



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 01:14 PM UTC

PDB ID : 6R86 / pdb_00006r86
EMDB ID : EMD-4752
Title : Yeast Vms1-60S ribosomal subunit complex (post-state)
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;
Neupert, W.; Beckmann, R.
Deposited on : 2019-03-31
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

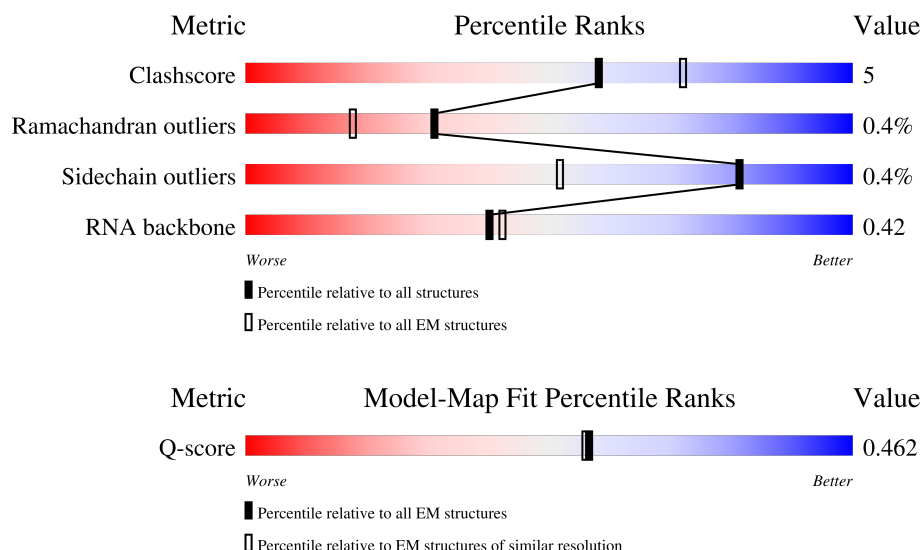
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



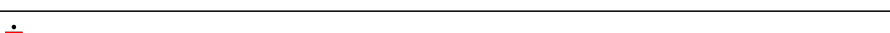
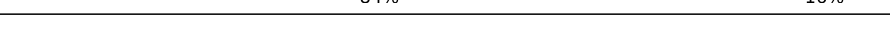
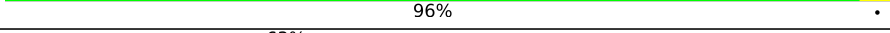
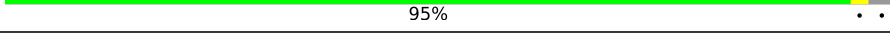
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	R	475	
2	X	224	
3	i	112	

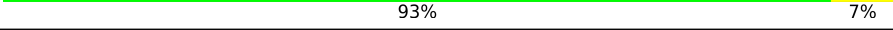
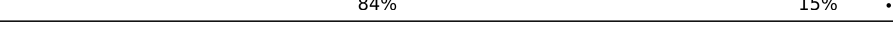
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	J	222	
5	j	119	
6	K	233	
7	k	99	
8	7	191	
9	l	87	
10	M	169	
11	m	77	
12	N	193	
13	n	50	
14	O	136	
15	o	52	
16	p	203	
17	Q	197	
18	5	183	
19	S	185	
20	s	220	
21	T	152	
22	U	172	
23	V	159	
24	W	100	
25	P	155	
26	r	197	
27	x	136	
28	3	121	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Y	62	
30	4	158	
31	Z	121	
32	a	126	
33	b	135	
34	C	105	
35	c	148	
36	D	91	
37	d	58	
38	E	252	
39	e	97	
40	F	386	
41	f	109	
42	G	361	
43	g	127	
44	H	296	
45	h	106	
46	I	175	
47	L	204	
48	1	3260	

2 Entry composition [i](#)

There are 49 unique types of molecules in this entry. The entry contains 132446 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	356	Total	C	N	O	S	Se	0	0
			2784	1776	495	500	12	1		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 3 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 5 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 6 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 7 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 10 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 13 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	P	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 26 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 28 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 29 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 34 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 36 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	D	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 37 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 38 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 39 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 43 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 44 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 45 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 46 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	I	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 47 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 48 is a RNA chain called 25S ribosomal RNA.

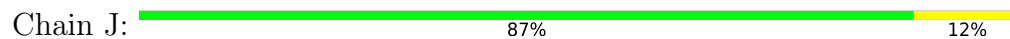
Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	3260	Total	C	N	O	P	0	0
			69730	31146	12569	22755	3260		

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

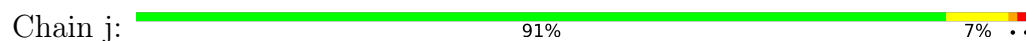
Mol	Chain	Residues	Atoms		AltConf
49	R	1	Total	Zn	0
			1	1	



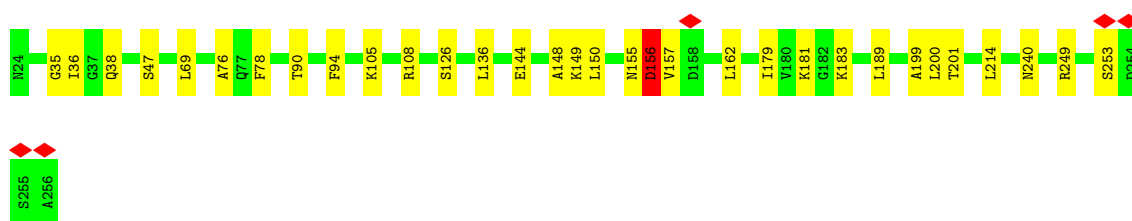
- Molecule 4: 60S ribosomal protein L7-A



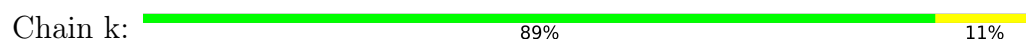
- Molecule 5: 60S ribosomal protein L35-A



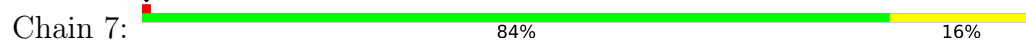
- Molecule 6: 60S ribosomal protein L8-A



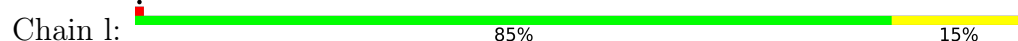
- Molecule 7: 60S ribosomal protein L36-A



- Molecule 8: 60S ribosomal protein L9-A

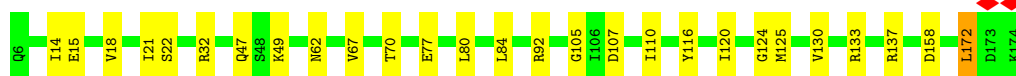
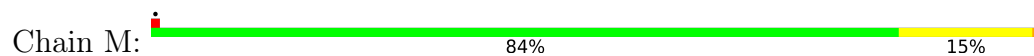


- Molecule 9: 60S ribosomal protein L37-A

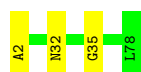




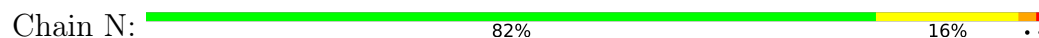
- Molecule 10: 60S ribosomal protein L11-B



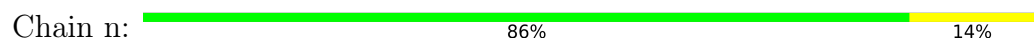
- Molecule 11: 60S ribosomal protein L38



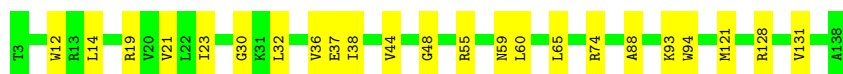
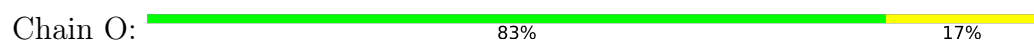
- Molecule 12: 60S ribosomal protein L13-A



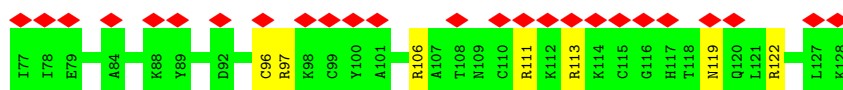
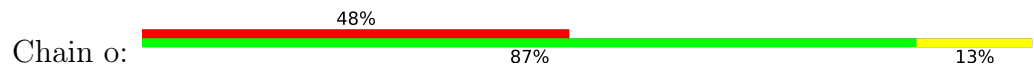
- Molecule 13: 60S ribosomal protein L39



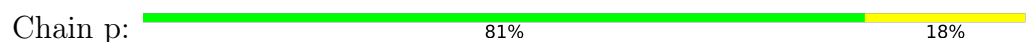
- Molecule 14: 60S ribosomal protein L14-A



- Molecule 15: Ubiquitin-60S ribosomal protein L40



- Molecule 16: 60S ribosomal protein L15-A





- Molecule 17: 60S ribosomal protein L16-A

Chain Q: 88% 12% .



- Molecule 18: 60S ribosomal protein L17-A

Chain 5: 84% 16%



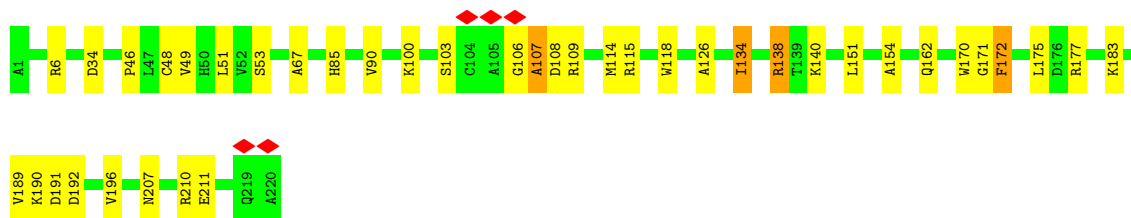
- Molecule 19: 60S ribosomal protein L18-A

Chain S: 87% 13%



- Molecule 20: 60S ribosomal protein L10

Chain s: 82% 16% .



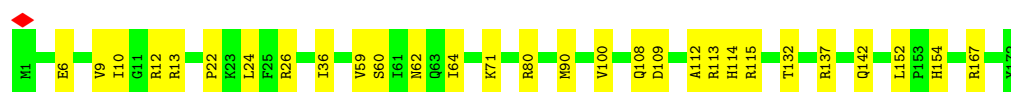
- Molecule 21: 60S ribosomal protein L19-A

Chain T: 89% 11%



- Molecule 22: 60S ribosomal protein L20-A

Chain U: 83% 17%



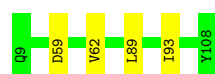
- Molecule 23: 60S ribosomal protein L21-A

Chain V: 83% 16%



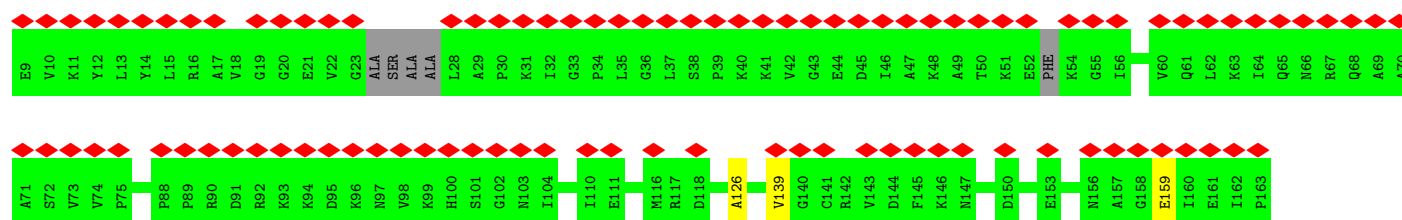
- Molecule 24: 60S ribosomal protein L22-A

Chain W: 96%



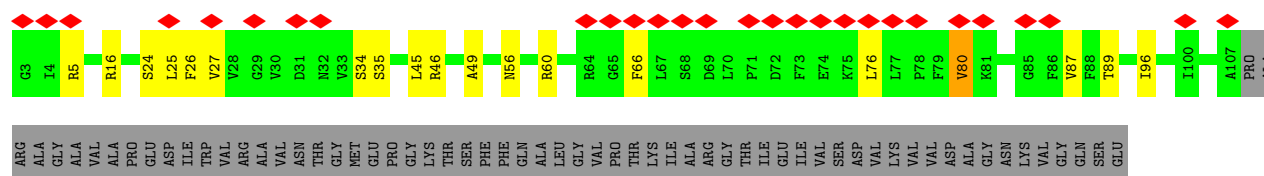
- Molecule 25: 60S ribosomal protein L12-A

Chain P: 63% 95%



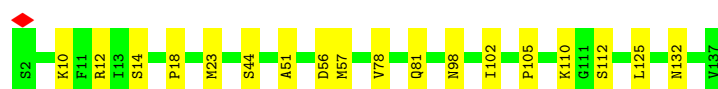
- Molecule 26: 60S acidic ribosomal protein P0

Chain r: 19% 51% 10% 39%

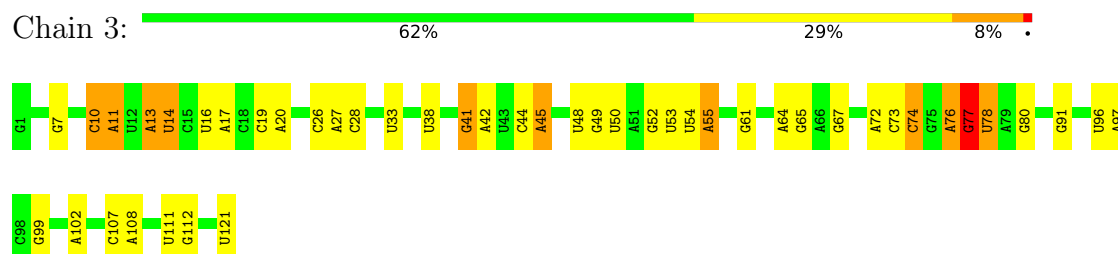


- Molecule 27: 60S ribosomal protein L23-A

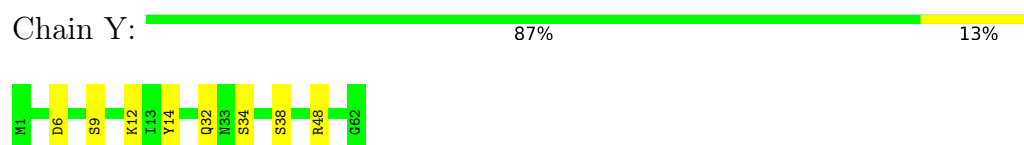
Chain x: 87% 13%



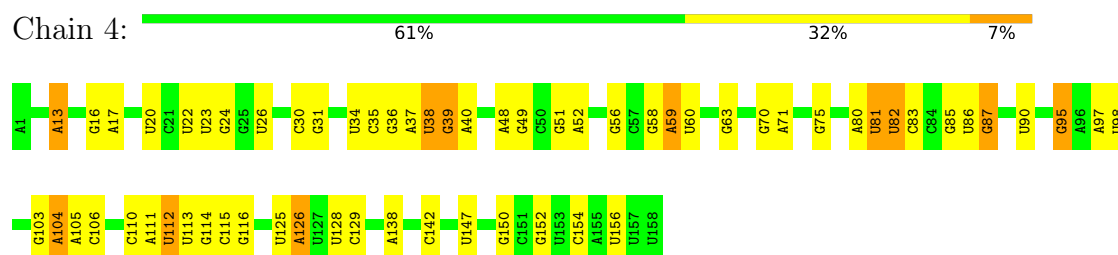
- Molecule 28: 5S ribosomal RNA



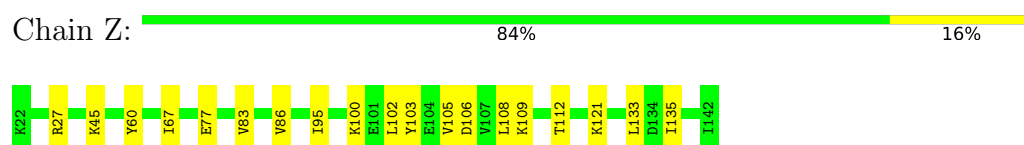
- Molecule 29: 60S ribosomal protein L24-A



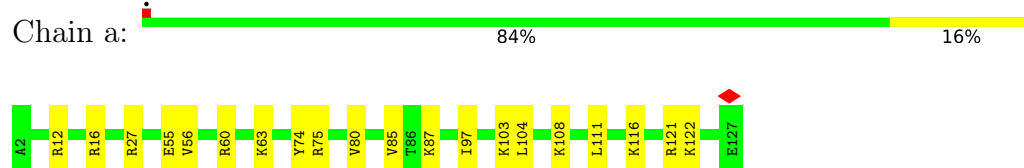
- Molecule 30: 5.8S ribosomal RNA



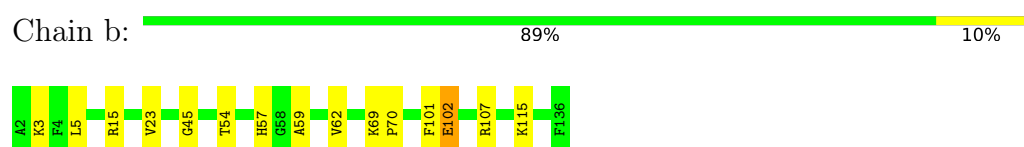
- Molecule 31: 60S ribosomal protein L25



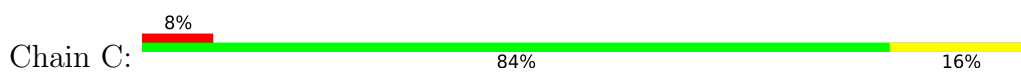
- Molecule 32: 60S ribosomal protein L26-A



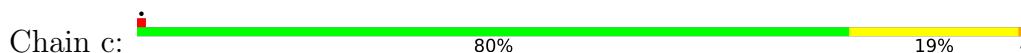
- Molecule 33: 60S ribosomal protein L27-A



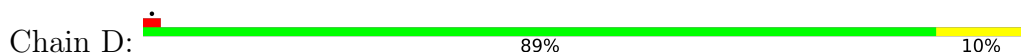
- Molecule 34: 60S ribosomal protein L42-A



- Molecule 35: 60S ribosomal protein L28



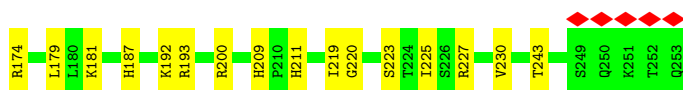
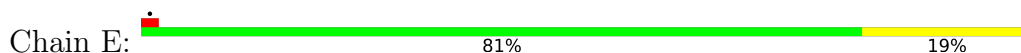
- Molecule 36: 60S ribosomal protein L43-A



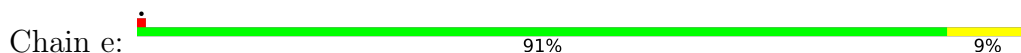
- Molecule 37: 60S ribosomal protein L29



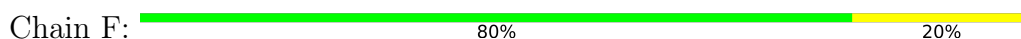
- Molecule 38: 60S ribosomal protein L2-A

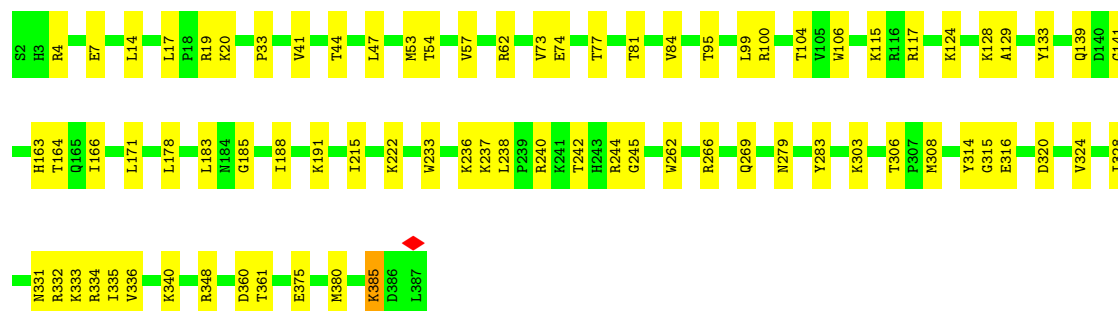


- Molecule 39: 60S ribosomal protein L30

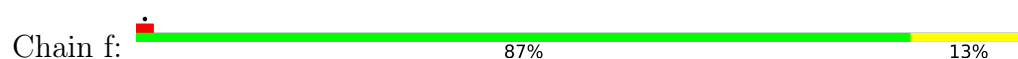


- Molecule 40: 60S ribosomal protein L3

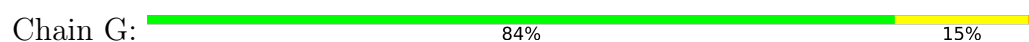




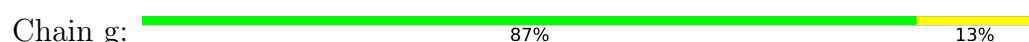
- Molecule 41: 60S ribosomal protein L31-A



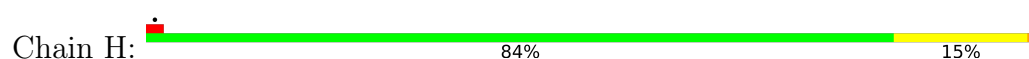
- Molecule 42: 60S ribosomal protein L4-A



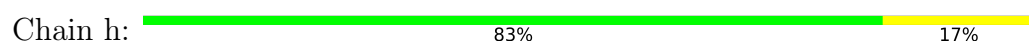
- Molecule 43: 60S ribosomal protein L32



