



Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 11:37 AM JST

PDB ID : 5ZWO
EMDB ID : EMD-6974
Title : Cryo-EM structure of the yeast B complex at average resolution of 3.9 angstrom
Authors : Bai, R.; Wan, R.; Yan, C.; Shi, Y.
Deposited on : 2018-05-16
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

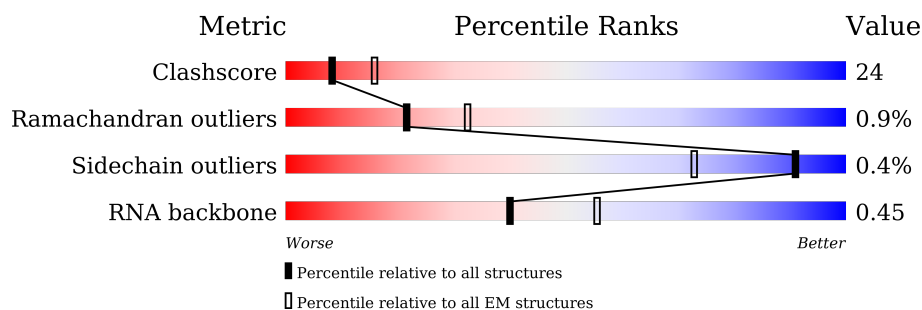
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.






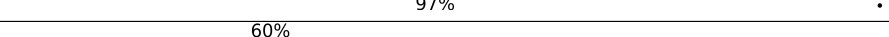



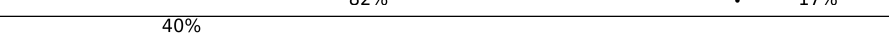


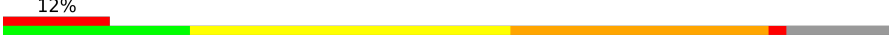
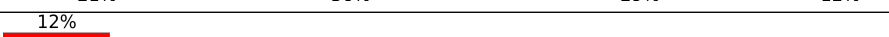













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2413	
2	K	465	
3	L	494	
4	N	899	
5	J	469	
6	E	143	
7	M	126	

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Mol	Chain	Length	Quality of chain
8	C	1008	
9	z	109	
10	q	95	
11	r	89	
12	x	86	
13	t	93	
14	y	115	
15	s	187	
16	F	112	
17	B	214	
18	O	587	
19	S	101	
19	d	101	
19	l	101	
20	P	196	
20	a	196	
20	h	196	
21	Q	146	
21	b	146	
21	m	146	
22	R	110	
22	c	110	
22	n	110	
23	T	94	
23	e	94	

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Mol	Chain	Length	Quality of chain
23	i	94	
24	U	86	
24	f	86	
24	j	86	
25	V	77	
25	g	77	
25	k	77	
26	I	161	
27	D	2163	
28	G	60	
29	1	971	
30	2	436	
31	3	1361	
32	4	213	
33	5	107	
34	6	85	
35	X	148	
36	Y	266	
37	Z	204	
38	H	1175	
39	o	238	
40	p	111	
41	u	530	
42	w	280	
43	v	266	

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Mol	Chain	Length	Quality of chain
44	W	194	<div><div></div><div>16%</div><div>44%</div><div>8%</div><div>48%</div></div>
45	0	242	<div><div></div><div>21%</div><div>66%</div><div>31%</div></div>
46	9	291	<div><div></div><div>16%</div><div>22%</div><div>78%</div></div>

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 91261 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2172	Total	C	N	O	S	0	0
			17092	10927	2976	3131	58		

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	429	Total	C	N	O	S	0	0
			3375	2101	610	650	14		

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	416	Total	C	N	O	S	0	0
			3171	2001	573	585	12		

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	725	Total	C	N	O	S	0	0
			4882	3036	902	930	14		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	308	Total	C	N	O	S	0	0
			2467	1557	451	445	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	138	Total	C	N	O	S	0	0
			1135	719	195	210	11		

- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	z	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 10 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	q	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 11 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	r	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 12 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	x	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 13 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	t	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 14 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	y	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	s	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	99	Total	C	N	O	P	0	0
			2043	913	341	690	99		

- Molecule 17 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	B	175	Total	C	N	O	P	0	0
			3677	1644	634	1225	174		

- Molecule 18 is a protein called 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	75	Total	C	N	O	S	0	0
			568	347	103	117	1		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	79	Total	C	N	O	0	0
			316	158	79	79		
19	S	82	Total	C	N	O	0	0
			404	240	82	82		
19	l	76	Total	C	N	O	0	0
			375	223	76	76		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	a	73	Total	C	N	O	0	0
			292	146	73	73		

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Mol	Chain	Residues	Atoms				AltConf	Trace
20	P	70	Total	C	N	O	0	0
			346	206	70	70		
20	h	76	Total	C	N	O	0	0
			376	224	76	76		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	b	77	Total	C	N	O	0	0
			308	154	77	77		
21	Q	99	Total	C	N	O	0	0
			491	293	99	99		
21	m	82	Total	C	N	O	0	0
			407	243	82	82		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	c	90	Total	C	N	O	0	0
			360	180	90	90		
22	R	92	Total	C	N	O	0	0
			457	273	92	92		
22	n	65	Total	C	N	O	0	0
			323	193	65	65		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	e	72	Total	C	N	O	0	0
			288	144	72	72		
23	T	77	Total	C	N	O	0	0
			379	225	77	77		
23	i	75	Total	C	N	O	0	0
			369	219	75	75		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	f	70	Total	C	N	O	0	0
			280	140	70	70		
24	U	73	Total	C	N	O	0	0
			359	213	73	73		

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Mol	Chain	Residues	Atoms				AltConf	Trace
24	j	70	Total	C	N	O	0	0
			344	204	70	70		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	g	70	Total	C	N	O	0	0
			280	140	70	70		
25	V	75	Total	C	N	O	0	0
			369	219	75	75		
25	k	69	Total	C	N	O	0	0
			340	202	69	69		

- Molecule 26 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	110	Total	C	N	O	P	0	0
			2334	1044	399	781	110		

- Molecule 27 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	D	1699	Total	C	N	O	1	0
			8422	5024	1699	1699		

- Molecule 28 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	60	Total	C	N	O	P	0	0
			1264	571	217	416	60		

- Molecule 29 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	1	816	Total	C	N	O	0	0
			4044	2412	816	816		

- Molecule 30 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	2	211	Total	C	N	O	0	0
			1042	620	211	211		

- Molecule 31 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	3	1180	Total	C	N	O	0	0
			5852	3492	1180	1180		

- Molecule 32 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	4	174	Total	C	N	O	0	0
			862	514	174	174		

- Molecule 33 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	5	103	Total	C	N	O	0	0
			507	301	103	103		

- Molecule 34 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	6	84	Total	C	N	O	0	0
			415	247	84	84		

- Molecule 35 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	X	128	Total	C	N	O	0	0
			631	375	128	128		

- Molecule 36 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	Y	89	Total	C	N	O	0	0
			439	261	89	89		

- Molecule 37 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	Z	22	Total	C	N	O	0	0
			109	65	22	22		

- Molecule 38 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	150	Total	C	N	O	P	0	0
			3169	1416	531	1072	150		

- Molecule 39 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	o	135	Total	C	N	O	0	0
			673	403	135	135		

- Molecule 40 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	p	73	Total	C	N	O	0	0
			361	215	73	73		

- Molecule 41 is a protein called Pre-mRNA-splicing factor PRP9.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	u	462	Total	C	N	O	0	0
			2298	1374	462	462		

- Molecule 42 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	w	127	Total	C	N	O	0	0
			633	379	127	127		

- Molecule 43 is a protein called Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	v	174	Total	C	N	O	0	0
			859	511	174	174		

- Molecule 44 is a protein called 23 kDa U4/U6.U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	100	Total	C	N	O	0	0
			497	297	100	100		

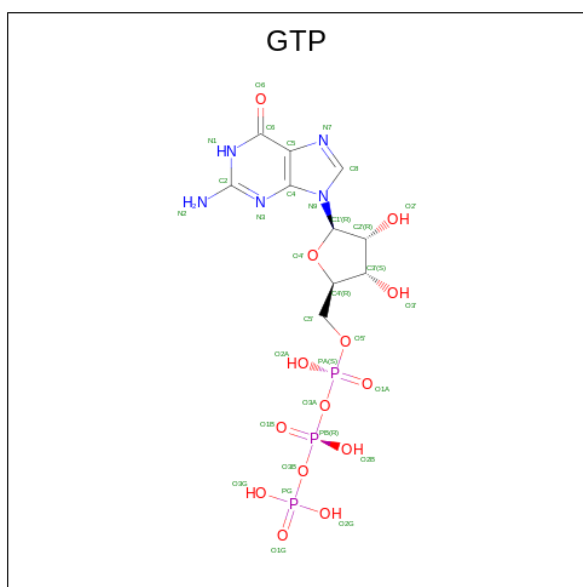
- Molecule 45 is a protein called Pre-mRNA-splicing factor 38.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	0	167	Total	C	N	O	0	0
			830	496	167	167		

- Molecule 46 is a protein called Pre-mRNA-splicing factor SPP381.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	9	64	Total	C	N	O	0	0
			320	192	64	64		

- Molecule 47 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
47	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

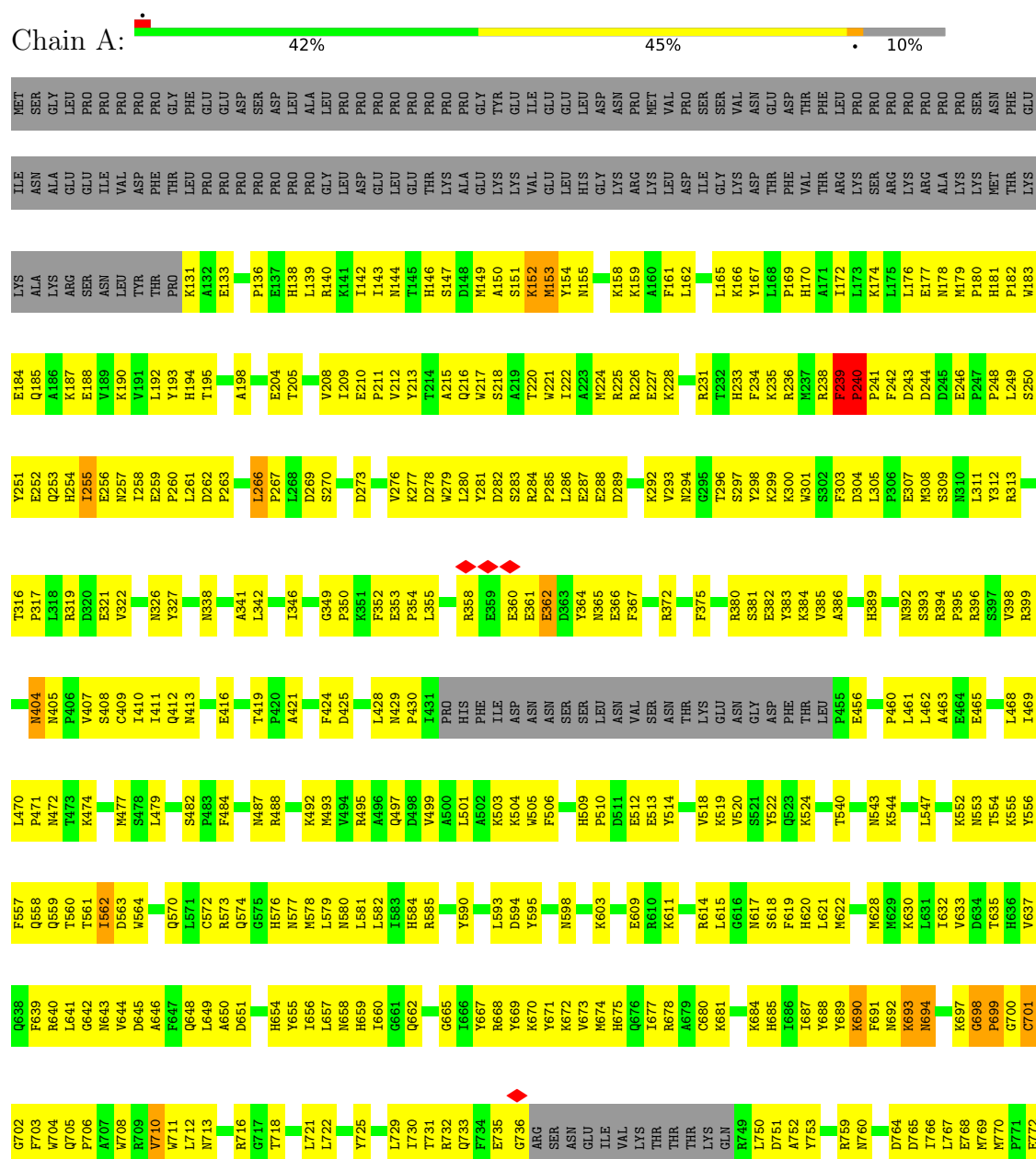
- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	C	1	Total	Mg	0
			1	1	

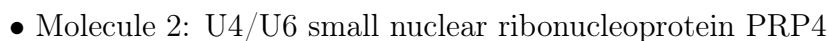
3 Residue-property plots

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

• Molecule 1: Pre-mRNA-splicing factor 8

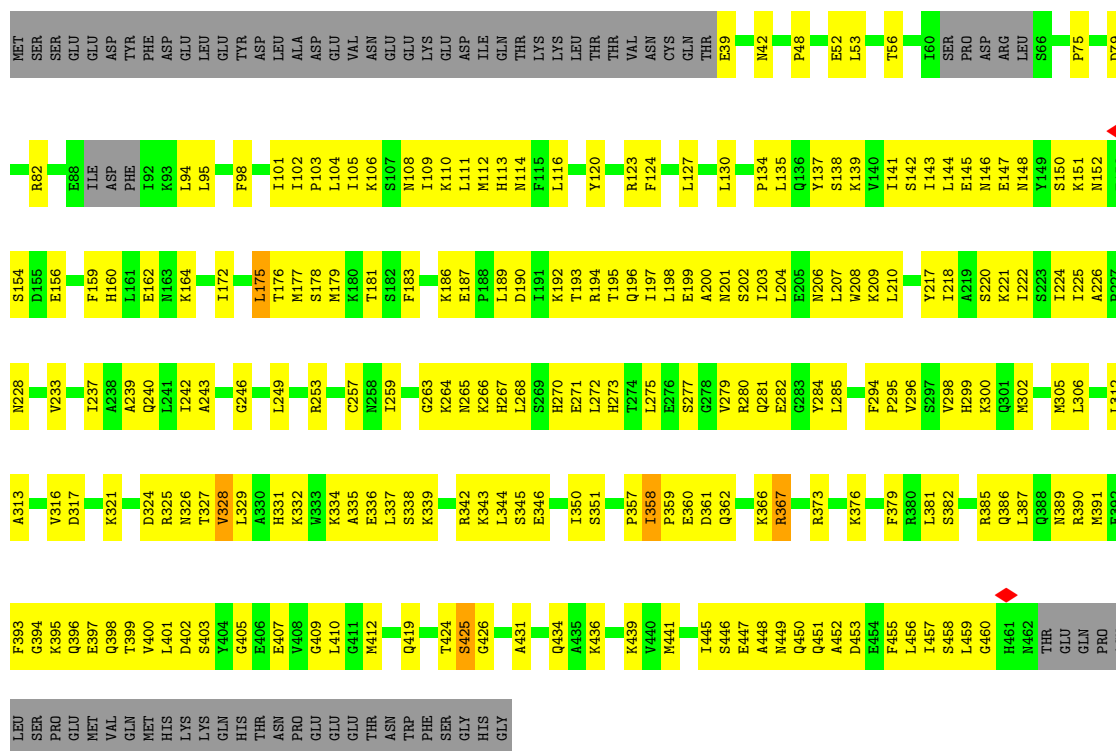


V1814	D1744	F1669	E1448	V1361	R1292	L1215	F1144	R1071	D996	V927	G850	S773
L1815	S1745	D1670	N1449	A1362	T1285	I1216	M1445	L1072	Q997	R928	R851	I774
R1817		L1676	E1450	G1363	K1294	R1217	F1146	I1073	Y998	L929	R852	R775
R1818	I1748	Q1677	F1606	G1364	T1297	Q1218	Q1147	V1074	L999	N930	T853	Q776
R1819	R1749	T1607	D1452	R1366	T1298	D1219	K1148	D1075	E1002	S932	R854	K777
R1820	R1750	T1608	D1453	Q1367	A1297	V1220	S1149			A931	K778	
R1821	W1609	W1609	S1454	Q1368	A1298	M1221				E333	L855	
W1610	Q1455	Q1455	Q1455	Q1369	Y1301	L1222	V1152	I1078	Q1005	R934	K858	T761
S1611	L1456	L1456	E1456	R1370	L1302	G1223	E1153	A1079	R1006	E935	L762	L762
P1612	W1537	W1537	W1458	V1371	K1303	R1224		Y1081	D1080	E936	L783	Q784
T1613	N1538	N1538	W1458	K1372	V1304	A1225	H1156		N1011	L937	T862	Q784
	L1539	L1539	A1459	L1373		V1226	I1157	K1085	K1014	A938	H785	H785
			E1460	G1374	E1307	F1227	I1158	M1086	P1015	L939	L786	L786
			Y1461	L1375	E1308	W1228	R1159	M1087	S1016	I940	Q864	S767
			A1462	L1376	K1309		L1160	V1088			I867	S767
			T1463	S1377	K1310	R1233	Y1161	V1089	Q1066	Y944	Q868	A789
			D1545	K1378	K1311		T1162	I1090			W790	W790
			R1465	M1379	F1312	T1236	R1163	M1091	I1020	P947	I874	R791
			Q1466	P1380	D1313	S1237	Y1164		P1022		T875	
				T1381		L1238	L1165	D1094	L1023	T950	E878	K794
			T1469	R1382		A1246	I1168	M1095	L1024	L951	A795	A795
			Q1470	F1383	G1317	F1247	Y1169	S1096	V1025	N952	N796	N796
				P1384	G1318	V1248	M1170	V1098	W1028	R953	T881	V801
			R1473	V1387	I1319	S1249	L1171	K955	T1029	I954	I882	P802
			R1474	F1388	L1320	W1250	F1172	K1100	Q1030	K956	S884	
			L1475	Y1389	M1321		H1173	Y1101	G1031	Y957	V885	P805
			A1476	F1392	S1323	K1253	E1175	G1102	I1032	L958	A806	A806
			F1477	G1324	G1324		E1176	L1033	N1034	L959	P807	P807
			E1478	E1393	E1393	P1256	E1177	I1104	N1034	T960	I808	I808
			E1479	L1394	L1394	M1257	D1177	R1105	L1035	Q961	W859	K809
			L1480	G1395	K1330		E1178	G1106		R962	K810	K810
			E1481	G1396	Y1331		G1179	L1107	I1038	V963	I811	I811
				L1397	A1332	F1260	E1180		W1039	F964	R893	I812
			W1484	L1398	K1334	M1262		A1110	D1040	K965	E813	E813
			I1488	I1400	M1335		T1183	S1111	V1041	P966	R894	R814
			P1489	S1401	N1336	V1267	D1184	F1112	S1042	Y967	F895	Y815
			R1490	A1402	T1337	R1268	E1185	I1113	R1043		S886	I816
			I1491	S1403	S1338	I1269	Y1186	F1114	G1044	T970	P897	K817
				L1406	L1340	P1270	L1187	Q1115	Q1045	M971	I898	S818
			L1494		S1341	R1272		Y1117	S1046	M972	P899	K817
			F1495		S1342		N1190		A1047	E973	P901	A820
				L1412	L1342	Q1273	F1195	G1118	V1048	N974	P902	
			D1498	S1413	F1343	R1274			L1049	Y976	W823	
			R1499	W1414	T1344	M1275	E1196	I1121	L1050	Q976	Y905	
			H500	W1414	T1344	E1276	N1197	D1122	E1051	N977	K906	Y829
			T1501	T1418	Y1346	E1277	S1198	L1123	T1052		N907	N830
			L1502	D1419	F1347	V1278		L1124	T1053	P980	D908	R831
				T1420	E1348	V1279	Y1201	L1125	L1054	V981	T909	E832
			D1505	G1421	A1349		N1202	L1126		Y982	K910	R833
			R1506		I1350	D1282	N1203	G1127	A1058		I911	
			G1507	L1436	V1351	E1283	R1204	Q1128	F1063	Y984	A838	A838
				I1437	A1352	G1284		F1129	T1064	D985	H839	H839
			I1510	T1440	T1353	V1285	W1207	R1130	T1064	P986	V840	V840
			R1512	F1441	K1356	D1287	K1209	D1133	L1065		E917	M844
			E1513	R1442	L1357	L1288	D1210	L1134	L1066		Y923	V845
			F1514		L1357	V1289	S1211	L1142	N1067		A924	A924
				T1446	D1358	D1290		M1142	L1068		N848	N848
			Y1517	W1447	L1360	E1291	R1214	E1143	L1070	L995	K926	K926

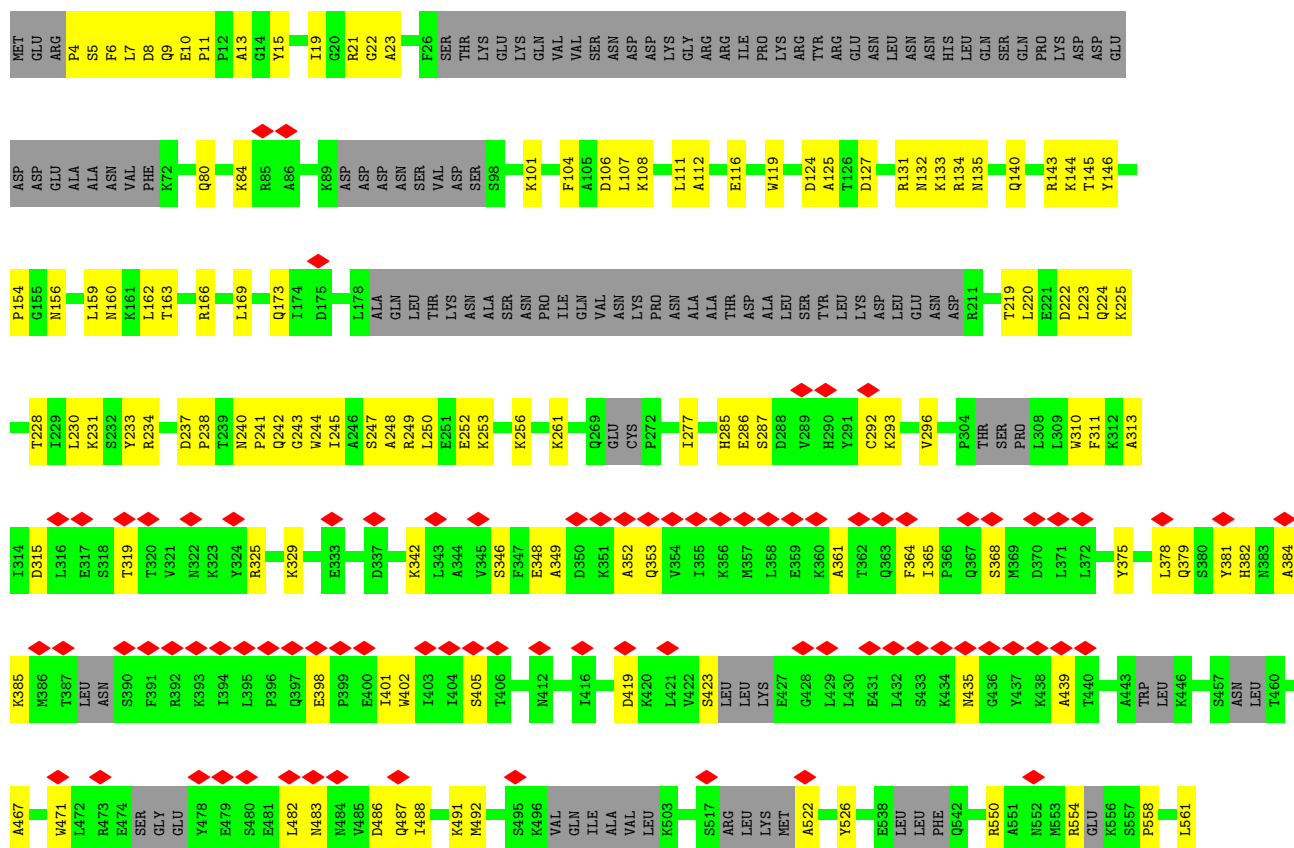
[illegible]

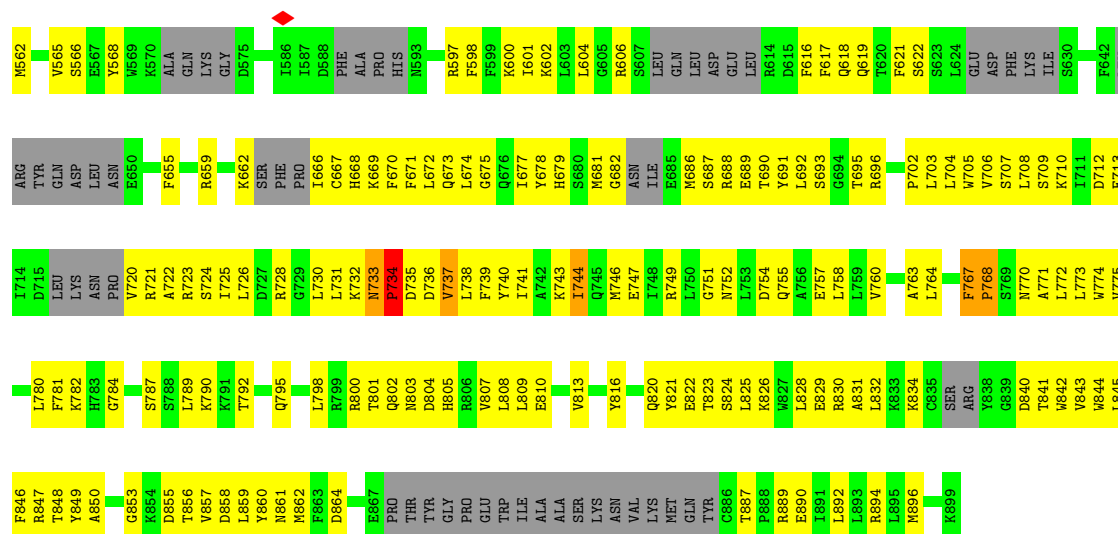
- Molecule 3: Pre-mRNA-processing factor 31

Chain L:  41% 43% • 16%



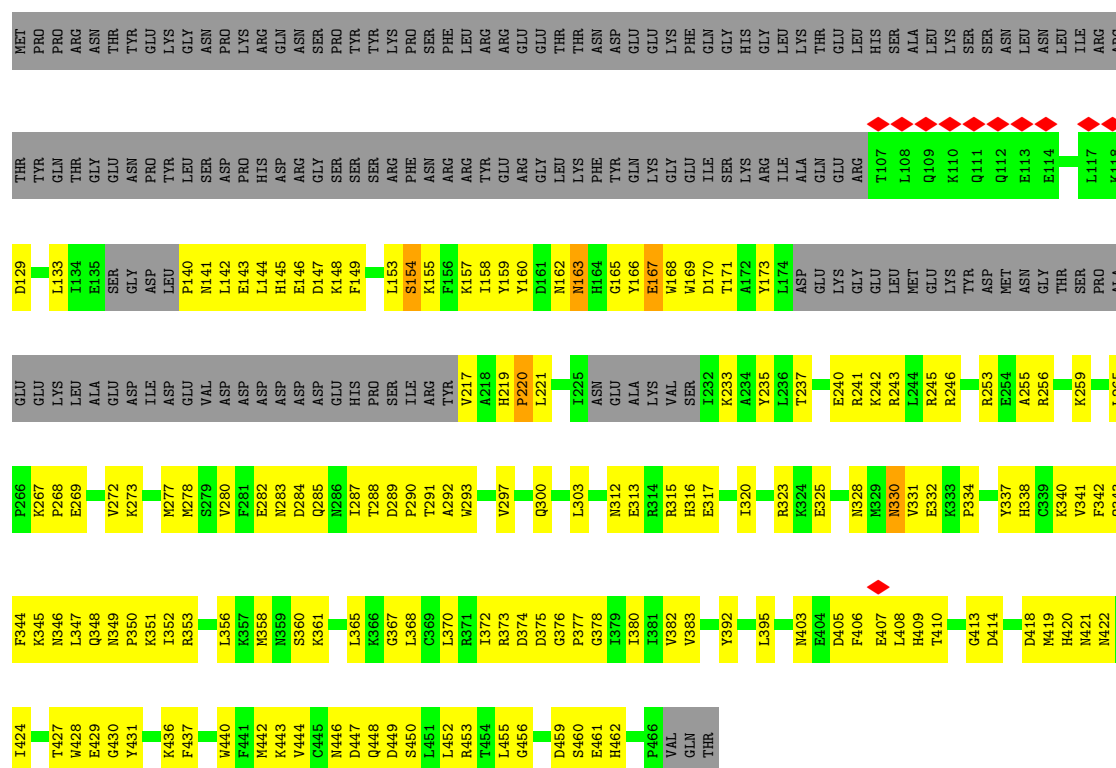
• Molecule 4: Pre-mRNA-splicing factor 4





- Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3

Chain J: 32% 32% 34%



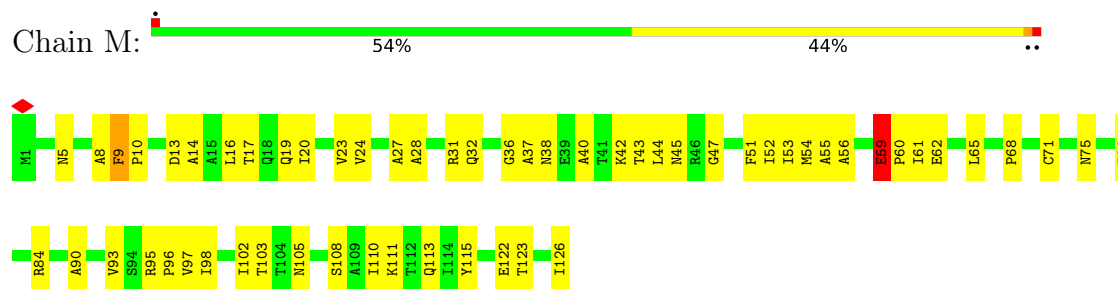
- Molecule 6: Spliceosomal protein DIB1

Chain E: 38% 58%



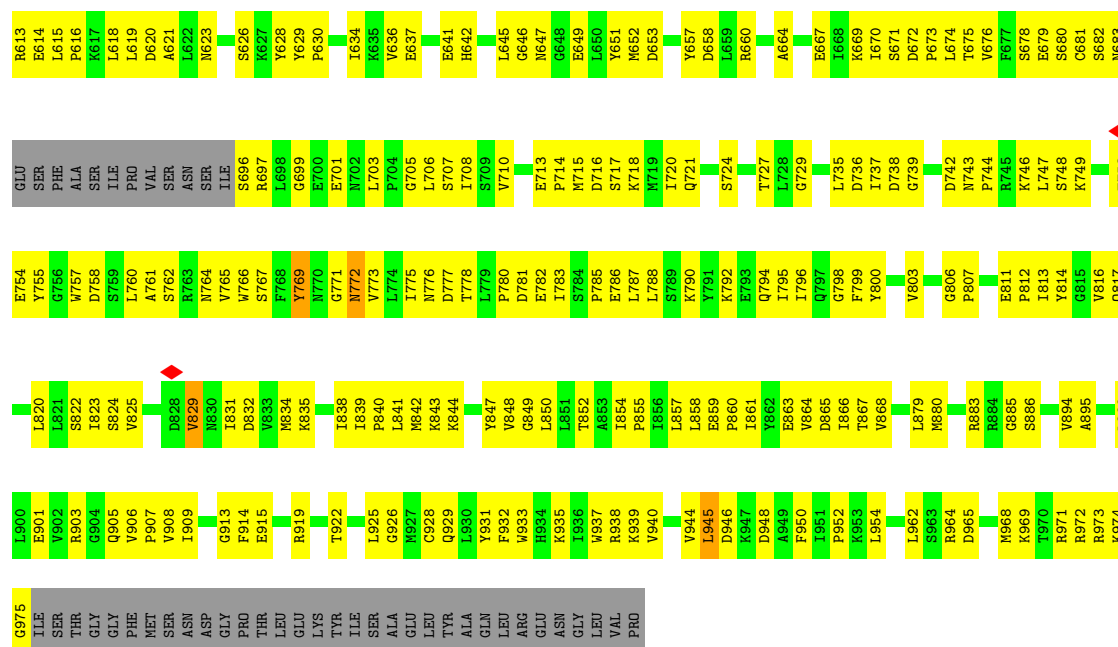


• Molecule 7: 13 kDa ribonucleoprotein-associated protein



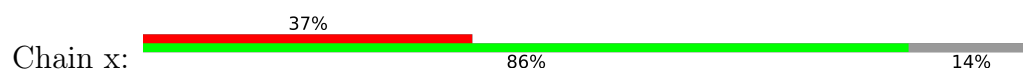
• Molecule 8: Pre-mRNA-splicing factor SNU114



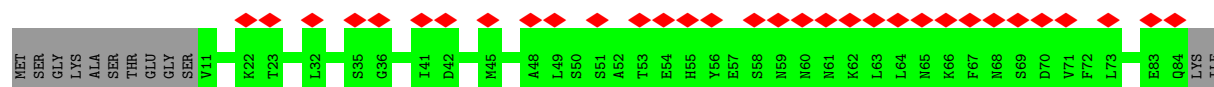




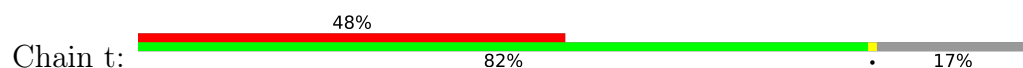
- Molecule 12: U6 snRNA-associated Sm-like protein LSm6



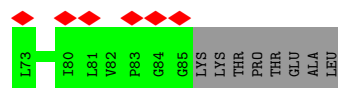
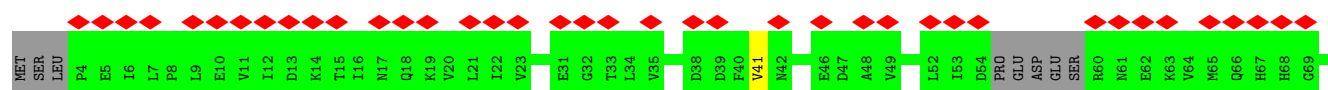
Chain x:



- Molecule 13: U6 snRNA-associated Sm-like protein LSm5



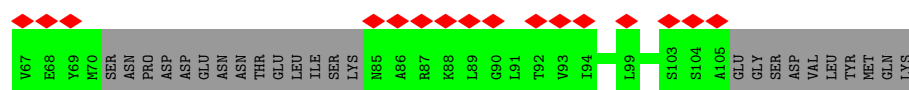
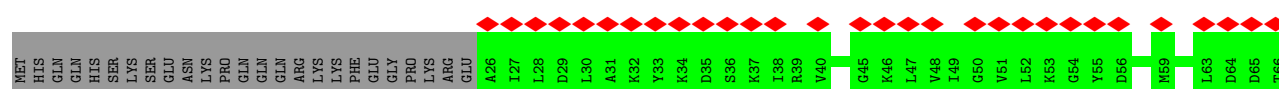
Chain t:



- Molecule 14: U6 snRNA-associated Sm-like protein LSm7



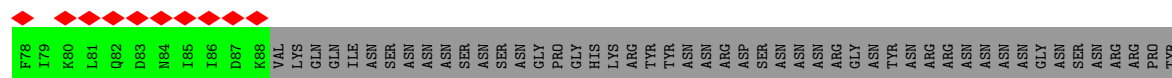
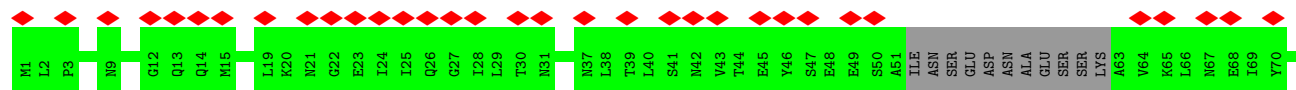
Chain y:



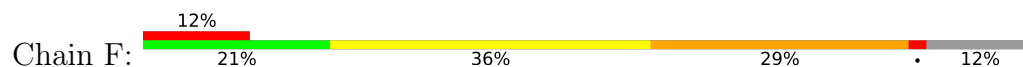
- Molecule 15: U6 snRNA-associated Sm-like protein LSm4



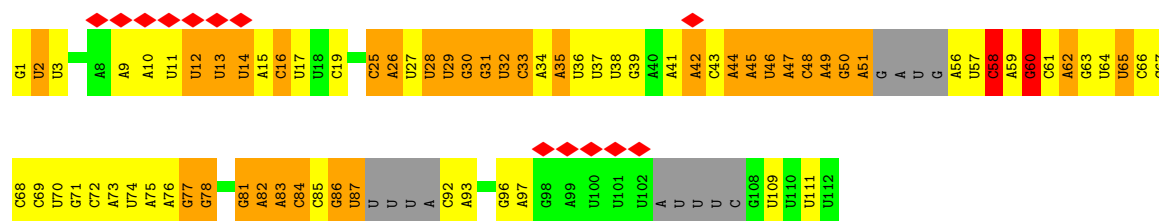
Chain s:



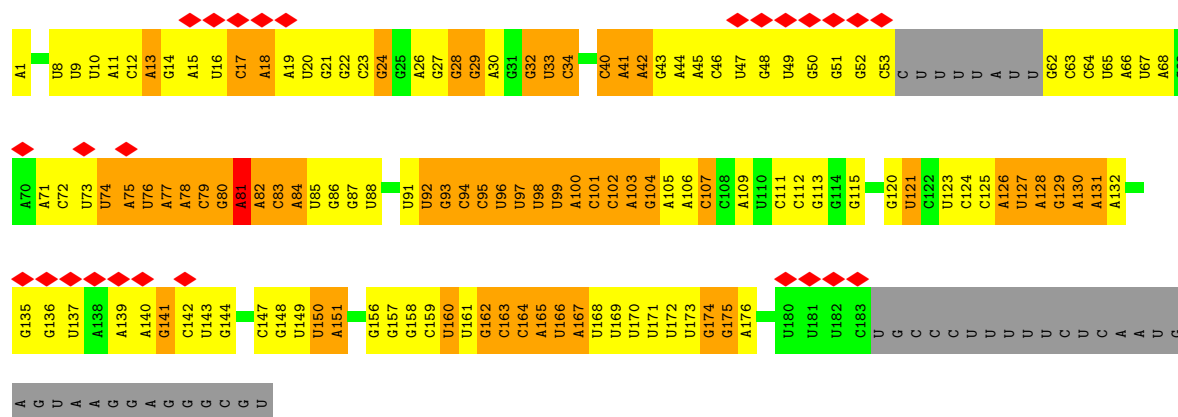
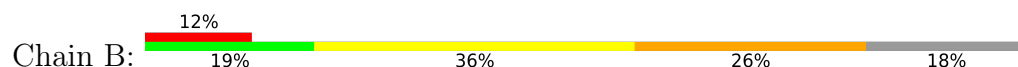
- Molecule 16: U6 snRNA



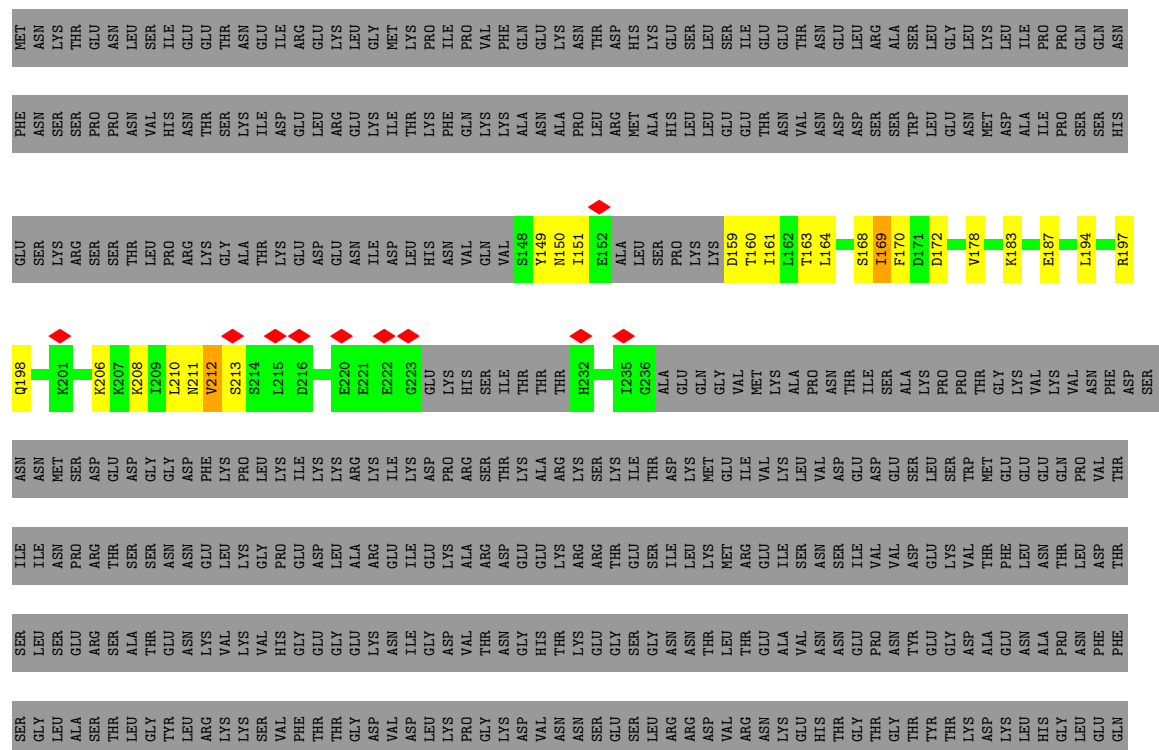
Chain F:



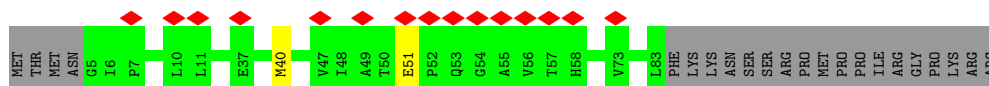
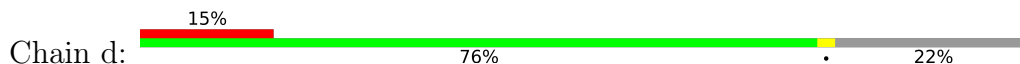
• Molecule 17: U5 snRNA



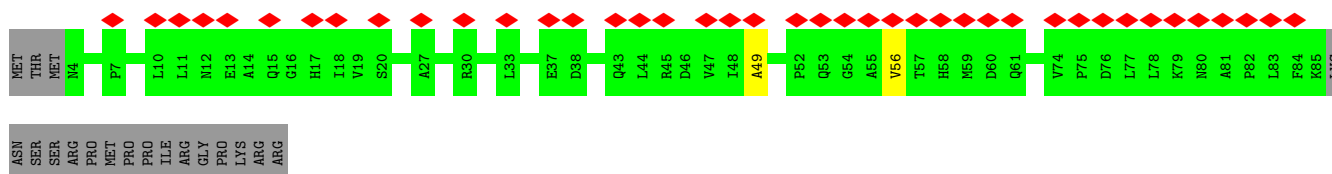
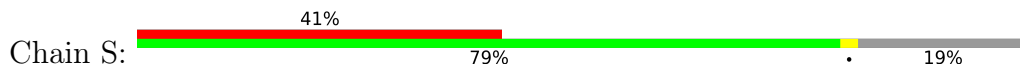
• Molecule 18: 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component



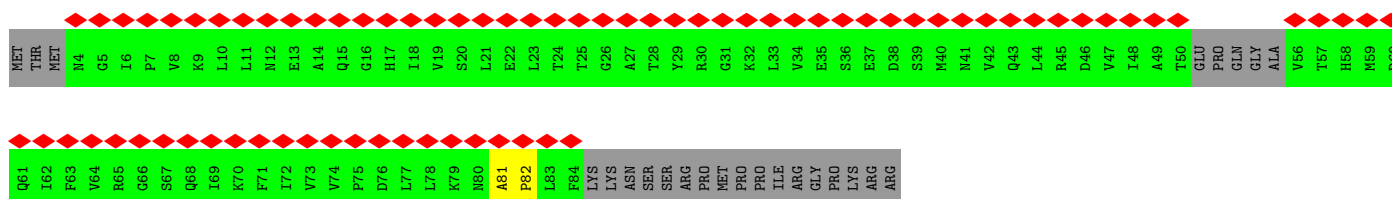
- Molecule 19: Small nuclear ribonucleoprotein Sm D3



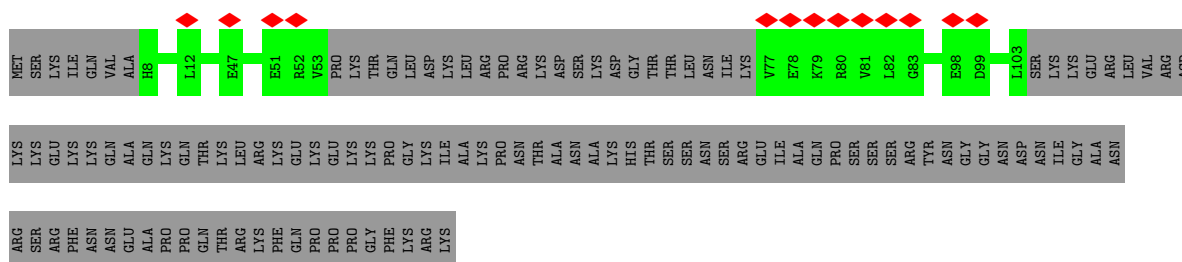
- Molecule 19: Small nuclear ribonucleoprotein Sm D3



- Molecule 19: Small nuclear ribonucleoprotein Sm D3

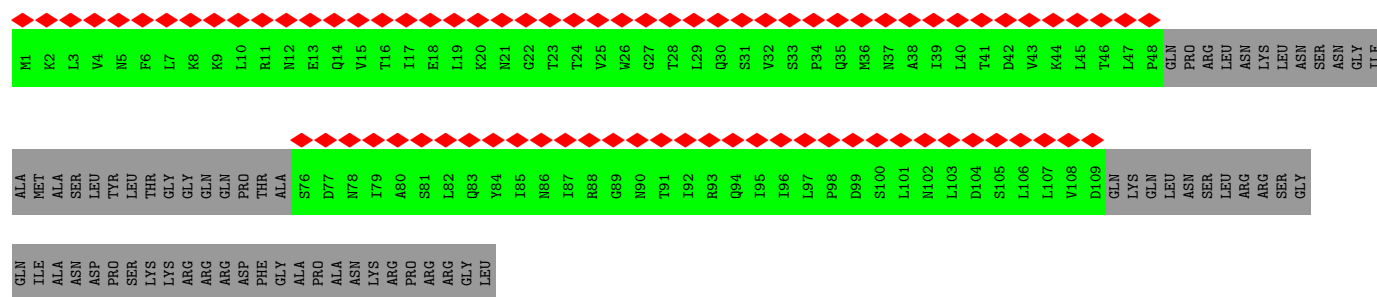


- Molecule 20: Small nuclear ribonucleoprotein-associated protein B

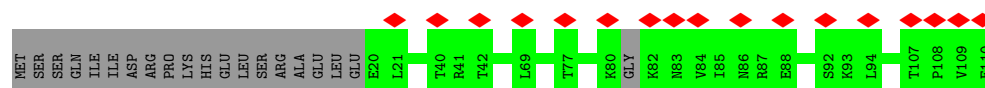
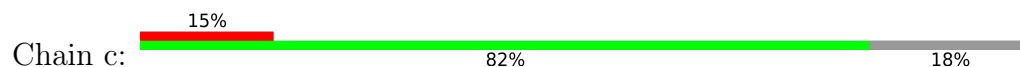


- Molecule 20: Small nuclear ribonucleoprotein-associated protein B

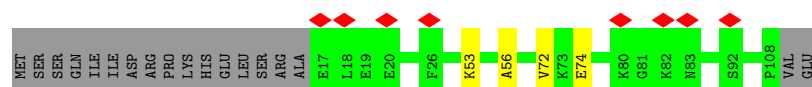
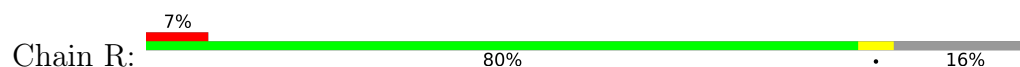




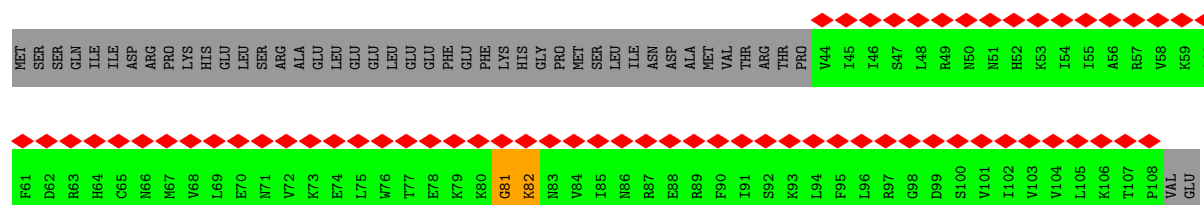
- Molecule 22: Small nuclear ribonucleoprotein Sm D2



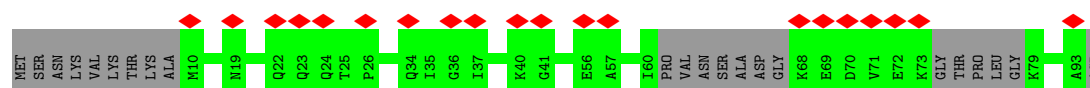
- Molecule 22: Small nuclear ribonucleoprotein Sm D2



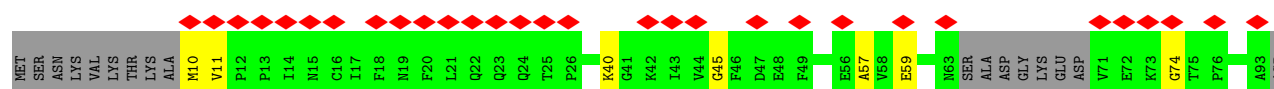
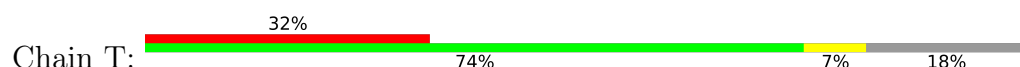
- Molecule 22: Small nuclear ribonucleoprotein Sm D2



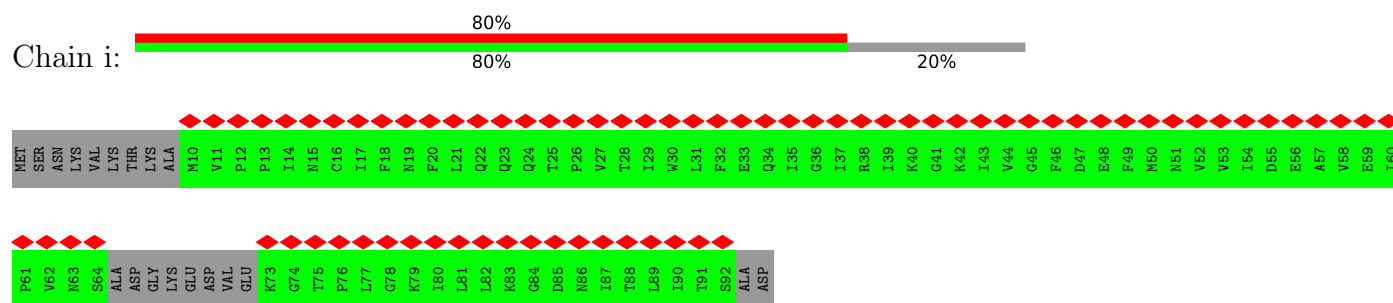
- Molecule 23: Small nuclear ribonucleoprotein E



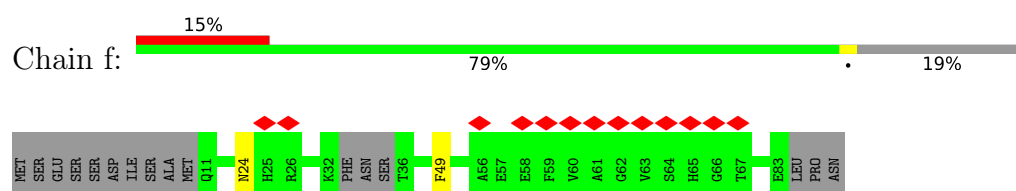
- Molecule 23: Small nuclear ribonucleoprotein E



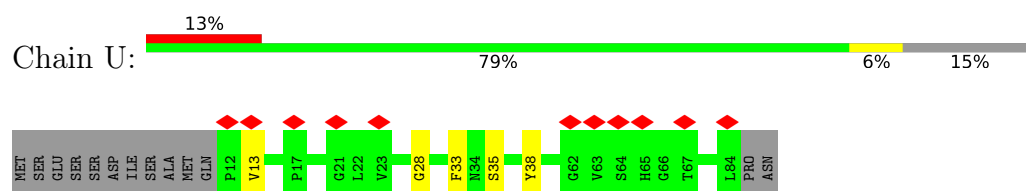
- Molecule 23: Small nuclear ribonucleoprotein E



