



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 01:35 PM UTC

PDB ID : 6FAI / pdb_00006fai
EMDB ID : EMD-4214
Title : Structure of a eukaryotic cytoplasmic pre-40S ribosomal subunit
Authors : Scaiola, A.; Pena, C.; Weisser, M.; Boehringer, D.; Leibundgut, M.; Klingauf-Nerurkar, P.; Gerhardt, S.; Panse, V.G.; Ban, N.
Deposited on : 2017-12-15
Resolution : 3.40 Å(reported)

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

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A user guide is available at

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

The types of validation reports are described at

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

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

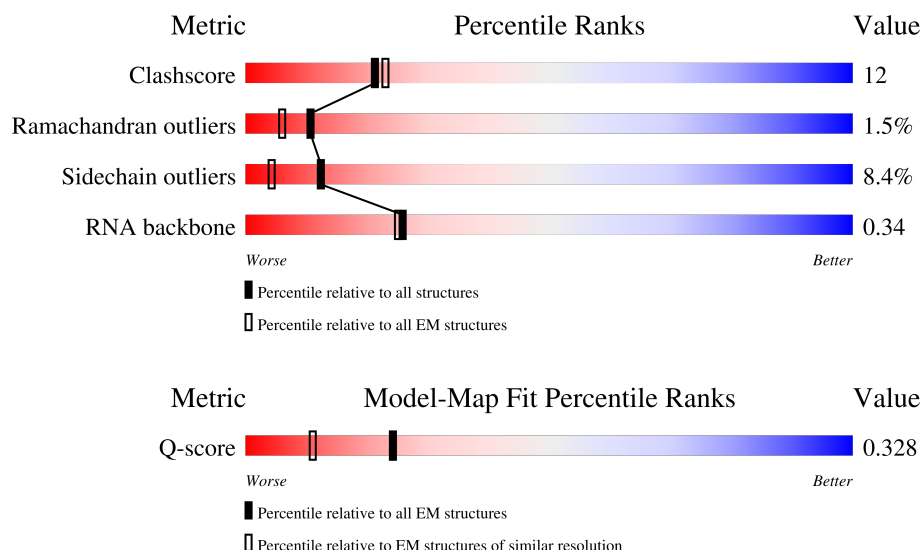
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 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.



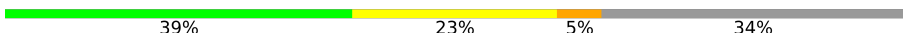
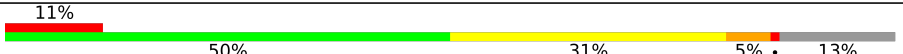
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	b	82	 76% 22% ..
2	c	67	 54% 36% • 6%
3	d	56	 7% 45% 20% • 34%

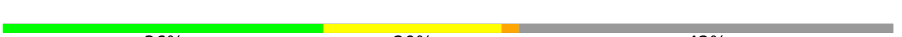
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Mol	Chain	Length	Quality of chain
4	e	63	
5	g	319	
6	h	274	
7	i	483	
8	j	463	
9	k	788	
10	l	425	
11	2	1800	
12	A	252	
13	B	255	
14	C	254	
15	D	240	
16	E	261	
17	F	225	
18	G	236	
19	H	190	
20	I	200	
21	J	197	
22	L	156	
23	M	143	
24	N	151	
25	O	137	
26	P	142	
27	Q	143	
28	R	136	

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Mol	Chain	Length	Quality of chain
29	S	146	 60%31%•8%
30	T	144	 65%31%••
31	U	121	 5%63%19%•15%
32	V	87	 64%29%7%
33	W	130	 62%28%6%••
34	X	145	 •59%36%••
35	Y	135	 69%26%••
36	Z	108	 36%20%•42%

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 84964 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 2 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 3 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	37	Total	C	N	O	S	0	0
			302	186	62	50	4		

- Molecule 4 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	48	Total	C	N	O	S	0	0
			384	242	81	59	2		

- Molecule 5 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	317	Total	C	N	O	S	0	0
			2431	1538	417	468	8		

- Molecule 6 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	181	Total	C	N	O	S	0	0
			1436	917	261	254	4		

- Molecule 7 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	i	262	Total	C	N	O	S	0	0
			2133	1388	364	378	3		

- Molecule 8 is a protein called Protein LTV1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	j	46	Total	C	N	O	S	0	0
			396	242	57	95	2		

- Molecule 9 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	k	670	Total	C	N	O	S	0	0
			5402	3449	937	1002	14		

- Molecule 10 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	286	Total	C	N	O	S	0	0
			2322	1464	410	430	18		

- Molecule 11 is a RNA chain called 20S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2	1775	Total	C	N	O	P	0	0
			37824	16909	6694	12446	1775		

- Molecule 12 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	206	Total	C	N	O	S	0	0
			1611	1036	285	288	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	PHE	ASP	conflict	UNP P32905

- Molecule 13 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 15 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D	202	Total	C	N	O	S	0	0
			1576	998	290	282	6		

- Molecule 16 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 17 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 18 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	232	Total	C	N	O	S	0	0
			1873	1172	366	332	3		

- Molecule 19 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	184	Total	C	N	O		0	0
			1481	951	265	265			

- Molecule 20 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	I	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 21 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	J	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 22 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	140	Total	C	N	O	S	0	0
			1129	724	215	187	3		

- Molecule 23 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	125	Total	C	N	O	S	0	0
			941	591	166	182	2		

- Molecule 24 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 25 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	127	Total	C	N	O	S	0	0
			1001	637	186	171	7		

- Molecule 27 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Q	127	Total	C	N	O		
			993	640	177	176	0	0

- Molecule 28 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	125	Total	C	N	O	S		
			1000	625	188	185	2	0	0

- Molecule 29 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	135	Total	C	N	O	S		
			1110	696	215	197	2	0	0

- Molecule 30 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	143	Total	C	N	O	S		
			1112	694	208	208	2	0	0

- Molecule 31 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	103	Total	C	N	O	S		
			819	519	148	151	1	0	0

- Molecule 32 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	87	Total	C	N	O	S		
			684	420	125	137	2	0	0

- Molecule 33 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	129	Total	C	N	O	S		
			1021	650	188	180	3	0	0

- Molecule 34 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 35 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 36 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	63	Total	C	N	O		0	0
			512	328	94	90			

- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	b	1	Total	Zn	0
			1	1	
37	d	1	Total	Zn	0
			1	1	

- Molecule 38 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
38	2	46	Total	Mg	0
			46	46	

3 Residue-property plots

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

- Molecule 1: 40S ribosomal protein S27-A

Chain b: 



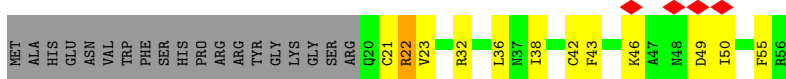
- Molecule 2: 40S ribosomal protein S28-A

Chain c: 



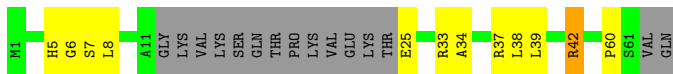
- Molecule 3: 40S ribosomal protein S29-A

Chain d: 



- Molecule 4: 40S ribosomal protein S30-A

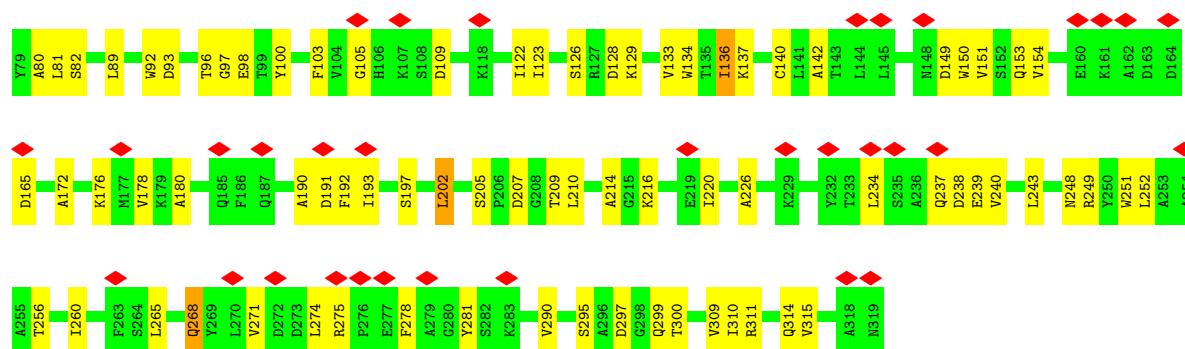
Chain e: 



- Molecule 5: Guanine nucleotide-binding protein subunit beta-like protein

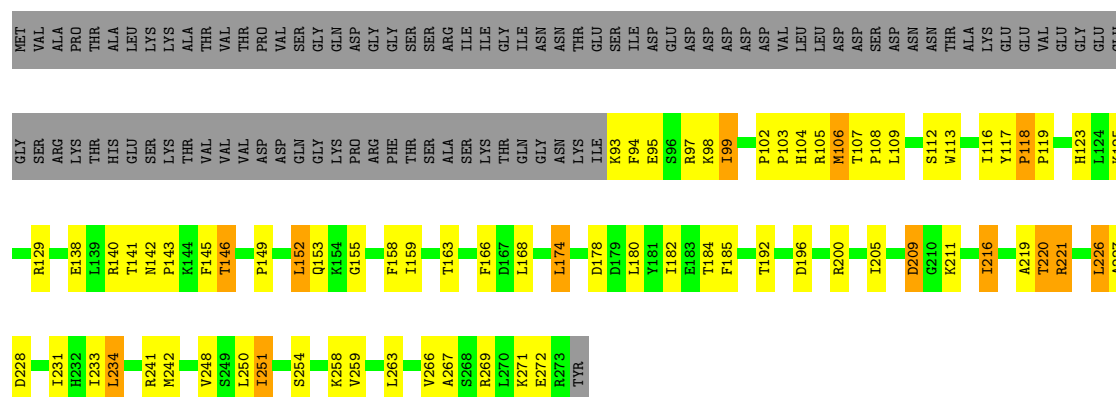
Chain g: 





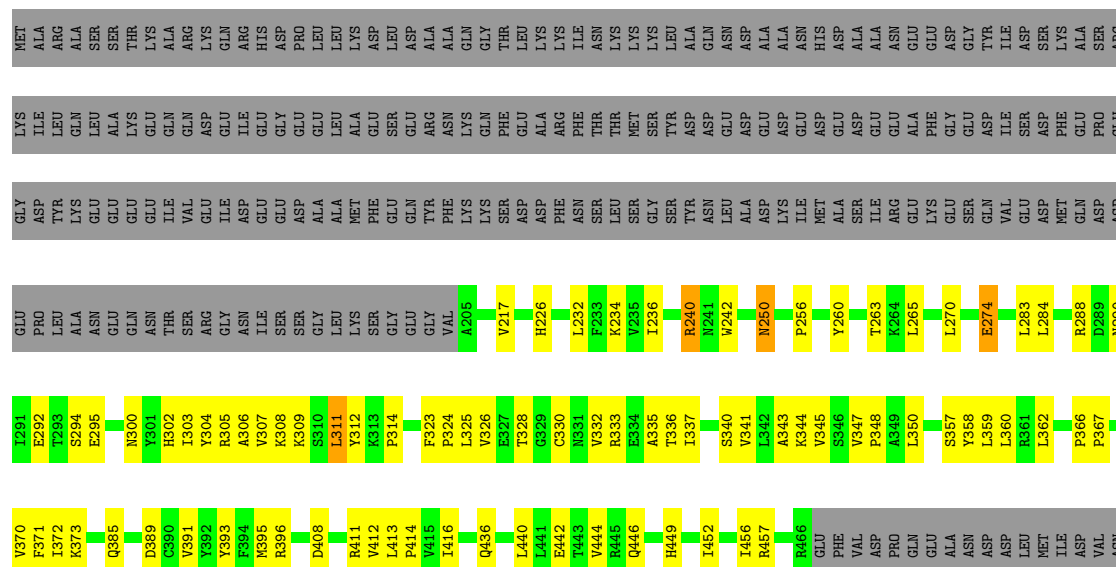
• Molecule 6: Pre-rRNA-processing protein PNO1

Chain h: 39% 23% 5% 34%



• Molecule 7: Essential nuclear protein 1

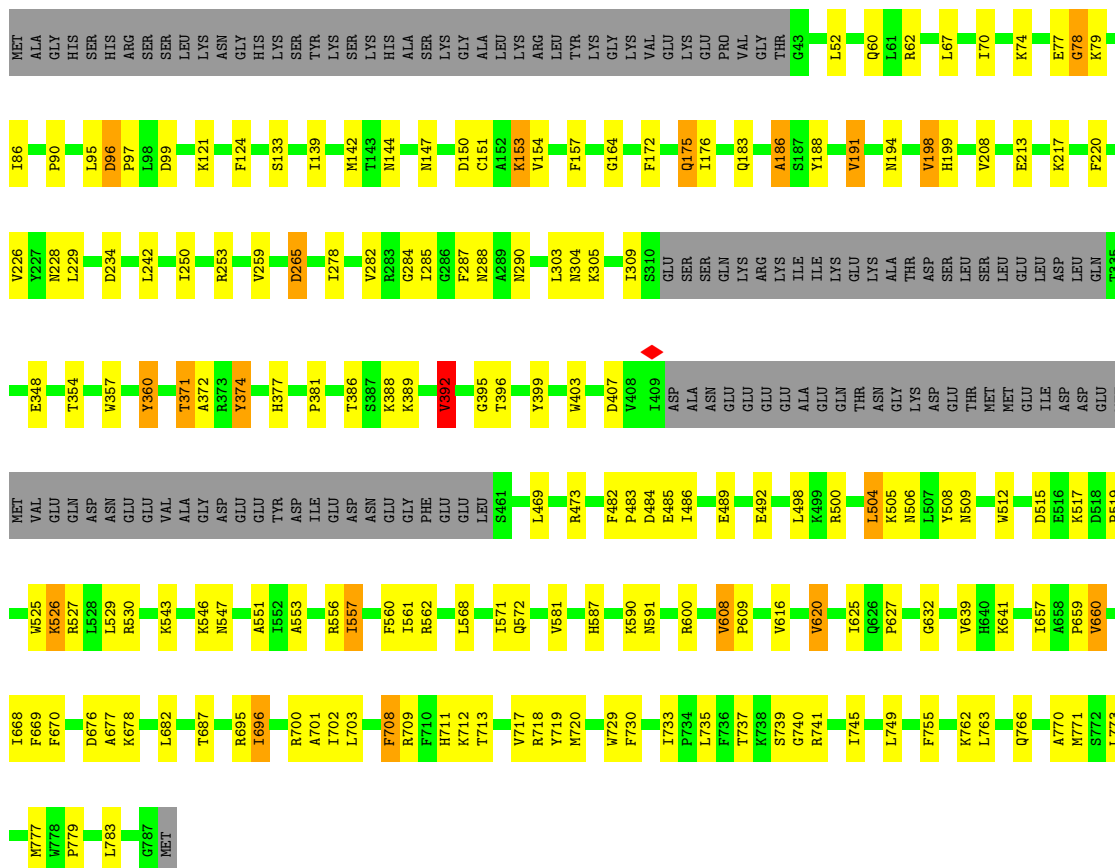
Chain i: 37% 17% 46%



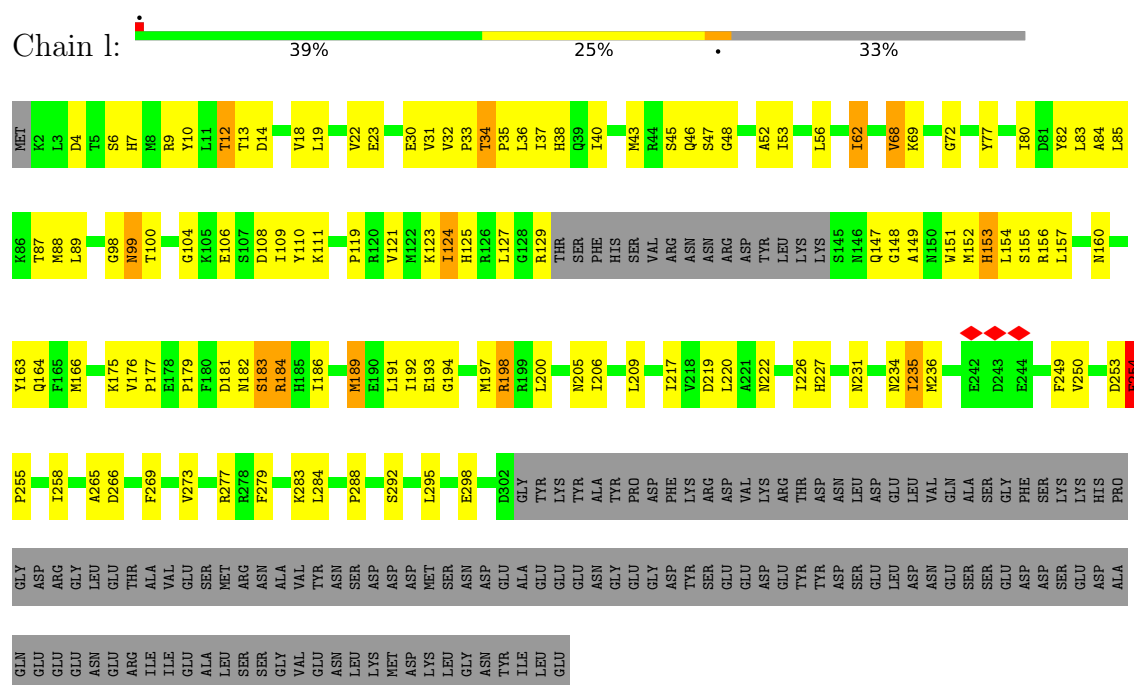
• Molecule 8: Protein LTV1

Chain j: 8% 90%

- Molecule 9: Ribosome biogenesis protein TSR1



• Molecule 10: Serine/threonine-protein kinase RIO2

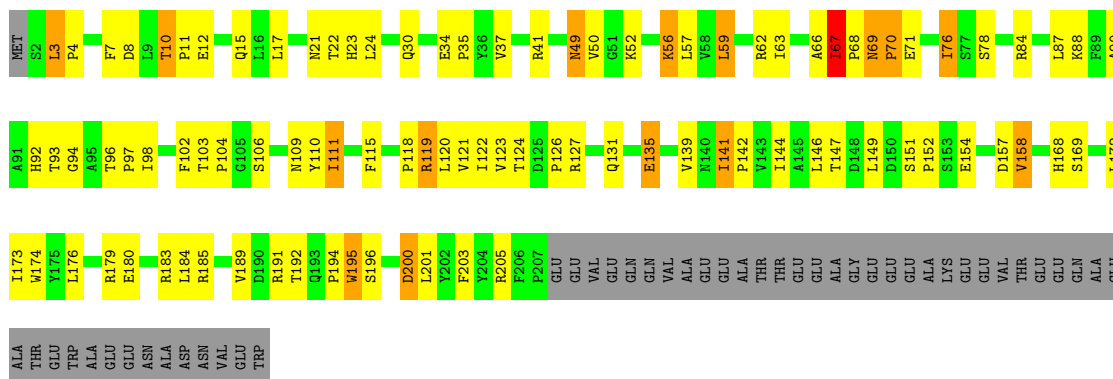


U1657	U1585	C1500	U1430	G1354	U1276	G1213	A1143	G1045	U958	A887	A814	C736	C653	C573
G1658	A1596	C1501	C1431	C1355	G1277	U1214	A1143	G1046	U959	U888	G815	A737	C654	G574
A1659	A1587	G1502	G1432	U1356	G1278	C1215	G1146	U1049	U960	U894	G816	G738	G855	C575
A1660	G1588	A1503	G1433	A1357	C1279	C1216	A1147	G1053	A963	G895	G819	G739	G856	C576
U1661	C1589	G1504	U1434	A1360	C1280	G1217	C1148	G1054	U965	G896	U820	C741	U657	A740
G1662	A1505	A1505	G1435	A1360	G1281	A1218	C1149	U1055	A966	C897	U821	U742	C658	U578
G1663	C1591	G1506	A1436	U1361	C1284	A1219	G1150	U1056	G880	A898	U822	U743	C	A579
	A1592		U1437	U1362	U1285	C1220	A1151	U1057	C969	G899	G823	U743	G	A580
A1671	A1593	U1511	G1438	U1363	U1286	A1221	C1152	U1058	U969	G901	U824	U749	A	U581
G1672	G1594	G1512	C1439	G1364	A1287	C1222	A1152	U1059	G980	G902	U825	U750	U	U582
G1673	U1595	C1440	C1365	C1365	U1287	A1223	G1155	U1060	G987	G903	U826	U751	U	C583
C1674	C1596	C1441	U1366	U1366	G1288	A1224	C1156	U1061	A988	G904	C827	A753	U	C584
G1675	A1597	U1514	G1367	G1367	U1289	U1225	A1157	A1062	U989	A905	U828	A754	U	A585
U1676	U1515	U1442	U1367		U1290	A1226	A1158	A1061	G987	A906	U829	A755	U	G586
U1677	U1598	U1443		U1370	U1291	A1227	C1159	A1062	A988	U988	U830	A756	C	C589
C1677	C1599	A1444		A1371	G1292	U1228	C1159	U1063	A988	A907	U831	A757	C	C590
G1679	G1601	A1446		U1372	U1293	G1229	A1160	G1064	C990	U908	U832	U758	G	A591
G1680		G1523	C1447	G1376	G1294	A1230	C1161	A1065	G991	U909	U833		G	A592
A1681	G1607	A1524	U1448		G1295	U1231	G1184	C1066	A992	C910	A834	A762	U	U593
U1682	U1608	A1525	U1449			U1232	G1185	C1067	A993	U911	U835	G763	U	A594
C1683	U1609	U1450	U1450	C1379	U1298	G1233	G1186		G997	U912	U836	G764	C	G595
U1684	G1610	C1451	U1380	U1380	G1299	A1234	G1167	G1072	A998	G913	U839	G765	U	
C1686	A1611	U1452	U1381	U1381	A1300	C1235	A1171	G1073	U999	G914	U840	U766	U	U602
U1687	G1615	G1534	A1382	A1382	U1301	A1236	G1172	A1076	A1001	A915	U841	U767	G676	U603
U1688		U1535	G1383	G1383	C1309	G1237	G1176	C1077	G1002	U916	C842	C768	G677	
A1689		G1536	A1384	A1384	U1310	A1238	U1175	C1078	A1003	U917	U843	G772	A678	A606
G1690		C1537	G1386	G1386	U1314	U1239	G1176	U1079	U1004	U918	G846	C773	U680	U607
		U1538	G1387	G1387	U1315	G1241	U1181	U1080	A1005	A919	U847	A774	U608	U608
G1696	U1621	G1539	A1388	A1388	U1316	A1242	U1182	A1081	C1006	U920	G875	C775	G610	G610
C1697	G1622	G1541	C1389	C1389	G1316	G1243	U1183	C1082	C1007	U921	G876	C776	U611	U611
U1698		G1482	U1390	U1390		A1244	U1184	G1083	G1008	A924	A850	C777	G686	U612
G1699		G1487			A1321	G1245	U1185	A1092	U1009	G925	U851	G778	G687	G612
C1700		U1488	U1397	U1397	A1322	U1247	A1186	A1093	G1010	A926	G852	G779	G613	C614
A1701		C1479	U1398	U1398	G1323	C1248	U1186	G1094	G1011	U927	U854	G780	U619	A619
		A1471	A1400	A1400	G1324	U1249	U1189	U1095	U1012	A928	U855	U781	A620	A620
C1706		A1472	A1401	A1401			C	U1096	C1016	A929	U856	U782	A621	A621
A1707		U1473			G1327	C1252	U	U1097	U1017	A930	U857	G783	U698	A622
U1712		G1409	G1409	G1409	G1328	U1253	C	U1098	U1018	C931	U860	C784	U699	A623
G1713		A1410	A1410	A1410	A1329	U1254	U	U1099	A1019	U932	U861	U785	C700	G624
A1714		G1411	A1411	A1411	A1330	G1255	A	G1100	A1020	A933	U862	C786	G624	C624
G1715		G1412	G1412	G1412	C1332	A1256	A	G1101	C1021	C934	A863	G787	C625	C625
		U1413	C1333	C1333	C1332	U1257	C	G1102	A1022	U935	U864	A788	U626	U626
U1724		U1414	U1334	U1334	U1334	U1258	A	G1111	C1022	A939	A865	U790	G712	A630
		U1415	U1335	U1335	U1335	U1259	C1197	U1097	A1025	A940	G866	A791	A713	G631
G1727		G1416	A1336	A1336	U1260	U1261	G1198	U1098	A1026	A941	G867	U792	G714	U632
A1728		A1417	A1337	A1337	G1261	G1262	G1199	U1099	A1027	G942	G868	U793	G715	A635
C1729		G1418	C1338	C1338	U1262	G1263	G1200	G1100	C1028	C943	A869	U794	U715	
A1730		G1419	C1339	C1339	G1263	G1264	G1201	U1120	U1031	A944	G870	U795	C716	C716
U1731		C1420	U1340	U1340	G1264	G1265	A1202	C1121	U1036	U945	G871	A799	C717	U638
		A1421			U1265	G1266	A1203	A1125	C1037	U946	G872	A804	U718	U640
A1732		U1343	U1343	U1343	U1266	G1267	U1206	G1130	G1041	U947	G873		U719	C645
C1733		A1422	A1344	A1344	G1267	U1268	C1207	U1135	G1042	U948	G876	G810	U720	
U1734		U1423	A1345	A1345	U1268	U1269	C1207	U1136	A1043	G949		A811	U721	U639
U1735		A1424	A1346	A1346	U1269	G1270	A1208	A1036	U1044			A812	G722	U640
G1736		A1425	U1347	U1347	U1270	G1271	C1209	C1037				A813	G723	
C1737		C1426	U1348	U1348	G1271	A1211	C1210	U1137				G810	U728	
U1738		A1427	A1349	A1349	G1271	A1211	C1210	A1138				A811		U649
C1739		G1428	G1349	G1349	A1275	G1212	G1212					A812		U650
A1740		G1429										U813		



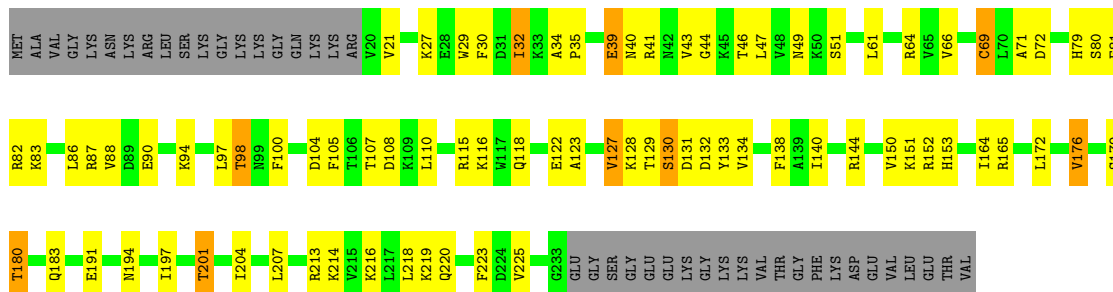
• Molecule 12: 40S ribosomal protein S0-A

Chain A: 44% 32% 6% 18%



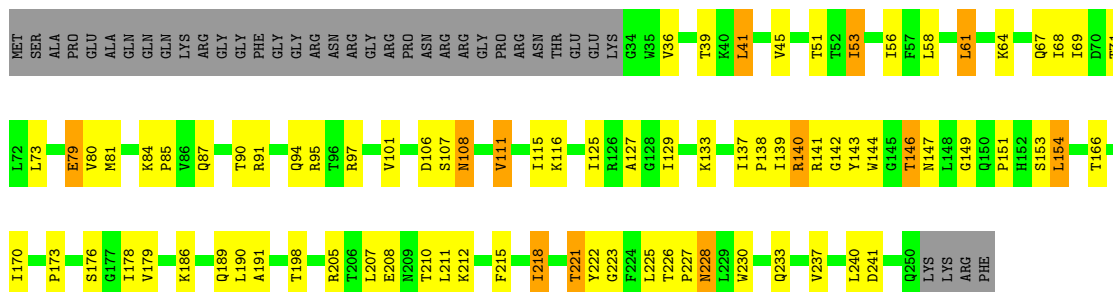
• Molecule 13: 40S ribosomal protein S1-A

Chain B: 52% 28% 16%



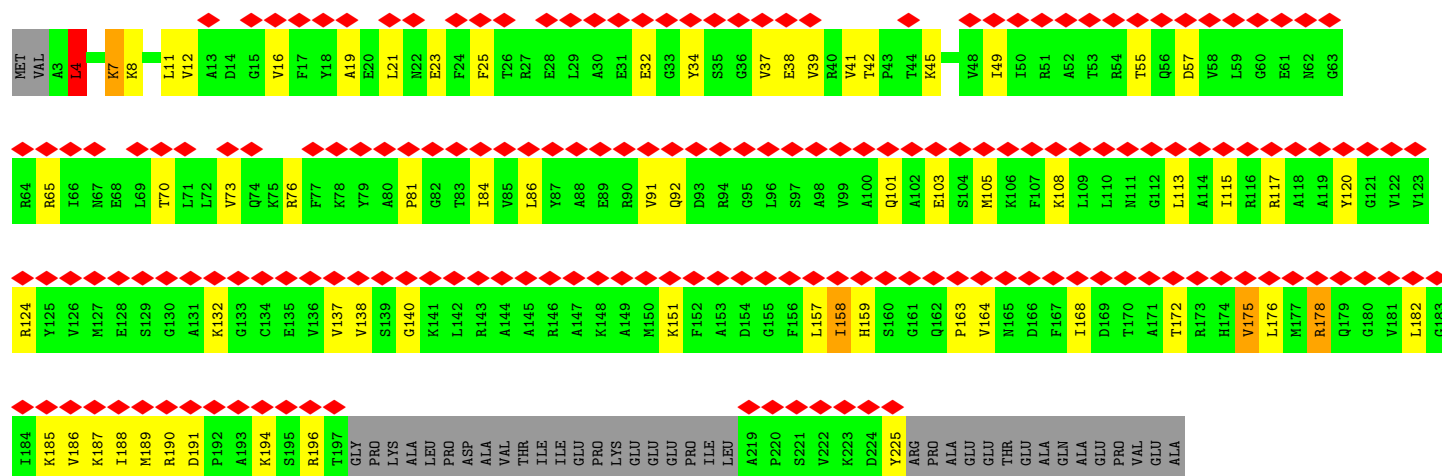
• Molecule 14: 40S ribosomal protein S2

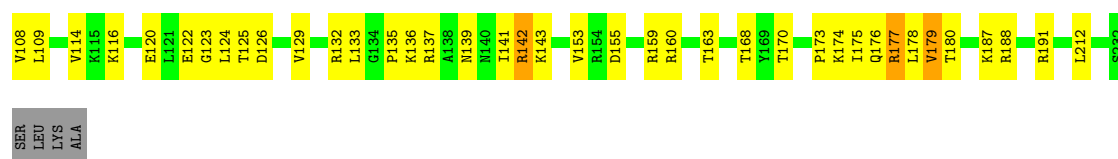
Chain C: 53% 28% 5% 15%



• Molecule 15: 40S ribosomal protein S3

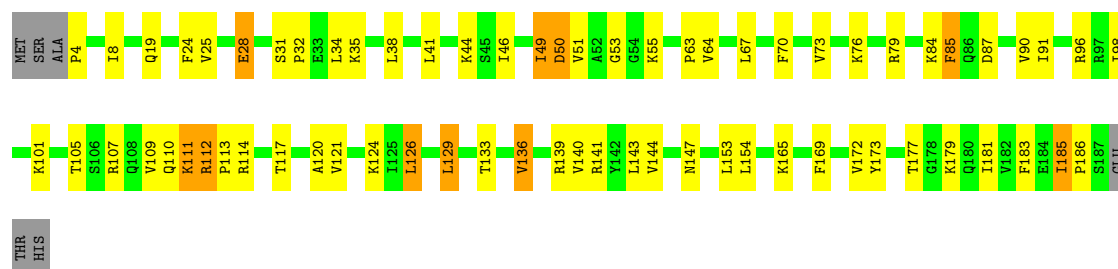
Chain D: 74% 57% 25% 16%





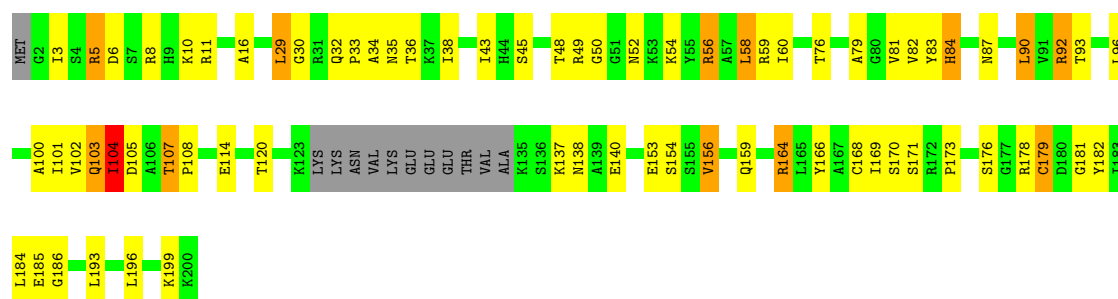
• Molecule 19: 40S ribosomal protein S7-A

Chain H: 61% 31% 5% .



