



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:08 PM UTC

PDB ID : 6ZMT / pdb_00006zmt
EMDB ID : EMD-11301
Title : SARS-CoV-2 Nsp1 bound to a pre-40S-like ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-03
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

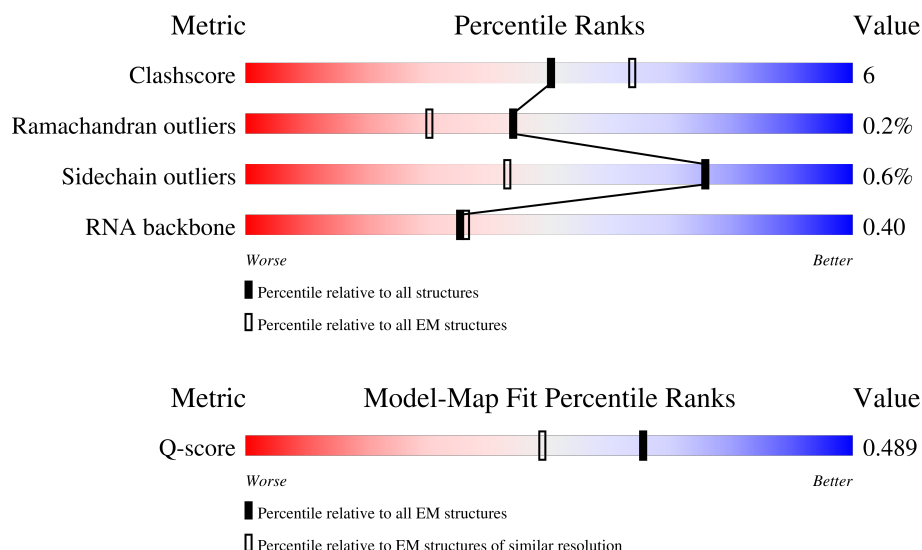
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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	B	295	
2	C	264	
3	D	293	

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Mol	Chain	Length	Quality of chain
4	E	263	
5	F	243	
6	G	249	
7	H	194	
8	I	208	
9	J	194	
10	K	204	
11	L	158	
12	M	165	
13	N	151	
14	O	132	
15	P	151	
16	Q	145	
17	R	146	
18	S	135	
19	T	152	
20	U	145	
21	V	119	
22	W	130	
23	X	143	
24	Y	133	
25	Z	83	
26	a	125	
27	b	84	
28	d	69	

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Mol	Chain	Length	Quality of chain
29	e	59	7% 86% 8% 5%
30	f	56	79% 16%
31	g	156	18% 31% 10% 59%
32	j	317	12% 81% 18%
33	2	1868	50% 28% 6% 16%
34	i	180	14% 84%
35	u	804	30% 62% 14% 24%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 76190 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	206	Total	C	N	O	S	0	0
			1624	1035	287	294	8		

- Molecule 2 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 3 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	218	Total	C	N	O	S	0	0
			1682	1090	289	293	10		

- Molecule 4 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	225	Total	C	N	O	S	0	0
			1748	1115	315	311	7		

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 9 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 10 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 12 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 15 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	122	Total	C	N	O	S	0	0
			897	555	166	170	6		

- Molecule 16 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 17 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 18 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	130	Total	C	N	O	S	0	0
			1050	661	196	189	4		

- Molecule 19 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 20 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	144	Total	C	N	O	S	0	0
			1122	703	217	199	3		

- Molecule 21 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 22 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 23 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 24 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 25 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 26 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 27 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 28 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	56	Total	C	N	O	S	0	0
			430	263	95	71	1		

- Molecule 30 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 31 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	64	Total	C	N	O	S	0	0
			477	298	87	85	7		

- Molecule 32 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 33 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	1569	Total	C	N	O	P	0	0
			33498	14952	6011	10966	1569		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1772	C	G	conflict	GB 337376

- Molecule 34 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	29	Total	C	N	O	S	0	0
			239	145	43	50	1		

- Molecule 35 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	u	615	Total	C	N	O	S	0	0
			4954	3179	885	866	24		

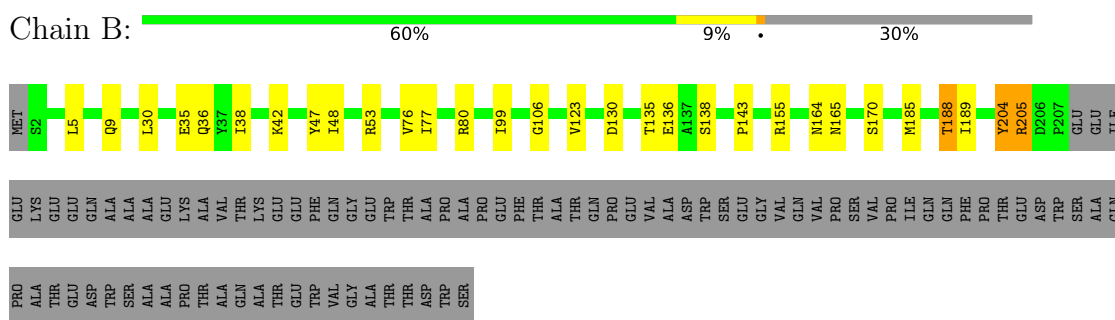
- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	f	1	Total	Zn	0
			1	1	
36	g	1	Total	Zn	0
			1	1	

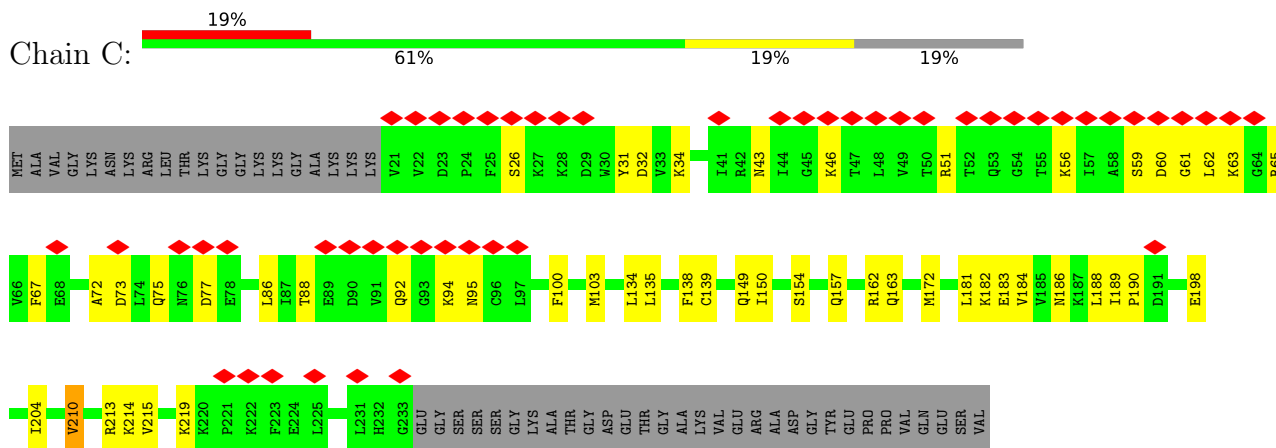
3 Residue-property plots

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

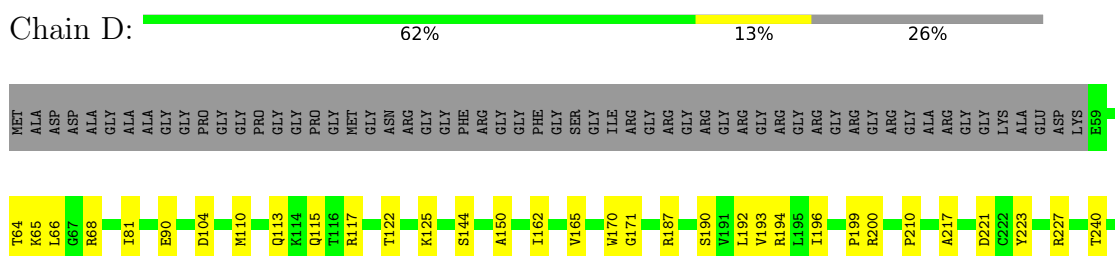
• Molecule 1: 40S ribosomal protein SA

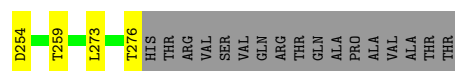


• Molecule 2: 40S ribosomal protein S3a

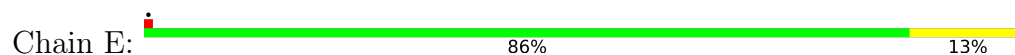


• Molecule 3: 40S ribosomal protein S2

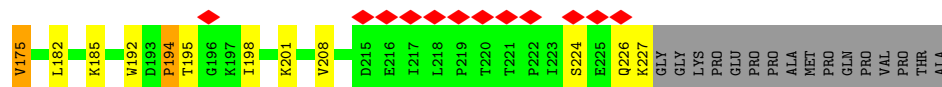
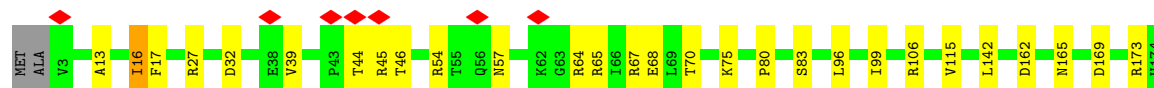
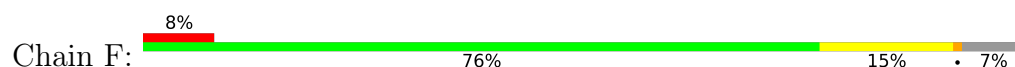




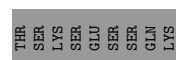
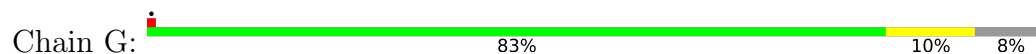
- Molecule 4: 40S ribosomal protein S4, X isoform



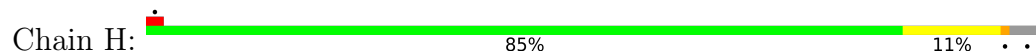
- Molecule 5: 40S ribosomal protein S3



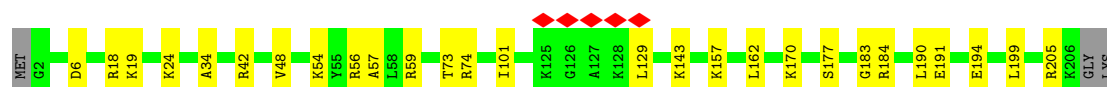
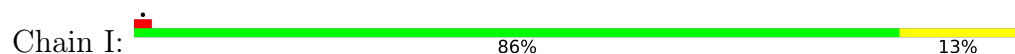
- Molecule 6: 40S ribosomal protein S6



- Molecule 7: 40S ribosomal protein S7

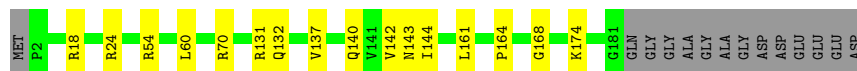


- Molecule 8: 40S ribosomal protein S8



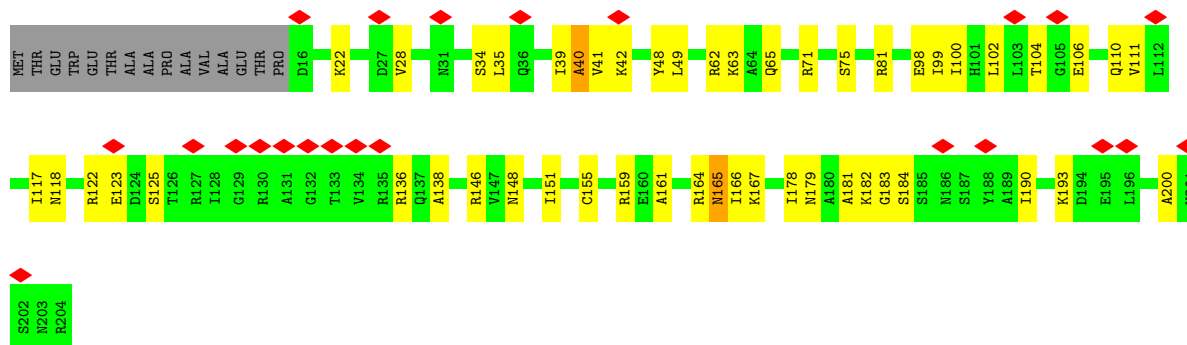
- Molecule 9: 40S ribosomal protein S9

Chain J: 



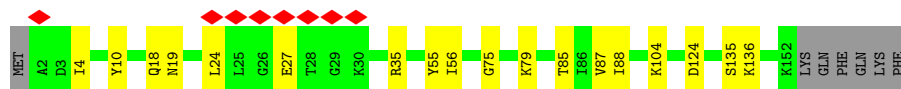
- Molecule 10: 40S ribosomal protein S5

Chain K: 

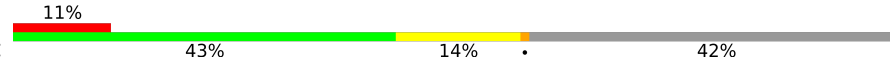


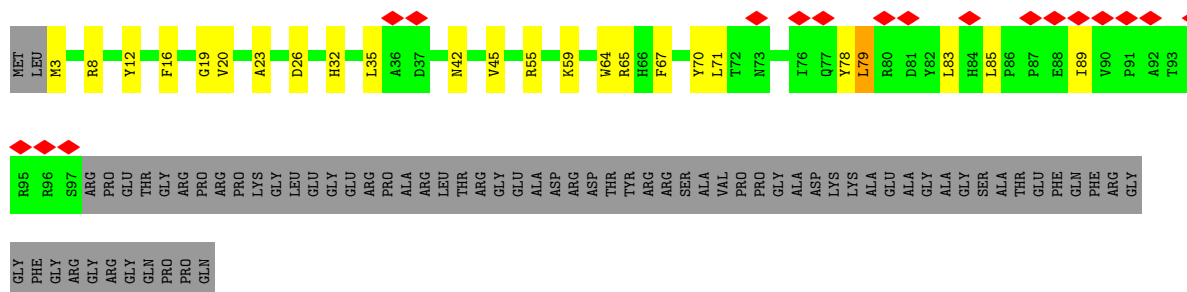
- Molecule 11: 40S ribosomal protein S11

Chain L: 



- Molecule 12: 40S ribosomal protein S10

Chain M: 



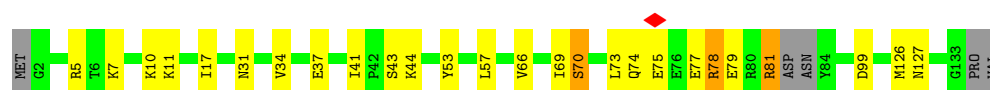
- Molecule 13: 40S ribosomal protein S13

Chain N: 



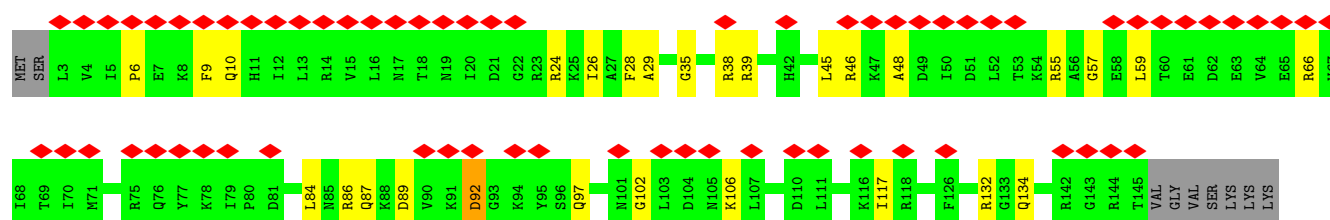
- Molecule 18: 40S ribosomal protein S17

Chain S:  77% 17% 6%



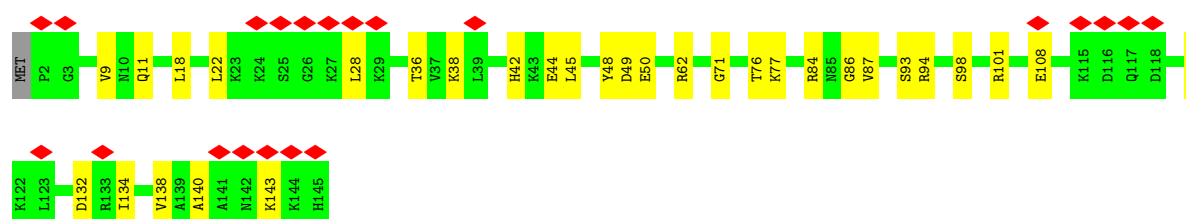
- Molecule 19: 40S ribosomal protein S18

Chain T:  45% 76% 18% 6%



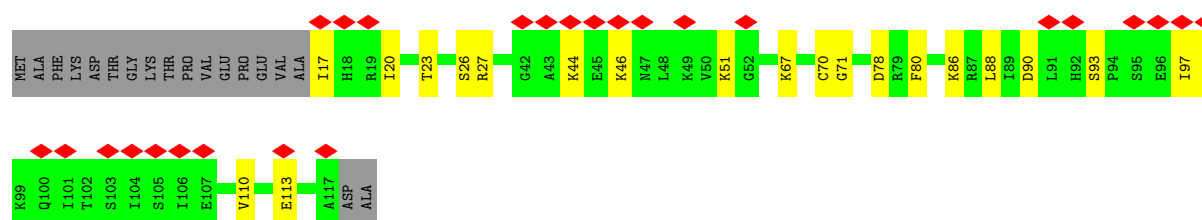
- Molecule 20: 40S ribosomal protein S19

Chain U:  14% 78% 21%



- Molecule 21: 40S ribosomal protein S20

Chain V:  22% 67% 18% 15%



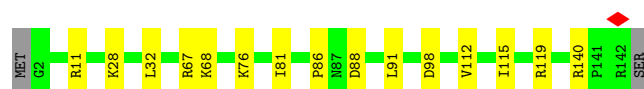
- Molecule 22: 40S ribosomal protein S15a

Chain W:  85% 14%



- Molecule 23: 40S ribosomal protein S23

Chain X:  88% 10%



- Molecule 24: 40S ribosomal protein S24

Chain Y:  74% 20% 7%

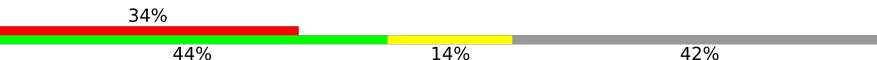


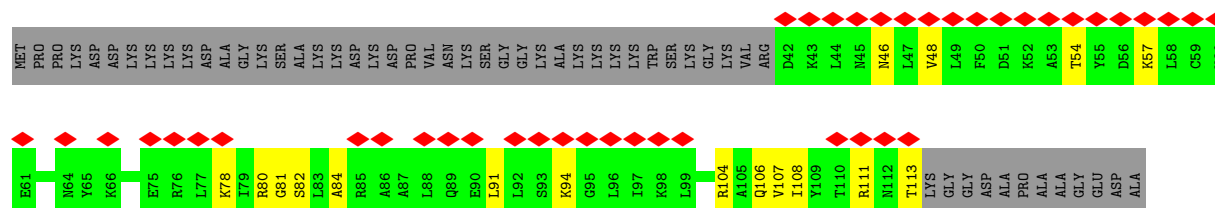
- Molecule 25: 40S ribosomal protein S21

