A:2222:G:H1'	2.20	0.56
32:H:22:PRO:HA	32:H:26:PRO:HD2	1.87	0.56
1:a:843:A:OP1	18:r:57:ARG:NH2	2.36	0.56
24:A:77:U:OP1	47:1:52:ARG:NH1	2.39	0.56
24:A:687:G:N2	24:A:690:U:OP2	2.35	0.56
30:G:43:ILE:HG22	30:G:52:VAL:HG12	1.87	0.56
1:a:1367:A:C6	1:a:1368:G:C5	2.94	0.56
6:f:26:ARG:O	6:f:30:ILE:HD12	2.05	0.56
23:v:148:ASN:ND2	58:v:601:HOH:O	2.31	0.56
24:A:1698:G:O2'	37:P:125:ASP:OD2	2.24	0.56
32:H:36:MET:O	32:H:41:GLU:N	2.38	0.56
1:a:1264:C:H4'	1:a:1265:G:H5'	1.87	0.56
21:x:51:U:O4	21:x:63:G:O6	2.23	0.56
24:A:891:U:O2'	24:A:893:A:OP1	2.24	0.56
24:A:1430:C:H2'	24:A:1431:A:H8	1.71	0.56
1:a:1014:C:H2'	1:a:1015:C:C6	2.41	0.56
1:a:1048:A:N6	1:a:1049:A:N6	2.54	0.56
1:a:1419:C:H2'	1:a:1420:A:C8	2.41	0.56
4:d:18:SER:OG	4:d:23:GLY:N	2.23	0.56
23:v:283:LEU:HD13	23:v:313:VAL:HB	1.86	0.56
44:W:71:ILE:HA	44:W:78:PRO:HA	1.86	0.56
1:a:547:A:H2'	1:a:548:G:C8	2.40	0.56
24:A:1880:A:H2	24:A:1881:A:H62	1.54	0.56
1:a:1260:G:H5'	10:j:47:SER:CB	2.36	0.56
1:a:1294:A:H2'	1:a:1295:A:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:97:ARG:CZ	23:v:261:LYS:HZ2	2.18	0.56
25:B:7:A:OP1	38:Q:19:ARG:NH1	2.38	0.56
1:a:1022:G:N2	1:a:1025:A:OP2	2.39	0.55
6:f:81:ALA:HB1	6:f:88:VAL:HG21	1.87	0.55
23:v:202:THR:HG21	23:v:231:LEU:HD23	1.88	0.55
24:A:2183:A:H2'	24:A:2184:U:C6	2.41	0.55
30:G:41:ILE:HG22	30:G:52:VAL:HB	1.88	0.55
1:a:969:U:H2'	1:a:1232:A:H62	1.72	0.55
1:a:1008:C:O2	1:a:1051:U:N3	2.34	0.55
24:A:1093:G:N2	24:A:1156:G:O2'	2.39	0.55
49:3:15:VAL:HG13	49:3:45:LEU:HD11	1.87	0.55
24:A:2127:A:H5''	24:A:2231:A:H61	1.70	0.55
30:G:33:LEU:HD22	30:G:75:MET:HG3	1.87	0.55
1:a:199:C:H2'	1:a:200:A:H8	1.71	0.55
12:l:52:THR:HG21	12:l:62:LEU:HG	1.87	0.55
23:v:79:SER:H	23:v:82:GLN:HE21	1.53	0.55
24:A:1187:U:H2'	33:L:66:THR:HG21	1.86	0.55
24:A:2348:U:O2	29:F:125:ARG:NH1	2.30	0.55
41:T:63:GLU:OE2	41:T:96:THR:OG1	2.22	0.55
5:e:113:ARG:O	5:e:117:GLU:HG3	2.07	0.55
20:t:32:ILE:HD11	20:t:57:LEU:HD21	1.87	0.55
23:v:367:THR:HG22	23:v:400:VAL:HG13	1.89	0.55
10:j:8:ILE:HA	10:j:100:ILE:HA	1.89	0.55
24:A:950:U:H2'	24:A:951:C:H6	1.71	0.55
24:A:2154:G:OP1	24:A:2203:G:N2	2.39	0.55
47:1:38:GLU:N	47:1:38:GLU:OE1	2.40	0.55
1:a:1275:G:N2	1:a:1319:G:H21	2.05	0.55
24:A:419:U:O2'	24:A:420:A:O5'	2.25	0.55
24:A:1172:A:H4'	24:A:1173:A:H5'	1.89	0.55
30:G:44:ASN:N	30:G:51:ASN:O	2.39	0.55
40:S:16:LYS:NZ	58:S:301:HOH:O	2.32	0.55
8:h:38:GLU:O	8:h:42:ARG:NH2	2.40	0.55
9:i:17:ALA:HB2	9:i:78:ALA:HB1	1.89	0.55
15:o:13:ALA:HA	15:o:16:ARG:CZ	2.36	0.55
5:e:89:HIS:O	5:e:89:HIS:ND1	2.40	0.55
1:a:277:U:H2'	1:a:278:A:C8	2.42	0.54
1:a:1073:G:H1'	1:a:1197:G:N2	2.22	0.54
8:h:9:ASP:OD2	8:h:13:ARG:NH2	2.36	0.54
50:4:28:ASN:N	50:4:37:ARG:O	2.40	0.54
1:a:984:A:H4'	1:a:985:G:H5''	1.88	0.54
24:A:344:C:H1'	44:W:12:ILE:HD12	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1336:U:H2'	24:A:1337:U:C6	2.42	0.54
24:A:1639:U:H2'	24:A:1640:A:C8	2.43	0.54
24:A:2346:C:H2'	24:A:2347:A:H8	1.72	0.54
24:A:2842:U:H2'	24:A:2843:C:H6	1.72	0.54
29:F:93:GLY:H	29:F:96:MET:HE1	1.73	0.54
30:G:123:ILE:HD11	30:G:144:LEU:HD21	1.88	0.54
1:a:1013:A:H5''	1:a:1033:U:H2'	1.89	0.54
1:a:1355:U:H2'	1:a:1356:A:C8	2.41	0.54
24:A:675:G:N2	24:A:678:A:OP2	2.33	0.54
27:D:8:ARG:NH1	27:D:197:LYS:O	2.37	0.54
29:F:101:ASP:O	29:F:105:THR:OG1	2.22	0.54
1:a:398:C:H4'	16:p:29:ARG:HH21	1.72	0.54
1:a:468:A:H2'	1:a:469:A:C8	2.42	0.54
1:a:967:A:H2'	1:a:968:A:C4	2.43	0.54
8:h:115:ASP:OD1	8:h:116:LYS:N	2.41	0.54
11:k:54:GLY:O	11:k:57:LYS:NZ	2.32	0.54
49:3:12:VAL:HG11	49:3:46:LEU:HG	1.89	0.54
49:3:48:VAL:HG22	49:3:49:GLU:H	1.72	0.54
1:a:928:A:O2'	1:a:929:U:O2	2.25	0.54
23:v:409:GLN:NE2	24:A:2693:A:N3	2.56	0.54
24:A:498:G:C8	28:E:58:ARG:HD3	2.43	0.54
29:F:58:ALA:O	29:F:62:GLY:N	2.31	0.54
1:a:1029:A:N6	1:a:1030:G:O6	2.41	0.54
1:a:1267:G:OP1	1:a:1291:C:O2'	2.19	0.54
5:e:96:LEU:HD21	5:e:127:LYS:HB3	1.88	0.54
8:h:5:ASP:OD2	8:h:79:ARG:NH1	2.41	0.54
24:A:1148:C:H2'	24:A:1149:A:H8	1.73	0.54
1:a:944:A:H2'	1:a:945:C:O4'	2.08	0.54
8:h:11:LEU:HD22	8:h:77:LEU:HD12	1.90	0.54
23:v:247:ASN:ND2	23:v:382:ASN:O	2.41	0.54
23:v:296:THR:HA	23:v:299:LYS:HE3	1.88	0.54
24:A:2052:U:OP2	50:4:6:ARG:NH2	2.41	0.54
24:A:2378:G:N3	24:A:2414:C:H2'	2.23	0.54
30:G:51:ASN:CG	30:G:52:VAL:H	2.15	0.54
44:W:33:VAL:HG23	44:W:65:VAL:HG22	1.90	0.54
1:a:382:A:H5''	1:a:460:A:H62	1.73	0.54
24:A:851:G:N2	24:A:875:A:OP1	2.41	0.54
25:B:41:C:OP1	49:3:1:MET:N	2.38	0.54
42:U:9:LYS:NZ	58:U:201:HOH:O	2.41	0.54
3:c:147:GLY:O	3:c:202:TYR:N	2.38	0.54
23:v:117:GLN:NE2	23:v:269:ALA:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:E:20:ASN:OD1	28:E:22:THR:N	2.40	0.54
30:G:17:VAL:HG22	30:G:26:VAL:HG22	1.89	0.54
1:a:1268:A:H8	1:a:1281:G:N2	1.99	0.53
23:v:18:ASP:OD1	23:v:19:TYR:N	2.40	0.53
24:A:2221:U:H3'	24:A:2222:G:C8	2.43	0.53
1:a:390:A:H2'	1:a:391:A:C8	2.43	0.53
1:a:415:U:H2'	1:a:416:A:H8	1.73	0.53
1:a:847:G:H2'	1:a:848:G:H8	1.72	0.53
1:a:1242:U:H2'	1:a:1243:A:O4'	2.08	0.53
1:a:1454:A:OP1	1:a:1455:C:N4	2.35	0.53
2:b:68:LEU:HD23	2:b:161:LEU:HG	1.90	0.53
17:q:70:SER:HB3	17:q:73:LYS:HB2	1.90	0.53
23:v:376:GLN:HG3	24:A:1141:A:C8	2.43	0.53
24:A:89:U:H3'	24:A:90:A:C8	2.43	0.53
24:A:2223:A:H2'	24:A:2224:C:C6	2.44	0.53
1:a:904:A:H2'	1:a:905:C:C6	2.44	0.53
1:a:995:A:H8	1:a:995:A:OP2	1.92	0.53
1:a:1178:G:H2'	1:a:1179:C:C6	2.42	0.53
18:r:40:ARG:HH21	18:r:76:ALA:HA	1.72	0.53
24:A:278:A:H2'	24:A:279:G:C8	2.43	0.53
48:2:15:ARG:HE	48:2:53:LEU:HD21	1.72	0.53
1:a:390:A:H2'	1:a:391:A:H8	1.72	0.53
1:a:726:A:C8	11:k:118:HIS:CD2	2.96	0.53
1:a:1171:G:H2'	1:a:1172:G:H8	1.73	0.53
24:A:1151:U:H2'	24:A:1152:G:C8	2.42	0.53
24:A:2134:G:O6	24:A:2221:U:O4	2.26	0.53
1:a:413:U:O4	4:d:3:ARG:NH2	2.41	0.53
24:A:597:U:H2'	24:A:598:G:O4'	2.09	0.53
5:e:89:HIS:HD2	5:e:94:GLU:OE1	1.91	0.53
24:A:193:A:H2'	24:A:194:C:C6	2.44	0.53
24:A:688:A:HO2'	24:A:689:A:P	2.32	0.53
23:v:164:LYS:HA	23:v:167:ILE:HG22	1.91	0.53
24:A:591:A:H4'	24:A:592:A:H5'	1.89	0.53
24:A:1903:U:O2'	24:A:1904:C:O2	2.24	0.53
42:U:40:ILE:HD13	50:4:24:LEU:HD11	1.91	0.53
45:Y:19:SER:O	45:Y:22:ARG:NH2	2.41	0.53
1:a:1174:G:N2	1:a:1177:A:OP2	2.42	0.53
4:d:60:MET:HE1	4:d:186:ALA:HB2	1.89	0.53
6:f:43:GLU:OE1	6:f:62:HIS:HD2	1.92	0.53
24:A:45:G:H5'	24:A:46:C:H5'	1.89	0.53
24:A:1117:G:H1'	24:A:1135:G:H2'	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2324:U:OP1	24:A:2413:U:O2'	2.26	0.53
24:A:27:G:HO2'	24:A:28:A:P	2.32	0.53
24:A:422:G:H2'	24:A:423:A:H8	1.74	0.53
24:A:1544:A:H2'	24:A:1545:A:C8	2.44	0.53
24:A:1823:C:O2'	26:C:208:ALA:HB2	2.09	0.53
24:A:2295:U:OP2	45:Y:24:SER:OG	2.21	0.53
24:A:2424:G:H2'	24:A:2457:C:H41	1.73	0.53
24:A:1187:U:H4'	24:A:1188:A:O4'	2.09	0.52
40:S:86:ALA:HB2	40:S:116:ALA:HB2	1.89	0.52
24:A:139:A:H2'	24:A:140:G:C8	2.45	0.52
24:A:789:A:O2'	24:A:1708:U:OP1	2.28	0.52
24:A:2446:G:N7	58:A:3319:HOH:O	2.34	0.52
28:E:13:ASN:OD1	28:E:14:ALA:N	2.43	0.52
49:3:31:SER:HB2	49:3:46:LEU:HD23	1.90	0.52
1:a:1159:A:HO2'	1:a:1160:A:H8	1.56	0.52
2:b:176:ALA:HB3	2:b:183:ILE:HD11	1.91	0.52
11:k:45:SER:HB2	11:k:70:ALA:HB2	1.91	0.52
15:o:3:LEU:HD23	15:o:35:GLU:HG2	1.91	0.52
44:W:24:LEU:HD11	44:W:36:GLU:HB3	1.90	0.52
1:a:376:U:H3'	1:a:377:C:H5'	1.91	0.52
8:h:68:ALA:O	8:h:69:THR:OG1	2.23	0.52
24:A:27:G:O2'	24:A:28:A:H8	1.91	0.52
24:A:2339:U:H5''	24:A:2340:G:H2'	1.91	0.52
53:7:62:VAL:HG23	53:7:62:VAL:O	2.09	0.52
24:A:292:U:H2'	24:A:293:G:C8	2.44	0.52
24:A:1535:A:H2'	24:A:1536:A:H8	1.75	0.52
1:a:670:A:H2'	1:a:671:A:C8	2.44	0.52
1:a:735:G:N2	1:a:738:G:OP2	2.35	0.52
17:q:22:THR:OG1	17:q:48:ALA:O	2.17	0.52
24:A:2360:A:H2'	24:A:2361:A:C8	2.45	0.52
38:Q:29:PRO:HG2	38:Q:92:VAL:HG12	1.91	0.52
45:Y:24:SER:OG	45:Y:25:GLU:N	2.40	0.52
1:a:633:G:H2'	1:a:634:G:H8	1.74	0.52
1:a:830:A:H2'	1:a:831:G:H5''	1.92	0.52
23:v:402:GLU:OE1	23:v:402:GLU:N	2.43	0.52
24:A:774:G:H4'	26:C:13:ARG:HD2	1.91	0.52
24:A:2159:A:C6	24:A:2196:A:H4'	2.45	0.52
24:A:2325:U:H2'	24:A:2326:C:H6	1.74	0.52
1:a:1258:A:H2'	1:a:1259:A:O4'	2.10	0.52
6:f:7:ILE:HG12	6:f:92:VAL:HG22	1.91	0.52
17:q:66:THR:N	17:q:74:HIS:O	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:48:VAL:HG13	18:r:49:THR:HG23	1.92	0.52
24:A:1010:C:O2'	24:A:2306:A:N3	2.43	0.52
24:A:1482:G:H2'	24:A:1483:A:C8	2.45	0.52
24:A:2511:A:OP2	54:8:2:LYS:NZ	2.40	0.52
1:a:291:U:C2	1:a:292:G:C8	2.98	0.52
15:o:39:LEU:HG	15:o:56:LEU:HD12	1.92	0.52
36:O:48:GLU:OE2	36:O:51:ARG:NH2	2.42	0.52
49:3:37:TRP:HE3	49:3:43:TYR:HD2	1.58	0.52
24:A:545:G:N1	24:A:548:A:OP2	2.38	0.52
24:A:2502:A:N6	24:A:2514:G:O2'	2.38	0.52
1:a:714:A:H4'	11:k:24:ARG:HD3	1.91	0.51
24:A:2668:U:O2'	27:D:82:GLU:OE2	2.25	0.51
30:G:95:ARG:HG2	30:G:128:ASN:HB2	1.92	0.51
44:W:9:VAL:CG1	44:W:68:VAL:HG13	2.38	0.51
1:a:931:G:H2'	1:a:932:A:C8	2.44	0.51
6:f:33:GLU:CD	6:f:34:ASN:H	2.19	0.51
1:a:113:G:H4'	1:a:114:A:O5'	2.10	0.51
1:a:194:C:N4	17:q:5:ASN:O	2.37	0.51
1:a:508:G:H2'	1:a:509:C:H6	1.75	0.51
1:a:1211:A:H2'	1:a:1212:U:O4'	2.10	0.51
20:t:74:ASN:OD1	20:t:75:LYS:N	2.44	0.51
24:A:1829:U:H2'	24:A:1830:C:C6	2.46	0.51
33:L:126:TYR:OH	33:L:133:HIS:NE2	2.40	0.51
34:M:63:VAL:HG12	34:M:106:LEU:HD11	1.92	0.51
1:a:691:G:H2'	1:a:692:U:C6	2.46	0.51
24:A:155:U:H2'	24:A:156:A:H8	1.76	0.51
24:A:632:U:H2'	24:A:633:A:H8	1.75	0.51
1:a:392:G:H2'	1:a:393:U:C6	2.46	0.51
17:q:30:TYR:HE1	17:q:41:LYS:HD2	1.75	0.51
24:A:1108:G:H2'	24:A:1109:G:H8	1.75	0.51
24:A:2064:A:N3	24:A:2488:G:O2'	2.36	0.51
24:A:2148:G:H4'	24:A:2200:U:H3	1.76	0.51
40:S:74:LEU:HD23	40:S:78:LYS:HE3	1.92	0.51
1:a:415:U:H2'	1:a:416:A:C8	2.45	0.51
1:a:1018:U:H2'	1:a:1019:C:C6	2.45	0.51
1:a:1099:U:H2'	1:a:1100:U:H6	1.75	0.51
1:a:1306:A:H8	1:a:1308:U:C2	2.29	0.51
1:a:1494:G:H2'	1:a:1495:G:C8	2.45	0.51
12:l:94:LEU:HD12	12:l:114:ALA:HB1	1.92	0.51
24:A:2:G:H2'	24:A:3:U:C6	2.46	0.51
24:A:2328:C:HO2'	24:A:2329:U:H6	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:F:2:ASN:N	29:F:98:ASP:OD1	2.44	0.51
47:1:58:ARG:NH1	47:1:62:LEU:O	2.43	0.51
15:o:40:ASN:HD21	24:A:761:A:H2	1.58	0.51
1:a:1261:G:H2'	1:a:1262:G:C8	2.46	0.51
1:a:1306:A:C2	1:a:1310:C:H1'	2.46	0.51
23:v:125:TYR:O	23:v:128:PRO:HD2	2.10	0.51
36:O:36:ALA:HB2	36:O:103:MET:HE2	1.93	0.51
42:U:11:VAL:HG12	42:U:109:THR:HG23	1.92	0.51
1:a:165:G:H2'	1:a:166:G:H8	1.75	0.51
1:a:964:U:H2'	1:a:965:U:N3	2.26	0.51
1:a:1373:C:H2'	1:a:1374:C:C6	2.46	0.51
24:A:1622:A:H2'	24:A:1623:A:C8	2.46	0.51
24:A:1922:A:H2'	24:A:1923:A:C8	2.46	0.51
24:A:2142:U:H2'	24:A:2143:G:C8	2.46	0.51
24:A:2333:A:H2'	24:A:2334:A:C8	2.46	0.51
24:A:2347:A:H2'	24:A:2348:U:C6	2.46	0.51
8:h:46:ILE:HG22	8:h:47:ARG:O	2.12	0.51
11:k:53:LYS:O	11:k:57:LYS:NZ	2.44	0.51
21:x:23:A:H2'	21:x:24:G:C8	2.46	0.51
24:A:341:A:N3	24:A:362:C:O2'	2.43	0.51
49:3:35:ILE:HD13	49:3:45:LEU:HD22	1.93	0.51
6:f:53:ILE:H	6:f:53:ILE:HD12	1.77	0.50
23:v:350:PHE:O	23:v:354:VAL:HG23	2.11	0.50
24:A:1133:G:O6	24:A:1135:G:N2	2.44	0.50
24:A:2139:G:H2'	24:A:2140:C:C6	2.46	0.50
24:A:2463:A:H2'	24:A:2463:A:N3	2.26	0.50
24:A:2522:G:N2	24:A:2524:U:O4	2.39	0.50
27:D:26:THR:OG1	27:D:190:GLY:O	2.29	0.50
49:3:34:THR:HG23	49:3:44:PRO:HA	1.92	0.50
1:a:56:U:H2'	1:a:57:G:H8	1.76	0.50
1:a:884:C:O2'	8:h:15:ARG:NH1	2.44	0.50
24:A:247:G:O2'	24:A:430:A:N1	2.39	0.50
24:A:1497:G:O2'	24:A:1596:A:N3	2.36	0.50
24:A:2624:C:H2'	24:A:2625:G:C8	2.46	0.50
24:A:2775:A:OP1	54:8:35:LYS:HE3	2.11	0.50
38:Q:96:ARG:NH1	38:Q:99:TYR:O	2.44	0.50
1:a:692:U:O2	11:k:41:ALA:N	2.45	0.50
1:a:1363:G:H2'	1:a:1364:A:C8	2.47	0.50
5:e:33:ARG:HD2	5:e:53:LYS:HE2	1.92	0.50
7:g:106:ASN:O	7:g:110:LEU:N	2.44	0.50
8:h:98:LEU:HD11	8:h:132:TRP:CD1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:x:52:G:H2'	21:x:53:G:C8	2.46	0.50
24:A:755:U:H2'	24:A:756:A:H8	1.76	0.50
24:A:2230:U:O2'	24:A:2231:A:O5'	2.29	0.50
1:a:1129:U:H2'	1:a:1130:U:C6	2.45	0.50
1:a:1266:C:H2'	1:a:1290:C:O2'	2.11	0.50
2:b:130:PRO:HB2	2:b:132:LYS:HG2	1.94	0.50
24:A:1456:A:H2'	24:A:1457:A:C8	2.47	0.50
28:E:157:ALA:HB2	28:E:198:ALA:HA	1.93	0.50
1:a:148:A:H2'	1:a:149:U:H6	1.77	0.50
11:k:128:ARG:NH1	22:w:13:A:O5'	2.44	0.50
17:q:70:SER:OG	17:q:71:ALA:N	2.44	0.50
18:r:67:ARG:HG2	18:r:72:LEU:HB2	1.92	0.50
23:v:47:ASN:HB3	23:v:50:THR:O	2.11	0.50
23:v:48:ARG:NH2	24:A:1997:G:OP1	2.44	0.50
24:A:1835:A:H2'	24:A:1836:A:C8	2.46	0.50
24:A:2276:U:H2'	24:A:2277:U:C6	2.46	0.50
1:a:1304:U:O2'	1:a:1305:C:OP2	2.21	0.50
7:g:92:ARG:O	7:g:96:ARG:N	2.37	0.50
18:r:52:SER:OG	18:r:53:ALA:N	2.44	0.50
21:x:70:G:H2'	21:x:71:G:H8	1.76	0.50
23:v:185:ARG:HG3	23:v:188:ARG:HH21	1.76	0.50
24:A:522:G:N1	24:A:525:A:OP2	2.41	0.50
24:A:2217:U:H2'	24:A:2218:G:C8	2.47	0.50
28:E:10:ASP:N	28:E:10:ASP:OD2	2.45	0.50
1:a:199:C:H2'	1:a:200:A:C8	2.46	0.50
23:v:203:ASN:O	23:v:321:LYS:NZ	2.43	0.50
23:v:340:PHE:HB2	23:v:347:SER:HB3	1.94	0.50
24:A:1320:G:OP2	24:A:1694:G:O2'	2.21	0.50
24:A:2095:A:H62	24:A:2536:A:H62	1.59	0.50
42:U:16:ARG:NH2	42:U:103:LYS:HD2	2.26	0.50
6:f:39:ILE:HG13	6:f:40:GLU:OE1	2.12	0.50
23:v:164:LYS:O	23:v:167:ILE:HG22	2.12	0.50
24:A:419:U:O2'	24:A:420:A:H8	1.79	0.50
1:a:931:G:O2'	1:a:932:A:OP1	2.30	0.50
1:a:1123:C:H2'	1:a:1124:U:C6	2.47	0.50
24:A:199:A:N6	24:A:2463:A:O2'	2.44	0.50
24:A:363:A:N3	28:E:169:ASN:ND2	2.60	0.50
24:A:1384:U:OP2	43:V:58:TYR:OH	2.26	0.50
24:A:2921:G:OP2	24:A:2921:G:N2	2.39	0.50
27:D:146:MET:HE2	27:D:154:VAL:HG21	1.94	0.50
1:a:1005:A:N6	1:a:1055:A:O2'	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1128:U:H3	1:a:1162:G:H1	1.58	0.49
2:b:23:TRP:CZ3	2:b:25:PRO:HA	2.47	0.49
8:h:88:TYR:CD1	8:h:126:GLU:HB3	2.46	0.49
23:v:219:GLU:N	23:v:219:GLU:OE1	2.44	0.49
24:A:2670:U:H2'	24:A:2671:G:O4'	2.11	0.49
30:G:46:GLU:H	30:G:50:ILE:HD13	1.77	0.49
26:C:144:ILE:HB	26:C:154:LEU:HB2	1.94	0.49
1:a:1264:C:H4'	1:a:1265:G:C5'	2.42	0.49
1:a:1394:G:H2'	1:a:1395:C:C6	2.47	0.49
7:g:142:HIS:O	7:g:146:ASP:N	2.40	0.49
16:p:70:VAL:O	16:p:72:ASN:N	2.43	0.49
24:A:688:A:O2'	24:A:689:A:OP1	2.26	0.49
24:A:2778:C:H2'	24:A:2779:U:C6	2.47	0.49
29:F:132:VAL:HG12	29:F:152:MET:HB2	1.95	0.49
1:a:726:A:C8	11:k:118:HIS:HD2	2.31	0.49
2:b:90:TYR:CE2	2:b:154:MET:HA	2.47	0.49
6:f:13:PRO:HG3	6:f:59:GLY:HA2	1.94	0.49
21:x:52:G:H2'	21:x:53:G:H8	1.77	0.49
24:A:31:C:O2'	24:A:1283:G:OP1	2.29	0.49
24:A:2144:U:OP2	24:A:2178:C:N4	2.46	0.49
24:A:2520:G:H2'	24:A:2521:A:H8	1.77	0.49
26:C:75:PRO:HB3	26:C:117:TYR:CZ	2.48	0.49
29:F:67:ILE:HG23	29:F:84:PRO:HB3	1.93	0.49
49:3:12:VAL:HG22	49:3:44:PRO:HB2	1.93	0.49
1:a:499:A:H2'	1:a:500:A:C8	2.48	0.49
1:a:572:U:P	12:l:12:ARG:HH21	2.36	0.49
1:a:994:C:OP2	1:a:1227:G:N2	2.25	0.49
24:A:277:A:H2'	24:A:278:A:H8	1.76	0.49
24:A:648:G:O6	35:N:103:ARG:NH1	2.46	0.49
24:A:2158:G:N2	24:A:2159:A:N1	2.59	0.49
1:a:1302:U:H2'	1:a:1303:C:C6	2.47	0.49
2:b:47:VAL:HA	2:b:50:VAL:HG12	1.95	0.49
24:A:410:G:O2'	24:A:412:U:O4	2.29	0.49
24:A:2624:C:H2'	24:A:2625:G:H8	1.77	0.49
32:H:6:ILE:N	32:H:60:VAL:O	2.46	0.49
37:P:115:ARG:HE	37:P:135:VAL:HG23	1.77	0.49
24:A:2107:U:H2'	24:A:2108:U:C6	2.48	0.49
30:G:102:LYS:HD2	30:G:116:VAL:HG22	1.94	0.49
35:N:105:GLU:OE2	35:N:108:GLY:N	2.46	0.49
1:a:159:A:N6	1:a:352:A:H62	2.11	0.49
24:A:1430:C:H2'	24:A:1431:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2167:A:N6	24:A:2191:A:O4'	2.46	0.49
1:a:504:G:N2	1:a:505:A:H3'	2.28	0.49
1:a:990:U:H5''	1:a:991:U:H3'	1.93	0.49
1:a:1434:C:H2'	1:a:1435:A:H8	1.78	0.49
24:A:579:U:O2'	40:S:49:ASP:OD1	2.30	0.49
24:A:943:A:H1'	24:A:945:C:C6	2.48	0.49
30:G:86:LYS:HD2	30:G:132:ILE:HG12	1.94	0.49
40:S:72:GLN:NE2	40:S:107:ASN:OD1	2.45	0.49
1:a:283:G:H5'	17:q:18:LYS:HD2	1.95	0.49
1:a:1131:U:O4	1:a:1132:A:N6	2.45	0.49
2:b:19:GLN:HG2	2:b:20:THR:H	1.78	0.49
10:j:29:ALA:O	10:j:33:GLY:N	2.45	0.49
21:x:51:U:H2'	21:x:52:G:C8	2.48	0.49
23:v:96:ASP:OD1	23:v:96:ASP:N	2.38	0.49
24:A:1699:A:O2'	24:A:1700:G:O5'	2.29	0.49
30:G:35:LYS:HE3	30:G:71:ILE:HD12	1.95	0.49
30:G:107:VAL:HB	30:G:152:ARG:HD3	1.94	0.49
1:a:722:G:H2'	1:a:723:A:C8	2.48	0.48
4:d:159:SER:OG	4:d:160:PHE:N	2.45	0.48
24:A:293:G:H2'	24:A:294:G:H8	1.78	0.48
24:A:330:A:H2'	24:A:331:G:H8	1.78	0.48
43:V:7:ILE:HG22	43:V:29:VAL:HG12	1.95	0.48
49:3:10:ARG:NH2	49:3:30:SER:OG	2.46	0.48
1:a:1047:A:H2'	1:a:1048:A:H8	1.77	0.48
1:a:1048:A:N6	1:a:1049:A:H62	2.11	0.48
23:v:153:GLU:HG3	23:v:154:LYS:H	1.79	0.48
24:A:1730:G:H21	24:A:1795:A:H3'	1.77	0.48
24:A:2346:C:H5''	29:F:88:LYS:HD3	1.95	0.48
25:B:21:G:H2'	25:B:22:G:C8	2.46	0.48
50:4:42:VAL:HG22	50:4:49:TYR:HB2	1.95	0.48
1:a:148:A:H2'	1:a:149:U:C6	2.48	0.48
1:a:800:A:O2'	1:a:802:A:N7	2.40	0.48
1:a:958:A:N1	1:a:1240:G:C2	2.81	0.48
23:v:391:GLU:HB2	23:v:398:GLN:HB3	1.95	0.48
24:A:155:U:H2'	24:A:156:A:C8	2.48	0.48
24:A:2829:U:H2'	24:A:2830:C:C4	2.48	0.48
29:F:63:GLN:OE1	29:F:95:ARG:NH1	2.46	0.48
30:G:103:LEU:HB3	30:G:115:PHE:HB2	1.94	0.48
1:a:755:U:H2'	1:a:756:A:C8	2.48	0.48
8:h:24:LYS:O	8:h:25:LEU:HD12	2.13	0.48
24:A:878:G:H2'	24:A:879:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2140:C:H2'	24:A:2141:U:H6	1.78	0.48
24:A:2362:A:H2'	24:A:2363:G:C8	2.48	0.48
50:4:33:CYS:SG	50:4:35:GLU:HG2	2.53	0.48
1:a:459:A:N1	1:a:488:U:O2'	2.34	0.48
1:a:1311:G:N2	1:a:1341:G:O6	2.46	0.48
1:a:1358:U:O2	1:a:1378:G:O6	2.31	0.48
11:k:33:MET:SD	11:k:44:TRP:HB3	2.54	0.48
24:A:487:U:O2'	28:E:46:GLN:NE2	2.46	0.48
24:A:703:U:H2'	24:A:704:A:C8	2.48	0.48
24:A:1731:A:H2'	24:A:1732:C:C6	2.48	0.48
24:A:2195:A:H5''	24:A:2205:U:H2'	1.96	0.48
24:A:2362:A:H2'	24:A:2363:G:H8	1.78	0.48
1:a:814:C:H2'	1:a:815:A:H8	1.78	0.48
5:e:84:HIS:CD2	8:h:98:LEU:HD22	2.49	0.48
12:l:85:HIS:HB3	12:l:112:ARG:HH12	1.78	0.48
24:A:575:G:O2'	24:A:577:A:N7	2.44	0.48
24:A:950:U:H2'	24:A:951:C:C6	2.49	0.48
31:I:26:VAL:O	31:I:83:ALA:N	2.35	0.48
47:1:10:SER:C	47:1:12:THR:H	2.22	0.48
1:a:8:A:N6	4:d:196:GLU:O	2.46	0.48
1:a:1201:U:C4	1:a:1202:C:N4	2.82	0.48
21:x:34:G:O2'	21:x:35:A:OP1	2.29	0.48
24:A:620:G:O2'	24:A:1299:A:OP1	2.32	0.48
24:A:1213:A:H2'	24:A:1214:A:C8	2.49	0.48
24:A:2325:U:H2'	24:A:2326:C:C6	2.48	0.48
28:E:49:HIS:ND1	28:E:92:PRO:HB2	2.28	0.48
30:G:98:LYS:HB2	30:G:125:VAL:HG11	1.94	0.48
1:a:329:A:H2'	1:a:330:C:H6	1.79	0.48
1:a:509:C:H2'	1:a:510:C:C6	2.49	0.48
23:v:372:PHE:HE2	32:H:29:GLY:HA3	1.79	0.48
1:a:46:G:O2'	1:a:373:U:O2	2.32	0.48
1:a:945:C:C4	1:a:946:A:C8	3.02	0.48
1:a:1019:C:H2'	1:a:1020:U:C6	2.48	0.48
24:A:2159:A:C5	24:A:2196:A:H4'	2.48	0.48
28:E:101:LEU:HG	28:E:102:PRO:HD2	1.94	0.48
50:4:20:VAL:HG12	50:4:20:VAL:O	2.13	0.48
54:8:11:CYS:HB3	54:8:32:HIS:HE1	1.79	0.48