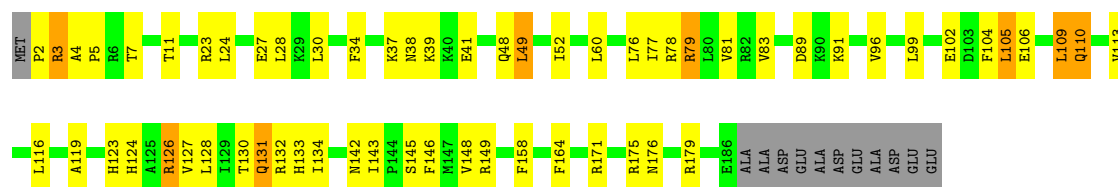
• Molecule 20: 40S ribosomal protein S8-A

Chain I: 58% 30% 6% 6%



• Molecule 21: 40S ribosomal protein S9-A

Chain J: 63% 27% 6%

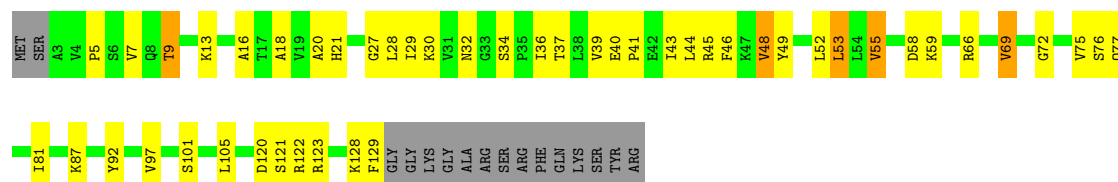


• Molecule 22: 40S ribosomal protein S11-A

Chain L: 69% 17% 10%

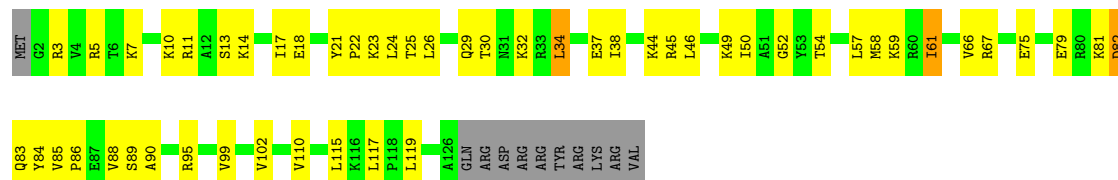






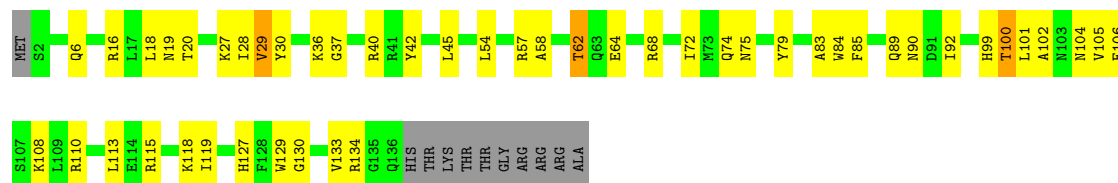
• Molecule 28: 40S ribosomal protein S17-A

Chain R: 54% 36% 8%



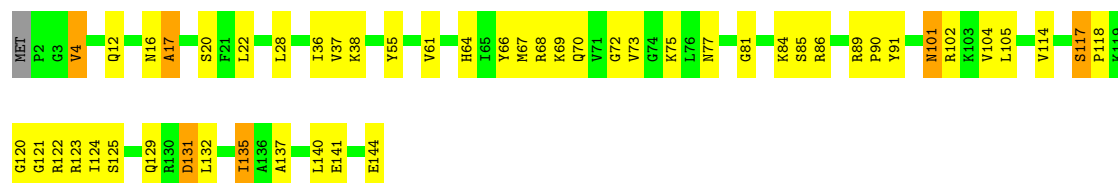
• Molecule 29: 40S ribosomal protein S18-A

Chain S: 60% 31% 8%



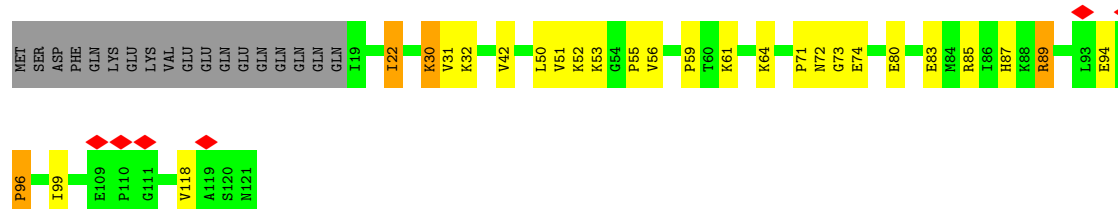
• Molecule 30: 40S ribosomal protein S19-A

Chain T: 65% 31% 4%



• Molecule 31: 40S ribosomal protein S20

Chain U: 5% 63% 19% 15%



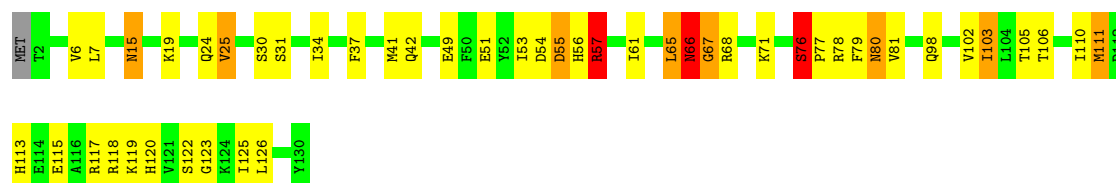
• Molecule 32: 40S ribosomal protein S21-A

Chain V: 



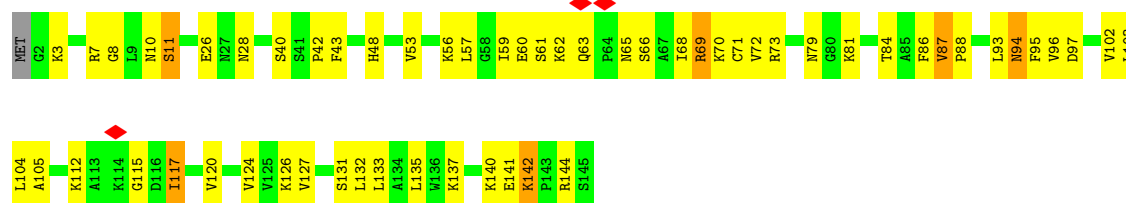
• Molecule 33: 40S ribosomal protein S22-A

Chain W: 



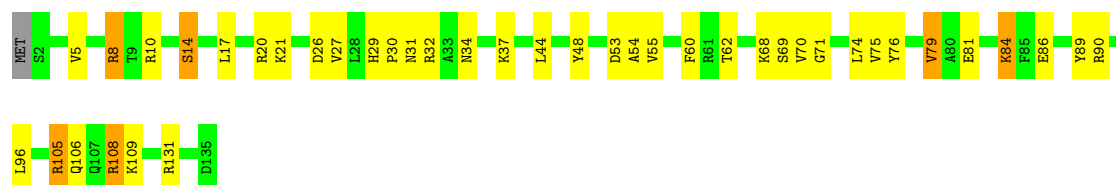
• Molecule 34: 40S ribosomal protein S23-A

Chain X: 



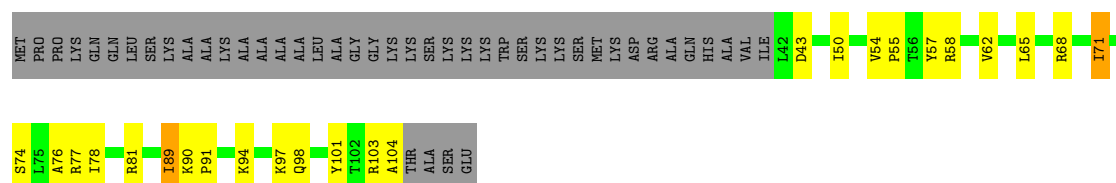
• Molecule 35: 40S ribosomal protein S24-A

Chain Y: 



• Molecule 36: 40S ribosomal protein S25-A

Chain Z: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	165168	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	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	0.393	Depositor
Minimum map value	-0.144	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	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, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.46	0/620	0.84	0/838
2	c	0.47	0/499	0.75	0/670
3	d	0.47	0/306	0.82	0/404
4	e	0.45	0/390	0.84	0/517
5	g	0.50	0/2484	0.77	1/3382 (0.0%)
6	h	0.41	0/1462	0.86	2/1969 (0.1%)
7	i	0.52	0/2188	0.78	2/2970 (0.1%)
8	j	0.49	0/403	0.65	0/543
9	k	0.37	0/5528	0.83	8/7477 (0.1%)
10	l	0.46	0/2368	0.83	5/3181 (0.2%)
11	2	0.30	0/42303	0.42	2/65912 (0.0%)
12	A	0.50	0/1653	0.97	8/2261 (0.4%)
13	B	0.45	0/1735	0.86	2/2335 (0.1%)
14	C	0.58	0/1665	0.94	2/2263 (0.1%)
15	D	0.54	0/1596	0.77	1/2142 (0.0%)
16	E	0.60	0/2109	0.94	8/2839 (0.3%)
17	F	0.47	0/1629	0.84	2/2202 (0.1%)
18	G	0.38	0/1897	0.83	5/2532 (0.2%)
19	H	0.42	0/1506	0.80	3/2028 (0.1%)
20	I	0.48	0/1514	0.88	2/2021 (0.1%)
21	J	0.56	0/1519	0.93	1/2035 (0.0%)
22	L	0.60	0/1155	0.92	3/1557 (0.2%)
23	M	0.57	0/949	0.81	0/1284
24	N	0.52	0/1215	0.85	0/1638
25	O	0.40	0/937	0.88	2/1261 (0.2%)
26	P	0.40	0/1022	0.84	2/1373 (0.1%)
27	Q	0.51	0/1011	0.85	4/1362 (0.3%)
28	R	0.50	0/1010	0.82	0/1355
29	S	0.44	0/1128	0.76	0/1518
30	T	0.45	0/1130	0.85	3/1517 (0.2%)
31	U	0.55	0/829	0.81	0/1121
32	V	0.48	0/693	0.89	1/935 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	W	0.76	0/1038	1.06	2/1395 (0.1%)
34	X	0.59	0/1139	0.92	5/1518 (0.3%)
35	Y	0.52	0/1087	0.86	0/1449
36	Z	0.52	0/519	0.84	0/696
All	All	0.41	0/90236	0.67	76/130500 (0.1%)

There are no bond length outliers.

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	W	76	SER	CA-C-N	-10.29	106.98	119.84
33	W	76	SER	C-N-CA	-10.29	106.98	119.84
11	2	1185	U	OP2-P-O3'	-8.65	82.04	108.00
9	k	392	VAL	CA-C-N	-7.98	111.52	119.90
9	k	392	VAL	C-N-CA	-7.98	111.52	119.90
11	2	1185	U	OP1-P-O3'	-7.81	84.56	108.00
17	F	66	GLN	CA-C-N	7.71	129.48	119.84
17	F	66	GLN	C-N-CA	7.71	129.48	119.84
12	A	3	LEU	CA-C-N	7.69	128.15	119.92
12	A	3	LEU	C-N-CA	7.69	128.15	119.92
30	T	117	SER	CA-C-N	7.41	129.10	119.84
30	T	117	SER	C-N-CA	7.41	129.10	119.84
18	G	38	GLY	N-CA-C	7.31	120.98	112.50
12	A	67	ILE	CA-C-N	7.28	127.62	119.32
12	A	67	ILE	C-N-CA	7.28	127.62	119.32
6	h	118	PRO	CA-C-N	-6.63	111.99	119.28
6	h	118	PRO	C-N-CA	-6.63	111.99	119.28
26	P	86	VAL	CA-C-N	6.50	127.97	119.84
26	P	86	VAL	C-N-CA	6.50	127.97	119.84
21	J	4	ALA	N-CA-C	-6.40	101.46	110.29
34	X	62	LYS	N-CA-C	6.34	119.42	111.24
9	k	96	ASP	CA-C-N	6.23	125.64	118.85
9	k	96	ASP	C-N-CA	6.23	125.64	118.85
12	A	69	ASN	CA-C-N	6.18	127.57	119.84
12	A	69	ASN	C-N-CA	6.18	127.57	119.84
27	Q	40	GLU	CA-C-N	-6.10	113.24	120.13
27	Q	40	GLU	C-N-CA	-6.10	113.24	120.13
34	X	87	VAL	CA-C-N	6.09	126.06	120.03
34	X	87	VAL	C-N-CA	6.09	126.06	120.03
32	V	82	VAL	N-CA-C	-6.09	107.01	112.12
22	L	99	ARG	N-CA-C	6.03	117.06	108.74
13	B	34	ALA	CA-C-N	6.02	127.37	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	34	ALA	C-N-CA	6.02	127.37	119.84
20	I	84	HIS	CA-C-N	5.99	125.87	119.28
20	I	84	HIS	C-N-CA	5.99	125.87	119.28
9	k	620	VAL	N-CA-C	-5.80	107.47	113.10
19	H	185	ILE	CA-C-N	5.78	126.12	119.93
19	H	185	ILE	C-N-CA	5.78	126.12	119.93
16	E	128	LYS	N-CA-C	5.71	117.69	108.32
10	l	205	ASN	CA-C-N	5.70	123.83	120.24
10	l	205	ASN	C-N-CA	5.70	123.83	120.24
7	i	250	ASN	CA-C-N	5.62	125.46	119.28
7	i	250	ASN	C-N-CA	5.62	125.46	119.28
14	C	41	LEU	N-CA-C	-5.61	106.99	113.88
25	O	56	SER	CA-C-N	5.53	125.88	119.47
25	O	56	SER	C-N-CA	5.53	125.88	119.47
10	l	184	ARG	CB-CA-C	-5.51	110.24	116.63
16	E	34	GLY	CA-C-N	5.50	125.16	119.05
16	E	34	GLY	C-N-CA	5.50	125.16	119.05
16	E	42	LEU	CA-C-N	5.47	125.39	119.76
16	E	42	LEU	C-N-CA	5.47	125.39	119.76
14	C	179	VAL	N-CA-C	5.46	112.05	106.21
30	T	37	VAL	N-CA-C	5.41	116.04	108.89
18	G	103	GLY	CA-C-N	5.39	126.44	120.45
18	G	103	GLY	C-N-CA	5.39	126.44	120.45
9	k	139	ILE	CA-C-N	5.33	125.31	120.03
9	k	139	ILE	C-N-CA	5.33	125.31	120.03
12	A	141	ILE	N-CA-C	5.33	113.75	107.77
19	H	64	VAL	CB-CA-C	-5.31	108.66	113.70
18	G	55	GLY	N-CA-C	5.26	118.08	111.09
12	A	78	SER	N-CA-C	-5.22	107.08	113.50
16	E	30	ARG	CA-C-N	5.20	125.11	119.76
16	E	30	ARG	C-N-CA	5.20	125.11	119.76
27	Q	123	ARG	CA-C-N	5.18	125.48	119.93
27	Q	123	ARG	C-N-CA	5.18	125.48	119.93
9	k	720	MET	N-CA-C	-5.16	108.01	114.56
18	G	71	THR	CB-CA-C	-5.15	107.09	114.87
5	g	56	VAL	N-CA-C	5.12	114.09	108.05
16	E	18	TRP	N-CA-C	-5.11	106.90	113.23
22	L	94	ILE	CA-C-N	5.09	125.91	120.47
22	L	94	ILE	C-N-CA	5.09	125.91	120.47
10	l	254	PHE	CA-C-N	-5.05	114.59	120.04
10	l	254	PHE	C-N-CA	-5.05	114.59	120.04
34	X	142	LYS	CA-C-N	5.03	126.13	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	X	142	LYS	C-N-CA	5.03	126.13	119.84
15	D	140	GLY	N-CA-C	5.02	116.83	110.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	610	0	629	13	0
2	c	497	0	535	14	0
3	d	302	0	297	9	0
4	e	384	0	423	9	0
5	g	2431	0	2381	48	0
6	h	1436	0	1515	53	0
7	i	2133	0	2172	59	0
8	j	396	0	322	10	0
9	k	5402	0	5276	104	0
10	l	2322	0	2305	78	0
11	2	37824	0	19031	638	0
12	A	1611	0	1616	76	0
13	B	1709	0	1784	52	0
14	C	1635	0	1723	59	0
15	D	1576	0	1650	41	0
16	E	2068	0	2154	66	0
17	F	1609	0	1675	72	0
18	G	1873	0	1980	51	0
19	H	1481	0	1572	45	0
20	I	1489	0	1525	55	0
21	J	1494	0	1573	42	0
22	L	1129	0	1196	19	0
23	M	941	0	982	42	0
24	N	1192	0	1255	26	0
25	O	926	0	950	39	0
26	P	1001	0	1042	36	0
27	Q	993	0	1051	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	R	1000	0	1063	38	0
29	S	1110	0	1134	33	0
30	T	1112	0	1124	33	0
31	U	819	0	885	19	0
32	V	684	0	672	22	0
33	W	1021	0	1060	35	0
34	X	1121	0	1196	43	0
35	Y	1073	0	1132	33	0
36	Z	512	0	551	20	0
37	b	1	0	0	0	0
37	d	1	0	0	0	0
38	2	46	0	0	0	0
All	All	84964	0	67431	1770	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 12.

