



Full wwPDB EM Validation Report ⓘ

Dec 12, 2022 – 09:17 PM EST

PDB ID : 3JCM
EMDB ID : EMD-6561
Title : Cryo-EM structure of the spliceosomal U4/U6.U5 tri-snRNP
Authors : Wan, R.; Yan, C.; Bai, R.; Wang, L.; Huang, M.; Wong, C.C.; Shi, Y.
Deposited on : 2015-12-23
Resolution : 3.80 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:

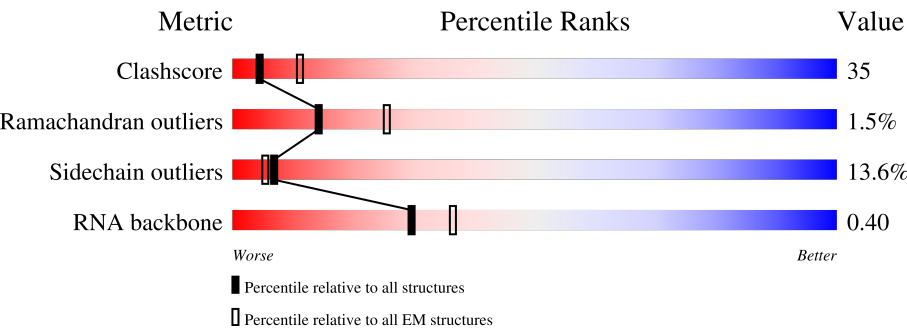
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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.








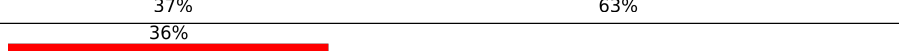
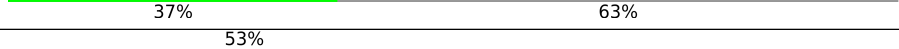









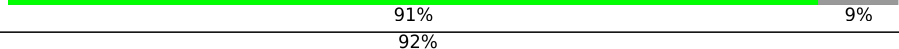
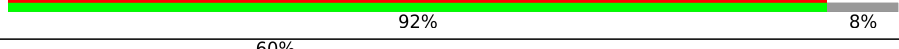

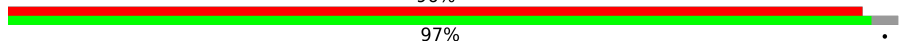




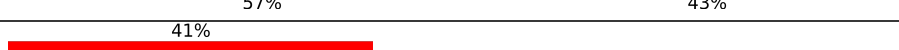
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	<div><div>11%</div><div><div>54%</div><div>28%</div><div>8%</div><div>10%</div></div></div>
2	B	465	<div><div>40%</div><div>43%</div><div>9%</div><div>8%</div></div>
3	I	494	<div><div>42%</div><div>31%</div><div>10%</div><div>16%</div></div>
4	G	899	<div><div>53%</div><div>22%</div><div>7%</div><div>18%</div></div>
5	K	469	<div><div>35%</div><div>20%</div><div>41%</div></div>
6	L	143	<div><div>50%</div><div>38%</div><div>8%</div></div>
7	M	126	<div><div>75%</div><div>21%</div><div>5%</div></div>

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Mol	Chain	Length	Quality of chain
8	H	1008	
9	N	2163	
10	J	101	
10	R	101	
11	O	196	
11	S	196	
12	P	146	
12	T	146	
13	Q	110	
13	U	110	
14	V	94	
14	Y	94	
15	W	86	
15	Z	86	
16	X	77	
16	a	77	
17	b	109	
18	c	95	
19	d	89	
20	e	86	
21	f	93	
22	g	115	
23	h	187	
24	C	20	
25	D	112	

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Mol	Chain	Length	Quality of chain
26	E	160	
27	F	214	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
28	GTP	H	1500	-	-	X	-

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 58253 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	2174	Total	C	N	O	S	0	0
			16889	10715	2978	3138	58		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3378	2102	610	652	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	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	G	734	Total	C	N	O	S	0	0
			4927	3063	911	939	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	279	Total	C	N	O	S	0	0
			2328	1476	422	416	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	139	Total	C	N	O	S	0	0
			1146	725	199	211	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	H	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	1686	Total	C	N	O	0	0
			6744	3372	1686	1686		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	79	Total	C	N	O	0	0
			316	158	79	79		
10	J	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	S	73	Total	C	N	O	0	0
			292	146	73	73		
11	O	73	Total	C	N	O	0	0
			292	146	73	73		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	77	Total	C	N	O	0	0
			308	154	77	77		
12	P	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	90	Total	C	N	O	0	0
			360	180	90	90		
13	Q	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	72	Total	C	N	O	0	0
			288	144	72	72		
14	Y	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	70	Total	C	N	O	0	0
			280	140	70	70		
15	Z	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	X	70	Total	C	N	O	0	0
			280	140	70	70		
16	a	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	f	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	g	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 24 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	20	Total	C	N	O	P	0	0
			429	193	79	137	20		

- Molecule 25 is a RNA chain called SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	45	Total	C	N	O	P	0	0
			945	422	170	308	45		

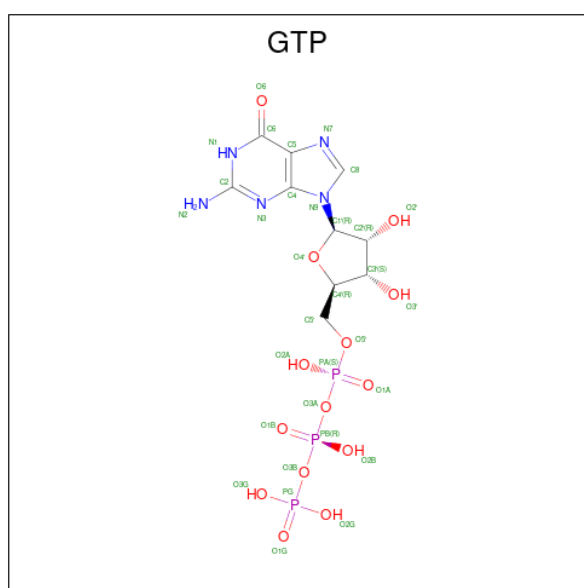
- Molecule 26 is a RNA chain called SNR14 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

- Molecule 27 is a RNA chain called SNR7-L snRNA.

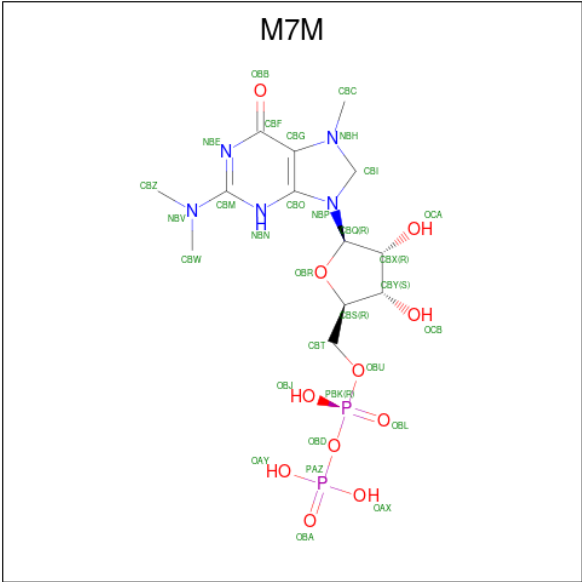
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 29 is N,N,7-trimethylguanosine 5'-(trihydrogen diphosphate) (three-letter code: M7M) (formula: $C_{13}H_{23}N_5O_{11}P_2$).

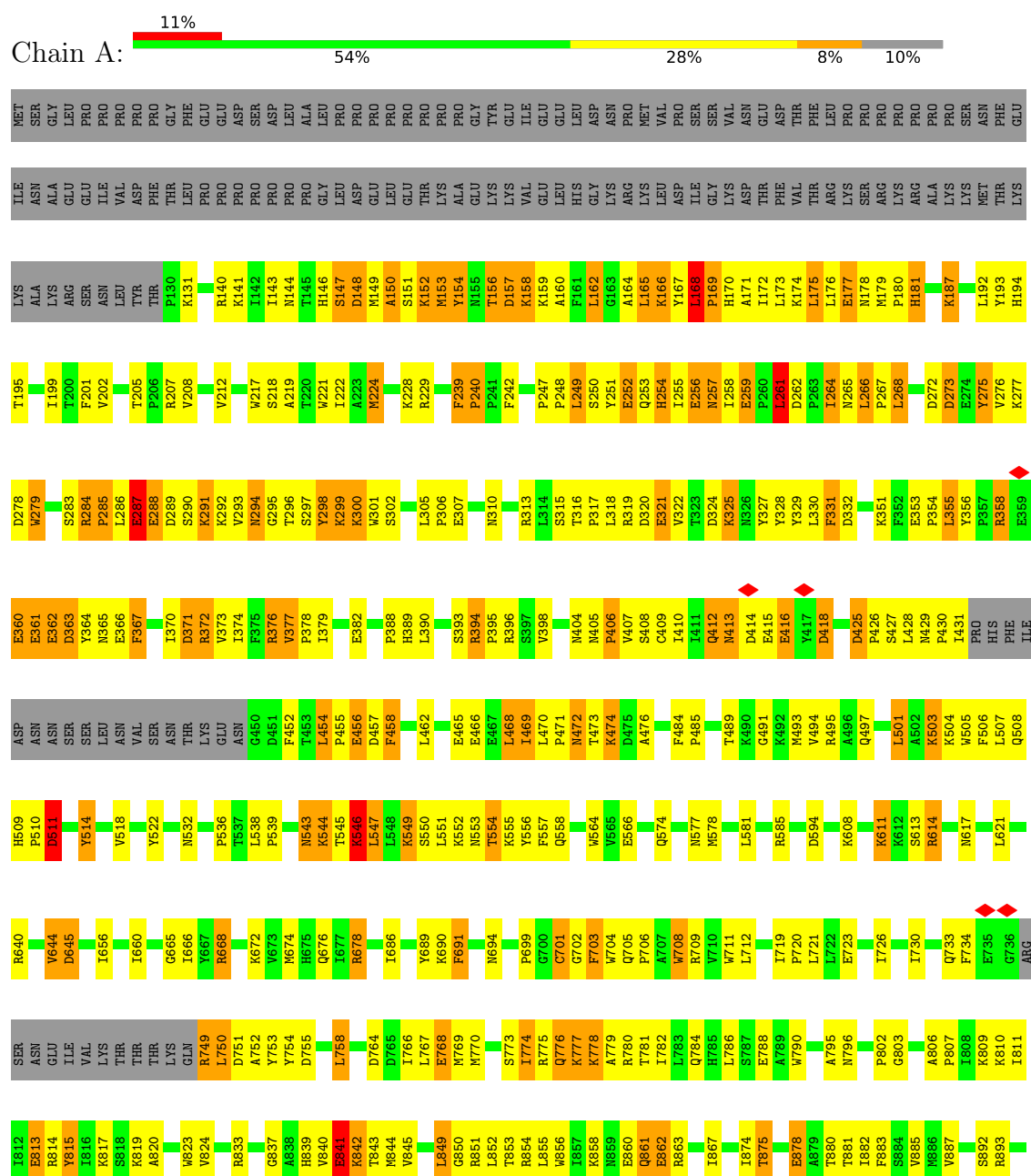


Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	

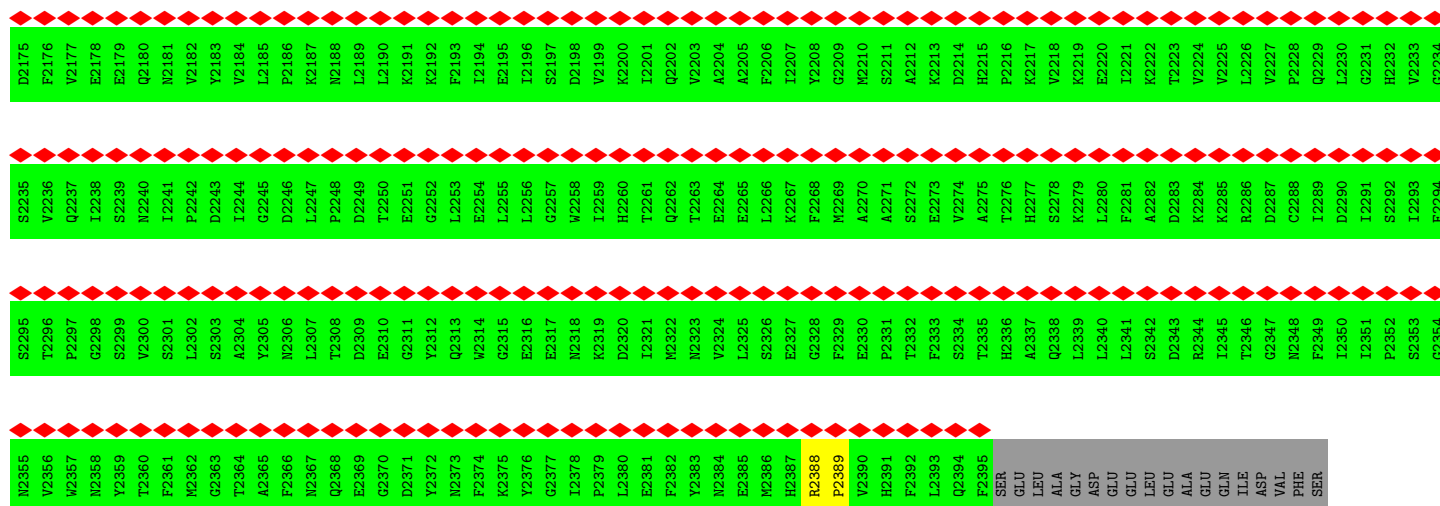
3 Residue-property plots

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

• Molecule 1: Pre-mRNA-splicing factor 8

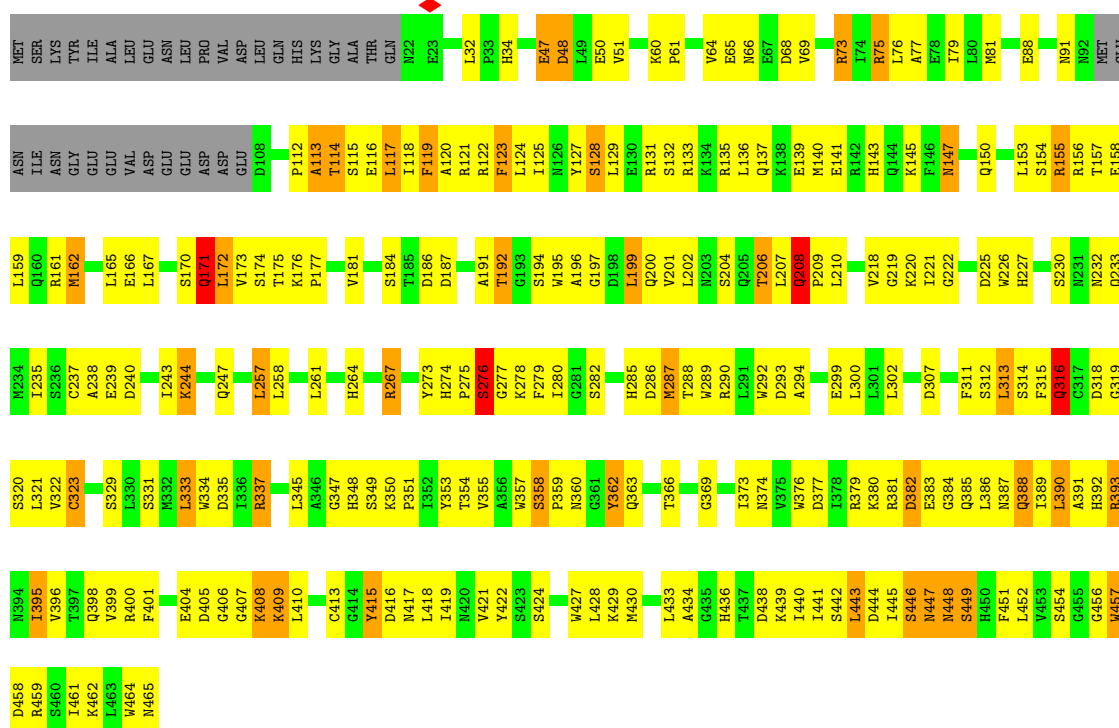


ALA	P2043	K1912	L1835	L1738	D1628	G1534	S1454	L1357	R1274	M1170	I1073	L995	P897
GLY	E2046	T1913	N1836	R1739	L1629	K1535	Q1455	D1358	E1275	L1171	V1074	Y998	F900
ALA		A1914	L1837	S1745	T1630	L1536	R1456	I1359	E1276	H1172	D1075	Y999	P901
SER		E1915	N1839	H1746	G1631	G1631	V1457		E1277	H1173	P1076		
THR		E1916	E1842	D1747	F1632	Y1542	A1458	T1364	V1278	E1175	I1078	E1002	D908
VAL		T2050		I1748	L1634	L1557	A1459	R1366	V1279		A1079	R1006	T909
MET			N1846	Y1751	H1635	E1558	Y1461	I1367		G1179	D1080	K1006	K910
LYS				V1752		H1560	A1462	Q1368	D1282	L1182	I1081	K1007	I911
THR			L1850	F1755	Q1647	L1561	T1463	N1369	E1283	T1183	I1082	K1008	L912
LYS			F1851	K1756	R1649	L1562	K1465		G1284	D1184	T1083	P1009	L912
ILE			D1854	F1756	F1650	F1574		L1373	V1285	F1195	M1087	M1011	D921
ASN			T1855	L1757	A1651	K1577	A1468	K1378	E1287	E1196	V1089	W1012	Y923
ALA			V1856	D1758	H1652	K1577	I1469	M1379		N1197	V1089	I1013	R928
GLN			V1857	Y1759	L1653	L1578	Q1470	P1380		K1014	P1015	K1014	L929
GLY				T1760	W1654	A1578	R1473	T1381		N1202	M1095	S1016	N930
GLU			H1863	T1761	I1657	S1579	R1474	R1382		N1203	S1096	D1017	A931
GLU			K1864	D1762	H1658	G1580	L1475	F1383		R1204	H1097	S1018	S932
ILE			T1865	Y1767		F1581	A1476	P1384		K1205	E1019	E1019	E933
VAL			E1867	T1775	I1661	E1582	F1477	A1386		W1207	Y1101	P1021	E936
VAL			G1868	T1771	V1662	M1585	E1478	Y1389		P1208	R1105	P1022	L937
VAL			V1869	G1772	F1663	Q1586	E1479	T1390		K1209	G1106	L1023	A938
SER			V1870	V1773	D1664		L1480	P1391		D1210	L1107	L1024	L939
ALA			A1871	H1774		K1589	E1481	E1392		S1211	F1109	V1025	I940
ASP						L1590		E1393		R1214	F1114	T1029	A943
TYR						G1776	W1484	E1393		L1215	Q1115	N1033	Y944
GLU			I1875	Y1787	S1697	T1591	T1488	T1400		L1216	Y1116	N1034	L951
GLU			N1876	G1788	A1698	H1592	P1489	S1401		R1217	G1118	L1035	A952
SER			C1877	N1789	A1699	Q1593	R1490	L1406		L1221	L1125	T1038	R953
THR			I1879	W1790		Q1594		E1497		V1234		W1039	K955
GLN			F1880	F1791	M1694	R1595	D1498	I1407			Q1128	D1040	K956
ASN			T1881			L1598	L1494	H1404		L1238		V1041	Y957
ILE			L1882	Y1787	S1697	T1601	R1495	T1414		A1246	E1143	G1044	L958
ALA			P1883	G1788	A1698	A1698	Q1496	S1415		F1247	F1144	A1047	L959
PRO			P1884	N1789	A1699	P1602	L1497	K1416		M1248	M1145	V1048	T960
SER			K1885	W1790			D1498	Q1417			Q1146	L1049	Q961
VAL			T1886	F1791	M1703	P1605	R1499	T1418		K1253	F1147	L1051	R962
LYS			G1887	K1795	E1704	F1606	H1500			N1254	E1153	E1051	V967
ARG			H1888	P1796	S1705	T1607	L1502			N1255	H1156	L1054	M971
GLN			L1889			L1608	L1501			N1256	P1157	L1054	E972
LYS				S1801	W1709	W1609	H1508			N1257	I1158	A1058	N974
MET			K1892		E1710	W1610				L1258	R1159	E1059	Y975
ALA			I1893		V1711	S1611	R1509			L1259	L1160	A1058	Q976
GLU			L1894		S1712	P1612	H1500			S1261	T1162	T1061	I978
LEU			H1895		K1713	T1613	I1510			M1262	H1163	L1065	Y862
GLU			T1896		P1714	I1614	R1512			G1264	Y1164	L1066	
ALA					S1715	N1615	L1519			F1265	L1165	L1066	
ALA						R1616	E1520			E1266	I1168	N1067	T991
ARG			W1899		E1719	A1617	E1520			V1267	Y1169	R1068	D992
SER			Q1902			N1618	L1521			G1268		L1065	
GLU										G1268		L1066	
LYS			L1905		K1730	V1621	F1525			G1268		L1066	
GLN			S1906		M1732	G1622	W1526			G1268		L1066	
ASN			Q1907		W1733	F1623	N1527			G1268		L1066	
ASP			L1908		F1734	L1624	T1528			G1268		L1066	
GLU			P1909		D1735	V1625	N1529			G1268		L1066	
GLU			A1910		V1736	Q1626	N1529			G1268		L1066	
ALA			W1911		Q1737	L1627	D1533			G1268		L1066	



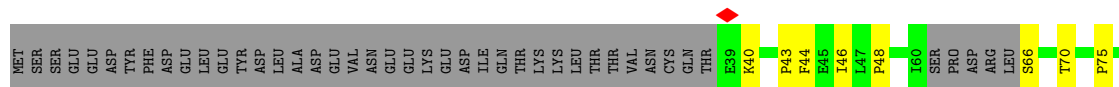
• Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

Chain B: 40% 43% 9% 8%



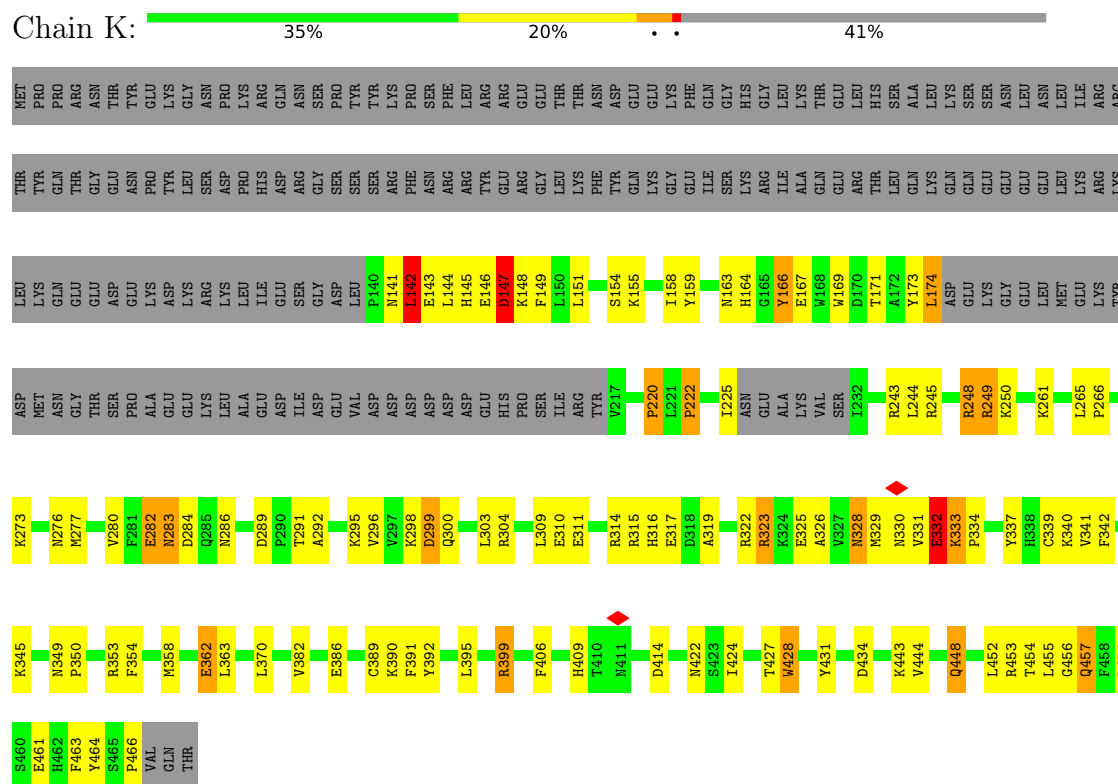
• Molecule 3: Pre-mRNA-processing factor 31

Chain I: 42% 31% 10% 16%

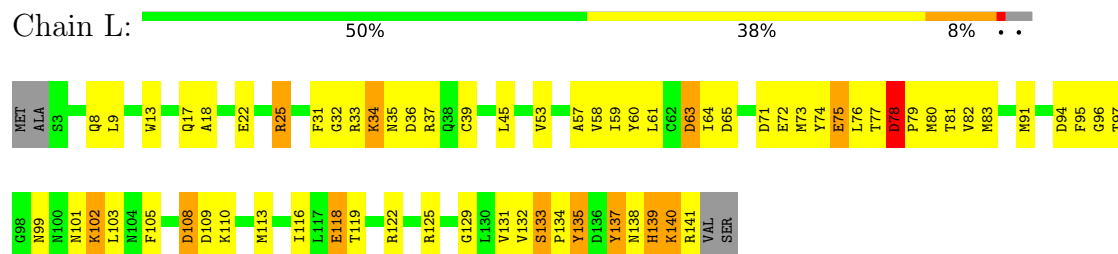




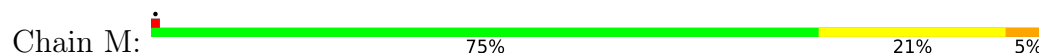
- Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3

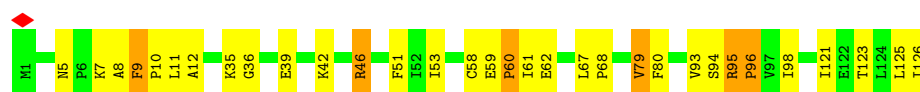


- Molecule 6: Spliceosomal protein DIB1

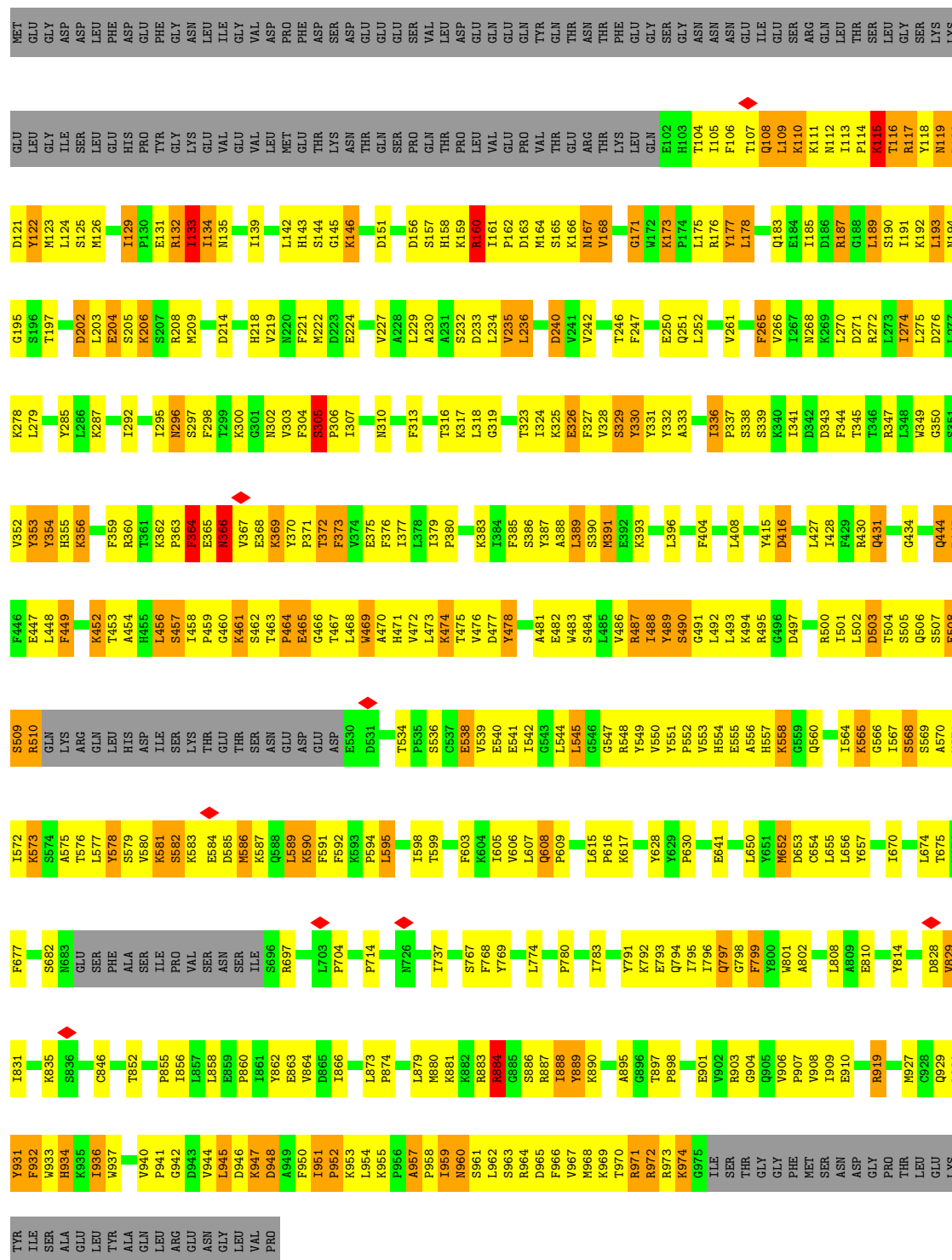


- Molecule 7: 13 kDa ribonucleoprotein-associated protein





• Molecule 8: Pre-mRNA-splicing factor SNU114

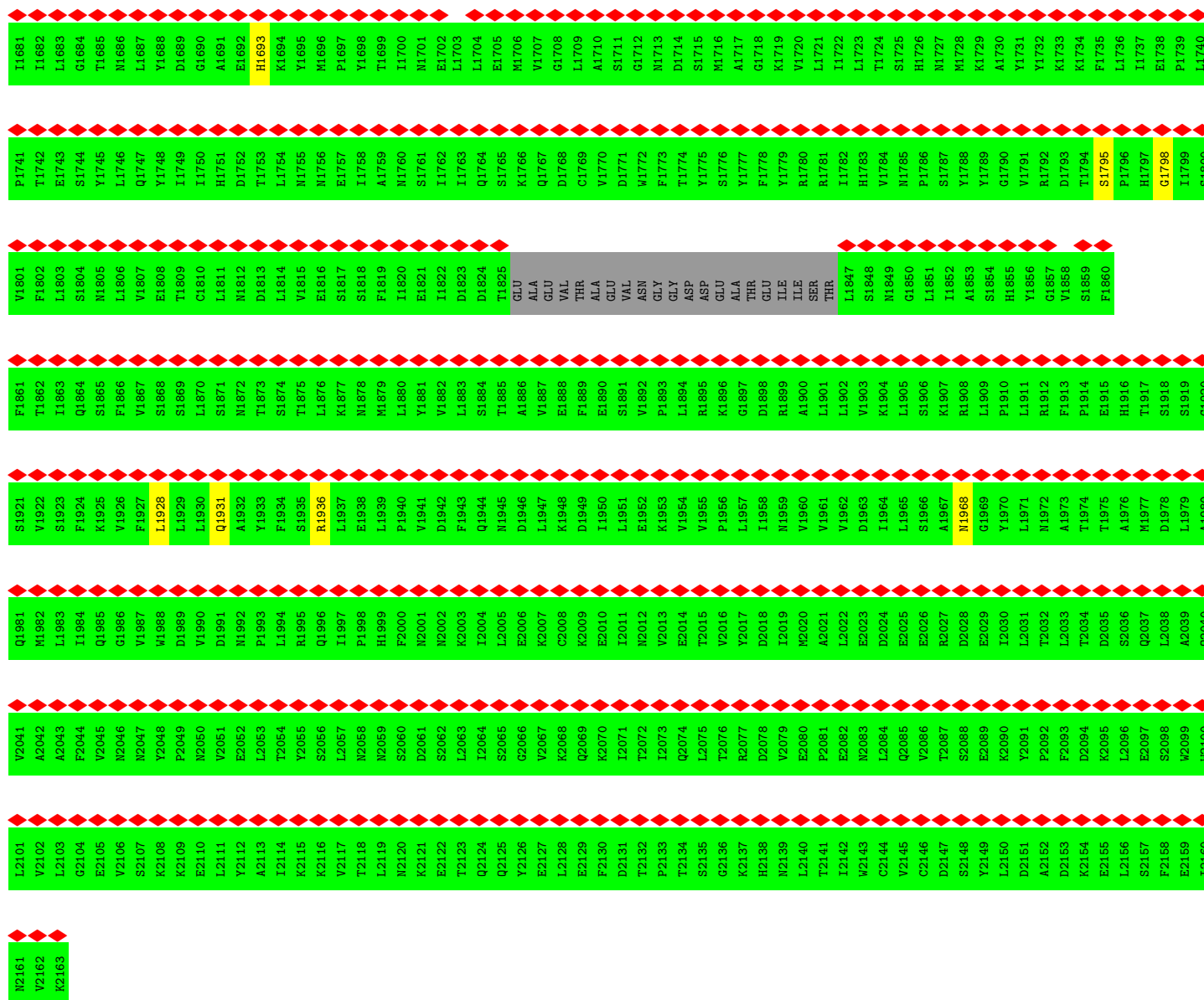


Chain N:

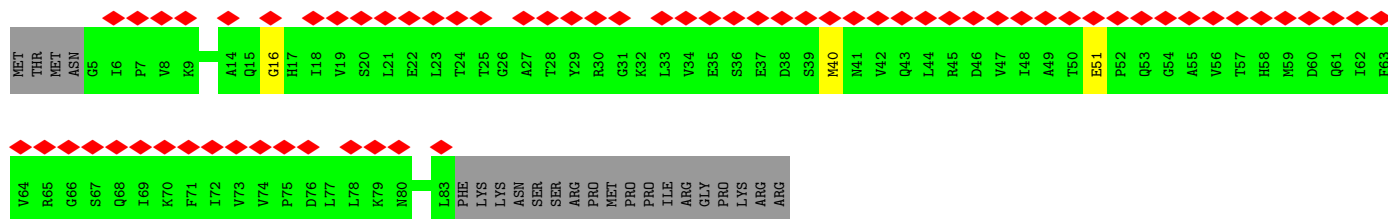
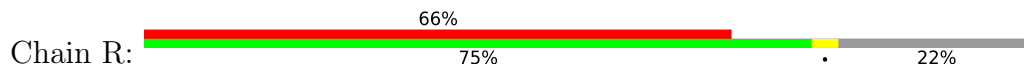


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H843	T783	N723	E663	Q603	H543	L483	PRO	LYS	GLY	ASN	ILE	ASN	GLN	GLY	HIS
T844	E784	D724	Y664	V604	H544	P484	PRO	SER	ASP	LYS	VAL	GLN	GLN	LEU	GLY
V845	A785	A725	P665	V606	H546	D485	VAL	THR	THR	THR	VAL	VAL	THR	CYS	THR
I846	A786	C726	R666	V606	H546	W486	ILE	GLU	SER	VAL	LYS	ASN	ASN	ASN	LYS
L847	N787	T727	I667	S607	T547	C487	ASP	ASN	VAL	SER	GLU	GLY	THR	GLY	LYS
K848	N788	E728	I668	T608	H548	Q488	LYS	PRO	ASN	VAL	VAL	ILE	ASN	GLY	LYS
G849	L789	K729	G669	P609	H549	E489	GLU	GLY	GLY	GLY	VAL	ILE	GLY	GLY	ALA
T850	D790	V730	L670	E610	L550	A490	ILE	ASN	PRO	ASN	GLY	ASN	LYS	LYS	ALA
D851	P791	L731	S671	K611	N551	F491	LYS	LEU	LEU	SER	THR	THR	ASN	LEU	ILE
V852	S792	E732	A672	W612	L552	P492	PHE	ILE	GLY	GLY	ASP	TYR	LYS	LYS	ARG
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S854	K794	I734	L674	I614	A554	S494	SER	VAL	VAL	ASN	HIS	THR	ASP	VAL	ARG
R855	K795	N735	P675	T615	F555	E495	LYS	ALA	ASN	LYS	PRO	ASP	PRO	ALA	TYR
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F883	G823	E763	L703	R643	T583	T523	P468	ARG	ARG	SER	ARG	ILE	ILE	SER	GLY
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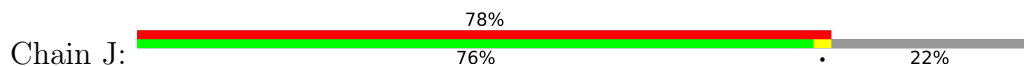
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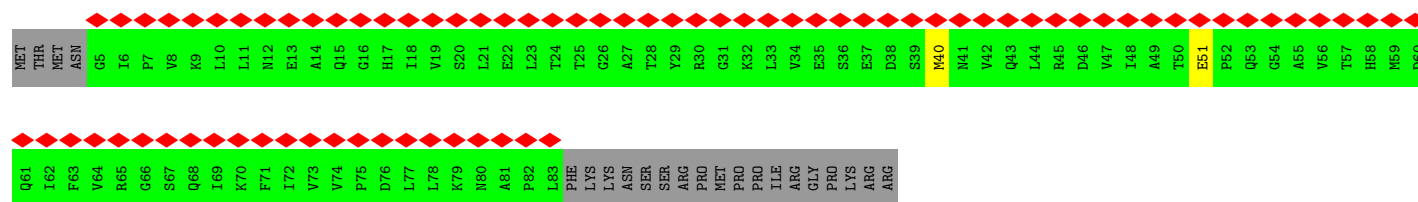


• Molecule 10: Small nuclear ribonucleoprotein Sm D3

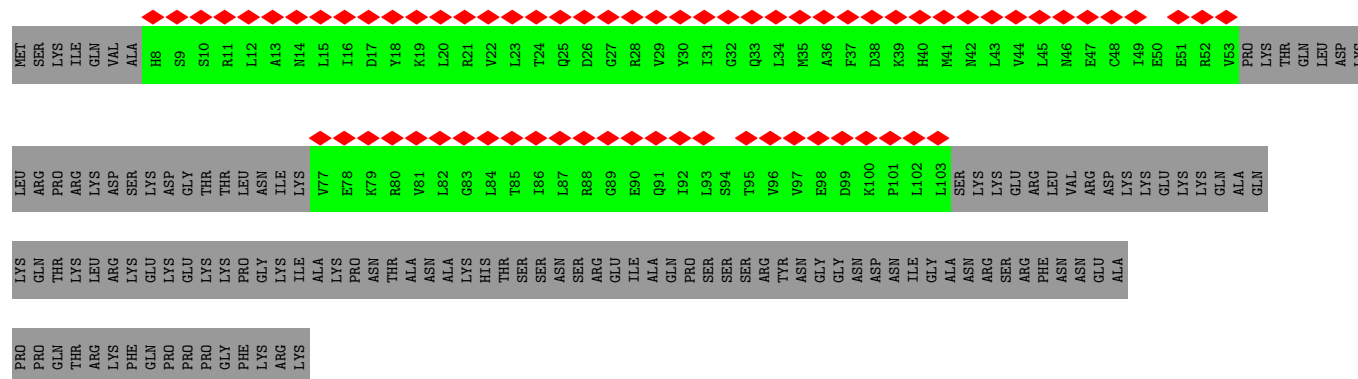


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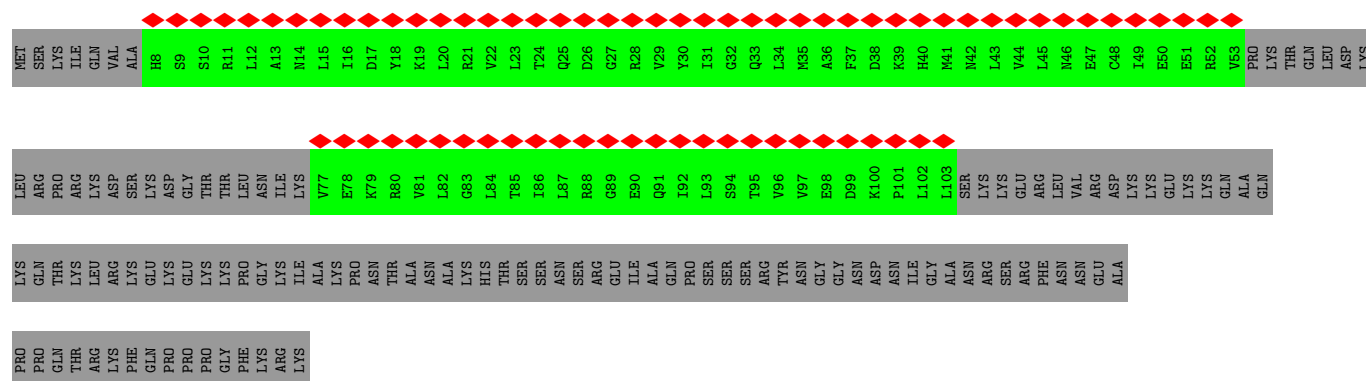




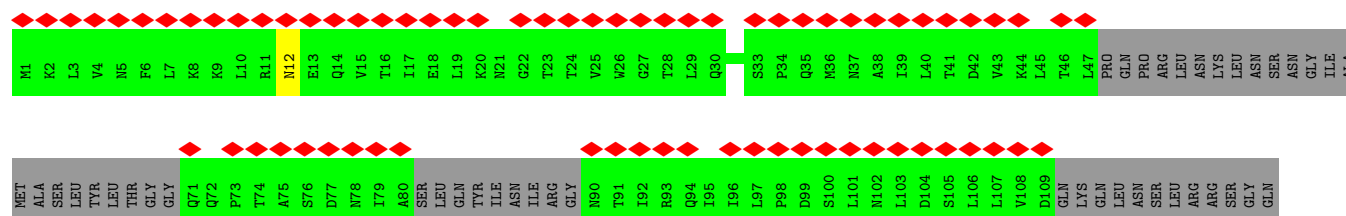
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B

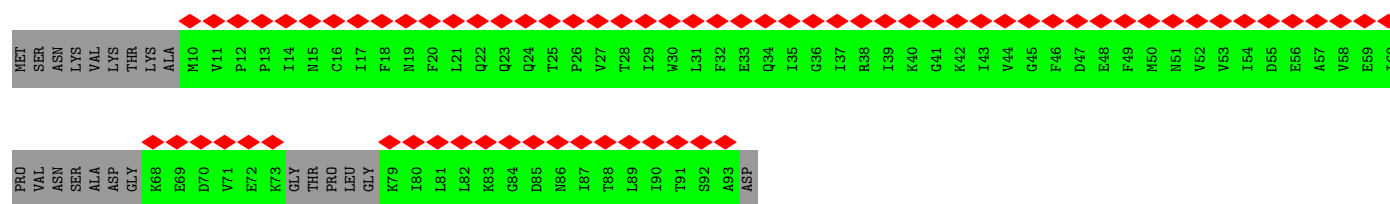
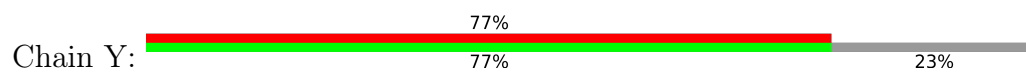


• Molecule 11: Small nuclear ribonucleoprotein-associated protein B

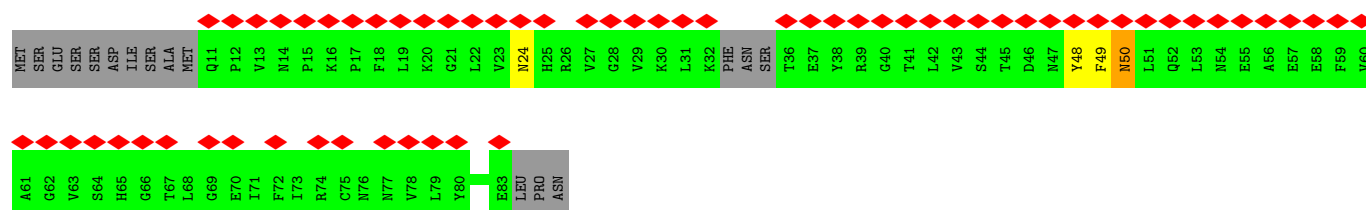
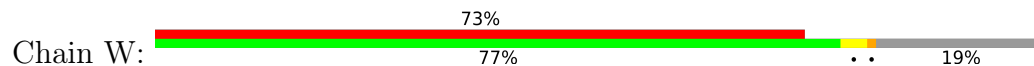


• Molecule 12: Small nuclear ribonucleoprotein Sm D1

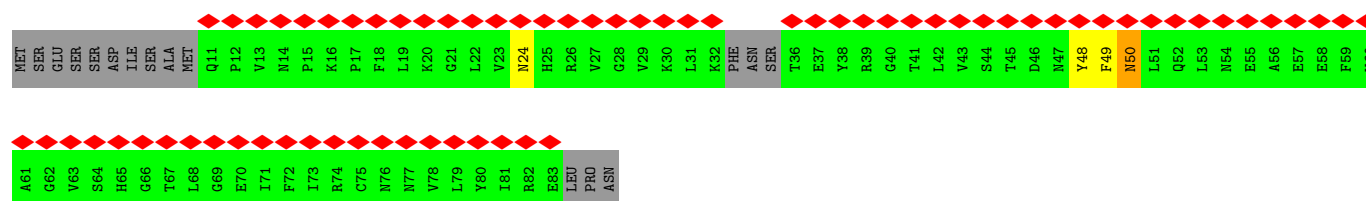
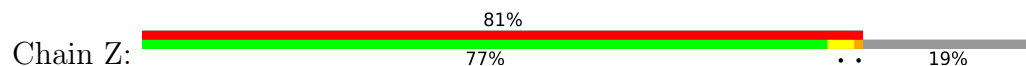




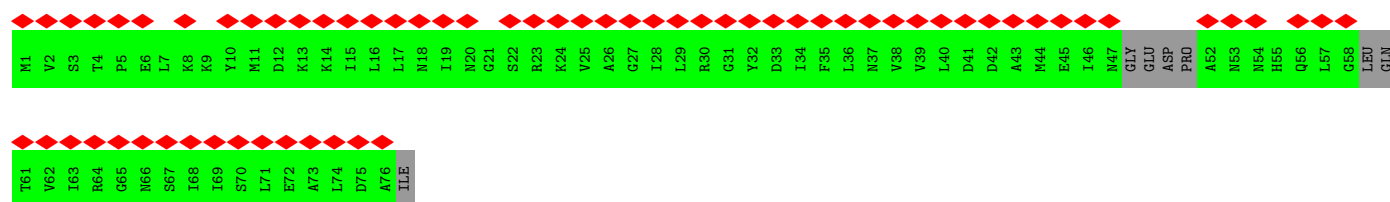
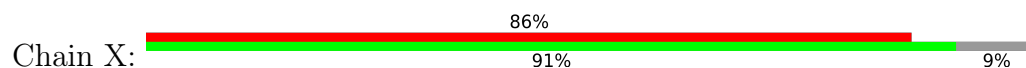
• Molecule 15: Small nuclear ribonucleoprotein F



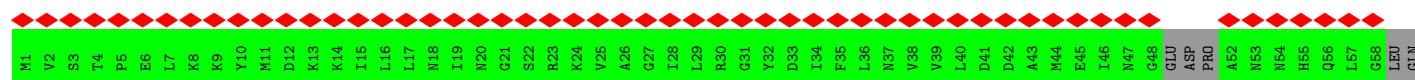
• Molecule 15: Small nuclear ribonucleoprotein F



• Molecule 16: Small nuclear ribonucleoprotein G

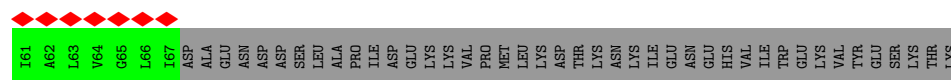


• Molecule 16: Small nuclear ribonucleoprotein G

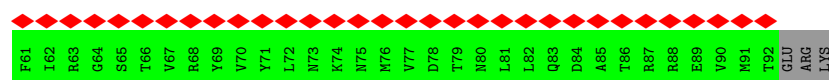
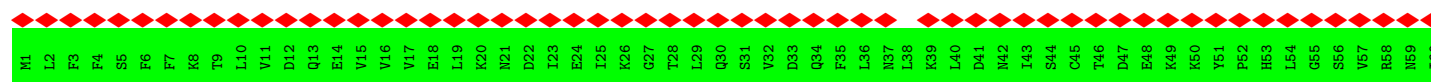




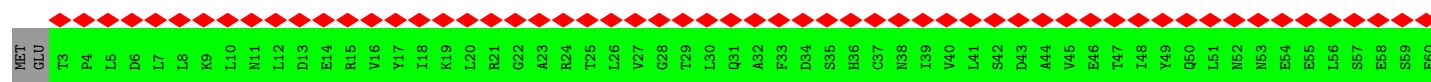
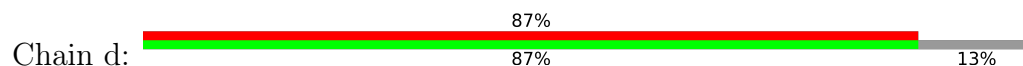
- Molecule 17: U6 snRNA-associated Sm-like protein LSm8



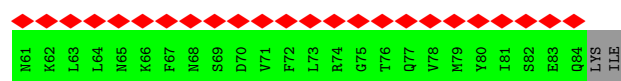
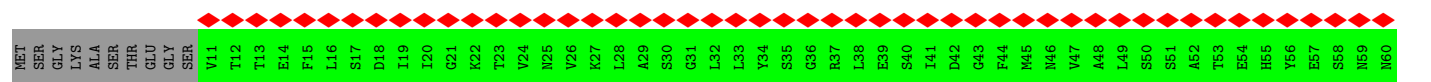
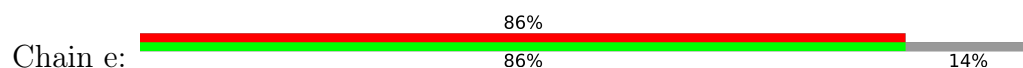
- Molecule 18: U6 snRNA-associated Sm-like protein LSm2



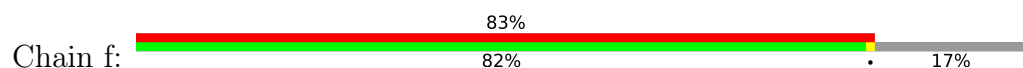
- Molecule 19: U6 snRNA-associated Sm-like protein LSm3

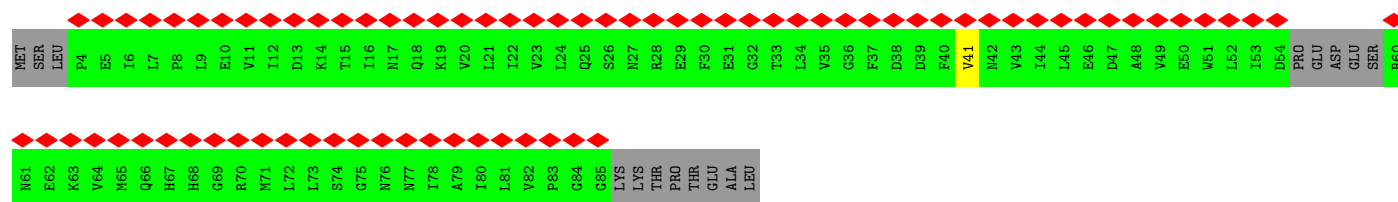


- Molecule 20: U6 snRNA-associated Sm-like protein LSm6



- Molecule 21: U6 snRNA-associated Sm-like protein LSm5





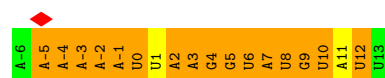
• Molecule 22: U6 snRNA-associated Sm-like protein LSm7



• Molecule 23: U6 snRNA-associated Sm-like protein LSm4



• Molecule 24: pre-mRNA

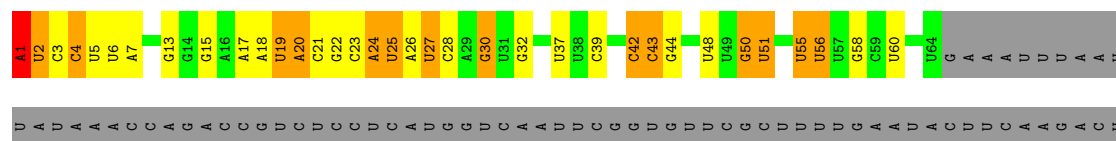


• Molecule 25: SNR6 snRNA

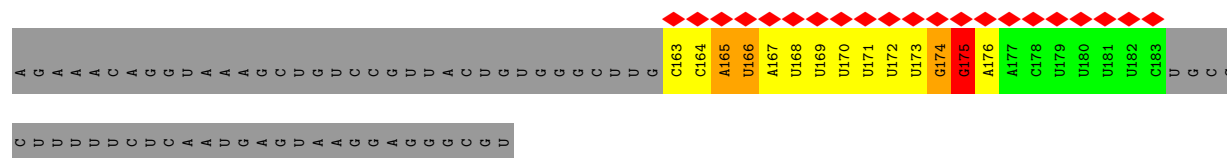
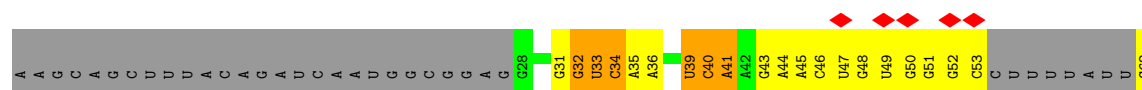
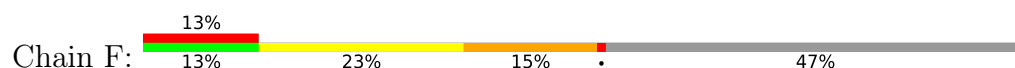




• Molecule 26: SNR14 snRNA



• Molecule 27: SNR7-L snRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	172134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
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	0.204	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0147	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: M7M, GTP

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	0.86	22/17296 (0.1%)	0.91	24/23336 (0.1%)
2	B	0.72	2/3434 (0.1%)	0.86	0/4635
3	I	0.84	1/3219 (0.0%)	0.99	13/4332 (0.3%)
4	G	0.62	3/4967 (0.1%)	0.79	14/6746 (0.2%)
5	K	0.67	1/2376 (0.0%)	0.83	3/3183 (0.1%)
6	L	0.73	0/1167	0.87	0/1571
7	M	0.95	0/963	1.02	2/1310 (0.2%)
8	H	0.55	2/6874 (0.0%)	0.78	8/9305 (0.1%)
9	N	0.52	0/6738	0.65	0/8412
10	J	0.29	0/315	0.46	0/392
10	R	0.29	0/315	0.46	0/392
11	O	0.28	0/290	0.46	0/359
11	S	0.28	0/290	0.46	0/359
12	P	0.27	0/305	0.47	0/376
12	T	0.27	0/305	0.46	0/376
13	Q	0.25	0/354	0.45	0/439
13	U	0.25	0/358	0.45	0/444
14	V	0.29	0/285	0.43	0/351
14	Y	0.29	0/285	0.43	0/351
15	W	0.30	0/278	0.45	0/344
15	Z	0.30	0/278	0.45	0/344
16	X	0.24	0/277	0.46	0/341
16	a	0.27	0/281	0.46	0/346
17	b	0.48	0/259	0.70	0/322
18	c	0.49	0/367	0.66	0/457
19	d	0.58	0/307	0.74	0/382
20	e	0.48	0/295	0.68	0/367
21	f	0.50	0/306	0.71	0/379
22	g	0.48	0/262	0.71	0/324
23	h	0.47	0/306	0.68	0/379
24	C	0.34	0/481	0.71	0/747
25	D	0.81	0/1054	0.93	3/1634 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	E	0.94	8/2016 (0.4%)	1.12	17/3136 (0.5%)
27	F	0.44	2/2659 (0.1%)	0.80	1/4131 (0.0%)
All	All	0.70	41/59562 (0.1%)	0.84	85/80302 (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	3
2	B	0	2
3	I	0	1
4	G	0	7
5	K	0	1
7	M	0	4
8	H	0	2
All	All	0	20

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	E	1	A	C5-C4	10.58	1.46	1.38
26	E	1	A	N7-C5	-8.64	1.34	1.39
1	A	1335	TRP	CG-CD2	-8.36	1.29	1.43
26	E	1	A	N9-C4	-8.09	1.32	1.37
26	E	1	A	C5-C6	7.52	1.47	1.41
1	A	1335	TRP	CE2-CZ2	-7.42	1.27	1.39
2	B	415	TYR	CE2-CZ	-7.38	1.28	1.38
5	K	428	TRP	CB-CG	-7.31	1.37	1.50
26	E	151	G	C1'-N9	-6.91	1.37	1.46
27	F	175	G	C1'-N9	-6.89	1.37	1.46
4	G	146	TYR	CE1-CZ	-6.75	1.29	1.38
26	E	142	G	C1'-N9	-6.75	1.37	1.46
1	A	856	TRP	CB-CG	-6.67	1.38	1.50
1	A	1335	TRP	CE3-CZ3	-6.46	1.27	1.38
1	A	1081	TYR	CE1-CZ	-6.35	1.30	1.38
1	A	1992	TYR	CE2-CZ	-6.32	1.30	1.38
4	G	146	TYR	CG-CD2	-6.10	1.31	1.39
26	E	155	A	C1'-N9	-6.08	1.38	1.46
1	A	1562	PHE	CB-CG	-6.06	1.41	1.51
1	A	1161	TYR	CB-CG	-5.89	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1383	PHE	CB-CG	-5.85	1.41	1.51
1	A	1012	TRP	CG-CD2	-5.79	1.33	1.43
2	B	415	TYR	CG-CD1	-5.71	1.31	1.39
26	E	17	A	O3'-P	-5.67	1.54	1.61
1	A	1542	TYR	CG-CD1	-5.61	1.31	1.39
1	A	1610	TRP	CD2-CE3	-5.56	1.32	1.40
4	G	774	TRP	CB-CG	-5.54	1.40	1.50
27	F	76	U	C1'-N1	5.45	1.56	1.48
1	A	1609	TRP	CB-CG	-5.42	1.40	1.50
1	A	708	TRP	CB-CG	-5.42	1.40	1.50
3	I	375	TYR	CG-CD1	-5.38	1.32	1.39
1	A	1116	TYR	CB-CG	-5.33	1.43	1.51
1	A	711	TRP	CB-CG	-5.32	1.40	1.50
8	H	958	PRO	N-CD	5.22	1.55	1.47
8	H	445	PRO	N-CD	5.15	1.55	1.47
1	A	1610	TRP	CG-CD2	-5.12	1.34	1.43
1	A	1117	TYR	CB-CG	-5.07	1.44	1.51
1	A	1542	TYR	CE1-CZ	-5.04	1.31	1.38
1	A	169	PRO	N-CD	5.04	1.54	1.47
1	A	1527	TRP	CE3-CZ3	-5.03	1.29	1.38
1	A	285	PRO	N-CD	5.01	1.54	1.47

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	E	1	A	C2-N3-C4	20.61	120.90	110.60
4	G	853	GLY	N-CA-C	12.86	145.25	113.10
26	E	1	A	N3-C4-C5	-11.57	118.70	126.80
8	H	951	ILE	C-N-CD	-10.75	96.95	120.60
1	A	1616	ARG	NE-CZ-NH1	10.12	125.36	120.30
26	E	1	A	N1-C2-N3	-9.87	124.37	129.30
26	E	1	A	N3-C4-N9	9.78	135.23	127.40
1	A	854	ARG	NE-CZ-NH2	-9.76	115.42	120.30
1	A	1268	ARG	NE-CZ-NH2	-9.14	115.73	120.30
25	D	61	C	O5'-P-OP2	-8.48	98.06	105.70
26	E	1	A	N9-C1'-C2'	-8.26	102.92	112.00
1	A	1616	ARG	NE-CZ-NH2	-8.16	116.22	120.30
4	G	852	LEU	N-CA-C	8.11	132.89	111.00
26	E	1	A	C4-C5-N7	-8.03	106.69	110.70
3	I	393	PHE	CB-CG-CD2	-7.84	115.31	120.80
26	E	50	G	O5'-P-OP2	7.67	119.91	110.70
3	I	393	PHE	CB-CG-CD1	7.51	126.06	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	E	1	A	C8-N9-C4	7.45	108.78	105.80
4	G	493	PRO	N-CA-CB	7.43	112.22	103.30
26	E	1	A	C5-N7-C8	7.38	107.59	103.90
1	A	1818	ARG	NE-CZ-NH2	-7.35	116.63	120.30
5	K	142	LEU	N-CA-C	7.25	130.59	111.00
1	A	1344	THR	CA-CB-CG2	-7.24	102.27	112.40
1	A	1095	MET	CG-SD-CE	-7.08	88.88	100.20
1	A	1263	CYS	CA-CB-SG	-7.00	101.40	114.00
3	I	304	ARG	NE-CZ-NH2	-6.98	116.81	120.30
4	G	396	PRO	N-CA-CB	6.84	111.51	103.30
4	G	399	PRO	N-CA-CB	6.77	111.42	103.30
7	M	79	VAL	CB-CA-C	-6.68	98.70	111.40
4	G	558	PRO	N-CA-CB	6.67	111.31	103.30
3	I	367	ARG	NE-CZ-NH1	-6.67	116.97	120.30
4	G	510	PRO	N-CA-CB	6.64	111.27	103.30
26	E	1	A	P-O3'-C3'	-6.63	111.74	119.70
5	K	222	PRO	N-CA-CB	6.58	111.20	103.30
1	A	668	ARG	NE-CZ-NH1	6.55	123.57	120.30
3	I	48	PRO	N-CA-CB	6.52	111.12	103.30
4	G	417	PRO	N-CA-CB	6.47	111.07	103.30
4	G	455	PRO	N-CA-CB	6.44	111.03	103.30
3	I	43	PRO	N-CA-CB	6.42	111.00	103.30
4	G	414	PRO	N-CA-CB	6.41	110.99	103.30
5	K	220	PRO	N-CA-CB	6.39	110.97	103.30
4	G	366	PRO	N-CA-CB	6.30	110.86	103.30
3	I	75	PRO	N-CA-CB	6.24	110.78	103.30
27	F	83	C	C4'-C3'-O3'	6.19	125.39	113.00
1	A	962	ARG	NE-CZ-NH1	-6.19	117.21	120.30
26	E	42	C	O5'-P-OP1	-6.15	100.16	105.70
1	A	1605	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	953	ARG	NE-CZ-NH2	-6.10	117.25	120.30
26	E	1	A	C6-C5-N7	6.00	136.50	132.30
8	H	464	PRO	N-CA-CB	5.95	110.44	103.30
3	I	390	ARG	NE-CZ-NH2	-5.94	117.33	120.30
3	I	401	LEU	CB-CG-CD1	-5.93	100.91	111.00
1	A	394	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	893	ARG	NE-CZ-NH2	-5.89	117.35	120.30
26	E	1	A	N7-C8-N9	-5.86	110.87	113.80
1	A	284	ARG	C-N-CD	5.80	140.57	128.40
8	H	370	TYR	C-N-CD	5.79	140.55	128.40
1	A	1823	LEU	CB-CG-CD1	-5.79	101.17	111.00
1	A	1335	TRP	CD1-NE1-CE2	-5.74	103.83	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	129	ILE	C-N-CD	5.74	140.45	128.40
1	A	168	LEU	C-N-CD	5.72	140.41	128.40
8	H	444	GLN	C-N-CD	5.68	140.34	128.40
8	H	957	ALA	C-N-CD	5.60	140.16	128.40
1	A	1089	VAL	N-CA-C	-5.58	95.92	111.00
4	G	152	LEU	CB-CG-CD1	-5.55	101.56	111.00
25	D	80	U	C5-C6-N1	-5.50	119.95	122.70
3	I	280	ARG	NE-CZ-NH2	-5.50	117.55	120.30
8	H	607	LEU	CB-CG-CD1	-5.49	101.67	111.00
1	A	1163	ARG	NE-CZ-NH2	-5.48	117.56	120.30
4	G	335	PRO	N-CA-CB	5.46	109.86	103.30
1	A	157	ASP	N-CA-C	5.46	125.73	111.00
26	E	1	A	O3'-P-O5'	5.40	114.25	104.00
3	I	429	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	1107	LEU	CB-CG-CD1	-5.26	102.06	111.00
1	A	1068	ARG	NE-CZ-NH2	-5.23	117.69	120.30
26	E	1	A	C3'-C2'-C1'	5.18	105.65	101.50
3	I	120	TYR	CB-CG-CD2	-5.17	117.90	121.00
26	E	50	G	O5'-P-OP1	-5.11	101.10	105.70
26	E	42	C	O5'-P-OP2	5.10	116.82	110.70
3	I	173	LEU	CB-CG-CD1	-5.09	102.35	111.00
25	D	80	U	N1-C2-N3	5.08	117.95	114.90
7	M	9	PHE	C-N-CD	-5.07	109.44	120.60
8	H	884	ARG	CG-CD-NE	-5.07	101.15	111.80
4	G	723	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	1739	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1867	GLU	Peptide
1	A	694	ASN	Peptide
2	B	208	GLN	Peptide
2	B	316	GLN	Peptide
4	G	12	PRO	Peptide
4	G	123	PRO	Peptide
4	G	733	ASN	Mainchain,Peptide
4	G	767	PHE	Mainchain,Peptide
4	G	802	GLN	Peptide
8	H	160	ARG	Peptide

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Mol	Chain	Res	Type	Group
8	H	171	GLY	Peptide
3	I	410	LEU	Peptide
5	K	282	GLU	Peptide
7	M	59	GLU	Mainchain,Peptide
7	M	9	PHE	Mainchain,Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16889	0	16134	1106	0
2	B	3378	0	3342	372	0
3	I	3171	0	3140	274	0
4	G	4927	0	4006	390	0
5	K	2328	0	2314	156	0
6	L	1146	0	1133	126	0
7	M	950	0	1004	27	0
8	H	6732	0	6904	868	0
9	N	6744	0	1759	27	0
10	J	316	0	86	0	0
10	R	316	0	86	2	0
11	O	292	0	78	0	0
11	S	292	0	78	0	0
12	P	308	0	78	0	0
12	T	308	0	78	0	0
13	Q	356	0	88	0	0
13	U	360	0	89	0	0
14	V	288	0	74	0	0
14	Y	288	0	74	0	0
15	W	280	0	77	1	0
15	Z	280	0	77	1	0
16	X	280	0	79	0	0
16	a	284	0	82	0	0
17	b	260	0	72	0	0
18	c	368	0	99	0	0
19	d	308	0	80	0	0
20	e	296	0	83	0	0
21	f	308	0	85	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	g	264	0	76	0	0
23	h	308	0	85	0	0
24	C	429	0	214	48	0
25	D	945	0	478	73	0
26	E	1806	0	907	49	0
27	F	2385	0	1209	210	0
28	H	32	0	12	10	0
29	E	31	0	20	6	0
All	All	58253	0	44280	3557	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 35.