1:a:899:G:O2'	1:a:915:G:O6	2.27	0.48
1:a:987:A:N1	1:a:1323:G:N3	2.61	0.48
1:a:1027:A:H2'	1:a:1028:G:C8	2.49	0.48
24:A:274:A:H5'	24:A:275:C:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:463:C:H2'	24:A:464:U:C6	2.49	0.48
24:A:2225:C:H2'	24:A:2226:A:H8	1.78	0.48
24:A:2628:G:N2	24:A:2631:A:OP2	2.43	0.48
27:D:32:GLN:HE22	27:D:55:ASP:CG	2.22	0.48
37:P:66:ILE:HG22	37:P:67:ARG:O	2.14	0.48
44:W:23:VAL:HG12	44:W:35:ILE:HG12	1.95	0.48
44:W:73:PRO:HG3	44:W:101:ILE:HG23	1.96	0.48
1:a:1021:G:O6	1:a:1027:A:C6	2.67	0.47
1:a:1247:U:H3	7:g:32:VAL:H	1.62	0.47
4:d:44:ILE:HG22	4:d:48:GLY:HA3	1.96	0.47
23:v:66:MET:SD	23:v:67:GLN:HG2	2.54	0.47
24:A:338:A:H2'	24:A:339:U:C6	2.49	0.47
24:A:1046:A:H2'	24:A:1047:A:C8	2.49	0.47
27:D:14:GLN:O	39:R:55:ILE:HD11	2.13	0.47
27:D:90:GLU:OE2	27:D:90:GLU:N	2.46	0.47
27:D:132:PRO:O	27:D:137:SER:OG	2.32	0.47
29:F:39:GLY:H	29:F:86:GLY:HA2	1.79	0.47
37:P:41:ARG:O	37:P:45:GLU:HG3	2.12	0.47
42:U:28:LEU:HD11	50:4:22:LEU:HD11	1.96	0.47
1:a:347:C:H2'	1:a:348:U:H6	1.79	0.47
6:f:38:ILE:HG13	6:f:39:ILE:N	2.28	0.47
6:f:52:GLU:HG2	6:f:57:ARG:HG2	1.96	0.47
8:h:47:ARG:HH21	8:h:63:PHE:HD1	1.60	0.47
25:B:47:C:H2'	25:B:48:G:H8	1.78	0.47
1:a:929:U:O2'	1:a:930:U:H5'	2.13	0.47
1:a:1129:U:H2'	1:a:1130:U:H6	1.79	0.47
23:v:73:ILE:HD13	23:v:95:MET:HB3	1.95	0.47
24:A:2324:U:H2'	24:A:2325:U:H6	1.78	0.47
24:A:2500:C:H2'	24:A:2501:A:O4'	2.14	0.47
1:a:904:A:H2'	1:a:905:C:H6	1.78	0.47
1:a:1379:U:OP1	9:i:73:THR:N	2.31	0.47
11:k:18:SER:O	11:k:37:THR:OG1	2.32	0.47
24:A:874:U:H2'	24:A:875:A:C8	2.49	0.47
24:A:2097:C:H2'	24:A:2098:C:C6	2.49	0.47
1:a:1248:G:H2'	1:a:1249:G:H8	1.77	0.47
1:a:1278:G:H2'	1:a:1279:U:H5'	1.97	0.47
24:A:404:A:H2'	24:A:405:G:C8	2.49	0.47
24:A:1112:U:N3	24:A:1115:A:OP2	2.37	0.47
24:A:2412:G:H2'	24:A:2413:U:C6	2.50	0.47
6:f:56:TYR:OH	6:f:87:ILE:HG12	2.14	0.47
23:v:222:ASP:OD1	23:v:222:ASP:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:214:G:H2'	24:A:215:A:O4'	2.14	0.47
24:A:1763:U:O2'	24:A:1764:A:H8	1.98	0.47
24:A:2830:C:H2'	24:A:2831:G:C4	2.49	0.47
29:F:58:ALA:HB2	29:F:65:PRO:HD3	1.96	0.47
30:G:38:ASN:OD1	30:G:39:PRO:HD2	2.15	0.47
38:Q:68:SER:O	38:Q:69:LYS:HG2	2.14	0.47
1:a:411:C:OP1	4:d:129:PRO:HD2	2.15	0.47
1:a:588:C:H2'	1:a:589:G:O4'	2.15	0.47
1:a:1240:G:OP1	9:i:126:GLN:HB3	2.15	0.47
17:q:31:LYS:NZ	17:q:42:TYR:HB2	2.30	0.47
24:A:27:G:H1'	24:A:558:A:H62	1.80	0.47
24:A:258:A:H2'	24:A:259:A:C8	2.49	0.47
24:A:277:A:H2'	24:A:278:A:C8	2.49	0.47
24:A:2173:G:H2'	24:A:2174:U:C6	2.50	0.47
24:A:2182:C:H2'	24:A:2183:A:C8	2.49	0.47
26:C:122:ALA:HB3	26:C:130:LEU:HD21	1.97	0.47
43:V:2:ASP:OD1	43:V:3:ALA:N	2.48	0.47
1:a:917:A:H2'	1:a:918:A:C8	2.45	0.47
4:d:101:LEU:HD22	4:d:167:PHE:HB2	1.97	0.47
17:q:21:LYS:NZ	17:q:51:GLU:O	2.32	0.47
24:A:632:U:H2'	24:A:633:A:C8	2.49	0.47
24:A:638:U:H2'	24:A:639:U:C6	2.50	0.47
24:A:1823:C:H2'	24:A:1824:A:N7	2.30	0.47
24:A:2193:G:H2'	24:A:2194:C:H6	1.80	0.47
1:a:36:C:OP1	12:l:133:LYS:NZ	2.31	0.47
1:a:509:C:H2'	1:a:510:C:H6	1.80	0.47
1:a:1123:C:H2'	1:a:1124:U:H6	1.80	0.47
4:d:91:GLU:OE2	4:d:100:ARG:NH1	2.48	0.47
23:v:303:GLU:O	23:v:307:VAL:HG23	2.15	0.47
24:A:2879:A:H2'	24:A:2880:A:H8	1.80	0.47
34:M:120:GLU:OE2	39:R:65:SER:OG	2.16	0.47
53:7:58:ILE:HB	53:7:61:MET:HE2	1.96	0.47
1:a:1086:G:N2	1:a:1089:A:OP2	2.45	0.47
2:b:74:LYS:O	2:b:77:GLN:HB2	2.15	0.47
21:x:62:C:H2'	21:x:63:G:H8	1.80	0.47
24:A:684:U:H2'	24:A:685:C:C6	2.50	0.47
24:A:1120:G:H2'	24:A:1121:C:C6	2.50	0.47
1:a:35:G:O2'	12:l:128:SER:O	2.30	0.46
1:a:732:G:OP2	1:a:840:G:N2	2.48	0.46
1:a:1133:G:N2	1:a:1134:U:O4	2.30	0.46
1:a:1268:A:N6	1:a:1281:G:O2'	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:162:PHE:HA	2:b:184:ILE:O	2.15	0.46
24:A:606:G:H21	40:S:37:GLN:NE2	2.10	0.46
24:A:1534:G:H2'	24:A:1535:A:H8	1.80	0.46
24:A:1700:G:HO2'	24:A:1701:A:H8	1.63	0.46
24:A:2879:A:H2'	24:A:2880:A:C8	2.50	0.46
31:I:123:ILE:O	31:I:127:ALA:N	2.41	0.46
1:a:1014:C:O2'	1:a:1047:A:O2'	2.04	0.46
14:n:23:ARG:HG2	14:n:30:PRO:HA	1.96	0.46
17:q:78:LEU:HG	17:q:79:GLU:HG2	1.97	0.46
23:v:41:GLN:HG2	23:v:43:ILE:HG23	1.97	0.46
24:A:278:A:H2'	24:A:279:G:H8	1.79	0.46
1:a:470:G:H2'	1:a:471:A:H8	1.79	0.46
1:a:723:A:H2'	1:a:724:A:C8	2.50	0.46
1:a:1360:G:H2'	1:a:1361:U:H6	1.81	0.46
1:a:1367:A:C4	1:a:1368:G:C8	3.04	0.46
1:a:1386:G:C2	1:a:1387:U:C4	3.03	0.46
2:b:117:ILE:HG13	2:b:118:GLU:N	2.31	0.46
3:c:148:ILE:HA	3:c:201:ILE:HA	1.97	0.46
24:A:380:G:C5	24:A:381:G:H1'	2.51	0.46
1:a:373:U:H5'	1:a:374:C:OP1	2.15	0.46
1:a:451:U:H2'	1:a:452:A:H8	1.80	0.46
1:a:1048:A:C4	1:a:1049:A:N7	2.84	0.46
23:v:70:ARG:HG2	23:v:70:ARG:HH11	1.80	0.46
24:A:629:A:H5'	28:E:89:VAL:HG21	1.97	0.46
24:A:1044:U:OP1	40:S:84:LYS:NZ	2.43	0.46
24:A:1087:U:O2	24:A:1160:G:N2	2.40	0.46
24:A:1364:G:OP2	24:A:1364:G:N2	2.30	0.46
24:A:2187:G:N2	24:A:2188:A:H62	2.13	0.46
43:V:56:MET:HE2	43:V:58:TYR:CE2	2.51	0.46
1:a:307:G:H2'	1:a:308:A:C8	2.51	0.46
1:a:642:C:H2'	1:a:643:A:H8	1.80	0.46
1:a:704:A:N3	1:a:794:G:O2'	2.42	0.46
1:a:1393:G:H2'	1:a:1394:G:C8	2.50	0.46
2:b:96:TRP:HH2	2:b:101:LEU:HD23	1.80	0.46
2:b:167:ARG:HD3	2:b:190:ASN:O	2.16	0.46
4:d:52:ALA:O	4:d:56:LYS:HG2	2.15	0.46
4:d:134:SER:OG	4:d:135:VAL:N	2.48	0.46
11:k:23:ILE:HG23	11:k:86:VAL:HA	1.97	0.46
17:q:26:VAL:HG22	17:q:45:LYS:HB3	1.98	0.46
24:A:292:U:H2'	24:A:293:G:H8	1.80	0.46
24:A:2166:G:N2	24:A:2190:G:O2'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2389:U:H2'	24:A:2390:G:O4'	2.16	0.46
35:N:75:ALA:HB3	35:N:109:ILE:HD13	1.98	0.46
1:a:1340:A:H2'	1:a:1341:G:O4'	2.16	0.46
17:q:19:MET:HE1	17:q:47:LYS:HD3	1.98	0.46
24:A:13:A:O2'	24:A:15:G:N7	2.48	0.46
24:A:2279:G:H2'	24:A:2280:A:C8	2.50	0.46
24:A:2398:G:N7	53:7:39:LYS:NZ	2.52	0.46
24:A:2915:G:O2'	50:4:28:ASN:OD1	2.32	0.46
27:D:54:GLU:O	27:D:78:ARG:N	2.49	0.46
29:F:134:GLU:OE2	29:F:136:LEU:HB2	2.15	0.46
30:G:137:ASN:HB3	30:G:140:HIS:HB2	1.97	0.46
39:R:24:ASP:HB2	39:R:88:ARG:O	2.16	0.46
1:a:1389:C:H2'	1:a:1390:C:H6	1.80	0.46
2:b:105:GLU:O	2:b:108:GLN:HG3	2.16	0.46
6:f:49:LEU:HD23	6:f:53:ILE:HD13	1.98	0.46
10:j:44:THR:HA	10:j:70:HIS:HA	1.98	0.46
16:p:9:ARG:HB3	16:p:29:ARG:NH1	2.31	0.46
24:A:139:A:H2	24:A:1453:G:H1'	1.81	0.46
24:A:231:A:H1'	24:A:232:U:O4'	2.15	0.46
24:A:1121:C:H2'	24:A:1122:C:C6	2.50	0.46
24:A:1578:G:N2	24:A:1596:A:OP2	2.38	0.46
24:A:1787:C:H5	39:R:94:ARG:NH2	2.14	0.46
29:F:103:LEU:O	29:F:108:LEU:HD12	2.15	0.46
1:a:209:A:H2'	1:a:210:A:C8	2.51	0.46
1:a:392:G:H2'	1:a:393:U:H6	1.81	0.46
21:x:9:A:C8	21:x:46:G7M:N2	2.84	0.46
28:E:157:ALA:HB1	28:E:201:LYS:HD3	1.98	0.46
1:a:1434:C:H2'	1:a:1435:A:C8	2.51	0.46
4:d:54:LYS:HD3	4:d:197:PHE:CE2	2.51	0.46
23:v:287:VAL:O	23:v:319:TYR:HA	2.16	0.46
24:A:407:G:H2'	24:A:408:U:H6	1.80	0.46
24:A:906:G:N2	24:A:964:A:OP2	2.30	0.46
30:G:68:THR:O	30:G:72:LEU:HD23	2.16	0.46
39:R:63:LYS:HE3	39:R:65:SER:HB2	1.97	0.46
1:a:160:A:H2'	1:a:161:A:C8	2.51	0.46
1:a:681:G:O3'	6:f:89:ARG:NH2	2.49	0.46
1:a:931:G:H2'	1:a:932:A:H8	1.81	0.46
1:a:1023:A:H2'	1:a:1024:G:C8	2.51	0.46
1:a:1116:C:C4	1:a:1117:G:C8	3.04	0.46
1:a:1231:U:H3'	1:a:1232:A:H5'	1.97	0.46
23:v:4:LYS:HG2	23:v:34:GLU:OE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2338:A:OP1	29:F:133:ARG:NH2	2.48	0.46
24:A:2743:C:OP1	37:P:11:SER:OG	2.33	0.46
23:v:138:ASP:HA	23:v:141:SER:HB2	1.96	0.45
24:A:1124:C:H5'	24:A:1125:C:OP1	2.16	0.45
24:A:1712:U:O2'	24:A:2719:G:H4'	2.16	0.45
24:A:1822:A:H2'	24:A:1823:C:O4'	2.16	0.45
24:A:2199:G:H2'	24:A:2200:U:H5	1.81	0.45
26:C:63:ARG:HG2	26:C:103:TYR:HE2	1.81	0.45
3:c:23:TYR:CA	10:j:95:GLY:H	2.29	0.45
23:v:165:HIS:HA	23:v:168:ARG:NH1	2.32	0.45
24:A:332:U:H3	24:A:393:G:H1	1.64	0.45
24:A:1123:A:H2'	24:A:1124:C:O4'	2.17	0.45
24:A:1685:U:H2'	24:A:1686:C:C6	2.51	0.45
24:A:2134:G:H1	24:A:2222:G:H1'	1.81	0.45
24:A:2350:C:H2'	24:A:2351:G:O4'	2.16	0.45
24:A:2781:A:N7	24:A:2787:U:O4	2.49	0.45
27:D:8:ARG:HG3	27:D:53:PHE:HE2	1.82	0.45
29:F:13:VAL:HG23	29:F:14:PRO:HD3	1.97	0.45
24:A:349:U:H2'	24:A:350:G:O4'	2.17	0.45
30:G:54:ARG:HD2	30:G:61:HIS:HB3	1.97	0.45
44:W:40:MET:SD	44:W:60:GLU:HG3	2.56	0.45
45:Y:79:ARG:HG2	45:Y:80:MET:O	2.16	0.45
1:a:1165:A:H4'	1:a:1166:C:O5'	2.16	0.45
1:a:1262:G:O2'	1:a:1265:G:N3	2.41	0.45
8:h:40:LEU:O	8:h:45:PHE:HB2	2.16	0.45
23:v:223:LYS:HD2	24:A:2507:C:H5'	1.97	0.45
24:A:859:U:H2'	24:A:860:C:C6	2.51	0.45
24:A:1535:A:H2'	24:A:1536:A:C8	2.52	0.45
24:A:2688:G:O2'	24:A:2697:G:O6	2.32	0.45
24:A:2886:G:N2	24:A:2889:A:OP2	2.49	0.45
30:G:80:SER:OG	30:G:81:GLU:OE1	2.25	0.45
1:a:721:G:H2'	1:a:722:G:C8	2.51	0.45
1:a:1213:G:H2'	1:a:1214:C:C6	2.52	0.45
24:A:330:A:H2'	24:A:331:G:C8	2.51	0.45
24:A:1806:A:N7	24:A:1862:A:H1'	2.31	0.45
24:A:2104:A:H2'	24:A:2105:G:C8	2.51	0.45
1:a:8:A:N1	4:d:200:ARG:NH2	2.65	0.45
1:a:158:G:N2	1:a:160:A:H3'	2.31	0.45
1:a:985:G:OP2	1:a:1365:U:O2'	2.33	0.45
1:a:992:A:O2'	14:n:2:ALA:N	2.44	0.45
1:a:1107:C:H2'	1:a:1108:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:44:PHE:O	14:n:48:ALA:HB3	2.16	0.45
15:o:41:GLU:HG3	15:o:44:ARG:NH2	2.26	0.45
20:t:8:ILE:O	20:t:11:VAL:HG22	2.17	0.45
24:A:5:A:H2'	24:A:6:A:C8	2.52	0.45
24:A:1569:U:H2'	24:A:1570:G:H8	1.81	0.45
28:E:75:GLN:HE21	28:E:83:TRP:HE1	1.62	0.45
1:a:424:G:H2'	1:a:425:G:C8	2.45	0.45
1:a:455:G:HO2'	1:a:456:A:P	2.38	0.45
1:a:650:A:N7	8:h:109:SER:HA	2.32	0.45
1:a:1014:C:H5	1:a:1033:U:H1'	1.82	0.45
1:a:1431:U:H2'	1:a:1432:A:C8	2.52	0.45
20:t:6:SER:O	20:t:10:ARG:HG2	2.17	0.45
21:x:26:A:H3'	21:x:27:G:H8	1.81	0.45
24:A:363:A:H4'	24:A:365:A:N7	2.32	0.45
24:A:1906:G:H2'	24:A:1907:C:H6	1.81	0.45
26:C:205:ILE:HD12	26:C:214:MET:HE1	1.98	0.45
30:G:125:VAL:HG13	30:G:125:VAL:O	2.16	0.45
1:a:98:U:H2'	1:a:99:A:H8	1.82	0.45
1:a:755:U:H2'	1:a:756:A:H8	1.82	0.45
1:a:960:G:C6	1:a:961:U:C4	3.05	0.45
1:a:1297:A:H3'	1:a:1298:C:C6	2.52	0.45
4:d:102:GLY:O	4:d:154:SER:OG	2.33	0.45
4:d:166:THR:OG1	4:d:177:ASN:ND2	2.44	0.45
24:A:283:C:H3'	24:A:284:U:H4'	1.98	0.45
24:A:301:A:H2'	24:A:302:G:C8	2.52	0.45
24:A:498:G:N7	28:E:58:ARG:HD3	2.32	0.45
24:A:1108:G:C2	24:A:1123:A:N1	2.85	0.45
24:A:1829:U:H2'	24:A:1830:C:H6	1.82	0.45
24:A:2195:A:H5''	24:A:2205:U:C6	2.52	0.45
24:A:2348:U:H2'	24:A:2349:U:C6	2.52	0.45
35:N:108:GLY:HA2	35:N:126:ASN:HD22	1.82	0.45
44:W:71:ILE:HG22	44:W:78:PRO:HB3	1.97	0.45
1:a:343:C:H2'	1:a:344:A:H8	1.82	0.45
1:a:532:G:H2'	1:a:533:C:C6	2.52	0.45
12:l:127:ARG:HG3	12:l:132:THR:HB	1.99	0.45
24:A:637:U:H2'	24:A:638:U:C6	2.51	0.45
24:A:735:A:H2'	24:A:736:C:C6	2.52	0.45
24:A:1886:A:N3	24:A:2266:A:O2'	2.44	0.45
1:a:155:C:H2'	1:a:156:G:H8	1.81	0.45
1:a:1438:C:H2'	1:a:1439:G:O4'	2.17	0.45
12:l:26:LYS:HB3	12:l:26:LYS:HE3	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:947:A:H2'	24:A:948:A:C8	2.52	0.45
38:Q:24:GLY:O	38:Q:47:ASP:N	2.50	0.45
38:Q:60:ASP:HB2	38:Q:63:PHE:HE2	1.82	0.45
1:a:347:C:H2'	1:a:348:U:C6	2.52	0.44
6:f:15:ILE:HD12	6:f:15:ILE:H	1.81	0.44
36:O:43:THR:HG22	36:O:94:VAL:HG12	1.99	0.44
1:a:971:C:C4	1:a:972:G:N7	2.85	0.44
24:A:2120:G:H2'	24:A:2121:A:H8	1.82	0.44
24:A:2141:U:H3	24:A:2214:G:N2	2.15	0.44
24:A:2333:A:H2'	24:A:2334:A:H8	1.82	0.44
25:B:49:G:H2'	25:B:50:U:C6	2.52	0.44
1:a:1017:C:O2'	1:a:1018:U:OP1	2.31	0.44
1:a:1220:A:C8	1:a:1222:G:C5	3.05	0.44
1:a:1439:G:O2'	1:a:1476:A:N6	2.50	0.44
24:A:2225:C:H2'	24:A:2226:A:C8	2.51	0.44
40:S:102:ASP:OD2	40:S:105:SER:OG	2.24	0.44
1:a:329:A:H2'	1:a:330:C:C6	2.52	0.44
1:a:945:C:N4	1:a:946:A:N7	2.65	0.44
1:a:1336:A:C5	1:a:1337:U:C5	3.05	0.44
1:a:1393:G:H2'	1:a:1394:G:H8	1.82	0.44
2:b:92:VAL:HG11	2:b:96:TRP:HE3	1.82	0.44
4:d:75:ALA:HB2	4:d:89:LEU:HD12	1.99	0.44
5:e:87:VAL:HA	5:e:96:LEU:HA	1.99	0.44
24:A:1276:U:H2'	24:A:1277:G:H8	1.81	0.44
24:A:1812:U:H5	24:A:1817:A:N7	2.16	0.44
24:A:2691:C:OP1	30:G:160:LYS:NZ	2.50	0.44
24:A:2731:U:H2'	24:A:2732:U:C6	2.53	0.44
25:B:59:U:H2'	25:B:60:U:C6	2.53	0.44
37:P:115:ARG:HE	37:P:135:VAL:CG2	2.29	0.44
46:Z:8:THR:O	46:Z:10:ARG:N	2.43	0.44
1:a:1165:A:C2	1:a:1188:G:C4	3.06	0.44
1:a:1496:G:H2'	1:a:1497:G:H8	1.82	0.44
2:b:96:TRP:CH2	2:b:101:LEU:HD23	2.53	0.44
17:q:61:VAL:HG11	17:q:77:LEU:HD11	1.99	0.44
24:A:1224:A:H2'	24:A:1225:G:C8	2.53	0.44
29:F:162:SER:OG	29:F:165:GLU:OE1	2.35	0.44
1:a:451:U:H2'	1:a:452:A:C8	2.53	0.44
1:a:572:U:OP2	12:l:12:ARG:NH2	2.43	0.44
1:a:1079:U:H2'	1:a:1080:C:C6	2.52	0.44
1:a:1124:U:H2'	1:a:1125:U:C6	2.53	0.44
1:a:1192:G:C6	1:a:1193:G:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1277:G:O2'	1:a:1322:U:OP1	2.32	0.44
11:k:46:SER:O	11:k:49:SER:OG	2.34	0.44
21:x:21:A:N7	21:x:48:C:N4	2.65	0.44
24:A:809:G:O2'	24:A:810:A:OP1	2.28	0.44
24:A:848:A:OP1	58:A:3302:HOH:O	2.21	0.44
24:A:2576:G:H2'	24:A:2577:G:C8	2.52	0.44
1:a:287:A:H4'	1:a:288:C:H5''	2.00	0.44
1:a:1252:G:C6	1:a:1300:A:N6	2.86	0.44
1:a:1262:G:H3'	1:a:1286:A:H61	1.83	0.44
19:s:51:VAL:O	19:s:58:VAL:N	2.50	0.44
23:v:117:GLN:O	23:v:120:ILE:HG22	2.17	0.44
24:A:873:U:O2'	24:A:2101:U:C2	2.71	0.44
24:A:911:G:H2'	24:A:912:C:C6	2.53	0.44
24:A:1227:U:H2'	24:A:1228:U:C6	2.52	0.44
24:A:1397:A:H2'	24:A:1398:A:C8	2.53	0.44
24:A:1823:C:H2'	24:A:1824:A:C8	2.52	0.44
27:D:108:ILE:HD12	27:D:202:ILE:HD12	1.98	0.44
28:E:154:ILE:HB	28:E:175:VAL:HG22	1.99	0.44
50:4:45:GLU:C	50:4:47:GLY:N	2.76	0.44
1:a:726:A:N7	11:k:118:HIS:HD2	2.16	0.44
1:a:988:C:H2'	1:a:989:C:C6	2.52	0.44
1:a:1071:U:H2'	1:a:1072:C:C5	2.53	0.44
5:e:158:ARG:NH1	5:e:160:LYS:O	2.51	0.44
24:A:1294:U:OP1	24:A:1294:U:H3'	2.18	0.44
24:A:1469:A:O2'	24:A:1471:G:N7	2.42	0.44
24:A:1637:A:H2'	24:A:1638:G:C8	2.53	0.44
24:A:1906:G:H2'	24:A:1907:C:C6	2.53	0.44
24:A:2215:G:H2'	24:A:2216:C:C6	2.53	0.44
27:D:146:MET:HG2	27:D:158:LYS:HE3	1.99	0.44
48:2:3:LYS:HB3	48:2:3:LYS:HE2	1.88	0.44
1:a:994:C:H5''	1:a:995:A:OP2	2.18	0.44
1:a:1318:A:N1	1:a:1334:A:C6	2.86	0.44
1:a:1333:U:H2'	1:a:1334:A:C8	2.45	0.44
6:f:15:ILE:HG23	6:f:19:GLU:HB3	2.00	0.44
11:k:25:SER:HB2	11:k:30:THR:HG22	2.00	0.44
23:v:368:PHE:N	23:v:399:ILE:O	2.32	0.44
24:A:339:U:H2'	24:A:340:G:O4'	2.18	0.44
24:A:1074:A:N3	24:A:2519:G:O2'	2.41	0.44
24:A:2346:C:H2'	24:A:2347:A:C8	2.53	0.44
28:E:135:LYS:HG3	28:E:138:GLU:H	1.83	0.44
31:I:24:SER:HA	31:I:113:ILE:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:N:58:PHE:CE2	35:N:59:ARG:HG3	2.53	0.44
39:R:83:LYS:HB2	39:R:83:LYS:HE2	1.73	0.44
1:a:459:A:H4'	1:a:460:A:O5'	2.18	0.43
1:a:683:A:H1'	11:k:118:HIS:CE1	2.52	0.43
9:i:46:GLU:O	9:i:50:GLN:N	2.36	0.43
24:A:842:U:H2'	24:A:843:U:C6	2.53	0.43
24:A:878:G:H2'	24:A:879:C:H6	1.82	0.43
24:A:1108:G:H2'	24:A:1109:G:C8	2.53	0.43
24:A:1122:C:O2'	32:H:91:GLU:O	2.36	0.43
24:A:1509:A:O2'	24:A:1511:G:OP2	2.34	0.43
24:A:2876:U:H2'	24:A:2877:G:O4'	2.18	0.43
29:F:121:ALA:HB3	29:F:128:TYR:HE1	1.83	0.43
39:R:32:VAL:HG23	39:R:32:VAL:O	2.18	0.43
52:6:43:SER:O	52:6:43:SER:OG	2.36	0.43
1:a:216:G:H2'	1:a:217:U:O4'	2.18	0.43
2:b:171:ILE:H	2:b:171:ILE:HD12	1.84	0.43
4:d:183:SER:OG	4:d:184:GLU:OE1	2.36	0.43
6:f:48:ARG:O	6:f:49:LEU:HB2	2.18	0.43
15:o:64:ARG:O	15:o:68:THR:HG23	2.18	0.43
24:A:525:A:N3	24:A:527:G:H5''	2.33	0.43
24:A:2829:U:H2'	24:A:2830:C:C5	2.53	0.43
33:L:50:ASP:OD1	33:L:122:LYS:NZ	2.49	0.43
35:N:10:GLU:H	35:N:10:GLU:CD	2.26	0.43
1:a:1096:G:C6	1:a:1108:G:N1	2.87	0.43
1:a:1260:G:OP1	10:j:46:LYS:N	2.50	0.43
4:d:36:HIS:C	4:d:38:PRO:HD2	2.43	0.43
22:w:12:A:H3'	22:w:13:A:H5''	2.00	0.43
23:v:113:GLU:O	23:v:117:GLN:HG3	2.19	0.43
23:v:199:VAL:HG21	23:v:305:LEU:HD11	1.99	0.43
23:v:350:PHE:HA	23:v:353:GLU:OE1	2.18	0.43
24:A:127:C:H2'	24:A:128:C:H6	1.84	0.43
24:A:2155:U:H2'	24:A:2156:A:H8	1.81	0.43
24:A:2590:G:H2'	24:A:2591:C:C6	2.54	0.43
31:I:42:ARG:O	31:I:46:ARG:N	2.51	0.43
1:a:1044:G:H2'	1:a:1045:A:C8	2.53	0.43
1:a:1326:A:OP1	19:s:3:ARG:N	2.51	0.43
2:b:183:ILE:HG21	2:b:196:ILE:HG22	2.01	0.43
8:h:7:ILE:HD11	8:h:32:ILE:HG21	2.01	0.43
11:k:122:ARG:HA	11:k:123:PRO:HD3	1.88	0.43
24:A:947:A:H2'	24:A:948:A:H8	1.84	0.43
24:A:1072:A:O2'	24:A:1073:A:OP2	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:2170:C:O2	24:A:2188:A:N6	2.52	0.43
24:A:2323:G:H2'	24:A:2324:U:C6	2.54	0.43
30:G:37:PHE:HE1	30:G:71:ILE:HD11	1.83	0.43
49:3:17:THR:HG23	49:3:48:VAL:O	2.18	0.43
1:a:562:U:H4'	12:l:39:ASN:HD22	1.84	0.43
1:a:1083:G:O3'	2:b:102:THR:HG21	2.18	0.43
1:a:1286:A:H1'	1:a:1289:C:H41	1.82	0.43
6:f:71:ALA:C	6:f:73:SER:H	2.26	0.43
14:n:34:ILE:N	14:n:39:LEU:O	2.52	0.43
23:v:181:ARG:HB3	23:v:181:ARG:CZ	2.49	0.43
24:A:2104:A:H2'	24:A:2105:G:H8	1.83	0.43
24:A:2126:G:O2'	24:A:2127:A:H5'	2.19	0.43
24:A:2199:G:H2'	24:A:2200:U:C5	2.53	0.43
24:A:2348:U:H5''	38:Q:2:ILE:HG12	2.00	0.43
24:A:2520:G:H2'	24:A:2521:A:C8	2.54	0.43
26:C:71:LYS:HD2	26:C:96:TYR:CD1	2.53	0.43
29:F:77:PHE:C	29:F:78:ARG:HD3	2.42	0.43
38:Q:117:LEU:HD23	38:Q:117:LEU:HA	1.89	0.43
1:a:107:A:H5'	1:a:108:C:H5	1.84	0.43
1:a:1052:G:O2'	1:a:1053:A:O4'	2.35	0.43
1:a:1318:A:C6	1:a:1334:A:N6	2.86	0.43
4:d:90:LEU:HD23	4:d:90:LEU:HA	1.92	0.43
24:A:775:G:H5'	24:A:776:U:H5''	2.01	0.43
24:A:1922:A:H2'	24:A:1923:A:H8	1.84	0.43
25:B:46:A:H2'	25:B:47:C:H6	1.84	0.43
27:D:10:VAL:HG11	39:R:4:LEU:HD23	2.00	0.43
36:O:51:ARG:O	36:O:55:THR:HG23	2.19	0.43
44:W:81:VAL:HG21	44:W:92:ARG:HB2	1.99	0.43
1:a:972:G:C6	1:a:982:G:O6	2.72	0.43
1:a:1268:A:O5'	1:a:1281:G:N2	2.52	0.43
1:a:1313:A:C5	1:a:1314:U:C2	3.07	0.43
4:d:142:ARG:O	4:d:142:ARG:HG3	2.19	0.43
4:d:151:ILE:O	4:d:155:LEU:HD23	2.18	0.43
18:r:54:LYS:O	18:r:58:LYS:HG2	2.19	0.43
23:v:340:PHE:HD2	23:v:347:SER:HB3	1.84	0.43
24:A:899:C:H2'	24:A:900:A:C8	2.54	0.43
24:A:926:G:N2	24:A:946:G:N7	2.66	0.43
24:A:2792:G:N2	30:G:139:GLU:OE2	2.41	0.43
26:C:205:ILE:O	26:C:210:ARG:HD3	2.19	0.43
1:a:504:G:H21	1:a:505:A:H5''	1.84	0.43
1:a:1021:G:O6	1:a:1027:A:N6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1139:A:H2'	1:a:1140:G:C8	2.54	0.43
1:a:1198:A:H2'	1:a:1199:C:H5'	2.01	0.43
2:b:111:ILE:O	2:b:115:LYS:HG2	2.19	0.43
4:d:126:VAL:HG12	4:d:128:ILE:H	1.84	0.43
24:A:755:U:H2'	24:A:756:A:C8	2.54	0.43
24:A:1623:A:H2'	24:A:1624:A:C8	2.54	0.43
39:R:4:LEU:HA	39:R:7:GLU:OE1	2.19	0.43
41:T:36:ASP:HA	41:T:57:THR:HG22	2.01	0.43
50:4:45:GLU:C	50:4:47:GLY:H	2.27	0.43
1:a:410:G:O2'	58:a:3201:HOH:O	2.21	0.43
1:a:847:G:H2'	1:a:848:G:C8	2.52	0.43
1:a:870:G:HO2'	1:a:883:G:HO2'	1.57	0.43
1:a:954:G:C2	1:a:955:A:C8	3.07	0.43
1:a:992:A:H5'	1:a:1228:G:C8	2.54	0.43
1:a:1024:G:H2'	1:a:1025:A:C8	2.54	0.43
1:a:1201:U:O4	1:a:1202:C:N4	2.52	0.43
1:a:1315:U:O4	1:a:1337:U:N3	2.51	0.43