Chain Z:  93% 6%



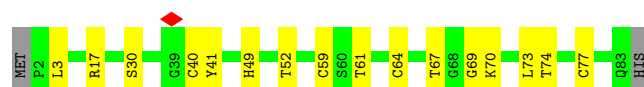
- Molecule 26: 40S ribosomal protein S25

Chain a:  34% 44% 14% 42%



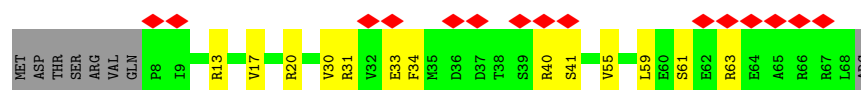
- Molecule 27: 40S ribosomal protein S27

Chain b:  79% 19%



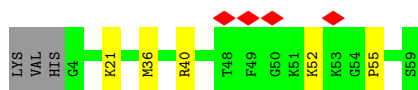
- Molecule 28: 40S ribosomal protein S28

Chain d:  22% 70% 19% 12%

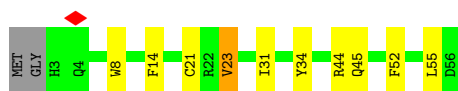
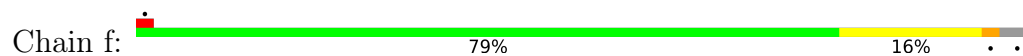


- Molecule 29: 40S ribosomal protein S30

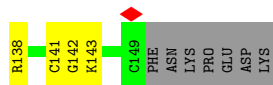
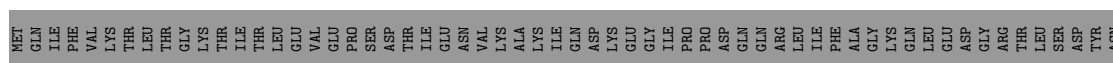
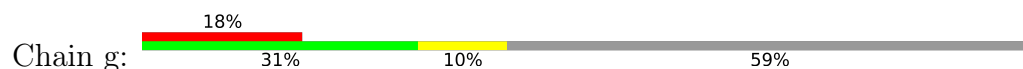
Chain e:  7% 86% 8% 5%



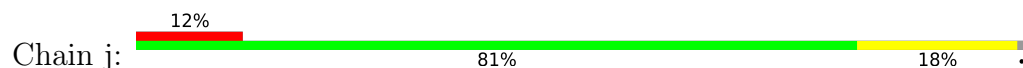
- Molecule 30: 40S ribosomal protein S29



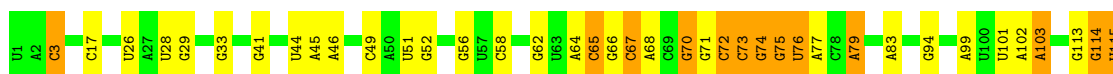
- Molecule 31: Ubiquitin-40S ribosomal protein S27a



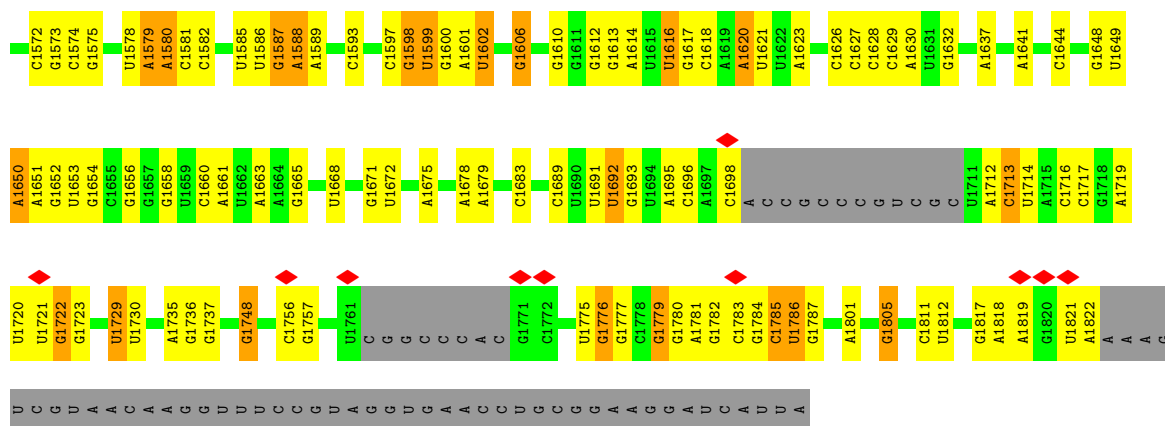
- Molecule 32: Receptor of activated protein C kinase 1



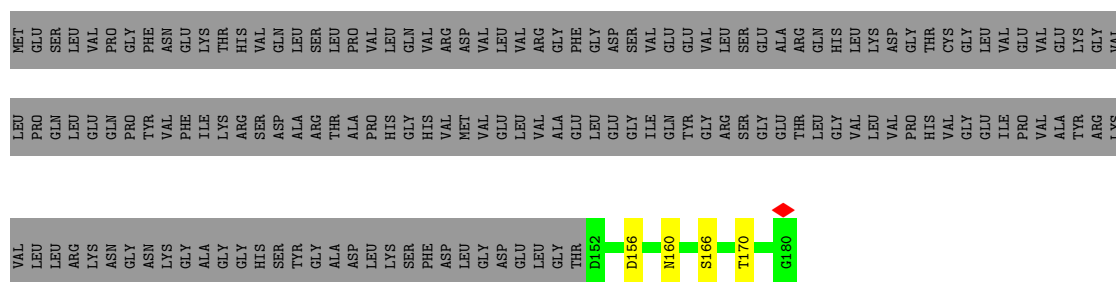
- Molecule 33: 18S ribosomal RNA



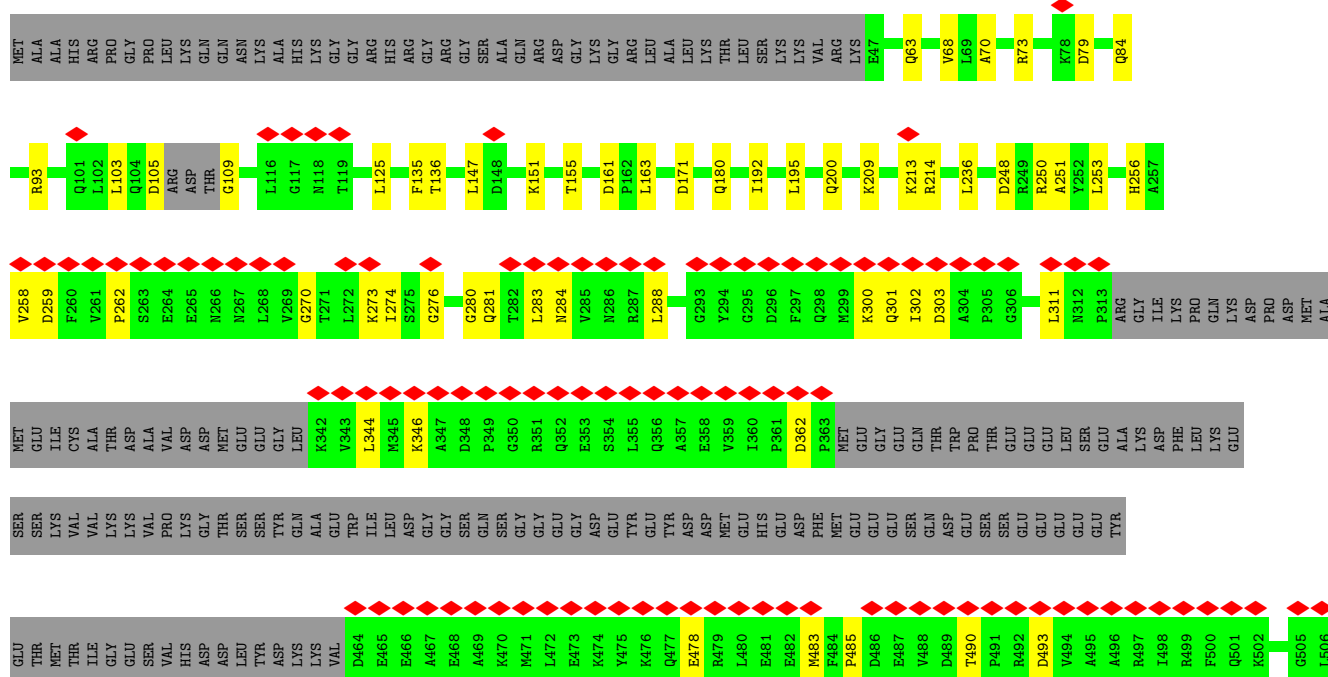
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G1507	C1416	G1322	U1241	U1505	C1415	U1319	A1241	G1501	A
G1510	C	G1325	A1242	U1506	C1416	G1321	U1242	U	U
U1511	C	U1326	U1243	G1507	C	G1322	U1244	U287	C
C1512	C	U1327	G1245	G1508	C	U1325	U1245	A292	A
G1514	C	U1328	A1250	G1509	C	U1326	A1251	C295	A
G1515	C	U1329	C1252	U1510	C	U1327	C1253	U296	A
C1516	C	U1330	A1253	U1511	C	U1328	A1254	A297	C
U1517	C	U1331	G1256	U1512	C	U1329	G1257	G307	C
G1520	C	U1332	U1257	U1513	C	U1330	A1258	G308	A
C1521	C	U1333	G1258	U1514	C	U1331	U1259	G309	C
G1527	C	U1334	A1260	U1515	C	U1332	C1261	C310	C
U1528	C	U1335	G1264	U1516	C	U1333	G1265	C311	C
C1529	C	U1336	A1265	U1517	C	U1334	G1266	C312	C
U1530	C	U1337	G1267	U1518	C	U1335	C1271	C	C
A1531	C	U1338	G1274	U1519	C	U1336	G1275	C	C
C1532	C	U1339	U1275	U1520	C	U1337	A1195	C	C
A1533	C	U1340	U1195	U1521	C	U1338	U1202	C	C
C1534	C	U1341	G1165	U1522	C	U1339	G1203	C	C
U1535	C	U1342	G1166	U1523	C	U1340	U1204	C	C
G1536	C	U1343	G1171	U1524	C	U1341	G1205	C	C
U1537	C	U1344	A1181	U1525	C	U1342	U1206	C	C
C1538	C	U1345	A1182	U1526	C	U1343	G1207	C	C
U1539	C	U1346	U1192	U1527	C	U1344	A1208	C	C
G1540	C	U1347	U1193	U1528	C	U1345	U1209	C	C
C1541	C	U1348	U1194	U1529	C	U1346	G1210	C	C
U1542	C	U1349	U1195	U1530	C	U1347	U1211	C	C
G1543	C	U1350	U1196	U1531	C	U1348	U1212	C	C
C1544	C	U1351	U1197	U1532	C	U1349	U1213	C	C
U1548	C	U1352	U1198	U1533	C	U1350	U1214	C	C
G1549	C	U1353	U1199	U1534	C	U1351	U1215	C	C
U1550	C	U1354	U1200	U1535	C	U1352	U1216	C	C
G1551	C	U1355	U1201	U1536	C	U1353	U1217	C	C
C	C	U1356	U1202	U1537	C	U1354	U1218	C	C
C	C	U1357	U1203	U1538	C	U1355	U1219	C	C
U	C	U1358	U1204	U1539	C	U1356	U1220	C	C
A	C	U1359	U1205	U1540	C	U1357	U1221	C	C
C	C	U1360	U1206	U1541	C	U1358	U1222	C	C
C1558	C	U1361	U1207	U1542	C	U1359	U1223	C	C
C1559	C	U1362	U1208	U1543	C	U1360	U1224	C	C
U1560	C	U1363	U1209	U1544	C	U1361	U1225	C	C
A1561	C	U1364	U1210	U1545	C	U1362	U1226	C	C
C1562	C	U1365	U1211	U1546	C	U1363	U1227	C	C
G1563	C	U1366	U1212	U1547	C	U1364	U1228	C	C
U1492	C	U1367	U1213	U1548	C	U1365	U1229	C	C
C1493	C	U1368	U1214	U1549	C	U1366	U1230	C	C
U1494	C	U1369	U1215	U1550	C	U1367	U1231	C	C
G1495	C	U1370	U1216	U1551	C	U1368	U1232	C	C
C	C	U1371	U1217	U1552	C	U1369	U1233	C	C
C	C	U1372	U1218	U1553	C	U1370	U1234	C	C
C	C	U1373	U1219	U1554	C	U1371	U1235	C	C
C	C	U1374	U1220	U1555	C	U1372	U1236	C	C
C	C	U1375	U1221	U1556	C	U1373	U1237	C	C
C	C	U1376	U1222	U1557	C	U1374	U1238	C	C
C	C	U1377	U1223	U1558	C	U1375	U1239	C	C
C	C	U1378	U1224	U1559	C	U1376	U1240	C	C
C	C	U1379	U1225	U1560	C	U1377	U1241	C	C
C	C	U1380	U1226	U1561	C	U1378	U1242	C	C
C	C	U1381	U1227	U1562	C	U1379	U1243	C	C
C	C	U1382	U1228	U1563	C	U1380	U1244	C	C
C	C	U1383	U1229	U1564	C	U1381	U1245	C	C
C	C	U1384	U1230	U1565	C	U1382	U1246	C	C
C	C	U1385	U1231	U1566	C	U1383	U1247	C	C
C	C	U1386	U1232	U1567	C	U1384	U1248	C	C
C	C	U1387	U1233	U1568	C	U1385	U1249	C	C
C	C	U1388	U1234	U1569	C	U1386	U1250	C	C
C	C	U1389	U1235	U1570	C	U1387	U1251	C	C
C	C	U1390	U1236	U1571	C	U1388	U1252	C	C
C	C	U1391	U1237	U1572	C	U1389	U1253	C	C
C	C	U1392	U1238	U1573	C	U1390	U1254	C	C
C	C	U1393	U1239	U1574	C	U1391	U1255	C	C
C	C	U1394	U1240	U1575	C	U1392	U1256	C	C
C	C	U1395	U1241	U1576	C	U1393	U1257	C	C
C	C	U1396	U1242	U1577	C	U1394	U1258	C	C
C	C	U1397	U1243	U1578	C	U1395	U1259	C	C
C	C	U1398	U1244	U1579	C	U1396	U1260	C	C
C	C	U1399	U1245	U1580	C	U1397	U1261	C	C
C	C	U1400	U1246	U1581	C	U1398	U1262	C	C
C	C	U1401	U1247	U1582	C	U1399	U1263	C	C
C	C	U1402	U1248	U1583	C	U1400	U1264	C	C
C	C	U1403	U1249	U1584	C	U1401	U1265	C	C
C	C	U1404	U1250	U1585	C	U1402	U1266	C	C
C	C	U1405	U1251	U1586	C	U1403	U1267	C	C
C	C	U1406	U1252	U1587	C	U1404	U1268	C	C
C	C	U1407	U1253	U1588	C	U1405	U1269	C	C
C	C	U1408	U1254	U1589	C	U1406	U1270	C	C
C	C	U1409	U1255	U1590	C	U1407	U1271	C	C
C	C	U1410	U1256	U1591	C	U1408	U1272	C	C
C	C	U1411	U1257	U1592	C	U1409	U1273	C	C
C	C	U1412	U1258	U1593	C	U1410	U1274	C	C
C	C	U1413	U1259	U1594	C	U1411	U1275	C	C
C	C	U1414	U1260	U1595	C	U1412	U1276	C	C
C	C	U1415	U1261	U1596	C	U1413	U1277	C	C
C	C	U1416	U1262	U1597	C	U1414	U1278	C	C
C	C	U1417	U1263	U1598	C	U1415	U1279	C	C
C	C	U1418	U1264	U1599	C	U1416	U1280	C	C
C	C	U1419	U1265	U1600	C	U1417	U1281	C	C
C	C	U1420	U1266	U1601	C	U1418	U1282	C	C
C	C	U1421	U1267	U1602	C	U1419	U1283	C	C
C	C	U1422	U1268	U1603	C	U1420	U1284	C	C
C	C	U1423	U1269	U1604	C	U1421	U1285	C	C
C	C	U1424	U1270	U1605	C	U1422	U1286	C	C
C	C	U1425	U1271	U1606	C	U1423	U1287	C	C
C	C	U1426	U1272	U1607	C	U1424	U1288	C	C
C	C	U1427	U1273	U1608	C	U1425	U1289	C	C
C	C	U1428	U1274	U1609	C	U1426	U1290	C	C
C	C	U1429	U1275	U1610	C	U1427	U1291	C	C
C	C	U1430	U1276	U1611	C	U1428	U1292	C	C
C	C	U1431	U1277	U1612	C	U1429	U1293	C	C
C	C	U1432	U1278	U1613	C	U1430	U1294	C	C
C	C	U1433	U1279	U1614	C	U1431	U1295	C	C
C	C	U1434	U1280	U1615	C	U1432	U1296	C	C
C	C	U1435	U1281	U1616	C	U1433	U1297	C	C
C	C	U1436	U1282	U1617	C	U1434	U1298	C	C
C	C	U1437	U1283	U1618	C	U1435	U1299	C	C
C	C	U1438	U1284	U1619	C	U1436	U1300	C	C
C	C	U1439	U1285	U1620	C	U1437	U1301	C	C
C	C	U1440	U1286	U1621	C	U1438	U1302	C	C
C	C	U1441	U1287	U1622	C	U1439	U1303	C	C
C	C	U1442	U1288	U1623	C	U1440	U1304	C	C
C	C	U1443	U1289	U1624	C	U1441	U1305	C	C
C	C	U1444	U1290	U1625	C	U1442	U1306	C	C
C	C	U1445	U1291	U1626	C	U1443	U1307	C	C
C	C	U1446	U1292	U1627	C	U1444	U1308	C	C
C	C	U1447	U1293	U1628	C	U1445	U1309	C	C
C	C	U1448	U1294	U1629	C	U1446	U1310	C	C
C	C	U1449	U1295	U1630	C	U1447	U1311	C	C
C	C	U1450	U1296	U1631	C	U1448	U1312	C	C
C	C	U1451	U1297	U1632	C	U1449	U1313	C	C
C	C	U1452	U1298	U1633	C	U1450	U1314	C	C
C	C	U1453	U1299	U1634	C	U1451	U1315	C	C
C	C	U1454	U1300	U1635	C	U1452	U1316	C	C
C	C	U1455	U1301	U1636	C	U1453	U1317	C	C
C	C	U1456	U1302	U1637	C	U1454	U1318	C	C
C	C	U1457	U1303	U1638	C	U1455	U1319	C	C
C	C	U1458	U1304	U1639	C	U1456	U1320	C	C
C	C	U1459	U1305	U1640	C	U1457	U1321	C	C
C	C	U1460	U1306	U1641	C	U1458	U1322	C	C
C	C	U1461	U1307	U1642	C	U1459	U1323	C	C
C	C	U1462	U1308	U1643	C	U1460	U1324	C	C
C	C	U1463	U1309	U1644	C	U1461	U1325	C	C
C	C	U1464	U1310	U1645	C	U1462	U1326	C	C
C	C	U1465	U1311	U1646	C	U1463	U1327	C	C
C	C	U1466	U1312	U1647	C	U1464	U1328	C	C
C	C	U1467	U1313	U1648	C	U1465	U1329	C	C
C	C	U1468	U1314	U1649	C	U1466	U1330	C	C
C	C	U1469	U1315	U1650	C	U1467	U1331	C	C
C	C	U1470	U1316	U1651	C	U1468	U1332	C	C
C	C	U1471	U1317	U1652	C	U1469	U1333	C	C
C	C	U1472	U1318	U1653	C	U1470	U1334	C	C
C	C	U1473	U1319						