All (3557) 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)
8:H:856:ILE:HA	8:H:944:VAL:CG1	1.17	1.58
4:G:672:LEU:HD21	4:G:704:LEU:CD2	1.29	1.58
8:H:168:VAL:HG13	8:H:173:LYS:CD	1.09	1.56
8:H:364:PHE:CB	8:H:369:LYS:HG3	1.34	1.54
4:G:672:LEU:CD2	4:G:704:LEU:CD2	1.82	1.52
4:G:274:SER:HB3	4:G:277:ILE:CD1	1.38	1.52
4:G:274:SER:CB	4:G:277:ILE:HD11	1.30	1.50
8:H:168:VAL:CG1	8:H:173:LYS:HD3	1.39	1.50
8:H:500:ARG:CD	8:H:534:THR:HG21	1.40	1.49
8:H:364:PHE:HB2	8:H:369:LYS:CG	1.42	1.49
9:N:807:GLY:CA	9:N:1093:ALA:H	1.28	1.46
8:H:500:ARG:NE	8:H:534:THR:HG21	1.31	1.41
8:H:364:PHE:HD2	8:H:369:LYS:CD	1.33	1.41
6:L:105:PHE:CB	6:L:141:ARG:HG2	1.52	1.38
9:N:807:GLY:HA2	9:N:1093:ALA:N	1.10	1.38
1:A:781:THR:CA	1:A:784:GLN:OE1	1.71	1.37
8:H:488:ILE:CG2	8:H:558:LYS:HA	1.54	1.37
8:H:856:ILE:CA	8:H:944:VAL:CG1	2.00	1.36
8:H:855:PRO:C	8:H:944:VAL:HG11	1.43	1.36
1:A:289:ASP:OD2	1:A:292:LYS:N	1.59	1.36
2:B:389:ILE:CD1	2:B:427:TRP:HB3	1.54	1.35
8:H:168:VAL:CG1	8:H:173:LYS:CD	1.97	1.35
8:H:458:ILE:CG2	8:H:459:PRO:HD2	1.56	1.35
4:G:846:PHE:CE1	4:G:859:LEU:HD21	1.62	1.35
1:A:285:PRO:HD2	1:A:298:TYR:OH	1.27	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:268:CYS:SG	4:G:278:TRP:CH2	2.21	1.34
1:A:162:LEU:HD21	1:A:730:ILE:CG2	0.88	1.33
8:H:500:ARG:CD	8:H:534:THR:CG2	2.07	1.33
8:H:855:PRO:O	8:H:944:VAL:CG1	1.75	1.33
8:H:856:ILE:CA	8:H:944:VAL:HG11	1.56	1.33
3:I:197:ILE:O	3:I:201:ASN:ND2	1.61	1.32
4:G:672:LEU:CD2	4:G:704:LEU:HD21	1.50	1.32
4:G:630:SER:CB	4:G:670:PHE:CZ	2.11	1.32
1:A:162:LEU:CD2	1:A:730:ILE:HG21	0.85	1.32
9:N:807:GLY:CA	9:N:1093:ALA:N	1.86	1.31
8:H:856:ILE:N	8:H:944:VAL:HG11	1.45	1.30
8:H:810:GLU:OE2	8:H:974:LYS:HG3	1.13	1.28
4:G:863:PHE:CZ	4:G:892:LEU:HD21	1.67	1.28
27:F:73:U:C2'	27:F:74:U:H5'	1.64	1.27
1:A:289:ASP:O	1:A:293:VAL:HG12	1.29	1.27
8:H:486:VAL:CG1	8:H:564:ILE:HD11	1.65	1.27
6:L:105:PHE:CZ	6:L:137:TYR:CE2	2.23	1.26
1:A:611:LYS:CE	24:C:4:G:OP1	1.85	1.25
9:N:807:GLY:CA	9:N:1093:ALA:CA	2.14	1.25
25:D:48:C:O3'	25:D:49:A:C8	1.89	1.24
1:A:165:LEU:HD12	1:A:578:MET:SD	1.78	1.24
1:A:195:THR:HG23	1:A:556:TYR:O	1.34	1.24
8:H:364:PHE:CD2	8:H:369:LYS:HD2	1.73	1.24
8:H:500:ARG:HD3	8:H:534:THR:CG2	1.66	1.23
9:N:807:GLY:HA2	9:N:1093:ALA:CA	1.67	1.23
5:K:350:PRO:HA	5:K:353:ARG:CG	1.68	1.22
8:H:364:PHE:CD2	8:H:369:LYS:CD	2.22	1.22
3:I:226:ALA:HA	3:I:317:ASP:OD2	1.31	1.22
8:H:330:TYR:HE1	8:H:430:ARG:NH2	1.36	1.22
24:C:8:U:C6	25:D:51:A:N6	2.05	1.22
6:L:105:PHE:CE1	6:L:137:TYR:CE2	2.28	1.21
8:H:889:TYR:CD1	8:H:890:LYS:HG2	1.77	1.20
5:K:354:PHE:HE1	5:K:358:MET:CE	1.52	1.20
4:G:630:SER:CB	4:G:670:PHE:CE2	2.24	1.20
4:G:672:LEU:CD2	4:G:704:LEU:HD23	1.48	1.20
4:G:846:PHE:HE1	4:G:859:LEU:CD2	1.55	1.20
6:L:105:PHE:CZ	6:L:137:TYR:CD2	2.29	1.20
8:H:454:ALA:O	8:H:457:SER:O	1.55	1.20
25:D:48:C:H3'	25:D:49:A:N7	1.57	1.19
3:I:123:ARG:HD3	3:I:189:LEU:CD1	1.70	1.19
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD12	1.78	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1748:ILE:HG22	1:A:1752:VAL:HG22	1.21	1.19
4:G:655:PHE:CB	4:G:674:LEU:HD21	1.71	1.19
8:H:116:THR:HG23	8:H:158:HIS:CD2	1.78	1.18
25:D:48:C:C3'	25:D:49:A:C8	2.25	1.18
8:H:492:LEU:HD21	8:H:557:HIS:ND1	1.57	1.18
27:F:75:A:C8	27:F:77:A:H5'	1.78	1.18
1:A:286:LEU:HD21	1:A:292:LYS:HB2	1.25	1.17
8:H:510:ARG:HB2	8:H:591:PHE:CE2	1.78	1.17
2:B:389:ILE:HD11	2:B:427:TRP:CB	1.73	1.17
1:A:1755:LYS:O	1:A:1759:TYR:HD2	1.22	1.17
5:K:350:PRO:HA	5:K:353:ARG:HG2	1.20	1.16
1:A:1035:LEU:HD12	1:A:1038:ILE:HG21	1.17	1.16
8:H:354:TYR:CB	8:H:359:PHE:HB3	1.76	1.16
8:H:855:PRO:O	8:H:944:VAL:CG2	1.94	1.15
8:H:163:ASP:OD2	8:H:548:ARG:NH1	1.79	1.15
2:B:316:GLN:HB2	2:B:357:TRP:CD2	1.81	1.15
1:A:468:LEU:HD13	1:A:469:ILE:HD13	1.21	1.15
8:H:117:ARG:HD2	8:H:157:SER:O	1.42	1.15
1:A:162:LEU:HD21	1:A:730:ILE:HG22	1.22	1.15
1:A:1880:PHE:CE2	1:A:1889:LEU:HD21	1.81	1.15
8:H:501:ILE:CD1	8:H:567:ILE:CG2	2.24	1.15
24:C:-3:A:H8	24:C:-2:A:C6	1.65	1.14
6:L:105:PHE:CE1	6:L:137:TYR:CD2	2.35	1.14
1:A:252:GLU:O	1:A:256:GLU:HG2	1.48	1.14
1:A:779:ALA:HA	1:A:782:ILE:HD12	1.30	1.14
1:A:781:THR:HA	1:A:784:GLN:OE1	0.97	1.14
8:H:364:PHE:HD2	8:H:369:LYS:HD2	1.01	1.13
8:H:488:ILE:CD1	8:H:560:GLN:HG2	1.78	1.13
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	1.62	1.13
1:A:1654:TRP:CZ3	1:A:1779:LEU:CD1	2.30	1.13
27:F:44:A:H2'	27:F:45:A:C8	1.83	1.13
8:H:501:ILE:HD11	8:H:567:ILE:CG2	1.78	1.12
8:H:330:TYR:CE1	8:H:430:ARG:NH2	2.17	1.12
8:H:810:GLU:OE2	8:H:974:LYS:CG	1.97	1.12
6:L:105:PHE:HB3	6:L:141:ARG:CG	1.79	1.11
27:F:44:A:H2'	27:F:45:A:H8	0.96	1.11
4:G:272:PRO:HB3	4:G:302:PHE:CD1	1.85	1.11
8:H:330:TYR:HE1	8:H:430:ARG:CZ	1.63	1.11
8:H:332:TYR:OH	8:H:376:PHE:HB3	1.50	1.11
8:H:488:ILE:HD12	8:H:560:GLN:HG2	1.29	1.11
25:D:48:C:O3'	25:D:49:A:H8	1.22	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:HA	1:A:144:ASN:ND2	1.64	1.11
1:A:362:GLU:HB3	1:A:1209:LYS:CE	1.81	1.11
2:B:329:SER:HB3	2:B:348:HIS:O	1.47	1.11
8:H:470:ALA:HB1	8:H:486:VAL:HG21	1.26	1.11
4:G:691:TYR:HB3	4:G:708:LEU:HD12	1.15	1.10
1:A:297:SER:HB3	27:F:32:G:OP1	1.48	1.10
8:H:486:VAL:HG12	8:H:564:ILE:HD11	1.13	1.10
1:A:162:LEU:HD23	1:A:730:ILE:HG21	1.20	1.10
8:H:168:VAL:HG13	8:H:173:LYS:HD2	1.18	1.10
8:H:677:PHE:CE1	8:H:966:PHE:CD2	2.39	1.10
1:A:2077:THR:O	1:A:2080:LYS:HG2	1.52	1.09
4:G:286:GLU:HB2	4:G:292:CYS:SG	1.90	1.09
8:H:364:PHE:HD2	8:H:369:LYS:HD3	1.17	1.08
1:A:141:LYS:HA	1:A:144:ASN:HD21	0.95	1.08
24:C:-3:A:H8	24:C:-2:A:C5	1.70	1.08
3:I:184:LYS:HD2	3:I:186:LYS:H	1.14	1.08
8:H:582:SER:CB	8:H:585:ASP:OD2	2.01	1.07
1:A:290:SER:OG	1:A:291:LYS:NZ	1.88	1.07
8:H:468:LEU:HD21	8:H:577:LEU:HD21	1.33	1.07
8:H:468:LEU:HD11	8:H:493:LEU:HD21	1.31	1.07
27:F:75:A:C8	27:F:77:A:C5'	2.37	1.07
2:B:323:CYS:SG	2:B:355:VAL:HG11	1.95	1.06
8:H:488:ILE:HD12	8:H:560:GLN:CG	1.82	1.06
4:G:252:GLU:HG2	4:G:256:LYS:HG3	1.37	1.06
8:H:598:ILE:HG22	8:H:933:TRP:CZ3	1.91	1.06
1:A:503:LYS:HA	1:A:506:PHE:CZ	1.89	1.06
8:H:197:THR:CG2	8:H:545:LEU:CD1	2.32	1.06
3:I:123:ARG:CD	3:I:189:LEU:HD13	1.84	1.06
4:G:668:HIS:HB3	4:G:698:VAL:HG11	1.32	1.06
4:G:672:LEU:HD23	4:G:704:LEU:CD2	1.68	1.06
8:H:458:ILE:HG23	8:H:459:PRO:HD2	1.08	1.06
3:I:135:LEU:HD23	3:I:136:GLN:N	1.70	1.06
5:K:354:PHE:HE1	5:K:358:MET:HE3	1.17	1.06
5:K:428:TRP:HZ2	5:K:463:PHE:CE2	1.74	1.06
8:H:168:VAL:HG13	8:H:173:LYS:CG	1.85	1.06
1:A:218:SER:N	1:A:318:LEU:HD21	1.71	1.05
4:G:274:SER:HB2	4:G:277:ILE:HD11	1.34	1.05
8:H:365:GLU:OE2	8:H:366:ASN:N	1.88	1.05
8:H:501:ILE:HD11	8:H:567:ILE:HG23	1.09	1.05
1:A:1755:LYS:O	1:A:1759:TYR:CD2	2.09	1.05
8:H:133:ILE:O	8:H:134:ILE:HG23	1.55	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1751:TYR:CE1	1:A:1755:LYS:HD3	1.92	1.05
1:A:1755:LYS:HG3	1:A:1759:TYR:HE2	1.19	1.05
6:L:116:ILE:HD11	6:L:137:TYR:OH	1.57	1.05
5:K:354:PHE:CE1	5:K:358:MET:CE	2.40	1.04
6:L:140:LYS:HG2	6:L:141:ARG:NH1	1.72	1.04
25:D:83:A:H1'	25:D:84:C:C5	1.93	1.04
24:C:-3:A:C8	24:C:-2:A:C6	2.45	1.04
8:H:501:ILE:CD1	8:H:567:ILE:HG23	1.87	1.04
4:G:846:PHE:CE1	4:G:859:LEU:CD2	2.35	1.04
1:A:611:LYS:HE2	24:C:4:G:OP1	1.55	1.03
1:A:1998:ARG:O	1:A:1999:ILE:HG13	1.58	1.03
1:A:1058:ALA:HB2	1:A:1114:PHE:HE1	1.23	1.03
8:H:500:ARG:NE	8:H:534:THR:CG2	2.15	1.03
2:B:389:ILE:HD11	2:B:427:TRP:HB3	1.04	1.03
8:H:510:ARG:HB2	8:H:591:PHE:HE2	0.86	1.03
1:A:611:LYS:HE3	24:C:4:G:OP1	1.54	1.02
8:H:488:ILE:HG22	8:H:558:LYS:CA	1.88	1.02
8:H:504:THR:HA	8:H:507:SER:OG	1.59	1.02
1:A:1748:ILE:O	1:A:1752:VAL:HG23	1.58	1.02
3:I:112:MET:HB3	3:I:204:LEU:HD21	1.38	1.02
4:G:695:THR:HB	4:G:705:TRP:NE1	1.73	1.02
8:H:227:VAL:HG11	8:H:474:LYS:HG3	1.37	1.02
1:A:1365:THR:O	1:A:1369:ASN:ND2	1.92	1.02
4:G:695:THR:O	4:G:699:PRO:HG3	1.58	1.02
27:F:78:A:O2'	27:F:79:C:O5'	1.76	1.02
1:A:1035:LEU:HD12	1:A:1038:ILE:CG2	1.90	1.02
3:I:217:TYR:HE1	3:I:221:LYS:NZ	1.58	1.02
8:H:110:LYS:HE2	8:H:552:PRO:HG2	1.42	1.02
1:A:294:ASN:HB2	1:A:299:LYS:O	1.59	1.02
9:N:807:GLY:N	9:N:1093:ALA:CA	2.22	1.02
1:A:470:LEU:O	1:A:473:THR:HG22	1.60	1.01
1:A:837:GLY:CA	1:A:1317:ARG:NH1	2.23	1.01
5:K:350:PRO:O	5:K:353:ARG:HG3	1.60	1.01
8:H:388:ALA:HA	8:H:396:LEU:HD11	1.42	1.01
27:F:95:C:O2'	27:F:96:U:H5'	1.60	1.01
8:H:472:VAL:HG11	8:H:571:TYR:CE2	1.96	1.01
2:B:127:TYR:CE2	2:B:276:SER:HB2	1.96	1.01
4:G:721:ARG:CD	4:G:725:ILE:HD11	1.90	1.01
8:H:354:TYR:HB2	8:H:359:PHE:HB3	1.40	1.01
8:H:504:THR:O	8:H:507:SER:OG	1.79	1.01
8:H:793:GLU:HA	8:H:796:ILE:HG22	1.39	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:283:ARG:HD2	4:G:284:LEU:HD22	1.43	1.00
8:H:608:GLN:HE22	8:H:641:GLU:HG2	1.25	1.00
1:A:192:LEU:HD11	1:A:557:PHE:HB3	1.42	1.00
2:B:446:SER:OG	2:B:451:PHE:HD2	1.42	1.00
27:F:43:G:H2'	27:F:44:A:C8	1.96	1.00
4:G:691:TYR:O	4:G:695:THR:HG23	1.62	1.00
27:F:39:U:H2'	27:F:40:C:H5'	1.43	1.00
1:A:837:GLY:HA3	1:A:1317:ARG:NH1	1.77	1.00
8:H:488:ILE:CG2	8:H:558:LYS:CA	2.39	1.00
27:F:73:U:H2'	27:F:74:U:C5'	1.90	1.00
1:A:1008:LEU:CD2	1:A:1073:ILE:HD11	1.91	0.99
8:H:488:ILE:HG21	8:H:557:HIS:C	1.81	0.99
8:H:862:TYR:HE1	8:H:908:VAL:HB	1.27	0.99
8:H:500:ARG:HD3	8:H:534:THR:HG23	1.42	0.99
8:H:481:ALA:HB3	8:H:565:LYS:HZ1	1.25	0.99
8:H:187:ARG:NH1	8:H:653:ASP:OD2	1.95	0.99
8:H:582:SER:HB2	8:H:585:ASP:HB2	1.44	0.99
8:H:133:ILE:O	8:H:134:ILE:CG2	2.11	0.99
8:H:304:PHE:HD2	8:H:310:ASN:CB	1.76	0.99
8:H:576:THR:HG22	8:H:592:PHE:HB2	1.40	0.99
8:H:901:GLU:OE2	8:H:903:ARG:NH2	1.95	0.99
1:A:912:LEU:HD11	1:A:951:LEU:HD21	1.42	0.98
4:G:274:SER:CB	4:G:277:ILE:CD1	2.13	0.98
8:H:387:TYR:O	8:H:391:MET:HB2	1.62	0.98
8:H:500:ARG:HE	8:H:534:THR:HG21	1.21	0.98
27:F:73:U:C2'	27:F:74:U:C5'	2.39	0.98
2:B:388:GLN:OE1	2:B:388:GLN:N	1.96	0.98
8:H:572:ILE:HD12	8:H:573:LYS:HG3	1.45	0.98
8:H:863:GLU:HB3	8:H:931:TYR:CE1	1.97	0.98
2:B:398:GLN:OE1	2:B:442:SER:OG	1.80	0.98
8:H:855:PRO:O	8:H:944:VAL:HG11	1.45	0.98
1:A:168:LEU:HB2	1:A:199:ILE:HD12	1.41	0.98
1:A:497:GLN:O	1:A:709:ARG:HD2	1.62	0.98
6:L:96:GLY:O	6:L:138:ASN:HB3	1.63	0.98
8:H:227:VAL:HG11	8:H:474:LYS:CG	1.92	0.98
8:H:677:PHE:HE1	8:H:966:PHE:CE2	1.82	0.98
4:G:230:LEU:HD12	4:G:247:SER:HA	1.40	0.98
8:H:168:VAL:CG1	8:H:173:LYS:CG	2.41	0.97
8:H:889:TYR:CE1	8:H:890:LYS:CG	2.47	0.97
3:I:358:ILE:HG23	3:I:359:PRO:HD2	1.44	0.97
8:H:855:PRO:HG2	8:H:944:VAL:HG21	1.42	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:465:GLU:OE1	8:H:466:GLY:N	1.97	0.97
1:A:322:VAL:HG21	1:A:327:TYR:CE2	1.99	0.97
2:B:235:ILE:CD1	2:B:280:ILE:HD13	1.95	0.97
3:I:266:LYS:HG3	3:I:267:HIS:H	1.26	0.97
8:H:855:PRO:C	8:H:944:VAL:CG1	2.26	0.97
24:C:-4:A:H1'	24:C:-3:A:OP1	1.64	0.97
8:H:304:PHE:HD2	8:H:310:ASN:HB3	1.25	0.97
27:F:43:G:H2'	27:F:44:A:H8	1.26	0.97
25:D:78:G:N2	26:E:4:C:C2	2.33	0.97
4:G:251:GLU:OE1	4:G:260:ALA:HB2	1.65	0.97
4:G:672:LEU:HD21	4:G:704:LEU:CG	1.93	0.97
3:I:282:GLU:HG2	3:I:286:PHE:CG	2.00	0.96
6:L:116:ILE:CD1	6:L:137:TYR:OH	2.13	0.96
8:H:677:PHE:CE1	8:H:966:PHE:CE2	2.53	0.96
4:G:846:PHE:HE1	4:G:859:LEU:HD21	0.91	0.96
8:H:492:LEU:CD2	8:H:557:HIS:ND1	2.28	0.96
1:A:773:SER:OG	1:A:774:ILE:CD1	2.13	0.96
8:H:576:THR:HG21	8:H:592:PHE:H	1.26	0.96
8:H:863:GLU:HB3	8:H:931:TYR:HE1	1.27	0.96
8:H:481:ALA:HB3	8:H:565:LYS:NZ	1.80	0.96
2:B:197:GLY:HA2	2:B:221:ILE:HG13	1.47	0.96
3:I:123:ARG:CD	3:I:189:LEU:CD1	2.41	0.96
8:H:324:ILE:O	8:H:328:VAL:HG23	1.66	0.96
1:A:1008:LEU:HD22	1:A:1073:ILE:HD11	1.46	0.95
3:I:226:ALA:CA	3:I:317:ASP:OD2	2.13	0.95
6:L:81:THR:HG21	6:L:102:LYS:NZ	1.80	0.95
6:L:105:PHE:CZ	6:L:137:TYR:HE2	1.72	0.95
8:H:458:ILE:CG2	8:H:459:PRO:CD	2.43	0.95
27:F:77:A:H4'	27:F:78:A:H5''	1.49	0.95
8:H:106:PHE:CE2	8:H:554:HIS:CE1	2.55	0.95
27:F:44:A:C2'	27:F:45:A:H8	1.78	0.95
4:G:663:SER:CA	4:G:667:CYS:SG	2.55	0.95
4:G:666:ILE:O	4:G:670:PHE:CD2	2.19	0.95
8:H:364:PHE:CD2	8:H:369:LYS:HD3	1.96	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE3	1.45	0.95
1:A:1654:TRP:HZ3	1:A:1779:LEU:HD12	1.29	0.95
8:H:131:GLU:OE1	8:H:445:PRO:HG3	1.66	0.95
8:H:458:ILE:HG22	8:H:459:PRO:HD2	1.47	0.95
8:H:501:ILE:CD1	8:H:567:ILE:HG22	1.95	0.95
25:D:49:A:H2'	25:D:50:G:H5''	1.46	0.95
8:H:331:TYR:CE1	8:H:404:PHE:HD1	1.84	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:372:THR:HG22	8:H:376:PHE:CD1	2.01	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE2	1.47	0.94
27:F:99:U:O2'	27:F:100:A:OP1	1.84	0.94
27:F:175:G:N2	27:F:176:A:H62	1.65	0.94
1:A:1658:HIS:HA	1:A:1661:ILE:HD12	1.49	0.94
8:H:168:VAL:HG11	8:H:173:LYS:HD3	1.46	0.94
4:G:107:LEU:O	4:G:110:SER:OG	1.86	0.94
6:L:105:PHE:CB	6:L:141:ARG:CG	2.42	0.94
1:A:366:GLU:HB2	1:A:372:ARG:NH1	1.81	0.94
1:A:1490:ARG:HH12	1:A:1536:LEU:HA	1.33	0.94
4:G:663:SER:C	4:G:667:CYS:SG	2.45	0.94
8:H:383:LYS:O	8:H:387:TYR:HB2	1.68	0.94
26:E:151:G:N2	26:E:152:A:H62	1.65	0.94
27:F:175:G:N2	27:F:176:A:N6	2.16	0.94
2:B:235:ILE:HD12	2:B:280:ILE:HD13	1.47	0.94
8:H:488:ILE:CD1	8:H:560:GLN:CG	2.42	0.94
8:H:608:GLN:NE2	8:H:641:GLU:HG2	1.82	0.94
27:F:73:U:H2'	27:F:74:U:H5'	0.95	0.94
1:A:162:LEU:HG	1:A:734:PHE:HE2	1.32	0.94
1:A:165:LEU:O	1:A:168:LEU:HB3	1.68	0.94
4:G:692:LEU:CD2	4:G:708:LEU:HD11	1.98	0.94
2:B:290:ARG:NE	2:B:302:LEU:HD13	1.82	0.93
3:I:199:GLU:O	3:I:203:ILE:HG13	1.68	0.93
8:H:332:TYR:HH	8:H:376:PHE:HD2	1.06	0.93
1:A:168:LEU:HA	1:A:199:ILE:HD11	1.48	0.93
1:A:1022:PRO:HD3	1:A:1345:TYR:HE1	1.32	0.93
3:I:123:ARG:HD3	3:I:189:LEU:HD13	0.94	0.93
8:H:197:THR:CG2	8:H:545:LEU:HD13	1.96	0.93
24:C:2:A:H2	27:F:98:U:H3	1.06	0.93
6:L:96:GLY:O	6:L:138:ASN:CB	2.16	0.93
26:E:151:G:N2	26:E:152:A:N6	2.16	0.93
8:H:489:TYR:HD2	8:H:592:PHE:HZ	1.11	0.93
4:G:286:GLU:O	4:G:288:ASP:N	2.02	0.93
8:H:219:VAL:HG21	8:H:931:TYR:HB3	1.51	0.93
8:H:486:VAL:HG12	8:H:564:ILE:CD1	1.99	0.93
25:D:48:C:H3'	25:D:49:A:C8	1.99	0.93
1:A:212:VAL:HG11	1:A:285:PRO:HB3	1.46	0.93
8:H:192:LYS:HA	8:H:224:GLU:OE1	1.67	0.93
8:H:855:PRO:O	8:H:944:VAL:HG21	1.67	0.93
4:G:843:VAL:HG21	4:G:895:LEU:HD13	1.51	0.93
5:K:341:VAL:HG21	5:K:428:TRP:HE1	1.32	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:510:ARG:CB	8:H:591:PHE:HE2	1.80	0.93
27:F:45:A:C2	27:F:46:C:C5	2.56	0.93
8:H:449:PHE:CE1	8:H:453:THR:HG21	2.04	0.92
1:A:1621:VAL:HG12	1:A:1622:GLY:H	1.34	0.92
6:L:105:PHE:HZ	6:L:137:TYR:CE2	1.82	0.92
27:F:98:U:H4'	27:F:99:U:OP1	1.69	0.92
1:A:703:PHE:CE1	1:A:706:PRO:HD3	2.04	0.92
1:A:455:PRO:HB2	1:A:457:ASP:OD1	1.70	0.92
1:A:773:SER:OG	1:A:774:ILE:HD12	1.68	0.92
2:B:358:SER:OG	2:B:401:PHE:CE1	2.20	0.92
3:I:112:MET:CB	3:I:204:LEU:HD21	2.00	0.92
4:G:285:HIS:CE1	4:G:291:TYR:CE2	2.57	0.92
6:L:140:LYS:C	6:L:141:ARG:HD2	1.90	0.92
8:H:468:LEU:HD21	8:H:577:LEU:CD2	1.99	0.92
1:A:781:THR:HA	1:A:784:GLN:CD	1.89	0.92
1:A:1748:ILE:HG22	1:A:1752:VAL:CG2	1.98	0.92
5:K:154:SER:O	5:K:158:ILE:HG23	1.68	0.92
8:H:506:GLN:O	8:H:509:SER:HB2	1.69	0.92
8:H:500:ARG:HE	8:H:534:THR:CG2	1.77	0.92
8:H:856:ILE:HA	8:H:944:VAL:HG12	0.94	0.92
4:G:274:SER:HB3	4:G:277:ILE:HD12	1.50	0.92
8:H:458:ILE:HG23	8:H:459:PRO:CD	1.99	0.92
2:B:115:SER:HA	2:B:118:ILE:CD1	1.99	0.91
8:H:330:TYR:CE1	8:H:430:ARG:CZ	2.52	0.91
8:H:372:THR:CG2	8:H:376:PHE:CE1	2.52	0.91
8:H:889:TYR:CE1	8:H:890:LYS:HG2	2.04	0.91
1:A:1256:PRO:HA	1:A:1274:ARG:HH21	1.31	0.91
4:G:668:HIS:CB	4:G:698:VAL:HG11	2.00	0.91
4:G:663:SER:HA	4:G:667:CYS:SG	2.09	0.91
1:A:1755:LYS:HG3	1:A:1759:TYR:CE2	2.06	0.91
8:H:132:ARG:HG2	8:H:132:ARG:HH11	1.35	0.91
8:H:488:ILE:HG22	8:H:558:LYS:HA	0.93	0.91
8:H:582:SER:HB2	8:H:585:ASP:OD2	1.69	0.91
1:A:286:LEU:CD2	1:A:292:LYS:HB2	2.01	0.91
8:H:489:TYR:CD2	8:H:592:PHE:HZ	1.88	0.91
1:A:288:GLU:OE1	1:A:288:GLU:N	2.04	0.91
4:G:105:ALA:O	4:G:108:LYS:HG3	1.71	0.91
8:H:889:TYR:CD1	8:H:890:LYS:CG	2.53	0.90
7:M:95:ARG:HG2	7:M:95:ARG:HH11	1.34	0.90
8:H:329:SER:HA	8:H:333:ALA:HB2	1.53	0.90
1:A:298:TYR:O	1:A:493:MET:HG3	1.70	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:GLN:OE1	1:A:412:GLN:N	2.05	0.90
2:B:389:ILE:HD13	2:B:427:TRP:HB3	1.53	0.90
4:G:695:THR:HB	4:G:705:TRP:HE1	1.33	0.90
8:H:185:ILE:HD13	27:F:75:A:OP2	1.72	0.90
2:B:173:VAL:HG13	2:B:200:GLN:OE1	1.70	0.90
1:A:317:PRO:HG2	1:A:318:LEU:HD12	1.51	0.90
6:L:81:THR:HG21	6:L:102:LYS:HZ1	1.35	0.90
1:A:322:VAL:HG21	1:A:327:TYR:CD2	2.06	0.90
27:F:75:A:N7	27:F:77:A:C5'	2.35	0.90
2:B:313:LEU:CD1	2:B:322:VAL:HG23	2.02	0.90
4:G:668:HIS:O	4:G:672:LEU:HG	1.72	0.90
27:F:75:A:O2'	27:F:76:U:OP2	1.89	0.90
2:B:316:GLN:HB2	2:B:357:TRP:CE2	2.07	0.90
8:H:481:ALA:CB	8:H:565:LYS:NZ	2.35	0.90
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.51	0.89
8:H:168:VAL:HG13	8:H:173:LYS:HD3	0.93	0.89
3:I:184:LYS:CE	3:I:186:LYS:HB2	2.03	0.89
4:G:695:THR:O	4:G:699:PRO:CG	2.20	0.89
8:H:355:HIS:O	8:H:356:LYS:CG	2.19	0.89
1:A:218:SER:CA	1:A:318:LEU:HD21	2.02	0.89
4:G:272:PRO:HB3	4:G:302:PHE:HD1	1.35	0.89
6:L:105:PHE:CZ	6:L:137:TYR:HD2	1.84	0.89
8:H:598:ILE:HG22	8:H:933:TRP:HZ3	1.32	0.89
8:H:674:LEU:HD13	8:H:973:ARG:HH12	1.35	0.89
6:L:105:PHE:HB3	6:L:141:ARG:HG2	0.89	0.89
25:D:48:C:H4'	25:D:49:A:OP1	1.73	0.89
8:H:500:ARG:CG	8:H:534:THR:HG21	2.03	0.89
4:G:721:ARG:HD3	4:G:725:ILE:HD11	1.53	0.89
8:H:855:PRO:O	8:H:944:VAL:CB	2.21	0.89
4:G:266:ASN:O	4:G:269:GLN:HG3	1.73	0.88
8:H:889:TYR:CE1	8:H:890:LYS:HG3	2.06	0.88
1:A:294:ASN:CB	1:A:299:LYS:O	2.22	0.88
1:A:923:TYR:CE1	1:A:933:GLU:HG3	2.08	0.88
2:B:274:HIS:HD2	2:B:276:SER:H	1.20	0.88
8:H:855:PRO:O	8:H:944:VAL:HG13	1.72	0.88
25:D:83:A:O2'	25:D:84:C:OP2	1.92	0.88
4:G:277:ILE:HD12	4:G:277:ILE:H	1.36	0.88
5:K:428:TRP:CZ2	5:K:463:PHE:CE2	2.61	0.88
8:H:304:PHE:CD2	8:H:310:ASN:HB3	2.07	0.88
24:C:7:A:O2'	24:C:8:U:O5'	1.92	0.88
25:D:50:G:O2'	25:D:51:A:O5'	1.91	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:LEU:O	2:B:128:SER:OG	1.90	0.88
3:I:373:ARG:HB3	3:I:373:ARG:HH11	1.38	0.88
8:H:855:PRO:CG	8:H:944:VAL:HG21	2.03	0.88
1:A:466:GLU:N	1:A:466:GLU:OE2	2.06	0.88
1:A:850:GLY:O	1:A:853:THR:HG22	1.73	0.88
2:B:393:ARG:HG2	2:B:393:ARG:HH21	1.37	0.88
3:I:98:PHE:HE2	3:I:217:TYR:CD2	1.91	0.88