All (1770) 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)
7:i:444:VAL:HG11	7:i:457:ARG:HB2	1.54	0.89
11:2:885:G:N2	25:O:124:ASP:OD2	2.06	0.88
23:M:43:ARG:HD2	23:M:103:LEU:HD21	1.54	0.88
19:H:177:THR:HG23	19:H:179:LYS:H	1.40	0.86
9:k:486:ILE:HD11	9:k:701:ALA:HB1	1.57	0.86
11:2:863:A:OP1	33:W:57:ARG:NH1	2.09	0.86
11:2:1186:U:O4	11:2:1200:G:N2	2.08	0.86
16:E:240:LYS:HE2	16:E:240:LYS:H	1.40	0.86
34:X:61:SER:HB2	34:X:117:ILE:HB	1.58	0.85
29:S:6:GLN:HB3	36:Z:43:ASP:HB2	1.54	0.85
11:2:538:A:OP2	21:J:171:ARG:NH2	2.09	0.85
11:2:1672:G:H2'	11:2:1673:G:C8	2.12	0.85
13:B:90:GLU:HB2	13:B:97:LEU:HB3	1.58	0.84
21:J:110:GLN:HE22	21:J:126:ARG:HG2	1.42	0.83
11:2:1213:G:H1'	11:2:1243:G:H1	1.43	0.83
11:2:789:A:OP1	16:E:108:ARG:NH1	2.12	0.83
12:A:183:ARG:HH21	12:A:191:ARG:HD3	1.42	0.83
7:i:242:TRP:HE1	7:i:274:GLU:HG3	1.44	0.82
11:2:519:C:N4	11:2:533:U:O2	2.11	0.82
9:k:632:GLY:HA2	9:k:695:ARG:HH22	1.44	0.82
21:J:143:ILE:HG22	21:J:145:SER:H	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1238:A:H61	11:2:1247:U:H3	1.23	0.81
11:2:1067:C:H5''	13:B:150:VAL:HG23	1.61	0.81
11:2:867:G:OP2	24:N:3:ARG:NH1	2.12	0.81
10:l:88:MET:HE3	10:l:183:SER:HB3	1.62	0.81
9:k:285:ILE:HD11	9:k:546:LYS:HG2	1.63	0.81
11:2:1330:G:H22	11:2:1421:A:H61	1.28	0.81
8:j:392:ARG:HG3	8:j:395:PHE:HB2	1.63	0.80
14:C:53:ILE:HD11	14:C:73:LEU:HG	1.61	0.80
13:B:130:SER:HB2	13:B:180:THR:HG23	1.61	0.80
11:2:782:U:O2	35:Y:21:LYS:NZ	2.13	0.80
11:2:1151:A:H62	11:2:1627:U:H3	1.27	0.79
11:2:829:A:H4'	11:2:830:U:H5'	1.64	0.79
11:2:1789:G:OP2	25:O:132:ARG:NH2	2.14	0.79
6:h:95:GLU:HB3	6:h:141:THR:HG22	1.65	0.79
11:2:59:C:N4	11:2:63:G:O6	2.16	0.79
8:j:360:GLN:HA	23:M:37:VAL:HG11	1.65	0.79
11:2:1542:G:H1	11:2:1568:C:HO2'	1.31	0.79
11:2:337:G:O2'	20:I:10:LYS:NZ	2.17	0.78
12:A:124:THR:HG22	12:A:174:TRP:HE1	1.49	0.78
1:b:20:LYS:HD3	24:N:15:ALA:HB2	1.66	0.77
17:F:64:VAL:HG21	17:F:89:ILE:H	1.49	0.77
18:G:137:ARG:HD3	18:G:177:ARG:HE	1.49	0.77
11:2:1552:U:OP2	26:P:43:ARG:NH2	2.18	0.77
27:Q:39:VAL:HG12	27:Q:41:PRO:HD2	1.67	0.77
11:2:1331:A:H61	11:2:1420:C:H42	1.33	0.76
6:h:93:LYS:HB2	6:h:143:PRO:HG3	1.67	0.76
11:2:1002:G:H21	11:2:1004:U:H5''	1.50	0.76
11:2:354:C:H5''	20:I:16:ALA:HB2	1.65	0.76
11:2:577:G:O2'	11:2:579:A:OP1	2.03	0.76
11:2:1689:A:H61	11:2:1712:A:H62	1.34	0.76
13:B:80:SER:O	13:B:82:ARG:N	2.18	0.76
5:g:133:VAL:HB	5:g:142:ALA:HB3	1.68	0.76
11:2:1594:G:OP2	11:2:1596:C:N4	2.19	0.76
4:e:60:PRO:HD2	11:2:559:C:H4'	1.67	0.75
11:2:570:A:H61	34:X:69:ARG:HA	1.52	0.75
14:C:226:THR:OG1	14:C:228:ASN:ND2	2.20	0.75
11:2:1345:A:O2'	11:2:1348:A:N6	2.20	0.74
15:D:115:ILE:HD11	15:D:138:VAL:HG11	1.69	0.74
17:F:80:LYS:HD2	17:F:83:ARG:HD2	1.69	0.74
11:2:885:G:H21	25:O:123:SER:HB2	1.53	0.74
17:F:42:LEU:HD12	17:F:48:PHE:H	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:62:VAL:HG13	17:F:89:ILE:HD12	1.69	0.73
11:2:742:U:O2'	19:H:107:ARG:NH1	2.21	0.73
25:O:20:TYR:HB3	25:O:27:PHE:HB2	1.70	0.73
10:l:231:ASN:HD22	11:2:1575:G:H1'	1.54	0.73
11:2:338:C:H5''	20:I:10:LYS:HD2	1.71	0.73
11:2:1002:G:N2	11:2:1004:U:H5''	2.02	0.73
11:2:1200:G:H4'	11:2:1201:G:H4'	1.71	0.73
11:2:939:A:H2'	11:2:940:A:C8	2.23	0.73
11:2:884:A:H2'	11:2:885:G:C8	2.24	0.73
9:k:164:GLY:H	9:k:194:ASN:HB2	1.54	0.73
15:D:55:THR:HG22	15:D:92:GLN:HB3	1.71	0.72
11:2:575:C:HO2'	11:2:582:U:H3	1.36	0.72
12:A:104:PRO:HB3	12:A:131:GLN:HE22	1.53	0.72
21:J:127:VAL:HG13	21:J:131:GLN:NE2	2.04	0.72
11:2:1563:C:OP1	30:T:84:LYS:NZ	2.23	0.72
16:E:9:LEU:HB2	16:E:30:ARG:HB2	1.70	0.72
34:X:103:LEU:HB3	34:X:126:LYS:HB2	1.72	0.72
11:2:1227:A:O4'	11:2:1255:G:N2	2.22	0.72
11:2:1473:U:O4	17:F:180:ARG:NE	2.20	0.72
7:i:344:LYS:HE2	11:2:1267:G:H4'	1.69	0.72
6:h:94:PHE:O	25:O:111:ARG:NH1	2.21	0.72
5:g:178:VAL:HB	5:g:192:PHE:HB2	1.72	0.71
6:h:104:HIS:NE2	11:2:1798:U:O2	2.23	0.71
11:2:1728:A:H1'	20:I:32:GLN:HE21	1.55	0.71
19:H:143:LEU:HD12	19:H:147:ASN:HB2	1.71	0.71
5:g:234:LEU:HD21	5:g:268:GLN:HE22	1.55	0.71
7:i:408:ASP:HA	7:i:411:ARG:HD2	1.73	0.71
28:R:24:LEU:HB2	28:R:58:MET:HE3	1.71	0.71
10:l:104:GLY:O	10:l:129:ARG:NH2	2.24	0.71
10:l:148:GLY:H	10:l:151:TRP:HD1	1.39	0.71
23:M:95:LYS:HA	23:M:117:GLY:HA3	1.71	0.71
25:O:92:LYS:HD3	25:O:121:VAL:HG22	1.72	0.70
11:2:66:U:H1'	18:G:160:ARG:HH21	1.56	0.70
11:2:1412:G:H4'	11:2:1415:U:H5''	1.73	0.70
30:T:86:ARG:HB2	30:T:89:ARG:HB2	1.71	0.70
11:2:513:U:H3	11:2:538:A:H62	1.39	0.70
30:T:73:VAL:HG13	30:T:101:ASN:HB2	1.74	0.70
11:2:1290:U:H5''	14:C:95:ARG:HH12	1.55	0.70
33:W:31:SER:HB2	33:W:34:ILE:HG13	1.73	0.70
5:g:299:GLN:NE2	5:g:315:VAL:O	2.25	0.70
11:2:884:A:H2'	11:2:885:G:H8	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1321:A:N6	12:A:135:GLU:OE1	2.24	0.69
11:2:511:A:OP2	21:J:176:ASN:ND2	2.24	0.69
11:2:1289:U:OP2	14:C:91:ARG:NH1	2.25	0.69
17:F:93:LEU:HD12	17:F:172:ILE:HG23	1.73	0.69
23:M:33:ARG:HB2	23:M:100:TRP:HE3	1.57	0.69
11:2:226:A:N6	11:2:834:G:O6	2.25	0.69
11:2:1175:U:H2'	11:2:1176:G:C8	2.27	0.69
13:B:179:SER:HB2	13:B:183:GLN:HB2	1.72	0.69
19:H:50:ASP:OD1	19:H:50:ASP:N	2.23	0.69
2:c:10:ALA:HB3	2:c:54:LEU:HB2	1.73	0.69
11:2:513:U:H2'	11:2:514:G:C8	2.27	0.69
5:g:89:LEU:HB2	5:g:103:PHE:HB2	1.73	0.69
8:j:362:ASP:O	8:j:366:ASN:ND2	2.25	0.69
10:l:33:PRO:HA	10:l:72:GLY:HA2	1.74	0.69
11:2:488:G:H22	11:2:499:U:H3	1.39	0.69
11:2:1585:U:H3	11:2:1611:A:H2	1.39	0.69
20:I:60:ILE:HD13	20:I:179:CYS:HB2	1.73	0.69
11:2:177:U:O2	18:G:191:ARG:NH1	2.26	0.69
27:Q:18:ALA:HB2	27:Q:69:VAL:HG13	1.74	0.69
9:k:70:ILE:HG22	9:k:74:LYS:HE3	1.75	0.69
11:2:1284:C:H42	11:2:1423:U:H3	1.40	0.69
11:2:780:A:H2	35:Y:8:ARG:HD3	1.58	0.68
11:2:1412:G:H21	28:R:3:ARG:HH22	1.41	0.68
29:S:92:ILE:HG21	29:S:115:ARG:HH22	1.57	0.68
1:b:20:LYS:NZ	24:N:13:SER:O	2.26	0.68
3:d:55:PHE:HB2	31:U:83:GLU:HB2	1.75	0.68
18:G:159:ARG:HH21	18:G:170:THR:HG23	1.58	0.68
11:2:630:A:N6	11:2:969:C:O2	2.19	0.68
24:N:42:ARG:HH21	24:N:80:LEU:HD21	1.58	0.68
11:2:1681:A:H1'	18:G:66:GLY:HA2	1.76	0.68
29:S:36:LYS:HB2	29:S:102:ALA:HA	1.75	0.68
11:2:248:U:H4'	22:L:36:LYS:HD3	1.75	0.68
11:2:656:G:O2'	11:2:657:U:O4'	2.12	0.68
11:2:780:A:H4'	11:2:781:U:H5'	1.76	0.68
16:E:192:ILE:HG13	16:E:243:GLY:HA3	1.75	0.68
11:2:1365:C:OP1	27:Q:66:ARG:NH2	2.27	0.68
15:D:172:THR:HG22	15:D:185:LYS:HG2	1.76	0.68
26:P:64:LYS:HE3	26:P:92:SER:HB2	1.74	0.68
11:2:1728:A:H1'	20:I:32:GLN:NE2	2.10	0.67
11:2:65:A:H2	11:2:84:A:H62	1.40	0.67
21:J:52:ILE:HG23	21:J:76:LEU:HD11	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:P:111:MET:HG2	29:S:119:ILE:HG23	1.75	0.67
26:P:18:ARG:HG3	26:P:36:LEU:HB3	1.75	0.67
34:X:69:ARG:NE	34:X:71:CYS:SG	2.67	0.67
30:T:77:ASN:OD1	30:T:101:ASN:ND2	2.28	0.67
15:D:108:LYS:HG2	15:D:113:LEU:HD12	1.76	0.67
33:W:66:ASN:HD22	33:W:68:ARG:HG3	1.59	0.67
6:h:216:ILE:O	6:h:220:THR:OG1	2.09	0.67
11:2:1610:G:H5''	17:F:107:LYS:HE3	1.75	0.67
10:l:89:LEU:HD11	26:P:142:LYS:HD2	1.77	0.67
11:2:1677:C:H42	11:2:1724:U:H3	1.42	0.67
18:G:102:VAL:HG13	18:G:106:LEU:HD12	1.77	0.67
11:2:568:G:H22	11:2:580:A:H2	1.40	0.66
11:2:1389:C:H4'	28:R:49:LYS:HA	1.75	0.66
35:Y:62:THR:HA	35:Y:69:SER:HB3	1.77	0.66
7:i:391:VAL:HG11	7:i:436:GLN:HB3	1.76	0.66
5:g:180:ALA:HB3	5:g:190:ALA:HB3	1.77	0.66
11:2:1387:G:OP1	28:R:32:LYS:NZ	2.28	0.66
20:I:114:GLU:HG2	20:I:120:THR:HA	1.76	0.66
15:D:101:GLN:HB2	15:D:186:VAL:HG11	1.77	0.66
11:2:153:G:OP2	35:Y:131:ARG:NH1	2.27	0.66
11:2:458:G:OP1	35:Y:109:LYS:NZ	2.29	0.66
11:2:614:C:OP1	34:X:3:LYS:NZ	2.25	0.66
11:2:1572:G:H1'	17:F:185:ARG:HH12	1.61	0.66
11:2:829:A:H61	11:2:843:U:H3	1.43	0.66
13:B:83:LYS:HG3	25:O:114:ARG:HH22	1.61	0.66
14:C:228:ASN:HD22	14:C:228:ASN:H	1.44	0.66
29:S:16:ARG:HE	29:S:19:ASN:HA	1.61	0.66
11:2:591:A:H2'	11:2:592:A:C8	2.30	0.65
12:A:142:PRO:HB3	32:V:34:ILE:HD11	1.77	0.65
11:2:717:C:H42	11:2:720:G:H22	1.42	0.65
29:S:37:GLY:O	29:S:99:HIS:NE2	2.26	0.65
11:2:1676:U:H5''	20:I:58:LEU:HD11	1.77	0.65
11:2:169:A:H5''	18:G:176:GLN:HG2	1.77	0.65
5:g:29:GLN:HE21	5:g:32:LEU:HD22	1.62	0.65
10:l:43:MET:HE1	10:l:48:GLY:HA3	1.78	0.65
10:l:177:PRO:HD3	10:l:250:VAL:HG13	1.77	0.65
11:2:1316:G:H21	11:2:1400:A:H2	1.45	0.65
11:2:1432:U:H5'	11:2:1433:G:H5'	1.79	0.65
23:M:33:ARG:NH1	23:M:33:ARG:O	2.30	0.65
33:W:80:ASN:OD1	33:W:80:ASN:N	2.27	0.65
7:i:311:LEU:HB3	7:i:345:VAL:HG11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:86:ILE:HG12	9:k:242:LEU:HD22	1.79	0.65
11:2:130:C:H42	11:2:136:C:H42	1.45	0.65
11:2:475:A:OP2	21:J:126:ARG:NH1	2.30	0.65
10:l:206:ILE:HD13	10:l:284:LEU:HB3	1.78	0.65
11:2:1331:A:H61	11:2:1420:C:N4	1.94	0.65
35:Y:54:ALA:HB2	35:Y:79:VAL:HG22	1.77	0.65
11:2:502:U:H2'	11:2:503:G:H8	1.62	0.65
11:2:1219:A:H62	11:2:1264:G:H1	1.44	0.65
10:l:209:LEU:HD22	10:l:249:PHE:HZ	1.62	0.64
35:Y:14:SER:HB3	35:Y:21:LYS:HE2	1.78	0.64
11:2:140:A:OP2	18:G:187:LYS:NZ	2.27	0.64
11:2:569:C:H5''	34:X:65:ASN:HB3	1.78	0.64
11:2:1042:G:H1	11:2:1076:A:H2	1.45	0.64
12:A:56:LYS:HZ1	12:A:158:VAL:HA	1.61	0.64
17:F:46:TRP:HE1	17:F:129:PRO:HG2	1.61	0.64
9:k:150:ASP:HA	9:k:153:LYS:HE2	1.79	0.64
11:2:1345:A:H4'	31:U:56:VAL:HG22	1.78	0.64
23:M:115:VAL:HG12	23:M:116:VAL:H	1.62	0.64
9:k:687:THR:OG1	34:X:144:ARG:NH2	2.30	0.64
11:2:1255:G:O2'	23:M:43:ARG:NH2	2.30	0.64
11:2:788:A:OP2	16:E:108:ARG:NH2	2.29	0.64
5:g:80:ALA:HB3	5:g:92:TRP:HB2	1.79	0.64
10:l:23:GLU:HG2	10:l:184:ARG:HH22	1.61	0.64
11:2:12:U:H2'	11:2:13:C:C6	2.32	0.64
30:T:86:ARG:HH21	30:T:89:ARG:HD3	1.62	0.64
7:i:270:LEU:HB3	7:i:274:GLU:HB3	1.78	0.64
10:l:226:ILE:HD12	10:l:265:ALA:HB1	1.78	0.64
11:2:113:U:O2'	11:2:115:G:O2'	2.13	0.64
11:2:1146:G:C8	11:2:1631:A:H2	2.15	0.64
12:A:59:LEU:HD12	32:V:79:LEU:HD11	1.79	0.64
14:C:137:ILE:HG13	14:C:138:PRO:HD2	1.80	0.64
17:F:92:ARG:NH2	17:F:169:ASN:OD1	2.30	0.64
36:Z:77:ARG:HD3	36:Z:81:ARG:HH12	1.62	0.64
12:A:49:ASN:HB3	12:A:52:LYS:HG3	1.80	0.64
21:J:109:LEU:HB2	21:J:146:PHE:HB3	1.78	0.64
34:X:112:LYS:H	34:X:117:ILE:HG12	1.61	0.64
10:l:119:PRO:HB2	10:l:191:LEU:HD22	1.80	0.63
11:2:1523:G:N7	30:T:68:ARG:NH1	2.45	0.63
16:E:175:PHE:HE2	16:E:198:LYS:HD2	1.63	0.63
20:I:104:ILE:HG12	20:I:105:ASP:H	1.63	0.63
10:l:277:ARG:HG2	10:l:288:PRO:HG3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:S:62:THR:HB	29:S:64:GLU:HG2	1.80	0.63
11:2:1254:U:H2'	11:2:1255:G:C8	2.33	0.63
11:2:1469:A:H4'	11:2:1541:G:H4'	1.80	0.63
13:B:27:LYS:HG2	13:B:49:ASN:HA	1.79	0.63
9:k:183:GLN:HB3	9:k:668:ILE:HD11	1.79	0.63
11:2:153:G:H21	18:G:56:ASN:HD21	1.46	0.63
11:2:913:G:H3'	11:2:914:G:H5''	1.80	0.63
24:N:136:PRO:HG2	24:N:139:TRP:HB2	1.80	0.63
7:i:343:ALA:O	11:2:1219:A:O2'	2.17	0.63
18:G:57:ASP:HA	18:G:106:LEU:HA	1.80	0.63
21:J:23:ARG:NH1	21:J:27:GLU:OE2	2.30	0.63
11:2:649:U:O2'	11:2:650:U:O5'	2.17	0.63
14:C:143:TYR:OH	14:C:149:GLY:O	2.16	0.63
16:E:184:THR:O	16:E:189:LEU:HD13	1.99	0.63
19:H:51:VAL:HG23	19:H:53:GLY:H	1.63	0.63
11:2:140:A:H1'	18:G:179:VAL:HG21	1.79	0.63
11:2:886:U:OP2	13:B:216:LYS:NZ	2.26	0.63
7:i:408:ASP:OD1	7:i:411:ARG:NH1	2.33	0.62
11:2:260:U:H5	20:I:43:ILE:HB	1.63	0.62
10:l:198:ARG:NE	11:2:1171:A:OP1	2.32	0.62
11:2:887:A:H5''	25:O:120:PRO:HB3	1.81	0.62
11:2:1137:A:H4'	11:2:1138:A:H4'	1.79	0.62
11:2:1291:G:OP1	14:C:97:ARG:NH2	2.33	0.62
12:A:110:TYR:CD2	12:A:111:ILE:HD13	2.34	0.62
17:F:23:VAL:HG11	27:Q:58:ASP:HA	1.80	0.62
11:2:1046:G:H1	11:2:1072:C:H42	1.46	0.62
11:2:1214:U:OP1	11:2:1245:G:N2	2.33	0.62
11:2:1788:G:OP2	25:O:132:ARG:NH1	2.33	0.62
29:S:29:VAL:HG22	29:S:54:LEU:HD22	1.81	0.62
5:g:14:GLU:HB3	5:g:309:VAL:HG22	1.80	0.62
6:h:97:ARG:HG3	6:h:152:LEU:HD21	1.82	0.62
11:2:1002:G:H21	11:2:1004:U:C5'	2.12	0.62
11:2:1553:G:O6	26:P:43:ARG:NH1	2.33	0.62
17:F:77:TYR:HD2	17:F:83:ARG:HG2	1.65	0.62
35:Y:14:SER:HA	35:Y:21:LYS:HG2	1.82	0.62
15:D:101:GLN:HG3	15:D:188:ILE:HD11	1.81	0.62
17:F:133:VAL:HG22	17:F:198:LEU:HD13	1.80	0.62
34:X:70:LYS:HB3	34:X:93:LEU:HD11	1.82	0.62
11:2:40:A:OP1	21:J:3:ARG:NH1	2.33	0.61
11:2:1310:U:O2'	11:2:1401:A:N1	2.32	0.61
11:2:1655:A:N1	11:2:1746:A:H2	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:J:127:VAL:HG13	21:J:131:GLN:HE21	1.64	0.61
11:2:115:G:OP1	22:L:67:ARG:NH1	2.33	0.61
11:2:1568:C:OP2	29:S:36:LYS:NZ	2.31	0.61
33:W:54:ASP:OD1	33:W:55:ASP:N	2.33	0.61
3:d:50:ILE:HG12	15:D:16:VAL:HG22	1.82	0.61
6:h:221:ARG:HH12	6:h:271:LYS:HG2	1.65	0.61
12:A:84:ARG:NH2	28:R:81:LYS:O	2.32	0.61
23:M:63:VAL:HG12	23:M:65:SER:H	1.65	0.61
7:i:449:HIS:CE1	11:2:1436:A:H61	2.18	0.61
11:2:1022:C:O2'	11:2:1125:A:N1	2.34	0.61
5:g:38:ARG:HG2	5:g:67:ILE:HD12	1.82	0.61
5:g:295:SER:HB2	5:g:300:THR:HB	1.83	0.61
5:g:248:ASN:ND2	5:g:297:ASP:O	2.34	0.61
9:k:90:PRO:HD2	9:k:142:MET:HE3	1.82	0.61
12:A:110:TYR:HD2	12:A:111:ILE:HD13	1.64	0.61
14:C:108:ASN:HD22	14:C:141:ARG:HH11	1.48	0.61
33:W:77:PRO:O	33:W:79:PHE:N	2.33	0.61
11:2:1268:G:H1'	11:2:1270:G:H5'	1.83	0.60
11:2:319:U:OP1	20:I:11:ARG:NH2	2.32	0.60
11:2:1299:G:H2'	11:2:1300:A:C8	2.36	0.60
11:2:1535:U:H5''	17:F:187:ILE:HD11	1.81	0.60
17:F:139:ASN:ND2	17:F:202:ALA:O	2.34	0.60
1:b:36:LYS:HE3	1:b:43:ILE:HG13	1.83	0.60
4:e:8:LEU:HD11	9:k:208:VAL:HG13	1.83	0.60
7:i:414:PRO:HB2	7:i:416:ILE:HG22	1.83	0.60
11:2:1537:C:O2'	11:2:1540:G:O6	2.14	0.60
11:2:1653:C:H2'	11:2:1654:G:C5	2.35	0.60
11:2:1003:A:HO2'	11:2:1004:U:H6	1.47	0.60
20:I:103:GLN:HG2	20:I:164:ARG:HG2	1.82	0.60
5:g:38:ARG:HA	5:g:67:ILE:HB	1.82	0.60
12:A:103:THR:O	12:A:106:SER:OG	2.14	0.60
24:N:3:ARG:HG2	24:N:6:SER:OG	2.02	0.60
9:k:52:LEU:HD13	11:2:1663:G:H4'	1.84	0.60
11:2:1238:A:N6	11:2:1247:U:H3	1.97	0.60
15:D:55:THR:HB	15:D:92:GLN:H	1.66	0.60
22:L:45:PRO:HG2	22:L:48:ALA:HB2	1.83	0.60
7:i:242:TRP:NE1	7:i:274:GLU:HG3	2.14	0.60
7:i:309:LYS:NZ	7:i:312:TYR:OH	2.32	0.60
11:2:1265:G:H8	11:2:1266:U:O2	1.84	0.60
15:D:8:LYS:HE2	31:U:61:LYS:NZ	2.17	0.60
16:E:104:ASP:OD1	16:E:105:VAL:N	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:l:33:PRO:HB2	10:l:35:PRO:HD2	1.83	0.60
11:2:1594:G:H5'	11:2:1596:C:H42	1.66	0.60
15:D:168:ILE:HD13	15:D:187:LYS:HE3	1.84	0.60
16:E:92:LEU:HD13	35:Y:17:LEU:HD11	1.83	0.60
11:2:1587:A:H2'	11:2:1588:G:H8	1.67	0.60
14:C:79:GLU:HG2	14:C:81:MET:HE3	1.82	0.60
27:Q:28:LEU:HD21	27:Q:30:LYS:HG3	1.82	0.60
11:2:197:A:H61	20:I:138:ASN:HD21	1.49	0.60
32:V:18:SER:OG	32:V:54:ALA:O	2.17	0.60
34:X:40:SER:O	34:X:81:LYS:NZ	2.34	0.60
11:2:78:A:H1'	18:G:175:ILE:HG12	1.84	0.59
14:C:106:ASP:OD1	14:C:107:SER:N	2.35	0.59
32:V:79:LEU:HD13	32:V:82:VAL:HG21	1.83	0.59
6:h:105:ARG:NH2	6:h:166:PHE:O	2.35	0.59
11:2:1219:A:C8	11:2:1266:U:H1'	2.36	0.59
12:A:180:GLU:O	12:A:184:LEU:HG	2.00	0.59
18:G:14:LYS:HD3	18:G:16:PHE:CZ	2.38	0.59
17:F:120:ILE:HD11	36:Z:98:GLN:HE22	1.66	0.59
23:M:52:LEU:HD11	23:M:60:VAL:HG21	1.84	0.59
17:F:222:LYS:HE2	17:F:225:ARG:HH12	1.67	0.59
23:M:28:LEU:HD21	23:M:61:VAL:HG13	1.84	0.59
10:l:156:ARG:HH11	10:l:184:ARG:HA	1.68	0.59
28:R:13:SER:HA	28:R:54:THR:HG22	1.85	0.59
28:R:17:ILE:HG23	28:R:58:MET:HE2	1.85	0.59
2:c:27:GLN:HE22	2:c:65:ARG:HD2	1.66	0.59
11:2:902:G:OP2	25:O:24:ASN:ND2	2.32	0.59
11:2:687:G:OP1	33:W:118:ARG:NH1	2.36	0.59
11:2:1096:C:OP2	33:W:71:LYS:NZ	2.28	0.59
12:A:126:PRO:HG3	12:A:147:THR:HG22	1.84	0.59
6:h:149:PRO:HB2	25:O:107:ARG:HA	1.83	0.59
25:O:15:GLY:O	25:O:80:HIS:N	2.35	0.59
11:2:639:U:H5'	19:H:101:LYS:HB2	1.84	0.58
17:F:89:ILE:HD11	17:F:137:ILE:HG13	1.85	0.58
19:H:44:LYS:HG3	19:H:63:PRO:HD3	1.84	0.58
23:M:66:VAL:HB	23:M:72:ILE:HD11	1.85	0.58
3:d:36:LEU:HD12	3:d:38:ILE:H	1.68	0.58
4:e:37:ARG:HB2	21:J:123:HIS:CE1	2.38	0.58
11:2:1291:G:H2'	11:2:1292:G:H8	1.69	0.58
17:F:112:ARG:HB2	27:Q:43:ILE:HD11	1.86	0.58
11:2:399:A:OP1	20:I:49:ARG:NH1	2.37	0.58
11:2:1635:A:H61	11:2:1769:U:H3	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:14:LYS:NZ	28:R:18:GLU:OE2	2.36	0.58
9:k:175:GLN:HG2	9:k:678:LYS:HZ3	1.67	0.58
18:G:57:ASP:HB3	18:G:98:ARG:HG3	1.86	0.58
18:G:137:ARG:HD3	18:G:177:ARG:NE	2.18	0.58
34:X:11:SER:O	34:X:11:SER:OG	2.21	0.58
36:Z:90:LYS:HE3	36:Z:104:ALA:HB2	1.85	0.58
10:l:226:ILE:HD13	10:l:269:PHE:HB2	1.86	0.58
11:2:1225:U:H3	11:2:1258:U:H3	1.51	0.58
11:2:1558:U:H3'	11:2:1559:A:H4'	1.85	0.58
16:E:46:VAL:HA	16:E:50:ASN:HD22	1.68	0.58
17:F:42:LEU:HD12	17:F:48:PHE:HB2	1.86	0.58
20:I:168:CYS:HB3	20:I:182:TYR:CE2	2.39	0.58
11:2:334:G:O6	20:I:5:ARG:NH2	2.35	0.58
11:2:789:A:O2'	16:E:106:LYS:NZ	2.34	0.58
11:2:1483:A:OP2	11:2:1521:G:N2	2.33	0.58
11:2:1082:C:O2'	11:2:1083:G:O4'	2.22	0.58
11:2:1149:G:O3'	11:2:1150:G:H2'	2.03	0.58
24:N:5:HIS:HB3	24:N:117:LEU:HD13	1.85	0.58
27:Q:7:VAL:HG21	27:Q:92:TYR:HA	1.86	0.58
6:h:182:ILE:HG12	6:h:234:LEU:HG	1.85	0.58
9:k:389:LYS:NZ	9:k:407:ASP:OD2	2.31	0.58
11:2:1066:C:H2'	11:2:1067:C:H6	1.69	0.58
11:2:1431:C:H3'	11:2:1432:U:H4'	1.84	0.58
13:B:164:ILE:HD13	13:B:207:LEU:HD11	1.85	0.58
14:C:218:ILE:O	14:C:221:THR:OG1	2.22	0.58
14:C:233:GLN:HE21	32:V:13:VAL:HG11	1.69	0.58
6:h:99:ILE:HD13	6:h:159:ILE:HG22	1.85	0.58
7:i:314:PRO:HG3	7:i:348:PRO:HD2	1.86	0.58
11:2:1322:A:O2'	12:A:104:PRO:HG2	2.03	0.58
22:L:67:ARG:HD3	22:L:67:ARG:N	2.18	0.58
11:2:217:A:H3'	11:2:218:A:H5''	1.85	0.57
28:R:88:VAL:O	28:R:95:ARG:NH2	2.34	0.57
29:S:130:GLY:O	29:S:134:ARG:HG2	2.04	0.57
31:U:96:PRO:HD2	31:U:99:ILE:HD12	1.86	0.57
34:X:102:VAL:HG22	34:X:127:VAL:HG12	1.85	0.57
11:2:197:A:H61	20:I:138:ASN:ND2	2.03	0.57
11:2:209:U:H2'	11:2:210:A:C8	2.39	0.57
11:2:513:U:H4'	21:J:131:GLN:HG3	1.86	0.57
11:2:919:A:H2'	11:2:920:U:H6	1.69	0.57
11:2:148:A:N6	11:2:167:U:O2	2.37	0.57
11:2:341:A:O2'	20:I:87:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1156:C:O2'	11:2:1157:A:OP2	2.22	0.57
17:F:42:LEU:HB3	17:F:67:PRO:HB3	1.86	0.57
18:G:78:THR:HG23	18:G:92:ARG:HG2	1.86	0.57
25:O:86:THR:HG21	25:O:90:ARG:HD2	1.86	0.57
14:C:143:TYR:CD1	14:C:147:ASN:HA	2.39	0.57
9:k:505:LYS:HG3	9:k:506:ASN:H	1.70	0.57
11:2:869:A:H61	11:2:958:U:H3	1.51	0.57
11:2:1288:G:H8	11:2:1314:U:O2'	1.88	0.57
14:C:53:ILE:O	14:C:56:ILE:N	2.37	0.57
17:F:120:ILE:HD11	36:Z:98:GLN:NE2	2.20	0.57
5:g:96:THR:HB	5:g:98:GLU:HG3	1.87	0.57
9:k:708:PHE:HB2	9:k:718:ARG:HB2	1.87	0.57
11:2:76:A:N6	11:2:80:A:O2'	2.37	0.57
11:2:569:C:OP2	34:X:66:SER:N	2.38	0.57
23:M:59:LEU:HD22	23:M:133:LEU:HD23	1.86	0.57
2:c:25:VAL:HG21	2:c:66:LEU:HD22	1.86	0.57
9:k:90:PRO:HB3	9:k:95:LEU:HD23	1.87	0.57
11:2:570:A:N6	34:X:69:ARG:HA	2.19	0.57
11:2:1198:G:H3'	11:2:1200:G:C8	2.40	0.57
14:C:106:ASP:CG	14:C:108:ASN:H	2.12	0.57
10:l:19:LEU:HD13	10:l:56:LEU:HD13	1.87	0.57
11:2:246:G:N2	22:L:66:ILE:O	2.25	0.57
11:2:1329:A:H61	28:R:7:LYS:NZ	2.02	0.57
13:B:71:ALA:HB2	13:B:80:SER:H	1.69	0.57
10:l:33:PRO:HG3	11:2:1634:C:H5	1.70	0.57
11:2:860:U:O4'	19:H:114:ARG:HG3	2.05	0.57
11:2:45:U:O2'	11:2:46:A:H2'	2.04	0.57
11:2:160:C:O3'	18:G:95:LYS:NZ	2.38	0.57
5:g:10:ARG:HE	5:g:314:GLN:HB2	1.70	0.56
10:l:236:MET:HB3	10:l:250:VAL:HB	1.87	0.56
11:2:753:A:OP1	16:E:187:ARG:N	2.38	0.56
13:B:129:THR:O	13:B:132:ASP:N	2.38	0.56
26:P:59:LYS:HE2	26:P:76:VAL:HG13	1.87	0.56
32:V:36:VAL:HB	32:V:51:VAL:HG23	1.87	0.56
36:Z:50:ILE:O	36:Z:54:VAL:HG23	2.05	0.56
9:k:386:THR:HG22	9:k:388:LYS:HG3	1.86	0.56
11:2:79:C:H1'	18:G:174:LYS:HD3	1.86	0.56
11:2:717:C:H42	11:2:720:G:N2	2.02	0.56
11:2:1175:U:H2'	11:2:1176:G:H8	1.68	0.56
13:B:27:LYS:HB3	13:B:47:LEU:HD11	1.86	0.56
7:i:307:VAL:HG12	7:i:341:VAL:HG11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:918:U:O3'	25:O:18:ARG:NH1	2.38	0.56
14:C:140:ARG:HD3	14:C:222:TYR:CE1	2.40	0.56
17:F:57:SER:OG	17:F:167:ARG:NH2	2.38	0.56
22:L:80:MET:HG3	22:L:83:THR:HG23	1.86	0.56
27:Q:13:LYS:NZ	27:Q:120:ASP:OD2	2.33	0.56
23:M:62:LEU:HD11	23:M:88:LEU:HD13	1.88	0.56
27:Q:45:ARG:HG3	27:Q:49:TYR:HE1	1.70	0.56
32:V:71:ARG:HB2	32:V:83:TRP:CE2	2.41	0.56
11:2:1270:G:H2'	11:2:1271:G:C8	2.41	0.56
9:k:259:VAL:HG23	9:k:287:PHE:CE2	2.40	0.56
11:2:1009:U:H2'	11:2:1010:C:O4'	2.06	0.56
6:h:119:PRO:O	6:h:123:HIS:HB3	2.05	0.56
9:k:403:TRP:HE1	29:S:129:TRP:CG	2.23	0.56
9:k:766:GLN:HE21	11:2:1271:G:H22	1.53	0.56
15:D:55:THR:H	15:D:91:VAL:HB	1.71	0.56
26:P:121:ILE:HG22	26:P:123:TYR:H	1.70	0.56
27:Q:101:SER:O	27:Q:105:LEU:HD13	2.06	0.56
2:c:45:LYS:HB2	17:F:160:VAL:HG21	1.87	0.56
7:i:260:TYR:HA	7:i:306:ALA:HB2	1.87	0.56
11:2:589:C:H2'	11:2:590:C:H6	1.71	0.56
34:X:96:VAL:HG22	34:X:127:VAL:HG11	1.86	0.56
5:g:278:PHE:HB3	5:g:281:TYR:HD1	1.70	0.56
11:2:458:G:OP2	35:Y:105:ARG:NH2	2.39	0.56
11:2:1309:C:O2'	11:2:1398:U:O2	2.23	0.56
15:D:38:GLU:HG3	15:D:49:ILE:HB	1.87	0.56
16:E:71:LYS:HB2	16:E:91:THR:HB	1.87	0.56
16:E:87:MET:SD	16:E:123:LEU:HB2	2.46	0.56
17:F:76:ARG:NH1	27:Q:121:SER:OG	2.38	0.56
7:i:337:ILE:O	7:i:340:SER:OG	2.18	0.56
18:G:26:VAL:O	18:G:30:LYS:NZ	2.32	0.56
19:H:98:ILE:HG22	19:H:121:VAL:HG21	1.88	0.56
11:2:6:G:N7	14:C:205:ARG:NH1	2.54	0.55
11:2:445:A:H1'	11:2:525:A:H5'	1.88	0.55
11:2:463:U:H2'	11:2:464:A:H8	1.71	0.55
11:2:654:C:H3'	11:2:655:G:H5''	1.88	0.55
13:B:110:LEU:HD11	13:B:213:ARG:HD3	1.87	0.55
32:V:60:ARG:HA	32:V:65:SER:HB2	1.88	0.55
11:2:1226:A:C5	23:M:115:VAL:HG13	2.42	0.55
20:I:81:VAL:HA	20:I:102:VAL:HG12	1.88	0.55
11:2:335:U:H5'	11:2:336:G:OP2	2.06	0.55
11:2:514:G:O2'	11:2:515:A:H5''	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H:91:ILE:HD12	19:H:172:VAL:HG21	1.88	0.55
6:h:205:ILE:HA	6:h:250:LEU:HD13	1.87	0.55
10:l:4:ASP:O	10:l:82:TYR:OH	2.25	0.55
11:2:1727:G:H21	20:I:32:GLN:NE2	2.03	0.55
23:M:60:VAL:HG22	23:M:122:VAL:HG22	1.87	0.55
27:Q:21:HIS:HB2	27:Q:66:ARG:HB2	1.87	0.55
11:2:781:U:H4'	11:2:782:U:H5'	1.87	0.55
11:2:1006:C:H2'	11:2:1007:C:H5'	1.89	0.55
14:C:56:ILE:HA	14:C:61:LEU:HD12	1.88	0.55
11:2:1055:U:H3	11:2:1064:G:H1	1.55	0.55
20:I:166:TYR:HB3	20:I:184:LEU:HD12	1.88	0.55
8:j:361:TYR:CZ	8:j:365:ILE:HG21	2.41	0.55
9:k:587:HIS:HB3	9:k:590:LYS:HD2	1.87	0.55
11:2:610:G:O2'	11:2:613:G:O2'	2.22	0.55
11:2:1293:U:O2	12:A:109:ASN:ND2	2.39	0.55
25:O:92:LYS:HZ3	25:O:122:PRO:HD2	1.71	0.55
30:T:137:ALA:O	30:T:141:GLU:HG2	2.07	0.55
33:W:105:THR:OG1	33:W:126:LEU:HG	2.06	0.55
6:h:174:LEU:HD23	6:h:180:LEU:HB2	1.88	0.55
11:2:1684:U:H2'	11:2:1685:G:C8	2.42	0.55
19:H:8:ILE:HD13	19:H:24:PHE:HD1	1.71	0.55
6:h:112:SER:HB3	6:h:168:LEU:HD11	1.88	0.55
11:2:140:A:N3	11:2:140:A:H5''	2.22	0.55
9:k:377:HIS:HA	26:P:142:LYS:HG2	1.89	0.55
9:k:489:GLU:HB2	9:k:492:GLU:HG3	1.89	0.55
11:2:504:U:O4	11:2:505:A:N6	2.40	0.55
12:A:183:ARG:NH2	12:A:191:ARG:HD3	2.18	0.55
11:2:649:U:H3	11:2:685:A:H61	1.55	0.54
11:2:1696:G:N2	11:2:1706:C:O2	2.40	0.54
20:I:3:ILE:HB	20:I:30:GLY:O	2.07	0.54
14:C:81:MET:HE2	14:C:81:MET:HA	1.89	0.54
14:C:146:THR:OG1	14:C:147:ASN:N	2.40	0.54
18:G:98:ARG:HD2	18:G:106:LEU:HD21	1.89	0.54
20:I:34:ALA:O	20:I:36:THR:N	2.40	0.54
9:k:217:LYS:HE2	34:X:140:LYS:NZ	2.22	0.54
11:2:912:U:H4'	11:2:913:G:O5'	2.07	0.54
11:2:1223:A:H61	11:2:1260:U:H3	1.54	0.54
4:e:37:ARG:HB2	21:J:123:HIS:HE1	1.72	0.54
5:g:76:ASP:OD1	5:g:76:ASP:N	2.40	0.54
6:h:196:ASP:HB3	6:h:200:ARG:HH12	1.73	0.54
10:l:147:GLN:HB3	10:l:152:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:131:C:H42	11:2:135:A:H61	1.53	0.54
23:M:91:VAL:HG11	23:M:97:LEU:HD13	1.89	0.54
1:b:67:THR:O	1:b:69:GLY:N	2.41	0.54
6:h:178:ASP:OD1	25:O:103:ARG:NH1	2.40	0.54
9:k:304:ASN:HB2	9:k:562:ARG:HG3	1.89	0.54
11:2:502:U:H2'	11:2:503:G:C8	2.42	0.54
11:2:778:G:H22	35:Y:10:ARG:HH21	1.56	0.54
11:2:1535:U:O2'	11:2:1536:G:N3	2.41	0.54
16:E:72:VAL:HG22	16:E:90:ILE:HG12	1.90	0.54
17:F:29:ILE:O	17:F:34:GLN:NE2	2.40	0.54
11:2:1349:G:H21	11:2:1379:C:H42	1.55	0.54
11:2:1413:U:H3'	11:2:1414:U:H3'	1.89	0.54
14:C:230:TRP:CD2	33:W:68:ARG:HD3	2.41	0.54
35:Y:29:HIS:HB2	35:Y:32:ARG:HB3	1.90	0.54
1:b:8:LEU:HD23	33:W:53:ILE:HD11	1.90	0.54
11:2:319:U:H1'	11:2:323:A:C4	2.43	0.54
11:2:765:G:H5''	21:J:149:ARG:HH22	1.73	0.54
19:H:4:PRO:HD2	19:H:25:VAL:HG11	1.89	0.54
25:O:40:ALA:HB1	25:O:67:VAL:HG22	1.89	0.54
26:P:86:VAL:HG13	26:P:89:MET:HE3	1.88	0.54
34:X:102:VAL:HG13	34:X:124:VAL:HG13	1.89	0.54
2:c:12:VAL:HG22	2:c:28:VAL:HG11	1.88	0.54
11:2:576:G:H2'	11:2:577:G:O4'	2.08	0.54
9:k:153:LYS:NZ	9:k:183:GLN:OE1	2.41	0.54
11:2:418:G:H3'	11:2:418:G:N3	2.23	0.54
11:2:1653:C:H2'	11:2:1654:G:C4	2.43	0.54
11:2:1330:G:H3'	11:2:1331:A:C8	2.43	0.54
16:E:94:ALA:HB3	35:Y:17:LEU:HD23	1.89	0.54
20:I:100:ALA:HB3	20:I:169:ILE:HD12	1.90	0.54
6:h:125:LYS:HG2	6:h:145:PHE:HD1	1.72	0.53
11:2:793:A:H1'	11:2:795:U:OP2	2.08	0.53
11:2:895:G:H1	11:2:917:U:H3	1.56	0.53
9:k:506:ASN:HB3	9:k:509:ASN:HB3	1.91	0.53
9:k:639:VAL:HG22	9:k:696:ILE:HG12	1.90	0.53
11:2:92:A:OP1	16:E:7:LYS:NZ	2.37	0.53
11:2:209:U:H5''	20:I:170:SER:O	2.08	0.53
11:2:336:G:H2'	11:2:338:C:H5	1.73	0.53
11:2:574:G:H22	11:2:582:U:H1'	1.73	0.53
12:A:118:PRO:O	12:A:119:ARG:HG2	2.08	0.53
18:G:31:ARG:HB3	18:G:101:ILE:HG12	1.90	0.53
24:N:132:VAL:HG23	24:N:134:VAL:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:l:106:GLU:O	10:l:125:HIS:ND1	2.41	0.53
11:2:1628:U:H2'	11:2:1629:G:C8	2.44	0.53
12:A:76:ILE:HB	12:A:123:VAL:HG22	1.90	0.53
13:B:32:ILE:HD12	13:B:66:VAL:HG21	1.90	0.53
16:E:100:ARG:NH2	16:E:122:LYS:HA	2.23	0.53
34:X:57:LEU:HD11	34:X:73:ARG:HG3	1.90	0.53
34:X:63:GLN:HB2	34:X:115:GLY:HA3	1.90	0.53
7:i:304:TYR:HE1	7:i:341:VAL:HG22	1.72	0.53
9:k:469:LEU:HD21	9:k:473:ARG:HH21	1.72	0.53
11:2:895:G:H21	25:O:38:THR:HG21	1.72	0.53
11:2:1226:A:C6	23:M:115:VAL:HG13	2.44	0.53
11:2:1290:U:OP1	14:C:90:THR:HG21	2.09	0.53
11:2:1591:C:H2'	11:2:1592:A:C8	2.43	0.53
12:A:52:LYS:HD3	32:V:82:VAL:HA	1.89	0.53
12:A:179:ARG:O	12:A:183:ARG:HG3	2.09	0.53
21:J:127:VAL:O	21:J:131:GLN:HB2	2.09	0.53
26:P:81:ARG:NH1	26:P:120:SER:O	2.35	0.53
33:W:102:VAL:O	33:W:113:HIS:HB3	2.09	0.53
34:X:87:VAL:HG23	34:X:132:LEU:HD21	1.90	0.53
5:g:243:LEU:HD22	5:g:252:LEU:HD11	1.90	0.53
11:2:268:C:O2	11:2:287:G:N2	2.22	0.53
11:2:919:A:P	25:O:18:ARG:HH12	2.31	0.53
16:E:133:LYS:O	16:E:136:VAL:HG22	2.08	0.53
2:c:12:VAL:HB	2:c:52:ASP:HB2	1.91	0.53
20:I:82:VAL:HG21	20:I:166:TYR:HE1	1.73	0.53
20:I:83:TYR:HB3	20:I:101:ILE:HB	1.90	0.53
20:I:92:ARG:HG2	20:I:93:THR:HG23	1.90	0.53
35:Y:30:PRO:C	35:Y:32:ARG:H	2.16	0.53
11:2:154:G:H1'	18:G:56:ASN:HD22	1.74	0.53
11:2:570:A:N1	34:X:69:ARG:HG2	2.22	0.53
11:2:1231:U:O2'	11:2:1232:U:OP1	2.25	0.53
16:E:122:LYS:NZ	16:E:143:ASP:OD2	2.23	0.53
7:i:234:LYS:HA	7:i:265:LEU:HD21	1.91	0.53
10:l:163:TYR:CG	10:l:182:ASN:HB3	2.44	0.53
11:2:568:G:O6	11:2:575:C:H2'	2.09	0.53
11:2:1498:G:H5''	30:T:72:GLY:HA3	1.91	0.53
14:C:45:VAL:HG21	14:C:68:ILE:HG23	1.91	0.53
18:G:175:ILE:HG21	18:G:178:LEU:HD13	1.91	0.53
23:M:99:GLU:HA	23:M:105:LYS:H	1.74	0.53
2:c:42:ARG:NH1	2:c:61:ARG:O	2.42	0.53
9:k:737:THR:HG22	9:k:739:SER:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:l:127:LEU:HD13	10:l:155:SER:HA	1.91	0.53
13:B:134:VAL:HB	13:B:219:LYS:HB2	1.90	0.53
34:X:28:ASN:OD1	34:X:28:ASN:N	2.40	0.53
34:X:95:PHE:O	34:X:142:LYS:NZ	2.36	0.53
1:b:42:ASN:ND2	1:b:57:GLU:OE1	2.42	0.52
9:k:265:ASP:OD1	9:k:265:ASP:N	2.41	0.52
34:X:104:LEU:HD23	34:X:124:VAL:HA	1.91	0.52
11:2:322:G:C2	11:2:337:G:C5	2.98	0.52
11:2:871:G:H2'	11:2:872:G:C8	2.43	0.52
11:2:1631:A:OP1	11:2:1633:A:H5''	2.09	0.52
16:E:17:HIS:ND1	16:E:107:GLY:O	2.42	0.52
7:i:232:LEU:HD21	8:j:399:LEU:HA	1.92	0.52
11:2:1458:G:N3	11:2:1458:G:H2'	2.24	0.52
21:J:37:LYS:N	21:J:41:GLU:OE1	2.29	0.52
19:H:31:SER:OG	19:H:34:LEU:HB2	2.10	0.52
24:N:91:LEU:HD12	24:N:125:LEU:HD12	1.91	0.52
5:g:150:TRP:HE1	28:R:37:GLU:HG3	1.74	0.52
11:2:539:G:H4'	11:2:540:G:OP1	2.09	0.52
11:2:898:A:N3	11:2:899:G:H1'	2.24	0.52
11:2:1096:C:H4'	11:2:1099:U:H4'	1.90	0.52
16:E:68:ARG:HD3	16:E:76:VAL:HG11	1.92	0.52
26:P:17:TYR:HB3	26:P:25:LEU:HD13	1.90	0.52
36:Z:91:PRO:HA	36:Z:101:TYR:HD2	1.75	0.52
11:2:894:U:H2'	11:2:895:G:C8	2.45	0.52
16:E:230:GLU:HB2	16:E:233:LYS:HB2	1.92	0.52
29:S:75:ASN:HB2	29:S:79:TYR:HE1	1.74	0.52
7:i:357:SER:HA	7:i:360:LEU:HD12	1.92	0.52
11:2:463:U:H2'	11:2:464:A:C8	2.45	0.52
11:2:930:A:H5'	11:2:931:C:OP2	2.10	0.52
11:2:1389:C:H1'	28:R:52:GLY:HA3	1.92	0.52
11:2:1573:A:H4'	11:2:1574:G:O5'	2.10	0.52
27:Q:13:LYS:O	27:Q:76:SER:OG	2.27	0.52
7:i:240:ARG:HH22	8:j:387:ASP:HB3	1.75	0.52
7:i:292:GLU:HG3	15:D:76:ARG:HG3	1.92	0.52
11:2:1533:C:H5	36:Z:77:ARG:HH12	1.57	0.52
12:A:21:ASN:HA	12:A:23:HIS:CD2	2.45	0.52
15:D:175:VAL:HG13	15:D:182:LEU:HB2	1.92	0.52
36:Z:91:PRO:HB3	36:Z:94:LYS:HE3	1.92	0.52
10:l:80:ILE:HD11	10:l:152:MET:HE2	1.92	0.52
11:2:138:A:N6	11:2:266:A:H61	2.08	0.52
11:2:959:U:C6	24:N:61:THR:HB	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1267:G:H22	11:2:1442:U:HO2'	1.57	0.52
6:h:241:ARG:HG2	6:h:242:MET:HE2	1.90	0.52
11:2:1146:G:C8	11:2:1631:A:C2	2.98	0.52
11:2:1400:A:H2'	11:2:1401:A:C8	2.45	0.52
11:2:1538:U:O2'	11:2:1539:G:H2'	2.10	0.52
12:A:200:ASP:HA	12:A:203:PHE:CD1	2.45	0.52
9:k:360:TYR:HD2	9:k:517:LYS:HD2	1.75	0.51
11:2:1114:G:O2'	11:2:1130:G:O6	2.27	0.51
12:A:15:GLN:HG3	28:R:117:LEU:HD22	1.92	0.51
7:i:311:LEU:HD13	7:i:345:VAL:HB	1.91	0.51
11:2:788:A:P	16:E:108:ARG:HH22	2.33	0.51
11:2:1631:A:H5'	11:2:1633:A:H5''	1.91	0.51
11:2:1651:A:N6	11:2:1749:A:H61	2.08	0.51
15:D:8:LYS:HE2	31:U:61:LYS:HZ1	1.75	0.51
29:S:106:GLU:O	29:S:110:ARG:HG2	2.10	0.51
33:W:55:ASP:O	33:W:57:ARG:HG2	2.10	0.51
6:h:184:THR:HB	25:O:93:THR:HG21	1.92	0.51
11:2:773:C:H5''	16:E:21:ASP:HB2	1.93	0.51
11:2:1654:G:H4'	11:2:1655:A:H8	1.76	0.51
19:H:154:LEU:HD11	19:H:183:PHE:HD2	1.76	0.51
28:R:21:TYR:N	28:R:22:PRO:HD2	2.26	0.51
6:h:98:LYS:HG2	6:h:138:GLU:HG2	1.93	0.51
7:i:332:VAL:O	7:i:336:THR:OG1	2.23	0.51
11:2:717:C:H2'	11:2:718:U:H5''	1.91	0.51
11:2:906:A:OP1	25:O:52:ARG:HG2	2.10	0.51
16:E:15:PRO:HG2	16:E:18:TRP:CE2	2.46	0.51
16:E:43:PRO:HA	16:E:82:TYR:O	2.11	0.51
17:F:80:LYS:HB2	17:F:83:ARG:HB2	1.91	0.51
10:l:45:SER:OG	10:l:46:GLN:N	2.44	0.51
10:l:192:ILE:HD13	10:l:250:VAL:HG21	1.93	0.51
11:2:1081:A:O2'	11:2:1083:G:N7	2.40	0.51
11:2:1284:C:H2'	11:2:1286:U:O2'	2.10	0.51
13:B:127:VAL:HG13	13:B:176:VAL:HG11	1.93	0.51
15:D:70:THR:HG22	15:D:86:LEU:HB2	1.92	0.51
20:I:96:LEU:HD13	20:I:179:CYS:SG	2.51	0.51
5:g:36:ALA:HB2	5:g:71:CYS:HB3	1.91	0.51
10:l:273:VAL:HG11	10:l:292:SER:HB2	1.92	0.51
11:2:1054:U:H2'	11:2:1055:U:H6	1.76	0.51
11:2:1386:G:OP2	28:R:44:LYS:NZ	2.34	0.51
17:F:23:VAL:HG21	27:Q:58:ASP:HB3	1.92	0.51
17:F:46:TRP:NE1	17:F:129:PRO:HG2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:M:60:VAL:HB	23:M:88:LEU:HD22	1.92	0.51
26:P:63:ALA:HB1	26:P:74:ALA:HB3	1.91	0.51
30:T:105:LEU:HD22	30:T:122:ARG:HG2	1.93	0.51
36:Z:62:VAL:HG13	36:Z:76:ALA:HB3	1.91	0.51
6:h:102:PRO:HG2	6:h:105:ARG:HB3	1.92	0.51
9:k:529:LEU:HD23	9:k:660:VAL:HG21	1.92	0.51
10:l:33:PRO:HD2	10:l:36:LEU:HD12	1.92	0.51
11:2:1151:A:N6	11:2:1627:U:H3	2.03	0.51
5:g:191:ASP:OD2	15:D:225:TYR:OH	2.27	0.51
7:i:240:ARG:N	8:j:391:GLU:OE2	2.41	0.51
18:G:163:THR:HG22	18:G:168:THR:HG23	1.93	0.51
21:J:2:PRO:C	21:J:3:ARG:HD3	2.35	0.51
6:h:95:GLU:HG2	6:h:152:LEU:HD22	1.93	0.51
9:k:186:ALA:N	9:k:250:ILE:HD11	2.26	0.51
10:l:12:THR:HG22	10:l:13:THR:H	1.76	0.51
10:l:45:SER:HB2	34:X:66:SER:HB3	1.93	0.51
11:2:46:A:N6	11:2:433:C:H4'	2.26	0.51
11:2:1206:U:H3'	11:2:1207:C:H5''	1.92	0.51
11:2:1467:C:H4'	11:2:1601:G:H4'	1.93	0.51
16:E:118:GLU:HA	16:E:121:TYR:HE1	1.76	0.51
24:N:115:LEU:HD13	24:N:119:GLU:HG3	1.93	0.51
10:l:83:LEU:O	10:l:87:THR:OG1	2.27	0.50
11:2:1220:C:H2'	11:2:1221:A:C8	2.46	0.50
11:2:1384:A:H2'	11:2:1385:G:O4'	2.11	0.50
16:E:99:PHE:HE1	16:E:113:ARG:HE	1.60	0.50
19:H:173:TYR:O	19:H:177:THR:HG22	2.11	0.50
11:2:780:A:C2	35:Y:8:ARG:HD3	2.43	0.50
11:2:1561:U:H2'	11:2:1562:G:H8	1.77	0.50
29:S:18:LEU:HD21	29:S:101:LEU:HD13	1.93	0.50
29:S:68:ARG:O	29:S:72:ILE:HG13	2.12	0.50
11:2:324:U:C2	11:2:325:G:C8	2.99	0.50
11:2:1137:A:OP1	34:X:112:LYS:HA	2.12	0.50
11:2:1673:G:H2'	11:2:1674:C:C6	2.46	0.50
12:A:201:LEU:HA	12:A:205:ARG:HH21	1.74	0.50
30:T:118:PRO:HD2	30:T:123:ARG:NH2	2.26	0.50
7:i:326:VAL:HA	7:i:330:CYS:HB2	1.94	0.50
11:2:1042:G:H22	11:2:1076:A:H2	1.60	0.50
11:2:1043:A:O3'	13:B:152:ARG:NH1	2.42	0.50
11:2:1270:G:H1	11:2:1440:C:H42	1.60	0.50
28:R:50:ILE:O	28:R:54:THR:HG23	2.11	0.50
5:g:240:VAL:HG22	5:g:256:THR:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:709:ARG:HD3	11:2:1209:C:OP2	2.12	0.50
10:l:6:SER:O	10:l:9:ARG:HG2	2.11	0.50
10:l:149:ALA:O	10:l:153:HIS:HB2	2.10	0.50
15:D:32:GLU:HG3	15:D:57:ASP:HB2	1.94	0.50
2:c:11:LYS:HB2	2:c:31:GLU:O	2.12	0.50
7:i:303:ILE:O	7:i:307:VAL:HG23	2.12	0.50
11:2:86:A:H2'	11:2:87:C:H6	1.77	0.50
11:2:347:G:H5'	22:L:80:MET:HE1	1.92	0.50
11:2:1387:G:H1'	11:2:1410:A:N6	2.27	0.50
24:N:112:LYS:O	24:N:116:ILE:HG13	2.11	0.50
10:l:220:LEU:HD22	10:l:227:HIS:HE1	1.77	0.50
16:E:147:ILE:HG21	16:E:169:ILE:HG13	1.94	0.50
18:G:137:ARG:HH21	18:G:177:ARG:NE	2.09	0.50
23:M:108:ARG:O	23:M:110:GLY:N	2.44	0.50
11:2:30:G:H4'	34:X:131:SER:HB2	1.94	0.50
11:2:1057:U:H1'	11:2:1058:U:H2'	1.92	0.50
11:2:1229:G:H4'	11:2:1230:A:OP1	2.12	0.50
20:I:34:ALA:HB2	20:I:56:ARG:HD3	1.93	0.50
23:M:28:LEU:HD23	23:M:91:VAL:HG13	1.93	0.50
5:g:129:LYS:HA	5:g:151:VAL:HG23	1.93	0.50
11:2:564:G:N2	11:2:577:G:O2'	2.44	0.50
11:2:810:G:H2'	19:H:111:LYS:HB2	1.92	0.50
11:2:1488:G:H3'	11:2:1515:A:H61	1.76	0.50
11:2:1514:U:C6	15:D:4:LEU:HD11	2.46	0.50
12:A:30:GLN:HE22	12:A:152:PRO:HA	1.76	0.50
12:A:124:THR:HG22	12:A:174:TRP:NE1	2.23	0.50
27:Q:36:ILE:HD13	27:Q:52:LEU:HD11	1.92	0.50
6:h:158:PHE:HD2	6:h:159:ILE:HD13	1.77	0.49
9:k:525:TRP:NE1	9:k:530:ARG:HH22	2.10	0.49
9:k:543:LYS:O	9:k:547:ASN:ND2	2.45	0.49
10:l:266:ASP:HA	10:l:295:LEU:HD13	1.94	0.49
11:2:1735:U:H2'	11:2:1736:G:C8	2.47	0.49
14:C:111:VAL:HG13	14:C:191:ALA:HB2	1.94	0.49
19:H:141:ARG:HH21	19:H:143:LEU:HD21	1.77	0.49
28:R:26:LEU:HD22	28:R:59:LYS:HG3	1.93	0.49
9:k:399:TYR:HE2	26:P:100:LYS:HD3	1.77	0.49
11:2:625:C:H2'	11:2:626:U:C6	2.46	0.49
11:2:1254:U:OP2	23:M:124:LYS:NZ	2.44	0.49
11:2:1689:A:H61	11:2:1712:A:N6	2.07	0.49
15:D:137:VAL:HG22	15:D:151:LYS:HG2	1.95	0.49
10:l:163:TYR:CE1	10:l:179:PRO:HB2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:153:G:P	35:Y:131:ARG:HH22	2.35	0.49
12:A:76:ILE:HD13	12:A:98:ILE:HB	1.93	0.49
13:B:123:ALA:HB2	13:B:165:ARG:HG2	1.95	0.49
9:k:86:ILE:HG13	9:k:157:PHE:HB2	1.94	0.49
10:l:192:ILE:HG21	10:l:250:VAL:HG21	1.94	0.49
11:2:260:U:C5	20:I:43:ILE:HB	2.46	0.49
11:2:1263:G:H2'	11:2:1264:G:C8	2.47	0.49
11:2:1587:A:H2'	11:2:1588:G:C8	2.47	0.49
14:C:227:PRO:HA	14:C:230:TRP:CE2	2.47	0.49
27:Q:16:ALA:HB2	27:Q:72:GLY:HA3	1.94	0.49
11:2:214:G:O2'	11:2:242:U:O4	2.24	0.49
11:2:284:G:N7	18:G:188:ARG:NH1	2.61	0.49
11:2:1560:U:H2'	11:2:1561:U:O4'	2.13	0.49
11:2:1678:A:OP1	20:I:59:ARG:NH2	2.40	0.49
27:Q:36:ILE:HD11	27:Q:48:VAL:HG12	1.95	0.49
28:R:84:TYR:O	28:R:86:PRO:HD3	2.12	0.49
2:c:12:VAL:HG21	2:c:48:VAL:HG11	1.95	0.49
5:g:20:VAL:HG11	5:g:310:ILE:HG12	1.94	0.49
6:h:272:GLU:HG2	17:F:152:GLY:HA2	1.93	0.49
11:2:1330:G:H3'	11:2:1331:A:H8	1.77	0.49
12:A:37:VAL:HG22	12:A:149:LEU:HD13	1.94	0.49
17:F:146:THR:HG23	17:F:221:ALA:HA	1.95	0.49
19:H:129:LEU:HD13	19:H:169:PHE:HB3	1.94	0.49
20:I:48:THR:HG21	20:I:54:LYS:HE3	1.93	0.49
35:Y:53:ASP:HB3	35:Y:96:LEU:HD22	1.93	0.49
6:h:211:LYS:NZ	11:2:1628:U:H5''	2.27	0.49
11:2:839:U:H2'	11:2:840:U:H5'	1.95	0.49
11:2:903:U:H2'	11:2:905:A:OP2	2.11	0.49
13:B:86:LEU:HD13	13:B:100:PHE:HA	1.94	0.49
17:F:76:ARG:HD3	27:Q:122:ARG:HG3	1.94	0.49
19:H:114:ARG:HA	19:H:117:THR:HG23	1.93	0.49
3:d:38:ILE:HB	3:d:43:PHE:HB2	1.93	0.49
11:2:86:A:H2'	11:2:87:C:C6	2.47	0.49
11:2:195:G:H2'	11:2:196:G:H5'	1.94	0.49
19:H:90:VAL:O	19:H:165:LYS:NZ	2.45	0.49
27:Q:44:LEU:HD11	27:Q:75:VAL:HG22	1.94	0.49
30:T:28:LEU:HD12	30:T:55:TYR:HD1	1.78	0.49
11:2:791:A:OP1	16:E:187:ARG:NH2	2.46	0.49
11:2:1077:C:O2'	11:2:1078:C:H5'	2.13	0.49
12:A:63:ILE:O	12:A:67:ILE:HD12	2.12	0.49
16:E:22:LYS:O	16:E:23:LEU:HD23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G:14:LYS:HD2	18:G:123:GLY:HA3	1.95	0.49
7:i:263:THR:HG21	7:i:306:ALA:O	2.13	0.49
7:i:389:ASP:OD2	8:j:361:TYR:OH	2.29	0.49
9:k:737:THR:O	9:k:740:GLY:N	2.42	0.49
16:E:102:VAL:HG12	16:E:182:TYR:CE1	2.47	0.49
17:F:144:GLU:OE1	17:F:225:ARG:NH2	2.46	0.49
17:F:150:GLY:O	17:F:155:ALA:HA	2.13	0.49
28:R:30:THR:O	28:R:34:LEU:HB2	2.12	0.49
31:U:87:HIS:HB3	31:U:89:ARG:HH12	1.77	0.49
17:F:51:VAL:HG13	17:F:134:VAL:HG21	1.95	0.48
20:I:50:GLY:O	20:I:52:ASN:N	2.46	0.48
28:R:5:ARG:O	28:R:10:LYS:NZ	2.33	0.48
7:i:304:TYR:CE1	7:i:341:VAL:HG22	2.47	0.48
9:k:188:TYR:CE1	9:k:220:PHE:HB3	2.48	0.48
9:k:288:ASN:ND2	9:k:290:ASN:H	2.11	0.48
11:2:1511:U:H2'	11:2:1512:G:C8	2.48	0.48
16:E:103:TYR:CD2	16:E:189:LEU:HD11	2.47	0.48
21:J:49:LEU:HD23	21:J:104:PHE:HE1	1.77	0.48
25:O:61:MET:HE1	25:O:107:ARG:HH11	1.77	0.48
5:g:40:LYS:HG2	5:g:66:HIS:C	2.38	0.48
9:k:259:VAL:HG23	9:k:287:PHE:HE2	1.79	0.48
9:k:278:ILE:HD13	9:k:581:VAL:HG21	1.94	0.48
11:2:15:U:H2'	11:2:16:G:O4'	2.13	0.48
11:2:750:U:OP1	33:W:120:HIS:HE1	1.96	0.48
11:2:868:G:OP1	24:N:121:ARG:NH1	2.46	0.48
11:2:1590:G:H2'	11:2:1591:C:C6	2.49	0.48
13:B:223:PHE:HE2	13:B:225:VAL:HG22	1.78	0.48
20:I:83:TYR:HE1	20:I:199:LYS:NZ	2.10	0.48
20:I:153:GLU:HG2	20:I:154:SER:H	1.78	0.48
23:M:63:VAL:HG21	23:M:94:ALA:HA	1.95	0.48
23:M:126:TRP:CD1	23:M:133:LEU:HD13	2.48	0.48
5:g:209:THR:HG22	5:g:226:ALA:HB2	1.94	0.48
7:i:284:LEU:HD11	7:i:325:LEU:HB2	1.94	0.48
9:k:305:LYS:HB3	9:k:560:PHE:HB2	1.96	0.48
9:k:372:ALA:HB3	9:k:733:ILE:HD11	1.95	0.48
11:2:317:C:H2'	11:2:318:U:H6	1.77	0.48
11:2:418:G:H1'	18:G:59:GLN:NE2	2.29	0.48
12:A:104:PRO:HB3	12:A:131:GLN:NE2	2.22	0.48
13:B:122:GLU:O	13:B:165:ARG:HD3	2.13	0.48
21:J:30:LEU:HD21	21:J:102:GLU:HG2	1.96	0.48
9:k:121:LYS:HB3	9:k:124:PHE:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:l:31:VAL:HG12	10:l:72:GLY:HA3	1.95	0.48
11:2:1222:C:H2'	11:2:1223:A:C8	2.48	0.48
11:2:1382:A:H4'	31:U:89:ARG:NH1	2.28	0.48
27:Q:46:PHE:HA	27:Q:49:TYR:HD1	1.78	0.48
6:h:182:ILE:HA	6:h:233:ILE:O	2.13	0.48
9:k:504:LEU:HD11	9:k:512:TRP:HE1	1.78	0.48
10:l:100:THR:HG22	10:l:110:TYR:CD2	2.49	0.48
11:2:525:A:H5''	35:Y:89:TYR:CE2	2.48	0.48
13:B:134:VAL:HG12	13:B:218:LEU:HB2	1.96	0.48
14:C:189:GLN:C	14:C:191:ALA:H	2.22	0.48
18:G:135:PRO:HB2	18:G:141:ILE:HG12	1.96	0.48
11:2:283:U:H5''	18:G:188:ARG:HD3	1.95	0.48
11:2:406:U:H2'	11:2:407:A:C8	2.49	0.48
11:2:472:U:H5''	21:J:11:THR:OG1	2.13	0.48
11:2:1181:U:H2'	11:2:1182:U:O4'	2.14	0.48
11:2:1381:U:H4'	31:U:59:PRO:HG3	1.96	0.48
12:A:4:PRO:HD2	12:A:7:PHE:CE1	2.49	0.48
18:G:39:GLU:HB2	18:G:46:LYS:HA	1.96	0.48
22:L:78:THR:HG23	22:L:84:ILE:HG22	1.95	0.48
11:2:804:A:N3	33:W:105:THR:HG22	2.28	0.48
11:2:825:U:H3	11:2:847:A:H61	1.62	0.48
11:2:861:U:O2'	33:W:56:HIS:O	2.30	0.48
19:H:28:GLU:H	19:H:28:GLU:HG2	1.45	0.48
22:L:97:TYR:O	22:L:99:ARG:HG2	2.14	0.48
26:P:60:LEU:HA	26:P:76:VAL:HG21	1.96	0.48
26:P:90:ILE:HD13	26:P:109:PRO:HA	1.95	0.48
6:h:106:MET:O	6:h:109:LEU:HB3	2.13	0.48
7:i:226:HIS:CE1	11:2:1451:C:H5''	2.48	0.48
11:2:74:U:H1'	11:2:75:U:H5'	1.95	0.48
11:2:639:U:H1'	11:2:640:U:C5	2.49	0.48
11:2:799:A:H4'	16:E:201:HIS:CE1	2.49	0.48
12:A:70:PRO:HB3	12:A:185:ARG:NH2	2.28	0.48
34:X:95:PHE:CE2	34:X:135:LEU:HB3	2.49	0.48
7:i:300:ASN:HB3	7:i:303:ILE:HG12	1.96	0.48
7:i:337:ILE:HG23	11:2:1269:U:O4	2.13	0.48
7:i:358:TYR:CD2	8:j:369:GLU:HA	2.49	0.48
10:l:124:ILE:HG22	10:l:186:ILE:HG23	1.96	0.48
11:2:513:U:C4'	21:J:131:GLN:HG3	2.44	0.48
11:2:1524:A:H2'	11:2:1525:A:C8	2.48	0.48
11:2:1729:C:C5	11:2:1730:A:C8	3.02	0.48
12:A:195:TRP:HE3	12:A:196:SER:H	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:32:LYS:HE2	28:R:32:LYS:HB3	1.67	0.48
33:W:25:VAL:HG13	33:W:65:LEU:HD11	1.96	0.48
5:g:12:THR:HG22	5:g:311:ARG:HG2	1.96	0.47
10:l:234:ASN:HD21	10:l:253:ASP:HB2	1.79	0.47
11:2:95:G:H4'	16:E:8:HIS:CD2	2.48	0.47
11:2:212:U:H2'	11:2:213:A:H8	1.79	0.47
11:2:367:A:H2'	11:2:368:U:O4'	2.14	0.47
11:2:697:C:H42	11:2:741:C:H42	1.60	0.47
21:J:110:GLN:HE22	21:J:126:ARG:CG	2.22	0.47
24:N:34:ILE:HG13	24:N:67:THR:HG21	1.96	0.47
24:N:119:GLU:HA	24:N:122:ILE:HD12	1.95	0.47
7:i:311:LEU:HD12	7:i:341:VAL:HG12	1.95	0.47
9:k:500:ARG:HH22	9:k:519:PRO:HD2	1.78	0.47
9:k:551:ALA:HB1	9:k:557:ILE:HD11	1.96	0.47
9:k:670:PHE:HB3	9:k:682:LEU:HD23	1.96	0.47
9:k:711:HIS:O	9:k:713:THR:N	2.48	0.47
11:2:300:A:H2'	11:2:301:A:C8	2.49	0.47
11:2:333:A:H5'	20:I:48:THR:HB	1.95	0.47
11:2:539:G:C4'	11:2:540:G:H5'	2.44	0.47
11:2:1334:U:H3	11:2:1417:A:H61	1.62	0.47
11:2:1397:U:O2'	11:2:1400:A:N6	2.47	0.47