16:p:32:ARG:NH2	58:p:103:HOH:O	2.52	0.43
24:A:613:G:H2'	24:A:2063:A:N7	2.34	0.43
24:A:1015:G:H2'	24:A:1016:U:C6	2.54	0.43
24:A:2146:C:H2'	24:A:2147:A:H8	1.84	0.43
24:A:2164:A:O4'	24:A:2191:A:N6	2.51	0.43
24:A:2822:C:H1'	24:A:2920:A:H2	1.82	0.43
24:A:2908:A:O2'	24:A:2909:C:OP2	2.28	0.43
26:C:121:GLU:N	26:C:121:GLU:OE2	2.52	0.43
37:P:122:ARG:HD3	37:P:129:MET:HE2	2.01	0.43
1:a:601:U:H2'	1:a:602:U:C6	2.54	0.43
1:a:987:A:N6	1:a:1323:G:O2'	2.52	0.43
1:a:1271:C:N3	1:a:1279:U:C4	2.85	0.43
1:a:1295:A:H2'	1:a:1296:A:C8	2.51	0.43
4:d:115:ASN:ND2	4:d:129:PRO:HG3	2.34	0.43
24:A:622:A:H2'	24:A:623:C:C6	2.54	0.43
24:A:1184:G:N3	33:L:109:MET:HE2	2.34	0.43
24:A:1433:G:H2'	24:A:1434:U:O4'	2.19	0.43
24:A:2155:U:H2'	24:A:2156:A:C8	2.54	0.43
25:B:29:C:H2'	25:B:30:C:H6	1.84	0.43
26:C:2:ALA:N	26:C:20:ASP:OD1	2.52	0.43
47:1:10:SER:O	47:1:12:THR:N	2.52	0.43
1:a:956:G:C6	1:a:957:C:C4	3.07	0.42
1:a:958:A:C2	1:a:1240:G:C2	3.07	0.42
23:v:318:ALA:HB1	23:v:340:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:27:G:H1'	24:A:558:A:N6	2.34	0.42
24:A:281:A:H2'	24:A:282:G:C8	2.53	0.42
24:A:879:C:O2'	53:7:57:ARG:NH1	2.51	0.42
24:A:1172:A:H4'	24:A:1173:A:C5'	2.48	0.42
24:A:1202:A:C8	40:S:51:ARG:HG2	2.54	0.42
24:A:1289:A:OP1	35:N:7:LYS:NZ	2.51	0.42
24:A:1593:C:H2'	24:A:1594:G:O4'	2.18	0.42
24:A:2058:C:H2'	24:A:2059:U:C6	2.53	0.42
53:7:54:ASP:OD1	53:7:57:ARG:NH2	2.51	0.42
1:a:1152:G:N2	1:a:1154:A:H62	2.17	0.42
1:a:1298:C:H2'	1:a:1299:C:O4'	2.18	0.42
4:d:53:GLU:OE1	4:d:190:ASN:N	2.41	0.42
24:A:579:U:H2'	24:A:580:U:C6	2.54	0.42
24:A:1763:U:H3	24:A:1778:A:H62	1.67	0.42
49:3:13:VAL:HB	49:3:45:LEU:HD13	2.01	0.42
49:3:34:THR:HA	49:3:44:PRO:HA	2.01	0.42
1:a:339:G:H2'	20:t:4:ILE:HD11	2.01	0.42
1:a:489:G:O2'	1:a:491:C:N4	2.51	0.42
1:a:1267:G:O2'	1:a:1268:A:H5'	2.19	0.42
1:a:1349:C:C2	1:a:1350:G:N7	2.87	0.42
2:b:117:ILE:HA	2:b:120:MET:HG2	2.01	0.42
24:A:460:C:H2'	24:A:461:A:H8	1.83	0.42
24:A:1114:G:N2	24:A:1141:A:O2'	2.51	0.42
24:A:1319:A:N7	37:P:12:GLN:HG2	2.35	0.42
24:A:1774:C:H2'	24:A:1775:C:H6	1.84	0.42
24:A:2133:U:N3	24:A:2134:G:N7	2.67	0.42
24:A:2827:C:H5'	24:A:2828:U:OP2	2.19	0.42
25:B:41:C:O2'	29:F:92:ARG:HB3	2.19	0.42
37:P:40:ILE:HA	37:P:43:VAL:HG22	2.01	0.42
1:a:45:U:H2'	1:a:46:G:H8	1.84	0.42
1:a:439:A:C5	1:a:440:A:C8	3.08	0.42
1:a:993:C:H5'	1:a:1228:G:O6	2.20	0.42
1:a:1063:C:H4'	1:a:1064:A:OP1	2.20	0.42
1:a:1171:G:C6	1:a:1181:G:C6	3.07	0.42
1:a:1258:A:N6	1:a:1292:A:H61	2.18	0.42
1:a:1281:G:H8	1:a:1281:G:OP2	2.02	0.42
1:a:1350:G:O3'	9:i:124:ALA:HB3	2.18	0.42
12:l:5:ASN:HA	12:l:8:VAL:HG22	2.01	0.42
18:r:30:VAL:O	18:r:34:LYS:HG2	2.18	0.42
23:v:147:SER:HA	24:A:2096:C:H1'	2.00	0.42
23:v:342:ALA:C	23:v:343:ARG:HD3	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:491:C:H2'	24:A:492:G:O4'	2.19	0.42
24:A:899:C:H2'	24:A:900:A:H8	1.84	0.42
24:A:2828:U:H2'	24:A:2830:C:OP2	2.19	0.42
29:F:108:LEU:O	29:F:111:VAL:HG12	2.19	0.42
35:N:77:VAL:HG13	35:N:102:ILE:HD11	2.01	0.42
1:a:278:A:H2'	1:a:279:C:H6	1.85	0.42
1:a:1011:U:O2	1:a:1012:G:O2'	2.38	0.42
1:a:1030:G:H2'	1:a:1031:C:C6	2.55	0.42
1:a:1295:A:N3	1:a:1360:G:O2'	2.49	0.42
1:a:1322:U:H2'	1:a:1323:G:C8	2.55	0.42
1:a:1453:A:O2'	1:a:1454:A:H5'	2.20	0.42
11:k:61:PHE:CD2	11:k:65:MET:HE1	2.54	0.42
16:p:57:LEU:HA	16:p:57:LEU:HD23	1.84	0.42
24:A:756:A:H2'	24:A:757:A:H8	1.83	0.42
24:A:1404:G:N7	24:A:1405:G:C8	2.88	0.42
24:A:1851:U:H5'	26:C:157:SER:HB2	2.01	0.42
24:A:2114:C:H2'	24:A:2115:A:H8	1.84	0.42
24:A:2159:A:H61	24:A:2205:U:P	2.42	0.42
25:B:57:G:O2'	38:Q:6:ASP:OD2	2.37	0.42
1:a:155:C:H2'	1:a:156:G:C8	2.55	0.42
1:a:177:A:H2'	1:a:178:A:H8	1.84	0.42
1:a:1069:U:O2'	10:j:54:ALA:HA	2.19	0.42
1:a:1133:G:N7	1:a:1153:C:O2'	2.46	0.42
1:a:1156:U:H2'	1:a:1157:C:O4'	2.19	0.42
1:a:1166:C:C4	1:a:1168:G:C8	3.08	0.42
1:a:1262:G:H2'	1:a:1286:A:H61	1.85	0.42
23:v:48:ARG:NH1	24:A:1997:G:H2'	2.34	0.42
23:v:365:LYS:HE2	23:v:365:LYS:HB2	1.95	0.42
24:A:1041:C:O2	33:L:4:THR:OG1	2.26	0.42
24:A:1067:A:OP2	33:L:68:LYS:NZ	2.42	0.42
24:A:1879:G:H2'	24:A:1880:A:C8	2.55	0.42
24:A:2623:A:H2'	24:A:2624:C:H6	1.84	0.42
35:N:92:THR:HG23	35:N:95:LEU:H	1.85	0.42
38:Q:60:ASP:HB2	38:Q:63:PHE:CE2	2.54	0.42
42:U:87:LEU:HB2	42:U:103:LYS:HB2	2.01	0.42
1:a:1130:U:H2'	1:a:1131:U:C6	2.54	0.42
2:b:44:GLN:O	2:b:47:VAL:HG22	2.20	0.42
4:d:57:LEU:HD12	4:d:194:ILE:HD13	2.02	0.42
4:d:141:VAL:HG21	4:d:172:LEU:HD23	2.02	0.42
5:e:19:ILE:HD11	5:e:61:ILE:HD11	2.02	0.42
24:A:448:A:H2'	24:A:449:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1890:G:N2	24:A:1918:A:H62	2.16	0.42
24:A:2292:G:C8	24:A:2460:C:C4	3.07	0.42
26:C:173:LEU:HD11	26:C:271:VAL:HG21	2.02	0.42
33:L:60:ALA:HB3	33:L:127:GLY:HA2	2.02	0.42
1:a:180:G:C2	1:a:209:A:C5	3.08	0.42
1:a:381:A:C2	1:a:382:A:C8	3.07	0.42
1:a:943:C:N4	1:a:1352:U:C2	2.88	0.42
1:a:995:A:H2'	1:a:996:G:O4'	2.20	0.42
1:a:1303:C:H4'	1:a:1309:U:C4	2.55	0.42
1:a:1419:C:H2'	1:a:1420:A:H8	1.84	0.42
24:A:464:U:H2'	24:A:465:C:C6	2.55	0.42
24:A:1429:A:C4	24:A:1430:C:C5	3.08	0.42
24:A:2158:G:H22	24:A:2205:U:P	2.42	0.42
25:B:19:A:H2'	25:B:20:A:C8	2.55	0.42
41:T:29:VAL:HA	41:T:62:VAL:HG23	2.01	0.42
1:a:17:U:H2'	1:a:18:C:C6	2.53	0.42
1:a:1295:A:H2	1:a:1360:G:H1'	1.85	0.42
1:a:1339:A:C4	1:a:1340:A:C8	3.08	0.42
8:h:97:VAL:HG23	8:h:104:ALA:HB2	2.01	0.42
21:x:18:G:O2'	21:x:57:G:N1	2.37	0.42
23:v:376:GLN:HG3	24:A:1141:A:H8	1.84	0.42
24:A:305:C:H2'	24:A:306:A:H8	1.84	0.42
24:A:718:C:H2'	24:A:719:C:H6	1.85	0.42
24:A:1716:G:O2'	24:A:2024:U:O4	2.28	0.42
24:A:2198:G:H2'	24:A:2199:G:C8	2.55	0.42
24:A:2437:C:H2'	24:A:2438:G:O4'	2.20	0.42
25:B:58:C:C2	25:B:59:U:C5	3.08	0.42
26:C:154:LEU:HD23	26:C:154:LEU:HA	1.72	0.42
1:a:260:U:C2	1:a:261:U:C5	3.07	0.42
1:a:1020:U:C2	1:a:1021:G:N7	2.88	0.42
1:a:1279:U:H2'	1:a:1280:G:O4'	2.20	0.42
1:a:1367:A:C5	1:a:1368:G:N7	2.88	0.42
15:o:13:ALA:HA	15:o:16:ARG:NH1	2.34	0.42
17:q:65:GLU:HA	17:q:75:PHE:HA	2.02	0.42
23:v:108:ARG:NH1	23:v:231:LEU:O	2.53	0.42
24:A:162:A:H2	24:A:2250:G:N3	2.17	0.42
24:A:193:A:H2'	24:A:194:C:H6	1.84	0.42
24:A:661:A:OP1	28:E:106:ARG:HD2	2.20	0.42
24:A:2809:A:H4'	24:A:2810:G:O5'	2.19	0.42
48:2:11:SER:OG	48:2:12:LEU:N	2.53	0.42
1:a:712:A:C5	1:a:713:U:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1350:G:H2'	1:a:1351:C:O4'	2.20	0.41
2:b:23:TRP:HZ3	2:b:25:PRO:HA	1.84	0.41
6:f:18:ASP:OD1	6:f:19:GLU:N	2.53	0.41
6:f:38:ILE:C	6:f:40:GLU:H	2.28	0.41
8:h:79:ARG:NH2	8:h:81:SER:O	2.54	0.41
14:n:10:GLN:CB	14:n:23:ARG:HH21	2.33	0.41
21:x:19:G:O2'	24:A:2145:A:N3	2.52	0.41
23:v:6:LEU:HD11	23:v:63:LEU:HD22	2.01	0.41
24:A:529:A:H3'	24:A:530:C:H6	1.85	0.41
24:A:889:G:H2'	24:A:890:G:C8	2.55	0.41
25:B:30:C:C2	25:B:49:G:N2	2.88	0.41
41:T:21:TYR:CZ	41:T:94:LYS:HE3	2.55	0.41
43:V:65:MET:HE3	43:V:65:MET:HB2	1.97	0.41
1:a:467:U:N3	1:a:468:A:N7	2.69	0.41
1:a:892:C:O2'	1:a:893:U:H5'	2.20	0.41
1:a:1013:A:C5	1:a:1034:U:O4	2.73	0.41
1:a:1257:A:O2'	1:a:1258:A:H5'	2.20	0.41
1:a:1504:C:H2'	1:a:1505:G:C8	2.56	0.41
23:v:262:LEU:HD23	23:v:267:VAL:HG12	2.02	0.41
24:A:629:A:N1	24:A:855:G:O2'	2.52	0.41
24:A:1685:U:O2'	24:A:1793:A:N3	2.43	0.41
24:A:1886:A:H2'	24:A:1887:A:C8	2.55	0.41
24:A:2048:A:C2	50:4:3:VAL:HG22	2.55	0.41
26:C:93:LEU:HD11	26:C:101:LYS:HB3	2.02	0.41
30:G:86:LYS:CD	30:G:132:ILE:HG12	2.49	0.41
38:Q:73:ALA:HB1	38:Q:108:LEU:HB2	2.02	0.41
1:a:33:A:H2'	1:a:34:C:C6	2.55	0.41
1:a:520:U:H2'	1:a:521:A:H8	1.85	0.41
1:a:960:G:C2	1:a:1238:G:C2	3.08	0.41
1:a:1022:G:H2'	1:a:1024:G:OP2	2.19	0.41
1:a:1340:A:H3'	1:a:1341:G:H8	1.85	0.41
4:d:57:LEU:HD23	4:d:57:LEU:HA	1.78	0.41
23:v:15:LYS:NZ	24:A:1948:U:O2	2.53	0.41
24:A:291:U:H2'	24:A:292:U:C6	2.55	0.41
24:A:329:A:H2'	24:A:330:A:H8	1.86	0.41
24:A:1003:A:N6	24:A:2492:A:C8	2.88	0.41
24:A:1247:U:H2'	24:A:1248:A:H8	1.85	0.41
24:A:2319:A:H2'	51:5:26:ASN:HD21	1.84	0.41
24:A:2546:G:H2'	24:A:2547:U:C6	2.55	0.41
24:A:2548:C:H2'	24:A:2549:G:H8	1.85	0.41
24:A:2658:G:H2'	24:A:2659:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:G:154:PRO:HG3	30:G:163:ARG:HB3	2.02	0.41
34:M:70:ARG:HB3	34:M:76:TYR:CE1	2.55	0.41
35:N:73:GLU:O	35:N:107:SER:HB3	2.19	0.41
35:N:96:LEU:HD23	35:N:96:LEU:HA	1.92	0.41
46:Z:3:LYS:HE2	46:Z:33:LEU:HD12	2.01	0.41
1:a:651:C:H1'	8:h:126:GLU:OE2	2.20	0.41
1:a:1080:C:H2'	1:a:1081:G:H8	1.86	0.41
1:a:1139:A:C6	1:a:1154:A:C5	3.08	0.41
1:a:1266:C:H6	1:a:1266:C:O5'	2.02	0.41
1:a:1336:A:C6	1:a:1337:U:C5	3.08	0.41
24:A:66:C:C2	24:A:67:A:C8	3.09	0.41
24:A:685:C:H2'	24:A:686:U:C6	2.55	0.41
24:A:1478:C:O2'	24:A:1621:A:OP2	2.31	0.41
24:A:1833:C:H5	24:A:1852:A:H62	1.69	0.41
24:A:2109:U:OP2	24:A:2271:G:N2	2.44	0.41
24:A:2125:G:H4'	24:A:2126:G:H5''	2.02	0.41
51:5:15:ARG:H	51:5:15:ARG:HD2	1.84	0.41
1:a:35:G:N3	12:l:128:SER:OG	2.53	0.41
1:a:1102:A:H5''	1:a:1103:G:OP2	2.20	0.41
1:a:1238:G:O5'	1:a:1238:G:H8	2.03	0.41
2:b:52:GLU:O	2:b:198:TYR:OH	2.38	0.41
4:d:100:ARG:HA	4:d:100:ARG:HD3	1.89	0.41
20:t:7:ALA:O	20:t:11:VAL:HG13	2.20	0.41
23:v:207:SER:OG	57:v:503:GCP:O2B	2.38	0.41
24:A:59:G:H1'	24:A:73:A:H2'	2.02	0.41
24:A:407:G:H2'	24:A:408:U:C6	2.55	0.41
24:A:1462:U:H1'	24:A:1464:A:C4	2.55	0.41
39:R:92:VAL:HG11	39:R:97:LEU:HD21	2.02	0.41
40:S:95:LEU:HD23	40:S:95:LEU:HA	1.86	0.41
1:a:1192:G:C4	1:a:1193:G:C8	3.08	0.41
1:a:1255:A:N6	1:a:1295:A:C5	2.89	0.41
2:b:43:LEU:O	2:b:47:VAL:HG13	2.21	0.41
16:p:56:THR:O	16:p:60:MET:HG3	2.21	0.41
23:v:10:ILE:HD11	23:v:46:GLU:HB3	2.03	0.41
24:A:1487:A:H2'	24:A:1488:U:C6	2.56	0.41
24:A:2324:U:C2	24:A:2325:U:C5	3.09	0.41
26:C:30:GLU:HG2	26:C:33:LEU:HD13	2.02	0.41
30:G:149:ARG:NE	30:G:167:GLU:OE2	2.53	0.41
1:a:1153:C:H4'	1:a:1154:A:H5'	2.03	0.41
1:a:1228:G:C2	1:a:1229:G:N2	2.88	0.41
1:a:1320:G:C2	1:a:1332:C:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:115:ASN:HD21	4:d:129:PRO:HG3	1.86	0.41
23:v:294:TYR:HA	23:v:297:MET:HE3	2.03	0.41
24:A:288:U:O2'	24:A:289:U:O5'	2.38	0.41
24:A:1761:A:H4'	24:A:1762:U:H5'	2.02	0.41
24:A:2226:A:H2'	24:A:2227:U:C6	2.56	0.41
35:N:37:GLY:H	35:N:40:ALA:HB3	1.85	0.41
35:N:58:PHE:O	53:7:13:ARG:NH1	2.53	0.41
37:P:47:LEU:HD21	37:P:66:ILE:CD1	2.49	0.41
38:Q:94:PHE:HB2	38:Q:119:PHE:CE2	2.55	0.41
1:a:382:A:H5''	1:a:460:A:N6	2.35	0.41
1:a:456:A:H2	1:a:494:U:O4	2.04	0.41
1:a:761:A:H4'	1:a:762:C:O5'	2.21	0.41
1:a:955:A:N3	1:a:956:G:C8	2.88	0.41
1:a:1193:G:C4	1:a:1194:G:C8	3.07	0.41
1:a:1246:A:P	1:a:1246:A:H8	2.44	0.41
1:a:1339:A:H2'	1:a:1340:A:H8	1.85	0.41
1:a:1454:A:P	1:a:1455:C:H41	2.42	0.41
11:k:36:ASP:HB2	11:k:40:ASN:OD1	2.20	0.41
15:o:7:ARG:NH1	15:o:10:GLU:OE1	2.54	0.41
15:o:80:GLU:O	15:o:84:ARG:HB2	2.21	0.41
21:x:28:G:H2'	21:x:29:G:O4'	2.20	0.41
21:x:40:C:H2'	21:x:41:C:C6	2.56	0.41
23:v:329:MET:HB3	23:v:332:LYS:HE2	2.03	0.41
23:v:365:LYS:HA	23:v:402:GLU:HA	2.02	0.41
23:v:369:LEU:HD12	23:v:397:THR:O	2.21	0.41
24:A:396:U:H2'	24:A:397:U:C6	2.56	0.41
24:A:420:A:H2'	24:A:421:C:O4'	2.21	0.41
24:A:1224:A:H2'	24:A:1225:G:H8	1.86	0.41
24:A:1244:U:H2'	24:A:1245:U:C6	2.56	0.41
24:A:2152:A:N6	24:A:2201:G:N3	2.68	0.41
24:A:2181:G:H8	24:A:2181:G:OP2	2.04	0.41
35:N:76:ILE:HD12	35:N:112:LEU:HD11	2.02	0.41
1:a:612:G:H2'	1:a:613:U:O4'	2.20	0.41
1:a:822:A:H5'	1:a:1519:G:H4'	2.03	0.41
1:a:900:U:H2'	1:a:901:A:H8	1.86	0.41
1:a:980:G:OP1	1:a:980:G:H3'	2.21	0.41
1:a:1008:C:H5'	1:a:1009:U:OP2	2.21	0.41
1:a:1160:A:H2'	1:a:1161:A:H8	1.85	0.41
1:a:1262:G:H2'	1:a:1286:A:N1	2.36	0.41
1:a:1283:G:O2'	1:a:1289:C:O4'	2.35	0.41
1:a:1351:C:O2'	1:a:1352:U:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1496:G:H2'	1:a:1497:G:C8	2.56	0.41
4:d:182:ARG:HH12	4:d:187:ALA:HA	1.86	0.41
21:x:70:G:H2'	21:x:71:G:C8	2.54	0.41
23:v:413:GLU:HG2	23:v:414:TYR:CD1	2.56	0.41
24:A:951:C:H2'	24:A:952:A:C8	2.56	0.41
24:A:1131:A:OP2	24:A:1131:A:H8	2.03	0.41
24:A:1309:G:O5'	24:A:1309:G:H8	2.04	0.41
24:A:1727:A:C4	24:A:1728:A:C8	3.09	0.41
24:A:2719:G:H2'	24:A:2720:U:C6	2.56	0.41
25:B:3:U:H2'	25:B:4:G:C8	2.55	0.41
27:D:126:HIS:CE1	27:D:159:LEU:HD22	2.56	0.41
29:F:74:ILE:HG12	29:F:79:LEU:HB3	2.03	0.41
29:F:129:THR:OG1	29:F:130:LEU:N	2.54	0.41
32:H:92:PRO:HA	32:H:136:GLY:HA2	2.02	0.41
49:3:12:VAL:CG1	49:3:46:LEU:HG	2.50	0.41
1:a:633:G:H2'	1:a:634:G:C8	2.55	0.41
1:a:693:G:H2'	1:a:694:U:C5	2.56	0.41
1:a:1182:G:C2	1:a:1183:A:C8	3.09	0.41
15:o:85:LEU:HD11	15:o:87:LEU:HD22	2.03	0.41
21:x:11:C:H2'	21:x:12:U:C6	2.56	0.41
24:A:669:C:O2'	24:A:703:U:OP1	2.35	0.41
24:A:1095:C:C2	24:A:1096:A:C8	3.09	0.41
24:A:1483:A:H2'	24:A:1484:A:C8	2.55	0.41
1:a:225:A:H2'	1:a:226:U:C6	2.56	0.40
1:a:499:A:H2'	1:a:500:A:H8	1.86	0.40
1:a:962:G:C6	1:a:1236:A:C6	3.09	0.40
1:a:998:U:C2	1:a:999:C:C5	3.09	0.40
1:a:1012:G:H2'	1:a:1012:G:N3	2.36	0.40
1:a:1243:A:H5'	1:a:1244:C:OP2	2.22	0.40
1:a:1297:A:H3'	1:a:1298:C:C5	2.56	0.40
12:l:48:THR:OG1	12:l:67:ARG:HG2	2.21	0.40
23:v:96:ASP:OD2	23:v:125:TYR:OH	2.30	0.40
24:A:3:U:H2'	24:A:4:U:C6	2.55	0.40
24:A:348:C:H2'	24:A:349:U:C6	2.56	0.40
24:A:1117:G:H2'	24:A:1118:C:C6	2.56	0.40
24:A:1555:U:N3	24:A:1556:G:N7	2.69	0.40
24:A:2279:G:H2'	24:A:2280:A:H8	1.86	0.40
24:A:2570:U:H2'	24:A:2571:C:H6	1.86	0.40
24:A:2715:G:C2	27:D:24:PRO:HB3	2.56	0.40
24:A:2723:A:OP2	37:P:10:SER:OG	2.31	0.40
24:A:2908:A:O2'	24:A:2909:C:P	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:56:VAL:HA	32:H:70:THR:HA	2.03	0.40
1:a:583:G:O2'	1:a:829:G:OP2	2.16	0.40
1:a:691:G:C2	1:a:692:U:C4	3.09	0.40
1:a:960:G:N1	1:a:1238:G:C6	2.89	0.40
1:a:1003:A:N6	1:a:1056:G:O2'	2.54	0.40
1:a:1020:U:N3	1:a:1021:G:N7	2.68	0.40
1:a:1100:U:O2	1:a:1100:U:H2'	2.20	0.40
2:b:91:PHE:HE2	2:b:93:ASN:HB2	1.87	0.40
23:v:413:GLU:OE1	23:v:413:GLU:N	2.41	0.40
24:A:879:C:H2'	24:A:880:U:C6	2.56	0.40
24:A:1560:A:H3'	24:A:1561:G:H8	1.87	0.40
24:A:1566:A:H4'	24:A:1608:U:O2'	2.20	0.40
24:A:2217:U:H2'	24:A:2218:G:H8	1.86	0.40
25:B:30:C:C2	25:B:31:G:C8	3.10	0.40
27:D:106:ASP:H	27:D:176:ILE:CG2	2.34	0.40
30:G:103:LEU:HD22	30:G:123:ILE:HG21	2.02	0.40
52:6:17:GLY:O	52:6:21:ARG:HG2	2.22	0.40
1:a:45:U:H2'	1:a:46:G:C8	2.56	0.40
1:a:1022:G:O3'	1:a:1023:A:H8	2.04	0.40
1:a:1114:A:H2'	1:a:1115:G:H8	1.86	0.40
1:a:1273:G:C2	1:a:1276:A:N7	2.88	0.40
1:a:1373:C:H2'	1:a:1374:C:H6	1.86	0.40
6:f:12:ARG:HH11	6:f:86:ASP:CB	2.34	0.40
24:A:24:G:O2'	42:U:83:GLU:O	2.40	0.40
24:A:59:G:O2'	24:A:74:U:OP2	2.32	0.40
24:A:946:G:C5	24:A:947:A:H1'	2.55	0.40
24:A:1397:A:H2'	24:A:1398:A:H8	1.86	0.40
24:A:1467:C:H2'	24:A:1468:G:O4'	2.21	0.40
24:A:2353:A:H2'	24:A:2353:A:N3	2.37	0.40
24:A:2720:U:H2'	24:A:2721:G:O4'	2.22	0.40
24:A:2832:G:H2'	24:A:2833:A:H8	1.86	0.40
28:E:152:ALA:O	28:E:189:HIS:ND1	2.55	0.40
30:G:44:ASN:H	30:G:52:VAL:HA	1.86	0.40
35:N:91:VAL:HB	35:N:123:VAL:HG12	2.03	0.40
49:3:37:TRP:CE3	49:3:38:GLU:HG2	2.56	0.40
1:a:945:C:H1'	1:a:1389:C:H42	1.86	0.40
1:a:1027:A:C6	1:a:1028:G:C6	3.09	0.40
1:a:1079:U:H2'	1:a:1080:C:H6	1.86	0.40
1:a:1262:G:C2'	1:a:1286:A:H61	2.34	0.40
1:a:1389:C:H2'	1:a:1390:C:C6	2.56	0.40
8:h:7:ILE:HB	8:h:79:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:45:PHE:HB3	8:h:74:ILE:HD11	2.02	0.40
18:r:55:TYR:HA	18:r:58:LYS:HG2	2.04	0.40
24:A:40:U:H2'	24:A:41:A:H8	1.85	0.40
24:A:1369:C:OP1	24:A:1696:G:O2'	2.35	0.40
24:A:1831:U:OP2	26:C:274:ARG:NH2	2.45	0.40
24:A:2211:C:H2'	24:A:2212:C:C6	2.57	0.40
24:A:2438:G:O2'	24:A:2439:C:OP2	2.34	0.40
29:F:93:GLY:N	29:F:96:MET:HE1	2.37	0.40
30:G:124:GLU:HG2	30:G:132:ILE:HB	2.03	0.40
1:a:377:C:OP2	1:a:396:G:N2	2.45	0.40
1:a:989:C:O2	14:n:19:GLN:HA	2.21	0.40
1:a:1320:G:N1	1:a:1332:C:N3	2.70	0.40
5:e:16:VAL:HG22	5:e:38:VAL:HG22	2.04	0.40
12:l:29:ASN:ND2	12:l:32:LYS:HD3	2.37	0.40
23:v:189:LYS:HD3	23:v:189:LYS:HA	1.94	0.40
24:A:1784:C:O2'	24:A:1785:C:H5'	2.20	0.40
24:A:2890:U:H2'	24:A:2891:A:H8	1.86	0.40
27:D:175:GLU:HG2	27:D:176:ILE:N	2.37	0.40
30:G:147:ASN:HD22	30:G:147:ASN:HA	1.75	0.40
54:8:16:VAL:HG22	54:8:25:VAL:HG22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	207/249 (83%)	180 (87%)	26 (13%)	1 (0%)	24	57
3	c	202/218 (93%)	176 (87%)	26 (13%)	0	100	100
4	d	197/200 (98%)	181 (92%)	16 (8%)	0	100	100
5	e	150/167 (90%)	137 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	f	93/97 (96%)	72 (77%)	20 (22%)	1 (1%)	11	39
7	g	128/156 (82%)	118 (92%)	10 (8%)	0	100	100
8	h	129/132 (98%)	115 (89%)	14 (11%)	0	100	100
9	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
10	j	94/102 (92%)	71 (76%)	22 (23%)	1 (1%)	11	39
11	k	112/129 (87%)	100 (89%)	12 (11%)	0	100	100
12	l	133/137 (97%)	120 (90%)	13 (10%)	0	100	100
13	m	106/121 (88%)	92 (87%)	14 (13%)	0	100	100
14	n	48/61 (79%)	33 (69%)	15 (31%)	0	100	100
15	o	85/89 (96%)	78 (92%)	7 (8%)	0	100	100
16	p	86/90 (96%)	74 (86%)	11 (13%)	1 (1%)	10	37
17	q	78/87 (90%)	71 (91%)	7 (9%)	0	100	100
18	r	62/79 (78%)	56 (90%)	6 (10%)	0	100	100
19	s	72/92 (78%)	65 (90%)	7 (10%)	0	100	100
20	t	79/84 (94%)	77 (98%)	2 (2%)	0	100	100
23	v	415/418 (99%)	382 (92%)	33 (8%)	0	100	100
26	C	272/277 (98%)	261 (96%)	10 (4%)	1 (0%)	30	61
27	D	204/209 (98%)	194 (95%)	10 (5%)	0	100	100
28	E	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
29	F	173/179 (97%)	161 (93%)	12 (7%)	0	100	100
30	G	169/178 (95%)	156 (92%)	13 (8%)	0	100	100
31	I	127/166 (76%)	122 (96%)	5 (4%)	0	100	100
32	H	133/141 (94%)	122 (92%)	9 (7%)	2 (2%)	8	32
33	L	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
34	M	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	N	144/146 (99%)	133 (92%)	11 (8%)	0	100	100
36	O	133/144 (92%)	129 (97%)	4 (3%)	0	100	100
37	P	118/135 (87%)	113 (96%)	5 (4%)	0	100	100
38	Q	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
39	R	111/114 (97%)	104 (94%)	7 (6%)	0	100	100
40	S	116/119 (98%)	113 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	T	99/102 (97%)	96 (97%)	3 (3%)	0	100	100
42	U	110/118 (93%)	107 (97%)	3 (3%)	0	100	100
43	V	90/94 (96%)	84 (93%)	5 (6%)	1 (1%)	11	39
44	W	100/103 (97%)	98 (98%)	2 (2%)	0	100	100
45	Y	74/96 (77%)	68 (92%)	6 (8%)	0	100	100
46	Z	57/62 (92%)	53 (93%)	4 (7%)	0	100	100
47	1	58/63 (92%)	56 (97%)	2 (3%)	0	100	100
48	2	54/59 (92%)	51 (94%)	3 (6%)	0	100	100
49	3	69/81 (85%)	61 (88%)	7 (10%)	1 (1%)	9	34
50	4	51/57 (90%)	44 (86%)	7 (14%)	0	100	100
51	5	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
52	6	41/44 (93%)	41 (100%)	0	0	100	100
53	7	62/66 (94%)	57 (92%)	5 (8%)	0	100	100
54	8	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
All	All	5827/6270 (93%)	5350 (92%)	468 (8%)	9 (0%)	44	73