- Molecule 44: 60S ribosomal protein L5



- Molecule 45: 60S ribosomal protein L33-A



A1900	C1793	U1672	C1574	G1487	G1389	G1285	U1211	G1126	G1029	A933	G842	G728	C636
A1901	G1794	G1675	A1575	G1488	A1390	A1286	A1212	G1127	G1032	G937	A843	G737	C637
G1905	U1795	A1676	G1577	A1489	G1392	A1287	G1213	U1128	U1033	C938	G849	A738	C638
G1906	G1796	G1677	C1578	A1490	A1393	C1292	C1219	A1129	G1034	C944	U850	G742	G639
C1907	A1797	A1683	A1580	G1493	A1394	U1293	A1221	G1131	A1036	C949	C851	C743	C641
A1913	G1812	U1687	C1581	U1494	A1399	A1301	G1222	G1134	C1037	C953	G857	C744	A645
G1914	A1813	U1687	C1582	U1495	G1400	A1302	A1223	U1138	C1038	G953	A858	A744	A646
A1915	A1814	U1695	A1583	C1497	A1401	A1303	C1224	U1139	U1039	C959	G859	C753	A647
U1920	A1815	A1696	G1404	A1498	G1404	U1305	G1226	G1140	A1040	C961	G860	C758	C648
G1927	G1817	G1712	A1587	A1503	U1410	G1307	G1230	A1143	U1044	U960	C861	U759	A649
G1928	U1818	G1713	A1588	C1508	G1417	A1308	A1231	U1144	C1045	A962	U865	G760	A656
G1929	U1819	A1714	G1590	C1508	A1418	G1314	C1232	G1145	A1046	G964	G869	G763	G661
A1930	U1821	U1715	A1594	U1511	A1419	G1315	U1235	A1150	A1064	G971	G870	G764	U664
U1931	C1822	G1716	C1420	U1512	G1420	U1316	G1236	U1151	G1063	A972	U871	C765	A665
A1932	G1830	U1717	G1421	U1523	G1421	A1317	G1237	G1152	A1048	A973	U872	U766	A666
G1935	U1830	G1718	C1596	G1523	U1432	U1322	G1242	A1155	C1062	G978	G873	G767	C667
U1938	G1838	U1722	A1605	C1527	A1433	U1329	U1241	C1156	A1065	U979	U879	G770	G674
G1939	A1839	A1723	U1606	G1528	G1434	A1330	G1243	A1157	G1066	U981	G880	U776	C675
C1943	U1840	C1725	A1613	U1533	A1435	U1331	A1245	A1158	U1071	G982	C881	U777	G676
G1953	A1842	G1730	C1615	A1534	U1436	U1336	A1246	A1159	G1072	U985	U882	U777	A677
G1954	C1844	G1732	G1618	G1536	G1437	U1337	U1247	A1169	A1075	U989	G883	U781	G678
U1955	G1846	U1732	A1619	G1543	A1438	A1337	C1248	G1177	C1076	U990	U884	G783	U679
A1956	C1847	G1733	U1620	A1546	G1447	A1337	G1249	U1178	U1081	G991	G885	G784	U681
G1957	U1847	G1733	A1621	G1547	U1448	U1349	G1250	A1179	U1082	G994	C889	A784	U682
U1958	G1848	U1740	G1622	C1548	A1449	G1348	A1251	A1181	G1083	U995	U891	G786	U683
G1959	C1849	A1741	G1623	U1549	G1450	A1351	A1252	A1182	U1088	A996	G900	G789	G684
A1960	G1851	U1742	U1628	C1550	U1455	A1352	C1253	C1183	U1089	U999	G901	G800	U687
G1961	G1852	A1749	U1629	G1551	A1456	A1352	C1254	A1184	G1090	C1000	A906	A801	A690
A1962	U1861	A1750	U1630	U1553	A1460	A1355	G1256	U1190	A1091	G1001	G907	G804	A691
G1963	G1862	C1755	C1631	U1554	A1461	U1356	C1257	U1191	C1092	G1005	G908	G805	A692
C1964	A1863	G1761	C1632	U1555	A1462	G1357	U1258	C1192	U1093	A1006	G909	A806	C696
C1965	G1864	A1760	G1634	C1556	U1463	A1363	A1259	A1193	A1094	G1010	C911	A807	A699
U1966	A1865	C1761	U1641	A1557	G1464	C1364	A1260	G1194	U1095	G1015	G912	A808	A705
U1967	C1866	C1762	A1642	A1558	A1467	G1365	G1261	A1196	U1096	C1016	A913	U814	G708
G1968	A1867	U1763	U1643	A1559	A1468	A1366	G1262	C1197	C1097	C1017	A914	G824	A709
G1969	G1868	U1765	U1645	G1561	C1469	G1367	G1263	A1198	A1098	G1018	G915	U825	A710
U1970	A1874	G1766	G1646	C1562	A1474	U1368	U1265	C1199	A1102	G1019	A916	A830	G712
C1971	G1878	G1769	A1656	U1564	A1477	G1374	G1266	A1200	A1103	G1020	A917	G831	G713
A1972	U1879	G1770	C1657	G1565	A1477	A1380	U1267	C1201	G1104	G1021	A920	A832	A715
G1973	G1880	C1771	G1661	A1566	G1480	A1381	A1270	A1202	U1110	G1024	C923	G833	G716
A1974	U1886	G1775	G1662	U1568	A1481	G1382	C1277	A1203	G1115	A1025	G924	G832	A717
C1975	A1887	G1780	G1666	U1569	A1482	C1385	U1278	G1206	G1116	A1026	A925	G836	U719
G1976	U1887	U1667	A1667	U1570	G1483	A1386	C1279	G1207	G1117	A1027	G925	A837	A720
C1977	A1893	G1786	G1668	U1571	U1484	G1387	G1281	U1208	U1122	U1028	A929	G837	
A1978	U1894	U1787		U1572	U1485	U1388	G1282	U1210			U932		
G1979				G1573	G1486								
C1980													
U2043													
U2044													
G2045													

U3287	G3288	G3289	G3290	G3291	A3292	U3293	A3294	A3295	A3296	U3297	G3303	U3304	A3305	U3306	A3307	C3308	G3309	U3313	A3316	U3317	G3318	U3319	G3328	U3329	U3332	G3333	U3334	A3335	U3341	G3345	U3346	A3347	G3348	C3349	G3350	U3351	U3352	G3353	U3354	U3355	G3356	U3357	U3358	A3359	A3362	U3363	G3368	U3369		
C3212	A3213	U3214	A3215	U3216	A3217	G3218	A3219	A3220	A3221	U3222	G3225	A3226	A3227	U3231	G3232	C3233	A3234	U3237	G3238	G3239	G3242	A3243	A3244	A3245	G3246	G3247	G3253	G3254	U3255	G3256	G3257	U3258	U3259	G3260	A3267	A3268	U3269	U3270	G3271	C3272	A3273	A3274	G3275	G3276	U3277	C3278	A3279	U3280	U3281	G3282
U2319	A2320	A2321	G2322	A2323	G2324	U2325	U2334	G2335	C2336	U2337	A2338	U2339	U2340	U2347	A2356	A2361	A2367	G2371	A2372	A2373	C2374	G2375	U2376	G2377	C2383	A2384	G2385	A2386	U2387	U2388	G2391	C2392	G2393	A2397	A2401	A2402	G2403	A2404	C2405	C2406	U2411	G2418	U2419	U2423	A2424	U2428				
G2429	G2435	G2440	A2441	G2442	A2443	A2444	A2445	U2446	A2447	G2448	A2449	G2450	U2451	G2452	U2453	G2454	U2455	A2456	A2457	A2458	A2459	U2460	A2461	A2462	G2466	U2467	A2468	G2469	C2470	U2471	U2472	C2473	C2474	G2477	A2480	U2481	U2482	C2483	A2486	U2487	A2488	C2489	C2492	C2496	U2497	A2500	U2501	A2502	G2503	U2504
U2505	U2506	C2507	U2508	U2509	U2510	A2511	C2512	U2513	U2514	A2515	U2516	G2522	A2523	C2526	C2531	U2532	G2533	G2534	U2537	U2538	C2539	A2540	U2541	U2542	U2543	U2544	C2545	C2546	A2547	C2548	G2549	C2552	U2553	A2554	G2555	U2559	C2560	A2561	U2565	C2568	A2569	U2570	U2571	C2572	G2573	G2576	G2584	G2585	G2586	
U2587	A2593	C2594	A2595	G2603	G2606	G2607	G2614	G2615	C2616	U2617	G2618	G2619	C2625	A2626	U2629	U2630	U2631	A2635	A2636	A2642	G2645	G2648	G2651	U2652	U2655	A2656	A2657	G2660	U2665	C2666	A2674	C2675	A2676	G2677	A2678	U2681	G2687	U2688	A2689	G2690	U2691	G2697	A2698	G2699	A2700					
C2693	A2694	G2700	U2701	A2702	A2703	A2704	A2705	C2711	U2712	U2713	G2714	A2715	U2716	U2719	G2720	U2724	U2725	C2726	A2727	U2728	U2729	C2737	C2742	A2743	U2744	G2748	C2755	U2756	U2757	G2761	A2762	U2767	U2768	A2769	C2772	C2773	G2777	G2778	A2779	G2784	U2785	G2786	A2787	A2788	G2789	A2790				
G2796	C2797	A2798	G2799	G2800	A2801	A2802	A2804	C2810	G2814	G2815	A2817	C2825	U2826	U2827	U2828	U2829	G2830	U2842	U2843	A2844	A2845	U2846	A2847	G2850	A2851	U2860	A2864	C2867	G2871	A2872	U2873	U2875	U2882	A2887	U2888	C2889	G2895	A2896	A2897	C2898	G2901	U2907	A2908	G2909	U3010					
G2908	A2911	G2912	U2915	U2923	U2924	A2925	A2926	C2929	U2935	A2936	G2937	G2938	A2941	G2945	A2946	G2947	U2948	G2950	G2951	U2954	C2960	G2961	A2971	C2972	U2978	U2979	U2980	U2981	A2982	C2983	C2984	C2985	C2988	U2989	G2990	U2996	G2997	G3003	C3004	U3007	A3008	G3009	U3010							
A3011	A3012	A3016	A3017	A3021	G3022	U3023	A3024	C3025	G3026	G3030	U3037	U3038	C3039	A3040	U3041	U3042	G3045	A3046	U3047	U3055	U3056	U3057	U3058	G3059	C3060	C3067	C3068	C3069	A3070	G3074	G3075	U3078	U3079	G3080	C3084	G3085	A3086	C3092	C3093	A3094	G3098	U3104	G3108	G3109						
C3115	G3116	C3117	C3118	U3119	C3120	U3121	A3122	A3130	U3131	G3136	A3139	G3140	A3141	A3142	C3143	G3144	U3151	U3152	U3153	C3154	U3155	U3156	U3157	C3158	C3159	U3160	C3161	C3162	A3163	A3167	G3173	A3174	U3175	G3176	U3179	A3180	C3181	A3186	A3187	U3196	G3197	U3198	G3205	C3206	U3207	G3208	A3209	A3210	C3211	
U3287	G3288	C3289	G3290	G3291	A3292	U3293	A3294	A3295	A3296	U3297	G3303	U3304	A3305	U3306	A3307	C3308	G3309	U3313	A3316	U3317	G3318	U3319	G3328	U3329	U3332	G3333	U3334	A3335	U3341	G3345	U3346	A3347	G3348	C3349	G3350	U3351	U3352	G3353	U3354	U3355	G3356	U3357	U3358	A3359	A3362	U3363	G3368	U3369		

A3375	U3382
A3376	G3383
G3377	G3386
C3378	G3390
C3379	U3393
	U3396

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	115812	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.812	Depositor
Minimum map value	-0.588	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	R	0.21	0/2631	0.56	0/3532
2	X	0.24	0/1653	0.62	4/2255 (0.2%)
3	i	0.39	0/890	0.76	1/1189 (0.1%)
4	J	0.41	0/1821	0.72	0/2451
5	j	0.32	0/978	0.84	8/1301 (0.6%)
6	K	0.33	0/1836	0.77	4/2481 (0.2%)
7	k	0.35	0/778	0.75	0/1034
8	7	0.28	0/1539	0.62	0/2073
9	l	0.44	0/696	0.79	0/923
10	M	0.26	0/1374	0.72	0/1842
11	m	0.32	0/618	0.64	0/826
12	N	0.42	0/1568	0.84	2/2106 (0.1%)
13	n	0.44	0/443	0.73	0/588
14	O	0.31	0/1068	0.67	0/1438
15	o	0.25	0/423	0.68	0/562
16	p	0.46	0/1757	0.85	3/2354 (0.1%)
17	Q	0.38	0/1585	0.72	0/2128
18	5	0.38	0/1443	0.74	2/1944 (0.1%)
19	S	0.36	0/1465	0.78	1/1965 (0.1%)
20	s	0.32	0/1807	0.80	6/2425 (0.2%)
21	T	0.34	0/1245	0.73	0/1661
22	U	0.37	0/1481	0.74	0/1990
23	V	0.37	0/1300	0.70	2/1743 (0.1%)
24	W	0.27	0/812	0.68	0/1099
25	P	0.25	0/734	0.85	1/1015 (0.1%)
26	r	0.21	0/982	0.65	1/1320 (0.1%)
27	x	0.40	0/1018	0.71	0/1369
28	3	0.29	0/2883	0.46	1/4491 (0.0%)
29	Y	0.32	0/525	0.64	0/696
30	4	0.35	0/3746	0.47	0/5832
31	Z	0.35	0/979	0.66	0/1321
32	a	0.32	0/1004	0.70	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.30	0/1118	0.68	2/1497 (0.1%)
34	C	0.32	0/860	0.74	0/1136
35	c	0.42	0/1204	0.82	1/1612 (0.1%)
36	D	0.39	0/701	0.74	0/934
37	d	0.32	0/473	0.64	0/629
38	E	0.46	0/1948	0.77	0/2617
39	e	0.26	0/751	0.61	0/1008
40	F	0.44	1/3146 (0.0%)	0.73	1/4228 (0.0%)
41	f	0.40	0/890	0.68	0/1196
42	G	0.38	0/2800	0.77	2/3790 (0.1%)
43	g	0.35	0/1041	0.67	1/1394 (0.1%)
44	H	0.31	0/2425	0.70	2/3271 (0.1%)
45	h	0.40	0/868	0.66	0/1168
46	I	0.27	0/1260	0.61	0/1694
47	L	0.25	0/1634	0.74	1/2195 (0.0%)
48	1	0.35	0/78052	0.53	17/121690 (0.0%)
All	All	0.35	1/142253 (0.0%)	0.60	63/209354 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	X	0	1
4	J	0	2
5	j	0	2
6	K	0	3
7	k	0	1
8	7	0	1
10	M	0	1
11	m	0	2
12	N	0	3
14	O	0	1
20	s	0	4
33	b	0	1
35	c	0	3
36	D	0	1
37	d	0	1
38	E	0	1
40	F	0	1
42	G	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
44	H	0	1
All	All	0	34

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	F	237	LYS	C-N	-8.30	1.17	1.33

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	N	61	PRO	CA-C-N	7.76	136.36	121.54
12	N	61	PRO	C-N-CA	7.76	136.36	121.54
6	K	38	GLN	CA-C-N	6.80	131.44	121.31
6	K	38	GLN	C-N-CA	6.80	131.44	121.31
23	V	133	ALA	CA-C-N	6.78	130.98	120.60
23	V	133	ALA	C-N-CA	6.78	130.98	120.60
48	1	857	G	C2'-C3'-O3'	6.64	119.46	109.50
26	r	80	VAL	N-CA-C	-6.53	106.36	112.83
44	H	139	PRO	CA-C-N	6.36	130.33	120.60
44	H	139	PRO	C-N-CA	6.36	130.33	120.60
48	1	1900	A	C2'-C3'-O3'	6.32	118.98	109.50
18	5	157	VAL	CA-C-N	6.32	130.11	120.82
18	5	157	VAL	C-N-CA	6.32	130.11	120.82
5	j	91	ALA	CA-C-N	6.26	130.63	121.31
5	j	91	ALA	C-N-CA	6.26	130.63	121.31
33	b	101	PHE	CA-C-N	6.14	130.46	121.31
33	b	101	PHE	C-N-CA	6.14	130.46	121.31
48	1	269	G	C2'-C3'-O3'	6.14	118.71	109.50
20	s	172	PHE	N-CA-C	-6.13	106.44	114.04
16	p	120	TRP	CA-C-N	-6.11	116.74	122.66
16	p	120	TRP	C-N-CA	-6.11	116.74	122.66
2	X	161	VAL	CA-C-N	6.06	129.49	120.83
2	X	161	VAL	C-N-CA	6.06	129.49	120.83
19	S	99	THR	N-CA-C	6.00	117.64	110.19
40	F	245	GLY	N-CA-C	5.99	119.00	112.29
48	1	1391	C	C2'-C3'-O3'	5.98	118.47	109.50
16	p	75	VAL	CA-CB-CG2	5.93	120.49	110.40
28	3	77	G	C2'-C3'-O3'	5.83	118.25	109.50
20	s	106	GLY	CA-C-N	5.83	132.67	121.54
20	s	106	GLY	C-N-CA	5.83	132.67	121.54
5	j	90	ARG	CA-C-N	5.81	132.64	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	j	90	ARG	C-N-CA	5.81	132.64	121.54
6	K	156	ASP	CA-C-N	5.69	132.22	121.97
6	K	156	ASP	C-N-CA	5.69	132.22	121.97
20	s	134	ILE	CA-C-N	5.66	132.35	121.54
20	s	134	ILE	C-N-CA	5.66	132.35	121.54
48	1	1481	A	C2'-C3'-O3'	5.48	117.72	109.50
48	1	2541	U	P-O3'-C3'	5.48	128.41	120.20
48	1	156	G	P-O3'-C3'	5.47	128.41	120.20
5	j	84	LYS	CA-C-N	5.47	131.99	121.54
5	j	84	LYS	C-N-CA	5.47	131.99	121.54
35	c	47	LYS	N-CA-C	5.47	122.45	110.80
25	P	139	VAL	N-CA-C	-5.40	108.24	113.53
48	1	2313	A	C4'-C3'-O3'	5.40	117.50	109.40
48	1	2468	A	P-O3'-C3'	5.39	128.28	120.20
47	L	191	VAL	N-CA-C	-5.33	106.66	113.22
5	j	46	THR	CA-C-N	-5.32	115.83	121.84
5	j	46	THR	C-N-CA	-5.32	115.83	121.84
48	1	1483	G	C2'-C3'-O3'	5.28	117.42	109.50
20	s	138	ARG	CA-CB-CG	5.28	124.66	114.10
48	1	2447	A	P-O3'-C3'	5.27	128.11	120.20
48	1	2509	U	P-O3'-C3'	5.27	128.11	120.20
48	1	2727	A	P-O3'-C3'	5.27	128.10	120.20
2	X	7	PHE	CA-C-N	5.13	131.34	121.54
2	X	7	PHE	C-N-CA	5.13	131.34	121.54
48	1	1307	G	P-O3'-C3'	5.13	127.89	120.20
42	G	337	GLU	CA-C-N	5.11	131.30	121.54
42	G	337	GLU	C-N-CA	5.11	131.30	121.54
3	i	89	ILE	N-CA-C	-5.07	106.86	111.67
48	1	2267	C	P-O3'-C3'	5.04	127.77	120.20
48	1	3278	C	C2-N1-C1'	5.04	133.91	118.80
43	g	42	VAL	N-CA-C	-5.02	107.49	111.81
48	1	1900	A	P-O3'-C3'	5.02	127.72	120.20

There are no chirality outliers.

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	7	21	LYS	Peptide
36	D	51	ALA	Peptide
38	E	179	LEU	Peptide
40	F	385	LYS	Peptide
42	G	131	VAL	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
42	G	291	ASN	Peptide
42	G	318	LEU	Peptide
42	G	338	LYS	Peptide
44	H	259	LYS	Peptide
4	J	157	ASN	Peptide
4	J	232	ARG	Peptide
6	K	156	ASP	Peptide
6	K	35	GLY	Peptide
6	K	76	ALA	Peptide
10	M	172	LEU	Peptide
12	N	4	SER	Peptide
12	N	47	ALA	Peptide
12	N	61	PRO	Peptide
14	O	48	GLY	Peptide
2	X	8	GLU	Peptide
33	b	102	GLU	Peptide
35	c	116	GLY	Peptide
35	c	45	MET	Peptide
35	c	46	ASP	Peptide
37	d	19	ASN	Peptide
5	j	90	ARG	Peptide
5	j	91	ALA	Peptide
7	k	27	SER	Peptide
11	m	32	ASN	Peptide
11	m	35	GLY	Peptide
20	s	103	SER	Peptide
20	s	107	ALA	Peptide
20	s	134	ILE	Peptide
20	s	170	TRP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	2784	0	2683	38	0
2	X	1633	0	1596	16	0
3	i	880	0	945	10	0
4	J	1784	0	1862	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	j	969	0	1078	5	0
6	K	1804	0	1877	20	0
7	k	771	0	849	9	0
8	7	1518	0	1587	17	0
9	l	681	0	687	11	0
10	M	1353	0	1383	15	0
11	m	612	0	682	1	0
12	N	1543	0	1608	24	0
13	n	436	0	475	4	0
14	O	1053	0	1149	17	0
15	o	417	0	459	6	0
16	p	1720	0	1779	28	0
17	Q	1555	0	1659	16	0
18	5	1420	0	1437	18	0
19	S	1441	0	1543	21	0
20	s	1770	0	1808	21	0
21	T	1228	0	1314	14	0
22	U	1445	0	1487	21	0
23	V	1276	0	1323	21	0
24	W	796	0	812	2	0
25	P	737	0	341	1	0
26	r	967	0	991	15	0
27	x	1003	0	1048	13	0
28	3	2579	0	1304	23	0
29	Y	513	0	540	7	0
30	4	3353	0	1695	28	0
31	Z	964	0	1025	11	0
32	a	993	0	1081	12	0
33	b	1092	0	1155	8	0
34	C	847	0	918	12	0
35	c	1173	0	1215	20	0
36	D	694	0	738	8	0
37	d	462	0	491	2	0
38	E	1914	0	1981	35	0
39	e	743	0	797	6	0
40	F	3075	0	3142	56	0
41	f	876	0	912	9	0
42	G	2748	0	2859	37	0
43	g	1020	0	1090	12	0
44	H	2375	0	2325	33	0
45	h	850	0	880	11	0
46	I	1239	0	1326	8	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	L	1609	0	1701	26	0
48	1	69730	0	35041	530	0
49	R	1	0	0	0	0
All	All	132446	0	96678	1020	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 5.

