



Full wwPDB EM Validation Report ⓘ

Jul 8, 2026 – 12:34 PM JST

PDB ID : 9KMU / pdb_00009kmu
EMDB ID : EMD-62445
Title : Bat SARSr-CoV RaTG15 Nsp1 bound to the Human 40S Ribosomal subunit-State2
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.87 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.dev133
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) : 2.50

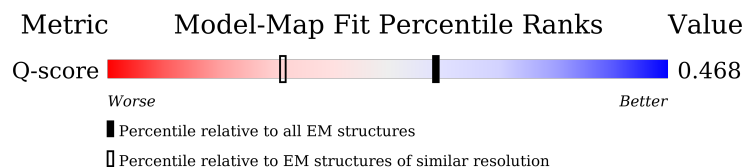
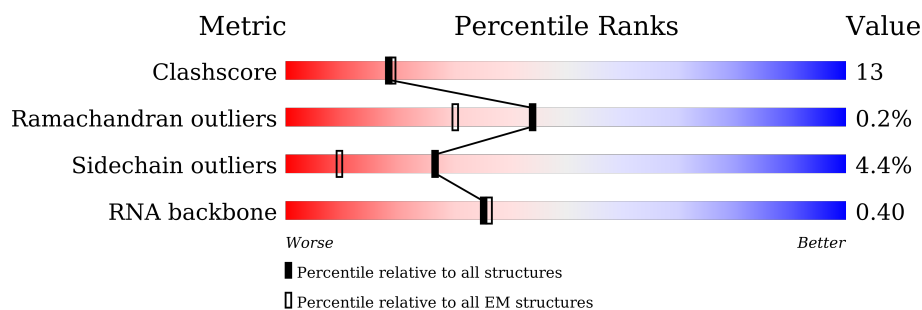
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

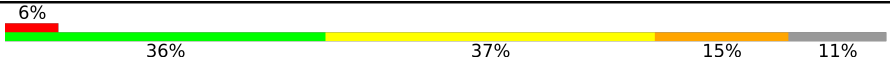
The reported resolution of this entry is 2.87 Å.

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.



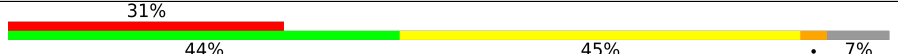
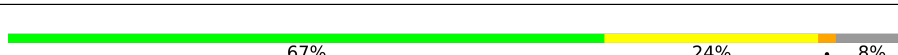
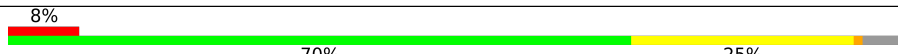
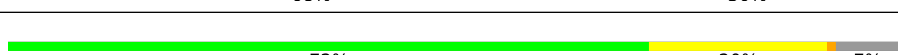
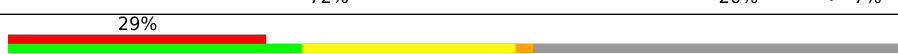
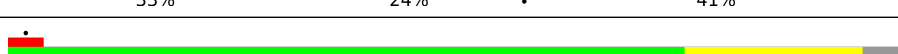
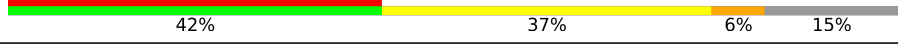
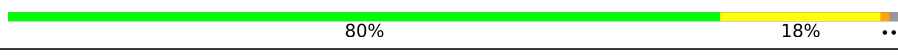
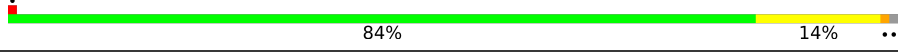
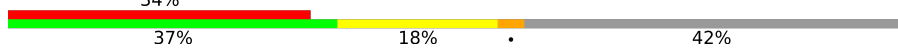
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12062 (2.37 - 3.37)

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	2	1869	
2	A	295	
3	B	264	

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	
30	c	62	
31	d	55	
32	e	56	
33	f	74	
34	g	315	
35	h	25	
36	n	180	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74574 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1660	Total	C	N	O	P	0	0
			35423	15824	6374	11575	1650		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

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

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

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

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

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

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

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

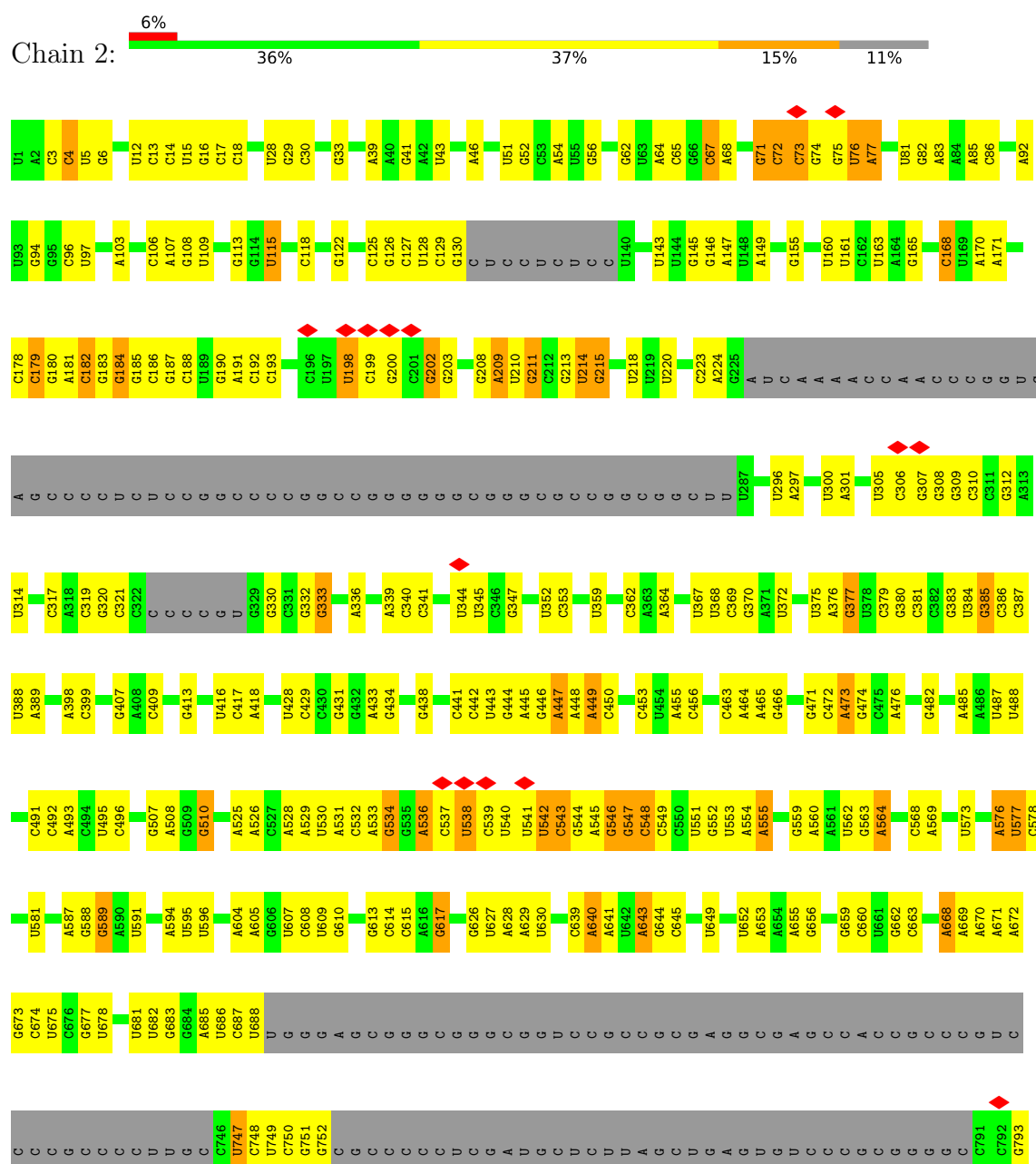
- Molecule 36 is a protein called ORF1ab polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	30	Total	C	N	O	S	0	0
			238	146	41	49	2		

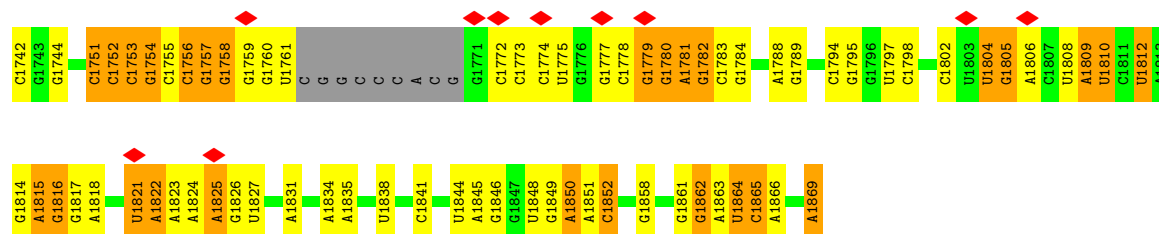
3 Residue-property plots

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.

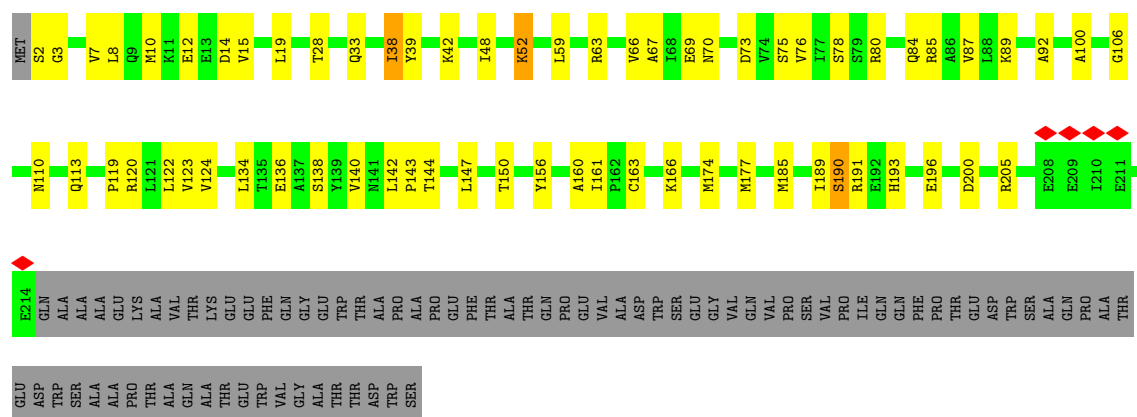
• Molecule 1: 18S ribosomal RNA



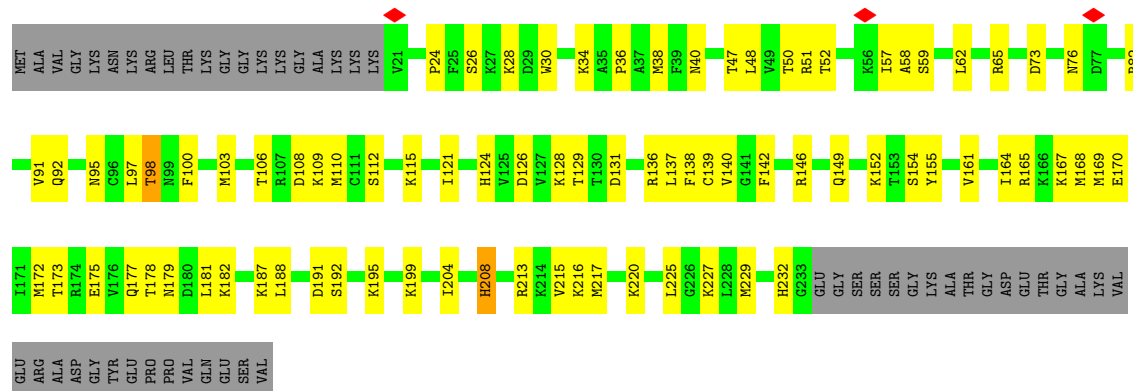
U1672	U1485	G1546	G1610	U1486	A	G1357	C1292	U1232	G1043	C953	U	A794
A1675	A1486	C1547	G1611	A1487	G	U1358	A1293	G1233	G1044	U954	U	A795
U1676	C1488	U1549	G1612	C1489	C	U1359	G1294	C1234	U1045	A955	C	G796
U1677	A1489	U1550	G1613	G1425	G1424	U1360	A1295	G1235	U1046	G956	U	C797
A1678	U1551	U1551	A1614	U1426	U1426	G1361	U1296	G1236	U1047	A957	A886	A886
A1679	G1490	G1552	U	C1427	C1427	U1362	C1237	C1237		G958	U887	U799
A1679	G1491	G1552	G1616	G1428	G1428	C1363	U1297	U1238		G959	U888	
A1679	G1492	C1553	G1617	G1429	G1429	U1364	U1298	U1239	C1053	U960	U889	U804
A1679	C1493	C1554	C1618	C1430	C1430	G1365	A1299	U1240	A1058	G961	U890	U805
A1680	U1494	U1555	G1619	G1431	G1431	G1366	U1300	A1241	G1059	A962	G891	A809
U1685	U1495	A1556	A1620	U1432	U1432	G1367	A1301	U1242	A1060	A963	U892	A810
G1686	U1496	C	U1621	C	C	U1367	U1302	U1243	U1061	U965	G895	A811
C1687	G1497	C	U1622	C	C	U1371	C1303	U1244	A1062	G971	U896	A812
C1688	A1498	C	A1623	C	C	U1372	G1304	G1245		G978	U897	G817
A1695	U1499	C	U1624	C	C	C1373	U1305	G1246	A1070	G979	U898	G817
A1699	G1500	C	U1625	C	C	G1374	C1306	A1247	A1071	G979	U899	G821
G1702	C1501	A1438	C	A1438	A1438	G1375	U1307	U1248	U1072	A980	C900	U822
C1703	C1502	A1439	C1627	A1440	A1440	U1376	U1308	A1249	U1073	A981	G901	U823
C1704	C1503	A1441	C1628	U1442	U1442	U1377		A1250	A1080	A982	G902	C824
C1705	U1504	U1443	G1629	C1443	C1443	A1378	C1311	A1251	A1083	A983	A903	A830
G1706	A1506	U1444	A1630	U1444	U1444	C1380	G1312	A1252	A1084	C984	A904	G831
G1709	G1507	U1445	U1631	A1445	A1445	G1381	A1313	C1253	C1085	G985	C905	
C1710	A1508	A1446	U1632	A1446	A1446		A1314	A1254	G1086	C989	U906	C834
U1711	U1509	G1447	G1633	G1447	G1447	G1385	U1315	G1255	A1087	A990	G907	C
U1712	G1510	A1448	G1634	A1448	A1448	A1386	C1316	G1256	U1088	G991	A908	G
C1713	U1511	G1449	G1635	G1449	G1449	G1387	C1317	A1257	G991	A992	G909	A
G1714	C1512	G1450	G1636	G1450	G1450	A1388	U1318	A1258	C1089		G910	C
U1715	G1513	G1451	G1637	G1451	G1451	C1389	U1319	A1259	G1091	A996	C911	C
C1716	C1514	A1452	G1638	A1452	A1452	U1390	G1320	C1261	G1092	A997	A913	
G1717	U1514	C1453	U1641	C1453	C1453	C1391	G1321	U1262	C1094	G999	U914	G841
C1718	G1517	A1454	U1642	A1454	A1454		A1263	U1263	G1095		U917	G846
U1720	A1518	A1455	U1643	A1455	A1455	C1395	G1322	A1265	G1096	U1002	G920	A847
A1719	U1519	G1456	G1644	G1456	G1456	A1396	U1323	G1266	G1097	C1007	A920	G852
U1721	G1520	U1457	C1645	U1457	U1457	U1397	G1324	C1267	C1098	A1008	G921	
G1722	C1521	G1458	C1646	G1458	G1458	G1398	U1325	C1268	A1100	A1009	A922	U857
A1724	A1522	U1462	U1647	U1462	U1462	U1400	U1326	G1269	G1101	G1010	G925	A858
U1725	C1523	U1463	U1648	U1463	U1463	A1401	G1327	G1270	G1102	A1011	G928	G859
G1726	G1524	G1466	U1649	G1466	G1466	A1402	U1328	C1271	C1109	A1012	G929	G860
C1727	C1525	C1467	A1650	C1467	C1467	C1403	U1329	C1272	U1016	U1013	G930	A861
U1728	G1526	A1468	A1651	A1468	A1468	U1404	G1330	C1273	U1017	G933	G940	G862
G1729	C1527	C1469	U1661	C1469	C1469	U1405	C1331	G1274	U1113		U940	G868
U1730	G1529	C1470	U1662	C1470	C1470	G1406	A1332	G1275	U1114	C941	G942	A870
A1731	U1530	C1471	G1663	C1471	C1471	U1407	U1333	A1276	U1115	A1023	G943	U871
G1732	A1531	G1472	U1664	G1472	G1472	U1408	G1334	G1277	C1116	U1024	A944	A872
C1733	C1532	G1473	U1665	G1473	G1473	C1409	U1335	A1278		A1025	U945	A873
U1734	A1533	A1474	U1666	A1474	A1474	C1410	G1338	C1279	A1119	U1026	G947	A874
G1735	C1534	G1475	U1667	G1475	G1475	C1411	U1339	G1280	U1120	C1027	U946	C876
C1736	U1535	A1476	U1668	A1476	A1476	G1412	G1340	G1281	A1121	A1027	G947	C877
G1738	G1536	U1477	U1669	U1477	U1477	A1413	U1341	U1225	A1122	A1028	G948	C878
C1739	A1537	U1478	U1670	U1478	U1478	A1414	G1342	G1226			G949	A875
U1741	C1538	G1479	G1604	G1479	G1479	C1415	U1343	A1282	G1129	G1033	C941	C876
	U1539	A1480	G1605	A1480	A1480	C1416	U1344	C1283	A1034	A1035	G947	C877
	G1540	C	G1606	C	C	C	A1344	A1284	C1138	A1036	G948	C878
	A	C	U	C	C	G	U1347	G1285	C1139	A1037	G949	C879
	U1541	A1483		A1483	A1483		G1348	G1286	G1140		G952	G880
	C1542	A1484		A1484	A1484		G1349	A1287				
	U1543						U1288	U1288				
	C1544						U1289	U1289				
	A1545						G1290	G1290				
							A1291	A1291				
							G1352	G1352				
							A1353	A1353				
							G1354	G1354				



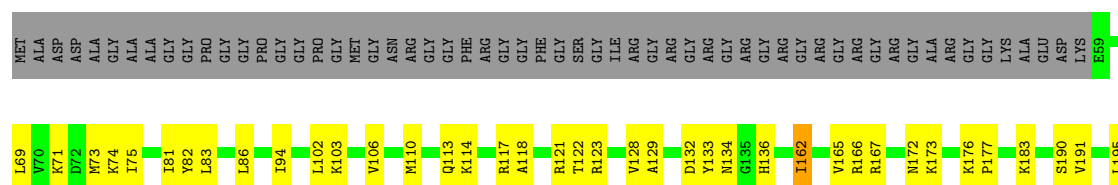
• Molecule 2: Small ribosomal subunit protein uS2



• Molecule 3: Small ribosomal subunit protein eS1

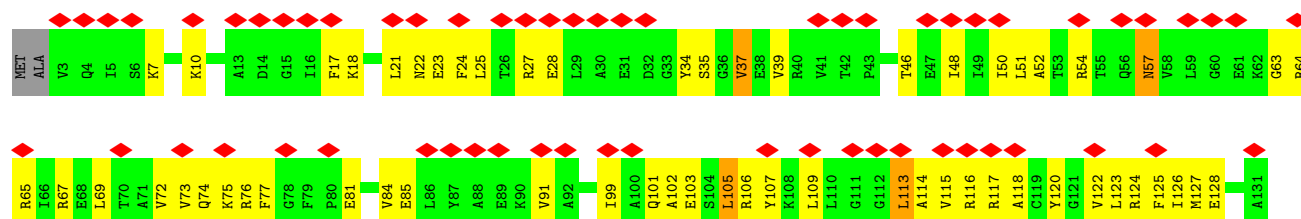


• Molecule 4: Small ribosomal subunit protein uS5

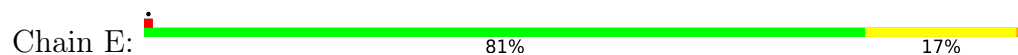




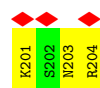
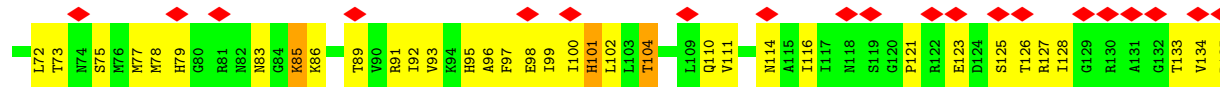
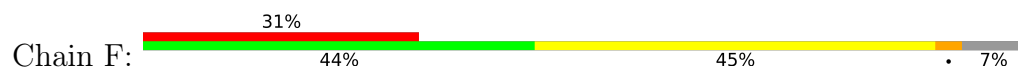
• Molecule 5: Small ribosomal subunit protein uS3



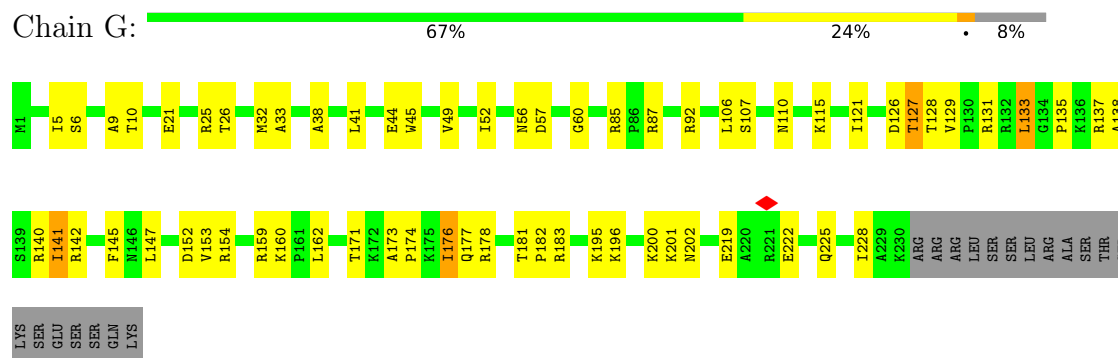
• Molecule 6: Small ribosomal subunit protein eS4, X isoform



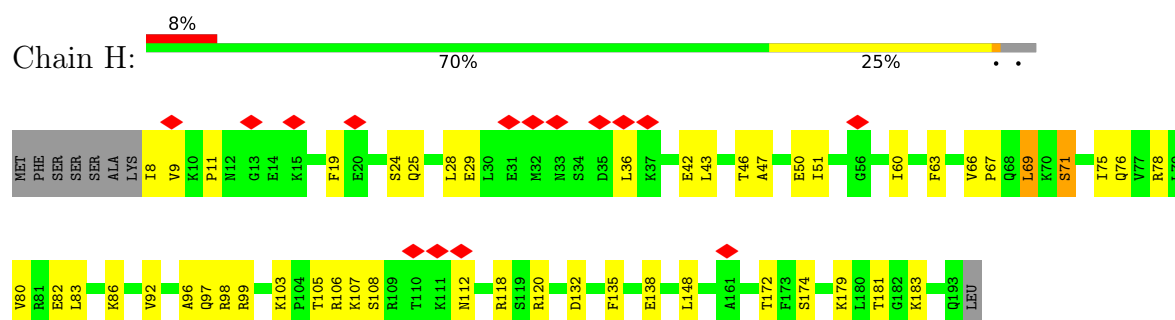
• Molecule 7: Small ribosomal subunit protein uS7



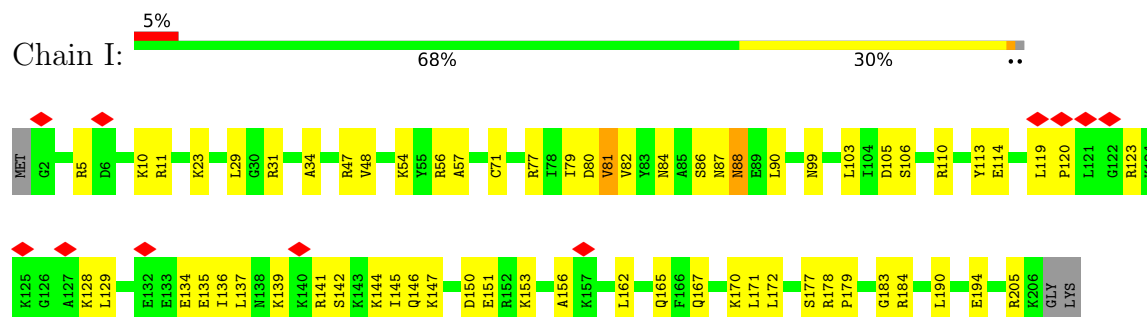
- Molecule 8: Small ribosomal subunit protein eS6



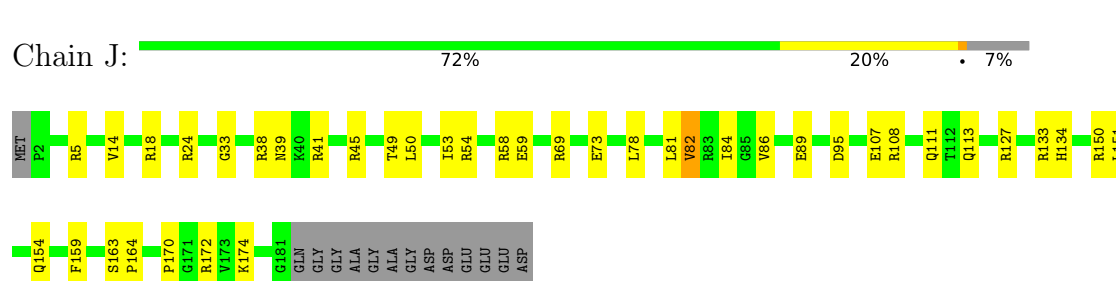
- Molecule 9: Small ribosomal subunit protein eS7



- Molecule 10: Small ribosomal subunit protein eS8



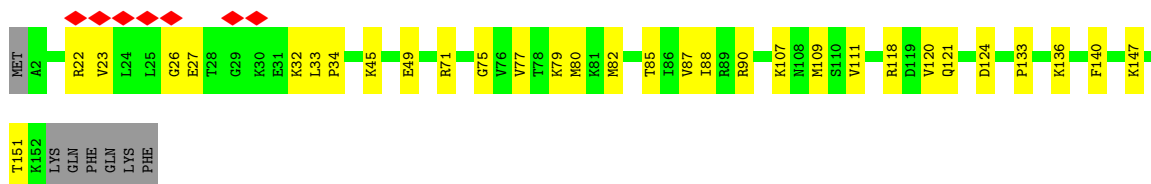
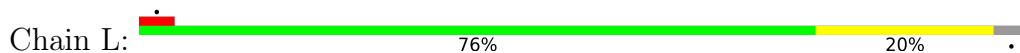
- Molecule 11: Small ribosomal subunit protein uS4



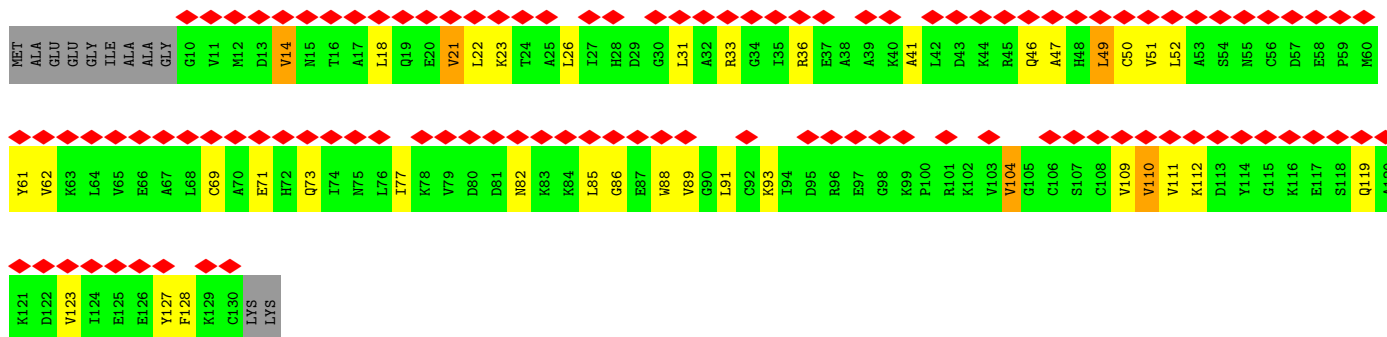
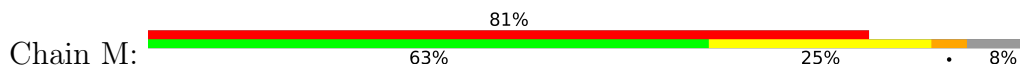
- Molecule 12: Small ribosomal subunit protein eS10



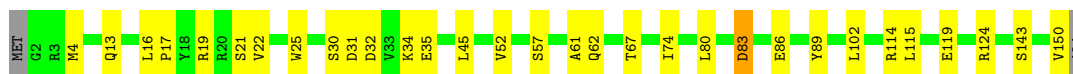
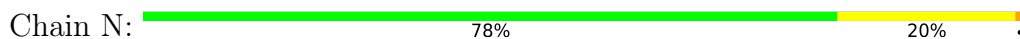
- Molecule 13: Small ribosomal subunit protein uS17



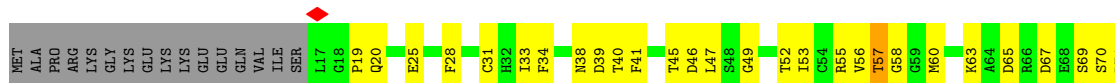
- Molecule 14: Small ribosomal subunit protein eS12



- Molecule 15: Small ribosomal subunit protein uS15

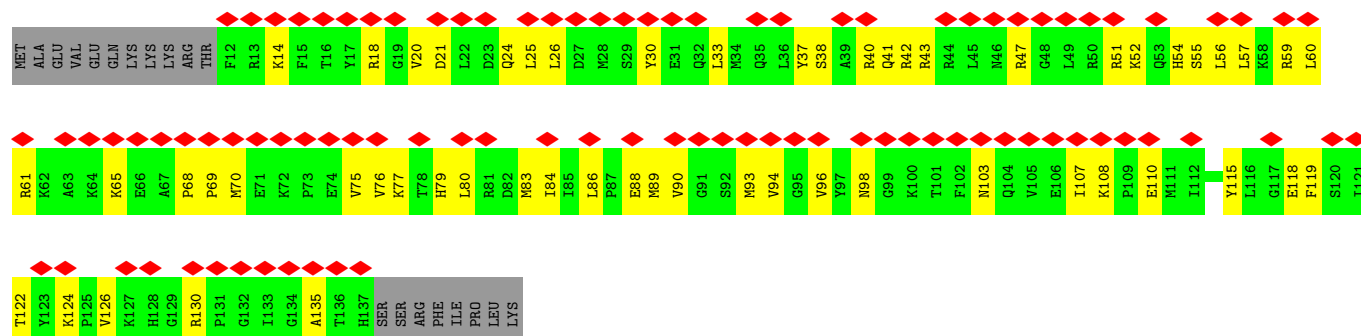


- Molecule 16: Small ribosomal subunit protein uS11

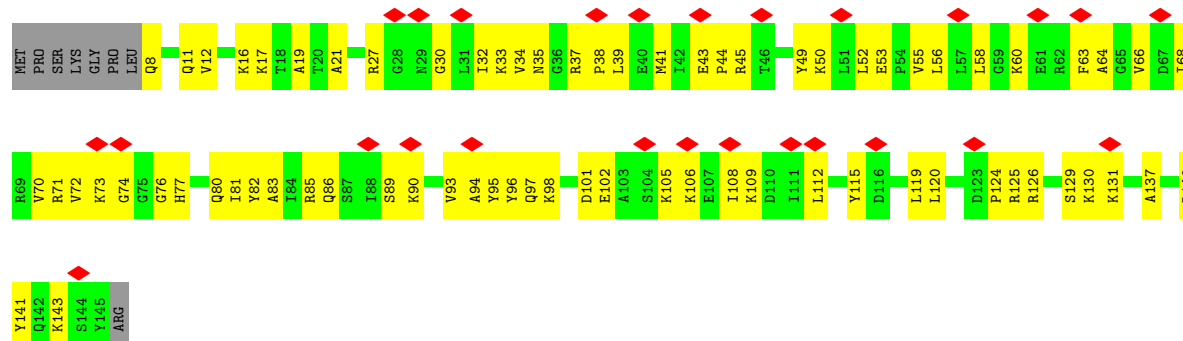
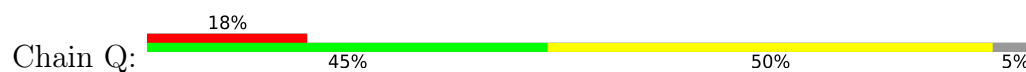