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	j	79	PRO
16	p	25	SER
32	H	92	PRO
49	3	56	PRO
2	b	129	LEU
6	f	39	ILE
43	V	91	PHE
32	H	5	VAL
26	C	252	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	104/214 (49%)	104 (100%)	0	100	100
4	d	162/170 (95%)	162 (100%)	0	100	100
5	e	104/131 (79%)	104 (100%)	0	100	100
6	f	81/85 (95%)	81 (100%)	0	100	100
7	g	4/130 (3%)	4 (100%)	0	100	100
8	h	109/110 (99%)	109 (100%)	0	100	100
9	i	4/102 (4%)	4 (100%)	0	100	100
11	k	58/100 (58%)	58 (100%)	0	100	100
12	l	101/118 (86%)	101 (100%)	0	100	100
14	n	5/52 (10%)	5 (100%)	0	100	100
15	o	71/81 (88%)	71 (100%)	0	100	100
16	p	63/80 (79%)	63 (100%)	0	100	100
17	q	72/78 (92%)	72 (100%)	0	100	100
18	r	47/67 (70%)	47 (100%)	0	100	100
20	t	55/66 (83%)	55 (100%)	0	100	100
23	v	351/365 (96%)	351 (100%)	0	100	100
26	C	215/225 (96%)	215 (100%)	0	100	100
27	D	158/171 (92%)	158 (100%)	0	100	100
28	E	161/174 (92%)	161 (100%)	0	100	100
29	F	93/155 (60%)	93 (100%)	0	100	100
30	G	139/147 (95%)	139 (100%)	0	100	100
32	H	4/111 (4%)	4 (100%)	0	100	100
33	L	116/121 (96%)	116 (100%)	0	100	100
34	M	92/101 (91%)	92 (100%)	0	100	100
35	N	105/115 (91%)	105 (100%)	0	100	100
36	O	105/113 (93%)	105 (100%)	0	100	100
37	P	102/111 (92%)	102 (100%)	0	100	100
38	Q	88/97 (91%)	88 (100%)	0	100	100
39	R	93/99 (94%)	93 (100%)	0	100	100
40	S	95/97 (98%)	95 (100%)	0	100	100
41	T	78/82 (95%)	78 (100%)	0	100	100
42	U	90/97 (93%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	V	76/84 (90%)	76 (100%)	0	100	100
44	W	83/88 (94%)	83 (100%)	0	100	100
45	Y	57/76 (75%)	57 (100%)	0	100	100
46	Z	45/53 (85%)	45 (100%)	0	100	100
47	1	48/55 (87%)	48 (100%)	0	100	100
48	2	50/52 (96%)	50 (100%)	0	100	100
49	3	48/73 (66%)	48 (100%)	0	100	100
50	4	44/50 (88%)	44 (100%)	0	100	100
51	5	44/48 (92%)	44 (100%)	0	100	100
52	6	39/39 (100%)	39 (100%)	0	100	100
53	7	54/56 (96%)	54 (100%)	0	100	100
54	8	32/35 (91%)	32 (100%)	0	100	100
All	All	3745/4674 (80%)	3745 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
4	d	70	ASN
4	d	85	ASN
4	d	115	ASN
4	d	137	GLN
5	e	84	HIS
5	e	89	HIS
8	h	16	ASN
8	h	22	HIS
8	h	56	ASN
8	h	99	ASN
11	k	118	HIS
12	l	29	ASN
12	l	59	ASN
15	o	18	HIS
15	o	40	ASN
17	q	33	HIS
20	t	24	GLN
23	v	82	GLN
23	v	117	GLN