8:H:582:SER:HB2	8:H:585:ASP:CB	2.03	0.88
1:A:501:LEU:HD12	1:A:501:LEU:H	1.38	0.88
4:G:702:PRO:HB3	4:G:739:PHE:CZ	2.09	0.88
6:L:101:ASN:O	6:L:102:LYS:HG2	1.73	0.88
6:L:105:PHE:HB2	6:L:141:ARG:HG2	1.56	0.88
8:H:364:PHE:HB3	8:H:369:LYS:HG3	1.53	0.88
8:H:415:TYR:O	8:H:416:ASP:OD1	1.92	0.88
8:H:501:ILE:HD13	8:H:567:ILE:HG22	1.55	0.88
2:B:124:LEU:HD21	2:B:274:HIS:CE1	2.08	0.88
8:H:189:LEU:HD12	8:H:190:SER:N	1.89	0.88
1:A:297:SER:HB2	27:F:32:G:O5'	1.74	0.87
4:G:891:ILE:O	4:G:894:ARG:N	2.07	0.87
8:H:168:VAL:CG1	8:H:173:LYS:HG3	2.04	0.87
2:B:380:LYS:O	2:B:381:ARG:HG2	1.73	0.87
2:B:395:ILE:HG22	2:B:396:VAL:H	1.38	0.87
1:A:141:LYS:CA	1:A:144:ASN:HD21	1.86	0.87
3:I:282:GLU:CD	3:I:286:PHE:CD2	2.48	0.87
2:B:446:SER:OG	2:B:451:PHE:CD2	2.19	0.87
4:G:212:VAL:H	4:G:215:LEU:HD23	1.39	0.87
4:G:282:ILE:O	4:G:286:GLU:HG2	1.73	0.87
4:G:691:TYR:HB3	4:G:708:LEU:CD1	2.03	0.87
5:K:350:PRO:HA	5:K:353:ARG:CD	2.04	0.87
5:K:141:ASN:OD1	5:K:142:LEU:N	2.07	0.87
1:A:266:LEU:HD23	1:A:267:PRO:HD2	1.55	0.87
1:A:358:ARG:HB3	1:A:358:ARG:HH11	1.37	0.87
4:G:692:LEU:HD23	4:G:708:LEU:HD11	1.55	0.87
24:C:8:U:C5	25:D:51:A:N6	2.34	0.87
8:H:306:PRO:HG2	8:H:349:TRP:CZ3	2.09	0.87
27:F:98:U:O2'	27:F:99:U:O5'	1.92	0.87
1:A:1353:THR:O	1:A:1357:LEU:HD12	1.73	0.87
1:A:1373:LEU:HD13	6:L:139:HIS:HE1	1.36	0.86
3:I:282:GLU:OE2	3:I:286:PHE:CD2	2.27	0.86
8:H:250:GLU:HB3	8:H:298:PHE:CE2	2.09	0.86
1:A:168:LEU:HB2	1:A:199:ILE:CD1	2.03	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:837:GLY:HA3	1:A:1317:ARG:HH12	1.37	0.86
2:B:274:HIS:CD2	2:B:276:SER:HB3	2.10	0.86
1:A:1364:GLU:OE1	1:A:1389:TYR:OH	1.92	0.86
8:H:968:MET:HE2	8:H:968:MET:HA	1.57	0.86
2:B:177:PRO:HB3	2:B:457:TRP:HA	1.56	0.86
3:I:191:ILE:H	3:I:191:ILE:HD12	1.38	0.86
8:H:488:ILE:HD13	8:H:557:HIS:O	1.74	0.86
8:H:489:TYR:CD2	8:H:592:PHE:CZ	2.64	0.86
6:L:140:LYS:HB3	6:L:141:ARG:HD2	1.55	0.86
2:B:313:LEU:HD13	2:B:322:VAL:HG23	1.57	0.86
3:I:282:GLU:CD	3:I:286:PHE:CE2	2.49	0.86
4:G:892:LEU:O	4:G:896:MET:HG2	1.75	0.86
1:A:1373:LEU:CD1	6:L:139:HIS:HE1	1.88	0.86
1:A:149:MET:HB3	1:A:154:TYR:HD2	1.39	0.86
3:I:231:PHE:CD2	3:I:330:ALA:HB1	2.10	0.86
4:G:886:CYS:SG	4:G:888:PRO:HD2	2.16	0.86
8:H:197:THR:HG23	8:H:545:LEU:O	1.76	0.86
8:H:489:TYR:HD2	8:H:592:PHE:CZ	1.93	0.86
1:A:162:LEU:CD2	1:A:730:ILE:CG2	1.74	0.85
1:A:1490:ARG:NH1	1:A:1536:LEU:HD23	1.91	0.85
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.41	0.85
2:B:159:LEU:HD13	2:B:430:MET:CE	2.05	0.85
4:G:688:ARG:HH12	4:G:721:ARG:HE	1.24	0.85
8:H:481:ALA:CB	8:H:565:LYS:HZ3	1.89	0.85
1:A:286:LEU:HD21	1:A:292:LYS:CB	2.05	0.85
1:A:823:TRP:HZ3	1:A:855:LEU:HD21	1.39	0.85
2:B:197:GLY:HA2	2:B:221:ILE:CG1	2.07	0.85
8:H:197:THR:CG2	8:H:545:LEU:HD12	2.06	0.85
8:H:608:GLN:HE22	8:H:641:GLU:CG	1.89	0.85
1:A:936:GLU:O	1:A:940:ILE:HD12	1.77	0.85
8:H:117:ARG:CD	8:H:157:SER:O	2.23	0.85
8:H:492:LEU:HD21	8:H:557:HIS:HD1	1.34	0.85
4:G:691:TYR:CB	4:G:708:LEU:HD12	2.04	0.85
1:A:1756:PHE:O	1:A:1760:THR:HG23	1.75	0.85
2:B:115:SER:HA	2:B:118:ILE:HD12	1.57	0.85
8:H:120:ARG:HG3	8:H:551:TYR:CE1	2.11	0.85
8:H:235:VAL:HG22	8:H:261:VAL:HG12	1.59	0.85
8:H:586:MET:O	8:H:589:LEU:HD23	1.77	0.85
1:A:224:MET:HG3	1:A:701:CYS:O	1.77	0.85
1:A:928:ARG:HH21	4:G:145:THR:HG21	1.42	0.85
8:H:106:PHE:HE2	8:H:554:HIS:CE1	1.93	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:951:ILE:HB	8:H:952:PRO:HD2	1.58	0.85
1:A:162:LEU:HD21	1:A:730:ILE:CB	2.06	0.85
1:A:166:LYS:O	1:A:169:PRO:HD2	1.76	0.85
1:A:1498:ASP:OD1	1:A:1502:LEU:CD1	2.25	0.85
8:H:247:PHE:HA	8:H:250:GLU:OE1	1.76	0.85
8:H:855:PRO:HG2	8:H:944:VAL:CG2	2.05	0.85
1:A:176:LEU:HD23	1:A:708:TRP:HE1	1.42	0.84
2:B:117:LEU:HD23	2:B:300:LEU:HB3	1.58	0.84
2:B:124:LEU:CD2	2:B:274:HIS:CE1	2.60	0.84
8:H:605:ILE:HG13	8:H:652:MET:SD	2.17	0.84
3:I:158:PHE:HA	3:I:161:LEU:HD12	1.57	0.84
8:H:449:PHE:HE1	8:H:453:THR:HG21	1.40	0.84
8:H:486:VAL:HG11	8:H:564:ILE:HD11	1.57	0.84
8:H:501:ILE:HD13	8:H:567:ILE:CG2	2.05	0.84
8:H:951:ILE:O	8:H:952:PRO:O	1.95	0.84
1:A:251:TYR:HA	1:A:255:ILE:HD12	1.58	0.84
4:G:278:TRP:CZ2	4:G:298:THR:HB	2.12	0.84
6:L:33:ARG:HD3	6:L:65:ASP:CG	1.98	0.84
8:H:793:GLU:HA	8:H:796:ILE:CG2	2.06	0.84
1:A:691:PHE:CZ	1:A:701:CYS:HA	2.13	0.84
1:A:703:PHE:HE1	1:A:706:PRO:HD3	1.40	0.84
8:H:862:TYR:HE1	8:H:908:VAL:CB	1.90	0.84
1:A:175:LEU:HD12	1:A:175:LEU:O	1.76	0.84
1:A:1877:GLY:O	1:A:1894:ILE:N	2.11	0.84
2:B:320:SER:HB2	2:B:337:ARG:NH2	1.92	0.84
2:B:320:SER:HB2	2:B:337:ARG:HH22	1.42	0.84
4:G:888:PRO:O	4:G:892:LEU:HD23	1.77	0.84
8:H:504:THR:CA	8:H:507:SER:OG	2.25	0.84
27:F:39:U:C2'	27:F:40:C:H5'	2.06	0.84
27:F:175:G:H21	27:F:176:A:H62	1.23	0.84
25:D:86:G:H8	25:D:86:G:H5''	1.41	0.84
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.56	0.84
8:H:332:TYR:OH	8:H:376:PHE:CB	2.25	0.84
1:A:195:THR:CG2	1:A:556:TYR:O	2.24	0.84
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	1.78	0.84
8:H:449:PHE:O	8:H:453:THR:HG23	1.77	0.84
8:H:576:THR:CG2	8:H:592:PHE:HB2	2.07	0.84
1:A:160:ALA:HB1	1:A:194:HIS:CE1	2.12	0.84
1:A:176:LEU:CD2	1:A:708:TRP:HE1	1.90	0.84
1:A:218:SER:N	1:A:318:LEU:CD2	2.41	0.84
1:A:1909:ALA:O	1:A:1913:THR:HG23	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:98:PHE:CE2	3:I:217:TYR:CD2	2.65	0.84
3:I:401:LEU:HD12	4:G:214:SER:HB3	1.58	0.84
24:C:-3:A:C8	24:C:-2:A:C5	2.61	0.84
27:F:78:A:N1	27:F:81:A:C5	2.46	0.84
4:G:122:ILE:HG13	4:G:123:PRO:HD2	1.57	0.84
5:K:354:PHE:CE1	5:K:358:MET:HE3	2.08	0.84
8:H:542:ILE:O	8:H:553:VAL:HB	1.77	0.84
1:A:170:HIS:ND1	1:A:547:LEU:HD23	1.93	0.83
1:A:286:LEU:CD2	1:A:292:LYS:CB	2.56	0.83
1:A:1459:ALA:O	1:A:1463:THR:HG23	1.78	0.83
6:L:105:PHE:HE1	6:L:137:TYR:CE2	1.92	0.83
8:H:576:THR:HG21	8:H:592:PHE:N	1.92	0.83
4:G:863:PHE:HB3	4:G:889:ARG:HH22	1.41	0.83
5:K:350:PRO:CA	5:K:353:ARG:HG2	2.06	0.83
4:G:863:PHE:CE2	4:G:892:LEU:HD21	2.13	0.83
27:F:75:A:C5	27:F:77:A:H5''	2.13	0.83
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	1.78	0.83
2:B:335:ASP:OD1	2:B:337:ARG:HD2	1.77	0.83
8:H:576:THR:HB	8:H:592:PHE:HD2	1.41	0.83
27:F:75:A:N7	27:F:77:A:H5'	1.91	0.83
1:A:1453:ASP:O	1:A:1456:ARG:HG2	1.77	0.83
8:H:120:ARG:HG3	8:H:551:TYR:CZ	2.13	0.83
1:A:923:TYR:CE1	1:A:933:GLU:CG	2.62	0.83
2:B:441:ILE:HD11	2:B:457:TRP:HE1	1.42	0.83
3:I:373:ARG:HH11	3:I:373:ARG:CB	1.91	0.83
4:G:268:CYS:SG	4:G:278:TRP:CZ2	2.72	0.83
9:N:807:GLY:N	9:N:1093:ALA:N	2.23	0.83
26:E:151:G:H21	26:E:152:A:H62	1.23	0.83
27:F:33:U:O2'	27:F:34:C:P	2.37	0.83
2:B:47:GLU:O	2:B:51:VAL:HG23	1.78	0.83
2:B:197:GLY:HA2	2:B:221:ILE:CD1	2.08	0.83
4:G:696:ARG:C	4:G:699:PRO:HD3	1.98	0.83
8:H:307:ILE:HD12	8:H:324:ILE:HD11	1.59	0.83
1:A:753:TYR:HE1	6:L:37:ARG:HB3	1.44	0.83
3:I:98:PHE:O	3:I:101:ILE:HG22	1.78	0.83
25:D:62:A:C2	26:E:58:G:C2	2.66	0.83
5:K:341:VAL:HG21	5:K:428:TRP:NE1	1.93	0.82
5:K:146:GLU:HA	5:K:149:PHE:CD2	2.14	0.82
1:A:289:ASP:OD2	1:A:292:LYS:CG	2.27	0.82
5:K:428:TRP:HZ2	5:K:463:PHE:HE2	1.27	0.82
8:H:372:THR:HG23	8:H:376:PHE:CE1	2.12	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:116:THR:HG23	8:H:158:HIS:HD2	1.37	0.82
27:F:103:A:O2'	27:F:104:G:O5'	1.96	0.82
1:A:795:ALA:HA	1:A:1095:MET:CE	2.09	0.82
2:B:170:SER:O	2:B:171:GLN:HB2	1.79	0.82
2:B:389:ILE:HD11	2:B:427:TRP:CG	2.14	0.82
4:G:251:GLU:OE2	4:G:259:VAL:HB	1.79	0.82
8:H:488:ILE:HG21	8:H:558:LYS:HA	1.59	0.82
8:H:230:ALA:CB	8:H:595:LEU:HD21	2.09	0.82
25:D:62:A:H2'	25:D:63:G:H5'	1.61	0.82
2:B:419:ILE:HD11	2:B:443:LEU:CD1	2.10	0.82
5:K:164:HIS:ND1	5:K:164:HIS:O	2.13	0.82
8:H:674:LEU:CD1	8:H:973:ARG:HH12	1.93	0.82
8:H:797:GLN:HA	8:H:797:GLN:NE2	1.94	0.82
1:A:1350:ILE:HG23	1:A:1356:LEU:CD1	2.09	0.82
2:B:446:SER:OG	2:B:451:PHE:HB2	1.78	0.82
3:I:184:LYS:HD2	3:I:186:LYS:N	1.93	0.82
8:H:113:ILE:HG22	8:H:114:PRO:HD2	1.62	0.82
1:A:218:SER:CA	1:A:318:LEU:CD2	2.55	0.82
2:B:202:LEU:HD23	2:B:207:LEU:CD2	2.09	0.82
4:G:671:PHE:HZ	4:G:693:SER:HG	1.26	0.82
1:A:149:MET:HG2	1:A:154:TYR:CE2	2.15	0.82
1:A:1415:SER:OG	1:A:1746:HIS:NE2	2.12	0.82
1:A:923:TYR:HE1	1:A:933:GLU:HG3	1.44	0.81
1:A:1908:LEU:HD12	1:A:1908:LEU:O	1.80	0.81
2:B:323:CYS:SG	2:B:355:VAL:CG1	2.68	0.81
4:G:283:ARG:HD2	4:G:284:LEU:CD2	2.09	0.81
8:H:194:ASN:OD1	8:H:547:GLY:HA2	1.80	0.81
1:A:404:ASN:OD1	8:H:927:MET:CE	2.28	0.81
1:A:809:LYS:O	1:A:813:GLU:HG2	1.80	0.81
2:B:459:ARG:NH2	4:G:758:LEU:HD22	1.95	0.81
5:K:350:PRO:CA	5:K:353:ARG:CG	2.56	0.81
8:H:373:PHE:CD1	8:H:377:ILE:HD12	2.14	0.81
4:G:104:PHE:O	4:G:107:LEU:N	2.14	0.81
4:G:702:PRO:HB3	4:G:739:PHE:CE1	2.16	0.81
6:L:33:ARG:CD	6:L:65:ASP:CG	2.49	0.81
8:H:230:ALA:HB2	8:H:595:LEU:HD21	1.60	0.81
8:H:492:LEU:CD2	8:H:557:HIS:CG	2.62	0.81
2:B:51:VAL:HG13	2:B:76:LEU:CD1	2.09	0.81
3:I:184:LYS:CD	3:I:186:LYS:HB2	2.10	0.81
8:H:810:GLU:CD	8:H:974:LYS:HG3	2.00	0.81
1:A:289:ASP:O	1:A:293:VAL:CG1	2.24	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:GLN:O	1:A:1499:ARG:HG2	1.81	0.81
2:B:195:TRP:O	2:B:219:GLY:O	1.99	0.81
4:G:721:ARG:HD2	4:G:725:ILE:HD11	1.60	0.81
8:H:183:GLN:OE1	8:H:657:TYR:CD2	2.34	0.81
8:H:946:ASP:O	8:H:964:ARG:HG2	1.80	0.81
1:A:176:LEU:HD23	1:A:176:LEU:O	1.79	0.81
8:H:471:HIS:O	8:H:486:VAL:HG23	1.81	0.81
25:D:49:A:H2'	25:D:50:G:C5'	2.11	0.81
27:F:32:G:H5''	27:F:32:G:C8	2.15	0.81
8:H:175:LEU:HD23	8:H:176:ARG:N	1.96	0.81
27:F:95:C:C4'	27:F:96:U:OP1	2.29	0.81
4:G:144:LYS:NZ	26:E:55:U:O5'	2.14	0.80
1:A:149:MET:HG2	1:A:154:TYR:HE2	1.46	0.80
1:A:361:GLU:N	1:A:361:GLU:OE2	2.13	0.80
25:D:48:C:C3'	25:D:49:A:N7	2.34	0.80
6:L:140:LYS:HB3	6:L:141:ARG:CD	2.11	0.80
8:H:568:SER:HA	8:H:571:TYR:HE1	1.45	0.80
8:H:769:TYR:CE1	8:H:799:PHE:HE2	1.99	0.80
8:H:336:ILE:HD11	8:H:341:ILE:HG22	1.61	0.80
8:H:369:LYS:HE2	8:H:369:LYS:O	1.80	0.80
8:H:598:ILE:CG2	8:H:933:TRP:CZ3	2.64	0.80
1:A:301:TRP:CD1	1:A:491:GLY:O	2.34	0.80
3:I:268:LEU:HD12	3:I:271:GLU:CG	2.11	0.80
4:G:295:LEU:O	4:G:298:THR:OG1	1.98	0.80
8:H:468:LEU:CD1	8:H:493:LEU:HD21	2.09	0.80
1:A:289:ASP:OD2	1:A:292:LYS:HG2	1.81	0.80
1:A:703:PHE:HE1	1:A:705:GLN:HB3	1.45	0.80
8:H:296:ASN:HD21	8:H:304:PHE:H	1.26	0.80
8:H:793:GLU:CA	8:H:796:ILE:HG22	2.11	0.80
2:B:446:SER:HB2	2:B:451:PHE:H	1.46	0.80
8:H:470:ALA:HB1	8:H:486:VAL:CG2	2.10	0.80
8:H:769:TYR:CE1	8:H:799:PHE:CE2	2.70	0.80
1:A:162:LEU:CG	1:A:730:ILE:CG2	2.58	0.80
4:G:846:PHE:CD1	4:G:859:LEU:HD21	2.17	0.80
8:H:121:ASP:OD1	8:H:122:TYR:N	2.15	0.80
1:A:781:THR:N	1:A:784:GLN:OE1	2.14	0.80
1:A:912:LEU:CD1	1:A:951:LEU:HD21	2.12	0.80
2:B:441:ILE:HD11	2:B:457:TRP:NE1	1.97	0.80
8:H:168:VAL:HG12	8:H:173:LYS:HG3	1.63	0.80
8:H:470:ALA:HB3	8:H:577:LEU:HB3	1.61	0.80
27:F:78:A:C6	27:F:81:A:N7	2.50	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:LEU:HD11	1:A:476:ALA:HB2	1.63	0.80
1:A:1654:TRP:CH2	1:A:1779:LEU:HD12	2.17	0.80
4:G:688:ARG:HH12	4:G:721:ARG:NE	1.79	0.80
1:A:166:LYS:HD3	1:A:167:TYR:CE1	2.17	0.79
1:A:837:GLY:CA	1:A:1317:ARG:HH11	1.95	0.79
2:B:316:GLN:HG3	2:B:357:TRP:CZ2	2.16	0.79
3:I:46:ILE:O	3:I:97:PHE:CZ	2.35	0.79
4:G:696:ARG:O	4:G:699:PRO:CD	2.30	0.79
4:G:863:PHE:CE2	4:G:892:LEU:HG	2.17	0.79
27:F:32:G:H1	27:F:121:U:H3	1.31	0.79
4:G:251:GLU:OE2	4:G:259:VAL:CG1	2.30	0.79
4:G:695:THR:O	4:G:699:PRO:CD	2.30	0.79
1:A:585:ARG:HD2	1:A:733:GLN:CD	2.03	0.79
4:G:691:TYR:HE2	4:G:711:ILE:HD11	1.47	0.79
8:H:488:ILE:HG21	8:H:558:LYS:CA	2.10	0.79
8:H:488:ILE:HG21	8:H:558:LYS:N	1.97	0.79
1:A:1264:GLY:HA3	1:A:1308:GLU:OE1	1.83	0.79
3:I:123:ARG:NH1	3:I:187:GLU:O	2.14	0.79
8:H:856:ILE:HA	8:H:944:VAL:HG13	1.59	0.79
8:H:856:ILE:CA	8:H:944:VAL:HG12	1.85	0.79
3:I:197:ILE:C	3:I:201:ASN:HD22	1.85	0.79
1:A:456:GLU:OE1	1:A:456:GLU:N	2.14	0.79
2:B:389:ILE:CD1	2:B:427:TRP:CB	2.46	0.79
3:I:217:TYR:HE1	3:I:221:LYS:HZ3	0.81	0.79
4:G:672:LEU:CG	4:G:704:LEU:HD21	2.13	0.79
8:H:189:LEU:HD13	28:H:1500:GTP:O1G	1.82	0.79
2:B:380:LYS:C	2:B:381:ARG:HG2	2.02	0.79
4:G:691:TYR:CE2	4:G:711:ILE:CD1	2.66	0.79
4:G:691:TYR:CE2	4:G:711:ILE:HD11	2.18	0.79
8:H:449:PHE:CE1	8:H:453:THR:CG2	2.65	0.79
4:G:274:SER:HB3	4:G:277:ILE:HD11	0.79	0.79
5:K:159:TYR:O	5:K:163:ASN:ND2	2.16	0.79
25:D:83:A:H1'	25:D:84:C:H5	1.47	0.79
1:A:285:PRO:CD	1:A:298:TYR:OH	2.21	0.78
4:G:98:SER:OG	4:G:99:ASN:ND2	2.16	0.78
6:L:140:LYS:CG	6:L:141:ARG:NH1	2.46	0.78
8:H:197:THR:HG21	8:H:545:LEU:HD12	1.64	0.78
8:H:500:ARG:HE	8:H:534:THR:CB	1.96	0.78
7:M:93:VAL:HG12	7:M:95:ARG:H	1.48	0.78
8:H:167:ASN:ND2	8:H:173:LYS:HG2	1.98	0.78
27:F:77:A:C4'	27:F:78:A:H5''	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1038:ILE:HD11	1:A:1039:TRP:CD2	2.17	0.78
8:H:468:LEU:HD11	8:H:493:LEU:CD2	2.09	0.78
2:B:51:VAL:HG13	2:B:76:LEU:HD11	1.66	0.78
3:I:138:SER:HA	3:I:141:ILE:HD12	1.64	0.78
8:H:467:THR:O	8:H:490:SER:HB3	1.82	0.78
1:A:923:TYR:HE1	1:A:933:GLU:CG	1.95	0.78
2:B:290:ARG:HE	2:B:302:LEU:HD13	1.45	0.78
8:H:863:GLU:CB	8:H:931:TYR:HE1	1.96	0.78
1:A:1755:LYS:CG	1:A:1759:TYR:HE2	1.96	0.78
3:I:266:LYS:HG3	3:I:267:HIS:N	1.98	0.78
6:L:33:ARG:HD2	6:L:65:ASP:OD2	1.83	0.78
9:N:565:ALA:CA	9:N:837:GLY:HA2	2.13	0.78
3:I:184:LYS:HD2	3:I:186:LYS:HB2	1.63	0.78
1:A:2079:ILE:HA	1:A:2082:ILE:HD12	1.64	0.78
3:I:266:LYS:CG	3:I:267:HIS:H	1.96	0.78
4:G:863:PHE:CE2	4:G:892:LEU:CG	2.67	0.78
1:A:1468:ALA:HB1	1:A:1473:ARG:O	1.83	0.78
5:K:457:GLN:OE1	5:K:457:GLN:N	2.17	0.78
8:H:116:THR:CG2	8:H:158:HIS:CD2	2.65	0.78
8:H:355:HIS:O	8:H:356:LYS:HG3	1.82	0.78
1:A:287:GLU:HB2	1:A:288:GLU:OE1	1.84	0.78
4:G:251:GLU:OE2	4:G:259:VAL:HG12	1.84	0.78
4:G:702:PRO:O	4:G:706:VAL:HG23	1.83	0.78
8:H:472:VAL:CG1	8:H:571:TYR:CE2	2.67	0.78
27:F:78:A:N1	27:F:81:A:C4	2.53	0.77
1:A:1697:SER:OG	1:A:1759:TYR:CD1	2.37	0.77
6:L:25:ARG:HB2	6:L:25:ARG:HH11	1.49	0.77
8:H:769:TYR:CZ	8:H:799:PHE:HE2	2.01	0.77
1:A:511:ASP:HB2	1:A:514:TYR:CE1	2.19	0.77
4:G:282:ILE:HA	4:G:295:LEU:HD12	1.66	0.77
8:H:862:TYR:CE1	8:H:908:VAL:HB	2.18	0.77
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.67	0.77
1:A:1877:GLY:O	1:A:1894:ILE:HB	1.83	0.77
5:K:428:TRP:CZ2	5:K:463:PHE:HE2	2.01	0.77
27:F:75:A:O2'	27:F:76:U:P	2.41	0.77
1:A:212:VAL:HG11	1:A:285:PRO:CB	2.15	0.77
1:A:823:TRP:CZ3	1:A:855:LEU:HD21	2.19	0.77
1:A:1313:ASP:CG	1:A:1359:ILE:HD13	2.05	0.77
4:G:212:VAL:HG13	4:G:215:LEU:HB3	1.66	0.77
6:L:139:HIS:NE2	27:F:96:U:C5'	2.48	0.77
8:H:195:GLY:HA3	8:H:545:LEU:HD22	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ASP:HB3	1:A:276:VAL:CG2	2.14	0.77
27:F:31:G:C2	27:F:32:G:H1'	2.19	0.77
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD11	2.17	0.77
4:G:695:THR:CB	4:G:705:TRP:HE1	1.98	0.77
8:H:794:GLN:OE1	8:H:835:LYS:HG3	1.84	0.77
8:H:947:LYS:CD	8:H:947:LYS:H	1.98	0.77
1:A:168:LEU:HA	1:A:199:ILE:CD1	2.14	0.77
5:K:146:GLU:O	5:K:148:LYS:N	2.18	0.77
1:A:1490:ARG:HH11	1:A:1536:LEU:HA	1.47	0.77
2:B:64:VAL:HG12	2:B:65:GLU:H	1.49	0.77
2:B:316:GLN:HG3	2:B:357:TRP:CE2	2.20	0.77
2:B:387:ASN:C	2:B:388:GLN:OE1	2.22	0.77
4:G:252:GLU:HG2	4:G:256:LYS:CG	2.15	0.77
8:H:151:ASP:OD1	8:H:175:LEU:HD22	1.85	0.77
1:A:317:PRO:HG2	1:A:318:LEU:CD1	2.15	0.77
1:A:2064:GLY:O	1:A:2068:ASN:N	2.18	0.77
9:N:1198:ARG:CA	9:N:1227:ILE:H	1.96	0.77
2:B:459:ARG:CZ	4:G:758:LEU:HD22	2.14	0.76
3:I:245:ALA:HB1	3:I:250:GLU:HB3	1.66	0.76
4:G:285:HIS:HE1	4:G:291:TYR:CE2	2.03	0.76
8:H:883:ARG:O	8:H:884:ARG:HB2	1.81	0.76
1:A:912:LEU:HD11	1:A:951:LEU:CD2	2.16	0.76
2:B:286:ASP:C	2:B:287:MET:HG2	2.05	0.76
8:H:189:LEU:HD21	8:H:218:HIS:HB2	1.67	0.76
8:H:265:PHE:CE2	8:H:295:ILE:HD12	2.20	0.76
8:H:492:LEU:HD23	8:H:557:HIS:HA	1.66	0.76
9:N:807:GLY:H	9:N:1093:ALA:CA	1.97	0.76
5:K:350:PRO:HB3	25:D:84:C:C5	2.21	0.76
8:H:492:LEU:HD21	8:H:557:HIS:CG	2.20	0.76
3:I:268:LEU:HD12	3:I:271:GLU:HG3	1.66	0.76
8:H:697:ARG:NE	8:H:697:ARG:HA	2.00	0.76
8:H:951:ILE:O	8:H:951:ILE:HD12	1.85	0.76
8:H:242:VAL:HG21	8:H:272:ARG:HD3	1.67	0.76
8:H:355:HIS:O	8:H:356:LYS:HG2	1.86	0.76
8:H:545:LEU:HD12	8:H:545:LEU:H	1.51	0.76
8:H:942:GLY:HA3	8:H:961:SER:HA	1.67	0.76
27:F:75:A:N7	27:F:77:A:H5''	2.00	0.76
27:F:106:A:C2'	27:F:107:C:H5'	2.16	0.76
1:A:162:LEU:HG	1:A:734:PHE:CE2	2.17	0.76
1:A:1073:ILE:HD12	1:A:1116:TYR:CE1	2.19	0.76
1:A:1902:GLN:O	1:A:1905:LEU:HD21	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2079:ILE:HG22	1:A:2083:ILE:HD11	1.65	0.76
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	1.85	0.76
4:G:251:GLU:OE2	4:G:259:VAL:CB	2.34	0.76
1:A:165:LEU:HD12	1:A:578:MET:CG	2.15	0.76
2:B:454:SER:HG	2:B:464:TRP:HE1	1.33	0.76
3:I:265:ASN:OD1	3:I:266:LYS:N	2.17	0.76
4:G:257:PHE:CG	4:G:258:SER:N	2.52	0.76
8:H:338:SER:HA	8:H:341:ILE:HD13	1.66	0.76
8:H:372:THR:HG22	8:H:376:PHE:CE1	2.16	0.76
1:A:218:SER:HA	1:A:318:LEU:HD21	1.66	0.76
1:A:217:TRP:C	1:A:318:LEU:HD21	2.05	0.75
8:H:197:THR:HG23	8:H:545:LEU:HD13	1.68	0.75
8:H:576:THR:HB	8:H:592:PHE:CD2	2.21	0.75
1:A:258:ILE:O	1:A:259:GLU:HB2	1.86	0.75
1:A:928:ARG:NH2	4:G:145:THR:HG21	2.00	0.75
1:A:1035:LEU:CD1	1:A:1038:ILE:HG21	2.09	0.75
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.67	0.75
2:B:154:SER:OG	2:B:155:ARG:HD3	1.85	0.75
1:A:253:GLN:O	1:A:257:ASN:ND2	2.19	0.75
8:H:118:TYR:HD1	8:H:119:ASN:O	1.69	0.75
8:H:468:LEU:CD1	8:H:493:LEU:CD2	2.63	0.75
1:A:296:THR:CG2	27:F:33:U:OP2	2.34	0.75
1:A:543:ASN:HD22	1:A:544:LYS:N	1.83	0.75
8:H:133:ILE:C	8:H:134:ILE:HG23	2.07	0.75
8:H:233:ASP:OD1	8:H:487:ARG:NH2	2.17	0.75
8:H:504:THR:C	8:H:507:SER:HG	1.89	0.75
2:B:345:LEU:HD13	2:B:376:TRP:CD2	2.20	0.75
8:H:146:LYS:HE2	28:H:1500:GTP:O3G	1.85	0.75
1:A:219:ALA:O	1:A:266:LEU:CD1	2.35	0.75
1:A:1058:ALA:HB2	1:A:1114:PHE:CE1	2.15	0.75
1:A:1647:GLN:HG2	25:D:52:G:OP2	1.86	0.75
8:H:304:PHE:CD2	8:H:310:ASN:CB	2.66	0.75
8:H:860:PRO:HB3	8:H:937:TRP:CZ3	2.21	0.75
1:A:276:VAL:HG11	1:A:310:ASN:HB3	1.68	0.75
1:A:322:VAL:CG2	1:A:327:TYR:CD2	2.69	0.75
4:G:672:LEU:HD21	4:G:704:LEU:HD23	1.15	0.75
6:L:139:HIS:CD2	27:F:96:U:H5"	2.21	0.75
8:H:331:TYR:CE1	8:H:404:PHE:CD1	2.73	0.75
8:H:456:LEU:N	8:H:456:LEU:HD23	2.02	0.75
1:A:1038:ILE:HD11	1:A:1039:TRP:CE3	2.21	0.75