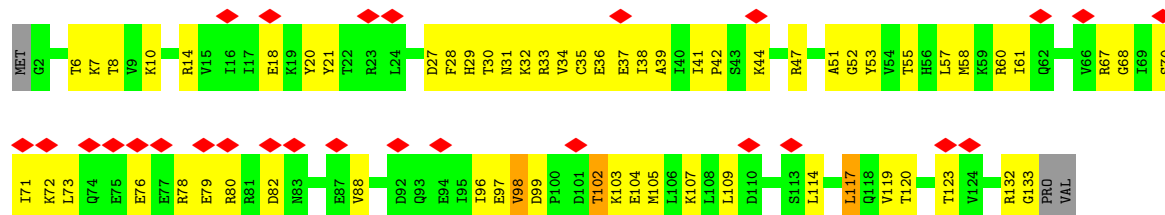
• Molecule 17: Small ribosomal subunit protein uS19



• Molecule 18: Small ribosomal subunit protein uS9

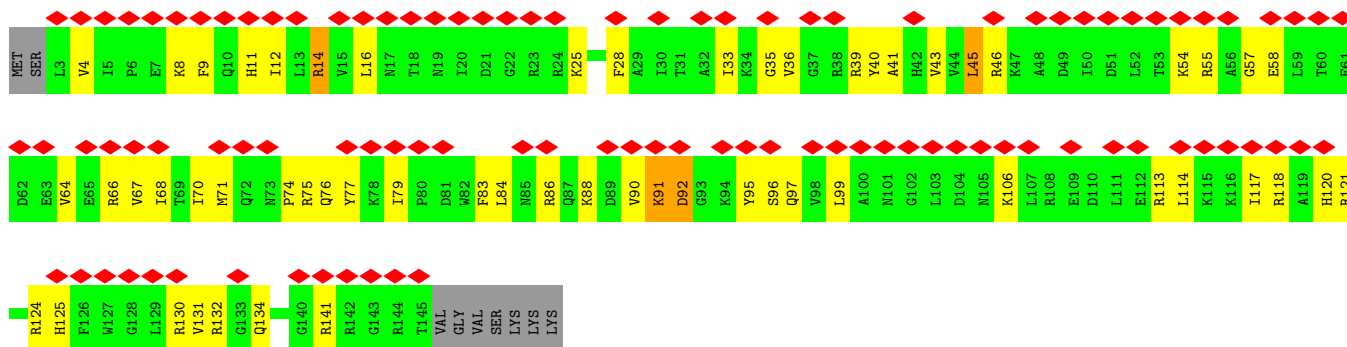


• Molecule 19: Small ribosomal subunit protein eS17

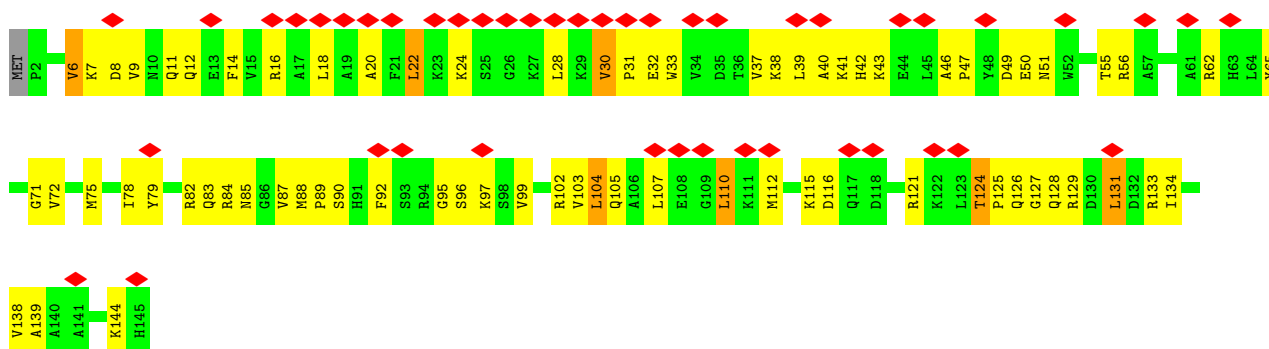


• Molecule 20: Small ribosomal subunit protein uS13

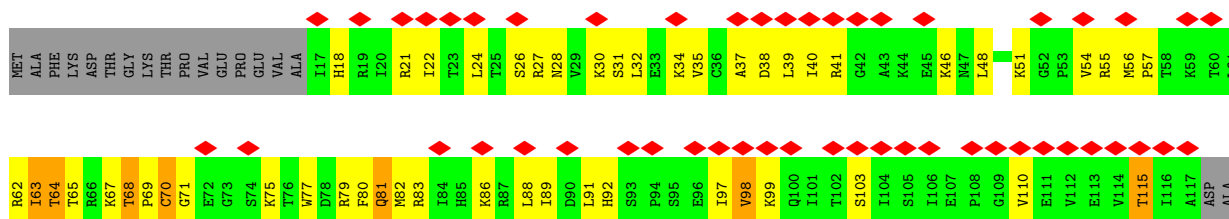




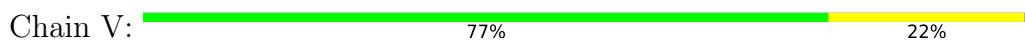
- Molecule 21: Small ribosomal subunit protein eS19



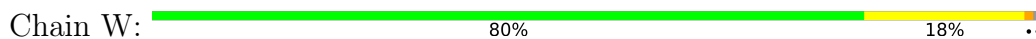
- Molecule 22: Small ribosomal subunit protein uS10



- Molecule 23: Small ribosomal subunit protein eS21

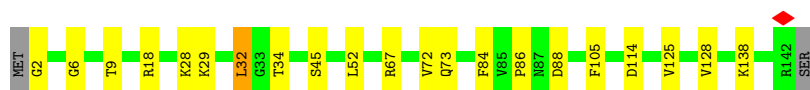


- Molecule 24: Small ribosomal subunit protein uS8



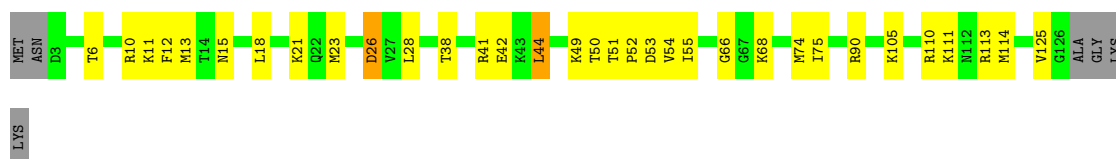
- Molecule 25: Small ribosomal subunit protein uS12

Chain X:  84% 14% ..



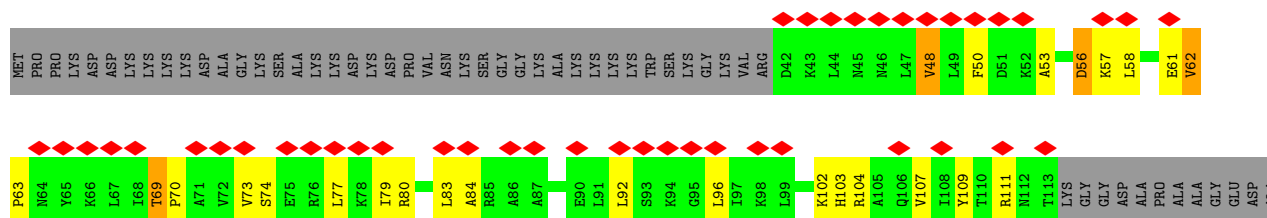
- Molecule 26: Small ribosomal subunit protein eS24

Chain Y:  70% 24% • 5%



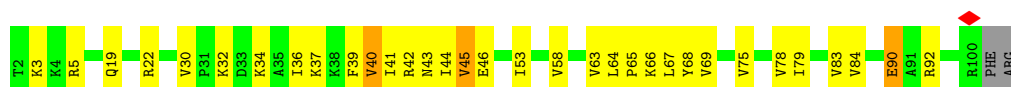
- Molecule 27: Small ribosomal subunit protein eS25

Chain Z:  34% 37% 18% • 42%



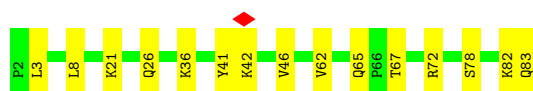
- Molecule 28: Small ribosomal subunit protein eS26

Chain a:  65% 30% • ..



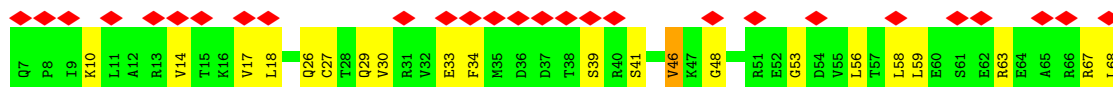
- Molecule 29: Small ribosomal subunit protein eS27

Chain b:  82% 18%

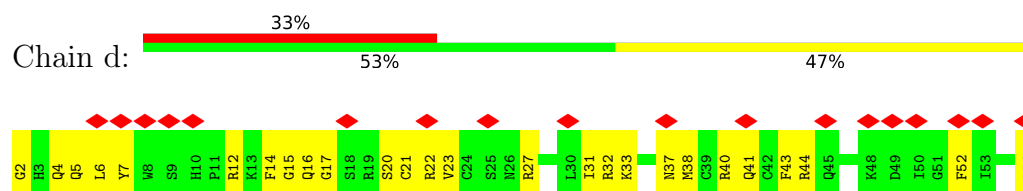


- Molecule 30: Small ribosomal subunit protein eS28

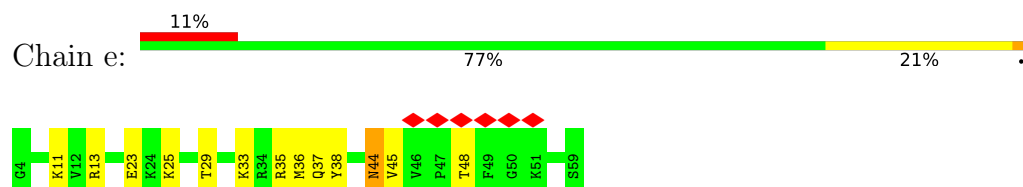
Chain c:  44% 66% 32% •



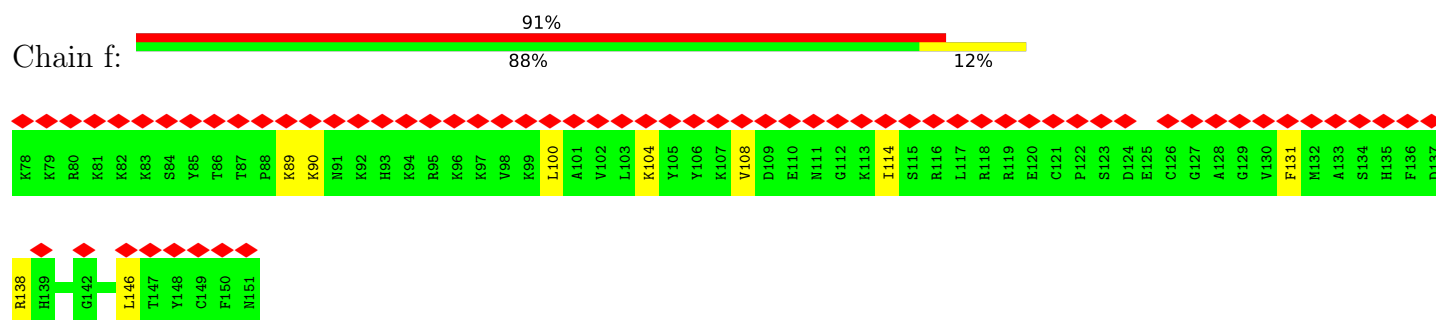
- Molecule 31: Small ribosomal subunit protein uS14



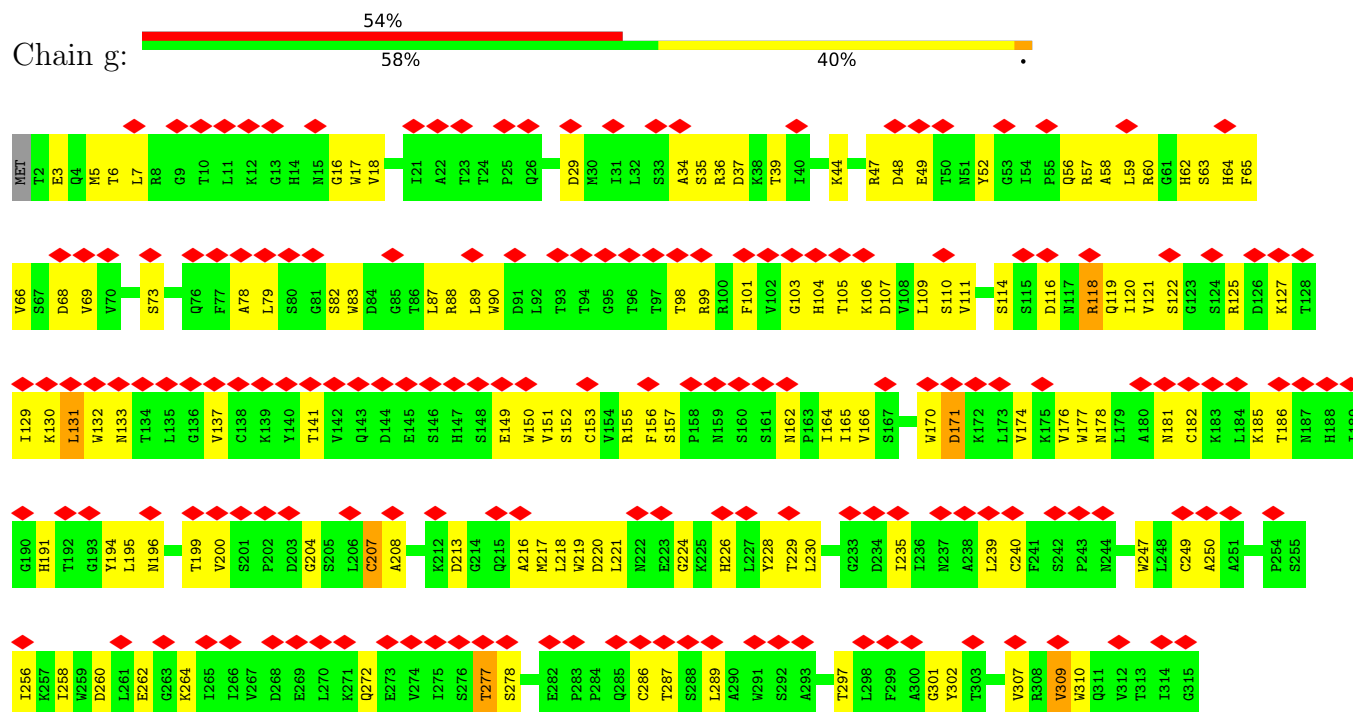
- Molecule 32: Small ribosomal subunit protein eS30



- Molecule 33: Small ribosomal subunit protein eS31



- Molecule 34: Small ribosomal subunit protein RACK1



- Molecule 35: Small ribosomal subunit protein eS32

Diagram illustrating the 22 amino acids in the genetic code, arranged in a grid corresponding to the 4th position of the codon (indicated by the number 4 in the top right corner). The amino acids are color-coded: yellow for the first 10, green for the next 10, and grey for the last 2.

M1	R2	W5	R9	M10	R11	R12	L13	R18	Q22	ARG	SER	LYS
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain n: 11% 5% 83%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51346	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.635	Depositor
Minimum map value	-0.792	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.24	1/39611 (0.0%)	0.31	0/61726
2	A	0.21	0/1723	0.33	0/2341
3	B	0.22	0/1756	0.34	0/2350
4	C	0.24	0/1726	0.36	0/2332
5	D	0.20	0/1780	0.50	1/2397 (0.0%)
6	E	0.25	0/2118	0.32	0/2849
7	F	0.21	0/1516	0.50	0/2037
8	G	0.19	0/1887	0.31	0/2513
9	H	0.17	0/1524	0.38	0/2042
10	I	0.21	0/1711	0.34	0/2282
11	J	0.25	0/1524	0.30	0/2035
12	K	0.14	0/840	0.38	0/1133
13	L	0.26	0/1250	0.37	0/1673
14	M	0.12	0/945	0.38	0/1269
15	N	0.20	0/1226	0.29	0/1649
16	O	0.22	0/1023	0.37	0/1372
17	P	0.15	0/1058	0.45	0/1414
18	Q	0.17	0/1114	0.49	0/1492
19	R	0.17	0/1082	0.47	0/1452
20	S	0.14	0/1202	0.43	0/1610
21	T	0.24	0/1143	0.51	1/1530 (0.1%)
22	U	0.14	0/813	0.39	0/1092
23	V	0.21	0/631	0.30	0/844
24	W	0.27	0/1051	0.35	0/1406
25	X	0.25	0/1116	0.37	0/1490
26	Y	0.24	0/1031	0.31	0/1370
27	Z	0.13	0/580	0.42	0/780
28	a	0.22	0/807	0.35	0/1082
29	b	0.21	0/654	0.42	0/876
30	c	0.13	0/491	0.36	0/656
31	d	0.14	0/470	0.43	0/623
32	e	0.20	0/447	0.34	0/587
33	f	0.11	0/623	0.33	0/822
34	g	0.14	0/2498	0.40	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.19	0/214	0.28	0/272
36	n	0.23	0/242	0.38	0/324
All	All	0.22	1/79427 (0.0%)	0.35	2/115121 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	510	G	C1'-N9	-6.03	1.39	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	198	ILE	N-CA-C	-5.91	106.73	111.81
21	T	110	LEU	N-CA-C	-5.05	106.71	112.92

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	2	35423	0	17912	703	0
2	A	1686	0	1688	44	0
3	B	1729	0	1803	54	0
4	C	1690	0	1777	51	0
5	D	1752	0	1848	87	0
6	E	2076	0	2177	27	0
7	F	1495	0	1549	75	0
8	G	1864	0	2018	49	0
9	H	1501	0	1593	36	0
10	I	1682	0	1769	50	0
11	J	1499	0	1618	29	0
12	K	816	0	841	40	0
13	L	1229	0	1302	21	0
14	M	935	0	964	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	N	1202	0	1289	18	0
16	O	1010	0	1034	53	0
17	P	1037	0	1082	51	0
18	Q	1097	0	1161	58	0
19	R	1068	0	1121	58	0
20	S	1184	0	1244	55	0
21	T	1123	0	1153	65	0
22	U	803	0	873	44	0
23	V	625	0	628	14	0
24	W	1034	0	1080	17	0
25	X	1098	0	1167	15	0
26	Y	1014	0	1082	25	0
27	Z	574	0	627	25	0
28	a	794	0	849	28	0
29	b	641	0	665	15	0
30	c	489	0	514	14	0
31	d	459	0	452	37	0
32	e	442	0	487	12	0
33	f	611	0	638	6	0
34	g	2441	0	2396	102	0
35	h	213	0	258	8	0
36	n	238	0	214	8	0
All	All	74574	0	58873	1718	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 13.