All (1020) 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)
48:1:3231:U:H3	48:1:3256:G:H1	1.13	0.96
48:1:196:G:H21	48:1:219:A:H61	1.08	0.96
48:1:3160:U:H3	48:1:3290:G:H1	1.14	0.92
48:1:196:G:N2	48:1:219:A:H61	1.71	0.89
48:1:1257:C:N4	48:1:1261:G:H22	1.73	0.86
48:1:182:U:H3	48:1:234:G:H1	1.24	0.84
48:1:1257:C:H42	48:1:1261:G:H22	1.22	0.83
40:F:81:THR:O	40:F:320:ASP:HB2	1.78	0.83
48:1:1257:C:H42	48:1:1261:G:N2	1.75	0.83
48:1:1564:U:H3	48:1:1576:G:H1	0.85	0.83
48:1:1958:U:C2	48:1:2083:G:O6	2.32	0.82
46:I:2:SER:N	48:1:1385:C:HO2'	1.76	0.81
48:1:3222:U:H3	48:1:3263:G:H1	1.31	0.79
48:1:2844:C:H42	48:1:2898:G:N2	1.82	0.78
22:U:6:GLU:O	22:U:64:ILE:HB	1.85	0.77
48:1:2844:C:N4	48:1:2898:G:H22	1.82	0.77
48:1:196:G:H21	48:1:219:A:N6	1.82	0.77
1:R:74:CYS:SG	1:R:96:HIS:CE1	2.77	0.77
48:1:3047:U:O4	48:1:3094:A:N1	2.18	0.77
48:1:1237:G:H1	48:1:1251:A:H61	1.33	0.77
48:1:1958:U:O2	48:1:2083:G:C6	2.38	0.76
48:1:3348:G:H1	48:1:3357:U:H3	1.34	0.75
48:1:170:G:H1	48:1:248:U:H3	1.32	0.74
12:N:35:ARG:HH12	48:1:684:G:H5''	1.52	0.74
12:N:91:ARG:HE	12:N:97:VAL:HB	1.52	0.73
48:1:437:G:H22	48:1:622:A:H61	1.37	0.71
17:Q:160:ARG:HD2	48:1:3243:A:H61	1.57	0.70
12:N:76:THR:HG22	12:N:101:ARG:HG3	1.73	0.69
42:G:98:ARG:NH2	48:1:804:C:OP1	2.26	0.69
48:1:2449:A:H61	48:1:2497:U:H3	1.40	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1:1562:C:H42	48:1:1578:C:H42	1.41	0.68
16:p:53:TYR:HB2	16:p:133:ILE:HD11	1.75	0.68
48:1:173:G:H1	48:1:245:U:H3	1.40	0.68
1:R:271:GLU:HB3	1:R:383:LYS:HD3	1.75	0.68
12:N:46:ILE:HG22	12:N:49:ARG:HB2	1.75	0.67
48:1:2193:U:H5'	48:1:2194:G:H5'	1.76	0.67
27:x:14:SER:O	27:x:81:GLN:NE2	2.29	0.66
27:x:81:GLN:O	27:x:98:ASN:ND2	2.28	0.66
26:r:25:LEU:HB3	26:r:191:TYR:HB3	1.78	0.65
42:G:334:PHE:HA	42:G:339:LEU:HD12	1.78	0.65
1:R:452:LYS:HG3	1:R:494:ILE:HG12	1.77	0.65
40:F:266:ARG:NH2	48:1:2392:C:O2'	2.30	0.64
17:Q:22:VAL:HG21	17:Q:120:VAL:HG11	1.80	0.64
48:1:2440:G:N2	48:1:2507:C:N3	2.45	0.64
35:c:58:MET:SD	48:1:2786:G:N2	2.68	0.64
21:T:103:ARG:NH1	21:T:124:TYR:OH	2.31	0.64
26:r:27:VAL:HB	26:r:189:GLN:HB2	1.80	0.64
30:4:81:U:H5''	30:4:82:U:H5'	1.80	0.64
48:1:2825:C:H42	48:1:2864:A:H61	1.43	0.64
30:4:156:U:H3	48:1:3:U:H3	1.44	0.63
20:s:207:ASN:HA	20:s:210:ARG:HG2	1.80	0.63
26:r:26:PHE:HB2	26:r:87:VAL:HB	1.81	0.63
17:Q:61:ALA:HA	17:Q:70:PRO:HD2	1.80	0.63
47:L:209:SER:HB2	48:1:2466:G:H21	1.63	0.63
16:p:201:ARG:HB3	42:G:110:ASN:HD22	1.64	0.63
48:1:2149:A:N6	48:1:2187:G:O2'	2.31	0.63
1:R:74:CYS:SG	1:R:77:CYS:HB2	2.39	0.63
34:C:41:ARG:NH1	48:1:284:A:OP2	2.32	0.62
14:O:36:VAL:HG11	14:O:55:ARG:HH12	1.63	0.62
9:l:72:ARG:NH1	30:4:95:G:OP2	2.33	0.62
1:R:436:ILE:HG12	1:R:461:ARG:HH11	1.64	0.62
10:M:47:GLN:HG2	10:M:67:VAL:HG12	1.80	0.62
30:4:17:A:N6	48:1:406:G:O2'	2.33	0.62
48:1:542:G:H1	48:1:549:U:H3	1.46	0.62
4:J:160:ARG:NH1	48:1:1363:A:OP1	2.33	0.62
19:S:12:ARG:NH2	48:1:972:A:OP1	2.33	0.62
48:1:3047:U:C4	48:1:3094:A:N1	2.67	0.62
42:G:206:LEU:HB2	42:G:246:ARG:HE	1.63	0.62
19:S:170:ARG:HD2	35:c:57:GLY:HA3	1.81	0.61
42:G:20:LEU:HD11	42:G:252:GLU:HG3	1.82	0.61
9:l:43:LYS:NZ	48:1:55:G:OP1	2.33	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:12:ARG:HB3	22:U:24:LEU:HD23	1.82	0.61
15:o:106:ARG:HH21	48:1:3118:C:H4'	1.65	0.61
48:1:2724:U:OP2	48:1:2726:C:N4	2.32	0.61
16:p:155:VAL:HG12	48:1:58:G:H4'	1.83	0.61
48:1:1958:U:O2	48:1:2083:G:O6	2.16	0.61
26:r:89:THR:HG21	26:r:96:ILE:HG13	1.83	0.61
48:1:2137:U:OP2	48:1:2142:A:N6	2.31	0.61
48:1:2534:G:H1	48:1:2545:C:H42	1.47	0.61
40:F:57:VAL:HG22	40:F:73:VAL:HG12	1.81	0.61
48:1:589:A:N6	48:1:610:G:O2'	2.32	0.60
1:R:344:ARG:HD2	48:1:2289:U:H4'	1.83	0.60
1:R:484:LYS:HD2	1:R:519:HIS:HB3	1.83	0.60
10:M:92:ARG:HA	10:M:172:LEU:HB2	1.84	0.60
42:G:71:VAL:HG22	42:G:76:ARG:HH22	1.66	0.60
45:h:13:HIS:ND1	45:h:93:THR:O	2.35	0.60
48:1:198:A:N3	48:1:218:G:O2'	2.35	0.60
18:5:135:ARG:NH2	48:1:879:U:O2'	2.34	0.60
26:r:46:ARG:HH22	48:1:1257:C:H4'	1.66	0.60
48:1:2844:C:N4	48:1:2898:G:N2	2.44	0.60
48:1:28:C:O2'	48:1:61:A:N3	2.32	0.60
20:s:46:PRO:HB2	20:s:177:ARG:HH22	1.67	0.59
40:F:139:GLN:HG3	40:F:141:GLY:H	1.67	0.59
40:F:53:MET:HG2	40:F:77:THR:HG22	1.84	0.59
48:1:2842:U:OP1	48:1:2844:C:N4	2.36	0.59
48:1:2761:G:O2'	48:1:2800:G:N2	2.35	0.59
12:N:36:ARG:NH2	48:1:687:U:OP2	2.34	0.59
20:s:190:LYS:NZ	20:s:211:GLU:OE1	2.36	0.59
40:F:115:LYS:NZ	40:F:129:ALA:O	2.36	0.59
48:1:2406:C:O2'	48:1:2619:G:N2	2.36	0.59
29:Y:12:LYS:O	29:Y:32:GLN:NE2	2.36	0.59
10:M:137:ARG:NH1	28:3:28:C:OP1	2.35	0.58
48:1:1237:G:H1	48:1:1251:A:N6	1.99	0.58
3:i:8:ARG:NH2	48:1:1606:U:O4'	2.36	0.58
6:K:126:SER:O	48:1:120:G:N2	2.37	0.58
7:k:30:LYS:NZ	48:1:317:A:OP2	2.35	0.58
38:E:126:LEU:HD13	38:E:150:LEU:HD21	1.85	0.58
12:N:59:ARG:NH1	48:1:73:C:N3	2.51	0.58
48:1:284:A:N7	48:1:305:U:O2'	2.37	0.58
48:1:645:A:O2'	48:1:647:A:OP2	2.20	0.58
18:5:56:ARG:NH1	18:5:75:GLU:OE2	2.37	0.58
48:1:1392:G:O2'	48:1:1418:A:N6	2.37	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:s:34:ASP:HB3	20:s:85:HIS:HE2	1.67	0.58
23:V:30:TYR:O	44:H:41:LYS:NZ	2.37	0.58
48:1:625:G:N2	48:1:1401:A:OP1	2.35	0.58
16:p:9:GLU:OE2	16:p:13:LYS:NZ	2.36	0.58
18:5:118:GLN:NE2	18:5:147:GLU:OE2	2.36	0.58
14:O:128:ARG:NH1	48:1:3214:U:OP2	2.37	0.58
19:S:86:THR:HG22	19:S:105:ARG:HB2	1.86	0.58
32:a:12:ARG:NH1	48:1:215:G:OP1	2.34	0.58
1:R:74:CYS:SG	1:R:96:HIS:HE1	2.25	0.58
6:K:148:ALA:HA	6:K:201:THR:HG22	1.86	0.58
48:1:1235:U:H4'	48:1:1236:G:H5'	1.86	0.57
19:S:92:ARG:NH1	48:1:784:A:O2'	2.36	0.57
23:V:93:VAL:HG11	44:H:41:LYS:HE3	1.85	0.57
30:4:39:G:O2'	30:4:104:A:N6	2.37	0.57
6:K:162:LEU:HA	16:p:7:LEU:HD11	1.86	0.57
12:N:18:TRP:NE1	48:1:799:G:O2'	2.32	0.57
16:p:68:ARG:NH2	48:1:292:U:OP2	2.37	0.57
43:g:38:ILE:O	43:g:44:ARG:NH2	2.37	0.57
4:J:207:LEU:HB3	4:J:243:MET:HB3	1.85	0.57
38:E:116:VAL:HG13	38:E:126:LEU:HB2	1.86	0.57
47:L:40:ASN:HB2	47:L:163:LEU:HB3	1.87	0.57
1:R:316:ASN:O	1:R:320:LEU:HB2	2.05	0.57
14:O:23:ILE:O	14:O:30:GLY:N	2.37	0.57
44:H:64:ILE:HD13	44:H:109:THR:HG21	1.86	0.57
44:H:123:GLU:HA	44:H:248:ARG:HH12	1.69	0.57
48:1:81:C:HO2'	48:1:683:U:HO2'	1.53	0.57
10:M:15:GLU:HB3	10:M:130:VAL:HG13	1.87	0.57
48:1:306:A:N6	48:1:2784:G:C2	2.73	0.57
30:4:150:G:OP1	31:Z:27:ARG:NH2	2.37	0.57
34:C:71:ARG:HH21	34:C:80:ARG:HH11	1.51	0.57
38:E:9:ARG:NH1	48:1:912:G:OP2	2.37	0.57
21:T:78:TYR:O	48:1:1914:G:N2	2.38	0.57
1:R:249:ALA:HB2	1:R:382:LEU:HD13	1.86	0.57
20:s:53:SER:HA	20:s:162:GLN:HB2	1.85	0.57
40:F:266:ARG:NH1	48:1:2988:C:O2	2.38	0.57
48:1:3060:C:O2	48:1:3332:U:O2'	2.23	0.57
7:k:40:VAL:HG11	16:p:5:LYS:HG3	1.87	0.56
48:1:2255:A:H2	48:1:2261:G:H1	1.53	0.56
31:Z:45:LYS:NZ	48:1:129:U:OP1	2.37	0.56
42:G:82:THR:HG23	42:G:84:ARG:H	1.69	0.56
4:J:88:ARG:NH1	4:J:109:THR:O	2.37	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:92:TYR:HB2	8:7:142:ASP:HB3	1.87	0.56
22:U:112:ALA:O	22:U:115:ARG:NH1	2.39	0.56
35:c:26:ARG:HH12	48:1:938:C:H3'	1.71	0.56
48:1:2085:U:H2'	48:1:2086:A:H8	1.71	0.56
1:R:235:ILE:HD12	1:R:250:ILE:HD12	1.87	0.56
42:G:188:ARG:NH1	48:1:1382:G:OP2	2.37	0.56
47:L:30:GLU:HB2	47:L:34:LEU:HD11	1.86	0.56
48:1:129:U:H3	48:1:139:G:H1	1.51	0.56
2:X:106:ASN:ND2	2:X:150:SER:OG	2.39	0.56
23:V:17:ARG:NH1	23:V:45:ASN:OD1	2.38	0.56
23:V:130:ARG:NH2	48:1:1062:A:N3	2.51	0.56
28:3:17:A:OP1	44:H:2:ALA:N	2.39	0.56
35:c:112:ILE:HB	35:c:130:VAL:HG12	1.87	0.56
48:1:984:G:N2	48:1:1138:U:OP1	2.39	0.56
4:J:67:ARG:NH2	48:1:517:G:OP1	2.39	0.56
6:K:69:LEU:HD21	16:p:24:ARG:HD2	1.88	0.56
33:b:54:THR:H	33:b:57:HIS:HD2	1.53	0.56
48:1:2307:G:O2'	48:1:2310:U:OP2	2.23	0.56
22:U:109:ASP:OD1	22:U:113:ARG:NH1	2.37	0.56
41:f:55:LEU:HB2	41:f:95:PRO:HD3	1.87	0.56
48:1:3333:G:N2	48:1:3369:G:O2'	2.38	0.56
48:1:397:A:O2'	48:1:400:G:OP2	2.23	0.56
38:E:21:ARG:HD3	48:1:824:C:H5''	1.87	0.56
5:j:77:PRO:HD2	5:j:80:LEU:HD12	1.88	0.56
10:M:133:ARG:NH2	10:M:158:ASP:OD2	2.39	0.56
47:L:35:GLN:HG3	47:L:169:VAL:HG22	1.87	0.56
6:K:36:ILE:HD13	38:E:34:TYR:HE2	1.71	0.55
27:x:12:ARG:HB2	48:1:3040:A:H5''	1.86	0.55
28:3:7:G:OP1	44:H:33:ARG:NH1	2.38	0.55
14:O:23:ILE:O	14:O:30:GLY:CA	2.54	0.55
21:T:62:ARG:NH2	48:1:3070:A:OP1	2.39	0.55
26:r:60:ARG:NH1	48:1:1222:G:N7	2.52	0.55
33:b:69:LYS:NZ	48:1:1632:A:OP1	2.37	0.55
47:L:122:ARG:NH1	48:1:2483:G:OP2	2.39	0.55
48:1:1455:U:OP1	48:1:1879:A:N6	2.39	0.55
48:1:1959:G:O6	48:1:2082:U:O2	2.24	0.55
1:R:239:PHE:HZ	1:R:328:LEU:HD21	1.70	0.55
48:1:1863:G:N1	48:1:1866:C:OP2	2.31	0.55
16:p:45:PRO:O	16:p:49:ARG:HB2	2.07	0.55
40:F:124:LYS:NZ	48:1:3297:U:O4	2.33	0.55
48:1:107:A:O2'	48:1:324:A:N3	2.35	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:100:ARG:NH1	48:1:76:G:O2'	2.37	0.55
19:S:141:ARG:NH1	48:1:743:C:N3	2.55	0.55
40:F:19:ARG:NH2	48:1:3045:G:OP1	2.39	0.55
1:R:74:CYS:SG	1:R:77:CYS:CB	2.95	0.55
40:F:385:LYS:NZ	48:1:3328:G:OP1	2.38	0.55
44:H:83:LEU:HB3	44:H:88:ILE:HB	1.89	0.55
1:R:325:GLN:NE2	1:R:353:ILE:O	2.40	0.55
7:k:74:LYS:HD3	7:k:80:PHE:HD1	1.72	0.55
48:1:370:U:H4'	48:1:404:G:H5'	1.89	0.55
12:N:2:ALA:HB3	35:c:41:HIS:HE1	1.72	0.55
1:R:350:ASP:HA	1:R:353:ILE:HD12	1.88	0.54
48:1:1497:C:H2'	48:1:1498:A:H8	1.72	0.54
48:1:2375:G:O2'	48:1:2377:G:OP2	2.22	0.54
17:Q:49:ARG:NH1	48:1:1193:A:OP2	2.35	0.54
22:U:9:VAL:O	22:U:26:ARG:HA	2.07	0.54
48:1:2116:G:OP1	48:1:2118:C:N4	2.40	0.54
48:1:2901:G:O2'	48:1:3024:A:N1	2.41	0.54
26:r:24:SER:HB2	26:r:89:THR:O	2.07	0.54
48:1:158:G:H2'	48:1:159:A:H8	1.73	0.54
20:s:192:ASP:OD2	48:1:1010:G:N2	2.40	0.54
39:e:16:LEU:HD23	39:e:98:SER:HB2	1.89	0.54
45:h:49:ILE:HG12	45:h:100:ILE:HG13	1.89	0.54
48:1:1226:G:H4'	48:1:3117:C:H1'	1.90	0.54
48:1:1551:C:O2'	48:1:2170:U:O2'	2.25	0.54
17:Q:164:SER:O	17:Q:167:TYR:HB3	2.08	0.54
46:I:26:ARG:NH1	48:1:502:U:O2'	2.41	0.54
48:1:1418:A:O2'	48:1:1419:A:O4'	2.25	0.54
5:j:67:ARG:NH2	30:4:97:A:OP1	2.40	0.54
36:D:4:ARG:NH2	48:1:837:A:OP2	2.40	0.54
42:G:73:ARG:NH2	48:1:2402:A:N7	2.53	0.54
43:g:82:LEU:HD11	43:g:112:ALA:HB2	1.88	0.54
23:V:39:ILE:HD12	23:V:102:ARG:HG3	1.89	0.54
26:r:5:ARG:NH2	48:1:1219:C:OP2	2.40	0.54
38:E:220:GLY:O	48:1:2245:C:O2'	2.25	0.54
48:1:2568:C:OP1	48:1:2569:A:N6	2.40	0.54
38:E:192:LYS:HB3	38:E:193:ARG:HE	1.73	0.54
18:5:36:ILE:HD11	18:5:95:LEU:HD11	1.90	0.54
48:1:873:C:H3'	48:1:874:U:H4'	1.90	0.54
1:R:101:LYS:NZ	2:X:120:ASP:OD1	2.40	0.53
1:R:256:LEU:HB2	1:R:273:ALA:HA	1.89	0.53
7:k:26:ILE:HD13	48:1:157:A:C8	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:s:6:ARG:NH2	48:1:2828:G:OP1	2.34	0.53
36:D:17:ARG:NH2	48:1:860:G:OP1	2.42	0.53
48:1:68:C:OP2	48:1:301:G:N2	2.40	0.53
6:K:155:ASN:HD21	6:K:181:LYS:HG2	1.73	0.53
38:E:79:ASN:ND2	38:E:166:ILE:O	2.41	0.53
48:1:532:A:N6	48:1:555:U:O2'	2.41	0.53
48:1:2234:G:HO2'	48:1:2603:G:HO2'	1.53	0.53
48:1:2565:U:H3	48:1:2576:G:H1	1.54	0.53
30:4:70:G:OP1	32:a:121:ARG:NH1	2.41	0.53
31:Z:112:THR:HA	31:Z:121:LYS:O	2.08	0.53
38:E:187:HIS:HB3	48:1:1794:G:H1'	1.89	0.53
48:1:170:G:N3	48:1:250:U:N3	2.56	0.53
48:1:1468:A:N6	48:1:1508:C:O2	2.40	0.53
11:m:2:ALA:N	48:1:1613:A:OP1	2.41	0.53
28:3:11:A:O2'	28:3:13:A:OP2	2.26	0.53
47:L:18:LYS:HG3	47:L:24:LYS:H	1.72	0.53
2:X:102:SER:OG	2:X:103:ALA:N	2.41	0.53
44:H:17:GLN:O	48:1:2688:U:N3	2.41	0.53
1:R:462:LEU:HD11	1:R:500:ILE:HD13	1.91	0.53
23:V:75:ILE:HG22	23:V:88:ARG:HG2	1.90	0.53
35:c:7:LYS:O	35:c:11:HIS:ND1	2.39	0.53
17:Q:173:ALA:O	17:Q:176:LYS:HB3	2.09	0.53
38:E:117:GLU:HG2	38:E:124:GLY:H	1.74	0.53
43:g:16:LYS:NZ	48:1:1404:G:O6	2.39	0.53
43:g:98:HIS:NE2	48:1:1394:A:OP1	2.40	0.53
44:H:210:GLU:O	44:H:214:ASP:HB2	2.08	0.53
10:M:49:LYS:HB3	10:M:62:ASN:HA	1.91	0.53
19:S:179:ARG:NH2	48:1:709:A:OP1	2.41	0.53
27:x:112:SER:O	27:x:132:ASN:ND2	2.41	0.53
32:a:16:ARG:NH1	48:1:216:G:OP1	2.41	0.53
48:1:91:G:OP2	48:1:93:C:N4	2.42	0.53
48:1:1447:G:N2	48:1:2356:A:OP2	2.42	0.53
42:G:193:LYS:HA	42:G:198:ARG:HA	1.91	0.53
5:j:86:ARG:NH1	30:4:37:A:OP2	2.36	0.53
8:7:62:ARG:NH2	48:1:3115:C:OP1	2.42	0.53
27:x:10:LYS:NZ	27:x:56:ASP:OD1	2.41	0.53
48:1:221:A:O2'	48:1:223:U:OP2	2.26	0.53
4:J:33:ARG:NH2	48:1:595:G:OP1	2.41	0.52
4:J:77:VAL:HG12	22:U:59:VAL:HA	1.91	0.52
40:F:244:ARG:NH2	48:1:2948:C:OP1	2.42	0.52
48:1:1672:U:H3	48:1:1775:G:H1	1.56	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:316:ASN:O	1:R:320:LEU:CB	2.57	0.52
21:T:79:GLY:N	48:1:1938:U:O2'	2.42	0.52
36:D:51:ALA:HB1	38:E:50:HIS:HB2	1.91	0.52
40:F:117:ARG:NH1	48:1:3313:U:OP1	2.42	0.52
48:1:2057:G:N2	48:1:2058:G:O6	2.41	0.52
48:1:2483:G:N2	48:1:2486:A:OP2	2.41	0.52
14:O:23:ILE:O	14:O:30:GLY:HA2	2.09	0.52
14:O:38:ILE:HG13	14:O:44:VAL:HG12	1.92	0.52
23:V:17:ARG:HG2	23:V:22:HIS:HA	1.89	0.52
23:V:18:ASP:HB2	23:V:21:LYS:HB2	1.91	0.52
35:c:42:ARG:NH1	48:1:2800:G:O6	2.40	0.52
27:x:12:ARG:NH1	48:1:3041:U:OP1	2.42	0.52
31:Z:100:LYS:NZ	31:Z:106:ASP:OD1	2.43	0.52
48:1:1351:U:H2'	48:1:1352:A:H2'	1.91	0.52
48:1:1477:A:OP1	48:1:3075:G:O2'	2.27	0.52
20:s:115:ARG:NH2	48:1:2617:U:O2'	2.42	0.52
47:L:36:VAL:HA	47:L:208:SER:HA	1.90	0.52
42:G:216:VAL:O	42:G:220:ARG:HB3	2.10	0.52
4:J:92:ILE:HD11	19:S:4:ASP:HB2	1.91	0.52
30:4:114:G:OP1	48:1:1831:U:O2'	2.28	0.52
47:L:18:LYS:HB2	47:L:23:THR:HB	1.92	0.52
48:1:824:C:O2'	48:1:1534:A:N3	2.40	0.52
6:K:47:SER:OG	48:1:2585:G:O6	2.28	0.52
8:7:9:GLN:HG2	8:7:54:LYS:HG2	1.92	0.52
16:p:62:TYR:HD2	16:p:134:LEU:HD13	1.75	0.52
30:4:103:G:OP2	30:4:105:A:O2'	2.28	0.52
45:h:99:ARG:NH1	48:1:3275:U:O2'	2.43	0.52
9:l:76:ASN:ND2	30:4:95:G:OP1	2.43	0.52
42:G:119:ARG:NH2	48:1:696:C:OP2	2.42	0.52
8:7:8:GLN:HB3	8:7:72:LYS:HD2	1.91	0.52
17:Q:157:GLU:HA	17:Q:160:ARG:HG2	1.92	0.52
19:S:43:PRO:HB2	48:1:728:G:H5''	1.91	0.52
25:P:126:ALA:HB3	25:P:159:GLU:HA	1.91	0.52
40:F:236:LYS:NZ	48:1:2338:C:OP1	2.35	0.52
42:G:122:THR:HG22	42:G:235:LEU:HB2	1.92	0.52
48:1:1564:U:O4	48:1:1576:G:O6	2.28	0.52
48:1:1966:U:O2	48:1:2057:G:N2	2.43	0.52
48:1:3353:G:O2'	48:1:3356:G:OP2	2.27	0.52
48:1:1433:A:O2'	48:1:1434:G:O4'	2.27	0.51
48:1:3152:U:N3	48:1:3155:U:O4	2.42	0.51
32:a:27:ARG:NH1	32:a:75:ARG:O	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:c:10:LYS:NZ	48:1:1374:G:O6	2.41	0.51
40:F:308:MET:HE2	48:1:3329:U:H5''	1.92	0.51
41:f:13:THR:HA	41:f:71:LEU:O	2.10	0.51
45:h:86:ARG:HH22	48:1:623:U:H4'	1.76	0.51
17:Q:171:LYS:O	17:Q:174:PHE:HB3	2.10	0.51
1:R:325:GLN:HA	1:R:328:LEU:HB2	1.93	0.51
7:k:11:LEU:HD11	12:N:180:ARG:HH11	1.75	0.51
38:E:174:ARG:NH2	48:1:2180:G:OP1	2.40	0.51
48:1:1464:G:H22	48:1:1467:A:H5''	1.75	0.51
4:J:178:ILE:HD11	4:J:187:GLU:HG3	1.92	0.51
14:O:37:GLU:OE2	14:O:74:ARG:NH2	2.43	0.51
43:g:100:ILE:O	43:g:125:ARG:NH1	2.44	0.51
48:1:2273:G:O2'	48:1:2311:G:N1	2.43	0.51
12:N:100:ARG:HH11	48:1:76:G:HO2'	1.58	0.51
13:n:28:ARG:NH1	13:n:36:ARG:O	2.44	0.51
15:o:119:ASN:ND2	48:1:1207:G:OP1	2.44	0.51
42:G:326:ARG:NH1	48:1:608:A:O3'	2.44	0.51
48:1:1223:A:H62	48:1:1285:G:H21	1.58	0.51
48:1:1460:A:H2'	48:1:1461:A:H8	1.76	0.51
48:1:3108:G:OP2	48:1:3120:C:N4	2.44	0.51
48:1:1974:A:N6	48:1:2049:A:O5'	2.43	0.51
41:f:44:MET:HB3	41:f:77:ARG:HD3	1.92	0.51
48:1:2196:C:O2'	48:1:2270:A:N3	2.38	0.51
47:L:36:VAL:HG12	47:L:168:ALA:H	1.75	0.51
7:k:44:VAL:HG21	16:p:9:GLU:HB3	1.93	0.51
1:R:343:ILE:HD12	1:R:367:ILE:HG23	1.93	0.50
31:Z:105:VAL:HG21	31:Z:135:ILE:HD12	1.93	0.50
33:b:107:ARG:NH1	48:1:1634:G:OP1	2.40	0.50
14:O:60:LEU:HD13	22:U:152:LEU:HD11	1.93	0.50
20:s:189:VAL:HG13	20:s:196:VAL:HG11	1.93	0.50
21:T:148:ASP:OD1	21:T:151:ARG:NH2	2.44	0.50
38:E:51:ASP:HB3	38:E:54:ARG:HB3	1.93	0.50
6:K:181:LYS:HE2	30:4:154:C:H5''	1.94	0.50
16:p:93:LYS:O	48:1:289:A:O2'	2.28	0.50
24:W:59:ASP:HB3	24:W:62:VAL:H	1.75	0.50
38:E:25:GLY:O	48:1:2175:U:O2'	2.29	0.50
42:G:92:ASN:HD22	42:G:100:PHE:HB2	1.75	0.50
45:h:75:HIS:HB2	45:h:82:ARG:HG3	1.94	0.50
4:J:219:LYS:HE2	48:1:1169:A:H4'	1.94	0.50
42:G:221:ASN:ND2	48:1:209:A:N3	2.59	0.50
47:L:210:MET:SD	48:1:2489:C:O2'	2.70	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1:2207:A:H3'	48:1:2208:A:H8	1.75	0.50
1:R:97:LEU:HD21	2:X:139:ARG:HD3	1.93	0.50
19:S:39:ARG:HH12	42:G:302:ALA:HA	1.76	0.50
40:F:100:ARG:NE	48:1:3244:A:OP1	2.43	0.50
44:H:8:LYS:NZ	48:1:2687:G:OP1	2.40	0.50
47:L:18:LYS:HZ2	47:L:24:LYS:HB3	1.77	0.50
26:r:34:SER:HA	48:1:1230:G:H4'	1.92	0.50
48:1:618:C:O2'	48:1:620:U:O2	2.29	0.50
10:M:105:GLY:HA3	48:1:2674:A:H5''	1.92	0.50
48:1:737:G:H2'	48:1:738:A:H8	1.77	0.50
48:1:2693:C:H5'	48:1:2694:A:H5''	1.94	0.50
48:1:2960:C:H2'	48:1:2961:G:C8	2.47	0.50
14:O:128:ARG:HH12	48:1:3213:A:H3'	1.76	0.50
17:Q:126:VAL:HG22	22:U:154:HIS:HE1	1.77	0.50
26:r:27:VAL:HG21	26:r:76:LEU:HD21	1.94	0.50
40:F:163:HIS:ND1	40:F:164:THR:O	2.43	0.50
40:F:380:MET:O	48:1:3369:G:N1	2.43	0.50
48:1:1239:C:N4	48:1:1244:A:O2'	2.45	0.50
2:X:107:VAL:HG13	2:X:118:HIS:H	1.76	0.50
44:H:261:THR:OG1	44:H:264:GLN:OE1	2.23	0.50
46:I:43:LEU:HD11	46:I:85:ILE:HG13	1.93	0.50
48:1:1845:G:H1	48:1:1849:C:H2'	1.77	0.50
48:1:2085:U:H2'	48:1:2086:A:C8	2.47	0.50
10:M:22:SER:HB2	48:1:2675:C:H42	1.78	0.49
41:f:10:ARG:HH11	41:f:44:MET:HE1	1.77	0.49
48:1:3157:U:H4'	48:1:3158:G:H8	1.77	0.49
40:F:128:LYS:HE2	48:1:3293:U:H5'	1.94	0.49
48:1:961:C:N4	48:1:2615:G:O2'	2.44	0.49
48:1:1157:G:O2'	48:1:1169:A:N3	2.44	0.49
48:1:1261:G:N2	48:1:1261:G:OP2	2.44	0.49
1:R:329:LYS:HB2	1:R:359:VAL:HG11	1.93	0.49
12:N:10:LEU:HD23	19:S:166:LEU:HD11	1.94	0.49
40:F:14:LEU:O	48:1:3009:G:O2'	2.28	0.49
40:F:54:THR:OG1	40:F:360:ASP:O	2.30	0.49
40:F:222:LYS:HD3	40:F:331:ASN:HB3	1.94	0.49
48:1:842:G:H2'	48:1:843:A:H8	1.77	0.49
48:1:865:U:OP2	48:1:893:C:N4	2.42	0.49
48:1:2092:A:H3'	48:1:2093:A:H4'	1.94	0.49
1:R:212:ASN:ND2	1:R:365:GLU:OE2	2.46	0.49
18:5:25:SER:OG	48:1:1447:G:N7	2.44	0.49
19:S:8:LYS:NZ	48:1:971:G:OP1	2.46	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:F:84:VAL:HG22	40:F:164:THR:HA	1.94	0.49
48:1:1492:G:H1'	48:1:1843:C:H5''	1.93	0.49
48:1:1579:C:H2'	48:1:1580:A:C8	2.47	0.49
48:1:2946:A:H5''	48:1:2947:G:H5'	1.95	0.49
20:s:67:ALA:HB1	20:s:154:ALA:HB1	1.95	0.49
21:T:102:LEU:HD22	21:T:138:LEU:HD13	1.92	0.49
39:e:57:GLU:OE1	48:1:2552:C:N4	2.45	0.49
48:1:3069:G:H2'	48:1:3070:A:H8	1.76	0.49
47:L:56:PRO:HG3	47:L:187:VAL:HG21	1.95	0.49
13:n:27:ILE:O	13:n:33:ASN:ND2	2.46	0.49
17:Q:34:VAL:HA	17:Q:103:LYS:O	2.13	0.49
18:5:122:ALA:HB3	18:5:143:PRO:HG2	1.95	0.49
20:s:51:LEU:HD12	20:s:151:LEU:HB3	1.95	0.49
48:1:2361:A:H61	48:1:2377:G:H1	1.60	0.49
39:e:16:LEU:HD21	39:e:97:ASP:HB3	1.94	0.49
48:1:269:G:O2'	48:1:270:U:OP2	2.28	0.49
3:i:20:ILE:HD12	3:i:32:ALA:HB1	1.94	0.49
28:3:44:C:H2'	28:3:45:A:H8	1.78	0.49
33:b:3:LYS:HE2	33:b:5:LEU:HB2	1.94	0.49
33:b:23:VAL:HG12	33:b:45:GLY:HA3	1.94	0.49
37:d:28:LYS:HD3	48:1:1065:A:H1'	1.94	0.49
40:F:269:GLN:NE2	48:1:3306:U:OP1	2.39	0.49
48:1:252:U:H5'	48:1:253:A:H5'	1.95	0.49
48:1:2371:G:N1	48:1:2375:G:OP1	2.39	0.49
48:1:3055:U:O2'	48:1:3057:U:OP1	2.31	0.49
9:l:48:ASN:OD1	9:l:54:LYS:NZ	2.44	0.49
22:U:108:GLN:NE2	48:1:1322:U:O2	2.41	0.49
40:F:238:LEU:HB3	40:F:242:THR:HG21	1.95	0.49
40:F:315:GLY:HA2	48:1:3379:C:H4'	1.93	0.49
48:1:655:C:H2'	48:1:656:A:H8	1.77	0.49
48:1:1497:C:H2'	48:1:1498:A:C8	2.48	0.49
10:M:18:VAL:HG22	10:M:70:THR:HG22	1.95	0.48
40:F:14:LEU:HA	40:F:17:LEU:HD13	1.94	0.48
33:b:59:ALA:O	33:b:62:VAL:HB	2.13	0.48
42:G:203:ARG:HE	42:G:246:ARG:HH12	1.59	0.48
44:H:28:THR:O	48:1:2703:A:N6	2.45	0.48
47:L:35:GLN:NE2	48:1:2466:G:O3'	2.46	0.48
48:1:1151:U:O4	48:1:1200:A:N6	2.46	0.48
8:7:28:VAL:HG22	8:7:33:THR:HG22	1.96	0.48
30:4:20:U:O2'	48:1:1419:A:OP1	2.30	0.48
38:E:59:ALA:HB2	38:E:78:ALA:HB2	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:G:349:THR:N	48:1:520:U:O4	2.44	0.48
48:1:1493:G:OP2	48:1:1493:G:N2	2.44	0.48
43:g:101:SER:HB3	48:1:1389:G:H5''	1.95	0.48
48:1:638:C:N4	48:1:639:G:O6	2.46	0.48
48:1:1712:G:N2	48:1:1733:G:O6	2.46	0.48
20:s:118:TRP:HZ3	48:1:1126:G:H5''	1.79	0.48
21:T:20:ARG:NH1	48:1:1874:A:N7	2.62	0.48
23:V:104:GLU:OE1	48:1:989:A:O2'	2.31	0.48
48:1:763:G:O6	48:1:769:G:N2	2.46	0.48
48:1:2127:U:O2'	48:1:2301:U:OP1	2.30	0.48
1:R:74:CYS:SG	1:R:96:HIS:ND1	2.86	0.48
13:n:42:ARG:NH1	48:1:1494:U:OP1	2.38	0.48
18:5:121:GLN:O	30:4:13:A:O2'	2.31	0.48
32:a:87:LYS:HB2	32:a:97:ILE:HD11	1.94	0.48
36:D:66:GLY:HA2	38:E:80:GLU:HG3	1.95	0.48
38:E:117:GLU:OE2	38:E:163:ARG:NH2	2.46	0.48
42:G:338:LYS:O	42:G:340:GLY:N	2.46	0.48
45:h:16:TYR:OH	45:h:89:LEU:O	2.28	0.48
48:1:900:G:H1'	48:1:1589:A:H62	1.79	0.48
48:1:3303:G:O2'	48:1:3305:A:N6	2.46	0.48
3:i:41:ARG:HG2	3:i:56:THR:HG21	1.95	0.48
23:V:99:SER:HG	23:V:101:CYS:HG	1.60	0.48
40:F:77:THR:HG21	40:F:328:ILE:HG22	1.96	0.48
42:G:150:LEU:HD22	42:G:249:ILE:HG12	1.94	0.48
47:L:35:GLN:HE22	48:1:2467:G:H5'	1.77	0.48
48:1:1549:U:H2'	48:1:1550:C:H6	1.78	0.48
1:R:237:ALA:HB2	1:R:335:LEU:HD21	1.96	0.48
16:p:4:TYR:OH	48:1:148:G:OP2	2.32	0.48
27:x:10:LYS:HD3	27:x:125:LEU:HD22	1.96	0.48
48:1:36:C:O2'	48:1:808:A:N1	2.42	0.48
48:1:515:C:H2'	48:1:516:A:H8	1.77	0.48
48:1:1277:C:H2'	48:1:1278:A:H8	1.77	0.48
48:1:1816:A:O2'	48:1:1817:G:O5'	2.31	0.48
48:1:2150:G:O2'	48:1:2189:U:OP1	2.29	0.48
48:1:2700:G:O2'	48:1:2705:A:N1	2.42	0.48
2:X:15:VAL:HA	2:X:61:ARG:HG2	1.95	0.48
4:J:155:LYS:NZ	48:1:1102:A:OP1	2.47	0.48
8:7:114:VAL:HB	8:7:124:ARG:HB2	1.95	0.48
40:F:303:LYS:HD2	40:F:361:THR:HG21	1.95	0.48
48:1:289:A:H2'	48:1:290:G:H8	1.77	0.48
48:1:2185:G:O2'	48:1:2314:U:OP2	2.32	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1:2323:G:O2'	48:1:2325:G:OP2	2.31	0.48
32:a:55:GLU:HB2	32:a:108:LYS:HB2	1.95	0.48
40:F:314:TYR:HD1	40:F:333:LYS:HG2	1.79	0.48
44:H:33:ARG:HH12	44:H:50:ARG:HH22	1.61	0.48
48:1:1127:G:N2	48:1:1130:A:OP2	2.43	0.48
48:1:1485:G:HO2'	48:1:1874:A:HO2'	1.56	0.48
6:K:240:ASN:ND2	48:1:2584:G:O2'	2.47	0.47
12:N:169:THR:O	12:N:173:ALA:N	2.47	0.47
48:1:2874:G:N2	48:1:2875:U:O4	2.35	0.47
19:S:32:LEU:HD12	42:G:286:VAL:HG13	1.95	0.47
39:e:22:LYS:HB2	39:e:94:GLU:HB2	1.96	0.47
48:1:3010:U:O2	48:1:3136:G:O6	2.31	0.47
6:K:144:GLU:OE1	7:k:36:ARG:NH1	2.48	0.47
46:I:70:LYS:NZ	48:1:3266:G:OP2	2.46	0.47
48:1:675:C:O2'	48:1:679:U:OP1	2.30	0.47
19:S:40:THR:OG1	19:S:45:ASN:ND2	2.46	0.47
40:F:332:ARG:NH1	40:F:333:LYS:HE2	2.30	0.47
42:G:48:GLN:NE2	48:1:336:A:O2'	2.47	0.47
48:1:237:G:H2'	48:1:238:A:H8	1.79	0.47
48:1:339:C:OP1	48:1:1380:G:O2'	2.31	0.47
48:1:2458:A:N6	48:1:2477:G:OP2	2.40	0.47
9:l:52:LYS:NZ	48:1:353:G:O6	2.41	0.47
19:S:169:GLY:O	19:S:174:ARG:NE	2.39	0.47
35:c:75:LEU:HB3	35:c:118:ILE:HG23	1.97	0.47
48:1:528:U:H2'	48:1:529:A:H8	1.79	0.47
31:Z:86:VAL:HG21	31:Z:95:ILE:HG12	1.97	0.47
38:E:146:THR:OG1	38:E:160:SER:OG	2.31	0.47
1:R:91:TYR:HB2	2:X:138:PHE:HD1	1.79	0.47
17:Q:64:PHE:O	40:F:262:TRP:N	2.48	0.47
18:5:36:ILE:HD12	18:5:48:LEU:HD11	1.96	0.47
20:s:90:VAL:HG12	20:s:126:ALA:HB1	1.96	0.47
21:T:99:LEU:HD21	21:T:103:ARG:HH21	1.79	0.47
29:Y:6:ASP:OD1	29:Y:32:GLN:N	2.42	0.47
29:Y:14:TYR:OH	40:F:375:GLU:OE2	2.33	0.47
34:C:82:GLN:NE2	48:1:2768:U:O2	2.45	0.47
44:H:211:LEU:HB3	44:H:219:PHE:HB2	1.96	0.47
48:1:371:G:N1	48:1:374:A:OP2	2.39	0.47
48:1:1190:A:C8	48:1:1193:A:H1'	2.50	0.47
48:1:2618:G:N2	48:1:2645:G:OP1	2.47	0.47
6:K:105:LYS:HA	6:K:108:ARG:HG2	1.96	0.47
8:7:90:MET:HE2	8:7:179:ILE:HG22	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:H:64:ILE:HG22	44:H:75:LEU:HB3	1.97	0.47
48:1:1257:C:N3	48:1:1261:G:N1	2.57	0.47
48:1:1956:A:H2'	48:1:1957:G:C8	2.49	0.47
2:X:62:MET:HE3	2:X:73:PRO:HG3	1.96	0.47
10:M:14:ILE:HD12	10:M:77:GLU:HG2	1.96	0.47
48:1:2768:U:H2'	48:1:2769:A:H8	1.78	0.47
48:1:3354:U:H5''	48:1:3355:U:H5'	1.97	0.47
7:k:33:ALA:O	7:k:38:LYS:NZ	2.48	0.47
28:3:77:G:O2'	28:3:78:U:OP2	2.30	0.47
48:1:41:G:N2	48:1:2803:A:H62	2.13	0.47
48:1:1463:U:H3	48:1:1467:A:H62	1.63	0.47
48:1:3042:U:OP2	48:1:3092:C:N4	2.46	0.47
22:U:60:SER:OG	22:U:62:ASN:OD1	2.33	0.46
40:F:95:THR:HG22	48:1:3243:A:H4'	1.97	0.46
48:1:994:G:N2	48:1:1054:A:OP2	2.37	0.46
48:1:1231:A:O2'	48:1:1261:G:O2'	2.29	0.46
48:1:2631:U:OP1	48:1:2757:U:O2'	2.32	0.46
6:K:149:LYS:N	6:K:200:LEU:O	2.47	0.46
10:M:110:ILE:HD13	10:M:116:TYR:HD1	1.80	0.46
14:O:59:ASN:HD22	48:1:1184:A:H5''	1.81	0.46
16:p:24:ARG:HH22	48:1:2435:G:H4'	1.80	0.46
30:4:126:A:O2'	30:4:128:U:OP2	2.34	0.46
38:E:3:ARG:HD3	48:1:911:C:H42	1.80	0.46
38:E:200:ARG:NH1	48:1:2146:C:OP1	2.48	0.46
48:1:920:A:OP1	48:1:923:C:N4	2.43	0.46
16:p:193:ARG:NH1	48:1:80:G:OP1	2.49	0.46
48:1:170:G:N2	48:1:248:U:O2	2.35	0.46
48:1:1642:A:O2'	48:1:1822:C:O2'	2.33	0.46
48:1:1661:G:H2'	48:1:1662:G:C8	2.50	0.46
22:U:22:PRO:O	23:V:146:ASN:ND2	2.48	0.46
32:a:111:LEU:HD23	32:a:116:LYS:HG2	1.97	0.46
34:C:30:ALA:O	48:1:2767:U:O2'	2.31	0.46
35:c:123:VAL:H	35:c:143:GLY:HA3	1.80	0.46
44:H:148:ILE:HG12	44:H:159:VAL:HG11	1.96	0.46
15:o:97:ARG:HH21	15:o:122:ARG:HB3	1.79	0.46
16:p:89:VAL:HB	48:1:2424:A:H5'	1.98	0.46
16:p:178:HIS:ND1	48:1:69:C:OP1	2.34	0.46
23:V:8:ARG:NH2	48:1:2756:C:O2	2.48	0.46
38:E:209:HIS:HD2	38:E:211:HIS:H	1.61	0.46
43:g:23:ASP:OD2	48:1:424:G:O2'	2.34	0.46
48:1:1093:A:O2'	48:1:1094:U:O4'	2.34	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:439:LEU:HD22	1:R:448:ILE:HD12	1.96	0.46
8:7:4:ILE:HB	22:U:142:GLN:HE21	1.80	0.46
12:N:2:ALA:HB3	35:c:41:HIS:CE1	2.49	0.46
27:x:18:PRO:HA	27:x:51:ALA:HA	1.96	0.46
48:1:1628:C:O5'	48:1:1814:A:N6	2.48	0.46
1:R:23:LEU:HD12	1:R:227:ASN:HD21	1.81	0.46
5:j:118:ILE:HG12	12:N:123:ILE:HG22	1.96	0.46
7:k:26:ILE:HG21	48:1:157:A:C8	2.51	0.46
10:M:21:ILE:HD11	10:M:125:MET:HE2	1.98	0.46
17:Q:60:LYS:NZ	48:1:1307:G:O4'	2.49	0.46
21:T:103:ARG:HG3	21:T:124:TYR:HE1	1.81	0.46
30:4:126:A:N1	48:1:1618:G:O2'	2.49	0.46
44:H:60:ILE:HG13	44:H:93:THR:HG22	1.98	0.46
48:1:1259:A:N3	48:1:1280:C:O2'	2.42	0.46
48:1:2516:U:O2'	48:1:2595:A:N6	2.46	0.46
9:l:49:TRP:O	48:1:929:A:O2'	2.33	0.46
30:4:75:G:OP2	32:a:74:TYR:OH	2.31	0.46
38:E:223:SER:OG	48:1:2244:A:O2'	2.32	0.46
40:F:215:ILE:HD11	40:F:324:VAL:HG21	1.98	0.46
43:g:43:ARG:NH1	48:1:1144:U:OP2	2.49	0.46
44:H:111:GLN:HA	44:H:116:ASP:HB2	1.97	0.46
45:h:52:VAL:HG22	45:h:66:VAL:HG22	1.97	0.46
48:1:1018:G:O6	48:1:1034:U:O4	2.32	0.46
48:1:1666:G:H2'	48:1:1667:A:H8	1.79	0.46
3:i:37:LYS:NZ	48:1:1656:A:OP2	2.49	0.46
15:o:111:ARG:NE	48:1:3121:U:OP2	2.46	0.46
16:p:112:ASN:OD1	16:p:112:ASN:N	2.49	0.46
18:5:23:ARG:HA	18:5:143:PRO:HB3	1.98	0.46
44:H:50:ARG:NH1	44:H:147:ASP:OD2	2.48	0.46
48:1:3259:U:H5''	48:1:3260:G:H3'	1.96	0.46
34:C:12:CYS:HB2	34:C:23:HIS:CE1	2.52	0.46
38:E:243:THR:HG23	48:1:2242:A:H5'	1.98	0.46
1:R:459:ASN:HB3	1:R:462:LEU:HD12	1.97	0.45
8:7:90:MET:HG2	8:7:181:VAL:HA	1.98	0.45
16:p:115:VAL:HG22	16:p:134:LEU:HG	1.98	0.45
26:r:45:LEU:HD22	26:r:49:ALA:HB3	1.97	0.45
28:3:67:G:O2'	44:H:13:SER:O	2.34	0.45
6:K:156:ASP:OD2	6:K:183:LYS:N	2.49	0.45
20:s:191:ASP:HA	20:s:196:VAL:HG22	1.97	0.45
26:r:56:ASN:HD22	48:1:1282:G:H5'	1.80	0.45
40:F:99:LEU:O	48:1:3004:C:O2'	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1:306:A:N6	48:1:2784:G:N2	2.64	0.45
48:1:373:A:C6	48:1:375:A:C6	3.04	0.45
48:1:3232:G:H1	48:1:3255:U:H3	1.63	0.45
6:K:183:LYS:NZ	48:1:147:U:O4	2.38	0.45
40:F:306:THR:HG21	40:F:316:GLU:HG2	1.99	0.45
48:1:307:A:O2'	48:1:2223:A:N3	2.43	0.45
48:1:3233:C:H2'	48:1:3234:A:C8	2.52	0.45
1:R:490:LEU:HD23	1:R:494:ILE:HD12	1.98	0.45
8:7:5:GLN:HA	8:7:57:VAL:O	2.16	0.45
22:U:132:THR:OG1	48:1:534:U:OP1	2.34	0.45
46:I:42:LEU:HD22	46:I:79:VAL:HG11	1.98	0.45
48:1:528:U:H2'	48:1:529:A:C8	2.50	0.45
48:1:1929:G:H4'	48:1:2321:A:H5''	1.99	0.45
5:j:85:THR:OG1	30:4:36:G:OP2	2.31	0.45
28:3:11:A:N1	28:3:67:G:O2'	2.46	0.45
47:L:101:LYS:NZ	47:L:122:ARG:O	2.49	0.45
48:1:1000:C:O2	48:1:1046:A:N6	2.49	0.45
48:1:1308:A:H61	48:1:2367:A:H2	1.64	0.45
48:1:1675:G:H2'	48:1:1676:A:H8	1.81	0.45
48:1:3258:U:O2'	48:1:3260:G:OP1	2.23	0.45
3:i:3:GLN:HB2	3:i:30:LEU:HD12	1.98	0.45
18:5:48:LEU:HD22	18:5:88:VAL:HG13	1.98	0.45
23:V:4:SER:OG	48:1:2631:U:OP2	2.34	0.45
23:V:17:ARG:HH22	23:V:25:VAL:HG12	1.81	0.45
48:1:1236:G:N1	48:1:1244:A:OP2	2.49	0.45
1:R:438:LEU:HD13	1:R:447:LEU:HB3	1.97	0.45
2:X:151:TYR:HE1	2:X:192:VAL:HG22	1.82	0.45
10:M:77:GLU:O	10:M:80:LEU:HB3	2.16	0.45
28:3:26:C:H5'	44:H:56:THR:HB	1.97	0.45
38:E:32:LEU:HD21	38:E:37:ARG:HD3	1.98	0.45
41:f:77:ARG:HG2	41:f:89:LEU:HD23	1.99	0.45
42:G:74:ILE:HD11	48:1:1438:U:H5'	1.98	0.45
45:h:21:ARG:NH2	48:1:1150:A:O2'	2.49	0.45
48:1:600:G:N2	48:1:603:A:OP2	2.35	0.45
48:1:2087:C:H2'	48:1:2088:A:H2'	1.99	0.45
22:U:71:LYS:HD3	48:1:562:C:H5''	1.98	0.45
38:E:9:ARG:NH2	48:1:912:G:N7	2.60	0.45
46:I:52:VAL:HG21	46:I:65:ILE:HD13	1.98	0.45
48:1:2844:C:H42	48:1:2898:G:H22	1.41	0.45
48:1:3187:A:H2	48:1:3205:G:H22	1.65	0.45
18:5:23:ARG:NH1	18:5:141:SER:OG	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:r:56:ASN:HB3	26:r:80:VAL:HG22	1.98	0.45
28:3:14:U:OP1	44:H:24:ARG:NH1	2.50	0.45
40:F:279:ASN:ND2	48:1:3098:G:OP1	2.50	0.45
9:l:9:GLY:HA3	48:1:1852:G:H1'	1.98	0.45
14:O:88:ALA:O	14:O:93:LYS:NZ	2.45	0.45
27:x:57:MET:HE1	27:x:105:PRO:HA	1.98	0.45
12:N:157:ARG:NH2	35:c:146:GLU:OE1	2.50	0.44
22:U:154:HIS:HD2	48:1:1316:C:H41	1.64	0.44
40:F:166:ILE:HD11	40:F:171:LEU:HD12	1.99	0.44
47:L:178:VAL:HG13	47:L:179:LEU:HG	1.99	0.44
48:1:109:A:N1	48:1:322:U:O2'	2.44	0.44
48:1:1194:G:H2'	48:1:1195:A:C8	2.51	0.44
48:1:1920:U:O2'	48:1:1932:A:N7	2.42	0.44
48:1:3152:U:H1'	48:1:3294:A:C5	2.52	0.44
4:J:86:VAL:O	4:J:114:GLY:HA2	2.17	0.44
8:7:18:VAL:HG12	8:7:27:VAL:HG22	1.98	0.44
16:p:38:ARG:NH1	30:4:142:C:OP1	2.47	0.44
38:E:27:ALA:HB3	38:E:128:ARG:HH21	1.82	0.44
40:F:240:ARG:NH2	48:1:1907:C:O2	2.44	0.44
41:f:26:LYS:NZ	48:1:1455:U:O2'	2.43	0.44
44:H:60:ILE:HB	44:H:80:SER:HB3	1.98	0.44
48:1:1786:G:H2'	48:1:1787:A:C8	2.51	0.44
6:K:105:LYS:NZ	48:1:123:A:OP1	2.35	0.44
21:T:84:THR:HG22	48:1:1915:A:H5''	1.98	0.44
38:E:209:HIS:CD2	38:E:211:HIS:H	2.36	0.44
40:F:33:PRO:HG2	40:F:340:LYS:HB2	1.99	0.44
48:1:2660:G:OP1	48:1:2750:U:O2'	2.34	0.44
48:1:3016:A:H2'	48:1:3017:A:H8	1.83	0.44
12:N:174:ARG:NH1	48:1:712:G:OP1	2.51	0.44
22:U:90:MET:HE1	22:U:114:HIS:NE2	2.33	0.44
35:c:91:LEU:HA	35:c:121:VAL:HG21	1.99	0.44
38:E:200:ARG:HD3	48:1:2186:U:H5	1.82	0.44
38:E:227:ARG:NH2	48:1:2155:G:O3'	2.50	0.44
46:I:40:LEU:HD13	46:I:84:VAL:HG11	1.99	0.44
3:i:92:ALA:HB2	48:1:2555:G:H1'	1.99	0.44
16:p:42:PRO:HG3	16:p:61:ILE:HG13	1.99	0.44
32:a:60:ARG:HB2	32:a:103:LYS:HD2	2.00	0.44
40:F:334:ARG:NH2	48:1:3305:A:OP1	2.50	0.44
48:1:1713:G:N2	48:1:1731:A:OP2	2.51	0.44
12:N:166:ALA:O	12:N:169:THR:HB	2.17	0.44
18:5:101:ASN:OD1	48:1:388:G:N2	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:71:A:N6	30:4:87:G:O2'	2.50	0.44
34:C:7:THR:HB	34:C:22:GLN:NE2	2.32	0.44
34:C:10:THR:O	34:C:20:HIS:HA	2.17	0.44
41:f:57:GLN:NE2	48:1:1474:A:O2'	2.47	0.44
42:G:11:LEU:HD21	42:G:156:LEU:HB2	2.00	0.44
48:1:122:A:O2'	48:1:123:A:O5'	2.32	0.44
48:1:170:G:H2'	48:1:171:G:C8	2.53	0.44
48:1:627:U:H2'	48:1:628:A:C8	2.52	0.44
48:1:907:G:N2	48:1:925:A:O2'	2.37	0.44
48:1:1593:A:N3	48:1:1615:C:O2'	2.49	0.44
48:1:1677:G:N2	48:1:1755:C:O2'	2.41	0.44
48:1:3152:U:O3'	48:1:3293:U:O2'	2.35	0.44
6:K:90:THR:HA	6:K:214:LEU:HD21	1.99	0.44
16:p:46:ASP:OD1	16:p:46:ASP:N	2.49	0.44
40:F:332:ARG:HH21	48:1:3377:G:N2	2.15	0.44
47:L:55:LEU:HD22	47:L:134:PHE:HD1	1.82	0.44
48:1:1018:G:H2'	48:1:1019:G:C8	2.53	0.44
48:1:1667:A:H2'	48:1:1668:G:C8	2.53	0.44
28:3:72:A:C6	28:3:74:C:C4	3.05	0.44
29:Y:38:SER:OG	48:1:3084:C:OP1	2.34	0.44
48:1:2660:G:O3'	48:1:2749:G:N2	2.50	0.44
48:1:2711:C:O2'	48:1:2744:U:OP1	2.34	0.44
4:J:120:THR:HB	23:V:132:PRO:HB2	2.00	0.44
12:N:73:ARG:NH1	48:1:110:G:OP2	2.51	0.44
39:e:88:GLY:N	48:1:1729:A:OP1	2.43	0.44
41:f:20:LEU:HD11	41:f:32:ALA:HB2	1.99	0.44
48:1:915:A:OP2	48:1:2145:A:O2'	2.31	0.44
48:1:2221:G:N2	48:1:2224:A:OP2	2.39	0.44
21:T:82:LYS:HD3	48:1:1863:G:H4'	1.99	0.43
27:x:44:SER:OG	48:1:2935:U:O4	2.35	0.43
35:c:59:ARG:NH1	48:1:283:G:O2'	2.50	0.43
44:H:60:ILE:HD11	44:H:93:THR:HA	2.00	0.43
48:1:90:C:O2'	48:1:282:G:OP1	2.33	0.43
48:1:1816:A:O2'	48:1:1817:G:O4'	2.36	0.43
23:V:51:GLY:HA3	23:V:92:ARG:HG3	1.99	0.43
42:G:3:ARG:HA	42:G:4:PRO:HD3	1.86	0.43
45:h:5:HIS:NE2	48:1:3219:G:O6	2.51	0.43
48:1:1071:U:H2'	48:1:1072:G:H8	1.82	0.43
48:1:1304:A:H61	48:1:2860:U:H5''	1.83	0.43
48:1:3162:C:H2'	48:1:3163:A:H8	1.83	0.43
10:M:32:ARG:NH1	10:M:120:ILE:O	2.44	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:62:ARG:HH12	48:1:3067:C:H3'	1.84	0.43
30:4:110:C:O2'	30:4:112:U:OP2	2.34	0.43
35:c:19:LYS:HB3	35:c:25:HIS:HB2	1.99	0.43
35:c:77:LYS:O	35:c:79:TRP:N	2.48	0.43
48:1:708:G:N2	48:1:711:A:OP2	2.40	0.43
48:1:1231:A:O2'	48:1:1278:A:N6	2.50	0.43
48:1:1569:U:H5''	48:1:1570:U:H6	1.82	0.43
48:1:3291:G:H2'	48:1:3292:A:C8	2.53	0.43
10:M:107:ASP:HA	10:M:124:GLY:HA2	2.01	0.43
42:G:107:ARG:HA	48:1:664:U:H5'	2.00	0.43
47:L:103:LEU:HG	47:L:128:LEU:HD22	1.99	0.43
8:7:89:LYS:HG2	8:7:145:VAL:HG22	1.98	0.43
8:7:134:ILE:HG13	8:7:146:LEU:HG	2.01	0.43
17:Q:119:VAL:HG11	22:U:167:ARG:HD2	2.00	0.43
21:T:100:ARG:NH1	48:1:1722:U:OP1	2.51	0.43
26:r:35:SER:OG	48:1:1230:G:O2'	2.25	0.43
40:F:47:LEU:HB3	40:F:335:ILE:HD11	2.01	0.43
42:G:35:VAL:HG21	42:G:244:LEU:HD21	1.99	0.43
48:1:2702:A:H5'	48:1:2704:A:H1'	2.00	0.43
15:o:96:CYS:SG	15:o:97:ARG:N	2.91	0.43
30:4:38:U:O2'	30:4:39:G:OP1	2.35	0.43
36:D:33:GLN:HG3	36:D:49:ARG:HD3	2.01	0.43
40:F:332:ARG:HH21	48:1:3377:G:H21	1.67	0.43
48:1:2250:G:O6	48:1:2266:U:O4	2.36	0.43
48:1:2393:G:H2'	48:1:2982:A:H61	1.84	0.43
18:5:179:GLN:O	18:5:184:ALA:N	2.50	0.43
20:s:138:ARG:HD3	20:s:172:PHE:HB2	2.01	0.43
31:Z:108:LEU:HB3	31:Z:109:LYS:H	1.73	0.43
33:b:70:PRO:HG3	33:b:115:LYS:HB2	2.01	0.43
40:F:74:GLU:OE1	40:F:283:TYR:OH	2.36	0.43
44:H:144:VAL:HG11	44:H:171:LEU:HD13	2.01	0.43
45:h:48:ARG:HG3	45:h:104:PRO:HD3	2.00	0.43
48:1:1975:C:N4	48:1:2049:A:OP1	2.52	0.43
2:X:146:ILE:HG13	2:X:147:LEU:HD12	1.99	0.43
14:O:14:LEU:H	14:O:19:ARG:NH1	2.16	0.43
16:p:71:ARG:HB2	16:p:94:TYR:HB2	2.00	0.43
18:5:116:HIS:O	18:5:148:LEU:HA	2.19	0.43
21:T:128:LYS:NZ	48:1:1724:U:OP2	2.33	0.43
28:3:76:A:H4'	28:3:77:G:H5'	2.01	0.43
29:Y:34:SER:OG	48:1:3085:G:OP1	2.32	0.43
44:H:31:TYR:O	44:H:35:ARG:NH1	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:L:17:LEU:HD12	47:L:214:PHE:HB3	2.00	0.43
4:J:156:ILE:N	4:J:158:LYS:O	2.52	0.43
4:J:186:HIS:O	4:J:190:THR:OG1	2.30	0.43
42:G:73:ARG:NH2	48:1:2402:A:H62	2.16	0.43
44:H:52:VAL:HA	44:H:147:ASP:HB3	2.00	0.43
48:1:3121:U:H1'	48:1:3122:A:H5''	1.99	0.43
1:R:238:LEU:O	1:R:248:GLY:HA2	2.19	0.43
20:s:48:CYS:SG	20:s:49:VAL:N	2.92	0.43
30:4:30:C:H2'	30:4:31:G:H8	1.82	0.43
31:Z:60:TYR:CE1	31:Z:102:LEU:HD21	2.54	0.43
48:1:307:A:H2'	48:1:308:A:C8	2.54	0.43
48:1:664:U:H2'	48:1:665:A:C8	2.54	0.43
48:1:714:G:O2'	48:1:753:C:O2'	2.31	0.43
48:1:1460:A:H2'	48:1:1461:A:C8	2.54	0.43
48:1:2565:U:O2	48:1:2576:G:N2	2.41	0.43
9:l:18:LEU:HD23	9:l:25:ARG:HB2	2.01	0.42
17:Q:97:ALA:O	17:Q:101:ARG:NH1	2.52	0.42
30:4:26:U:O2'	42:G:51:ALA:O	2.37	0.42
35:c:77:LYS:C	35:c:79:TRP:H	2.27	0.42
38:E:45:VAL:HG13	38:E:84:THR:HA	2.01	0.42
48:1:503:C:H2'	48:1:504:A:H8	1.84	0.42
48:1:1203:A:OP2	48:1:1301:A:N6	2.52	0.42
48:1:1250:G:H2'	48:1:1251:A:C8	2.54	0.42
48:1:2428:U:H2'	48:1:2429:G:C8	2.54	0.42
4:J:92:ILE:HD12	4:J:92:ILE:HA	1.83	0.42
40:F:17:LEU:HD11	40:F:233:TRP:HH2	1.85	0.42
48:1:1255:C:H2'	48:1:1256:G:C8	2.54	0.42
48:1:1666:G:H2'	48:1:1667:A:C8	2.54	0.42
1:R:193:PHE:HB2	1:R:204:LEU:O	2.18	0.42
3:i:86:LYS:HD2	33:b:15:ARG:HE	1.84	0.42
6:K:94:PHE:HB3	6:K:189:LEU:HD13	2.01	0.42
19:S:56:LYS:NZ	48:1:674:G:O6	2.52	0.42
38:E:219:ILE:HD11	48:1:2185:G:H4'	2.02	0.42
47:L:205:VAL:HG11	48:1:2492:C:H5'	2.02	0.42
48:1:961:C:N4	48:1:2615:G:HO2'	2.17	0.42
29:Y:6:ASP:OD2	29:Y:9:SER:N	2.34	0.42
47:L:54:LYS:HD3	47:L:187:VAL:HG13	2.01	0.42
48:1:411:U:H2'	48:1:412:G:H8	1.84	0.42
48:1:964:G:OP2	48:1:1115:G:N1	2.42	0.42
48:1:1861:G:O6	48:1:1870:C:N4	2.52	0.42
48:1:2171:G:H2'	48:1:2172:A:H8	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:4:ARG:HB3	2:X:208:LEU:HA	2.01	0.42
14:O:21:VAL:HG12	14:O:65:LEU:HD23	2.01	0.42
27:x:23:MET:HE1	27:x:78:VAL:HG22	2.00	0.42
30:4:115:C:OP2	48:1:1830:G:N2	2.38	0.42
43:g:99:ASN:O	48:1:1388:U:O2'	2.36	0.42
44:H:277:LEU:HD12	44:H:277:LEU:HA	1.81	0.42
45:h:14:LEU:HD11	45:h:31:LYS:HB2	2.01	0.42
48:1:19:U:H2'	48:1:20:A:C8	2.54	0.42
48:1:1381:A:H2'	48:1:1382:G:H8	1.84	0.42
48:1:1564:U:H2'	48:1:1565:G:H8	1.84	0.42
48:1:3348:G:O6	48:1:3357:U:O4	2.37	0.42
4:J:93:ASN:N	4:J:93:ASN:OD1	2.52	0.42
12:N:48:PRO:HB2	12:N:137:GLN:HB3	2.00	0.42
13:n:9:ILE:HG23	13:n:51:ILE:HG23	2.01	0.42
20:s:175:LEU:HD11	20:s:183:LYS:HE3	2.01	0.42
28:3:19:C:H2'	28:3:20:A:C8	2.55	0.42
35:c:74:ASN:ND2	48:1:705:A:H62	2.17	0.42
40:F:183:LEU:O	40:F:191:LYS:NZ	2.52	0.42
1:R:284:ARG:HD2	1:R:316:ASN:HD21	1.83	0.42
2:X:157:GLN:NE2	2:X:201:ASP:OD1	2.52	0.42
4:J:181:ILE:HG21	42:G:327:LEU:HD23	2.01	0.42
4:J:224:ILE:HA	22:U:36:ILE:HG12	2.01	0.42
8:7:44:THR:HG21	14:O:12:TRP:CH2	2.55	0.42
16:p:73:ARG:HH21	16:p:92:LEU:HD21	1.85	0.42
18:5:134:GLY:O	48:1:1846:C:N4	2.42	0.42
19:S:39:ARG:HB3	42:G:299:ILE:HG23	2.01	0.42
20:s:114:MET:HE3	48:1:1130:A:H61	1.85	0.42
28:3:19:C:H2'	28:3:20:A:H8	1.84	0.42
36:D:79:VAL:O	36:D:82:THR:HB	2.19	0.42
40:F:328:ILE:HD11	40:F:336:VAL:HG11	2.02	0.42
42:G:57:GLY:HA3	42:G:98:ARG:HB3	2.01	0.42
48:1:383:G:N2	48:1:386:A:OP2	2.45	0.42
48:1:408:A:N3	48:1:655:C:O2'	2.47	0.42
48:1:655:C:H2'	48:1:656:A:C8	2.54	0.42
48:1:937:G:N2	48:1:961:C:OP1	2.51	0.42
48:1:2532:U:H3	48:1:2547:A:H61	1.67	0.42
48:1:3007:U:H2'	48:1:3008:A:H8	1.84	0.42
48:1:3016:A:H2'	48:1:3017:A:C8	2.54	0.42
9:l:35:SER:HB2	48:1:814:U:H5''	2.02	0.42
12:N:62:THR:H	12:N:62:THR:HG23	1.51	0.42
20:s:107:ALA:O	20:s:109:ARG:N	2.53	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:G:337:GLU:HB2	42:G:339:LEU:HG	2.02	0.42
47:L:169:VAL:HB	47:L:172:VAL:HG23	2.02	0.42
48:1:500:C:H2'	48:1:501:A:H8	1.83	0.42
48:1:617:G:O4'	48:1:3274:A:N6	2.53	0.42
16:p:54:LYS:NZ	48:1:114:A:OP1	2.53	0.42
34:C:63:LYS:NZ	48:1:2796:G:N7	2.50	0.42
47:L:44:GLN:HE21	47:L:196:LYS:HE2	1.84	0.42
48:1:87:U:OP2	48:1:98:G:N1	2.39	0.42
48:1:155:G:H5''	48:1:156:G:H2'	2.01	0.42
48:1:825:U:H5''	48:1:1797:A:C6	2.54	0.42
48:1:1211:U:H2'	48:1:1212:A:C8	2.55	0.42
48:1:1959:G:C6	48:1:2082:U:O2	2.73	0.42
48:1:2907:G:H2'	48:1:2908:G:H8	1.84	0.42
15:o:113:ARG:HH22	48:1:1191:U:H5''	1.85	0.42
16:p:178:HIS:O	16:p:181:ASN:ND2	2.52	0.42
18:5:125:GLN:HB2	18:5:141:SER:HB2	2.02	0.42
28:3:41:G:O2'	28:3:44:C:N4	2.52	0.42
28:3:96:U:H2'	28:3:97:A:H8	1.85	0.42
42:G:53:SER:HB3	42:G:56:ALA:HB2	2.01	0.42
48:1:515:C:H2'	48:1:516:A:C8	2.53	0.42
48:1:783:A:H5''	48:1:784:A:H5''	2.02	0.42
48:1:1489:A:OP2	48:1:1838:G:N1	2.37	0.42
48:1:3157:U:H4'	48:1:3158:G:C8	2.54	0.42
8:7:11:GLU:HA	8:7:52:LEU:HD23	2.01	0.41
9:l:14:LYS:NZ	48:1:1491:A:OP1	2.50	0.41
17:Q:12:LYS:HB2	17:Q:37:ARG:HD2	2.01	0.41
32:a:122:LYS:HG2	48:1:185:C:H5''	2.02	0.41
40:F:348:ARG:HD3	48:1:3037:U:H5''	2.02	0.41
43:g:43:ARG:HA	43:g:52:GLN:HE22	1.85	0.41
46:I:51:ARG:O	46:I:72:ASN:ND2	2.53	0.41
48:1:27:C:H42	48:1:57:A:H61	1.68	0.41
16:p:37:HIS:HE1	16:p:63:ARG:HH11	1.67	0.41
18:5:126:ARG:HA	18:5:140:GLU:HG2	2.03	0.41
23:V:39:ILE:HG12	23:V:63:VAL:HG22	2.02	0.41
27:x:102:ILE:HG23	27:x:110:LYS:HB3	2.02	0.41
35:c:75:LEU:HG	35:c:114:GLY:HA2	2.02	0.41
48:1:358:G:N2	48:1:361:A:OP2	2.41	0.41
48:1:421:G:O6	48:1:2383:C:O2'	2.36	0.41
1:R:247:ALA:HB1	1:R:382:LEU:HD11	2.02	0.41
1:R:328:LEU:HD23	1:R:328:LEU:HA	1.92	0.41
19:S:141:ARG:HD2	48:1:744:A:H1'	2.00	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:3:10:C:O2'	28:3:13:A:N1	2.43	0.41
36:D:83:ILE:HG23	38:E:96:LEU:HD23	2.02	0.41
48:1:1574:C:H2'	48:1:1575:A:C8	2.53	0.41
1:R:520:ALA:HA	1:R:523:ILE:HG22	2.02	0.41
12:N:189:GLU:HA	12:N:192:GLU:HG2	2.01	0.41
23:V:102:ARG:HD2	23:V:102:ARG:HA	1.89	0.41
28:3:61:G:H5''	44:H:276:LYS:HA	2.01	0.41
38:E:134:VAL:HG12	38:E:151:PRO:HD3	2.01	0.41
48:1:1039:U:H2'	48:1:1040:A:C8	2.55	0.41
48:1:3231:U:O4	48:1:3256:G:O6	2.38	0.41
16:p:5:LYS:HA	16:p:5:LYS:HD2	1.88	0.41
42:G:22:LEU:HA	42:G:23:PRO:HD3	1.80	0.41
47:L:144:LEU:HD13	47:L:147:LYS:HD2	2.01	0.41
48:1:1134:G:O2'	48:1:2642:A:N3	2.41	0.41
48:1:1528:G:HO2'	48:1:1588:A:HO2'	1.63	0.41
8:7:141:LYS:NZ	8:7:142:ASP:OD2	2.52	0.41
23:V:30:TYR:HB3	44:H:38:THR:HG22	2.03	0.41
30:4:59:A:OP2	30:4:98:U:O2'	2.35	0.41
34:C:2:VAL:N	34:C:90:HIS:O	2.54	0.41
36:D:29:LEU:HD23	36:D:29:LEU:HA	1.94	0.41
42:G:10:SER:OG	42:G:13:GLY:O	2.31	0.41
44:H:85:ARG:HE	44:H:254:LYS:HE3	1.85	0.41
48:1:177:U:O2	48:1:241:G:N2	2.53	0.41
48:1:2403:G:O2'	48:1:2404:A:O5'	2.33	0.41
48:1:3238:G:H2'	48:1:3239:G:H8	1.86	0.41
2:X:88:LEU:HD23	2:X:92:VAL:HG11	2.02	0.41
3:i:11:ASN:O	3:i:18:ASN:ND2	2.43	0.41
14:O:121:MET:HE2	48:1:3215:A:H8	1.86	0.41
22:U:137:ARG:NE	48:1:1213:G:OP1	2.43	0.41
28:3:107:C:H2'	28:3:108:A:C8	2.56	0.41
31:Z:67:ILE:HD12	31:Z:83:VAL:HG12	2.02	0.41
34:C:10:THR:HG21	34:C:72:LEU:HD13	2.02	0.41
39:e:25:LEU:O	39:e:29:SER:OG	2.32	0.41
41:f:12:TYR:O	41:f:72:ARG:HA	2.20	0.41
48:1:825:U:H5''	48:1:1797:A:C5	2.55	0.41
48:1:972:A:H2'	48:1:973:A:C8	2.55	0.41
48:1:2502:A:H2'	48:1:2503:G:C8	2.55	0.41
48:1:3047:U:O4	48:1:3094:A:C6	2.74	0.41
3:i:7:PHE:HD2	48:1:1487:G:H21	1.67	0.41
19:S:164:ARG:NH2	48:1:1110:U:OP1	2.53	0.41
20:s:46:PRO:HD2	20:s:140:LYS:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:3:80:G:O2'	48:1:996:A:N3	2.52	0.41
31:Z:77:GLU:HG2	31:Z:133:LEU:HD12	2.03	0.41
35:c:73:LEU:HD11	35:c:77:LYS:HB2	2.02	0.41
40:F:4:ARG:HD2	40:F:7:GLU:HA	2.03	0.41
48:1:533:A:O2'	48:1:535:G:OP2	2.38	0.41
48:1:2443:A:O2'	48:1:2444:C:O5'	2.38	0.41
4:J:121:LYS:HB2	23:V:133:ALA:HB3	2.03	0.41
6:K:78:PHE:HD1	6:K:179:ILE:HD13	1.86	0.41
6:K:249:ARG:O	6:K:253:SER:N	2.54	0.41
12:N:27:ASP:O	12:N:31:LYS:N	2.44	0.41
12:N:27:ASP:OD1	12:N:27:ASP:N	2.53	0.41
18:5:108:ASP:N	18:5:152:GLU:OE2	2.44	0.41
19:S:145:ASN:HA	19:S:150:VAL:HG11	2.03	0.41
22:U:80:ARG:HE	23:V:156:TYR:HB2	1.86	0.41
26:r:16:ARG:HH21	26:r:66:PHE:HE1	1.69	0.41
29:Y:48:ARG:NH2	48:1:2111:G:OP2	2.49	0.41
32:a:63:LYS:HG2	32:a:85:VAL:HG13	2.03	0.41
38:E:93:LYS:NZ	48:1:2548:C:OP2	2.52	0.41
40:F:20:LYS:HB3	48:1:2990:G:H5'	2.02	0.41
40:F:62:ARG:HD3	48:1:3038:U:H5''	2.02	0.41
44:H:76:ALA:HB3	44:H:109:THR:HG22	2.03	0.41
48:1:842:G:H2'	48:1:843:A:C8	2.55	0.41
48:1:949:C:O2'	48:1:971:G:OP1	2.35	0.41
48:1:2768:U:H2'	48:1:2769:A:C8	2.55	0.41
48:1:2923:U:H2'	48:1:2924:U:H6	1.86	0.41
48:1:3358:U:H2'	48:1:3359:A:C8	2.56	0.41
2:X:151:TYR:OH	27:x:132:ASN:ND2	2.47	0.41
8:7:173:ARG:NH1	48:1:2897:A:OP2	2.51	0.41
20:s:100:LYS:HD2	20:s:100:LYS:HA	1.91	0.41
28:3:27:A:H2'	28:3:28:C:H6	1.86	0.41
48:1:255:A:H2'	48:1:256:G:C8	2.55	0.41
48:1:1543:G:O2'	48:1:2168:A:O2'	2.30	0.41
48:1:1570:U:O2	48:1:1571:A:N6	2.53	0.41
48:1:1596:C:H2'	48:1:1597:C:C6	2.55	0.41
48:1:3225:C:H2'	48:1:3226:A:H8	1.86	0.41
2:X:129:ILE:HG23	2:X:133:LEU:HD12	2.03	0.40
3:i:57:LEU:HB3	3:i:61:GLN:HB2	2.03	0.40
14:O:131:VAL:HG13	17:Q:181:ALA:HB1	2.01	0.40
37:d:47:LEU:HA	37:d:50:THR:HG22	2.03	0.40
40:F:106:TRP:HB2	40:F:133:TYR:CE2	2.55	0.40
48:1:147:U:O2'	48:1:148:G:OP1	2.37	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1:510:G:H1	48:1:581:U:H3	1.69	0.40
48:1:512:U:H2'	48:1:513:G:H8	1.87	0.40
48:1:636:C:O2	48:1:2375:G:N2	2.38	0.40
48:1:1071:U:H2'	48:1:1072:G:C8	2.56	0.40
48:1:2428:U:H2'	48:1:2429:G:H8	1.86	0.40
6:K:150:LEU:O	6:K:199:ALA:HA	2.21	0.40
14:O:32:LEU:HD11	14:O:94:TRP:CG	2.56	0.40
19:S:3:ILE:HD13	48:1:1364:C:H5''	2.03	0.40
22:U:10:ILE:HD12	22:U:60:SER:HB3	2.03	0.40
32:a:56:VAL:HG21	32:a:104:LEU:HD13	2.03	0.40
40:F:41:VAL:HG22	40:F:185:GLY:HA3	2.02	0.40
43:g:13:HIS:CE1	43:g:15:LYS:HB3	2.56	0.40
44:H:142:PHE:HD2	44:H:171:LEU:HD22	1.86	0.40
48:1:429:U:H2'	48:1:430:U:H6	1.86	0.40
48:1:1018:G:H2'	48:1:1019:G:H8	1.86	0.40
48:1:1224:C:H42	48:1:3116:G:H1	1.69	0.40
48:1:2168:A:N6	48:1:2170:U:O2	2.54	0.40
48:1:2295:A:N3	48:1:2929:C:O2'	2.49	0.40
48:1:2372:A:H5''	48:1:2373:A:H8	1.86	0.40
48:1:2441:A:H2'	48:1:2442:G:C8	2.56	0.40
4:J:206:LYS:NZ	48:1:1334:U:OP1	2.40	0.40
9:l:68:LYS:NZ	30:4:56:G:OP1	2.39	0.40
24:W:89:LEU:HB3	24:W:93:ILE:HD12	2.03	0.40
34:C:71:ARG:HH21	34:C:80:ARG:NH1	2.16	0.40
38:E:181:LYS:HB2	48:1:860:G:C5	2.56	0.40
40:F:33:PRO:HD2	40:F:44:THR:HB	2.04	0.40
40:F:106:TRP:HH2	40:F:178:LEU:HD21	1.86	0.40
47:L:35:GLN:HA	47:L:169:VAL:HA	2.03	0.40
48:1:1088:U:H2'	48:1:1089:G:H8	1.85	0.40
48:1:1336:U:H2'	48:1:1337:A:C8	2.56	0.40
48:1:1528:G:O2'	48:1:1588:A:O2'	2.27	0.40
48:1:3332:U:H2'	48:1:3333:G:O4'	2.21	0.40
19:S:2:GLY:HA3	48:1:1159:A:H5'	2.04	0.40
28:3:54:U:H4'	28:3:55:A:C8	2.56	0.40
47:L:103:LEU:HD11	47:L:128:LEU:HB3	2.02	0.40
48:1:1812:G:O3'	48:1:1817:G:O2'	2.39	0.40
48:1:1972:A:H62	48:1:2051:G:H21	1.68	0.40
2:X:51:THR:HG21	2:X:84:LEU:HD21	2.04	0.40
28:3:16:U:H2'	28:3:17:A:C8	2.57	0.40
31:Z:103:TYR:HB3	31:Z:135:ILE:HD11	2.02	0.40
34:C:74:CYS:SG	34:C:75:VAL:N	2.94	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:g:75:LEU:HD11	48:1:1410:U:H4'	2.03	0.40
48:1:210:U:HO2'	48:1:229:G:HO2'	1.63	0.40
48:1:1090:G:H2'	48:1:1091:A:C8	2.57	0.40
48:1:2270:A:H2'	48:1:2271:A:C8	2.56	0.40
48:1:2423:U:H2'	48:1:2424:A:C8	2.57	0.40
48:1:3060:C:H1'	48:1:3332:U:H1'	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	300/475 (63%)	284 (95%)	16 (5%)	0	100	100
2	X	222/224 (99%)	211 (95%)	11 (5%)	0	100	100
3	i	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
4	J	220/222 (99%)	202 (92%)	16 (7%)	2 (1%)	14	42
5	j	117/119 (98%)	109 (93%)	5 (4%)	3 (3%)	4	21
6	K	231/233 (99%)	215 (93%)	14 (6%)	2 (1%)	14	42
7	k	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
8	7	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
9	l	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
10	M	167/169 (99%)	145 (87%)	22 (13%)	0	100	100
11	m	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
12	N	191/193 (99%)	173 (91%)	14 (7%)	4 (2%)	5	24
13	n	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
14	O	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
15	o	50/52 (96%)	47 (94%)	3 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	p	201/203 (99%)	182 (90%)	16 (8%)	3 (2%)	8	30
17	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
18	5	181/183 (99%)	163 (90%)	18 (10%)	0	100	100
19	S	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
20	s	218/220 (99%)	194 (89%)	22 (10%)	2 (1%)	14	42
21	T	150/152 (99%)	141 (94%)	8 (5%)	1 (1%)	18	47
22	U	170/172 (99%)	158 (93%)	11 (6%)	1 (1%)	21	50
23	V	157/159 (99%)	145 (92%)	12 (8%)	0	100	100
24	W	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
25	P	144/155 (93%)	124 (86%)	20 (14%)	0	100	100
26	r	117/197 (59%)	108 (92%)	9 (8%)	0	100	100
27	x	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
29	Y	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
31	Z	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
32	a	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
33	b	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	44
34	C	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
35	c	146/148 (99%)	128 (88%)	16 (11%)	2 (1%)	9	31
36	D	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
37	d	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
38	E	250/252 (99%)	229 (92%)	21 (8%)	0	100	100
39	e	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
40	F	384/386 (100%)	354 (92%)	29 (8%)	1 (0%)	36	65
41	f	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
42	G	359/361 (99%)	325 (90%)	32 (9%)	2 (1%)	21	50
43	g	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
44	H	294/296 (99%)	274 (93%)	18 (6%)	2 (1%)	18	47
45	h	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
46	I	152/175 (87%)	147 (97%)	5 (3%)	0	100	100
47	L	202/204 (99%)	165 (82%)	37 (18%)	0	100	100
All	All	7086/7457 (95%)	6532 (92%)	528 (8%)	26 (0%)	31	59

