



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 12:42 AM UTC

PDB ID : 8UU4 / pdb_00008uu4
EMDB ID : EMD-42554
Title : Cryo-EM structure of the *Listeria innocua* 70S ribosome in complex with HPF (structure I-A)
Authors : Seely, S.M.; Basu, R.S.; Gagnon, M.G.
Deposited on : 2023-10-31
Resolution : 3.00 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

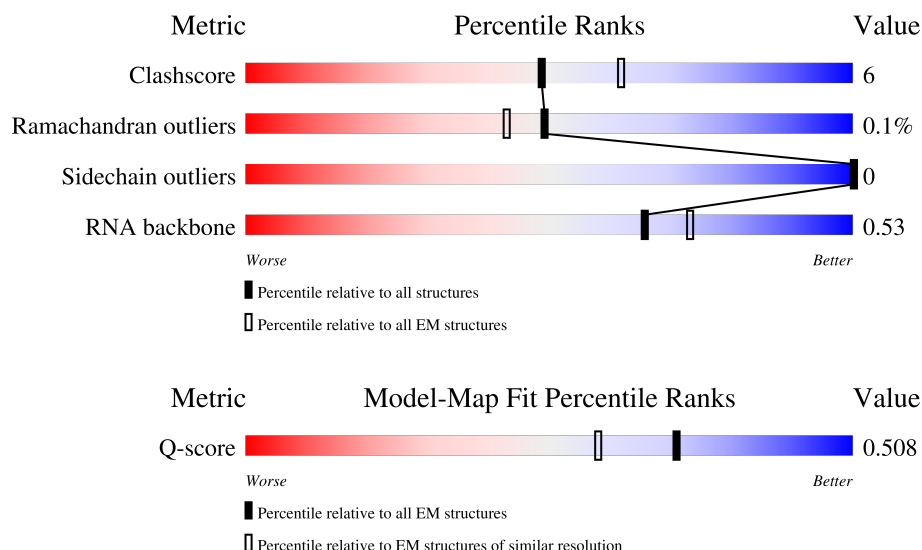
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



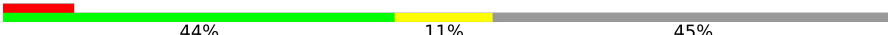
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	 63% 29% 5% .
2	b	249	 72% 17% 11%
3	c	218	 68% 26% 6%

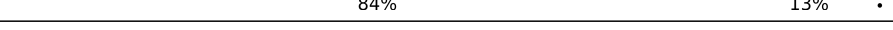
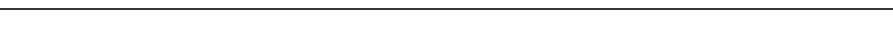
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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	167	
6	f	97	
7	g	156	
8	h	132	
9	i	130	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	90	
17	q	87	
18	r	79	
19	s	92	
20	t	84	
21	w	187	
22	A	2932	
23	B	116	
24	C	277	
25	D	209	
26	E	207	
27	F	179	
28	G	178	

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Mol	Chain	Length	Quality of chain
29	L	145	 90% 9% .
30	M	122	 89% 11%
31	N	146	 81% 19%
32	O	144	 80% 13% 7%
33	P	135	 79% 11% 10%
34	Q	119	 90% 10%
35	R	114	 87% 12% .
36	S	119	 92% 7% .
37	T	102	 92% 7% .
38	U	118	 77% 17% 6%
39	V	94	 90% 7% .
40	W	103	 75% 21% .
41	Y	96	 66% 14% 21%
42	Z	62	 84% 13% .
43	1	63	 81% 14% 5%
44	2	59	 83% 12% 5%
45	3	81	 81% 15% ..
46	4	57	 75% 18% 7%
47	5	49	 76% 22% .
48	6	44	 82% 18%
49	7	66	 88% 9% .
50	8	37	 76% 22% .

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 139761 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	221	Total	C	N	O	S	0	0
			1709	1087	301	314	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	204	Total	C	N	O	S	0	0
			1583	988	297	295	3		

- 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
			1499	938	282	277	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	156	Total	C	N	O	S	0	0
			1146	719	210	215	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	94	Total	C	N	O	S	0	0
			786	497	137	150	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	154	Total	C	N	O	S	0	0
			1167	728	220	210	9		

- 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	126	Total	C	N	O	S	0	0
			960	605	188	166	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	96	Total	C	N	O	S	0	0
			699	440	127	131	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			841	517	162	159	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	134	Total	C	N	O	S	0	0
			1040	645	209	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	109	Total	C	N	O	S	0	0
			767	471	155	140	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			490	313	97	75	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	86	Total	C	N	O	S	0	0
			722	448	145	127	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
			711	450	132	126	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
			656	413	123	119	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	65	Total	C	N	O	S	0	0
			527	339	96	90	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	81	Total	C	N	O	S	0	0
			634	406	117	109	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	82	Total	C	N	O	S	0	0
			624	378	127	118	1		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	102	Total	C	N	O	S	0	0
			847	536	150	160	1		

- Molecule 22 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	A	2903	Total	C	N	O	P	0	0
			62360	27830	11535	20092	2903		

- Molecule 23 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	273	Total	C	N	O	S	0	0
			2108	1307	415	379	7		

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	206	Total	C	N	O	S	0	0
			1583	995	291	293	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	204	Total	C	N	O		0	0
			1560	988	287	285			

- Molecule 27 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	174	Total	C	N	O	S	0	0
			1283	812	221	245	5		

- Molecule 28 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	172	Total	C	N	O	S	0	0
			1316	828	242	245	1		

- Molecule 29 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	143	Total	C	N	O	S	0	0
			1128	715	205	205	3		

- Molecule 30 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	122	Total	C	N	O	S	0	0
			925	573	175	172	5		

- Molecule 31 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	146	Total	C	N	O	S	0	0
			1112	687	216	208	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O	134	Total	C	N	O	S	0	0
			1063	680	206	171	6		

- Molecule 33 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	119	Total	C	N	O	S	0	0
			900	555	176	168	1		

- Molecule 35 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R	113	Total	C	N	O	S	0	0
			909	573	181	154	1		

- Molecule 36 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S	117	Total	C	N	O	S	0	0
			944	599	186	155	4		

- Molecule 37 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	T	101	Total	C	N	O	S	0	0
			785	506	134	144	1		

- Molecule 38 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	U	111	Total	C	N	O		0	0
			855	539	161	155			

- Molecule 39 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	92	Total	C	N	O	S	0	0
			751	477	131	140	3		

- Molecule 40 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	W	99	Total	C	N	O	S	0	0
			752	476	139	134	3		

- Molecule 41 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Y	76	Total	C	N	O	S	0	0
			585	357	114	113	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	60	Total	C	N	O	S	0	0
			467	289	98	78	2		

- Molecule 43 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1	60	Total	C	N	O	S	0	0
			495	304	95	95	1		

- Molecule 44 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	56	Total	C	N	O	S	0	0
			433	272	82	78	1		

- Molecule 45 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	79	Total	C	N	O	S	0	0
			491	308	89	93	1		

- Molecule 46 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	4	53	Total	C	N	O	S	0	0
			425	259	87	74	5		

- Molecule 47 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	48	Total	C	N	O	S	0	0
			408	248	82	74	4		

- Molecule 48 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	6	44	Total	C	N	O	S	0	0
			370	225	89	54	2		

- Molecule 49 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	64	Total	C	N	O	S	0	0
			520	322	114	79	5		

- Molecule 50 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	36	Total	C	N	O	S	0	0
			292	183	59	44	6		

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	a	167	Total	Mg	0
			167	167	
51	A	280	Total	Mg	0
			280	280	
51	B	1	Total	Mg	0
			1	1	
51	C	1	Total	Mg	0
			1	1	

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	n	1	Total	Zn	0
			1	1	
52	4	1	Total	Zn	0
			1	1	
52	5	1	Total	Zn	0
			1	1	
52	8	1	Total	Zn	0
			1	1	

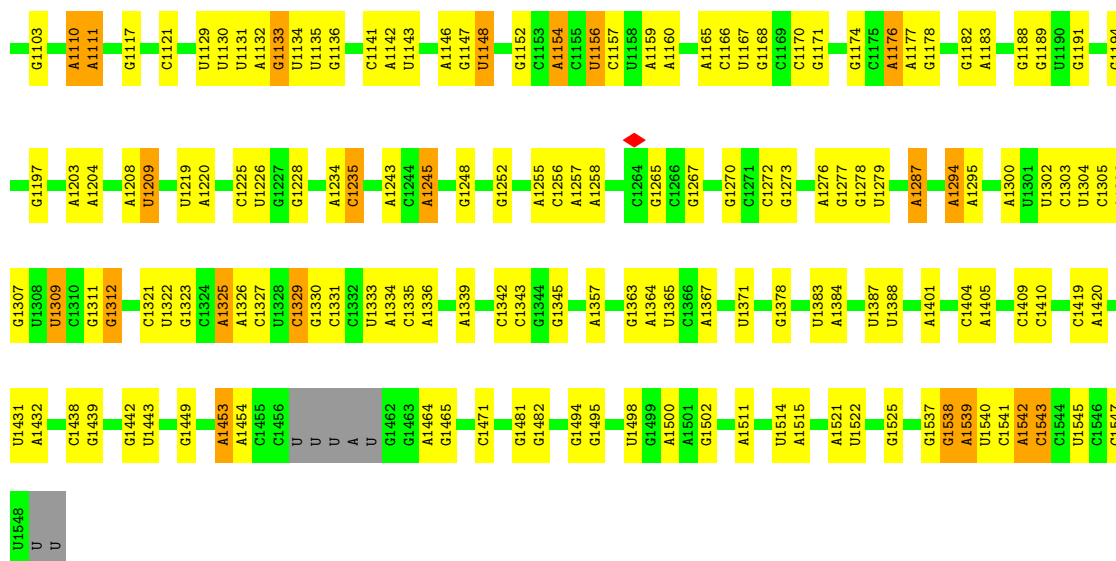
- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	a	47	Total	O	0
			47	47	
53	d	1	Total	O	0
			1	1	
53	t	1	Total	O	0
			1	1	

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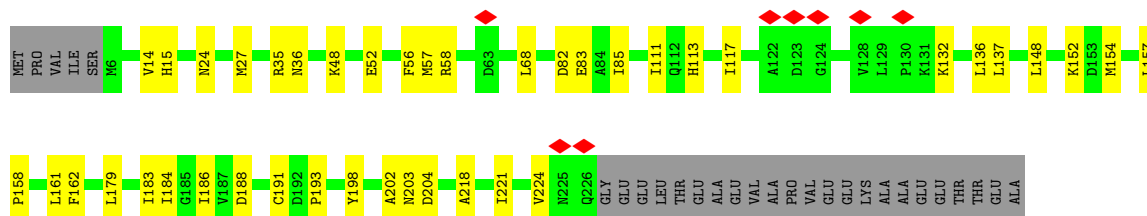
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Mol	Chain	Residues	Atoms		AltConf
53	A	80	Total 80	O 80	0
53	E	1	Total 1	O 1	0
53	N	1	Total 1	O 1	0
53	3	1	Total 1	O 1	0
53	6	1	Total 1	O 1	0



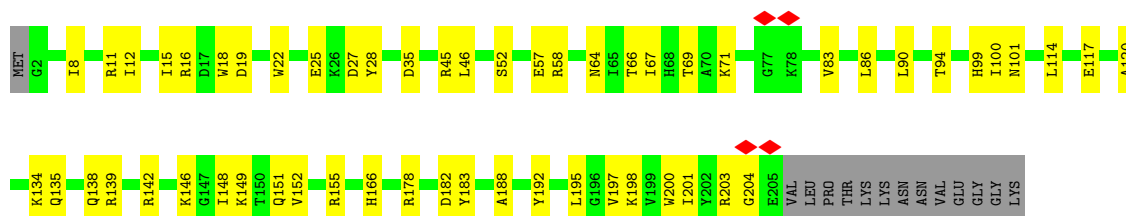
• Molecule 2: Small ribosomal subunit protein uS2

Chain b: 72% 17% 11%



• Molecule 3: Small ribosomal subunit protein uS3

Chain c: 68% 26% 6%

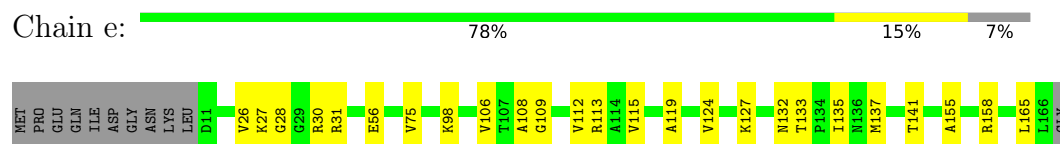


• Molecule 4: Small ribosomal subunit protein uS4

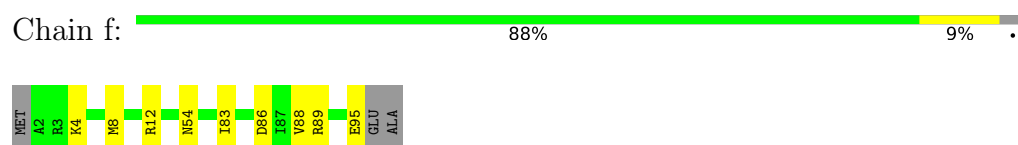
Chain d: 79% 20%



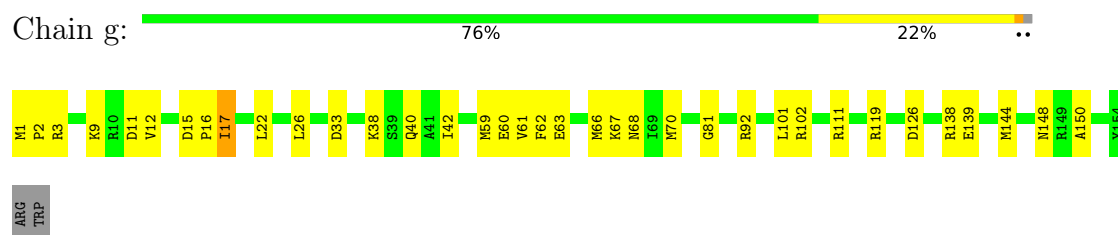
- Molecule 5: Small ribosomal subunit protein uS5



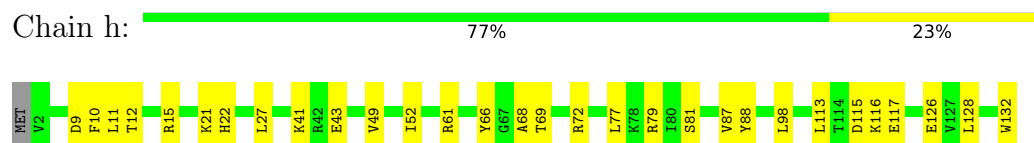
- Molecule 6: Small ribosomal subunit protein bS6



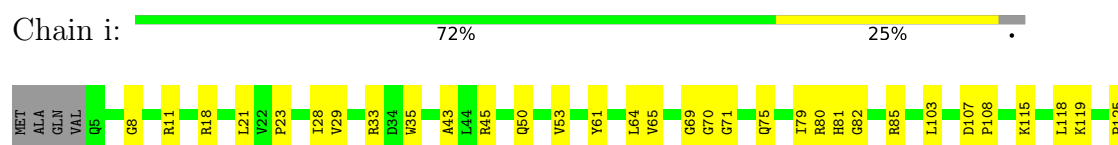
- Molecule 7: Small ribosomal subunit protein uS7



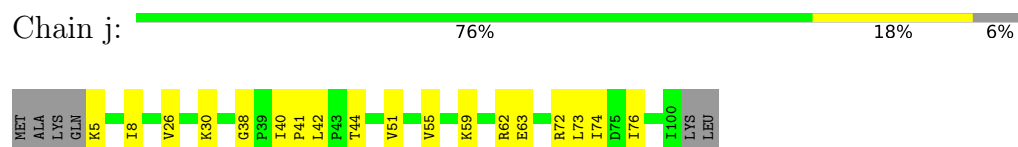
- Molecule 8: Small ribosomal subunit protein uS8



- Molecule 9: Small ribosomal subunit protein uS9

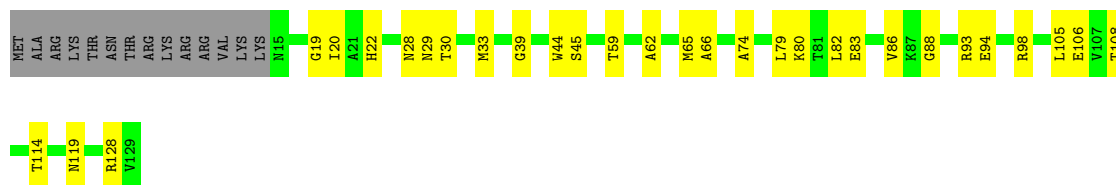


- Molecule 10: Small ribosomal subunit protein uS10



- Molecule 11: Small ribosomal subunit protein uS11

Chain k:  66% 23% 11%



- Molecule 12: Small ribosomal subunit protein uS12

Chain l:  77% 21% .



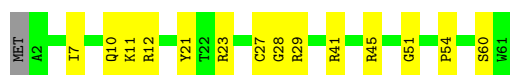
- Molecule 13: Small ribosomal subunit protein uS13

Chain m:  70% 20% 10%



- Molecule 14: Small ribosomal subunit protein uS14

Chain n:  75% 23% .



- Molecule 15: Small ribosomal subunit protein uS15

Chain o:  82% 15% .



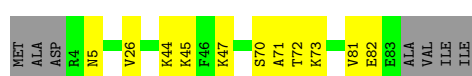
- Molecule 16: Small ribosomal subunit protein bS16

Chain p:  69% 29% .



- Molecule 17: Small ribosomal subunit protein uS17

Chain q:  79% 13% 8%



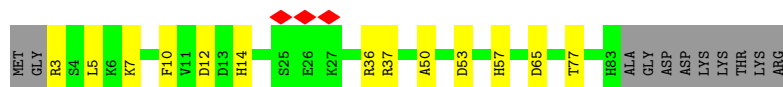
- Molecule 18: Small ribosomal subunit protein bS18

Chain r: 



- Molecule 19: Small ribosomal subunit protein uS19

Chain s: 

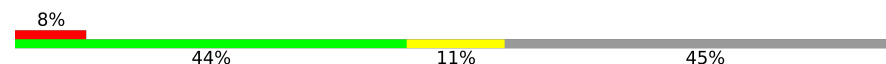


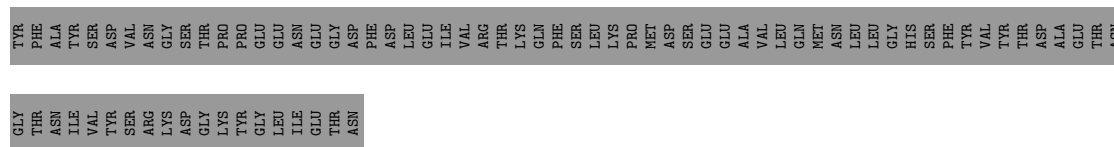
- Molecule 20: Small ribosomal subunit protein bS20

Chain t: 



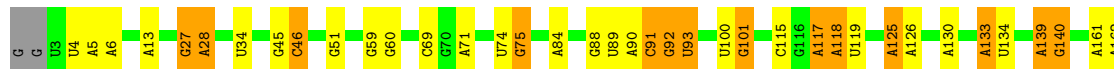
- Molecule 21: Ribosome hibernation promoting factor

Chain w: 

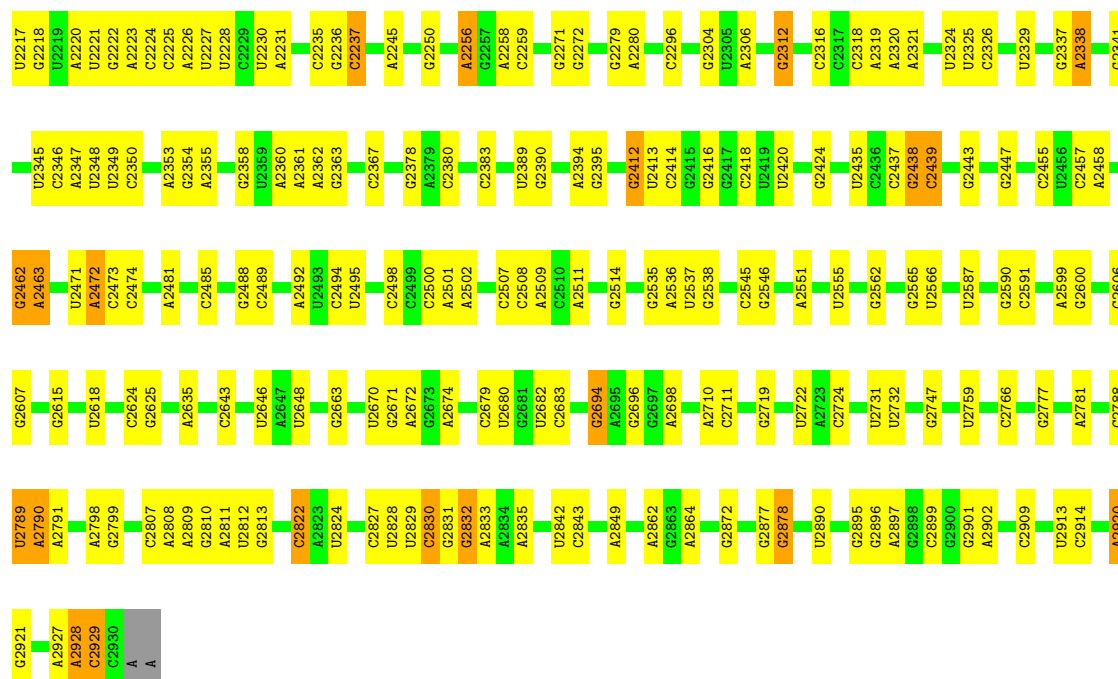


- Molecule 22: 23S Ribosomal RNA

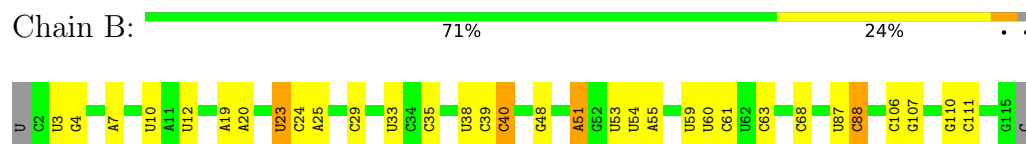
Chain A: 