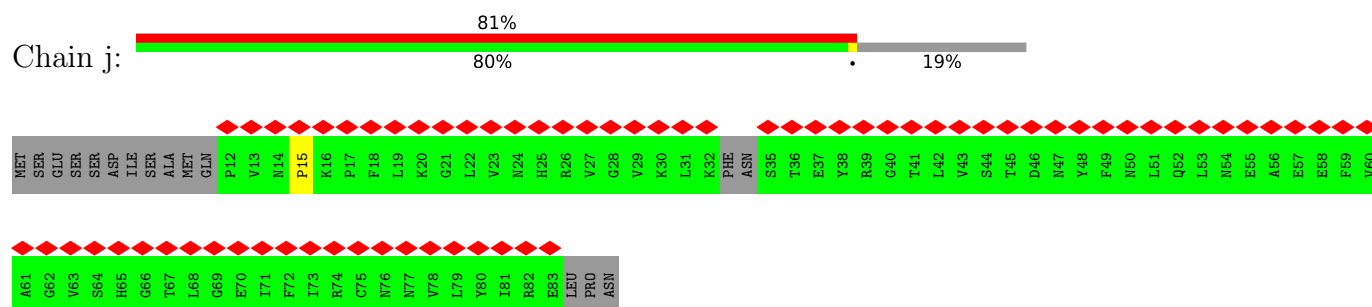
- Molecule 24: Small nuclear ribonucleoprotein F



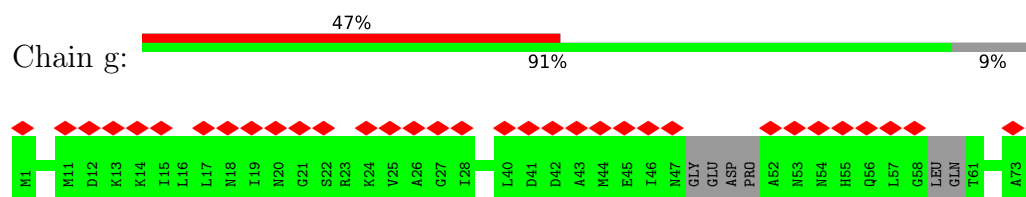
- Molecule 24: Small nuclear ribonucleoprotein F



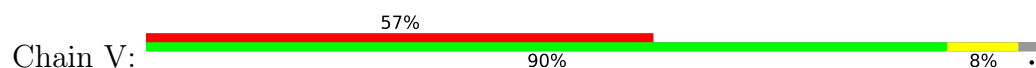
- Molecule 24: Small nuclear ribonucleoprotein F

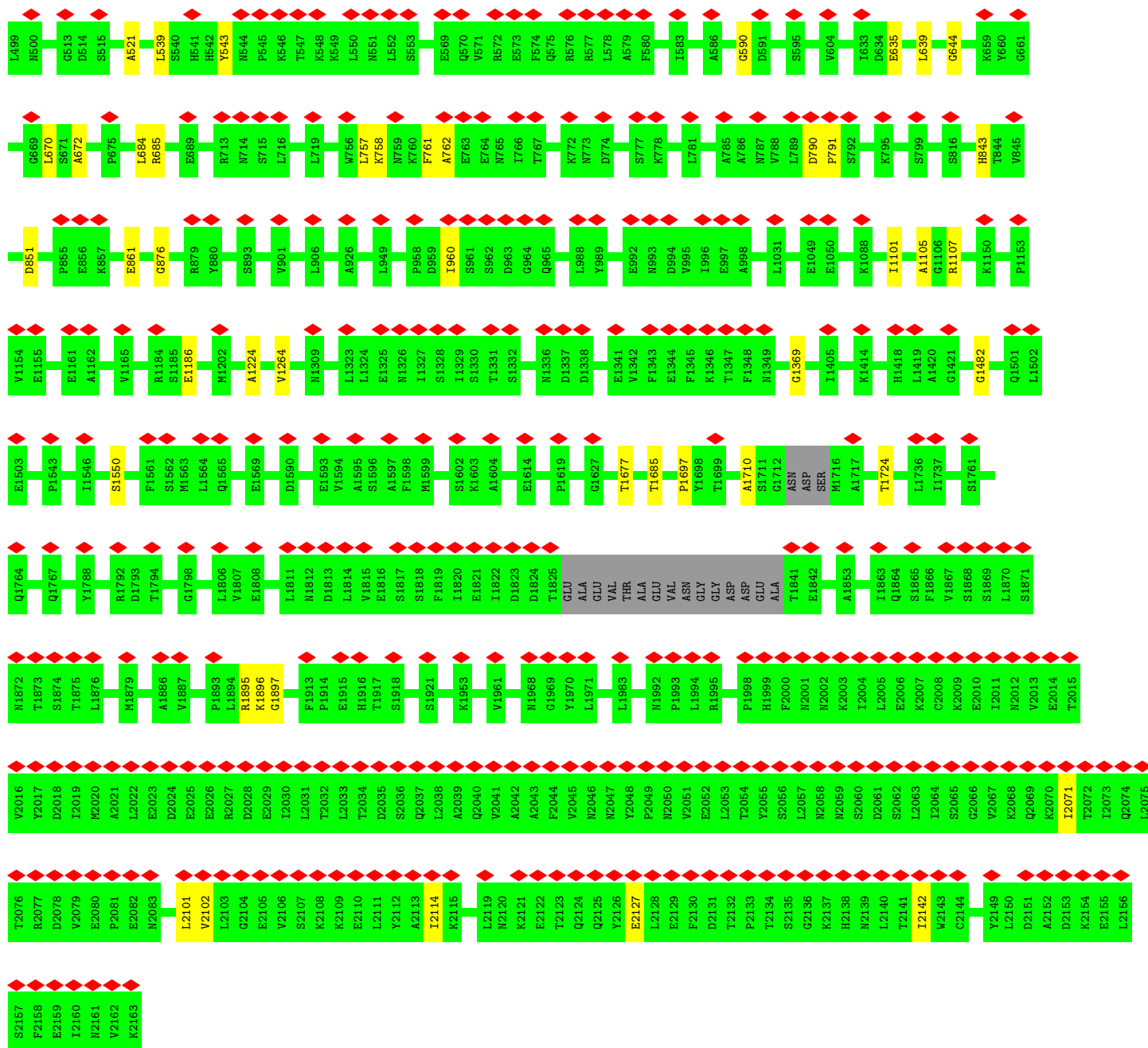


- Molecule 25: Small nuclear ribonucleoprotein G

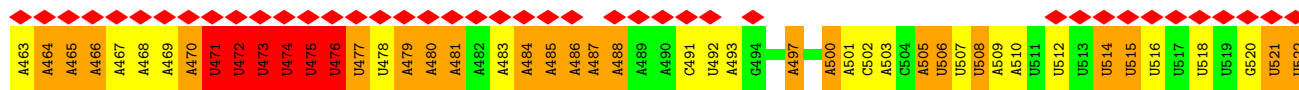
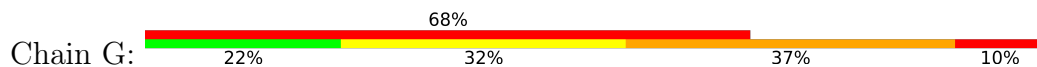


- Molecule 25: Small nuclear ribonucleoprotein G

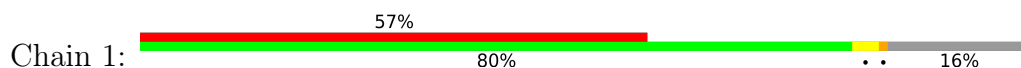




• Molecule 28: Pre-mRNA



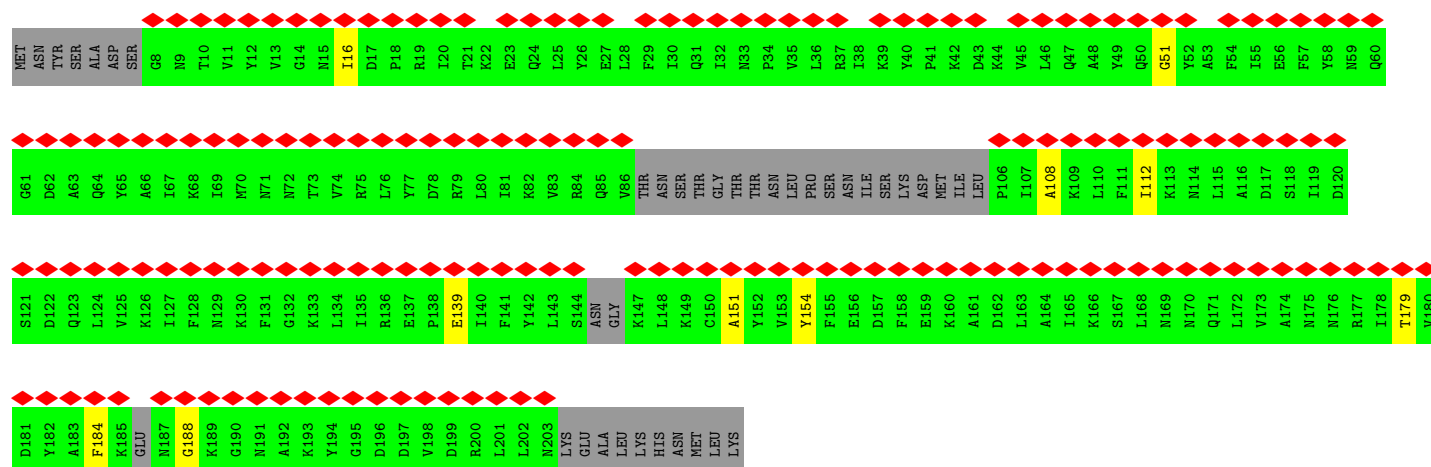
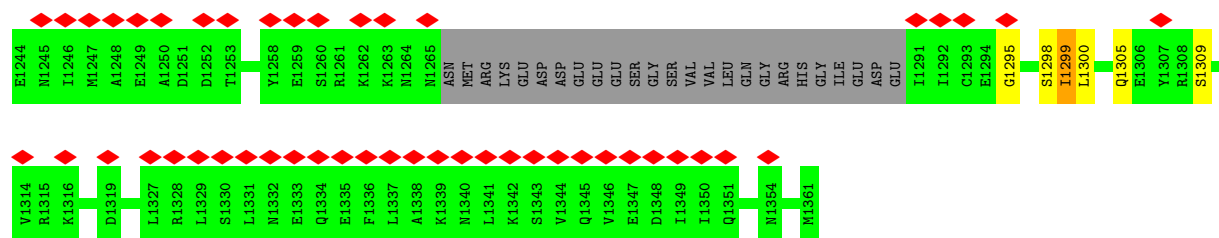
• Molecule 29: U2 snRNP component HSH155



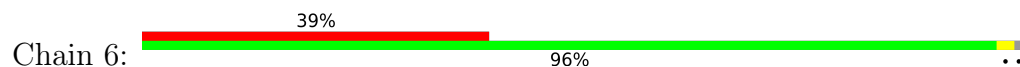
- Molecule 30: Cold sensitive U2 snRNA suppressor 1



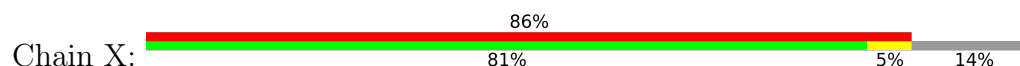


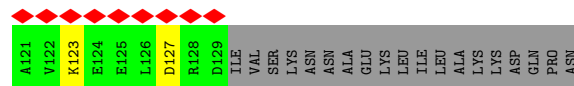
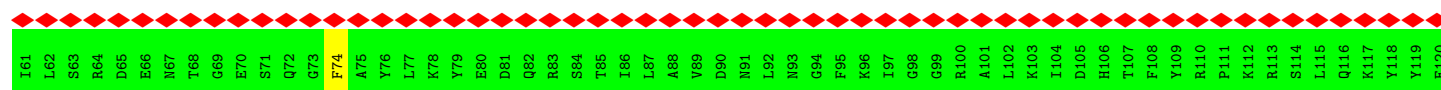


• Molecule 34: RDS3 complex subunit 10

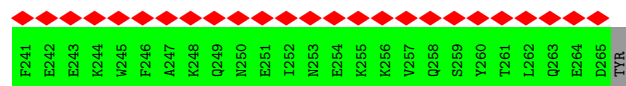
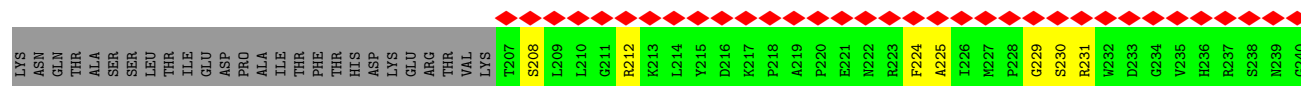
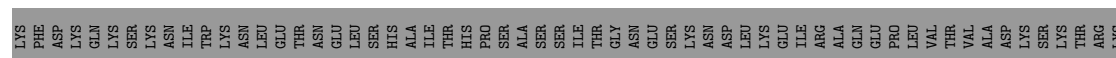


• Molecule 35: U2 snRNP component IST3

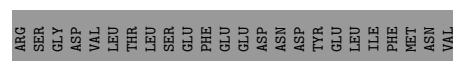
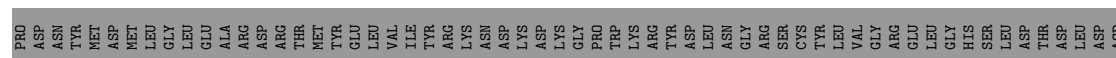
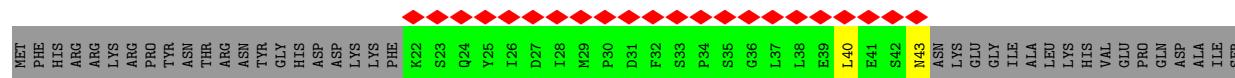




• Molecule 36: Pre-mRNA-splicing factor CWC26

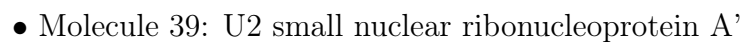


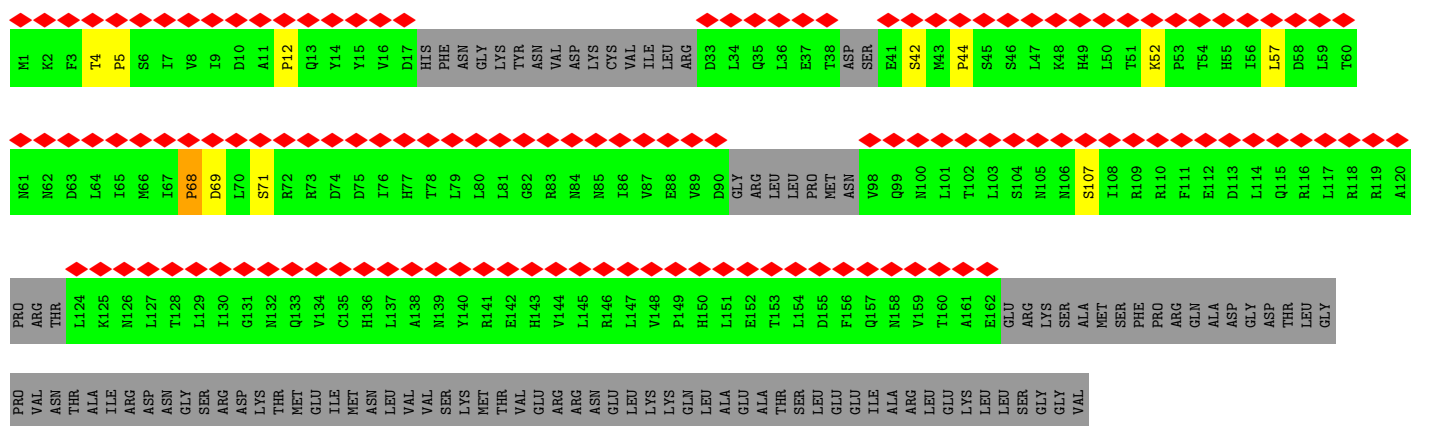
• Molecule 37: Pre-mRNA leakage protein 1



• Molecule 38: U2 snRNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	342588	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.249	Depositor
Minimum map value	-0.136	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.022	Depositor
Map size (\AA)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	A	0.78	12/17497 (0.1%)	0.73	18/23758 (0.1%)
2	K	0.60	0/3431	0.73	3/4631 (0.1%)
3	L	0.65	0/3219	0.71	1/4332 (0.0%)
4	N	0.44	0/4922	0.56	0/6683
5	J	0.50	0/2513	0.59	0/3374
6	E	0.72	0/1156	0.69	0/1557
7	M	0.80	0/963	0.78	0/1310
8	C	0.55	1/6874 (0.0%)	0.66	1/9305 (0.0%)
9	z	0.53	0/259	0.64	0/322
10	q	0.40	0/367	0.57	0/457
11	r	0.43	0/307	0.58	0/382
12	x	0.40	0/295	0.56	0/367
13	t	0.38	0/306	0.58	0/379
14	y	0.37	0/262	0.60	0/324
15	s	0.36	0/306	0.59	0/379
16	F	0.77	1/2277 (0.0%)	0.89	3/3534 (0.1%)
17	B	0.39	0/4106	0.78	2/6391 (0.0%)
18	O	0.58	0/567	0.65	0/757
19	S	0.27	0/403	0.53	0/559
19	d	0.46	0/315	0.52	0/392
19	l	0.42	0/373	0.70	0/516
20	P	0.28	0/344	0.54	0/476
20	a	0.42	0/290	0.47	0/359
20	h	0.36	0/374	0.57	0/518
21	Q	0.29	0/488	0.59	0/676
21	b	0.39	0/305	0.50	0/376
21	m	0.43	0/405	0.59	0/562
22	R	0.28	0/456	0.53	0/635
22	c	0.38	0/358	0.49	0/444
22	n	0.45	0/322	0.71	2/448 (0.4%)
23	T	0.28	0/377	0.55	0/521
23	e	0.40	0/285	0.48	0/351

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
23	i	0.43	0/367	0.61	0/507
24	U	0.29	0/358	0.58	0/496
24	f	0.42	0/278	0.46	0/344
24	j	0.42	0/342	0.63	0/472
25	V	0.28	0/368	0.61	0/510
25	g	0.38	0/277	0.49	0/341
25	k	0.38	0/338	0.61	0/467
26	I	1.17	9/2604 (0.3%)	1.25	19/4046 (0.5%)
27	D	0.29	0/8422	0.56	0/11741
28	G	0.61	7/1414 (0.5%)	0.83	0/2195
29	1	0.77	1/4043 (0.0%)	0.78	2/5637 (0.0%)
30	2	0.75	0/1039	0.78	0/1442
31	3	0.92	1/5844 (0.0%)	0.88	3/8140 (0.0%)
32	4	0.49	0/858	0.58	0/1190
33	5	0.91	0/506	0.79	0/702
34	6	0.97	0/414	0.84	0/575
35	X	0.47	0/630	0.60	0/875
36	Y	0.50	0/437	0.66	0/605
37	Z	0.47	0/108	0.55	0/149
38	H	1.06	30/3526 (0.9%)	1.42	76/5468 (1.4%)
39	o	0.76	1/668 (0.1%)	1.60	9/926 (1.0%)
40	p	0.63	0/359	1.32	1/497 (0.2%)
41	u	0.31	0/2294	0.45	0/3198
42	w	0.21	0/631	0.37	0/879
43	v	0.50	0/856	0.57	0/1187
44	W	0.24	0/494	0.46	0/685
45	0	0.24	0/825	0.44	0/1144
46	9	0.23	0/318	0.28	0/442
All	All	0.66	63/93340 (0.1%)	0.77	140/129935 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	10
2	K	0	6
3	L	0	3
4	N	0	4
5	J	0	3
7	M	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
8	C	0	6
19	l	0	2
22	n	0	2
25	V	0	1
25	k	0	1
27	D	0	4
29	1	0	2
30	2	0	3
31	3	0	15
41	u	0	1
45	0	0	2
All	All	0	67

All (63) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	H	1161	U	O3'-P	-15.67	1.42	1.61
38	H	1092	A	O3'-P	-14.82	1.43	1.61
38	H	1116	A	O3'-P	-11.49	1.47	1.61
38	H	1163	C	O5'-C5'	9.10	1.59	1.44
38	H	1116	A	C3'-O3'	-9.03	1.29	1.42
38	H	1127	A	O3'-P	-8.64	1.50	1.61
38	H	1167	U	O3'-P	8.57	1.71	1.61
38	H	1164	C	O3'-P	-8.12	1.51	1.61
26	I	142	G	N7-C5	-7.86	1.34	1.39
38	H	1162	U	P-O5'	7.58	1.67	1.59
38	H	1163	C	P-O5'	7.53	1.67	1.59
38	H	1117	G	P-O5'	7.19	1.67	1.59
38	H	1154	U	C1'-N1	7.06	1.59	1.48
39	o	69	ASP	CA-CB	-7.03	1.38	1.53
38	H	1096	C	O3'-P	7.00	1.69	1.61
38	H	1128	C	C5'-C4'	-6.97	1.43	1.51
38	H	1140	U	C1'-N1	6.90	1.59	1.48
1	A	266	LEU	C-N	6.57	1.46	1.34
38	H	1169	C	C1'-N1	6.55	1.58	1.48
38	H	1095	U	O3'-P	6.51	1.69	1.61
38	H	1117	G	C5'-C4'	6.33	1.58	1.51
38	H	1168	U	C5'-C4'	-6.25	1.43	1.51
38	H	1162	U	O3'-P	6.20	1.68	1.61
1	A	1609	TRP	CB-CG	-6.19	1.39	1.50
38	H	1162	U	O5'-C5'	6.09	1.54	1.44
26	I	142	G	C2-N2	-6.08	1.28	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	I	73	A	C1'-N9	-5.98	1.38	1.46
38	H	1165	C	O5'-C5'	5.96	1.53	1.44
1	A	1028	TRP	CB-CG	-5.95	1.39	1.50
38	H	1163	C	O3'-P	5.90	1.68	1.61
38	H	1151	U	O5'-C5'	-5.90	1.33	1.42
38	H	1162	U	C2-N3	5.89	1.41	1.37
38	H	1097	G	O3'-P	5.84	1.68	1.61
1	A	1169	TYR	CD2-CE2	-5.80	1.30	1.39
1	A	923	TYR	CD1-CE1	-5.79	1.30	1.39
38	H	1161	U	C3'-O3'	-5.76	1.34	1.42
8	C	214	ASP	C-N	-5.75	1.20	1.34
38	H	121	C	C1'-N1	5.73	1.57	1.48
26	I	26	A	N9-C4	-5.71	1.34	1.37
38	H	1162	U	C3'-C2'	-5.69	1.46	1.52
26	I	43	C	N1-C6	-5.66	1.33	1.37
26	I	74	U	C1'-N1	5.56	1.57	1.48
26	I	45	A	N7-C5	-5.55	1.35	1.39
1	A	923	TYR	CD2-CE2	-5.47	1.31	1.39
1	A	1610	TRP	CB-CG	-5.44	1.40	1.50
1	A	699	PRO	N-CD	5.30	1.55	1.47
1	A	1526	TRP	CB-CG	-5.29	1.40	1.50
1	A	899	PRO	N-CD	5.27	1.55	1.47
38	H	147	A	O3'-P	-5.26	1.54	1.61
16	F	16	C	P-OP1	-5.23	1.40	1.49
26	I	36	A	N9-C4	-5.23	1.34	1.37
29	1	548	LEU	CA-C	5.19	1.66	1.52
28	G	475	U	C1'-N1	5.19	1.56	1.48
28	G	477	U	C1'-N1	5.18	1.56	1.48
28	G	473	U	C1'-N1	5.17	1.56	1.48
28	G	476	U	C1'-N1	5.14	1.56	1.48
28	G	471	U	C1'-N1	5.13	1.56	1.48
28	G	472	U	C1'-N1	5.12	1.56	1.48
28	G	474	U	C1'-N1	5.10	1.56	1.48
1	A	1331	VAL	CB-CG1	-5.08	1.42	1.52
26	I	32	G	C5-C4	-5.07	1.34	1.38
31	3	1124	LEU	N-CA	-5.06	1.36	1.46
1	A	1345	TYR	CE2-CZ	-5.02	1.32	1.38

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	B	81	A	P-O3'-C3'	-15.08	101.61	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	H	1162	U	C5'-C4'-O4'	14.88	126.96	109.10
38	H	1093	C	P-O5'-C5'	14.75	144.50	120.90
38	H	1147	A	C5'-C4'-C3'	-14.15	93.36	116.00
38	H	1092	A	C2'-C3'-O3'	14.10	140.51	109.50
38	H	1098	C	N1-C1'-C2'	-13.34	96.66	114.00
29	1	548	LEU	CA-C-N	12.71	141.61	116.20
38	H	1151	U	C4'-C3'-O3'	-12.57	83.01	109.40
38	H	1151	U	P-O5'-C5'	11.64	139.52	120.90
38	H	1117	G	C5'-C4'-O4'	11.43	122.82	109.10
38	H	1117	G	C5'-C4'-C3'	-10.90	98.55	116.00
38	H	1163	C	C5'-C4'-O4'	10.53	121.74	109.10
29	1	548	LEU	O-C-N	-10.53	105.30	123.20
38	H	1126	G	N9-C1'-C2'	-10.01	100.99	114.00
26	I	142	G	N1-C6-O6	-9.86	113.98	119.90
38	H	1139	G	N9-C1'-C2'	-9.76	101.26	112.00
38	H	1163	C	C5'-C4'-C3'	-9.71	100.47	116.00
38	H	1147	A	P-O5'-C5'	9.63	136.31	120.90
1	A	1339	LEU	CB-CG-CD2	-9.46	94.91	111.00
38	H	1162	U	C5'-C4'-C3'	-9.16	101.34	116.00
38	H	1168	U	C4'-C3'-O3'	-9.00	90.51	109.40
39	o	44	PRO	N-CA-CB	8.81	113.87	103.30
38	H	142	C	N1-C1'-C2'	-8.79	102.33	112.00
26	I	142	G	C5-C6-O6	8.78	133.87	128.60
38	H	1152	U	P-O5'-C5'	8.71	134.83	120.90
38	H	1151	U	O4'-C1'-N1	8.62	115.10	108.20
38	H	1092	A	P-O5'-C5'	8.58	134.63	120.90
38	H	1148	U	C4'-C3'-O3'	-8.53	91.48	109.40
38	H	1165	C	C5'-C4'-C3'	-8.28	102.76	116.00
38	H	148	G	C5'-C4'-C3'	-8.26	102.78	116.00
26	I	142	G	N1-C2-N3	8.15	128.79	123.90
38	H	1151	U	C5'-C4'-O4'	8.04	118.75	109.10
38	H	1168	U	P-O5'-C5'	-7.92	108.22	120.90
38	H	1167	U	C2'-C3'-O3'	7.88	126.84	109.50
38	H	1092	A	C4'-C3'-O3'	-7.87	92.88	109.40
38	H	1165	C	C5'-C4'-O4'	7.86	118.53	109.10
26	I	71	U	C2-N1-C1'	7.84	127.11	117.70
38	H	1093	C	C5'-C4'-C3'	-7.75	103.59	116.00
38	H	1147	A	C4'-C3'-O3'	7.75	128.50	113.00
38	H	1161	U	C5'-C4'-C3'	-7.73	103.63	116.00
38	H	1169	C	P-O5'-C5'	-7.65	108.66	120.90
38	H	1097	G	C3'-C2'-O2'	7.62	135.39	113.30
38	H	1165	C	C4'-C3'-O3'	7.57	128.14	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	H	1115	G	O5'-P-OP1	-7.33	99.10	105.70
38	H	1168	U	C2'-C3'-O3'	7.29	125.53	109.50
39	o	5	PRO	N-CA-CB	7.27	112.03	103.30
38	H	1089	G	C4'-C3'-O3'	7.25	127.51	113.00
38	H	1128	C	C5'-C4'-O4'	7.25	117.79	109.10
39	o	42	SER	N-CA-CB	-7.24	99.63	110.50
38	H	1159	U	O5'-P-OP1	-7.19	99.23	105.70
26	I	71	U	N1-C2-O2	7.18	127.83	122.80
38	H	1089	G	O5'-P-OP1	-7.16	99.25	105.70
38	H	1159	U	O5'-P-OP2	-7.16	99.26	105.70
1	A	1539	LEU	CA-CB-CG	-7.15	98.85	115.30
1	A	1054	LEU	CA-CB-CG	-7.14	98.88	115.30
38	H	139	G	O5'-P-OP2	-7.11	99.31	105.70
38	H	139	G	O5'-P-OP1	-7.10	99.31	105.70
38	H	1089	G	O5'-P-OP2	-7.09	99.32	105.70
38	H	1115	G	C4'-C3'-O3'	7.04	127.07	113.00
38	H	1115	G	O5'-P-OP2	-6.98	99.42	105.70
39	o	12	PRO	N-CA-CB	6.77	111.42	103.30
38	H	1096	C	C1'-C2'-O2'	-6.68	90.56	110.60
26	I	4	C	N1-C2-O2	6.67	122.91	118.90
38	H	1129	U	C5'-C4'-O4'	6.64	117.07	109.10
26	I	32	G	C8-N9-C4	6.64	109.06	106.40
26	I	42	C	N3-C2-O2	-6.63	117.26	121.90
1	A	1557	LEU	CA-CB-CG	-6.58	100.17	115.30
38	H	140	G	N9-C1'-C2'	-6.52	104.83	112.00
38	H	148	G	C5'-C4'-O4'	6.49	116.89	109.10
1	A	1054	LEU	CB-CG-CD2	-6.47	99.99	111.00
26	I	142	G	C6-N1-C2	-6.47	121.22	125.10
26	I	59	C	N3-C4-C5	6.36	124.44	121.90
39	o	57	LEU	N-CA-CB	6.36	123.11	110.40
39	o	4	THR	N-CA-CB	-6.32	98.29	110.30
38	H	1092	A	N9-C1'-C2'	6.29	122.18	114.00
26	I	71	U	N3-C2-O2	-6.26	117.82	122.20
16	F	60	G	C8-N9-C4	6.25	108.90	106.40
38	H	1096	C	C4'-C3'-O3'	6.13	125.25	113.00
38	H	1152	U	C5'-C4'-C3'	-6.09	106.25	116.00
1	A	1123	LEU	CA-CB-CG	-6.09	101.30	115.30
38	H	1167	U	P-O3'-C3'	-6.04	112.46	119.70
38	H	1151	U	O3'-P-O5'	-6.01	92.58	104.00
1	A	916	LEU	CA-CB-CG	-5.97	101.56	115.30
38	H	1162	U	C4'-C3'-O3'	5.95	124.90	113.00
38	H	1167	U	C5'-C4'-O4'	-5.92	102.00	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	410	LEU	CA-CB-CG	-5.91	101.72	115.30
1	A	1125	LEU	CA-CB-CG	-5.91	101.72	115.30
17	B	81	A	O3'-P-O5'	5.89	115.19	104.00
38	H	1148	U	C5'-C4'-O4'	5.89	116.16	109.10
26	I	32	G	N9-C4-C5	-5.87	103.05	105.40
16	F	58	C	N1-C2-O2	5.84	122.40	118.90
38	H	1115	G	P-O3'-C3'	5.78	126.63	119.70
38	H	1162	U	C2'-C3'-O3'	-5.75	96.84	109.50
1	A	698	GLY	C-N-CD	5.75	140.48	128.40
26	I	4	C	N3-C2-O2	-5.73	117.89	121.90
1	A	898	ILE	C-N-CD	5.71	140.38	128.40
2	K	395	ILE	CG1-CB-CG2	-5.69	98.87	111.40
39	o	68	PRO	N-CA-CB	5.67	110.10	103.30
38	H	1162	U	P-O3'-C3'	5.62	126.45	119.70
26	I	142	G	C8-N9-C4	-5.62	104.15	106.40
26	I	71	U	C6-N1-C1'	-5.58	113.39	121.20
38	H	1167	U	C5'-C4'-C3'	5.57	124.91	116.00
22	n	81	GLY	CA-C-N	-5.56	104.97	117.20
8	C	598	ILE	CG1-CB-CG2	-5.55	99.20	111.40
38	H	1097	G	C2'-C3'-O3'	-5.54	97.31	109.50
38	H	1105	C	C4'-C3'-O3'	-5.49	97.87	109.40
38	H	1162	U	C4'-C3'-C2'	5.46	108.06	102.60
38	H	1168	U	C4'-C3'-C2'	-5.46	97.14	102.60
1	A	1412	LEU	CA-CB-CG	-5.41	102.86	115.30
38	H	1151	U	N1-C1'-C2'	5.39	121.01	114.00
1	A	1050	LEU	CA-CB-CG	5.38	127.68	115.30
38	H	1168	U	O3'-P-O5'	-5.36	93.82	104.00
26	I	36	A	C2-N3-C4	-5.34	107.93	110.60
38	H	1152	U	O4'-C4'-C3'	5.33	110.36	106.10
26	I	90	C	C2-N3-C4	5.31	122.55	119.90
31	3	1015	LEU	N-CA-C	5.28	125.27	111.00
1	A	1536	LEU	CA-CB-CG	-5.27	103.19	115.30
39	o	71	SER	N-CA-CB	-5.26	102.61	110.50
16	F	58	C	N3-C4-C5	5.26	124.00	121.90
1	A	1342	LEU	CB-CG-CD2	-5.24	102.09	111.00
31	3	856	ASP	N-CA-C	-5.22	96.90	111.00
31	3	667	THR	N-CA-CB	5.18	120.15	110.30
26	I	61	G	N9-C4-C5	-5.18	103.33	105.40
1	A	939	LEU	CB-CG-CD2	-5.16	102.23	111.00
38	H	1148	U	P-O5'-C5'	5.15	129.13	120.90
40	p	33	SER	N-CA-CB	5.12	118.19	110.50
39	o	107	SER	N-CA-CB	-5.12	102.83	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	H	1163	C	C4'-C3'-O3'	5.11	123.23	113.00
22	n	82	LYS	N-CA-C	5.11	124.81	111.00
3	L	367	ARG	NE-CZ-NH2	-5.11	117.75	120.30
38	H	1161	U	C5'-C4'-O4'	5.10	115.22	109.10
2	K	357	TRP	C-N-CA	-5.09	108.97	121.70
1	A	1122	ASP	CB-CG-OD1	-5.07	113.73	118.30
26	I	60	U	N3-C2-O2	-5.07	118.65	122.20
38	H	1147	A	O5'-C5'-C4'	5.06	121.31	111.70
38	H	146	A	C5'-C4'-C3'	-5.05	107.92	116.00
38	H	1169	C	O5'-C5'-C4'	-5.05	102.11	111.70
1	A	404	ASN	C-N-CA	-5.04	109.09	121.70
38	H	146	A	C5'-C4'-O4'	5.02	115.12	109.10
1	A	855	LEU	CA-CB-CG	-5.00	103.80	115.30

There are no chirality outliers.

All (67) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
45	0	15	LYS	Peptide
45	0	18	ASN	Peptide
29	1	389	GLY	Peptide
29	1	680	PRO	Mainchain
30	2	184	SER	Peptide
30	2	212	LEU	Mainchain,Peptide
31	3	1012	LYS	Mainchain,Peptide
31	3	1014	LYS	Mainchain,Peptide
31	3	1163	ALA	Peptide
31	3	1183	CYS	Mainchain,Peptide
31	3	185	ARG	Peptide
31	3	206	SER	Peptide
31	3	209	GLN	Peptide
31	3	666	LEU	Peptide
31	3	667	THR	Mainchain,Peptide
31	3	855	ALA	Mainchain,Peptide
1	A	1014	LYS	Peptide
1	A	1050	LEU	Peptide
1	A	1275	MET	Peptide
1	A	1346	PHE	Peptide
1	A	1352	ALA	Peptide
1	A	1388	PHE	Peptide
1	A	1528	THR	Peptide
1	A	239	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	A	240	PRO	Peptide
1	A	255	ILE	Peptide
8	C	170	LEU	Peptide
8	C	171	GLY	Peptide
8	C	177	TYR	Peptide
8	C	363	PRO	Peptide
8	C	365	GLU	Peptide
8	C	534	THR	Peptide
27	D	1369	GLY	Peptide
27	D	684	LEU	Peptide
27	D	685	ARG	Peptide
27	D	790	ASP	Peptide
5	J	163	ASN	Peptide
5	J	283	ASN	Peptide
5	J	330	ASN	Peptide
2	K	205	GLN	Peptide
2	K	208	GLN	Peptide
2	K	382	ASP	Peptide
2	K	383	GLU	Peptide
2	K	393	ARG	Peptide
2	K	64	VAL	Peptide
3	L	345	SER	Peptide
3	L	397	GLU	Peptide
3	L	425	SER	Peptide
7	M	59	GLU	Peptide
7	M	9	PHE	Peptide
4	N	733	ASN	Peptide
4	N	734	PRO	Peptide
4	N	767	PHE	Peptide
4	N	802	GLN	Peptide
25	V	50	ASP	Peptide
25	k	41	ASP	Peptide
19	l	81	ALA	Mainchain,Peptide
22	n	81	GLY	Mainchain,Peptide
41	u	458	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17092	0	16374	1323	0
2	K	3375	0	3343	293	0
3	L	3171	0	3140	204	0
4	N	4882	0	3988	259	0
5	J	2467	0	2365	181	0
6	E	1135	0	1120	91	0
7	M	950	0	1004	56	0
8	C	6732	0	6904	495	0
9	z	260	0	72	0	0
10	q	368	0	99	0	0
11	r	308	0	80	0	0
12	x	296	0	83	0	0
13	t	308	0	85	0	0
14	y	264	0	76	0	0
15	s	308	0	85	0	0
16	F	2043	0	1033	275	0
17	B	3677	0	1859	272	0
18	O	568	0	537	56	0
19	S	404	0	180	1	0
19	d	316	0	86	0	0
19	l	375	0	164	0	0
20	P	346	0	146	4	0
20	a	292	0	78	0	0
20	h	376	0	162	0	0
21	Q	491	0	207	6	0
21	b	308	0	78	0	0
21	m	407	0	171	0	0
22	R	457	0	192	2	0
22	c	360	0	89	0	0
22	n	323	0	136	0	0
23	T	379	0	159	6	0
23	e	288	0	74	0	0
23	i	369	0	152	0	0
24	U	359	0	155	3	0
24	f	280	0	77	0	0
24	j	344	0	148	0	0
25	V	369	0	168	3	0
25	g	280	0	79	0	0
25	k	340	0	152	0	0
26	I	2334	0	1173	184	0
27	D	8422	0	3689	23	0
28	G	1264	0	636	69	0
29	1	4044	0	1793	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	2	1042	0	435	4	0
31	3	5852	0	2487	30	0
32	4	862	0	384	5	0
33	5	507	0	215	1	0
34	6	415	0	183	1	0
35	X	631	0	276	3	0
36	Y	439	0	194	5	0
37	Z	109	0	42	1	0
38	H	3169	0	1608	155	0
39	o	673	0	276	0	0
40	p	361	0	159	0	0
41	u	2298	0	979	0	0
42	w	633	0	273	0	0
43	v	859	0	364	0	0
44	W	497	0	204	11	0
45	0	830	0	341	6	0
46	9	320	0	141	0	0
47	C	32	0	12	7	0
48	C	1	0	0	0	0
All	All	91261	0	60964	3655	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 24.