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Mol	Chain	Res	Type
23	v	264	HIS
23	v	382	ASN
26	C	53	HIS
26	C	70	ASN
26	C	114	GLN
26	C	204	ASN
27	D	32	GLN
27	D	33	ASN
27	D	126	HIS
27	D	152	ASN
28	E	46	GLN
28	E	75	GLN
28	E	119	ASN
28	E	162	ASN
30	G	73	ASN
30	G	99	GLN
30	G	147	ASN
33	L	118	GLN
35	N	126	ASN
37	P	75	GLN
37	P	89	ASN
38	Q	15	HIS
38	Q	43	GLN
38	Q	58	ASN
38	Q	102	HIS
38	Q	115	ASN
39	R	66	ASN
40	S	37	GLN
41	T	88	HIS
44	W	67	ASN
45	Y	48	GLN
45	Y	58	ASN
46	Z	16	ASN
46	Z	23	ASN
48	2	40	ASN
51	5	26	ASN
53	7	35	ASN

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550 (97%)	340 (22%)	0
21	x	72/76 (94%)	18 (25%)	0
22	w	8/21 (38%)	6 (75%)	0
24	A	2897/2932 (98%)	457 (15%)	29 (1%)
25	B	113/116 (97%)	12 (10%)	0
All	All	4602/4695 (98%)	833 (18%)	29 (0%)