3:I:151:LYS:O	3:I:152:ASN:HB2	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:ALA:O	1:A:810:LYS:HG2	1.87	0.75
8:H:510:ARG:HD3	8:H:591:PHE:CE2	2.21	0.75
1:A:180:PRO:HA	1:A:187:LYS:CD	2.17	0.74
2:B:121:ARG:O	2:B:125:ILE:HG13	1.86	0.74
2:B:155:ARG:O	2:B:159:LEU:HG	1.85	0.74
3:I:401:LEU:CD1	4:G:214:SER:HA	2.17	0.74
27:F:31:G:H2'	27:F:32:G:O4'	1.85	0.74
1:A:192:LEU:HD12	1:A:558:GLN:O	1.87	0.74
1:A:1035:LEU:HD21	1:A:1160:LEU:HD11	1.69	0.74
1:A:1629:LEU:HD23	1:A:1630:THR:HG23	1.68	0.74
3:I:192:LYS:O	3:I:195:THR:OG1	2.05	0.74
4:G:863:PHE:HB3	4:G:889:ARG:NH2	2.02	0.74
8:H:458:ILE:HG22	8:H:459:PRO:CD	2.14	0.74
1:A:1256:PRO:HA	1:A:1274:ARG:NH2	2.03	0.74
1:A:180:PRO:HA	1:A:187:LYS:HD3	1.67	0.74
1:A:289:ASP:OD2	1:A:292:LYS:CB	2.34	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:HE3	1.69	0.74
4:G:863:PHE:HZ	4:G:892:LEU:HD21	1.47	0.74
5:K:315:ARG:NH1	25:D:72:C:O2	2.18	0.74
8:H:476:VAL:CG1	8:H:478:TYR:HD1	2.01	0.74
8:H:489:TYR:CE2	8:H:592:PHE:CE1	2.76	0.74
24:C:2:A:H2	27:F:98:U:N3	1.84	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:CE	2.18	0.74
8:H:306:PRO:HG2	8:H:349:TRP:CE3	2.22	0.74
1:A:299:LYS:HA	1:A:493:MET:HG2	1.69	0.74
1:A:1922:ARG:HE	1:A:1951:PHE:HZ	1.35	0.74
8:H:504:THR:C	8:H:507:SER:OG	2.26	0.74
2:B:195:TRP:O	2:B:220:LYS:HA	1.86	0.74
26:E:139:A:O2'	26:E:140:G:OP2	2.05	0.74
4:G:281:ASN:ND2	4:G:295:LEU:CD1	2.51	0.74
24:C:-5:A:H4'	24:C:-4:A:OP2	1.88	0.74
1:A:173:LEU:HD11	1:A:712:LEU:HD11	1.68	0.74
1:A:404:ASN:OD1	8:H:927:MET:HE1	1.87	0.74
1:A:773:SER:OG	1:A:774:ILE:HD11	1.87	0.74
1:A:874:ILE:O	1:A:875:THR:OG1	2.06	0.74
2:B:410:LEU:HB2	2:B:422:TYR:HB2	1.68	0.74
3:I:231:PHE:HD2	3:I:330:ALA:HB1	1.50	0.74
3:I:272:LEU:O	3:I:272:LEU:HD13	1.87	0.74
4:G:863:PHE:CZ	4:G:892:LEU:CD2	2.61	0.74
5:K:146:GLU:HA	5:K:149:PHE:CE2	2.21	0.74
1:A:174:LYS:HD2	1:A:202:VAL:O	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:305:SER:OG	8:H:307:ILE:HG22	1.87	0.73
8:H:545:LEU:HD12	8:H:545:LEU:N	2.03	0.73
8:H:798:GLY:O	8:H:801:TRP:HB3	1.88	0.73
2:B:115:SER:HA	2:B:118:ILE:CG1	2.17	0.73
8:H:372:THR:HG23	8:H:376:PHE:HE1	1.53	0.73
1:A:297:SER:CB	27:F:32:G:OP1	2.33	0.73
1:A:365:ASN:OD1	1:A:366:GLU:N	2.22	0.73
2:B:374:ASN:HB3	2:B:376:TRP:HE1	1.53	0.73
8:H:354:TYR:CA	8:H:359:PHE:HB3	2.17	0.73
8:H:132:ARG:HG2	8:H:132:ARG:NH1	2.01	0.73
8:H:326:GLU:HG3	8:H:434:GLY:HA3	1.71	0.73
26:E:2:U:C5	26:E:3:C:C5	2.76	0.73
1:A:930:ASN:HB3	1:A:933:GLU:OE1	1.89	0.73
2:B:232:ASN:HB3	2:B:247:GLN:HE22	1.51	0.73
1:A:1498:ASP:OD1	1:A:1502:LEU:HD11	1.87	0.73
8:H:274:ILE:HG21	8:H:385:PHE:CE2	2.23	0.73
8:H:500:ARG:CG	8:H:534:THR:CG2	2.62	0.73
27:F:33:U:O2'	27:F:34:C:O5'	2.05	0.73
1:A:1065:LEU:HD23	1:A:1069:LEU:HD13	1.70	0.73
2:B:159:LEU:HD13	2:B:430:MET:HE2	1.71	0.73
4:G:99:ASN:O	4:G:103:GLN:HG3	1.88	0.73
1:A:1857:VAL:O	1:A:1877:GLY:HA3	1.89	0.73
3:I:123:ARG:O	3:I:183:PHE:HB2	1.89	0.73
4:G:655:PHE:CB	4:G:674:LEU:CD2	2.60	0.73
8:H:336:ILE:CD1	8:H:341:ILE:HG22	2.18	0.73
8:H:568:SER:HA	8:H:571:TYR:CE1	2.23	0.73
8:H:863:GLU:CB	8:H:931:TYR:CE1	2.71	0.73
24:C:8:U:H2'	24:C:9:G:H5'	1.68	0.73
1:A:151:SER:OG	1:A:152:LYS:N	2.22	0.73
1:A:289:ASP:OD2	1:A:292:LYS:CA	2.36	0.73
4:G:281:ASN:HD22	4:G:295:LEU:CD1	2.01	0.73
5:K:333:LYS:HE2	5:K:333:LYS:N	2.04	0.73
8:H:489:TYR:HE2	8:H:592:PHE:CE1	2.06	0.73
1:A:1414:TRP:HZ3	1:A:1416:LYS:HB2	1.54	0.72
2:B:127:TYR:CE2	2:B:276:SER:CB	2.71	0.72
9:N:1122:GLY:HA3	9:N:1249:ASP:CA	2.18	0.72
1:A:585:ARG:HD2	1:A:733:GLN:NE2	2.03	0.72
1:A:1195:PHE:HB3	1:A:1217:ARG:NH1	2.04	0.72
1:A:1461:TYR:CE2	1:A:1494:LEU:HD11	2.24	0.72
2:B:385:GLN:OE1	2:B:385:GLN:HA	1.88	0.72
27:F:44:A:C4	27:F:45:A:C8	2.76	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:751:ASP:OD1	1:A:752:ALA:N	2.22	0.72
1:A:842:LYS:O	1:A:842:LYS:HD2	1.89	0.72
1:A:1907:GLN:O	1:A:1910:LYS:HG2	1.89	0.72
8:H:197:THR:HG22	8:H:545:LEU:CD1	2.20	0.72
8:H:581:LYS:HZ2	8:H:581:LYS:HB3	1.52	0.72
8:H:959:ILE:CD1	8:H:960:ASN:H	2.00	0.72
1:A:1373:LEU:HD13	6:L:139:HIS:CE1	2.22	0.72
1:A:1464:LYS:O	1:A:1475:LEU:HD21	1.90	0.72
2:B:230:SER:HB2	2:B:232:ASN:HD22	1.53	0.72
8:H:274:ILE:HD13	8:H:274:ILE:O	1.90	0.72
8:H:336:ILE:CG1	8:H:341:ILE:HG22	2.19	0.72
8:H:476:VAL:HG12	8:H:478:TYR:HD1	1.55	0.72
24:C:2:A:C2	27:F:98:U:N3	2.57	0.72
1:A:286:LEU:HD12	1:A:287:GLU:N	2.05	0.72
2:B:199:LEU:N	2:B:199:LEU:HD23	2.04	0.72
8:H:197:THR:HG22	8:H:545:LEU:HD13	1.71	0.72
8:H:307:ILE:CD1	8:H:324:ILE:HD11	2.18	0.72
27:F:94:C:N4	27:F:96:U:O2'	2.22	0.72
1:A:468:LEU:HD13	1:A:469:ILE:CD1	2.10	0.72
1:A:1846:ASN:HA	1:A:1885:LYS:NZ	2.03	0.72
2:B:197:GLY:CA	2:B:221:ILE:HG13	2.18	0.72
2:B:374:ASN:OD1	2:B:388:GLN:HG3	1.90	0.72
3:I:346:GLU:O	3:I:347:ALA:HB3	1.87	0.72
3:I:427:SER:OG	3:I:428:ARG:N	2.20	0.72
5:K:354:PHE:CE1	5:K:358:MET:HE2	2.24	0.72
8:H:947:LYS:HG2	8:H:948:ASP:OD1	1.90	0.72
27:F:95:C:O4'	27:F:96:U:OP1	2.07	0.72
1:A:778:LYS:HA	1:A:778:LYS:CE	2.20	0.72
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.72	0.72
1:A:1008:LEU:HD21	1:A:1073:ILE:HD11	1.70	0.72
1:A:1880:PHE:CE1	1:A:1882:LEU:HD12	2.25	0.72
8:H:967:VAL:HG12	8:H:968:MET:CE	2.20	0.72
2:B:369:GLY:HA2	2:B:395:ILE:HG23	1.72	0.71
1:A:298:TYR:O	1:A:493:MET:CG	2.37	0.71
1:A:1069:LEU:HB3	1:A:1116:TYR:HE2	1.55	0.71
1:A:1751:TYR:CZ	1:A:1755:LYS:HD3	2.25	0.71
8:H:347:ARG:O	8:H:352:VAL:HG11	1.90	0.71
27:F:73:U:O2'	27:F:74:U:C5'	2.39	0.71
1:A:779:ALA:HA	1:A:782:ILE:CD1	2.15	0.71
1:A:1216:ILE:HD12	1:A:1254:ASN:HB3	1.72	0.71
1:A:1629:LEU:HD23	1:A:1630:THR:CG2	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1653:LEU:HD12	1:A:1653:LEU:O	1.90	0.71
2:B:135:ARG:NH1	2:B:139:GLU:OE2	2.23	0.71
1:A:298:TYR:CE1	1:A:493:MET:HE1	2.26	0.71
1:A:315:SER:C	1:A:317:PRO:HD2	2.11	0.71
2:B:153:LEU:O	2:B:157:THR:HG23	1.90	0.71
3:I:401:LEU:HD11	4:G:214:SER:HA	1.72	0.71
8:H:168:VAL:HG12	8:H:173:LYS:CG	2.18	0.71
2:B:220:LYS:HB3	2:B:239:GLU:HB3	1.71	0.71
2:B:127:TYR:CD2	2:B:276:SER:HB2	2.26	0.71
3:I:135:LEU:CD2	3:I:136:GLN:HG3	2.20	0.71
8:H:944:VAL:HG23	8:H:945:LEU:HG	1.71	0.71
1:A:778:LYS:O	1:A:782:ILE:HG13	1.90	0.71
2:B:443:LEU:O	2:B:443:LEU:HD23	1.90	0.71
5:K:350:PRO:O	5:K:353:ARG:CG	2.37	0.71
8:H:265:PHE:CD2	8:H:295:ILE:HD12	2.25	0.71
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.25	0.71
2:B:313:LEU:CD1	2:B:322:VAL:CG2	2.68	0.71
2:B:415:TYR:OH	7:M:126:ILE:HA	1.91	0.71
4:G:666:ILE:HG22	4:G:667:CYS:N	2.05	0.71
6:L:139:HIS:NE2	27:F:96:U:H5''	2.06	0.71
27:F:75:A:C8	27:F:77:A:H5''	2.22	0.71
8:H:332:TYR:CZ	8:H:376:PHE:HB3	2.26	0.71
8:H:799:PHE:CE1	8:H:846:CYS:SG	2.84	0.71
27:F:77:A:H1'	27:F:78:A:H5'	1.71	0.71
1:A:410:ILE:HG13	8:H:276:ASP:OD1	1.90	0.71
1:A:1415:SER:OG	1:A:1746:HIS:CD2	2.43	0.71
2:B:446:SER:CB	2:B:451:PHE:HB2	2.20	0.71
8:H:354:TYR:HA	8:H:359:PHE:HA	1.72	0.71
8:H:677:PHE:CE1	8:H:966:PHE:HD2	2.08	0.71
2:B:359:PRO:HD2	2:B:407:GLY:HA3	1.73	0.70
4:G:696:ARG:O	4:G:699:PRO:HD3	1.89	0.70
27:F:94:C:H6	27:F:94:C:C5'	2.04	0.70
1:A:162:LEU:HD23	1:A:730:ILE:HD13	1.71	0.70
1:A:614:ARG:CZ	24:C:3:A:OP1	2.39	0.70
1:A:770:MET:HE3	1:A:778:LYS:HB2	1.72	0.70
8:H:129:ILE:N	8:H:129:ILE:HD12	2.06	0.70
8:H:501:ILE:HG21	8:H:570:ALA:HB3	1.73	0.70
1:A:774:ILE:HG23	1:A:777:LYS:HE3	1.73	0.70
2:B:359:PRO:HB2	2:B:406:GLY:O	1.91	0.70
2:B:390:LEU:HG	2:B:390:LEU:O	1.91	0.70
5:K:154:SER:O	5:K:158:ILE:CG2	2.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:TRP:CZ2	1:A:851:ARG:HG2	2.26	0.70
1:A:1489:PRO:O	1:A:1533:ASP:O	2.10	0.70
1:A:1877:GLY:O	1:A:1894:ILE:CB	2.38	0.70
1:A:2071:ILE:O	1:A:2071:ILE:HD13	1.91	0.70
4:G:143:ARG:HB3	4:G:143:ARG:CZ	2.20	0.70
5:K:350:PRO:HG3	5:K:353:ARG:CZ	2.21	0.70
27:F:39:U:H3	27:F:115:G:H1	1.38	0.70
1:A:1846:ASN:HA	1:A:1885:LYS:HZ1	1.56	0.70
1:A:2080:LYS:HA	1:A:2083:ILE:HD12	1.74	0.70
2:B:446:SER:HG	2:B:451:PHE:HD2	0.72	0.70
8:H:488:ILE:HG21	8:H:557:HIS:O	1.91	0.70
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.74	0.70
1:A:1748:ILE:CG2	1:A:1752:VAL:HG22	2.12	0.70
3:I:145:GLU:OE2	3:I:145:GLU:HA	1.90	0.70
4:G:630:SER:CB	4:G:670:PHE:HZ	1.95	0.70
8:H:364:PHE:CB	8:H:369:LYS:CG	2.27	0.70
4:G:863:PHE:HE2	4:G:892:LEU:CG	2.04	0.70
27:F:31:G:C2	27:F:32:G:C4	2.80	0.70
1:A:149:MET:HB3	1:A:154:TYR:CD2	2.25	0.70
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.22	0.70
1:A:1615:ASN:HD21	1:A:1634:LEU:HD23	1.56	0.70
2:B:362:TYR:HD1	2:B:362:TYR:H	1.38	0.70
4:G:863:PHE:CE2	4:G:892:LEU:CD2	2.74	0.70
8:H:586:MET:HA	8:H:589:LEU:HD23	1.73	0.70
24:C:8:U:OP1	24:C:8:U:H4'	1.91	0.70
1:A:1647:GLN:O	1:A:1650:ARG:HG2	1.92	0.70
2:B:380:LYS:O	2:B:381:ARG:CG	2.39	0.70
4:G:98:SER:OG	4:G:99:ASN:N	2.24	0.70
6:L:31:PHE:O	6:L:80:MET:HA	1.92	0.70
1:A:1022:PRO:HD3	1:A:1345:TYR:CE1	2.22	0.69
8:H:132:ARG:O	8:H:133:ILE:HG12	1.91	0.69
8:H:135:ASN:HD22	8:H:487:ARG:NH2	1.90	0.69
4:G:251:GLU:OE2	4:G:260:ALA:N	2.25	0.69
4:G:666:ILE:HG22	4:G:667:CYS:H	1.57	0.69
8:H:105:ILE:HA	8:H:108:GLN:CD	2.12	0.69
8:H:474:LYS:NZ	8:H:630:PRO:HD3	2.06	0.69
8:H:580:VAL:HG22	8:H:582:SER:H	1.57	0.69
27:F:74:U:O2'	27:F:75:A:H5'	1.92	0.69
27:F:78:A:H61	27:F:81:A:N6	1.90	0.69
1:A:1756:PHE:CE1	1:A:1760:THR:HG21	2.27	0.69
4:G:862:MET:N	4:G:862:MET:SD	2.65	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:113:ILE:HG23	8:H:549:TYR:CD1	2.27	0.69
8:H:131:GLU:HA	8:H:131:GLU:OE2	1.92	0.69
26:E:4:C:O2'	26:E:5:U:H5'	1.92	0.69
1:A:1654:TRP:HZ3	1:A:1779:LEU:CD1	1.91	0.69
3:I:93:LYS:O	3:I:96:PRO:HD2	1.91	0.69
8:H:187:ARG:NH2	8:H:654:CYS:SG	2.66	0.69
8:H:959:ILE:N	8:H:959:ILE:HD12	2.06	0.69
27:F:78:A:C6	27:F:81:A:C5	2.80	0.69
1:A:305:LEU:HD11	1:A:476:ALA:CB	2.22	0.69
1:A:998:TYR:CE1	1:A:1002:GLU:HG3	2.28	0.69
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.75	0.69
8:H:143:HIS:HA	28:H:1500:GTP:O3B	1.91	0.69
8:H:161:ILE:HG23	8:H:162:PRO:HD2	1.75	0.69
2:B:115:SER:HA	2:B:118:ILE:HG13	1.75	0.69
2:B:177:PRO:HD2	2:B:195:TRP:CD1	2.28	0.69
2:B:274:HIS:CD2	2:B:276:SER:H	2.07	0.69
6:L:53:VAL:HG12	6:L:57:ALA:HB3	1.75	0.69
27:F:106:A:H2'	27:F:107:C:H5'	1.75	0.69
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.21	0.69
1:A:1647:GLN:O	1:A:1650:ARG:CG	2.40	0.69
4:G:666:ILE:O	4:G:670:PHE:HD2	1.73	0.69
8:H:488:ILE:HD12	8:H:560:GLN:HG3	1.73	0.69
27:F:32:G:H4'	27:F:33:U:OP2	1.92	0.69
1:A:1574:PHE:CE1	3:I:390:ARG:HD3	2.27	0.69
2:B:235:ILE:HD12	2:B:280:ILE:CD1	2.20	0.69
4:G:851:ARG:O	4:G:852:LEU:HD12	1.92	0.69
5:K:141:ASN:HD21	5:K:144:LEU:HD23	1.58	0.69
8:H:495:ARG:HH21	8:H:541:GLU:CD	1.96	0.69
9:N:807:GLY:HA2	9:N:1093:ALA:H	0.66	0.69
1:A:431:ILE:HD11	8:H:287:LYS:HA	1.74	0.69
2:B:176:LYS:HB3	2:B:195:TRP:HB2	1.75	0.69
8:H:349:TRP:HZ3	8:H:373:PHE:CE2	2.10	0.69
8:H:582:SER:HB2	8:H:585:ASP:CG	2.12	0.69
2:B:117:LEU:HG	2:B:300:LEU:O	1.93	0.69
3:I:217:TYR:CE1	3:I:221:LYS:NZ	2.45	0.69
8:H:117:ARG:HD2	8:H:157:SER:C	2.13	0.69
8:H:572:ILE:HD12	8:H:573:LYS:CG	2.22	0.69
8:H:948:ASP:OD1	8:H:948:ASP:N	2.26	0.69
25:D:109:U:H3'	25:D:110:U:H5''	1.75	0.69
1:A:1882:LEU:O	1:A:1882:LEU:HD13	1.93	0.68
4:G:19:ILE:HD12	4:G:20:GLY:N	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:33:U:O2'	27:F:34:C:OP2	2.11	0.68
1:A:354:PRO:O	1:A:355:LEU:HB3	1.93	0.68
1:A:428:LEU:HD13	8:H:279:LEU:HD11	1.74	0.68
2:B:274:HIS:HD2	2:B:276:SER:N	1.89	0.68
4:G:687:SER:O	4:G:690:THR:HG22	1.92	0.68
5:K:350:PRO:HG3	5:K:353:ARG:NH1	2.07	0.68
6:L:101:ASN:O	6:L:102:LYS:CG	2.41	0.68
8:H:495:ARG:HG2	8:H:540:GLU:O	1.94	0.68
1:A:168:LEU:CA	1:A:199:ILE:HD11	2.21	0.68
1:A:431:ILE:HA	8:H:895:ALA:HB1	1.74	0.68
4:G:666:ILE:C	4:G:670:PHE:CD2	2.67	0.68
8:H:332:TYR:OH	8:H:376:PHE:CD2	2.44	0.68
27:F:78:A:N6	27:F:81:A:C5	2.61	0.68
2:B:419:ILE:HD11	2:B:443:LEU:HD12	1.73	0.68
3:I:183:PHE:CE2	3:I:185:ASN:ND2	2.58	0.68
5:K:303:LEU:C	5:K:303:LEU:HD23	2.13	0.68
8:H:470:ALA:HB3	8:H:577:LEU:HD22	1.76	0.68
3:I:98:PHE:CE2	3:I:217:TYR:HD2	2.09	0.68
4:G:166:ARG:O	4:G:169:LEU:N	2.27	0.68
6:L:25:ARG:HH11	6:L:25:ARG:CB	2.07	0.68
8:H:105:ILE:O	8:H:109:LEU:HD23	1.93	0.68
1:A:2075:THR:HG22	1:A:2077:THR:H	1.58	0.68
3:I:124:PHE:CE2	3:I:127:LEU:HB2	2.28	0.68
3:I:268:LEU:CD1	3:I:271:GLU:HG2	2.24	0.68
1:A:837:GLY:HA2	1:A:1317:ARG:HH11	1.56	0.68
2:B:359:PRO:HB2	2:B:406:GLY:C	2.14	0.68
4:G:264:ILE:HG21	4:G:281:ASN:HA	1.75	0.68
8:H:477:ASP:HB2	8:H:628:TYR:CE1	2.29	0.68
8:H:444:GLN:HE21	8:H:444:GLN:HA	1.57	0.68
1:A:404:ASN:OD1	8:H:927:MET:HE3	1.92	0.68
1:A:753:TYR:CE1	6:L:37:ARG:HB3	2.28	0.68
4:G:693:SER:O	4:G:697:LEU:HG	1.94	0.68
5:K:354:PHE:CE1	5:K:358:MET:SD	2.87	0.68
6:L:39:CYS:SG	6:L:80:MET:HB3	2.34	0.68
8:H:113:ILE:HD11	8:H:550:VAL:O	1.94	0.68
8:H:142:LEU:HD12	8:H:929:GLN:HE21	1.57	0.68
8:H:330:TYR:HE1	8:H:430:ARG:NE	1.91	0.68
27:F:40:C:O2'	27:F:41:A:H5''	1.93	0.68
27:F:78:A:N6	27:F:81:A:N7	2.41	0.68
1:A:176:LEU:CD2	1:A:708:TRP:NE1	2.56	0.68
1:A:358:ARG:HH11	1:A:358:ARG:CB	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:ARG:O	1:A:377:VAL:HB	1.93	0.68
1:A:276:VAL:HG13	1:A:310:ASN:HD22	1.59	0.67
1:A:296:THR:HG21	27:F:33:U:OP2	1.94	0.67
2:B:374:ASN:HB3	2:B:376:TRP:NE1	2.09	0.67
8:H:317:LYS:HB2	28:H:1500:GTP:C6	2.29	0.67
8:H:461:LYS:HD2	8:H:461:LYS:C	2.15	0.67
8:H:577:LEU:HD23	8:H:577:LEU:C	2.15	0.67
8:H:855:PRO:O	8:H:944:VAL:HG22	1.92	0.67
1:A:325:LYS:HB3	1:A:405:ASN:ND2	2.09	0.67
3:I:179:MET:HG3	3:I:183:PHE:CE1	2.28	0.67
8:H:197:THR:HG23	8:H:545:LEU:CD1	2.20	0.67
1:A:795:ALA:HA	1:A:1095:MET:HE3	1.75	0.67
1:A:939:LEU:HD11	3:I:441:MET:CE	2.24	0.67
2:B:159:LEU:HD13	2:B:430:MET:HE1	1.75	0.67
4:G:238:PRO:HD2	4:G:239:THR:H	1.59	0.67
4:G:281:ASN:ND2	4:G:295:LEU:HD13	2.10	0.67
8:H:246:THR:O	8:H:250:GLU:HG3	1.94	0.67
9:N:1122:GLY:CA	9:N:1249:ASP:CA	2.73	0.67
1:A:276:VAL:HG11	1:A:310:ASN:CB	2.24	0.67
1:A:691:PHE:HZ	1:A:701:CYS:HA	1.55	0.67
1:A:774:ILE:HG23	1:A:777:LYS:CE	2.24	0.67
1:A:1654:TRP:CH2	1:A:1779:LEU:CD1	2.78	0.67
8:H:116:THR:OG1	8:H:120:ARG:NH2	2.24	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CB	2.21	0.67
8:H:488:ILE:CD1	8:H:560:GLN:HG3	2.23	0.67
8:H:936:ILE:HD13	8:H:936:ILE:H	1.59	0.67
4:G:863:PHE:HE2	4:G:892:LEU:HG	1.58	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CD	2.22	0.67
8:H:677:PHE:CZ	8:H:966:PHE:CD2	2.82	0.67
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.27	0.67
3:I:312:LEU:HB3	3:I:333:TRP:CH2	2.29	0.67
6:L:33:ARG:HD2	6:L:65:ASP:CG	2.15	0.67
1:A:175:LEU:HD12	1:A:175:LEU:C	2.15	0.67
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.60	0.67
3:I:280:ARG:NH2	26:E:37:U:OP2	2.27	0.67
4:G:224:GLN:O	4:G:228:THR:HG23	1.95	0.67
8:H:105:ILE:HA	8:H:108:GLN:OE1	1.95	0.67
8:H:959:ILE:HD12	8:H:960:ASN:H	1.58	0.67
1:A:165:LEU:CD1	1:A:578:MET:SD	2.72	0.67
1:A:1651:ALA:C	1:A:1652:HIS:CD2	2.68	0.67
3:I:92:ILE:HD12	3:I:92:ILE:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:105:PHE:HZ	6:L:137:TYR:HE2	1.18	0.67
8:H:330:TYR:CE1	8:H:430:ARG:NE	2.61	0.67
8:H:338:SER:O	8:H:341:ILE:HG12	1.95	0.67
27:F:48:G:H1	27:F:67:U:H3	1.41	0.67
27:F:77:A:H4'	27:F:78:A:OP1	1.95	0.67
3:I:123:ARG:CD	3:I:189:LEU:HD12	2.23	0.67
8:H:486:VAL:CG1	8:H:564:ILE:CD1	2.59	0.67
1:A:1703:MET:HB2	1:A:1732:MET:HB2	1.75	0.67
5:K:350:PRO:CB	25:D:84:C:C5	2.78	0.67
8:H:316:THR:OG1	28:H:1500:GTP:N7	2.28	0.67
27:F:32:G:H5''	27:F:32:G:H8	1.60	0.67
1:A:371:ASP:O	8:H:969:LYS:HG3	1.94	0.66
1:A:511:ASP:HB2	1:A:514:TYR:HE1	1.60	0.66
1:A:1892:LYS:HD2	1:A:1916:GLU:CG	2.25	0.66
4:G:672:LEU:HD23	4:G:704:LEU:HD21	1.41	0.66
4:G:688:ARG:HH22	4:G:721:ARG:NH2	1.93	0.66
8:H:271:ASP:O	8:H:274:ILE:HG22	1.94	0.66
8:H:331:TYR:OH	8:H:428:ILE:HG23	1.95	0.66
8:H:415:TYR:C	8:H:416:ASP:OD1	2.33	0.66
1:A:362:GLU:HB2	1:A:1209:LYS:HG2	1.77	0.66
1:A:909:THR:CG2	1:A:910:LYS:N	2.57	0.66
2:B:360:ASN:HB3	2:B:362:TYR:CE1	2.31	0.66
3:I:231:PHE:CD2	3:I:330:ALA:CB	2.78	0.66
4:G:692:LEU:HD22	4:G:708:LEU:HD11	1.75	0.66
4:G:721:ARG:CD	4:G:725:ILE:CD1	2.72	0.66
5:K:292:ALA:O	5:K:296:VAL:HG23	1.94	0.66
8:H:189:LEU:HD12	8:H:189:LEU:C	2.14	0.66
8:H:329:SER:O	8:H:333:ALA:HB3	1.96	0.66
27:F:31:G:N2	27:F:32:G:H1'	2.10	0.66
27:F:31:G:N3	27:F:32:G:H1'	2.10	0.66
2:B:202:LEU:HD23	2:B:207:LEU:HD22	1.77	0.66
3:I:112:MET:HB3	3:I:204:LEU:CD2	2.22	0.66
3:I:358:ILE:HG23	3:I:359:PRO:CD	2.21	0.66
8:H:329:SER:HA	8:H:333:ALA:CB	2.25	0.66
8:H:472:VAL:HG11	8:H:571:TYR:CZ	2.30	0.66
1:A:1417:GLN:OE1	1:A:1422:ILE:HD11	1.96	0.66
2:B:380:LYS:O	2:B:382:ASP:OD1	2.13	0.66
2:B:456:GLY:O	2:B:459:ARG:N	2.21	0.66
8:H:219:VAL:CG2	8:H:931:TYR:HB3	2.25	0.66
8:H:317:LYS:HB2	28:H:1500:GTP:C5	2.30	0.66
8:H:354:TYR:HB3	8:H:359:PHE:HB3	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:458:ILE:HB	8:H:590:LYS:HD3	1.76	0.66
2:B:314:SER:OG	2:B:355:VAL:O	2.10	0.66
3:I:197:ILE:C	3:I:201:ASN:ND2	2.44	0.66
8:H:495:ARG:CG	8:H:540:GLU:O	2.43	0.66
25:D:51:A:H4'	25:D:51:A:OP1	1.96	0.66
1:A:558:GLN:OE1	1:A:558:GLN:HA	1.95	0.66
1:A:862:GLU:HA	1:A:862:GLU:OE2	1.96	0.66
2:B:177:PRO:HD2	2:B:195:TRP:HD1	1.61	0.66
8:H:444:GLN:HA	8:H:444:GLN:NE2	2.11	0.66
25:D:109:U:H4'	25:D:110:U:OP2	1.95	0.66
1:A:362:GLU:CB	1:A:1209:LYS:HE2	2.22	0.66
1:A:923:TYR:CE1	1:A:933:GLU:HG2	2.30	0.66
1:A:1657:ILE:O	1:A:1661:ILE:HG13	1.95	0.66
2:B:274:HIS:CD2	2:B:275:PRO:HD2	2.30	0.66
2:B:313:LEU:HD11	2:B:322:VAL:CG2	2.26	0.66
27:F:50:G:H1	27:F:65:U:H3	1.41	0.66
1:A:366:GLU:HB2	1:A:372:ARG:HH11	1.59	0.66
1:A:1038:ILE:CD1	1:A:1039:TRP:CE3	2.78	0.66
1:A:1041:VAL:HG11	1:A:1253:LYS:N	2.11	0.66
2:B:316:GLN:CB	2:B:357:TRP:CE2	2.78	0.66
4:G:256:LYS:HG2	4:G:257:PHE:H	1.61	0.66
5:K:141:ASN:O	5:K:142:LEU:HD22	1.96	0.66
8:H:126:MET:CE	8:H:132:ARG:HH12	2.09	0.66
3:I:124:PHE:CD2	3:I:127:LEU:HB2	2.30	0.66
5:K:349:ASN:HB2	5:K:406:PHE:CE1	2.31	0.66
8:H:564:ILE:CG2	8:H:567:ILE:HG12	2.26	0.66
25:D:78:G:N2	26:E:4:C:O2	2.28	0.66
27:F:73:U:O2'	27:F:74:U:H5''	1.96	0.66
1:A:1591:THR:HG22	1:A:1592:HIS:N	2.11	0.65
4:G:99:ASN:ND2	4:G:99:ASN:H	1.94	0.65
8:H:855:PRO:C	8:H:944:VAL:HG21	2.16	0.65
1:A:325:LYS:HB3	1:A:405:ASN:HD22	1.59	0.65