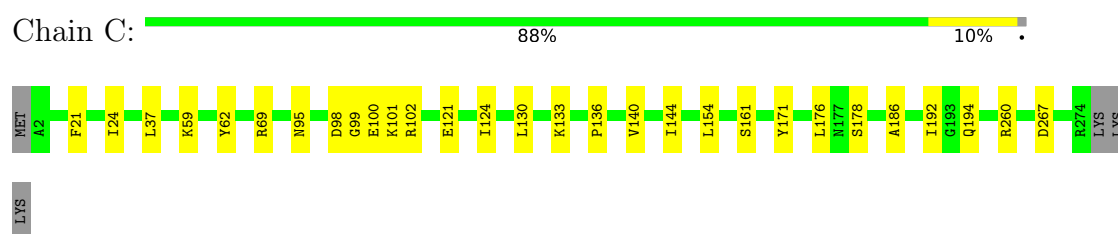
G534	G535	A536	G539	A550	U553	C554	C555	A558	U566	G567	G575	U576	A577	G578	U579	U580	A591	A592	U593	G594	U597	G598	G606	G613	G616	A617	A618	A629	G630	U631	U632	A633	U637	U638	A646	A657	A658	A659	A660	A661	G665	C666	G667																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A672	G679	C680	G681	A682	G683	U684	C685	U686	G687	A688	A689	U690	A700	U703	A704	C717	C718	C719	G720	U732	U733	G746	A756	A757	G758	A761	G775	U776	C786	A789	C790	G791	U792	U793	G794	G799	G809	A810	G811	A860	G821	G824	C830	A828																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
A829	U830	U831	C832	C833	A834	A835	U836	C837	G838	G847	C851	C852	U853	G854	G855	C858	U859	C860	A865	C871	U872	U873	U874	A875	G878	C879	U880	G890	U891	A892	A893	A894	G895	G896	G905	G906	C923	U924	A925	G926	G927	G928	G929	C930	C931																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
C932	U	C	U	C	U	C	G	G939	G940	U941	U942	A943	C944	C945	G946	A947	U948	U949	U950	C951	A957	A958	C959	G963	A964	A970	U971	G972	U973	A974	C975	U976	U979	A980	A987	G992	A993	C994	A1003	G1005	G1007	C1010	G1015	U1016	U1017	C1017	G1018	A1019	A1020	A1025	A1026																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
A1029	G1030	A1036	A1039	G1040	A1041	A1042	A1046	A1047	C1051	A1055	U1058	A1059	A1067	G1068	A1072	A1073	U1079	G1080	U1081	G972	U1087	U1090	U1091	A1092	G1093	A1094	C1095	A1100	G1101	G1102	A1103	U1104	G1105	U1106	U1107	G1108	G1109	G1110	U1111	U1112	A1113	G1114	A1115	G1117	C1121																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
C1122	A1123	C1124	C1125	A1126	U1127	U1128	U1129	A1130	A1131	A1132	G1133	A1134	G1135	U1136	G1137	C1138	G1139	U1140	A1141	A1142	U1143	A1144	G1145	U1151	G1152	G1153	U1154	C1155	G1156	A1157	G1158	U1159	G1160	A1161	C1162	C1163	G1171	U1178	A1179	C1180	C1181	G1182	G1185	C1186	U1187	A1188	C1199	A1203	C1216																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
U	C	U	U	C	G	A	G1225	G1230	U1234	U1245	U1249	A1249	G1250	C1253	G1254	G1257	A1265	G1268	U1283	U1294	G1295	A1298	G1301	C1302	G1309	U1310	G1311	G1316	A1317	G1320	C1328	C1333	U1336	U1337	A1344	A1345	A1352	G1353	U1362	U1363	U1364	U1365	U1366	U1367	U1368	U1369	U1370	U1371	U1372	U1373	U1374	U1375	U1376	U1377	U1378	U1379	U1380	U1381	U1382	U1383	U1384	U1385	U1386	U1387	U1388	U1389	U1390	U1391	U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453	U1454	U1455	U1456	U1457	U1458	U1459	U1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	U1468	U1469	U1470	U1471	U1472	U1473	U1474	U1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494	U1495	U1496	U1497	U1498	U1499	U1500	U1501	U1502	U1503	U1504	U1505	U1506	U1507	U1508	U1509	U1510	U1511	U1512	U1513	U1514	U1515	U1516	U1517	U1518	U1519	U1520	U1521	U1522	U1523	U1524	U1525	U1526	U1527	U1528	U1529	U1530	U1531	U1532	U1533	U1534	U1535	U1536	U1537	U1538	U1539	U1540	U1541	U1542	U1543	U1544	U1545	U1546	U1547	U1548	U1549	U1550	U1551	U1552	U1553	U1554	U1555	U1556	U1557	U1558	U1559	U1560	U1561	U1562	U1563	U1564	U1565	U1566	U1567	U1568	U1569	U1570	U1571	U1572	U1573	U1574	U1575	U1576	U1577	U1578	U1579	U1580	U1581	U1582	U1583	U1584	U1585	U1586	U1587	U1588	U1589	U1590	U1591	U1592	U1593	U1594	U1595	U1596	U1597	U1598	U1599	U1600	U1601	U1602	U1603	U1604	U1605	U1606	U1607	U1608	U1609	U1610	U1611	U1612	U1613	U1614	U1615	U1616	U1617	U1618	U1619	U1620	U1621	U1622	U1623	U1624	U1625	U1626	U1627	U1628	U1629	U1630	U1631	U1632	U1633	U1634	U1635	U1636	U1637	U1638	U1639	U1640	U1641	U1642	U1643	U1644	U1645	U1646	U1647	U1648	U1649	U1650	U1651	U1652	U1653	U1654	U1655	U1656	U1657	U1658	U1659	U1660	U1661	U1662	U1663	U1664	U1665	U1666	U1667	U1668	U1669	U1670	U1671	U1672	U1673	U1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1682	U1683	U1684	U1685	U1686	U1687	U1688	U1689	U1690	U1691	U1692	U1693	U1694	U1695	U1696	U1697	U1698	U1699	U1700	U1701	U1702	U1703	U1704	U1705	U1706	U1707	U1708	U1709	U1710	U1711	U1712	U1713	U1714	U1715	U1716	U1717	U1718	U1719	U1720	U1721	U1722	U1723	U1724	U1725	U1726	U1727	U1728	U1729	U1730	U1731	U1732	U1733	U1734	U1735	U1736	U1737	U1738	U1739	U1740	U1741	U1742	U1743	U1744	U1745	U1746	U1747	U1748	U1749	U1750	U1751	U1752	U1753	U1754	U1755	U1756	U1757	U1758	U1759	U1760	U1761	U1762	U1763	U1764	U1765	U1766	U1767	U1768	U1769	U1770	U1771	U1772	U1773	U1774	U1775	U1776	U1777	U1778	U1779	U1780	U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	U1790	U1791	U1792	U1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	U1801	U1802	U1803	U1804	U1805	U1806	U1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1831	U1832	U1833	U1834	U1835	U1836	U1837	U1838	U1839	U1840	U1841	U1842	U1843	U1844	U1845	U1846	U1847	U1848	U1849	U1850	U1851	U1852	U1853	U1854	U1855	U1856	U1857	U1858	U1859	U1860	U1861	U1862	U1863	U1864	U1865	U1866	U1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875	U1876	U1877	U1878	U1879	U1880	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1901	U1902	U1903	U1904	U1905	U1906	U1907	U1908	U1909	U1910	U1911	U1912	U1913	U1914	U1915	U1916	U1917	U1918	U1919	U1920	U1921	U1922	U1923	U1924	U1925	U1926	U1927	U1928	U1929	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938	U1939	U1940	U1941	U1942	U1943	U1944	U1945	U1946	U1947	U1948	U1949	U1950	U1951	U1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1967	U1968	U1969	U1970	U1971	U1972	U1973	U1974	U1975	U1976	U1977	U1978	U1979	U1980	U1981	U1982	U1983	U1984	U1985	U1986	U1987	U1988	U1989	U1990	U1991	U1992	U1993	U1994	U1995	U1996	U1997	U1998	U1999	U2000	U2001	U2002	U2003	U2004	U2005	U2006	U2007	U2008	U2009	U2010	U2011	U2012	U2013	U2014	U2015	U2016	U2017	U2018	U2019	U2020	U2021	U2022	U2023	U2024	U2025	U2026	U2027	U2028	U2029	U2030	U2031	U2032	U2033	U2034	U2035	U2036	U2037	U2038	U2039	U2040	U2041	U2042	U2043	U2044	U2045	U2046	U2047	U2048	U2049	U2050	U2051	U2052	U2053	U2054	U2055	U2056	U2057	U2058	U2059	U2060	U2061	U2062	U2063	U2064	U2065	U2066	U2067	U2068	U2069	U2070	U2071	U2072	U2073	U2074	U2075	U2076	U2077	U2078	U2079	U2080	U2081	U2082	U2083	U2084	U2085	U2086	U2087	U2088	U2089	U2090	U2091	U2092	U2093	U2094	U2095	U2096	U2097	U2098	U2099	U2100	U2101	U2102	U2103	U2104	U2105	U2106	U2107	U2108	U2109	U2110	U2111	U2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2120	U2121	U2122	U2123	U2124	U2125	U2126	U2127	U2128	U2129	U2130	U2131	U2132	U2133	U2134	U2135	U2136	U2137	U2138	U2139	U2140	U2141	U2142	U2143	U2144	U2145	U2146	U2147	U2148	U2149	U2150	U2151	U2152	U2153	U2154	U2155	U2156	U2157	U2158	U2159	U2160	U2161	U2162	U2163	U2164	U2165	U2166	U2167	U2168	U2169	U2170	U2171	U2172	U2173	U2174	U2175	U2176	U2177	U2178	U2179	U2180	U2181	U2182	U2183	U2184	U2185	U2186	U2187	U2188	U2189	U2190	U2191	U2192	U2193	U2194	U2195	U2196	U2197	U2198	U2199	U2200	U2201	U2202	U2203	U2204	U2205	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2213	U2214	U2215	U2216	U2217	U2218	U2219	U2220	U2221	U2222	U2223	U2224	U2225	U2226	U2227	U2228	U2229	U2230	U2231	U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2241	U2242	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2259	U2260	U2261	U2262	U2263	U2264	U2265	U2266	U2267	U2268	U2269	U2270	U2271	U2272	U2273	U2274	U2275	U2276	U2277	U2278	U2279	U2280	U2281	U2282	U2283	U2284	U2285	U2286	U2287	U2288	U2289	U2290	U2291	U2292	U2293	U2294	U2295	U2296	U2297	U2298	U2299	U2300	U2301	U2302	U2303	U2304	U2305	U2306	U2307	U2308



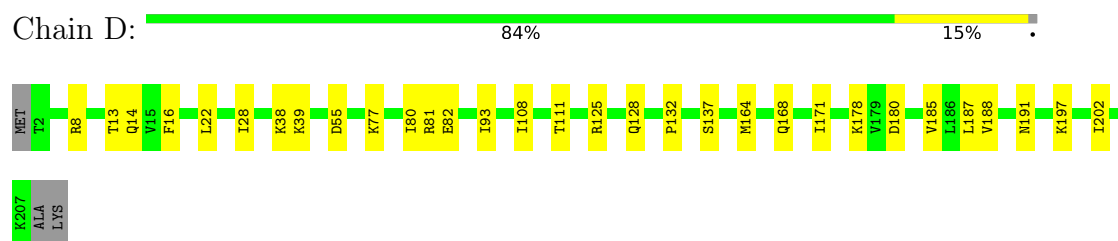
• Molecule 23: 5S Ribosomal RNA



• Molecule 24: Large ribosomal subunit protein uL2



• Molecule 25: Large ribosomal subunit protein uL3



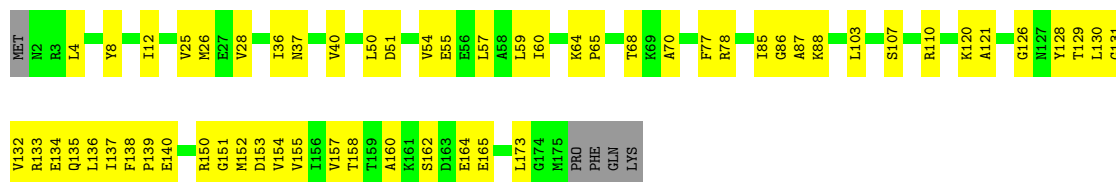
• Molecule 26: Large ribosomal subunit protein uL4





- Molecule 27: Large ribosomal subunit protein uL5

Chain F: 65% 32% .



- Molecule 28: Large ribosomal subunit protein uL6

Chain G: 75% 21% .



- Molecule 29: Large ribosomal subunit protein uL13

Chain L: 90% 9% .



- Molecule 30: Large ribosomal subunit protein uL14

Chain M: 89% 11% .



- Molecule 31: Large ribosomal subunit protein uL15

Chain N: 81% 19% .

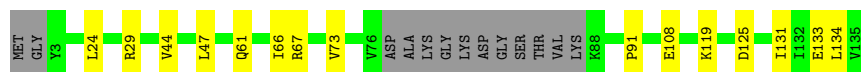
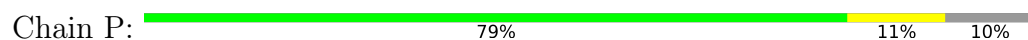


- Molecule 32: Large ribosomal subunit protein uL16

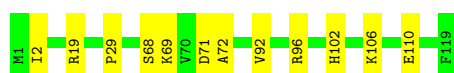
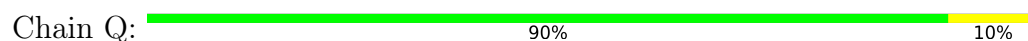
Chain O: 80% 13% 7% .



- Molecule 33: Large ribosomal subunit protein bL17



- Molecule 34: Large ribosomal subunit protein uL18



- Molecule 35: Large ribosomal subunit protein bL19



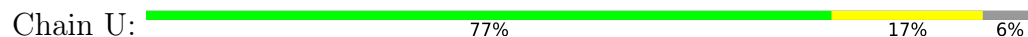
- Molecule 36: Large ribosomal subunit protein bL20



- Molecule 37: Large ribosomal subunit protein bL21



- Molecule 38: Large ribosomal subunit protein uL22



- Molecule 39: Large ribosomal subunit protein uL23





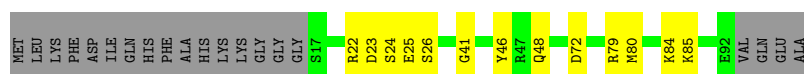
- Molecule 40: Large ribosomal subunit protein uL24

Chain W: 75% 21% .



- Molecule 41: Large ribosomal subunit protein bL27

Chain Y: 66% 14% 21%



- Molecule 42: Large ribosomal subunit protein bL28

Chain Z: 84% 13% .



- Molecule 43: Large ribosomal subunit protein uL29

Chain 1: 81% 14% 5%



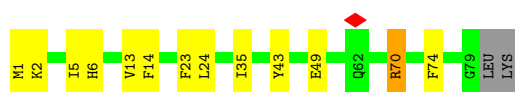
- Molecule 44: Large ribosomal subunit protein uL30

Chain 2: 83% 12% 5%



- Molecule 45: Large ribosomal subunit protein bL31B

Chain 3: 81% 15% ..



- Molecule 46: Large ribosomal subunit protein bL32

Chain 4: 75% 18% 7%



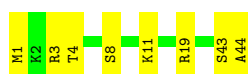
- Molecule 47: Large ribosomal subunit protein bL33

Chain 5: 76% 22% .



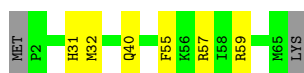
- Molecule 48: Large ribosomal subunit protein bL34

Chain 6: 82% 18%



- Molecule 49: Large ribosomal subunit protein bL35

Chain 7: 88% 9% .



- Molecule 50: Large ribosomal subunit protein bL36

Chain 8: 76% 22% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	303270	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	1.498	Depositor
Minimum map value	-0.520	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.078	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.20	0/36403	0.28	0/56778
2	b	0.16	0/1736	0.37	0/2341
3	c	0.15	0/1608	0.33	0/2173
4	d	0.16	0/1526	0.30	0/2065
5	e	0.19	0/1159	0.30	0/1565
6	f	0.21	0/798	0.39	0/1069
7	g	0.14	0/1182	0.33	0/1591
8	h	0.20	0/1035	0.32	0/1392
9	i	0.13	0/978	0.29	0/1321
10	j	0.13	0/709	0.24	0/962
11	k	0.16	0/855	0.31	0/1155
12	l	0.19	0/1056	0.36	0/1418
13	m	0.13	0/773	0.29	0/1046
14	n	0.16	0/500	0.33	0/664
15	o	0.19	0/732	0.29	0/980
16	p	0.18	0/724	0.31	0/970
17	q	0.16	0/665	0.33	0/889
18	r	0.20	0/535	0.27	0/716
19	s	0.13	0/650	0.24	0/878
20	t	0.16	0/627	0.28	0/835
21	w	0.17	0/859	0.40	0/1157
22	A	0.32	0/69865	0.34	0/108989
23	B	0.19	0/2711	0.24	0/4224
24	C	0.36	0/2144	0.44	0/2875
25	D	0.34	0/1605	0.42	0/2156
26	E	0.30	0/1580	0.37	0/2129
27	F	0.18	0/1298	0.39	0/1758
28	G	0.16	0/1338	0.34	0/1807
29	L	0.29	0/1151	0.31	0/1546
30	M	0.31	0/932	0.38	0/1248
31	N	0.29	0/1123	0.38	0/1492
32	O	0.25	0/1085	0.29	0/1449

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	P	0.31	0/993	0.40	0/1328
34	Q	0.17	0/908	0.31	0/1214
35	R	0.30	0/921	0.35	0/1234
36	S	0.34	0/957	0.37	0/1273
37	T	0.30	0/798	0.38	0/1071
38	U	0.30	0/865	0.36	0/1170
39	V	0.29	0/760	0.44	0/1017
40	W	0.20	0/762	0.29	0/1017
41	Y	0.28	0/592	0.38	0/788
42	Z	0.32	0/472	0.34	0/626
43	1	0.21	0/496	0.33	0/662
44	2	0.28	0/436	0.38	0/585
45	3	0.11	0/498	0.30	0/681
46	4	0.34	0/433	0.44	0/577
47	5	0.23	0/412	0.32	0/551
48	6	0.37	0/373	0.39	0/486
49	7	0.32	0/527	0.42	0/685
50	8	0.26	0/295	0.48	0/387
All	All	0.27	0/151440	0.33	0/226990