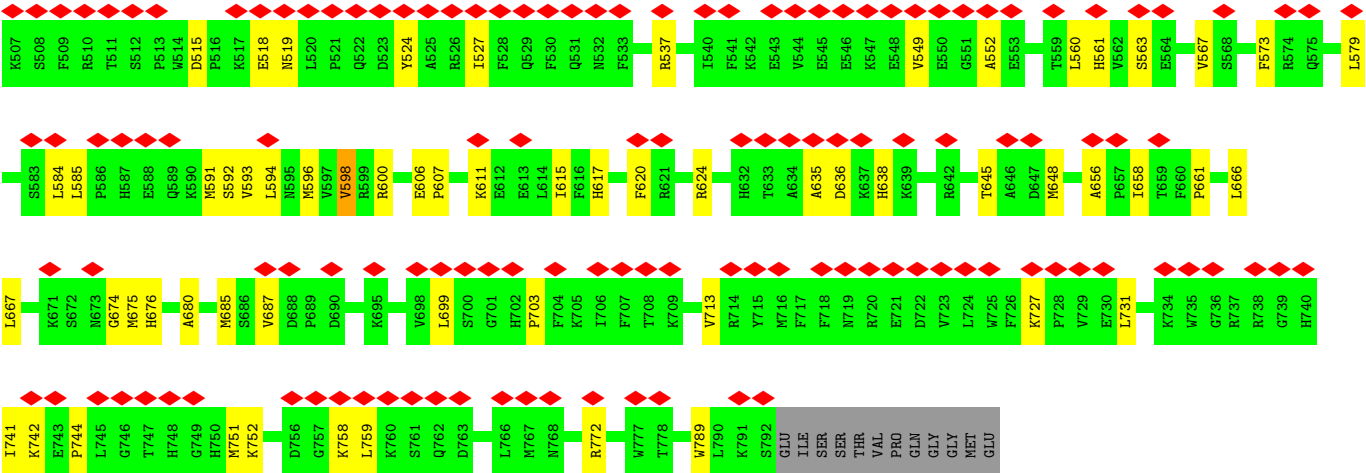


• Molecule 34: Non-structural protein 1



• Molecule 35: Pre-rRNA-processing protein TSR1 homolog





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35506	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.380	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.038	Depositor
Map size (Å)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	B	0.52	1/1661 (0.1%)	0.56	0/2259
2	C	0.24	0/1756	0.51	0/2350
3	D	0.48	0/1718	0.59	0/2322
4	E	0.50	0/2118	0.60	0/2849
5	F	0.30	0/1776	0.54	0/2392
6	G	0.37	0/1885	0.49	0/2510
7	H	0.35	0/1524	0.56	2/2042 (0.1%)
8	I	0.45	1/1711 (0.1%)	0.56	0/2282
9	J	0.49	0/1524	0.63	2/2035 (0.1%)
10	K	0.24	0/1516	0.57	0/2037
11	L	0.48	0/1250	0.55	0/1673
12	M	0.23	0/824	0.55	1/1112 (0.1%)
13	N	0.35	0/1226	0.46	0/1649
14	O	0.21	0/963	0.57	0/1291
15	P	0.17	0/910	0.43	0/1228
16	Q	0.21	0/1003	0.49	0/1341
17	R	0.26	0/1126	0.56	0/1506
18	S	0.48	0/1063	0.68	4/1424 (0.3%)
19	T	0.20	0/1202	0.53	0/1610
20	U	0.21	0/1142	0.48	0/1530
21	V	0.27	0/813	0.54	0/1092
22	W	0.55	0/1051	0.60	0/1406
23	X	0.48	0/1116	0.61	0/1490
24	Y	0.43	0/1031	0.58	0/1370
25	Z	0.46	0/631	0.51	0/844
26	a	0.24	0/580	0.62	0/780
27	b	0.39	0/653	0.62	0/876
28	d	0.19	0/481	0.47	0/643
29	e	0.38	0/434	0.76	0/571
30	f	0.30	0/466	0.63	0/618
31	g	0.19	0/485	0.52	0/650
32	j	0.21	0/2497	0.49	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	2	0.44	0/37453	0.50	6/58357 (0.0%)
34	i	0.39	0/244	0.48	0/328
35	u	0.21	0/5076	0.50	0/6860
All	All	0.40	2/80909 (0.0%)	0.53	15/116726 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
5	F	0	1
10	K	0	2
17	R	0	1
22	W	0	1
23	X	0	1
24	Y	0	1
29	e	0	1
All	All	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	204	TYR	CA-C	-6.57	1.44	1.53
8	I	18	ARG	C-N	-5.24	1.22	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	J	137	VAL	CA-C-N	6.71	134.35	121.54
9	J	137	VAL	C-N-CA	6.71	134.35	121.54
33	2	114	G	P-O3'-C3'	6.42	129.84	120.20
7	H	65	PRO	CA-C-N	6.41	124.28	120.24
7	H	65	PRO	C-N-CA	6.41	124.28	120.24
18	S	43	SER	CA-C-N	6.26	129.51	120.38
18	S	43	SER	C-N-CA	6.26	129.51	120.38
33	2	114	G	C2'-C3'-O3'	6.13	118.70	109.50
12	M	45	VAL	N-CA-C	-5.89	107.07	112.96
18	S	43	SER	N-CA-C	5.23	117.67	110.35
33	2	1403	C	P-O3'-C3'	5.19	127.98	120.20
33	2	1373	C	C4'-C3'-O3'	5.10	120.65	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	S	70	SER	N-CA-C	5.05	117.62	110.10
33	2	1494	U	P-O3'-C3'	5.04	127.76	120.20
33	2	1308	U	P-O3'-C3'	5.01	127.72	120.20