All (3655) 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)
1:A:1861:THR:CG2	18:O:161:ILE:HG12	1.34	1.56
1:A:1652:HIS:HE1	16:F:48:C:C6	1.21	1.53
5:J:350:PRO:CB	16:F:83:A:C8	1.94	1.51
1:A:1652:HIS:CE1	16:F:48:C:C6	1.95	1.50
5:J:350:PRO:HB2	16:F:83:A:C8	1.00	1.50
1:A:1650:ARG:HB2	16:F:49:A:C5'	1.52	1.38
1:A:1861:THR:HG22	18:O:161:ILE:CB	1.53	1.37
1:A:1861:THR:HG21	18:O:161:ILE:CG1	1.56	1.33
1:A:1861:THR:CG2	18:O:161:ILE:CG1	2.06	1.32
1:A:1861:THR:HG22	18:O:161:ILE:CG2	1.58	1.31
5:J:350:PRO:CG	16:F:84:C:H5	1.45	1.29
1:A:1861:THR:CG2	18:O:161:ILE:HG23	1.62	1.29
1:A:146:HIS:CD2	1:A:149:MET:HG3	1.67	1.28
1:A:146:HIS:HD2	1:A:149:MET:CG	1.45	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:B:73:U:C2'	17:B:74:U:H5'	1.64	1.27
1:A:1650:ARG:CB	16:F:49:A:C5'	2.13	1.26
16:F:31:G:H1'	16:F:32:U:OP1	1.36	1.25
1:A:654:HIS:CD2	1:A:701:CYS:SG	2.28	1.24
1:A:668:ARG:HB3	16:F:27:U:C1'	1.65	1.24
1:A:1664:ASP:OD1	18:O:213:SER:HB3	1.20	1.24
16:F:34:A:N6	16:F:47:A:N7	1.83	1.23
5:J:350:PRO:HB2	16:F:83:A:N7	1.53	1.22
1:A:668:ARG:HG2	16:F:27:U:O4'	1.07	1.22
1:A:667:TYR:HE1	16:F:26:A:O2'	1.20	1.21
1:A:1664:ASP:OD1	18:O:213:SER:CB	1.91	1.18
1:A:146:HIS:HD2	1:A:149:MET:CB	1.55	1.18
1:A:668:ARG:CG	16:F:27:U:O4'	1.91	1.18
1:A:614:ARG:CZ	16:F:29:U:OP1	1.92	1.17
1:A:1650:ARG:CB	16:F:49:A:H5'	1.70	1.17
16:F:29:U:O2'	16:F:30:G:H5'	1.45	1.16
28:G:487:A:H2'	28:G:488:A:H5'	1.27	1.15
38:H:1099:G:O2'	38:H:1100:A:H5'	1.42	1.15
5:J:350:PRO:CG	16:F:84:C:C5	2.29	1.15
8:C:472:VAL:HB	8:C:575:ALA:O	1.45	1.14
1:A:716:ARG:NH2	17:B:111:C:O2	1.82	1.13
1:A:1652:HIS:HE1	16:F:48:C:C5	1.65	1.12
1:A:1861:THR:CG2	18:O:161:ILE:CG2	2.23	1.12
1:A:153:MET:HE3	1:A:153:MET:H	1.15	1.11
17:B:74:U:H3'	17:B:75:A:H5'	1.18	1.11
1:A:668:ARG:CB	16:F:27:U:H1'	1.80	1.10
16:F:15:A:C6	16:F:16:C:N4	2.20	1.10
17:B:92:U:C5	17:B:93:G:N7	2.20	1.10
38:H:47:U:H2'	38:H:48:U:H5''	1.32	1.10
1:A:1651:ALA:N	16:F:49:A:OP2	1.84	1.10
1:A:146:HIS:CD2	1:A:149:MET:CG	2.29	1.09
5:J:350:PRO:HB3	16:F:84:C:C6	1.87	1.09
16:F:15:A:C4	16:F:16:C:C5	2.39	1.09
1:A:668:ARG:HE	16:F:27:U:H4'	1.12	1.08
17:B:44:A:H2'	17:B:45:A:C8	1.88	1.08
17:B:98:U:C2'	17:B:99:U:H5'	1.84	1.08
5:J:350:PRO:HG3	16:F:84:C:C5	1.86	1.08
17:B:44:A:H2'	17:B:45:A:H8	1.03	1.08
1:A:234:PHE:CZ	1:A:651:ASP:OD2	2.08	1.07
16:F:81:G:H2'	16:F:82:A:H5''	1.16	1.07
4:N:780:LEU:O	4:N:784:GLY:HA3	1.55	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:B:99:U:C5	17:B:100:A:H1'	1.90	1.06
1:A:1861:THR:CG2	18:O:161:ILE:CB	2.31	1.06
5:J:158:ILE:O	5:J:162:ASN:HB2	1.56	1.05
17:B:102:C:C4	17:B:103:A:N7	2.25	1.05
1:A:1861:THR:HG22	18:O:161:ILE:CA	1.86	1.04
1:A:701:CYS:SG	1:A:702:GLY:N	2.22	1.04
2:K:218:VAL:HG21	2:K:238:ALA:HB1	1.35	1.04
1:A:1862:VAL:O	18:O:160:THR:N	1.90	1.04
16:F:29:U:C2'	16:F:30:G:H5'	1.87	1.04
38:H:48:U:C5	38:H:49:U:C6	2.46	1.04
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.15	1.04
28:G:514:U:H4'	28:G:515:U:H5'	1.40	1.04
1:A:146:HIS:CD2	1:A:149:MET:CB	2.40	1.03
1:A:1861:THR:HG22	18:O:161:ILE:HG23	1.22	1.02
16:F:31:G:C1'	16:F:32:U:OP1	2.08	1.02
17:B:41:A:H5'	17:B:41:A:H8	1.23	1.02
38:H:110:A:H4'	38:H:111:C:C5'	1.89	1.02
1:A:1862:VAL:N	18:O:160:THR:O	1.93	1.02
1:A:1907:GLN:NE2	18:O:169:ILE:O	1.93	1.02
8:C:867:THR:O	8:C:926:GLY:HA2	1.58	1.02
1:A:665:GLY:HA3	1:A:668:ARG:NH1	1.74	1.01
1:A:1652:HIS:NE2	16:F:48:C:H2'	1.75	1.01
38:H:110:A:C4'	38:H:111:C:H5'	1.91	0.99
1:A:1664:ASP:CG	18:O:213:SER:HB3	1.82	0.99
1:A:146:HIS:CD2	1:A:149:MET:HB2	1.95	0.99
17:B:74:U:H3'	17:B:75:A:C5'	1.92	0.99
1:A:1650:ARG:HB2	16:F:49:A:H5'	1.02	0.99
17:B:162:G:H3'	17:B:163:C:H4'	1.45	0.99
4:N:675:GLY:O	4:N:679:HIS:HB2	1.63	0.98
17:B:73:U:H2'	17:B:74:U:H5'	0.99	0.98
16:F:36:U:H6	16:F:36:U:H5''	1.28	0.97
26:I:91:U:O2	26:I:142:G:N2	1.95	0.97
17:B:43:G:H2'	17:B:44:A:C8	1.98	0.97
17:B:41:A:H5'	17:B:41:A:C8	1.99	0.96
1:A:149:MET:SD	1:A:154:TYR:CE2	2.58	0.96
8:C:133:ILE:HA	8:C:209:MET:O	1.64	0.96
1:A:667:TYR:CE1	16:F:26:A:O2'	2.05	0.96
17:B:73:U:C2'	17:B:74:U:C5'	2.44	0.96
1:A:789:ALA:HB1	1:A:816:ILE:HD11	1.47	0.96
2:K:232:ASN:HB3	2:K:247:GLN:HE22	1.30	0.96
4:N:826:LYS:O	4:N:830:ARG:HB2	1.63	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:46:U:C4	16:F:47:A:C2	2.54	0.96
1:A:152:LYS:HA	1:A:155:ASN:HB2	1.48	0.95
44:W:116:LEU:O	45:O:50:ARG:HA	1.65	0.95
28:G:479:A:H2'	28:G:480:A:C8	2.01	0.95
8:C:218:HIS:HE1	8:C:220:ASN:HD22	1.13	0.95
17:B:43:G:H2'	17:B:44:A:H8	1.28	0.95
16:F:27:U:H2'	16:F:28:U:O4'	1.66	0.94
1:A:900:PHE:CD2	1:A:901:PRO:HD2	2.02	0.94
17:B:98:U:H2'	17:B:99:U:H5'	1.49	0.94
1:A:603:LYS:NZ	16:F:43:C:C5'	2.31	0.94
1:A:1646:ILE:HD13	16:F:49:A:C6	2.02	0.94
26:I:91:U:H3	26:I:142:G:H1	0.94	0.94
8:C:603:PHE:HB3	8:C:646:GLY:O	1.68	0.94
38:H:1099:G:C2'	38:H:1100:A:H5'	1.97	0.94
17:B:96:U:H2'	17:B:97:U:C6	2.03	0.93
28:G:487:A:O2'	28:G:488:A:OP1	1.85	0.93
1:A:1710:GLU:HG2	1:A:1728:ILE:HG12	1.50	0.93
38:H:41:C:H6	38:H:41:C:H5''	1.33	0.93
1:A:1650:ARG:HB3	16:F:49:A:C5'	1.98	0.92
5:J:350:PRO:HB3	16:F:84:C:C5	2.04	0.92
17:B:74:U:C3'	17:B:75:A:H5'	1.98	0.92
38:H:110:A:H4'	38:H:111:C:H5'	0.95	0.92
1:A:668:ARG:HG2	16:F:27:U:C4'	1.99	0.92
38:H:1165:C:H2'	38:H:1166:G:H8	1.32	0.92
17:B:73:U:H2'	17:B:74:U:C5'	1.94	0.92
38:H:47:U:C2'	38:H:48:U:H5''	1.99	0.92
1:A:2398:LEU:O	44:W:60:ARG:HA	1.70	0.92
1:A:668:ARG:CB	16:F:27:U:C1'	2.43	0.92
17:B:44:A:C2'	17:B:45:A:H8	1.83	0.91
28:G:483:A:O2'	28:G:484:A:OP2	1.88	0.91
1:A:689:TYR:CE1	1:A:693:LYS:HG3	2.05	0.91
5:J:159:TYR:HH	5:J:168:TRP:HD1	1.18	0.91
1:A:1861:THR:HG23	18:O:161:ILE:HG23	1.49	0.91
16:F:11:U:H2'	16:F:12:U:H5''	1.50	0.91
28:G:487:A:N3	28:G:488:A:H4'	1.85	0.91
5:J:408:LEU:O	5:J:414:ASP:HA	1.71	0.91
17:B:22:G:H1	17:B:149:U:H3	0.98	0.91
1:A:603:LYS:NZ	16:F:43:C:H5'	1.86	0.91
38:H:1165:C:H2'	38:H:1166:G:C8	2.06	0.90
1:A:146:HIS:HA	1:A:149:MET:HG2	1.52	0.90
1:A:668:ARG:NE	16:F:27:U:H4'	1.85	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:350:PRO:CB	16:F:83:A:N7	2.20	0.90
1:A:1861:THR:CB	18:O:161:ILE:HG12	2.01	0.90
16:F:47:A:H3'	16:F:48:C:H5'	1.54	0.90
5:J:350:PRO:CG	16:F:83:A:N7	2.35	0.90
1:A:2067:TYR:HB3	18:O:194:LEU:HD22	1.50	0.90
5:J:350:PRO:HB3	16:F:84:C:H6	1.34	0.90
17:B:92:U:C5	17:B:93:G:C8	2.59	0.90
17:B:45:A:C2	17:B:46:C:C5	2.60	0.90
1:A:665:GLY:HA3	1:A:668:ARG:HH11	1.33	0.90
8:C:707:SER:O	8:C:823:ILE:HA	1.71	0.89
16:F:15:A:C4	16:F:16:C:H5	1.83	0.89
5:J:350:PRO:CB	16:F:84:C:C5	2.54	0.89
16:F:15:A:C2	16:F:16:C:C5	2.60	0.89
16:F:46:U:C5	16:F:47:A:C2	2.61	0.89
38:H:48:U:C5	38:H:49:U:N1	2.41	0.89
17:B:94:C:H3'	17:B:95:C:H5''	1.55	0.88
1:A:1689:ARG:NH2	16:F:45:A:H5'	1.89	0.88
1:A:900:PHE:CE1	1:A:959:LEU:CD1	2.57	0.88
1:A:1860:VAL:HA	1:A:1873:LYS:O	1.73	0.88
1:A:1652:HIS:NE2	16:F:48:C:OP2	2.06	0.88
29:1:830:MET:O	29:1:832:LYS:N	2.06	0.88
1:A:1701:ILE:O	1:A:1733:TRP:HA	1.74	0.88
4:N:780:LEU:O	4:N:784:GLY:CA	2.21	0.88
31:3:690:LEU:HA	31:3:703:MET:O	1.73	0.88
31:3:656:ILE:HA	31:3:662:SER:O	1.72	0.88
1:A:900:PHE:CE1	1:A:959:LEU:HD11	2.08	0.88
16:F:11:U:O4	16:F:15:A:N6	2.06	0.88
1:A:681:LYS:O	1:A:684:LYS:HB3	1.74	0.87
17:B:98:U:C4	17:B:99:U:C4	2.62	0.87
1:A:234:PHE:HZ	1:A:651:ASP:OD2	1.52	0.87
1:A:1652:HIS:CE1	16:F:48:C:H6	1.68	0.87
1:A:149:MET:SD	1:A:154:TYR:HE2	1.98	0.87
1:A:1774:MET:O	1:A:1786:ALA:HA	1.73	0.87
17:B:175:G:N2	17:B:176:A:H62	1.70	0.87
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.57	0.87
1:A:1650:ARG:HB3	16:F:49:A:H5''	1.54	0.87
3:L:366:LYS:O	16:F:59:A:N6	2.07	0.87
16:F:81:G:C2'	16:F:82:A:H5''	2.05	0.86
1:A:353:GLU:HG2	17:B:104:G:OP1	1.75	0.86
1:A:1689:ARG:HH22	16:F:45:A:H5'	1.40	0.86
16:F:10:A:N6	16:F:11:U:O4	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:487:A:C2'	28:G:488:A:H5'	2.05	0.86
44:W:116:LEU:O	45:O:50:ARG:CA	2.24	0.86
5:J:158:ILE:O	5:J:162:ASN:CB	2.23	0.86
5:J:350:PRO:HB2	16:F:83:A:H8	1.07	0.86
16:F:15:A:N3	16:F:16:C:C5	2.43	0.86
16:F:83:A:O2'	16:F:84:C:OP2	1.92	0.86
2:K:439:LYS:NZ	7:M:122:GLU:OE1	2.09	0.86
1:A:934:ARG:HH21	3:L:436:LYS:H	1.23	0.86
26:I:97:U:H3	26:I:135:A:H61	1.23	0.86
1:A:614:ARG:NH2	16:F:29:U:OP1	2.08	0.86
26:I:146:U:H5''	26:I:147:U:H5'	1.56	0.86
5:J:442:MET:O	16:F:86:G:OP1	1.94	0.85
8:C:458:ILE:HB	8:C:590:LYS:HE2	1.58	0.85
8:C:316:THR:OG1	47:C:1500:GTP:N7	2.10	0.85
1:A:654:HIS:NE2	1:A:701:CYS:SG	2.45	0.85
1:A:1861:THR:HG22	18:O:161:ILE:HA	1.58	0.85
17:B:175:G:N2	17:B:176:A:N6	2.22	0.85
29:1:544:THR:O	29:1:548:LEU:N	2.07	0.85
1:A:668:ARG:HB3	16:F:27:U:H1'	0.86	0.85
28:G:514:U:O2'	28:G:515:U:OP2	1.93	0.85
1:A:964:PHE:CD2	1:A:1085:LYS:HD2	2.11	0.85
5:J:315:ARG:NH2	16:F:72:C:O2	2.10	0.85
1:A:1063:PHE:O	1:A:1066:LEU:N	2.10	0.85
17:B:92:U:C6	17:B:93:G:C8	2.65	0.85
28:G:487:A:C2	28:G:488:A:H4'	2.12	0.85
17:B:98:U:O2'	17:B:99:U:H5'	1.76	0.85
2:K:220:LYS:HB3	2:K:239:GLU:HB3	1.56	0.85
1:A:140:ARG:NH2	1:A:252:GLU:OE1	2.10	0.85
1:A:963:VAL:O	1:A:964:PHE:CD1	2.30	0.84
4:N:21:ARG:NH2	6:E:74:TYR:OH	2.09	0.84
1:A:603:LYS:HZ2	16:F:43:C:C5'	1.87	0.84
26:I:63:U:H2'	26:I:64:U:C5'	2.07	0.84
28:G:487:A:H2'	28:G:488:A:C5'	2.07	0.84
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.42	0.84
1:A:1911:TRP:CZ2	18:O:169:ILE:HD13	2.12	0.84
17:B:74:U:C3'	17:B:75:A:C5'	2.55	0.84
1:A:928:ARG:NH1	1:A:1586:GLN:OE1	2.10	0.84
28:G:479:A:O2'	28:G:480:A:H5'	1.76	0.84
1:A:581:LEU:O	1:A:585:ARG:HB2	1.77	0.84
1:A:1650:ARG:HB2	16:F:49:A:O5'	1.78	0.84
1:A:1916:GLU:O	1:A:1920:LEU:HB2	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:350:PRO:HG2	16:F:84:C:H5	1.42	0.84
1:A:900:PHE:CZ	1:A:959:LEU:HD11	2.12	0.84
8:C:765:VAL:HA	8:C:775:ILE:HG12	1.58	0.84
1:A:1214:ARG:HH12	1:A:1256:PRO:HD2	1.43	0.83
8:C:121:ASP:O	8:C:125:SER:HB2	1.77	0.83
1:A:152:LYS:O	1:A:155:ASN:HB3	1.79	0.83
16:F:36:U:H5''	16:F:36:U:C6	2.12	0.83
16:F:46:U:C5	16:F:47:A:H2	1.96	0.83
1:A:1378:LYS:NZ	16:F:30:G:N7	2.26	0.83
5:J:140:PRO:HA	5:J:146:GLU:HB2	1.59	0.83
8:C:501:ILE:HG21	8:C:570:ALA:HB1	1.59	0.83
1:A:1646:ILE:CD1	16:F:49:A:C6	2.61	0.83
2:K:116:GLU:O	2:K:119:PHE:HB3	1.78	0.83
1:A:150:ALA:HB3	1:A:153:MET:SD	2.19	0.82
5:J:167:GLU:HB3	5:J:169:TRP:HE3	1.42	0.82
1:A:1628:ASP:OD2	16:F:48:C:O2	1.96	0.82
3:L:147:GLU:HA	3:L:150:SER:HB2	1.60	0.82
5:J:350:PRO:HG2	16:F:83:A:N7	1.91	0.82
16:F:81:G:H2'	16:F:82:A:C5'	2.06	0.82
38:H:1099:G:O2'	38:H:1100:A:C5'	2.24	0.82
17:B:102:C:H42	17:B:103:A:H62	1.27	0.82
1:A:614:ARG:NH1	16:F:29:U:OP1	2.11	0.82
3:L:456:LEU:O	3:L:459:LEU:N	2.12	0.82
8:C:915:GLU:HG2	8:C:928:CYS:HB3	1.60	0.82
17:B:92:U:H2'	17:B:93:G:H5''	1.60	0.82
26:I:6:U:H2'	26:I:7:A:C8	2.15	0.82
16:F:15:A:C5	16:F:16:C:C5	2.68	0.82
3:L:160:HIS:O	3:L:164:LYS:HB3	1.79	0.81
5:J:350:PRO:CB	16:F:84:C:H5	1.91	0.81
17:B:102:C:N4	17:B:103:A:H62	1.78	0.81
8:C:220:ASN:O	8:C:647:ASN:ND2	2.12	0.81
26:I:134:U:H2'	26:I:135:A:H8	1.46	0.81
1:A:296:THR:HB	17:B:33:U:OP2	1.80	0.81
1:A:152:LYS:O	1:A:155:ASN:CB	2.28	0.81
1:A:1629:LEU:HD22	1:A:1652:HIS:ND1	1.95	0.81
3:L:376:LYS:NZ	26:I:55:U:O2'	2.13	0.81
3:L:281:GLN:NE2	26:I:37:U:O4	2.13	0.81
1:A:716:ARG:HE	17:B:112:C:H1'	1.46	0.81
2:K:395:ILE:HG22	2:K:396:VAL:H	1.45	0.81
8:C:274:ILE:HD13	8:C:385:PHE:HD2	1.46	0.80
1:A:1861:THR:HG21	18:O:161:ILE:HG12	0.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:MET:H	1:A:153:MET:CE	1.94	0.80
5:J:340:LYS:NZ	5:J:429:GLU:OE1	2.13	0.80
5:J:372:ILE:HB	5:J:376:GLY:HA3	1.63	0.80
1:A:1748:ILE:O	1:A:1751:TYR:N	2.14	0.80
2:K:213:LYS:NZ	2:K:215:ASP:OD1	2.13	0.80
17:B:8:U:H3	17:B:157:G:H1	1.30	0.80
38:H:1149:G:H5''	38:H:1149:G:C8	2.16	0.80
1:A:923:TYR:OH	1:A:936:GLU:OE1	1.99	0.80
2:K:316:GLN:NE2	2:K:320:SER:OG	2.15	0.80
1:A:1652:HIS:NE2	16:F:48:C:H6	1.80	0.80
29:1:835:ILE:O	29:1:837:PHE:N	2.15	0.80
1:A:299:LYS:HE3	17:B:115:G:OP1	1.82	0.80
1:A:900:PHE:CZ	1:A:959:LEU:CD1	2.64	0.80
8:C:605:ILE:HG13	8:C:652:MET:HE1	1.64	0.80
1:A:355:LEU:HD13	17:B:105:A:H5''	1.63	0.80
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.14	0.80
1:A:1863:HIS:ND1	1:A:1864:LYS:N	2.29	0.80
1:A:900:PHE:CD2	1:A:901:PRO:CD	2.65	0.79
1:A:1652:HIS:CE1	16:F:48:C:H2'	2.16	0.79
2:K:121:ARG:HD3	2:K:337:ARG:O	1.81	0.79
16:F:46:U:H6	16:F:46:U:H5''	1.44	0.79
8:C:142:LEU:HD12	8:C:929:GLN:HE21	1.48	0.79
17:B:33:U:H6	17:B:33:U:H3'	1.47	0.79
1:A:699:PRO:HB2	16:F:1:G:P	2.22	0.79
4:N:792:THR:O	4:N:795:GLN:HB2	1.81	0.79
8:C:185:ILE:HD13	17:B:75:A:OP1	1.82	0.79
8:C:465:GLU:CD	8:C:466:GLY:H	1.85	0.79
27:D:539:LEU:O	27:D:543:TYR:CB	2.31	0.79
28:G:485:A:C2	28:G:486:A:C8	2.70	0.79
1:A:1651:ALA:H	16:F:49:A:P	2.06	0.79
8:C:603:PHE:O	8:C:645:LEU:HA	1.82	0.79
8:C:742:ASP:HB3	8:C:746:LYS:HD3	1.65	0.79
26:I:21:C:H2'	26:I:22:G:O4'	1.83	0.79
38:H:49:U:O4	38:H:66:A:N6	2.16	0.79
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.46	0.79
4:N:845:LEU:O	4:N:848:THR:OG1	1.99	0.79
16:F:11:U:H2'	16:F:12:U:C5'	2.13	0.79
28:G:505:A:O4'	28:G:505:A:OP1	2.00	0.79
2:K:460:SER:OG	2:K:462:LYS:NZ	2.15	0.78
8:C:107:THR:HA	8:C:110:LYS:HG2	1.66	0.78
2:K:177:PRO:O	2:K:194:SER:OG	2.02	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:486:A:H3'	28:G:486:A:N3	1.98	0.78
1:A:1511:ARG:O	1:A:1514:PHE:N	2.17	0.78
2:K:321:LEU:HD11	5:J:169:TRP:HE1	1.47	0.78
2:K:410:LEU:HB2	2:K:422:TYR:HB2	1.66	0.78
17:B:158:G:N2	17:B:160:U:O4	2.16	0.78
8:C:187:ARG:NH1	8:C:653:ASP:OD2	2.17	0.78
26:I:12:C:H2'	26:I:13:G:H8	1.48	0.78
26:I:30:G:OP1	26:I:31:U:O2'	1.99	0.78
8:C:219:VAL:HG21	8:C:931:TYR:HB3	1.63	0.78
8:C:236:LEU:HD21	8:C:435:LEU:HD11	1.64	0.78
8:C:727:THR:H	8:C:736:ASP:HB2	1.49	0.78
1:A:1689:ARG:HH22	16:F:45:A:C5'	1.97	0.78
17:B:33:U:O2'	17:B:34:C:OP2	2.00	0.78
8:C:132:ARG:NH2	8:C:207:SER:O	2.17	0.78
1:A:791:ARG:O	1:A:794:LYS:N	2.16	0.78
1:A:243:ASP:HB3	1:A:246:GLU:HB2	1.66	0.78
1:A:681:LYS:HE2	16:F:25:C:H42	1.49	0.77
4:N:522:ALA:O	4:N:526:TYR:CB	2.32	0.77
16:F:29:U:O2'	16:F:30:G:C5'	2.31	0.77
1:A:693:LYS:HA	1:A:693:LYS:HZ2	1.49	0.77
1:A:1134:LEU:O	1:A:1142:ASN:ND2	2.17	0.77
8:C:218:HIS:CE1	8:C:220:ASN:HD22	2.02	0.77
38:H:48:U:C6	38:H:49:U:C6	2.73	0.77
1:A:855:LEU:O	1:A:858:LYS:N	2.17	0.77
1:A:1800:ASN:O	1:A:1804:THR:HG23	1.85	0.77
1:A:713:ASN:HB3	17:B:84:A:H5'	1.67	0.77
1:A:770:MET:O	1:A:775:ARG:NH2	2.14	0.77
2:K:243:ILE:HB	2:K:261:LEU:HB2	1.65	0.77
17:B:166:U:O2'	17:B:167:A:OP1	2.00	0.77
8:C:273:LEU:HD11	8:C:279:LEU:HD22	1.65	0.77
1:A:358:ARG:NE	1:A:361:GLU:OE2	2.14	0.77
1:A:654:HIS:CE1	1:A:701:CYS:HG	2.02	0.77
5:J:345:LYS:HA	5:J:377:PRO:HB3	1.67	0.77
1:A:238:ARG:NH2	1:A:241:PRO:O	2.18	0.77
2:K:112:PRO:HA	5:J:217:VAL:N	2.00	0.77
26:I:98:G:H1	26:I:134:U:H3	1.31	0.76
2:K:44:ILE:HG13	2:K:45:PRO:HD2	1.67	0.76
4:N:598:PHE:O	4:N:602:LYS:CB	2.33	0.76
4:N:678:TYR:O	4:N:682:GLY:N	2.17	0.76
16:F:15:A:N1	16:F:16:C:C4	2.52	0.76
8:C:223:ASP:O	8:C:226:ALA:HB3	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:292:ILE:O	8:C:296:ASN:ND2	2.19	0.76
4:N:746:MET:HG2	4:N:749:ARG:HH22	1.50	0.76
5:J:242:LYS:O	5:J:245:ARG:N	2.18	0.76
6:E:30:ARG:HH21	6:E:61:LEU:HD13	1.50	0.76
8:C:193:LEU:HD23	8:C:224:GLU:HB3	1.67	0.76
8:C:233:ASP:OD1	8:C:487:ARG:NH2	2.19	0.76
1:A:1682:THR:HG1	1:A:1702:THR:HG1	1.28	0.76
2:K:44:ILE:O	2:K:73:ARG:NH2	2.18	0.76
8:C:452:LYS:HZ1	8:C:487:ARG:HH22	1.30	0.76
17:B:175:G:H21	17:B:176:A:H62	1.31	0.76
16:F:15:A:C5	16:F:16:C:H5	2.02	0.75
1:A:225:ARG:HH21	1:A:694:ASN:CG	1.87	0.75
28:G:485:A:C2	28:G:486:A:H8	2.04	0.75
1:A:1130:ARG:HH22	1:A:1153:GLU:HA	1.51	0.75
17:B:94:C:H2'	17:B:96:U:OP1	1.87	0.75
1:A:1709:TRP:N	1:A:1729:THR:O	2.20	0.75
1:A:2050:THR:O	1:A:2053:SER:OG	2.03	0.75
1:A:225:ARG:HG2	1:A:691:PHE:HB2	1.68	0.75
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.18	0.75
1:A:1907:GLN:HA	1:A:1910:LYS:HD2	1.68	0.75
4:N:230:LEU:HD13	4:N:247:SER:HA	1.66	0.75
5:J:157:LYS:O	5:J:160:TYR:N	2.20	0.75
8:C:931:TYR:CD1	8:C:933:TRP:HD1	2.04	0.75
16:F:10:A:H61	16:F:16:C:H42	1.33	0.75
28:G:514:U:H4'	28:G:515:U:C5'	2.16	0.75
1:A:146:HIS:O	1:A:149:MET:N	2.19	0.75
1:A:1889:LEU:HD12	1:A:1989:PHE:HB2	1.68	0.75
17:B:162:G:H3'	17:B:163:C:C4'	2.16	0.75
1:A:1652:HIS:CE1	16:F:48:C:C5	2.53	0.75
8:C:328:VAL:HG13	8:C:332:TYR:HB2	1.66	0.75
8:C:603:PHE:CB	8:C:646:GLY:O	2.34	0.75
4:N:286:GLU:HG3	4:N:287:SER:H	1.52	0.75
17:B:96:U:H3'	17:B:97:U:H6	1.52	0.75
29:1:680:PRO:N	29:1:681:PRO:HA	2.00	0.75
1:A:1330:LYS:O	1:A:1333:ALA:N	2.20	0.75
28:G:500:A:H5'	28:G:500:A:C8	2.22	0.75
1:A:1376:ASN:OD1	1:A:1377:SER:N	2.20	0.74
4:N:401:ILE:O	4:N:405:SER:N	2.20	0.74
26:I:5:U:H2'	26:I:6:U:H6	1.52	0.74
1:A:694:ASN:ND2	1:A:694:ASN:H	1.85	0.74
1:A:1910:LYS:O	1:A:1913:THR:OG1	2.04	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:193:THR:O	3:L:196:GLN:N	2.20	0.74
6:E:51:GLU:OE1	6:E:51:GLU:N	2.19	0.74
17:B:83:C:O2'	17:B:84:A:O5'	2.05	0.74
44:W:131:PHE:O	44:W:135:TYR:CB	2.35	0.74
1:A:1861:THR:O	1:A:1872:THR:HA	1.85	0.74
1:A:1681:VAL:HA	1:A:1702:THR:O	1.87	0.74
6:E:138:ASN:OD1	6:E:139:HIS:N	2.20	0.74
16:F:15:A:H2'	16:F:16:C:H6	1.52	0.74
38:H:1138:G:P	38:H:1138:G:O4'	2.45	0.74
1:A:881:THR:O	1:A:884:SER:OG	2.06	0.74
8:C:484:SER:O	8:C:563:LEU:HA	1.88	0.74
1:A:146:HIS:HD2	1:A:149:MET:HB2	1.34	0.74
1:A:152:LYS:C	1:A:155:ASN:H	1.90	0.74
1:A:346:ILE:HD11	1:A:385:VAL:HG21	1.70	0.74
4:N:15:TYR:HE2	6:E:13:TRP:HD1	1.33	0.74
16:F:15:A:N6	16:F:16:C:N4	2.36	0.74
17:B:103:A:O2'	17:B:104:G:O5'	2.05	0.74
1:A:1356:LEU:O	1:A:1359:ILE:N	2.20	0.74
1:A:2069:VAL:HG22	18:O:198:GLN:NE2	2.02	0.74
16:F:46:U:H6	16:F:46:U:C5'	2.00	0.74
17:B:93:G:O3'	17:B:94:C:O4'	2.05	0.74
26:I:134:U:H2'	26:I:135:A:C8	2.23	0.74
28:G:487:A:HO2'	28:G:488:A:P	2.09	0.74
1:A:1717:LEU:O	1:A:1799:GLN:NE2	2.20	0.74
26:I:46:G:H2'	26:I:47:A:H8	1.53	0.74
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.20	0.74
8:C:636:VAL:HG22	8:C:642:HIS:HD1	1.52	0.74
16:F:15:A:C6	16:F:16:C:C4	2.75	0.74
1:A:146:HIS:O	1:A:149:MET:HB2	1.88	0.73
1:A:961:GLN:HG3	1:A:964:PHE:CE1	2.23	0.73
1:A:1087:ASN:HD21	3:L:272:LEU:HG	1.52	0.73
17:B:33:U:H4'	17:B:34:C:O5'	1.88	0.73
1:A:1883:ASN:ND2	1:A:1886:THR:OG1	2.20	0.73
2:K:119:PHE:O	2:K:122:ARG:HB2	1.88	0.73
5:J:344:PHE:O	5:J:377:PRO:HA	1.88	0.73
16:F:33:C:H42	16:F:51:A:H61	1.36	0.73
17:B:92:U:H2'	17:B:93:G:O4'	1.88	0.73
2:K:309:GLY:H	2:K:327:MET:HE2	1.50	0.73
8:C:445:PRO:O	8:C:449:PHE:HB2	1.88	0.73
16:F:15:A:N6	16:F:16:C:H41	1.85	0.73
1:A:1861:THR:HA	18:O:161:ILE:HA	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:327:THR:HG22	3:L:328:VAL:H	1.54	0.73
4:N:311:PHE:O	4:N:315:ASP:CB	2.36	0.73
1:A:900:PHE:CE1	1:A:959:LEU:HD12	2.23	0.73
16:F:15:A:C2	16:F:16:C:C4	2.76	0.73
1:A:1068:ARG:O	1:A:1071:ARG:N	2.21	0.73
1:A:1907:GLN:O	1:A:1910:LYS:HG2	1.88	0.73
17:B:32:G:H4'	17:B:33:U:OP2	1.88	0.73
38:H:48:U:H5	38:H:49:U:C6	2.02	0.73
1:A:1652:HIS:CD2	16:F:48:C:OP2	2.42	0.73
3:L:455:PHE:O	3:L:458:SER:OG	2.06	0.73
4:N:325:ARG:O	4:N:329:LYS:CB	2.36	0.73
1:A:1952:PRO:HB2	3:L:426:GLY:H	1.52	0.73
38:H:142:C:H2'	38:H:143:G:H8	1.52	0.73
1:A:1002:GLU:O	1:A:1005:GLN:N	2.22	0.72
1:A:1020:ILE:HG22	1:A:1022:PRO:HD2	1.71	0.72
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.23	0.72
17:B:80:G:C2	17:B:82:A:C2	2.77	0.72
2:K:446:SER:OG	2:K:451:PHE:HB2	1.90	0.72
17:B:92:U:C4	17:B:93:G:C5	2.76	0.72
1:A:787:SER:O	1:A:790:TRP:N	2.23	0.72
2:K:154:SER:O	2:K:157:THR:OG1	2.07	0.72
16:F:72:C:H2'	16:F:73:A:H8	1.53	0.72
2:K:271:VAL:HA	2:K:281:GLY:O	1.89	0.72
3:L:221:LYS:HA	3:L:224:ILE:HD12	1.71	0.72
1:A:228:LYS:NZ	1:A:698:GLY:HA3	2.05	0.72
2:K:395:ILE:HD11	7:M:123:THR:HA	1.70	0.72
38:H:1093:C:H2'	38:H:1094:G:O4'	1.90	0.72
1:A:603:LYS:HZ2	16:F:43:C:H5''	1.53	0.72
4:N:15:TYR:CE2	6:E:13:TRP:HD1	2.08	0.72
26:I:76:A:OP2	27:D:590:GLY:HA3	1.89	0.72
38:H:48:U:C2'	38:H:49:U:H5'	2.19	0.72
3:L:335:ALA:O	3:L:338:SER:OG	2.06	0.72
4:N:695:THR:HG22	4:N:704:LEU:HB3	1.72	0.72
31:3:547:ASN:HA	31:3:563:ILE:O	1.90	0.72
38:H:140:G:H1	38:H:1168:U:H3	1.37	0.72
38:H:142:C:H2'	38:H:143:G:C8	2.24	0.72
1:A:570:GLN:O	1:A:574:GLN:HB2	1.89	0.71
1:A:964:PHE:CE2	1:A:1085:LYS:HD2	2.24	0.71
28:G:500:A:H5'	28:G:500:A:H8	1.54	0.71
38:H:68:U:C4	38:H:69:G:N7	2.58	0.71
1:A:689:TYR:CE1	1:A:693:LYS:CG	2.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2398:LEU:O	44:W:59:LYS:O	2.06	0.71
17:B:162:G:O3'	17:B:164:C:OP1	2.08	0.71
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.24	0.71
2:K:223:ALA:N	2:K:237:CYS:SG	2.63	0.71
8:C:306:PRO:HG2	8:C:349:TRP:CD2	2.25	0.71
17:B:44:A:C4	17:B:45:A:C8	2.79	0.71
17:B:102:C:H2'	17:B:103:A:H5'	1.71	0.71
1:A:151:SER:OG	1:A:152:LYS:HG3	1.90	0.71
1:A:1277:GLU:OE1	1:A:1277:GLU:N	2.24	0.71
5:J:368:LEU:HD23	5:J:437:PHE:HE1	1.55	0.71
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	1.72	0.71
17:B:92:U:C4	17:B:93:G:N7	2.57	0.71
1:A:152:LYS:O	1:A:155:ASN:N	2.23	0.71
1:A:319:ARG:HH22	1:A:504:LYS:HE2	1.55	0.71
3:L:120:TYR:CZ	3:L:141:ILE:HG21	2.25	0.71
1:A:693:LYS:HA	1:A:693:LYS:NZ	2.05	0.71
3:L:359:PRO:O	6:E:122:ARG:NH1	2.23	0.71
38:H:119:G:H4'	38:H:119:G:OP1	1.90	0.71
1:A:372:ARG:HB3	8:C:973:ARG:HE	1.56	0.71
1:A:1145:MET:O	1:A:1146:GLN:HG3	1.90	0.70
17:B:98:U:C5	17:B:99:U:C5	2.79	0.70
1:A:654:HIS:CG	1:A:701:CYS:SG	2.84	0.70
1:A:776:GLN:N	1:A:776:GLN:OE1	2.24	0.70
4:N:562:MET:O	4:N:566:SER:CB	2.39	0.70
8:C:452:LYS:HZ2	8:C:487:ARG:HH12	1.40	0.70
1:A:252:GLU:HG2	1:A:253:GLN:HG3	1.73	0.70
1:A:1507:GLY:O	1:A:1511:ARG:NH2	2.24	0.70
1:A:1585:MET:SD	1:A:1588:LYS:NZ	2.63	0.70
1:A:1862:VAL:HG22	1:A:1872:THR:HG22	1.74	0.70
38:H:48:U:H2'	38:H:49:U:O4'	1.90	0.70
1:A:338:ASN:ND2	1:A:399:ARG:O	2.18	0.70
1:A:1861:THR:HG21	18:O:161:ILE:CD1	2.20	0.70
1:A:2268:PHE:CB	1:A:2331:PRO:CB	2.69	0.70
4:N:781:PHE:HA	4:N:784:GLY:HA3	1.73	0.70
1:A:1737:GLN:O	1:A:1776:GLY:HA2	1.91	0.70
2:K:375:VAL:O	2:K:386:LEU:HA	1.92	0.70
17:B:93:G:H5'	17:B:94:C:OP2	1.92	0.70
4:N:821:TYR:O	4:N:824:SER:OG	2.08	0.70
5:J:436:LYS:NZ	5:J:459:ASP:OD2	2.25	0.70
8:C:274:ILE:HD12	8:C:382:TYR:HD1	1.56	0.70
38:H:1138:G:HO2'	38:H:1139:G:H8	1.36	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:GLN:HG2	1:A:263:PRO:HD3	1.71	0.70
1:A:863:ARG:HG3	1:A:864:GLN:N	2.07	0.70
8:C:341:ILE:O	8:C:344:PHE:N	2.23	0.70
8:C:544:LEU:HG	8:C:553:VAL:HG21	1.74	0.70
17:B:83:C:H4'	17:B:84:A:OP1	1.91	0.70
17:B:163:C:H4'	17:B:164:C:OP1	1.91	0.70
26:I:12:C:H2'	26:I:13:G:C8	2.27	0.70
1:A:174:LYS:O	1:A:178:ASN:ND2	2.21	0.70
5:J:259:LYS:HB3	5:J:265:LEU:HD13	1.73	0.70
8:C:499:VAL:HG13	8:C:579:SER:HB2	1.74	0.70
26:I:97:U:H2'	26:I:98:G:C8	2.26	0.70
1:A:153:MET:HE3	1:A:153:MET:N	1.99	0.70
8:C:365:GLU:HG3	8:C:366:ASN:H	1.56	0.70
16:F:33:C:O2'	16:F:34:A:O5'	2.09	0.70
38:H:118:U:H4'	38:H:119:G:OP1	1.91	0.70
1:A:1339:LEU:HD21	1:A:1440:ILE:HD11	1.73	0.70
4:N:602:LYS:O	4:N:606:ARG:N	2.24	0.70
4:N:826:LYS:O	4:N:830:ARG:CB	2.40	0.70
27:D:1895:ARG:O	27:D:1897:GLY:N	2.16	0.70
1:A:934:ARG:NH2	3:L:436:LYS:H	1.90	0.69
1:A:1951:PHE:HB3	1:A:1954:ILE:HD12	1.74	0.69
4:N:238:PRO:O	4:N:244:TRP:NE1	2.25	0.69
17:B:91:U:H2'	17:B:92:U:H5''	1.73	0.69
1:A:639:PHE:HA	1:A:644:VAL:HB	1.73	0.69
1:A:956:LYS:HD3	3:L:452:ALA:HA	1.73	0.69
1:A:1323:SER:O	1:A:1370:ARG:NH2	2.24	0.69
4:N:124:ASP:OD1	4:N:125:ALA:N	2.25	0.69
16:F:28:U:H2'	16:F:29:U:H5'	1.75	0.69
38:H:48:U:H5	38:H:49:U:C5	2.10	0.69
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.26	0.69
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.25	0.69
4:N:9:GLN:HB3	4:N:11:PRO:HD3	1.74	0.69
8:C:133:ILE:CA	8:C:209:MET:O	2.39	0.69
8:C:142:LEU:HD11	8:C:218:HIS:CD2	2.27	0.69
8:C:223:ASP:HB3	8:C:630:PRO:HG2	1.75	0.69
26:I:91:U:O2'	26:I:92:C:OP1	2.08	0.69
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.74	0.69
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.25	0.69
1:A:2069:VAL:CG2	18:O:198:GLN:HE21	2.05	0.69
4:N:690:THR:O	4:N:693:SER:OG	2.07	0.69
1:A:2006:SER:O	1:A:2009:THR:OG1	2.09	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1101:ILE:O	27:D:1105:ALA:HB2	1.92	0.69
23:T:40:LYS:O	23:T:57:ALA:HA	1.93	0.69
1:A:194:HIS:HA	1:A:557:PHE:HD1	1.58	0.69
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.24	0.69
1:A:1341:SER:HA	1:A:1525:PHE:HE1	1.58	0.69
1:A:1446:THR:OG1	1:A:1449:ASN:ND2	2.25	0.69
4:N:482:LEU:O	4:N:486:ASP:CB	2.40	0.69
5:J:443:LYS:HG2	5:J:444:VAL:H	1.58	0.69
7:M:56:ALA:HB2	7:M:80:PHE:HB3	1.73	0.69
16:F:47:A:C3'	16:F:48:C:H5'	2.22	0.69
17:B:75:A:H3'	17:B:77:A:OP2	1.93	0.69
1:A:886:MET:O	1:A:889:TRP:N	2.26	0.69
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	1.93	0.69
3:L:192:LYS:O	3:L:195:THR:OG1	2.11	0.69
4:N:10:GLU:HG2	6:E:14:HIS:CE1	2.28	0.69
8:C:718:LYS:NZ	8:C:754:GLU:O	2.26	0.69
1:A:668:ARG:CG	16:F:27:U:C1'	2.71	0.69
4:N:706:VAL:O	4:N:710:LYS:HB2	1.93	0.69
7:M:24:VAL:O	7:M:27:ALA:N	2.22	0.69
8:C:266:VAL:HG22	8:C:312:ILE:HB	1.75	0.69
17:B:95:C:O3'	17:B:96:U:O4'	2.11	0.69
26:I:99:G:H4'	27:D:1186:GLU:CB	2.23	0.69
29:1:541:VAL:O	29:1:545:VAL:N	2.26	0.69
1:A:1347:ARG:NH1	1:A:1450:GLU:OE2	2.26	0.68
1:A:1861:THR:CG2	18:O:161:ILE:HA	2.23	0.68
8:C:794:GLN:HG2	8:C:835:LYS:HG2	1.74	0.68
17:B:95:C:H1'	17:B:96:U:O4'	1.92	0.68
17:B:95:C:H4'	17:B:96:U:OP1	1.91	0.68
38:H:1149:G:H2'	38:H:1150:U:H6	1.58	0.68
2:K:137:GLN:O	2:K:140:MET:HB3	1.93	0.68
4:N:666:ILE:HG22	4:N:667:CYS:H	1.58	0.68
4:N:842:TRP:HA	4:N:845:LEU:HD12	1.74	0.68
8:C:400:LEU:HB3	8:C:406:VAL:HB	1.73	0.68
2:K:232:ASN:O	2:K:247:GLN:NE2	2.26	0.68
8:C:222:MET:O	8:C:225:THR:OG1	2.11	0.68
8:C:748:SER:HB2	8:C:762:SER:HB2	1.75	0.68
17:B:73:U:O2'	17:B:74:U:C5'	2.41	0.68
38:H:1092:A:H3'	38:H:1093:C:H6	1.58	0.68
1:A:497:GLN:OE1	1:A:497:GLN:N	2.22	0.68
1:A:1118:GLY:HA3	1:A:1163:ARG:HH12	1.58	0.68
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:400:ARG:NH1	2:K:444:ASP:OD1	2.25	0.68
4:N:80:GLN:O	4:N:84:LYS:CB	2.41	0.68
4:N:809:LEU:HD12	4:N:841:THR:HG22	1.74	0.68
27:D:757:LEU:O	27:D:761:PHE:CB	2.41	0.68
1:A:353:GLU:CG	17:B:104:G:OP1	2.40	0.68
1:A:1819:ILE:O	1:A:1822:GLY:N	2.26	0.68
4:N:116:GLU:HA	4:N:119:TRP:HD1	1.59	0.68
4:N:668:HIS:HA	4:N:671:PHE:HD2	1.58	0.68
8:C:843:LYS:HG2	8:C:847:TYR:CE2	2.29	0.68
27:D:639:LEU:HA	27:D:644:GLY:HA3	1.74	0.68
1:A:1043:ARG:O	1:A:1045:GLN:N	2.26	0.68
1:A:1666:CYS:O	1:A:1670:ASP:HB2	1.91	0.68
1:A:1094:ASP:OD1	4:N:134:ARG:NH1	2.26	0.68
1:A:1303:LYS:HG2	1:A:1304:VAL:H	1.59	0.68
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.75	0.68
4:N:813:VAL:O	4:N:816:TYR:N	2.27	0.68
8:C:341:ILE:HG13	8:C:342:ASP:H	1.58	0.68
8:C:398:ASN:OD1	8:C:401:ARG:NH2	2.26	0.68
26:I:46:G:H2'	26:I:47:A:C8	2.28	0.68
1:A:1384:PRO:HG2	1:A:1387:VAL:HG23	1.75	0.68
1:A:2069:VAL:CG2	18:O:198:GLN:NE2	2.57	0.68
8:C:234:LEU:HB3	8:C:262:ALA:HB3	1.76	0.68
8:C:493:LEU:HB2	8:C:556:ALA:HB3	1.74	0.68
28:G:485:A:N3	28:G:486:A:H8	1.91	0.68
16:F:50:G:H4'	16:F:51:A:OP2	1.92	0.67
1:A:327:TYR:HH	1:A:509:HIS:HD1	1.41	0.67
8:C:769:TYR:HA	8:C:800:TYR:HE1	1.58	0.67
8:C:850:LEU:HG	8:C:855:PRO:HB3	1.74	0.67
2:K:120:ALA:O	2:K:123:PHE:HB3	1.94	0.67
4:N:293:LYS:HA	4:N:296:VAL:HB	1.75	0.67
8:C:761:ALA:O	8:C:765:VAL:N	2.26	0.67
17:B:147:C:H2'	17:B:148:G:H8	1.56	0.67
38:H:41:C:H6	38:H:41:C:C5'	2.03	0.67
1:A:217:TRP:HE1	1:A:703:PHE:HD1	1.41	0.67
5:J:344:PHE:HB3	5:J:424:ILE:HD13	1.77	0.67
8:C:637:GLU:OE1	8:C:974:LYS:NZ	2.28	0.67
26:I:77:U:C2	27:D:1107:ARG:HA	2.28	0.67
28:G:485:A:N3	28:G:486:A:C8	2.62	0.67
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.58	0.67
3:L:361:ASP:OD1	3:L:362:GLN:N	2.27	0.67
16:F:15:A:N1	16:F:16:C:N4	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Z:40:LEU:O	37:Z:43:ASN:O	2.12	0.67
8:C:185:ILE:HG21	17:B:75:A:OP1	1.93	0.67
8:C:697:ARG:CZ	8:C:849:GLY:HA2	2.25	0.67
17:B:100:A:H5'	17:B:101:C:OP2	1.95	0.67
30:2:185:GLY:O	30:2:188:LEU:N	2.27	0.67
1:A:251:TYR:O	1:A:256:GLU:N	2.26	0.67
2:K:314:SER:OG	2:K:355:VAL:O	2.12	0.67
1:A:1876:ASN:ND2	1:A:1981:ALA:O	2.28	0.67
5:J:246:ARG:HH22	26:I:23:C:P	2.18	0.67
1:A:594:ASP:OD1	1:A:598:ASN:N	2.27	0.67
1:A:1118:GLY:HA3	1:A:1163:ARG:NH1	2.10	0.67
1:A:1420:THR:O	1:A:1718:HIS:ND1	2.27	0.67
1:A:1798:ILE:O	1:A:1801:SER:OG	2.06	0.67
2:K:170:SER:O	2:K:171:GLN:HB2	1.93	0.67
8:C:775:ILE:HD12	8:C:817:GLN:HE21	1.58	0.67
26:I:47:A:H2'	26:I:48:U:H6	1.58	0.67
16:F:69:C:H2'	16:F:70:U:C6	2.30	0.67
28:G:479:A:O2'	28:G:480:A:C5'	2.43	0.67
3:L:237:ILE:O	3:L:240:GLN:N	2.28	0.66
8:C:193:LEU:N	8:C:224:GLU:OE1	2.25	0.66
1:A:1694:MET:O	1:A:1759:TYR:OH	2.12	0.66
1:A:1816:ARG:O	1:A:1820:ARG:NE	2.21	0.66
2:K:60:LYS:HG3	2:K:79:ILE:HD13	1.77	0.66
2:K:269:SER:OG	2:K:311:PHE:O	2.13	0.66
3:L:112:MET:HB2	3:L:204:LEU:HD21	1.77	0.66
3:L:357:PRO:O	3:L:358:ILE:HG13	1.94	0.66
4:N:127:ASP:OD2	4:N:131:ARG:N	2.26	0.66
1:A:195:THR:N	1:A:556:TYR:O	2.22	0.66
1:A:482:SER:OG	1:A:487:ASN:N	2.28	0.66
5:J:167:GLU:HB3	5:J:169:TRP:CE3	2.29	0.66
8:C:629:TYR:OH	8:C:658:ASP:OD2	2.13	0.66
1:A:1078:ILE:O	1:A:1081:TYR:N	2.28	0.66
2:K:175:THR:O	2:K:176:LYS:HG2	1.95	0.66
3:L:358:ILE:HG22	3:L:360:GLU:H	1.58	0.66
4:N:361:ALA:O	4:N:365:ILE:CB	2.43	0.66
8:C:500:ARG:HB3	8:C:534:THR:HG21	1.77	0.66
4:N:342:LYS:O	4:N:346:SER:CB	2.44	0.66
6:E:96:GLY:O	16:F:31:G:OP2	2.13	0.66
8:C:137:GLY:O	8:C:235:VAL:HA	1.96	0.66
17:B:147:C:H2'	17:B:148:G:C8	2.30	0.66
26:I:141:G:C2'	26:I:142:G:H5'	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:116:GLU:OE1	2:K:116:GLU:N	2.29	0.66
2:K:360:ASN:HB3	2:K:362:TYR:CE2	2.31	0.66
1:A:1616:ARG:NE	1:A:1744:ASP:OD1	2.27	0.66
4:N:713:GLU:HA	4:N:720:VAL:HG11	1.78	0.66
8:C:302:ASN:OD1	8:C:303:VAL:N	2.27	0.66
8:C:316:THR:O	8:C:319:GLY:N	2.28	0.66
1:A:304:ASP:OD1	1:A:305:LEU:N	2.25	0.66
1:A:1090:ILE:O	1:A:1096:SER:HA	1.96	0.66
1:A:1561:LEU:O	1:A:1564:GLY:N	2.24	0.66
1:A:1590:LEU:HB2	1:A:1595:ARG:HH21	1.60	0.66
1:A:2069:VAL:HG22	18:O:198:GLN:HE21	1.60	0.66
7:M:62:GLU:O	7:M:65:LEU:N	2.26	0.66
8:C:697:ARG:NH2	8:C:852:THR:OG1	2.28	0.66
17:B:126:A:H5'	17:B:127:U:OP2	1.96	0.66
1:A:632:ILE:O	1:A:635:THR:OG1	2.11	0.66
2:K:420:ASN:ND2	2:K:422:TYR:OH	2.29	0.66
3:L:120:TYR:O	3:L:123:ARG:N	2.29	0.66
3:L:124:PHE:CD2	3:L:127:LEU:HB2	2.31	0.66
1:A:193:TYR:O	1:A:557:PHE:HA	1.94	0.66
1:A:326:ASN:HB2	1:A:405:ASN:HB2	1.77	0.66
1:A:976:GLN:NE2	1:A:1310:LYS:HB3	2.00	0.66
1:A:1830:VAL:HG12	1:A:1832:GLU:H	1.61	0.66
2:K:270:ASP:OD1	2:K:271:VAL:N	2.28	0.66
38:H:1115:G:H1	38:H:1130:U:H3	1.43	0.66
3:L:124:PHE:CE2	3:L:127:LEU:HB2	2.31	0.65
17:B:95:C:O2	17:B:95:C:O2'	2.12	0.65
38:H:1149:G:H5''	38:H:1149:G:H8	1.56	0.65
45:O:194:TRP:O	45:O:198:GLN:CB	2.44	0.65
1:A:764:ASP:HA	1:A:767:LEU:HD12	1.78	0.65
1:A:805:PRO:HG2	1:A:808:ILE:HD12	1.79	0.65
1:A:1554:GLU:OE1	1:A:1554:GLU:N	2.24	0.65
2:K:135:ARG:NH1	2:K:139:GLU:OE2	2.29	0.65
8:C:342:ASP:O	8:C:345:THR:OG1	2.14	0.65
1:A:152:LYS:CA	1:A:155:ASN:HB2	2.24	0.65
3:L:113:HIS:CD2	3:L:134:PRO:HB3	2.31	0.65
4:N:241:PRO:HG3	4:N:277:ILE:HD11	1.78	0.65
1:A:1023:LEU:HB2	1:A:1451:PHE:HE1	1.60	0.65
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.24	0.65
5:J:233:LYS:HE2	5:J:235:TYR:HE1	1.60	0.65
8:C:397:LYS:HE3	8:C:413:LEU:HD21	1.77	0.65
38:H:1120:G:H2'	38:H:1121:U:H6	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:HD13	1:A:392:ASN:HD22	1.61	0.65
1:A:674:MET:HA	1:A:677:ILE:HD12	1.78	0.65
1:A:939:LEU:HD11	3:L:441:MET:HE2	1.79	0.65
1:A:1071:ARG:NH2	1:A:1080:ASP:OD1	2.29	0.65
1:A:1339:LEU:HD21	1:A:1440:ILE:CD1	2.25	0.65
7:M:71:CYS:O	7:M:75:ASN:N	2.29	0.65
1:A:970:THR:O	1:A:981:VAL:HB	1.97	0.65
1:A:1207:TRP:HB3	1:A:1211:SER:OG	1.97	0.65
1:A:1418:THR:OG1	1:A:1421:GLY:O	2.09	0.65
1:A:1450:GLU:O	1:A:1453:ASP:N	2.30	0.65
2:K:115:SER:O	2:K:118:ILE:N	2.25	0.65
3:L:350:ILE:HG13	3:L:351:SER:H	1.62	0.65
38:H:66:A:H2'	38:H:66:A:N3	2.10	0.65
1:A:1313:ASP:O	1:A:1316:ILE:N	2.29	0.65
1:A:1733:TRP:NE1	1:A:1769:SER:O	2.21	0.65
4:N:789:LEU:HD11	7:M:45:ASN:HB3	1.79	0.65
17:B:92:U:H2'	17:B:93:G:C5'	2.25	0.65
38:H:1138:G:O2'	38:H:1139:G:H8	1.79	0.65
1:A:1070:LEU:O	1:A:1073:ILE:N	2.29	0.65
1:A:1498:ASP:HA	4:N:160:ASN:HB2	1.77	0.65
3:L:187:GLU:OE1	3:L:187:GLU:N	2.30	0.65
4:N:825:LEU:HA	4:N:828:LEU:HD12	1.77	0.65
8:C:271:ASP:OD1	8:C:272:ARG:N	2.29	0.65
8:C:308:ASP:HB3	8:C:310:ASN:HD22	1.62	0.65
17:B:102:C:H42	17:B:103:A:N6	1.95	0.65
1:A:151:SER:OG	1:A:152:LYS:N	2.29	0.65
1:A:900:PHE:HE1	1:A:959:LEU:HD12	1.60	0.65
1:A:1834:PHE:HB3	1:A:1959:THR:HA	1.77	0.65
8:C:867:THR:O	8:C:926:GLY:CA	2.43	0.65
1:A:308:MET:O	1:A:311:LEU:N	2.29	0.65
1:A:900:PHE:HD2	1:A:901:PRO:N	1.95	0.65
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.61	0.65
3:L:98:PHE:HA	3:L:101:ILE:HG22	1.78	0.65
3:L:302:MET:O	3:L:306:LEU:N	2.24	0.65
4:N:550:ARG:O	4:N:554:ARG:N	2.29	0.65
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.22	0.64
1:A:1272:ARG:N	1:A:1297:THR:O	2.29	0.64
2:K:322:VAL:HG13	2:K:334:TRP:HB2	1.79	0.64
16:F:36:U:H6	16:F:36:U:C5'	2.05	0.64
26:I:151:G:H4'	26:I:152:A:O4'	1.97	0.64
45:0:191:LEU:O	45:0:195:LEU:CB	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ARG:HH21	1:A:699:PRO:HG2	1.63	0.64
1:A:300:LYS:HA	1:A:492:LYS:HA	1.78	0.64
1:A:1646:ILE:HD13	16:F:49:A:C5	2.31	0.64
4:N:234:ARG:HD2	4:N:244:TRP:CE3	2.33	0.64
8:C:139:ILE:O	8:C:237:ILE:HA	1.97	0.64
17:B:50:G:H1	17:B:65:U:H3	1.44	0.64
38:H:48:U:H2'	38:H:49:U:C4'	2.27	0.64
3:L:159:PHE:O	3:L:162:GLU:N	2.31	0.64
3:L:439:LYS:HE3	26:I:21:C:P	2.38	0.64
6:E:95:PHE:HE2	6:E:103:LEU:HD13	1.63	0.64
8:C:251:GLN:HG2	8:C:933:TRP:CE2	2.33	0.64
8:C:393:LYS:NZ	8:C:413:LEU:O	2.27	0.64
16:F:29:U:H2'	16:F:30:G:H5'	1.79	0.64
17:B:102:C:N4	17:B:103:A:N7	2.44	0.64
2:K:247:GLN:NE2	2:K:248:TYR:O	2.30	0.64
4:N:233:TYR:CE2	4:N:243:GLY:HA2	2.33	0.64
16:F:29:U:C4	17:B:98:U:N3	2.66	0.64
28:G:475:U:O3'	28:G:476:U:O4'	2.15	0.64
1:A:667:TYR:HE1	16:F:26:A:HO2'	0.78	0.64
1:A:1414:TRP:CD1	1:A:1555:THR:HG22	2.32	0.64
3:L:424:THR:HG21	4:N:156:ASN:HA	1.79	0.64
8:C:697:ARG:HH11	8:C:848:VAL:HG12	1.62	0.64
16:F:15:A:N3	16:F:16:C:C6	2.65	0.64
18:O:149:TYR:HD2	18:O:178:VAL:HG12	1.61	0.64
1:A:716:ARG:NH2	17:B:111:C:C2	2.63	0.64
8:C:534:THR:OG1	8:C:578:TYR:OH	2.13	0.64
8:C:583:LYS:HA	8:C:586:MET:HB3	1.80	0.64
17:B:99:U:H3'	17:B:100:A:H4'	1.79	0.64
28:G:486:A:C6	28:G:487:A:N7	2.66	0.64
38:H:1098:C:H2'	38:H:1099:G:H8	1.63	0.64
1:A:162:LEU:HG	1:A:730:ILE:HG21	1.77	0.64
1:A:923:TYR:O	1:A:926:LYS:N	2.29	0.64
1:A:1907:GLN:O	1:A:1910:LYS:CG	2.45	0.64
2:K:35:GLU:O	2:K:38:GLN:N	2.30	0.64
29:1:388:TYR:O	31:3:276:GLY:O	2.16	0.64
38:H:1097:G:C2	38:H:1146:G:C4	2.86	0.64
1:A:1863:HIS:HA	18:O:159:ASP:N	2.12	0.64
2:K:291:LEU:HB3	2:K:301:LEU:HB3	1.79	0.64
8:C:618:LEU:O	8:C:621:ALA:HB3	1.98	0.64
17:B:94:C:H3'	17:B:94:C:H6	1.63	0.64
2:K:112:PRO:HB3	5:J:217:VAL:N	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:316:GLN:HE21	2:K:320:SER:H	1.46	0.64
26:I:52:G:C6	26:I:53:U:O4	2.51	0.64
1:A:972:MET:HG2	1:A:981:VAL:HG21	1.80	0.64
1:A:1794:LEU:O	1:A:1798:ILE:N	2.24	0.64
4:N:734:PRO:O	4:N:736:ASP:N	2.31	0.64
8:C:398:ASN:HA	8:C:401:ARG:HH21	1.63	0.64
8:C:761:ALA:HA	8:C:764:ASN:HB2	1.78	0.64
8:C:880:MET:HB3	8:C:886:SER:HA	1.80	0.64
8:C:931:TYR:HD1	8:C:933:TRP:HD1	1.46	0.64
17:B:99:U:H3'	17:B:100:A:C4'	2.27	0.64
2:K:194:SER:H	2:K:221:ILE:HD12	1.63	0.63
2:K:232:ASN:HB3	2:K:247:GLN:NE2	2.08	0.63
6:E:26:LEU:HD23	6:E:86:TYR:HB2	1.80	0.63
16:F:86:G:C5'	16:F:86:G:H8	2.10	0.63
1:A:572:CYS:O	1:A:576:HIS:HB2	1.99	0.63
1:A:611:LYS:HE2	16:F:32:U:C5	2.33	0.63
1:A:620:HIS:HB3	1:A:669:TYR:CZ	2.33	0.63
1:A:785:HIS:NE2	4:N:124:ASP:O	2.31	0.63
8:C:778:THR:HG23	8:C:781:ASP:H	1.64	0.63
1:A:1811:ALA:O	1:A:1814:VAL:N	2.28	0.63
3:L:398:GLN:NE2	3:L:419:GLN:HG3	2.14	0.63
3:L:450:GLN:HG3	3:L:451:GLN:N	2.13	0.63
4:N:675:GLY:O	4:N:679:HIS:CB	2.41	0.63
8:C:232:SER:OG	8:C:234:LEU:O	2.17	0.63
17:B:98:U:C4	17:B:99:U:C5	2.86	0.63
1:A:1041:VAL:HG11	1:A:1253:LYS:HA	1.79	0.63
1:A:1603:ASN:O	1:A:1606:PHE:N	2.31	0.63
1:A:1790:TRP:CD2	1:A:1795:LYS:HE3	2.34	0.63
2:K:274:HIS:ND1	2:K:275:PRO:HD2	2.14	0.63
8:C:425:LEU:HA	8:C:428:ILE:HG22	1.81	0.63
17:B:73:U:O2'	17:B:74:U:H5'	1.98	0.63
1:A:552:LYS:NZ	1:A:559:GLN:OE1	2.32	0.63
1:A:934:ARG:NH2	3:L:436:LYS:O	2.32	0.63
1:A:1033:ASN:ND2	1:A:1288:LEU:HB3	2.14	0.63
2:K:261:LEU:HB3	2:K:292:TRP:CZ3	2.33	0.63
3:L:228:ASN:ND2	3:L:317:ASP:OD1	2.32	0.63
4:N:488:ILE:O	4:N:492:MET:CB	2.46	0.63
5:J:141:ASN:HB3	5:J:144:LEU:HB2	1.78	0.63
17:B:48:G:H1	17:B:67:U:H3	1.44	0.63
26:I:20:A:H2'	26:I:21:C:O4'	1.96	0.63
1:A:382:GLU:OE1	1:A:382:GLU:N	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1773:VAL:HG22	1:A:1788:GLY:HA3	1.81	0.63
3:L:218:ILE:O	3:L:221:LYS:N	2.31	0.63
5:J:129:ASP:O	5:J:133:LEU:CB	2.46	0.63
6:E:112:GLU:HG2	6:E:135:TYR:CE2	2.34	0.63
8:C:701:GLU:HG2	8:C:703:LEU:H	1.62	0.63
1:A:1195:PHE:HB3	1:A:1217:ARG:HE	1.64	0.63
8:C:717:SER:HA	8:C:720:ILE:HD12	1.81	0.63
38:H:48:U:H2'	38:H:49:U:H5'	1.79	0.63
1:A:194:HIS:HA	1:A:557:PHE:CD1	2.34	0.63
1:A:899:PRO:HD3	1:A:1006:ARG:HH22	1.64	0.63
1:A:1861:THR:CB	18:O:161:ILE:HA	2.29	0.63
2:K:260:ASP:OD1	2:K:261:LEU:N	2.32	0.63
7:M:44:LEU:O	7:M:47:GLY:N	2.32	0.63
8:C:697:ARG:NH1	8:C:848:VAL:O	2.30	0.63
26:I:22:G:C6	26:I:23:C:C4	2.86	0.63
4:N:704:LEU:O	4:N:707:SER:OG	2.16	0.63
4:N:861:ASN:OD1	4:N:862:MET:N	2.31	0.63
4:N:771:ALA:O	4:N:774:TRP:N	2.32	0.62
17:B:33:U:H3'	17:B:33:U:C6	2.32	0.62
28:G:492:U:O2	38:H:43:G:N2	2.32	0.62
38:H:1099:G:H2'	38:H:1100:A:H5'	1.80	0.62
1:A:1714:PRO:HA	1:A:1788:GLY:O	1.98	0.62
3:L:402:ASP:OD1	3:L:403:SER:N	2.30	0.62
8:C:576:THR:HG22	8:C:592:PHE:HD2	1.64	0.62
38:H:49:U:H3	38:H:66:A:N6	1.97	0.62
1:A:1583:ASP:O	1:A:1586:GLN:N	2.28	0.62
1:A:1861:THR:CG2	18:O:161:ILE:CA	2.72	0.62
1:A:2047:GLN:O	1:A:2050:THR:OG1	2.15	0.62
26:I:63:U:H2'	26:I:64:U:H5''	1.78	0.62
1:A:617:ASN:ND2	17:B:99:U:O2'	2.32	0.62
2:K:311:PHE:H	2:K:326:GLY:HA2	1.64	0.62
2:K:317:CYS:SG	2:K:359:PRO:HA	2.39	0.62
38:H:65:A:C5	38:H:66:A:N7	2.67	0.62
38:H:1149:G:H2'	38:H:1150:U:C6	2.34	0.62
3:L:257:CYS:SG	26:I:42:C:N4	2.72	0.62
6:E:30:ARG:HE	6:E:61:LEU:HD22	1.65	0.62
8:C:715:MET:SD	8:C:772:ASN:HB3	2.39	0.62
16:F:92:C:H2'	16:F:93:A:H8	1.63	0.62
26:I:63:U:H2'	26:I:64:U:H5'	1.81	0.62
28:G:471:U:O2	28:G:471:U:C2'	2.45	0.62
1:A:961:GLN:HG3	1:A:964:PHE:HE1	1.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1144:PHE:CZ	1:A:1162:THR:HG21	2.34	0.62
1:A:1697:SER:OG	1:A:1767:TYR:OH	2.16	0.62
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.00	0.62
1:A:2007:ARG:NH2	5:J:291:THR:OG1	2.32	0.62
8:C:412:ALA:HA	8:C:415:TYR:CE2	2.34	0.62
16:F:69:C:N4	26:I:12:C:H42	1.98	0.62
17:B:102:C:C5	17:B:103:A:N7	2.68	0.62
26:I:33:A:C5	26:I:45:A:N7	2.68	0.62
8:C:766:TRP:HB2	8:C:776:ASN:ND2	2.15	0.62
26:I:6:U:H2'	26:I:7:A:H8	1.60	0.62
26:I:141:G:O2'	26:I:142:G:H5'	1.99	0.62
1:A:1043:ARG:O	1:A:1043:ARG:HG3	2.00	0.62
2:K:452:LEU:HB3	2:K:464:TRP:HB2	1.82	0.62
8:C:269:LYS:HG2	47:C:1500:GTP:C6	2.35	0.62
8:C:699:GLY:N	8:C:708:ILE:O	2.32	0.62
1:A:900:PHE:CE2	1:A:901:PRO:HD2	2.35	0.62
3:L:75:PRO:O	3:L:79:ASP:N	2.24	0.62
6:E:105:PHE:CE2	6:E:137:TYR:CZ	2.87	0.62
17:B:44:A:N3	17:B:45:A:C8	2.68	0.62
17:B:98:U:HO2'	17:B:99:U:H5'	1.62	0.62
26:I:142:G:H5''	26:I:143:A:OP2	1.99	0.62
28:G:470:A:H2'	28:G:470:A:N3	2.13	0.62
1:A:815:TYR:O	1:A:818:SER:OG	2.13	0.62
4:N:131:ARG:O	4:N:135:ASN:HB2	2.00	0.62
8:C:400:LEU:O	8:C:405:ARG:N	2.33	0.62
1:A:413:ASN:ND2	1:A:419:THR:OG1	2.32	0.61
1:A:1043:ARG:O	1:A:1045:GLN:HG3	1.99	0.61
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.65	0.61
1:A:1775:ILE:HG12	1:A:1786:ALA:HB2	1.80	0.61
5:J:346:ASN:N	5:J:422:ASN:OD1	2.29	0.61
8:C:429:PHE:HB3	8:C:432:GLN:HE22	1.64	0.61
16:F:10:A:N6	16:F:11:U:C4	2.68	0.61
1:A:185:GLN:NE2	1:A:262:ASP:OD1	2.33	0.61
1:A:1733:TRP:CD2	1:A:1772:GLY:HA3	2.35	0.61
3:L:139:LYS:O	3:L:142:SER:OG	2.13	0.61
8:C:860:PRO:HG2	8:C:908:VAL:HG11	1.81	0.61
17:B:102:C:C2'	17:B:103:A:H5'	2.30	0.61
28:G:487:A:H2'	28:G:487:A:N3	2.13	0.61
38:H:1098:C:O5'	38:H:1098:C:H6	1.82	0.61
1:A:289:ASP:O	1:A:292:LYS:N	2.33	0.61
1:A:1942:ASP:OD2	18:O:170:PHE:HE2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:10:GLU:HG2	6:E:14:HIS:HE1	1.64	0.61
5:J:406:PHE:HE1	5:J:408:LEU:HB2	1.65	0.61
8:C:468:LEU:HA	8:C:490:SER:O	2.00	0.61
16:F:48:C:H2'	16:F:48:C:OP2	2.00	0.61
1:A:153:MET:HG2	1:A:154:TYR:H	1.65	0.61
1:A:609:GLU:OE2	16:F:43:C:OP1	2.18	0.61
1:A:1650:ARG:CB	16:F:49:A:O5'	2.42	0.61
3:L:264:LYS:NZ	26:I:39:C:O2	2.28	0.61
4:N:703:LEU:HA	4:N:706:VAL:HB	1.81	0.61
1:A:304:ASP:N	1:A:307:GLU:OE1	2.24	0.61
3:L:146:ASN:HD21	3:L:148:ASN:HB2	1.64	0.61
5:J:350:PRO:CB	16:F:84:C:C6	2.72	0.61
8:C:246:THR:HG23	8:C:248:VAL:HG12	1.83	0.61
44:W:46:TYR:O	44:W:50:ILE:N	2.31	0.61
1:A:236:ARG:HH21	1:A:699:PRO:CG	2.13	0.61
1:A:276:VAL:HA	1:A:279:TRP:CZ2	2.36	0.61