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32515	0	16371	299	0
2	b	1709	0	1688	28	0
3	c	1583	0	1560	35	0
4	d	1499	0	1419	35	0
5	e	1146	0	1202	15	0
6	f	786	0	780	8	0
7	g	1167	0	1183	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	h	1022	0	1078	19	0
9	i	960	0	965	25	0
10	j	699	0	656	14	0
11	k	841	0	848	23	0
12	l	1040	0	1108	18	0
13	m	767	0	722	19	0
14	n	490	0	525	12	0
15	o	722	0	747	9	0
16	p	711	0	740	16	0
17	q	656	0	687	8	0
18	r	527	0	566	6	0
19	s	634	0	624	10	0
20	t	624	0	659	7	0
21	w	847	0	878	14	0
22	A	62360	0	31356	463	0
23	B	2428	0	1229	18	0
24	C	2108	0	2184	23	0
25	D	1583	0	1646	16	0
26	E	1560	0	1653	18	0
27	F	1283	0	1269	49	0
28	G	1316	0	1352	26	0
29	L	1128	0	1158	9	0
30	M	925	0	982	7	0
31	N	1112	0	1162	21	0
32	O	1063	0	1137	13	0
33	P	982	0	1043	14	0
34	Q	900	0	922	10	0
35	R	909	0	982	8	0
36	S	944	0	1016	7	0
37	T	785	0	823	6	0
38	U	855	0	914	16	0
39	V	751	0	786	4	0
40	W	752	0	823	14	0
41	Y	585	0	586	10	0
42	Z	467	0	509	5	0
43	1	495	0	515	6	0
44	2	433	0	479	6	0
45	3	491	0	359	10	0
46	4	425	0	423	8	0
47	5	408	0	422	11	0
48	6	370	0	422	6	0
49	7	520	0	571	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	8	292	0	334	6	0
51	A	280	0	0	0	0
51	B	1	0	0	0	0
51	C	1	0	0	0	0
51	a	167	0	0	0	0
52	4	1	0	0	0	0
52	5	1	0	0	0	0
52	8	1	0	0	0	0
52	n	1	0	0	0	0
53	3	1	0	0	0	0
53	6	1	0	0	0	0
53	A	80	0	0	0	0
53	E	1	0	0	0	0
53	N	1	0	0	0	0
53	a	47	0	0	2	0
53	d	1	0	0	1	0
53	t	1	0	0	0	0
All	All	139761	0	92063	1300	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1300) 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)
22:A:1763:U:H3	22:A:1778:A:N6	1.52	1.06
22:A:1580:A:H62	22:A:1594:G:N2	1.55	1.04
22:A:1580:A:N6	22:A:1594:G:H21	1.58	1.01
1:a:418:G:H21	1:a:440:A:H62	0.96	0.94
22:A:419:U:HO2'	22:A:420:A:H8	0.95	0.94
23:B:53:U:H1'	27:F:26:MET:HE1	1.48	0.93
1:a:418:G:N2	1:a:440:A:H62	1.68	0.91
1:a:849:U:H3	1:a:854:G:H1	0.95	0.90
26:E:6:LEU:HD21	26:E:127:GLU:HB3	1.58	0.86
1:a:467:U:H3	1:a:482:G:H1	0.85	0.84
1:a:187:U:H3	1:a:202:G:H1	0.88	0.83
22:A:1087:U:H3	22:A:1160:G:H1	1.25	0.83
1:a:418:G:H21	1:a:440:A:N6	1.75	0.83
1:a:1270:G:H1	1:a:1279:U:H3	1.25	0.81
1:a:218:U:H2'	1:a:219:U:H2'	1.63	0.81
22:A:1580:A:H62	22:A:1594:G:H21	0.83	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:74:LEU:HD22	16:p:79:ILE:HD11	1.64	0.80
38:U:16:ARG:O	38:U:16:ARG:NH1	2.18	0.77
38:U:14:THR:H	38:U:107:HIS:HD2	1.32	0.77
1:a:1156:U:H1'	9:i:18:ARG:HH21	1.50	0.76
5:e:132:ASN:HA	5:e:137:MET:HE3	1.68	0.76
22:A:929:G:H1	22:A:941:U:H3	1.34	0.76
22:A:1106:U:H4'	22:A:1107:U:H2'	1.67	0.76
22:A:1132:A:O2'	22:A:1133:G:N7	2.19	0.76
1:a:158:G:H2'	1:a:159:A:H5''	1.67	0.75
22:A:2424:G:O2'	22:A:2462:G:N2	2.19	0.75
1:a:1047:A:H2'	1:a:1048:A:H8	1.51	0.74
2:b:184:ILE:HG22	2:b:198:TYR:HB2	1.69	0.74
22:A:928:G:O6	22:A:942:U:O2	2.06	0.74
22:A:2166:G:N2	22:A:2190:G:O2'	2.20	0.74
31:N:87:ASP:HB3	31:N:119:LYS:HB2	1.68	0.74
31:N:19:VAL:HG23	31:N:27:ASN:HB3	1.69	0.74
3:c:35:ASP:OD1	3:c:58:ARG:NH2	2.20	0.74
25:D:125:ARG:HG3	25:D:164:MET:HG3	1.68	0.74
27:F:40:VAL:HG22	27:F:86:GLY:H	1.52	0.73
47:5:19:THR:HG22	47:5:20:THR:H	1.54	0.73
1:a:412:G:N7	4:d:3:ARG:NH1	2.37	0.72
5:e:158:ARG:HH21	8:h:43:GLU:HB3	1.55	0.71
4:d:100:ARG:HD2	4:d:162:PRO:HG2	1.71	0.71
22:A:125:A:H5''	48:6:19:ARG:HG3	1.73	0.71
1:a:839:U:O2'	1:a:1547:C:OP1	2.09	0.71
28:G:27:LYS:NZ	28:G:28:GLY:O	2.24	0.71
7:g:60:GLU:O	7:g:62:PHE:N	2.23	0.70
22:A:228:A:O2'	22:A:231:A:N6	2.24	0.70
22:A:1130:A:N3	22:A:1151:U:O2'	2.24	0.70
22:A:1253:C:HO2'	22:A:1254:G:H8	1.39	0.70
46:4:30:CYS:HB3	46:4:33:CYS:HB2	1.72	0.70
48:6:43:SER:OG	48:6:44:ALA:N	2.24	0.70
2:b:35:ARG:NH2	2:b:36:ASN:O	2.25	0.69
40:W:9:VAL:HG13	40:W:68:VAL:HG13	1.74	0.69
22:A:2318:C:OP2	47:5:2:ARG:NH2	2.25	0.69
24:C:260:ARG:NH1	24:C:267:ASP:OD1	2.24	0.69
22:A:2927:A:N1	22:A:2928:A:N6	2.41	0.69
40:W:13:THR:OG1	40:W:67:ASN:ND2	2.23	0.69
22:A:2345:U:O2	27:F:37:ASN:ND2	2.25	0.69
1:a:412:G:OP2	4:d:115:ASN:ND2	2.25	0.69
3:c:146:LYS:NZ	3:c:204:GLY:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:942:G:N7	7:g:2:PRO:HG3	2.07	0.69
22:A:2196:A:OP1	22:A:2204:A:O2'	2.09	0.69
22:A:2338:A:N3	27:F:133:ARG:NH2	2.41	0.69
22:A:1114:G:N2	22:A:1141:A:O3'	2.26	0.68
3:c:138:GLN:OE1	3:c:142:ARG:NH2	2.26	0.68
22:A:1763:U:O4	22:A:1778:A:N7	2.26	0.68
22:A:2134:G:H1	22:A:2221:U:H3	1.39	0.68
1:a:726:A:H5'	11:k:119:ASN:HB2	1.75	0.68
2:b:117:ILE:HD12	2:b:137:LEU:HD11	1.75	0.68
22:A:419:U:O2'	22:A:420:A:H8	1.72	0.68
27:F:40:VAL:HG21	27:F:50:LEU:HD13	1.76	0.68
1:a:681:G:H2'	1:a:682:G:C8	2.28	0.68
1:a:1002:G:O2'	1:a:1003:A:N7	2.26	0.68
22:A:84:A:N6	22:A:101:G:O2'	2.27	0.68
31:N:124:LYS:HB3	31:N:146:ILE:HD11	1.76	0.68
31:N:55:LEU:O	31:N:60:ARG:NH1	2.26	0.67
26:E:148:VAL:HG12	26:E:191:LYS:HD3	1.76	0.67
3:c:152:VAL:HG22	3:c:197:VAL:HG12	1.77	0.67
1:a:224:U:O2'	1:a:476:C:N4	2.27	0.67
1:a:1024:G:N2	1:a:1225:C:O2	2.27	0.67
22:A:487:U:O2'	26:E:46:GLN:NE2	2.28	0.67
25:D:28:ILE:HD13	25:D:202:ILE:HD11	1.75	0.67
22:A:2167:A:H2'	22:A:2168:G:H8	1.59	0.67
1:a:194:C:N4	17:q:5:ASN:O	2.28	0.67
1:a:555:A:OP2	4:d:3:ARG:NH2	2.28	0.67
6:f:83:ILE:HD11	24:C:124:ILE:HG13	1.77	0.67
22:A:1295:G:OP2	31:N:21:ARG:NH1	2.27	0.67
1:a:1133:G:N2	1:a:1134:U:O4	2.19	0.66
22:A:2167:A:N6	22:A:2190:G:N3	2.43	0.66
38:U:64:GLU:HB2	38:U:71:ILE:HD11	1.76	0.66
22:A:1087:U:O2	22:A:1160:G:N2	2.24	0.66
1:a:691:G:N2	11:k:39:GLY:O	2.29	0.66
26:E:23:VAL:HA	26:E:111:LYS:HD2	1.76	0.66
9:i:28:ILE:HB	9:i:35:TRP:CD1	2.30	0.66
9:i:35:TRP:HZ3	9:i:45:ARG:HD3	1.60	0.66
22:A:1117:G:N2	22:A:1137:G:OP2	2.26	0.66
1:a:499:A:H2'	1:a:500:A:H8	1.60	0.66
9:i:65:VAL:HG21	9:i:79:ILE:HD11	1.76	0.66
22:A:789:A:O2'	22:A:1708:U:OP1	2.13	0.66
35:R:22:PRO:HA	35:R:47:VAL:HG23	1.77	0.66
3:c:148:ILE:HD13	3:c:201:ILE:HG12	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:14:ARG:NH1	13:m:42:ASP:OD1	2.29	0.65
22:A:1253:C:O2'	22:A:1254:G:H8	1.78	0.65
5:e:108:ALA:HB1	5:e:112:VAL:HG13	1.79	0.64
22:A:1812:U:OP2	22:A:1817:A:N6	2.30	0.64
2:b:58:ARG:HH22	2:b:224:VAL:HB	1.62	0.64
22:A:274:A:H62	22:A:295:G:H21	1.43	0.64
1:a:519:C:H1'	4:d:36:HIS:HE1	1.62	0.64
46:4:37:ARG:NH1	46:4:38:LEU:O	2.30	0.64
1:a:72:G:N2	1:a:94:A:O2'	2.29	0.64
22:A:665:G:H4'	22:A:666:A:H5'	1.80	0.64
22:A:879:C:O2'	49:7:57:ARG:NH1	2.31	0.64
2:b:157:LEU:HD21	2:b:179:LEU:HD21	1.79	0.64
22:A:311:A:H2'	22:A:312:U:H5''	1.80	0.64
22:A:2173:G:H1	22:A:2184:U:H3	1.43	0.64
1:a:1404:C:OP2	5:e:30:ARG:NH2	2.31	0.63
11:k:94:GLU:OE2	11:k:98:ARG:NH2	2.32	0.63
1:a:962:G:O6	13:m:103:LYS:NZ	2.32	0.63
7:g:144:MET:HE3	7:g:148:ASN:HD21	1.64	0.63
22:A:2438:G:O2'	22:A:2439:C:OP2	2.15	0.63
1:a:159:A:H8	1:a:159:A:OP1	1.81	0.63
1:a:383:U:O2	16:p:29:ARG:NH1	2.32	0.63
1:a:437:U:OP2	4:d:29:ARG:NH2	2.29	0.63
22:A:2177:G:O2'	22:A:2180:A:N6	2.31	0.63
27:F:110:ARG:NH2	45:3:49:GLU:OE1	2.32	0.63
1:a:499:A:H2'	1:a:500:A:C8	2.34	0.63
22:A:2043:G:H5''	38:U:47:SER:HB3	1.79	0.63
22:A:1579:A:N6	22:A:1595:G:O2'	2.31	0.63
22:A:2256:A:OP1	24:C:171:TYR:OH	2.16	0.63
8:h:11:LEU:HD12	8:h:77:LEU:HB3	1.80	0.63
22:A:2361:A:H2'	22:A:2362:A:C8	2.34	0.63
1:a:1245:A:OP1	1:a:1342:C:O2'	2.11	0.62
3:c:155:ARG:NH1	3:c:192:TYR:O	2.32	0.62
22:A:199:A:N6	22:A:2463:A:O2'	2.32	0.62
1:a:722:G:H2'	1:a:723:A:C8	2.35	0.62
1:a:1384:A:OP2	7:g:9:LYS:NZ	2.32	0.62
8:h:41:LYS:HD3	8:h:49:VAL:HG12	1.81	0.62
36:S:43:TYR:HB3	37:T:74:TYR:HB3	1.80	0.62
6:f:54:ASN:HD22	6:f:88:VAL:HG23	1.63	0.62
1:a:1182:G:H2'	1:a:1183:A:H8	1.64	0.62
7:g:111:ARG:NH2	7:g:126:ASP:OD2	2.33	0.62
22:A:1072:A:OP2	22:A:1180:C:O2'	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1112:U:H3	22:A:1115:A:H8	1.47	0.62
2:b:52:GLU:O	2:b:56:PHE:N	2.26	0.62
27:F:8:TYR:HA	27:F:12:ILE:HD13	1.81	0.62
33:P:47:LEU:HD21	33:P:66:ILE:HD11	1.80	0.62
27:F:64:LYS:HD3	45:3:5:ILE:HD12	1.82	0.62
22:A:1253:C:O2'	22:A:1254:G:O5'	2.17	0.62
22:A:2296:C:N4	41:Y:23:ASP:OD1	2.32	0.62
22:A:2471:U:O3'	22:A:2472:A:H3'	2.00	0.62
27:F:25:VAL:O	27:F:28:VAL:HG12	2.00	0.62
1:a:660:U:O4	1:a:760:G:O2'	2.15	0.61
30:M:63:VAL:HG23	30:M:106:LEU:HD11	1.82	0.61
10:j:51:VAL:HG13	14:n:41:ARG:HB2	1.82	0.61
22:A:1094:A:H1'	22:A:1158:G:H21	1.65	0.61
10:j:26:VAL:HG12	10:j:30:LYS:HZ2	1.65	0.61
1:a:147:G:O2'	1:a:1453:A:N3	2.30	0.61
1:a:1007:C:H2'	1:a:1008:C:H5''	1.82	0.61
1:a:1157:C:OP1	9:i:11:ARG:NH1	2.34	0.61
4:d:87:MET:HE1	4:d:191:GLU:HB3	1.82	0.61
23:B:38:U:O4	45:3:1:MET:N	2.32	0.61
1:a:38:G:H22	1:a:405:A:H5'	1.64	0.61
22:A:2182:C:H2'	22:A:2183:A:C8	2.36	0.61
4:d:115:ASN:ND2	53:d:301:HOH:O	2.30	0.61
22:A:2152:A:N6	22:A:2203:G:N7	2.48	0.61
22:A:2214:G:H2'	22:A:2215:G:C8	2.36	0.61
11:k:74:ALA:HB1	11:k:79:LEU:HD21	1.82	0.61
2:b:48:LYS:NZ	2:b:52:GLU:OE2	2.34	0.61
21:w:29:GLU:OE2	21:w:35:THR:OG1	2.18	0.61
1:a:849:U:O2	1:a:854:G:N2	2.24	0.60
27:F:54:VAL:HG13	27:F:65:PRO:HG2	1.83	0.60
1:a:1442:G:H2'	1:a:1443:U:C6	2.37	0.60
1:a:959:U:H2'	1:a:960:G:H8	1.65	0.60
12:l:91:SER:OG	12:l:116:ASP:OD2	2.19	0.60
50:8:16:VAL:HG22	50:8:25:VAL:HG12	1.83	0.60
1:a:17:U:H2'	1:a:18:C:C6	2.36	0.60
22:A:2318:C:H5	47:5:2:ARG:HH12	1.49	0.60
2:b:161:LEU:HB2	2:b:183:ILE:HG22	1.82	0.60
22:A:929:G:O2'	22:A:930:C:OP1	2.19	0.60
9:i:35:TRP:CZ3	9:i:45:ARG:HD3	2.36	0.60
16:p:5:ILE:HG22	16:p:22:VAL:HG22	1.84	0.60
22:A:1456:A:H2'	22:A:1457:A:C8	2.35	0.60
28:G:55:PRO:HD2	28:G:61:HIS:HE1	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:60:LEU:HB2	21:w:63:LEU:HB3	1.84	0.60
15:o:26:GLU:HA	15:o:81:LEU:HD11	1.84	0.59
26:E:13:ASN:OD1	26:E:14:ALA:N	2.36	0.59
1:a:1471:C:OP1	35:R:109:ARG:NH1	2.34	0.59
22:A:1530:G:H3'	22:A:1531:U:H5''	1.83	0.59
22:A:1763:U:H3	22:A:1778:A:H62	0.69	0.59
3:c:99:HIS:NE2	3:c:101:ASN:OD1	2.35	0.59
22:A:1151:U:H2'	22:A:1152:G:H8	1.66	0.59
22:A:2545:C:H5''	25:D:128:GLN:OE1	2.02	0.59
22:A:1897:U:OP1	22:A:2443:G:O2'	2.20	0.59
27:F:103:LEU:HA	27:F:107:SER:HB3	1.84	0.59
22:A:859:U:H2'	22:A:860:C:C6	2.38	0.59
1:a:409:C:O2'	1:a:629:A:N3	2.33	0.59
1:a:467:U:O4	1:a:482:G:O6	2.20	0.59
1:a:1159:A:HO2'	1:a:1160:A:H8	1.50	0.59
28:G:17:VAL:HG12	28:G:26:VAL:HG22	1.84	0.59
31:N:76:ILE:HG23	31:N:112:LEU:HD23	1.85	0.59
1:a:1255:A:H4'	9:i:33:ARG:HH22	1.68	0.59
22:A:1139:G:N2	22:A:1145:G:O6	2.36	0.58
1:a:187:U:O4	1:a:202:G:O6	2.21	0.58
1:a:1225:C:H2'	1:a:1226:U:C6	2.38	0.58
8:h:113:LEU:HD13	8:h:117:GLU:HB2	1.85	0.58
10:j:8:ILE:HB	10:j:74:ILE:HB	1.83	0.58
1:a:199:C:H2'	1:a:200:A:H8	1.67	0.58
1:a:847:G:H2'	1:a:848:G:H8	1.67	0.58
1:a:193:G:H2'	1:a:194:C:H5''	1.85	0.58
1:a:682:G:H2'	1:a:683:A:H8	1.67	0.58
1:a:721:G:H2'	1:a:722:G:C8	2.38	0.58
1:a:1050:G:H2'	1:a:1051:U:C6	2.39	0.58
1:a:1194:G:H21	14:n:60:SER:HB3	1.68	0.58
1:a:1387:U:O2'	7:g:1:MET:HA	2.03	0.58
13:m:86:TYR:OH	13:m:90:ARG:NH2	2.33	0.58
22:A:2125:G:H4'	22:A:2126:G:H5'	1.85	0.58
12:l:24:LEU:O	12:l:40:SER:OG	2.22	0.58
22:A:1248:A:H2'	22:A:1249:A:C8	2.39	0.58
22:A:2502:A:N6	22:A:2514:G:O2'	2.37	0.58
1:a:959:U:H2'	1:a:960:G:C8	2.39	0.58
7:g:26:LEU:HD13	7:g:101:LEU:HD22	1.85	0.58
22:A:2511:A:OP2	50:8:2:LYS:NZ	2.33	0.58
27:F:50:LEU:O	27:F:54:VAL:HG23	2.04	0.58
8:h:15:ARG:NH1	8:h:77:LEU:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:B:3:U:H2'	23:B:4:G:H8	1.68	0.58
1:a:1322:U:O2'	1:a:1367:A:N3	2.37	0.57
19:s:3:ARG:HG3	19:s:10:PHE:HB2	1.86	0.57
22:A:926:G:H2'	22:A:927:G:H8	1.69	0.57
22:A:2319:A:H61	47:5:19:THR:HG21	1.69	0.57
1:a:212:G:H2'	1:a:213:A:H8	1.68	0.57
1:a:1131:U:O4	1:a:1132:A:N6	2.37	0.57
1:a:1012:G:H3'	1:a:1035:C:H5	1.69	0.57
1:a:1159:A:H5''	10:j:44:THR:HG23	1.85	0.57
22:A:1685:U:H2'	22:A:1686:C:C6	2.39	0.57
1:a:870:G:HO2'	1:a:883:G:HO2'	1.51	0.57
1:a:1011:U:H2'	1:a:1012:G:H1'	1.86	0.57
3:c:151:GLN:HB3	3:c:166:HIS:HB3	1.86	0.57
22:A:1090:U:O2'	22:A:1157:A:N1	2.33	0.57
22:A:2217:U:H2'	22:A:2218:G:C8	2.39	0.57
42:Z:58:LYS:HG3	42:Z:59:VAL:H	1.69	0.57
9:i:81:HIS:CE1	9:i:85:ARG:HH21	2.22	0.57
22:A:1245:U:H1'	36:S:4:VAL:HG22	1.86	0.57
22:A:1549:G:N2	24:C:98:ASP:O	2.35	0.57
1:a:1419:C:H2'	1:a:1420:A:C8	2.39	0.57
21:w:31:TYR:O	21:w:93:LYS:NZ	2.38	0.57
1:a:947:A:N3	1:a:1383:U:O2'	2.32	0.57
22:A:1136:U:H2'	22:A:1137:G:C8	2.40	0.57
24:C:133:LYS:HB3	24:C:186:ALA:HB1	1.86	0.57
33:P:29:ARG:HE	33:P:131:ILE:HD11	1.70	0.57
4:d:101:LEU:HD22	4:d:167:PHE:HB2	1.87	0.57
12:l:67:ARG:NH1	12:l:77:THR:OG1	2.38	0.57
22:A:2184:U:H2'	22:A:2185:A:C8	2.40	0.57
5:e:115:VAL:HG21	5:e:141:THR:HG21	1.86	0.57
22:A:1812:U:H5	22:A:1817:A:N7	2.03	0.57
22:A:2182:C:H2'	22:A:2183:A:H8	1.70	0.57
25:D:178:LYS:HE3	25:D:187:LEU:HD22	1.87	0.57
1:a:1080:C:H2'	1:a:1081:G:H8	1.69	0.56
22:A:591:A:H4'	22:A:592:A:H5'	1.86	0.56
1:a:1146:A:N6	1:a:1148:U:O2'	2.38	0.56
50:8:11:CYS:SG	50:8:13:LYS:HG2	2.45	0.56
1:a:953:G:N1	1:a:1345:G:OP2	2.23	0.56
1:a:1021:G:O6	1:a:1027:A:N6	2.38	0.56
1:a:1256:C:O2'	9:i:70:GLY:O	2.23	0.56
22:A:1081:U:OP1	28:G:59:LYS:NZ	2.37	0.56
22:A:2412:G:H2'	22:A:2413:U:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:46:GLU:OE2	28:G:49:GLU:N	2.39	0.56
34:Q:106:LYS:O	34:Q:110:GLU:HG2	2.05	0.56
11:k:80:LYS:HA	11:k:105:LEU:HD22	1.88	0.56
22:A:791:G:O2'	22:A:794:G:O2'	2.15	0.56
22:A:1133:G:H2'	22:A:1135:G:H4'	1.86	0.56
22:A:1700:G:HO2'	22:A:1701:A:H8	1.53	0.56
24:C:161:SER:HB3	24:C:194:GLN:HG3	1.86	0.56
26:E:148:VAL:HG23	26:E:149:ASP:H	1.69	0.56
40:W:74:LYS:HG3	40:W:75:THR:HG23	1.87	0.56
1:a:422:A:P	1:a:436:G:H22	2.28	0.56
1:a:424:G:H2'	1:a:425:G:H8	1.70	0.56
3:c:135:GLN:HB3	3:c:139:ARG:HH12	1.71	0.56
22:A:2208:U:H2'	22:A:2209:A:H8	1.69	0.56
32:O:32:TYR:HH	32:O:111:GLU:CD	2.13	0.56
30:M:64:ARG:HG2	30:M:83:ALA:HB3	1.87	0.56
1:a:121:C:OP1	1:a:319:C:O2'	2.24	0.56
2:b:57:MET:HE2	2:b:221:ILE:HB	1.87	0.56
27:F:126:GLY:O	27:F:158:THR:OG1	2.23	0.56
22:A:1509:A:O2'	22:A:1511:G:OP2	2.24	0.56
1:a:280:C:H2'	1:a:281:A:H8	1.71	0.55
6:f:89:ARG:NH1	18:r:68:GLN:O	2.39	0.55
22:A:185:C:H2'	22:A:186:C:H5'	1.88	0.55
22:A:1151:U:H2'	22:A:1152:G:C8	2.41	0.55
22:A:1700:G:O2'	22:A:1701:A:H8	1.89	0.55
19:s:65:ASP:O	45:3:70:ARG:NH2	2.38	0.55
22:A:1482:G:H2'	22:A:1483:A:C8	2.41	0.55
22:A:1483:A:H2'	22:A:1484:A:C8	2.41	0.55
22:A:1903:U:O2'	22:A:1904:C:O2	2.17	0.55
22:A:2788:C:O2'	22:A:2789:U:O2	2.16	0.55
38:U:16:ARG:HH21	38:U:103:LYS:HD2	1.72	0.55
10:j:5:LYS:N	10:j:76:ILE:O	2.39	0.55
22:A:341:A:N3	22:A:362:C:O2'	2.37	0.55
25:D:55:ASP:OD1	25:D:77:LYS:NZ	2.38	0.55
7:g:16:PRO:HB2	7:g:17:ILE:HD12	1.87	0.55
11:k:20:ILE:HG22	11:k:83:GLU:HB3	1.89	0.55
1:a:436:G:H4'	1:a:437:U:H4'	1.89	0.55
22:A:2221:U:H2'	22:A:2222:G:H8	1.71	0.55
27:F:57:LEU:HA	27:F:60:ILE:HG22	1.88	0.55
1:a:1132:A:H4'	10:j:38:GLY:HA3	1.87	0.55
22:A:1058:U:O2'	29:L:144:ARG:NH1	2.40	0.55
22:A:1763:U:C2	22:A:1778:A:N6	2.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:B:29:C:O2'	23:B:51:A:N1	2.36	0.55
1:a:1121:C:H1'	3:c:178:ARG:HH11	1.71	0.55
1:a:1043:G:H2'	1:a:1044:G:C8	2.41	0.55
21:w:52:ALA:C	21:w:53:LYS:HD3	2.32	0.55
22:A:929:G:O6	22:A:941:U:O4	2.24	0.55
22:A:2789:U:H5	22:A:2791:A:N7	2.05	0.55
22:A:834:A:H1'	48:6:4:THR:HG21	1.89	0.55
22:A:2832:G:H2'	22:A:2833:A:H8	1.70	0.55
1:a:41:G:H2'	1:a:42:G:H8	1.72	0.54
7:g:111:ARG:HB3	7:g:119:ARG:HD2	1.89	0.54
22:A:1142:A:H2'	22:A:1143:U:O4'	2.06	0.54
22:A:2670:U:H2'	22:A:2671:G:O4'	2.07	0.54
28:G:89:LEU:HG	28:G:162:ILE:HG12	1.90	0.54
34:Q:29:PRO:HG2	34:Q:92:VAL:HG12	1.89	0.54
1:a:701:G:O2'	7:g:81:GLY:O	2.24	0.54
1:a:1273:G:N2	1:a:1276:A:OP2	2.24	0.54
1:a:1363:G:H2'	1:a:1364:A:C8	2.42	0.54
22:A:2052:U:OP2	46:4:6:ARG:NH2	2.40	0.54
2:b:24:ASN:ND2	2:b:191:CYS:O	2.31	0.54
33:P:24:LEU:HD23	33:P:44:VAL:HG21	1.88	0.54
1:a:105:G:O6	20:t:10:ARG:NH1	2.41	0.54
1:a:414:G:H21	4:d:112:GLN:HE22	1.55	0.54
22:A:1139:G:H21	22:A:1144:A:H62	1.56	0.54
22:A:2097:C:H2'	22:A:2098:C:C6	2.43	0.54
27:F:162:SER:N	27:F:165:GLU:OE2	2.40	0.54
22:A:1039:A:OP1	36:S:50:ARG:NH1	2.40	0.54
25:D:108:ILE:HD11	25:D:188:VAL:HG21	1.90	0.54
26:E:8:LYS:NZ	26:E:13:ASN:O	2.40	0.54
27:F:70:ALA:HB2	27:F:85:ILE:HD12	1.90	0.54
1:a:1014:C:H4'	1:a:1047:A:H1'	1.89	0.54
4:d:143:GLU:HA	4:d:146:ALA:HB2	1.89	0.54
22:A:419:U:O2'	22:A:420:A:O5'	2.25	0.54
22:A:1763:U:HO2'	22:A:1764:A:H8	1.54	0.54
28:G:46:GLU:OE1	28:G:47:GLY:N	2.40	0.54
28:G:154:PRO:HG3	28:G:163:ARG:HB3	1.90	0.54
1:a:1073:G:O2'	1:a:1197:G:N2	2.40	0.54
20:t:73:ARG:O	20:t:77:ARG:HG3	2.08	0.54
22:A:1103:A:OP1	22:A:1135:G:N2	2.39	0.54
22:A:1111:U:H2'	22:A:1112:U:C6	2.43	0.54
26:E:143:LEU:HD22	26:E:148:VAL:HG21	1.90	0.54
41:Y:80:MET:HE3	41:Y:84:LYS:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1170:C:H2'	1:a:1171:G:H8	1.74	0.53
1:a:1209:U:O2'	14:n:27:CYS:SG	2.66	0.53
3:c:28:TYR:OH	14:n:54:PRO:O	2.26	0.53
22:A:1716:G:O2'	22:A:2024:U:O4	2.23	0.53
22:A:2225:C:H2'	22:A:2226:A:H8	1.73	0.53
30:M:120:GLU:HG2	30:M:122:LEU:HG	1.90	0.53
1:a:1086:G:N2	1:a:1089:A:OP2	2.33	0.53
22:A:1116:A:H4'	22:A:1117:G:H5''	1.90	0.53
22:A:1172:A:H4'	22:A:1173:A:H5'	1.90	0.53
22:A:2149:G:N1	22:A:2195:A:OP1	2.42	0.53
22:A:2208:U:H2'	22:A:2209:A:C8	2.42	0.53
38:U:14:THR:H	38:U:107:HIS:CD2	2.21	0.53
1:a:1157:C:P	9:i:11:ARG:HH12	2.31	0.53
11:k:88:GLY:H	11:k:114:THR:HG22	1.72	0.53
25:D:8:ARG:NH1	25:D:197:LYS:O	2.42	0.53
22:A:2438:G:HO2'	22:A:2439:C:P	2.31	0.53
7:g:40:GLN:HE22	9:i:43:ALA:HB2	1.73	0.53
27:F:129:THR:HG23	27:F:155:VAL:HG22	1.90	0.53
31:N:94:GLU:HA	31:N:97:ILE:HG22	1.90	0.53
32:O:43:THR:HG22	32:O:94:VAL:HG12	1.90	0.53
38:U:53:GLU:OE2	38:U:57:LYS:HE3	2.08	0.53
1:a:68:G:N2	1:a:99:A:H61	2.07	0.53
2:b:14:VAL:C	2:b:15:HIS:HD1	2.17	0.53
12:l:52:THR:HG22	12:l:64:LYS:HA	1.91	0.53
27:F:133:ARG:NH2	27:F:153:ASP:OD1	2.41	0.53
39:V:6:ILE:HD11	39:V:41:ALA:HB2	1.90	0.53
2:b:111:ILE:HD12	2:b:152:LYS:HA	1.89	0.53
22:A:45:G:H5'	22:A:46:C:OP1	2.08	0.53
22:A:1459:U:H2'	22:A:1460:G:H8	1.73	0.53
1:a:1321:C:H2'	1:a:1322:U:C6	2.44	0.53
22:A:214:G:H2'	22:A:215:A:O4'	2.09	0.53
22:A:2148:G:O2'	22:A:2199:G:N2	2.33	0.53
22:A:2199:G:H2'	22:A:2200:U:C6	2.44	0.53
27:F:135:GLN:HG2	27:F:150:ARG:H	1.74	0.53
22:A:939:G:H2'	22:A:940:G:C8	2.44	0.53
22:A:1107:U:H1'	22:A:1116:A:H1'	1.91	0.53
23:B:40:C:OP2	45:3:2:LYS:NZ	2.34	0.53
40:W:33:VAL:HG23	40:W:65:VAL:HG22	1.89	0.53
9:i:50:GLN:OE1	9:i:80:ARG:NH1	2.42	0.53
22:A:292:U:H2'	22:A:293:G:H8	1.73	0.53
22:A:1517:C:OP2	22:A:1598:G:O2'	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:15:ASP:OD1	7:g:15:ASP:N	2.41	0.52
19:s:12:ASP:OD2	19:s:14:HIS:NE2	2.42	0.52
21:w:32:PHE:HD2	21:w:35:THR:HG22	1.73	0.52
22:A:2324:U:H2'	22:A:2325:U:C6	2.43	0.52
23:B:19:A:H2'	23:B:20:A:C8	2.44	0.52
28:G:94:TYR:O	28:G:95:ARG:NE	2.42	0.52
39:V:47:ASP:O	39:V:87:LYS:NZ	2.32	0.52
1:a:983:A:OP1	14:n:29:ARG:NH2	2.42	0.52
7:g:138:ARG:NH1	7:g:139:GLU:OE2	2.42	0.52
22:A:139:A:H2'	22:A:140:G:C8	2.44	0.52
22:A:897:G:H21	44:2:46:MET:HE2	1.72	0.52
22:A:1459:U:H2'	22:A:1460:G:C8	2.44	0.52
9:i:50:GLN:HA	9:i:53:VAL:HG12	1.92	0.52
22:A:228:A:H2'	22:A:229:A:C8	2.44	0.52
22:A:1121:C:H2'	22:A:1122:C:C6	2.43	0.52
23:B:19:A:H2'	23:B:20:A:H8	1.75	0.52
25:D:180:ASP:HB3	25:D:185:VAL:HG22	1.91	0.52
1:a:17:U:H2'	1:a:18:C:H6	1.75	0.52
1:a:955:A:H2'	1:a:956:G:C8	2.44	0.52
1:a:1511:A:C4	1:a:1539:A:H2	2.27	0.52
22:A:525:A:N3	22:A:527:G:H5''	2.25	0.52
22:A:2148:G:H1'	22:A:2200:U:O2	2.09	0.52
50:8:25:VAL:HG22	50:8:34:GLN:HB2	1.91	0.52
40:W:48:SER:OG	40:W:49:ASN:N	2.42	0.52
47:5:29:ARG:NH1	47:5:47:GLU:O	2.42	0.52
1:a:1419:C:H2'	1:a:1420:A:H8	1.73	0.52
22:A:1055:A:N3	22:A:1199:C:O2'	2.40	0.52
22:A:1320:G:OP2	22:A:1694:G:O2'	2.19	0.52
40:W:6:GLY:H	40:W:23:VAL:HG23	1.74	0.52
1:a:146:G:H2'	1:a:147:G:C8	2.44	0.52
1:a:985:G:OP2	1:a:1365:U:O2'	2.28	0.52
7:g:11:ASP:OD1	7:g:12:VAL:N	2.41	0.52
17:q:26:VAL:HG22	17:q:45:LYS:HB3	1.91	0.52
22:A:687:G:N1	22:A:690:U:OP2	2.42	0.52
1:a:1542:A:H2'	1:a:1543:C:C5	2.44	0.52
25:D:132:PRO:O	25:D:137:SER:OG	2.23	0.52
1:a:263:G:OP1	17:q:73:LYS:NZ	2.37	0.52
16:p:16:PRO:HD2	16:p:43:LEU:HD11	1.92	0.52
22:A:1593:C:H2'	22:A:1594:G:C8	2.45	0.52
33:P:73:VAL:HA	33:P:91:PRO:HA	1.91	0.52
8:h:22:HIS:O	8:h:66:TYR:OH	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:m:4:ILE:HD13	13:m:8:ASP:HA	1.91	0.51
22:A:2195:A:H5''	22:A:2205:U:C6	2.45	0.51
26:E:49:HIS:ND1	26:E:92:PRO:HB2	2.24	0.51
27:F:4:LEU:HD21	27:F:173:LEU:HD22	1.92	0.51
1:a:1047:A:H2'	1:a:1048:A:C8	2.40	0.51
1:a:1257:A:H2'	1:a:1258:A:C8	2.45	0.51
1:a:1294:A:H2'	1:a:1295:A:C8	2.46	0.51
22:A:1199:C:OP1	36:S:92:ARG:NH2	2.41	0.51
24:C:100:GLU:OE2	24:C:102:ARG:NH2	2.41	0.51
29:L:7:ALA:HB3	29:L:49:ILE:HD11	1.91	0.51
3:c:90:LEU:O	3:c:94:THR:OG1	2.21	0.51
4:d:182:ARG:NE	4:d:191:GLU:OE2	2.43	0.51
12:l:134:LYS:HD3	12:l:135:PRO:HD2	1.92	0.51
16:p:52:ASP:OD2	16:p:55:ALA:N	2.37	0.51
22:A:1115:A:H4'	22:A:1116:A:H2'	1.91	0.51
28:G:94:TYR:HD1	28:G:107:VAL:HA	1.74	0.51
1:a:1538:G:H21	1:a:1539:A:H61	1.58	0.51
3:c:22:TRP:NE1	3:c:35:ASP:OD2	2.41	0.51
22:A:90:A:H4'	22:A:91:C:H5'	1.91	0.51
22:A:1760:U:H3'	22:A:1761:A:H5''	1.93	0.51
22:A:1835:A:H2'	22:A:1836:A:C8	2.46	0.51
22:A:2789:U:OP2	50:8:19:ARG:NE	2.35	0.51
1:a:429:U:H5'	1:a:430:C:C5	2.45	0.51
1:a:723:A:H2'	1:a:724:A:C8	2.46	0.51
6:f:4:LYS:NZ	6:f:95:GLU:HB3	2.25	0.51
22:A:221:A:N3	22:A:236:U:O2'	2.39	0.51
22:A:305:C:H2'	22:A:306:A:H8	1.75	0.51
22:A:1268:G:OP2	37:T:89:ARG:NH1	2.42	0.51
9:i:23:PRO:HA	9:i:61:TYR:HD1	1.75	0.51
13:m:14:ARG:HD2	13:m:42:ASP:HA	1.92	0.51
22:A:1539:A:H2'	24:C:98:ASP:OD1	2.11	0.51
22:A:1452:U:H2'	22:A:1453:G:C8	2.46	0.51
1:a:1029:A:H2'	1:a:1030:G:C8	2.46	0.51
9:i:80:ARG:HD3	9:i:103:LEU:HG	1.92	0.51
27:F:110:ARG:HD2	27:F:137:ILE:O	2.10	0.51
38:U:55:VAL:HG12	38:U:110:VAL:HG12	1.91	0.51
41:Y:46:TYR:HD2	41:Y:48:GLN:HG2	1.76	0.51
1:a:212:G:H2'	1:a:213:A:C8	2.46	0.51
22:A:308:U:H3'	22:A:309:C:H5''	1.93	0.51
27:F:77:PHE:O	27:F:78:ARG:HD3	2.11	0.51
1:a:1363:G:H2'	1:a:1364:A:H8	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:109:GLY:O	5:e:113:ARG:HG3	2.11	0.50
23:B:3:U:H2'	23:B:4:G:C8	2.46	0.50
36:S:102:ASP:OD2	37:T:2:TYR:OH	2.11	0.50
38:U:23:ARG:NH1	38:U:81:VAL:O	2.44	0.50
41:Y:79:ARG:HG2	41:Y:80:MET:O	2.11	0.50
45:3:13:VAL:HG12	45:3:24:LEU:HD13	1.92	0.50
8:h:68:ALA:O	8:h:69:THR:OG1	2.25	0.50
22:A:2195:A:H4'	22:A:2205:U:H5''	1.92	0.50
24:C:37:LEU:HG	24:C:62:TYR:HB2	1.93	0.50
12:l:100:VAL:HG13	12:l:103:LEU:HB2	1.93	0.50
22:A:1763:U:O2'	22:A:1764:A:O5'	2.30	0.50
22:A:2135:U:O4	22:A:2136:A:N6	2.44	0.50
2:b:14:VAL:O	2:b:15:HIS:ND1	2.45	0.50
4:d:26:LEU:O	4:d:28:ARG:N	2.42	0.50
15:o:21:ASP:OD2	15:o:24:SER:OG	2.27	0.50
22:A:366:G:O2'	26:E:171:GLN:OE1	2.26	0.50
22:A:905:G:OP2	41:Y:85:LYS:NZ	2.43	0.50
22:A:1712:U:O2'	22:A:2719:G:H4'	2.12	0.50
1:a:982:G:OP1	10:j:59:LYS:NZ	2.29	0.50
1:a:1174:G:N2	1:a:1177:A:OP2	2.32	0.50
2:b:82:ASP:HA	2:b:85:ILE:HG12	1.94	0.50
3:c:182:ASP:OD2	3:c:203:ARG:NH1	2.44	0.50
17:q:81:VAL:HG12	17:q:82:GLU:HG3	1.93	0.50
22:A:2225:C:H2'	22:A:2226:A:C8	2.46	0.50
32:O:34:LEU:HB2	32:O:118:LEU:HD22	1.93	0.50
38:U:16:ARG:NH2	38:U:103:LYS:HD2	2.26	0.50
1:a:1129:U:H2'	1:a:1130:U:C6	2.47	0.50
16:p:45:ASP:HB3	16:p:46:PRO:HD3	1.93	0.50
22:A:1851:U:O2'	24:C:154:LEU:O	2.30	0.50
22:A:2500:C:H2'	22:A:2501:A:O4'	2.12	0.50
26:E:10:ASP:O	26:E:145:ASN:ND2	2.44	0.50
27:F:40:VAL:HA	27:F:150:ARG:HH12	1.76	0.50
9:i:29:VAL:HB	9:i:64:LEU:HD13	1.92	0.50
22:A:292:U:H2'	22:A:293:G:C8	2.46	0.50
22:A:720:G:H1'	26:E:74:ARG:HD3	1.93	0.50
22:A:2463:A:H2'	22:A:2463:A:N3	2.25	0.50
28:G:69:ARG:NH1	28:G:73:ASN:HB2	2.26	0.50
8:h:81:SER:HB3	8:h:87:VAL:HG22	1.93	0.50
22:A:1171:G:OP2	22:A:1172:A:O2'	2.21	0.50
22:A:2347:A:H2'	22:A:2348:U:C6	2.46	0.50
23:B:7:A:OP1	34:Q:19:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:77:PHE:C	27:F:78:ARG:HD3	2.37	0.50
31:N:2:LYS:HB3	31:N:4:HIS:CE1	2.47	0.50
22:A:2136:A:N6	22:A:2220:A:H61	2.10	0.50
23:B:48:G:OP1	34:Q:68:SER:OG	2.30	0.50
24:C:130:LEU:HD12	24:C:192:ILE:HD11	1.92	0.50
27:F:133:ARG:HD3	27:F:151:GLY:HA3	1.94	0.50
14:n:7:ILE:O	14:n:11:LYS:HG2	2.12	0.49
22:A:859:U:H2'	22:A:860:C:H6	1.76	0.49
22:A:928:G:O6	22:A:942:U:C2	2.64	0.49
41:Y:24:SER:OG	41:Y:25:GLU:N	2.45	0.49
1:a:439:A:H3'	1:a:440:A:H8	1.78	0.49
4:d:134:SER:OG	4:d:135:VAL:N	2.45	0.49
22:A:288:U:O2'	22:A:289:U:O5'	2.30	0.49
22:A:1046:A:H2'	22:A:1047:A:C8	2.47	0.49
26:E:6:LEU:HD12	26:E:17:ILE:HB	1.94	0.49
50:8:13:LYS:HE3	50:8:28:GLU:OE2	2.12	0.49
1:a:318:G:H5''	16:p:32:ARG:HG3	1.95	0.49
6:f:8:MET:HE1	18:r:28:LYS:HG2	1.94	0.49
22:A:1309:G:OP1	46:4:16:ARG:NH2	2.37	0.49
43:1:19:LYS:O	43:1:23:GLU:HG3	2.13	0.49
5:e:75:VAL:HG11	5:e:119:ALA:HB1	1.95	0.49
22:A:1102:G:H4'	22:A:1132:A:C8	2.48	0.49
38:U:40:ILE:HD12	46:4:24:LEU:HD11	1.94	0.49
1:a:159:A:H61	1:a:355:G:H21	1.60	0.49
1:a:1012:G:H3'	1:a:1035:C:C5	2.46	0.49
1:a:1539:A:H2'	1:a:1540:U:O4'	2.13	0.49
8:h:98:LEU:HD22	8:h:132:TRP:HB2	1.93	0.49
22:A:1126:A:H2'	22:A:1127:U:C6	2.48	0.49
22:A:1136:U:H2'	22:A:1137:G:H8	1.77	0.49
25:D:80:ILE:O	25:D:81:ARG:NH1	2.39	0.49
1:a:532:G:H2'	1:a:533:C:C6	2.48	0.49
14:n:23:ARG:HD2	14:n:28:GLY:O	2.12	0.49
26:E:194:ILE:HG12	26:E:199:VAL:HG23	1.95	0.49
39:V:8:LYS:NZ	39:V:30:ASP:OD1	2.45	0.49
22:A:687:G:N2	22:A:690:U:OP2	2.45	0.49
22:A:1187:U:H4'	22:A:1188:A:O4'	2.12	0.49
27:F:60:ILE:HD11	27:F:138:PHE:CG	2.47	0.49
28:G:94:TYR:CD1	28:G:107:VAL:HA	2.48	0.49
7:g:150:ALA:HB1	11:k:59:THR:HG21	1.94	0.49
22:A:613:G:H2'	22:A:2063:A:N7	2.28	0.49
28:G:68:THR:O	28:G:72:LEU:HD23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:583:G:O2'	1:a:829:G:OP2	2.30	0.49
22:A:2378:G:N3	22:A:2414:C:H2'	2.28	0.49
1:a:1050:G:H2'	1:a:1051:U:H6	1.78	0.48
1:a:1076:A:N1	1:a:1117:G:O2'	2.42	0.48
22:A:410:G:O2'	22:A:412:U:O4	2.29	0.48
22:A:1761:A:H8	22:A:1761:A:OP1	1.96	0.48
27:F:157:VAL:HG12	34:Q:2:ILE:HD11	1.95	0.48
29:L:43:PRO:HB3	36:S:68:ALA:HB2	1.95	0.48
1:a:262:G:O6	1:a:281:A:N6	2.46	0.48
1:a:588:C:H2'	1:a:589:G:O4'	2.13	0.48
4:d:84:GLU:HG2	4:d:182:ARG:HG2	1.95	0.48
22:A:2921:G:OP2	22:A:2921:G:N2	2.37	0.48
22:A:404:A:N6	22:A:405:G:O6	2.46	0.48
22:A:926:G:C2	22:A:946:G:H1'	2.49	0.48
24:C:95:ASN:HB3	24:C:101:LYS:HG2	1.93	0.48
27:F:60:ILE:HD11	27:F:138:PHE:CD2	2.48	0.48
47:5:2:ARG:HD2	47:5:20:THR:HB	1.94	0.48
3:c:66:THR:HG22	3:c:101:ASN:HB2	1.94	0.48
3:c:134:LYS:NZ	5:e:56:GLU:OE1	2.46	0.48
18:r:41:GLY:O	18:r:67:ARG:NH2	2.41	0.48
22:A:637:U:H2'	22:A:638:U:C6	2.48	0.48
22:A:1041:C:O2	29:L:4:THR:OG1	2.29	0.48
22:A:1532:G:HO2'	22:A:1533:A:H8	1.60	0.48
35:R:88:ARG:HH12	35:R:112:GLU:HB2	1.76	0.48
43:1:58:ARG:NH1	43:1:61:GLU:OE2	2.47	0.48
1:a:1030:G:H2'	1:a:1031:C:C6	2.49	0.48
22:A:629:A:N1	22:A:855:G:O2'	2.45	0.48
22:A:897:G:H21	44:2:46:MET:CE	2.26	0.48
22:A:1172:A:H4'	22:A:1173:A:C5'	2.44	0.48
22:A:1764:A:H2'	22:A:1765:G:O4'	2.14	0.48
22:A:2227:U:H2'	22:A:2228:U:C6	2.48	0.48
1:a:9:G:OP2	5:e:127:LYS:NZ	2.29	0.48
1:a:329:A:H2'	1:a:330:C:H6	1.78	0.48
1:a:392:G:H2'	1:a:393:U:C6	2.49	0.48
1:a:736:A:H2'	1:a:737:A:C8	2.47	0.48
2:b:27:MET:HE2	2:b:188:ASP:O	2.13	0.48
2:b:83:GLU:OE1	2:b:218:ALA:HB2	2.13	0.48
2:b:132:LYS:O	2:b:136:LEU:HG	2.14	0.48
3:c:57:GLU:HB3	3:c:64:ASN:HB2	1.96	0.48
22:A:305:C:H2'	22:A:306:A:C8	2.49	0.48
22:A:597:U:H2'	22:A:598:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2134:G:C6	22:A:2222:G:C6	3.02	0.48
22:A:2216:C:H2'	22:A:2217:U:H6	1.78	0.48
36:S:86:ALA:HB2	36:S:116:ALA:HB2	1.96	0.48
47:5:31:GLU:OE2	47:5:46:ARG:NH1	2.46	0.48
1:a:1121:C:H1'	3:c:178:ARG:NH1	2.29	0.48
3:c:12:ILE:HG22	3:c:18:TRP:HE3	1.77	0.48
3:c:188:ALA:HB3	3:c:195:LEU:HB2	1.96	0.48
10:j:59:LYS:HE3	10:j:62:ARG:NH2	2.28	0.48
11:k:65:MET:N	11:k:65:MET:HE2	2.29	0.48
12:l:43:LYS:NZ	12:l:72:ASN:HD22	2.11	0.48
17:q:47:LYS:HB3	17:q:73:LYS:HG2	1.96	0.48
22:A:703:U:H2'	22:A:704:A:C8	2.48	0.48
24:C:154:LEU:HD13	24:C:176:LEU:HD21	1.96	0.48
1:a:1335:C:C2	1:a:1336:A:C8	3.01	0.48
22:A:939:G:H2'	22:A:940:G:H8	1.79	0.48
45:3:5:ILE:HG13	45:3:6:HIS:CD2	2.49	0.48
5:e:30:ARG:C	5:e:31:ARG:HD3	2.39	0.48
10:j:55:VAL:O	14:n:41:ARG:NH2	2.44	0.48
22:A:1094:A:H1'	22:A:1158:G:N2	2.28	0.48
22:A:1100:A:H2'	22:A:1101:G:O4'	2.14	0.48
22:A:1546:U:H5''	22:A:1547:C:H5	1.78	0.48
22:A:2914:C:O2	46:4:37:ARG:NH2	2.46	0.48
1:a:8:A:N6	4:d:196:GLU:O	2.47	0.48
1:a:384:G:H5''	16:p:6:ARG:HB2	1.96	0.48
2:b:111:ILE:HD13	2:b:148:LEU:HD13	1.95	0.48
5:e:106:VAL:HG12	5:e:124:VAL:HG12	1.96	0.48
20:t:10:ARG:HA	20:t:13:THR:HG22	1.96	0.48
22:A:680:C:O2'	22:A:684:U:OP1	2.28	0.48
22:A:1987:G:O2'	22:A:1989:U:O4	2.25	0.48
23:B:23:U:O2'	23:B:25:A:OP2	2.26	0.48
27:F:40:VAL:HG22	27:F:86:GLY:N	2.26	0.48
41:Y:46:TYR:CD2	41:Y:48:GLN:HG2	2.49	0.48
1:a:307:G:H2'	1:a:308:A:C8	2.49	0.47
1:a:682:G:H2'	1:a:683:A:C8	2.48	0.47
1:a:1228:G:O3'	19:s:77:THR:HG21	2.13	0.47
1:a:1321:C:OP2	19:s:5:LEU:HD22	2.14	0.47
7:g:66:MET:HB3	7:g:70:MET:HE2	1.95	0.47
20:t:48:ASP:OD1	20:t:48:ASP:N	2.47	0.47
22:A:2195:A:H2'	22:A:2196:A:H8	1.79	0.47
27:F:131:GLY:O	27:F:133:ARG:HG2	2.14	0.47
40:W:40:MET:SD	40:W:60:GLU:HG3	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:975:G:C8	21:w:66:ARG:NH1	2.82	0.47
1:a:1333:U:H2'	1:a:1334:A:H8	1.79	0.47
3:c:149:LYS:HZ2	3:c:200:TRP:HZ2	1.61	0.47
19:s:50:ALA:HB1	19:s:57:HIS:HB3	1.96	0.47
22:A:1025:A:H5'	22:A:1026:A:H5''	1.96	0.47
22:A:2389:U:H2'	22:A:2390:G:O4'	2.14	0.47
22:A:2624:C:H2'	22:A:2625:G:C8	2.49	0.47
24:C:144:ILE:HB	24:C:154:LEU:HB2	1.96	0.47
35:R:49:LYS:HB2	35:R:96:LYS:HD2	1.97	0.47
47:5:1:MET:HG3	47:5:2:ARG:H	1.78	0.47
1:a:21:G:H2'	1:a:22:G:C8	2.49	0.47
1:a:664:G:O2'	15:o:28:GLN:NE2	2.43	0.47
12:l:86:ASN:HD21	12:l:118:ALA:H	1.61	0.47
22:A:873:U:O2'	22:A:2101:U:C2	2.67	0.47
22:A:929:G:HO2'	22:A:930:C:P	2.35	0.47
22:A:1397:A:H2'	22:A:1398:A:C8	2.50	0.47
22:A:1456:A:H2'	22:A:1457:A:H8	1.77	0.47
22:A:1497:G:O2'	22:A:1596:A:N3	2.45	0.47
27:F:134:GLU:HB3	27:F:137:ILE:HG12	1.96	0.47
33:P:66:ILE:HG22	33:P:67:ARG:O	2.15	0.47
1:a:7:G:N7	5:e:98:LYS:NZ	2.49	0.47
1:a:277:U:H2'	1:a:278:A:C8	2.49	0.47
1:a:383:U:OP1	16:p:69:THR:OG1	2.29	0.47
22:A:1112:U:N3	22:A:1114:G:O2'	2.44	0.47
27:F:134:GLU:OE2	27:F:136:LEU:HD23	2.13	0.47
33:P:24:LEU:HG	33:P:134:LEU:HD23	1.96	0.47
1:a:500:A:H2'	1:a:501:C:C6	2.48	0.47
6:f:4:LYS:HE3	6:f:95:GLU:C	2.40	0.47