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	s	108	ASP
35	c	47	LYS
35	c	78	LEU
42	G	339	LEU
4	J	158	LYS
4	J	233	GLU
6	K	157	VAL
12	N	62	THR
16	p	74	PRO
21	T	131	ALA
5	j	85	THR
5	j	91	ALA
12	N	48	PRO
5	j	90	ARG
6	K	156	ASP
22	U	13	ARG
12	N	61	PRO
42	G	292	SER
44	H	276	LYS
12	N	47	ALA
16	p	146	ALA
33	b	102	GLU
44	H	260	PHE
16	p	75	VAL
40	F	188	ILE
20	s	171	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	288/392 (74%)	287 (100%)	1 (0%)	86	84
2	X	177/192 (92%)	177 (100%)	0	100	100
3	i	95/95 (100%)	95 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	J	186/186 (100%)	186 (100%)	0	100	100
5	j	104/104 (100%)	103 (99%)	1 (1%)	68	75
6	K	187/191 (98%)	186 (100%)	1 (0%)	81	81
7	k	81/81 (100%)	81 (100%)	0	100	100
8	7	171/171 (100%)	170 (99%)	1 (1%)	78	80
9	l	70/70 (100%)	70 (100%)	0	100	100
10	M	147/147 (100%)	146 (99%)	1 (1%)	76	78
11	m	68/68 (100%)	68 (100%)	0	100	100
12	N	154/154 (100%)	151 (98%)	3 (2%)	50	66
13	n	45/45 (100%)	45 (100%)	0	100	100
14	O	107/107 (100%)	107 (100%)	0	100	100
15	o	47/47 (100%)	47 (100%)	0	100	100
16	p	175/175 (100%)	174 (99%)	1 (1%)	78	80
17	Q	160/160 (100%)	159 (99%)	1 (1%)	78	80
18	5	140/145 (97%)	138 (99%)	2 (1%)	59	70
19	S	150/150 (100%)	150 (100%)	0	100	100
20	s	184/186 (99%)	184 (100%)	0	100	100
21	T	126/126 (100%)	126 (100%)	0	100	100
22	U	156/156 (100%)	155 (99%)	1 (1%)	78	80
23	V	136/136 (100%)	134 (98%)	2 (2%)	57	69
24	W	87/87 (100%)	87 (100%)	0	100	100
26	r	105/166 (63%)	105 (100%)	0	100	100
27	x	104/104 (100%)	104 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
31	Z	104/105 (99%)	104 (100%)	0	100	100
32	a	109/109 (100%)	108 (99%)	1 (1%)	70	76
33	b	115/115 (100%)	115 (100%)	0	100	100
34	C	90/90 (100%)	90 (100%)	0	100	100
35	c	118/118 (100%)	117 (99%)	1 (1%)	73	77
36	D	71/71 (100%)	71 (100%)	0	100	100
37	d	46/46 (100%)	46 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	E	193/194 (100%)	190 (98%)	3 (2%)	55	68
39	e	81/81 (100%)	81 (100%)	0	100	100
40	F	319/322 (99%)	318 (100%)	1 (0%)	86	84
41	f	92/96 (96%)	92 (100%)	0	100	100
42	G	288/288 (100%)	288 (100%)	0	100	100
43	g	109/109 (100%)	109 (100%)	0	100	100
44	H	244/244 (100%)	243 (100%)	1 (0%)	84	83
45	h	90/90 (100%)	90 (100%)	0	100	100
46	I	134/152 (88%)	134 (100%)	0	100	100
47	L	185/185 (100%)	184 (100%)	1 (0%)	81	81
All	All	5892/6110 (96%)	5869 (100%)	23 (0%)	81	83