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	188	THR	Peptide
5	F	194	PRO	Peptide
10	K	165	ASN	Peptide
10	K	40	ALA	Peptide
17	R	15	ARG	Peptide
22	W	54	ASP	Peptide
23	X	112	VAL	Peptide
24	Y	118	ARG	Peptide
29	e	55	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1624	0	1634	22	0
2	C	1729	0	1803	35	0
3	D	1682	0	1769	24	0
4	E	2076	0	2177	22	0
5	F	1748	0	1844	28	0
6	G	1862	0	2018	20	0
7	H	1501	0	1593	15	0
8	I	1682	0	1769	20	0
9	J	1499	0	1618	11	0
10	K	1495	0	1549	33	0
11	L	1229	0	1302	12	0
12	M	800	0	818	16	0
13	N	1202	0	1289	13	0
14	O	953	0	990	15	0
15	P	897	0	907	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	Q	984	0	1028	19	0
17	R	1109	0	1174	19	0
18	S	1050	0	1105	20	0
19	T	1184	0	1244	20	0
20	U	1122	0	1153	24	0
21	V	803	0	873	16	0
22	W	1034	0	1080	11	0
23	X	1098	0	1167	9	0
24	Y	1014	0	1082	16	0
25	Z	625	0	628	5	0
26	a	574	0	627	15	0
27	b	640	0	665	10	0
28	d	479	0	507	9	0
29	e	430	0	464	3	0
30	f	455	0	446	9	0
31	g	477	0	439	10	0
32	j	2440	0	2396	35	0
33	2	33498	0	16915	241	0
34	i	239	0	211	2	0
35	u	4954	0	5014	67	0
36	f	1	0	0	0	0
36	g	1	0	0	0	0
All	All	76190	0	61298	727	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 (727) 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)
18:S:66:VAL:N	18:S:74:GLN:OE1	1.82	1.11
33:2:1206:G:H1	33:2:1692:U:H3	1.04	0.93
33:2:531:A:H2	33:2:552:G:H1	1.21	0.86
33:2:1656:G:H1	33:2:1668:U:H3	1.26	0.83
33:2:197:U:H3	33:2:202:G:H1	1.25	0.80
33:2:1533:A:H62	33:2:1602:U:H3	1.32	0.78
33:2:1227:G:H1	33:2:1531:A:H61	1.32	0.76
33:2:1748:G:H1	33:2:1786:U:H3	1.32	0.75
33:2:70:G:H21	33:2:79:A:H62	1.36	0.74
19:T:102:GLY:O	19:T:106:LYS:HB2	1.90	0.70
33:2:531:A:C2	33:2:552:G:N1	2.52	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:13:GLN:HE22	33:2:153:G:H21	1.41	0.69
33:2:925:G:H1	33:2:1017:U:H3	1.41	0.68
18:S:78:ARG:CZ	18:S:78:ARG:HB3	2.25	0.66
22:W:2:VAL:N	33:2:1091:C:HO2'	1.93	0.66
23:X:119:ARG:NH2	33:2:1192:U:OP2	2.28	0.66
3:D:210:PRO:HB3	3:D:240:THR:HG21	1.77	0.65
1:B:205:ARG:HH11	1:B:205:ARG:HB3	1.62	0.64
18:S:77:GLU:HA	18:S:77:GLU:OE1	1.95	0.64
20:U:62:ARG:HH12	33:2:1542:C:H5''	1.62	0.64
32:j:159:ASN:HB3	32:j:204:GLY:HA3	1.78	0.64
3:D:200:ARG:O	9:J:54:ARG:NH2	2.31	0.64
22:W:71:LYS:NZ	33:2:1153:C:OP2	2.31	0.64
35:u:258:VAL:HG13	35:u:274:ILE:HG22	1.80	0.64
13:N:124:ARG:NH1	33:2:677:G:OP1	2.31	0.63
16:Q:111:MET:HE2	19:T:117:ILE:HG23	1.81	0.63
26:a:81:GLY:H	33:2:1598:G:H2'	1.64	0.63
2:C:181:LEU:HA	2:C:184:VAL:HG22	1.81	0.63
11:L:124:ASP:OD1	11:L:124:ASP:N	2.32	0.63
33:2:957:A:H3'	33:2:958:G:H21	1.62	0.63
35:u:303:ASP:HB3	35:u:344:LEU:HD13	1.80	0.63
35:u:527:ILE:HG22	35:u:591:MET:HG3	1.82	0.62
31:g:118:ARG:HG2	31:g:134:SER:H	1.64	0.62
5:F:195:THR:HG22	5:F:201:LYS:HZ3	1.64	0.62
6:G:57:ASP:HB3	6:G:98:ARG:HD2	1.82	0.62
24:Y:29:HIS:NE2	24:Y:69:THR:OG1	2.32	0.62
33:2:1079:C:H4'	33:2:1182:A:H61	1.64	0.62
33:2:64:A:H2	33:2:83:A:H62	1.47	0.62
26:a:80:ARG:HE	33:2:1598:G:H5'	1.64	0.61
6:G:198:ARG:NH1	33:2:126:G:OP1	2.32	0.61
15:P:30:VAL:HG12	15:P:94:HIS:HB2	1.81	0.61
2:C:139:CYS:HB2	2:C:172:MET:HE1	1.83	0.61
4:E:100:ARG:NH2	4:E:121:TYR:O	2.32	0.61
20:U:101:ARG:NH1	33:2:1565:C:OP2	2.34	0.60
33:2:1227:G:H1	33:2:1531:A:N6	1.99	0.60
1:B:80:ARG:NH2	1:B:165:ASN:O	2.34	0.60
26:a:48:VAL:HG22	26:a:80:ARG:HD2	1.83	0.60
33:2:1811:C:O2'	35:u:63:GLN:NE2	2.35	0.60
35:u:283:LEU:HB3	35:u:552:ALA:HB3	1.83	0.60
12:M:3:MET:N	33:2:1314:U:HO2'	1.99	0.60
33:2:1284:A:O2'	33:2:1312:G:N2	2.35	0.60
31:g:135:HIS:HD2	31:g:138:ARG:HE	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:24:LEU:HA	11:L:27:GLU:HB3	1.82	0.60
15:P:83:GLN:HA	15:P:86:LYS:HE2	1.83	0.60
35:u:151:LYS:HB3	35:u:180:GLN:HE22	1.67	0.59
1:B:155:ARG:NH2	33:2:1138:C:OP1	2.35	0.59
18:S:7:LYS:O	18:S:11:LYS:HB2	2.02	0.59
20:U:98:SER:OG	33:2:1566:G:N7	2.34	0.59
13:N:64:ARG:NH2	33:2:919:A:OP2	2.36	0.59
30:f:55:LEU:HD13	33:2:1391:C:H4'	1.84	0.59
21:V:51:LYS:HB2	21:V:90:ASP:HB3	1.83	0.59
33:2:928:G:H1	33:2:1013:U:H3	1.50	0.59
33:2:1286:G:O2'	33:2:1313:A:N6	2.36	0.59
2:C:103:MET:HG3	2:C:188:LEU:HD21	1.85	0.58
33:2:1722:G:O6	33:2:1812:U:O2	2.21	0.58
9:J:174:LYS:HE2	33:2:560:A:H5'	1.83	0.58
15:P:55:ARG:NH2	33:2:954:U:O2	2.37	0.58
19:T:55:ARG:HH22	26:a:82:SER:HB3	1.69	0.58
33:2:103:A:OP2	33:2:356:C:N4	2.35	0.58
27:b:40:CYS:SG	27:b:41:TYR:N	2.77	0.58
32:j:89:LEU:HB2	32:j:99:ARG:HB2	1.86	0.58
10:K:122:ARG:HE	28:d:59:LEU:HD21	1.68	0.58
20:U:86:GLY:HA2	33:2:1606:G:H5'	1.85	0.58
33:2:531:A:N1	33:2:552:G:O6	2.36	0.58
1:B:188:THR:OG1	1:B:189:ILE:N	2.34	0.58
33:2:71:G:H21	33:2:72:C:H41	1.52	0.58
1:B:205:ARG:HH11	1:B:205:ARG:CB	2.17	0.58
7:H:66:VAL:HG22	7:H:96:ALA:HB1	1.86	0.58
20:U:108:GLU:OE2	20:U:121:ARG:NH1	2.36	0.58
24:Y:29:HIS:HE2	24:Y:69:THR:HG1	1.51	0.58
33:2:1589:A:N3	33:2:1653:U:O2'	2.35	0.58
35:u:105:ASP:OD1	35:u:109:GLY:N	2.37	0.58
4:E:182:MET:HB2	4:E:228:ILE:HD11	1.86	0.57
31:g:123:SER:OG	31:g:126:CYS:SG	2.62	0.57
35:u:744:PRO:HA	35:u:751:MET:HA	1.86	0.57
14:O:93:LYS:HE2	14:O:102:LYS:HB3	1.86	0.57
16:Q:42:ARG:NH2	33:2:1614:A:OP2	2.37	0.57
33:2:115:U:OP1	33:2:382:C:O2'	2.20	0.57
17:R:126:ARG:NH1	33:2:1394:G:OP1	2.37	0.57
32:j:31:ILE:HB	32:j:43:TRP:HB2	1.85	0.57
33:2:594:A:H61	33:2:643:A:H5''	1.70	0.57
8:I:6:ASP:OD1	8:I:6:ASP:N	2.35	0.57
11:L:104:LYS:O	23:X:11:ARG:NH2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:48:ALA:O	19:T:66:ARG:NH2	2.37	0.57
35:u:125:LEU:HD11	35:u:311:LEU:HA	1.85	0.57
9:J:132:GLN:HB2	33:2:562:U:H4'	1.87	0.57
29:e:36:MET:SD	29:e:40:ARG:NH2	2.75	0.57
35:u:302:ILE:HD11	35:u:346:LYS:HB2	1.87	0.57
5:F:57:ASN:O	5:F:65:ARG:NH2	2.38	0.57
6:G:134:GLY:O	33:2:65:C:N4	2.38	0.57
6:G:181:THR:HG23	6:G:183:ARG:H	1.70	0.57
18:S:70:SER:OG	18:S:73:LEU:HB3	2.04	0.57
22:W:30:CYS:SG	22:W:31:SER:N	2.78	0.57
16:Q:93:MET:HE1	16:Q:106:GLU:HG3	1.86	0.57
35:u:742:LYS:HD3	35:u:752:LYS:HB3	1.86	0.57
27:b:49:HIS:ND1	27:b:69:GLY:O	2.37	0.57
32:j:107:ASP:HB2	32:j:125:ARG:HG3	1.86	0.57
35:u:301:GLN:HB3	35:u:561:HIS:HB2	1.86	0.57
10:K:35:LEU:HD21	10:K:146:ARG:HD2	1.87	0.56
19:T:38:ARG:HE	20:U:45:LEU:HD21	1.70	0.56
33:2:885:U:O2	33:2:901:G:N2	2.34	0.56
35:u:703:PRO:HA	35:u:713:VAL:HA	1.87	0.56
33:2:1441:U:O2	33:2:1443:C:N4	2.37	0.56
35:u:667:LEU:HB2	35:u:680:ALA:HB3	1.87	0.56
12:M:85:LEU:HD13	12:M:89:ILE:HD11	1.88	0.56
21:V:17:ILE:HG12	21:V:20:ILE:HD11	1.86	0.56
2:C:198:GLU:HB3	2:C:210:VAL:HG11	1.87	0.56
5:F:106:ARG:HE	5:F:175:VAL:HA	1.71	0.56
19:T:24:ARG:HB2	19:T:29:ALA:HB2	1.88	0.56
21:V:80:PHE:HB3	30:f:52:PHE:HB3	1.87	0.56
35:u:93:ARG:HH22	35:u:163:LEU:HD12	1.70	0.56
10:K:71:ARG:NH2	10:K:148:ASN:OD1	2.39	0.55
16:Q:23:ASP:OD1	16:Q:23:ASP:N	2.38	0.55
33:2:536:A:H61	33:2:548:C:H42	1.55	0.55
35:u:284:ASN:HD21	35:u:549:VAL:HG21	1.72	0.55
10:K:34:SER:HA	28:d:55:VAL:HG23	1.88	0.55
16:Q:126:VAL:HB	33:2:1521:C:H5'	1.88	0.55
22:W:19:LYS:O	25:Z:22:ARG:NH2	2.40	0.55
2:C:73:ASP:OD1	15:P:128:ARG:NH2	2.39	0.55
33:2:1206:G:O6	33:2:1692:U:O4	2.24	0.55
35:u:256:HIS:HD2	35:u:276:GLY:HA2	1.71	0.55
35:u:573:PHE:HB2	35:u:579:LEU:HD11	1.89	0.55
33:2:197:U:O2	33:2:202:G:N2	2.34	0.55
35:u:251:ALA:HA	35:u:280:GLY:HA3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:72:LYS:HD3	16:Q:93:MET:HE3	1.88	0.55
33:2:940:U:H3	33:2:1002:U:H3	1.54	0.55
10:K:62:ARG:NH1	10:K:65:GLN:OE1	2.40	0.55
20:U:87:VAL:O	33:2:1529:C:O2'	2.24	0.55
6:G:201:LYS:NZ	33:2:125:C:OP2	2.40	0.55
15:P:54:CYS:SG	15:P:55:ARG:N	2.80	0.55
17:R:52:LEU:HB3	17:R:56:LEU:HD13	1.89	0.55
33:2:190:G:O2'	33:2:209:A:N6	2.38	0.55
11:L:4:ILE:HG21	11:L:56:ILE:HD12	1.89	0.55
15:P:55:ARG:NH1	33:2:973:C:N3	2.55	0.55
18:S:81:ARG:HG3	18:S:81:ARG:O	2.07	0.55
33:2:436:G:OP2	33:2:471:G:O2'	2.24	0.55
14:O:91:LEU:HB3	14:O:104:VAL:HB	1.89	0.55
27:b:67:THR:OG1	27:b:70:LYS:O	2.25	0.55
33:2:1722:G:O6	33:2:1812:U:C2	2.60	0.55
8:I:184:ARG:NH2	33:2:218:U:O2	2.40	0.54
16:Q:61:ARG:NH2	16:Q:88:GLU:O	2.40	0.54
23:X:68:LYS:HB3	23:X:91:LEU:HD22	1.89	0.54
26:a:46:ASN:OD1	26:a:78:LYS:NZ	2.40	0.54
1:B:77:ILE:HG12	1:B:99:ILE:HB	1.88	0.54
7:H:105:THR:OG1	7:H:106:ARG:N	2.40	0.54
2:C:182:LYS:O	2:C:186:ASN:ND2	2.40	0.54
19:T:55:ARG:NH2	33:2:1597:C:OP1	2.40	0.54
10:K:81:ARG:NH1	33:2:1533:A:O2'	2.41	0.54
4:E:211:LYS:HE3	4:E:215:GLY:HA2	1.89	0.54
5:F:175:VAL:HG22	5:F:182:LEU:HB2	1.88	0.54
9:J:164:PRO:HA	9:J:168:GLY:HA2	1.89	0.54
12:M:65:ARG:NH1	30:f:21:CYS:O	2.40	0.54
33:2:531:A:N1	33:2:552:G:C6	2.76	0.54
3:D:117:ARG:NH1	33:2:1689:C:OP1	2.40	0.54
7:H:66:VAL:HB	33:2:913:A:H1'	1.90	0.54
16:Q:43:ARG:NH2	33:2:1616:U:OP2	2.39	0.54
16:Q:81:ARG:NH2	16:Q:117:GLY:O	2.40	0.54
32:j:251:ALA:HB2	32:j:289:LEU:HD22	1.89	0.54
9:J:18:ARG:O	9:J:24:ARG:NH1	2.41	0.54
32:j:18:VAL:HA	32:j:35:SER:HA	1.90	0.54
23:X:88:ASP:HB3	33:2:617:G:H4'	1.89	0.54
33:2:1757:G:O6	33:2:1775:U:C2	2.61	0.54
5:F:169:ASP:N	5:F:169:ASP:OD1	2.40	0.54
15:P:85:CYS:HB3	15:P:90:ILE:HB	1.89	0.54
20:U:77:LYS:NZ	33:2:1587:G:OP1	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:45:GLN:HE21	33:2:1495:G:H22	1.56	0.54
35:u:300:LYS:HD3	35:u:563:SER:HA	1.90	0.54
7:H:58:LYS:HB2	7:H:90:LYS:HG2	1.90	0.53
33:2:1821:U:O4	33:2:1822:A:N6	2.40	0.53
35:u:171:ASP:OD1	35:u:214:ARG:NH1	2.41	0.53
2:C:214:LYS:NZ	33:2:943:U:OP1	2.41	0.53
13:N:112:LYS:NZ	33:2:1031:A:O3'	2.41	0.53
17:R:130:LYS:NZ	17:R:134:GLY:O	2.40	0.53
18:S:37:GLU:OE1	32:j:106:LYS:NZ	2.41	0.53
33:2:1566:G:H21	33:2:1569:A:H62	1.57	0.53
4:E:182:MET:HE2	4:E:192:ILE:HD11	1.91	0.53
21:V:70:CYS:SG	21:V:71:GLY:N	2.81	0.53
35:u:151:LYS:HE2	35:u:620:PHE:HA	1.89	0.53
4:E:192:ILE:HB	4:E:243:GLY:HA3	1.90	0.53
12:M:55:ARG:NH1	12:M:78:TYR:OH	2.42	0.53
20:U:140:ALA:HA	20:U:143:LYS:HE2	1.89	0.53
32:j:154:VAL:O	32:j:155:ARG:NH1	2.41	0.53
13:N:29:THR:OG1	13:N:31:ASP:OD1	2.26	0.53
19:T:24:ARG:NH2	19:T:28:PHE:O	2.42	0.53
33:2:1606:G:H22	33:2:1632:G:H2'	1.72	0.53
33:2:1748:G:O6	33:2:1786:U:O4	2.26	0.53
15:P:125:LYS:NZ	15:P:126:ILE:O	2.42	0.53
26:a:54:THR:HA	26:a:57:LYS:HE2	1.90	0.53
33:2:480:G:H4'	35:u:68:VAL:HG11	1.91	0.53
10:K:123:GLU:HG3	10:K:200:ALA:HB1	1.90	0.53
10:K:178:ILE:O	10:K:182:LYS:NZ	2.42	0.53
18:S:17:ILE:HG13	18:S:57:LEU:HD23	1.91	0.53
15:P:66:ARG:NH2	33:2:961:G:O2'	2.41	0.53
6:G:136:LYS:NZ	6:G:175:LYS:O	2.41	0.52
8:I:143:LYS:NZ	33:2:203:G:OP2	2.42	0.52
33:2:1283:C:O2'	33:2:1313:A:N6	2.42	0.52
33:2:1776:G:H2'	33:2:1777:G:H8	1.74	0.52
2:C:65:ARG:NH1	15:P:48:SER:OG	2.38	0.52
33:2:1396:A:O2'	33:2:1398:G:N7	2.41	0.52
12:M:3:MET:N	33:2:1314:U:O2'	2.42	0.52
18:S:126:MET:O	33:2:1124:C:O2'	2.26	0.52
22:W:3:ARG:HD3	22:W:6:VAL:HG23	1.91	0.52
27:b:64:CYS:HB3	27:b:73:LEU:HD23	1.91	0.52
3:D:187:ARG:NH2	33:2:1143:A:OP2	2.43	0.52
4:E:246:LEU:HB3	4:E:250:GLU:HG3	1.91	0.52
12:M:19:GLY:HA3	12:M:71:LEU:HD23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:83:ASP:OD1	13:N:83:ASP:N	2.43	0.52
24:Y:46:LYS:O	24:Y:49:LYS:NZ	2.42	0.52
35:u:161:ASP:OD1	35:u:161:ASP:N	2.42	0.52
15:P:34:PHE:HB3	15:P:41:PHE:HB2	1.90	0.52
17:R:37:ARG:NH2	20:U:11:GLN:OE1	2.43	0.52
28:d:13:ARG:HB2	28:d:33:GLU:HB3	1.92	0.52
33:2:531:A:H2	33:2:552:G:N1	1.97	0.52
5:F:162:ASP:OD1	5:F:165:ASN:ND2	2.39	0.52
35:u:259:ASP:HB2	35:u:273:LYS:HB2	1.91	0.52
35:u:731:LEU:HD11	35:u:741:ILE:HG23	1.92	0.52
1:B:205:ARG:CB	1:B:205:ARG:NH1	2.73	0.52
14:O:86:GLY:HA3	14:O:105:GLY:HA2	1.92	0.52
33:2:1757:G:O6	33:2:1775:U:O2	2.27	0.52
3:D:192:LEU:HB3	3:D:227:ARG:HB3	1.92	0.52
17:R:86:GLN:HE22	17:R:122:ALA:HB2	1.73	0.52
21:V:67:LYS:NZ	21:V:78:ASP:OD1	2.37	0.52
35:u:301:GLN:NE2	35:u:346:LYS:O	2.43	0.52
35:u:478:GLU:HG2	35:u:607:PRO:HG3	1.91	0.52
35:u:493:ASP:N	35:u:493:ASP:OD1	2.43	0.52
10:K:164:ARG:NH1	33:2:1533:A:OP2	2.43	0.52
13:N:70:LYS:HB2	13:N:73:ARG:HD2	1.92	0.52
19:T:132:ARG:HB2	19:T:134:GLN:HE22	1.75	0.52
21:V:23:THR:HB	21:V:113:GLU:HB3	1.92	0.52
24:Y:103:SER:O	24:Y:107:ARG:NH1	2.43	0.52
5:F:13:ALA:HA	5:F:16:ILE:HD12	1.91	0.51
28:d:17:VAL:HA	28:d:30:VAL:HA	1.92	0.51
3:D:193:VAL:HG11	3:D:240:THR:HG22	1.92	0.51
5:F:17:PHE:HE2	5:F:39:VAL:HG11	1.74	0.51
6:G:126:ASP:OD1	6:G:126:ASP:N	2.41	0.51
32:j:35:SER:OG	32:j:36:ARG:N	2.43	0.51
33:2:1650:A:H3'	33:2:1651:A:H8	1.76	0.51
19:T:6:PRO:HB2	19:T:9:PHE:HB2	1.92	0.51
19:T:92:ASP:OD1	19:T:92:ASP:N	2.34	0.51
16:Q:110:GLU:HB2	19:T:117:ILE:HD11	1.93	0.51
33:2:382:C:H2'	33:2:383:G:H8	1.75	0.51
33:2:1261:C:OP1	33:2:1518:C:N4	2.43	0.51
5:F:194:PRO:HA	5:F:201:LYS:HA	1.92	0.51
25:Z:64:GLU:HG3	27:b:3:LEU:HD13	1.92	0.51
9:J:140:GLN:NE2	24:Y:64:PHE:O	2.42	0.51
10:K:49:LEU:HD12	17:R:50:LYS:HG2	1.91	0.51
12:M:23:ALA:HB3	12:M:67:PHE:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:j:159:ASN:ND2	32:j:161:SER:OG	2.44	0.51
33:2:960:U:N3	33:2:963:A:OP2	2.43	0.51
7:H:60:ILE:HB	7:H:92:VAL:HG12	1.92	0.51
10:K:125:SER:O	10:K:136:ARG:NH2	2.44	0.51
12:M:32:HIS:HD2	12:M:35:LEU:H	1.58	0.51
16:Q:29:SER:H	16:Q:32:GLN:HE21	1.58	0.51
17:R:19:ALA:HB2	17:R:75:GLY:HA3	1.92	0.51
2:C:34:LYS:HA	2:C:43:ASN:HA	1.93	0.51
33:2:587:A:H5'	33:2:592:C:H41	1.76	0.51
35:u:209:LYS:O	35:u:213:LYS:NZ	2.44	0.51
3:D:190:SER:HB2	33:2:1143:A:H5'	1.93	0.51
5:F:227:LYS:O	32:j:183:LYS:NZ	2.44	0.51
17:R:139:ALA:O	17:R:140:ARG:NH1	2.44	0.51
9:J:142:VAL:HG12	9:J:144:ILE:H	1.76	0.51
13:N:32:ASP:OD1	13:N:32:ASP:N	2.38	0.51
19:T:39:ARG:NH2	20:U:36:THR:O	2.44	0.51
35:u:615:ILE:HA	35:u:624:ARG:HG2	1.92	0.51
14:O:69:CYS:HA	14:O:74:ILE:HD13	1.92	0.50
33:2:1550:G:H3'	33:2:1579:A:H61	1.76	0.50
32:j:11:LEU:HB2	32:j:307:VAL:HB	1.93	0.50
4:E:49:ARG:HB3	4:E:55:ALA:HB3	1.93	0.50
10:K:100:ILE:HA	10:K:178:ILE:HD11	1.91	0.50
14:O:83:LYS:HA	14:O:105:GLY:HA3	1.94	0.50
20:U:18:LEU:HD13	20:U:134:ILE:HG21	1.92	0.50
4:E:133:THR:H	33:2:297:A:H5''	1.75	0.50
9:J:60:LEU:HD22	9:J:70:ARG:HA	1.91	0.50
13:N:55:ARG:NH1	13:N:56:ASP:OD1	2.44	0.50
32:j:294:ASP:OD1	32:j:294:ASP:N	2.44	0.50
35:u:594:LEU:HD11	35:u:658:ILE:HA	1.92	0.50
31:g:104:LYS:O	31:g:118:ARG:NH1	2.44	0.50
33:2:201:C:H3'	33:2:202:G:H8	1.77	0.50
14:O:20:GLU:HG3	14:O:119:GLN:HE22	1.75	0.50
33:2:28:U:H2'	33:2:29:G:H8	1.76	0.50
15:P:85:CYS:HB2	15:P:124:MET:HE1	1.93	0.50
26:a:104:ARG:NH1	33:2:1593:C:OP2	2.43	0.50
1:B:36:GLN:O	1:B:53:ARG:NH1	2.45	0.50
3:D:194:ARG:HD3	3:D:196:ILE:HD11	1.94	0.50
5:F:54:ARG:HH11	5:F:57:ASN:HD22	1.58	0.50
6:G:170:ARG:HH12	33:2:73:C:H41	1.58	0.50
10:K:102:LEU:HD12	26:a:108:ILE:HD11	1.94	0.50
27:b:59:CYS:HG	27:b:61:THR:HG1	1.53	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:874:G:H2'	33:2:875:A:H8	1.77	0.49
35:u:155:THR:HG21	35:u:236:LEU:HD22	1.93	0.49
7:H:9:VAL:HG21	7:H:20:GLU:HB3	1.95	0.49
13:N:63:VAL:HG21	13:N:71:ILE:HD11	1.95	0.49
33:2:972:A:OP2	33:2:973:C:N4	2.38	0.49
35:u:70:ALA:HA	35:u:73:ARG:HE	1.77	0.49
35:u:515:ASP:HB3	35:u:518:GLU:HB2	1.94	0.49
2:C:157:GLN:NE2	33:2:1103:C:OP1	2.43	0.49
20:U:71:GLY:HA3	33:2:1562:C:H5''	1.94	0.49
10:K:28:VAL:O	10:K:42:LYS:NZ	2.35	0.49
18:S:10:LYS:NZ	33:2:1373:C:O2'	2.45	0.49
26:a:111:ARG:NH1	26:a:113:THR:O	2.44	0.49
2:C:162:ARG:NH2	33:2:1005:G:OP2	2.45	0.49
9:J:18:ARG:NH2	33:2:3:C:O2	2.43	0.49
19:T:46:ARG:NE	20:U:50:GLU:OE1	2.45	0.49
33:2:1652:G:H1	33:2:1672:U:H3	1.61	0.49
5:F:226:GLN:HA	32:j:186:THR:HA	1.95	0.49
6:G:135:PRO:HG2	6:G:141:ILE:HD13	1.94	0.49
19:T:35:GLY:O	19:T:97:GLN:NE2	2.45	0.49
31:g:141:CYS:SG	31:g:142:GLY:N	2.85	0.49
32:j:72:SER:OG	32:j:73:SER:N	2.45	0.49
35:u:600:ARG:NH2	35:u:606:GLU:O	2.45	0.49
5:F:64:ARG:HH12	12:M:71:LEU:HD11	1.78	0.49
10:K:48:TYR:HB3	17:R:49:TYR:HB3	1.95	0.49
10:K:138:ALA:O	28:d:63:ARG:NH2	2.46	0.49
33:2:164:A:H3'	33:2:165:G:H21	1.77	0.49
35:u:192:ILE:O	35:u:200:GLN:NE2	2.46	0.49
33:2:613:G:N2	33:2:626:G:OP1	2.42	0.48
3:D:196:ILE:HB	3:D:223:TYR:HB2	1.94	0.48
5:F:224:SER:OG	32:j:224:GLY:O	2.31	0.48
26:a:46:ASN:ND2	33:2:1599:U:OP2	2.45	0.48
2:C:67:PHE:HB2	2:C:86:LEU:HB2	1.95	0.48
15:P:44:VAL:O	15:P:52:THR:OG1	2.30	0.48
33:2:955:A:N6	33:2:971:G:O2'	2.45	0.48
3:D:171:GLY:O	22:W:98:GLN:NE2	2.43	0.48
7:H:35:ASP:OD1	7:H:35:ASP:N	2.44	0.48
10:K:104:THR:HG23	10:K:106:GLU:HG3	1.93	0.48
18:S:5:ARG:NH1	33:2:1466:G:OP2	2.46	0.48
22:W:60:LYS:NZ	33:2:921:G:O6	2.47	0.48
32:j:63:SER:HB3	33:2:1398:G:H1'	1.95	0.48
17:R:140:ARG:HA	17:R:140:ARG:HH11	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:a:91:LEU:HA	26:a:94:LYS:HE2	1.96	0.48
33:2:1562:C:H2'	33:2:1563:G:H8	1.78	0.48
3:D:165:VAL:HG11	3:D:217:ALA:HB1	1.95	0.48
20:U:44:GLU:N	33:2:1539:U:OP1	2.44	0.48
23:X:28:LYS:HD2	23:X:32:LEU:HD22	1.96	0.48
35:u:758:LYS:NZ	35:u:759:LEU:O	2.45	0.48
5:F:64:ARG:NH2	5:F:68:GLU:OE2	2.47	0.48
7:H:109:ARG:HD3	7:H:111:LYS:HD3	1.94	0.48
15:P:135:ILE:O	33:2:943:U:O2'	2.32	0.48
33:2:1776:G:H2'	33:2:1777:G:C8	2.49	0.48
4:E:179:ASN:HD22	4:E:231:GLY:H	1.60	0.48
21:V:46:LYS:NZ	21:V:97:ILE:O	2.47	0.48
35:u:594:LEU:HD13	35:u:656:ALA:HB3	1.96	0.48
21:V:26:SER:HB2	21:V:110:VAL:HG12	1.96	0.48
8:I:34:ALA:HB3	8:I:56:ARG:HD2	1.96	0.47
32:j:174:VAL:HB	32:j:188:HIS:HB2	1.96	0.47
33:2:1289:U:H3	33:2:1310:U:H3	1.62	0.47
32:j:124:SER:OG	32:j:125:ARG:N	2.47	0.47
33:2:94:G:O2'	33:2:508:A:O2'	2.29	0.47
6:G:193:ALA:HB2	33:2:332:G:H5'	1.96	0.47
2:C:72:ALA:HB3	15:P:128:ARG:HH22	1.79	0.47
3:D:64:THR:OG1	3:D:90:GLU:OE2	2.28	0.47
11:L:35:ARG:NH2	11:L:55:TYR:O	2.34	0.47
14:O:33:ARG:HG3	14:O:89:VAL:HG11	1.96	0.47
21:V:67:LYS:O	30:f:44:ARG:NH1	2.47	0.47
32:j:50:THR:OG1	32:j:51:ASN:OD1	2.32	0.47
33:2:1569:A:HO2'	33:2:1626:C:HO2'	1.60	0.47
34:i:156:ASP:O	34:i:160:ASN:ND2	2.43	0.47
12:M:26:ASP:O	12:M:42:ASN:ND2	2.48	0.47
17:R:10:VAL:HG21	17:R:95:TYR:HA	1.97	0.47
23:X:98:ASP:OD2	23:X:140:ARG:NH2	2.42	0.47
4:E:220:THR:OG1	4:E:221:ARG:O	2.31	0.47
6:G:1:MET:HE3	6:G:24:LEU:HD13	1.96	0.47
8:I:101:ILE:HD12	8:I:190:LEU:HD11	1.96	0.47
11:L:135:SER:OG	11:L:136:LYS:N	2.47	0.47
32:j:87:LEU:HB2	32:j:101:PHE:HB2	1.97	0.47
33:2:1228:A:H2'	33:2:1229:G:C8	2.49	0.47
33:2:1653:U:H3	33:2:1671:G:H1	1.63	0.47
35:u:617:HIS:HB2	35:u:666:LEU:HB2	1.95	0.47
3:D:66:LEU:HD21	3:D:81:ILE:HD13	1.97	0.47
11:L:75:GLY:HA3	11:L:88:ILE:HD12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:22:LEU:HD13	20:U:28:LEU:HD11	1.97	0.47
33:2:793:G:H2'	33:2:794:A:H8	1.79	0.47
33:2:1239:U:O2'	33:2:1241:A:N7	2.44	0.47
19:T:10:GLN:NE2	19:T:59:LEU:O	2.48	0.47
20:U:42:HIS:ND1	20:U:93:SER:OG	2.46	0.47
25:Z:81:LYS:HD3	25:Z:81:LYS:HA	1.77	0.47
33:2:641:A:O2'	33:2:645:C:OP1	2.33	0.47
2:C:59:SER:O	2:C:63:LYS:HB2	2.14	0.47
10:K:118:ASN:ND2	10:K:181:ALA:O	2.48	0.47
15:P:85:CYS:O	15:P:90:ILE:N	2.47	0.47
23:X:67:ARG:HG3	23:X:115:ILE:HG12	1.97	0.47
35:u:84:GLN:HE21	35:u:136:THR:HG21	1.80	0.47
2:C:61:GLY:O	15:P:50:LYS:NZ	2.44	0.47
3:D:221:ASP:N	3:D:221:ASP:OD1	2.47	0.47
1:B:143:PRO:HG3	25:Z:32:ILE:HG23	1.98	0.46
2:C:56:LYS:HB3	2:C:56:LYS:HE3	1.73	0.46
4:E:22:LYS:NZ	33:2:814:U:OP1	2.48	0.46
28:d:20:ARG:NH2	33:2:1679:A:OP1	2.48	0.46
1:B:205:ARG:H	1:B:205:ARG:HG2	1.42	0.46
8:I:57:ALA:HB2	8:I:183:GLY:HA2	1.98	0.46
32:j:245:ARG:NH1	32:j:295:GLY:O	2.42	0.46
33:2:1786:U:H2'	33:2:1787:G:H8	1.81	0.46
35:u:248:ASP:O	35:u:281:GLN:NE2	2.48	0.46
2:C:62:LEU:O	2:C:88:THR:OG1	2.31	0.46
4:E:9:LEU:HB2	4:E:30:ARG:HD3	1.98	0.46
5:F:96:LEU:HG	5:F:198:ILE:HD11	1.97	0.46
13:N:9:LYS:O	33:2:1130:G:O2'	2.34	0.46
21:V:26:SER:OG	21:V:27:ARG:N	2.48	0.46
33:2:541:U:O2'	33:2:542:U:O4'	2.33	0.46
33:2:1213:C:H2'	33:2:1214:A:C8	2.51	0.46
33:2:1514:G:H2'	33:2:1515:G:H8	1.81	0.46
35:u:362:ASP:OD1	35:u:362:ASP:N	2.39	0.46
2:C:32:ASP:HB2	2:C:46:LYS:HZ2	1.80	0.46
32:j:162:ASN:OD1	32:j:162:ASN:N	2.49	0.46
15:P:21:VAL:HG11	15:P:27:VAL:HG22	1.98	0.46
15:P:74:ALA:HA	15:P:77:ALA:HB3	1.98	0.46
33:2:1536:G:H2'	33:2:1537:A:H8	1.79	0.46
4:E:143:ASP:OD1	4:E:143:ASP:N	2.49	0.46
20:U:49:ASP:OD1	20:U:49:ASP:N	2.49	0.46
10:K:161:ALA:O	10:K:165:ASN:ND2	2.49	0.46
10:K:183:GLY:HA2	10:K:190:ILE:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:1265:A:O2'	33:2:1327:G:OP2	2.30	0.46
33:2:1562:C:H2'	33:2:1563:G:C8	2.51	0.46
16:Q:60:LEU:O	16:Q:64:LYS:NZ	2.45	0.45
32:j:111:VAL:O	32:j:155:ARG:NH1	2.49	0.45
33:2:28:U:H2'	33:2:29:G:C8	2.51	0.45
2:C:100:PHE:HD2	2:C:181:LEU:HD23	1.82	0.45
2:C:150:ILE:HG12	33:2:1124:C:H5''	1.98	0.45
10:K:22:LYS:NZ	10:K:98:GLU:OE2	2.47	0.45
10:K:151:ILE:O	10:K:155:CYS:HB2	2.16	0.45
11:L:85:THR:HG21	33:2:373:G:H4'	1.98	0.45
16:Q:38:SER:OG	16:Q:39:ALA:N	2.49	0.45
3:D:104:ASP:OD1	3:D:104:ASP:N	2.49	0.45
33:2:941:C:H2'	33:2:942:G:H8	1.81	0.45
35:u:79:ASP:OD1	35:u:79:ASP:N	2.49	0.45
6:G:132:ARG:O	33:2:168:C:O2'	2.34	0.45
18:S:53:TYR:O	18:S:57:LEU:HB2	2.16	0.45
28:d:31:ARG:NE	28:d:41:SER:OG	2.49	0.45
33:2:941:C:H2'	33:2:942:G:C8	2.51	0.45
35:u:274:ILE:HG13	35:u:560:LEU:HD13	1.99	0.45
2:C:182:LYS:HG3	2:C:183:GLU:HG3	1.98	0.45
8:I:48:VAL:HG11	8:I:54:LYS:HD2	1.98	0.45
15:P:27:VAL:N	15:P:91:THR:OG1	2.49	0.45
27:b:17:ARG:HE	27:b:17:ARG:HB3	1.63	0.45
6:G:155:GLN:HB3	33:2:75:G:H22	1.82	0.45
10:K:179:ASN:O	10:K:184:SER:OG	2.32	0.45
18:S:44:LYS:NZ	33:2:1451:G:N7	2.62	0.45
21:V:20:ILE:HG21	21:V:98:VAL:HG11	1.99	0.45
32:j:10:THR:HG22	32:j:308:ARG:HG2	1.97	0.45
33:2:1259:A:H1'	33:2:1264:C:H41	1.82	0.45
3:D:110:MET:HB3	3:D:125:LYS:HB3	1.99	0.45
7:H:34:SER:O	7:H:37:LYS:NZ	2.38	0.45
11:L:79:LYS:HB2	11:L:87:VAL:HB	1.99	0.45
15:P:43:HIS:HD2	15:P:55:ARG:HB2	1.82	0.45
20:U:48:TYR:OH	33:2:1538:C:O2	2.31	0.45
24:Y:12:PHE:HZ	24:Y:21:LYS:HD3	1.82	0.45
24:Y:89:HIS:CD2	33:2:574:A:H5'	2.52	0.45
31:g:108:VAL:HG22	31:g:114:ILE:HA	1.98	0.45
33:2:1588:A:H2'	33:2:1589:A:C8	2.51	0.45
2:C:219:LYS:HA	2:C:219:LYS:HD3	1.74	0.45
15:P:57:THR:HG23	15:P:60:MET:H	1.82	0.45
17:R:37:ARG:NH2	33:2:1543:U:OP1	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:20:ILE:HD13	21:V:93:SER:H	1.82	0.45
32:j:212:LYS:HA	32:j:235:ILE:HG23	1.98	0.45
33:2:1716:C:H2'	33:2:1717:C:C6	2.52	0.45
1:B:135:THR:O	1:B:138:SER:OG	2.32	0.44
4:E:204:SER:OG	4:E:205:PHE:N	2.48	0.44
12:M:16:PHE:HB2	12:M:79:LEU:HD22	1.99	0.44
14:O:41:ALA:O	14:O:112:LYS:NZ	2.50	0.44
17:R:8:GLN:OE1	17:R:27:ARG:NE	2.45	0.44
20:U:38:LYS:NZ	33:2:1628:C:OP1	2.40	0.44
33:2:1244:U:H2'	33:2:1245:G:H8	1.82	0.44
33:2:1539:U:H2'	33:2:1540:G:H8	1.82	0.44
35:u:250:ARG:HG2	35:u:585:LEU:HD11	1.99	0.44
35:u:253:LEU:HD22	35:u:560:LEU:HD21	1.99	0.44
3:D:254:ASP:OD1	3:D:254:ASP:N	2.50	0.44
5:F:67:ARG:O	5:F:70:THR:OG1	2.33	0.44
19:T:84:LEU:O	19:T:87:GLN:NE2	2.44	0.44
27:b:30:SER:OG	33:2:1016:U:O2	2.33	0.44
28:d:34:PHE:HZ	28:d:61:SER:HB3	1.81	0.44
33:2:640:A:H2'	33:2:641:A:C8	2.52	0.44
33:2:1536:G:H2'	33:2:1537:A:C8	2.52	0.44
1:B:5:LEU:O	1:B:9:GLN:NE2	2.47	0.44
2:C:149:GLN:HE22	2:C:154:SER:HB2	1.81	0.44
14:O:69:CYS:HB3	14:O:76:LEU:HD21	1.98	0.44
16:Q:108:LYS:HB2	16:Q:111:MET:HE3	1.98	0.44
33:2:1298:G:H2'	33:2:1299:A:C8	2.52	0.44
2:C:134:LEU:HD12	2:C:134:LEU:HA	1.90	0.44
8:I:162:LEU:HD11	8:I:191:GLU:HG2	1.99	0.44
12:M:8:ARG:HG2	12:M:12:TYR:HE1	1.82	0.44
34:i:166:SER:O	34:i:170:THR:OG1	2.31	0.44
35:u:598:VAL:HG11	35:u:680:ALA:HB1	1.98	0.44
35:u:675:MET:HG2	35:u:789:TRP:HA	2.00	0.44
3:D:113:GLN:HE21	3:D:122:THR:HG1	1.63	0.44
14:O:31:LEU:HD21	14:O:109:VAL:HG13	2.00	0.44
24:Y:114:MET:O	24:Y:122:LYS:NZ	2.45	0.44
31:g:137:ASP:N	31:g:137:ASP:OD1	2.48	0.44
33:2:1280:G:H2'	33:2:1281:G:H8	1.82	0.44
4:E:254:LYS:HB3	4:E:254:LYS:HE3	1.75	0.44
11:L:136:LYS:HB2	33:2:385:G:H3'	1.98	0.44
16:Q:81:ARG:HB3	16:Q:117:GLY:HA3	1.99	0.44
33:2:1329:U:O4	33:2:1500:G:O6	2.35	0.44
33:2:1330:G:O2'	33:2:1492:U:OP2	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:u:262:PRO:HA	35:u:270:GLY:HA3	2.00	0.44
13:N:132:LYS:HB3	13:N:132:LYS:HE2	1.81	0.44
33:2:1568:C:O2	33:2:1627:C:O2'	2.36	0.44
2:C:60:ASP:OD1	2:C:60:ASP:N	2.51	0.44
2:C:138:PHE:O	2:C:213:ARG:N	2.47	0.44
6:G:181:THR:HG22	6:G:184:VAL:HG23	1.99	0.44
10:K:75:SER:O	10:K:159:ARG:NH2	2.42	0.44
35:u:635:ALA:O	35:u:638:HIS:NE2	2.51	0.44
2:C:31:TYR:HA	2:C:94:LYS:HD2	1.99	0.44
8:I:42:ARG:HB3	8:I:59:ARG:HB2	2.00	0.44
10:K:159:ARG:NH1	33:2:1535:U:O4	2.45	0.44
12:M:59:LYS:HB3	12:M:70:TYR:HD2	1.83	0.44
30:f:8:TRP:HZ3	33:2:1512:C:H5'	1.82	0.44
33:2:367:U:H4'	33:2:371:A:C8	2.53	0.44
4:E:11:ARG:HA	4:E:28:ALA:HB2	2.00	0.43
17:R:112:LEU:HD13	17:R:120:LEU:HD21	2.00	0.43
18:S:31:ASN:HA	18:S:34:VAL:HG12	2.00	0.43
33:2:685:A:H62	33:2:917:U:H3	1.66	0.43
33:2:1427:C:H2'	33:2:1429:G:H8	1.83	0.43
33:2:1785:C:O2'	33:2:1786:U:O4'	2.34	0.43
1:B:204:TYR:CD2	1:B:204:TYR:O	2.71	0.43
16:Q:41:GLN:HG3	16:Q:84:ILE:HD13	2.00	0.43
18:S:5:ARG:HB2	18:S:10:LYS:HE3	1.99	0.43
20:U:9:VAL:HG21	20:U:138:VAL:HG13	2.00	0.43
20:U:76:THR:HG22	20:U:94:ARG:HB3	1.99	0.43
26:a:81:GLY:HA2	26:a:84:ALA:HB3	2.01	0.43
33:2:1514:G:H2'	33:2:1515:G:C8	2.52	0.43
33:2:1533:A:N6	33:2:1602:U:H3	2.08	0.43
3:D:115:GLN:O	33:2:1202:U:O2'	2.32	0.43
8:I:170:LYS:HB2	8:I:170:LYS:HE3	1.77	0.43
17:R:21:ALA:HB2	17:R:72:VAL:HG23	2.00	0.43
17:R:140:ARG:HB2	33:2:1644:C:H4'	1.99	0.43
32:j:88:ARG:HD3	32:j:88:ARG:HA	1.89	0.43
33:2:1329:U:C4	33:2:1500:G:O6	2.71	0.43
33:2:1658:G:OP2	33:2:1660:C:N4	2.51	0.43
35:u:288:LEU:HB3	35:u:584:LEU:HB2	2.00	0.43
1:B:38:ILE:HG21	1:B:47:TYR:HD2	1.83	0.43
1:B:42:LYS:HD3	1:B:48:ILE:HD11	2.00	0.43
4:E:79:ASP:HB3	4:E:82:TYR:HB2	1.99	0.43
4:E:95:THR:HG22	24:Y:16:ARG:HB2	2.00	0.43
7:H:57:ARG:NH1	7:H:89:GLY:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:190:LEU:HD22	8:I:194:GLU:HG2	2.01	0.43
35:u:490:THR:HG22	35:u:699:LEU:HD12	2.01	0.43
35:u:519:ASN:HD21	35:u:772:ARG:HB3	1.83	0.43
1:B:76:VAL:HG12	1:B:123:VAL:HB	2.01	0.43
5:F:115:VAL:HG21	5:F:142:LEU:HD22	2.01	0.43
22:W:30:CYS:HB2	22:W:61:ILE:HG13	2.00	0.43
24:Y:37:LYS:HB2	24:Y:37:LYS:HE2	1.94	0.43
32:j:156:PHE:HE1	32:j:179:LEU:HD21	1.84	0.43
33:2:1617:G:N2	33:2:1620:A:OP2	2.36	0.43
35:u:636:ASP:OD1	35:u:636:ASP:N	2.51	0.43
3:D:68:ARG:NH1	3:D:276:THR:OG1	2.51	0.43
5:F:80:PRO:O	5:F:83:SER:OG	2.36	0.43
8:I:73:THR:O	8:I:74:ARG:NH1	2.52	0.43
10:K:35:LEU:HD12	10:K:117:ILE:HG12	1.99	0.43
30:f:31:ILE:HG12	33:2:1256:G:H1	1.84	0.43
4:E:100:ARG:HH12	4:E:118:GLU:HG2	1.82	0.43
19:T:86:ARG:HH21	19:T:89:ASP:HB2	1.83	0.43
1:B:30:LEU:HD21	1:B:35:GLU:HG3	2.00	0.43
1:B:164:ASN:O	1:B:170:SER:OG	2.29	0.43
4:E:171:ASP:OD1	4:E:171:ASP:N	2.51	0.43
29:e:21:LYS:HE2	29:e:21:LYS:HB3	1.89	0.43
33:2:1729:U:H3	33:2:1805:G:H1	1.67	0.43
5:F:208:VAL:HG13	18:S:41:ILE:HG12	2.01	0.43
7:H:9:VAL:HG23	7:H:24:SER:HB3	2.01	0.43
15:P:39:ASP:OD1	15:P:39:ASP:N	2.52	0.43
21:V:44:LYS:HA	21:V:44:LYS:HD3	1.80	0.43
29:e:52:LYS:HA	29:e:52:LYS:HD2	1.92	0.43
32:j:178:ASN:HB3	32:j:181:ASN:HB3	2.01	0.43
33:2:1779:G:H2'	33:2:1780:G:C8	2.54	0.43
10:K:28:VAL:HG12	10:K:110:GLN:HB2	2.01	0.43
11:L:10:TYR:OH	11:L:18:GLN:NE2	2.52	0.43
26:a:80:ARG:NE	33:2:1598:G:H5'	2.33	0.43
28:d:40:ARG:NH2	28:d:61:SER:O	2.52	0.43
9:J:143:ASN:HB2	33:2:823:U:H5	1.83	0.42
33:2:1511:U:H2'	33:2:1512:C:C6	2.54	0.42
33:2:1786:U:H2'	33:2:1787:G:C8	2.54	0.42
17:R:28:GLY:HA3	17:R:67:ASP:HB2	2.01	0.42
32:j:71:ILE:HA	32:j:78:ALA:HA	2.01	0.42
35:u:611:LYS:HA	35:u:611:LYS:HD2	1.81	0.42
14:O:52:LEU:HD22	14:O:76:LEU:HD12	2.02	0.42
31:g:135:HIS:HB2	31:g:138:ARG:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:979:C:H2'	33:2:980:A:C8	2.54	0.42
35:u:592:SER:OG	35:u:593:VAL:N	2.51	0.42
3:D:65:LYS:HE2	3:D:273:LEU:HD13	2.01	0.42
5:F:27:ARG:NH2	33:2:1498:A:OP2	2.52	0.42
5:F:75:LYS:NZ	12:M:20:VAL:O	2.47	0.42
7:H:99:ARG:H	33:2:913:A:H2	1.68	0.42
7:H:116:ARG:NH2	33:2:687:C:O3'	2.52	0.42
17:R:13:PHE:HA	17:R:22:VAL:HA	2.01	0.42
20:U:84:ARG:NH2	33:2:1531:A:OP1	2.47	0.42
33:2:1775:U:H2'	33:2:1776:G:H8	1.83	0.42
5:F:195:THR:H	5:F:201:LYS:HG2	1.85	0.42
10:K:165:ASN:O	10:K:167:LYS:N	2.52	0.42
17:R:112:LEU:HA	17:R:112:LEU:HD23	1.87	0.42
22:W:18:GLU:HG2	22:W:69:LEU:HB3	2.01	0.42
24:Y:74:MET:HB2	24:Y:74:MET:HE3	1.73	0.42
33:2:928:G:H2'	33:2:929:G:C8	2.54	0.42
35:u:195:LEU:O	35:u:200:GLN:NE2	2.53	0.42
35:u:727:LYS:HA	35:u:741:ILE:HD11	2.01	0.42
15:P:130:GLU:HG3	15:P:132:VAL:HG23	2.01	0.42
19:T:26:ILE:HD12	19:T:45:LEU:HD23	2.01	0.42
20:U:132:ASP:OD2	33:2:1415:C:O2'	2.28	0.42
22:W:90:GLN:HB2	22:W:94:LEU:HD12	2.01	0.42
24:Y:55:ILE:HG22	24:Y:75:ILE:HG23	2.02	0.42
32:j:300:ALA:O	32:j:308:ARG:N	2.49	0.42
33:2:878:G:H1	33:2:908:A:H2	1.62	0.42
33:2:886:A:C4	33:2:887:U:H1'	2.54	0.42
9:J:131:ARG:HA	9:J:131:ARG:HD2	1.93	0.42
1:B:185:MET:HE2	1:B:185:MET:HB3	1.86	0.42
4:E:115:THR:HG23	4:E:118:GLU:H	1.83	0.42
8:I:191:GLU:O	11:L:19:ASN:ND2	2.53	0.42
14:O:61:TYR:OH	14:O:108:CYS:SG	2.66	0.42
21:V:93:SER:HB3	21:V:97:ILE:HD11	2.01	0.42
33:2:51:U:H2'	33:2:52:G:C8	2.55	0.42
33:2:612:U:O2'	33:2:615:C:N3	2.49	0.42
33:2:1004:U:H2'	33:2:1005:G:C8	2.55	0.42
1:B:42:LYS:NZ	18:S:99:ASP:OD2	2.41	0.42
3:D:144:SER:HB2	3:D:150:ALA:HB2	2.02	0.42
5:F:32:ASP:OD1	5:F:54:ARG:NH1	2.53	0.42
15:P:44:VAL:HG13	15:P:53:ILE:HB	2.01	0.42
16:Q:59:ARG:NH2	33:2:1297:U:O4	2.44	0.42
33:2:472:C:O2'	33:2:474:G:OP1	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:189:ILE:HG13	2:C:190:PRO:HD3	2.01	0.42
6:G:203:LYS:HE3	6:G:203:LYS:HB3	1.86	0.42
8:I:19:LYS:HD2	33:2:101:U:H5''	2.02	0.42
27:b:74:THR:OG1	27:b:77:CYS:SG	2.70	0.42
32:j:24:THR:HG23	32:j:27:PHE:H	1.84	0.42
33:2:1286:G:N2	33:2:1288:U:O4	2.53	0.42
35:u:537:ARG:HD2	35:u:661:PRO:HD2	2.01	0.42
3:D:170:TRP:CE2	3:D:199:PRO:HG3	2.55	0.41
5:F:44:THR:OG1	5:F:45:ARG:N	2.53	0.41
5:F:185:LYS:NZ	33:2:1336:C:OP2	2.36	0.41
7:H:34:SER:OG	7:H:35:ASP:N	2.53	0.41
14:O:94:ILE:HD12	14:O:94:ILE:HA	1.95	0.41
32:j:82:SER:OG	32:j:83:TRP:N	2.50	0.41
33:2:1289:U:H2'	33:2:1290:G:C8	2.55	0.41
35:u:524:TYR:HA	35:u:527:ILE:HG12	2.01	0.41
26:a:106:GLN:NE2	26:a:107:VAL:O	2.53	0.41
33:2:634:A:H2'	33:2:635:G:H8	1.84	0.41
33:2:1402:A:N6	33:2:1441:U:O2'	2.53	0.41
2:C:26:SER:O	2:C:51:ARG:NH1	2.54	0.41
2:C:183:GLU:HA	2:C:186:ASN:HD22	1.85	0.41
8:I:129:LEU:HD12	8:I:129:LEU:HA	1.89	0.41
12:M:64:TRP:HB3	30:f:23:VAL:HA	2.03	0.41
22:W:88:LYS:O	22:W:92:ASN:ND2	2.53	0.41
33:2:1181:A:H2'	33:2:1182:A:C8	2.56	0.41
8:I:177:SER:HB3	33:2:220:U:H5'	2.02	0.41
18:S:10:LYS:HD2	33:2:1374:C:OP1	2.20	0.41
33:2:554:A:H2'	33:2:556:U:H6	1.85	0.41
33:2:614:C:H4'	33:2:615:C:H5''	2.02	0.41
33:2:1232:U:H2'	33:2:1233:G:H8	1.85	0.41
2:C:75:GLN:NE2	2:C:77:ASP:OD2	2.44	0.41
33:2:1781:A:H2'	33:2:1782:G:C8	2.56	0.41
35:u:596:MET:HA	35:u:685:MET:H	1.84	0.41
35:u:645:THR:OG1	35:u:648:MET:O	2.38	0.41
2:C:163:GLN:HB3	2:C:204:ILE:HD13	2.02	0.41
5:F:46:THR:O	5:F:46:THR:OG1	2.36	0.41
10:K:190:ILE:HA	10:K:193:LYS:HB3	2.03	0.41
32:j:209:SER:OG	32:j:219:TRP:NE1	2.43	0.41
33:2:178:C:H2'	33:2:179:C:H6	1.86	0.41
1:B:205:ARG:NH1	1:B:205:ARG:HB2	2.36	0.41
8:I:199:LEU:HD23	8:I:199:LEU:HA	1.93	0.41
14:O:51:VAL:HG12	14:O:77:ILE:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:18:ARG:HG3	16:Q:36:LEU:HB3	2.03	0.41
32:j:26:GLN:HG2	32:j:75:GLY:H	1.86	0.41
33:2:1712:A:H2'	33:2:1713:C:C6	2.56	0.41
1:B:106:GLY:N	1:B:136:GLU:OE2	2.47	0.41
2:C:92:GLN:O	2:C:95:ASN:ND2	2.53	0.41
3:D:259:THR:HG21	25:Z:16:LYS:H	1.86	0.41
4:E:42:LEU:HD23	4:E:42:LEU:HA	1.95	0.41
5:F:99:ILE:HD12	5:F:173:ARG:HH21	1.85	0.41
6:G:57:ASP:HA	6:G:106:LEU:HA	2.02	0.41
10:K:99:ILE:HG13	26:a:108:ILE:HD12	2.02	0.41
19:T:10:GLN:HG2	19:T:57:GLY:HA2	2.03	0.41
24:Y:33:ALA:HB2	33:2:582:U:H1'	2.02	0.41
27:b:59:CYS:SG	27:b:61:THR:OG1	2.65	0.41
33:2:74:G:O2'	33:2:76:U:N3	2.54	0.41
33:2:907:G:H2'	33:2:908:A:C8	2.56	0.41
33:2:1027:A:H3'	33:2:1028:A:H8	1.85	0.41
35:u:103:LEU:HD21	35:u:135:PHE:CG	2.55	0.41
35:u:674:GLY:O	35:u:676:HIS:ND1	2.45	0.41
10:K:39:ILE:HD13	10:K:39:ILE:HA	1.93	0.41
21:V:86:LYS:NZ	33:2:1580:A:OP1	2.44	0.41
33:2:145:G:H2'	33:2:146:G:C8	2.55	0.41
33:2:1144:A:H2'	33:2:1145:A:C8	2.56	0.41
8:I:157:LYS:HD3	8:I:157:LYS:HA	1.76	0.40
8:I:205:ARG:HA	8:I:205:ARG:HD2	1.83	0.40
12:M:83:LEU:HG	12:M:85:LEU:HG	2.02	0.40
13:N:101:HIS:CE1	13:N:105:ASN:HD22	2.40	0.40
13:N:140:LYS:HD2	13:N:140:LYS:HA	1.80	0.40
16:Q:40:ARG:HH21	33:2:1620:A:H2'	1.87	0.40
18:S:127:ASN:OD1	18:S:127:ASN:N	2.52	0.40
23:X:68:LYS:NZ	33:2:617:G:OP2	2.37	0.40
33:2:1424:G:H2'	33:2:1425:G:H8	1.86	0.40
2:C:103:MET:HE3	2:C:215:VAL:HG23	2.03	0.40
7:H:120:ARG:NH2	33:2:915:G:OP1	2.48	0.40
10:K:63:LYS:NZ	33:2:1678:A:OP2	2.39	0.40
21:V:23:THR:HA	21:V:88:LEU:HD23	2.02	0.40
24:Y:78:SER:OG	24:Y:80:ASP:OD1	2.33	0.40
30:f:34:TYR:OH	33:2:1549:U:OP1	2.37	0.40
31:g:97:LYS:HD3	33:2:1286:G:C4	2.57	0.40
33:2:885:U:H3	33:2:901:G:H1	1.69	0.40
6:G:163:ASN:HA	33:2:67:C:H41	1.84	0.40
6:G:183:ARG:HH12	33:2:316:G:H3'	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:111:VAL:H	10:K:111:VAL:HG12	1.63	0.40
14:O:77:ILE:HG12	14:O:127:TYR:HE2	1.86	0.40
23:X:76:LYS:HB3	33:2:482:G:H5'	2.04	0.40
31:g:126:CYS:HB3	31:g:143:LYS:HG3	2.03	0.40
33:2:1817:G:H2'	33:2:1818:A:C4	2.56	0.40
35:u:483:MET:HE3	35:u:483:MET:HB2	1.96	0.40
6:G:221:LYS:HA	6:G:221:LYS:HD3	1.80	0.40
8:I:24:LYS:NZ	33:2:440:G:OP1	2.51	0.40
15:P:26:ASN:HD22	15:P:92:ALA:HB2	1.87	0.40
33:2:975:G:H2'	33:2:976:G:H8	1.85	0.40
33:2:1736:G:H2'	33:2:1737:G:C8	2.56	0.40
35:u:147:LEU:O	35:u:151:LYS:NZ	2.35	0.40
2:C:135:LEU:HD12	2:C:215:VAL:HG12	2.04	0.40
18:S:74:GLN:HE21	18:S:74:GLN:HB2	1.70	0.40
24:Y:47:MET:HE2	24:Y:47:MET:HB3	1.91	0.40
24:Y:66:GLY:HA2	33:2:581:U:H4'	2.02	0.40
33:2:406:U:H2'	33:2:408:A:H5''	2.04	0.40
33:2:980:A:H2'	33:2:981:A:C8	2.56	0.40
33:2:1344:A:N1	33:2:1385:G:O2'	2.45	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	204/295 (69%)	193 (95%)	11 (5%)	0	100	100
2	C	211/264 (80%)	200 (95%)	11 (5%)	0	100	100
3	D	216/293 (74%)	205 (95%)	11 (5%)	0	100	100
4	E	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
5	F	223/243 (92%)	212 (95%)	10 (4%)	1 (0%)	30	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	G	228/249 (92%)	218 (96%)	10 (4%)	0	100	100
7	H	184/194 (95%)	175 (95%)	9 (5%)	0	100	100
8	I	203/208 (98%)	198 (98%)	5 (2%)	0	100	100
9	J	178/194 (92%)	167 (94%)	10 (6%)	1 (1%)	21	56
10	K	187/204 (92%)	170 (91%)	14 (8%)	3 (2%)	7	34
11	L	149/158 (94%)	141 (95%)	8 (5%)	0	100	100
12	M	93/165 (56%)	86 (92%)	7 (8%)	0	100	100
13	N	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
14	O	121/132 (92%)	114 (94%)	7 (6%)	0	100	100
15	P	120/151 (80%)	116 (97%)	4 (3%)	0	100	100
16	Q	118/145 (81%)	114 (97%)	4 (3%)	0	100	100
17	R	137/146 (94%)	132 (96%)	5 (4%)	0	100	100
18	S	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
19	T	141/152 (93%)	132 (94%)	9 (6%)	0	100	100
20	U	142/145 (98%)	139 (98%)	3 (2%)	0	100	100
21	V	99/119 (83%)	96 (97%)	3 (3%)	0	100	100
22	W	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
23	X	139/143 (97%)	135 (97%)	3 (2%)	1 (1%)	18	53
24	Y	122/133 (92%)	114 (93%)	7 (6%)	1 (1%)	16	50
25	Z	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
26	a	70/125 (56%)	67 (96%)	3 (4%)	0	100	100
27	b	80/84 (95%)	74 (92%)	5 (6%)	1 (1%)	9	38
28	d	59/69 (86%)	56 (95%)	3 (5%)	0	100	100
29	e	54/59 (92%)	48 (89%)	6 (11%)	0	100	100
30	f	52/56 (93%)	47 (90%)	4 (8%)	1 (2%)	6	30
31	g	62/156 (40%)	55 (89%)	7 (11%)	0	100	100
32	j	312/317 (98%)	292 (94%)	20 (6%)	0	100	100
34	i	27/180 (15%)	24 (89%)	3 (11%)	0	100	100
35	u	607/804 (76%)	569 (94%)	37 (6%)	1 (0%)	43	76
All	All	5278/6345 (83%)	4996 (95%)	272 (5%)	10 (0%)	44	76