13:m:7:VAL:HG12	13:m:22:ILE:HG22	1.96	0.47
22:A:281:A:H2'	22:A:282:G:C8	2.49	0.47
22:A:1407:C:O2'	22:A:1842:A:N3	2.39	0.47
22:A:2125:G:H4'	22:A:2126:G:C5'	2.44	0.47
43:1:5:ASP:OD1	43:1:5:ASP:N	2.42	0.47
47:5:7:LEU:HD21	47:5:32:LEU:HD12	1.96	0.47
48:6:8:SER:HB3	48:6:11:LYS:HB2	1.95	0.47
2:b:58:ARG:NH2	2:b:224:VAL:HB	2.29	0.47
22:A:579:U:H2'	22:A:580:U:C6	2.49	0.47
22:A:1015:G:H2'	22:A:1016:U:C6	2.50	0.47
22:A:1139:G:H2'	22:A:1140:U:C6	2.50	0.47
27:F:120:LYS:O	27:F:120:LYS:HG3	2.14	0.47
28:G:64:LEU:HA	28:G:67:THR:HG22	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:3:70:ARG:O	45:3:74:PHE:N	2.37	0.47
1:a:670:A:H2'	1:a:671:A:C8	2.50	0.47
1:a:763:G:OP2	15:o:65:ASN:ND2	2.48	0.47
1:a:948:G:OP1	7:g:102:ARG:NH1	2.43	0.47
1:a:1272:C:H2'	1:a:1273:G:C8	2.50	0.47
1:a:1538:G:O2'	1:a:1539:A:OP2	2.30	0.47
4:d:71:THR:HG23	4:d:86:PHE:HE1	1.79	0.47
11:k:45:SER:OG	11:k:66:ALA:O	2.32	0.47
11:k:82:LEU:O	11:k:108:THR:OG1	2.30	0.47
22:A:247:G:O2'	22:A:430:A:N1	2.41	0.47
22:A:274:A:H62	22:A:295:G:N2	2.09	0.47
22:A:407:G:H2'	22:A:408:U:C6	2.49	0.47
22:A:1699:A:O2'	22:A:1700:G:O5'	2.32	0.47
22:A:2312:G:N7	41:Y:22:ARG:NH2	2.51	0.47
22:A:2362:A:H2'	22:A:2363:G:C8	2.49	0.47
32:O:63:LYS:HD3	32:O:65:TRP:CZ2	2.50	0.47
22:A:688:A:O2'	22:A:689:A:OP1	2.31	0.47
23:B:88:C:H5'	32:O:18:ARG:HG2	1.97	0.47
37:T:67:ARG:HB3	37:T:89:ARG:HG2	1.96	0.47
1:a:35:G:H2'	1:a:36:C:C6	2.49	0.47
1:a:421:G:H4'	1:a:422:A:H5'	1.96	0.47
1:a:955:A:H2'	1:a:956:G:H8	1.80	0.47
7:g:59:MET:O	7:g:63:GLU:HG2	2.15	0.47
11:k:86:VAL:HG11	11:k:93:ARG:HE	1.79	0.47
22:A:684:U:H2'	22:A:685:C:C6	2.50	0.47
22:A:871:C:O2'	31:N:54:GLN:HG3	2.15	0.47
22:A:2226:A:H2'	22:A:2227:U:H6	1.80	0.47
22:A:2227:U:H2'	22:A:2228:U:H6	1.80	0.47
1:a:373:U:H5'	1:a:374:C:OP1	2.15	0.47
1:a:954:G:C2	1:a:955:A:C8	3.03	0.47
4:d:182:ARG:O	4:d:182:ARG:NH1	2.37	0.47
11:k:86:VAL:HG11	11:k:93:ARG:NE	2.30	0.47
22:A:2207:C:H2'	22:A:2208:U:H6	1.79	0.47
22:A:2731:U:H2'	22:A:2732:U:C6	2.50	0.47
1:a:280:C:H2'	1:a:281:A:C8	2.50	0.46
1:a:422:A:OP2	1:a:436:G:N2	2.41	0.46
7:g:22:LEU:HD13	7:g:66:MET:HE2	1.96	0.46
22:A:1771:A:H8	22:A:1771:A:OP2	1.99	0.46
27:F:130:LEU:HD23	27:F:132:VAL:H	1.78	0.46
1:a:1009:U:H2'	1:a:1010:U:C6	2.50	0.46
22:A:1124:C:O2'	22:A:1134:A:H5''	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:36:ILE:HG21	27:F:152:MET:HE3	1.97	0.46
1:a:199:C:H2'	1:a:200:A:C8	2.49	0.46
1:a:1006:U:H2'	1:a:1007:C:C6	2.50	0.46
1:a:1026:C:N4	1:a:1027:A:H62	2.13	0.46
1:a:1136:G:H5'	1:a:1287:A:O2'	2.14	0.46
10:j:63:GLU:OE1	14:n:45:ARG:NH1	2.42	0.46
22:A:1138:C:H2'	22:A:1139:G:O4'	2.15	0.46
1:a:224:U:H2'	1:a:225:A:H8	1.80	0.46
1:a:534:C:OP2	12:l:101:LYS:NZ	2.48	0.46
3:c:52:SER:HB3	3:c:114:LEU:HD21	1.97	0.46
21:w:90:ARG:O	21:w:94:THR:OG1	2.26	0.46
22:A:539:G:H4'	38:U:11:VAL:HG22	1.97	0.46
22:A:851:G:N2	22:A:875:A:OP1	2.49	0.46
22:A:891:U:O2'	22:A:893:A:OP1	2.28	0.46
28:G:95:ARG:HD3	28:G:128:ASN:HB2	1.98	0.46
31:N:105:GLU:O	31:N:105:GLU:HG2	2.15	0.46
1:a:262:G:OP1	17:q:72:THR:OG1	2.26	0.46
1:a:480:U:H2'	1:a:481:U:H6	1.80	0.46
1:a:1188:G:H1'	1:a:1189:G:C4	2.50	0.46
9:i:115:LYS:HB2	9:i:118:LEU:HD12	1.97	0.46
18:r:66:SER:OG	18:r:72:LEU:HD12	2.16	0.46
22:A:92:G:O2'	22:A:93:U:OP1	2.27	0.46
22:A:271:C:H5''	22:A:297:U:O4	2.15	0.46
22:A:906:G:O2'	22:A:963:G:O6	2.22	0.46
22:A:1827:U:H2'	22:A:1828:C:C6	2.50	0.46
22:A:2130:G:C2	22:A:2131:U:C4	3.03	0.46
22:A:2134:G:O6	22:A:2221:U:O4	2.33	0.46
22:A:2682:U:H2'	22:A:2683:C:C6	2.51	0.46
33:P:108:GLU:N	33:P:108:GLU:OE2	2.47	0.46
40:W:6:GLY:O	40:W:22:LYS:NZ	2.48	0.46
1:a:1071:U:H2'	1:a:1072:C:C6	2.51	0.46
1:a:1321:C:C5	19:s:5:LEU:HD21	2.51	0.46
1:a:1325:A:H1'	19:s:37:ARG:HH11	1.80	0.46
27:F:36:ILE:O	27:F:88:LYS:HA	2.16	0.46
27:F:162:SER:OG	27:F:165:GLU:OE1	2.33	0.46
32:O:54:MET:HE2	32:O:118:LEU:HD23	1.96	0.46
32:O:76:SER:HB3	32:O:91:GLU:CD	2.39	0.46
1:a:697:C:OP1	11:k:29:ASN:ND2	2.45	0.46
2:b:157:LEU:HD12	2:b:158:PRO:HD2	1.98	0.46
4:d:91:GLU:OE2	4:d:164:TYR:OH	2.28	0.46
8:h:9:ASP:HA	8:h:12:THR:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:10:PHE:CD1	8:h:27:LEU:HD21	2.51	0.46
22:A:4:U:H2'	22:A:5:A:H8	1.81	0.46
22:A:1469:A:O2'	22:A:1471:G:N7	2.47	0.46
22:A:1477:A:H4'	22:A:1478:C:O5'	2.15	0.46
48:6:3:ARG:HA	48:6:3:ARG:HD3	1.62	0.46
3:c:12:ILE:HD13	3:c:16:ARG:HD2	1.97	0.46
22:A:799:G:OP1	48:6:1:MET:HE2	2.16	0.46
22:A:831:U:H2'	22:A:832:C:C6	2.50	0.46
22:A:1639:U:H2'	22:A:1640:A:C8	2.51	0.46
22:A:2216:C:H2'	22:A:2217:U:C6	2.50	0.46
1:a:245:C:OP2	17:q:44:LYS:NZ	2.48	0.46
1:a:1134:U:HO2'	1:a:1135:U:P	2.39	0.46
12:l:120:VAL:HG13	12:l:123:ARG:HB2	1.97	0.46
16:p:7:LEU:HD23	16:p:18:TYR:CG	2.50	0.46
22:A:944:C:H2'	22:A:945:C:C6	2.51	0.46
22:A:2181:G:H2'	22:A:2182:C:C6	2.50	0.46
28:G:37:PHE:CE2	28:G:71:ILE:HD11	2.51	0.46
33:P:134:LEU:HD12	33:P:134:LEU:O	2.15	0.46
49:7:31:HIS:CE1	49:7:32:MET:HE2	2.51	0.46
1:a:447:U:H1'	4:d:115:ASN:HD21	1.81	0.46
1:a:1481:G:H2'	1:a:1482:G:C8	2.50	0.46
3:c:11:ARG:HD3	3:c:15:ILE:HD11	1.98	0.46
15:o:17:VAL:HG22	15:o:21:ASP:OD2	2.15	0.46
19:s:36:ARG:NH1	19:s:53:ASP:HA	2.30	0.46
22:A:279:G:H2'	22:A:280:A:C8	2.50	0.46
22:A:2107:U:H2'	22:A:2108:U:C6	2.51	0.46
22:A:2149:G:H5''	22:A:2150:A:N7	2.30	0.46
22:A:2304:G:OP1	41:Y:26:SER:HB3	2.16	0.46
22:A:2424:G:H2'	22:A:2457:C:H41	1.80	0.46
23:B:63:C:O2'	23:B:106:C:N4	2.49	0.46
1:a:975:G:N7	21:w:66:ARG:NH1	2.63	0.45
22:A:1105:G:H2'	22:A:1106:U:C5	2.51	0.45
22:A:1763:U:N3	22:A:1778:A:N6	2.27	0.45
22:A:2047:A:H2'	22:A:2048:A:C8	2.51	0.45
22:A:2136:A:H2'	22:A:2137:C:H6	1.80	0.45
43:1:10:SER:O	43:1:12:THR:N	2.49	0.45
1:a:62:U:OP1	1:a:393:U:O2'	2.34	0.45
1:a:931:G:H2'	1:a:932:A:C8	2.51	0.45
1:a:1014:C:C5	1:a:1033:U:H1'	2.51	0.45
1:a:1330:G:H2'	1:a:1331:C:C6	2.51	0.45
8:h:52:ILE:HD11	8:h:61:ARG:HH12	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:27:G:O2'	22:A:28:A:O5'	2.31	0.45
22:A:1072:A:O2'	22:A:1073:A:H5'	2.17	0.45
22:A:1294:U:OP1	22:A:1294:U:H3'	2.16	0.45
22:A:1815:C:O2'	22:A:1816:A:O5'	2.34	0.45
28:G:95:ARG:N	28:G:106:ASN:OD1	2.33	0.45
35:R:105:GLY:C	35:R:107:ALA:H	2.25	0.45
42:Z:37:ARG:O	42:Z:60:GLU:HB2	2.16	0.45
1:a:62:U:H2'	1:a:63:C:C6	2.51	0.45
1:a:1309:U:OP1	13:m:13:LYS:NZ	2.34	0.45
3:c:19:ASP:N	14:n:51:GLY:O	2.48	0.45
13:m:78:LYS:HD2	13:m:81:ILE:HD12	1.98	0.45
22:A:522:G:N1	22:A:525:A:OP2	2.44	0.45
22:A:534:G:H4'	38:U:54:LYS:HE2	1.98	0.45
22:A:911:G:H2'	22:A:912:C:C6	2.51	0.45
22:A:1108:G:H2'	22:A:1109:G:H8	1.82	0.45
22:A:1639:U:H2'	22:A:1640:A:H8	1.81	0.45
22:A:1832:G:N7	24:C:178:SER:OG	2.47	0.45
47:5:2:ARG:HD3	47:5:21:LYS:O	2.16	0.45
1:a:238:G:H5'	16:p:24:ASP:OD2	2.15	0.45
1:a:725:C:H4'	11:k:119:ASN:HD22	1.81	0.45
1:a:744:U:H2'	1:a:745:C:C6	2.52	0.45
1:a:1165:A:H4'	1:a:1166:C:O4'	2.17	0.45
1:a:1321:C:H2'	1:a:1322:U:H6	1.81	0.45
1:a:1431:U:H2'	1:a:1432:A:C8	2.51	0.45
22:A:244:G:N2	22:A:257:A:OP2	2.37	0.45
22:A:1433:G:H2'	22:A:1434:U:O4'	2.16	0.45
22:A:2555:U:O2'	22:A:2680:U:OP1	2.27	0.45
22:A:2877:G:O2'	22:A:2897:A:N6	2.49	0.45
1:a:1130:U:H2'	1:a:1131:U:C6	2.52	0.45
1:a:1277:G:H2'	1:a:1278:G:H8	1.81	0.45
15:o:71:ARG:HG3	15:o:78:TYR:CD2	2.51	0.45
22:A:301:A:H2'	22:A:302:G:C8	2.52	0.45
22:A:529:A:H5''	40:W:46:LYS:HD3	1.98	0.45
22:A:2226:A:H2'	22:A:2227:U:C6	2.51	0.45
22:A:2674:A:H5''	29:L:79:SER:HB3	1.97	0.45
33:P:29:ARG:HG3	33:P:133:GLU:HB3	1.98	0.45
45:3:35:ILE:N	45:3:43:TYR:O	2.49	0.45
1:a:1378:G:O3'	9:i:71:GLY:HA3	2.16	0.45
1:a:1539:A:O5'	1:a:1539:A:H8	1.99	0.45
11:k:33:MET:SD	11:k:44:TRP:HB3	2.56	0.45
22:A:1103:A:N7	22:A:1132:A:H2'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2104:A:H2'	22:A:2105:G:C8	2.52	0.45
22:A:2160:G:H2'	22:A:2161:C:C6	2.52	0.45
27:F:121:ALA:HB3	27:F:128:TYR:CE1	2.52	0.45
43:1:38:GLU:N	43:1:38:GLU:OE1	2.46	0.45
1:a:686:U:H2'	1:a:687:C:C6	2.51	0.45
1:a:1539:A:H8	1:a:1539:A:P	2.40	0.45
2:b:162:PHE:HD1	2:b:184:ILE:HG13	1.82	0.45
12:l:47:CYS:HA	12:l:68:VAL:HA	1.99	0.45
21:w:22:GLU:O	21:w:26:ASP:HB2	2.16	0.45
22:A:878:G:H2'	22:A:879:C:C6	2.51	0.45
22:A:1113:A:H2	22:A:1141:A:C4	2.35	0.45
22:A:1947:C:O2'	22:A:1948:U:O5'	2.32	0.45
22:A:2565:G:N2	22:A:2696:G:O2'	2.50	0.45
29:L:126:TYR:OH	29:L:133:HIS:NE2	2.48	0.45
1:a:129:A:O2'	1:a:130:C:O5'	2.32	0.45
1:a:917:A:H2'	1:a:918:A:C8	2.52	0.45
1:a:917:A:H2'	1:a:918:A:H8	1.81	0.45
1:a:1235:C:OP2	13:m:110:LYS:NZ	2.39	0.45
1:a:1323:G:N1	1:a:1326:A:OP2	2.42	0.45
8:h:115:ASP:OD1	8:h:116:LYS:N	2.50	0.45
22:A:27:G:H1'	22:A:558:A:N6	2.31	0.45
22:A:2214:G:H2'	22:A:2215:G:H8	1.81	0.45
22:A:2671:G:O2'	22:A:2672:A:H8	1.99	0.45
28:G:41:ILE:HD12	28:G:61:HIS:HE2	1.82	0.45
29:L:32:GLU:HG2	29:L:143:LEU:HD22	1.99	0.45
32:O:109:VAL:HB	32:O:113:VAL:HG23	1.98	0.45
34:Q:68:SER:OG	34:Q:68:SER:O	2.31	0.45
1:a:35:G:O2'	12:l:128:SER:O	2.30	0.45
1:a:480:U:H2'	1:a:481:U:C6	2.51	0.45
7:g:38:LYS:O	7:g:42:ILE:HG23	2.17	0.45
22:A:224:A:N1	22:A:235:A:H5''	2.31	0.45
22:A:630:G:OP2	31:N:21:ARG:NH2	2.47	0.45
22:A:2112:U:O2'	42:Z:23:ASN:ND2	2.49	0.45
27:F:40:VAL:HA	27:F:150:ARG:NH1	2.32	0.45
6:f:83:ILE:HG13	24:C:136:PRO:HG3	1.98	0.45
22:A:1092:A:H3'	22:A:1093:G:H5'	1.99	0.45
22:A:2157:G:H2'	22:A:2158:G:O4'	2.17	0.45
22:A:2822:C:H1'	22:A:2920:A:H2	1.81	0.45
26:E:8:LYS:HG3	26:E:14:ALA:HB2	1.99	0.45
47:5:1:MET:HG3	47:5:2:ARG:N	2.32	0.45
1:a:437:U:O2'	1:a:438:A:OP2	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:941:C:N4	7:g:1:MET:HE3	2.32	0.44
9:i:69:GLY:O	9:i:75:GLN:NE2	2.46	0.44
13:m:11:ARG:CZ	13:m:11:ARG:HB3	2.47	0.44
22:A:310:U:H2'	22:A:311:A:C8	2.52	0.44
22:A:1112:U:H2'	22:A:1114:G:C8	2.52	0.44
22:A:1137:G:H2'	22:A:1138:C:C6	2.52	0.44
27:F:65:PRO:HB2	27:F:87:ALA:HB1	1.98	0.44
1:a:1003:A:O2'	14:n:12:ARG:NH2	2.47	0.44
3:c:8:ILE:HG22	3:c:12:ILE:HD11	1.99	0.44
22:A:278:A:H2'	22:A:279:G:C8	2.52	0.44
22:A:1137:G:H2'	22:A:1138:C:H6	1.83	0.44
22:A:1777:G:HO2'	22:A:1778:A:P	2.40	0.44
22:A:2181:G:H2'	22:A:2182:C:H6	1.82	0.44
22:A:2682:U:H2'	22:A:2683:C:H6	1.83	0.44
24:C:154:LEU:HD23	24:C:154:LEU:HA	1.82	0.44
1:a:95:A:H3'	1:a:96:G:C8	2.53	0.44
1:a:221:G:OP2	1:a:221:G:N2	2.43	0.44
1:a:1174:G:N2	1:a:1176:A:H3'	2.32	0.44
2:b:186:ILE:HG23	2:b:202:ALA:HB3	1.99	0.44
17:q:70:SER:OG	17:q:71:ALA:N	2.46	0.44
22:A:27:G:HO2'	22:A:28:A:P	2.40	0.44
22:A:2710:A:H2'	22:A:2711:C:C6	2.52	0.44
27:F:160:ALA:HB1	27:F:165:GLU:HG2	1.98	0.44
28:G:16:THR:HB	28:G:27:LYS:HB3	1.99	0.44
1:a:442:U:H2'	1:a:443:A:C8	2.53	0.44
1:a:1110:A:H4'	1:a:1111:A:O5'	2.18	0.44
1:a:1225:C:H2'	1:a:1226:U:H6	1.80	0.44
22:A:809:G:O2'	22:A:810:A:OP1	2.30	0.44
22:A:1763:U:O2'	22:A:1764:A:H8	1.99	0.44
23:B:110:G:H2'	23:B:111:C:C6	2.53	0.44
35:R:24:ASP:HB2	35:R:88:ARG:O	2.18	0.44
40:W:1:MET:HE3	40:W:65:VAL:HG21	1.98	0.44
44:2:58:GLU:OE2	44:2:58:GLU:N	2.50	0.44
1:a:508:G:H2'	1:a:509:C:C6	2.52	0.44
1:a:684:A:H2'	1:a:685:U:H6	1.82	0.44
1:a:1304:U:H1'	1:a:1305:C:H5	1.82	0.44
12:l:94:LEU:HB3	12:l:111:VAL:CG1	2.48	0.44
22:A:117:A:H5'	22:A:118:A:H8	1.81	0.44
22:A:631:U:H2'	22:A:632:U:C6	2.53	0.44
22:A:2349:U:H2'	22:A:2350:C:H6	1.82	0.44
1:a:765:U:H2'	1:a:766:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1021:G:C6	1:a:1027:A:C6	3.06	0.44
19:s:3:ARG:HD3	19:s:7:LYS:HG3	1.99	0.44
22:A:1549:G:O2'	24:C:99:GLY:O	2.34	0.44
22:A:2829:U:H2'	22:A:2830:C:C6	2.53	0.44
27:F:59:LEU:HG	27:F:140:GLU:OE2	2.18	0.44
31:N:96:LEU:HD22	31:N:101:ILE:HD11	1.99	0.44
33:P:47:LEU:HD21	33:P:66:ILE:CD1	2.46	0.44
1:a:41:G:H2'	1:a:42:G:C8	2.51	0.44
1:a:263:G:H2'	1:a:264:U:C6	2.53	0.44
1:a:1080:C:H2'	1:a:1081:G:C8	2.51	0.44
1:a:1272:C:H2'	1:a:1273:G:H8	1.83	0.44
4:d:185:LEU:O	4:d:187:ALA:N	2.49	0.44
5:e:26:VAL:O	5:e:28:GLY:N	2.51	0.44
22:A:463:C:H2'	22:A:464:U:C6	2.52	0.44
22:A:2694:G:OP2	22:A:2694:G:H8	2.00	0.44
25:D:111:THR:CG2	25:D:168:GLN:HE21	2.30	0.44
28:G:167:GLU:N	28:G:167:GLU:OE1	2.51	0.44
41:Y:41:GLY:N	41:Y:72:ASP:OD1	2.48	0.44
1:a:111:G:OP1	53:a:3201:HOH:O	2.21	0.44
1:a:519:C:H1'	4:d:36:HIS:CE1	2.48	0.44
22:A:930:C:H2'	22:A:931:C:O4'	2.17	0.44
22:A:1369:C:OP1	22:A:1696:G:O2'	2.32	0.44
22:A:1598:G:OP2	22:A:1598:G:N2	2.35	0.44
22:A:2215:G:H2'	22:A:2216:C:C6	2.53	0.44
35:R:63:LYS:HE3	35:R:65:SER:HB3	1.98	0.44
38:U:93:ARG:HA	38:U:93:ARG:HD2	1.83	0.44
1:a:392:G:H2'	1:a:393:U:H6	1.83	0.44
1:a:695:A:H61	1:a:711:G:H1'	1.82	0.44
1:a:1303:C:H4'	1:a:1309:U:O4	2.18	0.44
4:d:50:GLN:OE1	4:d:200:ARG:NH2	2.49	0.44
26:E:111:LYS:HE3	26:E:111:LYS:HB2	1.75	0.44
28:G:117:ALA:HB1	28:G:121:VAL:HG23	2.00	0.44
29:L:115:LEU:O	29:L:119:LEU:HG	2.18	0.44
1:a:1494:G:H2'	1:a:1495:G:C8	2.53	0.43
22:A:220:G:H22	22:A:237:U:H4'	1.83	0.43
22:A:231:A:O2'	22:A:232:U:O4'	2.28	0.43
22:A:688:A:HO2'	22:A:689:A:P	2.41	0.43
22:A:1094:A:H2'	22:A:1095:C:H6	1.82	0.43
22:A:2566:U:OP1	22:A:2698:A:O2'	2.36	0.43
22:A:2842:U:H2'	22:A:2843:C:H6	1.82	0.43
28:G:55:PRO:HD2	28:G:61:HIS:CE1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:936:G:O2'	1:a:1511:A:N7	2.48	0.43
22:A:5:A:H2'	22:A:6:A:C8	2.52	0.43
22:A:1569:U:H2'	22:A:1570:G:H8	1.82	0.43
22:A:1823:C:H2'	22:A:1824:A:C8	2.52	0.43
22:A:2167:A:N6	22:A:2190:G:H1'	2.33	0.43
22:A:2230:U:O2'	22:A:2231:A:C8	2.70	0.43
22:A:2624:C:H2'	22:A:2625:G:H8	1.82	0.43
25:D:171:ILE:HD11	25:D:191:ASN:O	2.19	0.43
1:a:113:G:H4'	1:a:114:A:O5'	2.17	0.43
1:a:1438:C:H2'	1:a:1439:G:O4'	2.18	0.43
4:d:19:LEU:HG	4:d:60:MET:HE3	2.00	0.43
13:m:22:ILE:O	13:m:25:ILE:HG22	2.19	0.43
26:E:111:LYS:HE2	26:E:206:LEU:HD13	2.00	0.43
28:G:125:VAL:HG13	28:G:125:VAL:O	2.18	0.43
30:M:24:VAL:HG13	30:M:33:ALA:HB2	2.00	0.43
44:2:16:PRO:HD2	44:2:19:GLN:HG3	2.00	0.43
8:h:21:LYS:CE	8:h:72:ARG:HE	2.32	0.43
8:h:88:TYR:CD1	8:h:126:GLU:HG3	2.54	0.43
22:A:1827:U:H2'	22:A:1828:C:H6	1.82	0.43
42:Z:3:LYS:HE2	42:Z:33:LEU:HD12	2.00	0.43
1:a:266:G:H2'	1:a:267:G:H8	1.83	0.43
1:a:390:A:H2'	1:a:391:A:C8	2.54	0.43
3:c:67:ILE:HG13	3:c:100:ILE:HD11	1.99	0.43
4:d:67:GLN:O	4:d:71:THR:HG22	2.19	0.43
10:j:40:ILE:HD13	10:j:73:LEU:HD22	2.01	0.43
18:r:56:GLN:O	18:r:60:THR:HG23	2.19	0.43
22:A:947:A:C5	22:A:948:A:C8	3.06	0.43
22:A:950:U:H2'	22:A:951:C:H6	1.83	0.43
22:A:2175:G:H2'	22:A:2176:C:C6	2.54	0.43
22:A:2545:C:H2'	22:A:2546:G:O4'	2.17	0.43
27:F:130:LEU:HB3	27:F:154:VAL:HG13	2.00	0.43
31:N:113:SER:O	31:N:113:SER:OG	2.31	0.43
1:a:642:C:H2'	1:a:643:A:H8	1.82	0.43
1:a:695:A:N6	1:a:711:G:H1'	2.34	0.43
1:a:1243:A:H4'	1:a:1311:G:H4'	2.00	0.43
1:a:1521:A:H2'	1:a:1522:U:C6	2.53	0.43
12:l:87:LEU:HD11	12:l:117:THR:HB	2.01	0.43
22:A:59:G:O2'	22:A:74:U:OP2	2.30	0.43
22:A:162:A:H2	22:A:2250:G:N3	2.16	0.43
22:A:1010:C:O2'	22:A:2306:A:N3	2.49	0.43
22:A:1815:C:HO2'	22:A:1816:A:P	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2349:U:H2'	22:A:2350:C:C6	2.53	0.43
22:A:2899:C:C5'	33:P:61:GLN:HE22	2.31	0.43
23:B:35:C:O2	34:Q:102:HIS:NE2	2.43	0.43
1:a:901:A:H2'	1:a:902:C:H6	1.83	0.43
1:a:1357:A:O2'	7:g:33:ASP:OD1	2.36	0.43
3:c:183:TYR:OH	3:c:198:LYS:HD3	2.18	0.43
22:A:75:G:N3	22:A:75:G:H2'	2.34	0.43
22:A:2170:C:H2'	22:A:2171:G:C8	2.54	0.43
22:A:2326:C:H5''	34:Q:96:ARG:HH12	1.83	0.43
49:7:55:PHE:O	49:7:59:ARG:HG3	2.18	0.43
1:a:901:A:H2'	1:a:902:C:C6	2.54	0.43
1:a:1409:C:H2'	1:a:1410:C:O4'	2.18	0.43
12:l:79:TYR:HB2	12:l:106:VAL:HG11	2.00	0.43
13:m:20:THR:HA	13:m:25:ILE:HG23	2.00	0.43
22:A:1187:U:OP2	29:L:66:THR:OG1	2.36	0.43
22:A:1532:G:N7	22:A:1556:G:N1	2.67	0.43
22:A:2097:C:H2'	22:A:2098:C:H6	1.81	0.43
22:A:2170:C:H2'	22:A:2171:G:H8	1.84	0.43
22:A:2325:U:H2'	22:A:2326:C:C6	2.54	0.43
28:G:86:LYS:HZ2	28:G:132:ILE:HD11	1.83	0.43
31:N:92:THR:HG23	31:N:94:GLU:HG2	2.01	0.43
1:a:409:C:OP2	4:d:66:ARG:HD3	2.18	0.43
1:a:508:G:H2'	1:a:509:C:H6	1.84	0.43
1:a:944:A:N6	7:g:2:PRO:HG2	2.34	0.43
8:h:21:LYS:HE3	8:h:72:ARG:HE	1.84	0.43
16:p:57:LEU:HD23	16:p:86:GLN:HE22	1.83	0.43
22:A:632:U:H2'	22:A:633:A:C8	2.54	0.43
22:A:1384:U:OP2	39:V:58:TYR:OH	2.34	0.43
22:A:1568:C:C2	22:A:1569:U:C5	3.07	0.43
22:A:1777:G:O2'	22:A:1778:A:OP2	2.35	0.43
22:A:2054:G:H2'	22:A:2054:G:N3	2.34	0.43
22:A:2145:A:N6	22:A:2202:G:N7	2.67	0.43
22:A:2200:U:H2'	22:A:2201:G:O4'	2.19	0.43
22:A:2395:G:OP1	49:7:40:GLN:NE2	2.47	0.43
35:R:89:ARG:O	35:R:113:ILE:HG22	2.18	0.43
38:U:9:LYS:HB3	38:U:111:VAL:HG22	2.01	0.43
1:a:224:U:H2'	1:a:225:A:C8	2.54	0.43
3:c:69:THR:HG22	3:c:71:LYS:H	1.83	0.43
22:A:275:C:O2'	22:A:305:C:OP1	2.34	0.43
22:A:509:G:N2	22:A:512:A:OP2	2.42	0.43
22:A:944:C:H2'	22:A:945:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1123:A:H2'	22:A:1124:C:O4'	2.18	0.43
22:A:1154:U:H2'	22:A:1155:C:O4'	2.19	0.43
22:A:1906:G:H2'	22:A:1907:C:C6	2.54	0.43
22:A:2928:A:C2	22:A:2929:C:N4	2.86	0.43
32:O:109:VAL:HB	32:O:113:VAL:CG2	2.49	0.43
1:a:336:C:H4'	1:a:337:A:H5'	2.01	0.42
1:a:686:U:H2'	1:a:687:C:H6	1.84	0.42
1:a:759:U:H2'	1:a:760:G:O4'	2.19	0.42
1:a:777:G:H4'	1:a:1521:A:H4'	2.00	0.42
22:A:331:G:H2'	22:A:332:U:C6	2.54	0.42
22:A:1249:A:N3	31:N:4:HIS:HB3	2.34	0.42
22:A:1640:A:H2'	22:A:1641:G:C8	2.54	0.42
44:2:9:LYS:HD3	44:2:55:ASP:OD2	2.19	0.42
1:a:942:G:OP2	7:g:2:PRO:HB2	2.19	0.42
3:c:8:ILE:HG12	3:c:183:TYR:HB3	2.01	0.42
9:i:8:GLY:O	9:i:82:GLY:HA2	2.18	0.42
11:k:29:ASN:OD1	11:k:30:THR:N	2.51	0.42
22:A:1094:A:H2'	22:A:1095:C:C6	2.54	0.42
22:A:1162:C:H2'	22:A:1163:C:C6	2.54	0.42
22:A:2163:G:O2'	22:A:2191:A:N1	2.41	0.42
22:A:2198:G:H2'	22:A:2199:G:C8	2.55	0.42
22:A:2928:A:H2'	22:A:2929:C:C5	2.54	0.42
23:B:59:U:H2'	23:B:60:U:C6	2.54	0.42
31:N:97:ILE:HD12	31:N:102:ILE:O	2.19	0.42
1:a:523:G:H2'	1:a:524:U:C6	2.54	0.42
1:a:941:C:H41	7:g:1:MET:HB2	1.85	0.42
22:A:1336:U:H2'	22:A:1337:U:C6	2.54	0.42
22:A:2176:C:H2'	22:A:2177:G:O4'	2.20	0.42
22:A:2501:A:HO2'	22:A:2502:A:P	2.42	0.42
1:a:479:C:C2	1:a:480:U:C5	3.07	0.42
1:a:486:C:H2'	1:a:487:U:C6	2.54	0.42
3:c:25:GLU:C	3:c:27:ASP:H	2.27	0.42
22:A:894:A:H5'	22:A:895:G:OP2	2.19	0.42
22:A:926:G:H2'	22:A:927:G:C8	2.52	0.42
22:A:1620:G:H4'	24:C:59:LYS:HG3	2.00	0.42
22:A:2142:U:H2'	22:A:2143:G:O4'	2.19	0.42
22:A:2830:C:H2'	22:A:2831:G:O4'	2.20	0.42
30:M:115:VAL:HG13	30:M:121:VAL:HG21	2.02	0.42
1:a:187:U:O2	1:a:202:G:N2	2.35	0.42
1:a:847:G:H2'	1:a:848:G:C8	2.51	0.42
1:a:1152:G:N2	1:a:1154:A:H62	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:113:HIS:O	2:b:117:ILE:HG12	2.19	0.42
11:k:19:GLY:O	11:k:82:LEU:HA	2.19	0.42
13:m:30:ALA:O	13:m:34:LEU:HD23	2.19	0.42
22:A:197:A:C8	22:A:199:A:OP1	2.72	0.42
22:A:578:G:H2'	22:A:579:U:C6	2.54	0.42
22:A:1129:G:H21	22:A:1131:A:P	2.42	0.42
27:F:138:PHE:HA	27:F:139:PRO:HD3	1.94	0.42
27:F:164:GLU:HG2	27:F:165:GLU:N	2.33	0.42
31:N:94:GLU:O	31:N:97:ILE:HG22	2.18	0.42
1:a:409:C:H2'	1:a:410:G:H8	1.85	0.42
1:a:550:U:OP1	4:d:10:LYS:NZ	2.39	0.42
1:a:693:G:H2'	1:a:694:U:C6	2.54	0.42
9:i:107:ASP:HA	9:i:108:PRO:HD3	1.92	0.42
15:o:6:GLU:O	15:o:10:GLU:HG3	2.19	0.42
16:p:4:LYS:HB2	16:p:65:LYS:O	2.19	0.42
21:w:66:ARG:O	21:w:88:GLN:NE2	2.43	0.42
22:A:2878:G:O2'	22:A:2895:G:N2	2.53	0.42
27:F:51:ASP:O	27:F:55:GLU:OE1	2.37	0.42
34:Q:68:SER:O	34:Q:69:LYS:HG2	2.19	0.42
1:a:974:A:C4	21:w:7:ARG:HG3	2.55	0.42
4:d:92:GLN:NE2	4:d:133:VAL:O	2.53	0.42
22:A:290:C:H2'	22:A:291:U:C6	2.54	0.42
22:A:1829:U:H2'	22:A:1830:C:H6	1.85	0.42
22:A:1829:U:H2'	22:A:1830:C:C6	2.55	0.42
7:g:63:GLU:OE1	7:g:67:LYS:NZ	2.53	0.42
22:A:661:A:OP1	26:E:106:ARG:HD2	2.20	0.42
22:A:873:U:O2'	22:A:2101:U:N3	2.51	0.42
24:C:121:GLU:N	24:C:121:GLU:OE2	2.53	0.42
1:a:437:U:O5'	4:d:9:TRP:CD1	2.73	0.42
1:a:439:A:C5	1:a:440:A:C8	3.08	0.42
1:a:626:C:H5'	1:a:627:U:H5''	2.02	0.42
1:a:699:G:OP2	11:k:28:ASN:ND2	2.43	0.42
1:a:1335:C:H2'	1:a:1336:A:H8	1.85	0.42
3:c:198:LYS:HB3	3:c:200:TRP:CZ3	2.54	0.42
16:p:20:ILE:N	16:p:38:GLY:O	2.52	0.42
22:A:491:C:H2'	22:A:492:G:O4'	2.19	0.42
22:A:879:C:H2'	22:A:880:U:C6	2.55	0.42
22:A:2207:C:H2'	22:A:2208:U:C6	2.55	0.42
30:M:98:ILE:HD13	30:M:114:ILE:HG23	2.01	0.42
46:4:33:CYS:HB3	46:4:35:GLU:H	1.84	0.42
1:a:1014:C:OP2	1:a:1033:U:H2'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:45:ARG:HG3	3:c:46:LEU:HG	2.02	0.42
12:l:123:ARG:HA	12:l:123:ARG:HD2	1.84	0.42
21:w:20:TYR:HA	21:w:23:LYS:HE3	2.02	0.42
22:A:74:U:H5''	22:A:75:G:O4'	2.20	0.42
22:A:575:G:N3	22:A:575:G:H2'	2.35	0.42
22:A:1019:A:H5'	22:A:1234:U:H1'	2.02	0.42
22:A:2279:G:H2'	22:A:2280:A:C8	2.55	0.42
1:a:170:A:OP2	53:a:3202:HOH:O	2.21	0.41
1:a:531:A:C2	12:l:101:LYS:HB3	2.55	0.41
1:a:987:A:O2'	1:a:1329:C:H5	2.02	0.41
7:g:92:ARG:H	7:g:92:ARG:HG2	1.69	0.41
8:h:10:PHE:HD1	8:h:27:LEU:HD21	1.84	0.41
20:t:45:ASN:O	20:t:49:LEU:HG	2.20	0.41
22:A:927:G:H2'	22:A:928:G:C8	2.55	0.41
22:A:2189:G:H4'	22:A:2190:G:OP1	2.20	0.41
22:A:2437:C:H2'	22:A:2438:G:O4'	2.20	0.41
1:a:647:G:O6	1:a:648:A:N6	2.53	0.41
2:b:136:LEU:HD12	2:b:137:LEU:N	2.35	0.41
3:c:117:GLU:HA	3:c:120:ALA:HB3	2.02	0.41
13:m:19:LEU:HD23	13:m:19:LEU:HA	1.92	0.41
22:A:115:C:O2'	22:A:125:A:N3	2.43	0.41
22:A:139:A:H2	22:A:1453:G:H1'	1.85	0.41
22:A:422:G:H2'	22:A:423:A:H8	1.85	0.41
22:A:746:G:O2'	22:A:1681:A:N3	2.41	0.41
22:A:2213:U:H2'	22:A:2214:G:C8	2.55	0.41
22:A:2361:A:H2'	22:A:2362:A:H8	1.82	0.41
22:A:2488:G:H2'	22:A:2489:C:C6	2.55	0.41
32:O:65:TRP:HB2	32:O:105:GLU:HB2	2.01	0.41
1:a:470:G:H2'	1:a:471:A:C8	2.55	0.41
1:a:935:G:C6	21:w:91:LYS:HG3	2.55	0.41
1:a:1014:C:H2'	1:a:1015:C:O4'	2.21	0.41
9:i:28:ILE:HB	9:i:35:TRP:CG	2.55	0.41
13:m:30:ALA:HA	13:m:33:VAL:HG22	2.03	0.41
20:t:20:ARG:O	20:t:24:GLN:HG2	2.20	0.41
25:D:13:THR:OG1	25:D:14:GLN:N	2.53	0.41
30:M:1:MET:HA	30:M:32:THR:HG23	2.02	0.41
42:Z:54:LEU:HD23	42:Z:58:LYS:HG2	2.01	0.41
1:a:927:A:H2'	1:a:928:A:C8	2.55	0.41
1:a:1302:U:H2'	1:a:1303:C:C6	2.55	0.41
7:g:66:MET:O	7:g:70:MET:HG3	2.20	0.41
7:g:68:ASN:O	7:g:138:ARG:NE	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:h:21:LYS:HD3	8:h:72:ARG:HE	1.86	0.41
15:o:18:HIS:CE1	15:o:21:ASP:HB3	2.56	0.41
16:p:87:LYS:HE3	16:p:87:LYS:HB3	1.92	0.41
22:A:338:A:H2'	22:A:339:U:C6	2.56	0.41
22:A:1139:G:N2	22:A:1144:A:H62	2.17	0.41
22:A:2202:G:H2'	22:A:2203:G:C4	2.55	0.41
22:A:2324:U:H2'	22:A:2325:U:H6	1.85	0.41
22:A:2362:A:H2'	22:A:2363:G:H8	1.86	0.41
1:a:523:G:H2'	1:a:524:U:H6	1.84	0.41
11:k:59:THR:HG23	11:k:62:ALA:H	1.85	0.41
22:A:1039:A:H1'	37:T:90:GLN:NE2	2.36	0.41
22:A:1178:U:H3'	22:A:1179:A:H5''	2.03	0.41
22:A:2134:G:H2'	22:A:2135:U:C6	2.55	0.41
22:A:2494:C:H2'	22:A:2495:U:C6	2.56	0.41
27:F:68:THR:O	27:F:85:ILE:N	2.51	0.41
1:a:8:A:N6	4:d:200:ARG:HB3	2.36	0.41
1:a:509:C:H2'	1:a:510:C:C6	2.56	0.41
1:a:1464:A:H2'	1:a:1465:G:O4'	2.20	0.41
22:A:349:U:H2'	22:A:350:G:O4'	2.20	0.41
22:A:994:C:H1'	22:A:1030:G:C8	2.55	0.41
22:A:1439:A:O2'	22:A:1440:U:H5''	2.21	0.41
22:A:2044:U:H2'	22:A:2045:G:O4'	2.21	0.41
23:B:12:U:OP2	23:B:68:C:O2'	2.37	0.41
23:B:60:U:H2'	23:B:61:C:C6	2.55	0.41
31:N:58:PHE:CE2	31:N:59:ARG:HG3	2.56	0.41
40:W:13:THR:HG1	40:W:67:ASN:ND2	2.17	0.41
1:a:150:A:H3'	1:a:151:A:H8	1.85	0.41
1:a:1208:A:H1'	1:a:1209:U:OP2	2.20	0.41
2:b:27:MET:SD	2:b:193:PRO:HG3	2.60	0.41
2:b:68:LEU:HD13	2:b:154:MET:HE1	2.01	0.41
4:d:167:PHE:CE1	4:d:172:LEU:HA	2.55	0.41
9:i:119:LYS:HE3	9:i:125:PRO:HB3	2.02	0.41
22:A:1622:A:H2'	22:A:1623:A:C8	2.55	0.41
22:A:2198:G:H2'	22:A:2199:G:H8	1.86	0.41
22:A:2235:C:O2'	22:A:2237:C:OP1	2.38	0.41
22:A:2507:C:H5''	22:A:2508:C:H5	1.84	0.41
22:A:2807:C:H2'	22:A:2808:A:O4'	2.20	0.41
28:G:11:ILE:HD11	28:G:50:ILE:HD11	2.03	0.41
1:a:760:G:H5''	15:o:73:LYS:NZ	2.36	0.41
1:a:1312:G:H1'	1:a:1339:A:N6	2.36	0.41
2:b:203:ASN:OD1	2:b:204:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:46:GLU:OE2	4:d:46:GLU:HA	2.21	0.41
12:l:75:GLU:OE1	12:l:75:GLU:HA	2.21	0.41
13:m:90:ARG:HH11	13:m:95:LEU:HB3	1.86	0.41
22:A:1430:C:H2'	22:A:1431:A:C8	2.56	0.41
22:A:2175:G:H2'	22:A:2176:C:H6	1.86	0.41
25:D:38:LYS:HB2	25:D:93:ILE:HD11	2.03	0.41
31:N:118:GLU:OE1	31:N:118:GLU:N	2.54	0.41
33:P:66:ILE:HD12	33:P:66:ILE:HG23	1.87	0.41
1:a:203:C:H2'	1:a:204:U:H6	1.85	0.41
1:a:434:U:H4'	4:d:34:GLY:O	2.20	0.41
1:a:726:A:H2	18:r:42:LYS:HG2	1.86	0.41
1:a:1134:U:O2'	1:a:1135:U:O5'	2.28	0.41
1:a:1335:C:H2'	1:a:1336:A:C8	2.56	0.41
2:b:204:ASP:N	2:b:204:ASP:OD1	2.54	0.41
4:d:71:THR:HG21	4:d:90:LEU:HD21	2.03	0.41
7:g:16:PRO:HG2	9:i:43:ALA:HA	2.03	0.41
8:h:79:ARG:HD2	8:h:128:LEU:O	2.21	0.41
10:j:42:LEU:HD11	10:j:73:LEU:HD12	2.03	0.41
11:k:22:HIS:HB2	11:k:33:MET:HB3	2.03	0.41
14:n:10:GLN:NE2	14:n:21:TYR:O	2.50	0.41
22:A:717:C:O2'	22:A:718:C:P	2.79	0.41
22:A:993:A:H2'	22:A:994:C:C6	2.55	0.41
22:A:1003:A:N6	22:A:2492:A:C8	2.88	0.41
22:A:1478:C:O2'	22:A:1621:A:OP2	2.36	0.41
22:A:1483:A:H2'	22:A:1484:A:H8	1.82	0.41
22:A:1947:C:HO2'	22:A:1948:U:P	2.43	0.41
22:A:2130:G:H2'	22:A:2131:U:C6	2.55	0.41
22:A:2149:G:H1	22:A:2195:A:P	2.44	0.41
22:A:2590:G:H2'	22:A:2591:C:C6	2.56	0.41
22:A:2671:G:HO2'	22:A:2672:A:P	2.43	0.41
22:A:2789:U:O2'	22:A:2790:A:OP2	2.31	0.41
24:C:140:VAL:HG13	24:C:161:SER:HB2	2.03	0.41
25:D:39:LYS:HE2	25:D:82:GLU:OE2	2.20	0.41
32:O:109:VAL:HG23	32:O:114:ALA:HB2	2.02	0.41
46:4:15:LYS:O	46:4:18:THR:HG22	2.20	0.41
1:a:1160:A:P	10:j:72:ARG:HH22	2.44	0.41
5:e:133:THR:HG22	5:e:135:ILE:HG22	2.02	0.41
5:e:155:ALA:HB2	5:e:165:LEU:HD12	2.03	0.41
9:i:21:LEU:HD11	9:i:61:TYR:HB3	2.03	0.41
13:m:82:GLU:OE1	13:m:82:GLU:N	2.54	0.41
16:p:71:ARG:NH1	16:p:75:SER:HB3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:w:89:ILE:H	21:w:89:ILE:HG13	1.71	0.41
22:A:27:G:O2'	22:A:28:A:H8	2.03	0.41
22:A:351:G:H2'	22:A:352:A:C8	2.56	0.41
22:A:1352:A:H2'	22:A:1353:G:O4'	2.21	0.41
22:A:1640:A:H2'	22:A:1641:G:H8	1.86	0.41
22:A:2064:A:N3	22:A:2488:G:O2'	2.43	0.41
22:A:2188:A:H2'	22:A:2189:G:C8	2.55	0.41
22:A:2325:U:H2'	22:A:2326:C:H6	1.86	0.41
1:a:97:U:H2'	1:a:98:U:C6	2.55	0.40
1:a:804:C:OP1	11:k:128:ARG:N	2.55	0.40
4:d:91:GLU:OE1	4:d:96:ASN:ND2	2.55	0.40
13:m:19:LEU:O	13:m:22:ILE:HG12	2.21	0.40
22:A:2424:G:H2'	22:A:2457:C:N4	2.36	0.40
24:C:21:PHE:HB3	24:C:24:ILE:HD13	2.01	0.40
33:P:125:ASP:N	33:P:125:ASP:OD1	2.54	0.40
37:T:62:VAL:HA	37:T:95:LEU:HD23	2.02	0.40
1:a:989:C:H2'	1:a:990:U:O4'	2.22	0.40
7:g:60:GLU:C	7:g:62:PHE:N	2.77	0.40
11:k:80:LYS:HB3	11:k:106:GLU:OE2	2.21	0.40
22:A:286:G:H4'	22:A:287:C:O5'	2.21	0.40
22:A:2345:U:O3'	27:F:68:THR:HG21	2.20	0.40
25:D:16:PHE:CE1	25:D:22:LEU:HD13	2.56	0.40
28:G:46:GLU:CD	28:G:48:ASN:H	2.30	0.40
38:U:11:VAL:HG12	38:U:109:THR:HG23	2.03	0.40
40:W:16:ASP:OD2	40:W:19:LYS:HD2	2.22	0.40
44:2:44:ARG:HG2	44:2:44:ARG:HH11	1.85	0.40
1:a:1252:G:O6	1:a:1300:A:N6	2.54	0.40
22:A:942:U:O2'	22:A:944:C:N4	2.51	0.40
22:A:950:U:H2'	22:A:951:C:C6	2.56	0.40
22:A:972:G:O3'	22:A:973:U:H2'	2.21	0.40
22:A:1458:U:H2'	22:A:1459:U:C6	2.56	0.40
22:A:1552:U:H2'	22:A:1553:C:C6	2.56	0.40
27:F:40:VAL:HG12	27:F:150:ARG:NH1	2.36	0.40
32:O:31:GLU:HG2	32:O:32:TYR:CD2	2.56	0.40
43:1:14:ILE:HD12	43:1:14:ILE:HA	1.89	0.40
45:3:14:PHE:N	45:3:23:PHE:O	2.53	0.40
6:f:12:ARG:NH1	6:f:86:ASP:OD1	2.54	0.40
20:t:8:ILE:O	20:t:11:VAL:HG12	2.22	0.40
22:A:69:C:H4'	22:A:75:G:N7	2.37	0.40
22:A:133:A:H2'	22:A:134:U:C6	2.56	0.40
22:A:390:A:H2'	22:A:391:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1497:G:H2'	22:A:1498:C:C6	2.56	0.40
24:C:69:ARG:HE	24:C:69:ARG:HB3	1.73	0.40
31:N:90:GLU:OE1	31:N:122:THR:OG1	2.38	0.40
32:O:1:MET:SD	32:O:45:ARG:HG3	2.62	0.40
34:Q:71:ASP:OD1	34:Q:72:ALA:N	2.55	0.40
40:W:24:LEU:HD11	40:W:36:GLU:HB3	2.02	0.40
1:a:1159:A:O4'	10:j:41:PRO:HB2	2.22	0.40
1:a:1453:A:O2'	1:a:1454:A:H5'	2.20	0.40
3:c:83:VAL:O	3:c:86:LEU:HB2	2.21	0.40
13:m:83:ILE:HG23	13:m:85:SER:H	1.86	0.40
22:A:344:C:H1'	40:W:12:ILE:HD12	2.03	0.40
31:N:79:LEU:HA	31:N:79:LEU:HD23	1.85	0.40
33:P:119:LYS:HE2	33:P:119:LYS:HB3	1.85	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	219/249 (88%)	198 (90%)	21 (10%)	0	100	100
3	c	202/218 (93%)	190 (94%)	12 (6%)	0	100	100
4	d	197/200 (98%)	182 (92%)	15 (8%)	0	100	100
5	e	154/167 (92%)	148 (96%)	5 (3%)	1 (1%)	21	56
6	f	92/97 (95%)	87 (95%)	5 (5%)	0	100	100
7	g	152/156 (97%)	139 (91%)	10 (7%)	3 (2%)	6	28
8	h	129/132 (98%)	127 (98%)	2 (2%)	0	100	100
9	i	124/130 (95%)	116 (94%)	8 (6%)	0	100	100
10	j	94/102 (92%)	84 (89%)	10 (11%)	0	100	100
11	k	113/129 (88%)	108 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	l	132/137 (96%)	125 (95%)	7 (5%)	0	100	100
13	m	107/121 (88%)	99 (92%)	8 (8%)	0	100	100
14	n	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
15	o	84/89 (94%)	83 (99%)	1 (1%)	0	100	100
16	p	86/90 (96%)	82 (95%)	4 (5%)	0	100	100
17	q	78/87 (90%)	75 (96%)	3 (4%)	0	100	100
18	r	63/79 (80%)	62 (98%)	1 (2%)	0	100	100
19	s	79/92 (86%)	74 (94%)	5 (6%)	0	100	100
20	t	80/84 (95%)	80 (100%)	0	0	100	100
21	w	100/187 (54%)	93 (93%)	7 (7%)	0	100	100
24	C	271/277 (98%)	260 (96%)	11 (4%)	0	100	100
25	D	204/209 (98%)	189 (93%)	15 (7%)	0	100	100
26	E	202/207 (98%)	186 (92%)	16 (8%)	0	100	100
27	F	172/179 (96%)	160 (93%)	12 (7%)	0	100	100
28	G	170/178 (96%)	156 (92%)	14 (8%)	0	100	100
29	L	141/145 (97%)	137 (97%)	4 (3%)	0	100	100
30	M	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
31	N	144/146 (99%)	134 (93%)	10 (7%)	0	100	100
32	O	132/144 (92%)	130 (98%)	2 (2%)	0	100	100
33	P	118/135 (87%)	110 (93%)	8 (7%)	0	100	100
34	Q	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
35	R	111/114 (97%)	102 (92%)	9 (8%)	0	100	100
36	S	115/119 (97%)	113 (98%)	2 (2%)	0	100	100
37	T	99/102 (97%)	94 (95%)	5 (5%)	0	100	100
38	U	109/118 (92%)	104 (95%)	5 (5%)	0	100	100
39	V	90/94 (96%)	81 (90%)	9 (10%)	0	100	100
40	W	97/103 (94%)	93 (96%)	4 (4%)	0	100	100
41	Y	74/96 (77%)	66 (89%)	8 (11%)	0	100	100
42	Z	58/62 (94%)	54 (93%)	4 (7%)	0	100	100
43	1	58/63 (92%)	55 (95%)	3 (5%)	0	100	100
44	2	54/59 (92%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	3	77/81 (95%)	57 (74%)	19 (25%)	1 (1%)	9	38
46	4	51/57 (90%)	47 (92%)	4 (8%)	0	100	100
47	5	46/49 (94%)	46 (100%)	0	0	100	100
48	6	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
49	7	62/66 (94%)	57 (92%)	5 (8%)	0	100	100
50	8	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
All	All	5311/5732 (93%)	4980 (94%)	326 (6%)	5 (0%)	49	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	e	27	LYS
45	3	70	ARG
7	g	17	ILE
7	g	61	VAL
7	g	3	ARG