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	212	ASN
5	j	36	LEU
6	K	136	LEU
8	7	68	LEU
10	M	84	LEU
12	N	58	VAL
12	N	85	LEU
12	N	124	ILE
16	p	183	THR
17	Q	34	VAL
18	5	24	VAL
18	5	114	VAL
22	U	100	VAL
23	V	80	VAL
23	V	128	LEU
32	a	80	VAL
35	c	78	LEU
38	E	101	VAL
38	E	225	ILE
38	E	230	VAL
40	F	104	THR
44	H	64	ILE
47	L	108	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	16	ASN
1	R	212	ASN
1	R	227	ASN
1	R	316	ASN
2	X	6	GLN
2	X	50	HIS
2	X	106	ASN
3	i	69	HIS
3	i	98	GLN
4	J	80	GLN
5	j	59	ASN
5	j	99	GLN
6	K	240	ASN
6	K	243	GLN
7	k	63	ASN
8	7	183	HIS
9	l	57	HIS
10	M	43	GLN
11	m	40	GLN
14	O	126	GLN
15	o	109	ASN
16	p	37	HIS
16	p	181	ASN
17	Q	31	GLN
18	5	116	HIS
18	5	133	HIS
19	S	73	GLN
21	T	66	HIS
22	U	88	HIS
23	V	122	GLN
23	V	146	ASN
24	W	87	ASN
26	r	32	ASN
26	r	56	ASN
27	x	98	ASN
29	Y	32	GLN
29	Y	58	HIS
29	Y	59	HIS
31	Z	111	ASN
32	a	120	GLN
33	b	36	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
33	b	57	HIS
34	C	22	GLN
35	c	64	GLN
35	c	74	ASN
37	d	12	GLN
38	E	79	ASN
38	E	132	ASN
38	E	205	ASN
38	E	209	HIS
40	F	109	HIS
40	F	231	HIS
42	G	5	GLN
42	G	48	GLN
42	G	110	ASN
42	G	361	HIS
43	g	52	GLN
43	g	88	HIS
44	H	81	HIS
45	h	42	GLN
46	I	28	GLN
47	L	21	ASN
47	L	44	GLN
47	L	57	ASN
47	L	96	ASN
47	L	108	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	3	120/121 (99%)	28 (23%)	1 (0%)
30	4	157/158 (99%)	36 (22%)	5 (3%)
48	1	3257/3260 (99%)	908 (27%)	158 (4%)
All	All	3534/3539 (99%)	972 (27%)	164 (4%)