5:K:154:SER:O	5:K:158:ILE:CG1	2.44	0.65
5:K:155:LYS:O	5:K:158:ILE:HG13	1.96	0.65
8:H:110:LYS:HE2	8:H:552:PRO:CG	2.20	0.65
8:H:797:GLN:HA	8:H:797:GLN:HE21	1.61	0.65
1:A:319:ARG:NH1	1:A:485:PRO:HG2	2.11	0.65
2:B:227:HIS:HD2	2:B:273:TYR:CE1	2.14	0.65
3:I:93:LYS:HA	3:I:93:LYS:HZ1	1.61	0.65
3:I:197:ILE:CG2	3:I:201:ASN:HD21	2.09	0.65
5:K:154:SER:O	5:K:158:ILE:HG12	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:165:SER:OG	8:H:168:VAL:HG22	1.96	0.65
25:D:48:C:C2'	25:D:49:A:C8	2.79	0.65
1:A:875:THR:OG1	1:A:878:GLU:HB2	1.96	0.65
2:B:316:GLN:HB2	2:B:357:TRP:CE3	2.30	0.65
6:L:141:ARG:HD2	6:L:141:ARG:N	2.11	0.65
7:M:95:ARG:HG3	7:M:96:PRO:HD2	1.78	0.65
8:H:129:ILE:HG12	10:R:16:GLY:HA3	1.78	0.65
8:H:888:ILE:H	8:H:888:ILE:HD12	1.60	0.65
1:A:809:LYS:O	1:A:813:GLU:CG	2.43	0.65
2:B:202:LEU:HB3	2:B:207:LEU:HD23	1.79	0.65
3:I:120:TYR:HE2	3:I:141:ILE:HG12	1.59	0.65
2:B:147:ASN:HB3	2:B:150:GLN:OE1	1.95	0.65
2:B:280:ILE:O	2:B:292:TRP:N	2.29	0.65
2:B:329:SER:CB	2:B:348:HIS:O	2.36	0.65
3:I:358:ILE:CG2	3:I:360:GLU:H	2.10	0.65
4:G:212:VAL:CG1	4:G:215:LEU:HB3	2.25	0.65
8:H:274:ILE:O	8:H:278:LYS:HA	1.96	0.65
1:A:404:ASN:HA	8:H:919:ARG:HH12	1.61	0.65
1:A:1279:VAL:HG11	1:A:1301:TYR:OH	1.96	0.65
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.78	0.65
4:G:278:TRP:CH2	4:G:298:THR:HB	2.31	0.65
8:H:306:PRO:HG2	8:H:349:TRP:CH2	2.31	0.65
1:A:366:GLU:HB2	1:A:372:ARG:HH12	1.59	0.65
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.78	0.65
3:I:179:MET:HG3	3:I:183:PHE:HE1	1.62	0.65
8:H:799:PHE:HE1	8:H:846:CYS:SG	2.20	0.65
1:A:173:LEU:HD11	1:A:712:LEU:CD1	2.27	0.65
1:A:770:MET:CE	1:A:775:ARG:O	2.45	0.65
1:A:875:THR:OG1	1:A:878:GLU:OE1	2.15	0.65
2:B:381:ARG:HG3	2:B:382:ASP:OD1	1.97	0.65
8:H:503:ASP:OD1	8:H:571:TYR:HB2	1.97	0.65
1:A:1145:MET:O	1:A:1146:GLN:HG3	1.97	0.64
2:B:218:VAL:HG21	2:B:238:ALA:HB3	1.80	0.64
4:G:843:VAL:HG21	4:G:895:LEU:CD1	2.27	0.64
8:H:160:ARG:HB3	8:H:161:ILE:HA	1.78	0.64
27:F:95:C:O2'	27:F:96:U:C5'	2.43	0.64
27:F:97:U:C6	27:F:97:U:H5''	2.33	0.64
1:A:767:LEU:HD21	1:A:779:ALA:CB	2.27	0.64
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.31	0.64
3:I:184:LYS:HE2	3:I:186:LYS:HB2	1.78	0.64
1:A:168:LEU:CB	1:A:199:ILE:CD1	2.74	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:LEU:HD12	1:A:173:LEU:O	1.98	0.64
1:A:174:LYS:NZ	1:A:177:GLU:OE2	2.30	0.64
1:A:207:ARG:NH1	1:A:299:LYS:HG2	2.13	0.64
8:H:500:ARG:NE	8:H:534:THR:CB	2.57	0.64
8:H:599:THR:CG2	8:H:933:TRP:CZ3	2.80	0.64
8:H:599:THR:HG22	8:H:932:PHE:O	1.98	0.64
8:H:862:TYR:OH	8:H:908:VAL:HG23	1.98	0.64
1:A:250:SER:O	1:A:254:HIS:HB2	1.96	0.64
1:A:676:GLN:N	1:A:676:GLN:OE1	2.31	0.64
1:A:780:ARG:O	1:A:784:GLN:OE1	2.15	0.64
2:B:313:LEU:HD11	2:B:322:VAL:HG23	1.78	0.64
3:I:266:LYS:CG	3:I:267:HIS:N	2.56	0.64
5:K:146:GLU:HA	5:K:149:PHE:HD2	1.62	0.64
6:L:76:LEU:HD12	6:L:76:LEU:N	2.11	0.64
27:F:44:A:N3	27:F:45:A:C8	2.66	0.64
1:A:1017:ASP:O	1:A:1509:ARG:NH1	2.31	0.64
2:B:48:ASP:OD2	2:B:69:VAL:HG21	1.96	0.64
2:B:235:ILE:HD13	2:B:280:ILE:HD13	1.78	0.64
2:B:374:ASN:CB	2:B:376:TRP:HE1	2.11	0.64
2:B:393:ARG:HH21	2:B:393:ARG:CG	2.09	0.64
3:I:401:LEU:HD12	4:G:214:SER:CB	2.27	0.64
6:L:91:MET:HE1	6:L:129:GLY:HA2	1.79	0.64
8:H:129:ILE:HD12	8:H:129:ILE:H	1.59	0.64
26:E:24:A:C2	26:E:50:G:C2	2.86	0.64
1:A:273:ASP:O	1:A:276:VAL:HG22	1.97	0.64
1:A:784:GLN:O	1:A:788:GLU:HG2	1.98	0.64
1:A:1876:ASN:OD1	1:A:1896:THR:HG23	1.97	0.64
2:B:311:PHE:CE2	7:M:126:ILE:HD13	2.32	0.64
2:B:316:GLN:CG	2:B:357:TRP:CE2	2.81	0.64
4:G:281:ASN:ND2	4:G:295:LEU:HD11	2.13	0.64
4:G:721:ARG:HD3	4:G:725:ILE:CD1	2.26	0.64
8:H:197:THR:HG21	8:H:545:LEU:CD1	2.21	0.64
26:E:1:A:N6	29:E:201:M7M:HBZB	2.13	0.64
8:H:164:MET:HG2	8:H:175:LEU:HD12	1.80	0.64
8:H:292:ILE:O	8:H:295:ILE:HG12	1.97	0.64
27:F:76:U:OP2	27:F:76:U:H4'	1.97	0.64
1:A:294:ASN:OD1	1:A:300:LYS:CE	2.45	0.64
1:A:703:PHE:CE1	1:A:705:GLN:HB3	2.30	0.64
1:A:1621:VAL:HG12	1:A:1622:GLY:N	2.07	0.64
8:H:167:ASN:HD21	8:H:173:LYS:HG2	1.62	0.64
1:A:506:PHE:HA	1:A:522:TYR:CE1	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:304:ARG:NH1	26:E:13:G:OP1	2.31	0.64
5:K:325:GLU:HA	5:K:328:ASN:OD1	1.97	0.64
8:H:470:ALA:CB	8:H:577:LEU:HD22	2.28	0.64
3:I:120:TYR:CE2	3:I:141:ILE:HG12	2.33	0.64
4:G:693:SER:HA	4:G:696:ARG:HD2	1.80	0.64
26:E:23:C:O2'	26:E:24:A:H5'	1.97	0.64
1:A:1076:PRO:O	1:A:1080:ASP:OD2	2.16	0.63
1:A:1458:TRP:CZ3	1:A:1461:TYR:CD2	2.86	0.63
2:B:415:TYR:HD2	2:B:439:LYS:HD3	1.61	0.63
4:G:843:VAL:CG2	4:G:895:LEU:HD13	2.27	0.63
8:H:105:ILE:HA	8:H:108:GLN:NE2	2.13	0.63
1:A:273:ASP:N	1:A:273:ASP:OD1	2.31	0.63
1:A:293:VAL:HG13	1:A:295:GLY:N	2.13	0.63
1:A:767:LEU:HD21	1:A:779:ALA:HB2	1.78	0.63
8:H:227:VAL:O	8:H:473:LEU:HD13	1.99	0.63
25:D:62:A:C2'	25:D:63:G:H5'	2.28	0.63
1:A:1613:THR:O	1:A:1616:ARG:HD3	1.97	0.63
2:B:114:THR:O	2:B:118:ILE:HG13	1.99	0.63
2:B:273:TYR:CZ	2:B:280:ILE:HD11	2.33	0.63
3:I:197:ILE:HG23	3:I:201:ASN:HD21	1.61	0.63
8:H:118:TYR:CD1	8:H:119:ASN:O	2.50	0.63
8:H:463:THR:CB	8:H:585:ASP:OD1	2.47	0.63
8:H:880:MET:HB3	8:H:886:SER:HA	1.81	0.63
8:H:947:LYS:H	8:H:947:LYS:HD3	1.62	0.63
27:F:78:A:HO2'	27:F:79:C:P	2.18	0.63
1:A:173:LEU:CD1	1:A:712:LEU:CD1	2.76	0.63
6:L:25:ARG:HH11	6:L:25:ARG:CG	2.10	0.63
8:H:484:SER:HB3	8:H:571:TYR:OH	1.97	0.63
24:C:10:U:O2'	24:C:11:A:H5'	1.99	0.63
25:D:49:A:C2'	25:D:50:G:H5''	2.23	0.63
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.81	0.63
3:I:98:PHE:CZ	3:I:217:TYR:HD2	2.15	0.63
3:I:225:ILE:C	3:I:325:ARG:HH12	2.01	0.63
3:I:282:GLU:OE1	3:I:286:PHE:CE2	2.52	0.63
4:G:134:ARG:HB3	4:G:134:ARG:CZ	2.28	0.63
8:H:945:LEU:HD12	8:H:945:LEU:H	1.63	0.63
27:F:40:C:H3'	27:F:40:C:OP2	1.99	0.63
1:A:175:LEU:HD11	1:A:564:TRP:CZ2	2.33	0.63
1:A:1317:ARG:HH21	1:A:1366:ARG:HH22	1.45	0.63
3:I:206:ASN:O	3:I:209:LYS:HG2	1.98	0.63
3:I:320:GLN:HG2	3:I:325:ARG:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:358:ILE:HG22	3:I:360:GLU:H	1.64	0.63
8:H:469:TRP:CD1	8:H:578:TYR:HB3	2.34	0.63
8:H:968:MET:HE2	8:H:968:MET:CA	2.29	0.63
1:A:1618:ASN:N	1:A:1618:ASN:OD1	2.31	0.63
2:B:230:SER:OG	2:B:233:GLN:OE1	2.16	0.63
2:B:391:ALA:O	2:B:392:HIS:HB2	1.97	0.63
3:I:268:LEU:HD12	3:I:271:GLU:HG2	1.80	0.63
3:I:402:ASP:OD1	3:I:403:SER:N	2.31	0.63
4:G:886:CYS:C	4:G:888:PRO:HD2	2.19	0.63
8:H:363:PRO:O	8:H:364:PHE:HB3	1.98	0.63
8:H:889:TYR:HE1	8:H:890:LYS:HG3	1.57	0.63
27:F:94:C:H6	27:F:94:C:H5''	1.63	0.63
1:A:393:SER:O	1:A:394:ARG:HG2	1.98	0.63
1:A:1658:HIS:CA	1:A:1661:ILE:HD12	2.27	0.63
1:A:1748:ILE:O	1:A:1752:VAL:CG2	2.41	0.63
2:B:239:GLU:HA	2:B:267:ARG:HB2	1.81	0.63
3:I:429:ARG:CB	3:I:429:ARG:HH11	2.11	0.63
4:G:279:LEU:N	4:G:279:LEU:HD23	2.13	0.63
5:K:452:LEU:O	5:K:456:GLY:N	2.31	0.63
1:A:874:ILE:HD11	1:A:1062:ASP:HB2	1.81	0.63
1:A:1118:GLY:HA3	1:A:1163:ARG:NH2	2.14	0.63
4:G:666:ILE:C	4:G:670:PHE:HD2	2.02	0.63
4:G:702:PRO:HA	4:G:739:PHE:CE2	2.33	0.63
8:H:942:GLY:O	8:H:963:SER:OG	2.17	0.63
27:F:92:U:H6	27:F:92:U:H5''	1.64	0.63
1:A:297:SER:CB	27:F:32:G:O5'	2.47	0.62
1:A:1916:GLU:HA	1:A:1916:GLU:OE2	1.98	0.62
24:C:2:A:H8	24:C:2:A:O5'	1.82	0.62
1:A:1653:LEU:HD21	1:A:1815:LEU:HD23	1.80	0.62
4:G:703:LEU:HD13	4:G:703:LEU:C	2.19	0.62
4:G:859:LEU:O	4:G:862:MET:HG2	1.99	0.62
8:H:178:LEU:N	8:H:178:LEU:HD23	2.14	0.62
8:H:959:ILE:CD1	8:H:960:ASN:N	2.61	0.62
1:A:770:MET:HE1	1:A:779:ALA:N	2.15	0.62
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.00	0.62
2:B:405:ASP:OD2	2:B:408:LYS:HD3	1.98	0.62
3:I:102:ILE:HB	3:I:103:PRO:HD3	1.81	0.62
6:L:96:GLY:O	6:L:138:ASN:HB2	1.96	0.62
8:H:126:MET:SD	8:H:132:ARG:NH1	2.72	0.62
8:H:936:ILE:H	8:H:936:ILE:CD1	2.12	0.62
9:N:807:GLY:H	9:N:1093:ALA:N	1.93	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1275:MET:HE3	1:A:1299:LYS:HD2	1.81	0.62
3:I:146:ASN:ND2	3:I:148:ASN:ND2	2.47	0.62
4:G:268:CYS:SG	4:G:278:TRP:HH2	2.15	0.62
5:K:141:ASN:ND2	5:K:144:LEU:HD23	2.14	0.62
8:H:129:ILE:HB	8:H:132:ARG:HB2	1.81	0.62
8:H:793:GLU:O	8:H:796:ILE:HG22	1.99	0.62
24:C:3:A:H8	24:C:3:A:O5'	1.81	0.62
1:A:1880:PHE:CD2	1:A:1889:LEU:HD21	2.32	0.62
3:I:321:LYS:HD2	3:I:324:ASP:HB3	1.79	0.62
3:I:433:ASN:O	3:I:434:GLN:C	2.37	0.62
4:G:124:ASP:N	4:G:124:ASP:OD1	2.32	0.62
4:G:223:LEU:HD23	4:G:223:LEU:O	2.00	0.62
5:K:166:TYR:OH	5:K:174:LEU:HD12	2.00	0.62
1:A:376:ARG:NE	8:H:910:GLU:OE2	2.32	0.62
1:A:840:VAL:O	1:A:840:VAL:HG22	2.00	0.62
2:B:292:TRP:CD1	2:B:299:GLU:HA	2.34	0.62
3:I:373:ARG:HB3	3:I:373:ARG:NH1	2.14	0.62
3:I:433:ASN:O	3:I:434:GLN:O	2.18	0.62
4:G:857:VAL:O	4:G:860:TYR:HB2	1.99	0.62
8:H:202:ASP:N	8:H:202:ASP:OD1	2.31	0.62
8:H:483:TRP:CH2	8:H:565:LYS:HG3	2.34	0.62
24:C:5:G:H4'	24:C:6:U:OP1	1.98	0.62
1:A:219:ALA:O	1:A:266:LEU:HD12	1.99	0.62
1:A:1022:PRO:CD	1:A:1345:TYR:HE1	2.09	0.62
4:G:167:GLU:HG3	4:G:168:LYS:N	2.13	0.62
8:H:379:ILE:O	8:H:383:LYS:HG3	1.99	0.62
8:H:931:TYR:O	8:H:931:TYR:HD1	1.83	0.62
1:A:1458:TRP:CE3	1:A:1461:TYR:HD2	2.18	0.62
1:A:1887:GLY:HA3	1:A:1992:TYR:HD1	1.64	0.62
5:K:311:GLU:HA	5:K:311:GLU:OE1	2.00	0.62
1:A:175:LEU:CD1	1:A:564:TRP:CE2	2.83	0.62
1:A:286:LEU:CD2	1:A:292:LYS:HB3	2.28	0.62
1:A:780:ARG:C	1:A:784:GLN:OE1	2.38	0.62
2:B:165:LEU:N	2:B:165:LEU:HD23	2.14	0.62
4:G:688:ARG:HD3	4:G:692:LEU:HD21	1.81	0.62
8:H:326:GLU:OE1	8:H:330:TYR:HD2	1.82	0.62
8:H:582:SER:OG	8:H:585:ASP:OD2	2.17	0.62
8:H:674:LEU:CD1	8:H:973:ARG:HH22	2.12	0.62
9:N:487:CYS:O	9:N:490:ALA:N	2.33	0.62
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.82	0.62
4:G:281:ASN:HD22	4:G:295:LEU:HD13	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:280:VAL:O	5:K:286:ASN:ND2	2.33	0.62
5:K:282:GLU:O	5:K:284:ASP:N	2.32	0.62
6:L:34:LYS:HD2	6:L:35:ASN:H	1.64	0.62
8:H:129:ILE:HG12	10:R:16:GLY:CA	2.30	0.62
1:A:1658:HIS:HA	1:A:1661:ILE:CD1	2.26	0.61
4:G:230:LEU:HD12	4:G:247:SER:CA	2.23	0.61
4:G:285:HIS:CE1	4:G:291:TYR:CZ	2.87	0.61
5:K:147:ASP:OD1	5:K:147:ASP:N	2.31	0.61
8:H:114:PRO:C	8:H:115:LYS:HG3	2.20	0.61
8:H:389:LEU:N	8:H:389:LEU:HD23	2.15	0.61
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.81	0.61
2:B:124:LEU:CD2	2:B:274:HIS:HE1	2.10	0.61
2:B:192:THR:HB	2:B:461:ILE:HD11	1.82	0.61
2:B:313:LEU:HD13	2:B:322:VAL:CG2	2.26	0.61
3:I:400:VAL:HG21	4:G:154:PRO:HG2	1.81	0.61
4:G:671:PHE:CE2	4:G:694:GLY:HA2	2.35	0.61
4:G:721:ARG:HD2	4:G:725:ILE:CD1	2.30	0.61
4:G:888:PRO:O	4:G:892:LEU:CD2	2.48	0.61
8:H:373:PHE:CE1	8:H:377:ILE:HD12	2.34	0.61
8:H:881:LYS:HA	8:H:886:SER:CB	2.30	0.61
27:F:31:G:N1	27:F:32:G:C4	2.68	0.61
3:I:184:LYS:CD	3:I:186:LYS:H	2.01	0.61
8:H:168:VAL:HG12	8:H:173:LYS:O	2.00	0.61
8:H:581:LYS:HB3	8:H:581:LYS:NZ	2.11	0.61
24:C:11:A:H8	24:C:11:A:O5'	1.83	0.61
1:A:207:ARG:NH1	1:A:299:LYS:CG	2.63	0.61
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.34	0.61
1:A:1907:GLN:O	1:A:1910:LYS:CG	2.48	0.61
2:B:395:ILE:HD11	7:M:123:THR:HG23	1.80	0.61
3:I:93:LYS:HA	3:I:93:LYS:NZ	2.15	0.61
3:I:263:GLY:O	3:I:283:GLY:HA2	2.00	0.61
3:I:450:GLN:HG3	3:I:451:GLN:N	2.14	0.61
4:G:143:ARG:HH21	4:G:143:ARG:CG	2.14	0.61
4:G:215:LEU:C	4:G:215:LEU:HD12	2.20	0.61
8:H:471:HIS:C	8:H:486:VAL:HG23	2.19	0.61
1:A:769:MET:CE	4:G:112:ALA:HA	2.29	0.61
1:A:843:THR:HG21	6:L:108:ASP:HB3	1.83	0.61
1:A:956:LYS:HD2	1:A:956:LYS:C	2.21	0.61
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.18	0.61
4:G:6:PHE:CD1	4:G:7:LEU:N	2.68	0.61
4:G:238:PRO:CD	4:G:239:THR:H	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:674:LEU:HD13	8:H:973:ARG:NH1	2.13	0.61
1:A:147:SER:O	1:A:150:ALA:HB2	2.00	0.61
1:A:322:VAL:CG2	1:A:327:TYR:CE2	2.80	0.61
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.83	0.61
1:A:892:SER:CB	1:A:1128:GLN:HE22	2.13	0.61
8:H:139:ILE:HD12	8:H:252:LEU:HD22	1.81	0.61
8:H:379:ILE:HG22	8:H:383:LYS:HE3	1.81	0.61
9:N:807:GLY:C	9:N:1093:ALA:H	2.00	0.61
1:A:141:LYS:CA	1:A:144:ASN:ND2	2.54	0.61
1:A:1350:ILE:HG23	1:A:1356:LEU:HD12	1.81	0.61
2:B:206:THR:HB	2:B:208:GLN:OE1	2.00	0.61
2:B:320:SER:CB	2:B:337:ARG:HH22	2.13	0.61
2:B:456:GLY:O	2:B:458:ASP:N	2.34	0.61
8:H:106:PHE:O	8:H:110:LYS:HG2	2.00	0.61
8:H:968:MET:HA	8:H:968:MET:CE	2.30	0.61
27:F:32:G:O2'	27:F:33:U:OP1	2.19	0.61
1:A:217:TRP:CD1	1:A:703:PHE:CE2	2.89	0.61
1:A:1275:MET:CE	1:A:1299:LYS:HD2	2.31	0.61
1:A:1468:ALA:CB	1:A:1473:ARG:O	2.49	0.61
3:I:393:PHE:CD1	3:I:393:PHE:C	2.73	0.61
8:H:606:VAL:HG21	8:H:973:ARG:HH21	1.66	0.61
24:C:11:A:O2'	24:C:12:U:H5'	2.01	0.61
27:F:74:U:H5'	27:F:74:U:H6	1.65	0.61
1:A:355:LEU:HD13	1:A:356:TYR:N	2.16	0.61
1:A:495:ARG:CZ	1:A:497:GLN:HE21	2.12	0.61
1:A:1282:ASP:O	1:A:1285:VAL:HG23	2.01	0.61
1:A:1830:VAL:HG11	1:A:1958:PRO:HG3	1.80	0.61
8:H:132:ARG:HH21	8:H:206:LYS:HG3	1.66	0.61
8:H:235:VAL:HG22	8:H:261:VAL:CG1	2.29	0.61
8:H:369:LYS:NZ	8:H:369:LYS:H	1.99	0.61
8:H:883:ARG:NH2	8:H:910:GLU:O	2.34	0.61
1:A:293:VAL:HG22	1:A:294:ASN:H	1.65	0.61
1:A:1887:GLY:HA3	1:A:1992:TYR:CD1	2.35	0.61
3:I:135:LEU:HD23	3:I:136:GLN:HG3	1.83	0.61
3:I:402:ASP:O	3:I:405:GLY:N	2.33	0.61
4:G:668:HIS:HB3	4:G:698:VAL:CG1	2.21	0.61
4:G:702:PRO:CB	4:G:739:PHE:CZ	2.83	0.61
5:K:334:PRO:HG2	5:K:337:TYR:CE1	2.36	0.61
8:H:576:THR:CB	8:H:592:PHE:HD2	2.11	0.61
1:A:547:LEU:HD12	1:A:547:LEU:O	2.00	0.60
2:B:175:THR:HA	2:B:459:ARG:HD2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:389:ILE:HD11	2:B:427:TRP:CD1	2.36	0.60
8:H:862:TYR:CE1	8:H:908:VAL:HG23	2.36	0.60
1:A:497:GLN:O	1:A:709:ARG:CD	2.46	0.60
1:A:547:LEU:HD12	1:A:547:LEU:C	2.20	0.60
1:A:1998:ARG:C	1:A:1999:ILE:HG13	2.21	0.60
1:A:842:LYS:HD2	1:A:842:LYS:C	2.19	0.60
1:A:1158:ILE:HG13	1:A:1172:PHE:HE1	1.65	0.60
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.60
3:I:158:PHE:HA	3:I:161:LEU:CD1	2.28	0.60
1:A:293:VAL:HG13	1:A:295:GLY:H	1.65	0.60
1:A:358:ARG:CD	1:A:360:GLU:HB2	2.31	0.60
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.66	0.60
4:G:6:PHE:CE1	4:G:7:LEU:HD12	2.36	0.60
4:G:692:LEU:HD23	4:G:692:LEU:N	2.17	0.60
7:M:95:ARG:HG2	7:M:95:ARG:NH1	2.01	0.60
27:F:95:C:HO2'	27:F:96:U:H5'	1.63	0.60
1:A:325:LYS:HE2	1:A:325:LYS:HA	1.83	0.60
2:B:127:TYR:CE2	2:B:276:SER:CA	2.85	0.60
2:B:320:SER:HB2	2:B:337:ARG:CZ	2.30	0.60
4:G:630:SER:CA	4:G:670:PHE:CZ	2.84	0.60
5:K:457:GLN:CD	5:K:457:GLN:H	1.98	0.60
6:L:71:ASP:HA	6:L:76:LEU:HD13	1.82	0.60
3:I:123:ARG:HD2	3:I:189:LEU:CD1	2.31	0.60
5:K:244:LEU:O	5:K:248:ARG:HB2	2.02	0.60
6:L:74:TYR:CD1	6:L:83:MET:HE3	2.37	0.60
24:C:8:U:C5	25:D:51:A:C6	2.90	0.60
27:F:44:A:C4	27:F:45:A:N7	2.69	0.60
27:F:102:C:O5'	27:F:102:C:H6	1.85	0.60
2:B:187:ASP:OD2	2:B:447:ASN:HB3	2.01	0.60
3:I:135:LEU:HD23	3:I:136:GLN:H	1.62	0.60
4:G:855:ASP:N	4:G:855:ASP:OD1	2.34	0.60
5:K:341:VAL:CG2	5:K:428:TRP:NE1	2.65	0.60
8:H:113:ILE:HG23	8:H:549:TYR:CG	2.37	0.60
8:H:352:VAL:HG13	8:H:372:THR:OG1	2.02	0.60
2:B:331:SER:HB3	2:B:345:LEU:HB2	1.83	0.60
3:I:123:ARG:HD2	3:I:189:LEU:HD12	1.83	0.60
8:H:113:ILE:HG22	8:H:114:PRO:CD	2.30	0.60
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.83	0.60
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.41	0.60
2:B:47:GLU:HB2	2:B:50:GLU:HG3	1.82	0.60
3:I:282:GLU:CG	3:I:286:PHE:CG	2.80	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:702:PRO:HB3	4:G:739:PHE:CE2	2.37	0.60
8:H:349:TRP:HZ3	8:H:373:PHE:HE2	1.47	0.60
24:C:8:U:N1	25:D:51:A:N6	2.48	0.60
27:F:32:G:N2	27:F:122:C:C2	2.70	0.60
27:F:97:U:C6	27:F:97:U:C5'	2.85	0.60
4:G:143:ARG:HH21	4:G:143:ARG:HG3	1.66	0.60
8:H:324:ILE:O	8:H:328:VAL:CG2	2.46	0.60
1:A:173:LEU:CD1	1:A:712:LEU:HD11	2.32	0.59
1:A:266:LEU:HD23	1:A:267:PRO:CD	2.32	0.59
1:A:1025:VAL:O	1:A:1029:THR:HG23	2.01	0.59
1:A:1354:GLU:N	1:A:1354:GLU:OE2	2.35	0.59
3:I:265:ASN:O	3:I:266:LYS:HB2	2.02	0.59
4:G:6:PHE:CZ	6:L:18:ALA:HB2	2.37	0.59
5:K:342:PHE:HB3	5:K:424:ILE:HD11	1.84	0.59
6:L:71:ASP:OD1	6:L:76:LEU:HB2	2.02	0.59
8:H:492:LEU:HD22	8:H:557:HIS:CG	2.36	0.59
27:F:97:U:H5''	27:F:97:U:H6	1.67	0.59
1:A:505:TRP:CZ3	1:A:690:LYS:HG3	2.37	0.59
1:A:1275:MET:CE	1:A:1299:LYS:CE	2.80	0.59
1:A:1450:GLU:HB3	1:A:1488:ILE:HD11	1.83	0.59
2:B:177:PRO:HB2	2:B:195:TRP:HE1	1.66	0.59
2:B:177:PRO:CD	2:B:195:TRP:CD1	2.85	0.59
4:G:863:PHE:HE2	4:G:892:LEU:CD1	2.16	0.59
6:L:81:THR:HG21	6:L:102:LYS:HZ3	1.62	0.59
1:A:1458:TRP:CZ3	1:A:1461:TYR:HD2	2.20	0.59
1:A:1857:VAL:O	1:A:1877:GLY:CA	2.49	0.59
3:I:98:PHE:CE2	3:I:217:TYR:CE2	2.91	0.59
3:I:184:LYS:HD2	3:I:186:LYS:CB	2.31	0.59
3:I:347:ALA:HB1	3:I:348:PRO:CD	2.31	0.59
5:K:350:PRO:HB3	5:K:353:ARG:HD2	1.84	0.59
7:M:125:LEU:O	7:M:126:ILE:C	2.39	0.59
2:B:177:PRO:HB2	2:B:195:TRP:NE1	2.17	0.59
3:I:98:PHE:HE2	3:I:217:TYR:CE2	2.19	0.59
8:H:332:TYR:OH	8:H:376:PHE:HD2	1.81	0.59
8:H:364:PHE:HB2	8:H:369:LYS:HG3	0.63	0.59
2:B:131:ARG:HG2	2:B:131:ARG:HH11	1.67	0.59
2:B:227:HIS:CD2	2:B:273:TYR:CE1	2.90	0.59
2:B:320:SER:CB	2:B:337:ARG:NH2	2.65	0.59
3:I:282:GLU:OE2	3:I:286:PHE:CE2	2.52	0.59
3:I:423:ALA:O	3:I:424:THR:HB	2.03	0.59
6:L:34:LYS:HD2	6:L:35:ASN:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ASN:OD1	1:A:300:LYS:HE2	2.01	0.59
1:A:362:GLU:OE2	1:A:1209:LYS:HE3	2.01	0.59
3:I:112:MET:CB	3:I:204:LEU:CD2	2.79	0.59
8:H:500:ARG:HD3	8:H:534:THR:CB	2.32	0.59
1:A:175:LEU:CD1	1:A:564:TRP:NE1	2.64	0.59
2:B:124:LEU:O	2:B:128:SER:N	2.31	0.59
3:I:301:GLN:OE1	3:I:344:LEU:HD13	2.01	0.59
5:K:146:GLU:O	5:K:149:PHE:N	2.33	0.59
8:H:385:PHE:O	8:H:389:LEU:HG	2.03	0.59
8:H:608:GLN:HG3	8:H:609:PRO:HD2	1.85	0.59
1:A:332:ASP:C	1:A:332:ASP:OD1	2.41	0.59
1:A:766:ILE:O	1:A:770:MET:HG2	2.03	0.59
2:B:177:PRO:CD	2:B:195:TRP:HD1	2.15	0.59
3:I:233:VAL:HG12	3:I:237:ILE:HB	1.84	0.59
3:I:393:PHE:C	3:I:393:PHE:HD1	2.05	0.59
8:H:230:ALA:HB3	8:H:473:LEU:HD13	1.84	0.59
8:H:323:THR:OG1	8:H:326:GLU:HB2	2.03	0.59
8:H:369:LYS:HE2	8:H:369:LYS:H	1.67	0.59
8:H:932:PHE:O	8:H:933:TRP:CE3	2.56	0.59
1:A:149:MET:O	1:A:153:MET:CG	2.51	0.59
1:A:316:THR:N	1:A:317:PRO:CD	2.66	0.59
1:A:390:LEU:HD13	8:H:652:MET:SD	2.42	0.59
1:A:546:LYS:O	1:A:550:SER:OG	2.18	0.59
1:A:1414:TRP:CZ3	1:A:1416:LYS:HB2	2.37	0.59