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	172/214 (80%)	172 (100%)	0	100	100
3	c	156/177 (88%)	156 (100%)	0	100	100
4	d	142/170 (84%)	142 (100%)	0	100	100
5	e	122/131 (93%)	122 (100%)	0	100	100
6	f	83/85 (98%)	83 (100%)	0	100	100
7	g	116/130 (89%)	116 (100%)	0	100	100
8	h	109/110 (99%)	109 (100%)	0	100	100
9	i	91/102 (89%)	91 (100%)	0	100	100
10	j	66/93 (71%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	k	86/100 (86%)	86 (100%)	0	100	100
12	l	115/118 (98%)	115 (100%)	0	100	100
13	m	66/102 (65%)	66 (100%)	0	100	100
14	n	51/52 (98%)	51 (100%)	0	100	100
15	o	79/81 (98%)	79 (100%)	0	100	100
16	p	78/80 (98%)	78 (100%)	0	100	100
17	q	73/78 (94%)	73 (100%)	0	100	100
18	r	58/67 (87%)	58 (100%)	0	100	100
19	s	64/78 (82%)	64 (100%)	0	100	100
20	t	64/66 (97%)	64 (100%)	0	100	100
21	w	96/170 (56%)	96 (100%)	0	100	100
24	C	221/225 (98%)	221 (100%)	0	100	100
25	D	169/171 (99%)	169 (100%)	0	100	100
26	E	168/174 (97%)	168 (100%)	0	100	100
27	F	130/155 (84%)	130 (100%)	0	100	100
28	G	140/147 (95%)	140 (100%)	0	100	100
29	L	120/121 (99%)	120 (100%)	0	100	100
30	M	101/101 (100%)	101 (100%)	0	100	100
31	N	115/115 (100%)	115 (100%)	0	100	100
32	O	106/113 (94%)	106 (100%)	0	100	100
33	P	102/111 (92%)	102 (100%)	0	100	100
34	Q	91/97 (94%)	91 (100%)	0	100	100
35	R	98/99 (99%)	98 (100%)	0	100	100
36	S	95/97 (98%)	95 (100%)	0	100	100
37	T	82/82 (100%)	82 (100%)	0	100	100
38	U	92/97 (95%)	92 (100%)	0	100	100
39	V	82/84 (98%)	82 (100%)	0	100	100
40	W	84/88 (96%)	84 (100%)	0	100	100
41	Y	61/76 (80%)	61 (100%)	0	100	100
42	Z	50/53 (94%)	50 (100%)	0	100	100
43	1	53/55 (96%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	2	50/52 (96%)	50 (100%)	0	100	100
45	3	29/73 (40%)	29 (100%)	0	100	100
46	4	47/50 (94%)	47 (100%)	0	100	100
47	5	47/48 (98%)	47 (100%)	0	100	100
48	6	39/39 (100%)	39 (100%)	0	100	100
49	7	54/56 (96%)	54 (100%)	0	100	100
50	8	35/35 (100%)	35 (100%)	0	100	100
All	All	4348/4818 (90%)	4348 (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 (86) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	103	ASN
3	c	95	GLN
3	c	118	ASN
4	d	36	HIS
4	d	55	GLN
4	d	59	HIS
4	d	70	ASN
4	d	73	ASN
4	d	82	HIS
4	d	85	ASN
4	d	92	GLN
4	d	112	GLN
4	d	115	ASN
4	d	137	GLN
4	d	177	ASN
5	e	44	ASN
5	e	84	HIS
6	f	34	ASN
6	f	54	ASN
7	g	40	GLN
7	g	52	GLN
7	g	129	ASN
7	g	148	ASN
8	h	56	ASN
9	i	81	HIS