1:A:1752:VAL:O	1:A:1755:LYS:N	2.32	0.61
1:A:1389:TYR:CE2	1:A:1437:ILE:HD13	2.35	0.61
3:L:410:LEU:O	3:L:410:LEU:HD12	2.00	0.61
4:N:381:TYR:HA	4:N:384:ALA:HB3	1.83	0.61
31:3:368:GLY:HA2	31:3:380:LEU:O	2.01	0.61
1:A:144:ASN:O	1:A:147:SER:OG	2.18	0.61
1:A:1348:GLU:OE2	1:A:1447:TRP:N	2.34	0.61
2:K:347:GLY:HA3	2:K:374:ASN:ND2	2.15	0.61
3:L:207:LEU:O	3:L:210:LEU:N	2.34	0.61
4:N:11:PRO:HD2	6:E:13:TRP:CH2	2.35	0.61
5:J:159:TYR:O	5:J:163:ASN:ND2	2.33	0.61
8:C:247:PHE:HB2	8:C:903:ARG:CZ	2.31	0.61
28:G:471:U:O2	28:G:471:U:H2'	2.01	0.61
28:G:514:U:H5''	28:G:515:U:H5''	1.83	0.61
38:H:1161:U:O2'	38:H:1162:U:H5'	2.01	0.61
1:A:218:SER:O	1:A:221:TRP:HB3	2.00	0.61
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.35	0.61
1:A:710:VAL:O	1:A:713:ASN:N	2.34	0.61
1:A:1554:GLU:H	1:A:1554:GLU:CD	2.04	0.61
1:A:1730:ASN:HB3	1:A:1731:LYS:HG3	1.82	0.61
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.82	0.61
4:N:667:CYS:HA	4:N:670:PHE:HD2	1.66	0.61
8:C:744:PRO:O	8:C:748:SER:OG	2.13	0.61
16:F:86:G:H8	16:F:86:G:O5'	1.83	0.61
17:B:162:G:C3'	17:B:163:C:H4'	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1208:PRO:O	1:A:1211:SER:OG	2.19	0.60
1:A:1851:PHE:O	1:A:1881:THR:HA	2.01	0.60
2:K:168:ALA:O	4:N:724:SER:OG	2.17	0.60
4:N:764:LEU:HD12	4:N:768:PRO:HA	1.81	0.60
5:J:146:GLU:HA	5:J:149:PHE:HD2	1.66	0.60
17:B:80:G:N1	17:B:82:A:C2	2.69	0.60
1:A:689:TYR:CZ	1:A:693:LYS:HG3	2.36	0.60
1:A:1657:ILE:O	1:A:1661:ILE:HD12	2.01	0.60
1:A:1916:GLU:O	1:A:1920:LEU:CB	2.49	0.60
2:K:458:ASP:OD1	2:K:458:ASP:N	2.32	0.60
17:B:94:C:H2'	17:B:95:C:H4'	1.83	0.60
26:I:26:A:O2'	26:I:27:U:O4'	2.18	0.60
32:4:184:PHE:HA	32:4:188:GLY:HA2	1.81	0.60
1:A:689:TYR:CD1	1:A:693:LYS:CG	2.84	0.60
1:A:699:PRO:CB	16:F:1:G:P	2.89	0.60
2:K:280:ILE:O	2:K:291:LEU:HD12	2.00	0.60
2:K:345:LEU:HD13	2:K:376:TRP:CD2	2.36	0.60
8:C:104:THR:O	8:C:107:THR:OG1	2.12	0.60
8:C:671:SER:OG	8:C:672:ASP:N	2.33	0.60
17:B:92:U:C2'	17:B:93:G:H5''	2.31	0.60
1:A:934:ARG:HH21	3:L:436:LYS:N	1.98	0.60
1:A:1962:ARG:O	1:A:2013:ARG:NH2	2.26	0.60
3:L:106:LYS:HA	3:L:109:ILE:HD12	1.81	0.60
3:L:296:VAL:HA	3:L:299:HIS:CE1	2.36	0.60
8:C:121:ASP:O	8:C:125:SER:CB	2.48	0.60
16:F:63:G:C2	26:I:57:U:C4	2.89	0.60
26:I:25:U:C3'	26:I:26:A:H5''	2.31	0.60
38:H:48:U:C5	38:H:49:U:C2	2.88	0.60
38:H:143:G:H2'	38:H:144:G:H8	1.65	0.60
1:A:136:PRO:O	1:A:140:ARG:HG3	2.01	0.60
1:A:400:ILE:HG22	8:C:187:ARG:HE	1.67	0.60
1:A:482:SER:O	1:A:487:ASN:ND2	2.34	0.60
1:A:1014:LYS:HE3	1:A:1144:PHE:CD1	2.35	0.60
2:K:141:GLU:OE2	2:K:145:LYS:NZ	2.29	0.60
2:K:316:GLN:HG3	2:K:319:GLY:N	2.16	0.60
17:B:28:G:H2'	17:B:29:G:C5'	2.31	0.60
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.83	0.60
1:A:180:PRO:HA	1:A:187:LYS:HD2	1.83	0.60
1:A:1021:PRO:O	1:A:1024:LEU:HB3	2.01	0.60
1:A:1377:SER:OG	16:F:31:G:OP1	2.17	0.60
3:L:400:VAL:O	3:L:407:GLU:HA	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:289:ASP:HB3	5:J:292:ALA:HB3	1.83	0.60
8:C:176:ARG:HB3	8:C:179:ASP:HB2	1.82	0.60
16:F:59:A:O2'	16:F:60:G:H5'	2.02	0.60
38:H:1139:G:H2'	38:H:1140:U:C6	2.36	0.60
1:A:217:TRP:O	1:A:220:THR:OG1	2.19	0.60
1:A:900:PHE:CD2	1:A:901:PRO:N	2.69	0.60
2:K:112:PRO:CA	5:J:217:VAL:N	2.64	0.60
2:K:392:HIS:HD2	2:K:396:VAL:HG22	1.67	0.60
8:C:251:GLN:NE2	8:C:255:GLN:HE21	1.99	0.60
8:C:580:VAL:HG22	8:C:582:SER:H	1.66	0.60
17:B:127:U:H1'	17:B:128:A:C8	2.36	0.60
17:B:136:G:O2'	17:B:137:U:O4'	2.19	0.60
18:O:183:LYS:O	18:O:187:GLU:HB2	2.02	0.60
35:X:123:LYS:O	35:X:127:ASP:N	2.34	0.60
1:A:753:TYR:CE1	6:E:37:ARG:HB3	2.36	0.60
2:K:170:SER:O	2:K:207:LEU:HD13	2.02	0.60
2:K:316:GLN:HG3	2:K:319:GLY:H	1.66	0.60
6:E:120:ILE:HA	6:E:131:VAL:HG21	1.82	0.60
8:C:678:SER:O	8:C:858:LEU:N	2.27	0.60
8:C:922:THR:OG1	8:C:925:LEU:O	2.08	0.60
38:H:47:U:C3'	38:H:48:U:H5''	2.31	0.60
1:A:149:MET:SD	1:A:154:TYR:CD2	2.94	0.60
1:A:621:LEU:HD23	1:A:722:LEU:HD21	1.84	0.60
5:J:350:PRO:HB3	16:F:83:A:C8	2.28	0.60
16:F:10:A:C6	16:F:11:U:C4	2.90	0.60
1:A:1414:TRP:HB2	1:A:1558:GLU:HG3	1.84	0.60
4:N:558:PRO:O	4:N:562:MET:N	2.35	0.60
5:J:407:GLU:HG2	5:J:414:ASP:HB3	1.83	0.60
8:C:811:GLU:HB3	8:C:812:PRO:HD2	1.83	0.60
16:F:63:G:C2	16:F:64:U:C6	2.90	0.60
16:F:72:C:H2'	16:F:73:A:C8	2.36	0.60
17:B:19:A:N6	17:B:151:A:N1	2.48	0.60
28:G:488:A:O5'	28:G:488:A:H8	1.85	0.60
1:A:365:ASN:OD1	1:A:366:GLU:N	2.34	0.59
1:A:693:LYS:N	1:A:693:LYS:HZ3	1.99	0.59
1:A:694:ASN:H	1:A:694:ASN:HD22	1.49	0.59
1:A:1600:GLN:O	1:A:1603:ASN:N	2.29	0.59
17:B:103:A:O2'	17:B:104:G:O4'	2.20	0.59
26:I:5:U:H2'	26:I:6:U:C6	2.36	0.59
38:H:1149:G:C8	38:H:1149:G:C5'	2.85	0.59
1:A:477:MET:HE2	8:C:278:LYS:HE2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1307:GLU:O	1:A:1310:LYS:N	2.35	0.59
2:K:305:GLY:HA2	5:J:221:LEU:O	2.01	0.59
4:N:805:HIS:HA	4:N:808:LEU:HD12	1.84	0.59
8:C:142:LEU:HD12	8:C:929:GLN:NE2	2.16	0.59
17:B:96:U:C2'	17:B:97:U:C6	2.80	0.59
2:K:140:MET:HA	2:K:143:HIS:HD2	1.68	0.59
2:K:345:LEU:HD13	2:K:376:TRP:CG	2.37	0.59
8:C:415:TYR:HB2	8:C:420:PHE:HB2	1.85	0.59
17:B:32:G:C4'	17:B:33:U:OP2	2.51	0.59
28:G:473:U:C2'	28:G:473:U:O2	2.50	0.59
1:A:689:TYR:CD1	1:A:693:LYS:HG2	2.37	0.59
1:A:1285:VAL:HG22	1:A:1301:TYR:CD1	2.38	0.59
2:K:283:ALA:HB1	2:K:310:VAL:HG12	1.85	0.59
24:U:28:GLY:HA2	24:U:38:TYR:O	2.02	0.59
38:H:1149:G:H8	38:H:1149:G:C5'	2.15	0.59
1:A:367:PHE:HB2	8:C:608:GLN:NE2	2.17	0.59
1:A:581:LEU:O	1:A:585:ARG:CB	2.48	0.59
1:A:1667:GLN:NE2	18:O:211:ASN:OD1	2.36	0.59
1:A:2081:ASP:O	1:A:2085:GLY:N	2.35	0.59
7:M:62:GLU:HA	7:M:65:LEU:HD12	1.83	0.59
8:C:168:VAL:HG12	8:C:173:LYS:HG3	1.84	0.59
8:C:208:ARG:NH1	8:C:440:THR:O	2.36	0.59
16:F:34:A:N6	16:F:47:A:C5	2.66	0.59
16:F:74:U:H2'	16:F:75:A:C8	2.37	0.59
26:I:96:A:H2'	26:I:97:U:O4'	2.02	0.59
38:H:1140:U:C2	38:H:1141:C:C5	2.91	0.59
44:W:116:LEU:O	45:O:50:ARG:C	2.40	0.59
4:N:600:LYS:O	4:N:604:LEU:CB	2.50	0.59
8:C:274:ILE:HD12	8:C:382:TYR:CD1	2.37	0.59
8:C:410:GLN:HA	8:C:413:LEU:HD12	1.84	0.59
17:B:33:U:C6	17:B:33:U:C3'	2.86	0.59
38:H:68:U:C5	38:H:69:G:N7	2.70	0.59
38:H:1141:C:H2'	38:H:1142:G:H8	1.67	0.59
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.37	0.59
1:A:668:ARG:HE	16:F:27:U:C4'	2.01	0.59
2:K:117:LEU:HD22	2:K:300:LEU:O	2.03	0.59
3:L:424:THR:HG22	3:L:425:SER:H	1.67	0.59
4:N:116:GLU:HA	4:N:119:TRP:CD1	2.37	0.59
5:J:342:PHE:HB2	5:J:380:ILE:HB	1.84	0.59
8:C:933:TRP:C	8:C:935:LYS:H	2.06	0.59
17:B:1:A:H61	17:B:164:C:N4	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:619:PHE:O	1:A:622:MET:N	2.35	0.59
1:A:681:LYS:HE2	16:F:25:C:N4	2.17	0.59
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.68	0.59
1:A:1389:TYR:CD2	1:A:1437:ILE:HG21	2.37	0.59
1:A:1473:ARG:HH11	1:A:1474:ARG:H	1.51	0.59
2:K:316:GLN:NE2	2:K:318:ASP:HB2	2.18	0.59
3:L:439:LYS:HE2	26:I:20:A:H5'	1.83	0.59
8:C:270:LEU:HD11	8:C:313:PHE:HB3	1.85	0.59
16:F:46:U:H2'	16:F:47:A:H1'	1.84	0.59
26:I:57:U:H2'	26:I:58:G:H8	1.68	0.59
38:H:48:U:H2'	38:H:49:U:C5'	2.33	0.59
38:H:49:U:H3	38:H:66:A:H61	1.49	0.59
1:A:654:HIS:HE2	1:A:688:TYR:HE1	1.49	0.59
1:A:1091:ASN:HA	1:A:1095:MET:O	2.03	0.59
1:A:1646:ILE:HD11	16:F:49:A:C6	2.38	0.59
1:A:1889:LEU:HD11	1:A:1991:ILE:HG13	1.85	0.59
4:N:795:GLN:O	4:N:798:LEU:HB2	2.03	0.59
8:C:697:ARG:NH1	8:C:848:VAL:HG12	2.17	0.59
38:H:1152:U:H2'	38:H:1153:C:C6	2.38	0.59
1:A:184:GLU:OE1	1:A:283:SER:OG	2.20	0.59
1:A:1666:CYS:O	1:A:1670:ASP:CB	2.51	0.59
2:K:112:PRO:CB	5:J:217:VAL:N	2.66	0.59
5:J:272:VAL:HG22	5:J:280:VAL:HG21	1.84	0.59
6:E:95:PHE:HB3	6:E:137:TYR:CE2	2.37	0.59
8:C:135:ASN:OD1	8:C:211:ASN:ND2	2.33	0.59
8:C:452:LYS:NZ	8:C:487:ARG:HH12	2.00	0.59
8:C:835:LYS:HB3	8:C:839:ILE:HD12	1.83	0.59
16:F:46:U:H2'	16:F:47:A:C1'	2.32	0.59
28:G:465:A:O5'	28:G:465:A:H8	1.83	0.59
1:A:808:ILE:HA	1:A:811:ILE:HD12	1.85	0.58
1:A:905:TYR:OH	1:A:1002:GLU:OE2	2.16	0.58
1:A:964:PHE:CE2	1:A:1085:LYS:CD	2.85	0.58
1:A:1652:HIS:CE1	16:F:48:C:C2'	2.84	0.58
4:N:13:ALA:HB3	4:N:15:TYR:HD2	1.68	0.58
38:H:65:A:H8	38:H:65:A:O5'	1.86	0.58
1:A:1853:ASP:OD2	1:A:1965:PHE:HB2	2.02	0.58
2:K:227:HIS:CG	2:K:228:PRO:HD2	2.39	0.58
2:K:372:ILE:HD11	5:J:428:TRP:HH2	1.67	0.58
3:L:189:LEU:H	3:L:194:ARG:HH22	1.50	0.58
4:N:655:PHE:O	4:N:659:ARG:CB	2.51	0.58
8:C:132:ARG:O	8:C:133:ILE:HG12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASP:O	1:A:595:TYR:N	2.20	0.58
1:A:1890:PHE:HB3	1:A:1986:MET:HE1	1.85	0.58
2:K:459:ARG:CZ	4:N:758:LEU:HD21	2.33	0.58
8:C:803:VAL:HG13	8:C:813:ILE:HB	1.84	0.58
1:A:657:LEU:HD23	1:A:660:ILE:HD11	1.86	0.58
1:A:1575:TRP:HB2	3:L:391:MET:HB3	1.86	0.58
2:K:370:ASP:OD1	2:K:371:GLY:N	2.36	0.58
4:N:230:LEU:O	4:N:234:ARG:HG3	2.03	0.58
4:N:832:LEU:HD21	4:N:845:LEU:HD11	1.85	0.58
5:J:345:LYS:NZ	5:J:421:ASN:OD1	2.31	0.58
8:C:140:GLY:H	8:C:146:LYS:HD3	1.69	0.58
8:C:474:LYS:NZ	8:C:628:TYR:O	2.28	0.58
8:C:840:PRO:O	8:C:843:LYS:HB3	2.03	0.58
31:3:427:LEU:N	31:3:439:PHE:O	2.25	0.58
44:W:130:GLU:O	44:W:134:CYS:CB	2.51	0.58
1:A:404:ASN:ND2	8:C:142:LEU:HD13	2.19	0.58
1:A:671:TYR:CD2	17:B:101:C:O2'	2.56	0.58
1:A:716:ARG:CZ	17:B:111:C:O2	2.50	0.58
3:L:367:ARG:HG3	3:L:367:ARG:O	2.04	0.58
8:C:272:ARG:HG3	8:C:276:ASP:OD2	2.03	0.58
8:C:494:LYS:N	8:C:497:ASP:OD2	2.36	0.58
1:A:2020:GLU:O	1:A:2023:LYS:N	2.37	0.58
3:L:135:LEU:O	3:L:138:SER:OG	2.19	0.58
4:N:375:TYR:O	4:N:379:GLN:CB	2.51	0.58
5:J:418:ASP:OD1	5:J:420:HIS:ND1	2.32	0.58
8:C:120:ARG:O	8:C:123:MET:N	2.37	0.58
8:C:474:LYS:HZ3	8:C:630:PRO:HD3	1.69	0.58
26:I:57:U:H2'	26:I:58:G:C8	2.38	0.58
29:1:548:LEU:O	29:1:549:GLY:O	2.21	0.58
1:A:138:HIS:O	1:A:142:ILE:HG12	2.03	0.58
1:A:250:SER:OG	1:A:253:GLN:HB2	2.04	0.58
1:A:296:THR:CB	17:B:33:U:OP2	2.51	0.58
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.39	0.58
1:A:1861:THR:CA	18:O:161:ILE:HA	2.34	0.58
3:L:199:GLU:O	3:L:202:SER:HB3	2.04	0.58
8:C:387:TYR:O	8:C:390:SER:N	2.37	0.58
8:C:682:SER:O	8:C:854:ILE:HB	2.03	0.58
28:G:463:A:H2'	28:G:464:A:C8	2.38	0.58
1:A:181:HIS:HA	1:A:704:TRP:CZ2	2.38	0.58
1:A:617:ASN:ND2	1:A:669:TYR:O	2.30	0.58
1:A:997:GLN:OE1	1:A:1511:ARG:NH1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:285:HIS:O	2:K:287:MET:N	2.37	0.58
8:C:608:GLN:HE21	8:C:641:GLU:HG2	1.67	0.58
1:A:751:ASP:OD1	1:A:752:ALA:N	2.34	0.58
1:A:1556:ILE:O	1:A:1559:HIS:N	2.17	0.58
1:A:1689:ARG:HH12	16:F:45:A:P	2.27	0.58
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	1.86	0.58
8:C:201:THR:HG22	8:C:207:SER:HB3	1.84	0.58
8:C:598:ILE:HG22	8:C:933:TRP:CZ3	2.39	0.58
8:C:678:SER:HB2	8:C:858:LEU:HB2	1.84	0.58
26:I:22:G:C6	26:I:52:G:C6	2.92	0.58
27:D:2102:VAL:O	27:D:2142:ILE:HA	2.03	0.58
1:A:140:ARG:NH2	1:A:252:GLU:HB3	2.19	0.57
1:A:1830:VAL:HG21	1:A:1941:LEU:HD13	1.85	0.57
1:A:1880:PHE:CE2	1:A:1965:PHE:HB3	2.39	0.57
4:N:702:PRO:HB3	4:N:739:PHE:CE1	2.38	0.57
7:M:9:PHE:CD2	7:M:10:PRO:HD3	2.39	0.57
8:C:348:LEU:HD12	8:C:372:THR:HG22	1.86	0.57
8:C:437:ASP:O	8:C:440:THR:HB	2.02	0.57
2:K:288:THR:HA	2:K:303:GLN:O	2.04	0.57
8:C:385:PHE:HE1	8:C:425:LEU:HD11	1.68	0.57
17:B:44:A:C4	17:B:45:A:N7	2.72	0.57
1:A:140:ARG:HH22	1:A:252:GLU:HB3	1.69	0.57
1:A:898:ILE:HD12	1:A:1002:GLU:HB2	1.85	0.57
1:A:1066:LEU:O	1:A:1069:LEU:N	2.37	0.57
2:K:32:LEU:HD23	2:K:34:HIS:H	1.70	0.57
16:F:57:U:H3	26:I:62:G:H22	1.52	0.57
17:B:99:U:C6	17:B:100:A:H1'	2.36	0.57
1:A:1023:LEU:HD13	1:A:1451:PHE:CD1	2.39	0.57
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.39	0.57
1:A:1834:PHE:O	1:A:1839:ASN:ND2	2.36	0.57
4:N:250:LEU:HA	4:N:253:LYS:HE2	1.86	0.57
5:J:341:VAL:HA	5:J:380:ILE:O	2.04	0.57
38:H:1097:G:H1'	38:H:1146:G:N2	2.20	0.57
1:A:1149:SER:OG	1:A:1152:VAL:HG23	2.04	0.57
1:A:1360:LEU:O	1:A:1363:GLY:N	2.37	0.57
1:A:1369:ASN:O	1:A:1372:LYS:N	2.37	0.57
1:A:1703:MET:HB2	1:A:1732:MET:HB2	1.87	0.57
1:A:2062:GLU:HG3	1:A:2065:ARG:HH21	1.70	0.57
2:K:285:HIS:C	2:K:287:MET:H	2.08	0.57
2:K:419:ILE:HD11	2:K:443:LEU:CD1	2.34	0.57
5:J:349:ASN:HB3	5:J:352:ILE:HD12	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:626:SER:HB2	8:C:634:ILE:HD13	1.86	0.57
29:1:935:TRP:CB	34:6:23:ASP:O	2.53	0.57
1:A:153:MET:HG2	1:A:154:TYR:N	2.18	0.57
1:A:341:ALA:HA	1:A:355:LEU:HD23	1.86	0.57
1:A:940:ILE:O	1:A:944:TYR:HB2	2.04	0.57
2:K:185:THR:OG1	2:K:231:ASN:ND2	2.37	0.57
5:J:360:SER:HA	5:J:365:LEU:HD12	1.86	0.57
8:C:313:PHE:HB2	8:C:322:PHE:HB2	1.86	0.57
8:C:706:LEU:HA	8:C:824:SER:O	2.04	0.57
1:A:691:PHE:CD1	1:A:692:ASN:N	2.73	0.57
1:A:1847:ASP:O	1:A:1885:LYS:NZ	2.37	0.57
2:K:422:TYR:CD1	2:K:429:LYS:HA	2.40	0.57
5:J:409:HIS:HB2	16:F:83:A:H61	1.69	0.57
8:C:315:SER:HB3	8:C:320:PHE:CE2	2.39	0.57
8:C:329:SER:HA	8:C:333:ALA:HB2	1.86	0.57
28:G:480:A:O2'	28:G:481:A:H8	1.87	0.57
1:A:410:ILE:HG13	8:C:276:ASP:CG	2.25	0.57
4:N:688:ARG:HE	4:N:712:ASP:HB2	1.70	0.57
16:F:9:A:H2'	16:F:10:A:H8	1.70	0.57
17:B:96:U:C3'	17:B:97:U:H6	2.17	0.57
1:A:266:LEU:HG	1:A:267:PRO:HD2	1.87	0.57
1:A:654:HIS:CD2	1:A:701:CYS:HG	1.89	0.57
2:K:359:PRO:HB2	2:K:406:GLY:HA2	1.87	0.57
2:K:415:TYR:HD1	2:K:439:LYS:HD3	1.69	0.57
3:L:376:LYS:NZ	26:I:55:U:HO2'	2.02	0.57
6:E:105:PHE:H	6:E:105:PHE:HD2	1.53	0.57
1:A:287:GLU:OE1	1:A:287:GLU:N	2.38	0.57
1:A:413:ASN:HD21	1:A:474:LYS:HE3	1.69	0.57
1:A:425:ASP:HB3	1:A:428:LEU:HG	1.86	0.57
1:A:699:PRO:CB	16:F:1:G:OP1	2.53	0.57
1:A:907:ASN:O	1:A:911:ILE:N	2.38	0.57
1:A:1501:THR:HG21	4:N:163:THR:HG21	1.87	0.57
3:L:120:TYR:OH	3:L:141:ILE:HG21	2.05	0.57
3:L:366:LYS:HD3	16:F:58:C:H41	1.68	0.57
6:E:8:GLN:HG2	6:E:61:LEU:HB2	1.87	0.57
8:C:938:ARG:HG2	8:C:939:LYS:N	2.20	0.57
20:P:40:HIS:O	20:P:89:GLY:HA3	2.05	0.57
1:A:961:GLN:O	1:A:962:ARG:NH1	2.33	0.56
6:E:11:THR:N	6:E:14:HIS:HD2	2.03	0.56
27:D:1101:ILE:O	27:D:1105:ALA:CB	2.53	0.56
1:A:1815:LEU:O	1:A:1818:ARG:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:206:THR:OG1	2:K:207:LEU:N	2.38	0.56
2:K:218:VAL:HG22	2:K:239:GLU:HG2	1.86	0.56
5:J:146:GLU:HA	5:J:149:PHE:CD2	2.40	0.56
8:C:185:ILE:HD13	17:B:75:A:P	2.46	0.56
16:F:51:A:H5'	16:F:51:A:C8	2.40	0.56
36:Y:229:GLY:O	36:Y:231:ARG:N	2.38	0.56
1:A:250:SER:OG	1:A:254:HIS:ND1	2.29	0.56
1:A:294:ASN:ND2	17:B:32:G:OP1	2.38	0.56
1:A:360:GLU:O	1:A:362:GLU:HG2	2.06	0.56
1:A:468:LEU:HB3	8:C:383:LYS:HG2	1.86	0.56
5:J:353:ARG:HH21	16:F:84:C:H1'	1.69	0.56
16:F:27:U:O5'	16:F:27:U:H6	1.86	0.56
1:A:519:LYS:HA	1:A:522:TYR:HD2	1.70	0.56
6:E:95:PHE:CE2	6:E:103:LEU:HD13	2.40	0.56
8:C:133:ILE:O	8:C:134:ILE:HG23	2.04	0.56
8:C:224:GLU:O	8:C:228:ALA:N	2.33	0.56
16:F:50:G:OP2	16:F:51:A:H2'	2.05	0.56
1:A:1214:ARG:NH1	1:A:1256:PRO:HD2	2.19	0.56
1:A:1353:THR:O	1:A:1353:THR:OG1	2.24	0.56
2:K:227:HIS:CD2	2:K:228:PRO:HD2	2.41	0.56
2:K:261:LEU:HD22	2:K:292:TRP:CE3	2.41	0.56
2:K:287:MET:HA	2:K:310:VAL:HG23	1.87	0.56
8:C:251:GLN:HE21	8:C:255:GLN:HE21	1.51	0.56
2:K:263:GLY:O	2:K:290:ARG:NH2	2.37	0.56
5:J:259:LYS:HE2	5:J:265:LEU:HD11	1.87	0.56
6:E:22:GLU:OE1	6:E:27:VAL:HG22	2.06	0.56
8:C:273:LEU:HD12	8:C:277:LEU:HD12	1.87	0.56
17:B:14:G:C2	17:B:15:A:C8	2.93	0.56
17:B:45:A:C2	17:B:46:C:C4	2.94	0.56
18:O:194:LEU:HD13	18:O:197:ARG:NH1	2.20	0.56
26:I:23:C:O2'	26:I:24:A:H5'	2.04	0.56
26:I:37:U:O2'	26:I:38:U:H2'	2.06	0.56
1:A:816:ILE:O	1:A:820:ALA:HB2	2.05	0.56
1:A:1414:TRP:CB	1:A:1558:GLU:HG3	2.36	0.56
2:K:415:TYR:OH	7:M:126:ILE:O	2.18	0.56
6:E:39:CYS:SG	6:E:80:MET:HB3	2.46	0.56
1:A:1585:MET:HA	1:A:1588:LYS:HZ3	1.70	0.56
5:J:350:PRO:HG2	16:F:83:A:C5	2.40	0.56
8:C:119:ASN:OD1	8:C:120:ARG:N	2.38	0.56
8:C:362:LYS:HG3	8:C:363:PRO:HD2	1.87	0.56
8:C:472:VAL:CB	8:C:575:ALA:O	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:865:ASP:HB2	8:C:931:TYR:HE2	1.71	0.56
16:F:15:A:C6	16:F:16:C:C5	2.93	0.56
17:B:80:G:C6	17:B:82:A:C6	2.94	0.56
38:H:1126:G:O2'	38:H:1127:A:C5'	2.54	0.56
38:H:1146:G:O2'	38:H:1147:A:O5'	2.15	0.56
1:A:161:PHE:O	1:A:165:LEU:HB2	2.06	0.56
1:A:1739:ARG:HH22	1:A:1745:SER:HG	1.52	0.56
2:K:176:LYS:O	2:K:459:ARG:HG2	2.06	0.56
17:B:28:G:H2'	17:B:29:G:H5'	1.88	0.56
26:I:47:A:H2'	26:I:48:U:C6	2.39	0.56
26:I:77:U:H2'	26:I:78:A:C8	2.41	0.56
1:A:672:LYS:NZ	17:B:86:G:OP2	2.39	0.56
1:A:716:ARG:NH1	17:B:84:A:C4	2.74	0.56
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.41	0.56
2:K:190:VAL:O	2:K:201:VAL:HA	2.06	0.56
2:K:239:GLU:HA	2:K:267:ARG:HG3	1.88	0.56
2:K:415:TYR:CD1	2:K:439:LYS:HB3	2.41	0.56
5:J:405:ASP:OD1	5:J:419:MET:N	2.34	0.56
8:C:312:ILE:HG12	8:C:323:THR:HG22	1.88	0.56
8:C:792:LYS:HD2	8:C:795:ILE:HD12	1.88	0.56
17:B:44:A:N1	17:B:71:A:N1	2.54	0.56
1:A:861:GLN:HG2	1:A:1097:HIS:HB3	1.88	0.55
1:A:940:ILE:O	1:A:944:TYR:CB	2.54	0.55
1:A:1748:ILE:HG22	1:A:1752:VAL:HG23	1.87	0.55
1:A:1963:LEU:HB3	1:A:1965:PHE:CE2	2.41	0.55
38:H:143:G:H2'	38:H:144:G:C8	2.41	0.55
1:A:1616:ARG:HB2	1:A:1744:ASP:OD2	2.05	0.55
2:K:360:ASN:HB3	2:K:362:TYR:CD2	2.40	0.55
6:E:53:VAL:HG13	6:E:56:PHE:CZ	2.41	0.55
8:C:696:SER:OG	8:C:697:ARG:N	2.40	0.55
16:F:56:A:H2'	16:F:57:U:C6	2.40	0.55
36:Y:208:SER:CB	36:Y:212:ARG:O	2.54	0.55
1:A:465:GLU:OE1	8:C:387:TYR:OH	2.24	0.55
1:A:829:TYR:OH	1:A:833:ARG:NH1	2.40	0.55
1:A:1339:LEU:HD23	1:A:1340:ILE:N	2.22	0.55
1:A:1680:SER:N	1:A:1704:GLU:OE1	2.40	0.55
1:A:1734:PHE:HD1	1:A:1773:VAL:HB	1.71	0.55
3:L:366:LYS:HD3	16:F:58:C:N4	2.21	0.55
3:L:367:ARG:NH2	26:I:57:U:C4	2.71	0.55
4:N:798:LEU:O	4:N:801:THR:HG22	2.06	0.55
4:N:887:THR:O	4:N:890:GLU:HB3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:93:VAL:HG12	7:M:95:ARG:H	1.71	0.55
8:C:233:ASP:HB3	8:C:443:TYR:CE1	2.41	0.55
8:C:452:LYS:HZ1	8:C:487:ARG:NH2	2.03	0.55
17:B:73:U:O2'	17:B:74:U:H5''	2.05	0.55
1:A:413:ASN:ND2	1:A:416:GLU:O	2.39	0.55
1:A:1169:TYR:CZ	1:A:1262:MET:HG2	2.41	0.55
1:A:1225:ALA:O	1:A:1228:TRP:N	2.38	0.55
1:A:1341:SER:OG	1:A:1342:LEU:N	2.38	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.70	0.55
1:A:1619:VAL:HG12	1:A:1620:TYR:CD2	2.40	0.55
1:A:1690:LYS:HA	1:A:1693:LYS:HG2	1.89	0.55
1:A:2044:THR:N	1:A:2047:GLN:OE1	2.31	0.55
4:N:398:GLU:O	4:N:402:TRP:CB	2.54	0.55
8:C:738:ASP:OD1	8:C:739:GLY:N	2.40	0.55
8:C:772:ASN:CG	8:C:816:VAL:H	2.09	0.55
16:F:83:A:O2'	16:F:84:C:P	2.65	0.55
17:B:149:U:H2'	17:B:150:U:O4'	2.07	0.55
26:I:26:A:H5'	26:I:26:A:H8	1.71	0.55
1:A:553:ASN:OD1	1:A:554:THR:N	2.38	0.55
1:A:731:THR:O	1:A:735:GLU:N	2.39	0.55
1:A:1608:LEU:O	1:A:1611:SER:N	2.23	0.55
1:A:1759:TYR:O	1:A:1765:SER:OG	2.24	0.55
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.41	0.55
4:N:286:GLU:HB2	4:N:292:CYS:SG	2.47	0.55
4:N:487:GLN:O	4:N:491:LYS:CB	2.54	0.55
7:M:111:LYS:HG2	7:M:115:TYR:CE2	2.42	0.55
8:C:287:LYS:HE2	8:C:895:ALA:O	2.06	0.55
8:C:778:THR:OG1	8:C:780:PRO:HD2	2.05	0.55
17:B:161:U:H2'	17:B:162:G:C8	2.41	0.55
26:I:36:A:H2	26:I:42:C:C2	2.24	0.55
1:A:146:HIS:O	1:A:149:MET:CB	2.54	0.55
1:A:250:SER:OG	1:A:254:HIS:N	2.37	0.55
1:A:252:GLU:HG2	1:A:253:GLN:N	2.22	0.55
1:A:618:SER:O	1:A:621:LEU:HB3	2.07	0.55
1:A:917:GLU:CD	4:N:159:LEU:HD21	2.27	0.55
1:A:1563:LYS:HD2	1:A:1781:TYR:HD1	1.72	0.55
1:A:1640:THR:OG1	1:A:1641:LEU:N	2.40	0.55
1:A:1709:TRP:HD1	1:A:1730:ASN:O	1.90	0.55
3:L:367:ARG:NH1	26:I:58:G:N7	2.55	0.55
7:M:105:ASN:HB3	7:M:108:SER:HB2	1.87	0.55
17:B:125:C:H2'	17:B:126:A:O4'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ILE:O	1:A:257:ASN:N	2.40	0.55
1:A:656:ILE:O	1:A:660:ILE:HG13	2.07	0.55
1:A:868:GLN:OE1	1:A:1100:LYS:NZ	2.39	0.55
1:A:1051:GLU:HG2	1:A:1169:TYR:CD1	2.42	0.55
1:A:1054:LEU:HD21	1:A:1168:ILE:HD11	1.88	0.55
1:A:1087:ASN:ND2	3:L:272:LEU:HG	2.22	0.55
1:A:1680:SER:H	1:A:1704:GLU:HB2	1.71	0.55
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.06	0.55
1:A:1759:TYR:HB3	1:A:1767:TYR:CE2	2.42	0.55
2:K:170:SER:OG	2:K:171:GLN:N	2.40	0.55
2:K:408:LYS:O	2:K:424:SER:HB3	2.07	0.55
8:C:231:ALA:O	8:C:487:ARG:NH1	2.39	0.55
8:C:265:PHE:CD2	8:C:295:ILE:HD12	2.42	0.55
16:F:83:A:H2'	16:F:83:A:N3	2.22	0.55
1:A:961:GLN:OE1	1:A:963:VAL:N	2.29	0.55
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.34	0.55
2:K:121:ARG:HA	2:K:124:LEU:HD12	1.89	0.55
3:L:146:ASN:O	3:L:150:SER:N	2.40	0.55
3:L:266:LYS:HG2	3:L:267:HIS:H	1.71	0.55
4:N:730:LEU:O	4:N:732:LYS:N	2.40	0.55
5:J:153:LEU:O	5:J:157:LYS:HB3	2.07	0.55
8:C:938:ARG:HG2	8:C:939:LYS:H	1.71	0.55
32:4:139:GLU:O	32:4:151:ALA:HA	2.07	0.55
1:A:297:SER:HB3	17:B:32:G:OP1	2.06	0.55
1:A:1268:ARG:HD3	1:A:1301:TYR:HB2	1.89	0.55
1:A:1275:MET:O	1:A:1277:GLU:N	2.39	0.55
1:A:1419:ASP:HB3	1:A:1803:ARG:NH2	2.22	0.55
1:A:1646:ILE:HD13	16:F:49:A:N1	2.22	0.55
4:N:669:LYS:HA	4:N:672:LEU:HD12	1.88	0.55
8:C:356:LYS:N	8:C:358:ASN:OD1	2.39	0.55
8:C:362:LYS:O	8:C:364:PHE:N	2.39	0.55
8:C:421:LEU:O	8:C:424:VAL:HB	2.05	0.55
8:C:483:TRP:HB3	8:C:563:LEU:HB3	1.88	0.55
8:C:735:LEU:HD21	8:C:739:GLY:HA3	1.89	0.55
16:F:51:A:C5'	16:F:51:A:H8	2.19	0.55
17:B:10:U:H2'	17:B:11:A:N7	2.22	0.55
17:B:98:U:C6	17:B:99:U:C5	2.94	0.55
26:I:14:G:H2'	26:I:15:G:H8	1.70	0.55
19:S:49:ALA:O	19:S:56:VAL:HA	2.07	0.55
38:H:1139:G:C4	38:H:1140:U:C5	2.94	0.55
38:H:1139:G:C5	38:H:1140:U:C5	2.94	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:W:80:PHE:O	44:W:88:THR:HA	2.07	0.55
1:A:225:ARG:NH2	1:A:694:ASN:CG	2.60	0.55
1:A:350:PRO:HG2	1:A:352:PHE:HE2	1.72	0.55
1:A:667:TYR:O	16:F:26:A:H2	1.90	0.55
1:A:852:LEU:O	1:A:855:LEU:N	2.37	0.55
1:A:1574:PHE:HE1	1:A:1826:TYR:HD2	1.55	0.55
1:A:1992:TYR:CD1	1:A:2004:ALA:HB1	2.42	0.55
2:K:140:MET:HE1	5:J:153:LEU:HD22	1.88	0.55
3:L:154:SER:HB2	3:L:156:GLU:HB2	1.89	0.55
5:J:347:LEU:HD21	5:J:442:MET:SD	2.47	0.55
1:A:150:ALA:CB	1:A:153:MET:SD	2.94	0.54
1:A:355:LEU:HD13	17:B:105:A:C5'	2.34	0.54
2:K:119:PHE:HA	2:K:122:ARG:HD3	1.88	0.54
4:N:702:PRO:HB3	4:N:739:PHE:HE1	1.71	0.54
5:J:358:MET:O	5:J:361:LYS:N	2.39	0.54
8:C:133:ILE:HG22	8:C:209:MET:HB3	1.89	0.54
28:G:505:A:OP1	28:G:505:A:C4'	2.55	0.54
1:A:1014:LYS:HE3	1:A:1144:PHE:CE1	2.43	0.54
2:K:401:PHE:CE1	2:K:410:LEU:HD21	2.41	0.54
5:J:382:VAL:HG11	5:J:392:TYR:CE2	2.42	0.54
8:C:265:PHE:N	8:C:310:ASN:O	2.33	0.54
1:A:228:LYS:HZ1	1:A:698:GLY:HA3	1.72	0.54
1:A:228:LYS:HZ3	1:A:698:GLY:C	2.11	0.54
1:A:408:SER:HB3	1:A:410:ILE:HD12	1.89	0.54
1:A:767:LEU:HD22	1:A:775:ARG:HD3	1.88	0.54
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.17	0.54
1:A:1394:LEU:HD21	3:L:394:GLY:HA2	1.90	0.54
1:A:2041:PRO:HG2	1:A:2043:PHE:HE2	1.72	0.54
2:K:284:SER:OG	2:K:285:HIS:N	2.36	0.54
4:N:808:LEU:HD11	4:N:834:LYS:HZ2	1.72	0.54
8:C:148:SER:O	8:C:151:ASP:HB3	2.08	0.54
8:C:620:ASP:HA	8:C:623:ASN:ND2	2.21	0.54
16:F:86:G:C5'	16:F:86:G:C8	2.90	0.54
26:I:20:A:N1	26:I:54:U:O2	2.40	0.54
1:A:234:PHE:CZ	1:A:648:GLN:HG2	2.42	0.54
1:A:338:ASN:OD1	1:A:399:ARG:N	2.34	0.54
6:E:70:PHE:HA	6:E:73:MET:HG2	1.89	0.54
38:H:1139:G:HO2'	38:H:1140:U:H6	1.54	0.54
7:M:14:ALA:O	7:M:17:THR:N	2.39	0.54
16:F:56:A:H2'	16:F:57:U:H6	1.72	0.54
1:A:194:HIS:HB3	1:A:198:ALA:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:GLN:OE1	1:A:412:GLN:N	2.41	0.54
1:A:893:ARG:O	1:A:894:SER:OG	2.26	0.54
1:A:1144:PHE:HD2	1:A:1145:MET:HG2	1.72	0.54
1:A:1650:ARG:HD2	16:F:49:A:H5'	1.89	0.54
1:A:1712:SER:HA	1:A:1723:SER:O	2.07	0.54
5:J:452:LEU:O	5:J:461:GLU:HG2	2.08	0.54
8:C:835:LYS:O	8:C:839:ILE:HB	2.07	0.54
1:A:603:LYS:NZ	16:F:43:C:H5''	2.12	0.54
1:A:965:LYS:HG3	1:A:985:ASP:OD2	2.08	0.54
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.89	0.54
1:A:1657:ILE:HG12	1:A:1811:ALA:HB1	1.90	0.54
1:A:2070:ASN:ND2	1:A:2072:SER:OG	2.41	0.54
2:K:51:VAL:HG13	2:K:76:LEU:HD11	1.89	0.54
2:K:441:ILE:HD11	2:K:457:TRP:HE1	1.73	0.54
3:L:273:HIS:ND1	3:L:273:HIS:O	2.41	0.54
4:N:349:ALA:O	4:N:353:GLN:CB	2.56	0.54
8:C:775:ILE:HD12	8:C:817:GLN:NE2	2.23	0.54
28:G:500:A:C2	38:H:36:A:C2	2.95	0.54
38:H:41:C:C5'	38:H:41:C:C6	2.89	0.54
38:H:1097:G:C5	38:H:1146:G:C6	2.96	0.54
44:W:93:LEU:O	44:W:97:ASP:CB	2.56	0.54
1:A:784:GLN:O	1:A:787:SER:N	2.41	0.54
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.41	0.54
1:A:1869:ASN:CG	1:A:1870:VAL:HG22	2.27	0.54
4:N:237:ASP:OD2	4:N:240:ASN:ND2	2.38	0.54
6:E:95:PHE:HD2	6:E:137:TYR:HH	1.55	0.54
7:M:9:PHE:HD2	7:M:10:PRO:HD3	1.72	0.54
7:M:113:GLN:HE21	16:F:77:G:H4'	1.73	0.54
8:C:118:TYR:CZ	8:C:199:LEU:HB3	2.43	0.54
8:C:140:GLY:N	8:C:146:LYS:HD3	2.23	0.54
8:C:470:ALA:HB1	8:C:487:ARG:O	2.08	0.54
16:F:29:U:N3	17:B:98:U:C2	2.76	0.54
38:H:1126:G:O2'	38:H:1127:A:O5'	2.24	0.54
1:A:188:GLU:HA	1:A:562:ILE:O	2.08	0.54
1:A:297:SER:HB2	17:B:32:G:H5'	1.90	0.54
1:A:503:LYS:NZ	17:B:83:C:OP1	2.36	0.54
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.08	0.54
8:C:794:GLN:HG2	8:C:835:LYS:CG	2.37	0.54
16:F:51:A:C8	16:F:51:A:C5'	2.90	0.54
33:5:103:LYS:O	33:5:104:LYS:CB	2.56	0.54
1:A:1020:ILE:O	1:A:1023:LEU:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1582:GLU:OE1	1:A:1583:ASP:N	2.41	0.54
1:A:1878:CYS:HB2	1:A:1891:LEU:HD22	1.88	0.54
2:K:46:GLU:HB2	2:K:73:ARG:NH1	2.23	0.54
2:K:200:GLN:HB3	2:K:213:LYS:HA	1.90	0.54
3:L:280:ARG:HH21	26:I:37:U:H5	1.56	0.54
4:N:688:ARG:HA	4:N:691:TYR:HD2	1.73	0.54
4:N:807:VAL:O	4:N:810:GLU:N	2.40	0.54
4:N:840:ASP:N	4:N:840:ASP:OD1	2.40	0.54
7:M:37:ALA:HB2	7:M:98:ILE:HD11	1.90	0.54
7:M:40:ALA:O	7:M:43:THR:OG1	2.21	0.54
8:C:249:VAL:HA	8:C:252:LEU:HD12	1.89	0.54
8:C:488:ILE:HG22	8:C:558:LYS:HA	1.90	0.54
8:C:542:ILE:HG22	8:C:553:VAL:HB	1.88	0.54
17:B:41:A:C8	17:B:41:A:C5'	2.85	0.54
1:A:1389:TYR:HD2	1:A:1437:ILE:HG21	1.71	0.53
1:A:1925:PRO:O	1:A:1928:GLU:N	2.38	0.53
2:K:218:VAL:CG2	2:K:239:GLU:HG2	2.37	0.53
4:N:310:TRP:O	4:N:313:ALA:N	2.41	0.53
4:N:738:LEU:O	4:N:741:ILE:N	2.41	0.53
5:J:392:TYR:O	5:J:395:LEU:HB3	2.08	0.53
6:E:32:GLY:HA3	6:E:39:CYS:SG	2.48	0.53
8:C:287:LYS:NZ	8:C:291:ILE:HD11	2.23	0.53
17:B:74:U:H5'	17:B:74:U:H6	1.73	0.53
1:A:750:LEU:HG	1:A:751:ASP:H	1.73	0.53
1:A:1908:LEU:O	1:A:1912:LYS:HG2	2.08	0.53
3:L:79:ASP:O	3:L:82:ARG:N	2.42	0.53
8:C:234:LEU:HA	8:C:262:ALA:O	2.09	0.53
8:C:326:GLU:HG2	8:C:330:TYR:CE2	2.43	0.53
1:A:346:ILE:HB	1:A:349:GLY:HA3	1.90	0.53
1:A:499:VAL:HG12	1:A:501:LEU:HD12	1.89	0.53
1:A:769:MET:HG3	4:N:111:LEU:HB2	1.90	0.53
1:A:1690:LYS:O	1:A:1693:LYS:HG2	2.08	0.53
2:K:247:GLN:HE21	2:K:248:TYR:C	2.12	0.53
3:L:105:ILE:O	3:L:109:ILE:HG13	2.09	0.53
4:N:687:SER:O	4:N:690:THR:HG22	2.08	0.53
4:N:692:LEU:HD23	4:N:708:LEU:HD11	1.90	0.53
4:N:702:PRO:HA	4:N:705:TRP:CE3	2.43	0.53
8:C:445:PRO:O	8:C:449:PHE:CB	2.56	0.53
17:B:28:G:C6	17:B:126:A:C2	2.96	0.53
31:3:153:ASP:O	31:3:154:SER:CB	2.56	0.53
1:A:495:ARG:HH12	17:B:112:C:C2'	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:693:SER:O	4:N:696:ARG:HG2	2.08	0.53
23:T:59:GLU:O	23:T:74:GLY:HA2	2.08	0.53
1:A:930:ASN:HB3	1:A:933:GLU:OE1	2.07	0.53
2:K:112:PRO:HB3	5:J:217:VAL:CA	2.38	0.53
2:K:383:GLU:HA	2:K:385:GLN:HG2	1.91	0.53
8:C:201:THR:HA	8:C:207:SER:HA	1.90	0.53
8:C:296:ASN:OD1	8:C:304:PHE:N	2.36	0.53
29:1:526:LEU:CB	29:1:564:ALA:HB1	2.38	0.53
31:3:520:SER:O	31:3:874:GLY:HA2	2.09	0.53
38:H:1089:G:H2'	38:H:1090:A:O5'	2.09	0.53
45:0:190:GLU:O	45:0:194:TRP:CB	2.57	0.53
1:A:321:GLU:OE1	1:A:321:GLU:N	2.42	0.53
1:A:645:ASP:CG	1:A:646:ALA:H	2.11	0.53
1:A:844:MET:O	1:A:848:ASN:HB2	2.09	0.53
1:A:1041:VAL:O	1:A:1041:VAL:HG12	2.09	0.53
1:A:1332:ALA:HB2	1:A:1397:LEU:HB3	1.90	0.53
1:A:1379:MET:SD	1:A:1380:PRO:HD2	2.49	0.53
4:N:616:PHE:O	4:N:619:GLN:N	2.40	0.53
5:J:269:GLU:OE1	5:J:269:GLU:N	2.42	0.53
38:H:47:U:H3'	38:H:48:U:C5'	2.37	0.53
38:H:1098:C:H2'	38:H:1099:G:C8	2.41	0.53
1:A:327:TYR:OH	1:A:509:HIS:ND1	2.32	0.53
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.23	0.53
3:L:239:ALA:O	3:L:243:ALA:CB	2.55	0.53
4:N:828:LEU:HB3	4:N:845:LEU:HD21	1.91	0.53
5:J:166:TYR:CE1	5:J:171:THR:HA	2.43	0.53
8:C:265:PHE:CE2	8:C:295:ILE:HD12	2.44	0.53
29:1:927:ALA:C	29:1:929:ASN:H	2.12	0.53
38:H:1126:G:HO2'	38:H:1127:A:H8	1.56	0.53
1:A:269:ASP:OD1	1:A:270:SER:N	2.42	0.53
1:A:1574:PHE:HD2	1:A:1828:SER:HG	1.55	0.53
2:K:274:HIS:HD2	2:K:276:SER:CB	2.22	0.53
2:K:327:MET:HA	2:K:351:PRO:HB3	1.91	0.53
4:N:242:GLN:HA	4:N:245:ILE:HD12	1.90	0.53
5:J:145:HIS:HB3	5:J:148:LYS:NZ	2.24	0.53
6:E:30:ARG:NE	6:E:61:LEU:HD22	2.24	0.53
6:E:32:GLY:HA2	6:E:79:PRO:O	2.08	0.53
8:C:323:THR:OG1	8:C:326:GLU:HB3	2.09	0.53
8:C:505:SER:O	8:C:508:GLU:N	2.41	0.53
28:G:483:A:O3'	28:G:484:A:H4'	2.07	0.53
31:3:855:ALA:HA	31:3:856:ASP:C	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:SER:O	1:A:384:LYS:N	2.42	0.53
1:A:404:ASN:HA	8:C:919:ARG:HH12	1.73	0.53
1:A:482:SER:HG	1:A:487:ASN:H	1.55	0.53
1:A:833:ARG:HG3	1:A:838:ALA:HB3	1.90	0.53
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.43	0.53
1:A:1372:LYS:HG2	1:A:1383:PHE:CE2	2.44	0.53
1:A:1574:PHE:CE1	1:A:1826:TYR:HD2	2.27	0.53
4:N:15:TYR:HE2	6:E:13:TRP:CD1	2.22	0.53
4:N:261:LYS:HE2	4:N:285:HIS:HA	1.90	0.53
5:J:315:ARG:HH21	16:F:72:C:H1'	1.73	0.53
8:C:341:ILE:HG13	8:C:342:ASP:N	2.22	0.53
8:C:396:LEU:O	8:C:400:LEU:HG	2.09	0.53
1:A:165:LEU:HG	1:A:578:MET:SD	2.49	0.53
1:A:225:ARG:HH21	1:A:694:ASN:ND2	2.07	0.53
1:A:671:TYR:HD2	17:B:101:C:HO2'	1.55	0.53
1:A:947:PRO:O	1:A:950:THR:HG22	2.09	0.53
1:A:1378:LYS:O	1:A:1379:MET:HB3	2.08	0.53
1:A:1491:ILE:O	1:A:1494:LEU:N	2.42	0.53
1:A:1623:PHE:CE2	16:F:31:G:C6	2.96	0.53
2:K:227:HIS:CE1	2:K:230:SER:H	2.27	0.53
3:L:265:ASN:O	3:L:266:LYS:HB2	2.08	0.53
16:F:46:U:H5'	16:F:47:A:OP2	2.09	0.53
26:I:9:G:H2'	26:I:10:C:C6	2.44	0.53
38:H:1148:U:H2'	38:H:1149:G:C8	2.43	0.53
1:A:248:PRO:HG3	1:A:573:ARG:HD2	1.91	0.52
1:A:772:GLU:HG2	1:A:775:ARG:CZ	2.40	0.52
3:L:48:PRO:O	3:L:52:GLU:CB	2.57	0.52
1:A:971:MET:SD	1:A:980:PRO:HA	2.48	0.52
1:A:1303:LYS:HG2	1:A:1304:VAL:N	2.23	0.52
6:E:118:GLU:OE2	6:E:122:ARG:NH2	2.41	0.52
6:E:121:PHE:HZ	6:E:125:ARG:HH21	1.57	0.52
8:C:713:GLU:N	8:C:817:GLN:O	2.41	0.52
17:B:28:G:H2'	17:B:29:G:H5''	1.92	0.52
17:B:72:C:H2'	17:B:73:U:H6	1.74	0.52
17:B:102:C:H2'	17:B:103:A:C5'	2.38	0.52
28:G:485:A:H2'	28:G:486:A:OP2	2.09	0.52
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.44	0.52
1:A:2018:ASN:ND2	1:A:2058:LEU:HB3	2.23	0.52
3:L:294:PHE:HB3	3:L:295:PRO:HD2	1.92	0.52
3:L:366:LYS:CD	16:F:58:C:H41	2.22	0.52
4:N:668:HIS:CE1	4:N:669:LYS:HG3	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:757:TRP:HZ2	8:C:775:ILE:HD11	1.74	0.52
8:C:776:ASN:OD1	8:C:792:LYS:NZ	2.43	0.52
16:F:81:G:H22	26:I:1:A:H1'	1.73	0.52
1:A:231:ARG:NE	1:A:233:HIS:O	2.41	0.52
1:A:1201:TYR:HB2	1:A:1224:ARG:HH21	1.75	0.52
2:K:207:LEU:HD11	2:K:463:LEU:HB2	1.91	0.52
4:N:617:PHE:O	4:N:621:PHE:CB	2.57	0.52
6:E:44:GLU:O	6:E:47:SER:OG	2.18	0.52
17:B:16:U:O2'	17:B:18:A:N7	2.42	0.52
17:B:91:U:C2'	17:B:92:U:H5''	2.37	0.52
26:I:140:G:H2'	26:I:141:G:O4'	2.09	0.52
38:H:68:U:H2'	38:H:69:G:O4'	2.10	0.52
38:H:1127:A:O2'	38:H:1128:C:H5'	2.08	0.52
1:A:769:MET:HG3	4:N:111:LEU:CB	2.40	0.52
1:A:1575:TRP:NE1	3:L:393:PHE:HD1	2.07	0.52
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.45	0.52
3:L:321:LYS:HG3	3:L:324:ASP:H	1.74	0.52
4:N:726:LEU:HD21	4:N:746:MET:SD	2.49	0.52
5:J:320:ILE:O	5:J:323:ARG:HB2	2.09	0.52
5:J:343:GLN:HA	5:J:378:GLY:O	2.08	0.52
26:I:92:C:H2'	26:I:93:C:H6	1.75	0.52
22:R:56:ALA:HB2	22:R:72:VAL:HA	1.90	0.52
28:G:470:A:N3	28:G:470:A:C2'	2.73	0.52
31:3:68:GLN:HA	31:3:1223:GLY:O	2.09	0.52
1:A:133:GLU:HG3	1:A:560:THR:HA	1.92	0.52
1:A:654:HIS:CD2	1:A:701:CYS:CB	2.92	0.52
1:A:693:LYS:NZ	1:A:693:LYS:CA	2.73	0.52
4:N:755:GLN:HA	4:N:758:LEU:HD13	1.92	0.52
8:C:410:GLN:OE1	8:C:410:GLN:N	2.35	0.52
8:C:755:TYR:HB2	8:C:757:TRP:HB2	1.92	0.52
8:C:780:PRO:HA	8:C:783:ILE:HD12	1.92	0.52
16:F:13:U:H3'	16:F:14:U:C5	2.45	0.52
16:F:47:A:H2'	16:F:48:C:C5'	2.40	0.52
17:B:29:G:H2'	17:B:30:A:O4'	2.09	0.52
38:H:1140:U:H2'	38:H:1141:C:H6	1.75	0.52
1:A:643:ASN:OD1	1:A:643:ASN:N	2.38	0.52
1:A:1661:ILE:HG13	1:A:1809:ASN:ND2	2.24	0.52
1:A:1973:LYS:O	1:A:1976:ASP:HB2	2.10	0.52
2:K:76:LEU:O	2:K:79:ILE:N	2.42	0.52
2:K:347:GLY:HA3	2:K:374:ASN:HD21	1.73	0.52
2:K:412:SER:OG	2:K:420:ASN:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:108:ASN:HA	3:L:111:LEU:HD12	1.90	0.52
4:N:890:GLU:O	4:N:894:ARG:HB2	2.09	0.52
6:E:42:MET:HE1	6:E:106:ILE:HA	1.92	0.52
7:M:38:ASN:HB2	26:I:32:G:O6	2.10	0.52
17:B:96:U:O5'	17:B:96:U:H6	1.92	0.52
27:D:851:ASP:HA	27:D:861:GLU:O	2.10	0.52
38:H:139:G:H2'	38:H:140:G:O5'	2.09	0.52
1:A:228:LYS:HZ3	1:A:698:GLY:CA	2.23	0.52
1:A:840:VAL:HG11	1:A:845:VAL:HG23	1.92	0.52
1:A:1014:LYS:HD2	1:A:1144:PHE:HE1	1.74	0.52
1:A:1478:GLU:O	1:A:1481:GLU:HB2	2.10	0.52
1:A:1575:TRP:NE1	3:L:393:PHE:CD1	2.78	0.52
1:A:1857:VAL:HG13	1:A:1894:ILE:HD12	1.91	0.52
1:A:1877:GLY:O	1:A:1893:ILE:HA	2.09	0.52
2:K:166:GLU:H	2:K:465:ASN:HB2	1.73	0.52
2:K:176:LYS:HB3	2:K:195:TRP:HB2	1.91	0.52
2:K:274:HIS:HB3	2:K:279:PHE:HB2	1.92	0.52
7:M:42:LYS:HZ3	26:I:43:C:H5	1.57	0.52
8:C:115:LYS:O	8:C:116:THR:OG1	2.23	0.52
8:C:197:THR:H	8:C:545:LEU:HD12	1.75	0.52
8:C:798:GLY:HA2	8:C:839:ILE:HG23	1.91	0.52
17:B:33:U:O2'	17:B:34:C:P	2.66	0.52
17:B:33:U:HO2'	17:B:34:C:P	2.30	0.52
26:I:35:G:N2	26:I:36:A:N3	2.58	0.52
28:G:471:U:O2'	28:G:472:U:C5	2.63	0.52
1:A:409:CYS:SG	8:C:272:ARG:NH2	2.80	0.52
1:A:1844:PHE:HB2	5:J:278:MET:SD	2.49	0.52
2:K:70:GLN:CD	2:K:70:GLN:H	2.12	0.52
3:L:379:PHE:N	3:L:379:PHE:CD1	2.77	0.52
4:N:15:TYR:OH	6:E:13:TRP:HA	2.09	0.52
5:J:410:THR:OG1	5:J:413:GLY:O	2.17	0.52
8:C:362:LYS:CG	8:C:363:PRO:HD2	2.39	0.52
17:B:94:C:C3'	17:B:94:C:C6	2.93	0.52
28:G:491:C:H2'	28:G:492:U:O4'	2.10	0.52
1:A:139:LEU:O	1:A:142:ILE:N	2.43	0.52
1:A:143:ILE:HD13	1:A:570:GLN:HE21	1.74	0.52
1:A:1038:ILE:HD11	1:A:1039:TRP:CE2	2.45	0.52
1:A:1144:PHE:HZ	1:A:1162:THR:HG21	1.72	0.52
1:A:1771:THR:HA	1:A:1789:ASN:ND2	2.24	0.52
2:K:160:GLN:O	2:K:164:ASN:N	2.38	0.52
2:K:206:THR:HB	2:K:208:GLN:OE1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:362:TYR:CD1	2:K:363:GLN:HG3	2.45	0.52
3:L:200:ALA:O	3:L:203:ILE:N	2.43	0.52
4:N:737:VAL:HA	4:N:767:PHE:CE2	2.45	0.52
8:C:501:ILE:HB	8:C:535:PRO:O	2.10	0.52
8:C:546:GLY:HA3	8:C:549:TYR:CE1	2.45	0.52
16:F:83:A:N3	16:F:83:A:C2'	2.73	0.52
17:B:84:A:H2'	17:B:85:U:C6	2.45	0.52
38:H:1097:G:C2	38:H:1146:G:C5	2.98	0.52
1:A:814:ARG:NH2	4:N:107:LEU:HD13	2.25	0.51
1:A:1835:LEU:HD11	1:A:1843:LEU:HD21	1.91	0.51
1:A:1887:GLY:HA3	1:A:1992:TYR:HD2	1.74	0.51
3:L:206:ASN:HA	3:L:209:LYS:HE2	1.92	0.51
3:L:239:ALA:O	3:L:243:ALA:HB2	2.09	0.51
3:L:390:ARG:O	3:L:412:MET:HG2	2.10	0.51
4:N:169:LEU:O	4:N:173:GLN:HG3	2.11	0.51
6:E:36:ASP:HB2	6:E:39:CYS:HB2	1.92	0.51
8:C:601:ALA:HB1	8:C:645:LEU:HB3	1.92	0.51
17:B:80:G:C6	17:B:82:A:N1	2.78	0.51
17:B:91:U:H3'	17:B:92:U:C5'	2.39	0.51
26:I:49:U:H2'	26:I:50:G:C8	2.44	0.51
38:H:1139:G:HO2'	38:H:1140:U:C5'	2.23	0.51
1:A:282:ASP:HB3	1:A:284:ARG:O	2.10	0.51
1:A:389:HIS:NE2	8:C:657:TYR:HD1	2.09	0.51
1:A:1649:PHE:HE1	1:A:1815:LEU:HD21	1.75	0.51
1:A:2019:GLU:O	1:A:2023:LYS:HG3	2.10	0.51
2:K:230:SER:OG	2:K:233:GLN:OE1	2.21	0.51
3:L:339:LYS:O	3:L:342:ARG:N	2.43	0.51
8:C:436:VAL:O	8:C:440:THR:N	2.35	0.51
8:C:649:GLU:OE2	8:C:913:GLY:N	2.39	0.51
16:F:69:C:C4	16:F:70:U:C4	2.98	0.51
28:G:486:A:N3	28:G:486:A:C3'	2.73	0.51
28:G:506:U:O2	28:G:506:U:H3'	2.11	0.51
1:A:936:GLU:O	1:A:939:LEU:N	2.43	0.51
1:A:960:THR:O	1:A:962:ARG:HG2	2.10	0.51
1:A:961:GLN:CG	1:A:964:PHE:HE1	2.22	0.51
1:A:1342:LEU:HD23	1:A:1343:PHE:CD1	2.45	0.51
1:A:1650:ARG:HB2	16:F:49:A:P	2.49	0.51
1:A:1857:VAL:O	1:A:1877:GLY:HA3	2.11	0.51
1:A:2025:ILE:HD12	1:A:2058:LEU:HD11	1.91	0.51
2:K:176:LYS:H	2:K:459:ARG:HD3	1.75	0.51
8:C:814:TYR:HB3	8:C:858:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:91:U:H2'	26:I:92:C:C6	2.45	0.51
31:3:1117:HIS:O	31:3:1133:ASP:HA	2.09	0.51
38:H:1125:U:O2'	38:H:1126:G:C8	2.57	0.51
1:A:152:LYS:HE3	1:A:584:HIS:CD2	2.45	0.51
1:A:394:ARG:HB2	8:C:667:GLU:OE2	2.11	0.51
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.92	0.51
1:A:1184:ASP:O	1:A:1187:LEU:N	2.43	0.51
2:K:270:ASP:O	2:K:282:SER:HA	2.10	0.51
3:L:101:ILE:HA	3:L:104:LEU:HD12	1.93	0.51
3:L:108:ASN:O	3:L:111:LEU:HB2	2.10	0.51
8:C:202:ASP:OD1	8:C:205:SER:N	2.43	0.51
8:C:248:VAL:O	8:C:252:LEU:HG	2.11	0.51
8:C:675:THR:HG22	8:C:909:ILE:HD13	1.91	0.51
16:F:81:G:H22	26:I:1:A:C1'	2.23	0.51
17:B:1:A:H61	17:B:164:C:H42	1.56	0.51
17:B:74:U:C5'	17:B:74:U:H6	2.24	0.51
1:A:984:VAL:HB	1:A:989:LYS:HG3	1.92	0.51
1:A:1044:GLY:HA3	1:A:1176:GLU:OE2	2.11	0.51
1:A:1664:ASP:OD2	18:O:213:SER:HB3	2.10	0.51
1:A:1705:SER:HA	1:A:1709:TRP:HE1	1.75	0.51
1:A:1734:PHE:CD1	1:A:1773:VAL:HB	2.46	0.51
1:A:1858:TYR:HD2	18:O:164:LEU:HG	1.74	0.51
1:A:1911:TRP:HZ2	18:O:169:ILE:HD13	1.69	0.51
1:A:2062:GLU:HG3	1:A:2065:ARG:NH2	2.26	0.51
2:K:308:LYS:HD2	2:K:328:ASP:HA	1.92	0.51
3:L:137:TYR:O	3:L:141:ILE:HG13	2.11	0.51
5:J:409:HIS:CB	16:F:83:A:H61	2.23	0.51
16:F:32:U:O2	16:F:32:U:O2'	2.21	0.51
26:I:19:U:O2'	26:I:20:A:OP2	2.26	0.51
26:I:50:G:C6	26:I:51:U:C4	2.99	0.51
36:Y:224:PHE:O	36:Y:225:ALA:HB3	2.11	0.51
1:A:668:ARG:NE	16:F:27:U:C4'	2.67	0.51
1:A:1907:GLN:HA	1:A:1910:LYS:CD	2.38	0.51
2:K:358:SER:HB3	2:K:360:ASN:HD22	1.75	0.51
3:L:445:ILE:O	3:L:449:ASN:ND2	2.44	0.51
5:J:141:ASN:CG	5:J:142:LEU:H	2.14	0.51
8:C:508:GLU:OE2	8:C:594:PRO:HG2	2.11	0.51
8:C:681:CYS:SG	8:C:816:VAL:HG22	2.51	0.51
26:I:2:U:H2'	26:I:3:C:H6	1.75	0.51
31:3:477:ILE:O	31:3:479:SER:N	2.41	0.51
1:A:287:GLU:CG	1:A:288:GLU:H	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1014:LYS:HG3	1:A:1016:SER:H	1.75	0.51
2:K:44:ILE:HG22	2:K:73:ARG:HE	1.76	0.51
3:L:144:LEU:HD21	3:L:183:PHE:CE1	2.46	0.51
5:J:345:LYS:HB2	5:J:422:ASN:OD1	2.11	0.51
38:H:41:C:H5''	38:H:41:C:C6	2.26	0.51
38:H:47:U:C3'	38:H:48:U:C5'	2.89	0.51
1:A:1267:VAL:HG22	1:A:1302:LEU:HD23	1.93	0.51
3:L:177:MET:O	3:L:181:THR:HG23	2.11	0.51
4:N:286:GLU:HG3	4:N:287:SER:N	2.24	0.51
5:J:163:ASN:HB2	5:J:165:GLY:H	1.75	0.51
5:J:280:VAL:HG12	5:J:282:GLU:H	1.76	0.51
26:I:43:C:H2'	26:I:44:G:H5'	1.91	0.51
38:H:1125:U:HO2'	38:H:1126:G:H8	1.49	0.51
1:A:170:HIS:CD2	1:A:547:LEU:HD23	2.46	0.51
1:A:520:VAL:HG12	1:A:524:LYS:HE2	1.93	0.51
1:A:540:THR:CG2	17:B:40:C:N4	2.74	0.51
1:A:1463:THR:O	1:A:1466:GLN:N	2.44	0.51
2:K:232:ASN:CB	2:K:247:GLN:HE22	2.12	0.51
3:L:457:ILE:C	3:L:460:GLY:H	2.14	0.51
4:N:828:LEU:HD11	4:N:848:THR:HG21	1.93	0.51
5:J:141:ASN:OD1	5:J:142:LEU:N	2.43	0.51
8:C:133:ILE:HG13	8:C:134:ILE:N	2.26	0.51
8:C:340:LYS:O	8:C:343:ASP:HB3	2.11	0.51
8:C:613:ARG:NH1	8:C:614:GLU:OE2	2.44	0.51
16:F:57:U:H3	26:I:62:G:H1	1.58	0.51
28:G:475:U:H2'	28:G:476:U:C2	2.45	0.51
1:A:240:PRO:O	1:A:242:PHE:N	2.44	0.51
1:A:639:PHE:O	1:A:642:GLY:N	2.43	0.51
1:A:964:PHE:CZ	1:A:1081:TYR:HE1	2.29	0.51
1:A:1609:TRP:HE3	1:A:1823:LEU:HD13	1.76	0.51
1:A:1821:LYS:O	1:A:1824:GLN:N	2.41	0.51
4:N:597:ARG:O	4:N:601:ILE:CB	2.59	0.51
5:J:373:ARG:NH1	5:J:446:ASN:O	2.44	0.51
5:J:406:PHE:CE1	5:J:408:LEU:HB2	2.46	0.51
6:E:7:PRO:HG2	6:E:60:TYR:CD1	2.46	0.51
7:M:8:ALA:HA	7:M:80:PHE:HE2	1.75	0.51
8:C:326:GLU:HG2	8:C:330:TYR:CD2	2.46	0.51
8:C:713:GLU:HB2	8:C:817:GLN:HB3	1.92	0.51
8:C:772:ASN:ND2	8:C:816:VAL:H	2.09	0.51
16:F:47:A:C3'	16:F:48:C:C5'	2.89	0.51
27:D:2071:ILE:O	27:D:2127:GLU:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:ASN:O	1:A:580:ASN:N	2.44	0.50
2:K:388:GLN:HB2	5:J:462:HIS:NE2	2.26	0.50
5:J:351:LYS:N	16:F:83:A:H8	2.09	0.50
7:M:52:ILE:HG22	7:M:53:ILE:N	2.26	0.50
8:C:175:LEU:HD23	8:C:176:ARG:N	2.26	0.50
8:C:192:LYS:HA	8:C:224:GLU:OE2	2.11	0.50
8:C:570:ALA:HB3	8:C:571:TYR:HD2	1.75	0.50
17:B:91:U:OP2	17:B:91:U:H6	1.94	0.50
1:A:181:HIS:HA	1:A:704:TRP:HZ2	1.76	0.50
1:A:665:GLY:HA2	1:A:667:TYR:CE2	2.47	0.50
2:K:266:ARG:HB3	2:K:285:HIS:HB2	1.93	0.50
4:N:659:ARG:O	4:N:662:LYS:N	2.43	0.50
7:M:95:ARG:O	7:M:97:VAL:HG23	2.12	0.50
8:C:360:ARG:CZ	8:C:362:LYS:HD3	2.41	0.50
8:C:474:LYS:HG3	8:C:476:VAL:HG22	1.92	0.50
16:F:65:U:H2'	16:F:66:C:C6	2.46	0.50
38:H:142:C:O2'	38:H:143:G:O4'	2.29	0.50
1:A:543:ASN:OD1	1:A:544:LYS:N	2.43	0.50
1:A:1063:PHE:HE2	1:A:1100:LYS:O	1.94	0.50
1:A:1121:ILE:O	1:A:1124:LEU:HB2	2.10	0.50
1:A:1952:PRO:HB2	3:L:426:GLY:N	2.25	0.50
1:A:1971:ILE:HB	1:A:1974:LEU:HD12	1.94	0.50
1:A:2067:TYR:HB3	18:O:194:LEU:CD2	2.34	0.50
2:K:110:PHE:HA	5:J:219:HIS:HA	1.93	0.50
2:K:247:GLN:HB2	2:K:258:LEU:HD21	1.93	0.50
3:L:313:ALA:O	3:L:316:VAL:HB	2.11	0.50
5:J:159:TYR:OH	5:J:168:TRP:N	2.44	0.50
6:E:32:GLY:O	6:E:63:ASP:HA	2.11	0.50
6:E:42:MET:CE	6:E:106:ILE:HA	2.40	0.50
8:C:117:ARG:NH1	8:C:158:HIS:O	2.43	0.50
8:C:703:LEU:O	8:C:705:GLY:N	2.38	0.50
17:B:99:U:C4	17:B:100:A:H1'	2.45	0.50
28:G:485:A:H2	28:G:486:A:C8	2.28	0.50
28:G:515:U:O2	28:G:515:U:H2'	2.11	0.50
31:3:1136:GLY:HA2	31:3:1197:ASP:O	2.11	0.50
38:H:1097:G:C2	38:H:1098:C:C4	3.00	0.50
1:A:644:VAL:O	1:A:648:GLN:HB2	2.12	0.50
1:A:899:PRO:O	1:A:998:TYR:OH	2.29	0.50
1:A:1559:HIS:ND1	1:A:1613:THR:HG21	2.26	0.50
1:A:1708:GLU:HG2	1:A:1730:ASN:OD1	2.12	0.50
1:A:1860:VAL:HG22	1:A:1874:ALA:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:274:HIS:CB	2:K:279:PHE:HB2	2.42	0.50