11:2:1561:U:H2'	11:2:1562:G:C8	2.49	0.47
12:A:127:ARG:NH2	12:A:152:PRO:HD3	2.29	0.47
14:C:129:ILE:O	14:C:133:LYS:HG2	2.15	0.47
11:2:1064:G:H2'	11:2:1065:A:C8	2.49	0.47
13:B:191:GLU:HB3	13:B:194:ASN:HD21	1.79	0.47
16:E:65:LEU:HD23	16:E:65:LEU:HA	1.76	0.47
17:F:26:ALA:HB3	27:Q:28:LEU:HB2	1.96	0.47
20:I:107:THR:HG23	20:I:108:PRO:HD3	1.96	0.47
30:T:66:TYR:HA	30:T:124:ILE:HG21	1.96	0.47
11:2:919:A:H2'	11:2:920:U:C6	2.48	0.47
11:2:1573:A:H61	17:F:102:ARG:HH12	1.62	0.47
12:A:90:ALA:O	12:A:94:GLY:N	2.44	0.47
12:A:168:HIS:CG	12:A:203:PHE:HE2	2.32	0.47
17:F:77:TYR:CD2	17:F:83:ARG:HG2	2.48	0.47
3:d:42:CYS:O	3:d:46:LYS:HG2	2.15	0.47
9:k:357:TRP:HE3	9:k:526:LYS:HB3	1.79	0.47
10:l:197:MET:HB3	10:l:279:PHE:CZ	2.48	0.47
11:2:209:U:O3'	20:I:170:SER:OG	2.28	0.47
11:2:388:G:OP2	11:2:423:G:O2'	2.33	0.47
11:2:574:G:N2	11:2:582:U:H1'	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:27:LYS:HA	13:B:49:ASN:O	2.15	0.47
13:B:30:PHE:CD2	13:B:94:LYS:HA	2.49	0.47
13:B:88:VAL:HA	13:B:98:THR:HG23	1.96	0.47
13:B:115:ARG:H	13:B:118:GLN:HE21	1.62	0.47
25:O:47:LYS:NZ	25:O:62:LEU:HB3	2.29	0.47
30:T:86:ARG:NH2	30:T:89:ARG:HD3	2.28	0.47
9:k:482:PHE:HB3	9:k:485:GLU:CD	2.40	0.47
11:2:1043:A:C6	11:2:1044:U:N3	2.83	0.47
11:2:1780:G:N2	11:2:1782:A:H5''	2.30	0.47
12:A:200:ASP:OD1	12:A:200:ASP:N	2.47	0.47
13:B:61:LEU:O	13:B:88:VAL:HB	2.15	0.47
28:R:45:ARG:CZ	28:R:49:LYS:HE2	2.45	0.47
7:i:290:ASN:O	7:i:294:SER:OG	2.29	0.47
10:l:36:LEU:HD22	10:l:40:ILE:HD11	1.97	0.47
11:2:94:U:OP1	16:E:2:ALA:HB1	2.14	0.47
11:2:407:A:H2'	11:2:408:C:C6	2.50	0.47
11:2:1143:A:H8	11:2:1143:A:O5'	1.98	0.47
11:2:1349:G:H1	11:2:1376:C:H42	1.63	0.47
11:2:1457:C:O2'	11:2:1458:G:O5'	2.28	0.47
14:C:116:LYS:HG2	14:C:127:ALA:HB3	1.97	0.47
16:E:185:GLY:H	16:E:224:ASN:HB3	1.80	0.47
17:F:54:LYS:HB2	17:F:138:THR:HG21	1.97	0.47
26:P:108:ARG:NH1	29:S:118:LYS:O	2.48	0.47
27:Q:129:PHE:HB2	31:U:80:GLU:HA	1.97	0.47
30:T:73:VAL:HG22	30:T:105:LEU:HD12	1.97	0.47
34:X:53:VAL:HG22	34:X:72:VAL:HG11	1.97	0.47
10:l:22:VAL:HG11	10:l:62:ILE:HD11	1.97	0.47
11:2:1266:U:H3'	11:2:1267:G:C8	2.50	0.47
11:2:1654:G:H5''	11:2:1655:A:OP1	2.15	0.47
11:2:1760:G:H3'	11:2:1761:U:H5''	1.95	0.47
12:A:56:LYS:HA	12:A:56:LYS:HD2	1.71	0.47
12:A:121:VAL:HG23	12:A:141:ILE:HG21	1.95	0.47
12:A:168:HIS:HE1	28:R:90:ALA:HB3	1.80	0.47
17:F:99:MET:HB3	17:F:180:ARG:CZ	2.44	0.47
17:F:222:LYS:HG2	17:F:225:ARG:NH2	2.30	0.47
21:J:37:LYS:HG3	21:J:38:ASN:OD1	2.14	0.47
25:O:43:THR:O	25:O:46:MET:HG2	2.14	0.47
26:P:58:LYS:O	26:P:61:ARG:HG2	2.14	0.47
5:g:136:ILE:HD13	5:g:136:ILE:H	1.79	0.47
6:h:125:LYS:HD3	6:h:146:THR:H	1.80	0.47
9:k:374:TYR:CZ	9:k:377:HIS:HB2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:518:A:C2	11:2:519:C:H5	2.33	0.47
11:2:1461:C:H2'	11:2:1462:G:H8	1.79	0.47
14:C:233:GLN:NE2	32:V:13:VAL:HG11	2.29	0.47
21:J:79:ARG:HH11	21:J:79:ARG:HG3	1.79	0.47
30:T:85:SER:HB2	30:T:91:TYR:CE2	2.50	0.47
33:W:126:LEU:HA	33:W:126:LEU:HD23	1.70	0.47
7:i:358:TYR:CE2	8:j:369:GLU:HA	2.50	0.47
9:k:498:LEU:HD13	9:k:773:LEU:HD12	1.97	0.47
11:2:523:G:H5'	35:Y:60:PHE:O	2.15	0.47
14:C:215:PHE:HA	14:C:218:ILE:HD11	1.97	0.47
5:g:63:GLY:HA3	5:g:92:TRP:HH2	1.80	0.46
6:h:185:PHE:HD1	6:h:231:ILE:HD11	1.81	0.46
11:2:61:A:N1	11:2:62:A:N6	2.63	0.46
11:2:872:G:H2'	11:2:873:U:O4'	2.15	0.46
11:2:1286:U:H3'	11:2:1287:A:H5'	1.97	0.46
11:2:1684:U:H2'	11:2:1685:G:H8	1.81	0.46
13:B:223:PHE:CE2	13:B:225:VAL:HG22	2.50	0.46
11:2:928:U:H4'	11:2:929:A:H5'	1.97	0.46
11:2:1382:A:H2'	11:2:1383:G:O4'	2.15	0.46
11:2:1764:C:H2'	11:2:1765:A:C8	2.50	0.46
11:2:1783:C:H2'	11:2:1784:C:H6	1.79	0.46
12:A:144:ILE:HG12	12:A:158:VAL:HB	1.96	0.46
13:B:197:ILE:O	13:B:201:THR:HB	2.15	0.46
15:D:120:TYR:O	15:D:124:ARG:HB2	2.15	0.46
15:D:159:HIS:HD2	15:D:187:LYS:HE2	1.80	0.46
16:E:181:VAL:HG11	16:E:225:VAL:HG13	1.97	0.46
17:F:88:PRO:HG2	17:F:91:GLU:OE1	2.16	0.46
22:L:94:ILE:HA	22:L:95:PRO:HD3	1.64	0.46
26:P:78:THR:HG22	26:P:80:MET:H	1.81	0.46
28:R:79:GLU:O	28:R:83:GLN:HG3	2.15	0.46
30:T:22:LEU:HD13	30:T:28:LEU:HD11	1.96	0.46
36:Z:58:ARG:HH11	36:Z:103:ARG:HE	1.62	0.46
10:l:84:ALA:HB1	10:l:183:SER:HB2	1.97	0.46
11:2:1025:A:HO2'	11:2:1773:C:HO2'	1.62	0.46
11:2:1060:U:H2'	11:2:1061:A:O4'	2.16	0.46
12:A:111:ILE:HD12	12:A:111:ILE:HA	1.68	0.46
12:A:192:THR:O	12:A:194:PRO:HD3	2.15	0.46
12:A:200:ASP:OD2	28:R:89:SER:HB3	2.15	0.46
15:D:132:LYS:HB3	15:D:189:MET:HG3	1.97	0.46
17:F:117:THR:HG23	17:F:195:ALA:HB2	1.97	0.46
21:J:148:VAL:HG12	21:J:149:ARG:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Q:37:THR:HA	27:Q:49:TYR:OH	2.15	0.46
27:Q:59:LYS:HE2	27:Q:59:LYS:HB2	1.78	0.46
34:X:70:LYS:HA	34:X:70:LYS:HD3	1.65	0.46
5:g:61:PHE:CE2	5:g:97:GLY:HA2	2.50	0.46
7:i:366:PRO:O	7:i:370:VAL:HG23	2.15	0.46
10:l:52:ALA:O	10:l:56:LEU:HG	2.15	0.46
11:2:539:G:N2	11:2:539:G:OP2	2.49	0.46
11:2:829:A:N6	11:2:843:U:H3	2.11	0.46
11:2:1525:A:H2'	11:2:1526:A:C8	2.51	0.46
11:2:1534:G:O6	36:Z:77:ARG:NH2	2.48	0.46
16:E:216:ASN:OD1	16:E:217:THR:N	2.49	0.46
17:F:133:VAL:O	17:F:137:ILE:HG12	2.15	0.46
19:H:173:TYR:CE1	19:H:177:THR:HG21	2.50	0.46
7:i:335:ALA:CB	7:i:367:PRO:HB3	2.45	0.46
7:i:391:VAL:HG22	7:i:440:LEU:HD11	1.98	0.46
11:2:138:A:H61	11:2:266:A:H61	1.62	0.46
11:2:322:G:N1	11:2:337:G:C6	2.84	0.46
11:2:778:G:N2	35:Y:10:ARG:HH21	2.14	0.46
11:2:1254:U:O2'	11:2:1255:G:H5'	2.15	0.46
11:2:1285:U:H5'	11:2:1286:U:H4'	1.97	0.46
11:2:1590:G:OP1	30:T:91:TYR:HB2	2.15	0.46
12:A:66:ALA:HB2	32:V:37:ALA:HB2	1.96	0.46
12:A:88:LYS:O	12:A:92:HIS:HD2	1.99	0.46
2:c:19:THR:HB	2:c:66:LEU:HB2	1.97	0.46
10:l:46:GLN:HB3	11:2:568:G:O2'	2.16	0.46
10:l:69:LYS:NZ	14:C:87:GLN:HG3	2.30	0.46
11:2:459:G:OP2	35:Y:105:ARG:NH1	2.46	0.46
11:2:1256:A:H5'	11:2:1257:U:C5	2.50	0.46
13:B:151:LYS:C	13:B:153:HIS:H	2.23	0.46
17:F:36:ALA:O	17:F:41:LYS:HB2	2.15	0.46
17:F:187:ILE:H	17:F:187:ILE:HD12	1.80	0.46
18:G:2:LYS:HB3	18:G:108:VAL:HG22	1.98	0.46
26:P:86:VAL:O	26:P:89:MET:HG2	2.16	0.46
28:R:57:LEU:O	28:R:61:ILE:HG13	2.16	0.46
33:W:57:ARG:HG2	33:W:57:ARG:H	1.45	0.46
7:i:236:ILE:HG22	7:i:242:TRP:HB2	1.97	0.46
11:2:163:G:H2'	11:2:164:A:H8	1.80	0.46
11:2:328:A:H2'	11:2:329:G:C8	2.50	0.46
11:2:573:C:H2'	11:2:574:G:O4'	2.16	0.46
11:2:1548:G:H4'	29:S:90:ASN:HB2	1.98	0.46
12:A:10:THR:HG22	12:A:11:PRO:HD2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:63:ILE:HG22	12:A:120:LEU:HD22	1.97	0.46
18:G:18:ILE:HD12	18:G:24:ILE:HG12	1.98	0.46
33:W:81:VAL:O	33:W:122:SER:OG	2.30	0.46
3:d:22:ARG:HA	7:i:295:GLU:HG2	1.98	0.46
5:g:42:LEU:HD21	5:g:82:SER:HB3	1.97	0.46
9:k:484:ASP:OD2	9:k:700:ARG:NH1	2.48	0.46
9:k:676:ASP:OD1	9:k:677:ALA:N	2.48	0.46
11:2:66:U:H5'	18:G:173:PRO:HA	1.98	0.46
11:2:602:U:H2'	11:2:603:U:C6	2.50	0.46
11:2:654:C:H3'	11:2:655:G:C5'	2.46	0.46
11:2:687:G:H5'	33:W:119:LYS:HG2	1.97	0.46
11:2:1290:U:H2'	11:2:1291:G:C8	2.51	0.46
11:2:1539:G:H4'	29:S:40:ARG:CZ	2.46	0.46
15:D:34:TYR:HE1	15:D:37:VAL:HG13	1.80	0.46
16:E:43:PRO:HG2	16:E:46:VAL:CG2	2.45	0.46
19:H:126:LEU:HD11	19:H:181:ILE:HD12	1.98	0.46
23:M:33:ARG:HB2	23:M:100:TRP:CE3	2.44	0.46
23:M:33:ARG:HH21	23:M:108:ARG:HH21	1.64	0.46
28:R:82:ASP:O	28:R:85:VAL:HG23	2.16	0.46
6:h:112:SER:O	6:h:116:ILE:HG13	2.15	0.46
11:2:330:G:O2'	20:I:33:PRO:HB3	2.15	0.46
11:2:540:G:OP2	11:2:541:A:H5'	2.16	0.46
11:2:541:A:H4'	11:2:542:A:OP2	2.16	0.46
11:2:948:G:H2'	11:2:949:C:C6	2.51	0.46
11:2:1513:G:O2'	11:2:1515:A:N3	2.37	0.46
26:P:85:ILE:HG22	26:P:112:LEU:HD23	1.97	0.46
5:g:260:ILE:HB	5:g:274:LEU:HB2	1.98	0.46
6:h:97:ARG:HH12	6:h:153:GLN:HA	1.81	0.46
6:h:226:LEU:HD22	6:h:231:ILE:HG22	1.96	0.46
11:2:400:A:H4'	11:2:401:A:H5'	1.98	0.46
11:2:448:C:OP1	16:E:29:PRO:HD3	2.16	0.46
11:2:1005:A:H2'	11:2:1006:C:O2	2.16	0.46
15:D:57:ASP:O	15:D:65:ARG:HD2	2.16	0.46
16:E:67:GLN:HB2	16:E:69:HIS:CD2	2.52	0.46
17:F:164:PRO:O	17:F:168:VAL:HG23	2.16	0.46
19:H:28:GLU:HB2	19:H:35:LYS:HG3	1.96	0.46
28:R:61:ILE:HG12	28:R:66:VAL:HG21	1.97	0.46
30:T:131:ASP:O	30:T:135:ILE:HG23	2.16	0.46
6:h:142:ASN:HD22	6:h:145:PHE:HE2	1.64	0.45
10:l:192:ILE:O	10:l:194:GLY:N	2.48	0.45
11:2:331:A:H5'	20:I:33:PRO:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:332:U:OP1	20:I:56:ARG:NH2	2.49	0.45
11:2:1063:U:H3'	11:2:1064:G:H8	1.81	0.45
11:2:1102:G:OP1	33:W:76:SER:OG	2.32	0.45
11:2:1513:G:H2'	11:2:1514:U:H5''	1.98	0.45
18:G:31:ARG:HG2	18:G:34:GLN:NE2	2.31	0.45
20:I:153:GLU:HG2	20:I:154:SER:N	2.32	0.45
21:J:158:PHE:CD2	21:J:164:PHE:HB2	2.51	0.45
23:M:24:ILE:HG22	23:M:89:ILE:HD11	1.97	0.45
23:M:69:ALA:O	23:M:73:LYS:N	2.43	0.45
25:O:43:THR:O	25:O:45:GLY:N	2.50	0.45
30:T:67:MET:HE2	30:T:68:ARG:HH21	1.81	0.45
11:2:209:U:H2'	11:2:210:A:H8	1.80	0.45
12:A:120:LEU:HD12	12:A:121:VAL:N	2.31	0.45
16:E:178:GLY:HA2	16:E:194:THR:CG2	2.46	0.45
23:M:91:VAL:HG21	23:M:97:LEU:HD13	1.98	0.45
30:T:28:LEU:HD12	30:T:55:TYR:CD1	2.50	0.45
31:U:72:ASN:O	31:U:74:GLU:N	2.44	0.45
33:W:15:ASN:HD22	33:W:19:LYS:HE3	1.80	0.45
33:W:42:GLN:NE2	33:W:49:GLU:HA	2.32	0.45
5:g:248:ASN:OD1	5:g:249:ARG:N	2.44	0.45
11:2:852:C:O2'	11:2:853:G:H8	1.98	0.45
11:2:1120:U:H2'	11:2:1121:C:C6	2.52	0.45
13:B:32:ILE:HG23	13:B:44:GLY:O	2.16	0.45
15:D:25:PHE:CD2	15:D:37:VAL:HG11	2.51	0.45
22:L:124:THR:HB	22:L:141:LYS:HB3	1.97	0.45
32:V:73:ALA:HB1	32:V:78:LEU:HB2	1.99	0.45
2:c:32:PHE:HD2	2:c:35:ASP:H	1.65	0.45
11:2:207:U:O2	20:I:178:ARG:NH1	2.49	0.45
11:2:886:U:OP1	13:B:214:LYS:NZ	2.47	0.45
12:A:84:ARG:HH12	28:R:81:LYS:HB3	1.81	0.45
16:E:159:THR:OG1	16:E:227:VAL:HB	2.16	0.45
17:F:57:SER:HB2	17:F:164:PRO:HB3	1.99	0.45
35:Y:10:ARG:HD2	35:Y:26:ASP:OD2	2.17	0.45
36:Z:55:PRO:HA	36:Z:103:ARG:HB2	1.98	0.45
6:h:196:ASP:HB3	6:h:200:ARG:NH1	2.31	0.45
9:k:730:PHE:HB3	9:k:771:MET:HE1	1.98	0.45
11:2:896:U:O2	25:O:41:ARG:NH1	2.50	0.45
11:2:980:G:H4'	11:2:1776:A:H4'	1.97	0.45
11:2:1242:A:OP2	26:P:59:LYS:NZ	2.42	0.45
17:F:132:VAL:HG13	17:F:202:ALA:HB2	1.97	0.45
29:S:104:ASN:O	29:S:108:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:32:ARG:NH2	11:2:1596:C:OP2	2.48	0.45
9:k:357:TRP:CE3	9:k:526:LYS:HB3	2.52	0.45
9:k:702:ILE:HA	9:k:771:MET:O	2.16	0.45
10:l:37:ILE:HG21	10:l:53:ILE:HD11	1.98	0.45
10:l:108:ASP:HB2	10:l:124:ILE:HG12	1.97	0.45
11:2:48:G:C6	11:2:432:G:C2	3.05	0.45
11:2:765:G:N1	21:J:149:ARG:HG3	2.31	0.45
11:2:1533:C:H5	36:Z:77:ARG:HH22	1.64	0.45
13:B:131:ASP:CG	13:B:180:THR:HG22	2.42	0.45
14:C:178:ILE:HD12	14:C:189:GLN:HG3	1.98	0.45
19:H:109:VAL:HG12	19:H:110:GLN:O	2.15	0.45
25:O:64:ALA:HB1	25:O:105:LEU:HD23	1.99	0.45
29:S:45:LEU:HD11	30:T:36:ILE:HG12	1.98	0.45
32:V:16:LYS:HB2	32:V:16:LYS:HE3	1.74	0.45
36:Z:65:LEU:HD22	36:Z:71:ILE:HD12	1.99	0.45
11:2:320:U:O2'	11:2:321:C:H5'	2.16	0.45
11:2:1356:U:H2'	11:2:1357:A:H8	1.81	0.45
11:2:1615:C:C5	17:F:81:ARG:HB3	2.51	0.45
11:2:1799:U:H2'	11:2:1800:A:C8	2.51	0.45
14:C:39:THR:C	14:C:41:LEU:H	2.24	0.45
14:C:208:GLU:OE2	14:C:208:GLU:N	2.36	0.45
16:E:179:LYS:O	16:E:194:THR:HA	2.17	0.45
23:M:29:LYS:HB3	23:M:100:TRP:CD1	2.51	0.45
29:S:129:TRP:CE2	29:S:133:VAL:HG21	2.51	0.45
6:h:129:ARG:HD2	6:h:140:ARG:NH2	2.32	0.45
10:l:166:MET:HB2	10:l:166:MET:HE2	1.67	0.45
11:2:380:U:N3	21:J:5:PRO:HB3	2.31	0.45
11:2:585:A:H2'	11:2:586:G:C8	2.51	0.45
11:2:918:U:H2'	11:2:919:A:C8	2.52	0.45
11:2:1533:C:H4'	11:2:1539:G:N1	2.31	0.45
13:B:172:LEU:HD23	13:B:172:LEU:HA	1.84	0.45
14:C:211:LEU:HD23	14:C:211:LEU:HA	1.74	0.45
26:P:57:MET:HE1	26:P:89:MET:HE2	1.97	0.45
27:Q:49:TYR:HB3	27:Q:53:LEU:HD11	1.97	0.45
34:X:56:LYS:HE3	34:X:56:LYS:HB2	1.70	0.45
11:2:168:A:H2'	11:2:169:A:C8	2.52	0.45
11:2:718:U:H5	11:2:720:G:N7	2.15	0.45
12:A:126:PRO:HG2	12:A:151:SER:HB3	1.98	0.45
14:C:116:LYS:HG2	14:C:127:ALA:CB	2.47	0.45
14:C:153:SER:OG	14:C:154:LEU:N	2.47	0.45
17:F:121:ILE:HG23	17:F:199:ILE:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:123:VAL:HG12	36:Z:58:ARG:HG3	1.98	0.45
17:F:183:ALA:HB2	17:F:193:THR:OG1	2.16	0.45
19:H:49:ILE:HD12	19:H:172:VAL:HA	1.99	0.45
21:J:175:ARG:O	21:J:179:ARG:HG2	2.16	0.45
25:O:47:LYS:HA	25:O:47:LYS:HD2	1.68	0.45
30:T:4:VAL:HG12	30:T:140:LEU:HD13	1.99	0.45
33:W:66:ASN:HB2	33:W:67:GLY:H	1.56	0.45
36:Z:74:SER:O	36:Z:78:ILE:HG13	2.17	0.45
5:g:42:LEU:HD11	5:g:68:VAL:HG11	1.99	0.45
9:k:60:GLN:NE2	11:2:1661:U:O2	2.49	0.45
11:2:101:U:H5''	11:2:102:U:OP2	2.17	0.45
19:H:38:LEU:HD23	19:H:41:LEU:HD12	1.99	0.45
35:Y:8:ARG:HB2	35:Y:26:ASP:HB2	1.99	0.45
5:g:172:ALA:HB2	5:g:202:LEU:HB3	1.98	0.44
7:i:442:GLU:HG3	7:i:446:GLN:HE21	1.81	0.44
11:2:67:A:N6	11:2:83:G:O2'	2.50	0.44
11:2:106:U:OP1	20:I:8:ARG:NH2	2.50	0.44
11:2:205:U:H2'	11:2:206:A:H8	1.81	0.44
11:2:720:G:N3	11:2:720:G:H2'	2.31	0.44
14:C:106:ASP:OD1	14:C:108:ASN:N	2.42	0.44
15:D:7:LYS:O	15:D:11:LEU:HG	2.17	0.44
15:D:158:ILE:HG13	15:D:163:PRO:HB2	1.99	0.44
18:G:31:ARG:HG2	18:G:34:GLN:HE21	1.82	0.44
29:S:75:ASN:O	29:S:79:TYR:HD1	1.99	0.44
29:S:83:ALA:HB1	29:S:89:GLN:HG3	1.98	0.44
11:2:939:A:C6	11:2:940:A:C6	3.05	0.44
11:2:1066:C:H2'	11:2:1067:C:C6	2.52	0.44
11:2:1210:C:H2'	11:2:1211:A:C8	2.52	0.44
11:2:1229:G:O2'	11:2:1230:A:O5'	2.35	0.44
17:F:20:PHE:CE1	17:F:22:PRO:HG3	2.53	0.44
19:H:136:VAL:HG12	19:H:153:LEU:HB2	1.99	0.44
24:N:34:ILE:O	24:N:38:VAL:HG23	2.18	0.44
30:T:117:SER:OG	30:T:121:GLY:O	2.33	0.44
32:V:34:ILE:O	32:V:52:THR:HA	2.17	0.44
6:h:248:VAL:O	6:h:251:ILE:HG22	2.17	0.44
9:k:78:GLY:HA3	9:k:133:SER:HA	1.99	0.44
9:k:96:ASP:HA	9:k:97:PRO:HD2	1.80	0.44
9:k:213:GLU:HG2	9:k:226:VAL:H	1.82	0.44
10:l:175:LYS:O	10:l:250:VAL:HA	2.17	0.44
11:2:240:U:H5''	11:2:835:U:H5'	2.00	0.44
11:2:453:U:O2	11:2:453:U:H2'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:609:U:C4	34:X:26:GLU:HG3	2.51	0.44
27:Q:45:ARG:HG3	27:Q:49:TYR:CE1	2.52	0.44
35:Y:20:ARG:HB3	35:Y:76:TYR:CD2	2.52	0.44
10:l:7:HIS:HA	10:l:10:TYR:CD1	2.52	0.44
10:l:68:VAL:HG13	14:C:94:GLN:HE21	1.82	0.44
10:l:219:ASP:HA	10:l:222:ASN:HB2	1.98	0.44
11:2:344:A:C5	11:2:345:U:C5	3.06	0.44
11:2:522:U:OP1	35:Y:37:LYS:HB2	2.17	0.44
14:C:173:PRO:O	14:C:176:SER:OG	2.33	0.44
19:H:55:LYS:HB3	19:H:55:LYS:HE2	1.80	0.44
20:I:153:GLU:HB3	20:I:156:VAL:HG23	1.99	0.44
21:J:48:GLN:O	21:J:52:ILE:HG13	2.18	0.44
24:N:130:ARG:HG2	24:N:130:ARG:HH11	1.82	0.44
2:c:45:LYS:O	17:F:166:ARG:HD3	2.16	0.44
10:l:99:ASN:HB3	10:l:111:LYS:HB3	1.98	0.44
10:l:160:ASN:O	10:l:164:GLN:HG2	2.17	0.44
11:2:1414:U:H5''	28:R:3:ARG:N	2.33	0.44
11:2:1671:A:C4	11:2:1731:A:C2	3.06	0.44
13:B:107:THR:OG1	13:B:108:ASP:N	2.49	0.44
17:F:62:VAL:O	17:F:64:VAL:HG23	2.17	0.44
10:l:235:ILE:H	10:l:235:ILE:HG13	1.65	0.44
10:l:269:PHE:CZ	10:l:298:GLU:HG3	2.53	0.44
11:2:317:C:H2'	11:2:318:U:C6	2.52	0.44
12:A:34:GLU:N	12:A:35:PRO:HD2	2.33	0.44
12:A:69:ASN:C	12:A:71:GLU:H	2.25	0.44
16:E:141:THR:O	16:E:144:GLY:N	2.48	0.44
19:H:24:PHE:O	19:H:28:GLU:HG2	2.18	0.44
20:I:84:HIS:CD2	20:I:90:LEU:HD12	2.52	0.44
34:X:133:LEU:HD11	34:X:137:LYS:HE2	1.98	0.44
4:e:8:LEU:HD11	9:k:208:VAL:HG22	1.99	0.44
7:i:359:LEU:HD13	7:i:371:PHE:HB3	2.00	0.44
9:k:625:ILE:O	9:k:627:PRO:HD3	2.17	0.44
10:l:77:TYR:HD1	10:l:147:GLN:NE2	2.16	0.44
10:l:217:ILE:HG22	10:l:269:PHE:CE2	2.53	0.44
11:2:131:C:N4	11:2:135:A:H61	2.14	0.44
11:2:140:A:N6	11:2:281:G:OP2	2.38	0.44
11:2:894:U:H2'	11:2:895:G:H8	1.82	0.44
11:2:932:U:H4'	11:2:933:A:O4'	2.17	0.44
11:2:1267:G:N2	11:2:1442:U:O2'	2.35	0.44
11:2:1335:U:H5'	31:U:85:ARG:HH22	1.83	0.44
11:2:1500:C:OP1	30:T:122:ARG:NH2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:B:29:TRP:CE3	13:B:47:LEU:HD13	2.53	0.44
14:C:61:LEU:H	14:C:61:LEU:HG	1.46	0.44
36:Z:89:ILE:HG23	36:Z:101:TYR:HB3	1.99	0.44
1:b:31:TYR:H	1:b:48:SER:HG	1.65	0.44
6:h:209:ASP:OD1	6:h:209:ASP:N	2.49	0.44
11:2:717:C:N4	11:2:720:G:H22	2.14	0.44
11:2:856:A:N7	19:H:96:ARG:HA	2.32	0.44
11:2:1097:U:H5'	11:2:1097:U:O2	2.18	0.44
16:E:192:ILE:CG1	16:E:243:GLY:HA3	2.47	0.44
17:F:25:LEU:HB3	27:Q:27:GLY:O	2.18	0.44
19:H:185:ILE:HA	19:H:186:PRO:HD2	1.73	0.44
31:U:87:HIS:HB3	31:U:89:ARG:NH1	2.33	0.44
9:k:175:GLN:HG2	9:k:678:LYS:NZ	2.31	0.44
11:2:325:G:H2'	11:2:326:G:H8	1.83	0.44
11:2:1201:G:H2'	11:2:1202:A:O4'	2.18	0.44
11:2:1360:A:N3	11:2:1361:U:H1'	2.33	0.44
11:2:1502:G:O6	30:T:102:ARG:NH2	2.50	0.44
11:2:1555:A:OP2	26:P:47:ARG:NH1	2.51	0.44
11:2:1572:G:H1'	17:F:185:ARG:NH1	2.29	0.44
15:D:168:ILE:HG22	15:D:189:MET:HB2	2.00	0.44
16:E:112:HIS:HE1	16:E:237:SER:OG	2.01	0.44
19:H:154:LEU:HD11	19:H:183:PHE:CD2	2.53	0.44
21:J:105:LEU:HA	21:J:105:LEU:HD12	1.77	0.44
29:S:92:ILE:HB	29:S:115:ARG:HH12	1.83	0.44
10:l:156:ARG:NH1	10:l:184:ARG:HA	2.33	0.43
11:2:539:G:O4'	11:2:540:G:H5'	2.18	0.43
11:2:1521:G:O2'	11:2:1523:G:OP2	2.26	0.43
11:2:1588:G:H1	11:2:1608:U:H3	1.66	0.43
12:A:63:ILE:HD13	12:A:144:ILE:HD11	2.00	0.43
13:B:71:ALA:CB	13:B:79:HIS:HA	2.48	0.43
16:E:59:ARG:H	16:E:59:ARG:HG3	1.64	0.43
19:H:112:ARG:HA	19:H:113:PRO:HD3	1.85	0.43
25:O:78:ALA:HA	25:O:111:ARG:HB3	2.00	0.43
28:R:13:SER:HB3	28:R:57:LEU:HD12	1.99	0.43
29:S:42:TYR:HA	29:S:85:PHE:HE2	1.82	0.43
5:g:214:ALA:HB2	5:g:220:ILE:HA	2.01	0.43
7:i:323:PHE:HB2	7:i:324:PRO:HD3	2.00	0.43
11:2:87:C:O2'	11:2:169:A:N1	2.46	0.43
11:2:116:U:O2'	11:2:334:G:H1'	2.18	0.43
11:2:177:U:H1'	18:G:191:ARG:NH1	2.33	0.43
11:2:1366:U:H2'	11:2:1367:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1673:G:OP1	18:G:94:ARG:NH1	2.42	0.43
13:B:191:GLU:HB3	13:B:194:ASN:ND2	2.33	0.43
14:C:106:ASP:OD2	14:C:108:ASN:HB2	2.17	0.43
23:M:42:ALA:HB3	23:M:122:VAL:HB	1.99	0.43
26:P:38:PRO:O	26:P:42:ARG:HG3	2.18	0.43
2:c:5:THR:HA	2:c:6:PRO:HD3	1.83	0.43
11:2:296:U:H2'	11:2:297:U:C6	2.54	0.43
11:2:1265:G:C8	11:2:1266:U:O2	2.68	0.43
11:2:1551:U:H3'	26:P:43:ARG:HH21	1.82	0.43
15:D:21:LEU:HD23	15:D:21:LEU:HA	1.87	0.43
17:F:124:LEU:HD13	17:F:199:ILE:HD12	2.00	0.43
20:I:159:GLN:OE1	20:I:166:TYR:N	2.49	0.43
22:L:91:LEU:HD23	22:L:91:LEU:HA	1.85	0.43
25:O:81:VAL:HG13	25:O:115:ILE:HA	2.00	0.43
28:R:66:VAL:HG12	28:R:67:ARG:H	1.83	0.43
29:S:84:TRP:HE1	29:S:85:PHE:HD1	1.66	0.43
33:W:30:SER:HB3	33:W:61:ILE:HG13	2.00	0.43
2:c:49:ARG:HH21	17:F:81:ARG:HG3	1.83	0.43
6:h:155:GLY:O	6:h:159:ILE:HG12	2.18	0.43
9:k:469:LEU:O	9:k:473:ARG:HG3	2.18	0.43
9:k:500:ARG:NH2	9:k:519:PRO:HD2	2.34	0.43
10:l:200:LEU:O	10:l:283:LYS:HE2	2.18	0.43
11:2:278:U:H4'	11:2:279:G:O5'	2.18	0.43
11:2:959:U:O2	11:2:959:U:H2'	2.17	0.43
11:2:1171:A:H2'	11:2:1172:G:C8	2.54	0.43
11:2:1640:C:H4'	11:2:1641:C:H5'	1.98	0.43
12:A:17:LEU:HD23	12:A:172:LEU:HD21	2.00	0.43
13:B:127:VAL:HG22	13:B:176:VAL:HG11	2.00	0.43
18:G:139:ASN:HA	18:G:142:ARG:HB2	1.99	0.43
20:I:193:LEU:HD23	20:I:193:LEU:HA	1.80	0.43
23:M:103:LEU:HB2	23:M:104:GLY:H	1.48	0.43
27:Q:30:LYS:HD3	27:Q:34:SER:C	2.43	0.43
1:b:70:LYS:HG3	11:2:1049:U:H5''	2.01	0.43
6:h:254:SER:HB3	6:h:258:LYS:HD3	2.01	0.43
7:i:305:ARG:O	7:i:309:LYS:HG2	2.17	0.43
7:i:360:LEU:HD23	7:i:372:ILE:HD13	2.01	0.43
9:k:77:GLU:O	9:k:79:LYS:N	2.45	0.43
9:k:777:MET:HE2	9:k:777:MET:HA	2.01	0.43
11:2:687:G:H5'	33:W:119:LYS:HE2	1.99	0.43
11:2:992:A:C2	11:2:1012:U:N3	2.87	0.43
11:2:1363:U:O2	11:2:1363:U:H2'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1474:G:OP2	36:Z:97:LYS:NZ	2.51	0.43
11:2:1483:A:P	11:2:1521:G:H21	2.39	0.43
13:B:29:TRP:CZ3	13:B:47:LEU:HD13	2.54	0.43
15:D:70:THR:HG22	15:D:86:LEU:HD13	2.00	0.43
15:D:191:ASP:HB3	15:D:194:LYS:HD2	2.01	0.43
19:H:91:ILE:HG21	19:H:129:LEU:HD23	2.00	0.43
20:I:196:LEU:HD23	20:I:196:LEU:HA	1.87	0.43
31:U:30:LYS:H	31:U:30:LYS:HG2	1.65	0.43
34:X:61:SER:HB2	34:X:117:ILE:CB	2.37	0.43
35:Y:27:VAL:O	35:Y:68:LYS:HA	2.17	0.43
10:l:189:MET:HB3	10:l:189:MET:HE2	1.47	0.43
11:2:205:U:H2'	11:2:206:A:C8	2.53	0.43
11:2:289:U:H2'	11:2:290:G:O4'	2.18	0.43
11:2:1600:A:H2'	11:2:1600:A:N3	2.33	0.43
11:2:1651:A:H62	11:2:1749:A:H61	1.65	0.43
14:C:125:ILE:O	14:C:129:ILE:HG13	2.19	0.43
16:E:249:ALA:HA	16:E:252:ARG:NH1	2.34	0.43
17:F:100:ASN:HB3	17:F:103:ASN:ND2	2.34	0.43
20:I:100:ALA:O	20:I:168:CYS:HA	2.19	0.43
23:M:42:ALA:HB1	23:M:47:GLU:HG2	2.00	0.43
24:N:67:THR:C	24:N:69:ASN:H	2.27	0.43
5:g:7:LEU:HD13	5:g:274:LEU:HD11	1.99	0.43
7:i:256:PRO:HB2	7:i:302:HIS:HB2	2.01	0.43
11:2:333:A:C6	11:2:334:G:C6	3.06	0.43
11:2:645:C:O2	11:2:690:G:N2	2.51	0.43
11:2:1699:G:C2	11:2:1700:C:H1'	2.54	0.43
12:A:49:ASN:CB	12:A:52:LYS:HG3	2.48	0.43
12:A:168:HIS:CE1	12:A:203:PHE:HE2	2.36	0.43
14:C:143:TYR:HE2	14:C:151:PRO:HG3	1.82	0.43
18:G:69:LEU:HA	18:G:70:PRO:HD3	1.88	0.43
20:I:168:CYS:O	20:I:181:GLY:HA3	2.18	0.43
22:L:80:MET:HB3	22:L:80:MET:HE2	1.74	0.43
26:P:139:ILE:HA	26:P:140:PRO:HD3	1.91	0.43
32:V:46:ILE:H	32:V:46:ILE:HG13	1.63	0.43
6:h:211:LYS:HZ1	11:2:1628:U:H5''	1.83	0.43
11:2:100:A:H2'	11:2:101:U:O4'	2.18	0.43
11:2:152:U:H3	11:2:162:A:H61	1.67	0.43
11:2:455:C:H3'	11:2:456:A:C8	2.53	0.43
11:2:828:U:O4	11:2:829:A:N6	2.50	0.43
11:2:854:U:O2'	11:2:855:A:H5''	2.18	0.43
11:2:887:A:H2'	11:2:888:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:110:TYR:HA	12:A:115:PHE:CD1	2.54	0.43
14:C:67:GLN:O	14:C:71:THR:HG23	2.18	0.43
14:C:154:LEU:HD12	14:C:154:LEU:HA	1.78	0.43
26:P:86:VAL:O	26:P:88:GLU:N	2.51	0.43
27:Q:77:GLN:O	27:Q:81:ILE:HG23	2.19	0.43
28:R:110:VAL:HG21	28:R:119:LEU:HD11	2.00	0.43
7:i:413:LEU:HA	7:i:414:PRO:HD3	1.76	0.43
7:i:442:GLU:OE2	7:i:446:GLN:NE2	2.52	0.43
9:k:284:GLY:O	9:k:553:ALA:HB2	2.19	0.43
11:2:148:A:N6	11:2:167:U:C2	2.87	0.43
11:2:964:U:H5''	24:N:128:TYR:CE1	2.54	0.43
14:C:186:LYS:HA	14:C:186:LYS:HD2	1.87	0.43
18:G:137:ARG:HH21	18:G:177:ARG:CZ	2.32	0.43
23:M:131:ASP:OD1	23:M:131:ASP:N	2.52	0.43
29:S:30:TYR:HE2	29:S:40:ARG:HD3	1.84	0.43
34:X:8:GLY:O	34:X:11:SER:HB3	2.18	0.43
5:g:45:TRP:CZ3	5:g:57:PRO:HB3	2.54	0.43
5:g:251:TRP:CE2	5:g:271:VAL:HG21	2.54	0.43
9:k:67:LEU:HD23	9:k:67:LEU:HA	1.87	0.43
9:k:735:LEU:HD11	9:k:745:ILE:HG22	2.01	0.43
11:2:390:G:H5''	11:2:390:G:N3	2.33	0.43
11:2:763:G:C6	11:2:764:U:N3	2.87	0.43
11:2:896:U:H2'	11:2:897:C:C6	2.54	0.43
11:2:992:A:H2	11:2:1012:U:N3	2.16	0.43
11:2:1682:U:H2'	11:2:1683:C:O4'	2.19	0.43
11:2:1761:U:C2'	11:2:1762:A:H5'	2.48	0.43
15:D:21:LEU:HD21	15:D:73:VAL:HG13	2.00	0.43
19:H:120:ALA:O	19:H:124:LYS:HG2	2.19	0.43
21:J:109:LEU:HD23	21:J:148:VAL:HG22	2.00	0.43
23:M:46:ARG:O	23:M:50:LYS:HG2	2.19	0.43
26:P:57:MET:HE2	26:P:57:MET:HA	2.00	0.43
27:Q:32:ASN:ND2	27:Q:69:VAL:HG23	2.34	0.43
28:R:17:ILE:HG21	28:R:61:ILE:HD12	2.01	0.43
35:Y:60:PHE:CD2	35:Y:71:GLY:HA3	2.54	0.43
9:k:399:TYR:CE2	26:P:100:LYS:HD3	2.54	0.42
10:l:85:LEU:HB3	26:P:141:LEU:HD11	2.00	0.42
10:l:109:ILE:HG12	10:l:123:LYS:HG2	2.01	0.42
10:l:254:PHE:H	10:l:255:PRO:HD2	1.84	0.42
11:2:79:C:C4	11:2:80:A:C6	3.07	0.42
11:2:518:A:C2'	11:2:519:C:H5''	2.49	0.42
11:2:543:C:H3'	11:2:544:A:C5'	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:767:U:H5	21:J:142:ASN:OD1	2.02	0.42
11:2:1482:C:OP2	11:2:1521:G:N2	2.43	0.42
12:A:62:ARG:HD3	32:V:37:ALA:O	2.18	0.42
13:B:69:CYS:HB2	13:B:72:ASP:H	1.84	0.42
19:H:8:ILE:HD13	19:H:24:PHE:CD1	2.52	0.42
28:R:23:LYS:CB	28:R:34:LEU:HD11	2.49	0.42
32:V:1:MET:HB3	32:V:10:GLU:CD	2.43	0.42
34:X:56:LYS:NZ	34:X:97:ASP:HA	2.34	0.42
9:k:303:LEU:HD23	9:k:561:ILE:HG23	2.00	0.42
9:k:591:ASN:HA	9:k:659:PRO:HA	2.01	0.42
9:k:766:GLN:HE21	11:2:1271:G:N2	2.17	0.42
11:2:990:C:H2'	11:2:991:G:O4'	2.19	0.42
14:C:69:ILE:HG13	14:C:133:LYS:O	2.19	0.42
19:H:67:LEU:HA	19:H:70:PHE:HB2	2.01	0.42
19:H:126:LEU:HD13	19:H:126:LEU:HA	1.85	0.42
25:O:61:MET:HE1	25:O:107:ARG:NH1	2.34	0.42
32:V:38:LYS:HD2	32:V:49:GLU:HB3	2.00	0.42
1:b:52:THR:HG22	24:N:56:ASP:OD2	2.19	0.42
7:i:284:LEU:O	7:i:288:ARG:HG3	2.19	0.42
9:k:228:ASN:O	9:k:234:ASP:HB2	2.19	0.42
9:k:717:VAL:HB	9:k:755:PHE:CE2	2.54	0.42
10:l:34:THR:HG22	10:l:38:HIS:CE1	2.55	0.42
11:2:1455:G:H5'	11:2:1456:C:OP2	2.19	0.42
11:2:1570:A:HO2'	11:2:1571:C:P	2.43	0.42
12:A:3:LEU:HA	12:A:4:PRO:HD3	1.77	0.42
18:G:178:LEU:O	18:G:180:THR:HG23	2.19	0.42
33:W:122:SER:OG	33:W:123:GLY:N	2.52	0.42
1:b:20:LYS:O	1:b:20:LYS:HG2	2.19	0.42
5:g:126:SER:HB2	5:g:128:ASP:OD1	2.19	0.42
6:h:266:VAL:HG22	6:h:269:ARG:CZ	2.49	0.42
7:i:304:TYR:CZ	7:i:308:LYS:HD2	2.54	0.42
9:k:153:LYS:HD2	9:k:620:VAL:HG23	2.01	0.42
9:k:309:ILE:O	9:k:556:ARG:HB2	2.19	0.42
11:2:197:A:H2'	11:2:198:A:C8	2.54	0.42
11:2:455:C:H3'	11:2:456:A:H8	1.83	0.42
11:2:782:U:O4	35:Y:48:TYR:HA	2.20	0.42
11:2:1054:U:H2'	11:2:1055:U:C6	2.54	0.42
11:2:1548:G:O2'	29:S:89:GLN:OE1	2.33	0.42
11:2:1555:A:OP1	26:P:47:ARG:HD3	2.19	0.42
12:A:102:PHE:CZ	12:A:106:SER:HB2	2.54	0.42
15:D:157:LEU:HD22	15:D:187:LYS:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:F:76:ARG:NH2	27:Q:120:ASP:HA	2.34	0.42
26:P:80:MET:O	26:P:116:LEU:HD12	2.19	0.42
27:Q:9:THR:HG21	27:Q:87:LYS:HB3	2.01	0.42
27:Q:49:TYR:O	27:Q:53:LEU:HG	2.20	0.42
9:k:703:LEU:O	9:k:770:ALA:HA	2.20	0.42
9:k:741:ARG:NH1	9:k:762:LYS:O	2.53	0.42
11:2:152:U:O2'	18:G:4:ASN:OD1	2.35	0.42
11:2:1334:U:H3	11:2:1417:A:N6	2.17	0.42
11:2:1338:C:N3	11:2:1386:G:N2	2.60	0.42
12:A:67:ILE:HA	12:A:68:PRO:HD3	1.77	0.42
13:B:39:GLU:O	13:B:41:ARG:HG3	2.19	0.42
13:B:87:ARG:O	13:B:87:ARG:HG3	2.20	0.42
13:B:201:THR:HG21	13:B:207:LEU:HG	2.01	0.42
24:N:53:LEU:HD12	24:N:53:LEU:HA	1.73	0.42
35:Y:62:THR:HA	35:Y:69:SER:CB	2.47	0.42
1:b:28:PRO:HB3	11:2:959:U:H5'	2.01	0.42
5:g:176:LYS:HG2	5:g:197:SER:O	2.19	0.42
6:h:106:MET:HE2	6:h:106:MET:HB3	1.74	0.42
6:h:107:THR:HB	6:h:108:PRO:HD3	2.00	0.42
7:i:393:TYR:O	7:i:396:ARG:HG2	2.19	0.42
11:2:416:A:H5''	11:2:417:A:N7	2.34	0.42
11:2:1111:G:N2	11:2:1135:U:H1'	2.35	0.42
11:2:1161:C:H1'	11:2:1619:C:H42	1.85	0.42
11:2:1371:A:H61	31:U:53:LYS:HE3	1.83	0.42
15:D:34:TYR:CE1	15:D:37:VAL:HG13	2.54	0.42
33:W:37:PHE:CD2	33:W:103:ILE:HD12	2.54	0.42
33:W:77:PRO:HG2	33:W:79:PHE:CZ	2.54	0.42
9:k:191:VAL:HG12	9:k:229:LEU:HG	2.02	0.42
11:2:254:A:H2'	11:2:255:U:H6	1.85	0.42
11:2:862:A:C2	11:2:963:A:C4	3.08	0.42
11:2:1042:G:N1	11:2:1076:A:H2	2.15	0.42
11:2:1569:A:H2'	11:2:1570:A:O4'	2.20	0.42
12:A:119:ARG:HD3	14:C:240:LEU:HD23	2.01	0.42
12:A:168:HIS:ND1	12:A:203:PHE:HE2	2.17	0.42
15:D:42:THR:OG1	15:D:45:LYS:O	2.29	0.42
16:E:125:LYS:HB2	16:E:226:PHE:CD1	2.54	0.42
19:H:140:VAL:O	33:W:51:GLU:HG3	2.20	0.42
25:O:20:TYR:HE2	25:O:22:SER:HB2	1.85	0.42
33:W:103:ILE:HD13	33:W:126:LEU:HB2	2.02	0.42
6:h:103:PRO:HB3	13:B:115:ARG:NH2	2.34	0.42
9:k:144:ASN:ND2	9:k:147:ASN:HB2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:k:198:VAL:HG12	9:k:199:HIS:H	1.85	0.42
11:2:332:U:H4'	20:I:29:LEU:O	2.20	0.42
11:2:1287:A:H1'	11:2:1329:A:H5'	2.01	0.42
12:A:87:LEU:HD23	12:A:87:LEU:HA	1.90	0.42
13:B:204:ILE:HD13	13:B:204:ILE:HA	1.92	0.42
17:F:130:ILE:O	17:F:134:VAL:HG23	2.20	0.42
21:J:116:LEU:HA	21:J:116:LEU:HD23	1.82	0.42
29:S:113:LEU:HD13	29:S:127:HIS:NE2	2.35	0.42
33:W:105:THR:HG23	33:W:110:ILE:HG12	2.02	0.42
34:X:94:ASN:OD1	34:X:94:ASN:N	2.50	0.42
7:i:292:GLU:HG2	15:D:76:ARG:HB2	2.02	0.42
11:2:104:A:C5	11:2:308:C:C4	3.08	0.42
11:2:396:G:N2	11:2:399:A:OP2	2.52	0.42
11:2:912:U:H1'	11:2:913:G:OP2	2.20	0.42
11:2:1018:U:H2'	11:2:1019:A:C8	2.55	0.42
11:2:1298:U:C5	11:2:1299:G:C5	3.08	0.42
11:2:1443:U:O2'	11:2:1444:A:N3	2.52	0.42
14:C:101:VAL:HG22	14:C:115:ILE:HG12	2.02	0.42
16:E:42:LEU:HA	16:E:43:PRO:HD2	1.77	0.42
19:H:110:GLN:O	19:H:112:ARG:N	2.53	0.42
25:O:80:HIS:CE1	25:O:114:ARG:HB2	2.55	0.42
4:e:38:LEU:HD23	4:e:42:ARG:HG3	2.02	0.42
5:g:122:ILE:O	5:g:134:TRP:HD1	2.03	0.42
6:h:117:TYR:CG	6:h:118:PRO:HD3	2.55	0.42
10:l:124:ILE:HA	10:l:186:ILE:HA	2.01	0.42
11:2:749:U:H2'	11:2:750:U:C6	2.55	0.42
11:2:1470:C:OP1	11:2:1540:G:O2'	2.38	0.42
16:E:182:TYR:CD2	16:E:192:ILE:HG12	2.55	0.42
23:M:28:LEU:HD11	23:M:61:VAL:HG22	2.02	0.42
29:S:27:LYS:HD3	29:S:57:ARG:HG2	2.02	0.42
1:b:24:LEU:HD12	1:b:24:LEU:HA	1.80	0.41
6:h:113:TRP:HA	6:h:116:ILE:HD12	2.02	0.41
9:k:151:CYS:O	9:k:154:VAL:HG12	2.20	0.41
11:2:520:A:H2'	11:2:521:A:O4'	2.20	0.41
11:2:649:U:HO2'	11:2:650:U:P	2.43	0.41
13:B:61:LEU:HA	13:B:64:ARG:HG2	2.01	0.41
19:H:76:LYS:H	19:H:76:LYS:HG3	1.62	0.41
4:e:33:ARG:NH1	4:e:33:ARG:HB3	2.35	0.41
6:h:95:GLU:O	6:h:140:ARG:HA	2.20	0.41
6:h:259:VAL:O	6:h:263:LEU:HB2	2.20	0.41
11:2:68:A:N6	18:G:132:ARG:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:246:G:N3	22:L:40:LEU:HD13	2.34	0.41
11:2:336:G:O2'	11:2:338:C:OP1	2.33	0.41
11:2:1041:G:H2'	11:2:1042:G:C8	2.55	0.41
11:2:1213:G:H1	11:2:1450:U:H3	1.68	0.41
11:2:1338:C:H42	11:2:1386:G:H1	1.68	0.41
11:2:1388:A:H4'	11:2:1389:C:O5'	2.19	0.41
11:2:1635:A:N6	11:2:1769:U:H3	2.16	0.41
11:2:1740:A:H2'	11:2:1741:U:O4'	2.20	0.41
12:A:84:ARG:HG2	12:A:203:PHE:O	2.19	0.41
16:E:113:ARG:O	16:E:114:ILE:HD13	2.20	0.41
21:J:175:ARG:HH21	21:J:179:ARG:NH2	2.18	0.41
24:N:5:HIS:NE2	24:N:121:ARG:HG3	2.35	0.41
28:R:7:LYS:HB2	28:R:11:ARG:NH2	2.35	0.41
30:T:61:VAL:HG21	30:T:104:VAL:HG11	2.02	0.41
3:d:49:ASP:HB3	15:D:19:ALA:HB1	2.01	0.41
9:k:354:THR:OG1	9:k:527:ARG:HG3	2.20	0.41
9:k:657:ILE:HG13	9:k:779:PRO:HB2	2.02	0.41
11:2:393:C:H2'	11:2:394:C:C6	2.55	0.41
11:2:607:G:H5'	11:2:613:G:N2	2.35	0.41
11:2:1018:U:H2'	11:2:1019:A:H8	1.85	0.41
11:2:1360:A:C2	11:2:1361:U:H1'	2.55	0.41
11:2:1498:G:OP1	30:T:75:LYS:HG2	2.19	0.41
11:2:1514:U:H5'	11:2:1514:U:O2	2.21	0.41
11:2:1653:C:H2'	11:2:1654:G:C8	2.56	0.41
12:A:110:TYR:HE1	14:C:64:LYS:HB3	1.85	0.41
13:B:104:ASP:OD1	13:B:105:PHE:N	2.45	0.41
18:G:55:GLY:O	18:G:63:MET:HG3	2.21	0.41
19:H:28:GLU:O	19:H:35:LYS:HB2	2.20	0.41
20:I:171:SER:O	20:I:173:PRO:HD3	2.21	0.41
30:T:70:GLN:HB2	30:T:121:GLY:C	2.45	0.41
30:T:125:SER:O	30:T:129:GLN:HG3	2.19	0.41
34:X:42:PRO:O	34:X:79:ASN:ND2	2.53	0.41
36:Z:57:TYR:OH	36:Z:68:ARG:NH2	2.53	0.41
1:b:3:LEU:HD23	1:b:3:LEU:HA	1.61	0.41
9:k:172:PHE:CE2	9:k:176:ILE:HD11	2.55	0.41
10:l:166:MET:SD	10:l:189:MET:HE1	2.61	0.41
11:2:217:A:OP1	11:2:830:U:H4'	2.20	0.41
11:2:358:U:O2'	11:2:360:A:H5''	2.19	0.41
11:2:1092:A:O2'	11:2:1093:A:H3'	2.21	0.41
11:2:1155:G:C6	11:2:1156:C:N4	2.88	0.41
11:2:1291:G:H2'	11:2:1292:G:C8	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:1483:A:C2	11:2:1607:G:H1'	2.55	0.41
11:2:1541:G:C6	11:2:1542:G:N1	2.88	0.41
20:I:34:ALA:HB2	20:I:56:ARG:HG2	2.02	0.41
23:M:36:LEU:HD13	23:M:41:LEU:HD12	2.02	0.41
31:U:32:LYS:HA	31:U:32:LYS:HD3	1.94	0.41
31:U:42:VAL:O	31:U:52:LYS:NZ	2.53	0.41
11:2:39:A:H2'	11:2:40:A:C8	2.56	0.41
11:2:324:U:H2'	11:2:325:G:H8	1.86	0.41
11:2:989:U:H2'	11:2:990:C:O4'	2.19	0.41
14:C:84:LYS:HA	14:C:85:PRO:HD2	1.81	0.41
14:C:208:GLU:H	14:C:208:GLU:CD	2.24	0.41
17:F:164:PRO:HA	17:F:167:ARG:HB2	2.03	0.41
27:Q:28:LEU:CD2	27:Q:30:LYS:HG3	2.50	0.41
30:T:118:PRO:C	30:T:120:GLY:H	2.29	0.41
35:Y:5:VAL:HG21	35:Y:32:ARG:NH1	2.36	0.41
7:i:373:LYS:HG2	7:i:416:ILE:HD11	2.02	0.41
11:2:82:U:H2'	11:2:83:G:O4'	2.21	0.41
11:2:337:G:H3'	22:L:133:LYS:HB2	2.03	0.41
11:2:469:C:H2'	11:2:470:A:O4'	2.19	0.41
11:2:1082:C:N4	32:V:62:ARG:HH21	2.19	0.41
11:2:1343:U:H4'	11:2:1344:A:OP1	2.20	0.41
11:2:1363:U:H3'	11:2:1364:G:H8	1.86	0.41
11:2:1410:A:H2'	11:2:1411:A:O4'	2.21	0.41
11:2:1468:U:OP1	30:T:90:PRO:HB3	2.20	0.41
11:2:1534:G:N2	17:F:187:ILE:HG23	2.35	0.41
12:A:24:LEU:CD2	12:A:41:ARG:HH12	2.33	0.41
14:C:140:ARG:NH2	14:C:226:THR:OG1	2.53	0.41
14:C:144:TRP:CE2	14:C:173:PRO:HG3	2.55	0.41
16:E:43:PRO:HG2	16:E:46:VAL:HG23	2.02	0.41
17:F:66:GLN:HA	17:F:67:PRO:HD3	1.61	0.41
18:G:93:LYS:HB2	18:G:93:LYS:HE3	1.88	0.41
24:N:119:GLU:OE1	24:N:141:TYR:OH	2.19	0.41
29:S:100:THR:HG22	29:S:104:ASN:HB2	2.02	0.41
30:T:17:ALA:O	30:T:20:SER:OG	2.32	0.41
9:k:616:VAL:HG22	9:k:669:PHE:CD2	2.55	0.41
11:2:164:A:O2'	11:2:165:G:H5'	2.21	0.41
11:2:325:G:C2	11:2:326:G:C8	3.08	0.41
11:2:514:G:N3	11:2:515:A:C8	2.89	0.41
11:2:581:U:H6	11:2:581:U:H2'	1.67	0.41
11:2:632:U:H5''	34:X:10:ASN:O	2.20	0.41
13:B:128:LYS:HA	13:B:133:TYR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:D:159:HIS:CD2	15:D:187:LYS:HE2	2.56	0.41
16:E:173:ILE:HD13	16:E:229:GLY:HA2	2.02	0.41
17:F:222:LYS:HG2	17:F:225:ARG:CZ	2.51	0.41
18:G:116:LYS:HD2	18:G:125:THR:HG21	2.02	0.41
22:L:46:LYS:C	22:L:48:ALA:H	2.27	0.41
5:g:134:TRP:CZ3	5:g:140:CYS:HB2	2.56	0.41
9:k:741:ARG:HD2	9:k:763:LEU:HD21	2.01	0.41
11:2:162:A:C6	11:2:163:G:C6	3.08	0.41
11:2:1255:G:H5''	11:2:1257:U:O4	2.20	0.41
16:E:42:LEU:HD23	16:E:47:PHE:HB2	2.01	0.41
18:G:58:LYS:HB2	18:G:105:ASP:O	2.20	0.41
19:H:19:GLN:HB3	19:H:85:PHE:HZ	1.86	0.41
23:M:72:ILE:O	23:M:76:GLU:N	2.51	0.41
24:N:16:ILE:HD13	24:N:16:ILE:HA	1.87	0.41
26:P:124:THR:HG22	26:P:125:PRO:HD2	2.02	0.41
30:T:12:GLN:O	30:T:16:ASN:ND2	2.53	0.41
9:k:96:ASP:OD2	9:k:99:ASP:N	2.51	0.41
9:k:259:VAL:HG22	9:k:282:VAL:HA	2.01	0.41
11:2:66:U:OP2	18:G:136:LYS:NZ	2.53	0.41
11:2:142:G:H5'	18:G:139:ASN:ND2	2.35	0.41
11:2:776:G:N2	11:2:785:U:H1'	2.36	0.41
11:2:779:U:O2'	11:2:780:A:P	2.78	0.41
11:2:850:A:H2'	11:2:851:U:H5'	2.01	0.41
11:2:946:U:H2'	11:2:947:U:C6	2.55	0.41
11:2:998:A:H4'	11:2:998:A:OP1	2.21	0.41
11:2:1095:U:O2'	33:W:19:LYS:NZ	2.53	0.41
11:2:1197:C:H2'	11:2:1198:G:O4'	2.21	0.41
11:2:1543:A:H1'	11:2:1569:A:C2	2.55	0.41
11:2:1733:C:H2'	11:2:1734:U:C6	2.56	0.41
12:A:124:THR:HA	12:A:146:LEU:HD12	2.03	0.41
14:C:143:TYR:CE2	14:C:151:PRO:HG3	2.56	0.41
14:C:228:ASN:HD22	14:C:228:ASN:N	2.17	0.41
15:D:178:ARG:HE	15:D:178:ARG:N	2.18	0.41
16:E:21:ASP:OD1	16:E:24:SER:HB2	2.20	0.41
16:E:238:LEU:H	16:E:238:LEU:HG	1.59	0.41
19:H:129:LEU:HD22	19:H:169:PHE:CD1	2.56	0.41
21:J:34:PHE:HE1	21:J:106:GLU:OE1	2.04	0.41
21:J:128:LEU:HB3	21:J:134:ILE:HD11	2.02	0.41
23:M:129:GLU:O	23:M:133:LEU:HD12	2.21	0.41
26:P:74:ALA:HA	26:P:75:PRO:HD3	1.88	0.41
28:R:75:GLU:O	28:R:79:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:U:22:ILE:HG12	31:U:118:VAL:HA	2.02	0.41
31:U:50:LEU:HD22	31:U:94:GLU:O	2.21	0.41
34:X:63:GLN:H	34:X:115:GLY:HA3	1.85	0.41
9:k:360:TYR:N	9:k:360:TYR:CD1	2.89	0.41
9:k:608:VAL:HA	9:k:609:PRO:HD2	1.90	0.41
10:l:36:LEU:HD23	10:l:36:LEU:HA	1.84	0.41
10:l:154:LEU:HD23	10:l:157:LEU:HD12	2.03	0.41
11:2:772:G:C5	11:2:773:C:C4	3.09	0.41
11:2:1005:A:O2'	11:2:1006:C:O4'	2.29	0.41
11:2:1036:A:H2'	11:2:1037:C:O4'	2.21	0.41
11:2:1043:A:H5'	11:2:1044:U:OP2	2.21	0.41
11:2:1473:U:C2	17:F:190:ILE:HG13	2.57	0.41
11:2:1490:C:H6	11:2:1490:C:OP2	2.04	0.41
11:2:1534:G:H21	17:F:187:ILE:HG23	1.84	0.41
11:2:1535:U:H5	17:F:185:ARG:C	2.29	0.41
12:A:200:ASP:CG	28:R:89:SER:HB3	2.46	0.41
23:M:45:LEU:HA	23:M:120:VAL:HG22	2.03	0.41
27:Q:20:ALA:HA	27:Q:66:ARG:O	2.21	0.41
5:g:205:SER:HB3	5:g:210:LEU:HB2	2.03	0.40
6:h:95:GLU:OE1	25:O:111:ARG:NH1	2.54	0.40
11:2:169:A:C4	11:2:171:A:C8	3.09	0.40
11:2:448:C:OP2	16:E:49:ARG:NH2	2.53	0.40
11:2:987:G:H5''	11:2:988:A:OP1	2.20	0.40
11:2:1008:G:H2'	11:2:1009:U:C6	2.56	0.40
11:2:1243:G:N2	11:2:1451:C:O2	2.53	0.40
11:2:1471:A:N3	11:2:1474:G:O2'	2.49	0.40
11:2:1503:A:H2'	11:2:1504:G:O4'	2.20	0.40
11:2:1654:G:H1'	11:2:1655:A:N7	2.36	0.40
13:B:27:LYS:HD3	13:B:47:LEU:HD21	2.02	0.40
16:E:54:TYR:HD2	16:E:54:TYR:HA	1.74	0.40
16:E:82:TYR:HA	16:E:83:PRO:HD3	1.85	0.40
21:J:30:LEU:HA	21:J:30:LEU:HD23	1.65	0.40
21:J:110:GLN:NE2	21:J:126:ARG:HG2	2.21	0.40
23:M:51:ALA:HB1	23:M:122:VAL:HG11	2.03	0.40
24:N:125:LEU:HD22	24:N:129:TYR:CE2	2.56	0.40
26:P:90:ILE:HD11	26:P:112:LEU:HD21	2.02	0.40
32:V:37:ALA:HB1	32:V:45:ALA:HB1	2.03	0.40
34:X:48:HIS:CE1	34:X:105:ALA:HB2	2.55	0.40
4:e:39:LEU:HA	4:e:42:ARG:HB2	2.03	0.40
5:g:56:VAL:HA	5:g:57:PRO:HD3	1.87	0.40
7:i:452:ILE:O	7:i:456:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2:901:G:C6	11:2:902:G:N1	2.89	0.40
11:2:911:U:H1'	11:2:915:A:H1'	2.03	0.40
11:2:1002:G:C2	11:2:1004:U:H5''	2.54	0.40
11:2:1219:A:H3'	11:2:1220:C:O4'	2.21	0.40
16:E:178:GLY:HA2	16:E:194:THR:HG23	2.03	0.40
21:J:119:ALA:HA	21:J:124:HIS:HD2	1.87	0.40
22:L:131:ILE:HD13	22:L:131:ILE:HA	1.64	0.40
24:N:102:LEU:HD23	24:N:102:LEU:HA	1.88	0.40
32:V:71:ARG:HB2	32:V:83:TRP:NE1	2.35	0.40
33:W:111:MET:HE3	33:W:115:GLU:HG2	2.03	0.40
34:X:86:PHE:CZ	34:X:88:PRO:HA	2.56	0.40
35:Y:86:GLU:OE1	35:Y:90:ARG:HD2	2.22	0.40
35:Y:108:ARG:HE	35:Y:108:ARG:HB2	1.41	0.40
3:d:21:CYS:C	3:d:23:VAL:H	2.29	0.40
5:g:93:ASP:HB2	5:g:100:TYR:CE2	2.57	0.40
5:g:123:ILE:HD12	5:g:154:VAL:HB	2.03	0.40
5:g:216:LYS:HA	5:g:239:GLU:HG3	2.04	0.40
9:k:374:TYR:OH	9:k:505:LYS:HB3	2.22	0.40
10:l:295:LEU:O	10:l:295:LEU:HG	2.21	0.40
11:2:990:C:H4'	25:O:128:LYS:O	2.20	0.40
11:2:1218:G:O4'	11:2:1219:A:H2	2.04	0.40
11:2:1239:U:H2'	11:2:1240:U:H2'	2.02	0.40
12:A:22:THR:HG22	12:A:169:SER:OG	2.21	0.40
12:A:126:PRO:CG	12:A:151:SER:HB3	2.51	0.40
13:B:138:PHE:HB2	13:B:214:LYS:H	1.86	0.40
22:L:16:GLN:HG3	22:L:54:ILE:CD1	2.50	0.40
25:O:17:ALA:N	25:O:80:HIS:O	2.42	0.40
29:S:28:ILE:HG12	29:S:58:ALA:HA	2.03	0.40
34:X:59:ILE:HD13	34:X:59:ILE:HA	1.95	0.40
35:Y:81:GLU:HA	35:Y:84:LYS:HG2	2.04	0.40
6:h:153:GLN:HG2	25:O:103:ARG:HG2	2.02	0.40
6:h:219:ALA:HB1	6:h:267:ALA:HB2	2.03	0.40
9:k:718:ARG:HG2	9:k:719:TYR:CD1	2.57	0.40
10:l:18:VAL:O	10:l:22:VAL:HG23	2.22	0.40
11:2:955:A:H2'	11:2:956:C:O4'	2.21	0.40
11:2:1077:C:C2'	11:2:1078:C:H5'	2.51	0.40
11:2:1286:U:H6	11:2:1286:U:H2'	1.71	0.40
11:2:1409:G:H22	11:2:1412:G:C5'	2.34	0.40
11:2:1457:C:H6	11:2:1457:C:OP1	2.04	0.40
11:2:1689:A:H2'	11:2:1690:G:H8	1.87	0.40
12:A:176:LEU:O	12:A:180:GLU:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:142:GLY:HA2	14:C:151:PRO:HB3	2.02	0.40
16:E:87:MET:HE2	16:E:87:MET:HB3	1.90	0.40
17:F:64:VAL:HG22	17:F:88:PRO:HA	2.02	0.40
17:F:193:THR:HA	17:F:196:GLU:HB3	2.03	0.40
18:G:91:GLU:HG2	18:G:92:ARG:N	2.37	0.40
21:J:128:LEU:O	21:J:133:HIS:HB2	2.21	0.40
4:e:34:ALA:O	4:e:37:ARG:HB3	2.21	0.40
6:h:220:THR:O	6:h:221:ARG:HG2	2.22	0.40
7:i:359:LEU:HD23	7:i:362:LEU:HD12	2.04	0.40
9:k:288:ASN:HD22	9:k:290:ASN:H	1.70	0.40
9:k:371:THR:HG22	9:k:372:ALA:H	1.87	0.40
9:k:508:TYR:OH	9:k:641:LYS:HE3	2.21	0.40
11:2:793:A:H4'	11:2:794:U:C4	2.57	0.40
11:2:899:G:O2'	11:2:915:A:N1	2.40	0.40
11:2:1199:G:H1'	11:2:1201:G:OP1	2.22	0.40
12:A:71:GLU:O	12:A:96:THR:HG22	2.21	0.40
12:A:173:ILE:HD13	12:A:173:ILE:HA	1.90	0.40
15:D:12:VAL:O	15:D:16:VAL:HG23	2.22	0.40
22:L:113:PRO:C	22:L:115:PHE:H	2.29	0.40
23:M:135:MET:HG2	23:M:139:HIS:HD2	1.86	0.40
25:O:42:VAL:HG13	25:O:67:VAL:HG23	2.03	0.40
25:O:61:MET:HE2	25:O:65:GLN:NE2	2.37	0.40
27:Q:48:VAL:HG13	27:Q:81:ILE:HG13	2.04	0.40
27:Q:55:VAL:HG11	27:Q:105:LEU:HG	2.02	0.40
29:S:28:ILE:HB	29:S:54:LEU:HD23	2.02	0.40
31:U:30:LYS:HB3	31:U:30:LYS:HE2	1.83	0.40
32:V:72:LEU:HD23	32:V:72:LEU:HA	1.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	79/82 (96%)	69 (87%)	9 (11%)	1 (1%)	9	33
2	c	61/67 (91%)	53 (87%)	7 (12%)	1 (2%)	7	29
3	d	35/56 (62%)	32 (91%)	2 (6%)	1 (3%)	3	19
4	e	44/63 (70%)	36 (82%)	7 (16%)	1 (2%)	5	23
5	g	315/319 (99%)	279 (89%)	30 (10%)	6 (2%)	6	26
6	h	179/274 (65%)	165 (92%)	12 (7%)	2 (1%)	11	38
7	i	260/483 (54%)	247 (95%)	12 (5%)	1 (0%)	30	59
8	j	44/463 (10%)	42 (96%)	2 (4%)	0	100	100
9	k	664/788 (84%)	599 (90%)	54 (8%)	11 (2%)	7	28
10	l	282/425 (66%)	253 (90%)	21 (7%)	8 (3%)	4	19
12	A	204/252 (81%)	181 (89%)	17 (8%)	6 (3%)	3	19
13	B	212/255 (83%)	184 (87%)	24 (11%)	4 (2%)	6	26
14	C	215/254 (85%)	196 (91%)	15 (7%)	4 (2%)	6	26
15	D	198/240 (82%)	182 (92%)	14 (7%)	2 (1%)	12	40
16	E	258/261 (99%)	235 (91%)	20 (8%)	3 (1%)	10	35
17	F	204/225 (91%)	184 (90%)	19 (9%)	1 (0%)	24	54
18	G	230/236 (98%)	216 (94%)	14 (6%)	0	100	100
19	H	182/190 (96%)	162 (89%)	16 (9%)	4 (2%)	5	24
20	I	184/200 (92%)	160 (87%)	19 (10%)	5 (3%)	4	20
21	J	183/197 (93%)	163 (89%)	18 (10%)	2 (1%)	11	38
22	L	138/156 (88%)	129 (94%)	9 (6%)	0	100	100
23	M	123/143 (86%)	110 (89%)	9 (7%)	4 (3%)	3	17
24	N	148/151 (98%)	137 (93%)	10 (7%)	1 (1%)	18	47
25	O	125/137 (91%)	113 (90%)	10 (8%)	2 (2%)	7	29
26	P	125/142 (88%)	116 (93%)	8 (6%)	1 (1%)	16	44
27	Q	125/143 (87%)	112 (90%)	11 (9%)	2 (2%)	7	29
28	R	123/136 (90%)	114 (93%)	9 (7%)	0	100	100
29	S	133/146 (91%)	122 (92%)	11 (8%)	0	100	100
30	T	141/144 (98%)	131 (93%)	7 (5%)	3 (2%)	5	24
31	U	101/121 (84%)	93 (92%)	4 (4%)	4 (4%)	2	15
32	V	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
33	W	127/130 (98%)	110 (87%)	11 (9%)	6 (5%)	2	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	X	142/145 (98%)	128 (90%)	12 (8%)	2 (1%)	9	31
35	Y	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	16	44
36	Z	61/108 (56%)	56 (92%)	5 (8%)	0	100	100
All	All	5862/7354 (80%)	5305 (90%)	468 (8%)	89 (2%)	11	30