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Mol	Chain	Res	Type
10	j	56	HIS
11	k	40	ASN
12	l	72	ASN
12	l	86	ASN
13	m	76	ASN
13	m	104	ASN
15	o	18	HIS
15	o	28	GLN
16	p	61	HIS
16	p	72	ASN
16	p	85	ASN
16	p	86	GLN
18	r	56	GLN
21	w	5	ASN
21	w	41	HIS
21	w	97	ASN
24	C	15	HIS
24	C	53	HIS
24	C	143	ASN
24	C	153	GLN
24	C	163	GLN
25	D	37	GLN
25	D	68	HIS
25	D	126	HIS
25	D	152	ASN
25	D	168	GLN
25	D	172	GLN
25	D	191	ASN
25	D	201	GLN
26	E	46	GLN
28	G	51	ASN
28	G	130	GLN
29	L	41	ASN
29	L	96	ASN
31	N	17	ASN
31	N	27	ASN
31	N	78	ASN
33	P	61	GLN
33	P	75	GLN
34	Q	15	HIS
34	Q	43	GLN
34	Q	115	ASN

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Mol	Chain	Res	Type
36	S	36	ASN
37	T	65	GLN
37	T	90	GLN
38	U	107	HIS
40	W	67	ASN
41	Y	20	ASN
41	Y	58	ASN
42	Z	16	ASN
42	Z	23	ASN
43	1	31	GLN
43	1	36	GLN
44	2	19	GLN
44	2	40	ASN
45	3	6	HIS
47	5	4	ASN
47	5	16	ASN
47	5	26	ASN
49	7	35	ASN
49	7	38	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1512/1550 (97%)	255 (16%)	0
22	A	2899/2932 (98%)	474 (16%)	30 (1%)
23	B	113/116 (97%)	12 (10%)	0
All	All	4524/4598 (98%)	741 (16%)	30 (0%)

All (741) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	A
1	a	9	G
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

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Mol	Chain	Res	Type
1	a	64	G
1	a	66	A
1	a	67	C
1	a	68	G
1	a	69	A
1	a	70	A
1	a	72	G
1	a	95	A
1	a	96	G
1	a	97	U
1	a	98	U
1	a	99	A
1	a	100	G
1	a	101	U
1	a	107	A
1	a	114	A
1	a	119	C
1	a	128	A
1	a	129	A
1	a	130	C
1	a	141	G
1	a	143	U
1	a	159	A
1	a	161	A
1	a	162	C
1	a	173	A
1	a	182	U
1	a	187	U
1	a	188	G
1	a	189	U
1	a	190	G
1	a	192	C
1	a	194	C
1	a	197	G
1	a	209	A
1	a	212	G
1	a	219	U
1	a	220	C
1	a	239	G
1	a	248	U
1	a	249	G
1	a	255	G

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Mol	Chain	Res	Type
1	a	259	G
1	a	265	A
1	a	274	G
1	a	275	C
1	a	288	C
1	a	297	G
1	a	329	A
1	a	336	C
1	a	337	A
1	a	338	C
1	a	340	G
1	a	353	C
1	a	355	G
1	a	359	G
1	a	360	C
1	a	362	G
1	a	372	A
1	a	373	U
1	a	375	U
1	a	380	C
1	a	381	A
1	a	400	G
1	a	405	A
1	a	412	G
1	a	414	G
1	a	419	A
1	a	420	A
1	a	421	G
1	a	422	A
1	a	425	G
1	a	426	U
1	a	429	U
1	a	430	C
1	a	432	G
1	a	437	U
1	a	439	A
1	a	447	U
1	a	456	A
1	a	461	C
1	a	467	U
1	a	473	U
1	a	475	A

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Mol	Chain	Res	Type
1	a	492	G
1	a	493	G
1	a	494	U
1	a	498	U
1	a	499	A
1	a	501	C
1	a	503	A
1	a	504	G
1	a	505	A
1	a	508	G
1	a	511	A
1	a	517	A
1	a	518	A
1	a	519	C
1	a	520	U
1	a	521	A
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	552	G
1	a	553	C
1	a	555	A
1	a	556	G
1	a	567	A
1	a	572	U
1	a	576	G
1	a	580	A
1	a	581	A
1	a	584	C
1	a	585	G
1	a	587	G
1	a	596	G
1	a	604	A
1	a	625	G
1	a	626	C
1	a	657	G
1	a	661	G
1	a	673	A
1	a	680	U

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Mol	Chain	Res	Type
1	a	695	A
1	a	702	A
1	a	703	A
1	a	712	A
1	a	731	U
1	a	732	G
1	a	739	G
1	a	742	A
1	a	757	A
1	a	763	G
1	a	768	G
1	a	785	A
1	a	786	G
1	a	789	A
1	a	801	U
1	a	802	A
1	a	823	A
1	a	825	C
1	a	829	G
1	a	848	G
1	a	855	C
1	a	867	G
1	a	881	A
1	a	923	A
1	a	925	G
1	a	935	G
1	a	936	G
1	a	940	C
1	a	943	C
1	a	944	A
1	a	954	G
1	a	965	U
1	a	966	U
1	a	969	U
1	a	974	A
1	a	977	A
1	a	978	A
1	a	980	G
1	a	984	A
1	a	985	G
1	a	986	A
1	a	992	A

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Mol	Chain	Res	Type
1	a	1002	G
1	a	1008	C
1	a	1010	U
1	a	1012	G
1	a	1013	A
1	a	1016	A
1	a	1018	U
1	a	1029	A
1	a	1032	U
1	a	1033	U
1	a	1035	C
1	a	1045	A
1	a	1046	C
1	a	1050	G
1	a	1052	G
1	a	1053	A
1	a	1054	C
1	a	1059	G
1	a	1063	C
1	a	1074	U
1	a	1094	U
1	a	1103	G
1	a	1110	A
1	a	1111	A
1	a	1133	G
1	a	1141	C
1	a	1142	A
1	a	1143	U
1	a	1147	G
1	a	1148	U
1	a	1154	A
1	a	1156	U
1	a	1167	U
1	a	1168	G
1	a	1176	A
1	a	1178	G
1	a	1191	G
1	a	1203	A
1	a	1204	A
1	a	1209	U
1	a	1219	U
1	a	1220	A