All (833) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	9	G
1	a	17	U
1	a	22	G
1	a	31	G
1	a	32	A
1	a	39	G
1	a	44	G
1	a	47	C
1	a	48	C
1	a	51	A
1	a	54	C
1	a	55	A
1	a	57	G
1	a	58	C
1	a	68	G
1	a	69	A
1	a	70	A
1	a	71	C
1	a	97	U
1	a	98	U
1	a	99	A
1	a	106	G
1	a	114	A
1	a	119	C
1	a	128	A
1	a	130	C
1	a	143	U
1	a	150	A
1	a	158	G
1	a	159	A
1	a	161	A

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Mol	Chain	Res	Type
1	a	162	C
1	a	173	A
1	a	182	U
1	a	183	A
1	a	187	U
1	a	190	G
1	a	195	A
1	a	207	U
1	a	209	A
1	a	211	A
1	a	212	G
1	a	219	U
1	a	220	C
1	a	221	G
1	a	222	G
1	a	223	C
1	a	224	U
1	a	226	U
1	a	228	G
1	a	252	U
1	a	255	G
1	a	259	G
1	a	265	A
1	a	274	G
1	a	275	C
1	a	289	G
1	a	297	G
1	a	329	A
1	a	336	C
1	a	340	G
1	a	350	C
1	a	354	G
1	a	355	G
1	a	360	C
1	a	362	G
1	a	372	A
1	a	373	U
1	a	375	U
1	a	377	C
1	a	380	C
1	a	381	A
1	a	385	G

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Mol	Chain	Res	Type
1	a	400	G
1	a	405	A
1	a	406	C
1	a	412	G
1	a	414	G
1	a	420	A
1	a	421	G
1	a	429	U
1	a	430	C
1	a	432	G
1	a	437	U
1	a	447	U
1	a	454	A
1	a	456	A
1	a	457	A
1	a	460	A
1	a	461	C
1	a	467	U
1	a	470	G
1	a	475	A
1	a	476	C
1	a	485	C
1	a	487	U
1	a	488	U
1	a	489	G
1	a	490	A
1	a	492	G
1	a	493	G
1	a	494	U
1	a	505	A
1	a	507	A
1	a	517	A
1	a	519	C
1	a	526	C
1	a	529	G
1	a	535	G
1	a	538	G
1	a	539	U
1	a	540	A
1	a	550	U
1	a	555	A
1	a	567	A

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Mol	Chain	Res	Type
1	a	572	U
1	a	576	G
1	a	581	A
1	a	584	C
1	a	585	G
1	a	587	G
1	a	596	G
1	a	604	A
1	a	643	A
1	a	661	G
1	a	673	A
1	a	674	G
1	a	692	U
1	a	693	G
1	a	694	U
1	a	695	A
1	a	703	A
1	a	710	A
1	a	711	G
1	a	712	A
1	a	716	G
1	a	726	A
1	a	731	U
1	a	732	G
1	a	739	G
1	a	742	A
1	a	757	A
1	a	762	C
1	a	763	G
1	a	783	G
1	a	785	A
1	a	789	A
1	a	801	U
1	a	802	A
1	a	813	C
1	a	825	C
1	a	831	G
1	a	848	G
1	a	855	C
1	a	881	A
1	a	923	A
1	a	929	U

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Mol	Chain	Res	Type
1	a	930	U
1	a	931	G
1	a	932	A
1	a	935	G
1	a	936	G
1	a	938	G
1	a	943	C
1	a	944	A
1	a	948	G
1	a	958	A
1	a	964	U
1	a	965	U
1	a	968	A
1	a	969	U
1	a	975	G
1	a	977	A
1	a	978	A
1	a	980	G
1	a	981	C
1	a	983	A
1	a	984	A
1	a	985	G
1	a	986	A
1	a	987	A
1	a	990	U
1	a	991	U
1	a	992	A
1	a	993	C
1	a	994	C
1	a	998	U
1	a	1001	U
1	a	1002	G
1	a	1006	U
1	a	1008	C
1	a	1011	U
1	a	1012	G
1	a	1013	A
1	a	1014	C
1	a	1015	C
1	a	1017	C
1	a	1018	U
1	a	1023	A

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Mol	Chain	Res	Type
1	a	1027	A
1	a	1032	U
1	a	1033	U
1	a	1034	U
1	a	1035	C
1	a	1046	C
1	a	1049	A
1	a	1050	G
1	a	1052	G
1	a	1053	A
1	a	1055	A
1	a	1059	G
1	a	1062	G
1	a	1064	A
1	a	1067	G
1	a	1068	U
1	a	1070	G
1	a	1071	U
1	a	1074	U
1	a	1084	U
1	a	1102	A
1	a	1103	G
1	a	1104	U
1	a	1110	A
1	a	1111	A
1	a	1122	C
1	a	1133	G
1	a	1134	U
1	a	1136	G
1	a	1139	A
1	a	1141	C
1	a	1142	A
1	a	1147	G
1	a	1148	U
1	a	1154	A
1	a	1156	U
1	a	1160	A
1	a	1163	U
1	a	1167	U
1	a	1178	G
1	a	1181	G
1	a	1182	G

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Mol	Chain	Res	Type
1	a	1189	G
1	a	1191	G
1	a	1199	C
1	a	1202	C
1	a	1203	A
1	a	1204	A
1	a	1207	C
1	a	1208	A
1	a	1209	U
1	a	1219	U
1	a	1220	A
1	a	1223	A
1	a	1226	U
1	a	1227	G
1	a	1228	G
1	a	1229	G
1	a	1230	C
1	a	1231	U
1	a	1232	A
1	a	1234	A
1	a	1235	C
1	a	1239	U
1	a	1240	G
1	a	1243	A
1	a	1244	C
1	a	1245	A
1	a	1246	A
1	a	1247	U
1	a	1248	G
1	a	1255	A
1	a	1256	C
1	a	1258	A
1	a	1262	G
1	a	1263	U
1	a	1265	G
1	a	1267	G
1	a	1273	G
1	a	1274	C
1	a	1278	G
1	a	1279	U
1	a	1280	G
1	a	1281	G

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Mol	Chain	Res	Type
1	a	1283	G
1	a	1285	C
1	a	1286	A
1	a	1287	A
1	a	1288	U
1	a	1289	C
1	a	1293	U
1	a	1294	A
1	a	1297	A
1	a	1298	C
1	a	1302	U
1	a	1304	U
1	a	1305	C
1	a	1306	A
1	a	1307	G
1	a	1308	U
1	a	1312	G
1	a	1315	U
1	a	1321	C
1	a	1327	C
1	a	1328	U
1	a	1329	C
1	a	1330	G
1	a	1347	A
1	a	1355	U
1	a	1364	A
1	a	1366	C
1	a	1367	A
1	a	1371	U
1	a	1377	G
1	a	1381	A
1	a	1386	G
1	a	1388	U
1	a	1401	A
1	a	1405	A
1	a	1433	A
1	a	1447	U
1	a	1449	G
1	a	1450	G
1	a	1453	A
1	a	1495	G
1	a	1498	U

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Mol	Chain	Res	Type
1	a	1500	A
1	a	1501	A
1	a	1502	G
1	a	1511	A
1	a	1514	U
1	a	1515	A
1	a	1525	G
1	a	1537	G
1	a	1538	G
1	a	1539	A
1	a	1540	U
1	a	1541	C
1	a	1542	A
1	a	1543	C
1	a	1544	C
21	x	4	C
21	x	8	4SU
21	x	9	A
21	x	10	G
21	x	19	G
21	x	21	A
21	x	25	C
21	x	29	G
21	x	30	G
21	x	34	G
21	x	35	A
21	x	44	G
21	x	46	G7M
21	x	48	C
21	x	52	G
21	x	53	G
21	x	73	A
21	x	76	A
22	w	12	A
22	w	13	A
22	w	14	U
22	w	17	U
22	w	18	A
22	w	19	A
24	A	13	A
24	A	14	A
24	A	28	A

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Mol	Chain	Res	Type
24	A	34	U
24	A	46	C
24	A	51	G
24	A	60	G
24	A	71	A
24	A	75	G
24	A	89	U
24	A	92	G
24	A	100	U
24	A	101	G
24	A	117	A
24	A	119	U
24	A	125	A
24	A	126	A
24	A	130	A
24	A	140	G
24	A	141	U
24	A	159	U
24	A	161	A
24	A	162	A
24	A	164	A
24	A	182	A
24	A	186	C
24	A	187	C
24	A	198	A
24	A	199	A
24	A	201	A
24	A	215	A
24	A	218	A
24	A	223	A
24	A	224	A
24	A	230	A
24	A	231	A
24	A	232	U
24	A	241	U
24	A	247	G
24	A	250	G
24	A	257	A
24	A	271	C
24	A	274	A
24	A	283	C
24	A	284	U

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Mol	Chain	Res	Type
24	A	285	U
24	A	286	G
24	A	289	U
24	A	290	C
24	A	299	G
24	A	300	U
24	A	301	A
24	A	307	C
24	A	309	C
24	A	313	A
24	A	320	U
24	A	345	G
24	A	354	A
24	A	360	G
24	A	372	A
24	A	373	A
24	A	374	C
24	A	375	A
24	A	404	A
24	A	406	A
24	A	411	A
24	A	417	A
24	A	418	G
24	A	420	A
24	A	429	C
24	A	432	G
24	A	433	U
24	A	451	C
24	A	452	G
24	A	457	G
24	A	470	G
24	A	490	C
24	A	501	C
24	A	503	A
24	A	513	G
24	A	527	G
24	A	529	A
24	A	530	C
24	A	550	A
24	A	552	U
24	A	553	U
24	A	554	C

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Mol	Chain	Res	Type
24	A	555	C
24	A	567	G
24	A	575	G
24	A	576	U
24	A	577	A
24	A	578	G
24	A	591	A
24	A	592	A
24	A	593	U
24	A	594	G
24	A	606	G
24	A	616	G
24	A	618	A
24	A	646	A
24	A	657	A
24	A	658	A
24	A	659	A
24	A	666	A
24	A	667	G
24	A	672	A
24	A	679	G
24	A	682	A
24	A	689	A
24	A	690	U
24	A	698	A
24	A	699	U
24	A	700	A
24	A	718	C
24	A	732	U
24	A	776	U
24	A	786	C
24	A	791	G
24	A	793	U
24	A	794	G
24	A	810	A
24	A	811	G
24	A	821	G
24	A	823	G
24	A	828	A
24	A	830	U
24	A	836	U
24	A	838	G

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Mol	Chain	Res	Type
24	A	851	G
24	A	858	C
24	A	865	A
24	A	873	U
24	A	874	U
24	A	891	U
24	A	892	A
24	A	893	A
24	A	913	A
24	A	921	G
24	A	924	U
24	A	925	A
24	A	926	G
24	A	943	A
24	A	944	C
24	A	945	C
24	A	946	G
24	A	947	A
24	A	948	A
24	A	957	A
24	A	959	C
24	A	964	A
24	A	973	U
24	A	974	A
24	A	979	U
24	A	980	A
24	A	987	A
24	A	991	A
24	A	992	G
24	A	1007	G
24	A	1019	A
24	A	1020	A
24	A	1025	A
24	A	1029	A
24	A	1036	A
24	A	1042	A
24	A	1055	A
24	A	1058	U
24	A	1059	A
24	A	1072	A
24	A	1073	A
24	A	1074	A

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Mol	Chain	Res	Type
24	A	1079	U
24	A	1087	U
24	A	1092	A
24	A	1093	G
24	A	1106	U
24	A	1115	A
24	A	1116	A
24	A	1123	A
24	A	1124	C
24	A	1129	G
24	A	1130	A
24	A	1131	A
24	A	1134	A
24	A	1136	U
24	A	1157	A
24	A	1158	G
24	A	1159	U
24	A	1161	A
24	A	1173	A
24	A	1174	A
24	A	1178	U
24	A	1179	A
24	A	1181	C
24	A	1182	G
24	A	1188	A
24	A	1203	A
24	A	1230	G
24	A	1249	A
24	A	1250	G
24	A	1254	G
24	A	1257	G
24	A	1265	A
24	A	1283	G
24	A	1298	A
24	A	1301	G
24	A	1302	C
24	A	1311	G
24	A	1316	G
24	A	1317	A
24	A	1320	G
24	A	1344	A
24	A	1345	A

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Mol	Chain	Res	Type
24	A	1357	U
24	A	1358	C
24	A	1365	A
24	A	1369	C
24	A	1373	U
24	A	1385	U
24	A	1394	C
24	A	1396	U
24	A	1409	A
24	A	1422	A
24	A	1423	U
24	A	1429	A
24	A	1430	C
24	A	1435	A
24	A	1439	A
24	A	1447	A
24	A	1462	U
24	A	1463	U
24	A	1464	A
24	A	1465	A
24	A	1469	A
24	A	1478	C
24	A	1503	A
24	A	1505	G
24	A	1509	A
24	A	1517	C
24	A	1519	A
24	A	1528	G
24	A	1529	U
24	A	1531	U
24	A	1532	G
24	A	1534	G
24	A	1539	A
24	A	1542	C
24	A	1543	A
24	A	1546	U
24	A	1556	G
24	A	1558	G
24	A	1559	A
24	A	1562	C
24	A	1564	U
24	A	1570	G

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Mol	Chain	Res	Type
24	A	1571	U
24	A	1573	A
24	A	1574	U
24	A	1618	A
24	A	1621	A
24	A	1630	U
24	A	1635	A
24	A	1638	G
24	A	1656	C
24	A	1657	A
24	A	1659	A
24	A	1683	A
24	A	1695	A
24	A	1696	G
24	A	1697	C
24	A	1700	G
24	A	1701	A
24	A	1703	A
24	A	1704	A
24	A	1712	U
24	A	1723	G
24	A	1724	C
24	A	1749	A
24	A	1761	A
24	A	1762	U
24	A	1763	U
24	A	1764	A
24	A	1770	C
24	A	1771	A
24	A	1773	G
24	A	1780	A
24	A	1781	G
24	A	1782	A
24	A	1783	G
24	A	1787	C
24	A	1796	G
24	A	1797	G
24	A	1806	A
24	A	1809	G
24	A	1815	C
24	A	1818	A
24	A	1819	A

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Mol	Chain	Res	Type
24	A	1833	C
24	A	1834	A
24	A	1842	A
24	A	1849	C
24	A	1850	G
24	A	1851	U
24	A	1852	A
24	A	1862	A
24	A	1880	A
24	A	1886	A
24	A	1887	A
24	A	1889	A
24	A	1899	A
24	A	1903	U
24	A	1904	C
24	A	1915	C
24	A	1939	G
24	A	1947	C
24	A	1950	U
24	A	1962	G
24	A	1963	G
24	A	1967	C
24	A	1969	A
24	A	1973	U
24	A	1988	U
24	A	1998	C
24	A	2000	C
24	A	2003	A
24	A	2004	A
24	A	2005	G
24	A	2024	U
24	A	2026	U
24	A	2030	A
24	A	2054	G
24	A	2056	A
24	A	2064	A
24	A	2065	G
24	A	2066	A
24	A	2072	G
24	A	2076	C
24	A	2088	C
24	A	2089	G

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Mol	Chain	Res	Type
24	A	2093	A
24	A	2094	G
24	A	2095	A
24	A	2102	G
24	A	2126	G
24	A	2127	A
24	A	2149	G
24	A	2150	A
24	A	2151	U
24	A	2159	A
24	A	2165	A
24	A	2166	G
24	A	2178	C
24	A	2188	A
24	A	2191	A
24	A	2192	G
24	A	2200	U
24	A	2201	G
24	A	2205	U
24	A	2206	A
24	A	2223	A
24	A	2231	A
24	A	2236	G
24	A	2237	C
24	A	2245	A
24	A	2258	A
24	A	2271	G
24	A	2272	G
24	A	2299	A
24	A	2312	G
24	A	2316	C
24	A	2319	A
24	A	2320	A
24	A	2321	A
24	A	2329	U
24	A	2338	A
24	A	2341	G
24	A	2344	A
24	A	2353	A
24	A	2355	A
24	A	2358	G
24	A	2360	A

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Mol	Chain	Res	Type
24	A	2367	C
24	A	2368	A
24	A	2380	C
24	A	2383	C
24	A	2391	A
24	A	2394	A
24	A	2412	G
24	A	2416	G
24	A	2418	C
24	A	2435	U
24	A	2436	C
24	A	2439	C
24	A	2455	C
24	A	2458	A
24	A	2462	G
24	A	2463	A
24	A	2473	C
24	A	2474	C
24	A	2481	A
24	A	2492	A
24	A	2498	C
24	A	2506	U
24	A	2507	C
24	A	2509	A
24	A	2535	G
24	A	2536	A
24	A	2538	G
24	A	2551	A
24	A	2562	G
24	A	2568	G
24	A	2587	U
24	A	2599	A
24	A	2600	G
24	A	2643	C
24	A	2646	U
24	A	2648	U
24	A	2663	G
24	A	2679	C
24	A	2694	G
24	A	2696	G
24	A	2715	G
24	A	2722	U