All (972) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	3	10	C
28	3	11	A
28	3	13	A
28	3	14	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
28	3	33	U
28	3	38	U
28	3	41	G
28	3	42	A
28	3	45	A
28	3	48	U
28	3	49	G
28	3	50	U
28	3	52	G
28	3	53	U
28	3	55	A
28	3	64	A
28	3	65	G
28	3	73	C
28	3	74	C
28	3	76	A
28	3	77	G
28	3	78	U
28	3	91	G
28	3	99	G
28	3	102	A
28	3	111	U
28	3	112	G
28	3	121	U
30	4	13	A
30	4	16	G
30	4	22	U
30	4	23	U
30	4	24	G
30	4	34	U
30	4	35	C
30	4	39	G
30	4	40	A
30	4	49	G
30	4	51	G
30	4	52	A
30	4	59	A
30	4	60	U
30	4	63	G
30	4	80	A
30	4	81	U
30	4	82	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	4	83	C
30	4	85	G
30	4	86	U
30	4	87	G
30	4	90	U
30	4	95	G
30	4	104	A
30	4	106	C
30	4	111	A
30	4	112	U
30	4	113	U
30	4	116	G
30	4	125	U
30	4	126	A
30	4	129	C
30	4	138	A
30	4	147	U
30	4	152	G
48	1	6	A
48	1	13	A
48	1	14	U
48	1	15	C
48	1	22	G
48	1	25	U
48	1	26	A
48	1	30	G
48	1	40	A
48	1	41	G
48	1	43	A
48	1	44	U
48	1	48	A
48	1	49	A
48	1	57	A
48	1	59	G
48	1	60	A
48	1	65	A
48	1	66	A
48	1	67	A
48	1	72	C
48	1	73	C
48	1	77	A
48	1	86	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	87	U
48	1	92	G
48	1	109	A
48	1	110	G
48	1	116	A
48	1	117	U
48	1	118	U
48	1	119	U
48	1	121	A
48	1	122	A
48	1	123	A
48	1	134	U
48	1	135	C
48	1	136	G
48	1	146	U
48	1	147	U
48	1	148	G
48	1	150	A
48	1	155	G
48	1	156	G
48	1	157	A
48	1	166	C
48	1	167	U
48	1	168	U
48	1	169	U
48	1	170	G
48	1	187	A
48	1	188	U
48	1	189	G
48	1	190	U
48	1	191	U
48	1	197	G
48	1	200	C
48	1	206	G
48	1	210	U
48	1	211	A
48	1	212	G
48	1	213	A
48	1	218	G
48	1	219	A
48	1	220	G
48	1	234	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	238	A
48	1	240	U
48	1	241	G
48	1	252	U
48	1	266	A
48	1	269	G
48	1	270	U
48	1	281	G
48	1	283	G
48	1	285	A
48	1	286	U
48	1	295	A
48	1	297	G
48	1	298	U
48	1	304	G
48	1	305	U
48	1	323	A
48	1	329	U
48	1	330	G
48	1	337	G
48	1	338	A
48	1	339	C
48	1	342	A
48	1	343	U
48	1	350	C
48	1	352	A
48	1	353	G
48	1	354	U
48	1	375	A
48	1	376	G
48	1	385	A
48	1	390	G
48	1	395	A
48	1	398	A
48	1	399	A
48	1	401	U
48	1	403	C
48	1	406	G
48	1	420	G
48	1	421	G
48	1	422	A
48	1	429	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	439	C
48	1	440	A
48	1	495	G
48	1	517	G
48	1	521	A
48	1	523	A
48	1	535	G
48	1	536	U
48	1	547	G
48	1	548	G
48	1	555	U
48	1	556	U
48	1	558	U
48	1	559	A
48	1	560	G
48	1	566	G
48	1	578	A
48	1	579	G
48	1	581	U
48	1	589	A
48	1	592	A
48	1	597	G
48	1	600	G
48	1	603	A
48	1	604	G
48	1	609	G
48	1	611	A
48	1	620	U
48	1	621	A
48	1	622	A
48	1	623	U
48	1	637	C
48	1	641	C
48	1	645	A
48	1	646	A
48	1	648	C
48	1	649	A
48	1	661	G
48	1	667	C
48	1	677	A
48	1	678	G
48	1	681	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	683	U
48	1	690	A
48	1	691	A
48	1	692	A
48	1	699	A
48	1	705	A
48	1	708	G
48	1	709	A
48	1	712	G
48	1	715	A
48	1	716	A
48	1	719	U
48	1	720	A
48	1	742	G
48	1	758	C
48	1	760	G
48	1	764	U
48	1	765	C
48	1	766	U
48	1	767	U
48	1	768	C
48	1	770	G
48	1	776	U
48	1	777	U
48	1	781	G
48	1	784	A
48	1	785	G
48	1	786	A
48	1	798	G
48	1	799	G
48	1	800	G
48	1	801	A
48	1	806	A
48	1	817	A
48	1	825	U
48	1	830	A
48	1	832	G
48	1	835	G
48	1	837	A
48	1	849	C
48	1	851	C
48	1	857	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	858	A
48	1	860	G
48	1	861	C
48	1	869	G
48	1	870	G
48	1	871	U
48	1	874	U
48	1	875	G
48	1	879	U
48	1	880	G
48	1	882	A
48	1	884	A
48	1	885	U
48	1	895	A
48	1	907	G
48	1	909	G
48	1	914	A
48	1	915	A
48	1	916	G
48	1	917	A
48	1	920	A
48	1	925	A
48	1	932	U
48	1	933	A
48	1	937	G
48	1	944	C
48	1	953	G
48	1	959	C
48	1	960	U
48	1	962	A
48	1	963	G
48	1	978	G
48	1	980	A
48	1	981	U
48	1	982	C
48	1	985	U
48	1	991	G
48	1	995	U
48	1	1001	G
48	1	1005	G
48	1	1006	A
48	1	1015	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1016	C
48	1	1017	C
48	1	1018	G
48	1	1021	G
48	1	1025	A
48	1	1026	A
48	1	1029	G
48	1	1032	C
48	1	1036	A
48	1	1037	C
48	1	1038	C
48	1	1044	U
48	1	1045	C
48	1	1047	A
48	1	1049	C
48	1	1054	A
48	1	1065	A
48	1	1066	G
48	1	1075	A
48	1	1076	C
48	1	1081	U
48	1	1082	U
48	1	1083	G
48	1	1092	C
48	1	1093	A
48	1	1094	U
48	1	1095	U
48	1	1096	U
48	1	1097	G
48	1	1098	A
48	1	1103	A
48	1	1104	G
48	1	1117	G
48	1	1122	U
48	1	1128	U
48	1	1131	G
48	1	1140	G
48	1	1143	A
48	1	1144	U
48	1	1145	G
48	1	1151	U
48	1	1153	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1155	C
48	1	1159	A
48	1	1177	G
48	1	1178	G
48	1	1180	A
48	1	1181	U
48	1	1182	A
48	1	1190	A
48	1	1191	U
48	1	1192	C
48	1	1193	A
48	1	1196	C
48	1	1197	A
48	1	1199	C
48	1	1200	A
48	1	1201	C
48	1	1202	A
48	1	1206	G
48	1	1209	G
48	1	1219	C
48	1	1220	U
48	1	1221	A
48	1	1222	G
48	1	1223	A
48	1	1224	C
48	1	1232	C
48	1	1235	U
48	1	1236	G
48	1	1237	G
48	1	1238	C
48	1	1239	C
48	1	1241	U
48	1	1242	G
48	1	1244	A
48	1	1245	A
48	1	1246	G
48	1	1258	U
48	1	1259	A
48	1	1262	G
48	1	1263	A
48	1	1264	G
48	1	1265	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1282	G
48	1	1285	G
48	1	1287	A
48	1	1292	C
48	1	1293	U
48	1	1301	A
48	1	1303	A
48	1	1305	U
48	1	1306	G
48	1	1307	G
48	1	1308	A
48	1	1313	G
48	1	1315	U
48	1	1316	C
48	1	1317	A
48	1	1329	U
48	1	1330	A
48	1	1331	U
48	1	1349	G
48	1	1351	U
48	1	1352	A
48	1	1355	A
48	1	1356	U
48	1	1357	G
48	1	1366	A
48	1	1367	G
48	1	1368	U
48	1	1380	G
48	1	1386	A
48	1	1391	C
48	1	1392	G
48	1	1399	A
48	1	1400	G
48	1	1418	A
48	1	1419	A
48	1	1421	G
48	1	1432	C
48	1	1434	G
48	1	1435	A
48	1	1436	U
48	1	1437	C
48	1	1438	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1443	G
48	1	1447	G
48	1	1448	U
48	1	1450	G
48	1	1456	A
48	1	1467	A
48	1	1468	A
48	1	1469	C
48	1	1480	G
48	1	1482	A
48	1	1483	G
48	1	1484	U
48	1	1487	G
48	1	1494	U
48	1	1495	U
48	1	1496	C
48	1	1503	A
48	1	1508	C
48	1	1511	U
48	1	1512	U
48	1	1523	U
48	1	1527	C
48	1	1528	G
48	1	1533	U
48	1	1536	G
48	1	1546	A
48	1	1547	G
48	1	1554	U
48	1	1555	U
48	1	1556	C
48	1	1558	A
48	1	1559	A
48	1	1560	G
48	1	1561	G
48	1	1563	C
48	1	1565	G
48	1	1567	U
48	1	1568	U
48	1	1569	U
48	1	1570	U
48	1	1572	U
48	1	1573	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1575	A
48	1	1578	C
48	1	1579	C
48	1	1580	A
48	1	1581	C
48	1	1582	C
48	1	1583	A
48	1	1587	A
48	1	1588	A
48	1	1589	A
48	1	1590	G
48	1	1593	A
48	1	1595	U
48	1	1605	A
48	1	1613	A
48	1	1620	U
48	1	1621	A
48	1	1623	G
48	1	1629	U
48	1	1630	U
48	1	1641	U
48	1	1645	U
48	1	1646	G
48	1	1657	C
48	1	1683	A
48	1	1687	U
48	1	1696	A
48	1	1715	A
48	1	1717	U
48	1	1719	G
48	1	1724	U
48	1	1725	C
48	1	1730	G
48	1	1731	A
48	1	1741	A
48	1	1742	U
48	1	1749	A
48	1	1750	A
48	1	1760	A
48	1	1762	C
48	1	1763	U
48	1	1765	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1766	G
48	1	1769	G
48	1	1770	G
48	1	1771	C
48	1	1775	G
48	1	1780	G
48	1	1794	G
48	1	1795	U
48	1	1796	G
48	1	1797	A
48	1	1813	A
48	1	1814	A
48	1	1815	U
48	1	1816	A
48	1	1817	G
48	1	1818	U
48	1	1819	U
48	1	1820	U
48	1	1822	C
48	1	1839	A
48	1	1840	U
48	1	1841	A
48	1	1843	C
48	1	1845	G
48	1	1846	C
48	1	1847	A
48	1	1849	C
48	1	1850	A
48	1	1851	G
48	1	1864	A
48	1	1866	C
48	1	1867	A
48	1	1871	U
48	1	1878	G
48	1	1879	A
48	1	1880	U
48	1	1886	A
48	1	1887	A
48	1	1893	A
48	1	1894	U
48	1	1901	A
48	1	1905	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1906	G
48	1	1907	C
48	1	1913	A
48	1	1914	G
48	1	1927	G
48	1	1930	A
48	1	1931	U
48	1	1932	A
48	1	1935	G
48	1	1939	G
48	1	1943	C
48	1	1953	G
48	1	1954	G
48	1	1955	U
48	1	1959	G
48	1	1960	A
48	1	1961	G
48	1	1962	A
48	1	1963	G
48	1	1964	C
48	1	1972	A
48	1	1973	G
48	1	1976	G
48	1	2044	U
48	1	2045	G
48	1	2047	A
48	1	2048	G
48	1	2049	A
48	1	2050	C
48	1	2051	G
48	1	2058	G
48	1	2059	U
48	1	2081	U
48	1	2082	U
48	1	2087	C
48	1	2088	A
48	1	2093	A
48	1	2099	A
48	1	2100	A
48	1	2101	C
48	1	2102	U
48	1	2107	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2111	G
48	1	2112	U
48	1	2113	A
48	1	2116	G
48	1	2121	G
48	1	2122	G
48	1	2126	A
48	1	2131	A
48	1	2134	G
48	1	2138	A
48	1	2139	A
48	1	2140	U
48	1	2142	A
48	1	2143	A
48	1	2144	A
48	1	2145	A
48	1	2159	U
48	1	2160	G
48	1	2166	A
48	1	2169	G
48	1	2170	U
48	1	2175	U
48	1	2176	U
48	1	2178	A
48	1	2179	C
48	1	2184	U
48	1	2187	G
48	1	2188	A
48	1	2205	U
48	1	2206	G
48	1	2209	U
48	1	2210	G
48	1	2218	G
48	1	2223	A
48	1	2225	U
48	1	2230	C
48	1	2243	A
48	1	2244	A
48	1	2249	G
48	1	2253	G
48	1	2254	U
48	1	2256	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2257	C
48	1	2258	U
48	1	2260	U
48	1	2261	G
48	1	2262	A
48	1	2263	C
48	1	2267	C
48	1	2268	U
48	1	2269	U
48	1	2270	A
48	1	2272	G
48	1	2273	G
48	1	2274	U
48	1	2276	G
48	1	2279	A
48	1	2280	A
48	1	2281	A
48	1	2282	U
48	1	2283	G
48	1	2284	C
48	1	2285	C
48	1	2298	U
48	1	2299	A
48	1	2306	C
48	1	2307	G
48	1	2308	C
48	1	2310	U
48	1	2313	A
48	1	2314	U
48	1	2315	G
48	1	2319	U
48	1	2334	U
48	1	2335	G
48	1	2340	U
48	1	2347	U
48	1	2356	A
48	1	2361	A
48	1	2373	A
48	1	2374	C
48	1	2375	G
48	1	2376	G
48	1	2386	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2388	U
48	1	2391	G
48	1	2393	G
48	1	2397	A
48	1	2401	A
48	1	2402	A
48	1	2403	G
48	1	2404	A
48	1	2411	U
48	1	2418	G
48	1	2419	A
48	1	2435	G
48	1	2440	G
48	1	2441	A
48	1	2443	A
48	1	2444	C
48	1	2445	A
48	1	2446	U
48	1	2447	A
48	1	2448	G
48	1	2453	U
48	1	2454	G
48	1	2459	A
48	1	2462	A
48	1	2469	G
48	1	2471	U
48	1	2482	U
48	1	2486	A
48	1	2487	U
48	1	2488	A
48	1	2496	C
48	1	2500	A
48	1	2503	G
48	1	2504	U
48	1	2505	U
48	1	2506	U
48	1	2507	C
48	1	2509	U
48	1	2510	U
48	1	2512	C
48	1	2513	U
48	1	2514	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2515	A
48	1	2522	G
48	1	2523	A
48	1	2526	C
48	1	2531	C
48	1	2532	U
48	1	2533	G
48	1	2537	U
48	1	2538	U
48	1	2539	C
48	1	2540	A
48	1	2541	U
48	1	2542	U
48	1	2543	U
48	1	2544	U
48	1	2548	C
48	1	2549	G
48	1	2552	C
48	1	2554	A
48	1	2559	U
48	1	2561	A
48	1	2568	C
48	1	2569	A
48	1	2570	U
48	1	2571	U
48	1	2572	C
48	1	2573	G
48	1	2585	G
48	1	2587	U
48	1	2593	A
48	1	2594	C
48	1	2606	G
48	1	2607	G
48	1	2614	G
48	1	2618	G
48	1	2619	G
48	1	2626	A
48	1	2629	U
48	1	2635	A
48	1	2636	A
48	1	2648	G
48	1	2651	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2652	U
48	1	2655	U
48	1	2657	A
48	1	2666	C
48	1	2674	A
48	1	2676	A
48	1	2678	A
48	1	2681	U
48	1	2689	A
48	1	2691	A
48	1	2694	A
48	1	2704	A
48	1	2713	U
48	1	2716	U
48	1	2719	U
48	1	2720	G
48	1	2726	C
48	1	2727	A
48	1	2728	G
48	1	2729	U
48	1	2737	C
48	1	2742	C
48	1	2753	G
48	1	2755	C
48	1	2761	G
48	1	2762	A
48	1	2772	C
48	1	2773	C
48	1	2777	G
48	1	2778	G
48	1	2779	A
48	1	2796	G
48	1	2797	C
48	1	2798	C
48	1	2800	G
48	1	2801	A
48	1	2802	A
48	1	2804	A
48	1	2810	C
48	1	2814	G
48	1	2816	G
48	1	2817	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2827	U
48	1	2829	U
48	1	2830	G
48	1	2842	U
48	1	2845	A
48	1	2846	U
48	1	2847	A
48	1	2850	G
48	1	2851	A
48	1	2867	C
48	1	2871	G
48	1	2872	A
48	1	2873	U
48	1	2874	G
48	1	2882	U
48	1	2887	A
48	1	2888	U
48	1	2889	C
48	1	2895	G
48	1	2912	G
48	1	2915	U
48	1	2923	U
48	1	2926	A
48	1	2935	U
48	1	2936	A
48	1	2938	G
48	1	2941	A
48	1	2945	G
48	1	2946	A
48	1	2947	G
48	1	2951	G
48	1	2954	U
48	1	2971	A
48	1	2972	G
48	1	2978	U
48	1	2979	U
48	1	2980	U
48	1	2983	C
48	1	2985	C
48	1	2996	U
48	1	2997	G
48	1	3003	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	3011	A
48	1	3012	A
48	1	3021	A
48	1	3022	G
48	1	3023	U
48	1	3026	G
48	1	3030	G
48	1	3047	U
48	1	3056	U
48	1	3058	U
48	1	3059	G
48	1	3069	G
48	1	3074	G
48	1	3078	U
48	1	3079	U
48	1	3080	G
48	1	3086	A
48	1	3092	C
48	1	3104	U
48	1	3109	G
48	1	3117	C
48	1	3118	C
48	1	3119	U
48	1	3122	A
48	1	3130	A
48	1	3131	U
48	1	3139	A
48	1	3141	A
48	1	3142	A
48	1	3143	C
48	1	3144	G
48	1	3151	U
48	1	3152	U
48	1	3153	U
48	1	3154	C
48	1	3155	U
48	1	3156	U
48	1	3157	U
48	1	3158	G
48	1	3167	A
48	1	3173	G
48	1	3174	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	3175	U
48	1	3176	G
48	1	3179	U
48	1	3180	A
48	1	3181	C
48	1	3186	A
48	1	3187	A
48	1	3196	U
48	1	3198	U
48	1	3205	G
48	1	3206	C
48	1	3207	U
48	1	3208	G
48	1	3209	A
48	1	3210	A
48	1	3211	C
48	1	3215	A
48	1	3217	C
48	1	3218	A
48	1	3219	G
48	1	3220	G
48	1	3222	U
48	1	3227	A
48	1	3237	U
48	1	3242	G
48	1	3243	A
48	1	3244	A
48	1	3245	A
48	1	3246	G
48	1	3247	G
48	1	3253	G
48	1	3259	U
48	1	3260	G
48	1	3263	G
48	1	3268	A
48	1	3269	U
48	1	3270	U
48	1	3271	G
48	1	3272	C
48	1	3273	A
48	1	3275	U
48	1	3276	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	3277	U
48	1	3278	C
48	1	3280	U
48	1	3282	U
48	1	3287	U
48	1	3288	G
48	1	3289	G
48	1	3293	U
48	1	3294	A
48	1	3295	A
48	1	3303	G
48	1	3304	U
48	1	3305	A
48	1	3308	C
48	1	3309	G
48	1	3313	U
48	1	3316	A
48	1	3317	U
48	1	3318	G
48	1	3319	U
48	1	3335	A
48	1	3341	U
48	1	3345	G
48	1	3347	A
48	1	3349	C
48	1	3351	U
48	1	3352	U
48	1	3353	G
48	1	3355	U
48	1	3357	U
48	1	3358	U
48	1	3362	A
48	1	3363	U
48	1	3368	U
48	1	3369	G
48	1	3375	A
48	1	3376	A
48	1	3378	C
48	1	3382	U
48	1	3383	G
48	1	3386	G
48	1	3390	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	3393	U
48	1	3396	U