1:A:1577:LYS:NZ	3:I:397:GLU:OE2	2.36	0.59
2:B:51:VAL:HG13	2:B:76:LEU:HD12	1.85	0.59
3:I:94:LEU:HD13	3:I:98:PHE:CZ	2.38	0.59
4:G:277:ILE:HD12	4:G:277:ILE:N	2.15	0.59
5:K:141:ASN:HD21	5:K:144:LEU:CD2	2.15	0.59
5:K:249:ARG:HG2	5:K:249:ARG:HH11	1.67	0.59
6:L:75:GLU:C	6:L:76:LEU:HD12	2.24	0.59
8:H:959:ILE:HD13	8:H:960:ASN:N	2.17	0.59
27:F:44:A:C2'	27:F:45:A:C8	2.67	0.59
27:F:45:A:C2	27:F:46:C:C4	2.91	0.59
1:A:425:ASP:OD2	1:A:426:PRO:HD2	2.03	0.58
2:B:358:SER:OG	2:B:401:PHE:CZ	2.48	0.58
4:G:702:PRO:HG3	4:G:738:LEU:HB2	1.85	0.58
6:L:33:ARG:NE	6:L:64:ILE:HB	2.18	0.58
8:H:567:ILE:HD13	8:H:567:ILE:N	2.18	0.58
1:A:176:LEU:HD23	1:A:176:LEU:C	2.22	0.58
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:ILE:CG1	1:A:1172:PHE:CE1	2.86	0.58
1:A:1628:ASP:HB3	25:D:50:G:N2	2.18	0.58
2:B:405:ASP:OD2	2:B:408:LYS:CD	2.52	0.58
2:B:415:TYR:OH	7:M:126:ILE:CA	2.51	0.58
2:B:456:GLY:O	2:B:457:TRP:C	2.42	0.58
4:G:12:PRO:HB2	4:G:13:ALA:O	2.03	0.58
8:H:268:ASN:HD21	8:H:316:THR:CG2	2.17	0.58
8:H:362:LYS:HE2	8:H:365:GLU:HB2	1.84	0.58
8:H:386:SER:O	8:H:390:SER:HB3	2.03	0.58
8:H:449:PHE:CD1	8:H:453:THR:CG2	2.86	0.58
25:D:109:U:C3'	25:D:110:U:H5''	2.31	0.58
1:A:297:SER:HB3	27:F:32:G:P	2.41	0.58
2:B:115:SER:CA	2:B:118:ILE:HG13	2.32	0.58
1:A:165:LEU:CD2	1:A:730:ILE:HD11	2.29	0.58
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.38	0.58
1:A:1758:ASP:O	1:A:1762:ASP:HB2	2.04	0.58
1:A:1880:PHE:HE2	1:A:1889:LEU:HD21	1.57	0.58
2:B:127:TYR:OH	2:B:131:ARG:NH1	2.35	0.58
3:I:367:ARG:NH2	26:E:58:G:N7	2.52	0.58
6:L:74:TYR:CD1	6:L:83:MET:CE	2.86	0.58
8:H:191:ILE:HG23	8:H:221:PHE:CE1	2.38	0.58
8:H:881:LYS:HA	8:H:886:SER:HB2	1.84	0.58
1:A:168:LEU:CA	1:A:199:ILE:CD1	2.81	0.58
1:A:506:PHE:HA	1:A:522:TYR:CD1	2.39	0.58
1:A:1664:ASP:O	1:A:1668:ILE:HG13	2.04	0.58
1:A:1854:ASP:OD1	1:A:1879:ILE:HG23	2.04	0.58
5:K:363:LEU:HD11	5:K:391:PHE:HD2	1.68	0.58
8:H:145:GLY:N	28:H:1500:GTP:O2B	2.31	0.58
8:H:476:VAL:CG1	8:H:478:TYR:CD1	2.85	0.58
8:H:780:PRO:HA	8:H:783:ILE:HB	1.85	0.58
3:I:113:HIS:HD2	3:I:134:PRO:HA	1.68	0.58
1:A:1496:GLN:O	1:A:1499:ARG:CG	2.51	0.58
2:B:446:SER:HB2	2:B:451:PHE:N	2.16	0.58
4:G:630:SER:CA	4:G:670:PHE:HZ	2.16	0.58
4:G:849:TYR:O	4:G:853:GLY:N	2.35	0.58
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.38	0.58
8:H:572:ILE:HD12	8:H:572:ILE:O	2.03	0.58
24:C:-1:A:N3	24:C:-1:A:H2'	2.18	0.58
1:A:255:ILE:O	1:A:258:ILE:HG22	2.03	0.58
1:A:457:ASP:OD1	1:A:457:ASP:N	2.37	0.58
1:A:839:HIS:NE2	27:F:96:U:C4	2.71	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1998:ARG:O	1:A:1999:ILE:CG1	2.44	0.58
3:I:282:GLU:HG2	3:I:286:PHE:CD1	2.36	0.58
6:L:133:SER:OG	6:L:135:TYR:O	2.20	0.58
8:H:307:ILE:CD1	8:H:324:ILE:CD1	2.81	0.58
8:H:369:LYS:HE2	8:H:369:LYS:CA	2.33	0.58
8:H:489:TYR:CE2	8:H:592:PHE:HE1	2.20	0.58
8:H:862:TYR:HD2	8:H:930:LEU:HB3	1.67	0.58
1:A:149:MET:CG	1:A:154:TYR:HE2	2.16	0.58
1:A:286:LEU:O	1:A:287:GLU:O	2.22	0.58
1:A:1256:PRO:CA	1:A:1274:ARG:HH21	2.12	0.58
1:A:1313:ASP:OD2	1:A:1359:ILE:HD13	2.03	0.58
5:K:295:LYS:O	5:K:299:ASP:HB2	2.04	0.58
8:H:296:ASN:HD21	8:H:304:PHE:N	2.00	0.58
8:H:507:SER:O	8:H:510:ARG:N	2.37	0.58
1:A:249:LEU:HD23	1:A:249:LEU:H	1.69	0.58
1:A:261:LEU:C	1:A:261:LEU:HD12	2.23	0.58
1:A:1751:TYR:CE1	1:A:1755:LYS:CD	2.77	0.58
2:B:197:GLY:C	2:B:221:ILE:HD11	2.24	0.58
3:I:421:VAL:HG21	4:G:250:LEU:CD1	2.33	0.58
4:G:278:TRP:HA	4:G:278:TRP:CE3	2.38	0.58
4:G:401:ILE:O	4:G:405:SER:N	2.35	0.58
4:G:672:LEU:HD23	4:G:704:LEU:HD23	1.45	0.58
4:G:697:LEU:N	4:G:697:LEU:HD23	2.17	0.58
1:A:1073:ILE:CG2	1:A:1074:VAL:HG23	2.29	0.57
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.87	0.57
2:B:286:ASP:C	2:B:287:MET:CG	2.72	0.57
4:G:248:ALA:HB1	4:G:264:ILE:HD11	1.86	0.57
4:G:867:GLU:OE2	4:G:888:PRO:CG	2.52	0.57
8:H:354:TYR:HA	8:H:359:PHE:CB	2.33	0.57
8:H:489:TYR:HE2	8:H:592:PHE:HE1	1.52	0.57
8:H:586:MET:CA	8:H:589:LEU:HD23	2.33	0.57
26:E:19:U:O2'	26:E:20:A:OP2	2.21	0.57
1:A:552:LYS:HG3	1:A:553:ASN:N	2.19	0.57
1:A:1256:PRO:CA	1:A:1274:ARG:NH2	2.67	0.57
2:B:264:HIS:HE1	2:B:290:ARG:HD2	1.69	0.57
2:B:278:LYS:C	2:B:279:PHE:HD1	2.08	0.57
4:G:764:LEU:O	4:G:768:PRO:HB3	2.04	0.57
4:G:846:PHE:CE1	4:G:859:LEU:HD23	2.36	0.57
8:H:349:TRP:CZ3	8:H:373:PHE:CE2	2.92	0.57
8:H:353:TYR:O	8:H:359:PHE:HB2	2.04	0.57
8:H:500:ARG:HG2	8:H:534:THR:CG2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:ARG:HH21	1:A:840:VAL:HG23	1.69	0.57
2:B:124:LEU:C	2:B:128:SER:HG	2.01	0.57
2:B:443:LEU:HD11	2:B:452:LEU:HD11	1.86	0.57
3:I:147:GLU:CD	3:I:147:GLU:H	2.07	0.57
1:A:1283:GLU:HG2	1:A:1351:VAL:HB	1.84	0.57
4:G:170:LEU:C	4:G:170:LEU:HD13	2.24	0.57
6:L:119:THR:HG22	6:L:131:VAL:CG1	2.35	0.57
8:H:336:ILE:HG13	8:H:341:ILE:HG22	1.85	0.57
2:B:127:TYR:CE2	2:B:276:SER:HA	2.38	0.57
2:B:131:ARG:HG2	2:B:131:ARG:NH1	2.18	0.57
3:I:189:LEU:HD23	3:I:193:THR:OG1	2.03	0.57
3:I:346:GLU:O	3:I:347:ALA:CB	2.53	0.57
4:G:695:THR:CB	4:G:705:TRP:NE1	2.57	0.57
5:K:163:ASN:O	5:K:164:HIS:HB3	2.03	0.57
8:H:129:ILE:H	8:H:129:ILE:CD1	2.18	0.57
27:F:78:A:HO2'	27:F:79:C:C5'	2.10	0.57
1:A:251:TYR:CE2	1:A:566:GLU:OE1	2.58	0.57
1:A:1049:LEU:HD13	1:A:1260:PHE:HB3	1.87	0.57
1:A:2007:ARG:NH2	5:K:291:THR:OG1	2.35	0.57
3:I:217:TYR:O	3:I:220:SER:OG	2.18	0.57
5:K:144:LEU:HD22	5:K:144:LEU:H	1.69	0.57
6:L:74:TYR:HB2	6:L:76:LEU:HD11	1.86	0.57
8:H:132:ARG:NH2	8:H:206:LYS:HG3	2.19	0.57
8:H:369:LYS:H	8:H:369:LYS:CE	2.16	0.57
8:H:580:VAL:HG11	8:H:586:MET:HG2	1.85	0.57
1:A:224:MET:CE	1:A:702:GLY:HA3	2.34	0.57
1:A:301:TRP:CE2	1:A:491:GLY:HA3	2.40	0.57
4:G:698:VAL:N	4:G:699:PRO:HD3	2.20	0.57
8:H:227:VAL:CG1	8:H:474:LYS:HG3	2.25	0.57
8:H:306:PRO:O	8:H:324:ILE:HD13	2.04	0.57
1:A:258:ILE:O	1:A:259:GLU:CB	2.53	0.57
1:A:430:PRO:O	1:A:431:ILE:HG22	2.05	0.57
3:I:155:ASP:N	3:I:155:ASP:OD1	2.35	0.57
3:I:344:LEU:HD23	3:I:344:LEU:N	2.20	0.57
4:G:678:TYR:CZ	4:G:686:MET:HG2	2.40	0.57
4:G:846:PHE:CB	4:G:896:MET:SD	2.93	0.57
6:L:22:GLU:OE2	6:L:58:VAL:HG11	2.04	0.57
7:M:39:GLU:HB2	26:E:32:G:O6	2.05	0.57
8:H:488:ILE:HD13	8:H:560:GLN:HG2	1.81	0.57
1:A:165:LEU:CD2	1:A:726:ILE:HG21	2.35	0.57
1:A:543:ASN:ND2	1:A:544:LYS:N	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2068:ASN:N	1:A:2068:ASN:OD1	2.38	0.57
4:G:9:GLN:C	4:G:10:GLU:HG3	2.24	0.57
8:H:697:ARG:HA	8:H:697:ARG:CZ	2.35	0.57
27:F:99:U:HO2'	27:F:100:A:P	2.23	0.57
1:A:358:ARG:HD2	1:A:360:GLU:HB2	1.87	0.57
1:A:367:PHE:C	1:A:367:PHE:CD1	2.78	0.57
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.87	0.57
1:A:1378:LYS:O	1:A:1379:MET:CB	2.53	0.57
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.87	0.57
8:H:133:ILE:O	8:H:134:ILE:HG22	2.01	0.57
8:H:251:GLN:HG2	8:H:933:TRP:CE2	2.39	0.57
8:H:331:TYR:HE1	8:H:404:PHE:HD1	1.50	0.57
8:H:468:LEU:CD1	8:H:493:LEU:HD23	2.35	0.57
1:A:299:LYS:HA	1:A:493:MET:CG	2.33	0.56
1:A:389:HIS:HB2	8:H:653:ASP:OD1	2.05	0.56
1:A:1020:ILE:HD13	1:A:1488:ILE:HG21	1.87	0.56
1:A:1158:ILE:HG13	1:A:1172:PHE:CE1	2.40	0.56
2:B:362:TYR:HB2	2:B:379:ARG:HD2	1.85	0.56
3:I:158:PHE:CA	3:I:161:LEU:HD12	2.34	0.56
8:H:251:GLN:HG2	8:H:933:TRP:CZ2	2.40	0.56
8:H:307:ILE:HD13	8:H:324:ILE:CD1	2.35	0.56
8:H:599:THR:HG23	8:H:933:TRP:CZ3	2.40	0.56
1:A:219:ALA:O	1:A:266:LEU:HD11	2.05	0.56
1:A:1073:ILE:HG23	1:A:1074:VAL:CG2	2.33	0.56
1:A:1464:LYS:C	1:A:1475:LEU:HD21	2.25	0.56
3:I:191:ILE:HD12	3:I:191:ILE:N	2.14	0.56
3:I:455:PHE:O	3:I:458:SER:OG	2.19	0.56
4:G:296:VAL:HG12	4:G:300:ILE:HD12	1.86	0.56
5:K:146:GLU:CA	5:K:149:PHE:HD2	2.18	0.56
27:F:103:A:O2'	27:F:104:G:P	2.63	0.56
1:A:170:HIS:ND1	1:A:547:LEU:CD2	2.68	0.56
1:A:180:PRO:HA	1:A:187:LYS:HD2	1.87	0.56
1:A:208:VAL:HG22	1:A:494:VAL:O	2.05	0.56
1:A:224:MET:HE2	1:A:702:GLY:HA3	1.86	0.56
1:A:325:LYS:HA	1:A:325:LYS:CE	2.35	0.56
1:A:770:MET:CE	1:A:778:LYS:CB	2.84	0.56
1:A:779:ALA:O	1:A:782:ILE:HB	2.04	0.56
1:A:909:THR:HG22	1:A:910:LYS:N	2.20	0.56
1:A:1038:ILE:HD11	1:A:1039:TRP:CE2	2.39	0.56
1:A:1498:ASP:HB2	4:G:159:LEU:HB2	1.86	0.56
1:A:1628:ASP:CB	25:D:50:G:N2	2.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:227:PRO:HG3	3:I:325:ARG:HB3	1.86	0.56
3:I:418:GLN:NE2	3:I:425:SER:HB2	2.20	0.56
5:K:296:VAL:O	5:K:300:GLN:HB2	2.05	0.56
6:L:53:VAL:CG1	6:L:57:ALA:HB3	2.35	0.56
6:L:82:VAL:HB	6:L:103:LEU:HB3	1.87	0.56
6:L:116:ILE:HD12	6:L:137:TYR:OH	2.02	0.56
8:H:146:LYS:CE	28:H:1500:GTP:O3G	2.51	0.56
8:H:268:ASN:HD21	8:H:316:THR:HG23	1.69	0.56
8:H:328:VAL:O	8:H:333:ALA:N	2.38	0.56
8:H:476:VAL:HG11	8:H:478:TYR:CD1	2.40	0.56
25:D:49:A:N6	25:D:50:G:C5	2.73	0.56
1:A:1115:GLN:HA	1:A:1115:GLN:NE2	2.20	0.56
1:A:1773:VAL:HG22	1:A:1788:GLY:HA2	1.86	0.56
8:H:328:VAL:HG21	8:H:345:THR:HG22	1.87	0.56
8:H:468:LEU:CD2	8:H:577:LEU:CD2	2.80	0.56
8:H:495:ARG:NH2	8:H:541:GLU:OE2	2.38	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CB	2.80	0.56
24:C:-3:A:C8	24:C:-2:A:N6	2.73	0.56
1:A:272:ASP:HB2	1:A:273:ASP:OD1	2.05	0.56
1:A:1275:MET:O	1:A:1277:GLU:O	2.24	0.56
1:A:1364:GLU:O	1:A:1368:GLN:HG3	2.06	0.56
1:A:2050:THR:O	1:A:2053:SER:OG	2.20	0.56
2:B:192:THR:CB	2:B:461:ILE:HD11	2.35	0.56
5:K:300:GLN:OE1	5:K:300:GLN:HA	2.06	0.56
7:M:95:ARG:CG	7:M:96:PRO:HD2	2.36	0.56
8:H:307:ILE:HA	8:H:324:ILE:HD11	1.87	0.56
8:H:369:LYS:HE2	8:H:369:LYS:N	2.20	0.56
8:H:489:TYR:CE2	8:H:592:PHE:CZ	2.94	0.56
9:N:461:ASP:O	9:N:709:GLY:N	2.35	0.56
25:D:86:G:H5''	25:D:86:G:C8	2.32	0.56
27:F:41:A:H5'	27:F:41:A:H8	1.71	0.56
1:A:273:ASP:HB3	1:A:276:VAL:HG22	1.86	0.56
2:B:115:SER:O	2:B:118:ILE:HB	2.06	0.56
2:B:127:TYR:HE2	2:B:276:SER:HB2	1.63	0.56
8:H:132:ARG:HH21	8:H:206:LYS:CD	2.18	0.56
1:A:406:PRO:HG2	28:H:1500:GTP:O2'	2.04	0.56
2:B:162:MET:CG	2:B:421:VAL:HG11	2.35	0.56
3:I:95:LEU:HA	3:I:98:PHE:HB2	1.88	0.56
3:I:217:TYR:HE1	3:I:221:LYS:CE	2.18	0.56
4:G:671:PHE:HZ	4:G:693:SER:OG	1.86	0.56
6:L:109:ASP:OD1	6:L:110:LYS:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:11:LEU:HD23	7:M:12:ALA:O	2.06	0.56
8:H:582:SER:CB	8:H:585:ASP:HB2	2.28	0.56
8:H:901:GLU:OE2	8:H:903:ARG:CZ	2.53	0.56
25:D:46:U:H2'	25:D:47:A:H8	1.69	0.56
1:A:148:ASP:OD1	1:A:148:ASP:N	2.38	0.56
1:A:360:GLU:OE1	1:A:360:GLU:HA	2.06	0.56
1:A:371:ASP:OD2	8:H:972:ARG:NH1	2.38	0.56
1:A:1379:MET:HG3	1:A:1380:PRO:HD2	1.87	0.56
8:H:118:TYR:CD1	8:H:119:ASN:N	2.74	0.56
1:A:165:LEU:CD1	1:A:578:MET:HB3	2.35	0.56
2:B:206:THR:O	2:B:207:LEU:HB2	2.05	0.56
3:I:95:LEU:HD23	3:I:98:PHE:HD2	1.69	0.56
4:G:288:ASP:OD1	4:G:291:TYR:HB2	2.05	0.56
8:H:341:ILE:O	8:H:344:PHE:HB3	2.06	0.56
1:A:167:TYR:N	1:A:167:TYR:CD1	2.73	0.56
1:A:176:LEU:O	1:A:179:MET:HG3	2.06	0.56
1:A:749:ARG:HD2	1:A:750:LEU:N	2.20	0.56
1:A:1389:TYR:CE2	1:A:1401:SER:HB3	2.40	0.56
2:B:320:SER:HB2	2:B:337:ARG:NH1	2.21	0.56
8:H:572:ILE:CD1	8:H:573:LYS:HG3	2.28	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CG2	2.89	0.56
25:D:77:G:N2	26:E:4:C:O2	2.29	0.56
1:A:428:LEU:CD1	8:H:279:LEU:HD11	2.36	0.55
1:A:549:LYS:HG2	27:F:35:A:H5'	1.88	0.55
1:A:770:MET:CE	1:A:778:LYS:HB2	2.37	0.55
2:B:348:HIS:CD2	2:B:374:ASN:ND2	2.74	0.55
4:G:526:TYR:O	4:G:530:GLU:N	2.35	0.55
4:G:804:ASP:CG	4:G:805:HIS:H	2.10	0.55
1:A:355:LEU:HD13	1:A:355:LEU:C	2.26	0.55
1:A:939:LEU:HD11	3:I:441:MET:HE1	1.87	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.21	0.55
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.22	0.55
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.41	0.55
3:I:329:LEU:HD12	3:I:333:TRP:CZ2	2.41	0.55
8:H:483:TRP:CZ3	8:H:565:LYS:CG	2.89	0.55
8:H:862:TYR:CZ	8:H:908:VAL:HG23	2.41	0.55
9:N:1795:SER:O	9:N:1798:GLY:N	2.39	0.55
27:F:33:U:O2	27:F:33:U:H2'	2.05	0.55
27:F:44:A:N1	27:F:71:A:N1	2.54	0.55
1:A:149:MET:O	1:A:153:MET:HG2	2.07	0.55
1:A:749:ARG:HD2	1:A:750:LEU:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:ASP:OD2	1:A:1109:PHE:CE2	2.60	0.55
2:B:389:ILE:HD12	2:B:427:TRP:O	2.05	0.55
8:H:229:LEU:HD21	8:H:235:VAL:HG11	1.87	0.55
25:D:48:C:C4'	25:D:49:A:OP1	2.52	0.55
27:F:78:A:N1	27:F:81:A:C8	2.74	0.55
27:F:95:C:H4'	27:F:96:U:OP1	2.05	0.55
1:A:503:LYS:HA	1:A:506:PHE:CE1	2.38	0.55
1:A:849:LEU:HG	1:A:973:GLU:HB3	1.88	0.55
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.05	0.55
1:A:1831:GLN:HG2	1:A:1832:GLU:N	2.20	0.55
4:G:282:ILE:O	4:G:286:GLU:CG	2.51	0.55
4:G:298:THR:O	4:G:302:PHE:HD2	1.88	0.55
8:H:332:TYR:CE2	8:H:376:PHE:HB3	2.41	0.55
8:H:605:ILE:CG1	8:H:652:MET:SD	2.92	0.55
25:D:44:A:H2'	25:D:45:A:H8	1.71	0.55
1:A:382:GLU:OE1	1:A:382:GLU:N	2.34	0.55
1:A:1065:LEU:HD23	1:A:1065:LEU:O	2.06	0.55
2:B:360:ASN:CB	2:B:362:TYR:HE1	2.20	0.55
4:G:695:THR:O	4:G:699:PRO:HD3	2.06	0.55
8:H:380:PRO:HA	8:H:383:LYS:HG3	1.88	0.55
8:H:430:ARG:O	8:H:431:GLN:O	2.23	0.55
8:H:586:MET:O	8:H:589:LEU:CD2	2.52	0.55
8:H:951:ILE:CD1	8:H:955:LYS:HB2	2.37	0.55
1:A:536:PRO:HG2	27:F:76:U:O4	2.06	0.55
1:A:1356:LEU:O	1:A:1356:LEU:HD22	2.06	0.55
1:A:1882:LEU:C	1:A:1882:LEU:HD22	2.26	0.55
1:A:2065:ARG:CD	1:A:2066:LYS:HE2	2.36	0.55
2:B:389:ILE:CD1	2:B:427:TRP:O	2.54	0.55
8:H:468:LEU:HB3	8:H:579:SER:HB3	1.89	0.55
8:H:506:GLN:O	8:H:509:SER:CB	2.49	0.55
1:A:160:ALA:CB	1:A:194:HIS:CE1	2.89	0.55
1:A:456:GLU:CD	1:A:456:GLU:H	1.97	0.55
1:A:1163:ARG:NH1	1:A:1165:LEU:O	2.39	0.55
1:A:1341:SER:HA	1:A:1525:PHE:HE1	1.72	0.55
2:B:166:GLU:O	2:B:465:ASN:N	2.39	0.55
3:I:135:LEU:HD23	3:I:135:LEU:C	2.25	0.55
5:K:350:PRO:HB3	25:D:84:C:C6	2.41	0.55
5:K:452:LEU:HB3	5:K:461:GLU:HG2	1.88	0.55
8:H:387:TYR:HB3	8:H:396:LEU:HD21	1.88	0.55
8:H:564:ILE:HG21	8:H:567:ILE:CG1	2.36	0.55
1:A:297:SER:CB	27:F:32:G:P	2.95	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:VAL:CB	1:A:327:TYR:CD2	2.90	0.55
1:A:672:LYS:O	1:A:674:MET:N	2.39	0.55
1:A:770:MET:HE2	1:A:775:ARG:O	2.06	0.55
1:A:1074:VAL:HG12	1:A:1075:ASP:N	2.21	0.55
2:B:141:GLU:OE1	2:B:141:GLU:HA	2.07	0.55
4:G:161:LYS:HA	4:G:161:LYS:HE3	1.89	0.55
5:K:332:GLU:O	5:K:332:GLU:HG2	2.05	0.55
8:H:272:ARG:HG3	8:H:276:ASP:HB2	1.89	0.55
25:D:51:A:O2'	25:D:52:G:O5'	2.22	0.55
1:A:1038:ILE:CD1	1:A:1039:TRP:CD2	2.90	0.55
2:B:446:SER:HB2	2:B:451:PHE:HB2	1.89	0.55
6:L:140:LYS:CB	6:L:141:ARG:HD2	2.32	0.55
8:H:354:TYR:HA	8:H:359:PHE:CA	2.35	0.55
8:H:474:LYS:HZ2	8:H:630:PRO:HD3	1.71	0.55
1:A:150:ALA:O	1:A:153:MET:HG2	2.07	0.55
1:A:1389:TYR:HE2	1:A:1401:SER:HB3	1.72	0.55
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.07	0.55
1:A:1627:LEU:HB2	1:A:1630:THR:OG1	2.07	0.55
2:B:275:PRO:HG3	2:B:319:GLY:CA	2.37	0.55
2:B:363:GLN:HG2	2:B:377:ASP:HB3	1.89	0.55
2:B:452:LEU:HB3	2:B:464:TRP:HB2	1.89	0.55
3:I:282:GLU:OE1	3:I:286:PHE:CZ	2.60	0.55
4:G:230:LEU:CD1	4:G:247:SER:HA	2.25	0.55
4:G:691:TYR:CD2	4:G:711:ILE:CD1	2.90	0.55
5:K:289:ASP:HB3	5:K:292:ALA:HB3	1.89	0.55
8:H:461:LYS:HD2	8:H:462:SER:N	2.22	0.55
8:H:829:VAL:O	8:H:829:VAL:HG12	2.07	0.55
1:A:373:VAL:O	8:H:969:LYS:HG2	2.07	0.54
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.42	0.54
1:A:1458:TRP:HZ3	1:A:1461:TYR:CE2	2.24	0.54
2:B:441:ILE:HD11	2:B:457:TRP:CD1	2.41	0.54
3:I:338:SER:O	3:I:342:ARG:HG3	2.07	0.54
4:G:104:PHE:O	4:G:105:ALA:C	2.45	0.54
8:H:132:ARG:C	8:H:133:ILE:HG23	2.27	0.54
8:H:337:PRO:O	8:H:341:ILE:HG23	2.07	0.54
1:A:1910:LYS:HG3	1:A:1911:TRP:N	2.22	0.54
3:I:146:ASN:HD21	3:I:148:ASN:ND2	2.04	0.54
3:I:418:GLN:HE22	3:I:425:SER:HB2	1.71	0.54
6:L:140:LYS:HB3	6:L:141:ARG:HH11	1.70	0.54
8:H:303:VAL:HG23	8:H:303:VAL:O	2.07	0.54
8:H:968:MET:CE	8:H:968:MET:CA	2.85	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ILE:HD12	1:A:410:ILE:N	2.22	0.54
2:B:206:THR:CG2	2:B:208:GLN:HE22	2.21	0.54
3:I:267:HIS:HE1	3:I:273:HIS:CE1	2.25	0.54
3:I:433:ASN:ND2	3:I:433:ASN:H	2.04	0.54
4:G:528:LYS:O	4:G:532:LEU:N	2.39	0.54
4:G:668:HIS:NE2	4:G:669:LYS:HG3	2.21	0.54
8:H:379:ILE:CG2	8:H:383:LYS:CE	2.86	0.54
8:H:582:SER:HB3	8:H:585:ASP:OD2	2.03	0.54
8:H:767:SER:OG	8:H:796:ILE:HD11	2.07	0.54
1:A:256:GLU:HG3	1:A:257:ASN:N	2.22	0.54
1:A:770:MET:SD	4:G:119:TRP:CZ3	3.01	0.54
1:A:1892:LYS:HD2	1:A:1916:GLU:CD	2.28	0.54
2:B:135:ARG:NH2	5:K:167:GLU:OE2	2.40	0.54
4:G:688:ARG:O	4:G:692:LEU:HG	2.07	0.54
4:G:696:ARG:C	4:G:699:PRO:CD	2.74	0.54
8:H:564:ILE:HG21	8:H:567:ILE:HG12	1.89	0.54
25:D:87:U:P	25:D:87:U:H3'	2.47	0.54
27:F:40:C:H3'	27:F:40:C:P	2.48	0.54
1:A:293:VAL:HG22	1:A:294:ASN:N	2.22	0.54
1:A:296:THR:HG22	27:F:33:U:OP2	2.06	0.54
1:A:363:ASP:N	1:A:363:ASP:OD1	2.39	0.54
1:A:413:ASN:ND2	1:A:413:ASN:H	2.06	0.54
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.72	0.54
4:G:846:PHE:HB2	4:G:896:MET:SD	2.48	0.54
1:A:221:TRP:CZ2	1:A:691:PHE:HB3	2.42	0.54
1:A:264:ILE:O	1:A:265:ASN:HB2	2.08	0.54
1:A:860:GLU:HA	1:A:860:GLU:OE1	2.07	0.54
3:I:191:ILE:H	3:I:191:ILE:CD1	2.14	0.54
5:K:141:ASN:OD1	5:K:144:LEU:HD23	2.08	0.54
8:H:470:ALA:CB	8:H:486:VAL:HG21	2.19	0.54
8:H:810:GLU:OE2	8:H:974:LYS:CB	2.56	0.54
1:A:158:LYS:HG2	1:A:159:LYS:N	2.23	0.54
1:A:1995:TRP:CZ3	1:A:2007:ARG:HD2	2.43	0.54
2:B:161:ARG:O	2:B:165:LEU:HD21	2.07	0.54
4:G:863:PHE:CE2	4:G:892:LEU:HD11	2.43	0.54
5:K:249:ARG:HG2	5:K:249:ARG:NH1	2.22	0.54
5:K:276:ASN:OD1	25:D:61:C:OP1	2.26	0.54
8:H:589:LEU:HD11	8:H:591:PHE:CE1	2.43	0.54
8:H:944:VAL:CG2	8:H:945:LEU:HG	2.37	0.54
27:F:74:U:C5'	27:F:74:U:H6	2.20	0.54
6:L:72:GLU:OE2	6:L:72:GLU:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:140:LYS:HG2	6:L:141:ARG:CZ	2.37	0.54
25:D:78:G:C2	26:E:4:C:C2	2.96	0.54
1:A:322:VAL:HB	1:A:327:TYR:CD2	2.42	0.54
2:B:64:VAL:HG12	2:B:65:GLU:N	2.20	0.54
2:B:415:TYR:CD2	2:B:439:LYS:HD3	2.42	0.54
3:I:392:GLU:HB2	3:I:412:MET:SD	2.48	0.54
4:G:842:TRP:HA	4:G:845:LEU:HD12	1.90	0.54
8:H:769:TYR:CE1	8:H:799:PHE:CD2	2.96	0.54
8:H:862:TYR:HE1	8:H:908:VAL:CG2	2.20	0.54
27:F:31:G:C2	27:F:32:G:C1'	2.89	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CD	2.38	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CG	2.25	0.54
8:H:502:LEU:O	8:H:575:ALA:HB1	2.08	0.54
27:F:78:A:C6	27:F:81:A:C8	2.95	0.54
1:A:266:LEU:CD2	1:A:267:PRO:HD2	2.33	0.53
1:A:614:ARG:NH1	24:C:3:A:OP1	2.41	0.53