2:K:348:HIS:ND1	2:K:370:ASP:OD2	2.40	0.50
2:K:439:LYS:HB2	2:K:457:TRP:CD1	2.46	0.50
4:N:804:ASP:OD1	4:N:805:HIS:N	2.43	0.50
6:E:103:LEU:HD11	6:E:105:PHE:CE2	2.47	0.50
7:M:16:LEU:O	7:M:19:GLN:N	2.44	0.50
8:C:410:GLN:HA	8:C:413:LEU:HB2	1.93	0.50
8:C:429:PHE:HB3	8:C:432:GLN:NE2	2.27	0.50
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.44	0.50
1:A:1474:ARG:HH22	1:A:1499:ARG:NH1	2.10	0.50
1:A:1560:THR:O	1:A:1612:PRO:HG3	2.11	0.50
2:K:311:PHE:CZ	2:K:353:TYR:HD1	2.30	0.50
4:N:159:LEU:O	4:N:162:LEU:HB3	2.12	0.50
4:N:731:LEU:O	4:N:734:PRO:HD3	2.12	0.50
6:E:38:GLN:HB3	6:E:80:MET:SD	2.51	0.50
8:C:425:LEU:O	8:C:428:ILE:HG22	2.12	0.50
16:F:30:G:H1	17:B:96:U:H3	1.59	0.50
16:F:65:U:H2'	16:F:66:C:H6	1.76	0.50
17:B:96:U:H5''	17:B:97:U:C5	2.46	0.50
1:A:1033:ASN:HD21	1:A:1288:LEU:HB3	1.77	0.50
1:A:1058:ALA:HB2	1:A:1114:PHE:HE1	1.76	0.50
1:A:1477:PHE:O	1:A:1481:GLU:HG3	2.12	0.50
1:A:1805:ILE:O	1:A:1808:ALA:N	2.40	0.50
4:N:315:ASP:O	4:N:319:THR:N	2.45	0.50
6:E:6:LEU:HD11	6:E:47:SER:HA	1.94	0.50
8:C:608:GLN:HB2	8:C:669:LYS:HE3	1.92	0.50
38:H:1151:U:H2'	38:H:1152:U:C6	2.46	0.50
1:A:840:VAL:HG22	1:A:844:MET:HB2	1.92	0.50
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.26	0.50
1:A:967:VAL:HG13	1:A:983:SER:O	2.11	0.50
1:A:1118:GLY:HA3	1:A:1163:ARG:CZ	2.42	0.50
1:A:1627:LEU:HD13	1:A:1632:ILE:HB	1.94	0.50
1:A:1665:ILE:O	1:A:1668:ILE:N	2.42	0.50
1:A:1944:LEU:O	1:A:1948:MET:N	2.43	0.50
2:K:395:ILE:HD12	2:K:415:TYR:CD2	2.47	0.50
3:L:268:LEU:HD13	3:L:270:HIS:CE1	2.46	0.50
8:C:564:ILE:HG22	8:C:565:LYS:H	1.77	0.50
26:I:10:C:H2'	26:I:11:A:O4'	2.11	0.50
28:G:475:U:H5'	28:G:476:U:OP1	2.11	0.50
1:A:816:ILE:O	1:A:820:ALA:CB	2.60	0.50
1:A:1186:TYR:HE1	1:A:1190:ASN:HD22	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1646:ILE:CD1	16:F:49:A:N1	2.74	0.50
2:K:274:HIS:HD2	2:K:276:SER:HB3	1.77	0.50
3:L:110:LYS:HG2	3:L:114:ASN:ND2	2.27	0.50
3:L:189:LEU:HB2	3:L:194:ARG:NH2	2.27	0.50
7:M:111:LYS:HG2	7:M:115:TYR:HE2	1.76	0.50
17:B:32:G:H5'	17:B:33:U:OP2	2.12	0.50
17:B:64:C:C2	17:B:65:U:C5	3.00	0.50
24:U:33:PHE:C	24:U:35:SER:H	2.16	0.50
38:H:142:C:C2'	38:H:143:G:H8	2.23	0.50
1:A:456:GLU:HG3	8:C:356:LYS:O	2.12	0.50
1:A:1069:LEU:O	1:A:1072:LEU:HB2	2.11	0.50
1:A:1256:PRO:HB3	1:A:1274:ARG:HE	1.77	0.50
2:K:285:HIS:C	2:K:287:MET:N	2.65	0.50
6:E:93:CYS:HG	6:E:95:PHE:HE1	1.60	0.50
8:C:428:ILE:HG23	8:C:429:PHE:CD1	2.47	0.50
8:C:764:ASN:HB3	8:C:775:ILE:HG23	1.93	0.50
16:F:15:A:H2'	16:F:16:C:C6	2.41	0.50
17:B:62:G:H2'	17:B:63:C:H6	1.77	0.50
32:4:112:ILE:HA	32:4:179:THR:O	2.12	0.50
1:A:190:LYS:N	1:A:204:GLU:OE2	2.42	0.49
1:A:901:PRO:HG3	1:A:998:TYR:CZ	2.47	0.49
1:A:947:PRO:O	1:A:950:THR:N	2.45	0.49
1:A:1758:ASP:O	1:A:1762:ASP:N	2.45	0.49
2:K:379:ARG:HD3	5:J:159:TYR:CZ	2.47	0.49
3:L:146:ASN:ND2	3:L:148:ASN:HB2	2.27	0.49
3:L:381:LEU:HD22	3:L:385:ARG:HG2	1.94	0.49
8:C:274:ILE:HD13	8:C:385:PHE:CD2	2.36	0.49
17:B:128:A:H2'	17:B:129:G:H2'	1.94	0.49
31:3:391:LEU:HA	31:3:406:GLN:O	2.12	0.49
1:A:659:HIS:O	1:A:662:GLN:N	2.45	0.49
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.47	0.49
2:K:44:ILE:CG1	2:K:45:PRO:HD2	2.40	0.49
2:K:173:VAL:HG13	2:K:200:GLN:NE2	2.27	0.49
4:N:702:PRO:HA	4:N:705:TRP:HE3	1.75	0.49
8:C:894:VAL:HB	8:C:899:LEU:HB2	1.93	0.49
26:I:151:G:H21	26:I:152:A:N6	2.10	0.49
38:H:1089:G:C2'	38:H:1090:A:O5'	2.60	0.49
1:A:354:PRO:O	1:A:355:LEU:HB3	2.11	0.49
1:A:380:ARG:HB3	1:A:382:GLU:OE1	2.12	0.49
1:A:421:ALA:HB3	1:A:469:ILE:HG12	1.94	0.49
1:A:997:GLN:HE22	1:A:1511:ARG:HH12	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1065:LEU:HD23	1:A:1069:LEU:HD13	1.95	0.49
1:A:1565:THR:HG1	1:A:1567:PHE:HD2	1.58	0.49
1:A:1759:TYR:HB3	1:A:1767:TYR:HE2	1.76	0.49
1:A:1998:ARG:NH1	1:A:2043:PHE:O	2.45	0.49
2:K:375:VAL:HG11	2:K:427:TRP:CZ2	2.47	0.49
2:K:397:THR:N	2:K:413:CYS:O	2.30	0.49
5:J:320:ILE:HA	5:J:323:ARG:HD3	1.94	0.49
6:E:9:LEU:HD22	6:E:14:HIS:HB3	1.93	0.49
8:C:218:HIS:HE1	8:C:220:ASN:ND2	1.95	0.49
8:C:379:ILE:HA	8:C:382:TYR:HD2	1.77	0.49
16:F:83:A:HO2'	16:F:84:C:P	2.26	0.49
26:I:46:G:C2	26:I:47:A:C5	3.00	0.49
1:A:244:ASP:HB3	1:A:594:ASP:HB2	1.93	0.49
1:A:350:PRO:HG2	1:A:352:PHE:CE2	2.48	0.49
1:A:1051:GLU:HG2	1:A:1169:TYR:HD1	1.77	0.49
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.48	0.49
1:A:1736:VAL:HA	1:A:1775:ILE:O	2.13	0.49
1:A:1779:LEU:HD22	1:A:1815:LEU:HD11	1.95	0.49
2:K:415:TYR:CD1	2:K:439:LYS:HD3	2.47	0.49
2:K:426:THR:HG22	5:J:145:HIS:HB2	1.94	0.49
8:C:611:LEU:O	8:C:614:GLU:N	2.30	0.49
16:F:83:A:O2'	16:F:84:C:H5'	2.12	0.49
26:I:11:A:H2'	26:I:12:C:C6	2.47	0.49
1:A:154:TYR:HB3	1:A:161:PHE:HE2	1.77	0.49
1:A:215:ALA:O	1:A:218:SER:OG	2.22	0.49
1:A:287:GLU:HG2	1:A:288:GLU:OE1	2.12	0.49
1:A:326:ASN:ND2	1:A:405:ASN:O	2.46	0.49
1:A:628:MET:SD	1:A:660:ILE:HD13	2.51	0.49
1:A:1677:GLN:HB3	1:A:1706:VAL:HG21	1.95	0.49
1:A:1678:ILE:HG23	1:A:1704:GLU:H	1.77	0.49
1:A:1709:TRP:O	1:A:1729:THR:N	2.34	0.49
1:A:1853:ASP:HB2	1:A:1880:PHE:HB3	1.95	0.49
1:A:1859:ARG:HG2	18:O:163:THR:HG22	1.93	0.49
2:K:235:ILE:HA	2:K:244:LYS:O	2.12	0.49
8:C:660:ARG:HH22	8:C:670:ILE:HD12	1.78	0.49
17:B:64:C:H2'	17:B:65:U:H6	1.77	0.49
17:B:72:C:C2	17:B:73:U:C5	3.00	0.49
26:I:150:G:N2	26:I:152:A:H5'	2.28	0.49
1:A:1145:MET:SD	1:A:1160:LEU:HD13	2.53	0.49
2:K:171:GLN:NE2	2:K:207:LEU:O	2.46	0.49
2:K:382:ASP:OD1	2:K:383:GLU:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:427:THR:OG1	5:J:428:TRP:N	2.46	0.49
8:C:498:THR:HA	8:C:538:GLU:HA	1.94	0.49
16:F:73:A:C6	26:I:9:G:C6	3.00	0.49
17:B:102:C:N4	17:B:103:A:N6	2.56	0.49
29:1:156:LEU:O	29:1:160:GLU:N	2.42	0.49
31:3:406:GLN:HA	31:3:455:LEU:O	2.13	0.49
31:3:1090:ILE:O	31:3:1117:HIS:HA	2.12	0.49
38:H:46:C:H4'	38:H:47:U:OP2	2.13	0.49
38:H:1139:G:H2'	38:H:1140:U:H6	1.76	0.49
1:A:505:TRP:CZ3	1:A:690:LYS:HG3	2.47	0.49
1:A:590:TYR:OH	16:F:42:A:O3'	2.31	0.49
1:A:765:ASP:O	1:A:768:GLU:N	2.46	0.49
1:A:814:ARG:HH22	4:N:106:ASP:CG	2.16	0.49
1:A:1052:THR:HG22	1:A:1246:ALA:HB2	1.95	0.49
1:A:1118:GLY:HA3	1:A:1163:ARG:NH2	2.27	0.49
1:A:1650:ARG:CG	16:F:49:A:H5'	2.40	0.49
2:K:115:SER:O	2:K:117:LEU:N	2.46	0.49
2:K:216:SER:OG	2:K:217:HIS:N	2.46	0.49
2:K:285:HIS:O	2:K:309:GLY:HA2	2.12	0.49
8:C:859:GLU:O	8:C:937:TRP:HA	2.13	0.49
17:B:99:U:C3'	17:B:100:A:H4'	2.43	0.49
26:I:49:U:H2'	26:I:50:G:H8	1.77	0.49
29:1:338:GLN:O	29:1:341:GLY:N	2.45	0.49
1:A:411:ILE:O	8:C:278:LYS:NZ	2.32	0.49
1:A:514:TYR:HE1	1:A:689:TYR:CE2	2.30	0.49
1:A:813:GLU:OE1	1:A:817:LYS:NZ	2.46	0.49
1:A:923:TYR:O	1:A:925:SER:N	2.46	0.49
1:A:1058:ALA:HB2	1:A:1114:PHE:CE1	2.48	0.49
1:A:1650:ARG:CD	16:F:49:A:H5'	2.42	0.49
1:A:1887:GLY:HA3	1:A:1992:TYR:CD2	2.47	0.49
2:K:401:PHE:CD1	2:K:410:LEU:HD21	2.48	0.49
3:L:447:GLU:OE1	3:L:448:ALA:N	2.45	0.49
4:N:106:ASP:OD1	4:N:107:LEU:N	2.45	0.49
4:N:231:LYS:HA	4:N:234:ARG:CZ	2.43	0.49
4:N:733:ASN:HB2	4:N:734:PRO:HA	1.94	0.49
4:N:849:TYR:HB3	4:N:853:GLY:HA2	1.95	0.49
5:J:253:ARG:HA	5:J:256:ARG:HH21	1.78	0.49
5:J:443:LYS:HG2	5:J:444:VAL:N	2.26	0.49
8:C:147:THR:HA	8:C:214:ASP:OD2	2.13	0.49
8:C:226:ALA:HB2	8:C:598:ILE:HG13	1.95	0.49
8:C:494:LYS:HA	8:C:554:HIS:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:B:63:C:C2	17:B:64:C:C5	3.01	0.49
26:I:7:A:H2'	26:I:8:U:H6	1.77	0.49
26:I:101:C:H2'	26:I:102:A:H8	1.77	0.49
31:3:157:LEU:O	31:3:176:ASN:HA	2.13	0.49
1:A:650:ALA:HB1	1:A:702:GLY:HA3	1.95	0.49
1:A:1058:ALA:HB1	1:A:1103:LEU:HD23	1.94	0.49
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.13	0.49
1:A:1606:PHE:O	1:A:1609:TRP:N	2.46	0.49
1:A:1891:LEU:O	1:A:1986:MET:HA	2.12	0.49
2:K:28:ILE:HA	2:K:31:GLN:HB3	1.95	0.49
3:L:259:ILE:HG22	3:L:285:LEU:HD11	1.93	0.49
3:L:305:MET:HG2	3:L:337:LEU:HD22	1.94	0.49
4:N:721:ARG:O	4:N:725:ILE:HD12	2.12	0.49
8:C:360:ARG:NE	8:C:362:LYS:HD3	2.28	0.49
26:I:14:G:H2'	26:I:15:G:C8	2.47	0.49
26:I:63:U:C2'	26:I:64:U:C5'	2.86	0.49
38:H:48:U:C4	38:H:49:U:C2	3.00	0.49
1:A:651:ASP:HA	1:A:700:GLY:O	2.13	0.49
1:A:964:PHE:HZ	1:A:1081:TYR:HE1	1.60	0.49
6:E:95:PHE:CD1	6:E:133:SER:HB2	2.47	0.49
8:C:246:THR:HG1	8:C:901:GLU:CD	2.16	0.49
8:C:410:GLN:O	8:C:413:LEU:HB2	2.12	0.49
8:C:965:ASP:O	8:C:969:LYS:HG2	2.12	0.49
17:B:10:U:O2	17:B:156:G:N1	2.46	0.49
17:B:80:G:N1	17:B:82:A:N1	2.61	0.49
31:3:97:THR:O	31:3:98:GLU:C	2.51	0.49
1:A:166:LYS:HE3	1:A:167:TYR:CE1	2.48	0.48
1:A:287:GLU:HG2	1:A:288:GLU:H	1.77	0.48
1:A:382:GLU:H	1:A:382:GLU:CD	2.10	0.48
1:A:964:PHE:HZ	1:A:1081:TYR:CE1	2.30	0.48
1:A:1289:VAL:HG12	1:A:1290:ASP:O	2.13	0.48
1:A:1637:LYS:HG3	1:A:1639:PRO:HD3	1.94	0.48
1:A:1998:ARG:NH2	1:A:2043:PHE:O	2.46	0.48
2:K:52:ARG:HA	2:K:55:LEU:HD12	1.95	0.48
2:K:194:SER:OG	2:K:195:TRP:N	2.43	0.48
2:K:337:ARG:NH1	5:J:170:ASP:OD1	2.45	0.48
4:N:101:LYS:CE	4:N:108:LYS:HZ3	2.25	0.48
4:N:234:ARG:HD3	4:N:247:SER:OG	2.13	0.48
4:N:747:GLU:OE2	4:N:752:ASN:HB3	2.13	0.48
5:J:143:GLU:H	5:J:143:GLU:CD	2.15	0.48
8:C:202:ASP:OD1	8:C:206:LYS:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:608:GLN:NE2	8:C:641:GLU:OE2	2.47	0.48
16:F:84:C:H1'	16:F:85:C:C5	2.48	0.48
18:O:150:ASN:OD1	18:O:151:ILE:N	2.46	0.48
23:T:59:GLU:O	23:T:74:GLY:CA	2.59	0.48
38:H:68:U:H3'	38:H:68:U:H6	1.78	0.48
1:A:226:ARG:HH12	1:A:267:PRO:HG2	1.77	0.48
1:A:353:GLU:HG2	17:B:104:G:P	2.53	0.48
1:A:729:LEU:O	1:A:733:GLN:HB2	2.13	0.48
1:A:900:PHE:CD2	1:A:900:PHE:C	2.85	0.48
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.48	0.48
1:A:1603:ASN:O	1:A:1606:PHE:HB3	2.13	0.48
2:K:27:ASP:O	2:K:31:GLN:N	2.36	0.48
4:N:286:GLU:CG	4:N:287:SER:H	2.25	0.48
5:J:345:LYS:HB2	5:J:422:ASN:HA	1.95	0.48
6:E:103:LEU:HD11	6:E:105:PHE:HE2	1.79	0.48
8:C:109:LEU:HA	8:C:112:ASN:OD1	2.13	0.48
8:C:379:ILE:HA	8:C:382:TYR:CD2	2.48	0.48
8:C:387:TYR:HB3	8:C:396:LEU:HD21	1.95	0.48
8:C:679:GLU:OE1	8:C:806:GLY:HA3	2.13	0.48
8:C:721:GLN:O	8:C:724:SER:OG	2.26	0.48
17:B:62:G:C4	17:B:63:C:C5	3.01	0.48
38:H:1097:G:H2'	38:H:1098:C:H5	1.78	0.48
38:H:1138:G:O2'	38:H:1139:G:C8	2.50	0.48
1:A:131:LYS:NZ	1:A:553:ASN:HA	2.28	0.48
1:A:133:GLU:HG3	1:A:559:GLN:O	2.13	0.48
1:A:658:ASN:ND2	1:A:688:TYR:OH	2.46	0.48
1:A:674:MET:O	1:A:677:ILE:HB	2.14	0.48
1:A:911:ILE:O	1:A:912:LEU:C	2.52	0.48
1:A:1474:ARG:HH22	1:A:1499:ARG:HH12	1.60	0.48
1:A:1557:LEU:HA	1:A:1557:LEU:HD23	1.60	0.48
1:A:1646:ILE:HD11	16:F:49:A:N6	2.28	0.48
1:A:1815:LEU:O	1:A:1817:GLU:N	2.46	0.48
4:N:286:GLU:HB2	4:N:292:CYS:HA	1.94	0.48
8:C:397:LYS:NZ	8:C:413:LEU:HD11	2.28	0.48
17:B:97:U:O2	17:B:97:U:H2'	2.14	0.48
29:1:763:LEU:O	29:1:766:LEU:N	2.46	0.48
38:H:1116:A:O2'	38:H:1117:G:H5'	2.13	0.48
38:H:1120:G:H2'	38:H:1121:U:C6	2.45	0.48
1:A:300:LYS:H	1:A:493:MET:HG2	1.78	0.48
1:A:362:GLU:HB3	1:A:1209:LYS:HE2	1.96	0.48
1:A:540:THR:HG21	17:B:40:C:C4	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:ALA:O	1:A:649:LEU:N	2.46	0.48
1:A:773:SER:OG	1:A:774:ILE:HD12	2.14	0.48
1:A:965:LYS:HZ3	1:A:965:LYS:HB3	1.79	0.48
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.46	0.48
1:A:1111:SER:OG	1:A:1112:PHE:N	2.47	0.48
1:A:1216:ILE:H	1:A:1220:VAL:HG23	1.77	0.48
1:A:1339:LEU:O	1:A:1342:LEU:N	2.47	0.48
1:A:1861:THR:HG22	18:O:161:ILE:CG1	1.93	0.48
1:A:1964:PRO:HD3	1:A:2013:ARG:NH2	2.27	0.48
2:K:182:SER:O	2:K:190:VAL:HA	2.13	0.48
2:K:227:HIS:HE1	2:K:229:ASP:HB3	1.77	0.48
3:L:102:ILE:HA	3:L:105:ILE:HD12	1.94	0.48
4:N:252:GLU:HG2	4:N:256:LYS:HB2	1.94	0.48
38:H:145:G:H2'	38:H:146:A:H8	1.77	0.48
1:A:1393:GLU:OE1	1:A:1393:GLU:N	2.36	0.48
6:E:97:THR:HG23	6:E:99:ASN:H	1.79	0.48
8:C:142:LEU:HD11	8:C:218:HIS:HD2	1.76	0.48
8:C:354:TYR:HA	8:C:358:ASN:O	2.12	0.48
8:C:452:LYS:O	8:C:455:HIS:N	2.45	0.48
8:C:781:ASP:HA	8:C:788:LEU:HD11	1.95	0.48
16:F:46:U:C5'	16:F:46:U:C6	2.90	0.48
16:F:78:G:H2'	16:F:78:G:N3	2.28	0.48
26:I:36:A:C2	26:I:42:C:C2	3.00	0.48
27:D:635:GLU:N	27:D:670:LEU:O	2.47	0.48
38:H:1166:G:H8	38:H:1166:G:O5'	1.96	0.48
1:A:210:GLU:N	1:A:211:PRO:HD2	2.28	0.48
1:A:252:GLU:HA	1:A:256:GLU:HB2	1.95	0.48
1:A:461:LEU:HD23	8:C:403:ASN:HB3	1.96	0.48
1:A:930:ASN:CG	1:A:931:ALA:H	2.16	0.48
1:A:992:ASP:O	1:A:995:LEU:N	2.47	0.48
1:A:1197:ASN:O	1:A:1224:ARG:NH2	2.47	0.48
1:A:2018:ASN:O	1:A:2021:SER:OG	2.26	0.48
3:L:110:LYS:HG2	3:L:114:ASN:HD21	1.78	0.48
3:L:294:PHE:HE1	3:L:342:ARG:HH12	1.61	0.48
3:L:366:LYS:NZ	16:F:58:C:H41	2.12	0.48
4:N:673:GLN:O	4:N:677:ILE:HG13	2.12	0.48
5:J:235:TYR:HD2	7:M:90:ALA:HA	1.78	0.48
16:F:96:G:H2'	16:F:97:A:H8	1.78	0.48
26:I:62:G:H8	26:I:62:G:O5'	1.96	0.48
1:A:193:TYR:CZ	1:A:558:GLN:HB2	2.48	0.48
1:A:460:PRO:HB2	1:A:463:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:372:ILE:HD11	5:J:428:TRP:CH2	2.48	0.48
3:L:450:GLN:O	3:L:453:ASP:N	2.44	0.48
4:N:101:LYS:HE2	4:N:108:LYS:HZ3	1.78	0.48
5:J:448:GLN:HE21	5:J:452:LEU:HD11	1.79	0.48
8:C:245:VAL:HG11	8:C:295:ILE:HG22	1.95	0.48
8:C:338:SER:O	8:C:341:ILE:HG12	2.14	0.48
16:F:28:U:H2'	16:F:29:U:C5'	2.42	0.48
17:B:94:C:H3'	17:B:95:C:C5'	2.35	0.48
17:B:106:A:H2'	17:B:107:C:O4'	2.13	0.48
1:A:513:GLU:OE1	1:A:513:GLU:N	2.42	0.48
1:A:1574:PHE:CE1	1:A:1826:TYR:HB2	2.48	0.48
1:A:1629:LEU:HD22	1:A:1652:HIS:CE1	2.49	0.48
1:A:1661:ILE:O	1:A:1664:ASP:N	2.47	0.48
2:K:153:LEU:O	2:K:157:THR:HG23	2.14	0.48
2:K:390:LEU:HD22	5:J:428:TRP:HE1	1.79	0.48
3:L:431:ALA:HA	3:L:434:GLN:HG2	1.96	0.48
5:J:144:LEU:HB3	5:J:146:GLU:OE2	2.13	0.48
6:E:6:LEU:CD1	6:E:47:SER:HA	2.44	0.48
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.48	0.48
8:C:183:GLN:HE21	8:C:187:ARG:HG3	1.78	0.48
38:H:1162:U:O2'	38:H:1163:C:H5'	2.14	0.48
1:A:221:TRP:NE1	1:A:225:ARG:HD2	2.28	0.48
1:A:555:LYS:O	1:A:557:PHE:N	2.47	0.48
1:A:823:TRP:HE1	1:A:851:ARG:HD2	1.78	0.48
1:A:898:ILE:HD13	1:A:1002:GLU:HB3	1.96	0.48
1:A:1028:TRP:CG	1:A:1262:MET:HE1	2.48	0.48
1:A:1899:TRP:HZ3	1:A:1905:LEU:HB3	1.79	0.48
2:K:51:VAL:HG13	2:K:76:LEU:CD1	2.43	0.48
2:K:177:PRO:HB2	2:K:195:TRP:CD1	2.49	0.48
2:K:382:ASP:CG	2:K:383:GLU:H	2.17	0.48
4:N:709:SER:O	4:N:712:ASP:N	2.46	0.48
6:E:112:GLU:O	6:E:115:ASP:N	2.46	0.48
8:C:683:ASN:H	8:C:714:PRO:HG2	1.79	0.48
17:B:92:U:C4	17:B:93:G:C8	3.01	0.48
17:B:98:U:H2'	17:B:99:U:C5'	2.31	0.48
26:I:91:U:C2	26:I:142:G:N2	2.78	0.48
28:G:473:U:O2	28:G:473:U:H2'	2.13	0.48
1:A:269:ASP:N	1:A:273:ASP:OD2	2.47	0.48
1:A:293:VAL:HG22	1:A:294:ASN:H	1.77	0.48
1:A:618:SER:HB2	1:A:725:TYR:CE1	2.49	0.48
1:A:823:TRP:HE1	1:A:851:ARG:HH11	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:890:LEU:HD23	1:A:890:LEU:HA	1.65	0.48
1:A:958:LEU:HD21	1:A:995:LEU:HD12	1.95	0.48
1:A:963:VAL:HG21	3:L:280:ARG:HH12	1.79	0.48
1:A:1125:LEU:HD23	1:A:1125:LEU:HA	1.48	0.48
2:K:249:SER:HB3	2:K:252:GLU:HB2	1.95	0.48
2:K:316:GLN:NE2	2:K:320:SER:H	2.09	0.48
3:L:279:VAL:HG22	3:L:300:LYS:HA	1.95	0.48
4:N:245:ILE:O	4:N:248:ALA:HB3	2.14	0.48
4:N:892:LEU:O	4:N:896:MET:HG2	2.14	0.48
8:C:219:VAL:O	8:C:222:MET:HG2	2.14	0.48
8:C:460:GLY:HA3	8:C:461:LYS:HA	1.57	0.48
28:G:463:A:H2'	28:G:464:A:H8	1.78	0.48
1:A:654:HIS:CD2	1:A:658:ASN:HD21	2.31	0.47
1:A:898:ILE:CD1	1:A:1002:GLU:HB2	2.44	0.47
1:A:1052:THR:HG22	1:A:1246:ALA:CB	2.44	0.47
2:K:169:GLY:HA2	4:N:724:SER:OG	2.14	0.47
2:K:292:TRP:N	2:K:292:TRP:CD1	2.82	0.47
2:K:299:GLU:OE2	2:K:302:LEU:HB2	2.13	0.47
2:K:304:GLU:HB3	5:J:220:PRO:CB	2.44	0.47
2:K:336:ILE:O	2:K:339:GLY:N	2.41	0.47
5:J:145:HIS:O	5:J:147:ASP:N	2.46	0.47
16:F:57:U:H3	26:I:62:G:N2	2.10	0.47
17:B:41:A:H2'	17:B:42:A:H8	1.77	0.47
17:B:73:U:H2'	17:B:74:U:H6	1.79	0.47
26:I:24:A:C6	26:I:26:A:N6	2.81	0.47
26:I:24:A:H2'	26:I:26:A:C8	2.49	0.47
21:Q:34:PRO:C	21:Q:36:MET:H	2.17	0.47
28:G:475:U:H3'	28:G:475:U:H6	1.78	0.47
29:1:565:LEU:O	29:1:569:PHE:N	2.47	0.47
1:A:176:LEU:HD23	1:A:708:TRP:HE1	1.79	0.47
1:A:235:LYS:HB3	1:A:648:GLN:NE2	2.28	0.47
1:A:252:GLU:HG2	1:A:253:GLN:H	1.78	0.47
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.95	0.47
1:A:785:HIS:CD2	4:N:124:ASP:O	2.67	0.47
1:A:1389:TYR:HE2	1:A:1437:ILE:HD13	1.77	0.47
3:L:281:GLN:HE22	26:I:36:A:N6	2.12	0.47
3:L:336:GLU:O	3:L:339:LYS:N	2.46	0.47
6:E:10:ARG:H	6:E:14:HIS:CD2	2.31	0.47
7:M:59:GLU:O	7:M:60:PRO:C	2.52	0.47
8:C:154:VAL:HG21	8:C:177:TYR:HD2	1.79	0.47
8:C:780:PRO:HA	8:C:783:ILE:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:B:96:U:H2'	17:B:97:U:N1	2.27	0.47
17:B:130:A:H4'	17:B:131:A:O5'	2.13	0.47
26:I:19:U:O2'	26:I:20:A:P	2.73	0.47
26:I:52:G:H2'	26:I:53:U:C6	2.48	0.47
38:H:1093:C:C2	38:H:1094:G:C8	3.02	0.47
3:L:268:LEU:HD12	3:L:271:GLU:N	2.29	0.47
5:J:147:ASP:N	5:J:147:ASP:OD1	2.47	0.47
5:J:409:HIS:HA	5:J:414:ASP:OD1	2.14	0.47
8:C:320:PHE:HB2	8:C:429:PHE:HD2	1.80	0.47
8:C:761:ALA:O	8:C:765:VAL:HG23	2.14	0.47
8:C:857:LEU:HD23	8:C:940:VAL:HG21	1.96	0.47
17:B:52:G:C4	17:B:53:C:C5	3.03	0.47
26:I:22:G:C5	26:I:23:C:C5	3.01	0.47
38:H:139:G:C2'	38:H:140:G:O5'	2.62	0.47
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.45	0.47
1:A:814:ARG:NH2	4:N:106:ASP:OD1	2.43	0.47
1:A:1048:VAL:HG22	1:A:1250:VAL:HG22	1.97	0.47
1:A:1069:LEU:HB3	1:A:1116:TYR:OH	2.14	0.47
1:A:1536:LEU:HD23	1:A:1536:LEU:HA	1.59	0.47
1:A:1748:ILE:O	1:A:1749:SER:C	2.52	0.47
1:A:1769:SER:C	1:A:1771:THR:H	2.18	0.47
1:A:1862:VAL:HA	1:A:1871:ALA:O	2.15	0.47
3:L:298:VAL:HG12	3:L:302:MET:HG2	1.96	0.47
4:N:23:ALA:HB1	6:E:73:MET:HE1	1.96	0.47
4:N:733:ASN:HB2	4:N:734:PRO:O	2.14	0.47
7:M:65:LEU:HD23	7:M:65:LEU:HA	1.68	0.47
8:C:234:LEU:HD23	8:C:443:TYR:HB2	1.96	0.47
8:C:269:LYS:HG2	47:C:1500:GTP:N1	2.29	0.47
8:C:271:ASP:OD2	47:C:1500:GTP:N1	2.44	0.47
8:C:861:ILE:HG21	8:C:905:GLN:HB3	1.96	0.47
17:B:166:U:O2'	17:B:167:A:P	2.72	0.47
26:I:17:A:H2'	26:I:18:A:O4'	2.15	0.47
1:A:684:LYS:HG3	1:A:688:TYR:CE2	2.50	0.47
1:A:960:THR:O	1:A:962:ARG:NH1	2.47	0.47
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.49	0.47
1:A:1861:THR:HB	18:O:161:ILE:HG12	1.93	0.47
1:A:2056:ARG:HE	5:J:288:THR:HB	1.79	0.47
3:L:225:ILE:HG13	3:L:226:ALA:N	2.29	0.47
5:J:348:GLN:HG2	5:J:374:ASP:OD1	2.15	0.47
7:M:20:ILE:O	7:M:23:VAL:N	2.47	0.47
8:C:103:HIS:O	8:C:106:PHE:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:57:U:C2	26:I:62:G:N2	2.83	0.47
26:I:33:A:C4	26:I:45:A:C8	3.03	0.47
1:A:611:LYS:HE2	16:F:32:U:H5	1.78	0.47
1:A:630:LYS:O	1:A:633:VAL:N	2.48	0.47
1:A:687:ILE:HG21	1:A:703:PHE:HD2	1.80	0.47
1:A:954:ILE:O	1:A:957:TYR:N	2.47	0.47
1:A:1539:LEU:HD23	1:A:1539:LEU:HA	1.39	0.47
1:A:1705:SER:HB3	1:A:1709:TRP:CD1	2.49	0.47
2:K:376:TRP:CH2	2:K:386:LEU:HD23	2.49	0.47
5:J:285:GLN:HG2	5:J:293:TRP:HB2	1.96	0.47
5:J:353:ARG:HG3	5:J:442:MET:SD	2.54	0.47
8:C:486:VAL:CG1	8:C:564:ILE:HD11	2.44	0.47
8:C:507:SER:HB2	8:C:591:PHE:HB3	1.97	0.47
8:C:769:TYR:CE1	8:C:799:PHE:CE2	3.03	0.47
16:F:46:U:C6	16:F:46:U:C4'	2.98	0.47
17:B:63:C:H2'	17:B:64:C:H6	1.79	0.47
27:D:843:HIS:HA	27:D:876:GLY:HA2	1.96	0.47
28:G:485:A:C2'	28:G:486:A:OP2	2.63	0.47
29:1:873:HIS:O	29:1:875:ASP:N	2.43	0.47
38:H:65:A:C4	38:H:66:A:C8	3.03	0.47
38:H:1097:G:C6	38:H:1146:G:C6	3.02	0.47
1:A:143:ILE:HG13	1:A:144:ASN:N	2.29	0.47
1:A:307:GLU:O	1:A:311:LEU:HG	2.15	0.47
1:A:520:VAL:O	1:A:524:LYS:HG2	2.14	0.47
1:A:668:ARG:CG	16:F:27:U:C4'	2.79	0.47
1:A:1058:ALA:HB3	1:A:1105:ARG:HH21	1.79	0.47
1:A:1126:LEU:HD13	1:A:1134:LEU:HD12	1.97	0.47
1:A:1361:VAL:HG22	1:A:1403:SER:HB3	1.95	0.47
1:A:1462:ALA:O	1:A:1465:ARG:HB3	2.14	0.47
1:A:1682:THR:OG1	1:A:1702:THR:OG1	2.10	0.47
1:A:1710:GLU:HB3	1:A:1724:PHE:HB3	1.96	0.47
2:K:117:LEU:O	2:K:120:ALA:HB3	2.15	0.47
2:K:289:TRP:HB3	2:K:310:VAL:HG11	1.97	0.47
3:L:196:GLN:O	3:L:199:GLU:HB2	2.15	0.47
3:L:332:LYS:O	3:L:335:ALA:N	2.47	0.47
3:L:351:SER:HB2	4:N:132:ASN:HD21	1.80	0.47
4:N:5:SER:O	4:N:8:ASP:N	2.48	0.47
4:N:467:ALA:O	4:N:471:TRP:N	2.46	0.47
4:N:770:ASN:HB3	4:N:773:LEU:HD12	1.96	0.47
4:N:820:GLN:O	4:N:823:THR:OG1	2.13	0.47
5:J:428:TRP:HZ3	5:J:430:GLY:HA3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:105:PHE:CD2	6:E:105:PHE:N	2.80	0.47
8:C:142:LEU:HD23	8:C:142:LEU:HA	1.64	0.47
8:C:505:SER:O	8:C:508:GLU:HB2	2.14	0.47
17:B:8:U:O4	17:B:157:G:O6	2.32	0.47
17:B:28:G:C2'	17:B:29:G:H5''	2.45	0.47
17:B:73:U:C3'	17:B:74:U:C5'	2.90	0.47
17:B:96:U:OP1	17:B:96:U:H4'	2.15	0.47
26:I:26:A:H2'	26:I:27:U:C6	2.50	0.47
26:I:43:C:C2'	26:I:44:G:H5'	2.45	0.47
22:R:53:LYS:O	22:R:74:GLU:HA	2.15	0.47
28:G:472:U:O2	28:G:472:U:C2'	2.63	0.47
36:Y:167:VAL:O	36:Y:171:GLY:N	2.46	0.47
38:H:1094:G:C6	38:H:1149:G:C6	3.02	0.47
38:H:1165:C:C2	38:H:1166:G:N7	2.83	0.47
1:A:593:LEU:HA	1:A:593:LEU:HD23	1.74	0.47
1:A:898:ILE:CD1	1:A:1002:GLU:CB	2.93	0.47
1:A:899:PRO:CD	1:A:1006:ARG:HH22	2.27	0.47
1:A:953:ARG:HG2	1:A:957:TYR:CE2	2.50	0.47
1:A:1211:SER:HA	1:A:1257:ASN:HD21	1.79	0.47
1:A:1655:GLN:O	1:A:1658:HIS:N	2.48	0.47
1:A:1802:MET:O	1:A:1805:ILE:N	2.47	0.47
3:L:350:ILE:HG13	3:L:351:SER:N	2.29	0.47
4:N:737:VAL:HA	4:N:767:PHE:HE2	1.79	0.47
5:J:144:LEU:HB3	5:J:146:GLU:HG2	1.95	0.47
5:J:368:LEU:HD13	5:J:370:LEU:HG	1.97	0.47
8:C:195:GLY:HA3	8:C:212:PHE:O	2.14	0.47
8:C:199:LEU:HD12	8:C:208:ARG:O	2.15	0.47
8:C:600:GLU:OE1	8:C:935:LYS:HE3	2.15	0.47
26:I:62:G:N2	26:I:63:U:C2	2.83	0.47
27:D:1685:THR:O	27:D:1697:PRO:HA	2.15	0.47
28:G:473:U:H4'	28:G:474:U:OP1	2.14	0.47
29:1:389:GLY:O	29:1:391:GLU:N	2.48	0.47
38:H:1126:G:O2'	38:H:1127:A:H8	1.97	0.47
1:A:221:TRP:CZ2	1:A:691:PHE:HB3	2.50	0.47
1:A:974:ASN:HD22	1:A:977:ASN:HB2	1.79	0.47
1:A:1048:VAL:O	1:A:1171:LEU:HD12	2.15	0.47
1:A:1580:GLY:HA3	3:L:389:ASN:ND2	2.30	0.47
1:A:1630:THR:HB	1:A:1654:TRP:CE3	2.50	0.47
1:A:1762:ASP:HB3	1:A:1765:SER:OG	2.15	0.47
1:A:1863:HIS:CE1	1:A:1864:LYS:O	2.68	0.47
3:L:399:THR:HB	3:L:407:GLU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:483:ASN:O	4:N:487:GLN:CB	2.63	0.47
6:E:80:MET:HG3	6:E:80:MET:O	2.15	0.47
16:F:84:C:H1'	16:F:85:C:H5	1.79	0.47
17:B:48:G:C4	17:B:49:U:C5	3.03	0.47
17:B:95:C:O2'	17:B:96:U:H1'	2.14	0.47
26:I:7:A:H2'	26:I:8:U:C6	2.50	0.47
26:I:8:U:H2'	26:I:9:G:H8	1.80	0.47
28:G:505:A:O3'	28:G:506:U:O4'	2.33	0.47
28:G:506:U:OP1	28:G:506:U:H4'	2.15	0.47
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.97	0.47
1:A:280:LEU:HD23	1:A:281:TYR:CE2	2.50	0.47
1:A:488:ARG:NH1	17:B:81:A:N6	2.63	0.47
1:A:759:ARG:HG3	1:A:760:ASN:N	2.29	0.47
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	1.95	0.47
2:K:225:ASP:OD1	2:K:226:TRP:N	2.48	0.47
2:K:266:ARG:CB	2:K:285:HIS:HB2	2.44	0.47
2:K:287:MET:HG2	2:K:308:LYS:O	2.15	0.47
2:K:320:SER:CB	2:K:337:ARG:HH22	2.28	0.47
3:L:225:ILE:HG13	3:L:226:ALA:H	1.80	0.47
4:N:844:TRP:O	4:N:848:THR:HG23	2.15	0.47
5:J:348:GLN:NE2	5:J:375:ASP:HA	2.30	0.47
8:C:137:GLY:N	8:C:232:SER:OG	2.45	0.47
17:B:164:C:O2	17:B:164:C:H2'	2.14	0.47
1:A:190:LYS:H	1:A:204:GLU:CD	2.18	0.46
1:A:300:LYS:N	1:A:493:MET:HG2	2.30	0.46
1:A:396:ARG:NH1	8:C:667:GLU:OE2	2.48	0.46
1:A:603:LYS:HZ1	16:F:43:C:H5'	1.72	0.46
1:A:651:ASP:HB3	1:A:700:GLY:CA	2.45	0.46
1:A:895:PHE:HE2	1:A:1073:ILE:HG13	1.80	0.46
1:A:900:PHE:HD2	1:A:900:PHE:C	2.18	0.46
1:A:1421:GLY:HA2	1:A:1718:HIS:CD2	2.50	0.46
1:A:1474:ARG:NH2	1:A:1499:ARG:HH12	2.13	0.46
1:A:1553:ILE:O	1:A:1556:ILE:N	2.46	0.46
1:A:1621:VAL:HG12	1:A:1622:GLY:N	2.31	0.46
1:A:2393:LEU:O	1:A:2397:GLU:CB	2.63	0.46
3:L:379:PHE:CZ	4:N:144:LYS:HD3	2.50	0.46
4:N:764:LEU:HD21	4:N:774:TRP:CH2	2.50	0.46
6:E:71:ASP:HA	6:E:76:LEU:HD13	1.96	0.46
7:M:8:ALA:HB1	7:M:80:PHE:HD2	1.80	0.46
8:C:387:TYR:O	8:C:391:MET:N	2.48	0.46
8:C:544:LEU:HD23	8:C:562:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:885:GLY:CA	8:C:907:PRO:HD3	2.45	0.46
31:3:1295:GLY:O	31:3:1299:ILE:N	2.47	0.46
1:A:131:LYS:HZ3	1:A:553:ASN:HA	1.78	0.46
1:A:472:ASN:HB2	8:C:390:SER:OG	2.16	0.46
1:A:671:TYR:HD2	17:B:101:C:O2'	1.96	0.46
1:A:982:TYR:HD2	1:A:1106:GLY:HA3	1.81	0.46
1:A:1176:GLU:O	1:A:1179:GLY:N	2.48	0.46
2:K:236:SER:OG	2:K:244:LYS:HB2	2.16	0.46
2:K:274:HIS:CD2	2:K:276:SER:H	2.34	0.46
2:K:327:MET:O	2:K:351:PRO:HG3	2.14	0.46
3:L:225:ILE:O	3:L:325:ARG:NH1	2.41	0.46
3:L:329:LEU:HA	3:L:329:LEU:HD23	1.65	0.46
4:N:864:ASP:OD1	4:N:889:ARG:NH2	2.48	0.46
5:J:352:ILE:O	5:J:356:LEU:HG	2.15	0.46
8:C:220:ASN:HB3	8:C:651:TYR:HB2	1.97	0.46
8:C:598:ILE:HG22	8:C:933:TRP:HZ3	1.80	0.46
8:C:727:THR:HG23	8:C:729:GLY:H	1.79	0.46
8:C:792:LYS:O	8:C:796:ILE:HG22	2.15	0.46
16:F:10:A:H61	16:F:16:C:N4	2.06	0.46
17:B:29:G:C6	17:B:30:A:C6	3.03	0.46
17:B:44:A:C2'	17:B:45:A:C8	2.71	0.46
17:B:48:G:H2'	17:B:49:U:H6	1.79	0.46
17:B:66:A:C4	17:B:67:U:C5	3.03	0.46
26:I:3:C:H2'	26:I:4:C:C6	2.51	0.46
26:I:35:G:N1	26:I:36:A:C2	2.82	0.46
38:H:1143:C:H4'	38:H:1144:U:H2'	1.96	0.46
1:A:177:GLU:HA	1:A:708:TRP:HZ2	1.81	0.46
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.30	0.46
1:A:1889:LEU:HD21	1:A:1991:ILE:HD12	1.98	0.46
2:K:316:GLN:CD	2:K:321:LEU:H	2.18	0.46
6:E:63:ASP:HB2	6:E:66:GLU:HG2	1.98	0.46
17:B:76:U:O2'	17:B:78:A:H5'	2.15	0.46
26:I:150:G:O2'	26:I:152:A:OP1	2.32	0.46
20:P:50:GLU:O	20:P:79:LYS:HA	2.14	0.46
38:H:1098:C:HO2'	38:H:1099:G:C5'	2.28	0.46
1:A:924:ALA:O	4:N:154:PRO:HG3	2.14	0.46
1:A:1041:VAL:HG11	1:A:1253:LYS:CA	2.45	0.46
1:A:1608:LEU:O	1:A:1609:TRP:C	2.54	0.46
1:A:1967:ALA:O	1:A:1970:SER:OG	2.17	0.46
2:K:167:LEU:O	4:N:728:ARG:NH2	2.48	0.46
2:K:390:LEU:HB2	5:J:428:TRP:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:441:ILE:HD11	2:K:457:TRP:NE1	2.30	0.46
4:N:381:TYR:O	4:N:385:LYS:CB	2.63	0.46
4:N:730:LEU:HA	4:N:739:PHE:CD2	2.50	0.46
4:N:829:GLU:HA	4:N:832:LEU:HD12	1.97	0.46
7:M:61:ILE:O	7:M:65:LEU:HG	2.16	0.46
17:B:46:C:C2	17:B:47:U:C5	3.03	0.46
1:A:867:ILE:HG21	1:A:1101:TYR:CD1	2.50	0.46
1:A:1204:ARG:HH21	1:A:1260:PHE:HA	1.80	0.46
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.98	0.46
1:A:1368:GLN:NE2	1:A:1389:TYR:OH	2.49	0.46
1:A:1458:TRP:NE1	1:A:1489:PRO:HD2	2.30	0.46
1:A:2065:ARG:NH2	1:A:2066:LYS:HE2	2.31	0.46
2:K:205:GLN:HB2	2:K:206:THR:HG23	1.98	0.46
4:N:133:LYS:NZ	26:I:49:U:OP1	2.41	0.46
6:E:23:THR:OG1	6:E:24:LYS:HG3	2.15	0.46
8:C:602:VAL:HG21	8:C:932:PHE:CD2	2.50	0.46
26:I:63:U:C2'	26:I:64:U:H5''	2.44	0.46
38:H:120:G:H4'	38:H:121:C:O4'	2.15	0.46
1:A:239:PHE:CZ	1:A:655:TYR:CD2	3.04	0.46
1:A:383:TYR:O	1:A:386:ALA:N	2.40	0.46
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.96	0.46
1:A:1068:ARG:O	1:A:1069:LEU:C	2.54	0.46
1:A:1890:PHE:CD1	1:A:1920:LEU:HD11	2.51	0.46
1:A:1944:LEU:HA	1:A:1944:LEU:HD23	1.71	0.46
2:K:244:LYS:HB3	2:K:246:PHE:CE2	2.50	0.46
2:K:269:SER:H	2:K:284:SER:HA	1.80	0.46
3:L:294:PHE:HE1	3:L:342:ARG:NH1	2.13	0.46
4:N:688:ARG:NE	4:N:712:ASP:HB2	2.29	0.46
4:N:723:ARG:O	4:N:726:LEU:N	2.49	0.46
5:J:375:ASP:OD1	5:J:376:GLY:N	2.49	0.46
8:C:144:SER:OG	8:C:146:LYS:HG3	2.14	0.46
8:C:680:SER:OG	8:C:681:CYS:N	2.49	0.46
8:C:968:MET:O	8:C:972:ARG:HG3	2.16	0.46
26:I:1:A:C2	26:I:2:U:C2	3.04	0.46
26:I:1:A:N3	26:I:1:A:H2'	2.30	0.46
29:1:581:LYS:O	29:1:585:ALA:N	2.47	0.46
32:4:108:ALA:O	32:4:154:TYR:HA	2.16	0.46
1:A:510:PRO:HB3	1:A:514:TYR:HD2	1.79	0.46
1:A:785:HIS:CE1	4:N:125:ALA:HA	2.51	0.46
1:A:1267:VAL:HG22	1:A:1302:LEU:CD2	2.45	0.46
1:A:1309:ILE:O	1:A:1312:PHE:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:197:ILE:O	3:L:201:ASN:ND2	2.49	0.46
3:L:268:LEU:O	3:L:271:GLU:N	2.24	0.46
8:C:189:LEU:HD12	8:C:189:LEU:O	2.16	0.46
8:C:286:LEU:O	8:C:290:HIS:HB2	2.15	0.46
8:C:291:ILE:O	8:C:295:ILE:HG23	2.16	0.46
17:B:43:G:C2	17:B:44:A:C5	3.03	0.46
27:D:1482:GLY:HA3	21:Q:143:ARG:O	2.15	0.46
27:D:1677:THR:O	27:D:1710:ALA:HA	2.15	0.46
23:T:11:VAL:O	25:V:31:GLY:HA3	2.15	0.46
1:A:228:LYS:NZ	1:A:698:GLY:CA	2.76	0.46
1:A:309:SER:HA	1:A:479:LEU:HD11	1.98	0.46
1:A:487:ASN:OD1	1:A:488:ARG:N	2.49	0.46
1:A:603:LYS:HZ2	16:F:43:C:C4'	2.29	0.46
1:A:1029:THR:HG22	1:A:1260:PHE:HZ	1.81	0.46
1:A:1118:GLY:HA3	1:A:1163:ARG:HH22	1.81	0.46
1:A:1440:ILE:O	1:A:1442:ARG:N	2.49	0.46
1:A:1739:ARG:HD2	1:A:1751:TYR:CG	2.50	0.46
6:E:95:PHE:C	6:E:97:THR:H	2.19	0.46
8:C:294:ASN:O	8:C:297:SER:OG	2.31	0.46
8:C:462:SER:CB	8:C:588:GLN:HB3	2.45	0.46
8:C:576:THR:HG21	8:C:592:PHE:H	1.81	0.46
8:C:605:ILE:HD11	8:C:673:PRO:HA	1.97	0.46
26:I:141:G:H2'	26:I:142:G:H5'	1.97	0.46
1:A:152:LYS:HG2	1:A:584:HIS:CD2	2.50	0.46
1:A:1123:LEU:HD23	1:A:1123:LEU:HA	1.51	0.46
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.31	0.46
2:K:413:CYS:SG	2:K:443:LEU:HD13	2.56	0.46
8:C:449:PHE:CE2	8:C:453:THR:HG21	2.51	0.46
8:C:706:LEU:HD23	8:C:825:VAL:HA	1.98	0.46
16:F:46:U:C4	16:F:47:A:N1	2.83	0.46
26:I:33:A:C6	26:I:45:A:C8	3.04	0.46
21:Q:16:THR:HA	21:Q:25:VAL:O	2.16	0.46
1:A:574:GLN:O	1:A:577:ASN:HB2	2.15	0.46
1:A:795:ALA:O	1:A:796:ASN:HB2	2.16	0.46
1:A:1023:LEU:HD13	1:A:1451:PHE:CE1	2.50	0.46
1:A:1271:PRO:HA	1:A:1298:ALA:HB2	1.98	0.46
1:A:1625:VAL:O	1:A:1633:PHE:HA	2.16	0.46
2:K:290:ARG:CB	2:K:292:TRP:HE1	2.29	0.46
2:K:364:VAL:HG13	2:K:376:TRP:HB2	1.98	0.46
4:N:798:LEU:HB3	4:N:803:ASN:ND2	2.31	0.46
8:C:395:LYS:O	8:C:399:LEU:HG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:716:ASP:OD2	8:C:718:LYS:HB3	2.16	0.46
8:C:834:MET:O	8:C:838:ILE:HG22	2.15	0.46
17:B:46:C:H2'	17:B:47:U:H6	1.80	0.46
18:O:212:VAL:HG23	18:O:213:SER:H	1.80	0.46
26:I:36:A:C2	26:I:42:C:N3	2.84	0.46
26:I:64:U:H3'	26:I:64:U:H6	1.81	0.46
1:A:1679:GLU:OE2	1:A:1706:VAL:HA	2.16	0.45
2:K:179:SER:HA	2:K:441:ILE:HG21	1.96	0.45
4:N:4:PRO:O	4:N:7:LEU:HB2	2.16	0.45
4:N:104:PHE:O	4:N:108:LYS:HG2	2.16	0.45
4:N:249:ARG:O	4:N:253:LYS:HG3	2.16	0.45
8:C:287:LYS:HZ2	8:C:291:ILE:HD11	1.81	0.45
8:C:458:ILE:O	8:C:590:LYS:HG3	2.15	0.45
8:C:950:PHE:CE2	8:C:952:PRO:HA	2.52	0.45
17:B:73:U:C2	17:B:74:U:C5	3.05	0.45
26:I:6:U:C2	26:I:7:A:N7	2.84	0.45
26:I:22:G:C5	26:I:52:G:N1	2.84	0.45
31:3:379:VAL:O	31:3:390:LYS:HA	2.16	0.45
38:H:1140:U:H2'	38:H:1141:C:C6	2.50	0.45
1:A:182:PRO:HD3	1:A:704:TRP:CZ2	2.52	0.45
1:A:814:ARG:HH21	4:N:107:LEU:HD13	1.81	0.45
1:A:1104:ILE:HG22	1:A:1107:LEU:HG	1.98	0.45
1:A:1848:ILE:HB	1:A:1930:PRO:HA	1.97	0.45
1:A:1863:HIS:CB	18:O:159:ASP:N	2.79	0.45
2:K:388:GLN:HB2	5:J:462:HIS:CD2	2.51	0.45
3:L:268:LEU:HG	3:L:271:GLU:OE1	2.17	0.45
3:L:376:LYS:HA	3:L:376:LYS:HD2	1.70	0.45
4:N:144:LYS:O	4:N:145:THR:OG1	2.25	0.45
5:J:273:LYS:NZ	26:I:14:G:OP2	2.40	0.45
5:J:447:ASP:OD1	5:J:450:SER:N	2.49	0.45
8:C:501:ILE:HD13	8:C:570:ALA:HB2	1.98	0.45
8:C:925:LEU:HA	8:C:925:LEU:HD23	1.74	0.45
8:C:962:LEU:O	8:C:965:ASP:N	2.48	0.45
16:F:71:G:H2'	16:F:72:C:C6	2.51	0.45
17:B:71:A:H2'	17:B:72:C:H6	1.81	0.45
17:B:93:G:H2'	17:B:94:C:H1'	1.97	0.45
17:B:96:U:C3'	17:B:97:U:C6	2.98	0.45
26:I:33:A:C5	26:I:45:A:C8	3.04	0.45
26:I:33:A:H2'	26:I:34:G:O4'	2.15	0.45
31:3:820:VAL:HA	31:3:828:VAL:HA	1.98	0.45
1:A:208:VAL:HG11	1:A:213:TYR:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:LEU:HD21	1:A:289:ASP:HB3	1.98	0.45
1:A:794:LYS:HB3	1:A:854:ARG:NH1	2.31	0.45
1:A:1066:LEU:O	1:A:1067:ASN:C	2.54	0.45
1:A:1450:GLU:O	1:A:1451:PHE:C	2.54	0.45
1:A:1502:LEU:HA	1:A:1502:LEU:HD23	1.73	0.45
1:A:1645:LEU:HD23	1:A:1648:ILE:HD12	1.98	0.45
4:N:667:CYS:HA	4:N:670:PHE:CD2	2.49	0.45
4:N:686:MET:O	4:N:689:GLU:HB3	2.15	0.45
4:N:691:TYR:HB3	4:N:708:LEU:HD12	1.99	0.45
4:N:723:ARG:HA	4:N:726:LEU:HD12	1.99	0.45
6:E:40:MET:O	6:E:43:ASP:HB3	2.16	0.45
6:E:85:PHE:HE1	6:E:90:HIS:HD1	1.64	0.45
7:M:110:ILE:O	7:M:113:GLN:N	2.50	0.45
8:C:106:PHE:O	8:C:109:LEU:HB2	2.16	0.45
8:C:179:ASP:HA	8:C:184:GLU:OE1	2.17	0.45
8:C:366:ASN:OD1	8:C:367:VAL:HG23	2.15	0.45
8:C:760:LEU:O	8:C:764:ASN:N	2.47	0.45
8:C:775:ILE:HG22	8:C:777:ASP:HB2	1.98	0.45
8:C:787:LEU:HD11	8:C:825:VAL:HG11	1.98	0.45
8:C:971:ARG:HA	8:C:974:LYS:HB2	1.99	0.45
16:F:35:A:N1	16:F:46:U:O2	2.49	0.45
17:B:91:U:C3'	17:B:92:U:C5'	2.95	0.45
28:G:508:U:H3'	28:G:508:U:OP2	2.15	0.45
1:A:770:MET:HE1	1:A:775:ARG:HA	1.98	0.45
1:A:883:PHE:O	1:A:887:VAL:HG23	2.17	0.45
1:A:963:VAL:O	1:A:964:PHE:HD1	1.93	0.45
1:A:1676:LEU:O	1:A:1709:TRP:CH2	2.69	0.45
3:L:446:SER:HA	3:L:449:ASN:HD22	1.81	0.45
5:J:348:GLN:NE2	5:J:374:ASP:OD2	2.49	0.45
7:M:5:ASN:HD21	7:M:61:ILE:HG21	1.81	0.45
17:B:101:C:C2'	17:B:102:C:H5'	2.46	0.45
36:Y:167:VAL:O	36:Y:171:GLY:HA2	2.17	0.45
38:H:1139:G:C6	38:H:1140:U:C4	3.04	0.45
1:A:681:LYS:HE2	16:F:1:G:O6	2.17	0.45
1:A:753:TYR:CZ	6:E:37:ARG:HD3	2.51	0.45
1:A:886:MET:O	1:A:887:VAL:C	2.53	0.45
1:A:916:LEU:HD23	1:A:916:LEU:HA	1.61	0.45
1:A:1590:LEU:CB	1:A:1595:ARG:HH21	2.29	0.45
1:A:1912:LYS:O	1:A:1916:GLU:HG2	2.15	0.45
1:A:1995:TRP:CE3	1:A:2007:ARG:HD2	2.52	0.45
1:A:2080:LYS:HA	1:A:2083:ILE:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:203:ILE:O	3:L:206:ASN:N	2.50	0.45
3:L:206:ASN:O	3:L:209:LYS:HB3	2.16	0.45
3:L:424:THR:HG22	3:L:425:SER:N	2.32	0.45
4:N:733:ASN:HB2	4:N:734:PRO:CA	2.46	0.45
8:C:292:ILE:HG22	8:C:296:ASN:HD21	1.81	0.45
27:D:2101:LEU:O	27:D:2114:ILE:HA	2.16	0.45
1:A:1316:ILE:O	1:A:1317:ARG:C	2.54	0.45
2:K:118:ILE:HA	2:K:121:ARG:HD2	1.99	0.45
3:L:195:THR:O	3:L:198:LEU:HB3	2.16	0.45
3:L:344:LEU:HD23	3:L:344:LEU:HA	1.82	0.45
8:C:616:PRO:O	8:C:619:LEU:HB2	2.17	0.45
16:F:11:U:C2'	16:F:12:U:C5'	2.92	0.45
16:F:66:C:H2'	16:F:67:C:C6	2.52	0.45
17:B:71:A:C4	17:B:72:C:C5	3.04	0.45
26:I:48:U:H2'	26:I:49:U:H6	1.81	0.45
1:A:249:LEU:HD13	1:A:254:HIS:HB2	1.98	0.45
1:A:668:ARG:CD	16:F:27:U:H4'	2.45	0.45
1:A:1651:ALA:CA	16:F:49:A:OP2	2.63	0.45
1:A:1907:GLN:HG2	18:O:169:ILE:HA	1.98	0.45
2:K:135:ARG:NH2	2:K:318:ASP:OD2	2.47	0.45
2:K:267:ARG:O	2:K:284:SER:HB2	2.16	0.45
2:K:316:GLN:HA	2:K:357:TRP:NE1	2.31	0.45
2:K:392:HIS:HB3	2:K:416:ASP:HB2	1.98	0.45
3:L:399:THR:HG22	3:L:409:GLY:HA2	1.98	0.45
8:C:315:SER:OG	47:C:1500:GTP:O6	2.34	0.45
8:C:584:GLU:O	8:C:588:GLN:HG2	2.17	0.45
16:F:43:C:O2'	16:F:44:A:H8	2.00	0.45
17:B:135:G:N1	17:B:136:G:N2	2.65	0.45
26:I:150:G:H2'	26:I:151:G:H5''	1.98	0.45
1:A:152:LYS:HE3	1:A:584:HIS:NE2	2.31	0.45
1:A:194:HIS:HB3	1:A:198:ALA:N	2.31	0.45
1:A:657:LEU:HA	1:A:660:ILE:CD1	2.47	0.45
1:A:1033:ASN:O	1:A:1035:LEU:N	2.50	0.45
1:A:1652:HIS:CD2	16:F:48:C:H2'	2.48	0.45
2:K:161:ARG:O	2:K:164:ASN:HB3	2.17	0.45
2:K:173:VAL:HG21	2:K:461:ILE:HD12	1.99	0.45
3:L:264:LYS:HA	3:L:282:GLU:O	2.17	0.45
6:E:118:GLU:OE2	6:E:122:ARG:NE	2.50	0.45
8:C:116:THR:HG22	8:C:117:ARG:N	2.32	0.45
8:C:128:ASN:HB3	8:C:557:HIS:CE1	2.52	0.45
8:C:397:LYS:O	8:C:400:LEU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:B:98:U:C5	17:B:99:U:C4	3.01	0.45
20:P:33:GLN:O	20:P:45:LEU:HA	2.16	0.45
1:A:850:GLY:O	1:A:852:LEU:N	2.50	0.45
1:A:933:GLU:O	1:A:936:GLU:N	2.49	0.45
1:A:1014:LYS:HE3	1:A:1144:PHE:HD1	1.79	0.45
1:A:1177:ASP:N	1:A:1177:ASP:OD1	2.49	0.45
1:A:1198:SER:HB2	1:A:1215:LEU:HD13	1.99	0.45
1:A:1371:VAL:O	1:A:1374:GLY:N	2.50	0.45
1:A:2035:LYS:HD2	1:A:2038:HIS:CD2	2.52	0.45
2:K:204:SER:C	2:K:206:THR:H	2.20	0.45
3:L:240:GLN:O	3:L:243:ALA:HB3	2.17	0.45
4:N:755:GLN:O	4:N:758:LEU:N	2.50	0.45
5:J:237:THR:OG1	5:J:240:GLU:HG2	2.17	0.45
5:J:408:LEU:HD11	16:F:84:C:N4	2.31	0.45
6:E:41:ILE:O	6:E:44:GLU:N	2.50	0.45
8:C:196:SER:O	8:C:212:PHE:HB2	2.17	0.45
8:C:469:TRP:H	8:C:490:SER:HB2	1.80	0.45
8:C:841:LEU:O	8:C:844:LYS:N	2.50	0.45
17:B:22:G:O6	17:B:149:U:O4	2.35	0.45
38:H:1139:G:H2'	38:H:1140:U:C5	2.51	0.45
38:H:1152:U:H2'	38:H:1153:C:H6	1.80	0.45
1:A:681:LYS:HG2	1:A:685:HIS:NE2	2.32	0.45
1:A:964:PHE:CZ	1:A:1081:TYR:CE1	3.05	0.45
1:A:1201:TYR:HB2	1:A:1224:ARG:NH2	2.30	0.45
1:A:1236:THR:OG1	1:A:1237:SER:N	2.50	0.45
1:A:1458:TRP:O	1:A:1461:TYR:HB3	2.17	0.45
1:A:1795:LYS:N	1:A:1796:PRO:HD2	2.32	0.45
1:A:1992:TYR:HD1	1:A:2004:ALA:HB1	1.82	0.45
1:A:1993:ASP:OD2	1:A:2040:TRP:N	2.49	0.45
2:K:48:ASP:O	2:K:52:ARG:CB	2.65	0.45
2:K:68:ASP:OD1	2:K:69:VAL:N	2.45	0.45
2:K:397:THR:OG1	2:K:413:CYS:O	2.13	0.45
3:L:373:ARG:O	3:L:376:LYS:N	2.43	0.45
3:L:395:LYS:HE2	4:N:222:ASP:OD1	2.17	0.45
4:N:159:LEU:HD23	4:N:159:LEU:HA	1.66	0.45
4:N:666:ILE:HG22	4:N:667:CYS:N	2.28	0.45
4:N:678:TYR:HA	4:N:681:MET:HB2	1.99	0.45
4:N:723:ARG:O	4:N:726:LEU:HB2	2.17	0.45
8:C:769:TYR:CE2	8:C:772:ASN:HB2	2.52	0.45
8:C:769:TYR:HB2	8:C:771:GLY:N	2.32	0.45
8:C:865:ASP:HB2	8:C:931:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:945:LEU:HD12	8:C:945:LEU:O	2.17	0.45
16:F:81:G:N2	26:I:1:A:N3	2.65	0.45
16:F:82:A:O2'	16:F:83:A:OP2	2.32	0.45
26:I:11:A:C4	26:I:12:C:C5	3.05	0.45
1:A:143:ILE:HD13	1:A:570:GLN:NE2	2.32	0.44
1:A:1567:PHE:HE1	1:A:1827:GLN:HG3	1.82	0.44
1:A:1817:GLU:O	1:A:1820:ARG:N	2.50	0.44
2:K:232:ASN:O	2:K:248:TYR:N	2.40	0.44
2:K:410:LEU:HA	2:K:410:LEU:HD23	1.39	0.44
3:L:249:LEU:O	3:L:253:ARG:HG2	2.17	0.44
5:J:141:ASN:HB2	5:J:144:LEU:HD12	1.98	0.44
5:J:330:ASN:O	5:J:332:GLU:N	2.32	0.44
8:C:879:LEU:O	8:C:883:ARG:HG2	2.17	0.44
8:C:944:VAL:HG23	8:C:945:LEU:HG	1.98	0.44
17:B:17:C:O2'	17:B:18:A:OP2	2.31	0.44
17:B:32:G:C5'	17:B:33:U:OP2	2.65	0.44
17:B:98:U:H2'	17:B:99:U:H6	1.81	0.44
26:I:47:A:C4	26:I:48:U:C5	3.04	0.44
1:A:158:LYS:HG3	1:A:159:LYS:N	2.32	0.44
1:A:259:GLU:HG3	1:A:260:PRO:HD2	1.99	0.44
1:A:939:LEU:HA	1:A:939:LEU:HD23	1.78	0.44
1:A:1144:PHE:CE2	1:A:1145:MET:HE2	2.52	0.44
1:A:1312:PHE:CD1	1:A:1342:LEU:HD13	2.52	0.44
1:A:2003:THR:OG1	1:A:2004:ALA:N	2.51	0.44
2:K:44:ILE:CG2	2:K:73:ARG:HE	2.30	0.44
2:K:68:ASP:HB2	16:F:74:U:H4'	1.99	0.44
3:L:217:TYR:O	3:L:220:SER:OG	2.16	0.44
6:E:53:VAL:O	6:E:55:ASN:N	2.49	0.44
7:M:65:LEU:O	7:M:68:PRO:HD2	2.17	0.44
8:C:176:ARG:HD3	8:C:179:ASP:OD2	2.17	0.44
8:C:292:ILE:O	8:C:295:ILE:HG12	2.17	0.44
26:I:52:G:C2	26:I:53:U:C4	3.05	0.44
23:T:10:MET:HA	25:V:30:ARG:C	2.38	0.44
38:H:141:A:H2'	38:H:142:C:C6	2.52	0.44
1:A:140:ARG:O	1:A:143:ILE:HG12	2.17	0.44
1:A:375:PHE:CE2	8:C:954:LEU:HD23	2.52	0.44
1:A:750:LEU:HG	1:A:751:ASP:N	2.31	0.44
1:A:958:LEU:HD23	1:A:958:LEU:HA	1.61	0.44
1:A:1621:VAL:HG12	1:A:1622:GLY:H	1.82	0.44
1:A:1709:TRP:O	1:A:1728:ILE:HA	2.17	0.44
1:A:1893:ILE:HD13	1:A:1978:VAL:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:201:VAL:C	2:K:202:LEU:HD12	2.37	0.44
4:N:162:LEU:O	4:N:166:ARG:HG2	2.18	0.44
4:N:364:PHE:O	4:N:368:SER:N	2.51	0.44
4:N:730:LEU:HD12	4:N:739:PHE:HD2	1.82	0.44
4:N:747:GLU:HG3	4:N:751:GLY:O	2.17	0.44
5:J:300:GLN:O	5:J:303:LEU:HB3	2.17	0.44
8:C:113:ILE:HG12	8:C:549:TYR:CD1	2.52	0.44
8:C:271:ASP:HB3	8:C:318:LEU:HD12	2.00	0.44
8:C:282:MET:HB2	8:C:370:TYR:HE1	1.83	0.44
16:F:46:U:C6	16:F:46:U:C3'	2.99	0.44
17:B:28:G:C2'	17:B:29:G:C5'	2.95	0.44
26:I:15:G:C2	26:I:16:A:C8	3.06	0.44
27:D:521:ALA:O	27:D:672:ALA:HA	2.17	0.44
1:A:251:TYR:O	1:A:255:ILE:HB	2.18	0.44
1:A:576:HIS:HE1	1:A:594:ASP:O	2.00	0.44
1:A:844:MET:O	1:A:848:ASN:CB	2.66	0.44
1:A:1464:LYS:C	1:A:1475:LEU:HD21	2.37	0.44
1:A:1907:GLN:HA	1:A:1910:LYS:CG	2.47	0.44
1:A:2007:ARG:HA	1:A:2010:LEU:HD12	2.00	0.44
2:K:121:ARG:O	2:K:125:ILE:HG13	2.18	0.44
4:N:166:ARG:HA	4:N:166:ARG:HD3	1.78	0.44
8:C:145:GLY:N	47:C:1500:GTP:O1B	2.35	0.44
8:C:158:HIS:HB2	8:C:161:ILE:HG13	1.98	0.44
8:C:674:LEU:HA	8:C:674:LEU:HD23	1.78	0.44
8:C:715:MET:CE	8:C:773:VAL:HG12	2.48	0.44
8:C:743:ASN:O	8:C:747:LEU:N	2.34	0.44
1:A:158:LYS:HG3	1:A:159:LYS:H	1.83	0.44
1:A:316:THR:N	1:A:317:PRO:HD2	2.33	0.44
1:A:783:LEU:O	1:A:786:LEU:HB2	2.18	0.44
1:A:936:GLU:HG2	1:A:986:PRO:HB3	1.98	0.44
1:A:1348:GLU:HG2	1:A:1446:THR:HB	2.00	0.44
1:A:1502:LEU:O	1:A:1505:ASP:N	2.41	0.44
1:A:1910:LYS:HG2	1:A:1910:LYS:H	1.54	0.44
2:K:173:VAL:HB	2:K:178:ILE:HD11	1.98	0.44
2:K:335:ASP:OD1	2:K:336:ILE:N	2.50	0.44
2:K:380:LYS:O	2:K:382:ASP:N	2.51	0.44
2:K:422:TYR:HD1	2:K:429:LYS:HA	1.79	0.44
8:C:119:ASN:CG	8:C:120:ARG:H	2.21	0.44
8:C:621:ALA:HB2	8:C:664:ALA:HB2	1.98	0.44
8:C:681:CYS:HB3	8:C:850:LEU:CD1	2.48	0.44
16:F:2:U:H2'	16:F:3:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:33:C:N3	16:F:51:A:N1	2.65	0.44
16:F:51:A:OP2	16:F:51:A:O3'	2.21	0.44
17:B:45:A:H2'	17:B:45:A:N3	2.32	0.44
17:B:166:U:H4'	17:B:167:A:OP1	2.17	0.44
26:I:58:G:C2	26:I:59:C:C2	3.06	0.44
38:H:1150:U:C6	38:H:1150:U:OP2	2.70	0.44
1:A:807:PRO:HB2	4:N:111:LEU:HD23	2.00	0.44
1:A:901:PRO:HG3	1:A:998:TYR:CE2	2.53	0.44
1:A:1054:LEU:HA	1:A:1054:LEU:HD23	1.52	0.44
1:A:1067:ASN:HD22	3:L:270:HIS:HB3	1.81	0.44
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.33	0.44
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.32	0.44
4:N:10:GLU:CG	6:E:14:HIS:HE1	2.30	0.44
4:N:828:LEU:HB3	4:N:845:LEU:CD2	2.48	0.44
5:J:154:SER:OG	5:J:155:LYS:N	2.49	0.44
8:C:208:ARG:CZ	8:C:440:THR:HG23	2.48	0.44
8:C:736:ASP:OD1	8:C:737:ILE:N	2.50	0.44
16:F:61:C:C2	16:F:62:A:C8	3.05	0.44
26:I:15:G:N1	26:I:16:A:C5	2.86	0.44
1:A:1335:TRP:O	1:A:1336:ASN:C	2.56	0.44
1:A:1466:GLN:O	1:A:1470:GLN:HB2	2.18	0.44
1:A:1829:SER:OG	1:A:1830:VAL:N	2.50	0.44
2:K:309:GLY:O	2:K:327:MET:N	2.41	0.44
4:N:242:GLN:HA	4:N:245:ILE:HB	2.00	0.44
4:N:435:ASN:O	4:N:439:ALA:N	2.51	0.44
5:J:242:LYS:O	5:J:243:ARG:C	2.55	0.44
5:J:334:PRO:HG2	5:J:337:TYR:CE1	2.53	0.44
6:E:87:HIS:O	6:E:89:LYS:HG3	2.18	0.44
8:C:284:ALA:O	8:C:287:LYS:HB3	2.17	0.44