All (1718) 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)
5:D:195:THR:CG2	5:D:199:GLY:O	1.66	1.44
5:D:195:THR:HG23	5:D:199:GLY:CA	1.46	1.44
5:D:195:THR:HG23	5:D:199:GLY:C	1.57	1.26
5:D:195:THR:HG21	5:D:199:GLY:O	1.21	1.25
1:2:1172:U:H3	1:2:1188:A:N6	1.32	1.23
5:D:195:THR:CG2	5:D:199:GLY:C	2.14	1.17
5:D:191:PRO:HB2	5:D:194:PRO:HD2	1.29	1.14
5:D:195:THR:CG2	5:D:199:GLY:CA	2.31	1.08
5:D:195:THR:HG23	5:D:199:GLY:HA3	1.32	1.07
34:g:118:ARG:HH21	34:g:133:ASN:HB3	1.17	1.03
1:2:1605:G:N2	1:2:1634:A:H62	1.61	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1605:G:C2	1:2:1634:A:N6	2.34	0.96
1:2:1215:C:H42	1:2:1220:A:H61	1.06	0.96
5:D:105:LEU:HB2	5:D:118:ALA:HB1	1.48	0.96
32:e:44:ASN:C	32:e:44:ASN:HD22	1.73	0.96
1:2:1172:U:N3	1:2:1188:A:N6	2.01	0.95
13:L:80:MET:HE1	13:L:120:VAL:HG23	1.49	0.94
1:2:880:G:H22	1:2:907:G:H1'	1.36	0.90
1:2:1335:G:N2	1:2:1492:U:O2	2.04	0.89
5:D:195:THR:CG2	5:D:199:GLY:N	2.36	0.88
17:P:89:MET:HE1	17:P:107:ILE:HG13	1.55	0.87
1:2:1172:U:C2	1:2:1188:A:N6	2.42	0.86
1:2:64:A:H2	1:2:83:A:H62	1.22	0.86
1:2:1513:C:H5''	1:2:1514:G:H21	1.41	0.85
1:2:1864:U:H5'	28:a:79:ILE:HD11	1.57	0.85
5:D:195:THR:HG22	5:D:199:GLY:N	1.93	0.83
12:K:3:MET:HE1	12:K:8:ARG:HB2	1.58	0.83
7:F:201:LYS:HA	7:F:201:LYS:HE3	1.60	0.83
18:Q:97:GLN:HB2	18:Q:105:LYS:HE3	1.62	0.82
1:2:1323:U:OP2	1:2:1497:G:N2	2.13	0.82
1:2:880:G:N2	1:2:907:G:N3	2.28	0.82
7:F:104:THR:HG21	7:F:111:VAL:HG21	1.62	0.82
1:2:1211:G:H1	1:2:1688:C:H5	1.27	0.81
34:g:66:VAL:HA	34:g:82:SER:HA	1.62	0.81
14:M:26:LEU:HD11	14:M:91:LEU:HD13	1.62	0.81
31:d:23:VAL:HB	31:d:38:MET:HE3	1.63	0.81
1:2:1739:C:H5	1:2:1795:G:H1	1.27	0.81
1:2:1215:C:N4	1:2:1220:A:H61	1.78	0.80
8:G:141:ILE:HD11	8:G:153:VAL:HB	1.63	0.80
1:2:1335:G:H1	1:2:1492:U:H3	0.81	0.80
34:g:220:ASP:HB2	34:g:224:GLY:H	1.45	0.80
1:2:1537:A:H62	27:Z:104:ARG:HH21	1.30	0.80
27:Z:57:LYS:HD3	27:Z:77:LEU:HD13	1.63	0.79
5:D:191:PRO:HB2	5:D:194:PRO:CD	2.10	0.79
1:2:1230:C:O2'	1:2:1665:G:N2	2.15	0.79
13:L:77:VAL:HG11	13:L:80:MET:HE3	1.63	0.79
21:T:56:ARG:NH2	21:T:75:MET:O	2.16	0.79
34:g:16:GLY:HA3	34:g:37:ASP:HB3	1.66	0.78
5:D:136:VAL:HG22	5:D:186:VAL:HG12	1.65	0.78
9:H:69:LEU:HG	9:H:96:ALA:HB2	1.64	0.77
12:K:21:MET:HE3	12:K:22:VAL:H	1.50	0.77
1:2:1544:C:N3	1:2:1589:A:N1	2.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:125:PRO:O	21:T:128:GLN:HG3	1.84	0.77
1:2:1549:U:H2'	1:2:1550:G:H8	1.51	0.76
7:F:96:ALA:HA	7:F:99:ILE:HB	1.67	0.76
26:Y:52:PRO:HA	26:Y:55:ILE:HD12	1.67	0.76
20:S:39:ARG:HH21	20:S:83:PHE:HZ	1.34	0.76
1:2:1442:U:H1'	18:Q:11:GLN:HB3	1.68	0.76
21:T:18:LEU:HD23	21:T:134:ILE:HG21	1.67	0.76
5:D:195:THR:HG23	5:D:199:GLY:N	2.00	0.75
1:2:1215:C:H42	1:2:1220:A:N6	1.82	0.75
1:2:1545:A:H3'	1:2:1546:G:H21	1.51	0.75
1:2:1324:G:O2'	1:2:1510:G:N2	2.20	0.75
1:2:1517:G:H2'	1:2:1518:C:H5''	1.68	0.74
19:R:98:VAL:HG13	19:R:102:THR:HG23	1.68	0.74
7:F:92:ILE:HG13	7:F:170:ALA:HB2	1.68	0.74
3:B:126:ASP:OD2	3:B:136:ARG:NH1	2.21	0.74
5:D:51:LEU:HD11	5:D:91:VAL:HG22	1.70	0.74
9:H:19:PHE:HE2	9:H:50:GLU:HB2	1.52	0.74
30:c:17:VAL:HA	30:c:30:VAL:HG23	1.70	0.74
34:g:114:SER:HB3	34:g:119:GLN:HB3	1.69	0.74
22:U:64:THR:HG23	22:U:77:TRP:HB3	1.70	0.74
1:2:1496:U:O2'	12:K:64:TRP:NE1	2.21	0.73
1:2:1258:A:OP2	1:2:1664:A:N6	2.22	0.73
1:2:94:G:HO2'	1:2:508:A:HO2'	1.32	0.73
1:2:1224:G:H5'	1:2:1225:U:H5'	1.70	0.73
16:O:46:ASP:OD1	16:O:47:LEU:N	2.22	0.73
19:R:29:HIS:HA	19:R:32:LYS:NZ	2.04	0.73
1:2:1709:G:H5'	1:2:1710:C:H4'	1.71	0.73
1:2:617:G:H4'	25:X:88:ASP:HB3	1.71	0.73
1:2:1172:U:O4	1:2:1188:A:N7	2.22	0.73
1:2:385:G:O2'	10:I:10:LYS:NZ	2.21	0.73
21:T:107:LEU:HD23	21:T:112:MET:CE	2.19	0.73
1:2:1592:C:O2	21:T:12:GLN:NE2	2.22	0.72
8:G:159:ARG:HG2	8:G:173:ALA:HB2	1.72	0.72
10:I:88:ASN:HB3	10:I:205:ARG:HH12	1.53	0.72
1:2:1254:C:H1'	22:U:71:GLY:H	1.54	0.71
4:C:200:ARG:O	11:J:54:ARG:NH2	2.22	0.71
1:2:1470:C:OP2	7:F:59:LYS:NZ	2.22	0.71
1:2:878:G:H1	1:2:908:A:H61	1.38	0.71
1:2:1398:G:N3	34:g:63:SER:OG	2.23	0.71
7:F:137:GLN:OE1	30:c:63:ARG:NH2	2.23	0.71
34:g:118:ARG:NH2	34:g:133:ASN:HB3	1.99	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:952:G:H21	16:O:52:THR:HG21	1.54	0.71
5:D:7:LYS:HD2	5:D:10:LYS:HE3	1.72	0.71
3:B:73:ASP:OD1	16:O:128:ARG:NH1	2.23	0.71
1:2:1779:G:H1	8:G:9:ALA:HB2	1.55	0.71
34:g:109:LEU:HD22	34:g:152:SER:HA	1.73	0.71
28:a:40:VAL:HG22	28:a:69:VAL:HB	1.73	0.70
1:2:297:A:H5'	6:E:132:GLY:HA2	1.73	0.70
20:S:124:ARG:HE	20:S:131:VAL:HG23	1.56	0.70
1:2:747:U:O4	1:2:798:G:N2	2.23	0.70
5:D:39:VAL:HG12	5:D:48:ILE:HG13	1.74	0.70
1:2:1592:C:O2'	18:Q:45:ARG:NH1	2.25	0.70
7:F:77:MET:HB2	7:F:89:THR:HG21	1.72	0.70
2:A:66:VAL:HG21	2:A:185:MET:HB3	1.74	0.70
27:Z:57:LYS:HA	27:Z:61:GLU:HB3	1.74	0.70
20:S:46:ARG:NH2	21:T:50:GLU:OE1	2.25	0.70
1:2:747:U:H3'	1:2:796:G:H21	1.53	0.70
1:2:799:U:OP1	9:H:108:SER:OG	2.10	0.70
20:S:70:ILE:HG13	20:S:76:GLN:HG2	1.74	0.69
22:U:38:ASP:OD1	22:U:41:ARG:NH2	2.25	0.69
34:g:65:PHE:HB2	34:g:83:TRP:HE3	1.55	0.69
17:P:130:ARG:NH1	17:P:130:ARG:O	2.25	0.69
34:g:65:PHE:HB2	34:g:83:TRP:CE3	2.26	0.69
1:2:886:A:N6	1:2:901:G:O6	2.25	0.69
1:2:1550:G:N2	1:2:1577:G:H21	1.90	0.69
21:T:72:VAL:HG11	21:T:104:LEU:HD22	1.75	0.69
16:O:97:LEU:HD11	16:O:112:ALA:HB1	1.74	0.69
8:G:135:PRO:HB2	8:G:141:ILE:HG22	1.75	0.69
1:2:1648:G:N2	1:2:1675:A:OP2	2.26	0.69
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.26	0.69
16:O:113:GLN:HE22	28:a:45:VAL:HA	1.56	0.69
25:X:67:ARG:NH2	25:X:114:ASP:OD2	2.24	0.69
28:a:44:ILE:HD12	28:a:65:PRO:HG2	1.75	0.69
34:g:106:LYS:HG3	34:g:125:ARG:HG3	1.73	0.69
18:Q:93:VAL:HA	18:Q:105:LYS:HZ1	1.56	0.69
34:g:152:SER:OG	34:g:195:LEU:O	2.10	0.68
11:J:89:GLU:OE2	11:J:89:GLU:N	2.23	0.68
1:2:1542:C:OP1	21:T:62:ARG:NH2	2.26	0.68
18:Q:95:TYR:HA	18:Q:98:LYS:HE2	1.75	0.68
24:W:90:GLN:OE1	24:W:117:ARG:NH2	2.27	0.68
3:B:57:ILE:HG22	3:B:59:SER:H	1.59	0.68
7:F:32:ASP:O	7:F:34:SER:N	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1756:C:H1'	1:2:1758:G:H1	1.58	0.68
1:2:942:G:H21	16:O:137:SER:HB2	1.59	0.68
9:H:80:VAL:HG23	9:H:92:VAL:HB	1.75	0.67
15:N:83:ASP:OD1	15:N:83:ASP:N	2.26	0.67
18:Q:89:SER:O	18:Q:93:VAL:HG23	1.93	0.67
7:F:128:ILE:HD13	7:F:137:GLN:HB2	1.74	0.67
1:2:643:A:OP1	11:J:39:ASN:ND2	2.27	0.67
1:2:940:U:H3	1:2:1002:U:H3	1.41	0.67
5:D:65:ARG:HG3	5:D:69:LEU:HD12	1.76	0.67
1:2:73:C:O2'	1:2:76:U:O4	2.12	0.67
10:I:80:ASP:OD1	10:I:81:VAL:N	2.27	0.67
19:R:28:PHE:HA	19:R:31:ASN:HB2	1.76	0.67
30:c:33:GLU:HG2	30:c:41:SER:HB3	1.75	0.67
34:g:118:ARG:NH1	34:g:119:GLN:HB2	2.09	0.67
1:2:928:G:H1	1:2:1013:U:H3	1.41	0.67
1:2:1170:A:H5'	1:2:1172:U:H1'	1.75	0.67
3:B:47:THR:OG1	3:B:65:ARG:NH1	2.27	0.67
34:g:110:SER:HB2	34:g:153:CYS:HA	1.77	0.67
34:g:149:GLU:HB2	34:g:171:ASP:HB3	1.76	0.67
34:g:121:VAL:HG23	34:g:131:LEU:HB3	1.76	0.67
10:I:11:ARG:O	13:L:136:LYS:NZ	2.26	0.67
1:2:1289:U:OP2	1:2:1290:G:N2	2.28	0.67
19:R:6:THR:HG22	19:R:8:THR:H	1.59	0.67
2:A:84:GLN:HG2	2:A:100:ALA:HB1	1.76	0.66
1:2:1258:A:N6	1:2:1660:C:OP1	2.27	0.66
21:T:83:GLN:NE2	21:T:85:ASN:OD1	2.28	0.66
1:2:202:G:H3'	1:2:203:G:H8	1.59	0.66
1:2:1398:G:O6	1:2:1448:A:N1	2.29	0.66
9:H:19:PHE:CE2	9:H:50:GLU:HB2	2.30	0.66
12:K:29:MET:HE3	12:K:42:ASN:HB3	1.76	0.66
5:D:101:GLN:HB3	5:D:122:VAL:HG23	1.77	0.66
1:2:925:G:H1	1:2:1017:U:H3	1.43	0.66
1:2:1295:A:H2	33:f:138:ARG:HH12	1.44	0.66
1:2:1721:U:OP2	1:2:1814:G:N2	2.26	0.66
34:g:153:CYS:SG	34:g:155:ARG:NH1	2.69	0.66
1:2:1709:G:OP1	1:2:1710:C:O2'	2.13	0.66
19:R:29:HIS:HB2	34:g:36:ARG:HH12	1.60	0.66
11:J:134:HIS:ND1	11:J:163:SER:OG	2.27	0.66
1:2:1290:G:N2	1:2:1302:G:OP1	2.28	0.66
2:A:42:LYS:HG3	2:A:48:ILE:HD11	1.78	0.66
5:D:124:ARG:NH1	5:D:125:PHE:HB2	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:19:LEU:HB2	7:F:23:TRP:HB2	1.78	0.66
34:g:5:MET:HA	34:g:5:MET:HE3	1.76	0.66
1:2:171:A:H5'	8:G:177:GLN:HG2	1.77	0.65
1:2:1406:G:O2'	1:2:1443:C:N4	2.30	0.65
11:J:59:GLU:OE2	11:J:69:ARG:NH2	2.29	0.65
13:L:82:MET:HE3	13:L:85:THR:HB	1.78	0.65
20:S:121:ARG:O	20:S:125:HIS:ND1	2.30	0.65
1:2:909:G:H2'	1:2:910:G:C8	2.32	0.65
1:2:1296:U:O2'	1:2:1299:A:OP1	2.14	0.65
1:2:640:A:H2'	1:2:641:A:C8	2.32	0.65
1:2:1143:A:H5'	4:C:190:SER:HB3	1.78	0.65
14:M:14:VAL:HG21	14:M:127:TYR:HB2	1.79	0.65
1:2:536:A:H2'	1:2:538:U:H5	1.61	0.65
1:2:1328:G:H8	1:2:1502:C:H41	1.44	0.65
1:2:1375:G:OP1	19:R:67:ARG:NH1	2.30	0.65
1:2:1864:U:OP2	28:a:5:ARG:NH2	2.28	0.65
5:D:143:ARG:NH2	36:n:156:ASP:OD1	2.29	0.65
17:P:110:GLU:HB3	20:S:117:ILE:HD13	1.78	0.65
30:c:14:VAL:HB	30:c:53:GLY:H	1.62	0.65
1:2:507:G:O6	26:Y:105:LYS:NZ	2.31	0.64
20:S:74:PRO:HB3	20:S:97:GLN:HB2	1.80	0.64
1:2:1303:C:O2'	33:f:90:LYS:NZ	2.30	0.64
1:2:1657:G:H2'	1:2:1658:G:C8	2.31	0.64
2:A:38:ILE:HD11	2:A:150:THR:HG22	1.80	0.64
26:Y:55:ILE:HG12	26:Y:75:ILE:HG12	1.79	0.64
12:K:23:ALA:HB3	12:K:67:PHE:HB2	1.79	0.64
20:S:41:ALA:O	20:S:45:LEU:HD23	1.96	0.64
20:S:120:HIS:CD2	20:S:124:ARG:HH12	2.15	0.64
1:2:909:G:H2'	1:2:910:G:H8	1.62	0.64
21:T:107:LEU:HD23	21:T:112:MET:HE2	1.78	0.64
32:e:44:ASN:C	32:e:44:ASN:ND2	2.50	0.64
8:G:49:VAL:HB	8:G:115:LYS:HB2	1.79	0.64
34:g:62:HIS:HA	34:g:88:ARG:HH12	1.62	0.64
9:H:9:VAL:HG22	9:H:11:PRO:HD3	1.80	0.64
12:K:24:LYS:HE3	12:K:26:ASP:HB2	1.79	0.64
1:2:317:C:H5	1:2:333:G:H1	1.46	0.63
1:2:1406:G:OP1	1:2:1428:G:N2	2.31	0.63
1:2:1444:U:H1'	1:2:1545:A:H61	1.63	0.63
5:D:123:LEU:O	5:D:127:MET:HG2	1.98	0.63
15:N:115:LEU:O	15:N:119:GLU:HG2	1.98	0.63
1:2:1262:C:OP1	31:d:12:ARG:NH2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:77:A:H1'	8:G:176:ILE:HD12	1.80	0.63
17:P:90:VAL:HG22	17:P:107:ILE:HG22	1.80	0.63
30:c:46:VAL:HG11	30:c:56:LEU:HD13	1.80	0.63
1:2:1757:G:H22	1:2:1775:U:H2'	1.64	0.63
8:G:201:LYS:NZ	8:G:202:ASN:OD1	2.31	0.63
17:P:130:ARG:HD3	17:P:130:ARG:H	1.62	0.63
34:g:68:ASP:HB3	34:g:111:VAL:H	1.63	0.63
2:A:10:MET:HE2	2:A:15:VAL:HG22	1.80	0.63
7:F:121:PRO:HA	7:F:193:LYS:HG3	1.80	0.63
34:g:103:GLY:HA3	34:g:132:TRP:HH2	1.62	0.63
12:K:43:LEU:O	12:K:47:LYS:HG3	1.98	0.63
34:g:62:HIS:HA	34:g:88:ARG:NH1	2.13	0.63
1:2:178:C:H2'	1:2:179:C:C6	2.34	0.63
1:2:1373:C:O3'	19:R:10:LYS:NZ	2.32	0.63
1:2:1600:G:O2'	1:2:1602:U:N3	2.31	0.63
9:H:82:GLU:O	9:H:86:LYS:HG2	1.99	0.63
9:H:148:LEU:HD13	24:W:49:GLU:HG3	1.80	0.63
34:g:89:LEU:HD12	34:g:99:ARG:HB2	1.80	0.63
1:2:1500:G:O2'	1:2:1501:C:OP1	2.17	0.62
1:2:615:C:O2	32:e:11:LYS:NZ	2.29	0.62
1:2:1658:G:H5'	31:d:33:LYS:HE3	1.81	0.62
12:K:53:LYS:HB3	12:K:60:GLU:HB3	1.81	0.62
15:N:34:LYS:HE2	15:N:67:THR:HG23	1.80	0.62
1:2:1653:U:H2'	1:2:1654:G:H8	1.63	0.62
6:E:129:ILE:HD11	6:E:139:LEU:HD12	1.82	0.62
18:Q:96:TYR:HD2	18:Q:105:LYS:HZ3	1.47	0.62
1:2:1398:G:H1	1:2:1448:A:H2	1.46	0.62
10:I:150:ASP:HA	10:I:153:LYS:HG3	1.81	0.62
1:2:1318:G:H5'	1:2:1505:U:H3	1.65	0.62
1:2:1354:G:N2	1:2:1357:A:OP2	2.23	0.62
1:2:1412:C:H41	1:2:1413:G:H21	1.48	0.62
2:A:2:SER:OG	2:A:3:GLY:N	2.31	0.62
13:L:147:LYS:HD3	13:L:151:THR:HG21	1.81	0.62
34:g:29:ASP:HB3	34:g:44:LYS:HG3	1.81	0.62
1:2:1395:C:H1'	1:2:1450:G:H22	1.64	0.62
7:F:190:ILE:HD12	7:F:191:LYS:N	2.15	0.62
19:R:78:ARG:O	19:R:82:ASP:N	2.33	0.62
21:T:71:GLY:HA2	21:T:121:ARG:HE	1.64	0.62
2:A:200:ASP:O	2:A:205:ARG:NH2	2.32	0.62
16:O:67:ASP:O	16:O:70:SER:OG	2.15	0.62
1:2:1533:A:OP2	1:2:1636:G:N2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:131:LYS:HB2	18:Q:140:ARG:HH22	1.65	0.62
20:S:75:ARG:NH1	20:S:79:ILE:O	2.32	0.62
1:2:170:A:OP2	8:G:140:ARG:NH1	2.32	0.61
1:2:913:A:OP1	9:H:99:ARG:NH2	2.33	0.61
1:2:1171:G:N2	1:2:1188:A:OP2	2.28	0.61
1:2:1300:U:O2	31:d:2:GLY:N	2.33	0.61
1:2:1652:G:H1	1:2:1672:U:H3	1.46	0.61
7:F:96:ALA:HB1	7:F:174:ALA:HB2	1.82	0.61
11:J:107:GLU:O	11:J:113:GLN:NE2	2.32	0.61
29:b:65:GLN:HB2	29:b:72:ARG:HB3	1.82	0.61
34:g:48:ASP:OD1	34:g:49:GLU:N	2.33	0.61
1:2:796:G:O2'	1:2:797:C:O4'	2.17	0.61
1:2:1234:C:O2'	1:2:1526:G:N2	2.33	0.61
7:F:136:ARG:HB2	7:F:203:ASN:HD21	1.65	0.61
1:2:588:G:OP2	1:2:588:G:N2	2.29	0.61
1:2:1249:C:O2'	18:Q:143:LYS:NZ	2.32	0.61
2:A:52:LYS:N	2:A:52:LYS:HD3	2.15	0.61
1:2:531:A:H62	1:2:552:G:H21	1.47	0.61
1:2:1098:C:H2'	1:2:1099:G:C8	2.35	0.61
2:A:122:LEU:HD23	2:A:144:THR:HG23	1.82	0.61
34:g:17:TRP:O	34:g:35:SER:OG	2.15	0.61
11:J:18:ARG:O	11:J:24:ARG:NH1	2.34	0.61
1:2:491:C:C2	1:2:510:G:C2	2.89	0.61
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.83	0.61
1:2:878:G:H1	1:2:908:A:N6	1.98	0.61
1:2:1655:C:OP1	21:T:92:PHE:N	2.33	0.61
7:F:167:LYS:NZ	7:F:168:THR:O	2.34	0.61
12:K:72:THR:HG23	12:K:75:GLY:H	1.64	0.61
17:P:51:ARG:NH1	31:d:4:GLN:OE1	2.34	0.61
18:Q:12:VAL:HG13	18:Q:90:LYS:HE2	1.82	0.61
21:T:107:LEU:CD2	21:T:112:MET:HE2	2.31	0.61
34:g:216:ALA:HB3	34:g:230:LEU:HB3	1.82	0.61
1:2:178:C:H2'	1:2:179:C:H6	1.66	0.61
1:2:1249:C:H5'	1:2:1250:A:H5'	1.82	0.61
1:2:1601:A:O2'	1:2:1635:C:N4	2.34	0.61
2:A:80:ARG:HH22	2:A:166:LYS:HA	1.66	0.61
1:2:380:G:O6	10:I:178:ARG:NH2	2.33	0.61
22:U:81:GLN:HE21	22:U:83:ARG:HB2	1.66	0.61
3:B:139:CYS:HB3	3:B:172:MET:HE1	1.81	0.60
14:M:41:ALA:HA	14:M:46:GLN:HB2	1.82	0.60
26:Y:110:ARG:O	26:Y:114:MET:HG3	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:78:VAL:HG22	28:a:83:VAL:HB	1.83	0.60
1:2:639:C:HO2'	1:2:640:A:H8	1.50	0.60
26:Y:10:ARG:NH1	26:Y:26:ASP:OD2	2.35	0.60
10:I:134:GLU:HA	10:I:137:LEU:HD12	1.82	0.60
1:2:957:A:H3'	1:2:958:G:H21	1.65	0.60
1:2:1246:A:O2'	22:U:70:CYS:SG	2.59	0.60
1:2:1612:G:O2'	1:2:1613:G:OP1	2.14	0.60
1:2:1740:C:H42	1:2:1794:C:H42	1.49	0.60
11:J:84:ILE:HG13	11:J:86:VAL:HG23	1.83	0.60
34:g:37:ASP:OD1	34:g:39:THR:OG1	2.18	0.60
1:2:678:U:OP2	1:2:1026:C:N4	2.30	0.60
10:I:110:ARG:O	10:I:114:GLU:HG2	2.02	0.60
1:2:126:G:O6	8:G:196:LYS:NZ	2.34	0.60
1:2:546:G:OP1	1:2:547:G:N1	2.34	0.60
1:2:1546:G:H22	1:2:1588:A:H61	1.50	0.60
3:B:138:PHE:O	3:B:213:ARG:N	2.35	0.60
14:M:50:CYS:SG	14:M:51:VAL:N	2.75	0.60
16:O:56:VAL:HG22	16:O:81:VAL:HG23	1.83	0.60
22:U:27:ARG:NH2	22:U:82:MET:HB3	2.16	0.60
1:2:1091:C:HO2'	24:W:2:VAL:N	2.00	0.60
1:2:1657:G:N2	1:2:1667:U:O2	2.34	0.60
10:I:141:ARG:HB3	10:I:145:ILE:HD11	1.83	0.60
1:2:913:A:H1'	9:H:66:VAL:HB	1.83	0.60
5:D:167:TYR:HA	5:D:190:LEU:HB2	1.84	0.60
2:A:85:ARG:NH2	19:R:82:ASP:O	2.35	0.60
8:G:126:ASP:OD1	8:G:127:THR:N	2.35	0.60
1:2:617:G:N7	25:X:67:ARG:NH1	2.44	0.59
1:2:860:G:N2	24:W:107:SER:OG	2.34	0.59
34:g:199:THR:HG21	34:g:240:CYS:HA	1.83	0.59
1:2:581:U:OP1	11:J:133:ARG:NH2	2.35	0.59
1:2:749:U:O4	1:2:794:A:O2'	2.15	0.59
1:2:1600:G:H22	27:Z:80:ARG:HH21	1.49	0.59
6:E:259:LYS:O	6:E:259:LYS:NZ	2.31	0.59
8:G:129:VAL:HG12	8:G:131:ARG:H	1.66	0.59
19:R:29:HIS:HA	19:R:32:LYS:HZ2	1.67	0.59
10:I:119:LEU:HD22	10:I:156:ALA:HA	1.84	0.59
31:d:38:MET:HE2	31:d:38:MET:HA	1.83	0.59
1:2:1619:A:H5''	17:P:40:ARG:HA	1.84	0.59
5:D:106:ARG:HB2	5:D:173:ARG:HD3	1.84	0.59
15:N:25:TRP:HB3	29:b:82:LYS:HD3	1.84	0.59
34:g:109:LEU:HD11	34:g:125:ARG:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:3:MET:HG3	12:K:44:HIS:HB3	1.84	0.59
20:S:113:ARG:O	20:S:117:ILE:HG13	2.02	0.59
6:E:37:LYS:HB2	6:E:40:GLU:HG3	1.83	0.59
12:K:65:ARG:NH1	31:d:20:SER:OG	2.35	0.59
17:P:61:ARG:O	17:P:65:LYS:HB2	2.02	0.59
16:O:145:GLY:O	28:a:22:ARG:NH2	2.35	0.59
17:P:18:ARG:HH21	20:S:88:LYS:HD3	1.67	0.59
7:F:110:GLN:HE21	7:F:114:ASN:HD21	1.50	0.59
18:Q:19:ALA:HA	18:Q:74:GLY:HA3	1.84	0.59
22:U:81:GLN:HE21	22:U:83:ARG:H	1.48	0.59
1:2:917:U:H1'	9:H:118:ARG:HG2	1.85	0.59
4:C:165:VAL:HG21	4:C:217:ALA:HB1	1.83	0.59
27:Z:70:PRO:HB3	27:Z:84:ALA:HB1	1.84	0.59
1:2:107:A:H2'	1:2:108:G:C8	2.38	0.59
1:2:952:G:H2'	1:2:953:C:C6	2.37	0.59
1:2:1544:C:N4	1:2:1589:A:C2	2.71	0.59
1:2:1549:U:H2'	1:2:1550:G:C8	2.35	0.59
14:M:23:LYS:NZ	14:M:88:TRP:O	2.36	0.59
20:S:90:VAL:HG23	20:S:91:LYS:HG3	1.85	0.59
1:2:1204:A:H5''	4:C:117:ARG:NH1	2.18	0.58
1:2:1666:C:O2'	1:2:1667:U:OP1	2.21	0.58
17:P:20:VAL:HG13	17:P:24:GLN:HB2	1.85	0.58
1:2:1676:U:O3'	7:F:148:ASN:ND2	2.31	0.58
7:F:19:LEU:HD22	7:F:48:TYR:HA	1.86	0.58
17:P:77:LYS:HD2	17:P:79:HIS:CE1	2.39	0.58
24:W:57:ARG:NH1	29:b:26:GLN:OE1	2.35	0.58
28:a:32:LYS:O	28:a:37:LYS:NZ	2.36	0.58
34:g:78:ALA:O	34:g:89:LEU:HA	2.03	0.58
35:h:1:MET:HE1	35:h:9:ARG:HE	1.68	0.58
1:2:677:G:N1	1:2:1027:A:OP2	2.24	0.58
1:2:1203:G:H2'	1:2:1204:A:C8	2.38	0.58
1:2:1493:C:O2	1:2:1498:A:N6	2.36	0.58
4:C:263:LYS:HG3	4:C:267:GLN:HE21	1.67	0.58
1:2:562:U:H2'	1:2:563:G:C8	2.37	0.58
34:g:185:LYS:HG3	34:g:186:THR:HG23	1.84	0.58
1:2:613:G:N2	1:2:626:G:OP1	2.37	0.58
1:2:857:U:H2'	1:2:858:A:C8	2.38	0.58
1:2:1219:C:H42	1:2:1646:C:H42	1.51	0.58
1:2:1528:G:H21	1:2:1529:C:H5	1.49	0.58
4:C:75:ILE:HD11	4:C:265:PRO:HB3	1.85	0.58
1:2:1172:U:H3	1:2:1188:A:H62	0.61	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1237:C:H5'	17:P:130:ARG:HH22	1.69	0.58
5:D:75:LYS:HD2	12:K:22:VAL:HB	1.86	0.58
19:R:30:THR:O	19:R:34:VAL:HG13	2.04	0.58
16:O:28:PHE:HZ	28:a:58:VAL:HG21	1.67	0.58
31:d:16:GLN:OE1	31:d:27:ARG:NH2	2.36	0.58
17:P:51:ARG:HA	17:P:54:HIS:HE1	1.69	0.58
3:B:108:ASP:OD1	3:B:109:LYS:N	2.37	0.57
1:2:1594:A:OP2	27:Z:102:LYS:NZ	2.37	0.57
3:B:152:LYS:HE2	19:R:133:GLY:HA2	1.86	0.57
17:P:40:ARG:HH22	17:P:84:ILE:HG22	1.70	0.57
34:g:239:LEU:HD23	34:g:250:ALA:HB2	1.86	0.57
1:2:1533:A:N7	7:F:164:ARG:NH2	2.52	0.57
1:2:1342:U:H3	1:2:1483:A:H2'	1.70	0.57
3:B:26:SER:O	3:B:51:ARG:NH2	2.38	0.57
13:L:22:ARG:HH21	13:L:27:GLU:HG3	1.68	0.57
20:S:92:ASP:OD1	20:S:92:ASP:N	2.37	0.57
1:2:381:C:OP2	10:I:54:LYS:NZ	2.35	0.57
1:2:545:A:OP2	1:2:546:G:N2	2.37	0.57
1:2:1599:U:N3	7:F:165:ASN:O	2.37	0.57
8:G:5:ILE:HG21	8:G:45:TRP:HH2	1.69	0.57
12:K:80:ARG:HA	12:K:85:LEU:HD12	1.85	0.57
13:L:75:GLY:HA3	13:L:88:ILE:HD12	1.85	0.57
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.87	0.57
18:Q:130:LYS:HA	18:Q:137:ALA:HA	1.86	0.57
1:2:429:C:O2'	1:2:811:A:N1	2.37	0.57
1:2:996:A:H2'	1:2:997:A:C8	2.40	0.57
5:D:27:ARG:HH22	12:K:64:TRP:CD1	2.23	0.57
7:F:30:ILE:HG23	7:F:31:ASN:H	1.68	0.57
7:F:195:GLU:HG2	7:F:198:ARG:HH21	1.69	0.57
9:H:98:ARG:NH2	9:H:132:ASP:OD2	2.38	0.57
1:2:1255:G:N2	1:2:1494:U:O2	2.37	0.57
1:2:1512:C:O2'	1:2:1513:C:O2	2.21	0.57
1:2:1545:A:H3'	1:2:1546:G:N2	2.19	0.57
1:2:1817:G:H2'	1:2:1818:A:C8	2.40	0.57
1:2:928:G:H2'	1:2:929:G:C8	2.40	0.57
18:Q:37:ARG:HG3	21:T:7:LYS:HG3	1.87	0.57
18:Q:105:LYS:HZ3	18:Q:108:ILE:HD11	1.69	0.57
20:S:74:PRO:HB2	20:S:75:ARG:HH21	1.69	0.57
1:2:213:G:H2'	1:2:214:U:O4'	2.05	0.57
1:2:532:C:H2'	1:2:533:A:H8	1.70	0.57
1:2:1457:U:H2'	1:2:1458:G:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1468:C:H2'	1:2:1469:A:C8	2.40	0.57
6:E:54:TYR:OH	6:E:97:GLU:OE2	2.15	0.57
34:g:226:HIS:NE2	34:g:228:TYR:O	2.38	0.57
1:2:879:C:H2'	1:2:880:G:H4'	1.87	0.56
1:2:1844:U:P	35:h:11:ARG:HH22	2.27	0.56
3:B:40:ASN:ND2	3:B:76:ASN:OD1	2.38	0.56
7:F:69:VAL:O	7:F:72:LEU:HG	2.05	0.56
1:2:145:G:H2'	1:2:146:G:C8	2.40	0.56
17:P:98:ASN:HB2	17:P:122:THR:HG22	1.87	0.56
18:Q:131:LYS:HB2	18:Q:140:ARG:NH2	2.20	0.56
1:2:1567:G:H2'	1:2:1568:C:C5	2.40	0.56
5:D:138:VAL:HG22	5:D:182:LEU:HD22	1.88	0.56
8:G:57:ASP:HA	8:G:106:LEU:HA	1.88	0.56
20:S:33:ILE:HG22	20:S:35:GLY:H	1.70	0.56
21:T:110:LEU:HD23	21:T:112:MET:SD	2.46	0.56
25:X:29:LYS:HD2	25:X:29:LYS:C	2.31	0.56
1:2:943:U:O2'	16:O:135:ILE:O	2.23	0.56
1:2:1567:G:H5'	21:T:37:VAL:HG23	1.87	0.56
1:2:1824:A:H2'	1:2:1825:A:H4'	1.87	0.56
8:G:57:ASP:O	8:G:107:SER:OG	2.22	0.56
16:O:113:GLN:OE1	28:a:46:GLU:N	2.37	0.56
20:S:130:ARG:HD3	20:S:134:GLN:HB2	1.87	0.56
34:g:200:VAL:HG13	34:g:207:CYS:HB2	1.88	0.56
1:2:1560:U:O4	1:2:1572:C:N4	2.38	0.56
1:2:384:U:O4	10:I:5:ARG:NH2	2.33	0.56
1:2:846:G:H2'	6:E:19:MET:HG2	1.88	0.56
1:2:1231:C:N4	1:2:1666:C:O2'	2.39	0.56
18:Q:53:GLU:OE2	18:Q:115:TYR:OH	2.19	0.56
1:2:817:G:H4'	11:J:73:GLU:OE1	2.04	0.56
1:2:1013:U:OP1	1:2:1129:G:O2'	2.24	0.56
1:2:1329:U:O4	1:2:1501:C:N4	2.38	0.56
1:2:1653:U:H2'	1:2:1654:G:C8	2.40	0.56
9:H:25:GLN:O	9:H:29:GLU:HG2	2.06	0.56
19:R:104:GLU:OE1	19:R:107:LYS:NZ	2.38	0.56
1:2:1669:G:O2'	22:U:62:ARG:NH1	2.38	0.56
34:g:36:ARG:HB2	34:g:65:PHE:HB3	1.88	0.56
1:2:495:U:H2'	1:2:496:C:O4'	2.06	0.56
1:2:547:G:OP1	1:2:549:C:N4	2.32	0.56
1:2:1153:C:OP1	24:W:12:LYS:NZ	2.39	0.56
1:2:1235:G:H21	1:2:1524:G:H3'	1.71	0.56
1:2:1514:G:O6	31:d:12:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1614:A:N6	17:P:43:ARG:HD2	2.21	0.56
5:D:124:ARG:O	5:D:128:GLU:HG3	2.06	0.56
6:E:31:PRO:HG2	6:E:38:LEU:HG	1.87	0.56
7:F:33:ILE:HG23	7:F:34:SER:H	1.70	0.56
1:2:1546:G:N2	1:2:1588:A:H61	2.05	0.55
1:2:1562:C:N4	1:2:1563:G:O6	2.39	0.55
2:A:52:LYS:HE3	19:R:109:LEU:HB2	1.87	0.55
18:Q:34:VAL:HA	18:Q:70:VAL:HB	1.88	0.55
1:2:4:C:H4'	4:C:207:ALA:HB2	1.88	0.55
1:2:1480:A:H4'	18:Q:131:LYS:HD2	1.88	0.55
1:2:455:A:H2'	1:2:456:C:C6	2.41	0.55
1:2:1113:A:H2'	1:2:1114:U:C6	2.41	0.55
1:2:1657:G:H2'	1:2:1658:G:H8	1.71	0.55
5:D:195:THR:HG22	5:D:199:GLY:H	1.71	0.55
21:T:42:HIS:HB2	21:T:83:GLN:HA	1.87	0.55
22:U:31:SER:HA	22:U:34:LYS:HD3	1.87	0.55
28:a:19:GLN:H	28:a:19:GLN:CD	2.13	0.55
34:g:120:ILE:O	34:g:131:LEU:HA	2.06	0.55
1:2:77:A:C8	8:G:154:ARG:HG2	2.41	0.55
1:2:1468:C:H2'	1:2:1469:A:H8	1.71	0.55
17:P:40:ARG:HH21	17:P:115:TYR:HD1	1.54	0.55
21:T:75:MET:HA	21:T:78:ILE:HG12	1.88	0.55
21:T:124:THR:HG23	21:T:127:GLY:HA3	1.88	0.55
31:d:20:SER:HB2	31:d:27:ARG:HA	1.88	0.55
7:F:133:THR:O	7:F:136:ARG:NH1	2.39	0.55
1:2:29:G:H2'	1:2:30:C:C6	2.41	0.55
1:2:1414:A:H5''	21:T:128:GLN:HE22	1.72	0.55
1:2:1668:U:OP2	18:Q:141:TYR:OH	2.19	0.55
5:D:210:ILE:HG13	19:R:39:ALA:HB2	1.87	0.55
20:S:58:GLU:HG3	27:Z:50:PHE:CE2	2.42	0.55
1:2:1236:G:H1	1:2:1522:A:H62	1.54	0.55
12:K:28:HIS:CE1	31:d:12:ARG:HB2	2.42	0.55
16:O:135:ILE:O	16:O:135:ILE:HD12	2.06	0.55
1:2:186:C:H2'	1:2:187:G:C8	2.42	0.55
1:2:981:A:H2'	1:2:982:G:C8	2.42	0.55
1:2:1119:A:O3'	29:b:72:ARG:NH1	2.40	0.55
19:R:27:ASP:O	19:R:31:ASN:N	2.40	0.55
1:2:1275:G:H4'	1:2:1276:A:H8	1.71	0.55
7:F:100:ILE:O	7:F:104:THR:OG1	2.23	0.55
17:P:77:LYS:HD2	17:P:79:HIS:HE1	1.72	0.55
1:2:943:U:H2'	1:2:944:A:H8	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1190:A:N3	1:2:1714:U:O2'	2.38	0.55
1:2:1544:C:C4	1:2:1589:A:N1	2.75	0.55
11:J:113:GLN:OE1	11:J:154:GLN:NE2	2.39	0.55
1:2:109:U:O2	13:L:71:ARG:NH2	2.41	0.54
1:2:1753:C:N4	1:2:1781:A:OP2	2.39	0.54
1:2:1757:G:O2'	1:2:1758:G:OP1	2.23	0.54
2:A:52:LYS:HD2	19:R:109:LEU:HD22	1.89	0.54
7:F:55:ARG:NH2	18:Q:125:ARG:HB2	2.21	0.54
17:P:108:LYS:HG3	17:P:110:GLU:H	1.72	0.54
1:2:880:G:N1	1:2:906:U:C4	2.76	0.54
1:2:1217:A:H2'	1:2:1218:C:C6	2.42	0.54
1:2:1402:A:H4'	22:U:51:LYS:HD2	1.88	0.54
5:D:109:LEU:HD13	5:D:175:VAL:HG11	1.89	0.54
16:O:31:CYS:HB2	16:O:93:LEU:HD23	1.89	0.54
20:S:8:LYS:O	20:S:8:LYS:HD2	2.06	0.54
36:n:160:ASN:ND2	36:n:163:THR:OG1	2.35	0.54
1:2:223:C:H2'	1:2:224:A:C8	2.42	0.54
1:2:379:C:O2	10:I:5:ARG:NE	2.37	0.54
1:2:568:C:H2'	1:2:569:A:C8	2.42	0.54
1:2:1024:A:OP2	15:N:124:ARG:NH2	2.40	0.54
1:2:1544:C:O2	1:2:1589:A:N6	2.41	0.54
7:F:83:ASN:OD1	7:F:85:LYS:NZ	2.40	0.54
18:Q:49:TYR:HA	18:Q:52:LEU:HB3	1.87	0.54
20:S:70:ILE:HD11	20:S:77:TYR:HE2	1.72	0.54
1:2:118:C:H1'	1:2:445:A:C5	2.43	0.54
1:2:1254:C:O2'	22:U:69:PRO:O	2.25	0.54
5:D:54:ARG:HB3	5:D:57:ASN:HB2	1.89	0.54
10:I:172:LEU:HB3	10:I:190:LEU:HD12	1.90	0.54
22:U:24:LEU:HD13	22:U:35:VAL:HG11	1.88	0.54
22:U:81:GLN:HE21	22:U:83:ARG:N	2.05	0.54
1:2:1033:G:N1	1:2:1080:A:O2'	2.36	0.54
1:2:1546:G:H3'	1:2:1548:G:C2	2.43	0.54
7:F:93:VAL:O	7:F:97:PHE:HB2	2.08	0.54
1:2:388:U:H2'	1:2:389:A:H8	1.73	0.54
1:2:641:A:O2'	1:2:645:C:OP1	2.26	0.54
1:2:1628:C:O3'	21:T:38:LYS:NZ	2.41	0.54
1:2:1797:U:H2'	1:2:1798:C:C6	2.42	0.54
7:F:125:SER:HB2	7:F:203:ASN:HD22	1.73	0.54
17:P:56:LEU:O	17:P:59:ARG:HG3	2.07	0.54
34:g:170:TRP:HA	34:g:194:TYR:HB2	1.90	0.54
1:2:15:U:H2'	1:2:16:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1472:C:N4	1:2:1473:G:O6	2.41	0.54
1:2:1480:A:O2'	31:d:56:ASP:OD1	2.26	0.54
5:D:35:SER:HA	5:D:99:ILE:HG21	1.89	0.54
5:D:113:LEU:HD11	5:D:118:ALA:HB2	1.88	0.54
11:J:108:ARG:NH2	11:J:154:GLN:OE1	2.26	0.54
17:P:51:ARG:O	17:P:52:LYS:HG2	2.07	0.54
1:2:1190:A:OP1	25:X:34:THR:OG1	2.18	0.54
1:2:1623:A:H2	20:S:132:ARG:HH21	1.54	0.54
3:B:34:LYS:O	3:B:98:THR:OG1	2.26	0.54
3:B:97:LEU:HG	3:B:232:HIS:CE1	2.42	0.54
5:D:191:PRO:CB	5:D:194:PRO:HD2	2.20	0.54
23:V:62:MET:HG2	23:V:64:GLU:HG2	1.89	0.54
17:P:96:VAL:HB	17:P:103:ASN:HB2	1.89	0.54
36:n:155:GLU:HA	36:n:158:GLU:HB2	1.88	0.54
1:2:28:U:H2'	1:2:29:G:H8	1.72	0.53
1:2:942:G:H2'	1:2:943:U:C6	2.43	0.53
1:2:1219:C:H42	1:2:1646:C:N4	2.06	0.53
1:2:1589:A:O2'	1:2:1653:U:O2'	2.17	0.53
4:C:255:LEU:HD13	23:V:23:ILE:HD11	1.89	0.53
10:I:106:SER:HB3	10:I:171:LEU:HG	1.89	0.53
34:g:65:PHE:O	34:g:83:TRP:HB2	2.07	0.53
1:2:1406:G:H2'	1:2:1407:U:C6	2.43	0.53
2:A:76:VAL:HG12	2:A:123:VAL:HB	1.90	0.53
5:D:102:ALA:HB1	5:D:173:ARG:HE	1.72	0.53
13:L:49:GLU:HG2	13:L:118:ARG:NH2	2.23	0.53
30:c:18:LEU:HB2	30:c:29:GLN:HG2	1.88	0.53
1:2:1507:G:H21	33:f:89:LYS:HD2	1.73	0.53
3:B:139:CYS:HA	3:B:213:ARG:H	1.73	0.53
7:F:175:ASP:HA	7:F:178:ILE:HG12	1.90	0.53
14:M:50:CYS:O	14:M:77:ILE:N	2.32	0.53
20:S:46:ARG:NH1	21:T:47:PRO:O	2.37	0.53
1:2:85:A:H2'	1:2:86:C:C6	2.44	0.53
1:2:687:C:O2'	9:H:103:LYS:NZ	2.31	0.53
19:R:21:TYR:HE2	19:R:73:LEU:HD23	1.74	0.53
20:S:74:PRO:HG3	20:S:96:SER:HA	1.88	0.53
34:g:166:VAL:HB	34:g:221:LEU:HD21	1.91	0.53
1:2:747:U:H3'	1:2:796:G:N2	2.23	0.53
1:2:1188:A:H2'	1:2:1189:A:H8	1.73	0.53
1:2:1384:C:H5''	5:D:158:ILE:HG22	1.90	0.53
27:Z:79:ILE:HB	27:Z:83:LEU:HD23	1.90	0.53
1:2:127:C:O2'	1:2:215:G:O2'	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:177:SER:OG	10:I:184:ARG:O	2.26	0.53