All (164) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	3	77	G
30	4	22	U
30	4	38	U
30	4	48	A
30	4	51	G
30	4	58	G
48	1	14	U
48	1	43	A
48	1	66	A
48	1	71	A
48	1	86	G
48	1	116	A
48	1	122	A
48	1	147	U
48	1	155	G
48	1	156	G
48	1	189	G
48	1	211	A
48	1	218	G
48	1	219	A
48	1	239	G
48	1	268	A
48	1	269	G
48	1	282	G
48	1	337	G
48	1	341	G
48	1	342	A
48	1	352	A
48	1	353	G
48	1	400	G
48	1	494	G
48	1	547	G
48	1	558	U
48	1	621	A
48	1	645	A
48	1	648	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	661	G
48	1	677	A
48	1	715	A
48	1	764	U
48	1	857	G
48	1	870	G
48	1	884	A
48	1	906	A
48	1	914	A
48	1	916	G
48	1	920	A
48	1	924	G
48	1	932	U
48	1	962	A
48	1	979	U
48	1	994	G
48	1	1064	A
48	1	1075	A
48	1	1097	G
48	1	1116	G
48	1	1144	U
48	1	1152	G
48	1	1177	G
48	1	1192	C
48	1	1199	C
48	1	1241	U
48	1	1305	U
48	1	1307	G
48	1	1329	U
48	1	1348	U
48	1	1355	A
48	1	1365	G
48	1	1391	C
48	1	1417	G
48	1	1418	A
48	1	1433	A
48	1	1434	G
48	1	1455	U
48	1	1481	A
48	1	1483	G
48	1	1511	U
48	1	1553	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	1554	U
48	1	1557	A
48	1	1558	A
48	1	1580	A
48	1	1588	A
48	1	1589	A
48	1	1695	U
48	1	1716	U
48	1	1730	G
48	1	1740	U
48	1	1793	C
48	1	1795	U
48	1	1815	U
48	1	1816	A
48	1	1840	U
48	1	1849	C
48	1	1850	A
48	1	1866	C
48	1	1900	A
48	1	1906	G
48	1	1913	A
48	1	1938	U
48	1	1959	G
48	1	2086	A
48	1	2101	C
48	1	2111	G
48	1	2112	U
48	1	2139	A
48	1	2158	A
48	1	2175	U
48	1	2177	G
48	1	2178	A
48	1	2187	G
48	1	2208	A
48	1	2262	A
48	1	2267	C
48	1	2271	A
48	1	2282	U
48	1	2283	G
48	1	2298	U
48	1	2313	A
48	1	2385	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	2403	G
48	1	2447	A
48	1	2468	A
48	1	2487	U
48	1	2509	U
48	1	2513	U
48	1	2537	U
48	1	2541	U
48	1	2586	G
48	1	2593	A
48	1	2617	U
48	1	2625	C
48	1	2635	A
48	1	2656	A
48	1	2665	U
48	1	2715	A
48	1	2727	A
48	1	2796	G
48	1	2797	C
48	1	2803	A
48	1	2816	G
48	1	2850	G
48	1	2872	A
48	1	2911	A
48	1	2950	G
48	1	3022	G
48	1	3055	U
48	1	3078	U
48	1	3121	U
48	1	3154	C
48	1	3156	U
48	1	3175	U
48	1	3179	U
48	1	3208	G
48	1	3216	G
48	1	3218	A
48	1	3219	G
48	1	3246	G
48	1	3269	U
48	1	3293	U
48	1	3303	G
48	1	3334	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	1	3368	U
48	1	3375	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	4
48	1	3
40	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	173:UNK	C	188:SER	N	30.28
1	R	105:ARG	C	113:UNK	N	19.44
1	1	1980:C	O3'	2042:G	P	19.07
1	R	529:GLY	C	535:UNK	N	17.02
1	R	123:UNK	C	156:UNK	N	12.97
1	1	440:A	O3'	494:G	P	12.88
1	1	2059:U	O3'	2080:C	P	12.20
1	F	237:LYS	C	238:LEU	N	1.17

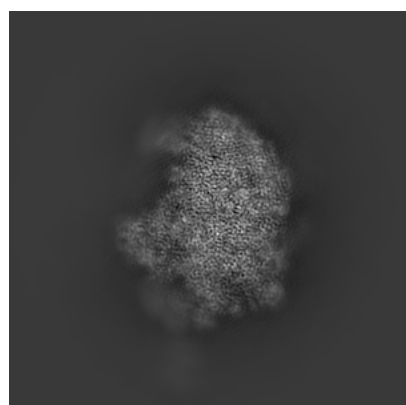
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4752. These allow visual inspection of the internal detail of the map and identification of artifacts.

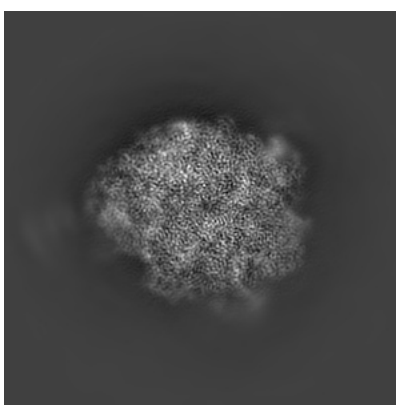
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

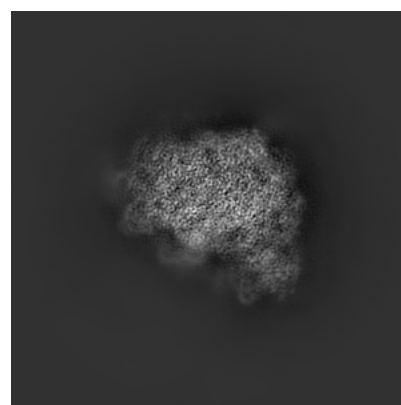
6.1.1 Primary map



X



Y

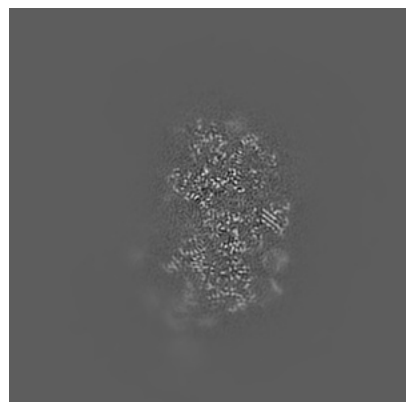


Z

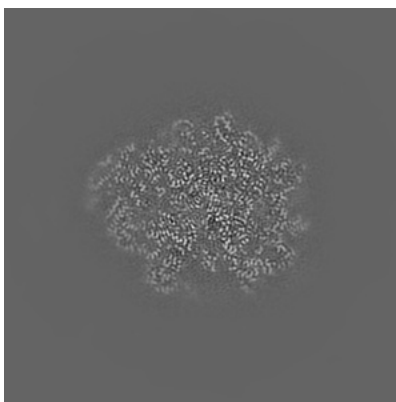
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

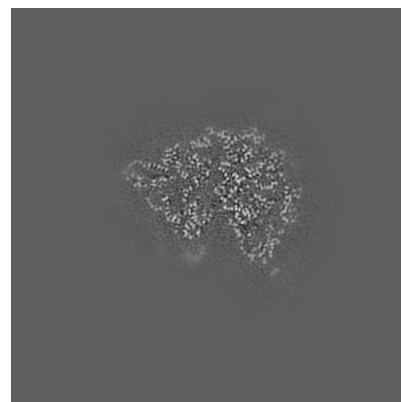
6.2.1 Primary map



X Index: 198



Y Index: 198

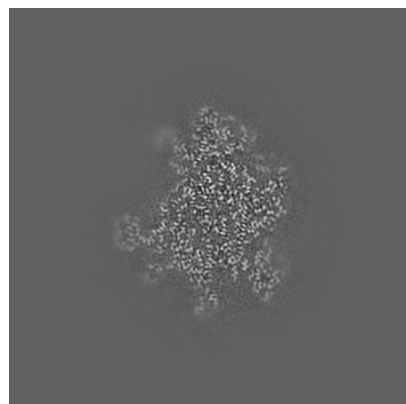


Z Index: 198

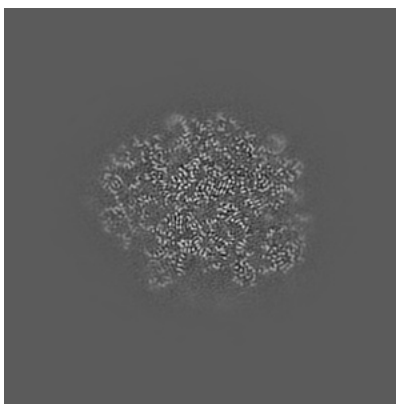
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

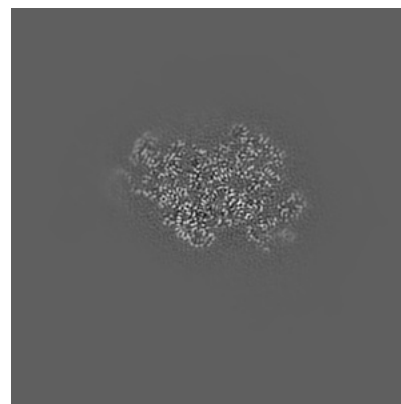
6.3.1 Primary map



X Index: 235



Y Index: 206

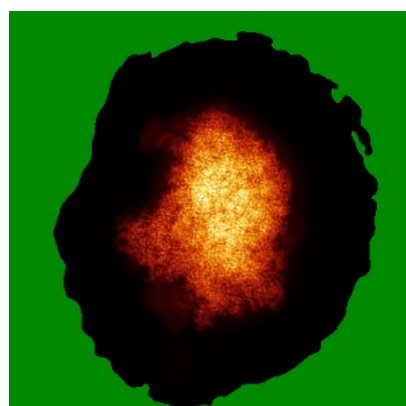


Z Index: 217

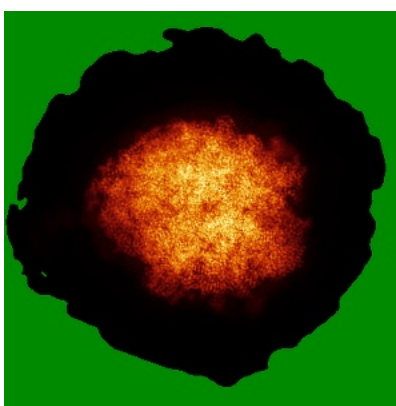
The images above show the largest variance slices of the map in three orthogonal directions.