8:C:295:ILE:O	8:C:298:PHE:N	2.51	0.44
8:C:422:LYS:O	8:C:425:LEU:N	2.50	0.44
8:C:914:PHE:HE2	8:C:928:CYS:HG	1.65	0.44
16:F:46:U:H5''	16:F:46:U:C6	2.36	0.44
23:T:45:GLY:HA3	24:U:13:VAL:O	2.18	0.44
28:G:487:A:C2	28:G:488:A:O3'	2.71	0.44
1:A:563:ASP:OD1	1:A:564:TRP:N	2.51	0.44
1:A:1068:ARG:HD3	1:A:1068:ARG:HA	1.39	0.44
1:A:1356:LEU:O	1:A:1357:LEU:C	2.56	0.44
1:A:1412:LEU:HD23	1:A:1412:LEU:HA	1.61	0.44
1:A:1645:LEU:HD23	1:A:1645:LEU:HA	1.78	0.44
1:A:1715:SER:O	1:A:1787:TYR:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:177:PRO:O	2:K:195:TRP:HD1	2.01	0.44
2:K:415:TYR:HD1	2:K:439:LYS:HB3	1.82	0.44
3:L:94:LEU:HD23	3:L:94:LEU:O	2.18	0.44
3:L:387:LEU:HA	3:L:387:LEU:HD23	1.72	0.44
5:J:365:LEU:O	5:J:440:TRP:HB2	2.17	0.44
8:C:135:ASN:HB2	8:C:233:ASP:CG	2.38	0.44
8:C:710:VAL:HG22	8:C:820:LEU:HD12	1.99	0.44
16:F:69:C:H42	26:I:12:C:N4	2.15	0.44
17:B:1:A:N6	17:B:164:C:H42	2.15	0.44
17:B:13:A:C2	17:B:14:G:H1'	2.52	0.44
17:B:92:U:O4	17:B:93:G:C6	2.71	0.44
26:I:22:G:H1	26:I:51:U:H3	1.66	0.44
26:I:30:G:N3	26:I:30:G:H5''	2.33	0.44
27:D:1550:SER:HA	27:D:1724:THR:O	2.18	0.44
28:G:480:A:O2'	28:G:481:A:H2'	2.18	0.44
38:H:60:A:H2'	38:H:61:A:O4'	2.18	0.44
1:A:699:PRO:HB2	16:F:1:G:OP1	2.18	0.44
1:A:1112:PHE:O	1:A:1113:ILE:C	2.55	0.44
1:A:1321:MET:HB3	1:A:1321:MET:HE3	1.91	0.44
1:A:1608:LEU:O	1:A:1610:TRP:N	2.50	0.44
2:K:180:ALA:CB	2:K:223:ALA:HA	2.48	0.44
2:K:287:MET:HG2	2:K:308:LYS:C	2.38	0.44
2:K:304:GLU:HG2	2:K:305:GLY:H	1.83	0.44
2:K:415:TYR:OH	7:M:126:ILE:C	2.57	0.44
3:L:328:VAL:HA	3:L:331:HIS:HD2	1.82	0.44
4:N:787:SER:O	4:N:790:LYS:HG2	2.18	0.44
5:J:312:ASN:ND2	16:F:71:G:O2'	2.51	0.44
6:E:42:MET:HG2	6:E:80:MET:HE3	1.99	0.44
16:F:29:U:H2'	16:F:30:G:O4'	2.18	0.44
17:B:80:G:C5	17:B:82:A:C6	3.06	0.44
26:I:51:U:H2'	26:I:52:G:C8	2.53	0.44
28:G:497:A:C2	38:H:39:A:N3	2.86	0.44
29:1:927:ALA:O	29:1:929:ASN:N	2.51	0.44
1:A:220:THR:O	1:A:224:MET:HG2	2.17	0.43
1:A:1393:GLU:OE2	3:L:396:GLN:HA	2.18	0.43
1:A:1591:THR:HB	1:A:1594:GLN:HG2	1.99	0.43
1:A:1814:VAL:O	1:A:1814:VAL:HG12	2.17	0.43
2:K:61:PRO:HG2	2:K:75:ARG:HH12	1.83	0.43
2:K:389:ILE:HD11	2:K:427:TRP:HB3	2.00	0.43
2:K:395:ILE:HG21	2:K:395:ILE:HD13	1.77	0.43
3:L:327:THR:O	3:L:328:VAL:HB	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:348:GLU:O	4:N:352:ALA:CB	2.66	0.43
4:N:808:LEU:HB2	4:N:831:ALA:HB2	2.00	0.43
6:E:117:LEU:HD23	6:E:117:LEU:HA	1.69	0.43
8:C:118:TYR:CE1	8:C:199:LEU:HB3	2.53	0.43
8:C:195:GLY:C	8:C:545:LEU:HD13	2.38	0.43
8:C:251:GLN:HG2	8:C:933:TRP:CZ2	2.53	0.43
8:C:363:PRO:O	8:C:364:PHE:CD2	2.70	0.43
8:C:864:VAL:HG12	8:C:866:ILE:HG13	2.00	0.43
17:B:32:G:C6	17:B:34:C:C4	3.06	0.43
17:B:106:A:H2'	17:B:107:C:C6	2.52	0.43
18:O:210:LEU:HB3	18:O:212:VAL:HG13	1.99	0.43
26:I:53:U:H2'	26:I:54:U:O4'	2.19	0.43
1:A:244:ASP:HB3	1:A:594:ASP:CB	2.49	0.43
1:A:276:VAL:O	1:A:280:LEU:HB2	2.18	0.43
1:A:460:PRO:HG3	8:C:376:PHE:CE1	2.53	0.43
1:A:692:ASN:HB3	1:A:693:LYS:HZ3	1.83	0.43
1:A:2058:LEU:O	1:A:2061:THR:N	2.51	0.43
1:A:2059:ILE:O	1:A:2063:TYR:CB	2.66	0.43
1:A:2060:LEU:HD13	1:A:2071:ILE:HD11	1.99	0.43
1:A:2076:GLN:HE22	5:J:288:THR:HG21	1.83	0.43
3:L:178:SER:O	3:L:181:THR:N	2.51	0.43
4:N:804:ASP:O	4:N:808:LEU:HG	2.18	0.43
8:C:195:GLY:CA	8:C:212:PHE:O	2.66	0.43
8:C:857:LEU:O	8:C:940:VAL:HG23	2.18	0.43
17:B:67:U:H2'	17:B:68:A:H8	1.83	0.43
35:X:35:ILE:O	35:X:74:PHE:HA	2.18	0.43
38:H:1099:G:H2'	38:H:1100:A:H8	1.82	0.43
38:H:1138:G:C6	38:H:1139:G:O6	2.71	0.43
1:A:889:TRP:HA	1:A:1128:GLN:HE22	1.83	0.43
1:A:997:GLN:NE2	1:A:1511:ARG:HH12	2.16	0.43
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.78	0.43
1:A:1144:PHE:HE2	1:A:1145:MET:HE2	1.82	0.43
1:A:1320:LEU:HD21	1:A:1367:ILE:HG12	1.99	0.43
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.49	0.43
1:A:1676:LEU:O	1:A:1709:TRP:HH2	2.01	0.43
1:A:1819:ILE:O	1:A:1821:LYS:N	2.51	0.43
2:K:117:LEU:O	2:K:121:ARG:HG3	2.18	0.43
3:L:401:LEU:HB3	3:L:405:GLY:HA2	2.00	0.43
4:N:740:TYR:O	4:N:743:LYS:N	2.51	0.43
5:J:285:GLN:HB2	5:J:289:ASP:HB2	2.00	0.43
7:M:28:ALA:O	7:M:31:ARG:N	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:102:ILE:HG23	7:M:102:ILE:HD12	1.68	0.43
8:C:318:LEU:HA	8:C:422:LYS:HG2	2.00	0.43
8:C:545:LEU:HD12	8:C:545:LEU:O	2.17	0.43
16:F:82:A:HO2'	16:F:83:A:P	2.42	0.43
16:F:87:U:H3'	16:F:87:U:H6	1.83	0.43
17:B:9:U:H2'	17:B:10:U:O4'	2.19	0.43
17:B:92:U:O4	17:B:93:G:C5	2.70	0.43
17:B:162:G:OP1	17:B:163:C:C6	2.71	0.43
27:D:1224:ALA:HB3	27:D:1264:VAL:HA	2.00	0.43
1:A:579:LEU:HD23	1:A:579:LEU:HA	1.90	0.43
1:A:694:ASN:ND2	1:A:694:ASN:N	2.60	0.43
1:A:769:MET:HE1	4:N:112:ALA:HA	1.99	0.43
1:A:1593:ALA:HB2	6:E:115:ASP:OD1	2.18	0.43
1:A:1710:GLU:HA	1:A:1728:ILE:HA	1.99	0.43
1:A:1920:LEU:O	1:A:1923:SER:OG	2.28	0.43
3:L:95:LEU:HD23	3:L:98:PHE:HD2	1.84	0.43
3:L:142:SER:O	3:L:145:GLU:N	2.49	0.43
3:L:209:LYS:HE2	3:L:209:LYS:HB3	1.82	0.43
5:J:237:THR:O	5:J:241:ARG:NH1	2.51	0.43
5:J:242:LYS:HD3	5:J:242:LYS:HA	1.80	0.43
6:E:11:THR:N	6:E:14:HIS:CD2	2.84	0.43
6:E:13:TRP:CZ2	6:E:17:GLN:OE1	2.71	0.43
8:C:229:LEU:HD13	8:C:259:ASN:HD22	1.84	0.43
8:C:948:ASP:O	8:C:950:PHE:N	2.51	0.43
17:B:10:U:O2	17:B:11:A:N6	2.51	0.43
26:I:2:U:H2'	26:I:3:C:C6	2.52	0.43
26:I:77:U:H2'	26:I:78:A:H8	1.83	0.43
29:1:540:ALA:O	29:1:544:THR:CB	2.66	0.43
38:H:149:A:H2'	38:H:150:G:H8	1.82	0.43
1:A:1048:VAL:HG21	1:A:1222:LEU:CD2	2.48	0.43
1:A:1480:LEU:HD12	1:A:1495:PHE:HZ	1.82	0.43
1:A:1689:ARG:HH22	16:F:45:A:H5''	1.81	0.43
2:K:50:GLU:O	2:K:54:LEU:HG	2.19	0.43
2:K:167:LEU:HD11	4:N:728:ARG:HB2	2.00	0.43
3:L:156:GLU:HB3	3:L:160:HIS:NE2	2.33	0.43
4:N:722:ALA:O	4:N:725:ILE:HB	2.18	0.43
6:E:23:THR:OG1	6:E:24:LYS:N	2.50	0.43
8:C:113:ILE:HG21	8:C:120:ARG:HH21	1.84	0.43
17:B:72:C:H2'	17:B:73:U:C6	2.54	0.43
17:B:126:A:C5	17:B:127:U:O4	2.72	0.43
17:B:166:U:C6	17:B:166:U:OP1	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:33:A:C2	26:I:45:A:C8	3.07	0.43
26:I:60:U:H2'	26:I:61:G:O4'	2.19	0.43
38:H:1094:G:H2'	38:H:1095:U:H6	1.83	0.43
1:A:462:LEU:HD21	8:C:404:PHE:HE2	1.83	0.43
1:A:674:MET:O	1:A:678:ARG:HG2	2.19	0.43
1:A:691:PHE:CD1	1:A:691:PHE:C	2.92	0.43
1:A:878:GLU:O	1:A:881:THR:OG1	2.29	0.43
1:A:1049:LEU:HD23	1:A:1050:LEU:O	2.18	0.43
1:A:1217:ARG:O	1:A:1221:ASN:HB2	2.18	0.43
1:A:1338:SER:O	1:A:1341:SER:OG	2.32	0.43
1:A:1601:ILE:O	1:A:1604:ARG:N	2.51	0.43
1:A:1616:ARG:HB2	1:A:1744:ASP:CG	2.37	0.43
1:A:1830:VAL:HG12	1:A:1832:GLU:N	2.28	0.43
1:A:1858:TYR:CD2	18:O:164:LEU:HG	2.52	0.43
2:K:443:LEU:HG	2:K:444:ASP:N	2.34	0.43
3:L:95:LEU:HD23	3:L:98:PHE:CD2	2.54	0.43
6:E:109:ASP:OD1	6:E:111:GLN:N	2.51	0.43
7:M:36:GLY:HA2	26:I:30:G:O2'	2.18	0.43
8:C:761:ALA:HB1	8:C:775:ILE:HD13	2.00	0.43
8:C:769:TYR:HA	8:C:800:TYR:CE1	2.47	0.43
26:I:33:A:C4	26:I:45:A:N7	2.86	0.43
26:I:145:U:H3	25:V:35:PHE:CB	2.32	0.43
1:A:153:MET:HE2	1:A:153:MET:HB3	1.76	0.43
1:A:205:THR:CG2	17:B:33:U:O2	2.67	0.43
1:A:393:SER:OG	1:A:394:ARG:N	2.50	0.43
1:A:424:PHE:CZ	1:A:428:LEU:HB2	2.54	0.43
1:A:963:VAL:HG21	3:L:280:ARG:NH1	2.34	0.43
1:A:1440:ILE:HD13	1:A:1440:ILE:HG21	1.75	0.43
1:A:1488:ILE:C	1:A:1490:ARG:H	2.21	0.43
1:A:1573:LEU:HD12	1:A:1573:LEU:N	2.34	0.43
1:A:2051:ILE:O	1:A:2054:GLN:N	2.51	0.43
2:K:204:SER:O	2:K:206:THR:N	2.52	0.43
3:L:386:GLN:O	3:L:389:ASN:N	2.52	0.43
4:N:419:ASP:O	4:N:423:SER:N	2.51	0.43
8:C:197:THR:HG21	8:C:544:LEU:HD22	2.00	0.43
8:C:769:TYR:C	8:C:771:GLY:H	2.21	0.43
17:B:50:G:H2'	17:B:51:G:H8	1.83	0.43
17:B:52:G:H2'	17:B:53:C:H6	1.83	0.43
30:2:363:TYR:C	30:2:365:GLY:H	2.22	0.43
38:H:67:A:O2'	38:H:68:U:C6	2.71	0.43
1:A:400:ILE:HD12	1:A:400:ILE:HG23	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:781:THR:HA	1:A:784:GLN:OE1	2.17	0.43
1:A:1490:ARG:HA	1:A:1490:ARG:HD3	1.85	0.43
1:A:2077:THR:OG1	1:A:2078:GLU:N	2.51	0.43
2:K:88:GLU:O	2:K:91:ASN:HB3	2.19	0.43
3:L:395:LYS:HG3	4:N:219:THR:HG21	2.01	0.43
4:N:772:LEU:O	4:N:775:VAL:N	2.51	0.43
5:J:284:ASP:HB2	5:J:293:TRP:CZ3	2.54	0.43
7:M:62:GLU:HA	7:M:65:LEU:HB2	2.01	0.43
8:C:133:ILE:C	8:C:209:MET:O	2.57	0.43
17:B:96:U:O5'	17:B:96:U:C6	2.70	0.43
17:B:164:C:OP2	17:B:165:A:OP1	2.36	0.43
17:B:175:G:H4'	17:B:176:A:O4'	2.18	0.43
18:O:149:TYR:CD2	18:O:178:VAL:HG12	2.48	0.43
38:H:1094:G:H2'	38:H:1095:U:C6	2.54	0.43
1:A:409:CYS:H	8:C:272:ARG:HH21	1.67	0.43
1:A:495:ARG:HH12	17:B:112:C:H2'	1.84	0.43
1:A:801:VAL:HG12	1:A:802:PRO:O	2.19	0.43
1:A:898:ILE:HA	1:A:1006:ARG:NH1	2.34	0.43
1:A:1110:ALA:O	1:A:1111:SER:C	2.56	0.43
1:A:2006:SER:OG	1:A:2007:ARG:N	2.51	0.43
2:K:263:GLY:HA3	2:K:290:ARG:HH12	1.84	0.43
2:K:457:TRP:O	2:K:459:ARG:HG3	2.19	0.43
3:L:53:LEU:O	3:L:56:THR:N	2.51	0.43
3:L:264:LYS:HZ3	3:L:281:GLN:HG2	1.84	0.43
4:N:841:THR:O	4:N:844:TRP:N	2.52	0.43
6:E:126:LYS:O	6:E:127:ASN:HB2	2.19	0.43
8:C:221:PHE:O	8:C:223:ASP:N	2.51	0.43
8:C:305:SER:O	8:C:308:ASP:N	2.52	0.43
8:C:306:PRO:HG2	8:C:349:TRP:CE3	2.54	0.43
8:C:729:GLY:HA3	8:C:735:LEU:HD13	1.99	0.43
8:C:838:ILE:HD12	8:C:841:LEU:HD23	2.01	0.43
16:F:9:A:H2'	16:F:10:A:C8	2.53	0.43
16:F:10:A:N6	16:F:16:C:H42	2.08	0.43
26:I:14:G:C2	26:I:15:G:C4	3.07	0.43
27:D:758:LYS:O	27:D:762:ALA:HB3	2.18	0.43
38:H:1148:U:H2'	38:H:1149:G:H8	1.83	0.43
1:A:194:HIS:CD2	1:A:557:PHE:HE1	2.36	0.43
1:A:654:HIS:CE1	1:A:701:CYS:SG	3.06	0.43
1:A:902:PRO:HG2	1:A:905:TYR:HB2	2.00	0.43
1:A:917:GLU:OE2	4:N:159:LEU:HD21	2.18	0.43
1:A:1277:GLU:O	1:A:1279:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1393:GLU:O	1:A:1395:GLY:N	2.52	0.43
1:A:1591:THR:HG22	1:A:1593:ALA:H	1.84	0.43
1:A:1819:ILE:HG22	1:A:1820:ARG:N	2.34	0.43
1:A:1907:GLN:O	1:A:1910:LYS:HG3	2.18	0.43
8:C:767:SER:OG	8:C:796:ILE:HD13	2.19	0.43
16:F:59:A:C2	26:I:61:G:C4	3.07	0.43
16:F:70:U:C2	16:F:71:G:C8	3.07	0.43
27:D:758:LYS:O	27:D:762:ALA:CB	2.67	0.43
28:G:465:A:H4'	28:G:466:A:OP1	2.19	0.43
35:X:27:TYR:O	35:X:29:ASP:N	2.48	0.43
38:H:1153:C:H2'	38:H:1154:U:H6	1.84	0.43
1:A:190:LYS:HD3	1:A:559:GLN:HE21	1.84	0.42
1:A:222:ILE:HD11	1:A:317:PRO:HG3	2.00	0.42
1:A:266:LEU:HD23	1:A:267:PRO:C	2.38	0.42
1:A:312:TYR:O	1:A:316:THR:HG23	2.18	0.42
1:A:705:GLN:HB3	1:A:706:PRO:HD3	2.01	0.42
1:A:954:ILE:O	1:A:955:LYS:C	2.57	0.42
1:A:1048:VAL:HG21	1:A:1222:LEU:HD22	2.02	0.42
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.54	0.42
1:A:1292:ARG:O	1:A:1294:LYS:HG3	2.19	0.42
1:A:1847:ASP:O	1:A:1849:LYS:NZ	2.47	0.42
1:A:2035:LYS:HD3	1:A:2037:TYR:HD2	1.84	0.42
2:K:233:GLN:OE1	2:K:233:GLN:N	2.51	0.42
2:K:249:SER:O	2:K:252:GLU:N	2.51	0.42
3:L:267:HIS:CE1	3:L:273:HIS:NE2	2.86	0.42
4:N:825:LEU:HD23	4:N:828:LEU:HD12	2.01	0.42
4:N:843:VAL:O	4:N:847:ARG:HG3	2.19	0.42
4:N:846:PHE:HE1	4:N:859:LEU:HD23	1.84	0.42
8:C:153:LEU:HD23	8:C:153:LEU:HA	1.71	0.42
8:C:616:PRO:HA	8:C:619:LEU:HD12	2.01	0.42
8:C:777:ASP:O	8:C:778:THR:HB	2.19	0.42
8:C:863:GLU:HB3	8:C:931:TYR:CE1	2.53	0.42
8:C:946:ASP:O	8:C:964:ARG:HG2	2.19	0.42
16:F:47:A:H2'	16:F:48:C:H5''	2.01	0.42
17:B:92:U:H2'	17:B:93:G:C4'	2.49	0.42
26:I:24:A:C6	26:I:50:G:C6	3.07	0.42
38:H:1097:G:C4	38:H:1146:G:C2	3.07	0.42
1:A:1023:LEU:HB2	1:A:1451:PHE:CE1	2.48	0.42
1:A:1392:LYS:O	1:A:1393:GLU:C	2.58	0.42
1:A:1406:LEU:HB3	1:A:1436:LEU:CD2	2.49	0.42
1:A:1543:ARG:CZ	3:L:396:GLN:HB3	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1848:ILE:HG22	1:A:1930:PRO:HB3	2.00	0.42
1:A:1870:VAL:O	1:A:1872:THR:HG23	2.19	0.42
2:K:172:LEU:HD13	4:N:723:ARG:NE	2.34	0.42
3:L:176:THR:O	3:L:179:MET:HB3	2.19	0.42
3:L:189:LEU:N	3:L:194:ARG:HH22	2.15	0.42
5:J:313:GLU:O	5:J:317:GLU:HG2	2.20	0.42
8:C:681:CYS:HB3	8:C:850:LEU:HD12	2.00	0.42
16:F:64:U:C2	16:F:65:U:C5	3.08	0.42
17:B:21:G:H2'	17:B:22:G:C8	2.54	0.42
17:B:93:G:C4	17:B:94:C:O2	2.72	0.42
26:I:61:G:H2'	26:I:61:G:N3	2.33	0.42
38:H:48:U:C3'	38:H:49:U:H5'	2.48	0.42
38:H:1143:C:H4'	38:H:1144:U:H3'	2.01	0.42
1:A:651:ASP:OD1	1:A:701:CYS:O	2.36	0.42
1:A:1499:ARG:HG3	1:A:1500:HIS:CD2	2.54	0.42
1:A:1611:SER:N	1:A:1612:PRO:HD2	2.33	0.42
1:A:1790:TRP:CE2	1:A:1795:LYS:HE3	2.54	0.42
1:A:1964:PRO:O	1:A:2012:LEU:HB3	2.19	0.42
2:K:189:VAL:HA	2:K:202:LEU:O	2.19	0.42
2:K:354:THR:HG21	2:K:399:VAL:HG23	2.01	0.42
3:L:312:LEU:HD23	3:L:312:LEU:HA	1.83	0.42
4:N:140:GLN:HE22	4:N:143:ARG:NH2	2.17	0.42
4:N:348:GLU:O	4:N:352:ALA:HB3	2.20	0.42
4:N:378:LEU:O	4:N:382:HIS:CB	2.68	0.42
4:N:822:GLU:HA	4:N:825:LEU:HG	2.00	0.42
5:J:267:LYS:HD2	5:J:268:PRO:HD2	2.01	0.42
16:F:33:C:N4	16:F:51:A:H61	2.08	0.42
16:F:70:U:H2'	16:F:71:G:H8	1.84	0.42
16:F:92:C:H2'	16:F:93:A:C8	2.48	0.42
31:3:520:SER:O	31:3:874:GLY:CA	2.68	0.42
1:A:654:HIS:CD2	1:A:701:CYS:HB3	2.54	0.42
1:A:732:ARG:O	1:A:736:GLY:N	2.53	0.42
1:A:1078:ILE:O	1:A:1081:TYR:HB3	2.19	0.42
1:A:1452:LEU:HD23	1:A:1452:LEU:HA	1.82	0.42
1:A:1456:ARG:O	1:A:1459:ALA:N	2.53	0.42
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.53	0.42
1:A:1788:GLY:O	1:A:1790:TRP:NE1	2.51	0.42
1:A:2043:PHE:HB2	1:A:2048:TRP:NE1	2.34	0.42
2:K:434:ALA:HB1	4:N:731:LEU:HD13	2.01	0.42
3:L:175:LEU:O	3:L:176:THR:C	2.56	0.42
3:L:190:ASP:O	3:L:193:THR:OG1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:266:LYS:HG2	3:L:267:HIS:N	2.33	0.42
4:N:618:GLN:O	4:N:622:SER:CB	2.66	0.42
5:J:255:ALA:O	5:J:259:LYS:HB2	2.19	0.42
5:J:373:ARG:HA	5:J:444:VAL:HG11	2.01	0.42
5:J:447:ASP:CG	5:J:450:SER:H	2.21	0.42
8:C:425:LEU:O	8:C:428:ILE:N	2.52	0.42
8:C:675:THR:OG1	8:C:676:VAL:N	2.52	0.42
26:I:12:C:C2	26:I:13:G:C8	3.07	0.42
28:G:479:A:C5	28:G:480:A:C6	3.08	0.42
1:A:140:ARG:HA	1:A:143:ILE:HG12	2.01	0.42
1:A:287:GLU:HG2	1:A:288:GLU:N	2.35	0.42
1:A:540:THR:HA	17:B:79:C:H41	1.84	0.42
1:A:635:THR:HG21	1:A:656:ILE:HD11	2.01	0.42
1:A:699:PRO:HB3	16:F:1:G:OP1	2.18	0.42
1:A:712:LEU:HD12	1:A:712:LEU:HA	1.75	0.42
1:A:718:THR:HA	1:A:721:LEU:HD12	2.02	0.42
1:A:965:LYS:HB3	1:A:965:LYS:NZ	2.34	0.42
1:A:1130:ARG:O	1:A:1133:ASP:HB2	2.19	0.42
1:A:1172:PHE:CE2	1:A:1226:VAL:HG11	2.54	0.42
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.34	0.42
1:A:1527:TRP:CD1	1:A:1527:TRP:N	2.88	0.42
1:A:1711:VAL:O	1:A:1724:PHE:HA	2.20	0.42
1:A:2014:ALA:O	1:A:2017:THR:N	2.30	0.42
1:A:2057:ASP:O	1:A:2061:THR:HG23	2.20	0.42
2:K:244:LYS:HA	2:K:244:LYS:HD2	1.89	0.42
2:K:316:GLN:HA	2:K:357:TRP:CD1	2.55	0.42
5:J:316:HIS:NE2	5:J:320:ILE:HD11	2.35	0.42
6:E:115:ASP:O	6:E:119:THR:OG1	2.18	0.42
7:M:32:GLN:O	7:M:103:THR:OG1	2.26	0.42
8:C:715:MET:HG2	8:C:817:GLN:HB2	2.01	0.42
16:F:29:U:C2	17:B:98:U:C2	3.08	0.42
17:B:66:A:H2'	17:B:67:U:H6	1.83	0.42
26:I:8:U:C2	26:I:9:G:C8	3.07	0.42
26:I:77:U:C2	26:I:78:A:N7	2.87	0.42
26:I:91:U:HO2'	26:I:92:C:P	2.35	0.42
1:A:140:ARG:HH22	1:A:252:GLU:N	2.18	0.42
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.51	0.42
1:A:470:LEU:HB3	1:A:471:PRO:HD2	2.00	0.42
1:A:681:LYS:NZ	16:F:1:G:O6	2.49	0.42
1:A:693:LYS:NZ	1:A:693:LYS:N	2.66	0.42
1:A:1070:LEU:O	1:A:1074:VAL:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1686:VAL:HG12	1:A:1687:HIS:O	2.19	0.42
1:A:1748:ILE:HD13	1:A:1748:ILE:HG21	1.84	0.42
2:K:239:GLU:HG3	2:K:240:ASP:OD1	2.20	0.42
2:K:393:ARG:O	2:K:394:ASN:C	2.58	0.42
4:N:261:LYS:HB3	4:N:285:HIS:HD2	1.84	0.42
4:N:561:LEU:O	4:N:565:VAL:CB	2.68	0.42
5:J:170:ASP:O	5:J:173:TYR:HD2	2.01	0.42
5:J:325:GLU:HG2	5:J:328:ASN:ND2	2.34	0.42
6:E:26:LEU:HB2	6:E:57:ALA:HB2	2.01	0.42
8:C:198:LEU:HA	8:C:198:LEU:HD12	1.85	0.42
8:C:749:LYS:O	8:C:753:THR:CB	2.68	0.42
8:C:835:LYS:HB3	8:C:839:ILE:CD1	2.50	0.42
8:C:933:TRP:C	8:C:935:LYS:N	2.71	0.42
17:B:80:G:C2	17:B:82:A:N3	2.87	0.42
17:B:98:U:C2	17:B:99:U:C6	3.07	0.42
17:B:174:G:C2	17:B:176:A:H4'	2.55	0.42
38:H:1097:G:N1	38:H:1146:G:C5	2.88	0.42
1:A:301:TRP:HD1	1:A:493:MET:SD	2.43	0.42
1:A:408:SER:HB3	1:A:410:ILE:CD1	2.49	0.42
1:A:460:PRO:HG3	8:C:375:GLU:HG3	2.00	0.42
1:A:468:LEU:HD12	1:A:469:ILE:N	2.35	0.42
1:A:963:VAL:C	1:A:964:PHE:CD1	2.93	0.42
1:A:1400:ILE:HG23	1:A:1542:TYR:CE2	2.55	0.42
1:A:1466:GLN:HA	1:A:1469:ILE:HB	2.01	0.42
1:A:1717:LEU:HD21	1:A:1786:ALA:HB3	2.02	0.42
1:A:1882:LEU:HD21	1:A:1965:PHE:CE1	2.55	0.42
2:K:399:VAL:HA	2:K:411:VAL:O	2.20	0.42
3:L:120:TYR:OH	3:L:197:ILE:HD13	2.19	0.42
3:L:233:VAL:CG1	3:L:237:ILE:HB	2.50	0.42
5:J:145:HIS:C	5:J:147:ASP:H	2.23	0.42
5:J:367:GLY:O	5:J:440:TRP:HA	2.20	0.42
6:E:95:PHE:HD1	6:E:133:SER:HB2	1.84	0.42
8:C:343:ASP:O	8:C:346:THR:OG1	2.25	0.42
8:C:365:GLU:CG	8:C:366:ASN:H	2.29	0.42
8:C:500:ARG:HG2	8:C:536:SER:OG	2.20	0.42
8:C:883:ARG:NH2	8:C:914:PHE:HB2	2.35	0.42
16:F:45:A:N3	16:F:45:A:H2'	2.35	0.42
16:F:59:A:C2'	16:F:60:G:H5'	2.50	0.42
17:B:47:U:H2'	17:B:48:G:H8	1.85	0.42
26:I:25:U:H3'	26:I:26:A:H5''	2.01	0.42
26:I:135:A:C6	26:I:136:U:C4	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:1146:G:H2'	38:H:1147:A:H8	1.84	0.42
1:A:293:VAL:HG22	1:A:294:ASN:N	2.35	0.42
1:A:484:PHE:CE1	1:A:488:ARG:HD2	2.54	0.42
1:A:641:LEU:HB2	1:A:643:ASN:OD1	2.20	0.42
1:A:770:MET:HE1	1:A:778:LYS:HB2	2.01	0.42
1:A:1222:LEU:O	1:A:1225:ALA:HB3	2.19	0.42
1:A:1282:ASP:HB2	1:A:1284:GLY:H	1.85	0.42
1:A:1544:THR:OG1	1:A:1545:ASP:N	2.52	0.42
1:A:1843:LEU:HD23	1:A:1843:LEU:HA	1.80	0.42
1:A:1850:LEU:HA	1:A:1882:LEU:O	2.20	0.42
1:A:1856:ASN:HB2	1:A:1878:CYS:SG	2.60	0.42
2:K:135:ARG:HE	2:K:318:ASP:CG	2.23	0.42
2:K:418:LEU:HD23	2:K:418:LEU:HA	1.85	0.42
4:N:21:ARG:NH2	6:E:74:TYR:HH	2.12	0.42
4:N:225:LYS:HE3	4:N:225:LYS:HB3	1.85	0.42
5:J:338:HIS:O	5:J:383:VAL:HA	2.20	0.42
8:C:861:ILE:HG23	8:C:906:VAL:O	2.20	0.42
17:B:150:U:H4'	17:B:151:A:OP1	2.19	0.42
1:A:766:ILE:O	1:A:770:MET:HG3	2.20	0.42
1:A:770:MET:HB3	1:A:770:MET:HE2	1.93	0.42
1:A:788:GLU:OE2	1:A:791:ARG:HD2	2.20	0.42
1:A:1035:LEU:O	1:A:1035:LEU:HD12	2.19	0.42
1:A:1319:ILE:HD11	1:A:1334:LYS:HB3	2.02	0.42
1:A:1681:VAL:HG22	1:A:1703:MET:SD	2.60	0.42
2:K:422:TYR:HE1	2:K:429:LYS:HG3	1.85	0.42
3:L:116:LEU:HD23	3:L:116:LEU:HA	1.86	0.42
3:L:147:GLU:OE1	3:L:147:GLU:N	2.43	0.42
3:L:172:ILE:O	3:L:176:THR:HG23	2.20	0.42
4:N:725:ILE:HA	4:N:728:ARG:NH1	2.34	0.42
4:N:847:ARG:O	4:N:850:ALA:HB3	2.20	0.42
5:J:277:MET:HG3	5:J:293:TRP:HE1	1.85	0.42
8:C:971:ARG:O	8:C:975:GLY:N	2.53	0.42
16:F:28:U:C2'	16:F:29:U:H5'	2.46	0.42
26:I:6:U:C2	26:I:7:A:C8	3.07	0.42
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.20	0.42
1:A:404:ASN:HA	8:C:919:ARG:NH1	2.35	0.42
1:A:603:LYS:HZ3	16:F:43:C:H5'	1.76	0.42
1:A:637:VAL:O	1:A:640:ARG:N	2.53	0.42
1:A:654:HIS:CE1	1:A:658:ASN:HD21	2.36	0.42
1:A:1022:PRO:O	1:A:1025:VAL:N	2.53	0.42
1:A:1028:TRP:CD2	1:A:1262:MET:HE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1270:LEU:HD23	1:A:1270:LEU:HA	1.59	0.42
1:A:1330:LYS:O	1:A:1331:VAL:C	2.58	0.42
1:A:1658:HIS:HD1	1:A:1691:SER:HG	0.56	0.42
2:K:289:TRP:CH2	2:K:322:VAL:HG11	2.54	0.42
2:K:306:HIS:CD2	2:K:310:VAL:HG22	2.55	0.42
3:L:329:LEU:O	3:L:332:LYS:N	2.53	0.42
7:M:52:ILE:HG23	7:M:52:ILE:HD12	1.77	0.42
7:M:55:ALA:HB1	7:M:84:ARG:HB3	2.00	0.42
7:M:95:ARG:CG	7:M:96:PRO:HD2	2.50	0.42
8:C:331:TYR:OH	8:C:428:ILE:O	2.38	0.42
8:C:488:ILE:O	8:C:559:GLY:N	2.50	0.42
8:C:885:GLY:HA3	8:C:906:VAL:HG23	2.02	0.42
17:B:10:U:H1'	17:B:156:G:N2	2.35	0.42
26:I:4:C:H2'	26:I:5:U:C6	2.54	0.42
26:I:135:A:C4	26:I:136:U:C5	3.08	0.42
20:P:31:ILE:O	20:P:48:CYS:HA	2.20	0.42
31:3:676:PRO:HA	31:3:694:ALA:O	2.20	0.42
1:A:152:LYS:HG2	1:A:584:HIS:HD2	1.84	0.41
1:A:234:PHE:CE2	1:A:651:ASP:OD2	2.68	0.41
1:A:572:CYS:O	1:A:576:HIS:CB	2.66	0.41
1:A:768:GLU:CD	4:N:108:LYS:HZ1	2.23	0.41
1:A:1478:GLU:HA	1:A:1481:GLU:OE1	2.20	0.41
1:A:1498:ASP:HB2	4:N:159:LEU:HB2	2.01	0.41
1:A:1567:PHE:CZ	1:A:1820:ARG:NH1	2.88	0.41
1:A:1600:GLN:O	1:A:1601:ILE:C	2.58	0.41
1:A:1890:PHE:HB3	1:A:1986:MET:CE	2.49	0.41
2:K:61:PRO:HG2	2:K:75:ARG:NH1	2.34	0.41
3:L:137:TYR:CZ	3:L:141:ILE:HD11	2.55	0.41
3:L:192:LYS:HE2	3:L:192:LYS:HB3	1.67	0.41
4:N:740:TYR:CD1	4:N:763:ALA:HB2	2.55	0.41
4:N:804:ASP:OD1	4:N:805:HIS:ND1	2.52	0.41
5:J:409:HIS:H	16:F:83:A:N6	2.18	0.41
5:J:453:ARG:O	5:J:456:GLY:N	2.53	0.41
5:J:456:GLY:C	5:J:459:ASP:H	2.22	0.41
7:M:42:LYS:NZ	26:I:43:C:H5	2.18	0.41
7:M:44:LEU:HA	7:M:44:LEU:HD23	1.72	0.41
7:M:108:SER:O	7:M:111:LYS:HB2	2.20	0.41
8:C:126:MET:SD	8:C:132:ARG:HG3	2.59	0.41
8:C:159:LYS:HG3	8:C:160:ARG:N	2.35	0.41
8:C:247:PHE:HB2	8:C:903:ARG:NH2	2.34	0.41
8:C:251:GLN:HG2	8:C:933:TRP:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:295:ILE:HG13	8:C:296:ASN:N	2.34	0.41
8:C:590:LYS:HA	8:C:590:LYS:HD2	1.71	0.41
8:C:708:ILE:HA	8:C:822:SER:O	2.20	0.41
17:B:10:U:H2'	17:B:11:A:C8	2.55	0.41
17:B:44:A:H61	17:B:71:A:H61	1.67	0.41
17:B:159:C:O2'	17:B:161:U:OP2	2.20	0.41
18:O:206:LYS:HB2	18:O:208:LYS:NZ	2.35	0.41
21:Q:19:LEU:HA	21:Q:93:ARG:H	1.85	0.41
31:3:1298:SER:C	31:3:1300:LEU:H	2.23	0.41
1:A:209:ILE:HG21	1:A:303:PHE:HE2	1.85	0.41
1:A:367:PHE:HB2	8:C:608:GLN:HE22	1.84	0.41
1:A:776:GLN:HG2	1:A:777:LYS:N	2.35	0.41
1:A:1899:TRP:CZ3	1:A:1905:LEU:HB3	2.56	0.41
1:A:1907:GLN:O	1:A:1911:TRP:HD1	2.03	0.41
1:A:2052:GLU:OE1	5:J:290:PRO:HG2	2.19	0.41
3:L:130:LEU:HA	3:L:130:LEU:HD23	1.84	0.41
3:L:193:THR:O	3:L:194:ARG:C	2.59	0.41
3:L:207:LEU:O	3:L:210:LEU:HB3	2.20	0.41
3:L:221:LYS:O	3:L:225:ILE:HG12	2.20	0.41
3:L:324:ASP:OD1	3:L:326:ASN:HB2	2.20	0.41
4:N:741:ILE:H	4:N:741:ILE:HD12	1.84	0.41
5:J:297:VAL:O	5:J:300:GLN:HB3	2.19	0.41
6:E:130:LEU:HA	6:E:130:LEU:HD23	1.79	0.41
8:C:381:LEU:O	8:C:384:ILE:N	2.53	0.41
8:C:868:VAL:HA	8:C:926:GLY:HA2	2.02	0.41
17:B:23:C:N4	17:B:24:G:O6	2.54	0.41
26:I:152:A:H2'	26:I:153:A:H8	1.85	0.41
26:I:152:A:H2'	26:I:153:A:C8	2.54	0.41
28:G:497:A:C2	38:H:39:A:C2	3.08	0.41
28:G:503:A:C2	38:H:34:G:C4	3.08	0.41
38:H:142:C:HO2'	38:H:143:G:H8	1.65	0.41
1:A:150:ALA:O	1:A:153:MET:SD	2.79	0.41
1:A:153:MET:CE	1:A:153:MET:N	2.73	0.41
1:A:255:ILE:O	1:A:258:ILE:N	2.42	0.41
1:A:298:TYR:O	1:A:493:MET:HG3	2.20	0.41
1:A:384:LYS:HB3	1:A:392:ASN:HB2	2.03	0.41
1:A:488:ARG:HG2	8:C:416:ASP:OD2	2.20	0.41
1:A:514:TYR:HB3	1:A:518:VAL:HG23	2.02	0.41
1:A:553:ASN:O	1:A:554:THR:OG1	2.28	0.41
1:A:615:LEU:HA	1:A:615:LEU:HD12	1.72	0.41
1:A:769:MET:HE2	4:N:111:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1464:LYS:HD3	1:A:1479:GLU:OE1	2.21	0.41
1:A:1863:HIS:HB2	18:O:159:ASP:HA	2.03	0.41
4:N:132:ASN:O	4:N:133:LYS:C	2.58	0.41
4:N:754:ASP:O	4:N:757:GLU:HB2	2.21	0.41
7:M:95:ARG:NE	26:I:30:G:OP2	2.42	0.41
8:C:381:LEU:HD12	8:C:384:ILE:HD12	2.03	0.41
8:C:444:GLN:O	8:C:448:LEU:HG	2.21	0.41
16:F:56:A:H2	26:I:63:U:O2	2.02	0.41
30:2:252:PHE:O	30:2:256:ALA:HB2	2.20	0.41
31:3:361:LYS:C	31:3:363:VAL:H	2.24	0.41
31:3:1012:LYS:HA	31:3:1013:ASP:HA	1.70	0.41
1:A:192:LEU:HD22	1:A:552:LYS:HB3	2.03	0.41
1:A:809:LYS:O	1:A:813:GLU:HG2	2.20	0.41
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.44	0.41
1:A:1406:LEU:HB3	1:A:1436:LEU:HD23	2.03	0.41
1:A:1600:GLN:HA	1:A:1603:ASN:HD22	1.85	0.41
1:A:1834:PHE:CZ	1:A:1958:PRO:HG2	2.56	0.41
1:A:1849:LYS:HE2	1:A:1849:LYS:HB2	1.84	0.41
1:A:1870:VAL:O	1:A:1870:VAL:HG23	2.21	0.41
2:K:350:LYS:NZ	5:J:431:TYR:CZ	2.86	0.41
3:L:450:GLN:CG	3:L:451:GLN:N	2.82	0.41
4:N:19:ILE:C	4:N:22:GLY:H	2.23	0.41
6:E:101:ASN:C	6:E:102:LYS:HG2	2.41	0.41
8:C:274:ILE:HG21	8:C:385:PHE:CE2	2.56	0.41
8:C:317:LYS:N	47:C:1500:GTP:O6	2.53	0.41
16:F:10:A:C6	16:F:11:U:C5	3.08	0.41
38:H:1098:C:O5'	38:H:1098:C:C6	2.69	0.41
1:A:680:CYS:HG	1:A:711:TRP:HE1	1.66	0.41
1:A:692:ASN:C	1:A:693:LYS:HZ3	2.23	0.41
1:A:850:GLY:C	1:A:852:LEU:N	2.74	0.41
1:A:951:LEU:HA	1:A:951:LEU:HD23	1.73	0.41
1:A:981:VAL:HG13	1:A:1517:TYR:O	2.21	0.41
1:A:1388:PHE:HB2	1:A:1389:TYR:CD1	2.56	0.41
1:A:1652:HIS:HE2	16:F:48:C:H6	1.61	0.41
1:A:1790:TRP:CG	1:A:1795:LYS:HE3	2.55	0.41
1:A:2035:LYS:HD2	1:A:2038:HIS:HD2	1.85	0.41
2:K:50:GLU:O	2:K:53:ARG:HB3	2.21	0.41
2:K:69:VAL:O	2:K:72:ARG:N	2.53	0.41
2:K:149:ARG:HA	2:K:152:LEU:HD12	2.02	0.41
2:K:172:LEU:HD21	4:N:755:GLN:OE1	2.21	0.41
2:K:175:THR:HA	2:K:459:ARG:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:242:ILE:O	3:L:246:GLY:N	2.42	0.41
3:L:373:ARG:NH1	16:F:60:G:OP1	2.54	0.41
4:N:108:LYS:HB2	4:N:108:LYS:HE3	1.81	0.41
4:N:145:THR:O	4:N:146:TYR:CG	2.74	0.41
4:N:774:TRP:CZ2	4:N:800:ARG:HD2	2.55	0.41
8:C:715:MET:CG	8:C:817:GLN:HB2	2.50	0.41
8:C:829:VAL:HA	8:C:832:ASP:HB2	2.02	0.41
16:F:11:U:O2	16:F:12:U:H5	2.03	0.41
17:B:26:A:N6	17:B:141:G:H8	2.17	0.41
17:B:91:U:C3'	17:B:92:U:H5''	2.50	0.41
29:1:835:ILE:C	29:1:837:PHE:H	2.23	0.41
38:H:42:U:H2'	38:H:43:G:H8	1.85	0.41
1:A:252:GLU:OE1	1:A:252:GLU:N	2.39	0.41
1:A:429:ASN:HB3	1:A:430:PRO:HD2	2.01	0.41
1:A:1028:TRP:O	1:A:1031:GLY:N	2.54	0.41
1:A:1219:ASP:HB3	1:A:1250:VAL:HG11	2.02	0.41
1:A:1311:LYS:O	1:A:1312:PHE:C	2.58	0.41
1:A:1344:THR:HG21	1:A:1537:TRP:CE3	2.56	0.41
1:A:1677:GLN:HB3	1:A:1706:VAL:CG2	2.49	0.41
1:A:1703:MET:CB	1:A:1732:MET:HB2	2.51	0.41
1:A:1735:ASP:HB2	1:A:1774:MET:SD	2.59	0.41
2:K:182:SER:OG	2:K:183:LEU:N	2.53	0.41
3:L:124:PHE:CE1	3:L:183:PHE:HB2	2.56	0.41
3:L:275:LEU:HB2	3:L:277:SER:HB2	2.02	0.41
4:N:671:PHE:HA	4:N:674:LEU:HD12	2.01	0.41
5:J:284:ASP:OD1	5:J:284:ASP:N	2.53	0.41
5:J:447:ASP:OD2	5:J:449:ASP:HB2	2.20	0.41
6:E:61:LEU:HA	6:E:61:LEU:HD23	1.73	0.41
7:M:62:GLU:H	7:M:62:GLU:CD	2.19	0.41
8:C:105:ILE:O	8:C:109:LEU:HG	2.21	0.41
8:C:172:TRP:CZ2	8:C:419:PRO:HD3	2.56	0.41
8:C:193:LEU:HB3	8:C:215:ALA:HA	2.02	0.41
8:C:238:VAL:HA	8:C:266:VAL:O	2.21	0.41
8:C:411:GLU:O	8:C:414:GLN:N	2.52	0.41
8:C:931:TYR:CD1	8:C:933:TRP:CD1	2.95	0.41
17:B:143:U:H2'	17:B:144:G:H8	1.85	0.41
18:O:194:LEU:HD13	18:O:197:ARG:HH11	1.86	0.41
38:H:66:A:O2'	38:H:67:A:OP1	2.27	0.41
38:H:1146:G:HO2'	38:H:1147:A:P	2.37	0.41
1:A:155:ASN:OD1	1:A:585:ARG:NH2	2.54	0.41
1:A:561:THR:O	1:A:562:ILE:HB	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:582:LEU:O	1:A:585:ARG:HB3	2.21	0.41
1:A:831:ARG:HD2	1:A:831:ARG:HA	1.74	0.41
1:A:1165:LEU:HA	1:A:1165:LEU:HD23	1.88	0.41
1:A:1353:THR:H	1:A:1353:THR:HG23	1.54	0.41
1:A:1585:MET:HA	1:A:1588:LYS:NZ	2.34	0.41
1:A:1802:MET:O	1:A:1803:ARG:C	2.58	0.41
1:A:2065:ARG:O	1:A:2068:ASN:ND2	2.53	0.41
1:A:2076:GLN:HE22	5:J:288:THR:CG2	2.34	0.41
2:K:37:LEU:O	2:K:40:VAL:N	2.54	0.41
2:K:70:GLN:OE1	2:K:70:GLN:N	2.43	0.41
2:K:86:ASP:HB3	2:K:90:ILE:HD12	2.01	0.41
3:L:382:SER:HG	3:L:385:ARG:H	1.61	0.41
4:N:277:ILE:H	4:N:277:ILE:HD12	1.86	0.41
4:N:671:PHE:O	4:N:674:LEU:HB2	2.20	0.41
4:N:861:ASN:OD1	4:N:862:MET:HG2	2.21	0.41
5:J:160:TYR:HA	5:J:163:ASN:ND2	2.36	0.41
5:J:342:PHE:HB3	5:J:424:ILE:HD11	2.01	0.41
6:E:9:LEU:HD13	6:E:15:VAL:HG22	2.02	0.41
6:E:109:ASP:OD1	6:E:110:LYS:N	2.54	0.41
7:M:54:MET:HB2	7:M:80:PHE:CD1	2.56	0.41
8:C:411:GLU:H	8:C:411:GLU:CD	2.22	0.41
16:F:64:U:H2'	16:F:65:U:C6	2.55	0.41
17:B:14:G:N3	17:B:14:G:H2'	2.36	0.41
17:B:62:G:H2'	17:B:63:C:C6	2.55	0.41
26:I:40:G:N3	26:I:40:G:H3'	2.36	0.41
26:I:47:A:C5	26:I:48:U:C5	3.09	0.41
38:H:68:U:H3'	38:H:68:U:C6	2.56	0.41
38:H:1149:G:C4	38:H:1150:U:C5	3.08	0.41
1:A:212:VAL:O	1:A:216:GLN:HG3	2.21	0.41
1:A:221:TRP:HH2	1:A:690:LYS:HB2	1.86	0.41
1:A:512:GLU:O	1:A:514:TYR:N	2.54	0.41
1:A:729:LEU:O	1:A:733:GLN:CB	2.69	0.41
1:A:935:GLU:O	1:A:938:ALA:HB3	2.21	0.41
1:A:940:ILE:O	1:A:944:TYR:HB3	2.21	0.41
1:A:947:PRO:HA	1:A:950:THR:HG22	2.03	0.41
1:A:1046:SER:OG	1:A:1174:PHE:HB2	2.21	0.41
1:A:1085:LYS:O	1:A:1085:LYS:HG3	2.21	0.41
1:A:1257:ASN:OD1	1:A:1270:LEU:HD21	2.21	0.41
1:A:1360:LEU:HA	1:A:1360:LEU:HD23	1.78	0.41
1:A:1839:ASN:HD21	1:A:1957:ARG:NH1	2.19	0.41
2:K:44:ILE:HD12	2:K:44:ILE:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:126:ASN:O	2:K:130:GLU:HG2	2.21	0.41
2:K:187:ASP:OD2	2:K:447:ASN:N	2.54	0.41
2:K:419:ILE:CG2	2:K:433:LEU:HB2	2.50	0.41
4:N:220:LEU:O	4:N:223:LEU:HB3	2.21	0.41
4:N:224:GLN:O	4:N:228:THR:HG23	2.21	0.41
4:N:706:VAL:O	4:N:710:LYS:CB	2.67	0.41
5:J:153:LEU:O	5:J:157:LYS:CB	2.68	0.41
5:J:287:ILE:HA	5:J:287:ILE:HD13	1.83	0.41
5:J:373:ARG:CZ	5:J:446:ASN:HB3	2.51	0.41
5:J:403:ASN:HA	5:J:419:MET:O	2.20	0.41
6:E:82:VAL:HB	6:E:103:LEU:HD23	2.02	0.41
8:C:128:ASN:OD1	8:C:129:ILE:HD12	2.20	0.41
8:C:378:LEU:HD23	8:C:378:LEU:HA	1.92	0.41
8:C:706:LEU:HD23	8:C:824:SER:O	2.20	0.41
8:C:746:LYS:O	8:C:749:LYS:HB3	2.21	0.41
8:C:792:LYS:HD2	8:C:792:LYS:HA	1.88	0.41
16:F:36:U:C6	16:F:36:U:C5'	2.91	0.41
17:B:120:G:H2'	17:B:121:U:O4'	2.20	0.41
17:B:123:U:H2'	17:B:124:C:C6	2.56	0.41
18:O:168:SER:O	18:O:172:ASP:CB	2.69	0.41
26:I:11:A:C6	26:I:12:C:N4	2.89	0.41
26:I:24:A:C4	26:I:26:A:N7	2.89	0.41
38:H:65:A:O5'	38:H:65:A:C8	2.71	0.41
1:A:176:LEU:O	1:A:179:MET:HG3	2.21	0.41
1:A:260:PRO:O	1:A:261:LEU:HB3	2.21	0.41
1:A:309:SER:O	1:A:313:ARG:HG3	2.20	0.41
1:A:462:LEU:HD23	8:C:403:ASN:HD22	1.86	0.41
1:A:681:LYS:HE3	1:A:685:HIS:NE2	2.36	0.41
1:A:796:ASN:OD1	1:A:858:LYS:HE2	2.21	0.41
1:A:861:GLN:HG2	1:A:1097:HIS:CB	2.49	0.41
1:A:890:LEU:O	1:A:893:ARG:N	2.54	0.41
1:A:923:TYR:CD2	1:A:937:LEU:HD12	2.55	0.41
1:A:1041:VAL:O	1:A:1042:SER:C	2.58	0.41
1:A:1063:PHE:O	1:A:1066:LEU:HB2	2.21	0.41
1:A:1087:ASN:O	1:A:1099:ASN:HB3	2.21	0.41
1:A:1203:ASN:OD1	1:A:1203:ASN:N	2.49	0.41
1:A:1271:PRO:HA	1:A:1298:ALA:CB	2.51	0.41
1:A:1346:PHE:O	1:A:1347:ARG:C	2.59	0.41
1:A:1366:ARG:O	1:A:1369:ASN:HB2	2.21	0.41
1:A:1451:PHE:O	1:A:1454:SER:N	2.53	0.41
1:A:1488:ILE:HD13	1:A:1488:ILE:HA	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1690:LYS:HA	1:A:1693:LYS:CD	2.50	0.41
1:A:1701:ILE:HB	1:A:1734:PHE:HD2	1.86	0.41
1:A:1732:MET:SD	1:A:1771:THR:HB	2.61	0.41
1:A:1801:SER:O	1:A:1805:ILE:HG13	2.20	0.41
1:A:2060:LEU:HA	1:A:2060:LEU:HD23	1.88	0.41
2:K:40:VAL:HG21	2:K:81:MET:SD	2.60	0.41
2:K:52:ARG:O	2:K:55:LEU:HB2	2.21	0.41
2:K:85:ILE:HG12	2:K:86:ASP:O	2.21	0.41
2:K:290:ARG:HB2	2:K:292:TRP:HE1	1.86	0.41
2:K:386:LEU:HD12	2:K:386:LEU:C	2.41	0.41
3:L:186:LYS:HB3	3:L:187:GLU:OE1	2.20	0.41
4:N:6:PHE:HB3	6:E:17:GLN:NE2	2.36	0.41
4:N:803:ASN:O	4:N:834:LYS:NZ	2.53	0.41
4:N:856:THR:HG22	4:N:860:TYR:CE2	2.55	0.41
5:J:346:ASN:O	5:J:422:ASN:ND2	2.54	0.41
5:J:428:TRP:CZ3	5:J:430:GLY:HA3	2.56	0.41
5:J:455:LEU:HB3	5:J:460:SER:C	2.41	0.41
6:E:7:PRO:HG2	6:E:60:TYR:HD1	1.86	0.41
6:E:20:VAL:HA	6:E:88:ASN:OD1	2.21	0.41
7:M:13:ASP:O	7:M:17:THR:OG1	2.30	0.41
7:M:16:LEU:HD12	7:M:16:LEU:HA	1.85	0.41
8:C:570:ALA:HB3	8:C:571:TYR:CD2	2.56	0.41
8:C:576:THR:HG22	8:C:592:PHE:CD2	2.50	0.41
8:C:612:PRO:O	8:C:615:LEU:HB2	2.21	0.41
8:C:758:ASP:HB3	8:C:761:ALA:HB3	2.02	0.41
8:C:769:TYR:CG	8:C:772:ASN:O	2.74	0.41
8:C:931:TYR:HD1	8:C:933:TRP:CD1	2.32	0.41
16:F:14:U:C6	16:F:15:A:C8	3.09	0.41
16:F:60:G:O2'	16:F:61:C:O5'	2.32	0.41
16:F:67:C:N3	26:I:15:G:N1	2.69	0.41
16:F:96:G:H2'	16:F:97:A:C8	2.55	0.41
17:B:10:U:H1'	17:B:156:G:H22	1.85	0.41
17:B:87:G:H2'	17:B:88:U:C6	2.55	0.41
26:I:28:C:C4	26:I:29:A:N7	2.89	0.41
26:I:92:C:H2'	26:I:93:C:C6	2.56	0.41
26:I:96:A:C6	26:I:137:G:C6	3.09	0.41
28:G:476:U:H6	28:G:476:U:H5''	1.86	0.41
28:G:488:A:O5'	28:G:488:A:C8	2.70	0.41
28:G:522:U:H3'	28:G:522:U:H6	1.86	0.41
30:2:367:LEU:C	30:2:369:SER:H	2.24	0.41
32:4:16:ILE:O	32:4:51:GLY:HA2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:9:C:H2'	38:H:10:U:H6	1.86	0.41
38:H:1125:U:O2'	38:H:1126:G:H8	2.00	0.41
38:H:1139:G:O2'	38:H:1140:U:O5'	2.33	0.41
1:A:131:LYS:NZ	1:A:552:LYS:O	2.53	0.41
1:A:342:LEU:HB3	1:A:392:ASN:ND2	2.35	0.41
1:A:1104:ILE:HG21	1:A:1104:ILE:HD13	1.82	0.41
1:A:1134:LEU:HA	1:A:1134:LEU:HD23	1.89	0.41
1:A:1324:GLY:O	1:A:1370:ARG:NH2	2.54	0.41
1:A:1348:GLU:HG2	1:A:1446:THR:CB	2.51	0.41
1:A:1714:PRO:HB2	1:A:1787:TYR:CZ	2.56	0.41
1:A:1739:ARG:HD2	1:A:1751:TYR:CD2	2.56	0.41
1:A:1914:ALA:HB2	1:A:1943:PRO:HB2	2.04	0.41
1:A:1977:VAL:HG11	1:A:1987:VAL:HG21	2.03	0.41
1:A:2027:LEU:HD23	1:A:2027:LEU:HA	1.87	0.41
2:K:114:THR:O	2:K:117:LEU:HG	2.21	0.41
2:K:165:LEU:HD23	2:K:165:LEU:HA	1.80	0.41
2:K:281:GLY:HA2	2:K:290:ARG:O	2.20	0.41
2:K:405:ASP:OD1	2:K:408:LYS:HE2	2.20	0.41
2:K:419:ILE:HG21	2:K:419:ILE:HD13	1.81	0.41
3:L:102:ILE:HB	3:L:103:PRO:HD3	2.02	0.41
3:L:263:GLY:HA3	3:L:284:TYR:N	2.36	0.41
7:M:51:PHE:CE2	7:M:102:ILE:HG13	2.56	0.41
8:C:150:MET:O	8:C:154:VAL:HG23	2.21	0.41
8:C:252:LEU:O	8:C:255:GLN:N	2.54	0.41
8:C:331:TYR:OH	8:C:428:ILE:HG12	2.21	0.41
8:C:364:PHE:HB2	8:C:369:LYS:HB3	2.02	0.41
8:C:786:GLU:O	8:C:790:LYS:HG3	2.20	0.41
8:C:831:ILE:HD12	8:C:831:ILE:HG23	1.87	0.41
17:B:16:U:H2'	17:B:17:C:O4'	2.21	0.41
26:I:47:A:C6	26:I:48:U:C4	3.09	0.41
26:I:58:G:C4	26:I:59:C:C6	3.10	0.41
26:I:133:C:H2'	26:I:134:U:C6	2.56	0.41
21:Q:26:TRP:O	21:Q:43:VAL:HA	2.21	0.41
21:Q:139:ASN:O	21:Q:140:LYS:CB	2.69	0.41
28:G:514:U:O4'	28:G:515:U:C5	2.74	0.41
28:G:521:U:O5'	28:G:521:U:H6	2.03	0.41
31:3:405:VAL:O	31:3:456:THR:HA	2.21	0.41
38:H:68:U:O2'	38:H:69:G:H5'	2.21	0.41
38:H:1166:G:H2'	38:H:1167:U:C6	2.56	0.41
1:A:221:TRP:HE1	1:A:225:ARG:HD2	1.86	0.40
1:A:322:VAL:HG11	1:A:327:TYR:CG	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:THR:OG1	1:A:561:THR:N	2.54	0.40
1:A:670:LYS:O	1:A:673:VAL:HG12	2.21	0.40
1:A:874:ILE:HG22	1:A:875:THR:O	2.21	0.40
1:A:1288:LEU:HD23	1:A:1288:LEU:HA	1.75	0.40
1:A:1748:ILE:HD11	1:A:1778:ASP:N	2.36	0.40
1:A:1834:PHE:CD1	1:A:1834:PHE:N	2.87	0.40
2:K:148:THR:OG1	2:K:149:ARG:N	2.54	0.40
2:K:211:THR:HG21	2:K:248:TYR:OH	2.21	0.40
2:K:400:ARG:HD3	2:K:400:ARG:HA	1.87	0.40
3:L:265:ASN:OD1	3:L:265:ASN:N	2.54	0.40
3:L:343:LYS:HG2	3:L:346:GLU:OE1	2.21	0.40
4:N:841:THR:OG1	4:N:842:TRP:N	2.55	0.40
4:N:860:TYR:HB3	4:N:889:ARG:NH2	2.37	0.40
5:J:233:LYS:O	5:J:233:LYS:HG3	2.21	0.40
5:J:350:PRO:C	16:F:83:A:H8	2.25	0.40
8:C:348:LEU:HD11	8:C:373:PHE:HA	2.04	0.40
8:C:604:LYS:O	8:C:674:LEU:HB2	2.21	0.40
8:C:782:GLU:O	8:C:785:PRO:HD3	2.22	0.40
8:C:885:GLY:HA3	8:C:907:PRO:HD3	2.03	0.40
17:B:48:G:H2'	17:B:49:U:C6	2.56	0.40
38:H:142:C:C2'	38:H:143:G:C8	3.00	0.40
38:H:1118:U:H2'	38:H:1119:C:H6	1.86	0.40
38:H:1139:G:O2'	38:H:1140:U:H6	2.04	0.40
1:A:277:LYS:NZ	1:A:278:ASP:OD1	2.36	0.40
1:A:929:LEU:HD23	1:A:929:LEU:HA	1.77	0.40
1:A:1111:SER:O	1:A:1112:PHE:C	2.59	0.40
1:A:1204:ARG:NH2	1:A:1260:PHE:HA	2.36	0.40
1:A:1381:THR:O	1:A:1382:ARG:HB3	2.21	0.40
1:A:1910:LYS:HE2	1:A:1910:LYS:HB3	1.82	0.40
1:A:1924:LEU:HB2	1:A:1929:GLN:HG2	2.03	0.40
2:K:60:LYS:HA	2:K:60:LYS:HD2	1.88	0.40
2:K:135:ARG:NH1	2:K:360:ASN:O	2.53	0.40
3:L:39:GLU:HA	3:L:42:ASN:CB	2.51	0.40
4:N:744:ILE:O	4:N:747:GLU:N	2.54	0.40
4:N:808:LEU:HD11	4:N:834:LYS:NZ	2.36	0.40
5:J:344:PHE:O	5:J:377:PRO:CA	2.63	0.40
8:C:197:THR:N	8:C:545:LEU:HD12	2.37	0.40
8:C:251:GLN:O	8:C:255:GLN:HG2	2.21	0.40
8:C:344:PHE:HA	8:C:347:ARG:HB2	2.03	0.40
8:C:715:MET:HE1	8:C:773:VAL:HG12	2.02	0.40
8:C:962:LEU:O	8:C:965:ASP:HB3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:19:U:HO2'	26:I:20:A:P	2.42	0.40
31:3:1101:PRO:O	31:3:1102:ALA:HB3	2.20	0.40
38:H:1166:G:C8	38:H:1166:G:O5'	2.75	0.40
1:A:183:TRP:HE3	1:A:220:THR:HG21	1.85	0.40
1:A:209:ILE:HG21	1:A:303:PHE:CE2	2.56	0.40
1:A:1690:LYS:HA	1:A:1693:LYS:HD3	2.02	0.40
1:A:1791:PHE:H	1:A:1794:LEU:HD12	1.86	0.40
1:A:1863:HIS:O	1:A:1870:VAL:HA	2.21	0.40
1:A:1899:TRP:HE3	1:A:1905:LEU:HD22	1.85	0.40
1:A:2005:PHE:O	1:A:2009:THR:HG23	2.21	0.40
2:K:200:GLN:NE2	2:K:202:LEU:HD11	2.36	0.40
3:L:189:LEU:H	3:L:194:ARG:NH2	2.18	0.40
3:L:296:VAL:HA	3:L:299:HIS:NE2	2.36	0.40
4:N:706:VAL:HA	4:N:746:MET:HE3	2.03	0.40
4:N:849:TYR:CE1	4:N:855:ASP:HB2	2.56	0.40
7:M:102:ILE:HG22	7:M:103:THR:N	2.37	0.40
8:C:582:SER:HB2	8:C:585:ASP:HB2	2.03	0.40
16:F:63:G:N1	26:I:57:U:O4	2.54	0.40
17:B:79:C:H3'	17:B:79:C:O2	2.22	0.40
26:I:12:C:C2	26:I:13:G:N7	2.90	0.40
26:I:26:A:H5'	26:I:26:A:C8	2.54	0.40
26:I:33:A:C8	26:I:34:G:C8	3.09	0.40
1:A:174:LYS:HD2	1:A:177:GLU:OE2	2.21	0.40
1:A:1034:ASN:ND2	1:A:1291:GLU:HB2	2.37	0.40
1:A:1268:ARG:HH21	1:A:1270:LEU:HD11	1.87	0.40
1:A:1382:ARG:O	1:A:1619:VAL:HG13	2.21	0.40
1:A:1559:HIS:HB3	1:A:1613:THR:HG21	2.02	0.40
2:K:80:LEU:HD22	2:K:85:ILE:HG21	2.04	0.40
2:K:156:ARG:HA	2:K:159:LEU:HD12	2.04	0.40
2:K:390:LEU:HD22	5:J:428:TRP:NE1	2.36	0.40
2:K:393:ARG:O	2:K:395:ILE:O	2.40	0.40
3:L:142:SER:OG	3:L:143:ILE:N	2.54	0.40
4:N:6:PHE:CZ	6:E:18:ALA:HA	2.57	0.40
4:N:826:LYS:HE2	4:N:826:LYS:HB2	1.91	0.40
4:N:857:VAL:HG23	4:N:858:ASP:N	2.36	0.40
5:J:145:HIS:C	5:J:147:ASP:N	2.75	0.40
6:E:86:TYR:CE2	6:E:87:HIS:HD2	2.39	0.40
8:C:123:MET:SD	8:C:199:LEU:HB2	2.61	0.40
8:C:710:VAL:HG21	8:C:842:MET:SD	2.62	0.40
16:F:63:G:H1	26:I:18:A:H61	1.68	0.40
17:B:29:G:H2'	17:B:30:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:48:U:H2'	26:I:49:U:C6	2.56	0.40
26:I:94:U:C4	26:I:95:C:C4	3.09	0.40
29:1:678:LEU:O	29:1:681:PRO:CB	2.69	0.40
38:H:48:U:C6	38:H:49:U:O4'	2.74	0.40
38:H:1139:G:C2'	38:H:1140:U:H6	2.34	0.40
1:A:645:ASP:OD1	1:A:646:ALA:N	2.54	0.40
1:A:681:LYS:NZ	16:F:1:G:N7	2.70	0.40
1:A:840:VAL:HG22	1:A:840:VAL:O	2.21	0.40
1:A:909:THR:HG23	1:A:910:LYS:N	2.36	0.40
1:A:1014:LYS:HB2	1:A:1014:LYS:HE2	1.86	0.40
1:A:1350:ILE:O	1:A:1352:ALA:N	2.54	0.40
1:A:1421:GLY:HA2	1:A:1718:HIS:CE1	2.57	0.40
2:K:162:MET:SD	2:K:409:LYS:HD2	2.62	0.40
2:K:184:SER:OG	2:K:186:ASP:OD1	2.37	0.40
2:K:274:HIS:CG	2:K:275:PRO:HD2	2.55	0.40
3:L:135:LEU:HD12	3:L:208:TRP:CG	2.57	0.40
3:L:334:LYS:HE3	3:L:334:LYS:HB3	1.89	0.40
4:N:285:HIS:O	4:N:285:HIS:ND1	2.54	0.40
5:J:373:ARG:NH2	5:J:446:ASN:HB3	2.37	0.40
6:E:49:ILE:HG22	6:E:49:ILE:O	2.22	0.40
7:M:51:PHE:O	7:M:52:ILE:HD13	2.21	0.40
8:C:142:LEU:HD21	8:C:218:HIS:HB2	2.03	0.40
8:C:557:HIS:H	8:C:560:GLN:HE21	1.69	0.40
8:C:679:GLU:OE1	8:C:807:PRO:HD2	2.21	0.40
16:F:36:U:C6	16:F:36:U:C4'	3.04	0.40
16:F:67:C:C2	26:I:15:G:C2	3.09	0.40
17:B:91:U:H2'	17:B:92:U:C5'	2.48	0.40
26:I:11:A:C6	26:I:12:C:C4	3.09	0.40
26:I:24:A:O2'	26:I:26:A:H5'	2.22	0.40
26:I:64:U:C3'	26:I:64:U:C6	3.05	0.40
31:3:336:LEU:HA	31:3:346:LEU:O	2.22	0.40
31:3:1305:GLN:O	31:3:1309:SER:CB	2.70	0.40
44:W:127:PRO:C	44:W:129:GLU:H	2.24	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	A	2164/2413 (90%)	1843 (85%)	298 (14%)	23 (1%)	14	51
2	K	425/465 (91%)	354 (83%)	68 (16%)	3 (1%)	22	60
3	L	410/494 (83%)	349 (85%)	55 (13%)	6 (2%)	10	45
4	N	675/899 (75%)	558 (83%)	109 (16%)	8 (1%)	13	49
5	J	300/469 (64%)	260 (87%)	36 (12%)	4 (1%)	12	48
6	E	136/143 (95%)	116 (85%)	19 (14%)	1 (1%)	22	60
7	M	124/126 (98%)	108 (87%)	15 (12%)	1 (1%)	19	57
8	C	837/1008 (83%)	727 (87%)	102 (12%)	8 (1%)	15	52
9	z	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
10	q	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
11	r	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
12	x	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
13	t	73/93 (78%)	68 (93%)	4 (6%)	1 (1%)	11	46
14	y	62/115 (54%)	62 (100%)	0	0	100	100
15	s	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
18	O	69/587 (12%)	65 (94%)	2 (3%)	2 (3%)	4	33
19	S	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
19	d	77/101 (76%)	71 (92%)	4 (5%)	2 (3%)	5	35
19	l	72/101 (71%)	63 (88%)	8 (11%)	1 (1%)	11	46
20	P	66/196 (34%)	62 (94%)	4 (6%)	0	100	100
20	a	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
20	h	72/196 (37%)	65 (90%)	7 (10%)	0	100	100
21	Q	93/146 (64%)	89 (96%)	3 (3%)	1 (1%)	14	51
21	b	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11	46
21	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	R	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
22	c	86/110 (78%)	81 (94%)	5 (6%)	0	100	100
22	n	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	9	44
23	T	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
23	e	66/94 (70%)	61 (92%)	5 (8%)	0	100	100
23	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
24	U	71/86 (83%)	68 (96%)	3 (4%)	0	100	100
24	f	66/86 (77%)	60 (91%)	4 (6%)	2 (3%)	4	33
24	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	10	45
25	V	73/77 (95%)	66 (90%)	5 (7%)	2 (3%)	5	35
25	g	64/77 (83%)	56 (88%)	8 (12%)	0	100	100
25	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	D	1694/2163 (78%)	1631 (96%)	60 (4%)	3 (0%)	47	79
29	1	814/971 (84%)	770 (95%)	32 (4%)	12 (2%)	10	45
30	2	205/436 (47%)	192 (94%)	10 (5%)	3 (2%)	10	45
31	3	1164/1361 (86%)	1039 (89%)	107 (9%)	18 (2%)	10	45
32	4	166/213 (78%)	166 (100%)	0	0	100	100
33	5	101/107 (94%)	87 (86%)	14 (14%)	0	100	100
34	6	82/85 (96%)	77 (94%)	4 (5%)	1 (1%)	13	49
35	X	126/148 (85%)	117 (93%)	7 (6%)	2 (2%)	9	44
36	Y	85/266 (32%)	80 (94%)	3 (4%)	2 (2%)	6	37
37	Z	20/204 (10%)	14 (70%)	6 (30%)	0	100	100
39	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	9	44
40	p	69/111 (62%)	67 (97%)	2 (3%)	0	100	100
41	u	454/530 (86%)	417 (92%)	35 (8%)	2 (0%)	34	71
42	w	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
43	v	168/266 (63%)	142 (84%)	23 (14%)	3 (2%)	8	42
44	W	94/194 (48%)	87 (93%)	7 (7%)	0	100	100
45	0	157/242 (65%)	135 (86%)	22 (14%)	0	100	100
46	9	60/291 (21%)	59 (98%)	1 (2%)	0	100	100
All	All	12887/17914 (72%)	11601 (90%)	1170 (9%)	116 (1%)	21	54