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Mol	Chain	Res	Type
1	a	1234	A
1	a	1235	C
1	a	1245	A
1	a	1248	G
1	a	1265	G
1	a	1267	G
1	a	1287	A
1	a	1294	A
1	a	1306	A
1	a	1307	G
1	a	1309	U
1	a	1312	G
1	a	1325	A
1	a	1327	C
1	a	1329	C
1	a	1343	C
1	a	1371	U
1	a	1388	U
1	a	1401	A
1	a	1405	A
1	a	1449	G
1	a	1453	A
1	a	1498	U
1	a	1500	A
1	a	1502	G
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	1541	C
1	a	1542	A
1	a	1543	C
1	a	1545	U
22	A	13	A
22	A	28	A
22	A	34	U
22	A	46	C
22	A	51	G
22	A	60	G
22	A	71	A

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Mol	Chain	Res	Type
22	A	75	G
22	A	89	U
22	A	91	C
22	A	93	U
22	A	100	U
22	A	101	G
22	A	117	A
22	A	118	A
22	A	119	U
22	A	125	A
22	A	126	A
22	A	130	A
22	A	133	A
22	A	140	G
22	A	161	A
22	A	164	A
22	A	167	U
22	A	186	C
22	A	187	C
22	A	198	A
22	A	199	A
22	A	201	A
22	A	215	A
22	A	217	G
22	A	218	A
22	A	223	A
22	A	224	A
22	A	230	A
22	A	231	A
22	A	232	U
22	A	235	A
22	A	241	U
22	A	247	G
22	A	250	G
22	A	257	A
22	A	267	A
22	A	274	A
22	A	282	G
22	A	283	C
22	A	285	U
22	A	286	G
22	A	287	C

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Mol	Chain	Res	Type
22	A	289	U
22	A	290	C
22	A	295	G
22	A	296	G
22	A	298	U
22	A	300	U
22	A	301	A
22	A	306	A
22	A	307	C
22	A	308	U
22	A	309	C
22	A	313	A
22	A	320	U
22	A	323	A
22	A	345	G
22	A	354	A
22	A	372	A
22	A	373	A
22	A	374	C
22	A	375	A
22	A	388	A
22	A	404	A
22	A	406	A
22	A	412	U
22	A	417	A
22	A	418	G
22	A	419	U
22	A	420	A
22	A	432	G
22	A	433	U
22	A	457	G
22	A	458	A
22	A	470	G
22	A	490	C
22	A	501	C
22	A	503	A
22	A	513	G
22	A	527	G
22	A	536	A
22	A	550	A
22	A	553	U
22	A	554	C

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Mol	Chain	Res	Type
22	A	555	C
22	A	566	U
22	A	567	G
22	A	576	U
22	A	577	A
22	A	578	G
22	A	591	A
22	A	592	A
22	A	593	U
22	A	594	G
22	A	606	G
22	A	616	G
22	A	618	A
22	A	629	A
22	A	646	A
22	A	657	A
22	A	658	A
22	A	659	A
22	A	666	A
22	A	667	G
22	A	672	A
22	A	679	G
22	A	682	A
22	A	689	A
22	A	690	U
22	A	699	U
22	A	700	A
22	A	718	C
22	A	732	U
22	A	758	G
22	A	761	A
22	A	775	G
22	A	776	U
22	A	786	C
22	A	793	U
22	A	794	G
22	A	810	A
22	A	811	G
22	A	821	G
22	A	824	G
22	A	828	A
22	A	830	U

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Mol	Chain	Res	Type
22	A	836	U
22	A	838	G
22	A	851	G
22	A	852	C
22	A	858	C
22	A	865	A
22	A	873	U
22	A	874	U
22	A	890	G
22	A	891	U
22	A	892	A
22	A	893	A
22	A	913	A
22	A	923	C
22	A	924	U
22	A	925	A
22	A	930	C
22	A	931	C
22	A	942	U
22	A	943	A
22	A	946	G
22	A	957	A
22	A	959	C
22	A	964	A
22	A	970	A
22	A	973	U
22	A	974	A
22	A	976	U
22	A	979	U
22	A	980	A
22	A	987	A
22	A	992	G
22	A	1007	G
22	A	1020	A
22	A	1025	A
22	A	1029	A
22	A	1036	A
22	A	1042	A
22	A	1051	C
22	A	1058	U
22	A	1059	A
22	A	1067	A

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Mol	Chain	Res	Type
22	A	1068	G
22	A	1072	A
22	A	1073	A
22	A	1079	U
22	A	1092	A
22	A	1093	G
22	A	1094	A
22	A	1101	G
22	A	1106	U
22	A	1113	A
22	A	1115	A
22	A	1116	A
22	A	1117	G
22	A	1129	G
22	A	1134	A
22	A	1141	A
22	A	1142	A
22	A	1153	G
22	A	1156	G
22	A	1157	A
22	A	1158	G
22	A	1161	A
22	A	1173	A
22	A	1174	A
22	A	1178	U
22	A	1179	A
22	A	1181	C
22	A	1182	G
22	A	1185	G
22	A	1187	U
22	A	1188	A
22	A	1203	A
22	A	1230	G
22	A	1249	A
22	A	1250	G
22	A	1254	G
22	A	1257	G
22	A	1265	A
22	A	1283	G
22	A	1298	A
22	A	1301	G
22	A	1302	C

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Mol	Chain	Res	Type
22	A	1311	G
22	A	1316	G
22	A	1317	A
22	A	1320	G
22	A	1328	A
22	A	1333	C
22	A	1344	A
22	A	1345	A
22	A	1365	A
22	A	1369	C
22	A	1373	U
22	A	1392	G
22	A	1394	C
22	A	1396	U
22	A	1409	A
22	A	1423	U
22	A	1429	A
22	A	1430	C
22	A	1435	A
22	A	1439	A
22	A	1462	U
22	A	1463	U
22	A	1464	A
22	A	1465	A
22	A	1466	C
22	A	1469	A
22	A	1478	C
22	A	1494	A
22	A	1509	A
22	A	1519	A
22	A	1528	G
22	A	1529	U
22	A	1530	G
22	A	1531	U
22	A	1532	G
22	A	1533	A
22	A	1534	G
22	A	1535	A
22	A	1539	A
22	A	1542	C
22	A	1543	A
22	A	1546	U

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Mol	Chain	Res	Type
22	A	1553	C
22	A	1556	G
22	A	1557	C
22	A	1558	G
22	A	1559	A
22	A	1562	C
22	A	1563	A
22	A	1564	U
22	A	1570	G
22	A	1571	U
22	A	1573	A
22	A	1574	U
22	A	1575	G
22	A	1610	A
22	A	1618	A
22	A	1619	A
22	A	1621	A
22	A	1630	U
22	A	1638	G
22	A	1656	C
22	A	1657	A
22	A	1659	A
22	A	1695	A
22	A	1696	G
22	A	1697	C
22	A	1700	G
22	A	1701	A
22	A	1723	G
22	A	1724	C
22	A	1749	A
22	A	1750	A
22	A	1761	A
22	A	1762	U
22	A	1763	U
22	A	1764	A
22	A	1771	A
22	A	1772	A
22	A	1773	G
22	A	1780	A
22	A	1781	G
22	A	1782	A
22	A	1783	G

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Mol	Chain	Res	Type
22	A	1787	C
22	A	1789	G
22	A	1795	A
22	A	1796	G
22	A	1797	G
22	A	1806	A
22	A	1809	G
22	A	1815	C
22	A	1816	A
22	A	1819	A
22	A	1833	C
22	A	1834	A
22	A	1842	A
22	A	1849	C
22	A	1862	A
22	A	1880	A
22	A	1886	A
22	A	1887	A
22	A	1889	A
22	A	1891	G
22	A	1899	A
22	A	1903	U
22	A	1938	C
22	A	1939	G
22	A	1946	A
22	A	1948	U
22	A	1962	G
22	A	1963	G
22	A	1969	A
22	A	1970	A
22	A	1971	A
22	A	1973	U
22	A	1988	U
22	A	1996	C
22	A	2000	C
22	A	2003	A
22	A	2004	A
22	A	2005	G
22	A	2024	U
22	A	2026	U
22	A	2030	A
22	A	2054	G

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Mol	Chain	Res	Type
22	A	2056	A
22	A	2064	A
22	A	2065	G
22	A	2066	A
22	A	2069	C
22	A	2072	G
22	A	2076	C
22	A	2088	C
22	A	2089	G
22	A	2093	A
22	A	2094	G
22	A	2095	A
22	A	2102	G
22	A	2103	G
22	A	2126	G
22	A	2127	A
22	A	2133	U
22	A	2144	U
22	A	2149	G
22	A	2150	A
22	A	2153	G
22	A	2159	A
22	A	2165	A
22	A	2178	C
22	A	2181	G
22	A	2190	G
22	A	2191	A
22	A	2202	G
22	A	2203	G
22	A	2205	U
22	A	2206	A
22	A	2223	A
22	A	2224	C
22	A	2236	G
22	A	2237	C
22	A	2245	A
22	A	2256	A
22	A	2258	A
22	A	2259	C
22	A	2271	G
22	A	2272	G
22	A	2312	G

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Mol	Chain	Res	Type
22	A	2316	C
22	A	2320	A
22	A	2321	A
22	A	2329	U
22	A	2337	G
22	A	2338	A
22	A	2341	G
22	A	2346	C
22	A	2353	A
22	A	2354	G
22	A	2355	A
22	A	2358	G
22	A	2360	A
22	A	2367	C
22	A	2380	C
22	A	2383	C
22	A	2394	A
22	A	2412	G
22	A	2416	G
22	A	2418	C
22	A	2420	U
22	A	2435	U
22	A	2439	C
22	A	2447	G
22	A	2455	C
22	A	2458	A
22	A	2462	G
22	A	2463	A
22	A	2473	C
22	A	2474	C
22	A	2481	A
22	A	2485	C
22	A	2498	C
22	A	2509	A
22	A	2535	G
22	A	2536	A
22	A	2537	U
22	A	2538	G
22	A	2551	A
22	A	2562	G
22	A	2587	U
22	A	2599	A

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Mol	Chain	Res	Type
22	A	2600	G
22	A	2606	C
22	A	2607	G
22	A	2615	G
22	A	2618	U
22	A	2635	A
22	A	2643	C
22	A	2646	U
22	A	2648	U
22	A	2663	G
22	A	2679	C
22	A	2694	G
22	A	2722	U
22	A	2724	C
22	A	2747	G
22	A	2759	U
22	A	2766	C
22	A	2777	G
22	A	2781	A
22	A	2790	A
22	A	2798	A
22	A	2799	G
22	A	2810	G
22	A	2811	A
22	A	2812	U
22	A	2813	G
22	A	2822	C
22	A	2824	U
22	A	2827	C
22	A	2828	U
22	A	2830	C
22	A	2832	G
22	A	2835	A
22	A	2849	A
22	A	2862	A
22	A	2864	A
22	A	2872	G
22	A	2878	G
22	A	2890	U
22	A	2896	G
22	A	2901	G
22	A	2902	A

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Mol	Chain	Res	Type
22	A	2909	C
22	A	2913	U
22	A	2920	A
22	A	2928	A
22	A	2929	C
23	B	10	U
23	B	23	U
23	B	24	C
23	B	33	U
23	B	39	C
23	B	40	C
23	B	51	A
23	B	54	U
23	B	55	A
23	B	87	U
23	B	88	C
23	B	107	G

All (30) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	A	27	G
22	A	88	G
22	A	92	G
22	A	139	A
22	A	553	U
22	A	688	A
22	A	756	A
22	A	809	G
22	A	847	G
22	A	854	G
22	A	929	G
22	A	979	U
22	A	1017	C
22	A	1172	A
22	A	1248	A
22	A	1249	A
22	A	1497	G
22	A	1528	G
22	A	1532	G
22	A	1533	A
22	A	1569	U

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Mol	Chain	Res	Type
22	A	1886	A
22	A	1888	G
22	A	2189	G
22	A	2320	A
22	A	2438	G
22	A	2472	A
22	A	2535	G
22	A	2789	U
22	A	2809	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 453 ligands modelled in this entry, 453 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

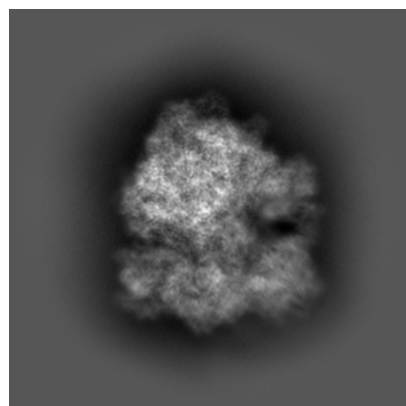
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42554. These allow visual inspection of the internal detail of the map and identification of artifacts.

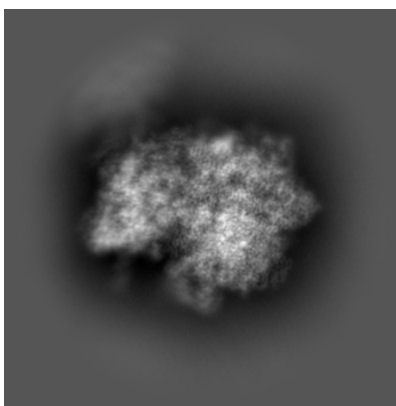
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

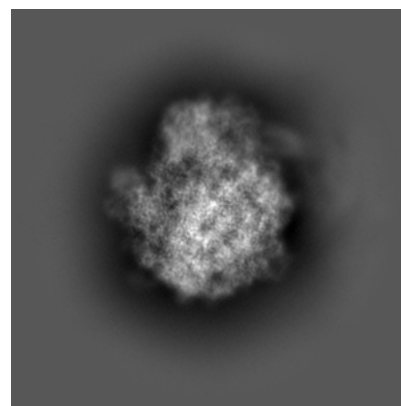
6.1.1 Primary map



X

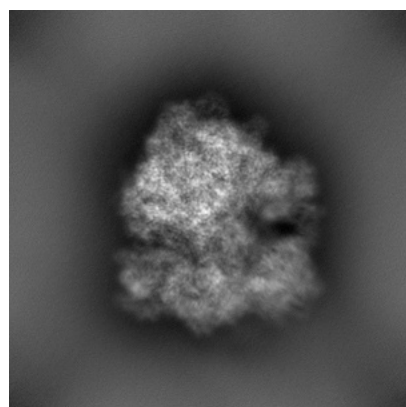


Y

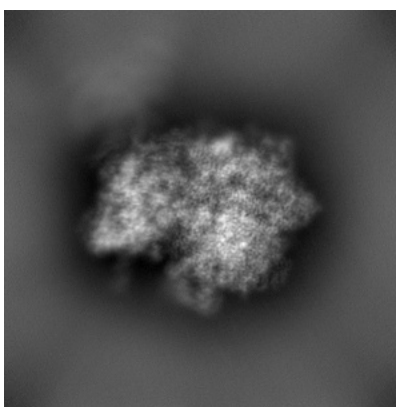


Z

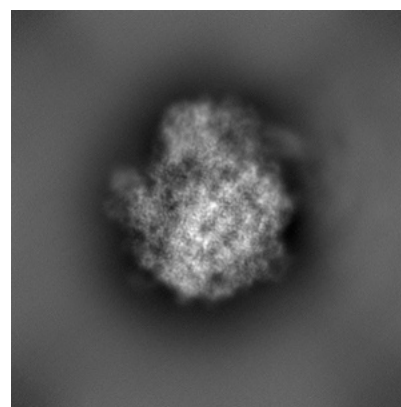
6.1.2 Raw map



X



Y

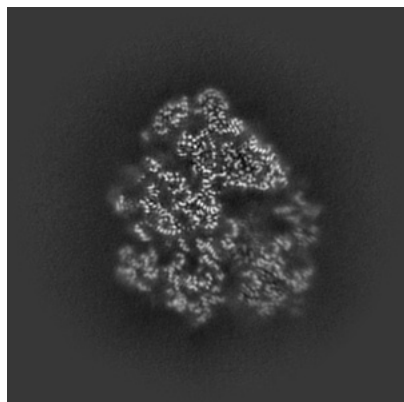


Z

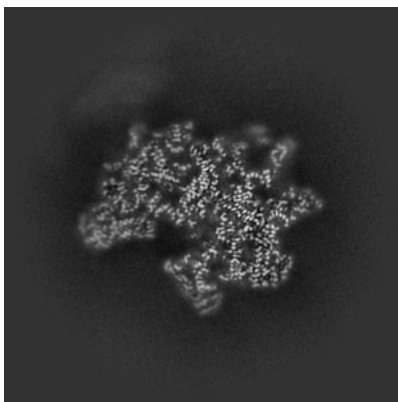
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

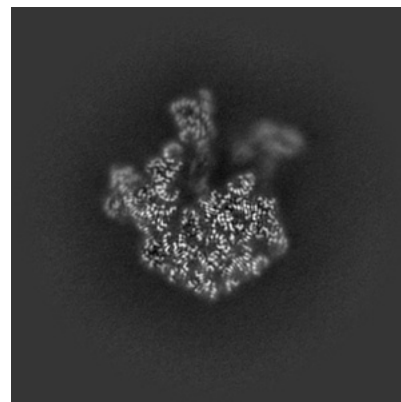
6.2.1 Primary map



X Index: 256

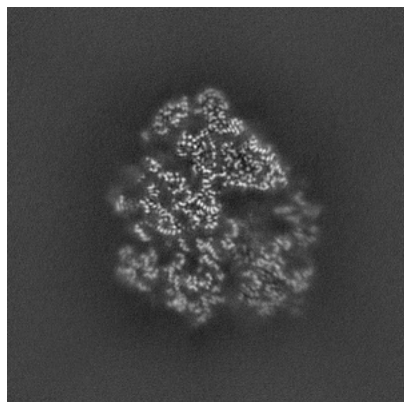


Y Index: 256

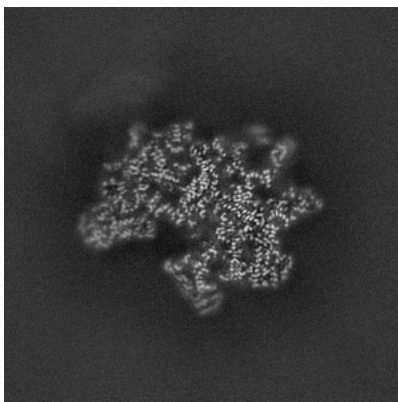


Z Index: 256

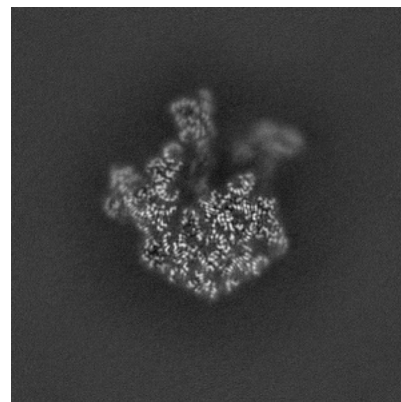
6.2.2 Raw map



X Index: 256



Y Index: 256

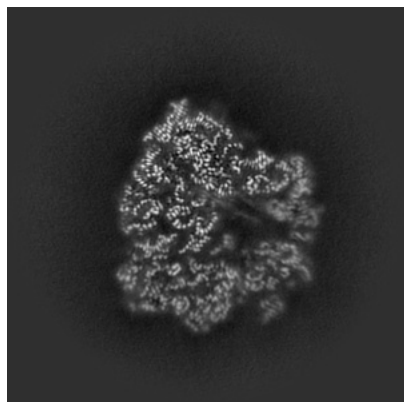


Z Index: 256

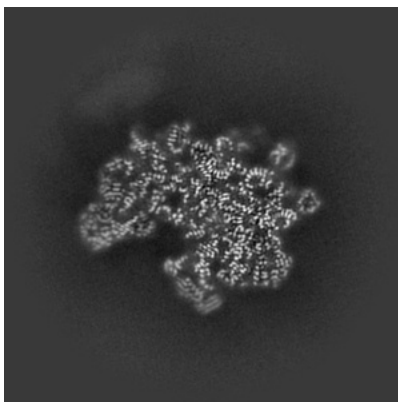
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

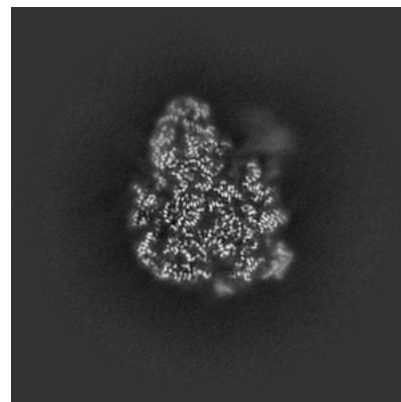
6.3.1 Primary map



X Index: 240

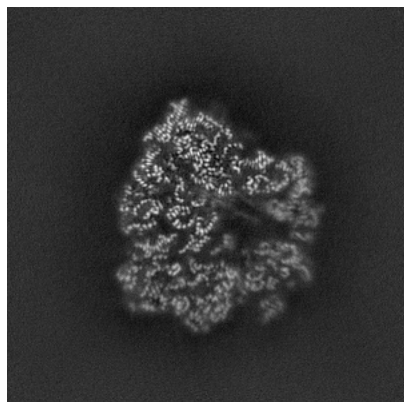


Y Index: 251

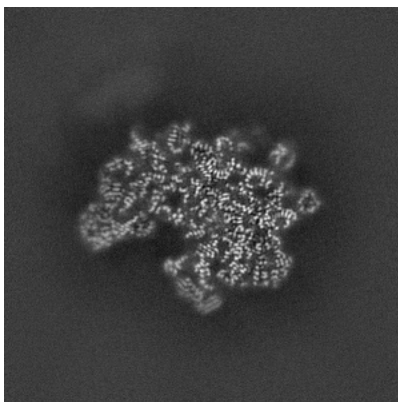


Z Index: 288

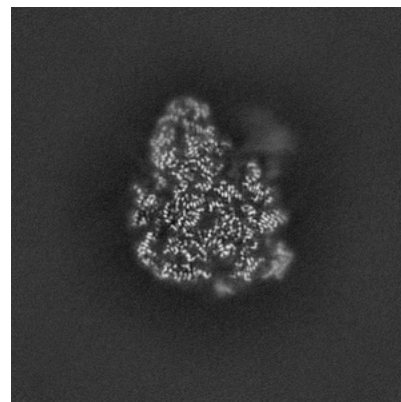
6.3.2 Raw map



X Index: 240



Y Index: 251

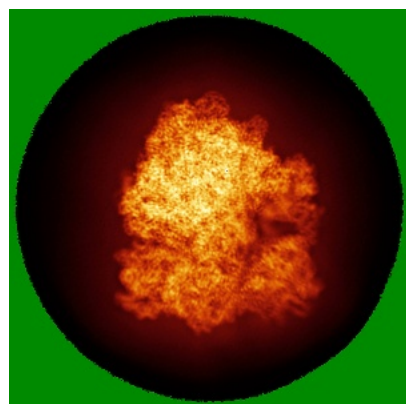


Z Index: 288

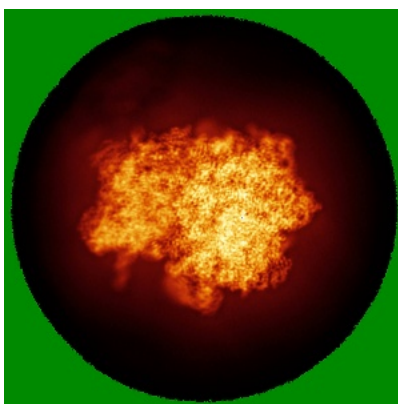
The images above show the largest variance slices of the map in three orthogonal directions.