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

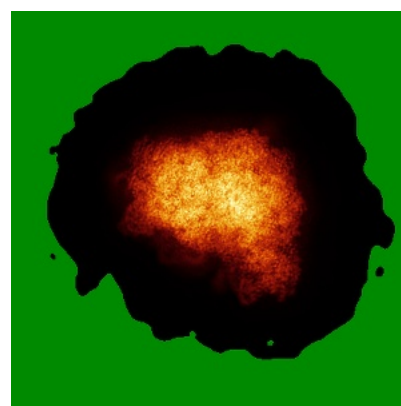
6.4.1 Primary map



X



Y

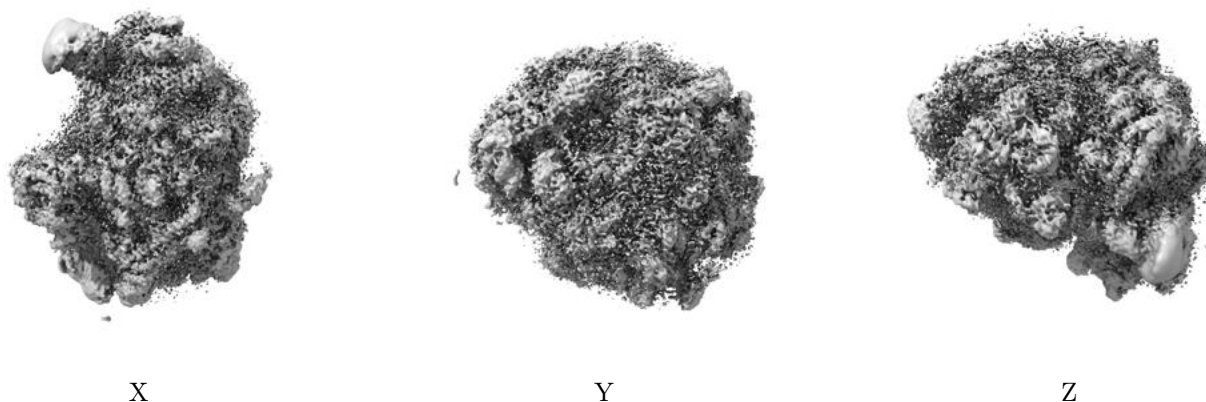


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

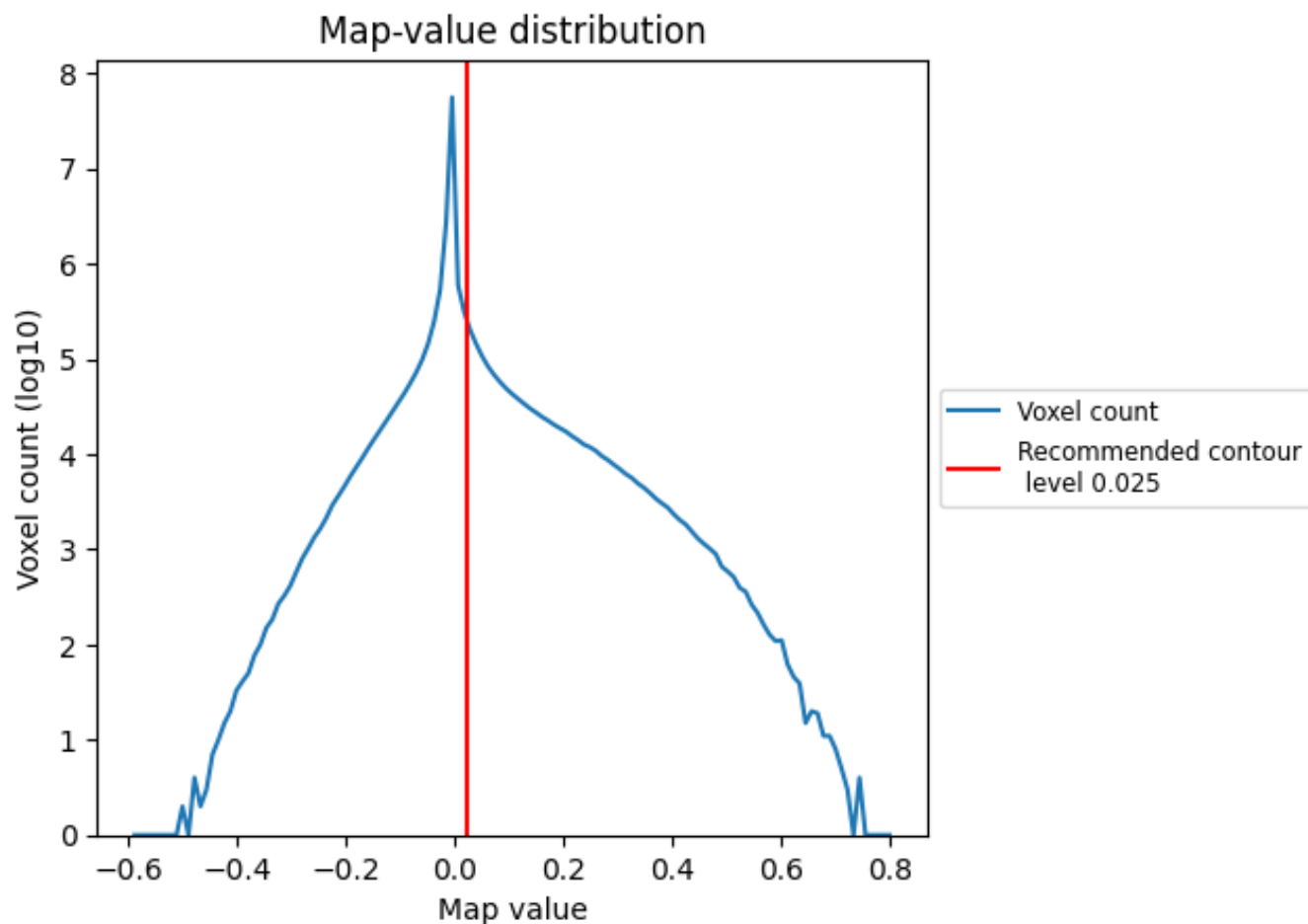
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

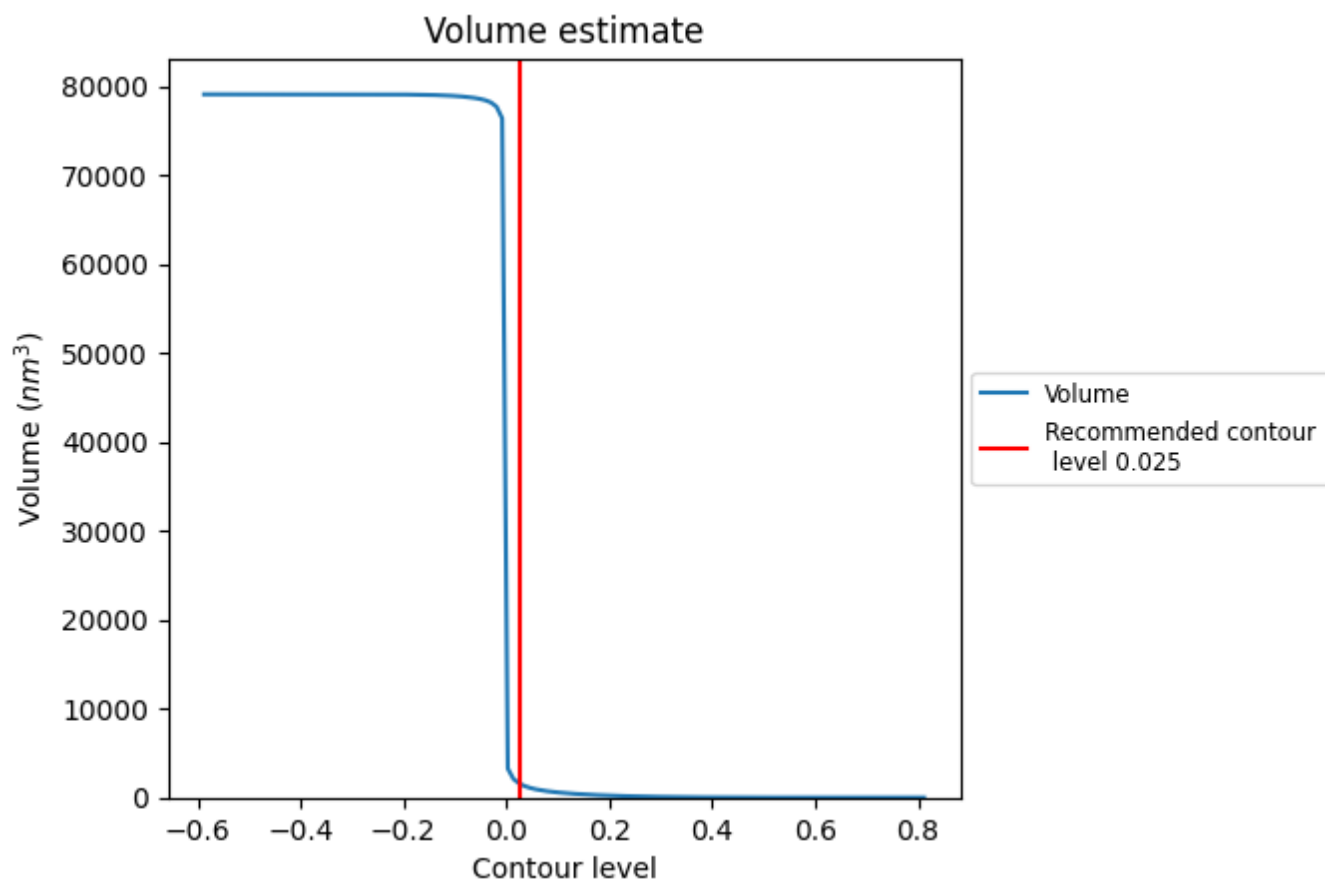
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

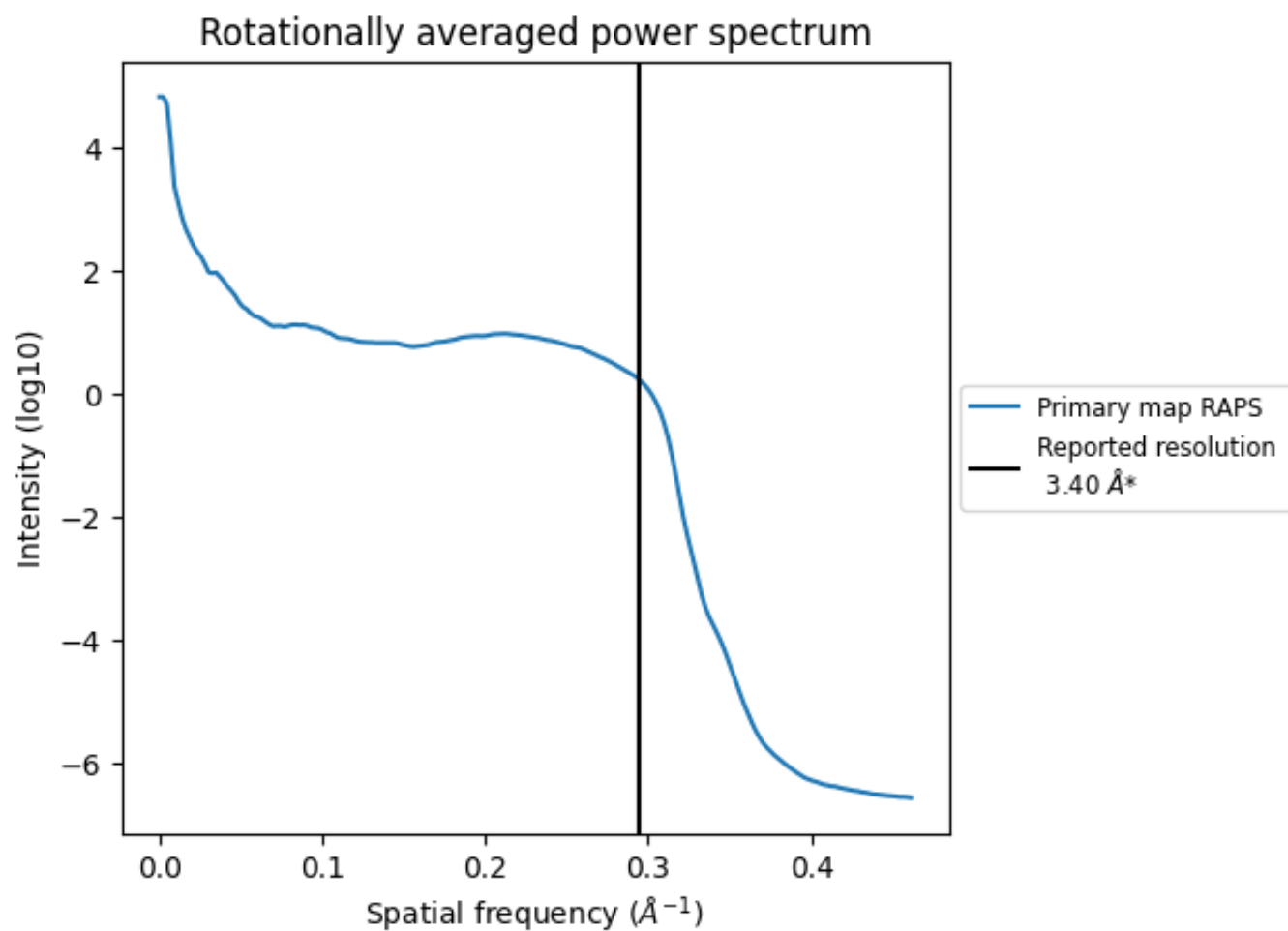
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1583 nm³; this corresponds to an approximate mass of 1430 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 0.294 Å⁻¹

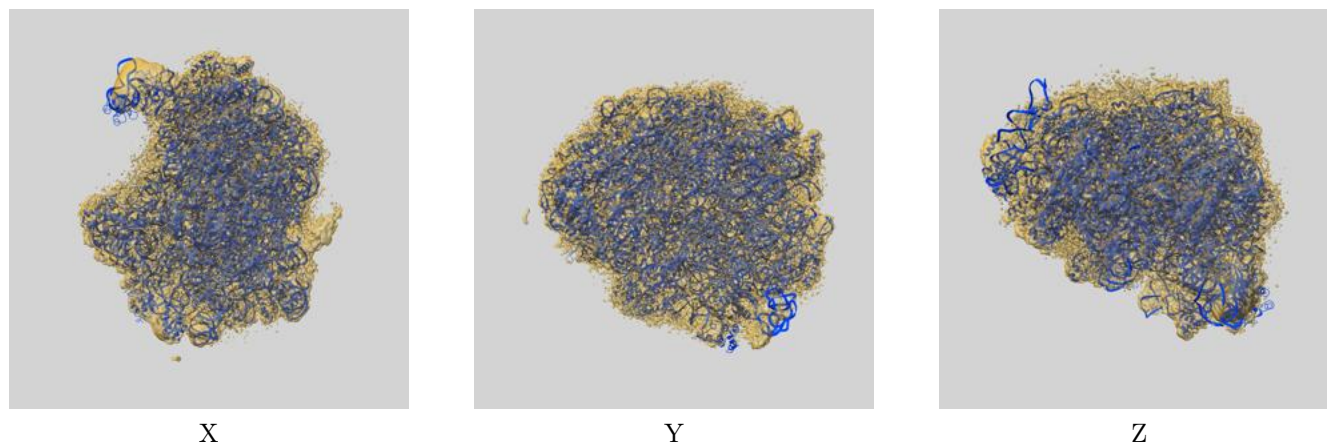
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

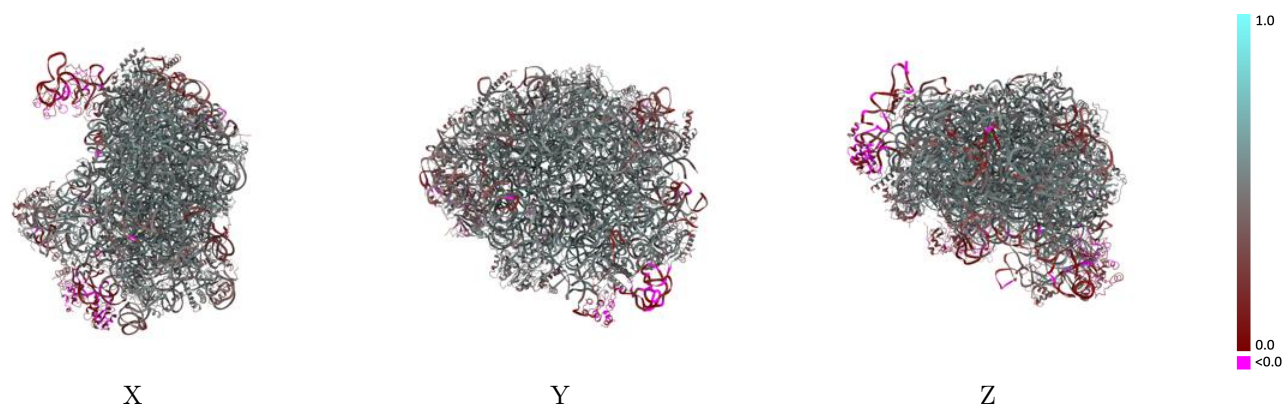
This section contains information regarding the fit between EMDB map EMD-4752 and PDB model 6R86. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



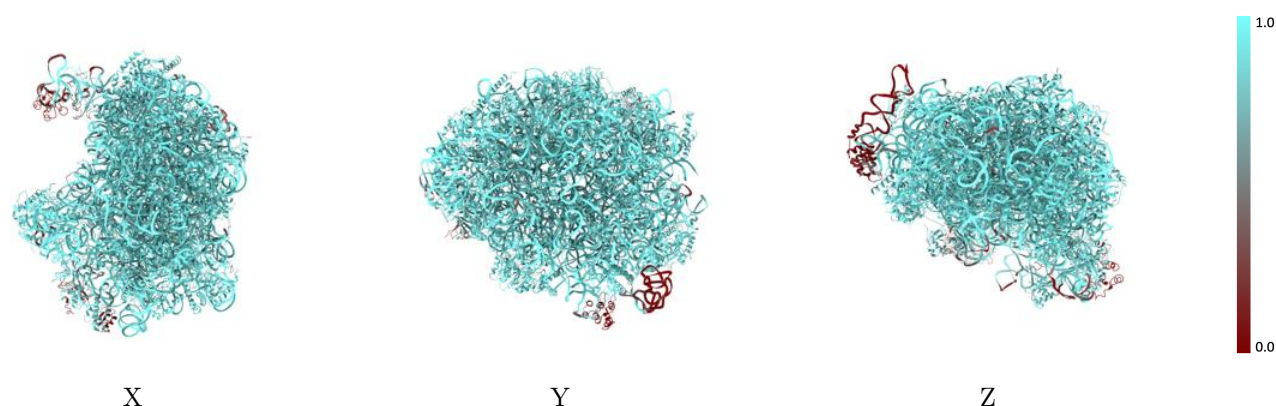
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



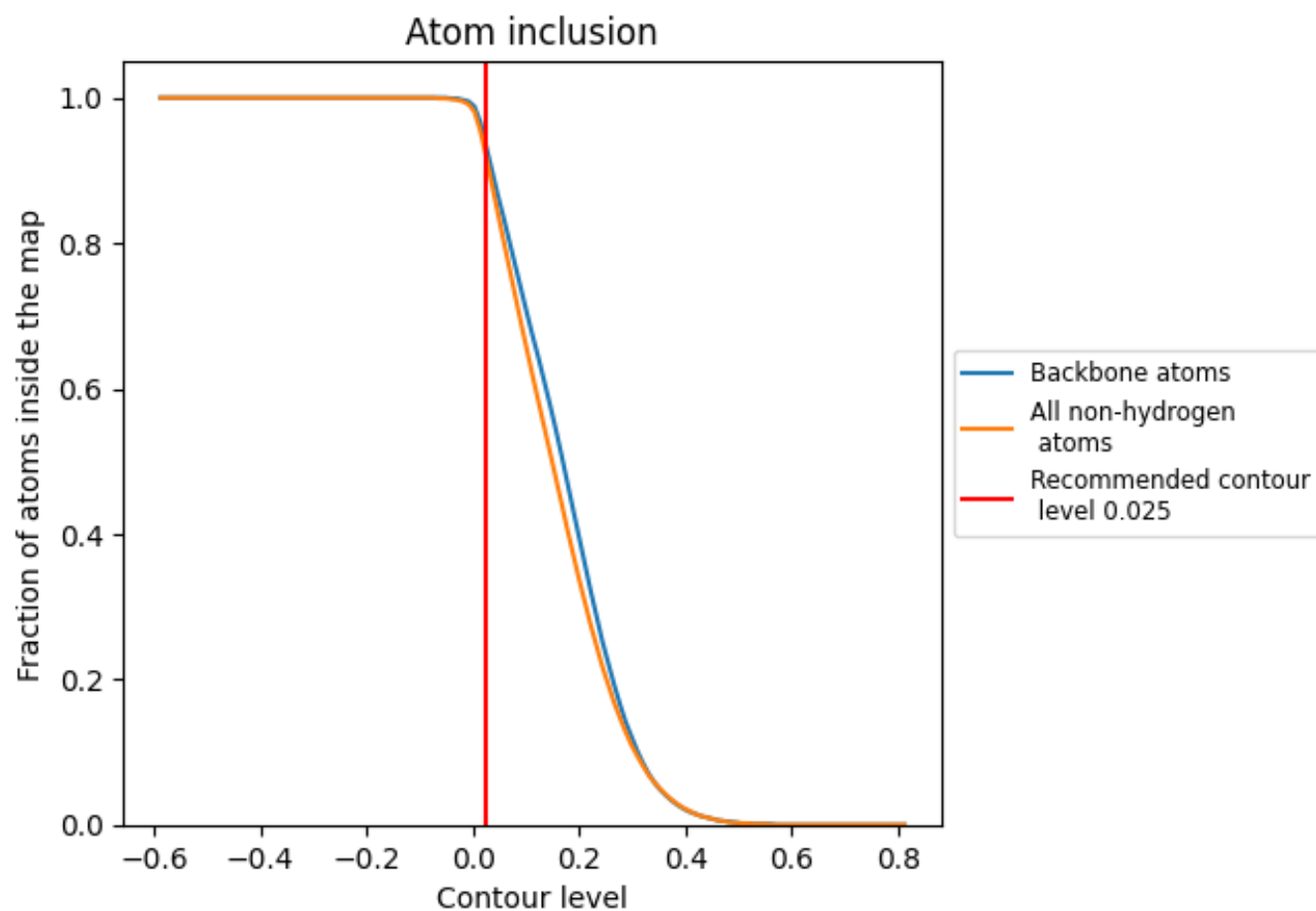
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4620
1	 0.9430	 0.4680
3	 0.9850	 0.4910
4	 0.9750	 0.5130
5	 0.9210	 0.4980
7	 0.9150	 0.4580
C	 0.8560	 0.4840
D	 0.9220	 0.5110
E	 0.9330	 0.5330
F	 0.9440	 0.5170
G	 0.9400	 0.5110
H	 0.9070	 0.4360
I	 0.9110	 0.4590
J	 0.9400	 0.5070
K	 0.9180	 0.4680
L	 0.3870	 0.0560
M	 0.8700	 0.3790
N	 0.9360	 0.5050
O	 0.9230	 0.4740
P	 0.3660	 0.0790
Q	 0.9510	 0.5190
R	 0.6070	 0.1760
S	 0.9340	 0.5090
T	 0.9300	 0.5060
U	 0.9180	 0.4900
V	 0.9430	 0.5100
W	 0.9050	 0.4440
X	 0.9220	 0.4450
Y	 0.9400	 0.5090
Z	 0.9440	 0.5110
a	 0.9250	 0.5030
b	 0.9240	 0.4710
c	 0.9560	 0.5330
d	 0.9180	 0.4880
e	 0.9040	 0.4580



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.9070	 0.4930
g	 0.9440	 0.5280
h	 0.9460	 0.5350
i	 0.9170	 0.5070
j	 0.9240	 0.4930
k	 0.9230	 0.4740
l	 0.9590	 0.5480
m	 0.9100	 0.4610
n	 0.9590	 0.5320
o	 0.4270	 0.1660
p	 0.9570	 0.5540
r	 0.6380	 0.0610
s	 0.8920	 0.4590
x	 0.9410	 0.5320