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	K	166	ILE
9	J	161	LEU
5	F	192	TRP
27	b	52	THR
30	f	14	PHE
23	X	86	PRO
10	K	40	ALA
35	u	485	PRO
10	K	41	VAL
24	Y	119	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	172/243 (71%)	170 (99%)	2 (1%)	63	82
2	C	194/231 (84%)	193 (100%)	1 (0%)	81	89
3	D	182/225 (81%)	181 (100%)	1 (0%)	81	89
4	E	224/225 (100%)	222 (99%)	2 (1%)	70	85
5	F	188/202 (93%)	186 (99%)	2 (1%)	65	83
6	G	200/218 (92%)	200 (100%)	0	100	100
7	H	167/174 (96%)	166 (99%)	1 (1%)	78	88
8	I	178/180 (99%)	178 (100%)	0	100	100
9	J	160/168 (95%)	160 (100%)	0	100	100
10	K	159/170 (94%)	159 (100%)	0	100	100
11	L	135/142 (95%)	135 (100%)	0	100	100
12	M	86/136 (63%)	85 (99%)	1 (1%)	63	82
13	N	130/131 (99%)	130 (100%)	0	100	100
14	O	104/108 (96%)	103 (99%)	1 (1%)	68	84
15	P	94/119 (79%)	94 (100%)	0	100	100
16	Q	107/130 (82%)	106 (99%)	1 (1%)	70	85
17	R	115/121 (95%)	115 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	S	116/122 (95%)	111 (96%)	5 (4%)	26	60
19	T	124/132 (94%)	123 (99%)	1 (1%)	73	86
20	U	114/115 (99%)	114 (100%)	0	100	100
21	V	93/107 (87%)	93 (100%)	0	100	100
22	W	112/113 (99%)	111 (99%)	1 (1%)	70	85
23	X	113/115 (98%)	112 (99%)	1 (1%)	70	85
24	Y	108/115 (94%)	106 (98%)	2 (2%)	50	76
25	Z	66/67 (98%)	66 (100%)	0	100	100
26	a	64/103 (62%)	64 (100%)	0	100	100
27	b	74/76 (97%)	74 (100%)	0	100	100
28	d	54/62 (87%)	54 (100%)	0	100	100
29	e	42/48 (88%)	42 (100%)	0	100	100
30	f	48/49 (98%)	47 (98%)	1 (2%)	47	75
31	g	46/140 (33%)	45 (98%)	1 (2%)	45	74
32	j	272/275 (99%)	272 (100%)	0	100	100
34	i	26/151 (17%)	26 (100%)	0	100	100
35	u	539/705 (76%)	536 (99%)	3 (1%)	78	88
All	All	4606/5418 (85%)	4579 (99%)	27 (1%)	76	88