17:P:118:GLU:O	20:S:120:HIS:ND1	2.39	0.53
21:T:30:VAL:HG12	21:T:31:PRO:HD2	1.89	0.53
1:2:449:A:OP1	10:I:23:LYS:NZ	2.38	0.53
1:2:953:C:O2	16:O:55:ARG:NH2	2.41	0.53
1:2:1400:U:O2	22:U:55:ARG:NH1	2.40	0.53
21:T:65:TYR:HD2	21:T:131:LEU:HD23	1.73	0.53
1:2:1301:A:H5'	31:d:6:LEU:HD12	1.91	0.53
12:K:29:MET:HG3	12:K:42:ASN:HD22	1.74	0.53
1:2:17:C:H2'	1:2:18:C:C6	2.44	0.53
3:B:173:THR:O	3:B:177:GLN:HG2	2.09	0.53
34:g:199:THR:OG1	34:g:239:LEU:O	2.22	0.53
1:2:860:G:N2	24:W:107:SER:HG	2.07	0.53
1:2:1809:A:H8	1:2:1810:U:C5	2.26	0.53
5:D:25:LEU:HD21	5:D:37:VAL:HG21	1.90	0.53
14:M:22:LEU:HD12	14:M:85:LEU:HD22	1.91	0.53
16:O:103:ASN:HB3	16:O:142:ARG:HG2	1.91	0.53
21:T:40:ALA:HA	21:T:95:GLY:HA2	1.90	0.53
2:A:78:SER:HB2	2:A:87:VAL:HG21	1.92	0.52
3:B:110:MET:HE1	3:B:140:VAL:HG11	1.91	0.52
4:C:73:MET:HE2	4:C:73:MET:N	2.24	0.52
12:K:32:HIS:HB3	12:K:35:LEU:HB2	1.90	0.52
1:2:115:U:O2'	1:2:381:C:O2	2.22	0.52
1:2:677:G:OP1	15:N:124:ARG:NH1	2.42	0.52
1:2:1285:G:N7	14:M:33:ARG:HB2	2.24	0.52
1:2:1509:U:H3'	1:2:1510:G:C8	2.44	0.52
3:B:52:THR:HG23	3:B:57:ILE:HA	1.90	0.52
17:P:76:VAL:HG23	17:P:94:VAL:HA	1.91	0.52
18:Q:38:PRO:HD2	18:Q:41:MET:HE1	1.90	0.52
1:2:17:C:O2'	1:2:1194:A:N1	2.37	0.52
8:G:56:ASN:ND2	8:G:60:GLY:O	2.43	0.52
34:g:60:ARG:H	34:g:60:ARG:HD2	1.74	0.52
1:2:81:U:H2'	1:2:82:G:O4'	2.09	0.52
1:2:155:G:N2	8:G:56:ASN:OD1	2.43	0.52
1:2:536:A:H2'	1:2:538:U:C5	2.44	0.52
1:2:1037:G:H4'	1:2:1845:A:H4'	1.91	0.52
1:2:1581:C:H5'	1:2:1582:C:H5	1.75	0.52
20:S:43:VAL:HA	20:S:46:ARG:HG2	1.92	0.52
32:e:45:VAL:O	32:e:48:THR:HG22	2.10	0.52
34:g:118:ARG:HH12	34:g:119:GLN:HB2	1.72	0.52
1:2:617:G:H4'	25:X:88:ASP:CB	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:52:LEU:HD21	14:M:62:VAL:HG23	1.91	0.52
20:S:84:LEU:HD13	20:S:95:TYR:HD1	1.74	0.52
1:2:1217:A:H2'	1:2:1218:C:H6	1.75	0.52
7:F:135:ARG:NH1	7:F:135:ARG:O	2.43	0.52
22:U:46:LYS:HD3	22:U:97:ILE:HG12	1.92	0.52
1:2:12:U:H2'	1:2:13:C:C6	2.45	0.52
1:2:902:G:OP1	1:2:904:A:N6	2.43	0.52
1:2:1188:A:H2'	1:2:1189:A:C8	2.44	0.52
1:2:1254:C:H2'	1:2:1255:G:H8	1.74	0.52
1:2:1613:G:C6	1:2:1614:A:H1'	2.45	0.52
22:U:31:SER:O	22:U:34:LYS:HG2	2.10	0.52
34:g:64:HIS:CG	34:g:83:TRP:HB3	2.45	0.52
1:2:5:U:H2'	1:2:6:G:H8	1.74	0.52
1:2:639:C:O2'	1:2:640:A:H8	1.92	0.52
2:A:19:LEU:HD13	19:R:117:LEU:HD11	1.91	0.52
21:T:20:ALA:O	21:T:24:LYS:HG2	2.10	0.52
1:2:1541:G:N2	1:2:1594:A:OP1	2.43	0.52
1:2:1720:U:H2'	1:2:1814:G:N2	2.25	0.52
20:S:39:ARG:HH12	21:T:46:ALA:HB2	1.75	0.52
20:S:55:ARG:HD2	27:Z:83:LEU:HD13	1.91	0.52
20:S:66:ARG:HG2	20:S:66:ARG:HH11	1.75	0.52
20:S:113:ARG:HE	20:S:114:LEU:HD22	1.74	0.52
1:2:39:A:OP2	11:J:5:ARG:NH1	2.43	0.52
1:2:1552:G:OP1	1:2:1578:U:N3	2.42	0.52
6:E:206:ASP:HB2	6:E:222:LEU:HB2	1.92	0.52
13:L:79:LYS:HB2	13:L:87:VAL:HB	1.92	0.52
20:S:57:GLY:HA3	27:Z:50:PHE:HD2	1.75	0.52
1:2:181:A:H3'	1:2:182:C:H5'	1.92	0.51
1:2:1010:G:H2'	1:2:1011:A:C8	2.45	0.51
1:2:1144:A:H2'	1:2:1145:A:C8	2.45	0.51
1:2:1493:C:N3	1:2:1499:U:O2	2.43	0.51
1:2:1686:G:H2'	1:2:1687:C:C6	2.45	0.51
1:2:1723:G:N1	1:2:1812:U:O2	2.43	0.51
1:2:1845:A:H2'	1:2:1846:G:C8	2.45	0.51
34:g:256:ILE:HD13	34:g:289:LEU:HD21	1.91	0.51
1:2:980:A:H2'	1:2:981:A:C8	2.44	0.51
1:2:1754:G:N2	1:2:1781:A:OP2	2.42	0.51
3:B:129:THR:OG1	3:B:131:ASP:OD1	2.22	0.51
4:C:113:GLN:OE1	4:C:122:THR:OG1	2.27	0.51
34:g:17:TRP:HB2	34:g:36:ARG:HD2	1.92	0.51
1:2:106:C:H2'	1:2:107:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1335:G:O6	1:2:1492:U:O4	2.28	0.51
35:h:1:MET:HE1	35:h:9:ARG:NE	2.26	0.51
1:2:5:U:H2'	1:2:6:G:C8	2.45	0.51
1:2:544:G:H2'	1:2:545:A:H8	1.76	0.51
1:2:1230:C:HO2'	1:2:1665:G:N2	2.05	0.51
1:2:1361:G:N2	1:2:1362:U:O2'	2.43	0.51
1:2:1519:U:O2	1:2:1622:U:O2'	2.29	0.51
5:D:21:LEU:HD12	5:D:22:ASN:N	2.26	0.51
9:H:47:ALA:HB3	9:H:63:PHE:HD2	1.75	0.51
13:L:33:LEU:HD12	13:L:34:PRO:HD2	1.92	0.51
1:2:372:U:O2'	13:L:82:MET:SD	2.59	0.51
1:2:555:A:H8	32:e:25:LYS:HE3	1.76	0.51
1:2:920:A:O2'	1:2:922:A:OP1	2.27	0.51
1:2:1260:A:H61	1:2:1620:A:H2	1.58	0.51
1:2:1709:G:O2'	1:2:1710:C:OP2	2.29	0.51
7:F:18:LYS:HB2	7:F:24:SER:HA	1.93	0.51
9:H:8:ILE:HD12	9:H:24:SER:HB2	1.91	0.51
16:O:25:GLU:OE1	16:O:25:GLU:N	2.44	0.51
28:a:42:ARG:NH1	28:a:43:ASN:O	2.43	0.51
1:2:85:A:H2'	1:2:86:C:H6	1.76	0.51
1:2:1160:U:O4	25:X:2:GLY:N	2.44	0.51
1:2:1486:A:H2'	1:2:1487:A:O4'	2.11	0.51
12:K:15:LEU:HD12	12:K:21:MET:HB2	1.93	0.51
1:2:184:G:H2'	1:2:185:G:C8	2.45	0.51
1:2:1472:C:N3	1:2:1476:A:N7	2.58	0.51
12:K:1:MET:H2	12:K:47:LYS:HD2	1.76	0.51
12:K:26:ASP:O	12:K:42:ASN:ND2	2.44	0.51
20:S:84:LEU:HD23	20:S:86:ARG:H	1.75	0.51
1:2:1589:A:H4'	21:T:82:ARG:HD3	1.93	0.51
1:2:1663:A:H2'	1:2:1664:A:H4'	1.93	0.51
1:2:1722:G:O6	1:2:1812:U:N3	2.43	0.51
19:R:103:LYS:HD2	19:R:119:VAL:HG22	1.93	0.51
34:g:166:VAL:HG23	34:g:176:VAL:HG22	1.93	0.51
1:2:388:U:H2'	1:2:389:A:C8	2.46	0.51
19:R:35:CYS:HB3	19:R:41:ILE:HD11	1.93	0.51
19:R:96:ILE:HD12	19:R:96:ILE:O	2.11	0.51
22:U:81:GLN:NE2	22:U:83:ARG:HB2	2.26	0.51
36:n:156:ASP:O	36:n:160:ASN:HB2	2.11	0.51
1:2:1101:U:H2'	1:2:1102:G:H8	1.76	0.51
1:2:1358:U:H5'	4:C:114:LYS:HD2	1.92	0.51
5:D:124:ARG:HH12	5:D:125:PHE:HB2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:154:LEU:HB3	7:F:189:ALA:HB2	1.92	0.51
25:X:6:GLY:O	25:X:9:THR:OG1	2.25	0.51
34:g:191:HIS:CD2	34:g:195:LEU:HD11	2.46	0.51
1:2:1487:A:H4'	4:C:118:ALA:HB1	1.92	0.50
1:2:1821:U:O2'	1:2:1822:A:OP1	2.27	0.50
4:C:132:ASP:OD1	4:C:136:HIS:HB2	2.10	0.50
4:C:236:PHE:O	4:C:240:THR:HG22	2.10	0.50
18:Q:82:TYR:HD1	18:Q:85:ARG:HH21	1.58	0.50
34:g:132:TRP:HE1	34:g:141:THR:HG22	1.76	0.50
1:2:1262:C:C2	31:d:15:GLY:HA2	2.46	0.50
1:2:1661:A:H2'	1:2:1662:U:H5	1.75	0.50
2:A:33:GLN:NE2	23:V:64:GLU:OE2	2.34	0.50
2:A:106:GLY:N	2:A:136:GLU:OE2	2.27	0.50
1:2:929:G:H2'	1:2:930:C:O4'	2.10	0.50
1:2:1736:G:H2'	1:2:1737:G:C8	2.47	0.50
14:M:33:ARG:HA	14:M:104:VAL:HG12	1.94	0.50
28:a:90:GLU:H	28:a:90:GLU:CD	2.18	0.50
34:g:217:MET:HB2	34:g:226:HIS:CD2	2.46	0.50
1:2:1373:C:OP1	19:R:7:LYS:HB3	2.12	0.50
7:F:78:MET:HE2	7:F:79:HIS:NE2	2.27	0.50
16:O:136:PRO:HG3	16:O:139:SER:HB3	1.94	0.50
1:2:880:G:N2	1:2:907:G:H1'	2.16	0.50
1:2:1088:U:H4'	1:2:1089:G:OP2	2.12	0.50
1:2:1256:G:C2	31:d:31:ILE:HG12	2.46	0.50
1:2:1349:G:H2'	1:2:1350:U:C6	2.47	0.50
1:2:1367:U:HO2'	1:2:1466:G:HO2'	1.57	0.50
2:A:7:VAL:HG13	2:A:8:LEU:HG	1.92	0.50
8:G:152:ASP:OD1	8:G:154:ARG:N	2.39	0.50
14:M:119:GLN:O	14:M:123:VAL:HG13	2.11	0.50
19:R:44:LYS:HA	19:R:47:ARG:HG2	1.93	0.50
1:2:902:G:N7	1:2:903:A:N6	2.57	0.50
1:2:1060:A:O2'	1:2:1062:A:N7	2.39	0.50
1:2:1235:G:H2'	1:2:1236:G:C8	2.46	0.50
1:2:1618:C:P	17:P:47:ARG:HH21	2.34	0.50
10:I:79:ILE:HD13	10:I:170:LYS:HZ3	1.76	0.50
1:2:1083:A:N7	1:2:1841:C:O2'	2.44	0.50
1:2:1366:G:O2'	1:2:1367:U:H5'	2.11	0.50
1:2:1446:A:O2'	1:2:1447:G:N7	2.34	0.50
1:2:1491:G:H2'	1:2:1492:U:C6	2.46	0.50
1:2:1605:G:N2	1:2:1606:G:O6	2.44	0.50
5:D:193:ASP:HB2	5:D:194:PRO:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:38:ALA:HB1	8:G:41:LEU:HD12	1.93	0.50
1:2:187:G:H2'	1:2:188:C:C6	2.47	0.50
1:2:681:U:O2'	1:2:1160:U:OP1	2.29	0.50
1:2:1222:G:H2'	1:2:1223:A:C8	2.47	0.50
1:2:1736:G:H2'	1:2:1737:G:H8	1.77	0.50
3:B:36:PRO:HA	3:B:232:HIS:CD2	2.47	0.50
8:G:33:ALA:N	8:G:52:ILE:O	2.33	0.50
20:S:55:ARG:CZ	27:Z:83:LEU:HD22	2.41	0.50
21:T:22:LEU:HD11	21:T:28:LEU:HB2	1.92	0.50
31:d:27:ARG:O	31:d:27:ARG:NH1	2.42	0.50
1:2:903:A:C8	1:2:903:A:H5'	2.47	0.50
1:2:1456:G:H2'	1:2:1457:U:C6	2.46	0.50
2:A:110:ASN:HB3	2:A:113:GLN:HG3	1.94	0.50
9:H:42:GLU:N	9:H:42:GLU:OE2	2.45	0.50
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.27	0.50
18:Q:53:GLU:OE1	18:Q:85:ARG:NH1	2.45	0.50
30:c:39:SER:O	30:c:39:SER:OG	2.30	0.50
34:g:109:LEU:HD13	34:g:151:VAL:O	2.11	0.50
34:g:247:TRP:NE1	34:g:260:ASP:OD1	2.45	0.50
1:2:3:C:O2	11:J:18:ARG:NH2	2.40	0.49
1:2:198:U:O4	1:2:202:G:N1	2.45	0.49
1:2:491:C:H1'	1:2:510:G:N2	2.26	0.49
1:2:656:G:N2	1:2:663:C:H5''	2.26	0.49
1:2:957:A:OP1	16:O:57:THR:OG1	2.23	0.49
1:2:1220:A:H2'	1:2:1221:G:O4'	2.12	0.49
1:2:1276:A:H1'	12:K:55:ARG:HA	1.93	0.49
3:B:82:ARG:HD3	3:B:103:MET:HE2	1.93	0.49
3:B:146:ARG:HB2	3:B:149:GLN:HB2	1.94	0.49
3:B:227:LYS:HB3	3:B:227:LYS:NZ	2.27	0.49
5:D:51:LEU:HD22	5:D:52:ALA:H	1.77	0.49
11:J:170:PRO:HB3	11:J:174:LYS:HD3	1.94	0.49
20:S:25:LYS:HG2	27:Z:80:ARG:HH11	1.77	0.49
21:T:14:PHE:HA	21:T:138:VAL:HG11	1.92	0.49
21:T:133:ARG:NE	21:T:133:ARG:HA	2.26	0.49
22:U:18:HIS:O	22:U:92:HIS:ND1	2.45	0.49
26:Y:28:LEU:HD13	26:Y:68:LYS:HB3	1.94	0.49
26:Y:38:THR:O	26:Y:42:GLU:HG2	2.11	0.49
26:Y:74:MET:HE1	26:Y:90:ARG:HH21	1.76	0.49
34:g:7:LEU:HD21	34:g:272:GLN:HG3	1.94	0.49
34:g:176:VAL:HB	34:g:186:THR:OG1	2.12	0.49
1:2:168:C:O2	8:G:133:LEU:HD23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1101:U:H2'	1:2:1102:G:C8	2.47	0.49
1:2:1366:G:H2'	1:2:1367:U:O4'	2.12	0.49
1:2:1457:U:H2'	1:2:1458:G:C8	2.45	0.49
1:2:1590:C:H5	18:Q:77:HIS:CE1	2.30	0.49
1:2:1794:C:H2'	1:2:1795:G:C8	2.47	0.49
2:A:163:CYS:SG	2:A:174:MET:HE2	2.52	0.49
5:D:72:VAL:HA	5:D:75:LYS:HE2	1.93	0.49
5:D:113:LEU:HD22	5:D:114:ALA:N	2.27	0.49
16:O:99:ALA:H	16:O:133:THR:HB	1.77	0.49
17:P:83:MET:HE2	17:P:83:MET:N	2.27	0.49
24:W:111:MET:HE3	24:W:116:ALA:HA	1.94	0.49
34:g:58:ALA:O	34:g:60:ARG:NH1	2.46	0.49
34:g:104:HIS:CD2	34:g:130:LYS:HD3	2.47	0.49
1:2:913:A:O2'	1:2:914:U:OP1	2.26	0.49
1:2:1351:G:H1	1:2:1360:U:H5	1.58	0.49
1:2:1407:U:O2	1:2:1439:A:N6	2.45	0.49
1:2:1409:A:H61	1:2:1432:U:H5''	1.76	0.49
28:a:78:VAL:HG13	28:a:84:VAL:HG22	1.94	0.49
1:2:126:G:H5'	8:G:195:LYS:NZ	2.27	0.49
1:2:589:G:N2	32:e:23:GLU:OE2	2.45	0.49
1:2:1236:G:H21	17:P:130:ARG:HH12	1.59	0.49
1:2:1488:C:H3'	1:2:1489:A:H4'	1.95	0.49
4:C:167:ARG:HB3	4:C:177:PRO:HB2	1.95	0.49
6:E:212:ASP:OD2	6:E:216:ASN:ND2	2.44	0.49
7:F:63:LYS:HG3	7:F:144:LEU:HD11	1.93	0.49
7:F:100:ILE:HG21	7:F:177:LEU:HD22	1.94	0.49
1:2:985:G:H4'	16:O:138:ASP:OD2	2.12	0.49
1:2:1330:G:H1	1:2:1493:C:H5	1.60	0.49
1:2:1557:C:C2	1:2:1661:A:H5'	2.48	0.49
1:2:1646:C:H1'	1:2:1678:A:H2	1.77	0.49
9:H:43:LEU:HD21	9:H:71:SER:HB2	1.93	0.49
15:N:67:THR:HG21	15:N:74:ILE:HD11	1.95	0.49
21:T:39:LEU:HD23	21:T:47:PRO:HD3	1.94	0.49
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.46	0.49
1:2:65:C:C2	8:G:133:LEU:HD12	2.48	0.49
1:2:1753:C:H5'	1:2:1754:G:H5''	1.94	0.49
21:T:65:TYR:CD2	21:T:131:LEU:HD23	2.48	0.49
26:Y:23:MET:HE1	26:Y:75:ILE:HD12	1.95	0.49
1:2:220:U:H5	1:2:301:A:N1	2.09	0.49
1:2:964:A:H2'	1:2:965:U:H6	1.78	0.49
1:2:1164:G:O2'	1:2:1165:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1815:A:H5'	1:2:1816:G:C8	2.48	0.49
6:E:126:VAL:HA	6:E:141:THR:HA	1.95	0.49
25:X:52:LEU:HD11	25:X:73:GLN:HB2	1.94	0.49
28:a:36:ILE:HD13	28:a:78:VAL:HG11	1.95	0.49
1:2:1587:G:OP1	1:2:1587:G:N2	2.46	0.49
19:R:34:VAL:O	19:R:37:GLU:HG2	2.13	0.49
1:2:528:A:H2'	1:2:529:A:C8	2.47	0.49
1:2:544:G:H2'	1:2:545:A:C8	2.48	0.49
1:2:1614:A:H62	17:P:43:ARG:HD2	1.77	0.49
17:P:38:SER:O	17:P:42:ARG:HB2	2.12	0.49
1:2:1235:G:O2'	1:2:1524:G:N2	2.45	0.49
4:C:272:HIS:O	4:C:276:THR:OG1	2.24	0.49
13:L:23:VAL:HG23	13:L:26:GLY:H	1.77	0.49
16:O:119:LEU:O	16:O:124:MET:HB2	2.13	0.49
1:2:125:C:OP1	8:G:202:ASN:ND2	2.46	0.48
1:2:340:C:H2'	1:2:341:C:C6	2.48	0.48
1:2:376:A:N3	10:I:86:SER:OG	2.36	0.48
1:2:1275:G:H4'	1:2:1276:A:C8	2.48	0.48
1:2:1397:U:H5'	1:2:1398:G:C8	2.47	0.48
1:2:1705:C:H2'	1:2:1706:G:C8	2.49	0.48
12:K:3:MET:CE	12:K:8:ARG:HB2	2.36	0.48
12:K:64:TRP:HB3	31:d:23:VAL:O	2.13	0.48
19:R:53:TYR:O	19:R:57:LEU:HD22	2.13	0.48
22:U:79:ARG:HD2	22:U:79:ARG:C	2.38	0.48
34:g:116:ASP:OD2	34:g:118:ARG:HG2	2.13	0.48
1:2:532:C:H2'	1:2:533:A:C8	2.48	0.48
1:2:1270:G:N2	1:2:1301:A:OP2	2.46	0.48
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.95	0.48
5:D:126:ILE:HG22	5:D:127:MET:SD	2.53	0.48
7:F:167:LYS:NZ	7:F:171:GLU:HB2	2.28	0.48
21:T:16:ARG:NH2	21:T:55:THR:HG23	2.28	0.48
28:a:36:ILE:HG21	28:a:78:VAL:HG21	1.94	0.48
34:g:62:HIS:CE1	34:g:66:VAL:HB	2.48	0.48
1:2:380:G:P	10:I:56:ARG:HH22	2.36	0.48
1:2:1238:U:C2	17:P:126:VAL:HA	2.47	0.48
5:D:206:ASP:OD1	5:D:206:ASP:N	2.46	0.48
7:F:123:GLU:CD	7:F:201:LYS:HZ3	2.21	0.48
19:R:97:GLU:HB3	19:R:120:THR:OG1	2.12	0.48
31:d:22:ARG:HG2	31:d:37:ASN:HB3	1.95	0.48
34:g:219:TRP:HA	34:g:219:TRP:CE3	2.48	0.48
1:2:555:A:C8	32:e:25:LYS:HE3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1815:A:H5'	1:2:1816:G:H8	1.79	0.48
15:N:19:ARG:HH12	29:b:83:GLN:CD	2.21	0.48
15:N:86:GLU:H	15:N:86:GLU:CD	2.19	0.48
19:R:28:PHE:O	19:R:31:ASN:N	2.45	0.48
19:R:51:ALA:O	19:R:55:THR:HG23	2.13	0.48
34:g:64:HIS:ND1	34:g:83:TRP:HB3	2.28	0.48
1:2:1495:G:O4'	31:d:41:GLN:NE2	2.45	0.48
8:G:32:MET:HA	8:G:52:ILE:HG22	1.96	0.48
18:Q:60:LYS:HE2	18:Q:60:LYS:HB2	1.68	0.48
27:Z:96:LEU:O	27:Z:111:ARG:HD3	2.14	0.48
34:g:301:GLY:HA2	34:g:307:VAL:HG22	1.94	0.48
1:2:822:U:H2'	1:2:824:C:OP2	2.13	0.48
1:2:1442:U:H2'	1:2:1443:C:O4'	2.14	0.48
1:2:1475:G:H5'	18:Q:124:PRO:HG2	1.96	0.48
1:2:1589:A:H5'	21:T:82:ARG:HH11	1.78	0.48
3:B:58:ALA:O	3:B:62:LEU:HB2	2.14	0.48
11:J:78:LEU:O	11:J:82:VAL:HG13	2.12	0.48
15:N:16:LEU:HD11	15:N:62:GLN:HG3	1.95	0.48
18:Q:112:LEU:HD22	18:Q:120:LEU:HG	1.96	0.48
20:S:16:LEU:HD23	20:S:16:LEU:H	1.79	0.48
4:C:199:PRO:O	4:C:202:THR:HG23	2.13	0.48
5:D:195:THR:HG22	5:D:199:GLY:O	1.93	0.48
10:I:144:LYS:HG3	10:I:145:ILE:N	2.27	0.48
20:S:84:LEU:HD23	20:S:86:ARG:N	2.28	0.48
28:a:53:ILE:HG21	28:a:64:LEU:HD21	1.95	0.48
1:2:907:G:N2	1:2:908:A:N7	2.61	0.48
1:2:1183:A:OP2	35:h:18:ARG:NH2	2.47	0.48
1:2:1390:U:H2'	1:2:1391:C:C6	2.48	0.48
1:2:1818:A:O2'	35:h:13:LEU:HD11	2.13	0.48
3:B:36:PRO:HB2	3:B:38:MET:SD	2.54	0.48
4:C:173:LYS:O	23:V:3:ASN:HB2	2.13	0.48
4:C:199:PRO:HG3	11:J:58:ARG:HD3	1.94	0.48
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.96	0.48
29:b:41:TYR:CE1	29:b:42:LYS:HG3	2.49	0.48
1:2:1284:A:N7	14:M:91:LEU:HD11	2.29	0.48
1:2:1397:U:H5'	1:2:1398:G:H8	1.79	0.48
1:2:1456:G:H2'	1:2:1457:U:H6	1.79	0.48
1:2:1532:C:O2'	1:2:1604:G:N2	2.47	0.48
1:2:1566:G:O3'	1:2:1567:G:N2	2.47	0.48
2:A:39:TYR:CD2	19:R:105:MET:HB2	2.49	0.48
2:A:147:LEU:HD23	2:A:161:ILE:HD12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:135:GLU:O	10:I:139:LYS:HG3	2.14	0.48
22:U:24:LEU:HD12	22:U:32:LEU:HD22	1.96	0.48
14:M:110:VAL:HG12	14:M:111:VAL:H	1.79	0.48
27:Z:62:VAL:HG13	27:Z:63:PRO:HD3	1.96	0.48
1:2:1600:G:H22	27:Z:80:ARG:NH2	2.12	0.47
1:2:1714:U:H2'	1:2:1715:A:C8	2.49	0.47
1:2:1727:G:O6	1:2:1805:G:O2'	2.30	0.47
13:L:45:LYS:HB3	13:L:45:LYS:HE2	1.64	0.47
15:N:16:LEU:HD12	15:N:17:PRO:HD2	1.96	0.47
29:b:62:VAL:HG21	29:b:65:GLN:NE2	2.29	0.47
34:g:122:SER:HB2	34:g:130:LYS:HE2	1.94	0.47
1:2:1254:C:H2'	1:2:1255:G:C8	2.49	0.47
1:2:1380:C:H2'	1:2:1381:G:O4'	2.14	0.47
1:2:1660:C:OP2	31:d:16:GLN:NE2	2.46	0.47
1:2:1678:A:O2'	1:2:1679:A:O4'	2.26	0.47
5:D:116:ARG:NH1	36:n:152:ASP:H	2.12	0.47
11:J:45:ARG:O	11:J:49:THR:HG23	2.14	0.47
16:O:56:VAL:HG12	16:O:60:MET:HE1	1.96	0.47
1:2:186:C:H2'	1:2:187:G:H8	1.79	0.47
1:2:656:G:H5'	1:2:662:G:N2	2.29	0.47
1:2:1539:U:H4'	21:T:47:PRO:HA	1.96	0.47
5:D:158:ILE:HG13	5:D:164:VAL:HG13	1.96	0.47
17:P:51:ARG:HE	17:P:51:ARG:H	1.63	0.47
19:R:28:PHE:CD1	19:R:28:PHE:C	2.92	0.47
19:R:33:ARG:O	19:R:36:GLU:HG2	2.14	0.47
20:S:68:ILE:HA	20:S:71:MET:HE3	1.95	0.47
1:2:659:G:HO2'	1:2:662:G:HO2'	1.57	0.47
1:2:1240:A:H2'	1:2:1241:A:C5	2.49	0.47
1:2:1285:G:O6	14:M:33:ARG:N	2.47	0.47
2:A:75:SER:HB3	2:A:119:PRO:HB3	1.97	0.47
1:2:28:U:H2'	1:2:29:G:C8	2.50	0.47
1:2:447:A:N3	6:E:3:ARG:NH1	2.62	0.47
1:2:1539:U:OP2	21:T:43:LYS:NZ	2.37	0.47
1:2:1848:U:H2'	1:2:1850:A:OP2	2.14	0.47
1:2:1865:C:O2	28:a:92:ARG:HB3	2.14	0.47
2:A:190:SER:HB3	2:A:193:HIS:CE1	2.50	0.47
5:D:109:LEU:HA	5:D:113:LEU:HB3	1.96	0.47
6:E:20:LEU:HD21	6:E:46:ILE:HD12	1.96	0.47
20:S:67:VAL:O	20:S:70:ILE:HG22	2.14	0.47
21:T:72:VAL:HA	21:T:75:MET:SD	2.53	0.47
22:U:63:ILE:HD13	31:d:43:PHE:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:17:TRP:N	34:g:17:TRP:CD1	2.82	0.47
1:2:984:C:O2'	16:O:138:ASP:HB3	2.14	0.47
1:2:1007:C:H2'	1:2:1008:A:C8	2.49	0.47
1:2:1414:A:H5''	21:T:128:GLN:NE2	2.28	0.47
1:2:1441:U:OP1	18:Q:8:GLN:NE2	2.34	0.47
6:E:122:LYS:NZ	6:E:143:ASP:OD2	2.33	0.47
10:I:141:ARG:HD3	10:I:146:GLN:OE1	2.14	0.47
17:P:30:TYR:HB3	17:P:33:LEU:HB3	1.96	0.47
20:S:11:HIS:ND1	20:S:11:HIS:O	2.48	0.47
20:S:121:ARG:HG2	20:S:131:VAL:HG21	1.96	0.47
1:2:463:C:O2'	1:2:466:G:O6	2.29	0.47
1:2:943:U:C2	1:2:944:A:C8	3.02	0.47
1:2:1242:U:O2'	1:2:1518:C:O4'	2.33	0.47
1:2:1267:C:H2'	1:2:1268:C:C4	2.50	0.47
1:2:1339:U:O2'	1:2:1340:U:OP1	2.30	0.47
1:2:1726:G:O6	1:2:1809:A:N6	2.47	0.47
1:2:1788:A:H2'	1:2:1789:G:O4'	2.14	0.47
4:C:183:LYS:HA	4:C:195:LEU:O	2.15	0.47
5:D:195:THR:CG2	5:D:199:GLY:HA3	2.23	0.47
6:E:45:ILE:HA	6:E:61:VAL:HG11	1.97	0.47
6:E:104:ASP:OD1	6:E:105:THR:N	2.47	0.47
7:F:32:ASP:O	7:F:35:LEU:N	2.40	0.47
7:F:49:LEU:HD22	7:F:50:PRO:HD2	1.96	0.47
16:O:78:ALA:HB3	16:O:118:ALA:HB3	1.96	0.47
22:U:80:PHE:CD1	31:d:52:PHE:HB3	2.50	0.47
24:W:18:GLU:OE2	24:W:67:GLY:HA2	2.14	0.47
26:Y:41:ARG:NH2	26:Y:52:PRO:O	2.46	0.47
1:2:594:A:H61	1:2:643:A:H5''	1.79	0.47
1:2:1043:G:H2'	1:2:1044:G:O4'	2.15	0.47
1:2:1618:C:H2'	1:2:1619:A:C5	2.50	0.47
1:2:1677:U:H5'	7:F:148:ASN:HD22	1.80	0.47
14:M:82:ASN:OD1	14:M:82:ASN:N	2.46	0.47
19:R:29:HIS:HA	19:R:32:LYS:HZ3	1.80	0.47
22:U:28:ASN:OD1	22:U:30:LYS:N	2.47	0.47
1:2:1344:A:N6	1:2:1386:A:H5'	2.30	0.47
1:2:1352:G:H1	1:2:1359:U:H5	1.63	0.47
1:2:1486:A:OP2	5:D:151:LYS:NZ	2.47	0.47
3:B:124:HIS:HA	3:B:137:LEU:O	2.15	0.47
3:B:142:PHE:O	3:B:208:HIS:N	2.48	0.47
9:H:36:LEU:HD12	9:H:36:LEU:O	2.15	0.47
19:R:79:GLU:HA	19:R:82:ASP:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:n:152:ASP:O	36:n:156:ASP:HB2	2.15	0.47
1:2:92:A:H1'	6:E:3:ARG:HB2	1.96	0.47
1:2:1296:U:H1'	1:2:1303:C:H42	1.79	0.47
1:2:1335:G:N1	1:2:1492:U:N3	2.25	0.47
1:2:1593:C:O2	1:2:1594:A:N6	2.48	0.47
6:E:107:GLY:HA2	6:E:189:LEU:HD22	1.96	0.47
8:G:142:ARG:HH21	8:G:153:VAL:HG11	1.80	0.47
8:G:219:GLU:O	8:G:222:GLU:HG3	2.15	0.47
21:T:32:GLU:HG3	21:T:33:TRP:CD1	2.50	0.47
21:T:43:LYS:HE2	21:T:43:LYS:HA	1.97	0.47
1:2:359:U:OP2	25:X:18:ARG:HD2	2.15	0.46
1:2:529:A:H2'	1:2:530:U:O4'	2.15	0.46
1:2:804:U:H2'	1:2:805:U:C6	2.49	0.46
1:2:903:A:H2'	1:2:903:A:N3	2.30	0.46
1:2:945:U:H2'	1:2:946:U:C6	2.50	0.46
1:2:1286:G:N2	1:2:1316:C:O2	2.48	0.46
1:2:1402:A:C2	22:U:54:VAL:HA	2.50	0.46
5:D:7:LYS:HA	5:D:10:LYS:HE3	1.97	0.46
5:D:69:LEU:O	5:D:73:VAL:HG12	2.14	0.46
8:G:138:ALA:O	8:G:141:ILE:HG13	2.15	0.46
19:R:27:ASP:OD2	19:R:30:THR:HG23	2.15	0.46
21:T:11:GLN:OE1	21:T:62:ARG:NH2	2.48	0.46
1:2:446:G:OP2	10:I:47:ARG:NH2	2.44	0.46
1:2:1010:G:H2'	1:2:1011:A:H8	1.79	0.46
1:2:1260:A:H5'	1:2:1517:G:O6	2.15	0.46
5:D:73:VAL:HG23	5:D:77:PHE:CD1	2.50	0.46
14:M:51:VAL:HG22	14:M:77:ILE:HB	1.98	0.46
16:O:39:ASP:C	16:O:39:ASP:OD1	2.58	0.46
27:Z:56:ASP:OD1	27:Z:56:ASP:N	2.47	0.46
1:2:380:G:N1	1:2:383:G:OP2	2.38	0.46
1:2:1447:G:H2'	1:2:1448:A:H8	1.79	0.46
12:K:15:LEU:O	12:K:19:GLY:N	2.41	0.46
19:R:67:ARG:HH11	19:R:67:ARG:HG3	1.80	0.46
25:X:28:LYS:O	25:X:32:LEU:HB2	2.14	0.46
1:2:16:G:H2'	1:2:17:C:C6	2.49	0.46
1:2:202:G:H3'	1:2:203:G:C8	2.46	0.46
1:2:1378:A:H4'	1:2:1379:A:O5'	2.15	0.46
1:2:1535:U:C4	7:F:159:ARG:HD3	2.50	0.46
1:2:1666:C:HO2'	1:2:1667:U:P	2.37	0.46
7:F:179:ASN:OD1	7:F:184:SER:HB3	2.15	0.46
9:H:138:GLU:OE2	15:N:21:SER:OG	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:52:LEU:HG	18:Q:56:LEU:HD22	1.98	0.46
21:T:56:ARG:HH22	21:T:78:ILE:HB	1.79	0.46
34:g:157:SER:HB2	34:g:204:GLY:HA2	1.98	0.46
34:g:286:CYS:HA	34:g:302:TYR:HA	1.97	0.46
1:2:573:U:H1'	1:2:577:U:O4	2.15	0.46
1:2:1253:A:O5'	1:2:1527:C:N4	2.48	0.46
1:2:1269:G:H22	1:2:1513:C:H1'	1.80	0.46
1:2:1568:C:H5'	21:T:41:LYS:NZ	2.31	0.46
5:D:23:GLU:OE2	5:D:27:ARG:NH2	2.47	0.46
9:H:112:ASN:OD1	9:H:112:ASN:N	2.48	0.46
18:Q:105:LYS:NZ	18:Q:108:ILE:HD11	2.29	0.46
22:U:75:LYS:H	22:U:75:LYS:HD2	1.80	0.46
1:2:563:G:O2'	1:2:564:A:H8	1.98	0.46
1:2:1046:U:H2'	1:2:1047:C:O4'	2.16	0.46
1:2:1215:C:O2'	1:2:1645:C:OP2	2.28	0.46
1:2:1262:C:H1'	31:d:17:GLY:H	1.81	0.46
1:2:1339:U:H2'	1:2:1340:U:C6	2.51	0.46
4:C:263:LYS:HG2	4:C:268:GLU:HB2	1.98	0.46
5:D:64:ARG:NH1	12:K:73:ASN:OD1	2.45	0.46
15:N:31:ASP:OD1	15:N:32:ASP:N	2.49	0.46
17:P:98:ASN:HB3	17:P:103:ASN:OD1	2.16	0.46
18:Q:112:LEU:HD21	18:Q:119:LEU:HB2	1.98	0.46
35:h:2:ARG:HB3	35:h:5:TRP:CD1	2.50	0.46
1:2:71:G:H1'	1:2:72:C:H6	1.80	0.46
1:2:908:A:H2'	1:2:908:A:N3	2.31	0.46
1:2:1084:A:OP1	1:2:1858:G:O2'	2.28	0.46
1:2:1256:G:H8	22:U:77:TRP:HZ3	1.64	0.46
1:2:1332:A:O4'	1:2:1500:G:N1	2.48	0.46
4:C:232:THR:O	4:C:232:THR:OG1	2.34	0.46
4:C:263:LYS:HD3	4:C:268:GLU:HA	1.97	0.46
7:F:147:VAL:O	7:F:151:ILE:HG13	2.15	0.46
7:F:167:LYS:HZ1	7:F:171:GLU:HB2	1.81	0.46
10:I:113:TYR:OH	10:I:119:LEU:HB2	2.16	0.46
14:M:49:LEU:HD13	14:M:128:PHE:HB2	1.98	0.46
14:M:61:TYR:HB2	33:f:100:LEU:HD13	1.98	0.46
18:Q:102:GLU:HA	18:Q:105:LYS:HB3	1.98	0.46
19:R:10:LYS:HD2	19:R:53:TYR:CE2	2.51	0.46
19:R:60:ARG:HD2	19:R:60:ARG:HA	1.75	0.46
19:R:67:ARG:HG3	19:R:68:GLY:N	2.29	0.46
20:S:106:LYS:HD3	20:S:106:LYS:HA	1.60	0.46
1:2:1523:C:H42	17:P:135:ALA:HB1	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1630:A:H2'	1:2:1631:U:H6	1.81	0.46
2:A:85:ARG:HH12	2:A:205:ARG:HH21	1.64	0.46
7:F:153:LEU:CD2	7:F:189:ALA:HA	2.46	0.46
22:U:37:ALA:HA	22:U:40:ILE:HG22	1.97	0.46
34:g:125:ARG:HB3	34:g:150:TRP:NE1	2.30	0.46
1:2:122:G:H1'	6:E:145:ARG:HA	1.97	0.46
1:2:160:U:O2'	1:2:161:U:H3'	2.16	0.46
1:2:352:U:H2'	1:2:353:C:C6	2.51	0.46
1:2:959:G:OP2	16:O:38:ASN:ND2	2.33	0.46
1:2:1016:U:C6	15:N:61:ALA:HB1	2.51	0.46
3:B:128:LYS:HB2	3:B:128:LYS:HE2	1.68	0.46
11:J:84:ILE:HA	11:J:150:ARG:HA	1.97	0.46
14:M:26:LEU:HD12	14:M:31:LEU:HD21	1.98	0.46
16:O:40:THR:O	16:O:58:GLY:N	2.46	0.46
16:O:45:THR:HA	16:O:52:THR:HA	1.97	0.46
17:P:59:ARG:NH1	17:P:76:VAL:HG12	2.31	0.46
20:S:117:ILE:O	20:S:118:ARG:HG3	2.16	0.46
1:2:1373:C:OP1	19:R:7:LYS:HE2	2.16	0.46
1:2:1445:U:H5''	1:2:1446:A:OP1	2.16	0.46
1:2:1606:G:N7	1:2:1632:G:H8	2.14	0.46
4:C:74:LYS:HA	4:C:74:LYS:HD3	1.65	0.46
8:G:10:THR:HB	8:G:128:THR:HA	1.98	0.46
21:T:16:ARG:NE	21:T:16:ARG:HA	2.31	0.46
25:X:128:VAL:HG12	25:X:138:LYS:HD3	1.98	0.46
1:2:376:A:H2'	1:2:377:G:O4'	2.16	0.45
1:2:526:A:OP1	32:e:35:ARG:NH1	2.49	0.45
1:2:943:U:H2'	1:2:944:A:C8	2.50	0.45
1:2:1606:G:C6	1:2:1632:G:H1'	2.51	0.45
12:K:13:GLU:HG3	12:K:83:LEU:HD21	1.97	0.45
20:S:33:ILE:HD13	20:S:99:LEU:HD13	1.97	0.45
31:d:44:ARG:HA	31:d:44:ARG:HE	1.80	0.45
1:2:170:A:OP1	8:G:137:ARG:N	2.41	0.45
1:2:1510:G:H2'	1:2:1511:U:C6	2.51	0.45
1:2:1617:G:H1'	31:d:14:PHE:CZ	2.51	0.45
1:2:1620:A:H8	1:2:1624:U:OP1	1.99	0.45
1:2:1852:C:OP2	35:h:1:MET:HG3	2.15	0.45
2:A:14:ASP:HB3	2:A:177:MET:HE1	1.97	0.45
9:H:181:THR:HG22	9:H:183:LYS:H	1.81	0.45
17:P:76:VAL:HG23	17:P:94:VAL:HG13	1.98	0.45
17:P:86:LEU:HG	17:P:88:GLU:H	1.81	0.45
1:2:314:U:H5	1:2:336:A:N1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1395:C:O2'	1:2:1450:G:N2	2.49	0.45
1:2:1733:U:H2'	1:2:1734:G:O4'	2.17	0.45
4:C:257:LYS:O	23:V:16:LYS:NZ	2.45	0.45
5:D:202:LYS:HE3	5:D:202:LYS:HB2	1.84	0.45
10:I:119:LEU:HB3	10:I:120:PRO:CD	2.47	0.45
11:J:95:ASP:OD1	11:J:95:ASP:N	2.50	0.45
12:K:14:LEU:HA	12:K:17:LYS:HG2	1.98	0.45
14:M:69:CYS:O	14:M:73:GLN:N	2.49	0.45
19:R:10:LYS:O	19:R:14:ARG:HG3	2.16	0.45
26:Y:26:ASP:OD1	26:Y:26:ASP:N	2.50	0.45
1:2:67:C:C6	8:G:162:LEU:HD11	2.51	0.45
1:2:1269:G:O2'	1:2:1270:G:O4'	2.26	0.45
1:2:1387:G:H2'	1:2:1388:A:O4'	2.17	0.45
1:2:1548:G:H1	1:2:1655:C:HO2'	1.64	0.45
3:B:164:ILE:O	3:B:168:MET:HG3	2.16	0.45
5:D:34:TYR:HA	5:D:52:ALA:HB2	1.99	0.45
18:Q:27:ARG:H	18:Q:27:ARG:HD2	1.81	0.45
26:Y:12:PHE:HZ	26:Y:21:LYS:HD3	1.82	0.45
26:Y:74:MET:HE1	26:Y:90:ARG:NH2	2.31	0.45
27:Z:74:SER:HA	27:Z:79:ILE:HG12	1.99	0.45
1:2:65:C:C6	8:G:174:PRO:HB3	2.51	0.45
1:2:546:G:H4'	1:2:548:C:N4	2.31	0.45
1:2:831:G:N7	26:Y:11:LYS:NZ	2.61	0.45
1:2:1364:U:H2'	1:2:1365:G:H5'	1.99	0.45
1:2:1375:G:H2'	1:2:1376:A:C8	2.51	0.45
1:2:1866:A:N6	28:a:84:VAL:HB	2.32	0.45
4:C:121:ARG:NH1	4:C:123:ARG:HG3	2.32	0.45
5:D:203:PRO:HG2	19:R:42:PRO:HG3	1.98	0.45
16:O:33:ILE:HD12	16:O:95:ILE:HG23	1.98	0.45
20:S:40:TYR:OH	20:S:83:PHE:O	2.33	0.45
21:T:6:VAL:HG22	21:T:14:PHE:CZ	2.52	0.45
22:U:26:SER:HB2	22:U:110:VAL:HG13	1.99	0.45
34:g:36:ARG:CB	34:g:65:PHE:HB3	2.46	0.45
34:g:65:PHE:N	34:g:65:PHE:CD1	2.83	0.45
34:g:181:ASN:OD1	34:g:182:CYS:N	2.49	0.45
1:2:106:C:H2'	1:2:107:A:C8	2.51	0.45
1:2:443:U:H2'	1:2:444:G:O4'	2.17	0.45
1:2:1869:A:C5	28:a:39:PHE:HE2	2.35	0.45
3:B:192:SER:HA	3:B:195:LYS:HE2	1.99	0.45
5:D:74:GLN:CD	5:D:81:GLU:HA	2.42	0.45
7:F:95:HIS:ND1	7:F:98:GLU:OE2	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:200:LYS:HB2	8:G:200:LYS:HE3	1.59	0.45
17:P:21:ASP:O	17:P:25:LEU:HD12	2.17	0.45
21:T:124:THR:HG23	21:T:127:GLY:H	1.82	0.45
1:2:1263:U:O2'	1:2:1264:C:OP1	2.30	0.45
1:2:1344:A:N1	1:2:1385:G:O2'	2.37	0.45
1:2:1548:G:N2	1:2:1655:C:HO2'	2.15	0.45
1:2:1630:A:H2'	1:2:1631:U:C6	2.52	0.45
3:B:225:LEU:HD11	3:B:229:MET:HE2	1.99	0.45
5:D:148:LYS:HG2	5:D:150:MET:HG2	1.98	0.45
8:G:85:ARG:O	8:G:87:ARG:NH1	2.49	0.45
14:M:41:ALA:HB1	14:M:47:ALA:HB2	1.99	0.45
16:O:103:ASN:OD1	16:O:139:SER:HB2	2.17	0.45
19:R:73:LEU:O	19:R:76:GLU:HG3	2.16	0.45
34:g:34:ALA:HB2	34:g:69:VAL:HB	1.98	0.45
34:g:114:SER:HA	34:g:156:PHE:CE2	2.51	0.45
1:2:551:U:H2'	1:2:552:G:O4'	2.16	0.45
1:2:904:A:H4'	1:2:905:C:C5	2.52	0.45