All (116) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	PRO
2	K	171	GLN
2	K	395	ILE
3	L	328	VAL
4	N	735	ASP
8	C	364	PHE
8	C	602	VAL
21	b	12	ASN
29	1	386	TYR
29	1	549	GLY
29	1	830	MET
29	1	831	SER
29	1	836	TYR
30	2	368	ILE
31	3	363	VAL
31	3	413	ILE
31	3	961	CYS
31	3	1233	SER
31	3	1299	ILE
35	X	17	LEU
39	o	68	PRO
43	v	55	ASN
43	v	56	PRO
1	A	1044	GLY
1	A	1088	VAL
2	K	286	ASP
3	L	151	LYS
5	J	167	GLU
5	J	220	PRO
5	J	331	VAL
8	C	133	ILE
8	C	134	ILE
19	d	40	MET
24	f	24	ASN
24	f	49	PHE
21	Q	140	LYS
29	1	835	ILE
31	3	773	LYS
36	Y	172	ILE
36	Y	230	SER
41	u	463	GLY
1	A	690	LYS

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Mol	Chain	Res	Type
1	A	1816	ARG
1	A	1869	ASN
3	L	152	ASN
4	N	768	PRO
27	D	791	PRO
27	D	1896	LYS
25	V	60	GLN
30	2	260	PRO
31	3	98	GLU
31	3	180	THR
31	3	247	PHE
31	3	667	THR
34	6	19	ILE
1	A	1313	ASP
1	A	1621	VAL
1	A	1628	ASP
1	A	2321	ILE
3	L	222	ILE
4	N	734	PRO
8	C	772	ASN
18	O	212	VAL
27	D	960	ILE
29	1	874	GLU
30	2	194	PHE
31	3	92	GLN
31	3	364	THR
31	3	434	ASN
31	3	1184	LYS
19	l	82	PRO
22	n	82	LYS
1	A	239	PHE
1	A	775	ARG
1	A	1015	PRO
1	A	1184	ASP
1	A	2330	GLU
3	L	175	LEU
4	N	782	LYS
5	J	154	SER
6	E	66	GLU
25	V	49	GLU
29	1	349	LEU
29	1	873	HIS