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	130	ASP
1	B	205	ARG
2	C	210	VAL
3	D	162	ILE
4	E	70	ILE
4	E	126	VAL
5	F	16	ILE
5	F	175	VAL
7	H	105	THR
12	M	79	LEU
14	O	110	VAL
16	Q	94	VAL
18	S	69	ILE
18	S	75	GLU

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Mol	Chain	Res	Type
18	S	78	ARG
18	S	79	GLU
18	S	81	ARG
19	T	92	ASP
22	W	25	VAL
23	X	81	ILE
24	Y	50	THR
24	Y	117	VAL
30	f	23	VAL
31	g	98	VAL
35	u	567	VAL
35	u	598	VAL
35	u	687	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	70	ASN
2	C	95	ASN
2	C	118	GLN
2	C	179	ASN
2	C	186	ASN
4	E	8	HIS
4	E	138	HIS
4	E	179	ASN
4	E	260	GLN
5	F	57	ASN
5	F	101	GLN
6	G	13	GLN
6	G	59	GLN
6	G	70	HIS
6	G	105	ASN
7	H	163	GLN
7	H	165	ASN
8	I	52	ASN
8	I	165	GLN
8	I	168	GLN
10	K	31	ASN
10	K	79	HIS
11	L	18	GLN
11	L	19	ASN
11	L	65	ASN

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Mol	Chain	Res	Type
13	N	36	GLN
13	N	62	GLN
13	N	105	ASN
14	O	119	GLN
15	P	32	HIS
15	P	43	HIS
15	P	79	GLN
16	Q	32	GLN
17	R	29	ASN
17	R	48	GLN
17	R	86	GLN
18	S	116	ASN
18	S	118	GLN
20	U	12	GLN
20	U	51	ASN
21	V	85	HIS
22	W	92	ASN
23	X	16	HIS
23	X	97	ASN
24	Y	63	HIS
26	a	89	GLN
29	e	44	ASN
29	e	58	ASN
30	f	26	ASN
30	f	45	GLN
31	g	135	HIS
32	j	15	ASN
32	j	20	GLN
32	j	117	ASN
32	j	133	ASN
32	j	215	GLN
34	i	158	GLN
34	i	162	ASN
35	u	55	HIS
35	u	63	GLN
35	u	84	GLN
35	u	131	HIS
35	u	180	GLN
35	u	239	GLN
35	u	241	GLN
35	u	256	HIS
35	u	284	ASN

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Mol	Chain	Res	Type
35	u	575	GLN
35	u	632	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	2	1559/1868 (83%)	423 (27%)	41 (2%)

All (423) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
33	2	3	C
33	2	17	C
33	2	26	U
33	2	33	G
33	2	41	G
33	2	44	U
33	2	45	A
33	2	46	A
33	2	49	C
33	2	56	G
33	2	58	C
33	2	62	G
33	2	66	G
33	2	67	C
33	2	68	A
33	2	70	G
33	2	72	C
33	2	73	C
33	2	74	G
33	2	75	G
33	2	76	U
33	2	77	A
33	2	79	A
33	2	99	A
33	2	103	A
33	2	113	G
33	2	114	G
33	2	115	U
33	2	126	G
33	2	130	G

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Mol	Chain	Res	Type
33	2	143	U
33	2	144	U
33	2	155	G
33	2	170	A
33	2	181	A
33	2	182	C
33	2	184	G
33	2	191	A
33	2	192	C
33	2	211	G
33	2	292	A
33	2	295	C
33	2	307	G
33	2	308	G
33	2	309	G
33	2	310	C
33	2	313	A
33	2	319	C
33	2	320	G
33	2	321	C
33	2	331	C
33	2	332	G
33	2	333	G
33	2	338	G
33	2	347	G
33	2	350	C
33	2	351	G
33	2	360	A
33	2	362	C
33	2	364	A
33	2	368	U
33	2	370	G
33	2	377	G
33	2	381	C
33	2	383	G
33	2	384	U
33	2	385	G
33	2	386	C
33	2	399	C
33	2	400	C
33	2	407	G
33	2	408	A

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Mol	Chain	Res	Type
33	2	409	C
33	2	418	A
33	2	436	G
33	2	438	G
33	2	441	C
33	2	448	A
33	2	449	A
33	2	450	C
33	2	464	A
33	2	466	G
33	2	467	G
33	2	471	G
33	2	472	C
33	2	473	A
33	2	474	G
33	2	476	A
33	2	482	G
33	2	483	C
33	2	487	U
33	2	492	C
33	2	493	A
33	2	502	C
33	2	516	A
33	2	525	A
33	2	533	A
33	2	534	G
33	2	535	G
33	2	538	U
33	2	541	U
33	2	542	U
33	2	546	G
33	2	547	G
33	2	548	C
33	2	553	U
33	2	554	A
33	2	555	A
33	2	556	U
33	2	557	U
33	2	559	G
33	2	560	A
33	2	563	G
33	2	568	C