1:2:948:C:H2'	1:2:949:G:H8	1.82	0.45
1:2:1330:G:H4'	1:2:1331:C:H3'	1.98	0.45
1:2:1544:C:N3	1:2:1589:A:C6	2.85	0.45
1:2:1666:C:H2'	1:2:1667:U:O4'	2.16	0.45
1:2:1704:C:H2'	1:2:1705:C:C6	2.51	0.45
1:2:1780:G:H4'	1:2:1781:A:C5	2.52	0.45
3:B:188:LEU:HD11	3:B:215:VAL:HG21	1.98	0.45
7:F:59:LYS:HG2	7:F:60:ARG:N	2.32	0.45
10:I:87:ASN:HB3	10:I:90:LEU:HG	1.98	0.45
14:M:18:LEU:O	14:M:21:VAL:HG12	2.17	0.45
18:Q:106:LYS:HA	18:Q:109:LYS:HG2	1.99	0.45
1:2:1335:G:OP2	5:D:185:LYS:HE3	2.17	0.45
1:2:1373:C:H2'	1:2:1374:C:C6	2.52	0.45
1:2:1493:C:N3	1:2:1499:U:C2	2.85	0.45
1:2:1548:G:N2	1:2:1655:C:O2'	2.50	0.45
7:F:204:ARG:HG2	30:c:63:ARG:CZ	2.47	0.45
18:Q:32:ILE:HG23	18:Q:68:ILE:HB	1.99	0.45
18:Q:96:TYR:HE2	18:Q:105:LYS:HA	1.82	0.45
19:R:99:ASP:O	19:R:103:LYS:HG3	2.17	0.45
20:S:12:ILE:CG2	20:S:14:ARG:HH21	2.29	0.45
21:T:8:ASP:OD1	21:T:9:VAL:N	2.50	0.45
1:2:106:C:OP1	1:2:431:G:O2'	2.32	0.45
1:2:685:A:H2'	1:2:686:U:O4'	2.16	0.45
1:2:1120:U:P	29:b:72:ARG:HH12	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1606:G:P	21:T:84:ARG:HH21	2.38	0.45
5:D:72:VAL:HG13	12:K:68:TYR:CD1	2.52	0.45
20:S:9:PHE:CE1	20:S:57:GLY:HA2	2.52	0.45
22:U:99:LYS:O	22:U:103:SER:OG	2.24	0.45
29:b:36:LYS:HB2	29:b:78:SER:OG	2.17	0.45
1:2:1439:A:C2	1:2:1440:C:H4'	2.52	0.44
2:A:73:ASP:HB3	2:A:120:ARG:HB2	1.99	0.44
13:L:107:LYS:HE2	13:L:107:LYS:HB3	1.80	0.44
17:P:75:VAL:HG22	17:P:93:MET:SD	2.56	0.44
20:S:54:LYS:HD2	20:S:58:GLU:HB2	1.99	0.44
27:Z:56:ASP:O	27:Z:57:LYS:HG2	2.17	0.44
28:a:66:LYS:HE2	28:a:66:LYS:HB2	1.69	0.44
34:g:5:MET:HE2	34:g:310:TRP:O	2.17	0.44
1:2:317:C:OP2	8:G:183:ARG:NH1	2.43	0.44
1:2:1258:A:N7	1:2:1661:A:N6	2.66	0.44
1:2:1618:C:H4'	17:P:41:GLN:HE21	1.82	0.44
2:A:160:ALA:HB3	23:V:66:ASP:OD2	2.16	0.44
3:B:199:LYS:HE3	3:B:199:LYS:HB3	1.49	0.44
5:D:201:LYS:HD3	5:D:201:LYS:HA	1.87	0.44
7:F:63:LYS:H	7:F:63:LYS:HG2	1.44	0.44
10:I:135:GLU:O	10:I:139:LYS:N	2.50	0.44
14:M:85:LEU:O	14:M:89:VAL:HG13	2.16	0.44
34:g:99:ARG:HD3	34:g:101:PHE:CZ	2.52	0.44
1:2:211:G:P	1:2:211:G:H8	2.41	0.44
1:2:1274:G:H21	12:K:47:LYS:HD3	1.82	0.44
2:A:138:SER:HB2	2:A:156:TYR:CE1	2.52	0.44
3:B:139:CYS:CB	3:B:172:MET:HE1	2.48	0.44
7:F:204:ARG:NH1	30:c:63:ARG:HG3	2.33	0.44
10:I:142:SER:O	10:I:146:GLN:HB2	2.18	0.44
13:L:121:GLN:N	13:L:124:ASP:OD2	2.47	0.44
21:T:49:ASP:C	21:T:51:ASN:H	2.24	0.44
28:a:41:ILE:HG12	28:a:68:TYR:CE1	2.52	0.44
34:g:208:ALA:HA	34:g:218:LEU:HA	1.99	0.44
1:2:444:G:N1	1:2:447:A:OP2	2.49	0.44
1:2:862:A:C8	24:W:107:SER:HA	2.52	0.44
1:2:1047:C:H4'	16:O:142:ARG:O	2.17	0.44
1:2:1862:G:O6	28:a:34:LYS:HE2	2.17	0.44
2:A:67:ALA:HB2	23:V:37:ALA:HB2	1.98	0.44
3:B:187:LYS:HB3	3:B:187:LYS:HE2	1.72	0.44
4:C:216:MET:HE3	4:C:216:MET:HB3	1.76	0.44
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:86:GLY:O	14:M:89:VAL:HG22	2.17	0.44
34:g:79:LEU:HB2	34:g:87:LEU:HD11	2.00	0.44
34:g:162:ASN:OD1	34:g:162:ASN:N	2.51	0.44
1:2:96:C:O2	1:2:473:A:O2'	2.33	0.44
1:2:531:A:H62	1:2:552:G:N2	2.13	0.44
1:2:952:G:N2	16:O:52:THR:HG21	2.28	0.44
1:2:1255:G:OP2	1:2:1257:G:N2	2.50	0.44
1:2:1511:U:OP1	1:2:1514:G:N1	2.44	0.44
1:2:1568:C:P	21:T:41:LYS:HZ1	2.40	0.44
2:A:59:LEU:HD23	2:A:59:LEU:HA	1.82	0.44
3:B:165:ARG:HG2	3:B:169:MET:HE2	2.00	0.44
7:F:33:ILE:HG23	7:F:34:SER:N	2.32	0.44
7:F:69:VAL:HA	7:F:72:LEU:HD21	1.99	0.44
7:F:100:ILE:HG13	7:F:101:HIS:N	2.32	0.44
10:I:147:LYS:O	10:I:151:GLU:HG3	2.17	0.44
10:I:162:LEU:HD23	10:I:162:LEU:HA	1.83	0.44
10:I:165:GLN:HB3	10:I:171:LEU:HD23	2.00	0.44
11:J:151:LEU:HD23	11:J:151:LEU:HA	1.90	0.44
20:S:33:ILE:HG21	20:S:99:LEU:HD13	1.99	0.44
34:g:18:VAL:HA	34:g:35:SER:HA	1.98	0.44
1:2:126:G:H5'	8:G:195:LYS:HZ2	1.82	0.44
1:2:1260:A:N7	1:2:1261:C:N4	2.66	0.44
1:2:1455:A:C6	1:2:1456:G:C8	3.05	0.44
2:A:70:ASN:C	2:A:70:ASN:HD22	2.25	0.44
5:D:57:ASN:OD1	5:D:57:ASN:N	2.49	0.44
5:D:185:LYS:HD2	5:D:187:LYS:NZ	2.33	0.44
6:E:73:ASP:HA	6:E:164:LEU:HD13	1.99	0.44
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.99	0.44
11:J:134:HIS:CE1	11:J:164:PRO:HD2	2.53	0.44
13:L:22:ARG:NH2	13:L:27:GLU:HG3	2.32	0.44
17:P:14:LYS:HE3	17:P:14:LYS:HB3	1.76	0.44
18:Q:32:ILE:HB	18:Q:39:LEU:HD11	2.00	0.44
22:U:21:ARG:HB3	22:U:115:THR:HG23	1.98	0.44
22:U:91:LEU:HD13	22:U:98:VAL:HG11	1.99	0.44
27:Z:92:LEU:HD11	27:Z:109:TYR:CE2	2.52	0.44
1:2:1593:C:OP1	27:Z:103:HIS:HA	2.17	0.44
10:I:123:ARG:HG2	10:I:128:LYS:NZ	2.33	0.44
32:e:33:LYS:O	32:e:37:GLN:HG3	2.18	0.44
1:2:43:U:OP2	1:2:485:A:N6	2.47	0.44
1:2:1279:C:H2'	1:2:1280:G:C8	2.53	0.44
28:a:19:GLN:OE1	28:a:19:GLN:N	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:78:ALA:HB3	34:g:90:TRP:HD1	1.83	0.44
7:F:91:ARG:HH21	7:F:95:HIS:CE1	2.35	0.44
18:Q:16:LYS:HB3	18:Q:83:ALA:HB2	1.99	0.44
22:U:68:THR:O	22:U:68:THR:OG1	2.36	0.44
34:g:277:THR:HG23	34:g:278:SER:H	1.83	0.44
34:g:297:THR:CG2	34:g:309:VAL:HG22	2.48	0.44
36:n:165:TYR:O	36:n:169:VAL:HG13	2.17	0.44
1:2:542:U:H3'	1:2:543:C:O4'	2.18	0.43
1:2:643:A:OP1	11:J:41:ARG:NH2	2.51	0.43
1:2:649:U:H1'	25:X:45:SER:HB3	2.00	0.43
1:2:1241:A:H2'	1:2:1242:U:C6	2.53	0.43
1:2:1252:C:H5''	1:2:1254:C:P	2.57	0.43
1:2:1254:C:H1'	22:U:71:GLY:N	2.27	0.43
5:D:116:ARG:NH1	5:D:117:ARG:HB2	2.33	0.43
7:F:86:LYS:O	7:F:89:THR:OG1	2.18	0.43
9:H:60:ILE:HD11	9:H:92:VAL:HG22	2.00	0.43
16:O:45:THR:OG1	16:O:49:GLY:HA2	2.18	0.43
22:U:62:ARG:HA	22:U:79:ARG:NH1	2.33	0.43
26:Y:23:MET:HE3	26:Y:23:MET:HB3	1.86	0.43
27:Z:58:LEU:O	27:Z:58:LEU:HD13	2.18	0.43
1:2:165:G:H1'	8:G:110:ASN:HD22	1.82	0.43
1:2:528:A:H2'	1:2:529:A:H8	1.83	0.43
1:2:1276:A:H61	1:2:1321:G:H1'	1.83	0.43
1:2:1581:C:OP2	1:2:1582:C:N4	2.49	0.43
1:2:1635:C:O2'	1:2:1638:G:N2	2.51	0.43
1:2:1660:C:H5	31:d:32:ARG:HB2	1.84	0.43
1:2:1705:C:H2'	1:2:1706:G:H8	1.83	0.43
4:C:75:ILE:HG21	4:C:81:ILE:CD1	2.48	0.43
5:D:46:THR:O	5:D:84:VAL:HA	2.18	0.43
5:D:109:LEU:HD13	5:D:175:VAL:HG21	2.00	0.43
7:F:126:THR:O	7:F:136:ARG:HB3	2.18	0.43
10:I:77:ARG:NH2	10:I:79:ILE:HG12	2.32	0.43
34:g:18:VAL:HG12	34:g:35:SER:HB2	2.00	0.43
1:2:630:U:H5	36:n:168:GLY:HA3	1.83	0.43
1:2:809:A:H2'	1:2:810:A:O4'	2.18	0.43
1:2:913:A:O2'	9:H:67:PRO:HD3	2.19	0.43
3:B:121:ILE:HG12	3:B:161:VAL:HG13	2.01	0.43
4:C:71:LYS:O	4:C:71:LYS:HG3	2.18	0.43
4:C:74:LYS:HB3	4:C:269:PHE:CD2	2.54	0.43
7:F:167:LYS:HA	7:F:167:LYS:HD2	1.59	0.43
9:H:107:LYS:HB2	9:H:107:LYS:HE3	1.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:90:ARG:HD2	13:L:109:MET:HE2	1.98	0.43
18:Q:53:GLU:O	18:Q:56:LEU:HD23	2.18	0.43
31:d:17:GLY:HA2	31:d:27:ARG:HD3	2.01	0.43
34:g:133:ASN:HD21	34:g:137:VAL:H	1.65	0.43
1:2:433:A:H2'	1:2:434:G:C8	2.53	0.43
1:2:913:A:N6	9:H:120:ARG:HD3	2.34	0.43
1:2:1225:U:H5	1:2:1641:A:C8	2.37	0.43
1:2:1496:U:O4	1:2:1498:A:N6	2.51	0.43
2:A:140:VAL:HG23	2:A:142:LEU:HB2	2.01	0.43
10:I:139:LYS:HB2	10:I:139:LYS:HE3	1.88	0.43
14:M:71:GLU:HG3	33:f:114:ILE:HD11	2.00	0.43
18:Q:35:ASN:HD21	18:Q:72:VAL:H	1.65	0.43
18:Q:43:GLU:HB2	18:Q:44:PRO:HD3	2.01	0.43
19:R:76:GLU:O	19:R:79:GLU:HG3	2.19	0.43
21:T:39:LEU:HD13	21:T:99:VAL:HG21	2.01	0.43
21:T:99:VAL:O	21:T:103:VAL:HG23	2.19	0.43
22:U:65:THR:HG23	31:d:40:ARG:HG2	1.99	0.43
34:g:191:HIS:NE2	34:g:195:LEU:HD11	2.34	0.43
1:2:145:G:O6	8:G:178:ARG:NH2	2.52	0.43
1:2:434:G:OP1	10:I:23:LYS:HG2	2.19	0.43
1:2:908:A:C5	1:2:909:G:C8	3.07	0.43
1:2:956:G:O5'	16:O:60:MET:HG2	2.19	0.43
1:2:1449:G:H2'	1:2:1450:G:C8	2.53	0.43
8:G:181:THR:HG22	8:G:182:PRO:HD2	2.01	0.43
16:O:75:MET:HE2	16:O:75:MET:HB3	1.81	0.43
16:O:119:LEU:HD23	16:O:119:LEU:HA	1.88	0.43
18:Q:86:GLN:HG2	18:Q:90:LYS:HD3	1.99	0.43
22:U:39:LEU:HD13	22:U:39:LEU:HA	1.90	0.43
22:U:81:GLN:NE2	22:U:83:ARG:H	2.15	0.43
23:V:1:MET:O	23:V:9:VAL:HG22	2.18	0.43
1:2:453:C:O2'	8:G:92:ARG:O	2.31	0.43
1:2:682:U:O2'	24:W:4:MET:SD	2.73	0.43
1:2:1258:A:OP2	1:2:1659:U:H1'	2.18	0.43
4:C:74:LYS:HD2	4:C:269:PHE:CD1	2.53	0.43
4:C:74:LYS:HE3	4:C:272:HIS:CE1	2.54	0.43
5:D:37:VAL:HG22	5:D:50:ILE:HG13	2.01	0.43
5:D:163:PRO:HA	5:D:166:TYR:CZ	2.54	0.43
9:H:46:THR:HG21	9:H:97:GLN:HG2	2.00	0.43
15:N:13:GLN:HG3	29:b:21:LYS:HE3	2.00	0.43
17:P:33:LEU:HD23	17:P:37:TYR:HD1	1.83	0.43
18:Q:101:ASP:HA	34:g:56:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:14:ARG:O	19:R:18:GLU:HB2	2.18	0.43
20:S:39:ARG:CZ	20:S:39:ARG:HB3	2.48	0.43
21:T:102:ARG:HA	21:T:105:GLN:OE1	2.19	0.43
22:U:46:LYS:HE2	22:U:48:LEU:HD11	1.99	0.43
23:V:28:ASP:OD2	23:V:31:SER:HB3	2.19	0.43
26:Y:6:THR:HB	26:Y:28:LEU:HB2	2.01	0.43
1:2:65:C:O2'	8:G:160:LYS:HE3	2.19	0.43
1:2:953:C:H2'	1:2:954:U:C6	2.54	0.43
3:B:92:GLN:O	3:B:95:ASN:HB2	2.19	0.43
3:B:112:SER:O	3:B:115:LYS:NZ	2.52	0.43
5:D:63:GLY:O	5:D:67:ARG:HG2	2.19	0.43
5:D:76:ARG:HB2	12:K:68:TYR:HE1	1.83	0.43
9:H:36:LEU:HD13	9:H:75:ILE:HD12	1.99	0.43
15:N:89:TYR:CE2	15:N:150:VAL:HG13	2.53	0.43
16:O:93:LEU:O	16:O:127:GLY:N	2.40	0.43
1:2:1025:U:H2'	1:2:1026:C:O4'	2.18	0.43
1:2:1087:A:OP1	28:a:3:LYS:HD2	2.19	0.43
1:2:1667:U:H5'	18:Q:141:TYR:CE2	2.54	0.43
2:A:69:GLU:OE1	2:A:69:GLU:N	2.50	0.43
7:F:201:LYS:HE3	7:F:201:LYS:CA	2.39	0.43
10:I:144:LYS:O	10:I:147:LYS:HG2	2.19	0.43
12:K:1:MET:SD	12:K:51:SER:HB3	2.59	0.43
20:S:75:ARG:HH22	20:S:84:LEU:HD12	1.84	0.43
27:Z:53:ALA:HB2	27:Z:77:LEU:HD11	2.00	0.43
33:f:104:LYS:HD3	33:f:131:PHE:CD2	2.54	0.43
34:g:297:THR:HG21	34:g:309:VAL:HG22	2.01	0.43
1:2:1139:C:H2'	1:2:1140:G:O4'	2.18	0.43
7:F:141:VAL:HB	7:F:146:ARG:HG3	2.01	0.43
10:I:177:SER:O	10:I:179:PRO:HD3	2.18	0.43
26:Y:44:LEU:HD13	26:Y:44:LEU:HA	1.85	0.43
34:g:127:LYS:HE3	34:g:127:LYS:HB2	1.80	0.43
1:2:1206:G:H1'	1:2:1834:A:C4	2.54	0.43
2:A:12:GLU:HG2	19:R:114:LEU:HD21	2.01	0.43
2:A:143:PRO:HG3	23:V:32:ILE:HB	2.00	0.43
4:C:129:ALA:C	4:C:216:MET:HE1	2.44	0.43
12:K:47:LYS:HA	12:K:50:GLN:HG2	2.01	0.43
16:O:53:ILE:HG23	16:O:88:LEU:HD13	2.01	0.43
17:P:130:ARG:HD3	17:P:130:ARG:N	2.32	0.43
18:Q:17:LYS:O	18:Q:126:ARG:NH1	2.40	0.43
18:Q:58:LEU:HD11	18:Q:63:PHE:CD2	2.54	0.43
29:b:36:LYS:HE2	29:b:36:LYS:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:249:CYS:HB2	34:g:258:ILE:HG12	2.00	0.43
1:2:387:C:OP2	10:I:10:LYS:HE3	2.19	0.42
1:2:476:A:N3	1:2:488:U:O2'	2.34	0.42
1:2:533:A:H2'	1:2:534:G:C8	2.54	0.42
1:2:961:G:OP1	16:O:149:ARG:NH2	2.47	0.42
1:2:1305:C:H2'	1:2:1306:U:H5	1.83	0.42
1:2:1319:U:OP1	1:2:1505:U:N3	2.52	0.42
1:2:1533:A:C8	1:2:1604:G:H1'	2.54	0.42
1:2:1542:C:H5'	21:T:62:ARG:HH21	1.84	0.42
1:2:1702:G:H2'	1:2:1703:C:O4'	2.19	0.42
1:2:1844:U:H2'	1:2:1845:A:C8	2.54	0.42
3:B:100:PHE:HB3	3:B:181:LEU:HD21	1.99	0.42
4:C:75:ILE:HG21	4:C:81:ILE:HD12	2.01	0.42
8:G:225:GLN:HA	8:G:228:ILE:HG22	2.01	0.42
9:H:51:ILE:HG21	9:H:179:LYS:HG2	2.00	0.42
34:g:260:ASP:HB2	34:g:264:LYS:H	1.84	0.42
1:2:398:A:OP1	1:2:399:C:O2'	2.31	0.42
1:2:1270:G:N2	1:2:1298:G:N7	2.67	0.42
2:A:2:SER:OG	23:V:80:SER:OG	2.36	0.42
3:B:82:ARG:NH1	3:B:191:ASP:OD2	2.52	0.42
3:B:97:LEU:HG	3:B:232:HIS:ND1	2.34	0.42
4:C:172:ASN:ND2	11:J:95:ASP:OD2	2.46	0.42
4:C:254:ASP:HB2	23:V:1:MET:HG2	2.01	0.42
16:O:113:GLN:NE2	28:a:45:VAL:HA	2.30	0.42
18:Q:52:LEU:O	18:Q:55:VAL:HG22	2.20	0.42
1:2:495:U:O2'	6:E:27:PHE:O	2.37	0.42
1:2:1272:C:H4'	12:K:2:LEU:HD12	2.01	0.42
1:2:1348:G:C8	1:2:1349:G:C8	3.07	0.42
1:2:1388:A:H2'	1:2:1389:C:H5'	1.99	0.42
1:2:1667:U:H2'	1:2:1668:U:C6	2.53	0.42
3:B:164:ILE:HG22	3:B:168:MET:HE3	2.01	0.42
5:D:24:PHE:O	5:D:28:GLU:HG3	2.19	0.42
5:D:123:LEU:HD11	5:D:154:ASP:HB2	2.01	0.42
7:F:20:PHE:HD2	7:F:23:TRP:CD1	2.37	0.42
10:I:153:LYS:O	10:I:156:ALA:HB2	2.19	0.42
14:M:21:VAL:HG23	14:M:112:LYS:NZ	2.34	0.42
24:W:39:THR:O	24:W:43:LYS:HG2	2.19	0.42
34:g:133:ASN:HD21	34:g:137:VAL:N	2.18	0.42
1:2:595:U:H2'	1:2:596:U:C6	2.54	0.42
1:2:643:A:OP1	11:J:38:ARG:NH1	2.52	0.42
1:2:1330:G:N2	1:2:1333:U:OP2	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1471:C:H2'	1:2:1472:C:O4'	2.20	0.42
4:C:203:GLY:H	4:C:221:ASP:HB3	1.84	0.42
7:F:75:SER:C	7:F:77:MET:H	2.28	0.42
7:F:138:ALA:HB3	7:F:204:ARG:HG3	2.01	0.42
16:O:56:VAL:HG22	16:O:81:VAL:CG2	2.48	0.42
16:O:74:ALA:HB1	16:O:115:ALA:HB2	2.02	0.42
20:S:58:GLU:HG3	27:Z:50:PHE:HE2	1.84	0.42
34:g:57:ARG:NH2	34:g:59:LEU:HD22	2.34	0.42
1:2:609:U:H2'	1:2:610:G:H8	1.83	0.42
1:2:1804:U:H4'	1:2:1805:G:OP1	2.19	0.42
3:B:178:THR:HG23	3:B:179:ASN:OD1	2.19	0.42
9:H:76:GLN:HG2	9:H:135:PHE:CD2	2.54	0.42
18:Q:21:ALA:HB2	18:Q:72:VAL:HG22	2.01	0.42
19:R:80:ARG:HD3	19:R:80:ARG:HA	1.84	0.42
34:g:3:GLU:HG3	34:g:247:TRP:CH2	2.54	0.42
1:2:96:C:H2'	1:2:97:U:C6	2.54	0.42
1:2:375:U:H2'	1:2:376:A:C8	2.54	0.42
1:2:1445:U:H4'	22:U:57:PRO:HG3	2.02	0.42
1:2:1526:G:H2'	1:2:1528:G:O6	2.19	0.42
3:B:136:ARG:HB3	3:B:216:LYS:HG3	2.01	0.42
7:F:79:HIS:CE1	7:F:156:THR:HG23	2.54	0.42
10:I:34:ALA:HB2	10:I:56:ARG:HD3	2.01	0.42
17:P:51:ARG:HH12	31:d:4:GLN:HB3	1.85	0.42
19:R:67:ARG:NH1	19:R:67:ARG:HG3	2.35	0.42
26:Y:53:ASP:OD1	26:Y:54:VAL:HG13	2.19	0.42
34:g:260:ASP:HB3	34:g:262:GLU:H	1.84	0.42
1:2:576:A:H4'	1:2:577:U:H5	1.84	0.42
1:2:682:U:H2'	1:2:683:G:O4'	2.19	0.42
1:2:909:G:C2	1:2:910:G:C5	3.07	0.42
5:D:75:LYS:NZ	12:K:20:VAL:HB	2.35	0.42
9:H:148:LEU:HA	9:H:148:LEU:HD12	1.84	0.42
1:2:51:U:H2'	1:2:52:G:C8	2.54	0.42
1:2:384:U:H5'	13:L:133:PRO:O	2.20	0.42
1:2:1285:G:C6	14:M:36:ARG:HB2	2.55	0.42
1:2:1666:C:O2'	1:2:1667:U:P	2.77	0.42
2:A:70:ASN:HB3	2:A:73:ASP:OD2	2.19	0.42
6:E:192:ILE:HB	6:E:243:GLY:HA3	2.00	0.42
8:G:133:LEU:HD12	8:G:133:LEU:HA	1.76	0.42
18:Q:21:ALA:HA	18:Q:71:ARG:O	2.19	0.42
19:R:58:MET:HA	19:R:61:ILE:HG22	2.02	0.42
22:U:67:LYS:HA	22:U:67:LYS:HD2	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:21:CYS:HB2	31:d:37:ASN:C	2.45	0.42
1:2:1300:U:C2	31:d:5:GLN:HG3	2.55	0.42
1:2:1447:G:H2'	1:2:1448:A:C8	2.54	0.42
1:2:1659:U:OP1	31:d:31:ILE:HG23	2.20	0.42
1:2:1723:G:H2'	1:2:1724:A:H8	1.85	0.42
1:2:1780:G:H4'	1:2:1781:A:N7	2.35	0.42
4:C:94:ILE:HG22	4:C:102:LEU:HD11	2.02	0.42
5:D:109:LEU:HD11	5:D:115:VAL:HB	2.01	0.42
5:D:158:ILE:HG12	5:D:189:MET:HE3	2.02	0.42
6:E:19:MET:HE3	6:E:19:MET:HB2	1.82	0.42
7:F:127:ARG:HA	7:F:136:ARG:HB3	2.02	0.42
9:H:76:GLN:HG2	9:H:135:PHE:HD2	1.85	0.42
10:I:129:LEU:HD11	10:I:134:GLU:HB3	2.01	0.42
16:O:20:GLN:H	16:O:20:GLN:HG2	1.72	0.42
18:Q:30:GLY:HA3	18:Q:64:ALA:HA	2.02	0.42
21:T:88:MET:SD	21:T:89:PRO:HD2	2.60	0.42
22:U:22:ILE:HD11	22:U:89:ILE:HB	2.00	0.42
22:U:54:VAL:HB	22:U:88:LEU:HB2	2.02	0.42
26:Y:13:MET:HE2	26:Y:13:MET:HB3	1.93	0.42
26:Y:49:LYS:HE2	26:Y:49:LYS:HB2	1.75	0.42
1:2:491:C:C2	1:2:510:G:N2	2.88	0.42
1:2:1546:G:N7	1:2:1654:G:N2	2.68	0.42
1:2:1618:C:N4	31:d:12:ARG:HA	2.35	0.42
8:G:145:PHE:HB3	8:G:147:LEU:HD23	2.01	0.42
23:V:19:ALA:HB2	23:V:68:SER:HB3	2.02	0.42
1:2:54:A:OP1	26:Y:111:LYS:NZ	2.28	0.41
1:2:190:G:N2	1:2:209:A:OP2	2.41	0.41
1:2:1204:A:H5''	4:C:117:ARG:HH11	1.84	0.41
4:C:103:LYS:HB3	4:C:103:LYS:HE3	1.78	0.41
12:K:14:LEU:O	12:K:17:LYS:HG2	2.20	0.41
21:T:40:ALA:HA	21:T:96:SER:H	1.85	0.41
24:W:101:PHE:HA	24:W:113:HIS:CE1	2.55	0.41
34:g:57:ARG:HH21	34:g:59:LEU:HD22	1.85	0.41
1:2:191:A:H62	1:2:208:G:H21	1.67	0.41
1:2:879:C:C2'	1:2:880:G:H4'	2.49	0.41
1:2:1121:G:O2'	3:B:204:ILE:O	2.25	0.41
1:2:1230:C:N4	1:2:1529:C:O2	2.54	0.41
1:2:1258:A:H61	1:2:1660:C:H4'	1.85	0.41
1:2:1493:C:O4'	1:2:1496:U:H5	2.03	0.41
2:A:190:SER:OG	2:A:191:ARG:N	2.53	0.41
7:F:44:LYS:HD3	7:F:44:LYS:HA	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:72:LEU:HD12	7:F:73:THR:N	2.35	0.41
11:J:113:GLN:CD	11:J:154:GLN:HE22	2.27	0.41
12:K:72:THR:OG1	12:K:73:ASN:N	2.53	0.41
17:P:68:PRO:HA	17:P:69:PRO:HD3	1.93	0.41
18:Q:73:LYS:HA	18:Q:73:LYS:HD3	1.72	0.41
18:Q:94:ALA:O	18:Q:98:LYS:HG2	2.20	0.41
19:R:70:SER:C	19:R:71:ILE:HD12	2.46	0.41
19:R:107:LYS:HE3	19:R:107:LYS:HB2	1.74	0.41
34:g:185:LYS:HG3	34:g:186:THR:N	2.35	0.41
34:g:194:TYR:CE1	34:g:196:ASN:HB2	2.55	0.41
1:2:340:C:H2'	1:2:341:C:H6	1.85	0.41
1:2:441:C:H2'	1:2:442:C:C6	2.56	0.41
1:2:674:C:H2'	1:2:675:U:C6	2.55	0.41
1:2:1288:U:H3'	1:2:1289:U:C6	2.55	0.41
1:2:1617:G:H8	17:P:43:ARG:HH22	1.68	0.41
4:C:82:TYR:OH	4:C:162:ILE:HG22	2.21	0.41
5:D:195:THR:CG2	5:D:199:GLY:H	2.23	0.41
21:T:124:THR:HG23	21:T:127:GLY:CA	2.49	0.41
24:W:62:VAL:HG11	29:b:8:LEU:HG	2.00	0.41
24:W:83:LEU:HA	24:W:83:LEU:HD23	1.79	0.41
26:Y:50:THR:OG1	26:Y:51:THR:N	2.52	0.41
1:2:1298:G:N2	1:2:1299:A:H61	2.17	0.41
1:2:1338:G:H2'	1:2:1339:U:C6	2.55	0.41
1:2:1649:U:O2'	1:2:1650:A:OP1	2.33	0.41
1:2:1753:C:C5'	1:2:1754:G:H5''	2.50	0.41
3:B:24:PRO:O	3:B:28:LYS:HG3	2.19	0.41
5:D:103:GLU:HG2	5:D:107:TYR:CD1	2.56	0.41
27:Z:69:THR:O	27:Z:73:VAL:HG23	2.19	0.41
29:b:67:THR:HG21	29:b:72:ARG:HE	1.86	0.41
34:g:47:ARG:NH2	34:g:52:TYR:O	2.53	0.41
1:2:959:G:O6	16:O:65:ASP:HB3	2.20	0.41
1:2:963:A:H2'	1:2:964:A:C8	2.55	0.41
1:2:1189:A:H4'	1:2:1190:A:OP1	2.21	0.41
1:2:1560:U:N3	1:2:1574:C:O2	2.53	0.41
1:2:1845:A:H2'	1:2:1846:G:H8	1.86	0.41
4:C:86:LEU:HD11	4:C:265:PRO:HG2	2.02	0.41
10:I:113:TYR:CE1	10:I:119:LEU:HB2	2.55	0.41
21:T:126:GLN:O	21:T:129:ARG:HB2	2.20	0.41
30:c:10:LYS:HE2	30:c:34:PHE:CE1	2.56	0.41
34:g:129:ILE:HD11	34:g:151:VAL:HG11	2.03	0.41
34:g:165:ILE:HG13	34:g:177:TRP:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:192:C:H2'	1:2:193:C:H6	1.86	0.41
1:2:218:U:H5	10:I:184:ARG:HH12	1.67	0.41
1:2:1683:C:H2'	1:2:1684:C:H2'	2.02	0.41
3:B:139:CYS:HB3	3:B:172:MET:CE	2.47	0.41
4:C:133:TYR:CZ	4:C:216:MET:HG2	2.55	0.41
6:E:183:VAL:HG13	6:E:220:THR:HG21	2.03	0.41
7:F:77:MET:O	7:F:77:MET:HG2	2.20	0.41
15:N:114:ARG:HD3	15:N:114:ARG:HA	1.74	0.41
17:P:57:LEU:HA	17:P:60:LEU:HG	2.02	0.41
18:Q:76:GLY:O	18:Q:80:GLN:HG3	2.20	0.41
32:e:44:ASN:ND2	32:e:44:ASN:O	2.43	0.41
1:2:65:C:C5	8:G:174:PRO:HB3	2.56	0.41
1:2:184:G:H2'	1:2:185:G:H8	1.84	0.41
1:2:491:C:C2	1:2:510:G:N1	2.89	0.41
1:2:868:G:O2'	1:2:869:A:OP1	2.33	0.41
1:2:1100:A:OP1	19:R:132:ARG:NH1	2.54	0.41
1:2:1299:A:C8	17:P:59:ARG:HB3	2.56	0.41
1:2:1469:A:H2'	1:2:1470:C:C6	2.56	0.41
1:2:1510:G:O2'	1:2:1511:U:O4'	2.39	0.41
1:2:1602:U:H2'	1:2:1603:G:N7	2.36	0.41
1:2:1809:A:H8	1:2:1810:U:H5	1.68	0.41
2:A:196:GLU:H	2:A:196:GLU:CD	2.28	0.41
3:B:217:MET:HE2	3:B:220:LYS:HG3	2.03	0.41
5:D:18:LYS:HA	5:D:21:LEU:HG	2.01	0.41
8:G:44:GLU:HG3	8:G:121:ILE:HG13	2.02	0.41
9:H:83:LEU:HB3	9:H:92:VAL:HG21	2.03	0.41
11:J:33:GLY:HA3	32:e:38:TYR:CG	2.56	0.41
17:P:20:VAL:HG13	17:P:24:GLN:CB	2.49	0.41
19:R:20:TYR:CD2	19:R:38:ILE:HB	2.55	0.41
1:2:381:C:OP1	10:I:31:ARG:NH2	2.54	0.41
1:2:1347:U:H2'	1:2:1348:G:N3	2.36	0.41
1:2:1551:U:H2'	1:2:1578:U:H3	1.86	0.41
1:2:1665:G:N2	21:T:87:VAL:HG11	2.35	0.41
1:2:1752:C:N4	1:2:1782:G:C2	2.89	0.41
2:A:2:SER:O	2:A:63:ARG:NH2	2.53	0.41
2:A:124:VAL:HG21	2:A:134:LEU:HD11	2.03	0.41
3:B:48:LEU:HD23	3:B:48:LEU:H	1.86	0.41
4:C:106:VAL:HG22	4:C:128:VAL:HG22	2.02	0.41
4:C:110:MET:HE3	4:C:110:MET:HB2	1.81	0.41
5:D:178:ARG:HD2	5:D:178:ARG:HA	1.84	0.41
21:T:56:ARG:NH2	21:T:78:ILE:HB	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:116:ASP:N	21:T:116:ASP:OD1	2.54	0.41
1:2:381:C:H5'	10:I:48:VAL:HB	2.03	0.41
1:2:1238:U:N3	17:P:124:LYS:O	2.32	0.41
1:2:1567:G:H21	1:2:1567:G:P	2.43	0.41
3:B:30:TRP:CE3	16:O:19:PRO:HG3	2.55	0.41
3:B:106:THR:OG1	3:B:108:ASP:OD1	2.31	0.41
4:C:83:LEU:O	23:V:15:ARG:HD3	2.20	0.41
4:C:166:ARG:HB2	4:C:248:TYR:CD2	2.56	0.41
4:C:270:THR:O	4:C:274:VAL:HG23	2.20	0.41
5:D:17:PHE:HD1	5:D:77:PHE:CD2	2.39	0.41
6:E:86:PHE:O	6:E:87:MET:HB2	2.21	0.41
7:F:41:VAL:HA	7:F:46:ALA:HB2	2.02	0.41
7:F:123:GLU:OE2	30:c:59:LEU:HD22	2.21	0.41
7:F:167:LYS:HZ2	7:F:168:THR:H	1.69	0.41
8:G:110:ASN:OD1	8:G:110:ASN:N	2.54	0.41
10:I:82:VAL:HG11	10:I:103:LEU:HG	2.02	0.41
15:N:80:LEU:HD23	15:N:80:LEU:H	1.86	0.41
16:O:71:PRO:O	16:O:114:SER:OG	2.33	0.41
18:Q:50:LYS:HB2	18:Q:50:LYS:HE2	1.84	0.41
19:R:28:PHE:C	19:R:31:ASN:H	2.28	0.41
21:T:115:LYS:HE2	21:T:115:LYS:HB2	1.86	0.41
21:T:139:ALA:O	21:T:144:LYS:N	2.49	0.41
22:U:56:MET:HG3	22:U:86:LYS:HD2	2.03	0.41
31:d:31:ILE:HD13	31:d:31:ILE:HA	1.90	0.41
1:2:300:U:H2'	1:2:301:A:C8	2.56	0.41
1:2:1070:A:H2'	1:2:1071:G:O4'	2.20	0.41
1:2:1284:A:H61	14:M:93:LYS:HB2	1.86	0.41
7:F:16:ASP:OD1	7:F:16:ASP:N	2.54	0.41
9:H:118:ARG:HD3	9:H:118:ARG:HA	1.86	0.41
12:K:55:ARG:HB3	12:K:57:TYR:CE2	2.55	0.41
16:O:125:LYS:HB3	28:a:58:VAL:HG13	2.03	0.41
18:Q:33:LYS:HE3	18:Q:35:ASN:N	2.36	0.41
18:Q:89:SER:HB3	18:Q:112:LEU:HD11	2.03	0.41
22:U:31:SER:O	22:U:35:VAL:HG23	2.21	0.41
30:c:10:LYS:HG3	30:c:58:LEU:HG	2.03	0.41
34:g:165:ILE:HD11	34:g:177:TRP:HB2	2.02	0.41
1:2:106:C:H5''	1:2:431:G:O2'	2.21	0.40
1:2:416:U:H2'	1:2:417:C:O4'	2.21	0.40
1:2:652:U:H2'	1:2:653:A:C8	2.56	0.40
1:2:1093:A:H2'	1:2:1094:C:C6	2.56	0.40
1:2:1218:C:H2'	1:2:1219:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1259:A:O2'	1:2:1264:C:OP1	2.28	0.40
1:2:1300:U:C4	17:P:55:SER:HB2	2.56	0.40
1:2:1654:G:H2'	1:2:1655:C:C6	2.56	0.40
1:2:1703:C:H2'	1:2:1704:C:O4'	2.21	0.40
10:I:79:ILE:HD11	10:I:105:ASP:OD1	2.20	0.40
16:O:63:LYS:HB2	16:O:63:LYS:HE3	1.79	0.40
24:W:84:LYS:HB2	24:W:84:LYS:HE3	1.75	0.40
25:X:88:ASP:OD2	32:e:13:ARG:HB2	2.20	0.40
1:2:1271:C:H4'	31:d:7:TYR:CD1	2.56	0.40
1:2:1350:U:C2	1:2:1351:G:C8	3.09	0.40
1:2:1453:C:O2'	19:R:52:GLY:HA3	2.20	0.40
1:2:1657:G:H1	1:2:1667:U:H3	1.67	0.40
1:2:1751:C:H1'	1:2:1784:G:H22	1.86	0.40
2:A:89:LYS:O	2:A:92:ALA:HB3	2.21	0.40
5:D:135:GLU:OE2	5:D:137:VAL:HB	2.21	0.40
7:F:142:SER:OG	30:c:48:GLY:HA3	2.20	0.40
9:H:28:LEU:HA	9:H:28:LEU:HD23	1.85	0.40
9:H:106:ARG:HH11	9:H:106:ARG:HG2	1.86	0.40
10:I:190:LEU:HD22	10:I:194:GLU:HG2	2.03	0.40
12:K:6:LYS:O	12:K:9:ILE:HG13	2.21	0.40
18:Q:81:ILE:C	18:Q:83:ALA:H	2.29	0.40
20:S:55:ARG:HH22	27:Z:48:VAL:HA	1.85	0.40
26:Y:113:ARG:HB3	26:Y:125:VAL:HG11	2.02	0.40
28:a:75:VAL:O	28:a:78:VAL:HG12	2.21	0.40
34:g:286:CYS:HB2	34:g:302:TYR:CE1	2.56	0.40
1:2:944:A:H5''	16:O:134:PRO:HB2	2.04	0.40
1:2:1517:G:H2'	1:2:1517:G:N3	2.37	0.40
3:B:167:LYS:HD3	3:B:170:GLU:OE1	2.22	0.40
4:C:69:LEU:O	4:C:74:LYS:HB2	2.21	0.40
4:C:132:ASP:C	4:C:134:ASN:H	2.29	0.40
12:K:66:HIS:NE2	31:d:22:ARG:HB2	2.36	0.40
16:O:60:MET:HE2	16:O:60:MET:HB2	1.72	0.40
19:R:71:ILE:HG22	19:R:72:LYS:N	2.37	0.40
20:S:64:VAL:HA	20:S:67:VAL:HG12	2.03	0.40
26:Y:15:ASN:ND2	26:Y:18:LEU:HB2	2.36	0.40
29:b:8:LEU:HD23	29:b:8:LEU:HA	1.83	0.40
34:g:83:TRP:HA	34:g:107:ASP:CG	2.45	0.40
35:h:2:ARG:HD3	35:h:5:TRP:NE1	2.37	0.40
1:2:14:C:O2'	1:2:668:A:N1	2.53	0.40
1:2:296:U:O2'	6:E:131:VAL:O	2.23	0.40
1:2:383:G:O2'	13:L:133:PRO:O	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:881:G:O6	1:2:904:A:O2'	2.25	0.40
1:2:989:C:OP2	3:B:155:TYR:OH	2.22	0.40
1:2:1660:C:H5''	31:d:32:ARG:HH11	1.87	0.40
3:B:175:GLU:OE2	3:B:175:GLU:HA	2.21	0.40
3:B:208:HIS:C	3:B:208:HIS:ND1	2.79	0.40
5:D:158:ILE:HG23	5:D:189:MET:HE1	2.03	0.40
5:D:160:SER:C	5:D:164:VAL:HG21	2.46	0.40
6:E:44:LEU:HD12	6:E:44:LEU:HA	1.84	0.40
6:E:104:ASP:HB2	6:E:110:ALA:HB2	2.04	0.40
19:R:72:LYS:HE3	19:R:72:LYS:HB2	1.97	0.40
20:S:75:ARG:NH2	20:S:84:LEU:HD12	2.36	0.40
24:W:9:ASP:OD1	24:W:9:ASP:N	2.54	0.40
29:b:65:GLN:OE1	29:b:65:GLN:HA	2.20	0.40
1:2:455:A:H2'	1:2:456:C:H6	1.83	0.40
1:2:1035:A:H2'	1:2:1036:A:O4'	2.21	0.40
1:2:1058:A:H2'	1:2:1059:G:C8	2.57	0.40
1:2:1445:U:H1'	1:2:1580:A:N6	2.37	0.40
1:2:1467:C:H2'	1:2:1468:C:C6	2.57	0.40
1:2:1566:G:O6	21:T:97:LYS:NZ	2.35	0.40
1:2:1576:G:N3	1:2:1582:C:O2'	2.55	0.40
1:2:1718:G:H4'	1:2:1816:G:N2	2.37	0.40
7:F:56:TYR:O	7:F:62:ARG:HB2	2.22	0.40
8:G:21:GLU:O	8:G:25:ARG:HG2	2.21	0.40
12:K:3:MET:CG	12:K:44:HIS:HB3	2.49	0.40
20:S:36:VAL:HG12	20:S:41:ALA:HB2	2.03	0.40
30:c:67:ARG:CZ	30:c:68:LEU:HG	2.52	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	A	211/295 (72%)	206 (98%)	4 (2%)	1 (0%)	24	51
3	B	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
4	C	216/293 (74%)	206 (95%)	10 (5%)	0	100	100
5	D	223/243 (92%)	206 (92%)	17 (8%)	0	100	100
6	E	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
7	F	187/204 (92%)	167 (89%)	19 (10%)	1 (0%)	24	51
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	177 (96%)	7 (4%)	0	100	100
10	I	203/208 (98%)	189 (93%)	14 (7%)	0	100	100
11	J	178/194 (92%)	168 (94%)	10 (6%)	0	100	100
12	K	95/165 (58%)	86 (90%)	9 (10%)	0	100	100
13	L	149/158 (94%)	144 (97%)	4 (3%)	1 (1%)	18	44
14	M	119/132 (90%)	107 (90%)	10 (8%)	2 (2%)	7	23
15	N	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
16	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
17	P	124/145 (86%)	109 (88%)	15 (12%)	0	100	100
18	Q	136/146 (93%)	123 (90%)	13 (10%)	0	100	100
19	R	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
20	S	141/152 (93%)	123 (87%)	17 (12%)	1 (1%)	18	44
21	T	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
22	U	99/119 (83%)	88 (89%)	11 (11%)	0	100	100
23	V	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
24	W	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
25	X	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
26	Y	122/130 (94%)	119 (98%)	3 (2%)	0	100	100
27	Z	70/125 (56%)	61 (87%)	9 (13%)	0	100	100
28	a	97/101 (96%)	93 (96%)	3 (3%)	1 (1%)	12	35
29	b	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
30	c	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
31	d	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
32	e	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
33	f	72/74 (97%)	61 (85%)	10 (14%)	1 (1%)	9	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	g	312/315 (99%)	285 (91%)	26 (8%)	1 (0%)	36	62
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	28/180 (16%)	25 (89%)	3 (11%)	0	100	100
All	All	4830/5567 (87%)	4534 (94%)	287 (6%)	9 (0%)	44	70