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

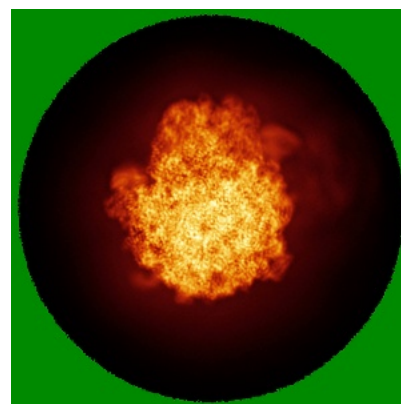
6.4.1 Primary map



X

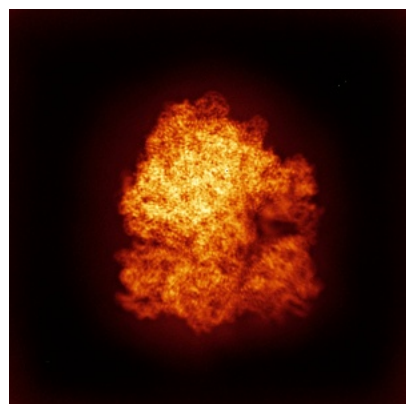


Y

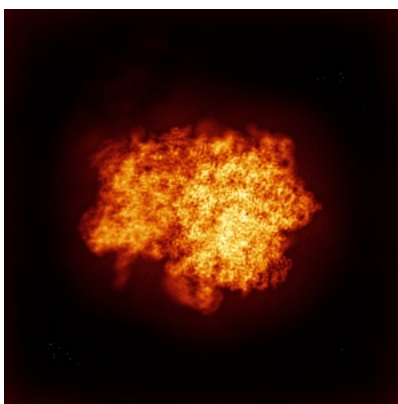


Z

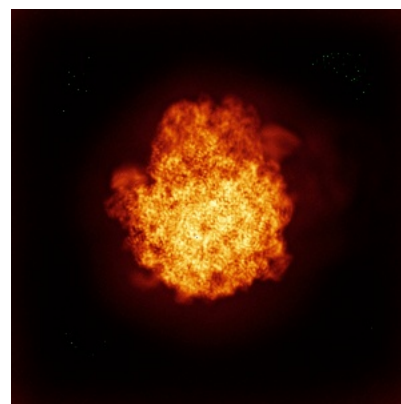
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

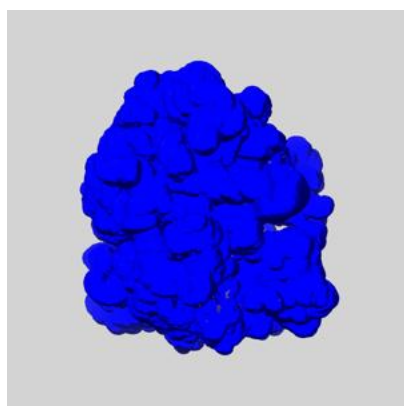
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

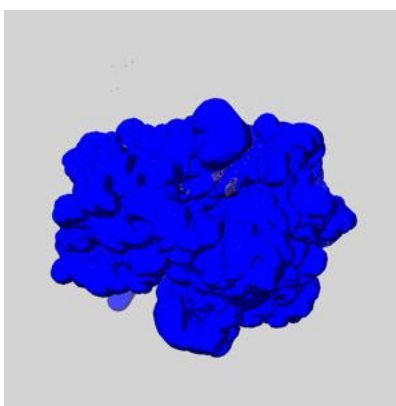
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

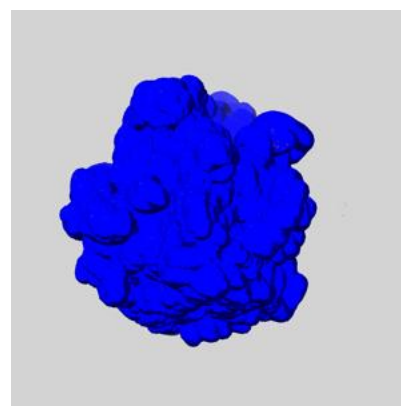
6.6.1 emd_42554_msk_1.map [i](#)



X



Y

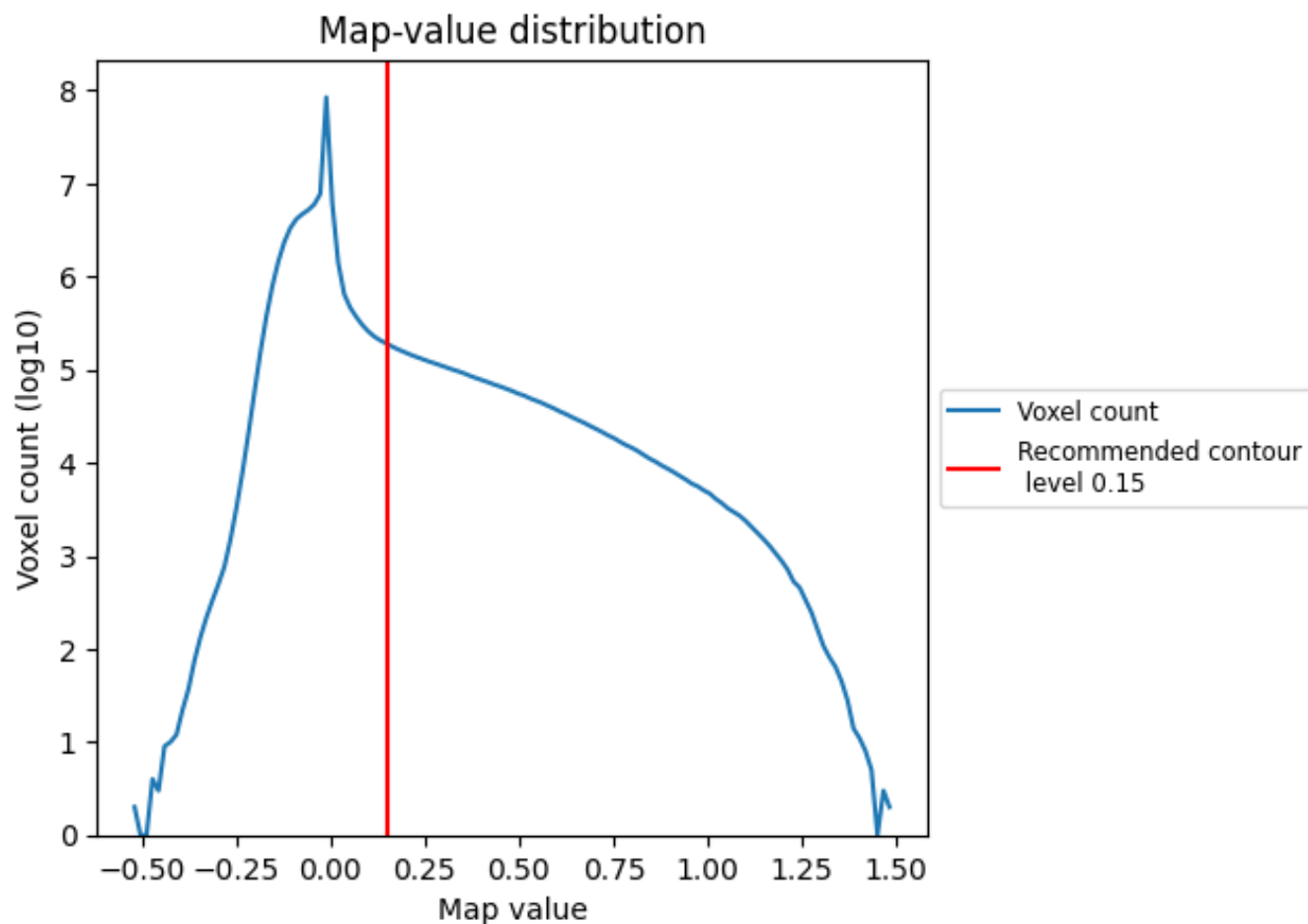


Z

7 Map analysis [i](#)

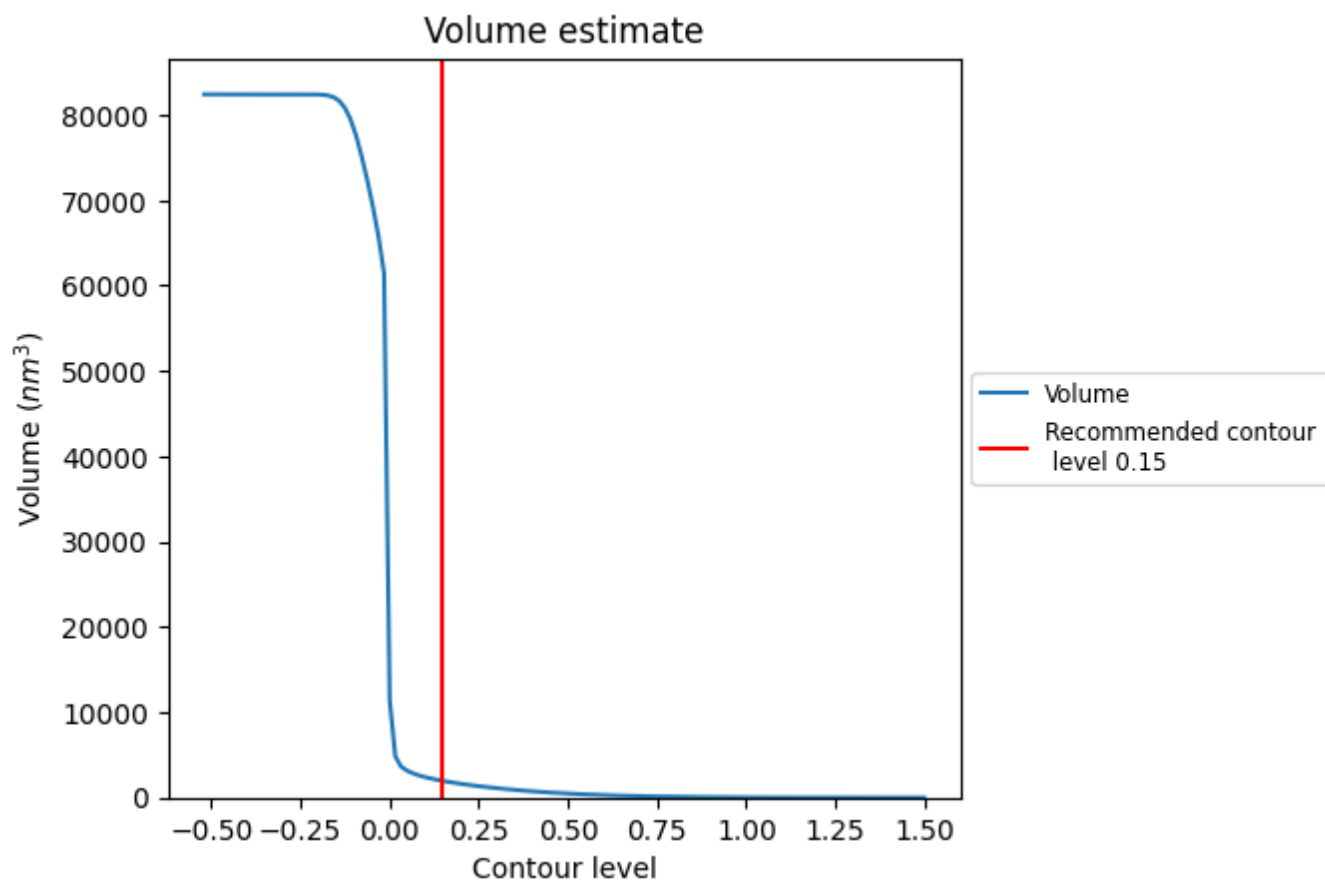
This section contains the results of statistical analysis of the map.

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.

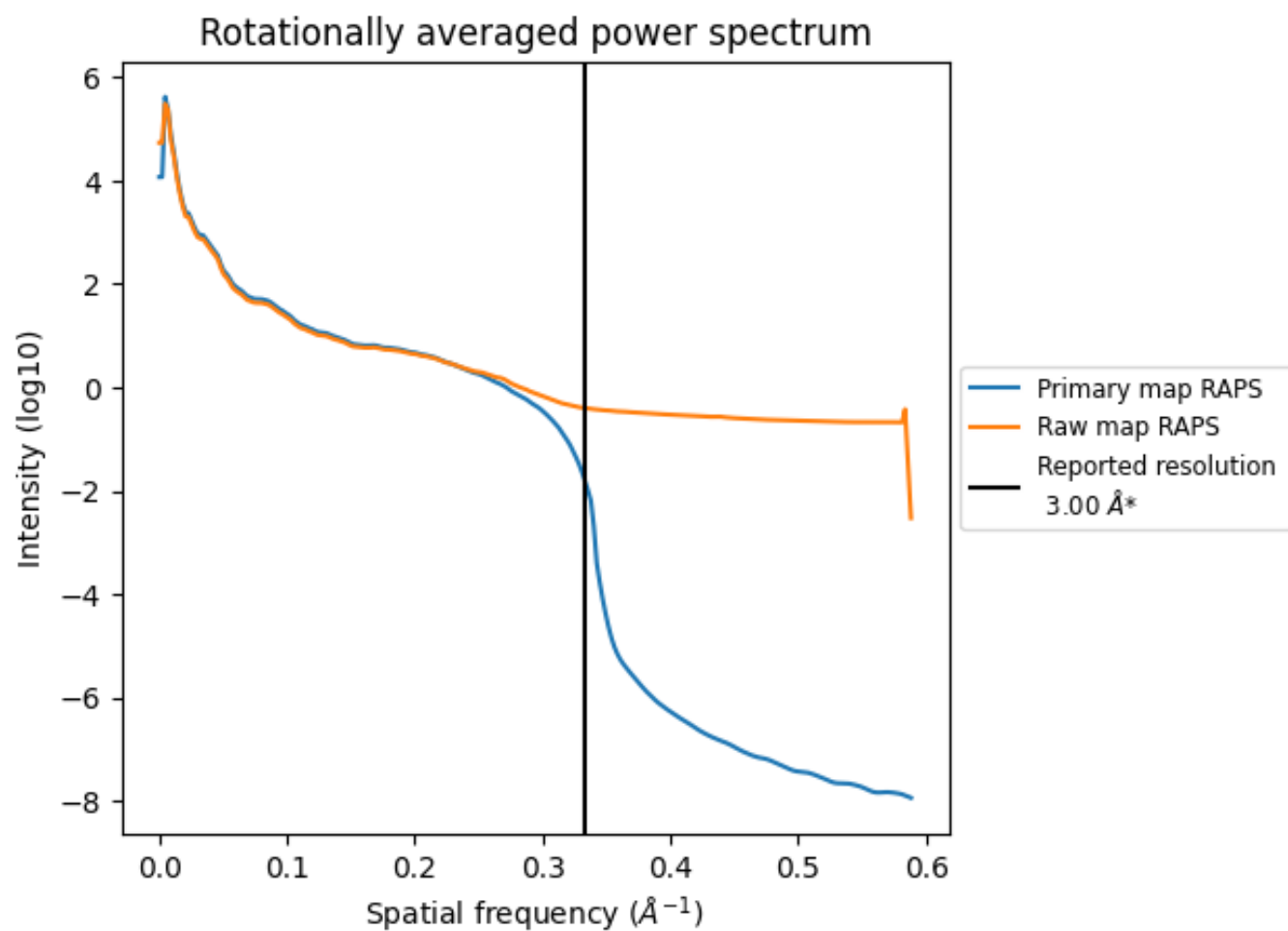
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1950 nm³; this corresponds to an approximate mass of 1761 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 ⓘ

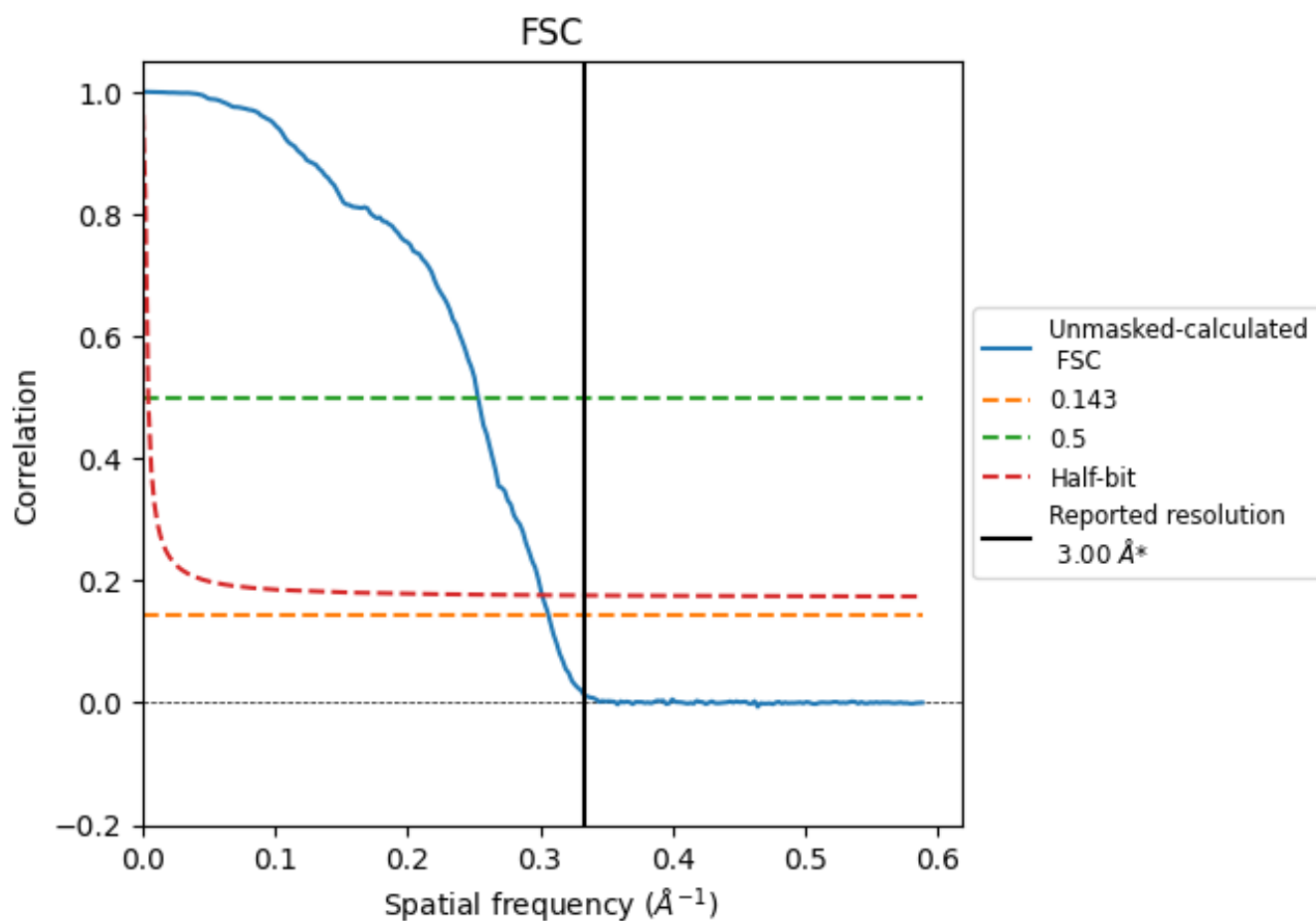


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

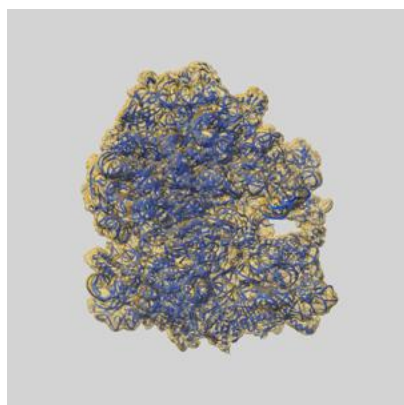
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.26	3.95	3.32

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

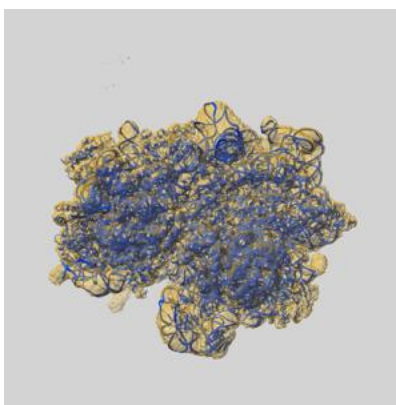
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42554 and PDB model 8UU4. Per-residue inclusion information can be found in section [3](#) on page [14](#).

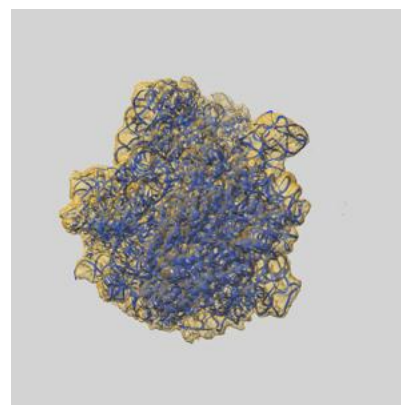
9.1 Map-model overlay [i](#)



X



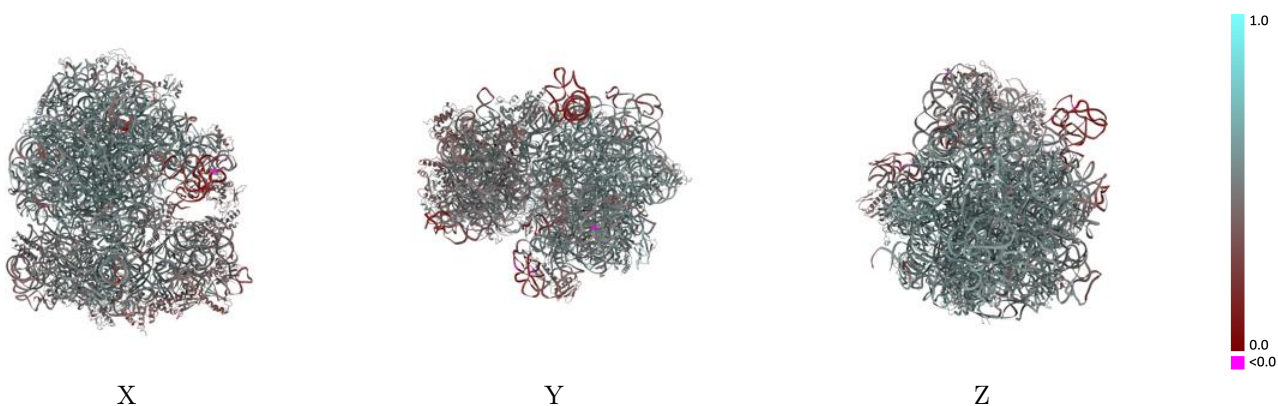
Y



Z

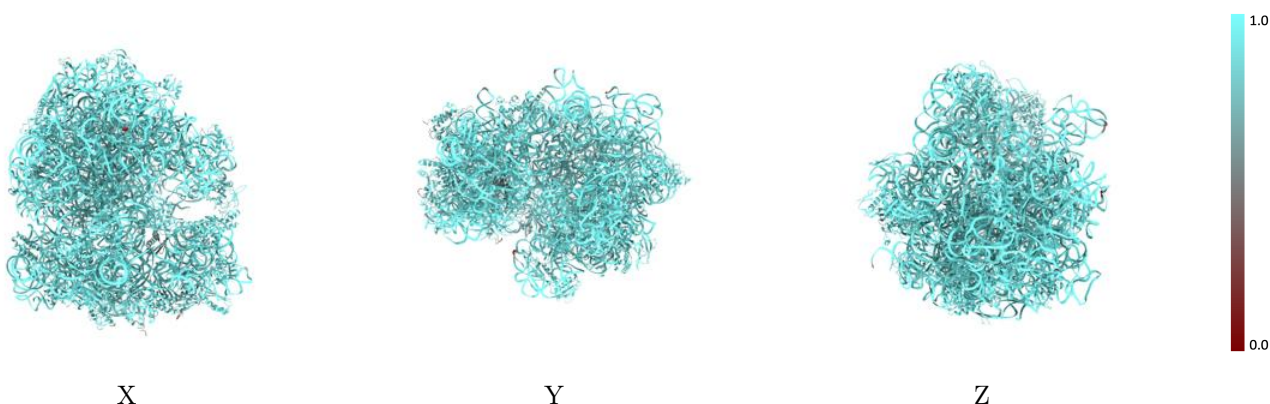
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



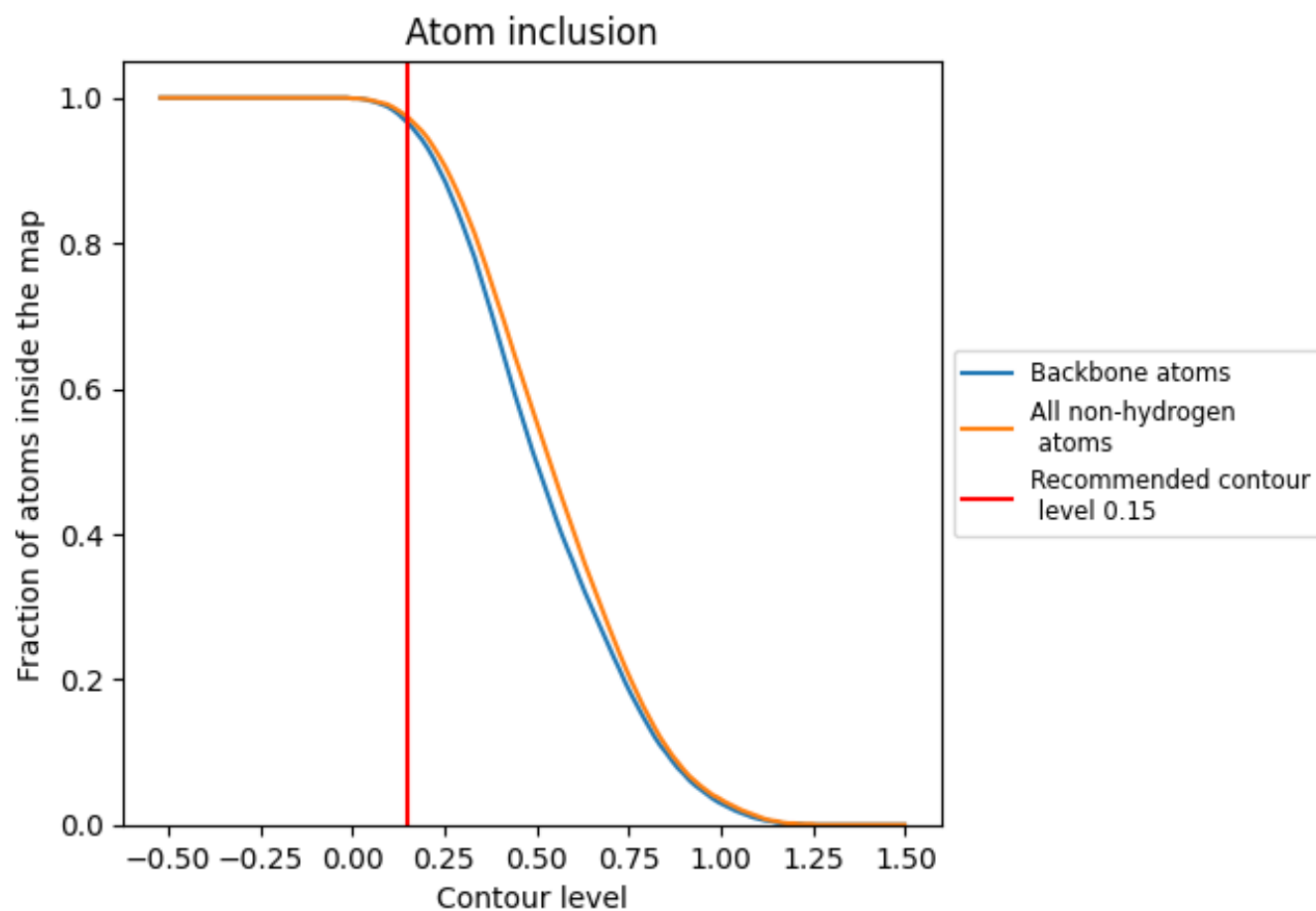
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9740	 0.5080
1	 0.9270	 0.4940
2	 0.9620	 0.5450
3	 0.9280	 0.4080
4	 0.9680	 0.5580
5	 0.9390	 0.5390
6	 0.9910	 0.5830
7	 0.9780	 0.5870
8	 0.9720	 0.5510
A	 0.9910	 0.5250
B	 0.9980	 0.4730
C	 0.9780	 0.5740
D	 0.9670	 0.5610
E	 0.9650	 0.5370
F	 0.9160	 0.4230
G	 0.9470	 0.4310
L	 0.9710	 0.5590
M	 0.9510	 0.5580
N	 0.9580	 0.5250
O	 0.9810	 0.5510
P	 0.9730	 0.5520
Q	 0.9590	 0.4660
R	 0.9550	 0.5570
S	 0.9790	 0.5620
T	 0.9670	 0.5570
U	 0.9760	 0.5610
V	 0.9580	 0.5390
W	 0.9150	 0.5000
Y	 0.9730	 0.5630
Z	 0.9850	 0.5540
a	 0.9930	 0.4850
b	 0.8180	 0.4100
c	 0.8480	 0.4510
d	 0.9400	 0.4670
e	 0.9090	 0.5050



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Chain	Atom inclusion	Q-score
f	 0.9280	 0.4860
g	 0.9250	 0.4230
h	 0.9320	 0.4960
i	 0.9360	 0.4400
j	 0.9180	 0.4420
k	 0.9330	 0.4740
l	 0.9190	 0.5080
m	 0.9500	 0.4450
n	 0.9070	 0.4810
o	 0.9610	 0.5000
p	 0.9390	 0.4680
q	 0.8980	 0.4720
r	 0.9280	 0.5080
s	 0.8830	 0.4430
t	 0.9340	 0.4600
w	 0.6900	 0.4350