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Mol	Chain	Res	Type
24	A	2724	C
24	A	2747	G
24	A	2759	U
24	A	2766	C
24	A	2768	G
24	A	2785	C
24	A	2790	A
24	A	2797	A
24	A	2798	A
24	A	2799	G
24	A	2802	C
24	A	2810	G
24	A	2811	A
24	A	2812	U
24	A	2813	G
24	A	2822	C
24	A	2826	U
24	A	2827	C
24	A	2828	U
24	A	2829	U
24	A	2831	G
24	A	2832	G
24	A	2835	A
24	A	2862	A
24	A	2864	A
24	A	2872	G
24	A	2877	G
24	A	2890	U
24	A	2896	G
24	A	2901	G
24	A	2909	C
24	A	2913	U
24	A	2920	A
24	A	2922	G
25	B	10	U
25	B	23	U
25	B	33	U
25	B	40	C
25	B	42	G
25	B	43	A
25	B	54	U
25	B	55	A

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Mol	Chain	Res	Type
25	B	84	G
25	B	87	U
25	B	88	C
25	B	107	G

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	27	G
24	A	88	G
24	A	139	A
24	A	384	G
24	A	553	U
24	A	688	A
24	A	756	A
24	A	809	G
24	A	847	G
24	A	854	G
24	A	1017	C
24	A	1172	A
24	A	1248	A
24	A	1249	A
24	A	1468	G
24	A	1497	G
24	A	1528	G
24	A	1530	G
24	A	1533	A
24	A	1569	U
24	A	1817	A
24	A	1851	U
24	A	1886	A
24	A	2320	A
24	A	2438	G
24	A	2472	A
24	A	2789	U
24	A	2809	A
24	A	2908	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	G7M	x	46	21	23,26,27	2.38	5 (21%)	34,39,42	3.07	11 (32%)
21	5MU	x	54	21	19,22,23	1.36	5 (26%)	27,32,35	2.13	6 (22%)
21	MIA	x	37	21	28,31,32	2.29	6 (21%)	38,44,47	2.79	14 (36%)
21	PSU	x	55	21	18,21,22	1.36	2 (11%)	21,30,33	2.02	4 (19%)
21	PSU	x	39	21	18,21,22	1.30	2 (11%)	21,30,33	2.13	4 (19%)
21	4SU	x	8	21	18,21,22	1.87	5 (27%)	25,30,33	2.45	6 (24%)
21	PSU	x	32	21	18,21,22	1.36	2 (11%)	21,30,33	2.03	3 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	G7M	x	46	21	-	4/7/25/26	0/3/3/3
21	5MU	x	54	21	-	0/7/25/26	0/2/2/2
21	MIA	x	37	21	-	1/15/33/34	0/3/3/3
21	PSU	x	55	21	-	0/7/25/26	0/2/2/2
21	PSU	x	39	21	-	0/7/25/26	0/2/2/2
21	4SU	x	8	21	-	2/7/25/26	0/2/2/2
21	PSU	x	32	21	-	0/7/25/26	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	46	G7M	C8-N7	7.49	1.45	1.33
21	x	37	MIA	C13-C14	6.81	1.52	1.32
21	x	37	MIA	C2-S10	-6.66	1.70	1.75
21	x	8	4SU	C4-S4	-5.03	1.59	1.68
21	x	46	G7M	C5-N7	-4.81	1.33	1.39
21	x	37	MIA	C5-C4	4.67	1.47	1.39
21	x	46	G7M	C8-N9	4.15	1.46	1.35
21	x	46	G7M	C5-C4	3.92	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	x	55	PSU	C6-C5	3.42	1.39	1.35
21	x	8	4SU	C4-N3	-3.32	1.34	1.37
21	x	39	PSU	C6-C5	3.25	1.38	1.35
21	x	32	PSU	C6-C5	2.99	1.38	1.35
21	x	37	MIA	C5-C6	2.78	1.48	1.41
21	x	8	4SU	C5-C4	-2.72	1.39	1.42
21	x	32	PSU	C4-N3	-2.68	1.33	1.38
21	x	54	5MU	C6-C5	2.59	1.38	1.34
21	x	55	PSU	C4-N3	-2.56	1.34	1.38
21	x	54	5MU	C4-N3	-2.51	1.34	1.38
21	x	39	PSU	C4-N3	-2.51	1.34	1.38
21	x	46	G7M	C6-N1	-2.49	1.34	1.38
21	x	37	MIA	C8-N7	2.31	1.36	1.31
21	x	54	5MU	C2-N1	2.28	1.42	1.38
21	x	37	MIA	C5-N7	-2.26	1.35	1.39
21	x	54	5MU	C4-C5	2.26	1.48	1.44
21	x	8	4SU	C2-N1	2.24	1.42	1.38
21	x	54	5MU	C6-N1	-2.22	1.34	1.38
21	x	8	4SU	C2-N3	-2.07	1.34	1.38

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	x	37	MIA	C12-C13-C14	-9.03	110.80	127.01
21	x	46	G7M	CN7-N7-C8	-8.14	112.46	124.79
21	x	37	MIA	C5-C4-N3	-8.05	118.70	127.18
21	x	8	4SU	C4-N3-C2	-7.15	120.46	127.31
21	x	46	G7M	N9-C4-N3	6.76	139.48	125.95
21	x	46	G7M	N9-C8-N7	-6.52	96.65	112.48
21	x	39	PSU	N1-C2-N3	6.47	121.99	115.17
21	x	37	MIA	N3-C4-N9	6.46	135.19	126.99
21	x	46	G7M	C8-N7-C5	6.45	115.85	107.78
21	x	32	PSU	N1-C2-N3	6.37	121.88	115.17
21	x	55	PSU	N1-C2-N3	6.32	121.83	115.17
21	x	8	4SU	C5-C4-N3	5.92	120.26	114.75
21	x	46	G7M	C5-C4-N3	-5.92	116.97	128.15
21	x	54	5MU	C4-N3-C2	-5.14	120.59	127.34
21	x	54	5MU	N3-C2-N1	4.84	121.19	114.89
21	x	46	G7M	C2-N3-C4	4.61	120.24	112.30
21	x	39	PSU	C4-N3-C2	-4.60	120.03	126.37
21	x	8	4SU	C5-C4-S4	-4.59	119.06	124.31
21	x	54	5MU	C5-C4-N3	4.44	119.18	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	x	54	5MU	O4-C4-C5	-4.34	119.95	124.92
21	x	8	4SU	N3-C2-N1	4.13	120.27	114.89
21	x	32	PSU	C4-N3-C2	-4.05	120.79	126.37
21	x	55	PSU	C4-N3-C2	-4.03	120.83	126.37
21	x	46	G7M	C1'-N9-C8	-4.02	113.17	126.74
21	x	46	G7M	C8-N9-C4	4.01	117.02	107.09
21	x	46	G7M	CN7-N7-C5	3.92	131.68	126.80
21	x	37	MIA	C15-C14-C13	-3.89	110.97	122.66
21	x	37	MIA	C16-C14-C13	-3.77	111.35	122.66
21	x	32	PSU	O2-C2-N1	-3.70	118.97	122.79
21	x	55	PSU	O2-C2-N1	-3.66	119.01	122.79
21	x	39	PSU	O2-C2-N1	-3.52	119.15	122.79
21	x	54	5MU	C5-C6-N1	-3.48	119.54	123.31
21	x	37	MIA	C2-N3-C4	3.47	121.38	112.29
21	x	37	MIA	C4-C5-N7	-3.46	106.63	110.58
21	x	37	MIA	C6-C5-N7	3.30	136.03	132.43
21	x	37	MIA	C4-N9-C8	2.85	108.73	105.74
21	x	37	MIA	C5-N7-C8	2.63	107.58	103.45
21	x	46	G7M	O6-C6-C5	-2.48	122.48	128.01
21	x	37	MIA	N3-C2-N1	-2.45	122.53	127.00
21	x	8	4SU	C3'-C2'-C1'	2.36	105.93	101.46
21	x	37	MIA	C2-N1-C6	2.32	121.94	117.54
21	x	54	5MU	O2-C2-N1	-2.26	119.86	122.80
21	x	39	PSU	C5-C6-N1	-2.22	119.06	122.14
21	x	37	MIA	N6-C6-N1	2.11	121.16	118.33
21	x	37	MIA	N9-C8-N7	-2.09	110.97	113.94
21	x	55	PSU	C5-C6-N1	-2.07	119.27	122.14
21	x	8	4SU	C1'-N1-C2	2.03	121.23	117.59
21	x	46	G7M	C5-C6-N1	2.02	116.02	111.84

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	x	37	MIA	C12-C13-C14-C16
21	x	46	G7M	O4'-C4'-C5'-O5'
21	x	8	4SU	O4'-C4'-C5'-O5'
21	x	46	G7M	C3'-C4'-C5'-O5'
21	x	8	4SU	C3'-C4'-C5'-O5'
21	x	46	G7M	O4'-C1'-N9-C4
21	x	46	G7M	O4'-C1'-N9-C8

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	x	46	G7M	2	0
21	x	37	MIA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 428 ligands modelled in this entry, 427 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	GCP	v	503	55	32,34,34	1.40	7 (21%)	49,54,54	1.77	8 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	GCP	v	503	55	-	5/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	v	503	GCP	C5-C4	2.90	1.46	1.38
57	v	503	GCP	PG-O3G	2.75	1.61	1.55
57	v	503	GCP	PG-O2G	2.70	1.61	1.55
57	v	503	GCP	C6-N1	-2.46	1.34	1.38
57	v	503	GCP	C5-N7	-2.36	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	v	503	GCP	PB-O3A	2.15	1.60	1.58
57	v	503	GCP	C4-N9	-2.02	1.32	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	v	503	GCP	C5-C4-N3	-5.96	118.91	128.39
57	v	503	GCP	C2-N3-C4	4.97	120.86	112.30
57	v	503	GCP	N9-C4-N3	4.45	134.85	125.95
57	v	503	GCP	C6-C5-N7	3.12	135.96	130.29
57	v	503	GCP	PB-O3A-PA	-2.87	122.99	132.37
57	v	503	GCP	O6-C6-C5	-2.36	120.31	126.53
57	v	503	GCP	C4-C5-N7	-2.35	106.94	110.67
57	v	503	GCP	C3'-C2'-C1'	2.23	105.68	101.46

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	v	503	GCP	C5'-O5'-PA-O3A
57	v	503	GCP	C5'-O5'-PA-O1A
57	v	503	GCP	O4'-C4'-C5'-O5'
57	v	503	GCP	C3'-C4'-C5'-O5'
57	v	503	GCP	C5'-O5'-PA-O2A

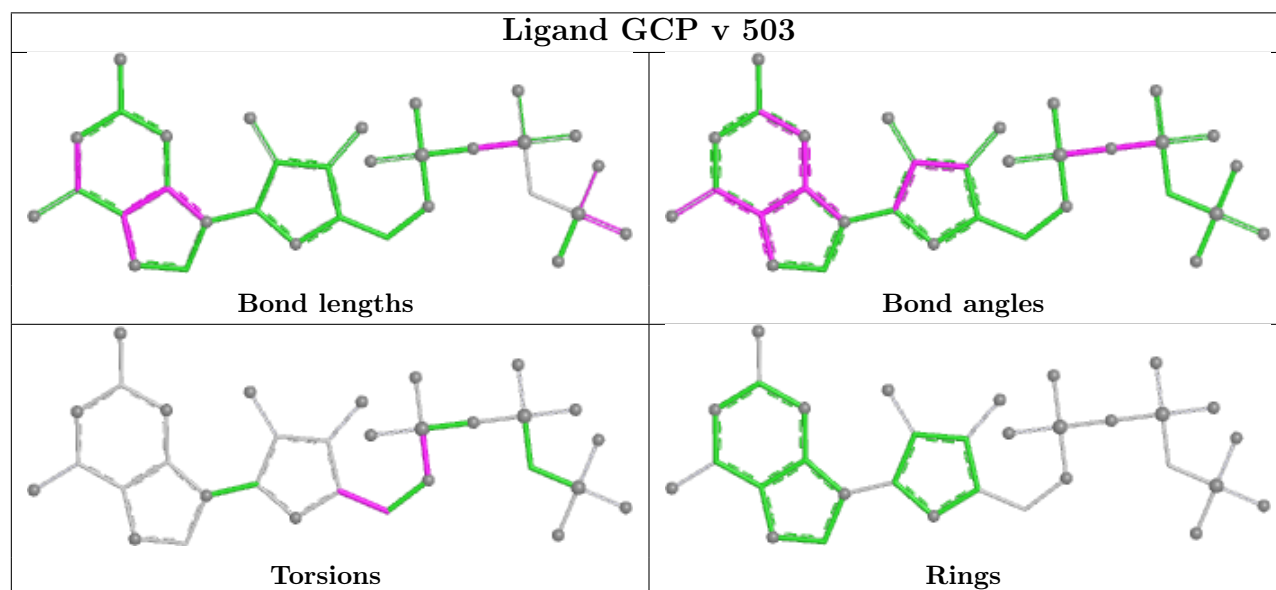
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	v	503	GCP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

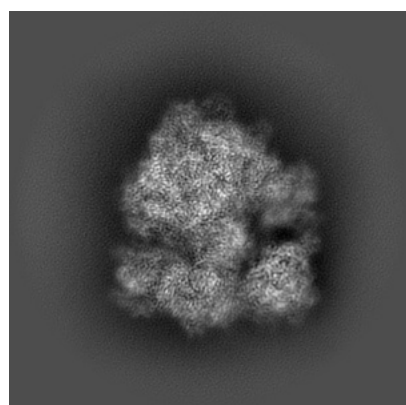
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42571. These allow visual inspection of the internal detail of the map and identification of artifacts.

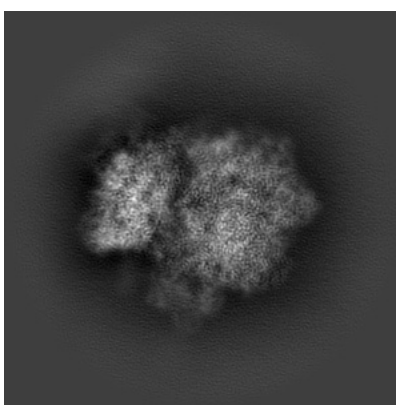
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

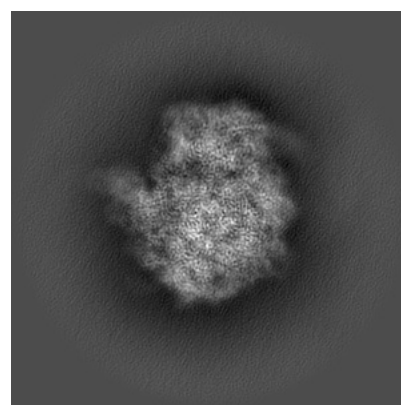
6.1.1 Primary map



X



Y

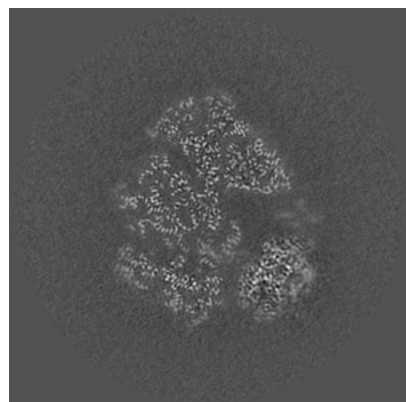


Z

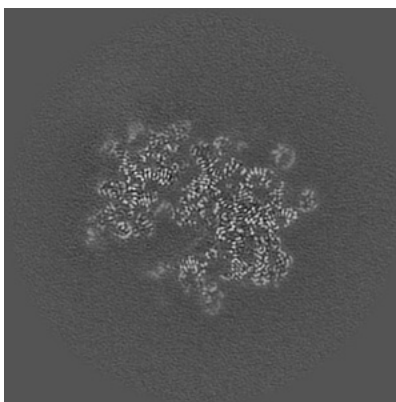
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

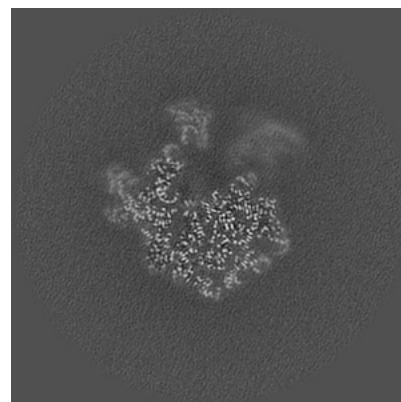
6.2.1 Primary map



X Index: 256



Y Index: 256

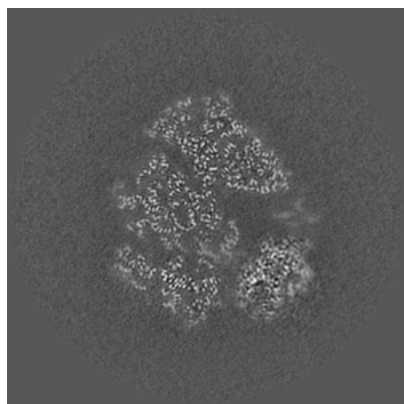


Z Index: 256

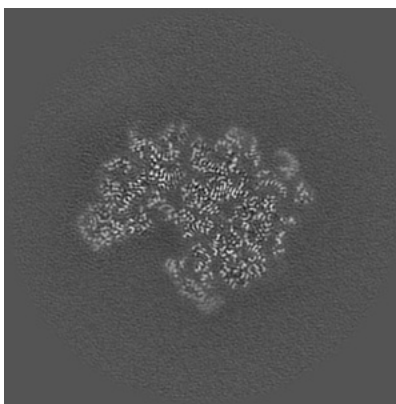
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

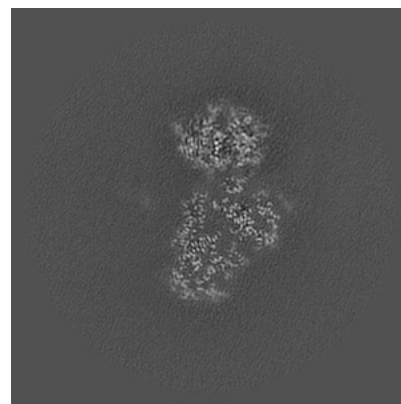
6.3.1 Primary map



X Index: 255



Y Index: 244

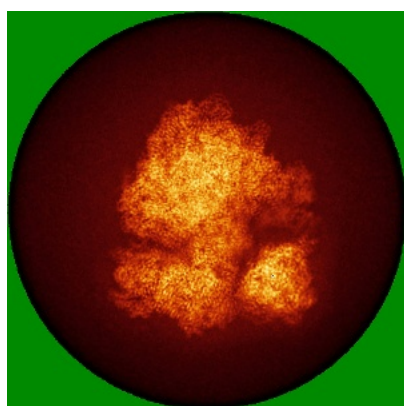


Z Index: 178

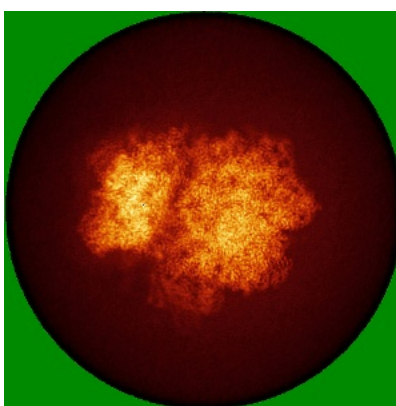
The images above show the largest variance slices of the map in three orthogonal directions.