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE
7	F	33	ILE
14	M	109	VAL
14	M	110	VAL
28	a	63	VAL
13	L	32	LYS
20	S	91	LYS
34	g	235	ILE
33	f	108	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	179/243 (74%)	175 (98%)	4 (2%)	45	75
3	B	194/231 (84%)	188 (97%)	6 (3%)	35	66
4	C	184/225 (82%)	178 (97%)	6 (3%)	33	65
5	D	189/202 (94%)	177 (94%)	12 (6%)	16	42
6	E	224/225 (100%)	213 (95%)	11 (5%)	22	51
7	F	159/170 (94%)	146 (92%)	13 (8%)	10	30
8	G	200/218 (92%)	193 (96%)	7 (4%)	32	63
9	H	167/174 (96%)	161 (96%)	6 (4%)	31	63
10	I	178/180 (99%)	170 (96%)	8 (4%)	24	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	J	160/168 (95%)	155 (97%)	5 (3%)	35	66
12	K	88/136 (65%)	84 (96%)	4 (4%)	24	55
13	L	135/142 (95%)	135 (100%)	0	100	100
14	M	102/108 (94%)	98 (96%)	4 (4%)	28	60
15	N	130/131 (99%)	120 (92%)	10 (8%)	12	33
16	O	105/119 (88%)	99 (94%)	6 (6%)	18	47
17	P	112/130 (86%)	108 (96%)	4 (4%)	31	63
18	Q	114/121 (94%)	112 (98%)	2 (2%)	51	78
19	R	119/122 (98%)	114 (96%)	5 (4%)	26	58
20	S	124/132 (94%)	118 (95%)	6 (5%)	23	53
21	T	114/115 (99%)	106 (93%)	8 (7%)	14	37
22	U	93/107 (87%)	86 (92%)	7 (8%)	12	34
23	V	66/67 (98%)	64 (97%)	2 (3%)	36	67
24	W	112/113 (99%)	106 (95%)	6 (5%)	20	49
25	X	113/115 (98%)	109 (96%)	4 (4%)	32	63
26	Y	108/112 (96%)	106 (98%)	2 (2%)	50	77
27	Z	64/103 (62%)	59 (92%)	5 (8%)	11	32
28	a	87/89 (98%)	82 (94%)	5 (6%)	18	47
29	b	74/74 (100%)	72 (97%)	2 (3%)	39	70
30	c	55/55 (100%)	52 (94%)	3 (6%)	19	48
31	d	48/48 (100%)	48 (100%)	0	100	100
32	e	45/45 (100%)	42 (93%)	3 (7%)	15	39
33	f	67/67 (100%)	66 (98%)	1 (2%)	57	82
34	g	272/273 (100%)	256 (94%)	16 (6%)	18	45
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	26/147 (18%)	24 (92%)	2 (8%)	12	33
All	All	4228/4731 (89%)	4043 (96%)	185 (4%)	27	56