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Mol	Chain	Res	Type
29	1	892	SER
35	X	18	SER
43	v	232	GLY
1	A	992	ASP
1	A	1238	LEU
1	A	1870	VAL
4	N	568	TYR
4	N	737	VAL
8	C	601	ALA
31	3	722	SER
41	u	458	SER
1	A	562	ILE
1	A	875	THR
8	C	829	VAL
19	d	51	GLU
29	1	681	PRO
24	j	15	PRO
39	o	52	LYS
1	A	407	VAL
4	N	760	VAL
7	M	59	GLU
13	t	41	VAL
29	1	348	VAL
31	3	299	PRO
31	3	523	ILE
1	A	1752	VAL
1	A	710	VAL
3	L	358	ILE
8	C	363	PRO
18	O	169	ILE
31	3	1031	ILE
4	N	744	ILE

5.3.2 Protein sidechains [i](#)

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	A	1743/2182 (80%)	1729 (99%)	14 (1%)	81	89
2	K	373/410 (91%)	373 (100%)	0	100	100
3	L	327/445 (74%)	327 (100%)	0	100	100
4	N	361/813 (44%)	361 (100%)	0	100	100
5	J	252/436 (58%)	252 (100%)	0	100	100
6	E	128/132 (97%)	128 (100%)	0	100	100
7	M	104/104 (100%)	104 (100%)	0	100	100
8	C	757/910 (83%)	753 (100%)	4 (0%)	88	93
18	O	57/534 (11%)	57 (100%)	0	100	100
All	All	4102/5966 (69%)	4084 (100%)	18 (0%)	91	94

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	LYS
1	A	153	MET
1	A	362	GLU
1	A	364	TYR
1	A	675	HIS
1	A	693	LYS
1	A	694	ASN
1	A	697	LYS
1	A	701	CYS
1	A	900	PHE
1	A	965	LYS
1	A	1177	ASP
1	A	1863	HIS
1	A	1910	LYS
8	C	190	SER
8	C	468	LEU
8	C	769	TYR
8	C	945	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	294	ASN
1	A	326	ASN

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Mol	Chain	Res	Type
1	A	344	ASN
1	A	368	ASN
1	A	392	ASN
1	A	429	ASN
1	A	584	HIS
1	A	592	HIS
1	A	617	ASN
1	A	648	GLN
1	A	658	ASN
1	A	659	HIS
1	A	694	ASN
1	A	974	ASN
1	A	976	GLN
1	A	1011	ASN
1	A	1045	GLN
1	A	1202	ASN
1	A	1368	GLN
1	A	1424	HIS
1	A	1449	ASN
1	A	1594	GLN
1	A	1603	ASN
1	A	1635	HIS
1	A	1652	HIS
1	A	1839	ASN
1	A	1888	HIS
1	A	2018	ASN
1	A	2068	ASN
1	A	2076	GLN
2	K	31	GLN
2	K	144	GLN
2	K	212	GLN
2	K	232	ASN
2	K	247	GLN
2	K	274	HIS
2	K	316	GLN
2	K	360	ASN
2	K	392	HIS
2	K	420	ASN
2	K	450	HIS
2	K	465	ASN
3	L	113	HIS
3	L	152	ASN

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Mol	Chain	Res	Type
3	L	185	ASN
3	L	228	ASN
3	L	331	HIS
3	L	449	ASN
4	N	132	ASN
4	N	140	GLN
4	N	770	ASN
4	N	783	HIS
4	N	803	ASN
5	J	145	HIS
5	J	163	ASN
5	J	247	ASN
5	J	433	GLN
5	J	448	GLN
6	E	14	HIS
6	E	87	HIS
6	E	111	GLN
7	M	45	ASN
7	M	113	GLN
8	C	183	GLN
8	C	218	HIS
8	C	251	GLN
8	C	260	ASN
8	C	432	GLN
8	C	623	ASN
8	C	721	GLN
8	C	817	GLN
8	C	837	GLN
8	C	929	GLN
18	O	198	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	F	95/112 (84%)	44 (46%)	3 (3%)
17	B	173/214 (80%)	66 (38%)	14 (8%)
26	I	106/161 (65%)	44 (41%)	6 (5%)
28	G	59/60 (98%)	39 (66%)	7 (11%)
38	H	142/1175 (12%)	54 (38%)	23 (16%)
All	All	575/1722 (33%)	247 (42%)	53 (9%)

All (247) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	F	2	U
16	F	12	U
16	F	13	U
16	F	14	U
16	F	17	U
16	F	19	C
16	F	25	C
16	F	26	A
16	F	28	U
16	F	29	U
16	F	30	G
16	F	31	G
16	F	32	U
16	F	33	C
16	F	35	A
16	F	37	U
16	F	38	U
16	F	39	G
16	F	41	A
16	F	42	A
16	F	44	A
16	F	45	A
16	F	46	U
16	F	47	A
16	F	48	C
16	F	49	A
16	F	50	G
16	F	51	A
16	F	58	C
16	F	60	G
16	F	62	A
16	F	65	U
16	F	68	C
16	F	76	A
16	F	77	G
16	F	78	G
16	F	81	G
16	F	82	A
16	F	83	A
16	F	84	C
16	F	86	G
16	F	87	U
16	F	109	U

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Mol	Chain	Res	Type
16	F	111	U
17	B	12	C
17	B	13	A
17	B	18	A
17	B	20	U
17	B	24	G
17	B	27	G
17	B	28	G
17	B	29	G
17	B	33	U
17	B	34	C
17	B	40	C
17	B	41	A
17	B	42	A
17	B	74	U
17	B	75	A
17	B	76	U
17	B	77	A
17	B	78	A
17	B	79	C
17	B	80	G
17	B	81	A
17	B	82	A
17	B	84	A
17	B	92	U
17	B	93	G
17	B	94	C
17	B	95	C
17	B	96	U
17	B	97	U
17	B	98	U
17	B	99	U
17	B	100	A
17	B	101	C
17	B	102	C
17	B	103	A
17	B	104	G
17	B	107	C
17	B	109	A
17	B	113	G
17	B	121	U
17	B	126	A

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Mol	Chain	Res	Type
17	B	127	U
17	B	128	A
17	B	129	G
17	B	131	A
17	B	132	A
17	B	139	A
17	B	140	A
17	B	141	G
17	B	142	C
17	B	151	A
17	B	160	U
17	B	162	G
17	B	163	C
17	B	164	C
17	B	165	A
17	B	166	U
17	B	167	A
17	B	168	U
17	B	169	U
17	B	170	U
17	B	171	U
17	B	172	U
17	B	173	U
17	B	174	G
17	B	175	G
26	I	6	U
26	I	11	A
26	I	18	A
26	I	19	U
26	I	20	A
26	I	22	G
26	I	24	A
26	I	25	U
26	I	26	A
26	I	27	U
26	I	28	C
26	I	29	A
26	I	30	G
26	I	31	U
26	I	32	G
26	I	33	A
26	I	35	G

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Mol	Chain	Res	Type
26	I	39	C
26	I	40	G
26	I	45	A
26	I	49	U
26	I	55	U
26	I	56	U
26	I	57	U
26	I	61	G
26	I	62	G
26	I	63	U
26	I	64	U
26	I	74	U
26	I	75	U
26	I	76	A
26	I	77	U
26	I	78	A
26	I	79	A
26	I	92	C
26	I	98	G
26	I	134	U
26	I	135	A
26	I	138	U
26	I	139	A
26	I	143	A
26	I	144	A
26	I	145	U
26	I	151	G
28	G	464	A
28	G	465	A
28	G	466	A
28	G	467	A
28	G	468	A
28	G	469	A
28	G	470	A
28	G	471	U
28	G	472	U
28	G	473	U
28	G	474	U
28	G	475	U
28	G	476	U
28	G	477	U
28	G	478	U

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Mol	Chain	Res	Type
28	G	479	A
28	G	481	A
28	G	484	A
28	G	485	A
28	G	486	A
28	G	487	A
28	G	488	A
28	G	493	A
28	G	497	A
28	G	501	A
28	G	502	C
28	G	505	A
28	G	506	U
28	G	507	U
28	G	508	U
28	G	509	A
28	G	510	A
28	G	512	U
28	G	515	U
28	G	516	U
28	G	518	U
28	G	520	G
28	G	521	U
28	G	522	U
38	H	32	G
38	H	38	U
38	H	41	C
38	H	46	C
38	H	47	U
38	H	48	U
38	H	52	A
38	H	65	A
38	H	66	A
38	H	67	A
38	H	68	U
38	H	83	U
38	H	111	C
38	H	115	U
38	H	116	U
38	H	117	U
38	H	118	U
38	H	119	G

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Mol	Chain	Res	Type
38	H	120	G
38	H	140	G
38	H	141	A
38	H	142	C
38	H	145	G
38	H	1090	A
38	H	1094	G
38	H	1095	U
38	H	1096	C
38	H	1097	G
38	H	1098	C
38	H	1100	A
38	H	1101	C
38	H	1102	C
38	H	1103	C
38	H	1104	U
38	H	1105	C
38	H	1106	G
38	H	1119	C
38	H	1120	G
38	H	1121	U
38	H	1122	U
38	H	1123	C
38	H	1124	U
38	H	1125	U
38	H	1126	G
38	H	1130	U
38	H	1139	G
38	H	1141	C
38	H	1142	G
38	H	1143	C
38	H	1144	U
38	H	1145	U
38	H	1146	G
38	H	1150	U
38	H	1166	G

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	F	31	G
16	F	82	A

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Mol	Chain	Res	Type
16	F	86	G
17	B	17	C
17	B	32	G
17	B	33	U
17	B	41	A
17	B	81	A
17	B	83	C
17	B	95	C
17	B	96	U
17	B	128	A
17	B	130	A
17	B	150	U
17	B	166	U
17	B	168	U
17	B	172	U
26	I	18	A
26	I	19	U
26	I	24	A
26	I	91	U
26	I	134	U
26	I	142	G
28	G	472	U
28	G	473	U
28	G	480	A
28	G	487	A
28	G	500	A
28	G	514	U
28	G	515	U
38	H	46	C
38	H	67	A
38	H	117	U
38	H	1095	U
38	H	1096	C
38	H	1097	G
38	H	1100	A
38	H	1101	C
38	H	1102	C
38	H	1105	C
38	H	1119	C
38	H	1120	G
38	H	1121	U
38	H	1122	U

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Mol	Chain	Res	Type
38	H	1123	C
38	H	1124	U
38	H	1125	U
38	H	1138	G
38	H	1141	C
38	H	1142	G
38	H	1144	U
38	H	1145	U
38	H	1149	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	GTP	C	1500	48	26,34,34	1.50	4 (15%)	32,54,54	2.11	7 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	GTP	C	1500	48	-	7/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	C	1500	GTP	C5-C6	-4.99	1.37	1.47
47	C	1500	GTP	C5-C4	-2.32	1.37	1.43
47	C	1500	GTP	C2'-C1'	-2.26	1.50	1.53
47	C	1500	GTP	O4'-C4'	-2.12	1.40	1.45

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	C	1500	GTP	PB-O3B-PG	-7.36	107.56	132.83
47	C	1500	GTP	PA-O3A-PB	-5.25	114.81	132.83
47	C	1500	GTP	C2-N1-C6	-3.09	119.40	125.10
47	C	1500	GTP	C5-C6-N1	2.93	119.12	113.95
47	C	1500	GTP	C8-N7-C5	2.87	108.46	102.99
47	C	1500	GTP	O6-C6-C5	-2.63	119.23	124.37
47	C	1500	GTP	O3'-C3'-C2'	-2.11	104.99	111.82

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	C	1500	GTP	PB-O3A-PA-O5'
47	C	1500	GTP	C5'-O5'-PA-O1A
47	C	1500	GTP	C5'-O5'-PA-O2A
47	C	1500	GTP	C3'-C4'-C5'-O5'
47	C	1500	GTP	O4'-C4'-C5'-O5'
47	C	1500	GTP	PA-O3A-PB-O1B
47	C	1500	GTP	C5'-O5'-PA-O3A

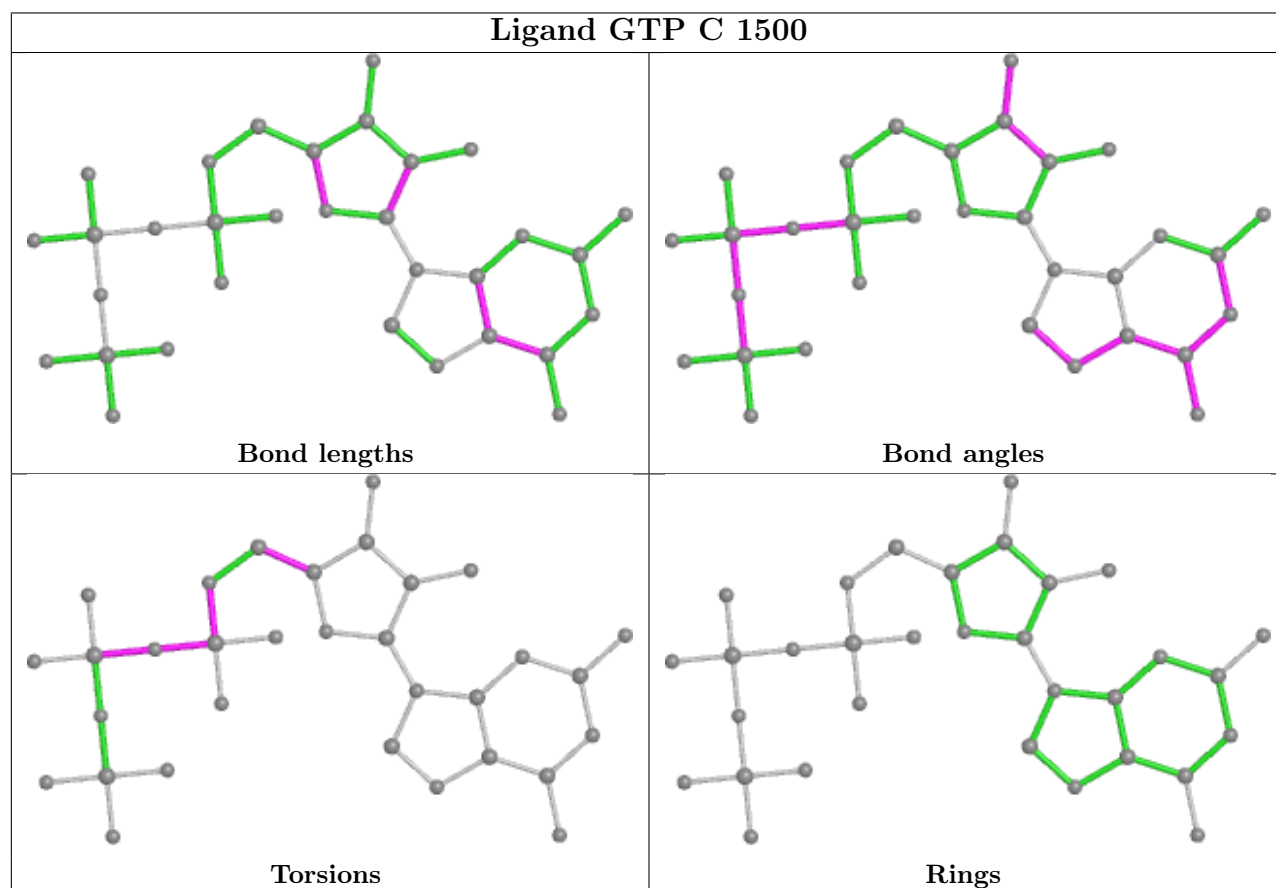
There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	C	1500	GTP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

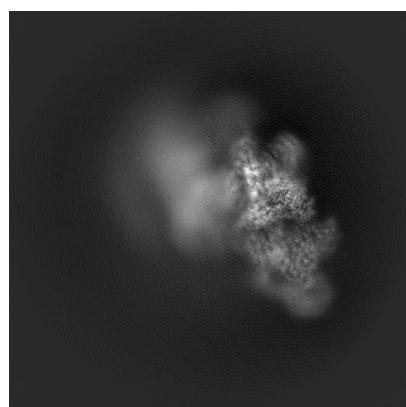
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6974. These allow visual inspection of the internal detail of the map and identification of artifacts.

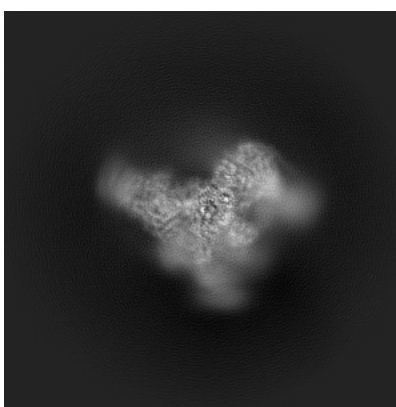
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

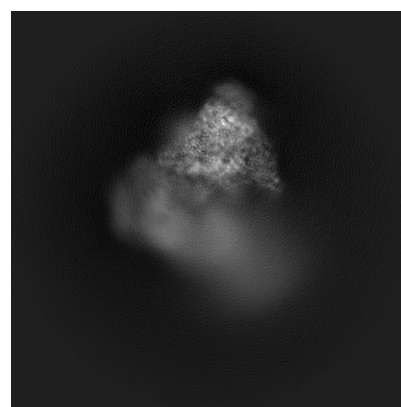
6.1.1 Primary map



X



Y

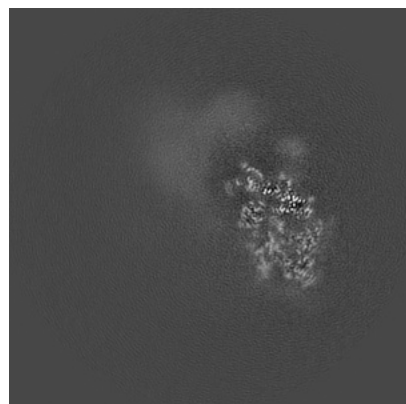


Z

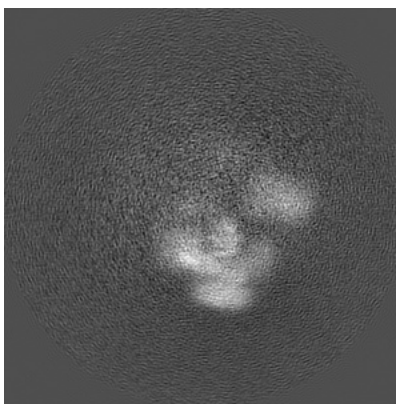
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

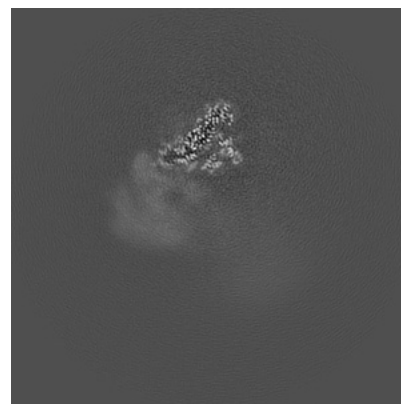
6.2.1 Primary map



X Index: 200



Y Index: 200

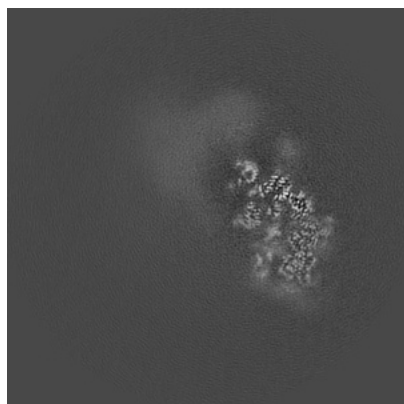


Z Index: 200

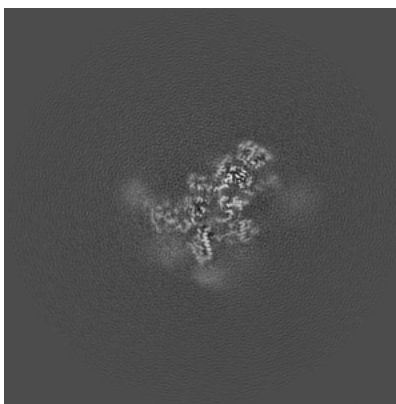
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

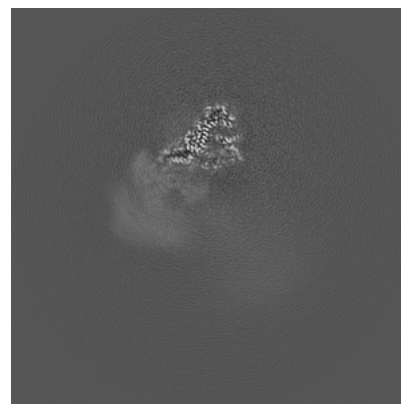
6.3.1 Primary map



X Index: 206



Y Index: 247



Z Index: 202

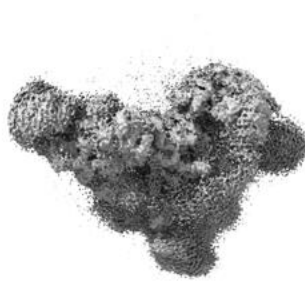
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

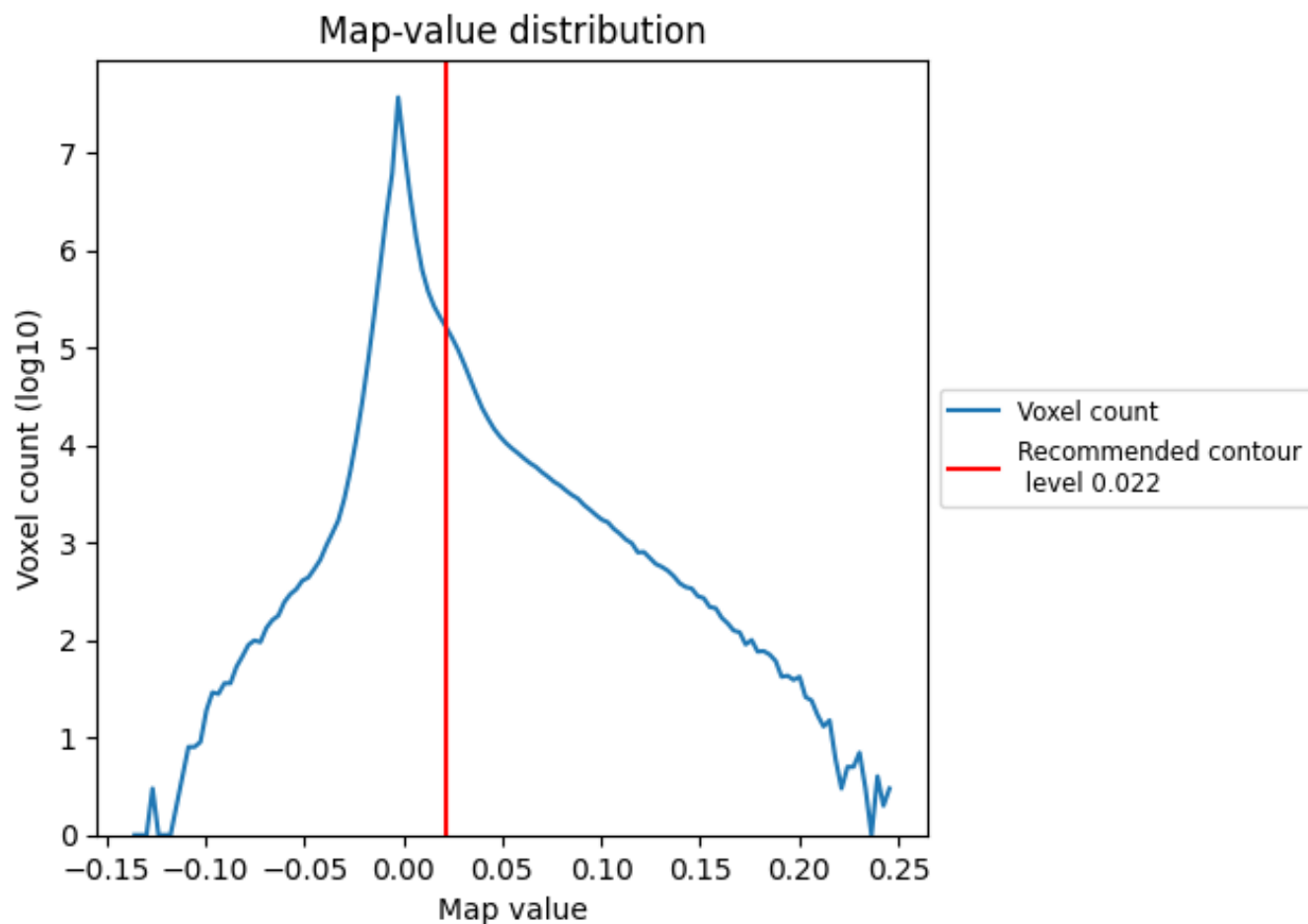
6.5 Mask visualisation

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

7 Map analysis [i](#)

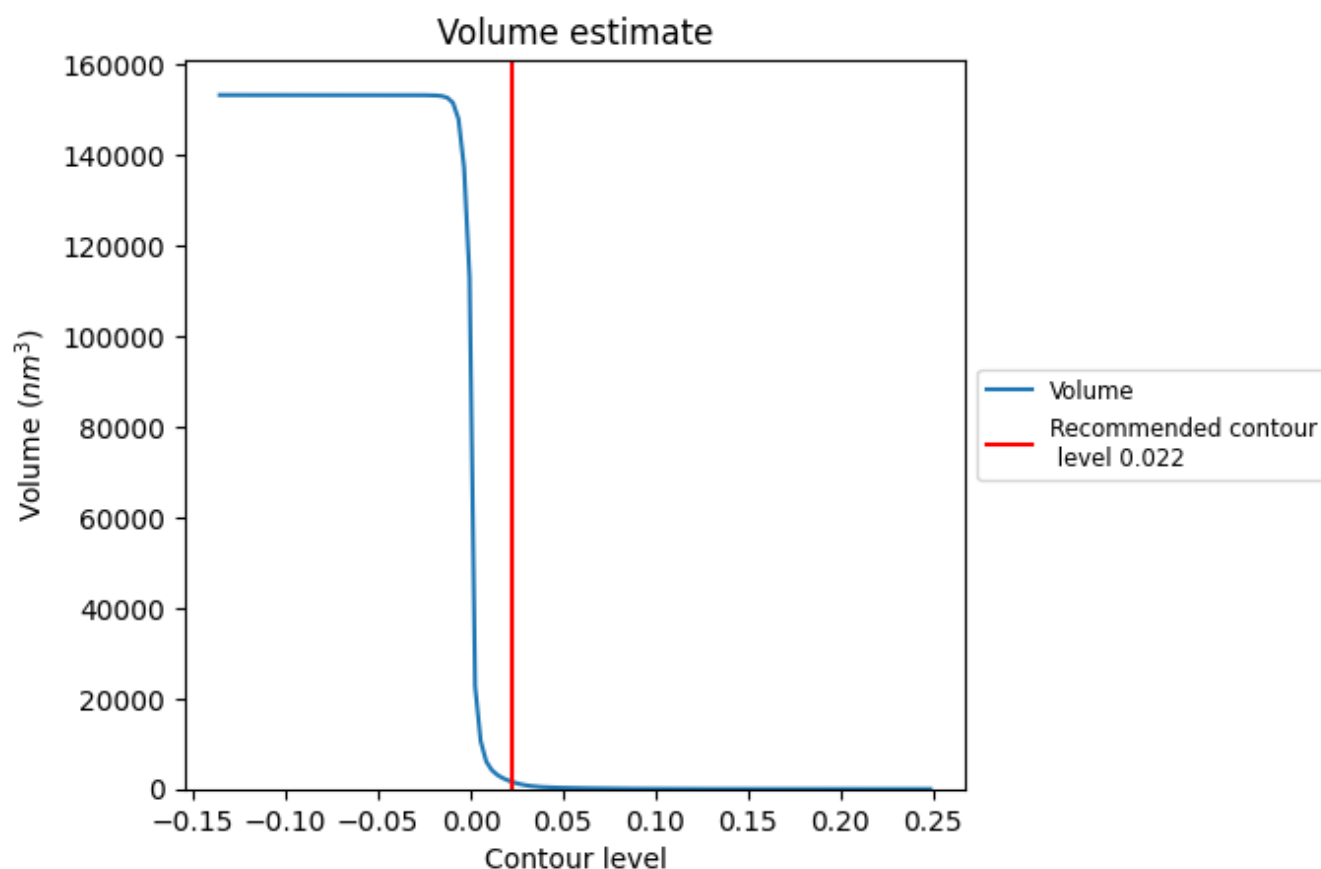
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

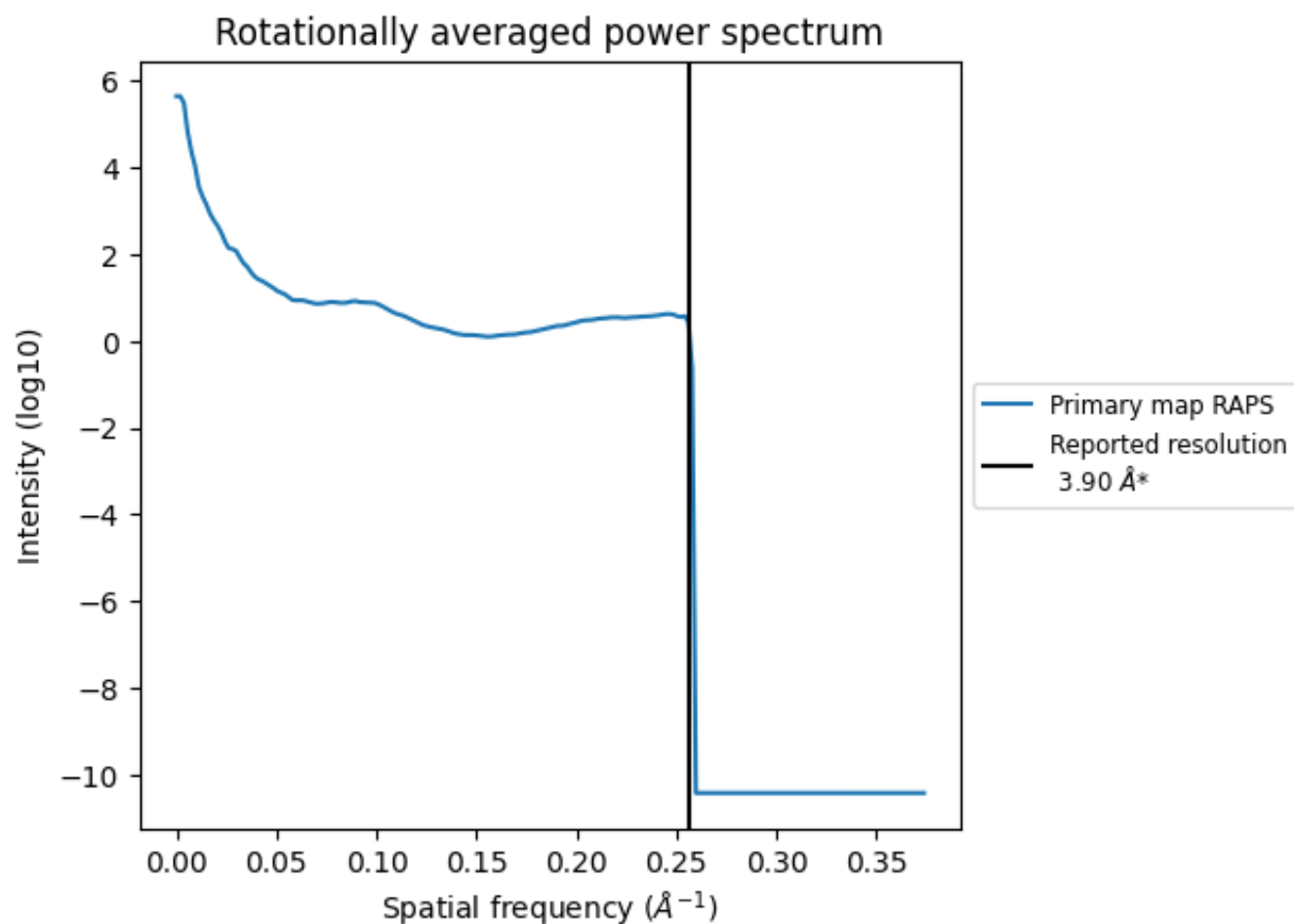
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1643 nm³; this corresponds to an approximate mass of 1484 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 0.256 Å⁻¹

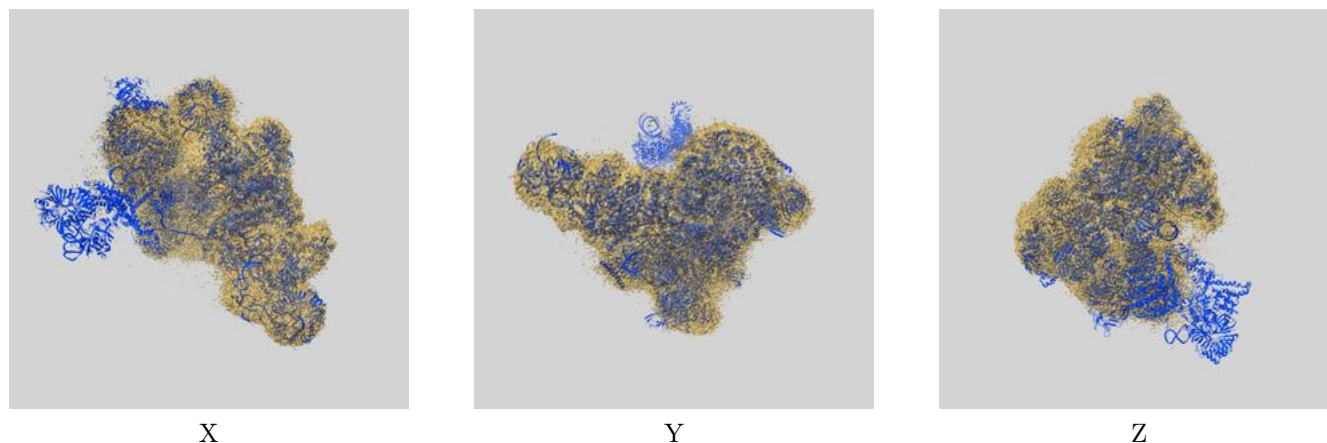
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

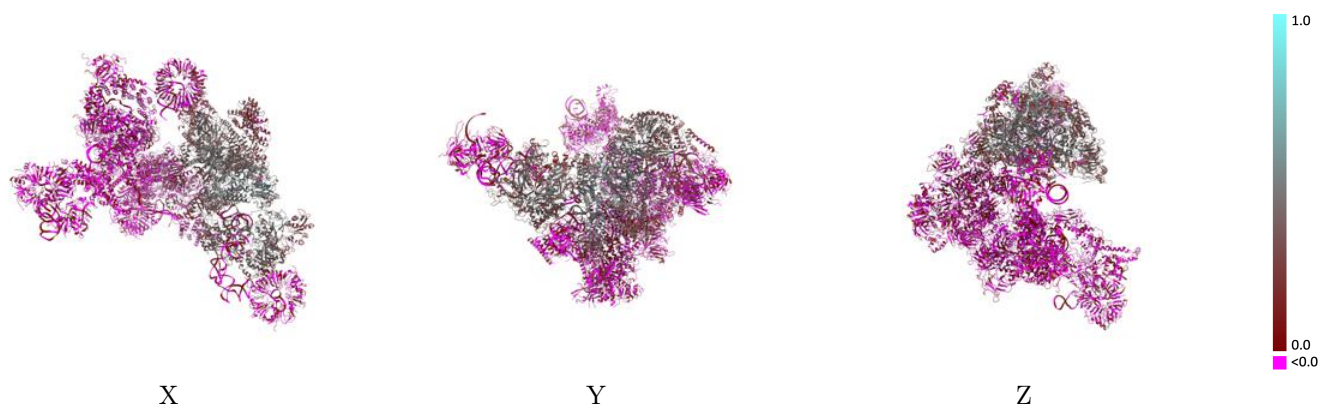
This section contains information regarding the fit between EMDB map EMD-6974 and PDB model 5ZWO. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



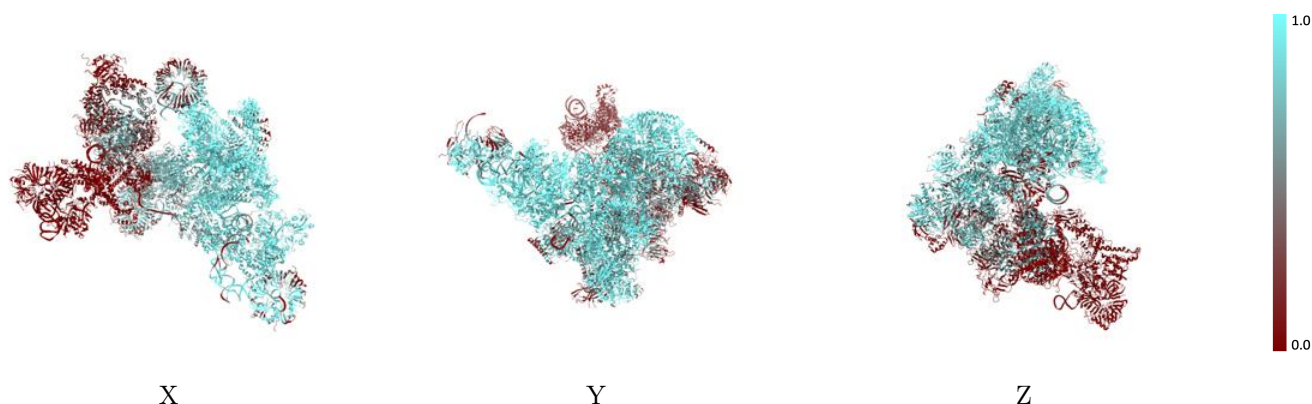
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



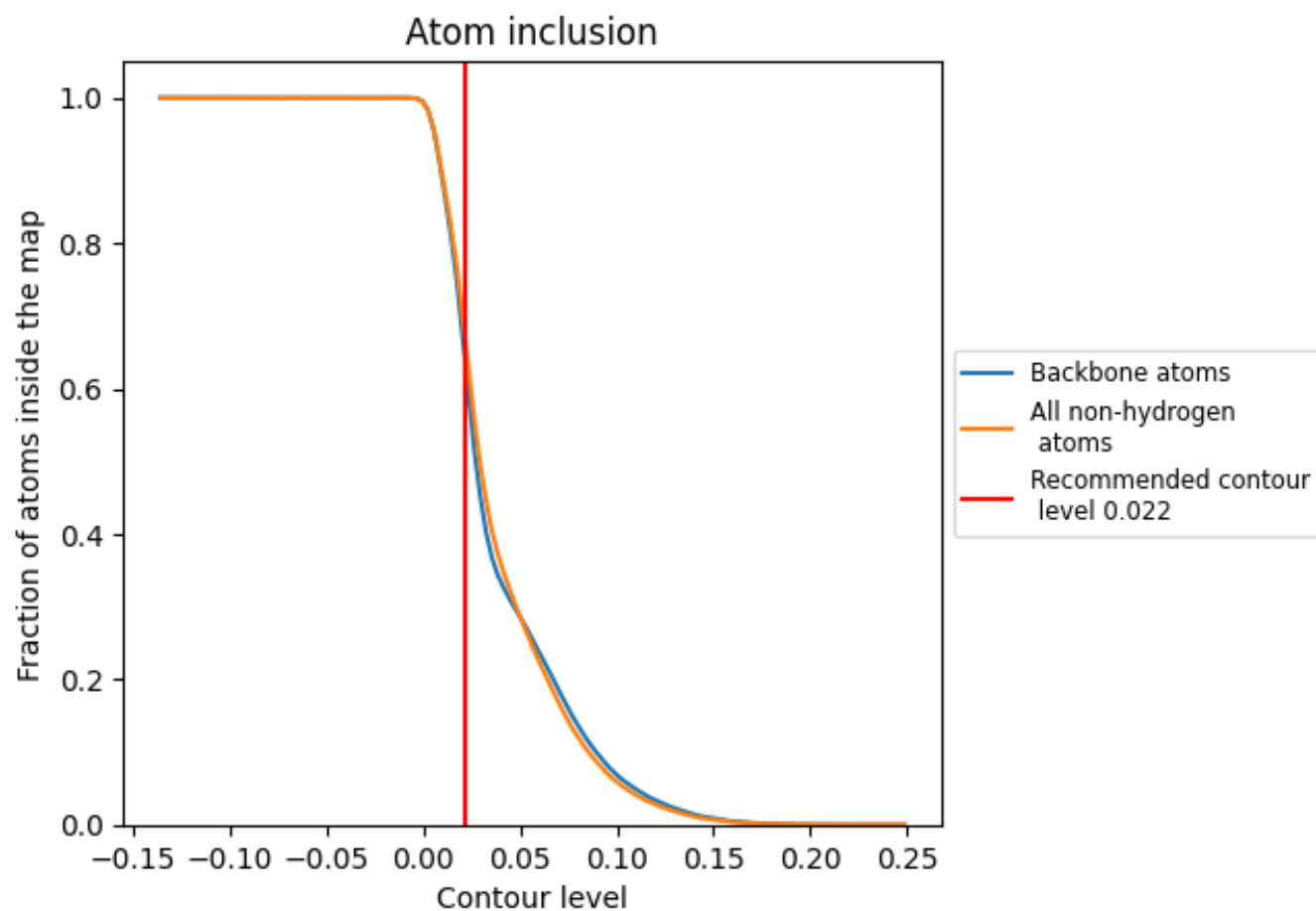
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 66% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6623	 0.1910
0	 0.6446	 0.0150
1	 0.3484	 0.0000
2	 0.2217	 0.0270
3	 0.3134	 -0.0030
4	 0.0696	 -0.0010
5	 0.6371	 -0.0140
6	 0.5566	 0.0050
9	 0.3156	 0.0410
A	 0.9460	 0.3990
B	 0.7987	 0.1080
C	 0.9413	 0.3770
D	 0.7403	 0.0420
E	 0.9334	 0.4360
F	 0.7885	 0.1650
G	 0.3078	 0.0070
H	 0.1278	 0.0120
I	 0.9666	 0.2600
J	 0.9200	 0.3510
K	 0.9365	 0.3910
L	 0.9433	 0.4200
M	 0.9563	 0.4810
N	 0.8601	 0.3180
O	 0.6499	 0.1870
P	 0.6965	 0.0150
Q	 0.7251	 0.0060
R	 0.8775	 0.0420
S	 0.5000	 0.0060
T	 0.5541	 0.0130
U	 0.8189	 0.0140
V	 0.4444	 0.0190
W	 0.6519	 0.0170
X	 0.0063	 0.0000
Y	 0.0000	 -0.0170
Z	 0.0000	 0.0380



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Chain	Atom inclusion	Q-score
a	 0.7671	 0.0500
b	 0.7825	 0.0160
c	 0.7583	 0.0350
d	 0.7278	 0.0790
e	 0.7014	 0.0630
f	 0.7286	 -0.0160
g	 0.4071	 -0.0160
h	 0.0000	 -0.0320
i	 0.0000	 0.0350
j	 0.0000	 -0.0450
k	 0.0000	 -0.0280
l	 0.0000	 0.0300
m	 0.0025	 0.0080
n	 0.0000	 0.0290
o	 0.0000	 -0.0170
p	 0.0000	 -0.0010
q	 0.3723	 0.0020
r	 0.2370	 -0.0630
s	 0.3604	 -0.0040
t	 0.3409	 -0.0020
u	 0.0187	 0.0050
v	 0.1059	 0.0160
w	 0.0047	 -0.0040
x	 0.4730	 0.0370
y	 0.2803	 0.0050
z	 0.5077	 0.0170