All (89) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	k	483	PRO
12	A	189	VAL
13	B	81	PHE
23	M	104	GLY
23	M	109	GLU
25	O	36	LYS
30	T	69	LYS
30	T	81	GLY
33	W	57	ARG
33	W	66	ASN
33	W	78	ARG
1	b	68	GLY
5	g	55	GLY
6	h	228	ASP
9	k	374	TYR
12	A	49	ASN
13	B	35	PRO
17	F	150	GLY
19	H	111	LYS
20	I	186	GLY
21	J	91	LYS
23	M	103	LEU
24	N	68	GLY
25	O	44	GLY
5	g	58	VAL
5	g	63	GLY
5	g	105	GLY
5	g	237	GLN
6	h	227	ALA
9	k	186	ALA
9	k	348	GLU
9	k	381	PRO
9	k	749	LEU

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Mol	Chain	Res	Type
10	l	30	GLU
10	l	254	PHE
12	A	70	PRO
14	C	190	LEU
16	E	170	THR
20	I	35	ASN
31	U	71	PRO
33	W	55	ASP
34	X	69	ARG
3	d	22	ARG
5	g	15	GLY
9	k	708	PHE
9	k	712	LYS
10	l	47	SER
10	l	68	VAL
10	l	193	GLU
13	B	40	ASN
14	C	146	THR
14	C	223	GLY
15	D	4	LEU
16	E	231	GLN
19	H	85	PHE
20	I	6	ASP
26	P	87	PRO
33	W	67	GLY
9	k	78	GLY
9	k	395	GLY
12	A	97	PRO
13	B	39	GLU
14	C	79	GLU
15	D	81	PRO
19	H	32	PRO
20	I	79	ALA
21	J	126	ARG
23	M	126	TRP
27	Q	128	LYS
30	T	17	ALA
35	Y	31	ASN
9	k	392	VAL
10	l	99	ASN
10	l	183	SER
12	A	158	VAL