All (185) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	28	THR
2	A	38	ILE

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Mol	Chain	Res	Type
2	A	52	LYS
2	A	190	SER
3	B	50	THR
3	B	91	VAL
3	B	98	THR
3	B	154	SER
3	B	182	LYS
3	B	208	HIS
4	C	162	ILE
4	C	176	LYS
4	C	232	THR
4	C	248	TYR
4	C	260	VAL
4	C	264	SER
5	D	37	VAL
5	D	57	ASN
5	D	85	GLU
5	D	105	LEU
5	D	113	LEU
5	D	120	TYR
5	D	142	LEU
5	D	148	LYS
5	D	156	LEU
5	D	176	LEU
5	D	178	ARG
5	D	223	ILE
6	E	91	SER
6	E	101	LEU
6	E	105	THR
6	E	126	VAL
6	E	159	THR
6	E	177	THR
6	E	199	GLU
6	E	204	SER
6	E	220	THR
6	E	236	ILE
6	E	256	LEU
7	F	49	LEU
7	F	68	ILE
7	F	69	VAL
7	F	85	LYS
7	F	101	HIS

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Mol	Chain	Res	Type
7	F	102	LEU
7	F	104	THR
7	F	116	ILE
7	F	134	VAL
7	F	139	VAL
7	F	167	LYS
7	F	169	ILE
7	F	199	VAL
8	G	6	SER
8	G	26	THR
8	G	127	THR
8	G	133	LEU
8	G	141	ILE
8	G	171	THR
8	G	176	ILE
9	H	69	LEU
9	H	71	SER
9	H	78	ARG
9	H	105	THR
9	H	172	THR
9	H	174	SER
10	I	29	LEU
10	I	71	CYS
10	I	81	VAL
10	I	84	ASN
10	I	88	ASN
10	I	99	ASN
10	I	136	ILE
10	I	167	GLN
11	J	14	VAL
11	J	50	LEU
11	J	82	VAL
11	J	159	PHE
11	J	172	ARG
12	K	3	MET
12	K	7	ASN
12	K	28	HIS
12	K	72	THR
14	M	14	VAL
14	M	21	VAL
14	M	49	LEU
14	M	104	VAL

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Mol	Chain	Res	Type
15	N	4	MET
15	N	22	VAL
15	N	30	SER
15	N	35	GLU
15	N	45	LEU
15	N	52	VAL
15	N	57	SER
15	N	83	ASP
15	N	102	LEU
15	N	143	SER
16	O	57	THR
16	O	69	SER
16	O	88	LEU
16	O	107	THR
16	O	126	ILE
16	O	129	ILE
17	P	26	LEU
17	P	70	MET
17	P	80	LEU
17	P	119	PHE
18	Q	66	VAL
18	Q	129	SER
19	R	88	VAL
19	R	98	VAL
19	R	102	THR
19	R	117	LEU
19	R	123	THR
20	S	4	VAL
20	S	14	ARG
20	S	28	PHE
20	S	45	LEU
20	S	92	ASP
20	S	141	ARG
21	T	6	VAL
21	T	22	LEU
21	T	30	VAL
21	T	79	TYR
21	T	90	SER
21	T	104	LEU
21	T	124	THR
21	T	131	LEU
22	U	63	ILE

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Mol	Chain	Res	Type
22	U	64	THR
22	U	68	THR
22	U	70	CYS
22	U	81	GLN
22	U	98	VAL
22	U	115	THR
23	V	39	VAL
23	V	42	VAL
24	W	30	CYS
24	W	41	MET
24	W	74	VAL
24	W	80	ASP
24	W	84	LYS
24	W	106	THR
25	X	32	LEU
25	X	72	VAL
25	X	105	PHE
25	X	125	VAL
26	Y	26	ASP
26	Y	44	LEU
27	Z	48	VAL
27	Z	56	ASP
27	Z	62	VAL
27	Z	69	THR
27	Z	107	VAL
28	a	30	VAL
28	a	40	VAL
28	a	45	VAL
28	a	67	LEU
28	a	90	GLU
29	b	3	LEU
29	b	46	VAL
30	c	26	GLN
30	c	27	CYS
30	c	46	VAL
32	e	29	THR
32	e	36	MET
32	e	44	ASN
33	f	146	LEU
34	g	6	THR
34	g	73	SER
34	g	98	THR

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Mol	Chain	Res	Type
34	g	105	THR
34	g	118	ARG
34	g	131	LEU
34	g	164	ILE
34	g	171	ASP
34	g	174	VAL
34	g	178	ASN
34	g	207	CYS
34	g	213	ASP
34	g	229	THR
34	g	277	THR
34	g	287	THR
34	g	309	VAL
36	n	154	PHE
36	n	160	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	70	ASN
2	A	113	GLN
2	A	131	HIS
2	A	132	GLN
3	B	158	HIS
3	B	159	GLN
3	B	232	HIS
5	D	159	HIS
5	D	179	GLN
7	F	65	GLN
7	F	110	GLN
7	F	203	ASN
8	G	227	GLN
9	H	33	ASN
9	H	91	HIS
12	K	7	ASN
12	K	28	HIS
13	L	13	GLN
14	M	46	GLN
14	M	48	HIS
17	P	53	GLN
17	P	54	HIS
17	P	103	ASN

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Mol	Chain	Res	Type
17	P	114	HIS
18	Q	35	ASN
21	T	12	GLN
21	T	51	ASN
21	T	83	GLN
21	T	126	GLN
22	U	81	GLN
25	X	23	HIS
25	X	26	GLN
25	X	31	HIS
25	X	73	GLN
26	Y	63	HIS
26	Y	85	ASN
29	b	26	GLN
32	e	15	GLN
32	e	44	ASN
34	g	104	HIS
36	n	160	ASN
36	n	172	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1645/1869 (88%)	549 (33%)	22 (1%)

All (549) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	33	G
1	2	41	G
1	2	46	A
1	2	56	G
1	2	62	G
1	2	67	C
1	2	68	A
1	2	71	G
1	2	72	C
1	2	73	C
1	2	74	G
1	2	75	G

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Mol	Chain	Res	Type
1	2	76	U
1	2	77	A
1	2	103	A
1	2	113	G
1	2	115	U
1	2	128	U
1	2	129	C
1	2	130	G
1	2	143	U
1	2	147	A
1	2	149	A
1	2	163	U
1	2	168	C
1	2	179	C
1	2	180	G
1	2	182	C
1	2	183	G
1	2	184	G
1	2	198	U
1	2	199	C
1	2	200	G
1	2	202	G
1	2	209	A
1	2	210	U
1	2	211	G
1	2	214	U
1	2	215	G
1	2	305	U
1	2	306	C
1	2	307	G
1	2	308	G
1	2	309	G
1	2	310	C
1	2	312	G
1	2	319	C
1	2	320	G
1	2	321	C
1	2	330	G
1	2	333	G
1	2	339	A
1	2	344	U
1	2	345	U

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Mol	Chain	Res	Type
1	2	347	G
1	2	362	C
1	2	364	A
1	2	367	U
1	2	368	U
1	2	369	C
1	2	370	G
1	2	377	G
1	2	385	G
1	2	386	C
1	2	407	G
1	2	409	C
1	2	413	G
1	2	418	A
1	2	428	U
1	2	438	G
1	2	447	A
1	2	448	A
1	2	449	A
1	2	450	C
1	2	464	A
1	2	465	A
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	482	G
1	2	487	U
1	2	492	C
1	2	493	A
1	2	525	A
1	2	534	G
1	2	536	A
1	2	537	C
1	2	538	U
1	2	539	C
1	2	540	U
1	2	541	U
1	2	542	U
1	2	543	C
1	2	546	G
1	2	547	G

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Mol	Chain	Res	Type
1	2	548	C
1	2	553	U
1	2	554	A
1	2	555	A
1	2	559	G
1	2	560	A
1	2	564	A
1	2	576	A
1	2	577	U
1	2	578	C
1	2	587	A
1	2	589	G
1	2	591	U
1	2	604	A
1	2	605	A
1	2	607	U
1	2	608	C
1	2	614	C
1	2	617	G
1	2	627	U
1	2	628	A
1	2	629	A
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	660	C
1	2	668	A
1	2	669	A
1	2	670	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	688	U
1	2	747	U
1	2	748	C
1	2	750	C
1	2	751	G
1	2	752	G
1	2	793	G
1	2	794	A
1	2	797	C

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Mol	Chain	Res	Type
1	2	798	G
1	2	799	U
1	2	811	A
1	2	812	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	830	A
1	2	834	C
1	2	847	A
1	2	852	G
1	2	869	A
1	2	870	A
1	2	872	A
1	2	873	G
1	2	874	G
1	2	876	C
1	2	878	G
1	2	880	G
1	2	881	G
1	2	887	U
1	2	889	U
1	2	890	U
1	2	891	G
1	2	893	U
1	2	894	G
1	2	896	U
1	2	897	U
1	2	898	U
1	2	899	U
1	2	902	G
1	2	903	A
1	2	904	A
1	2	905	C
1	2	906	U
1	2	907	G
1	2	912	C
1	2	913	A
1	2	914	U
1	2	917	U
1	2	920	A

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Mol	Chain	Res	Type
1	2	921	G
1	2	922	A
1	2	930	C
1	2	933	G
1	2	961	G
1	2	971	G
1	2	978	G
1	2	982	G
1	2	990	A
1	2	992	A
1	2	999	G
1	2	1017	U
1	2	1023	A
1	2	1027	A
1	2	1028	A
1	2	1045	U
1	2	1053	C
1	2	1061	U
1	2	1062	A
1	2	1073	U
1	2	1083	A
1	2	1085	C
1	2	1096	G
1	2	1100	A
1	2	1109	C
1	2	1115	U
1	2	1116	C
1	2	1121	G
1	2	1122	A
1	2	1138	C
1	2	1148	A
1	2	1149	A
1	2	1154	U
1	2	1157	G
1	2	1171	G
1	2	1172	U
1	2	1173	A
1	2	1175	G
1	2	1188	A
1	2	1190	A
1	2	1195	A
1	2	1207	G

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Mol	Chain	Res	Type
1	2	1212	G
1	2	1215	C
1	2	1216	C
1	2	1224	G
1	2	1225	U
1	2	1226	G
1	2	1227	G
1	2	1228	A
1	2	1229	G
1	2	1231	C
1	2	1232	U
1	2	1233	G
1	2	1235	G
1	2	1236	G
1	2	1237	C
1	2	1239	U
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1245	G
1	2	1247	C
1	2	1248	U
1	2	1250	A
1	2	1253	A
1	2	1254	C
1	2	1256	G
1	2	1257	G
1	2	1258	A
1	2	1259	A
1	2	1260	A
1	2	1261	C
1	2	1262	C
1	2	1263	U
1	2	1264	C
1	2	1265	A
1	2	1267	C
1	2	1268	C
1	2	1269	G
1	2	1271	C
1	2	1272	C
1	2	1273	C

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Mol	Chain	Res	Type
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1278	A
1	2	1279	C
1	2	1282	A
1	2	1283	C
1	2	1284	A
1	2	1285	G
1	2	1286	G
1	2	1287	A
1	2	1288	U
1	2	1289	U
1	2	1291	A
1	2	1293	A
1	2	1294	G
1	2	1295	A
1	2	1296	U
1	2	1297	U
1	2	1298	G
1	2	1299	A
1	2	1300	U
1	2	1301	A
1	2	1302	G
1	2	1305	C
1	2	1306	U
1	2	1308	U
1	2	1311	C
1	2	1312	G
1	2	1313	A
1	2	1314	U
1	2	1315	U
1	2	1316	C
1	2	1317	C
1	2	1319	U
1	2	1320	G
1	2	1323	U
1	2	1325	G
1	2	1326	U
1	2	1327	G
1	2	1328	G
1	2	1329	U

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Mol	Chain	Res	Type
1	2	1330	G
1	2	1331	C
1	2	1332	A
1	2	1333	U
1	2	1334	G
1	2	1335	G
1	2	1340	U
1	2	1348	G
1	2	1364	U
1	2	1371	U
1	2	1372	U
1	2	1378	A
1	2	1395	C
1	2	1396	A
1	2	1397	U
1	2	1398	G
1	2	1402	A
1	2	1403	C
1	2	1404	U
1	2	1405	A
1	2	1406	G
1	2	1409	A
1	2	1411	G
1	2	1412	C
1	2	1414	A
1	2	1415	C
1	2	1416	C
1	2	1425	G
1	2	1426	U
1	2	1429	G
1	2	1431	G
1	2	1432	U
1	2	1439	A
1	2	1440	C
1	2	1444	U
1	2	1445	U
1	2	1446	A
1	2	1447	G
1	2	1452	A
1	2	1454	A
1	2	1455	A
1	2	1456	G

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Mol	Chain	Res	Type
1	2	1463	U
1	2	1466	G
1	2	1472	C
1	2	1478	U
1	2	1480	A
1	2	1484	A
1	2	1485	U
1	2	1486	A
1	2	1488	C
1	2	1489	A
1	2	1494	U
1	2	1495	G
1	2	1497	G
1	2	1498	A
1	2	1500	G
1	2	1501	C
1	2	1502	C
1	2	1503	C
1	2	1504	U
1	2	1505	U
1	2	1506	A
1	2	1507	G
1	2	1509	U
1	2	1510	G
1	2	1512	C
1	2	1513	C
1	2	1514	G
1	2	1517	G
1	2	1518	C
1	2	1519	U
1	2	1520	G
1	2	1521	C
1	2	1522	A
1	2	1524	G
1	2	1525	C
1	2	1526	G
1	2	1527	C
1	2	1528	G
1	2	1529	C
1	2	1530	U
1	2	1534	C
1	2	1535	U

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Mol	Chain	Res	Type
1	2	1536	G
1	2	1537	A
1	2	1538	C
1	2	1539	U
1	2	1542	C
1	2	1545	A
1	2	1546	G
1	2	1547	C
1	2	1548	G
1	2	1552	G
1	2	1553	C
1	2	1555	U
1	2	1556	A
1	2	1557	C
1	2	1558	C
1	2	1561	A
1	2	1562	C
1	2	1563	G
1	2	1566	G
1	2	1571	G
1	2	1572	C
1	2	1573	G
1	2	1575	G
1	2	1576	G
1	2	1577	G
1	2	1578	U
1	2	1579	A
1	2	1580	A
1	2	1581	C
1	2	1582	C
1	2	1583	C
1	2	1584	G
1	2	1588	A
1	2	1590	C
1	2	1591	C
1	2	1592	C
1	2	1593	C
1	2	1595	U
1	2	1598	G
1	2	1599	U
1	2	1601	A
1	2	1604	G

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Mol	Chain	Res	Type
1	2	1605	G
1	2	1606	G
1	2	1611	G
1	2	1613	G
1	2	1614	A
1	2	1617	G
1	2	1619	A
1	2	1620	A
1	2	1621	U
1	2	1622	U
1	2	1623	A
1	2	1624	U
1	2	1625	U
1	2	1630	A
1	2	1631	U
1	2	1632	G
1	2	1636	G
1	2	1637	A
1	2	1639	G
1	2	1640	A
1	2	1641	A
1	2	1642	U
1	2	1643	U
1	2	1647	A
1	2	1648	G
1	2	1649	U
1	2	1650	A
1	2	1651	A
1	2	1656	G
1	2	1657	G
1	2	1659	U
1	2	1660	C
1	2	1661	A
1	2	1662	U
1	2	1664	A
1	2	1665	G
1	2	1666	C
1	2	1667	U
1	2	1672	U
1	2	1675	A
1	2	1676	U
1	2	1678	A

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Mol	Chain	Res	Type
1	2	1680	G
1	2	1683	C
1	2	1684	C
1	2	1685	U
1	2	1686	G
1	2	1695	A
1	2	1699	A
1	2	1709	G
1	2	1710	C
1	2	1711	U
1	2	1712	A
1	2	1717	C
1	2	1718	G
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1723	G
1	2	1724	A
1	2	1725	U
1	2	1728	U
1	2	1730	U
1	2	1731	A
1	2	1732	G
1	2	1742	C
1	2	1744	G
1	2	1751	C
1	2	1752	C
1	2	1753	C
1	2	1754	G
1	2	1755	C
1	2	1756	C
1	2	1758	G
1	2	1759	G
1	2	1760	G
1	2	1761	U
1	2	1772	C
1	2	1773	C
1	2	1774	C
1	2	1777	G
1	2	1778	C
1	2	1779	G
1	2	1780	G

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Mol	Chain	Res	Type
1	2	1781	A
1	2	1782	G
1	2	1783	C
1	2	1802	C
1	2	1804	U
1	2	1805	G
1	2	1806	A
1	2	1808	U
1	2	1809	A
1	2	1810	U
1	2	1812	U
1	2	1815	A
1	2	1816	G
1	2	1821	U
1	2	1822	A
1	2	1823	A
1	2	1825	A
1	2	1826	G
1	2	1827	U
1	2	1831	A
1	2	1835	A
1	2	1838	U
1	2	1849	G
1	2	1850	A
1	2	1851	A
1	2	1852	C
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1869	A

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	332	G
1	2	604	A
1	2	868	G
1	2	902	G
1	2	1189	A
1	2	1263	U

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Mol	Chain	Res	Type
1	2	1329	U
1	2	1339	U
1	2	1424	G
1	2	1500	G
1	2	1528	G
1	2	1546	G
1	2	1557	C
1	2	1571	G
1	2	1612	G
1	2	1647	A
1	2	1649	U
1	2	1666	C
1	2	1709	G
1	2	1757	G
1	2	1804	U
1	2	1821	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

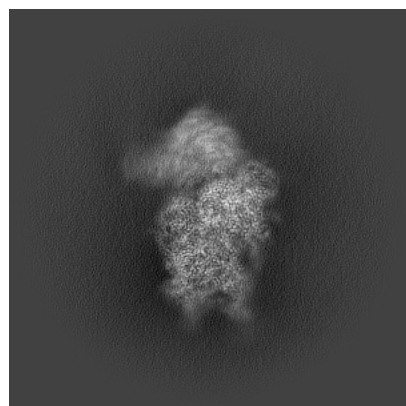
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62445. These allow visual inspection of the internal detail of the map and identification of artifacts.

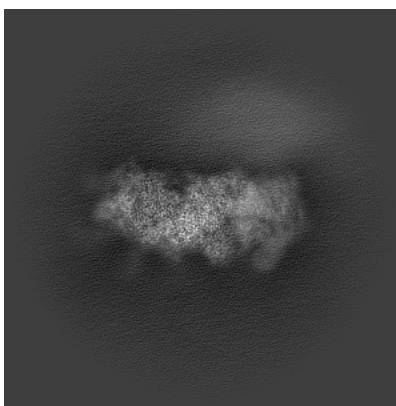
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

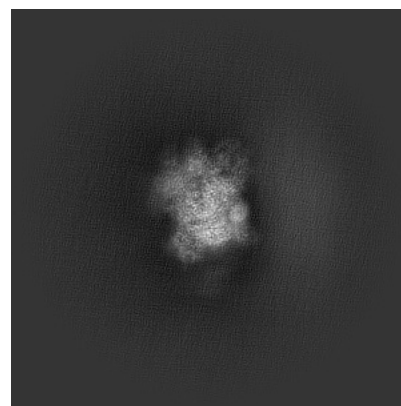
6.1.1 Primary map



X

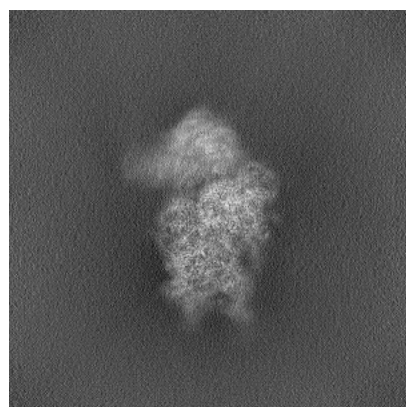


Y

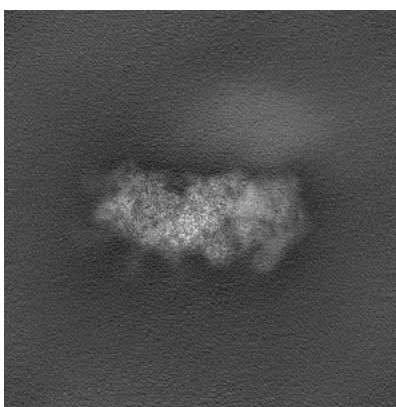


Z

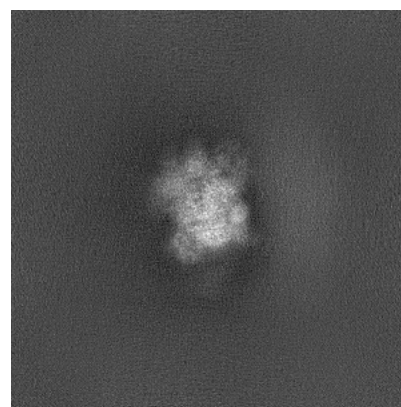
6.1.2 Raw map



X



Y

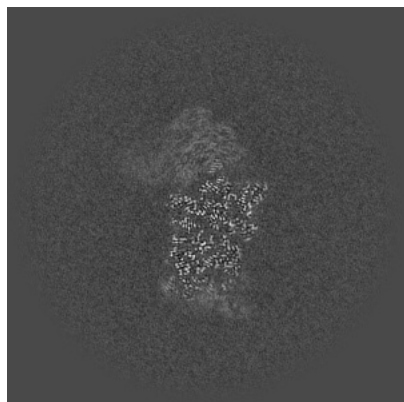


Z

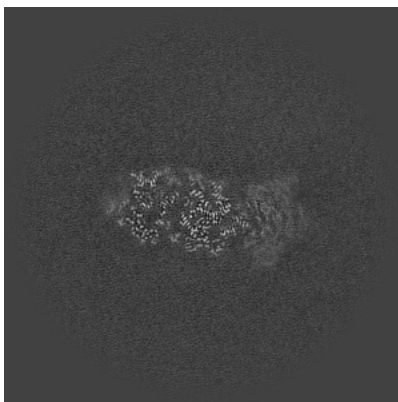
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

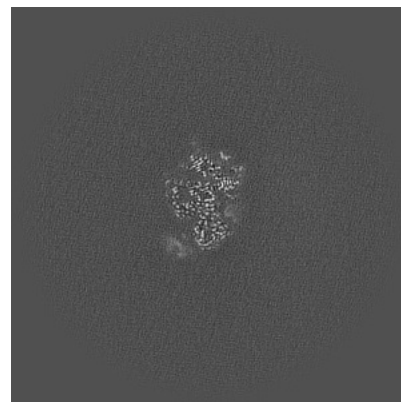
6.2.1 Primary map



X Index: 256

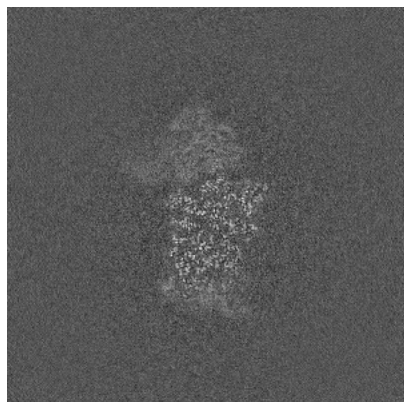


Y Index: 256

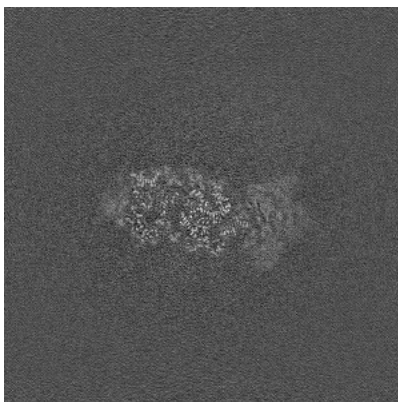


Z Index: 256

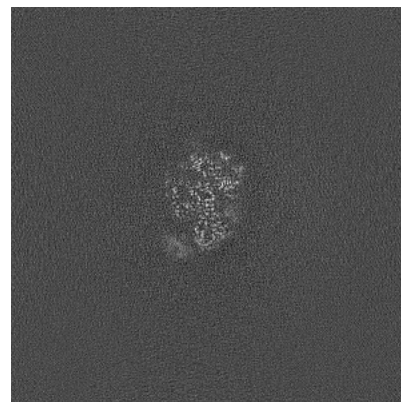
6.2.2 Raw map



X Index: 256



Y Index: 256

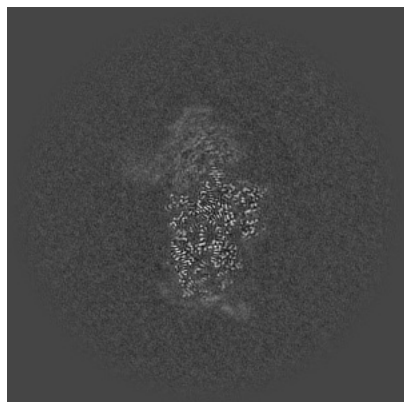


Z Index: 256

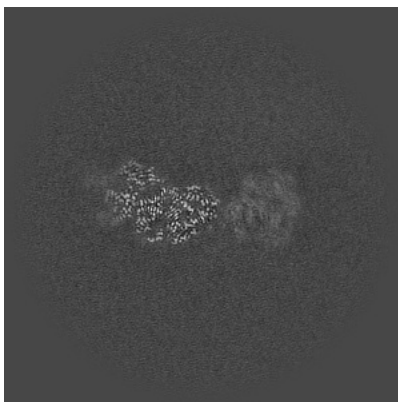
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

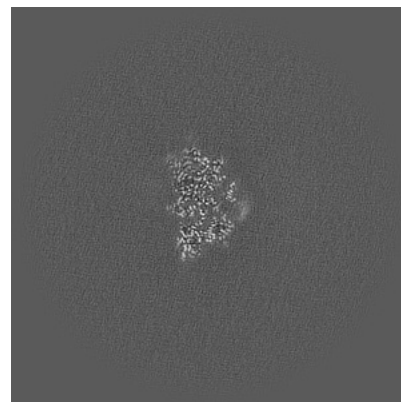
6.3.1 Primary map



X Index: 251

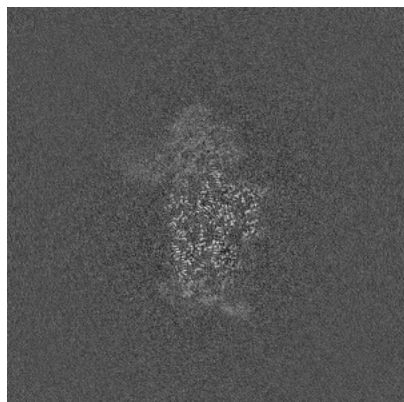


Y Index: 225

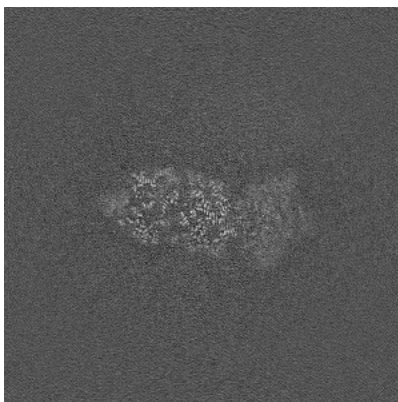


Z Index: 236

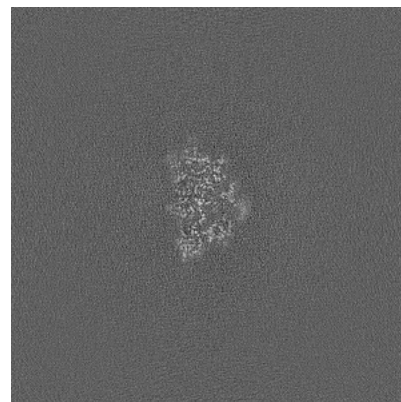
6.3.2 Raw map



X Index: 251



Y Index: 257

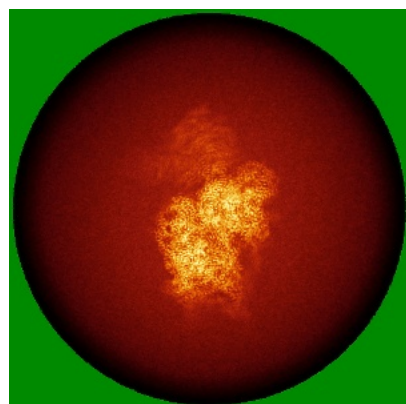


Z Index: 237

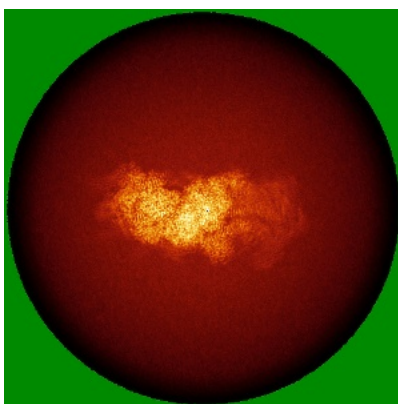
The images above show the largest variance slices of the map in three orthogonal directions.