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Mol	Chain	Res	Type
33	2	573	U
33	2	574	A
33	2	576	A
33	2	583	A
33	2	587	A
33	2	589	G
33	2	591	U
33	2	592	C
33	2	593	C
33	2	598	G
33	2	603	C
33	2	607	U
33	2	608	C
33	2	614	C
33	2	615	C
33	2	617	G
33	2	620	G
33	2	628	A
33	2	629	A
33	2	643	A
33	2	644	G
33	2	655	A
33	2	660	C
33	2	668	A
33	2	669	A
33	2	671	A
33	2	672	A
33	2	673	G
33	2	683	G
33	2	684	G
33	2	688	U
33	2	748	C
33	2	749	U
33	2	750	C
33	2	751	G
33	2	792	C
33	2	793	G
33	2	794	A
33	2	795	A
33	2	797	C
33	2	798	G
33	2	799	U

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Mol	Chain	Res	Type
33	2	801	U
33	2	809	A
33	2	810	A
33	2	821	G
33	2	822	U
33	2	830	A
33	2	847	A
33	2	853	C
33	2	859	G
33	2	869	A
33	2	870	A
33	2	871	U
33	2	872	A
33	2	873	G
33	2	874	G
33	2	878	G
33	2	879	C
33	2	880	G
33	2	881	G
33	2	887	U
33	2	888	U
33	2	890	U
33	2	891	G
33	2	898	U
33	2	899	U
33	2	901	G
33	2	903	A
33	2	904	A
33	2	906	U
33	2	913	A
33	2	914	U
33	2	917	U
33	2	920	A
33	2	930	C
33	2	933	G
33	2	954	U
33	2	955	A
33	2	959	G
33	2	963	A
33	2	965	U
33	2	967	C
33	2	968	U

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Mol	Chain	Res	Type
33	2	970	G
33	2	971	G
33	2	973	C
33	2	981	A
33	2	983	A
33	2	989	C
33	2	990	A
33	2	999	G
33	2	1002	U
33	2	1017	U
33	2	1023	A
33	2	1030	A
33	2	1039	C
33	2	1080	A
33	2	1083	A
33	2	1085	C
33	2	1086	G
33	2	1087	A
33	2	1088	U
33	2	1089	G
33	2	1096	G
33	2	1107	G
33	2	1112	U
33	2	1113	A
33	2	1115	U
33	2	1118	C
33	2	1119	A
33	2	1120	U
33	2	1121	G
33	2	1123	C
33	2	1130	G
33	2	1133	A
33	2	1138	C
33	2	1149	A
33	2	1153	C
33	2	1154	U
33	2	1155	U
33	2	1157	G
33	2	1158	G
33	2	1166	G
33	2	1171	G
33	2	1195	A

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Mol	Chain	Res	Type
33	2	1202	U
33	2	1203	G
33	2	1207	G
33	2	1208	A
33	2	1214	A
33	2	1215	C
33	2	1217	A
33	2	1221	G
33	2	1224	G
33	2	1227	G
33	2	1232	U
33	2	1235	G
33	2	1236	G
33	2	1237	C
33	2	1238	U
33	2	1242	U
33	2	1243	U
33	2	1250	A
33	2	1251	A
33	2	1253	A
33	2	1257	G
33	2	1259	A
33	2	1260	A
33	2	1261	C
33	2	1269	G
33	2	1271	C
33	2	1274	G
33	2	1275	G
33	2	1283	C
33	2	1284	A
33	2	1285	G
33	2	1286	G
33	2	1287	A
33	2	1297	U
33	2	1298	G
33	2	1300	U
33	2	1301	A
33	2	1302	G
33	2	1303	C
33	2	1308	U
33	2	1309	C
33	2	1312	G

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Mol	Chain	Res	Type
33	2	1313	A
33	2	1315	U
33	2	1317	C
33	2	1318	G
33	2	1320	G
33	2	1322	G
33	2	1325	G
33	2	1330	G
33	2	1331	C
33	2	1332	A
33	2	1341	C
33	2	1342	U
33	2	1348	G
33	2	1352	G
33	2	1354	G
33	2	1358	U
33	2	1364	U
33	2	1371	U
33	2	1372	U
33	2	1374	C
33	2	1376	A
33	2	1378	A
33	2	1381	G
33	2	1382	A
33	2	1401	A
33	2	1402	A
33	2	1404	U
33	2	1406	G
33	2	1411	G
33	2	1416	C
33	2	1426	U
33	2	1429	G
33	2	1430	C
33	2	1431	G
33	2	1432	U
33	2	1439	A
33	2	1441	U
33	2	1444	U
33	2	1452	A
33	2	1454	A
33	2	1462	U
33	2	1463	U

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Mol	Chain	Res	Type
33	2	1465	A
33	2	1466	G
33	2	1474	A
33	2	1477	U
33	2	1478	U
33	2	1488	C
33	2	1489	A
33	2	1490	G
33	2	1491	G
33	2	1494	U
33	2	1495	G
33	2	1498	A
33	2	1505	U
33	2	1507	G
33	2	1510	G
33	2	1512	C
33	2	1518	C
33	2	1519	U
33	2	1520	G
33	2	1521	C
33	2	1527	C
33	2	1528	G
33	2	1531	A
33	2	1533	A
33	2	1534	C
33	2	1535	U
33	2	1544	C
33	2	1548	G
33	2	1559	C
33	2	1560	U
33	2	1566	G
33	2	1567	G
33	2	1572	C
33	2	1573	G
33	2	1574	C
33	2	1575	G
33	2	1578	U
33	2	1579	A
33	2	1580	A
33	2	1581	C
33	2	1582	C
33	2	1585	U

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Mol	Chain	Res	Type
33	2	1586	U
33	2	1587	G
33	2	1588	A
33	2	1598	G
33	2	1599	U
33	2	1600	G
33	2	1601	A
33	2	1602	U
33	2	1606	G
33	2	1610	G
33	2	1612	G
33	2	1613	G
33	2	1616	U
33	2	1618	C
33	2	1620	A
33	2	1621	U
33	2	1623	A
33	2	1629	C
33	2	1630	A
33	2	1637	A
33	2	1641	A
33	2	1648	G
33	2	1649	U
33	2	1650	A
33	2	1654	G
33	2	1661	A
33	2	1663	A
33	2	1665	G
33	2	1675	A
33	2	1683	C
33	2	1691	U
33	2	1692	U
33	2	1693	G
33	2	1695	A
33	2	1696	C
33	2	1698	C
33	2	1713	C
33	2	1714	U
33	2	1719	A
33	2	1720	U
33	2	1721	U
33	2	1722	G

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Mol	Chain	Res	Type
33	2	1723	G
33	2	1729	U
33	2	1730	U
33	2	1735	A
33	2	1748	G
33	2	1756	C
33	2	1776	G
33	2	1779	G
33	2	1783	C
33	2	1784	G
33	2	1785	C
33	2	1786	U
33	2	1801	A
33	2	1805	G
33	2	1819	A

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	2	65	C
33	2	102	A
33	2	114	G
33	2	143	U
33	2	180	G
33	2	332	G
33	2	382	C
33	2	417	C
33	2	465	A
33	2	749	U
33	2	750	C
33	2	791	C
33	2	793	G
33	2	797	C
33	2	870	A
33	2	958	G
33	2	980	A
33	2	1137	U
33	2	1165	G
33	2	1231	C
33	2	1302	G
33	2	1308	U
33	2	1316	C

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Mol	Chain	Res	Type
33	2	1330	G
33	2	1373	C
33	2	1403	C
33	2	1415	C
33	2	1425	G
33	2	1430	C
33	2	1431	G
33	2	1438	A
33	2	1440	C
33	2	1464	C
33	2	1494	U
33	2	1511	U
33	2	1534	C
33	2	1558	C
33	2	1585	U
33	2	1587	G
33	2	1601	A
33	2	1648	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1200:A	O3'	1201:U	P	3.10

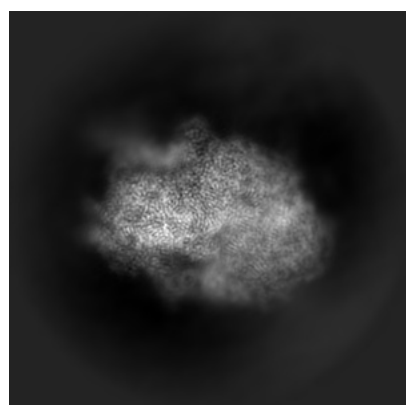
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11301. These allow visual inspection of the internal detail of the map and identification of artifacts.

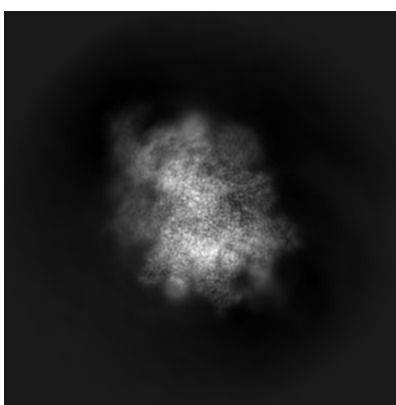
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

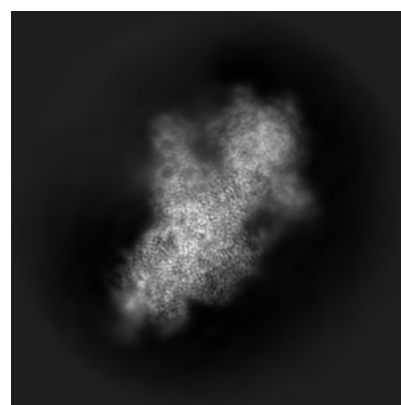
6.1.1 Primary map



X



Y

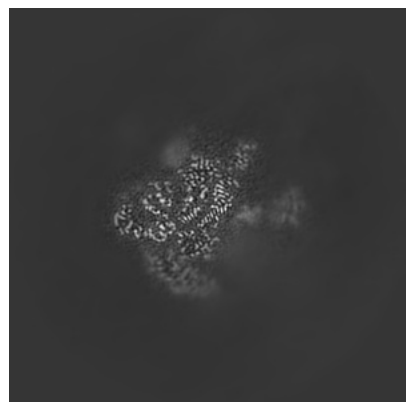


Z

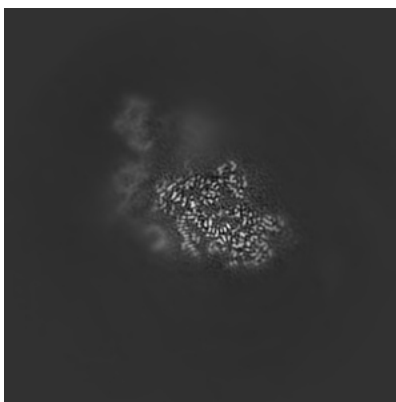
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

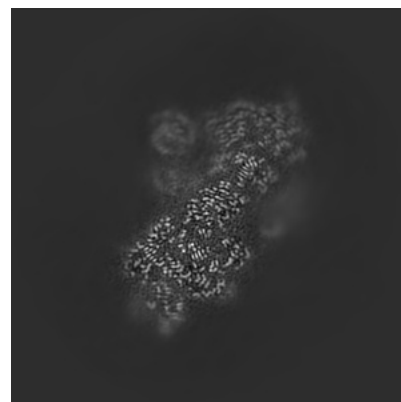
6.2.1 Primary map



X Index: 180



Y Index: 180

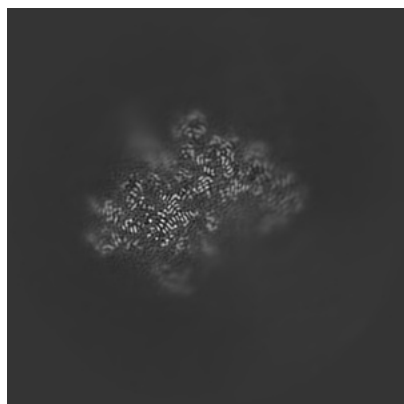


Z Index: 180

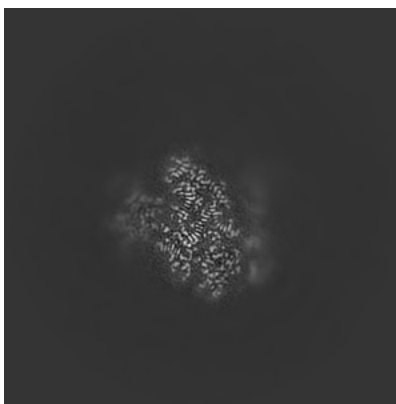
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

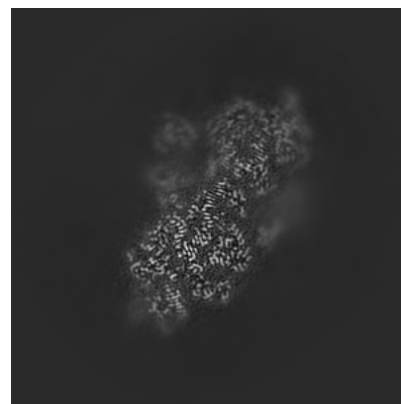
6.3.1 Primary map



X Index: 151



Y Index: 140

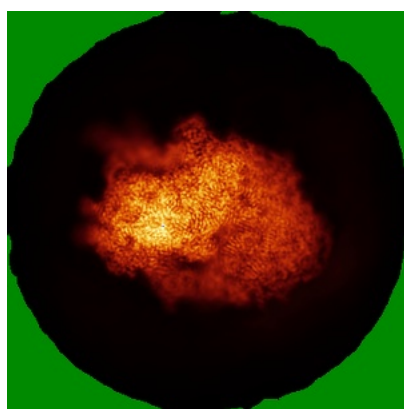


Z Index: 175

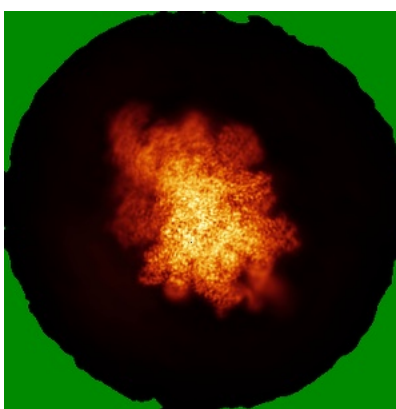
The images above show the largest variance slices of the map in three orthogonal directions.

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

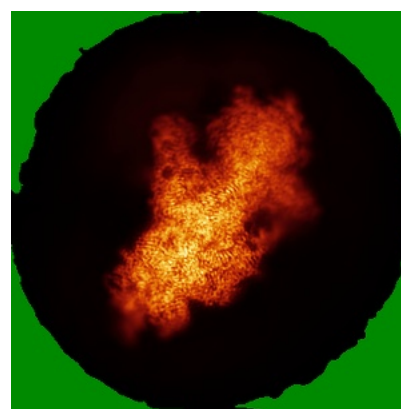
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