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Mol	Chain	Res	Type
19	H	84	LYS
4	e	6	GLY
12	A	139	VAL
27	Q	5	PRO
33	W	76	SER
34	X	68	ILE
2	c	24	GLY
7	i	250	ASN
10	l	98	GLY
31	U	96	PRO
16	E	29	PRO
20	I	104	ILE
31	U	55	PRO
31	U	73	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	70/71 (99%)	66 (94%)	4 (6%)	18	45
2	c	56/60 (93%)	48 (86%)	8 (14%)	3	13
3	d	33/49 (67%)	33 (100%)	0	100	100
4	e	40/54 (74%)	36 (90%)	4 (10%)	7	26
5	g	259/262 (99%)	239 (92%)	20 (8%)	12	37
6	h	158/238 (66%)	144 (91%)	14 (9%)	9	31
7	i	234/424 (55%)	222 (95%)	12 (5%)	21	48
8	j	44/419 (10%)	42 (96%)	2 (4%)	24	51
9	k	580/703 (82%)	556 (96%)	24 (4%)	27	52
10	l	260/384 (68%)	245 (94%)	15 (6%)	18	45
12	A	171/210 (81%)	153 (90%)	18 (10%)	6	23
13	B	191/224 (85%)	175 (92%)	16 (8%)	10	34
14	C	176/205 (86%)	153 (87%)	23 (13%)	4	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	D	164/195 (84%)	148 (90%)	16 (10%)	7	27
16	E	221/222 (100%)	200 (90%)	21 (10%)	8	29
17	F	173/191 (91%)	162 (94%)	11 (6%)	16	42
18	G	198/201 (98%)	174 (88%)	24 (12%)	5	19
19	H	165/170 (97%)	150 (91%)	15 (9%)	9	30
20	I	150/161 (93%)	131 (87%)	19 (13%)	4	17
21	J	158/166 (95%)	136 (86%)	22 (14%)	3	14
22	L	125/137 (91%)	111 (89%)	14 (11%)	6	21
23	M	101/119 (85%)	94 (93%)	7 (7%)	14	40
24	N	127/128 (99%)	115 (91%)	12 (9%)	8	29
25	O	91/105 (87%)	81 (89%)	10 (11%)	6	22
26	P	105/118 (89%)	98 (93%)	7 (7%)	15	41
27	Q	107/119 (90%)	100 (94%)	7 (6%)	15	42
28	R	113/124 (91%)	103 (91%)	10 (9%)	9	31
29	S	120/129 (93%)	114 (95%)	6 (5%)	22	49
30	T	115/116 (99%)	106 (92%)	9 (8%)	11	37
31	U	96/114 (84%)	90 (94%)	6 (6%)	16	42
32	V	74/74 (100%)	63 (85%)	11 (15%)	3	12
33	W	110/111 (99%)	94 (86%)	16 (14%)	3	13
34	X	119/120 (99%)	110 (92%)	9 (8%)	12	38
35	Y	112/113 (99%)	99 (88%)	13 (12%)	5	20
36	Z	56/89 (63%)	54 (96%)	2 (4%)	31	56
All	All	5072/6325 (80%)	4645 (92%)	427 (8%)	12	34

All (427) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	2	VAL
1	b	11	THR
1	b	48	SER
1	b	73	LEU
2	c	8	THR
2	c	15	VAL
2	c	19	THR

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Mol	Chain	Res	Type
2	c	28	VAL
2	c	33	LEU
2	c	48	VAL
2	c	55	VAL
2	c	56	LEU
4	e	5	HIS
4	e	7	SER
4	e	25	GLU
4	e	42	ARG
5	g	14	GLU
5	g	43	ILE
5	g	46	LYS
5	g	59	ARG
5	g	76	ASP
5	g	81	LEU
5	g	109	ASP
5	g	136	ILE
5	g	137	LYS
5	g	149	ASP
5	g	153	GLN
5	g	165	ASP
5	g	193	ILE
5	g	202	LEU
5	g	207	ASP
5	g	238	ASP
5	g	265	LEU
5	g	268	GLN
5	g	275	ARG
5	g	290	VAL
6	h	99	ILE
6	h	106	MET
6	h	146	THR
6	h	152	LEU
6	h	163	THR
6	h	174	LEU
6	h	192	THR
6	h	209	ASP
6	h	216	ILE
6	h	220	THR
6	h	221	ARG
6	h	226	LEU
6	h	234	LEU