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

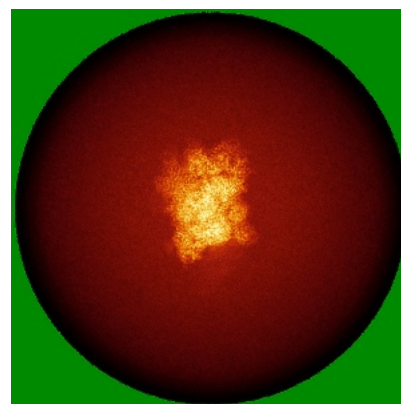
6.4.1 Primary map



X

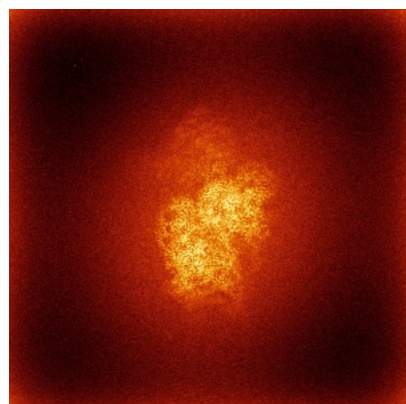


Y

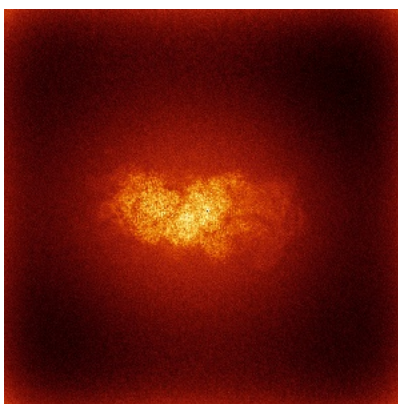


Z

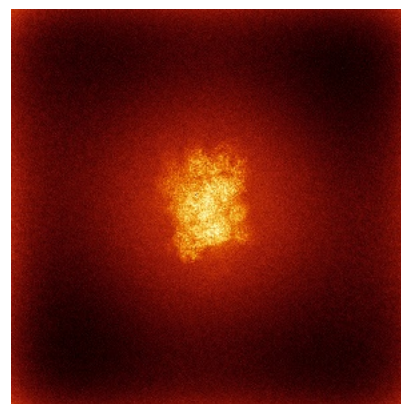
6.4.2 Raw map



X



Y

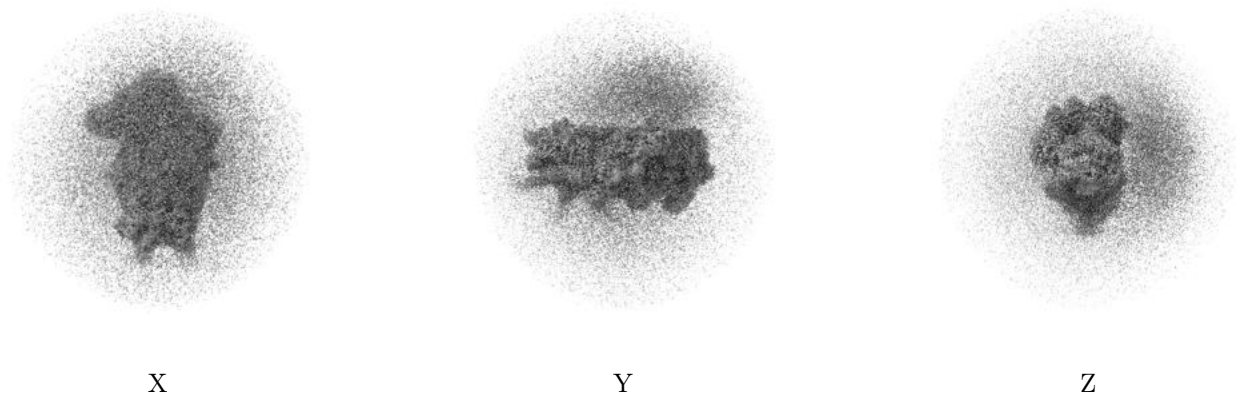


Z

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

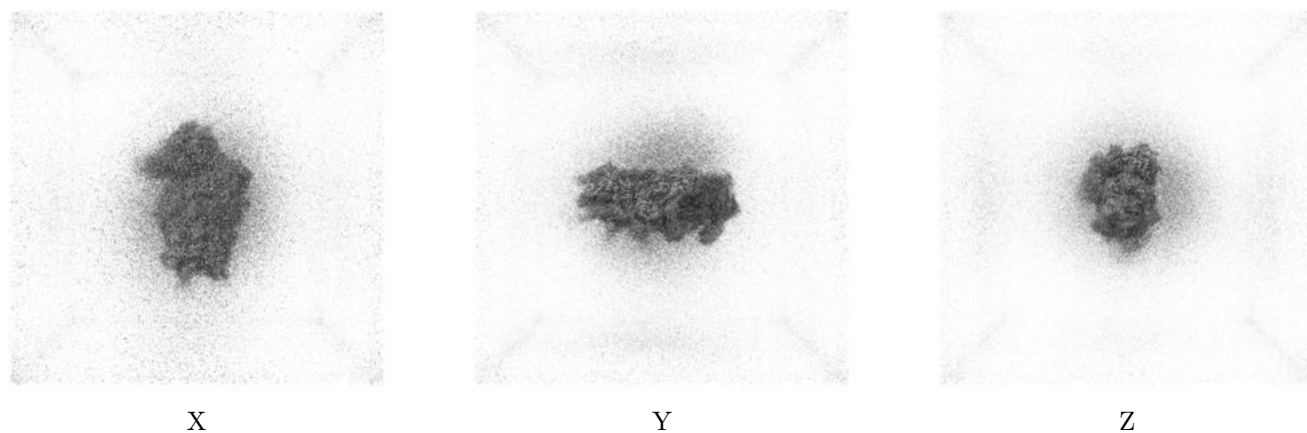
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 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



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

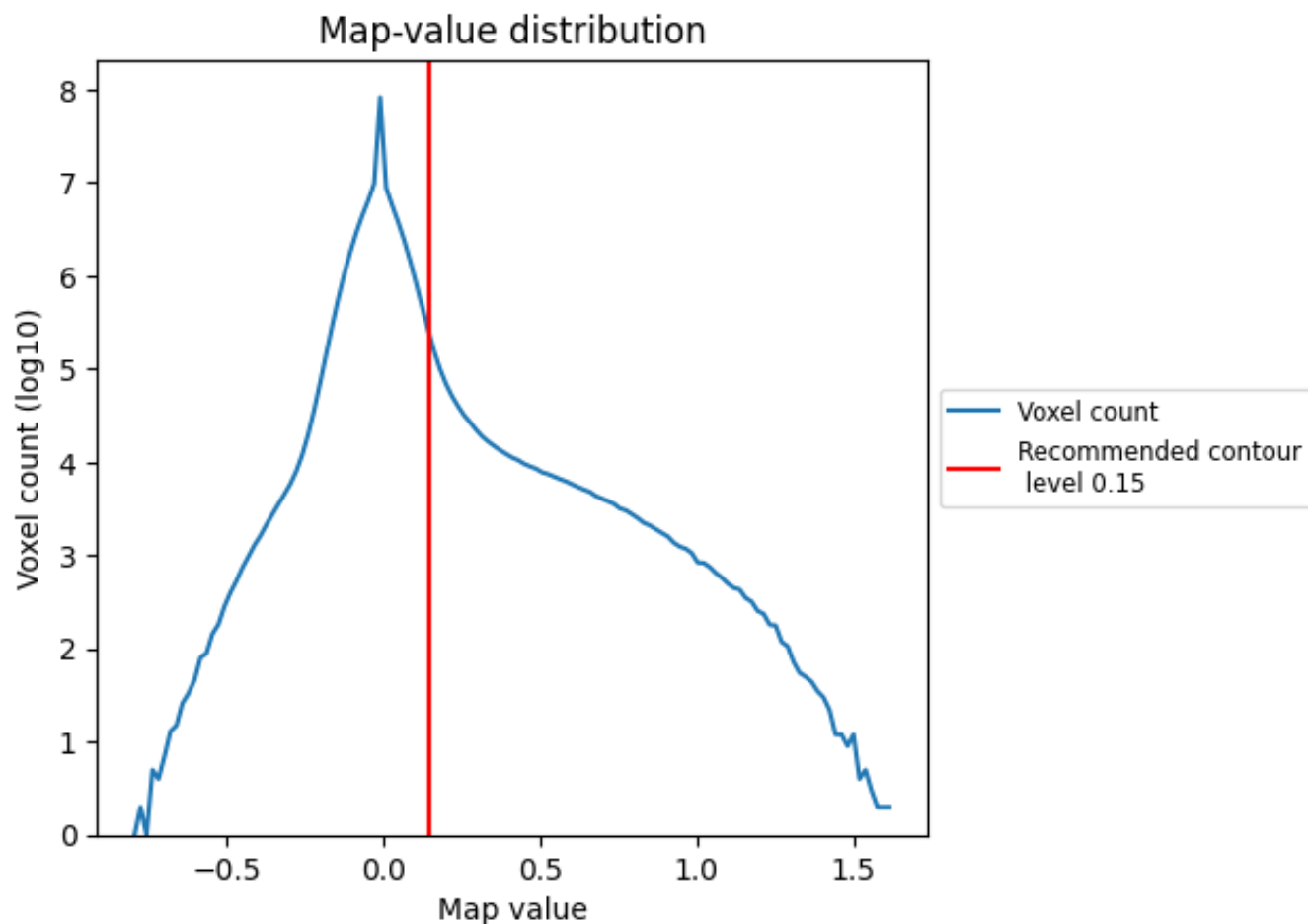
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

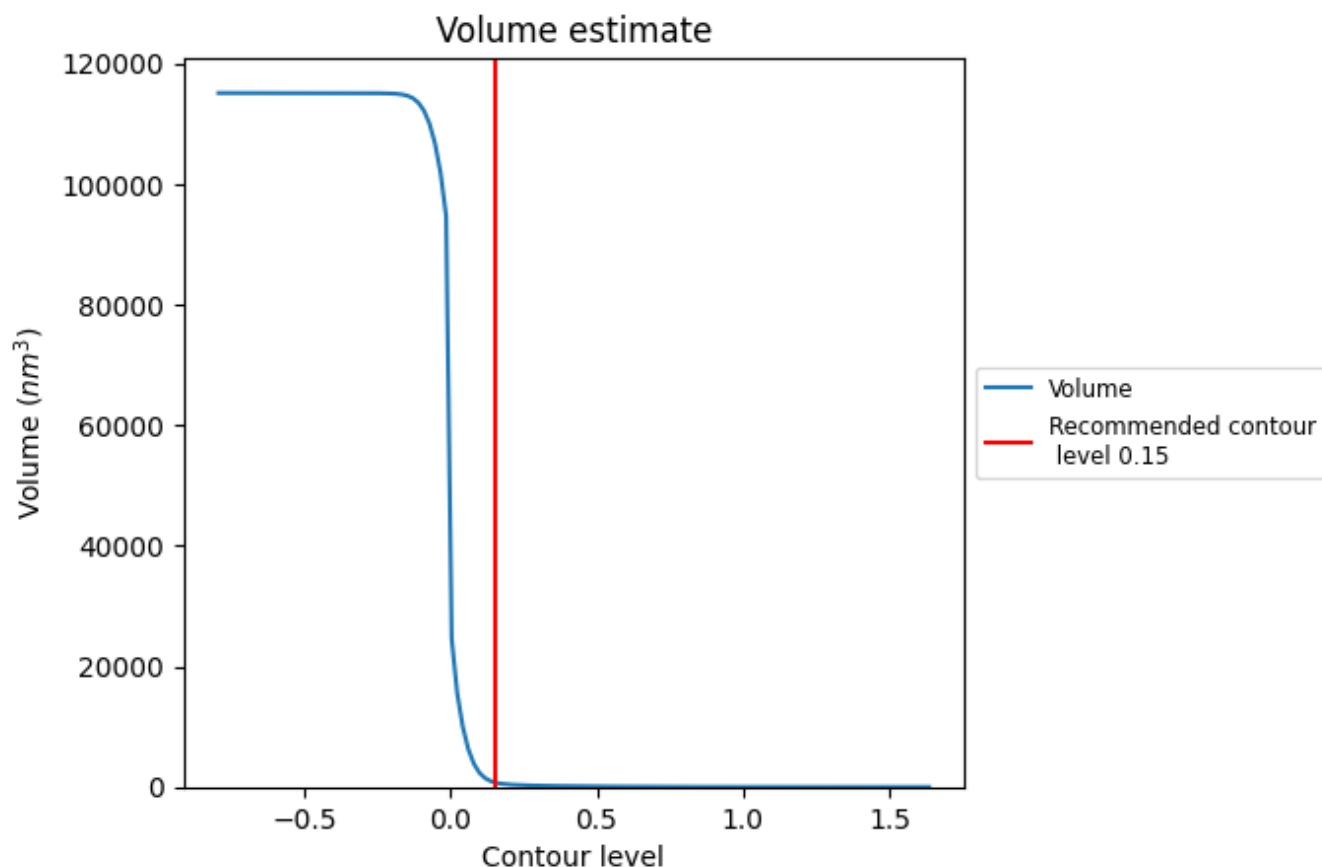
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

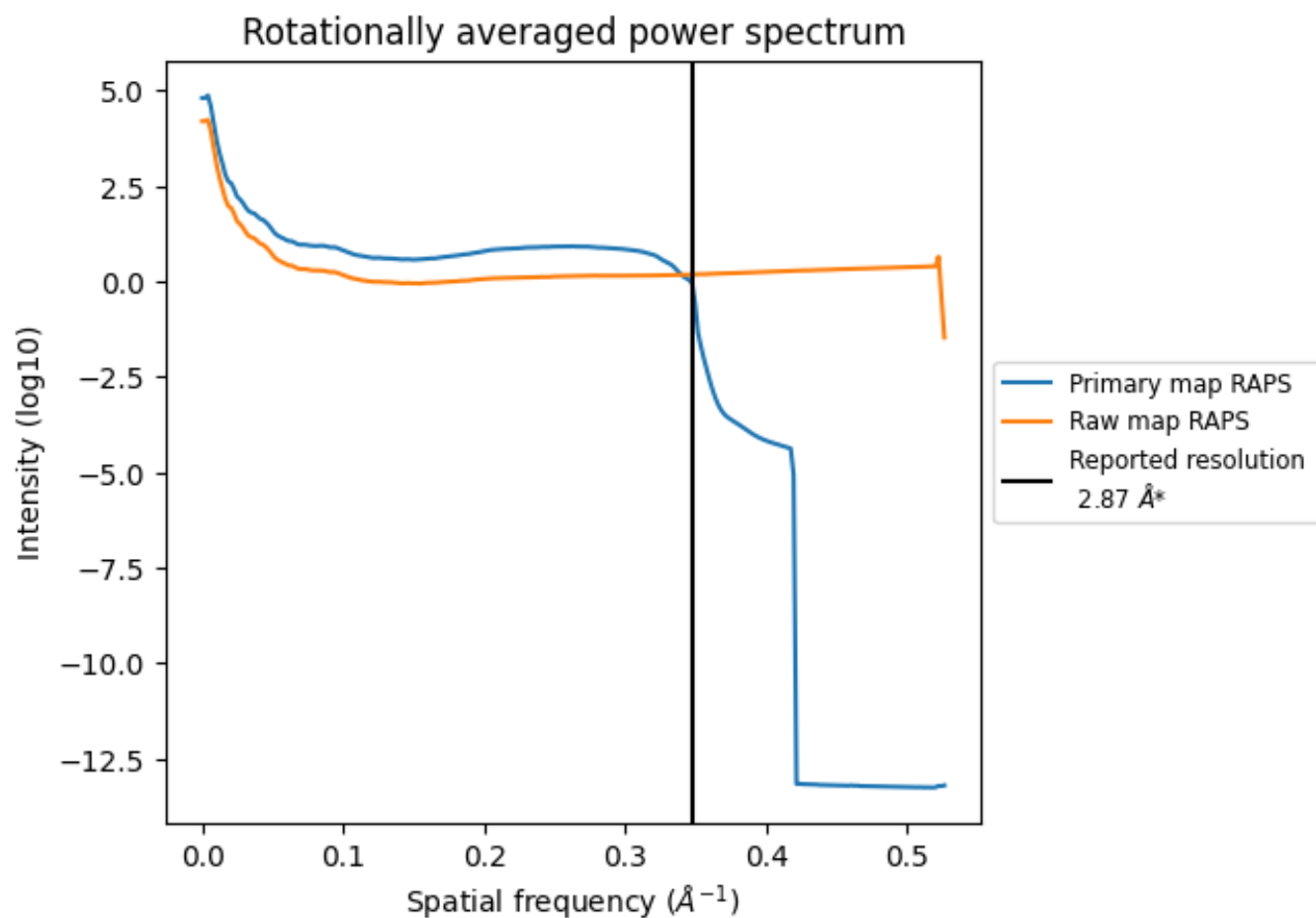
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 789 nm³; this corresponds to an approximate mass of 712 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 ⓘ

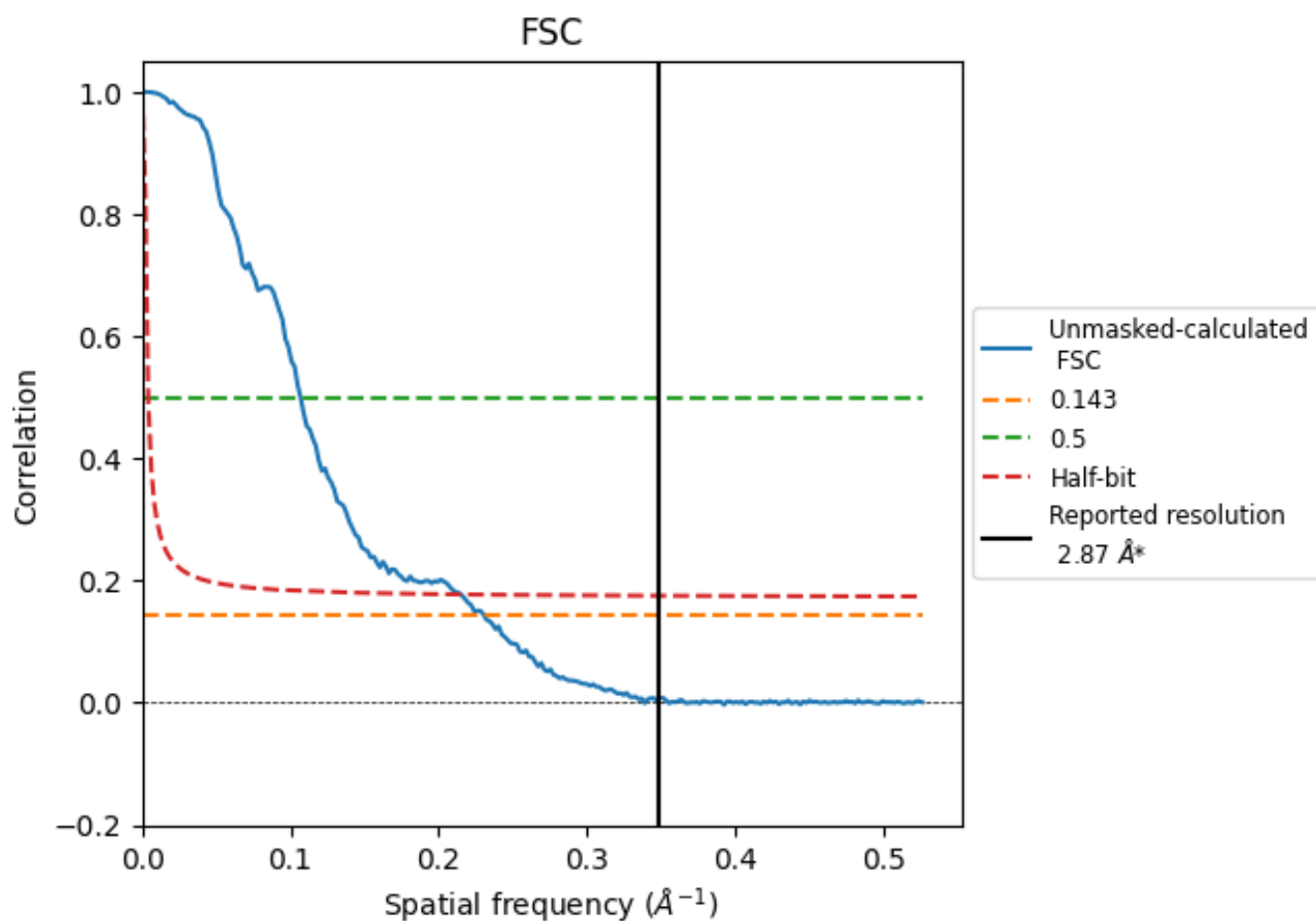


*Reported resolution corresponds to spatial frequency of 0.348 Å⁻¹

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 0.348 Å⁻¹

8.2 Resolution estimates [i](#)

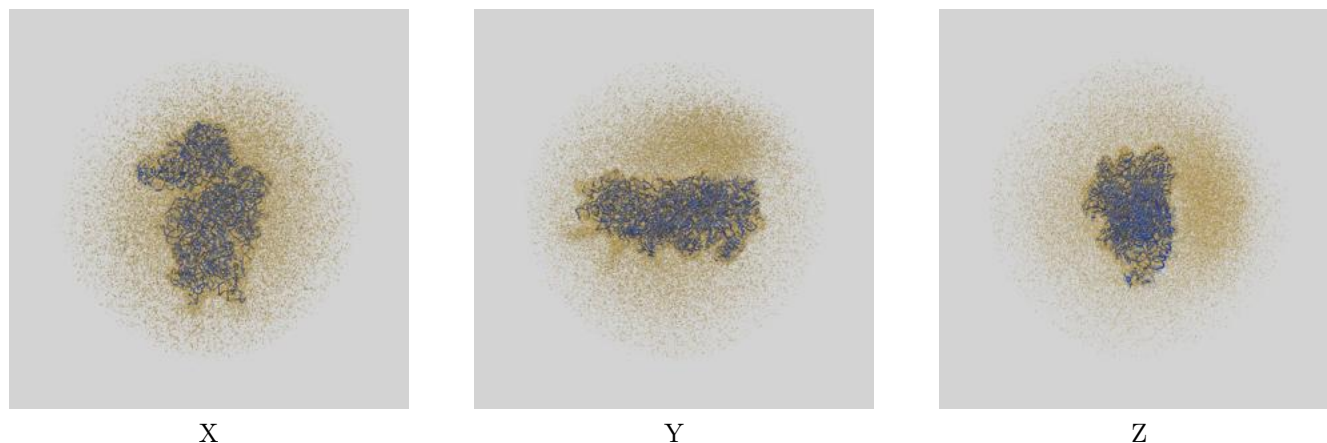
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.34	9.36	4.65

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.34 differs from the reported value 2.87 by more than 10 %

9 Map-model fit [i](#)

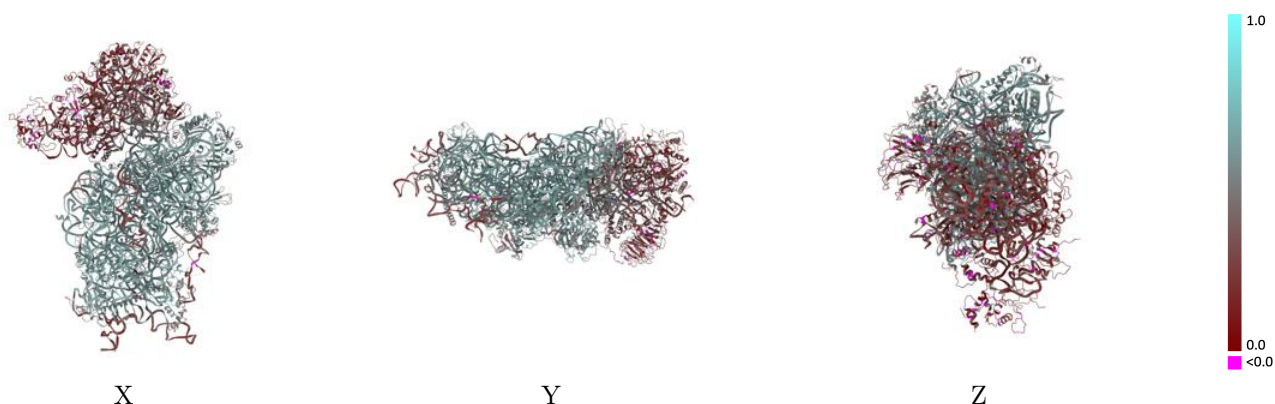
This section contains information regarding the fit between EMDB map EMD-62445 and PDB model 9KMU. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



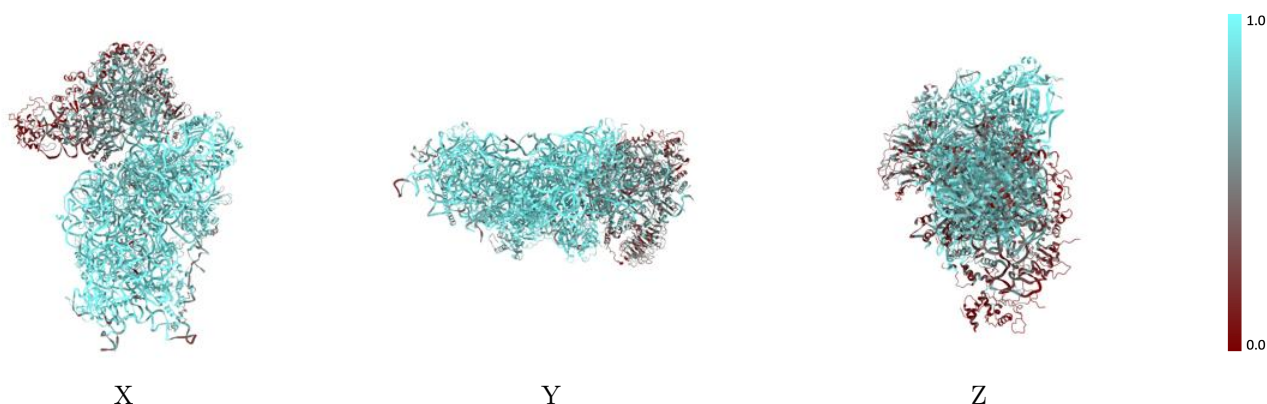
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



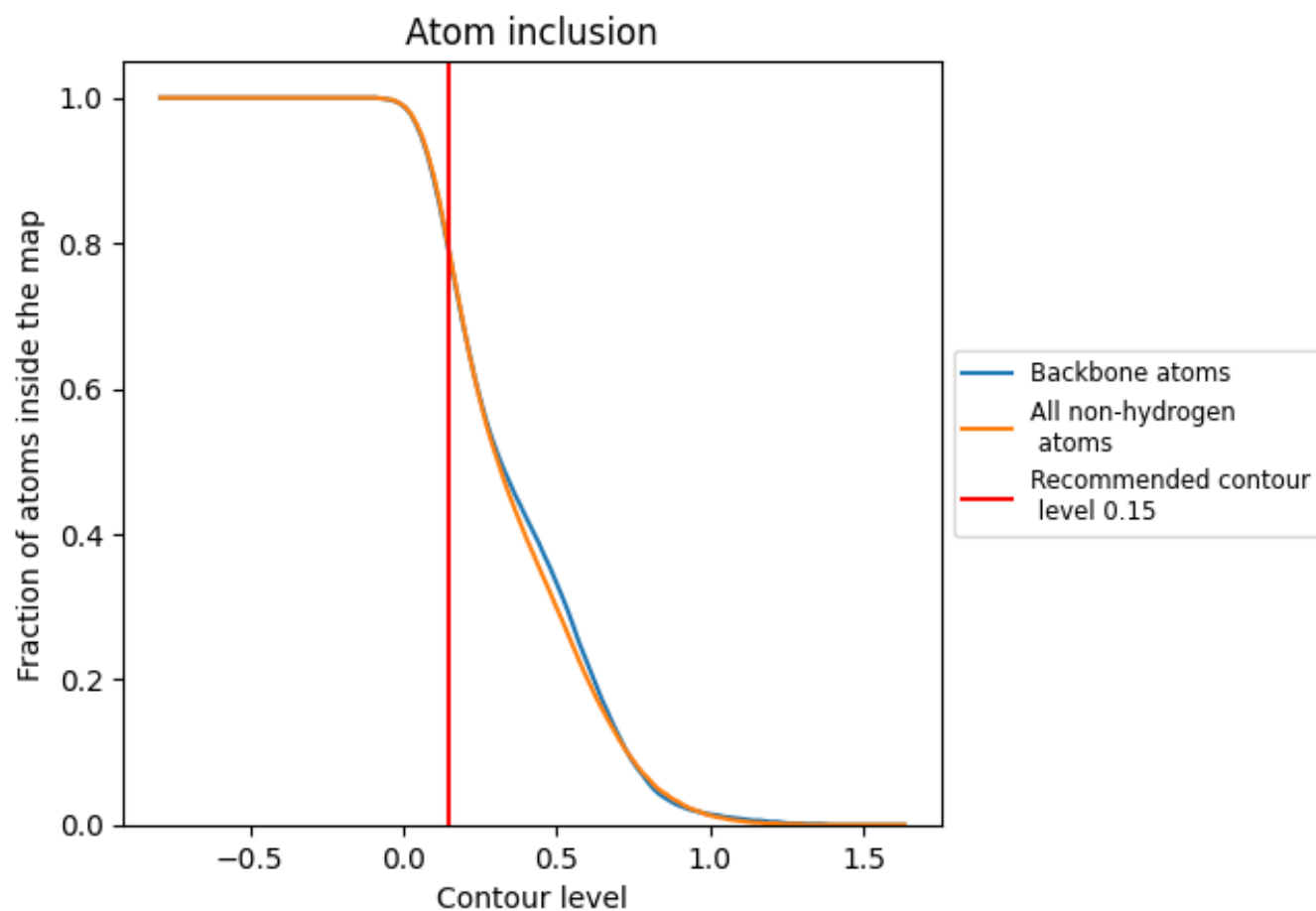
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 79% of all backbone atoms, 79% 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	 0.7880	 0.4680
2	 0.8650	 0.4840
A	 0.9250	 0.5710
B	 0.9180	 0.5660
C	 0.9360	 0.5890
D	 0.4620	 0.2810
E	 0.9600	 0.6080
F	 0.5200	 0.2980
G	 0.9150	 0.5400
H	 0.7850	 0.4920
I	 0.8730	 0.5390
J	 0.9700	 0.6040
K	 0.4080	 0.2480
L	 0.9200	 0.5810
M	 0.1630	 0.2130
N	 0.9530	 0.5810
O	 0.9060	 0.5630
P	 0.2580	 0.2430
Q	 0.6060	 0.3260
R	 0.6420	 0.3980
S	 0.2970	 0.2790
T	 0.5430	 0.2790
U	 0.4090	 0.2850
V	 0.9570	 0.5890
W	 0.9570	 0.6070
X	 0.9630	 0.5980
Y	 0.9630	 0.5990
Z	 0.3300	 0.2530
a	 0.9300	 0.5780
b	 0.8790	 0.5420
c	 0.4690	 0.3100
d	 0.5120	 0.2700
e	 0.8600	 0.5500
f	 0.1280	 0.2490
g	 0.3920	 0.2590



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Chain	Atom inclusion	Q-score
h	 0.8870	 0.5560
n	 0.8500	 0.5430