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

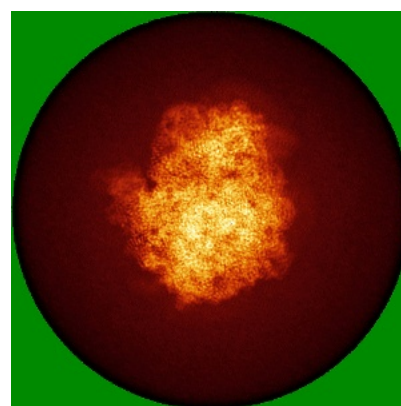
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

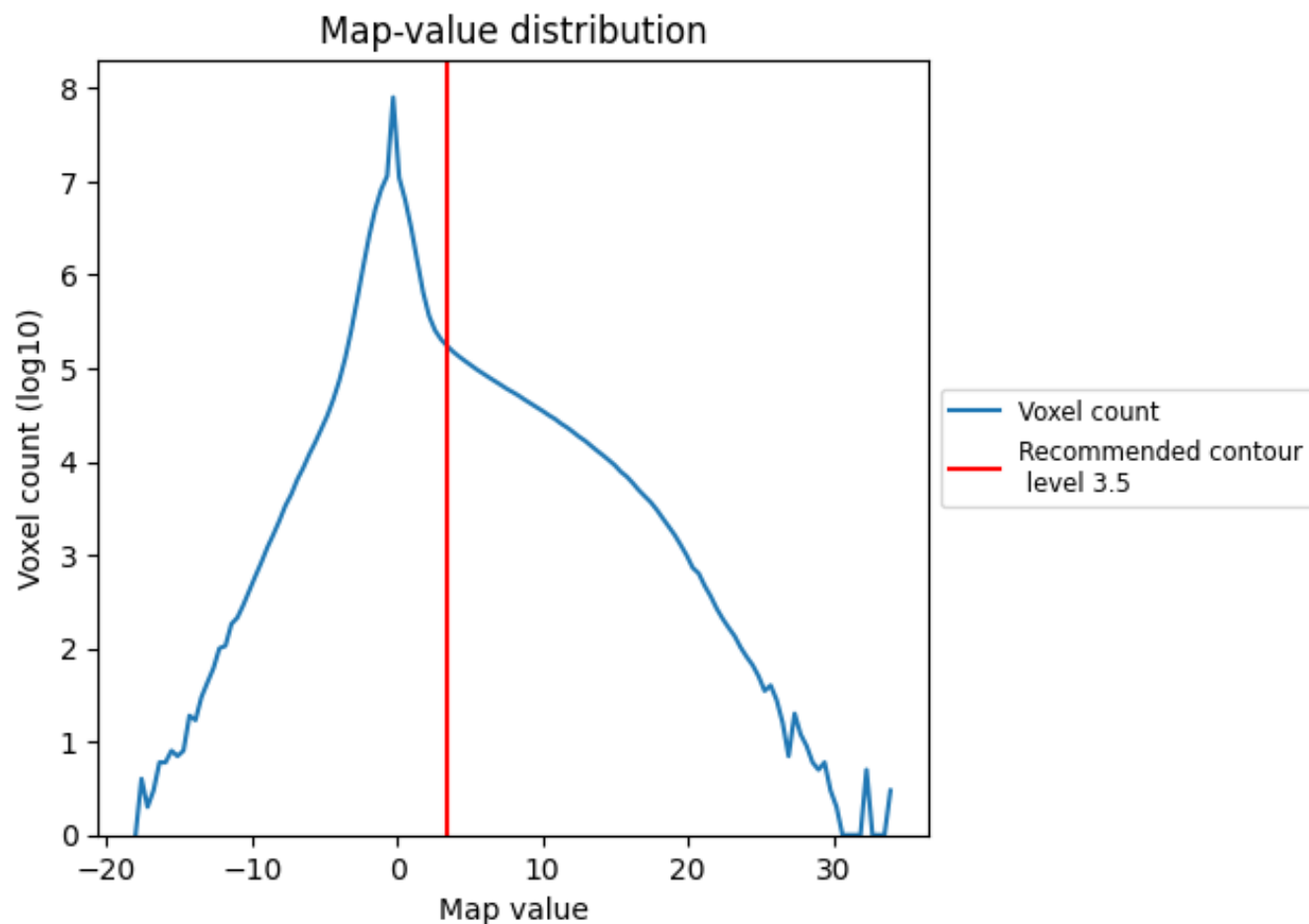
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

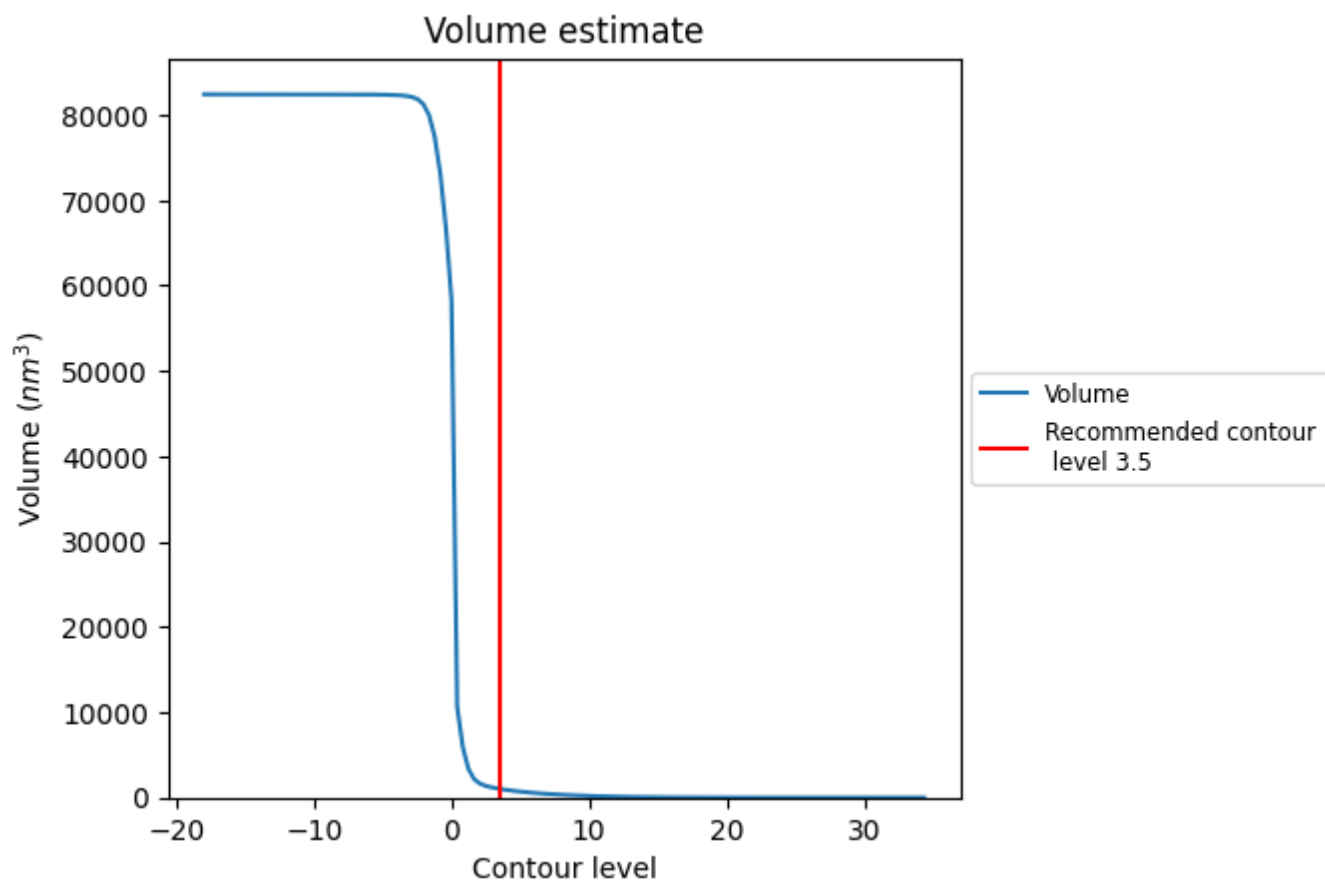
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

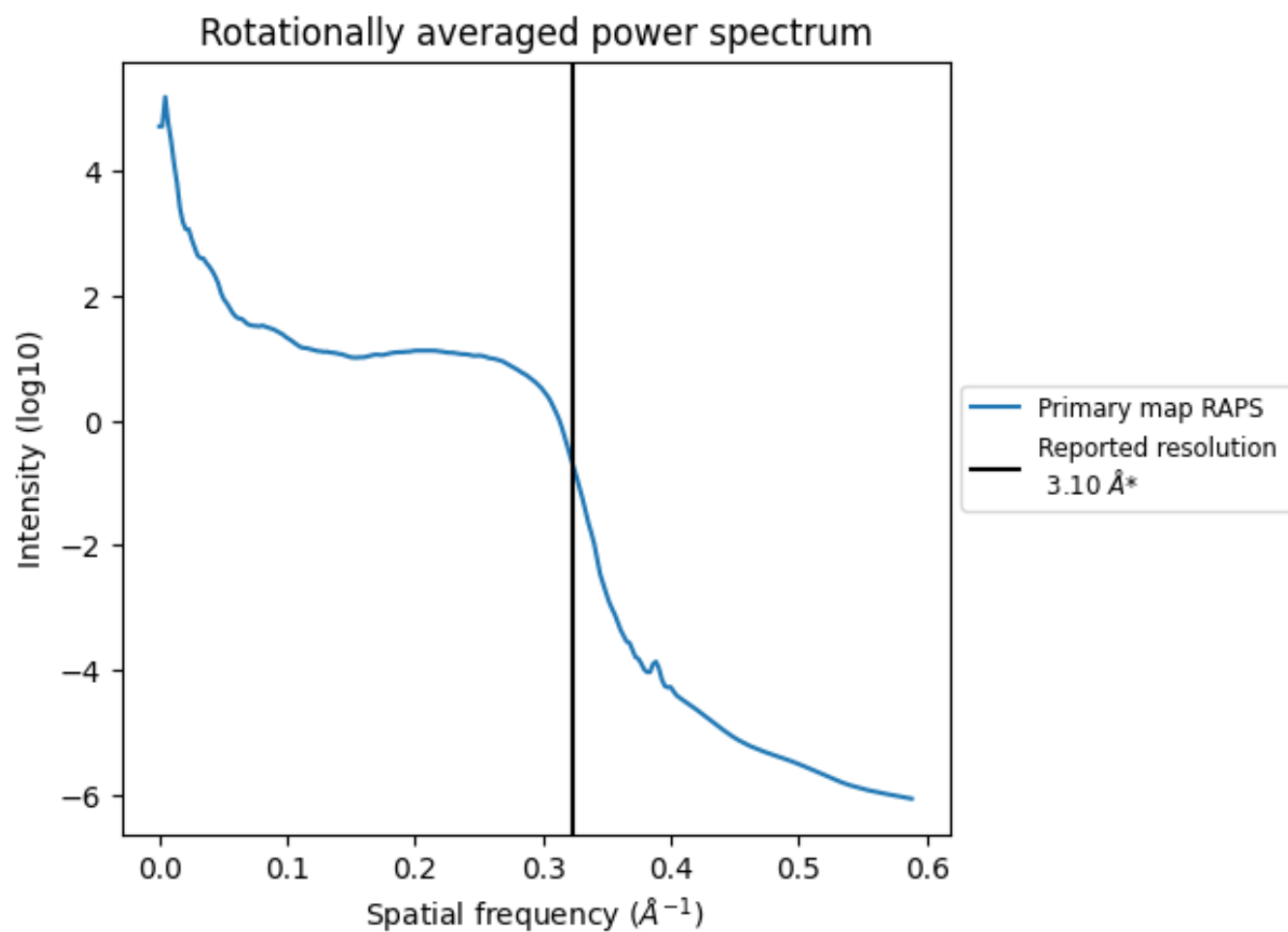
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1018 nm^3 ; this corresponds to an approximate mass of 919 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

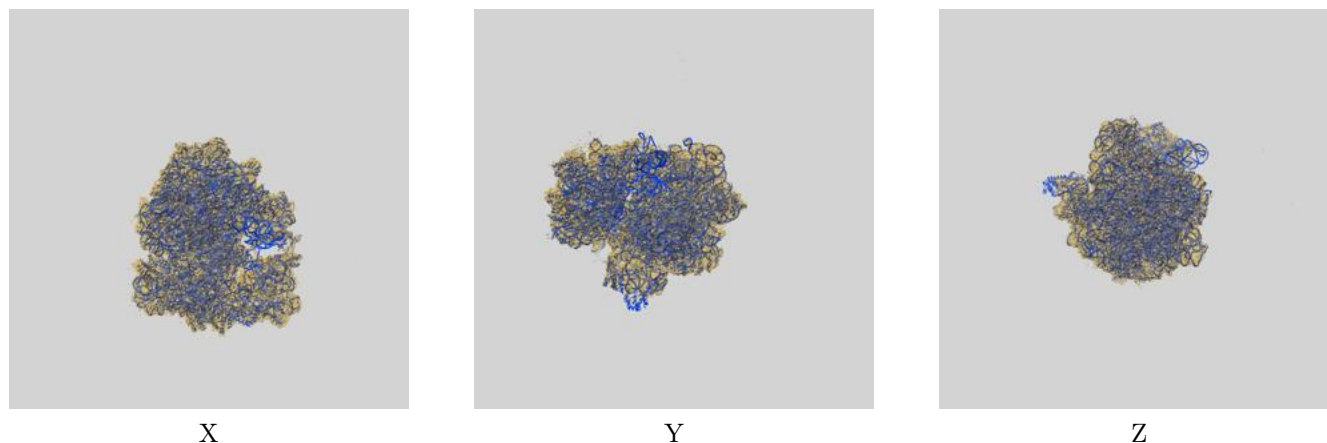
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

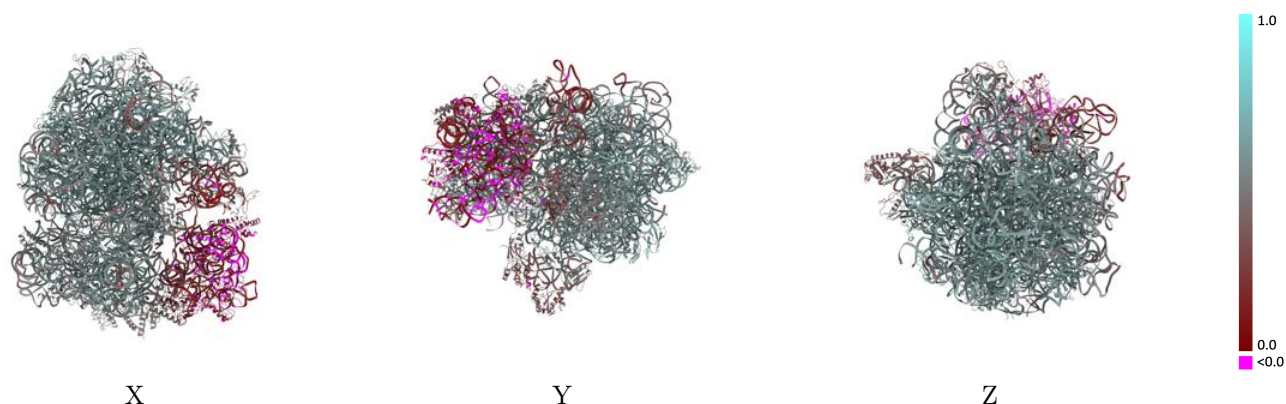
This section contains information regarding the fit between EMDB map EMD-42571 and PDB model 8UU8. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

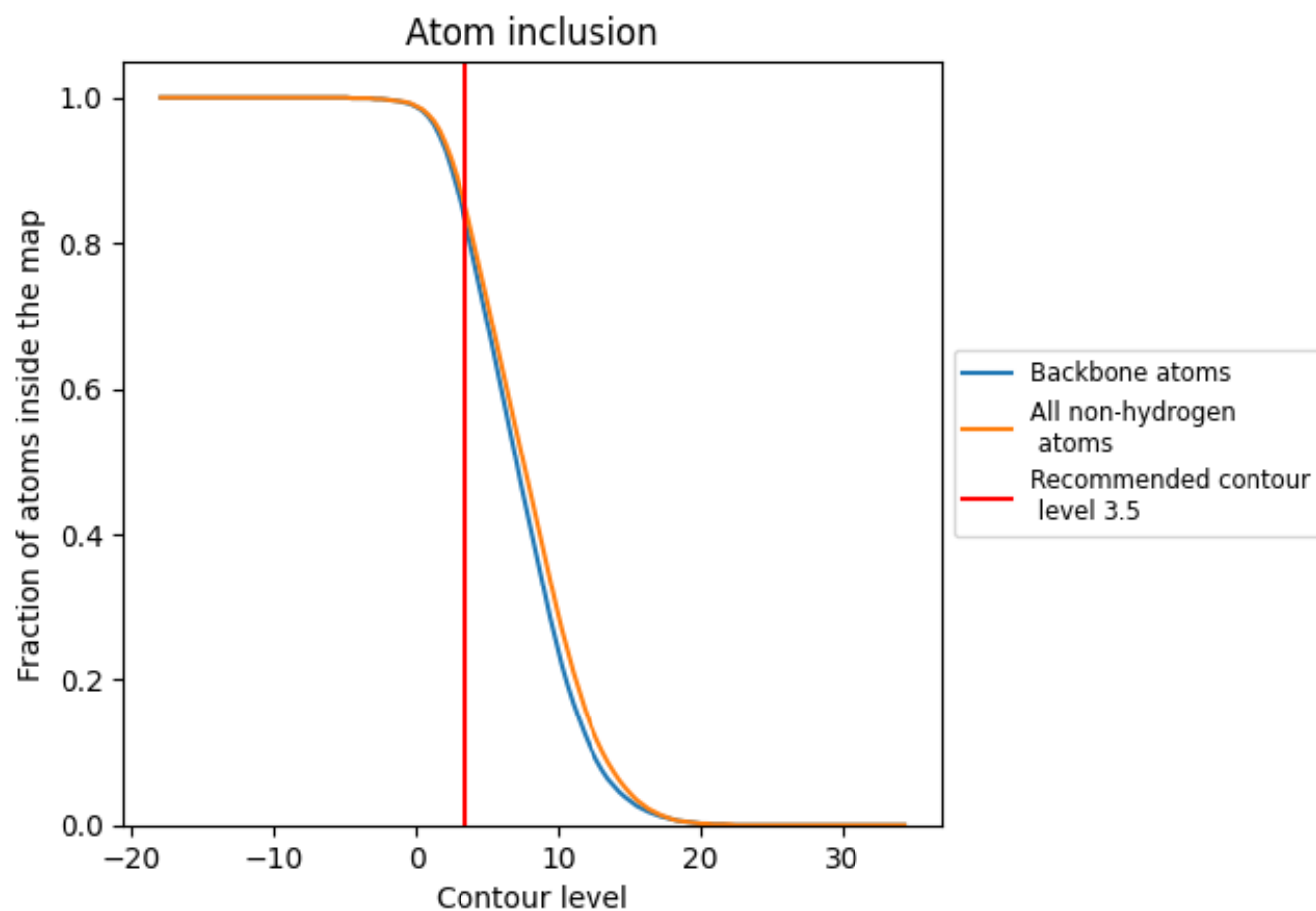


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.4960
1	 0.8590	 0.5500
2	 0.8820	 0.5800
3	 0.3020	 0.2860
4	 0.8910	 0.5710
5	 0.8390	 0.5660
6	 0.9360	 0.6050
7	 0.9240	 0.6010
8	 0.8910	 0.5920
A	 0.9200	 0.5500
B	 0.9080	 0.4850
C	 0.8710	 0.5900
D	 0.8960	 0.5870
E	 0.8740	 0.5700
F	 0.5140	 0.4000
G	 0.6820	 0.4780
H	 0.3860	 0.3430
I	 0.1510	 0.3370
L	 0.9260	 0.5950
M	 0.8450	 0.5760
N	 0.8600	 0.5600
O	 0.8680	 0.5810
P	 0.8770	 0.5780
Q	 0.7450	 0.5010
R	 0.8400	 0.5760
S	 0.9230	 0.5940
T	 0.9200	 0.5940
U	 0.8840	 0.5870
V	 0.8720	 0.5720
W	 0.7820	 0.5250
Y	 0.9120	 0.5890
Z	 0.8730	 0.5650
a	 0.8410	 0.4110
b	 0.6710	 0.4360
c	 0.5490	 0.1920



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Chain	Atom inclusion	Q-score
d	 0.8700	 0.5170
e	 0.8670	 0.5350
f	 0.7060	 0.4520
g	 0.3860	 0.0340
h	 0.8590	 0.5290
i	 0.6450	 0.1130
j	 0.6020	 0.0820
k	 0.7420	 0.4800
l	 0.8530	 0.5560
m	 0.4170	 0.1220
n	 0.6900	 0.0940
o	 0.7910	 0.5200
p	 0.8960	 0.5470
q	 0.8040	 0.5060
r	 0.8750	 0.5140
s	 0.2050	 0.0830
t	 0.8370	 0.5190
v	 0.7140	 0.4890
w	 0.3630	 0.3800
x	 0.1390	 0.3140