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Mol	Chain	Res	Type
6	h	251	ILE
7	i	217	VAL
7	i	240	ARG
7	i	274	GLU
7	i	283	LEU
7	i	311	LEU
7	i	328	THR
7	i	333	ARG
7	i	347	VAL
7	i	350	LEU
7	i	385	GLN
7	i	395	MET
7	i	412	VAL
8	j	360	GLN
8	j	362	ASP
9	k	62	ARG
9	k	153	LYS
9	k	175	GLN
9	k	191	VAL
9	k	198	VAL
9	k	253	ARG
9	k	265	ASP
9	k	360	TYR
9	k	371	THR
9	k	392	VAL
9	k	396	THR
9	k	504	LEU
9	k	515	ASP
9	k	526	LYS
9	k	557	ILE
9	k	568	LEU
9	k	571	ILE
9	k	572	GLN
9	k	600	ARG
9	k	608	VAL
9	k	660	VAL
9	k	696	ILE
9	k	729	TRP
9	k	783	LEU
10	l	12	THR
10	l	14	ASP
10	l	32	VAL

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Mol	Chain	Res	Type
10	l	34	THR
10	l	62	ILE
10	l	121	VAL
10	l	124	ILE
10	l	153	HIS
10	l	176	VAL
10	l	181	ASP
10	l	189	MET
10	l	198	ARG
10	l	235	ILE
10	l	254	PHE
10	l	258	ILE
12	A	8	ASP
12	A	10	THR
12	A	12	GLU
12	A	50	VAL
12	A	56	LYS
12	A	57	LEU
12	A	59	LEU
12	A	67	ILE
12	A	76	ILE
12	A	93	THR
12	A	111	ILE
12	A	119	ARG
12	A	122	ILE
12	A	135	GLU
12	A	154	GLU
12	A	157	ASP
12	A	195	TRP
12	A	200	ASP
13	B	21	VAL
13	B	32	ILE
13	B	43	VAL
13	B	46	THR
13	B	51	SER
13	B	69	CYS
13	B	98	THR
13	B	116	LYS
13	B	127	VAL
13	B	130	SER
13	B	140	ILE
13	B	144	ARG

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Mol	Chain	Res	Type
13	B	176	VAL
13	B	180	THR
13	B	201	THR
13	B	220	GLN
14	C	36	VAL
14	C	51	THR
14	C	53	ILE
14	C	58	LEU
14	C	61	LEU
14	C	80	VAL
14	C	108	ASN
14	C	111	VAL
14	C	139	ILE
14	C	140	ARG
14	C	154	LEU
14	C	166	THR
14	C	170	ILE
14	C	198	THR
14	C	207	LEU
14	C	210	THR
14	C	212	LYS
14	C	218	ILE
14	C	221	THR
14	C	225	LEU
14	C	228	ASN
14	C	237	VAL
14	C	241	ASP
15	D	4	LEU
15	D	7	LYS
15	D	23	GLU
15	D	39	VAL
15	D	41	VAL
15	D	84	ILE
15	D	103	GLU
15	D	105	MET
15	D	117	ARG
15	D	158	ILE
15	D	164	VAL
15	D	175	VAL
15	D	176	LEU
15	D	178	ARG
15	D	190	ARG

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Mol	Chain	Res	Type
15	D	196	ARG
16	E	6	LYS
16	E	9	LEU
16	E	38	LEU
16	E	39	ARG
16	E	45	ILE
16	E	49	ARG
16	E	54	TYR
16	E	59	ARG
16	E	78	THR
16	E	87	MET
16	E	95	THR
16	E	102	VAL
16	E	105	VAL
16	E	147	ILE
16	E	155	LYS
16	E	156	VAL
16	E	181	VAL
16	E	183	VAL
16	E	189	LEU
16	E	195	ILE
16	E	240	LYS
17	F	89	ILE
17	F	103	ASN
17	F	123	VAL
17	F	125	THR
17	F	146	THR
17	F	156	ARG
17	F	162	VAL
17	F	190	ILE
17	F	194	LEU
17	F	216	GLU
17	F	225	ARG
18	G	18	ILE
18	G	25	ARG
18	G	71	THR
18	G	73	ILE
18	G	77	LEU
18	G	78	THR
18	G	97	VAL
18	G	98	ARG
18	G	105	ASP

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Mol	Chain	Res	Type
18	G	109	LEU
18	G	114	VAL
18	G	120	GLU
18	G	122	GLU
18	G	124	LEU
18	G	126	ASP
18	G	129	VAL
18	G	133	LEU
18	G	142	ARG
18	G	143	LYS
18	G	153	VAL
18	G	155	ASP
18	G	177	ARG
18	G	179	VAL
18	G	212	LEU
19	H	28	GLU
19	H	46	ILE
19	H	49	ILE
19	H	50	ASP
19	H	73	VAL
19	H	79	ARG
19	H	87	ASP
19	H	105	THR
19	H	112	ARG
19	H	126	LEU
19	H	129	LEU
19	H	133	THR
19	H	136	VAL
19	H	139	ARG
19	H	144	VAL
20	I	5	ARG
20	I	29	LEU
20	I	38	ILE
20	I	45	SER
20	I	56	ARG
20	I	58	LEU
20	I	76	THR
20	I	90	LEU
20	I	92	ARG
20	I	103	GLN
20	I	104	ILE
20	I	107	THR

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Mol	Chain	Res	Type
20	I	137	LYS
20	I	140	GLU
20	I	156	VAL
20	I	164	ARG
20	I	176	SER
20	I	179	CYS
20	I	185	GLU
21	J	3	ARG
21	J	7	THR
21	J	24	LEU
21	J	28	LEU
21	J	39	LYS
21	J	49	LEU
21	J	60	LEU
21	J	77	ILE
21	J	78	ARG
21	J	79	ARG
21	J	81	VAL
21	J	83	VAL
21	J	89	ASP
21	J	96	VAL
21	J	99	LEU
21	J	105	LEU
21	J	109	LEU
21	J	110	GLN
21	J	113	VAL
21	J	130	THR
21	J	131	GLN
21	J	132	ARG
22	L	8	GLN
22	L	40	LEU
22	L	43	LYS
22	L	44	THR
22	L	58	CYS
22	L	66	ILE
22	L	67	ARG
22	L	77	SER
22	L	83	THR
22	L	109	VAL
22	L	117	VAL
22	L	123	VAL
22	L	129	ARG

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Mol	Chain	Res	Type
22	L	131	ILE
23	M	31	VAL
23	M	37	VAL
23	M	45	LEU
23	M	91	VAL
23	M	103	LEU
23	M	122	VAL
23	M	133	LEU
24	N	3	ARG
24	N	4	MET
24	N	20	ARG
24	N	39	LYS
24	N	53	LEU
24	N	64	ARG
24	N	66	ILE
24	N	67	THR
24	N	80	LEU
24	N	88	LEU
24	N	125	LEU
24	N	134	VAL
25	O	12	GLN
25	O	31	THR
25	O	43	THR
25	O	54	GLU
25	O	66	ASP
25	O	67	VAL
25	O	80	HIS
25	O	89	THR
25	O	105	LEU
25	O	124	ASP
26	P	20	VAL
26	P	50	THR
26	P	60	LEU
26	P	79	HIS
26	P	86	VAL
26	P	124	THR
26	P	141	LEU
27	Q	9	THR
27	Q	29	ILE
27	Q	48	VAL
27	Q	53	LEU
27	Q	55	VAL

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Mol	Chain	Res	Type
27	Q	69	VAL
27	Q	97	VAL
28	R	25	THR
28	R	29	GLN
28	R	34	LEU
28	R	38	ILE
28	R	46	LEU
28	R	61	ILE
28	R	82	ASP
28	R	99	VAL
28	R	102	VAL
28	R	115	LEU
29	S	20	THR
29	S	29	VAL
29	S	62	THR
29	S	74	GLN
29	S	100	THR
29	S	105	VAL
30	T	4	VAL
30	T	38	LYS
30	T	64	HIS
30	T	101	ASN
30	T	114	VAL
30	T	131	ASP
30	T	132	LEU
30	T	135	ILE
30	T	144	GLU
31	U	22	ILE
31	U	30	LYS
31	U	31	VAL
31	U	51	VAL
31	U	64	LYS
31	U	89	ARG
32	V	1	MET
32	V	8	LEU
32	V	20	THR
32	V	25	LYS
32	V	32	VAL
32	V	34	ILE
32	V	51	VAL
32	V	62	ARG
32	V	69	LEU

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Mol	Chain	Res	Type
32	V	71	ARG
32	V	81	ASN
33	W	6	VAL
33	W	7	LEU
33	W	15	ASN
33	W	24	GLN
33	W	25	VAL
33	W	41	MET
33	W	57	ARG
33	W	65	LEU
33	W	66	ASN
33	W	80	ASN
33	W	98	GLN
33	W	103	ILE
33	W	106	THR
33	W	111	MET
33	W	117	ARG
33	W	125	ILE
34	X	7	ARG
34	X	11	SER
34	X	43	PHE
34	X	60	GLU
34	X	84	THR
34	X	94	ASN
34	X	117	ILE
34	X	120	VAL
34	X	141	GLU
35	Y	8	ARG
35	Y	14	SER
35	Y	34	ASN
35	Y	44	LEU
35	Y	55	VAL
35	Y	70	VAL
35	Y	74	LEU
35	Y	75	VAL
35	Y	79	VAL
35	Y	84	LYS
35	Y	105	ARG
35	Y	106	GLN
35	Y	108	ARG
36	Z	71	ILE
36	Z	89	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	51	GLN
2	c	27	GLN
2	c	43	ASN
3	d	48	ASN
5	g	4	ASN
5	g	29	GLN
5	g	174	ASN
5	g	268	GLN
5	g	299	GLN
6	h	142	ASN
6	h	239	HIS
7	i	385	GLN
7	i	434	GLN
8	j	366	ASN
9	k	60	GLN
9	k	144	ASN
9	k	166	GLN
9	k	237	ASN
9	k	288	ASN
9	k	506	ASN
9	k	547	ASN
9	k	591	ASN
9	k	617	GLN
9	k	626	GLN
10	l	7	HIS
10	l	29	HIS
10	l	99	ASN
12	A	23	HIS
12	A	30	GLN
12	A	92	HIS
12	A	131	GLN
12	A	168	HIS
13	B	95	ASN
13	B	101	HIS
13	B	118	GLN
13	B	209	ASN
13	B	232	HIS
14	C	59	HIS
14	C	94	GLN
14	C	108	ASN
14	C	147	ASN

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Mol	Chain	Res	Type
14	C	228	ASN
14	C	233	GLN
15	D	159	HIS
16	E	50	ASN
16	E	98	ASN
16	E	112	HIS
16	E	188	ASN
16	E	201	HIS
16	E	209	HIS
17	F	34	GLN
17	F	103	ASN
17	F	116	HIS
18	G	34	GLN
18	G	56	ASN
18	G	80	ASN
18	G	201	GLN
19	H	5	GLN
19	H	71	HIS
19	H	108	GLN
19	H	110	GLN
20	I	32	GLN
20	I	84	HIS
20	I	87	ASN
21	J	110	GLN
21	J	123	HIS
21	J	131	GLN
22	L	14	GLN
22	L	104	HIS
23	M	80	ASN
23	M	139	HIS
24	N	58	HIS
25	O	29	HIS
25	O	80	HIS
25	O	99	GLN
26	P	128	HIS
27	Q	103	ASN
28	R	83	GLN
28	R	123	ASN
29	S	74	GLN
30	T	127	ASN
30	T	129	GLN
30	T	138	GLN

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Mol	Chain	Res	Type
31	U	44	ASN
31	U	72	ASN
33	W	24	GLN
33	W	44	HIS
33	W	56	HIS
33	W	66	ASN
33	W	113	HIS
33	W	120	HIS
34	X	27	ASN
35	Y	29	HIS
36	Z	82	HIS
36	Z	98	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	2	1771/1800 (98%)	632 (35%)	20 (1%)

All (632) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	2	4	C
11	2	17	C
11	2	25	C
11	2	26	A
11	2	34	G
11	2	42	G
11	2	45	U
11	2	47	A
11	2	50	C
11	2	51	A
11	2	57	G
11	2	60	U
11	2	66	U
11	2	67	A
11	2	68	A
11	2	72	A
11	2	73	U
11	2	74	U
11	2	75	U
11	2	77	U

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Mol	Chain	Res	Type
11	2	101	U
11	2	103	A
11	2	104	A
11	2	105	A
11	2	114	C
11	2	115	G
11	2	127	G
11	2	128	U
11	2	130	C
11	2	131	C
11	2	134	U
11	2	135	A
11	2	138	A
11	2	140	A
11	2	141	U
11	2	142	G
11	2	146	U
11	2	153	G
11	2	155	U
11	2	156	A
11	2	158	U
11	2	178	U
11	2	179	A
11	2	185	U
11	2	186	C
11	2	191	C
11	2	192	U
11	2	193	U
11	2	194	U
11	2	195	G
11	2	196	G
11	2	197	A
11	2	198	A
11	2	215	A
11	2	217	A
11	2	218	A
11	2	219	A
11	2	220	A
11	2	221	A
11	2	225	A
11	2	227	U
11	2	228	G

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Mol	Chain	Res	Type
11	2	229	U
11	2	230	C
11	2	231	U
11	2	232	U
11	2	233	C
11	2	234	G
11	2	235	G
11	2	236	A
11	2	237	C
11	2	238	U
11	2	240	U
11	2	241	U
11	2	242	U
11	2	250	C
11	2	257	A
11	2	261	U
11	2	265	A
11	2	267	U
11	2	269	G
11	2	271	A
11	2	272	U
11	2	275	C
11	2	276	C
11	2	277	U
11	2	278	U
11	2	279	G
11	2	280	U
11	2	281	G
11	2	288	A
11	2	304	U
11	2	305	C
11	2	308	C
11	2	309	C
11	2	314	C
11	2	316	A
11	2	318	U
11	2	319	U
11	2	320	U
11	2	322	G
11	2	334	G
11	2	335	U
11	2	337	G

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Mol	Chain	Res	Type
11	2	338	C
11	2	344	A
11	2	345	U
11	2	352	A
11	2	359	A
11	2	360	A
11	2	361	C
11	2	369	A
11	2	370	A
11	2	399	A
11	2	400	A
11	2	401	A
11	2	402	C
11	2	404	G
11	2	411	C
11	2	416	A
11	2	417	A
11	2	419	G
11	2	423	G
11	2	424	C
11	2	425	A
11	2	426	G
11	2	434	G
11	2	439	U
11	2	444	C
11	2	445	A
11	2	446	A
11	2	448	C
11	2	459	G
11	2	460	A
11	2	464	A
11	2	469	C
11	2	475	A
11	2	477	A
11	2	478	A
11	2	479	C
11	2	480	G
11	2	481	A
11	2	482	U
11	2	483	A
11	2	484	C
11	2	486	G

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Mol	Chain	Res	Type
11	2	490	C
11	2	492	A
11	2	493	U
11	2	494	U
11	2	495	C
11	2	497	G
11	2	498	G
11	2	500	C
11	2	504	U
11	2	505	A
11	2	506	A
11	2	507	U
11	2	514	G
11	2	519	C
11	2	527	A
11	2	532	U
11	2	534	A
11	2	540	G
11	2	541	A
11	2	542	A
11	2	543	C
11	2	544	A
11	2	545	A
11	2	548	G
11	2	549	G
11	2	555	A
11	2	556	A
11	2	557	G
11	2	558	U
11	2	559	C
11	2	563	U
11	2	564	G
11	2	565	C
11	2	566	C
11	2	567	A
11	2	568	G
11	2	571	G
11	2	575	C
11	2	576	G
11	2	577	G
11	2	578	U
11	2	579	A

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Mol	Chain	Res	Type
11	2	580	A
11	2	582	U
11	2	583	C
11	2	594	A
11	2	595	G
11	2	606	A
11	2	610	G
11	2	611	U
11	2	619	A
11	2	620	A
11	2	622	A
11	2	623	A
11	2	624	G
11	2	635	A
11	2	638	U
11	2	639	U
11	2	640	U
11	2	650	U
11	2	653	C
11	2	655	G
11	2	656	G
11	2	657	U
11	2	658	C
11	2	677	G
11	2	679	U
11	2	680	U
11	2	684	A
11	2	685	A
11	2	696	C
11	2	697	C
11	2	698	U
11	2	699	U
11	2	700	C
11	2	708	C
11	2	709	C
11	2	712	G
11	2	714	G
11	2	715	U
11	2	717	C
11	2	718	U
11	2	719	U
11	2	721	U

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Mol	Chain	Res	Type
11	2	722	G
11	2	723	G
11	2	728	U
11	2	736	C
11	2	737	A
11	2	738	G
11	2	739	G
11	2	740	A
11	2	741	C
11	2	742	U
11	2	743	U
11	2	754	A
11	2	756	A
11	2	758	U
11	2	762	A
11	2	765	G
11	2	766	U
11	2	767	U
11	2	768	C
11	2	774	A
11	2	775	G
11	2	777	C
11	2	780	A
11	2	781	U
11	2	782	U
11	2	783	G
11	2	784	C
11	2	786	C
11	2	787	G
11	2	789	A
11	2	793	A
11	2	794	U
11	2	811	A
11	2	812	A
11	2	813	U
11	2	815	G
11	2	816	G
11	2	819	G
11	2	820	U
11	2	821	U
11	2	822	U
11	2	824	G

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Mol	Chain	Res	Type
11	2	826	U
11	2	827	C
11	2	829	A
11	2	830	U
11	2	831	U
11	2	832	U
11	2	834	G
11	2	835	U
11	2	840	U
11	2	841	U
11	2	846	G
11	2	850	A
11	2	851	U
11	2	852	C
11	2	854	U
11	2	855	A
11	2	856	A
11	2	857	U
11	2	862	A
11	2	863	A
11	2	865	A
11	2	876	G
11	2	886	U
11	2	898	A
11	2	900	A
11	2	904	G
11	2	905	A
11	2	906	A
11	2	908	U
11	2	909	U
11	2	910	C
11	2	912	U
11	2	913	G
11	2	914	G
11	2	915	A
11	2	921	U
11	2	924	A
11	2	926	A
11	2	928	U
11	2	933	A
11	2	934	C
11	2	935	U

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Mol	Chain	Res	Type
11	2	942	G
11	2	944	A
11	2	959	U
11	2	960	U
11	2	966	A
11	2	969	C
11	2	988	A
11	2	992	A
11	2	993	A
11	2	997	G
11	2	998	A
11	2	1000	C
11	2	1001	A
11	2	1002	G
11	2	1003	A
11	2	1004	U
11	2	1005	A
11	2	1007	C
11	2	1009	U
11	2	1011	G
11	2	1012	U
11	2	1016	C
11	2	1020	A
11	2	1021	C
11	2	1026	A
11	2	1028	C
11	2	1031	U
11	2	1043	A
11	2	1044	U
11	2	1053	G
11	2	1058	U
11	2	1059	U
11	2	1060	U
11	2	1061	A
11	2	1063	U
11	2	1072	C
11	2	1073	G
11	2	1076	A
11	2	1078	C
11	2	1080	U
11	2	1081	A
11	2	1082	C

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Mol	Chain	Res	Type
11	2	1092	A
11	2	1096	C
11	2	1097	U
11	2	1098	U
11	2	1100	G
11	2	1137	A
11	2	1138	A
11	2	1143	A
11	2	1146	G
11	2	1148	C
11	2	1150	G
11	2	1151	A
11	2	1152	A
11	2	1155	G
11	2	1156	C
11	2	1157	A
11	2	1158	C
11	2	1160	A
11	2	1164	G
11	2	1165	G
11	2	1167	G
11	2	1183	A
11	2	1185	U
11	2	1186	U
11	2	1189	A
11	2	1198	G
11	2	1199	G
11	2	1200	G
11	2	1201	G
11	2	1203	A
11	2	1206	U
11	2	1207	C
11	2	1208	A
11	2	1210	C
11	2	1212	G
11	2	1214	U
11	2	1215	C
11	2	1216	C
11	2	1217	A
11	2	1218	G
11	2	1219	A
11	2	1220	C

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Mol	Chain	Res	Type
11	2	1227	A
11	2	1228	G
11	2	1229	G
11	2	1230	A
11	2	1232	U
11	2	1234	A
11	2	1235	C
11	2	1236	A
11	2	1238	A
11	2	1239	U
11	2	1240	U
11	2	1242	A
11	2	1243	G
11	2	1244	A
11	2	1245	G
11	2	1246	C
11	2	1249	U
11	2	1252	C
11	2	1254	U
11	2	1255	G
11	2	1256	A
11	2	1258	U
11	2	1262	U
11	2	1264	G
11	2	1266	U
11	2	1267	G
11	2	1268	G
11	2	1269	U
11	2	1270	G
11	2	1275	A
11	2	1276	U
11	2	1277	G
11	2	1278	G
11	2	1279	C
11	2	1280	C
11	2	1281	G
11	2	1284	C
11	2	1285	U
11	2	1286	U
11	2	1287	A
11	2	1288	G
11	2	1293	U

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Mol	Chain	Res	Type
11	2	1294	G
11	2	1295	G
11	2	1301	U
11	2	1309	C
11	2	1314	U
11	2	1315	U
11	2	1321	A
11	2	1324	G
11	2	1327	C
11	2	1328	G
11	2	1330	G
11	2	1331	A
11	2	1332	C
11	2	1333	C
11	2	1334	U
11	2	1336	A
11	2	1337	A
11	2	1339	C
11	2	1340	U
11	2	1343	U
11	2	1344	A
11	2	1345	A
11	2	1346	A
11	2	1347	U
11	2	1348	A
11	2	1354	G
11	2	1361	U
11	2	1362	U
11	2	1363	U
11	2	1364	G
11	2	1367	G
11	2	1370	U
11	2	1371	A
11	2	1372	U
11	2	1383	G
11	2	1387	G
11	2	1388	A
11	2	1390	U
11	2	1398	U
11	2	1399	C
11	2	1400	A
11	2	1412	G

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Mol	Chain	Res	Type
11	2	1413	U
11	2	1415	U
11	2	1418	G
11	2	1419	G
11	2	1420	C
11	2	1421	A
11	2	1422	A
11	2	1424	A
11	2	1425	A
11	2	1426	C
11	2	1427	A
11	2	1428	G
11	2	1429	G
11	2	1431	C
11	2	1432	U
11	2	1434	U
11	2	1435	G
11	2	1436	A
11	2	1437	U
11	2	1438	G
11	2	1439	C
11	2	1441	C
11	2	1442	U
11	2	1443	U
11	2	1444	A
11	2	1446	A
11	2	1447	C
11	2	1448	G
11	2	1449	U
11	2	1450	U
11	2	1452	U
11	2	1455	G
11	2	1457	C
11	2	1458	G
11	2	1459	C
11	2	1460	A
11	2	1469	A
11	2	1471	A
11	2	1473	U
11	2	1474	G
11	2	1475	A
11	2	1479	A

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Mol	Chain	Res	Type
11	2	1482	C
11	2	1486	G
11	2	1490	C
11	2	1492	A
11	2	1493	A
11	2	1506	G
11	2	1515	A
11	2	1516	A
11	2	1521	G
11	2	1523	G
11	2	1535	U
11	2	1536	G
11	2	1537	C
11	2	1538	U
11	2	1539	G
11	2	1540	G
11	2	1542	G
11	2	1557	U
11	2	1559	A
11	2	1568	C
11	2	1571	C
11	2	1573	A
11	2	1574	G
11	2	1584	G
11	2	1590	G
11	2	1595	U
11	2	1596	C
11	2	1597	A
11	2	1598	U
11	2	1601	G
11	2	1615	C
11	2	1618	C
11	2	1619	C
11	2	1620	C
11	2	1622	G
11	2	1624	C
11	2	1627	U
11	2	1630	U
11	2	1631	A
11	2	1632	C
11	2	1633	A
11	2	1634	C

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Mol	Chain	Res	Type
11	2	1635	A
11	2	1637	C
11	2	1638	G
11	2	1639	C
11	2	1640	C
11	2	1641	C
11	2	1642	G
11	2	1648	A
11	2	1649	G
11	2	1651	A
11	2	1652	C
11	2	1653	C
11	2	1655	A
11	2	1657	U
11	2	1658	G
11	2	1659	A
11	2	1680	G
11	2	1681	A
11	2	1683	C
11	2	1686	C
11	2	1687	U
11	2	1689	A
11	2	1697	G
11	2	1700	C
11	2	1701	A
11	2	1707	A
11	2	1712	A
11	2	1714	A
11	2	1715	G
11	2	1731	A
11	2	1732	A
11	2	1736	G
11	2	1738	U
11	2	1739	C
11	2	1741	U
11	2	1742	U
11	2	1743	U
11	2	1744	A
11	2	1745	G
11	2	1746	A
11	2	1748	G
11	2	1749	A

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Mol	Chain	Res	Type
11	2	1750	A
11	2	1753	A
11	2	1754	A
11	2	1755	A
11	2	1757	G
11	2	1758	U
11	2	1759	C
11	2	1760	G
11	2	1761	U
11	2	1762	A
11	2	1763	A
11	2	1765	A
11	2	1766	A
11	2	1767	G
11	2	1769	U
11	2	1770	U
11	2	1772	C
11	2	1779	U
11	2	1781	A
11	2	1782	A
11	2	1783	C
11	2	1792	G
11	2	1793	G
11	2	1795	U

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	2	155	U
11	2	278	U
11	2	418	G
11	2	539	G
11	2	567	A
11	2	721	U
11	2	779	U
11	2	782	U
11	2	912	U
11	2	1156	C
11	2	1200	G
11	2	1229	G
11	2	1231	U
11	2	1343	U

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Mol	Chain	Res	Type
11	2	1458	G
11	2	1481	C
11	2	1570	A
11	2	1573	A
11	2	1631	A
11	2	1652	C

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 48 ligands modelled in this entry, 48 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	2	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1377:U	O3'	1378:U	P	3.76
1	2	902:G	O3'	903:U	P	3.04

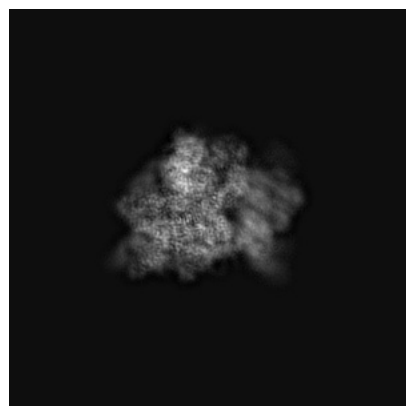
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4214. These allow visual inspection of the internal detail of the map and identification of artifacts.

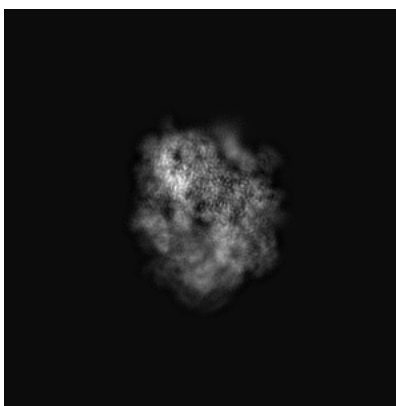
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

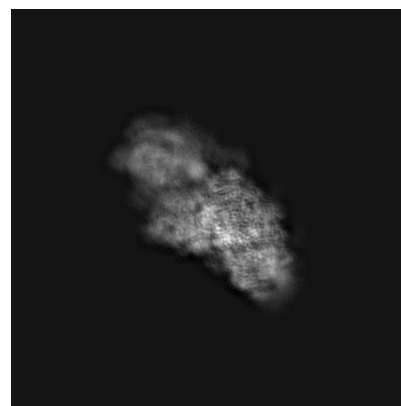
6.1.1 Primary map



X

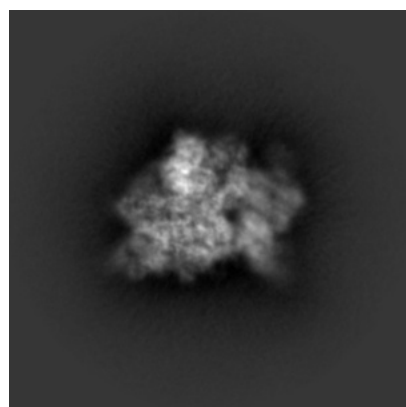


Y

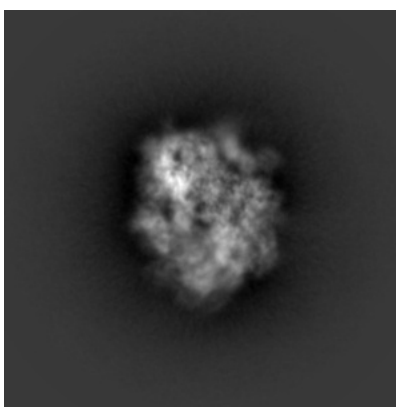


Z

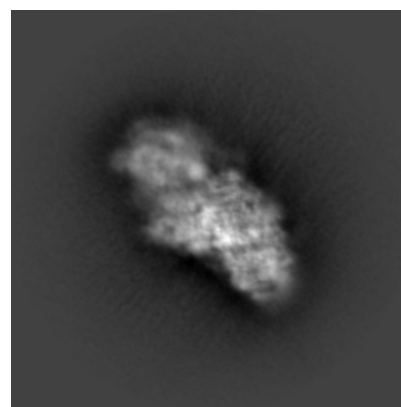
6.1.2 Raw map



X



Y

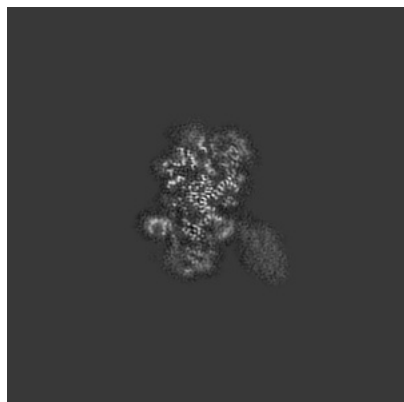


Z

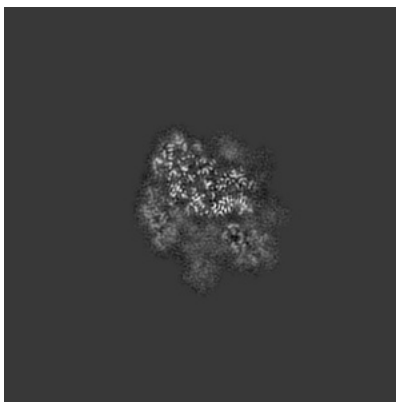
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

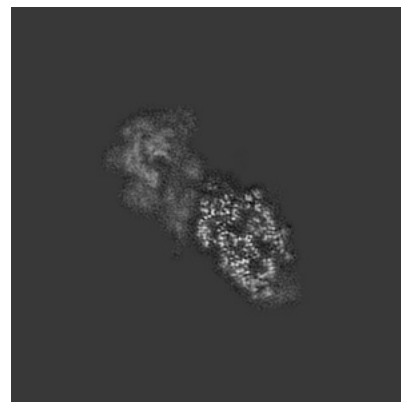
6.2.1 Primary map



X Index: 160

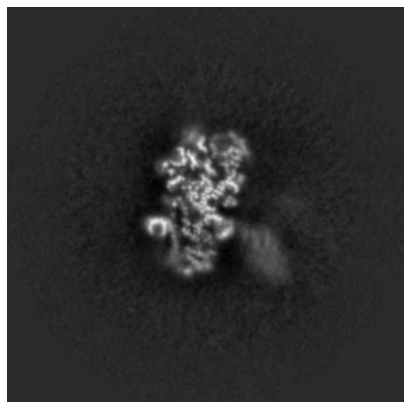


Y Index: 160

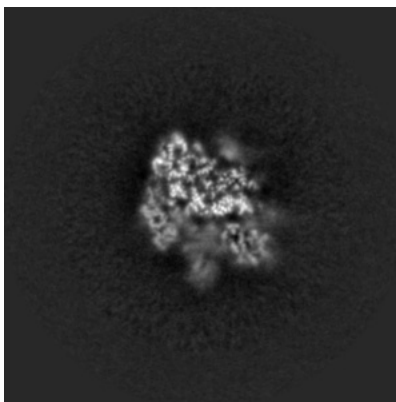


Z Index: 160

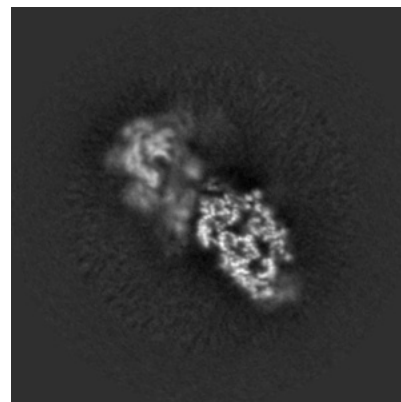
6.2.2 Raw map



X Index: 160



Y Index: 160

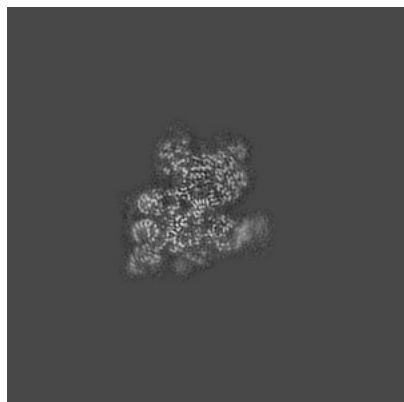


Z Index: 160

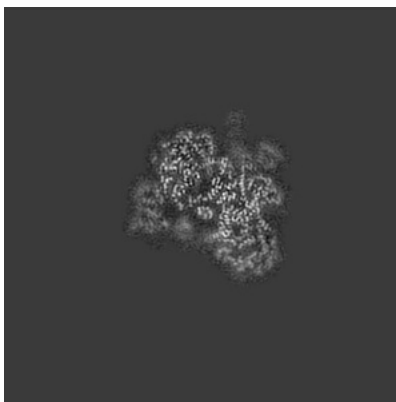
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

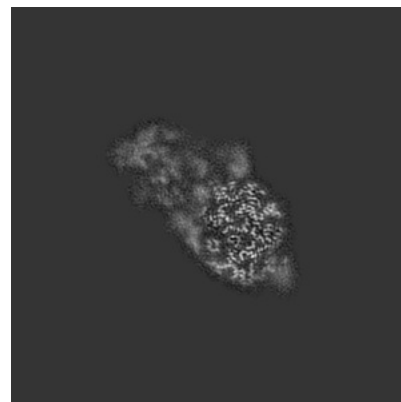
6.3.1 Primary map



X Index: 178

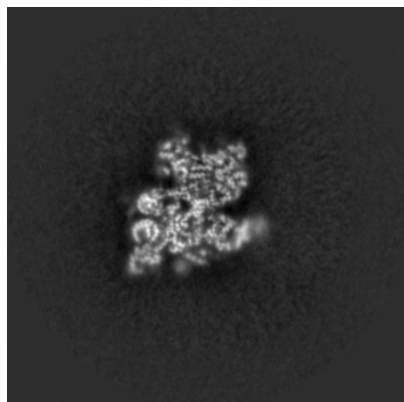


Y Index: 141

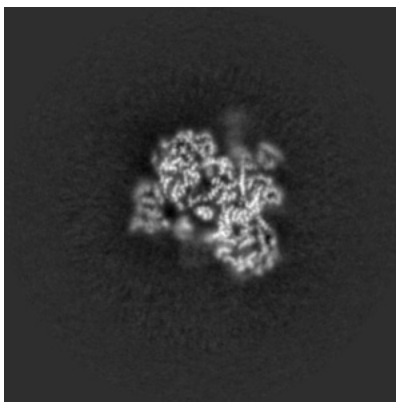


Z Index: 144

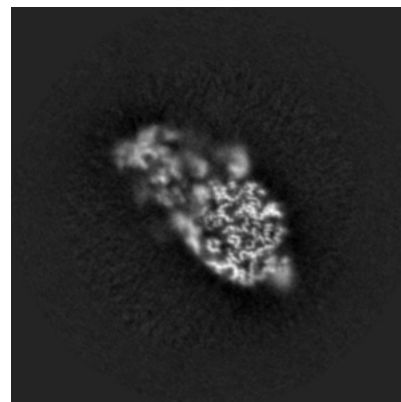
6.3.2 Raw map



X Index: 178



Y Index: 141

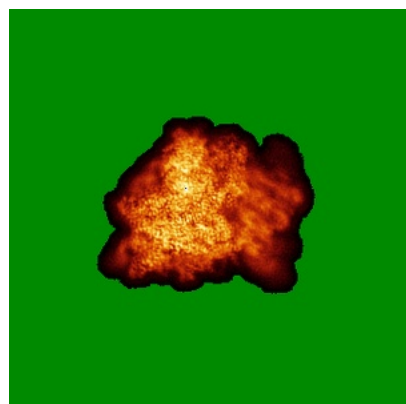


Z Index: 144

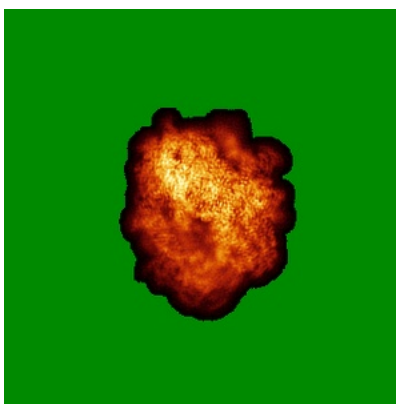
The images above show the largest variance slices of the map in three orthogonal directions.