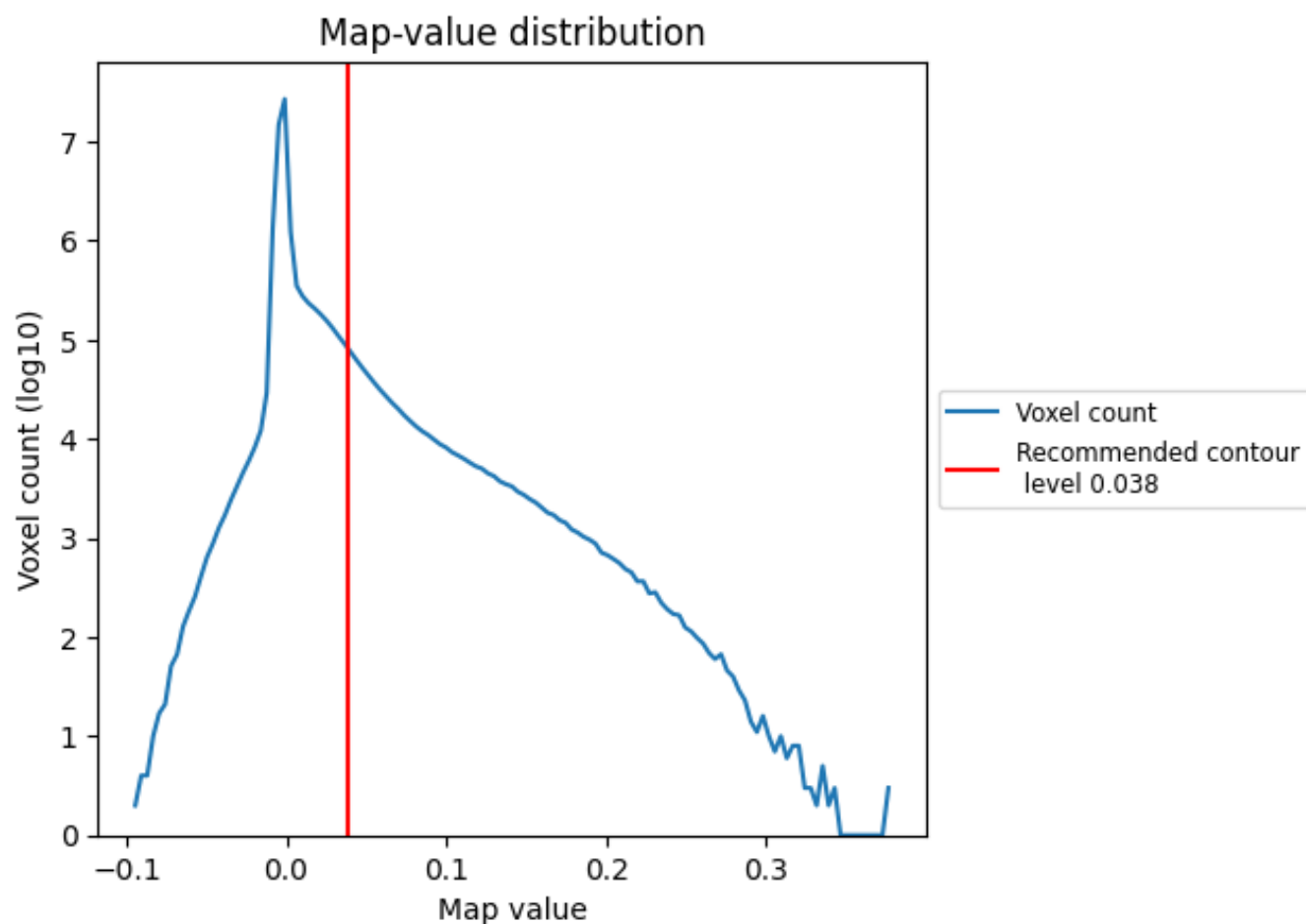
6.6 Mask visualisation

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

7 Map analysis [i](#)

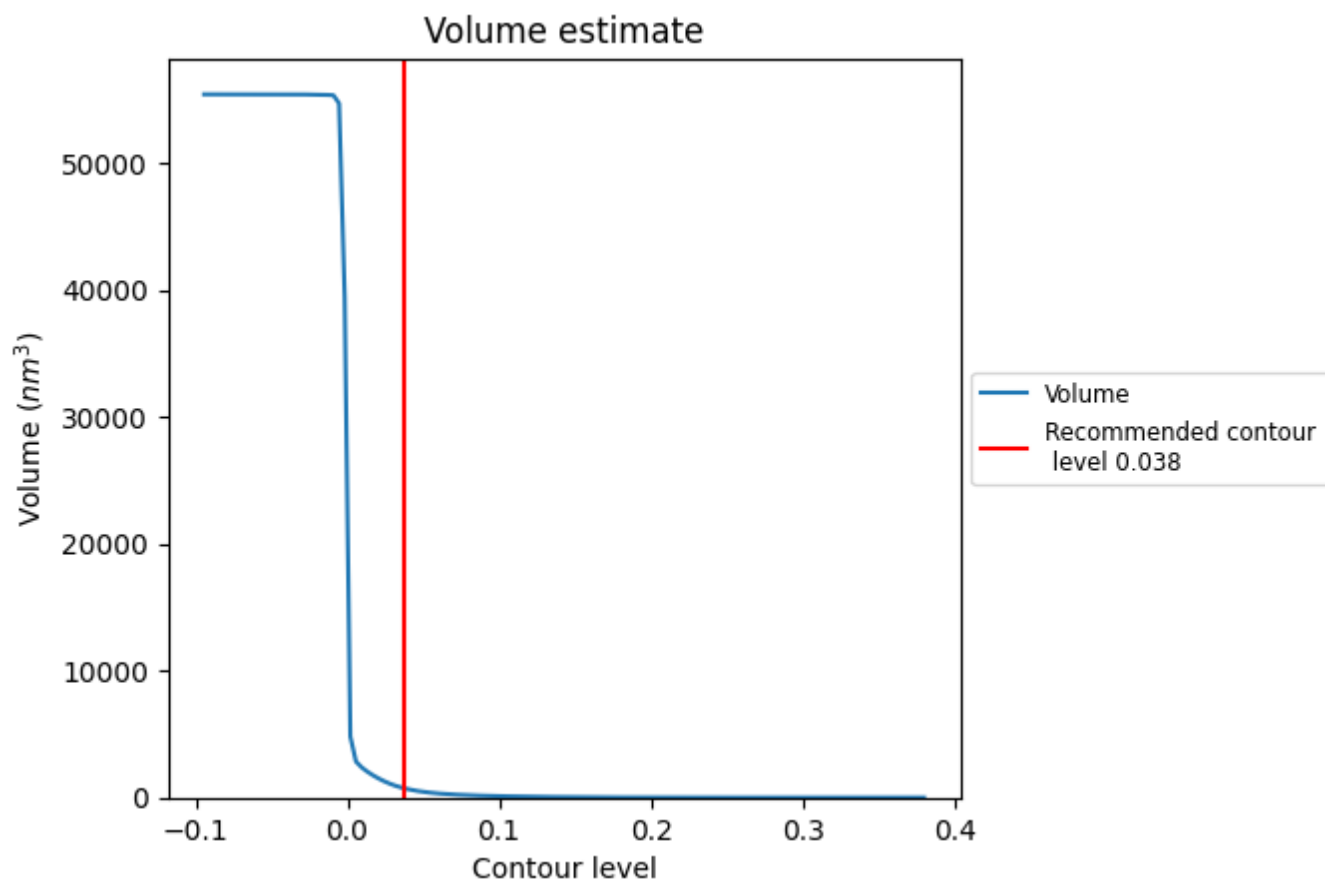
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

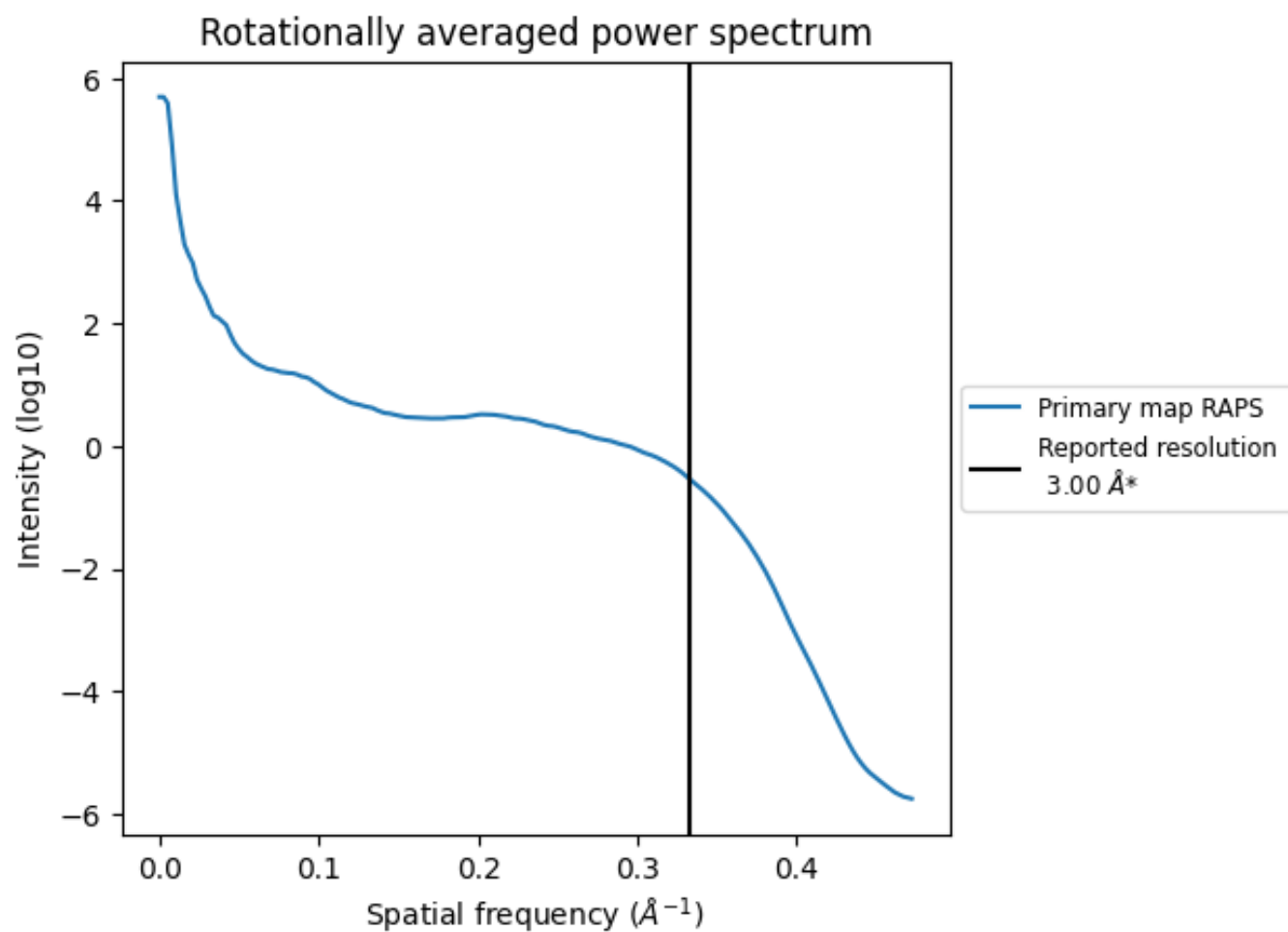
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 718 nm^3 ; this corresponds to an approximate mass of 649 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 ⓘ

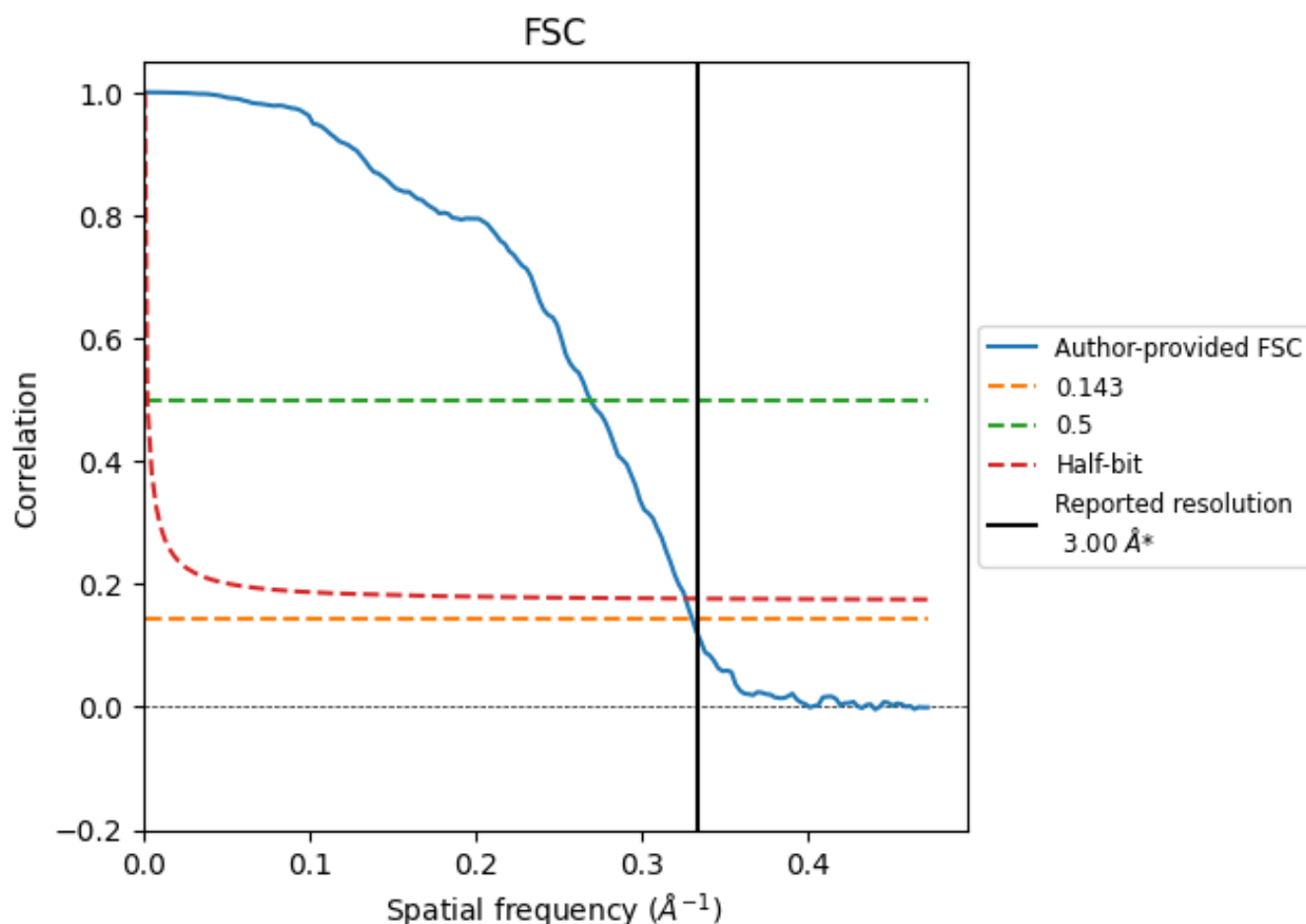


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

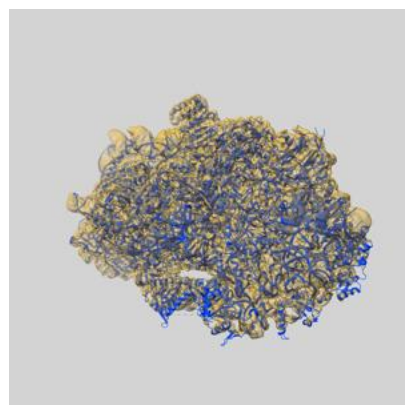
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.71	3.06
Unmasked-calculated*	-	-	-

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

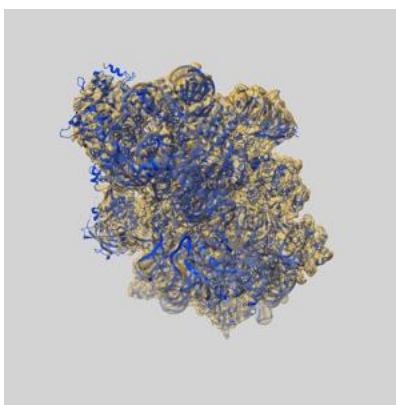
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11301 and PDB model 6ZMT. Per-residue inclusion information can be found in section [3](#) on page [11](#).

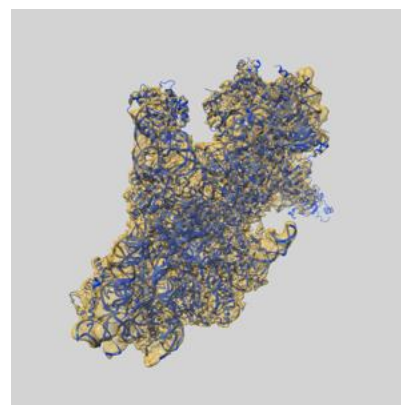
9.1 Map-model overlay [i](#)



X



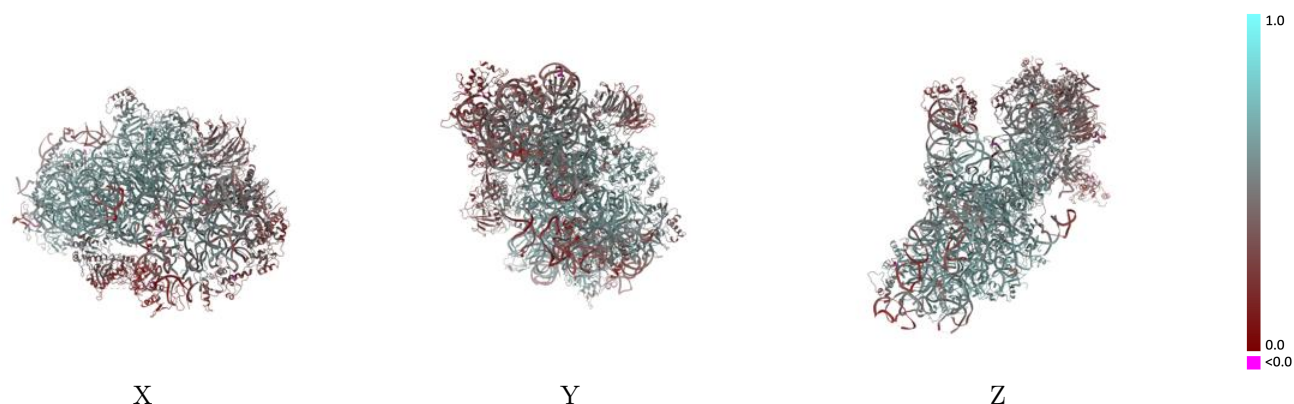
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.038 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](#)

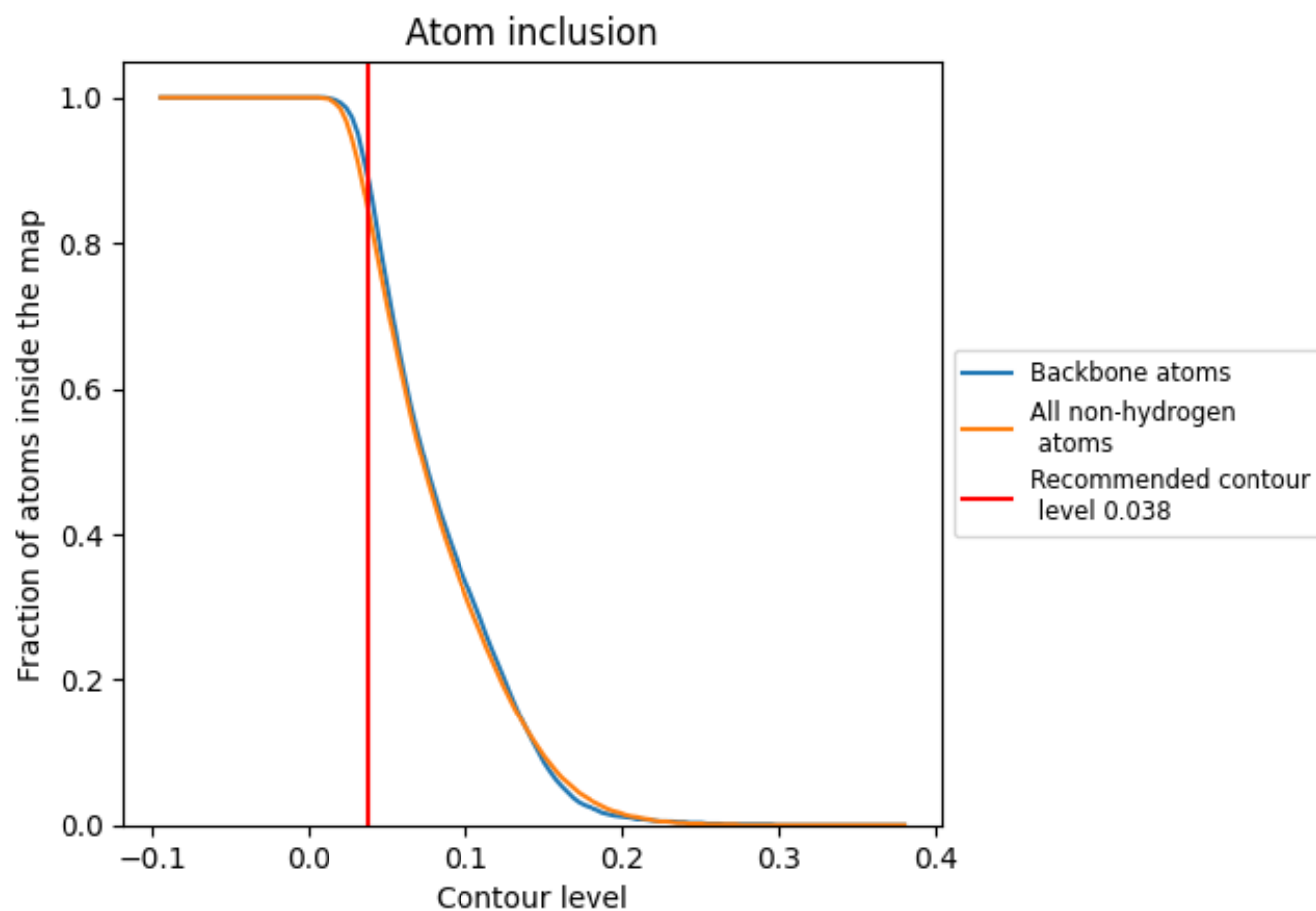


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.038) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8470	 0.4890
2	 0.9590	 0.5170
B	 0.9620	 0.5790
C	 0.6400	 0.3920
D	 0.9650	 0.5980
E	 0.9570	 0.6030
F	 0.8030	 0.4600
G	 0.8940	 0.5250
H	 0.8500	 0.4860
I	 0.9030	 0.5490
J	 0.9620	 0.5990
K	 0.7150	 0.4200
L	 0.9150	 0.5880
M	 0.6790	 0.3540
N	 0.9220	 0.5390
O	 0.1970	 0.2250
P	 0.4400	 0.3160
Q	 0.5430	 0.3680
R	 0.8210	 0.4660
S	 0.8810	 0.5250
T	 0.4490	 0.3320
U	 0.6700	 0.3880
V	 0.6820	 0.4250
W	 0.9820	 0.6230
X	 0.9630	 0.5920
Y	 0.9560	 0.5910
Z	 0.9390	 0.5870
a	 0.3640	 0.3070
b	 0.8930	 0.5420
d	 0.6250	 0.3960
e	 0.8870	 0.5280
f	 0.9360	 0.5200
g	 0.4530	 0.2200
i	 0.9230	 0.5820
j	 0.7100	 0.3800
u	 0.4910	 0.3530