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

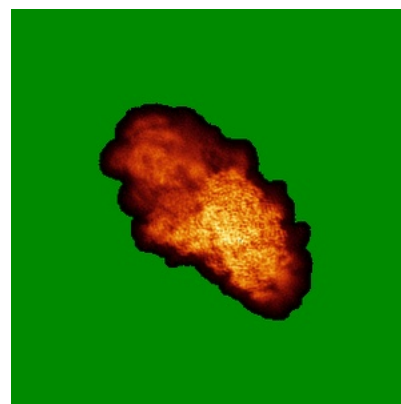
6.4.1 Primary map



X

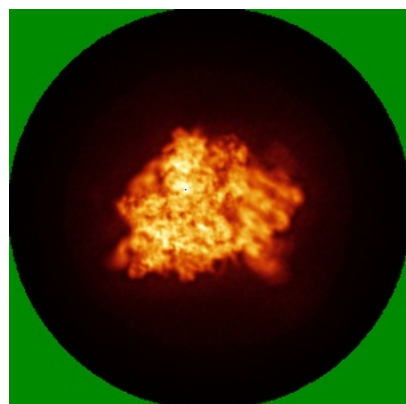


Y

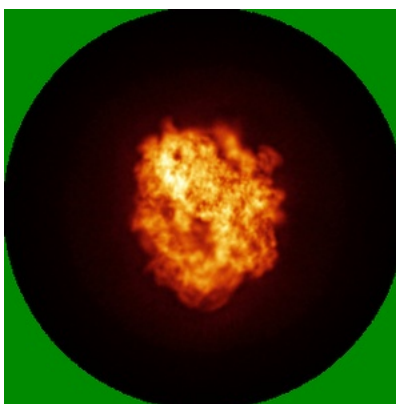


Z

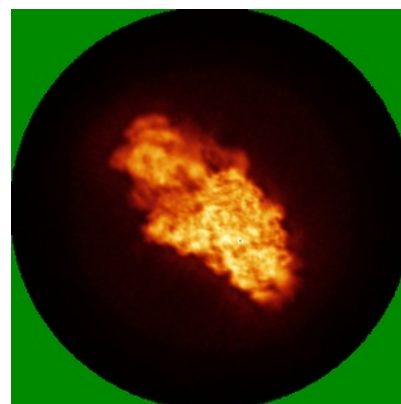
6.4.2 Raw map



X



Y

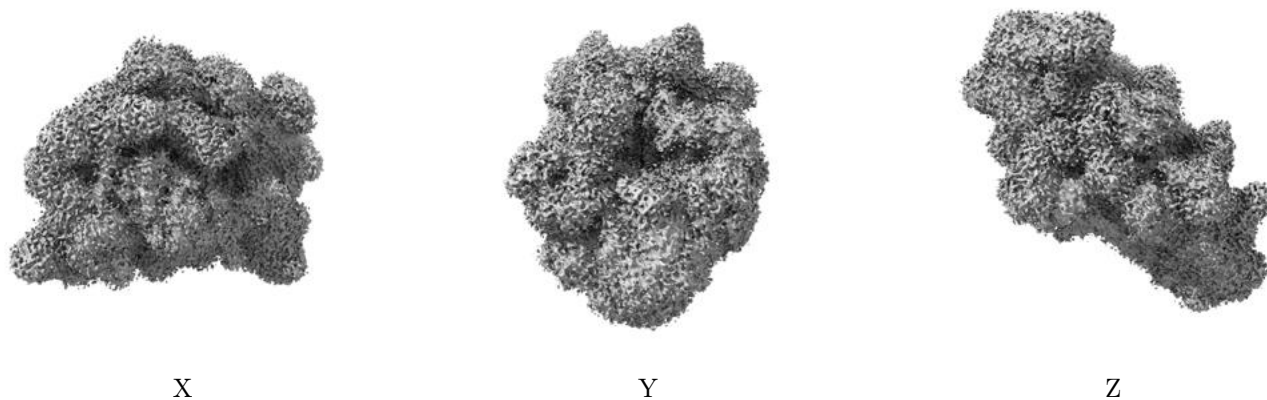


Z

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

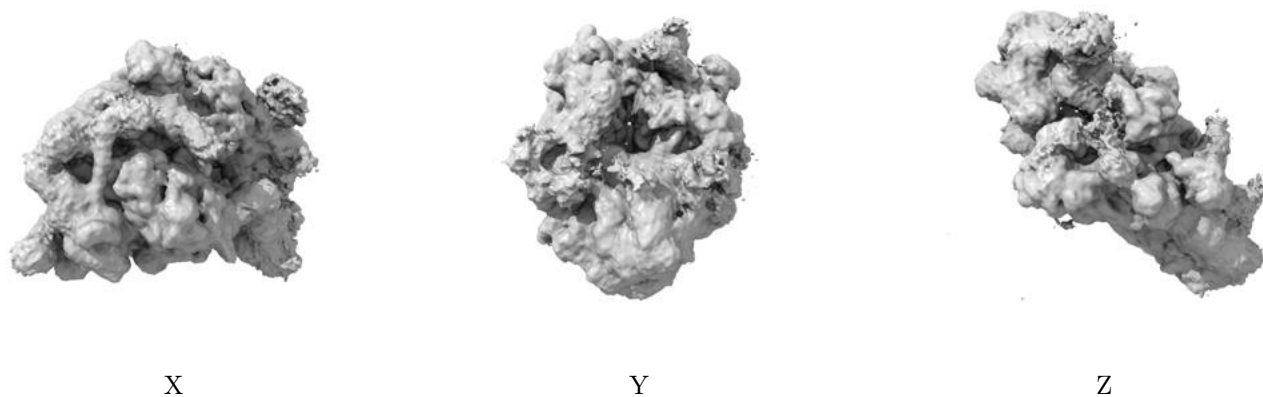
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

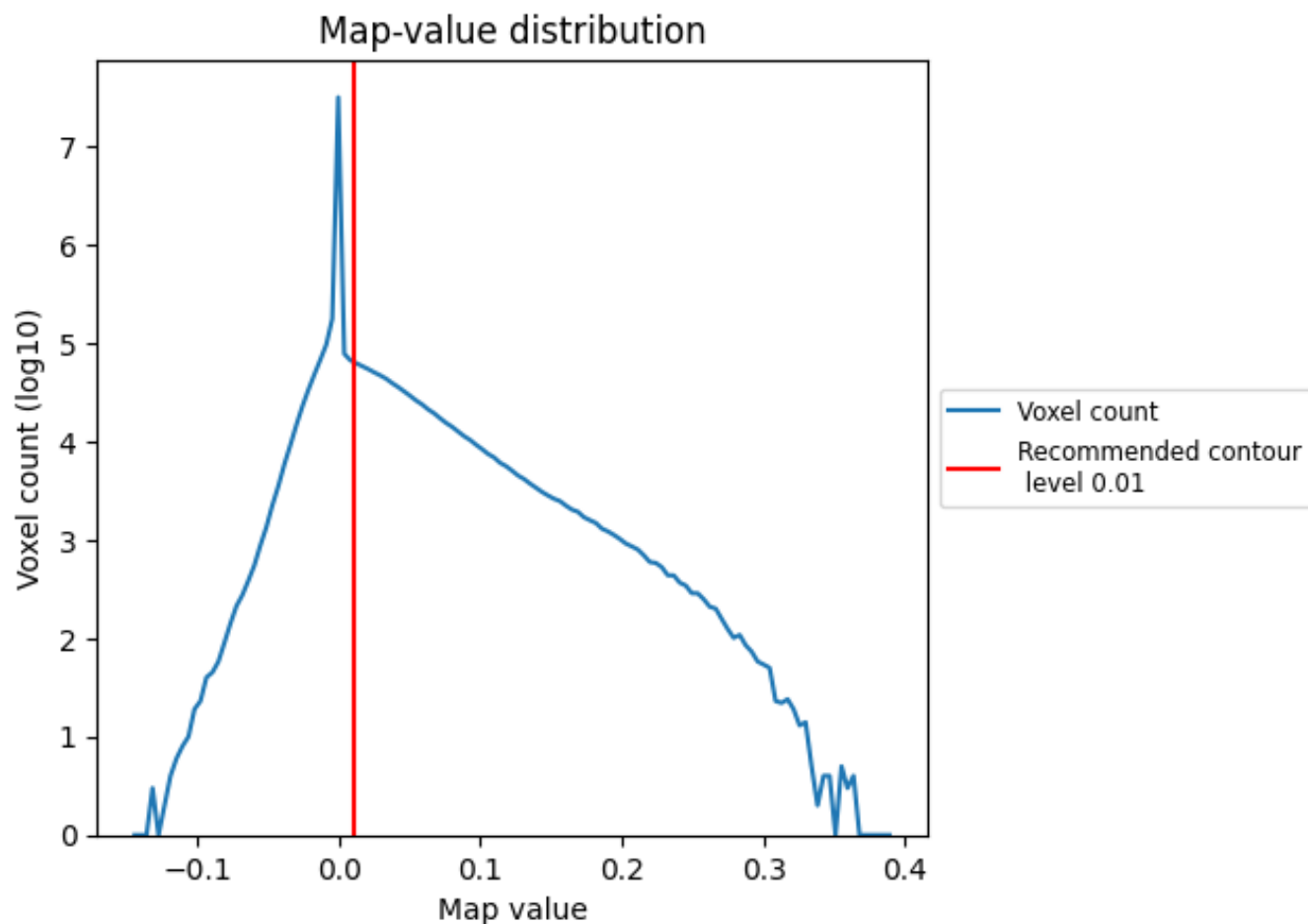
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

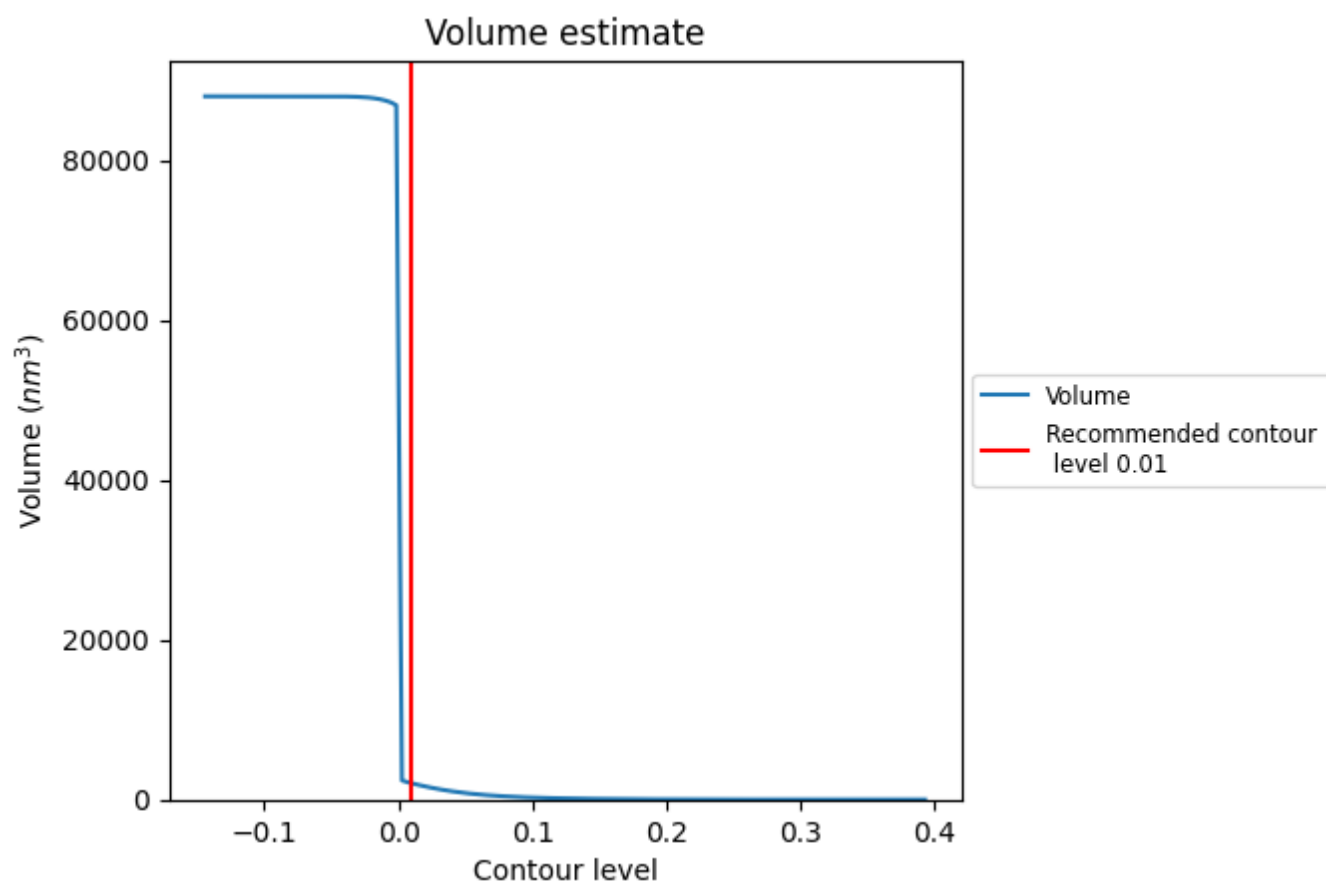
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

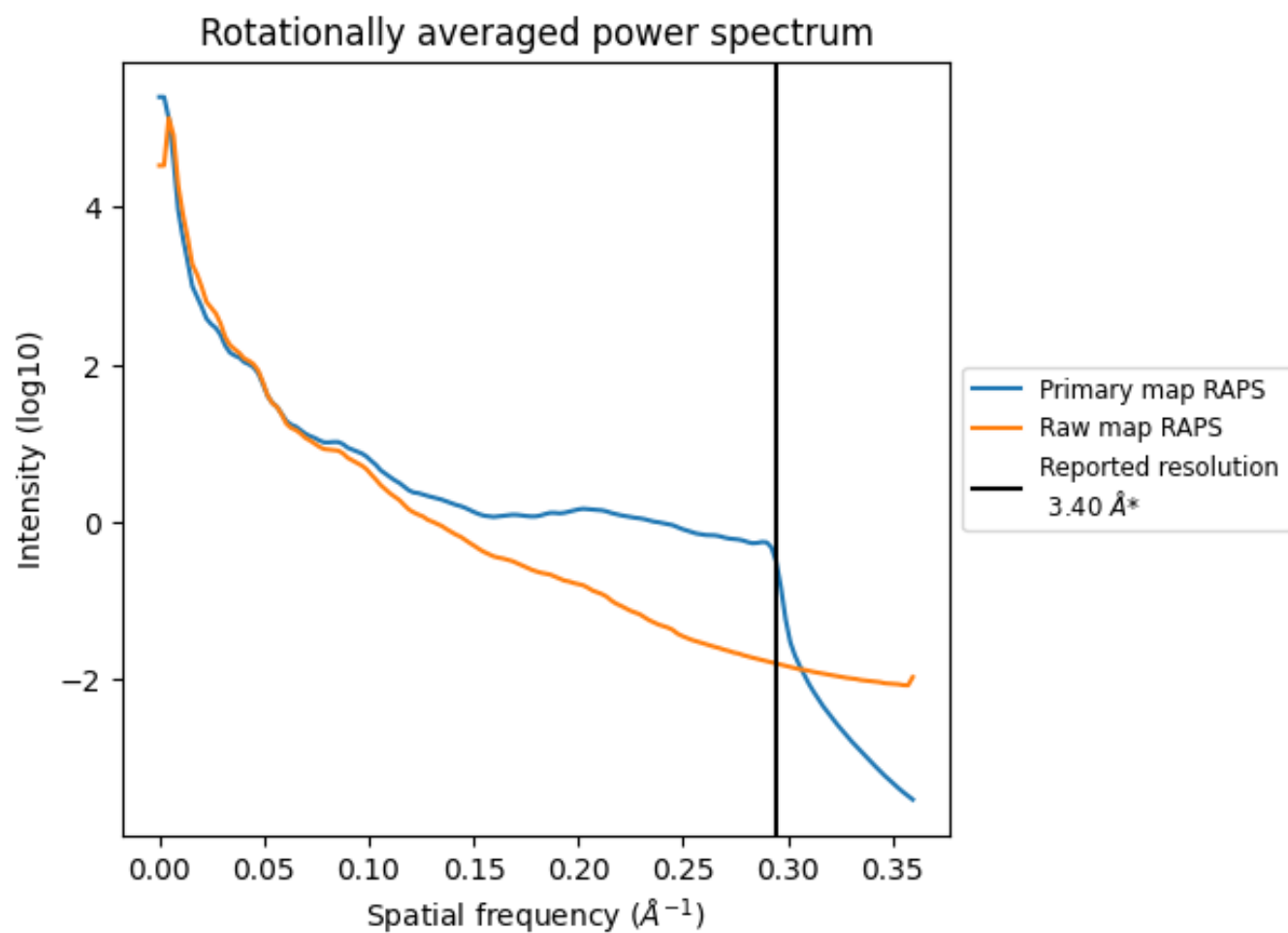
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2041 nm^3 ; this corresponds to an approximate mass of 1844 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 ⓘ

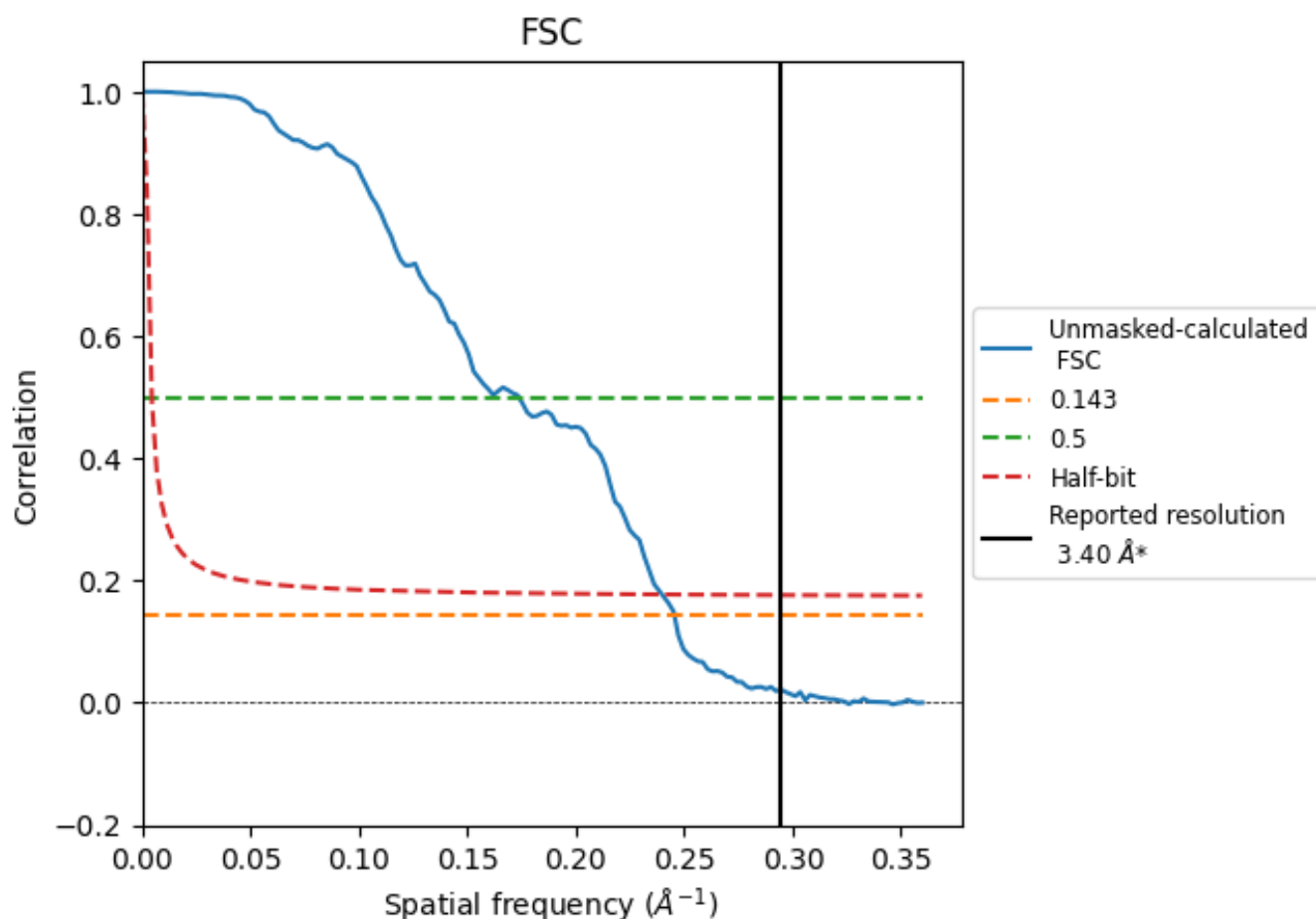


*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

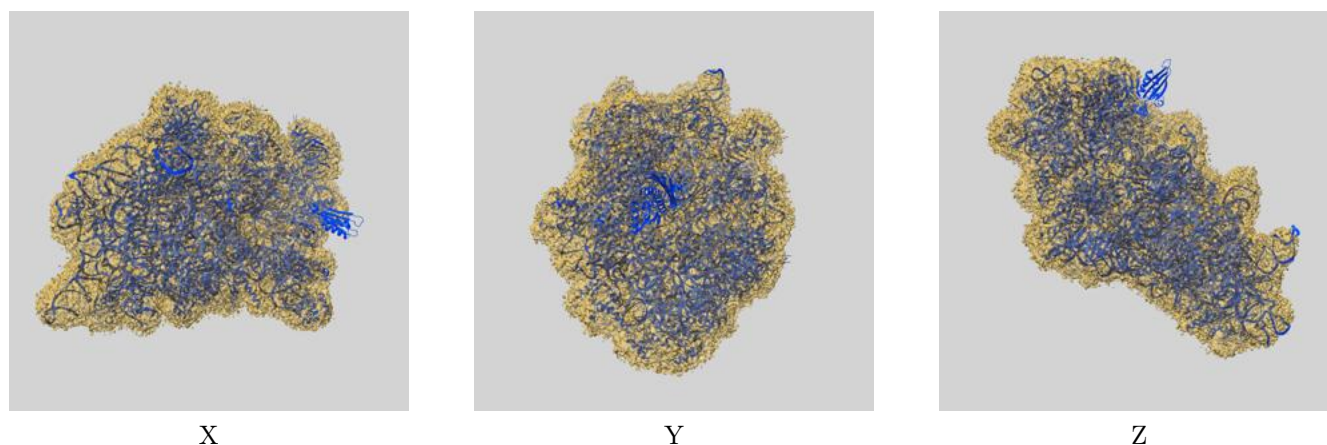
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	5.76	4.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.07 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

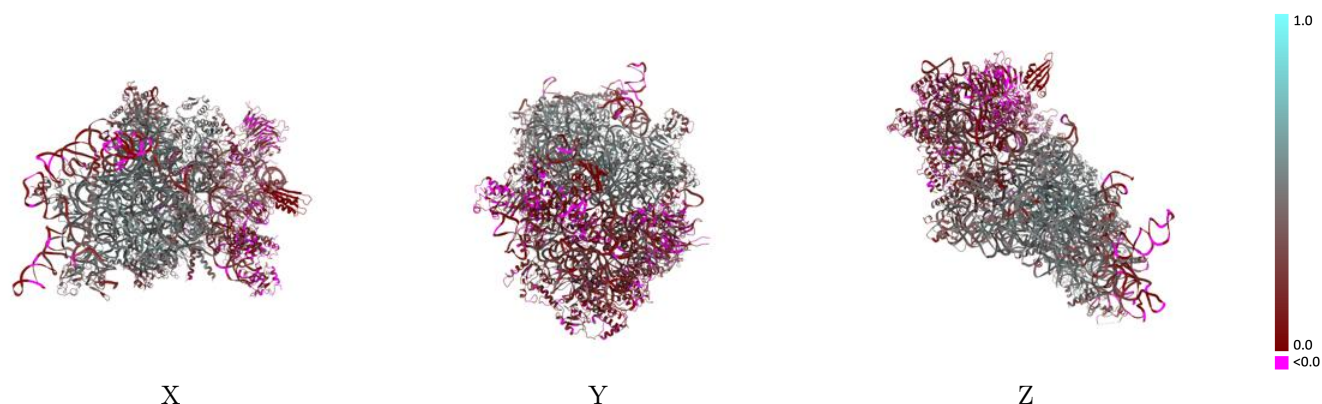
This section contains information regarding the fit between EMDB map EMD-4214 and PDB model 6FAI. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



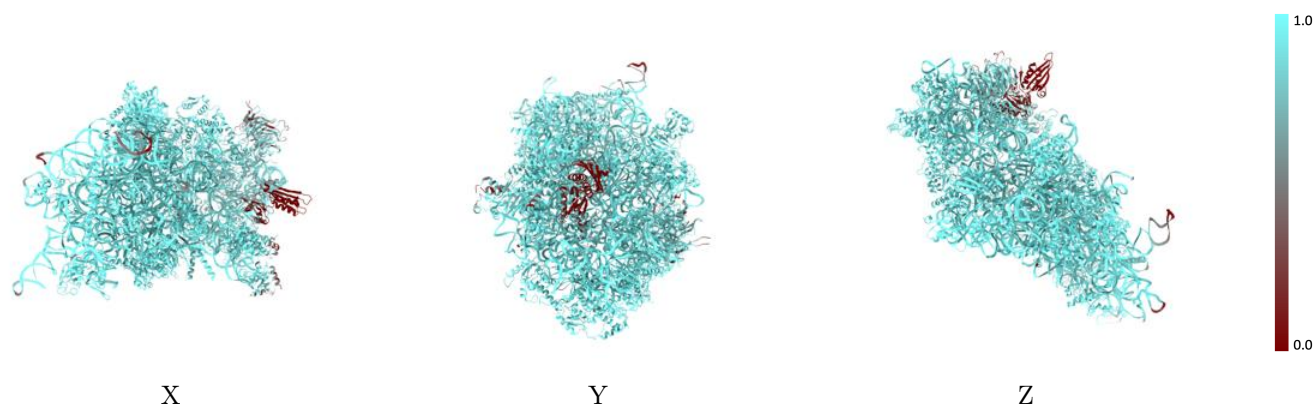
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



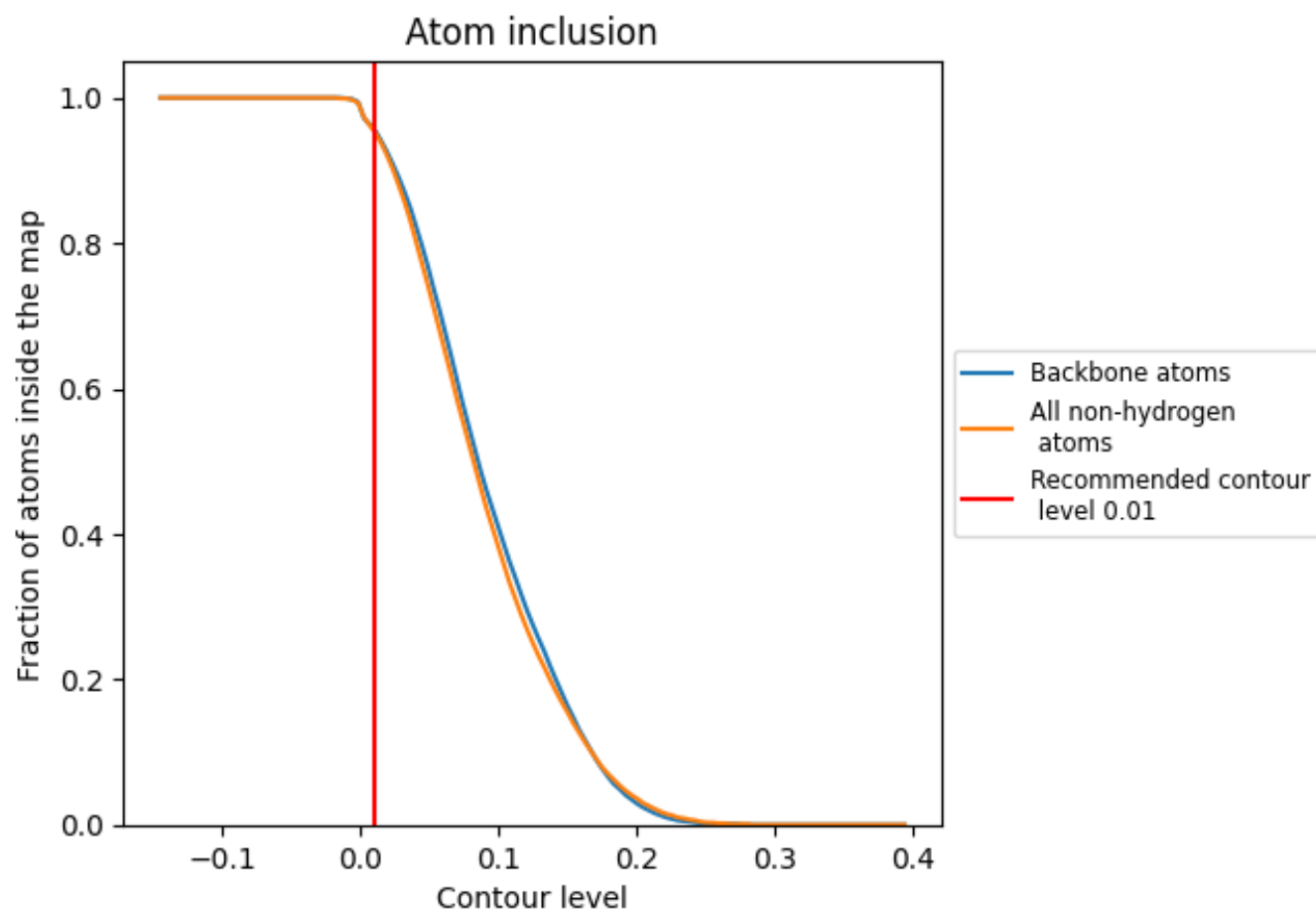
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.3280
2	 0.9860	 0.3450
A	 0.9940	 0.4650
B	 0.9870	 0.4070
C	 0.9910	 0.4910
D	 0.1160	 0.0110
E	 0.9910	 0.5140
F	 0.9810	 0.1790
G	 0.9930	 0.4050
H	 0.9880	 0.3830
I	 0.9940	 0.4530
J	 0.9900	 0.4900
L	 0.9950	 0.5100
M	 0.7850	 0.0600
N	 0.9860	 0.4620
O	 0.9920	 0.3990
P	 0.9730	 0.2270
Q	 0.9770	 0.1420
R	 0.9750	 0.2020
S	 0.9820	 0.1630
T	 0.9900	 0.1610
U	 0.8000	 0.0910
V	 0.9930	 0.4870
W	 0.9940	 0.5380
X	 0.9650	 0.4560
Y	 0.9920	 0.4780
Z	 0.9680	 0.1420
b	 0.9920	 0.4760
c	 0.9730	 0.1660
d	 0.8290	 0.0570
e	 0.9590	 0.3900
g	 0.7240	 0.0850
h	 0.9820	 0.3650
i	 0.9610	 0.0920
j	 0.6560	 0.0400



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Chain	Atom inclusion	Q-score
k	 0.9780	 0.3780
l	 0.9550	 0.1840