1:A:1038:ILE:HD11	1:A:1039:TRP:CZ3	2.44	0.53
2:B:267:ARG:HG3	2:B:285:HIS:CD2	2.42	0.53
2:B:279:PHE:N	2:B:279:PHE:CD1	2.76	0.53
3:I:257:CYS:HB2	26:E:42:C:H41	1.72	0.53
3:I:421:VAL:O	3:I:421:VAL:HG12	2.06	0.53
5:K:455:LEU:C	5:K:457:GLN:OE1	2.47	0.53
8:H:177:TYR:C	8:H:178:LEU:HD23	2.29	0.53
8:H:578:TYR:CD2	8:H:589:LEU:HD13	2.43	0.53
24:C:7:A:HO2'	24:C:8:U:P	2.26	0.53
27:F:72:C:H2'	27:F:73:U:H6	1.73	0.53
1:A:166:LYS:HE3	1:A:723:GLU:HB3	1.90	0.53
1:A:176:LEU:HD21	1:A:708:TRP:CD1	2.43	0.53
1:A:1379:MET:HG3	1:A:1380:PRO:CD	2.39	0.53
1:A:1586:GLN:HG2	1:A:1595:ARG:NH1	2.23	0.53
2:B:201:VAL:C	2:B:202:LEU:HD12	2.28	0.53
4:G:891:ILE:O	4:G:892:LEU:C	2.45	0.53
5:K:167:GLU:HB3	5:K:169:TRP:CE3	2.43	0.53
6:L:33:ARG:HE	6:L:64:ILE:HB	1.73	0.53
8:H:307:ILE:CD1	8:H:345:THR:O	2.55	0.53
8:H:331:TYR:OH	8:H:428:ILE:CG2	2.57	0.53
8:H:494:LYS:HE2	8:H:555:GLU:OE1	2.08	0.53
24:C:11:A:C2'	24:C:12:U:H5'	2.39	0.53
1:A:167:TYR:O	1:A:201:PHE:HE1	1.91	0.53
1:A:284:ARG:NH1	27:F:33:U:O4	2.40	0.53
7:M:60:PRO:HB2	7:M:62:GLU:OE1	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:862:TYR:CD2	8:H:930:LEU:HB3	2.42	0.53
27:F:31:G:C2	27:F:32:G:N9	2.76	0.53
1:A:168:LEU:CB	1:A:199:ILE:HD11	2.38	0.53
1:A:1880:PHE:HE1	1:A:1882:LEU:HD12	1.71	0.53
5:K:167:GLU:HB3	5:K:169:TRP:HE3	1.73	0.53
8:H:114:PRO:O	8:H:115:LYS:O	2.27	0.53
8:H:447:GLU:HA	8:H:447:GLU:OE2	2.08	0.53
8:H:468:LEU:CD2	8:H:577:LEU:HD21	2.23	0.53
8:H:873:LEU:HB3	8:H:874:PRO:HD3	1.90	0.53
1:A:755:ASP:OD2	1:A:819:LYS:HE3	2.08	0.53
3:I:123:ARG:O	3:I:183:PHE:CB	2.56	0.53
1:A:469:ILE:O	1:A:470:LEU:HD22	2.09	0.53
1:A:674:MET:CE	1:A:678:ARG:HD3	2.38	0.53
1:A:2074:LEU:N	1:A:2074:LEU:HD23	2.22	0.53
2:B:199:LEU:HD23	2:B:199:LEU:H	1.73	0.53
2:B:322:VAL:HG13	2:B:334:TRP:HB2	1.91	0.53
2:B:360:ASN:HB3	2:B:362:TYR:CD1	2.44	0.53
4:G:292:CYS:O	4:G:296:VAL:HG23	2.09	0.53
4:G:708:LEU:HD22	4:G:725:ILE:HG21	1.90	0.53
8:H:113:ILE:CG2	8:H:114:PRO:HD2	2.34	0.53
8:H:599:THR:HG22	8:H:933:TRP:CZ3	2.43	0.53
8:H:677:PHE:HE1	8:H:966:PHE:HE2	1.45	0.53
8:H:697:ARG:NE	8:H:697:ARG:CA	2.71	0.53
26:E:19:U:C6	26:E:19:U:H3'	2.44	0.53
1:A:239:PHE:O	1:A:240:PRO:C	2.47	0.53
1:A:468:LEU:N	1:A:468:LEU:HD12	2.24	0.53
1:A:837:GLY:C	1:A:1317:ARG:NH1	2.62	0.53
1:A:1500:HIS:HB2	4:G:160:ASN:HD21	1.74	0.53
2:B:75:ARG:HG2	2:B:75:ARG:HH21	1.74	0.53
3:I:357:PRO:O	3:I:358:ILE:HG13	2.08	0.53
4:G:158:ASP:OD1	4:G:158:ASP:N	2.40	0.53
4:G:688:ARG:NH1	4:G:721:ARG:NE	2.54	0.53
4:G:691:TYR:CD2	4:G:711:ILE:HD12	2.44	0.53
25:D:49:A:C2'	25:D:50:G:C5'	2.84	0.53
1:A:954:ILE:HG23	1:A:991:THR:HG22	1.89	0.53
2:B:176:LYS:HB2	2:B:194:SER:OG	2.09	0.53
4:G:672:LEU:HD21	4:G:704:LEU:HG	1.83	0.53
4:G:846:PHE:HB3	4:G:896:MET:SD	2.49	0.53
8:H:504:THR:OG1	8:H:594:PRO:HG3	2.09	0.53
27:F:64:C:H2'	27:F:65:U:H6	1.74	0.53
27:F:73:U:C3'	27:F:74:U:C5'	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:PHE:CE1	1:A:249:LEU:HD21	2.44	0.53
1:A:774:ILE:HD12	1:A:774:ILE:N	2.24	0.53
1:A:944:TYR:O	4:G:166:ARG:NH1	2.41	0.53
2:B:162:MET:HE2	2:B:162:MET:N	2.24	0.53
4:G:104:PHE:O	4:G:106:ASP:N	2.41	0.53
8:H:227:VAL:HG11	8:H:474:LYS:CB	2.39	0.53
1:A:166:LYS:HD3	1:A:167:TYR:CZ	2.43	0.53
1:A:1125:LEU:HD21	1:A:1234:VAL:HG23	1.90	0.53
1:A:2065:ARG:HD2	1:A:2066:LYS:HE2	1.91	0.53
3:I:358:ILE:HG22	3:I:360:GLU:N	2.24	0.53
4:G:170:LEU:HD13	4:G:171:GLN:N	2.24	0.53
8:H:176:ARG:O	8:H:548:ARG:NH2	2.41	0.53
8:H:326:GLU:OE1	8:H:330:TYR:CD2	2.61	0.53
8:H:488:ILE:CD1	8:H:557:HIS:O	2.51	0.53
1:A:721:LEU:HD11	27:F:85:U:O2'	2.09	0.52
1:A:1511:ARG:NH2	1:A:1511:ARG:HG3	2.24	0.52
3:I:82:ARG:O	3:I:86:GLN:N	2.35	0.52
3:I:257:CYS:SG	26:E:44:G:O6	2.61	0.52
4:G:630:SER:HA	4:G:670:PHE:HZ	1.72	0.52
5:K:349:ASN:HB2	5:K:406:PHE:CD1	2.44	0.52
6:L:33:ARG:HD3	6:L:65:ASP:N	2.24	0.52
8:H:265:PHE:HE2	8:H:295:ILE:HB	1.73	0.52
1:A:881:THR:O	1:A:885:VAL:HG23	2.08	0.52
1:A:928:ARG:HH21	4:G:145:THR:CG2	2.17	0.52
1:A:1262:MET:O	1:A:1263:CYS:HB2	2.09	0.52
2:B:316:GLN:O	2:B:316:GLN:NE2	2.42	0.52
4:G:126:THR:HB	4:G:128:PHE:CZ	2.44	0.52
4:G:666:ILE:CG2	4:G:667:CYS:H	2.18	0.52
25:D:64:U:H5''	25:D:64:U:H6	1.74	0.52
1:A:778:LYS:HA	1:A:778:LYS:HE2	1.90	0.52
1:A:921:ASP:HB3	3:I:403:SER:HB2	1.91	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CE1	2.45	0.52
1:A:1468:ALA:O	1:A:1473:ARG:N	2.37	0.52
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.09	0.52
3:I:327:THR:O	3:I:328:VAL:HG23	2.09	0.52
3:I:347:ALA:HA	4:G:130:ARG:HH11	1.74	0.52
5:K:143:GLU:HA	5:K:145:HIS:CE1	2.45	0.52
8:H:106:PHE:HE2	8:H:554:HIS:NE2	2.06	0.52
8:H:674:LEU:CD1	8:H:973:ARG:NH1	2.69	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CD1	2.44	0.52
1:A:1613:THR:O	1:A:1616:ARG:CD	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:83:LYS:C	4:G:85:ARG:H	2.12	0.52
4:G:252:GLU:CG	4:G:256:LYS:HG3	2.26	0.52
4:G:283:ARG:NH1	4:G:284:LEU:HD21	2.24	0.52
4:G:672:LEU:HD21	4:G:704:LEU:HD21	1.28	0.52
7:M:95:ARG:HG3	7:M:96:PRO:CD	2.40	0.52
25:D:44:A:H2'	25:D:45:A:C8	2.44	0.52
26:E:19:U:O2'	26:E:20:A:P	2.67	0.52
26:E:19:U:C6	26:E:19:U:C3'	2.93	0.52
1:A:1065:LEU:CD2	1:A:1069:LEU:HD13	2.39	0.52
1:A:1902:GLN:O	1:A:1905:LEU:CD2	2.56	0.52
3:I:336:GLU:O	3:I:340:LYS:HB2	2.09	0.52
3:I:398:GLN:NE2	3:I:419:GLN:HG3	2.25	0.52
4:G:234:ARG:O	4:G:237:ASP:O	2.28	0.52
4:G:288:ASP:OD1	4:G:291:TYR:CB	2.58	0.52
4:G:671:PHE:CE1	4:G:690:THR:O	2.62	0.52
5:K:314:ARG:NH2	5:K:314:ARG:HG2	2.23	0.52
6:L:140:LYS:HB3	6:L:141:ARG:NH1	2.25	0.52
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.91	0.52
8:H:942:GLY:C	8:H:963:SER:OG	2.47	0.52
24:C:-4:A:Cl'	24:C:-3:A:OP1	2.49	0.52
1:A:691:PHE:C	1:A:691:PHE:CD1	2.82	0.52
1:A:770:MET:HB2	1:A:775:ARG:HG3	1.92	0.52
1:A:1458:TRP:HZ3	1:A:1461:TYR:CD2	2.25	0.52
3:I:99:ASN:O	3:I:103:PRO:HD2	2.09	0.52
5:K:354:PHE:CE1	5:K:358:MET:HG2	2.45	0.52
6:L:140:LYS:CB	6:L:141:ARG:NH1	2.73	0.52
8:H:369:LYS:HE2	8:H:369:LYS:C	2.30	0.52
8:H:682:SER:HA	8:H:714:PRO:HG3	1.92	0.52
1:A:261:LEU:HD12	1:A:262:ASP:N	2.24	0.52
1:A:377:VAL:CG1	1:A:378:PRO:HD2	2.37	0.52
1:A:514:TYR:HD1	1:A:514:TYR:H	1.58	0.52
1:A:814:ARG:NH1	4:G:103:GLN:O	2.43	0.52
1:A:1342:LEU:C	1:A:1342:LEU:HD23	2.30	0.52
3:I:400:VAL:HG12	4:G:215:LEU:HA	1.92	0.52
4:G:712:ASP:OD2	4:G:721:ARG:HB3	2.09	0.52
4:G:863:PHE:HE2	4:G:892:LEU:HD11	1.73	0.52
8:H:126:MET:CE	8:H:132:ARG:NH1	2.73	0.52
27:F:95:C:O3'	27:F:96:U:C4'	2.58	0.52
8:H:332:TYR:CZ	8:H:376:PHE:HD2	2.27	0.52
8:H:884:ARG:HD3	8:H:884:ARG:C	2.30	0.52
1:A:362:GLU:CB	1:A:1209:LYS:CE	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.91	0.52
1:A:1468:ALA:HB1	1:A:1473:ARG:C	2.29	0.52
1:A:1899:TRP:CH2	1:A:1909:ALA:HB2	2.45	0.52
2:B:68:ASP:OD1	5:K:322:ARG:NH1	2.41	0.52
2:B:286:ASP:O	2:B:288:THR:HG23	2.10	0.52
2:B:438:ASP:HB2	2:B:458:ASP:HB3	1.91	0.52
3:I:101:ILE:O	3:I:105:ILE:HG13	2.10	0.52
3:I:217:TYR:CE1	3:I:221:LYS:CE	2.92	0.52
4:G:169:LEU:O	4:G:173:GLN:HG3	2.10	0.52
5:K:314:ARG:HG2	5:K:314:ARG:HH21	1.75	0.52
8:H:265:PHE:N	8:H:265:PHE:CD1	2.77	0.52
8:H:270:LEU:HD11	8:H:313:PHE:HB3	1.92	0.52
27:F:103:A:HO2'	27:F:104:G:P	2.29	0.52
1:A:644:VAL:O	1:A:645:ASP:HB2	2.10	0.52
1:A:703:PHE:HD1	1:A:704:TRP:N	2.08	0.52
1:A:1285:VAL:O	1:A:1448:GLU:OE2	2.29	0.52
2:B:316:GLN:HB2	2:B:357:TRP:CG	2.42	0.52
3:I:127:LEU:HD11	3:I:131:ILE:HD12	1.90	0.52
4:G:702:PRO:CA	4:G:739:PHE:CZ	2.93	0.52
8:H:168:VAL:HA	8:H:173:LYS:HG3	1.92	0.52
8:H:483:TRP:CZ3	8:H:565:LYS:HG2	2.45	0.52
1:A:321:GLU:HA	1:A:508:GLN:OE1	2.11	0.51
1:A:471:PRO:HG2	1:A:472:ASN:OD1	2.10	0.51
1:A:1416:LYS:HG2	1:A:1417:GLN:N	2.25	0.51
1:A:1992:TYR:CD2	1:A:2004:ALA:HB1	2.44	0.51
2:B:117:LEU:C	2:B:117:LEU:HD13	2.31	0.51
3:I:184:LYS:CD	3:I:186:LYS:CB	2.87	0.51
4:G:360:LYS:O	4:G:364:PHE:N	2.38	0.51
27:F:77:A:H4'	27:F:78:A:C5'	2.32	0.51
27:F:100:A:H5'	27:F:101:C:OP2	2.10	0.51
1:A:376:ARG:O	1:A:377:VAL:CB	2.56	0.51
1:A:769:MET:HE2	4:G:112:ALA:HA	1.91	0.51
2:B:360:ASN:CB	2:B:362:TYR:CE1	2.93	0.51
3:I:347:ALA:HB1	3:I:348:PRO:HD2	1.92	0.51
4:G:143:ARG:NH2	4:G:143:ARG:CB	2.73	0.51
8:H:227:VAL:HG13	8:H:473:LEU:HB3	1.90	0.51
8:H:497:ASP:O	8:H:538:GLU:HA	2.09	0.51
1:A:217:TRP:CD1	1:A:703:PHE:CZ	2.98	0.51
1:A:228:LYS:CD	1:A:691:PHE:HE1	2.23	0.51
1:A:286:LEU:HD12	1:A:287:GLU:H	1.72	0.51
1:A:1342:LEU:HD23	1:A:1350:ILE:HD11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2013:ARG:HG3	1:A:2083:ILE:O	2.11	0.51
2:B:275:PRO:CG	2:B:319:GLY:CA	2.88	0.51
8:H:369:LYS:CE	8:H:369:LYS:N	2.73	0.51
8:H:478:TYR:HB2	8:H:483:TRP:HD1	1.76	0.51
9:N:1928:LEU:O	9:N:1931:GLN:N	2.40	0.51
1:A:249:LEU:HD23	1:A:249:LEU:N	2.25	0.51
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.45	0.51
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.25	0.51
1:A:1464:LYS:NZ	1:A:1479:GLU:HB3	2.25	0.51
4:G:9:GLN:C	4:G:11:PRO:HD3	2.30	0.51
4:G:19:ILE:HD12	4:G:20:GLY:CA	2.40	0.51
4:G:327:VAL:O	4:G:331:LEU:N	2.39	0.51
8:H:135:ASN:HD22	8:H:487:ARG:HH21	1.57	0.51
8:H:354:TYR:CE1	8:H:376:PHE:HZ	2.28	0.51
8:H:478:TYR:HB2	8:H:483:TRP:CD1	2.45	0.51
8:H:860:PRO:HB3	8:H:937:TRP:HZ3	1.74	0.51
1:A:250:SER:HB2	1:A:252:GLU:OE1	2.11	0.51
1:A:1313:ASP:OD2	1:A:1359:ILE:CD1	2.59	0.51
1:A:1339:LEU:CD2	1:A:1440:ILE:HD12	2.40	0.51
5:K:316:HIS:C	5:K:316:HIS:CD2	2.83	0.51
5:K:350:PRO:C	5:K:353:ARG:HG3	2.30	0.51
6:L:135:TYR:N	6:L:135:TYR:CD1	2.79	0.51
8:H:113:ILE:CG2	8:H:114:PRO:CD	2.89	0.51
8:H:232:SER:OG	8:H:234:LEU:O	2.28	0.51
8:H:586:MET:C	8:H:589:LEU:HD23	2.30	0.51
8:H:951:ILE:CB	8:H:952:PRO:CD	2.88	0.51
8:H:959:ILE:HD13	8:H:960:ASN:H	1.72	0.51
27:F:62:G:H2'	27:F:63:C:H6	1.75	0.51
1:A:166:LYS:O	1:A:169:PRO:CD	2.53	0.51
1:A:366:GLU:HG3	1:A:367:PHE:N	2.26	0.51
2:B:171:GLN:O	2:B:172:LEU:CD1	2.59	0.51
2:B:436:HIS:CD2	2:B:440:ILE:HD11	2.45	0.51
3:I:401:LEU:HD12	4:G:214:SER:HA	1.93	0.51
4:G:101:LYS:O	4:G:105:ALA:N	2.36	0.51
6:L:94:ASP:OD1	6:L:132:VAL:HA	2.10	0.51
8:H:307:ILE:HD11	8:H:345:THR:C	2.30	0.51
8:H:354:TYR:HA	8:H:359:PHE:HB3	1.90	0.51
8:H:461:LYS:NZ	8:H:464:PRO:CB	2.73	0.51
1:A:291:LYS:NZ	1:A:291:LYS:H	2.09	0.51
1:A:497:GLN:HB3	1:A:712:LEU:HD23	1.92	0.51
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1065:LEU:CD2	1:A:1069:LEU:HD22	2.40	0.51
1:A:2067:TYR:N	1:A:2067:TYR:CD1	2.78	0.51
3:I:376:LYS:O	3:I:378:LYS:N	2.43	0.51
8:H:178:LEU:HD12	8:H:214:ASP:HB2	1.92	0.51
8:H:379:ILE:CG2	8:H:383:LYS:HE2	2.40	0.51
8:H:953:LYS:O	8:H:954:LEU:HB2	2.10	0.51
1:A:273:ASP:HB3	1:A:276:VAL:HG21	1.92	0.51
1:A:298:TYR:O	1:A:493:MET:SD	2.69	0.51
1:A:522:TYR:CE2	1:A:686:ILE:HD12	2.46	0.51
2:B:415:TYR:OH	7:M:126:ILE:C	2.49	0.51
27:F:74:U:H2'	27:F:75:A:H3'	1.92	0.51
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.76	0.51
2:B:274:HIS:HD2	2:B:276:SER:HB3	1.72	0.51
3:I:112:MET:HB2	3:I:204:LEU:HD21	1.91	0.51
3:I:265:ASN:O	3:I:266:LYS:CB	2.57	0.51
8:H:697:ARG:NH1	8:H:852:THR:OG1	2.44	0.51
8:H:883:ARG:CZ	8:H:910:GLU:O	2.59	0.51
8:H:945:LEU:O	8:H:945:LEU:HD13	2.11	0.51
9:N:1502:LEU:O	9:N:1503:GLU:C	2.47	0.51
24:C:11:A:C2	24:C:12:U:C4	2.99	0.51
27:F:64:C:C2	27:F:65:U:C5	2.99	0.51
1:A:621:LEU:HD12	1:A:666:ILE:HD11	1.91	0.51
1:A:774:ILE:CG2	1:A:777:LYS:HE3	2.38	0.51
1:A:1511:ARG:HH21	1:A:1511:ARG:CG	2.22	0.51
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.46	0.51
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.11	0.51
2:B:121:ARG:HD2	2:B:337:ARG:O	2.11	0.51
2:B:274:HIS:CD2	2:B:275:PRO:CD	2.93	0.51
7:M:46:ARG:NH1	26:E:43:C:OP1	2.44	0.51
8:H:143:HIS:HA	28:H:1500:GTP:PB	2.51	0.51
8:H:160:ARG:HB3	8:H:161:ILE:CA	2.40	0.51
8:H:376:PHE:CD1	8:H:376:PHE:N	2.79	0.51
27:F:72:C:C2	27:F:73:U:C5	2.98	0.51
1:A:767:LEU:CD2	1:A:779:ALA:HB2	2.40	0.50
1:A:806:ALA:N	1:A:807:PRO:HD2	2.26	0.50
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.44	0.50
2:B:127:TYR:HE2	2:B:276:SER:CB	2.19	0.50
2:B:167:LEU:O	4:G:728:ARG:NH2	2.44	0.50
2:B:243:ILE:HD12	2:B:292:TRP:CZ3	2.46	0.50
3:I:301:GLN:OE1	3:I:344:LEU:CD1	2.60	0.50
3:I:447:GLU:OE2	3:I:448:ALA:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:143:ARG:CG	4:G:143:ARG:NH2	2.73	0.50
8:H:116:THR:CG2	8:H:157:SER:OG	2.59	0.50
8:H:247:PHE:CB	8:H:931:TYR:OH	2.59	0.50
8:H:353:TYR:CE2	8:H:371:PRO:HG3	2.47	0.50
1:A:418:ASP:N	1:A:418:ASP:OD1	2.44	0.50
1:A:1477:PHE:O	1:A:1481:GLU:N	2.44	0.50
1:A:1498:ASP:OD1	1:A:1502:LEU:HD12	2.07	0.50
2:B:354:THR:HG21	2:B:399:VAL:H	1.75	0.50
3:I:210:LEU:O	3:I:214:ILE:HG13	2.12	0.50
3:I:447:GLU:HA	3:I:450:GLN:HG2	1.93	0.50
4:G:887:THR:N	4:G:888:PRO:CD	2.74	0.50
8:H:135:ASN:ND2	8:H:487:ARG:NH2	2.60	0.50
8:H:285:TYR:CD1	8:H:285:TYR:C	2.84	0.50
15:Z:48:TYR:O	15:Z:50:ASN:N	2.45	0.50
27:F:63:C:C2	27:F:64:C:C5	3.00	0.50
27:F:117:G:H2'	27:F:118:U:O4'	2.12	0.50
1:A:149:MET:CG	1:A:154:TYR:CE2	2.89	0.50
1:A:251:TYR:CA	1:A:255:ILE:HD12	2.34	0.50
1:A:774:ILE:O	1:A:774:ILE:HG22	2.11	0.50
1:A:1627:LEU:HD22	1:A:1632:ILE:HB	1.94	0.50
2:B:360:ASN:ND2	2:B:406:GLY:O	2.43	0.50
2:B:419:ILE:HD11	2:B:443:LEU:HD13	1.91	0.50
4:G:215:LEU:HD12	4:G:216:SER:O	2.11	0.50
8:H:305:SER:C	8:H:307:ILE:H	2.15	0.50
25:D:62:A:H2'	25:D:63:G:C5'	2.38	0.50
1:A:299:LYS:O	1:A:300:LYS:HB2	2.12	0.50
1:A:505:TRP:O	1:A:522:TYR:HE1	1.93	0.50
1:A:754:TYR:CE2	1:A:758:LEU:CD2	2.94	0.50
1:A:764:ASP:O	1:A:768:GLU:N	2.44	0.50
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.46	0.50
1:A:1336:ASN:O	1:A:1340:ILE:HG13	2.10	0.50
1:A:1373:LEU:HD21	1:A:1379:MET:SD	2.51	0.50
1:A:1461:TYR:CE2	1:A:1494:LEU:CD1	2.95	0.50
1:A:1709:TRP:HD1	1:A:1730:ASN:O	1.94	0.50
1:A:1735:ASP:O	1:A:1775:ILE:N	2.37	0.50
1:A:1880:PHE:CE2	1:A:1889:LEU:CD2	2.74	0.50
1:A:1882:LEU:HD22	1:A:1883:ASN:N	2.27	0.50
1:A:1892:LYS:HG3	1:A:1916:GLU:HG3	1.93	0.50
2:B:127:TYR:CZ	2:B:276:SER:HA	2.47	0.50
2:B:171:GLN:O	2:B:172:LEU:HD13	2.12	0.50
2:B:376:TRP:N	2:B:376:TRP:CD1	2.78	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:410:LEU:O	3:I:410:LEU:HD12	2.12	0.50
4:G:6:PHE:HE1	4:G:7:LEU:HD12	1.75	0.50
8:H:302:ASN:OD1	8:H:303:VAL:N	2.44	0.50
8:H:580:VAL:O	8:H:580:VAL:HG13	2.11	0.50
8:H:793:GLU:C	8:H:796:ILE:HG22	2.31	0.50
8:H:794:GLN:OE1	8:H:835:LYS:CG	2.57	0.50
1:A:1650:ARG:O	1:A:1651:ALA:HB3	2.12	0.50
6:L:32:GLY:O	6:L:63:ASP:HA	2.10	0.50
8:H:133:ILE:C	8:H:134:ILE:CG2	2.72	0.50
8:H:354:TYR:CA	8:H:359:PHE:CB	2.86	0.50
8:H:769:TYR:CD1	8:H:799:PHE:HD2	2.29	0.50
1:A:165:LEU:HD21	1:A:726:ILE:HG21	1.93	0.50
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.11	0.50
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.46	0.50
1:A:1778:ASP:HB2	1:A:1783:MET:HB2	1.94	0.50
4:G:252:GLU:O	4:G:256:LYS:HB2	2.11	0.50
4:G:274:SER:HB2	4:G:277:ILE:CD1	2.15	0.50
4:G:702:PRO:CB	4:G:739:PHE:CE2	2.95	0.50
5:K:144:LEU:HD22	5:K:144:LEU:N	2.27	0.50
6:L:140:LYS:HG2	6:L:141:ARG:HH12	1.69	0.50
8:H:160:ARG:NH1	8:H:160:ARG:HG3	2.26	0.50
8:H:349:TRP:CZ3	8:H:373:PHE:CD2	2.99	0.50
15:W:48:TYR:O	15:W:50:ASN:N	2.45	0.50
25:D:81:G:C6	25:D:82:A:N7	2.80	0.50
27:F:39:U:O2'	27:F:40:C:H5'	2.11	0.50
1:A:286:LEU:HD21	1:A:289:ASP:HB3	1.92	0.50
1:A:289:ASP:CG	1:A:292:LYS:CG	2.80	0.50
1:A:367:PHE:O	1:A:367:PHE:HD1	1.95	0.50
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.44	0.50
2:B:390:LEU:HD12	5:K:428:TRP:CD1	2.46	0.50
4:G:143:ARG:CZ	4:G:143:ARG:CB	2.86	0.50
4:G:241:PRO:HG3	4:G:274:SER:OG	2.12	0.50
8:H:133:ILE:HA	8:H:209:MET:O	2.11	0.50
8:H:379:ILE:HG22	8:H:383:LYS:CE	2.42	0.50
8:H:862:TYR:OH	8:H:908:VAL:CG2	2.59	0.50
1:A:547:LEU:O	1:A:551:LEU:HB2	2.12	0.50
2:B:290:ARG:NE	2:B:299:GLU:OE2	2.42	0.50
2:B:446:SER:OG	2:B:451:PHE:CB	2.54	0.50
2:B:462:LYS:HE2	4:G:727:ASP:OD2	2.12	0.50
4:G:161:LYS:O	4:G:165:GLU:HB2	2.12	0.50
26:E:139:A:O2'	26:E:140:G:P	2.69	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:97:U:O2	27:F:97:U:H2'	2.11	0.50
1:A:221:TRP:CH2	1:A:691:PHE:HB3	2.47	0.50
1:A:395:PRO:O	1:A:396:ARG:HG3	2.11	0.50
1:A:1008:LEU:HD21	1:A:1073:ILE:CD1	2.40	0.50
1:A:1264:GLY:HA3	1:A:1308:GLU:CD	2.33	0.50
4:G:141:LEU:O	4:G:141:LEU:HD13	2.11	0.50
4:G:299:ALA:O	4:G:303:ASN:N	2.43	0.50
5:K:363:LEU:HD11	5:K:391:PHE:CD2	2.47	0.50
6:L:140:LYS:CG	6:L:141:ARG:CZ	2.90	0.50
8:H:132:ARG:HH21	8:H:206:LYS:CG	2.25	0.50
8:H:347:ARG:HG3	8:H:359:PHE:CZ	2.47	0.50
8:H:501:ILE:HG21	8:H:570:ALA:CB	2.41	0.50
27:F:32:G:O3'	27:F:33:U:H4'	2.11	0.50
27:F:73:U:C2'	27:F:74:U:H5''	2.38	0.50
27:F:75:A:O2'	27:F:76:U:C3'	2.59	0.50
1:A:291:LYS:NZ	1:A:291:LYS:N	2.60	0.49
1:A:452:PHE:CZ	8:H:343:ASP:HB3	2.46	0.49
1:A:909:THR:HG22	1:A:910:LYS:H	1.77	0.49
1:A:1275:MET:CE	1:A:1299:LYS:NZ	2.75	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.27	0.49
3:I:275:LEU:N	3:I:275:LEU:HD23	2.27	0.49
4:G:798:LEU:O	4:G:802:GLN:HA	2.12	0.49
5:K:319:ALA:O	5:K:323:ARG:N	2.44	0.49
8:H:250:GLU:HB3	8:H:298:PHE:CD2	2.47	0.49
1:A:201:PHE:CE2	1:A:551:LEU:HD21	2.47	0.49
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.47	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
1:A:1759:TYR:HB3	1:A:1767:TYR:OH	2.12	0.49
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.48	0.49
1:A:2065:ARG:NE	1:A:2066:LYS:HE2	2.26	0.49
2:B:143:HIS:CE1	5:K:151:LEU:HD22	2.47	0.49
3:I:401:LEU:HD12	4:G:214:SER:CA	2.42	0.49
4:G:886:CYS:SG	4:G:888:PRO:CD	2.97	0.49
8:H:118:TYR:O	8:H:119:ASN:CB	2.60	0.49
8:H:474:LYS:HZ2	8:H:630:PRO:CD	2.25	0.49
8:H:503:ASP:OD1	8:H:571:TYR:CB	2.59	0.49
1:A:149:MET:O	1:A:153:MET:HG3	2.11	0.49
1:A:1490:ARG:HH11	1:A:1536:LEU:HD23	1.76	0.49
1:A:1591:THR:HG22	1:A:1592:HIS:H	1.76	0.49
2:B:448:ASN:O	2:B:449:SER:HB2	2.12	0.49
4:G:6:PHE:CD1	4:G:6:PHE:C	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:379:ILE:CG2	8:H:383:LYS:HE3	2.42	0.49
25:D:50:G:HO2'	25:D:51:A:P	2.27	0.49
26:E:141:G:O2'	26:E:142:G:OP2	2.27	0.49
27:F:62:G:C4	27:F:63:C:C5	3.00	0.49
1:A:1118:GLY:HA3	1:A:1163:ARG:CZ	2.42	0.49
8:H:336:ILE:HG13	8:H:341:ILE:CG2	2.43	0.49
8:H:430:ARG:O	8:H:431:GLN:C	2.50	0.49
1:A:356:TYR:HE2	1:A:396:ARG:HB2	1.76	0.49
1:A:470:LEU:HB2	1:A:473:THR:HB	1.95	0.49
1:A:908:ASP:HB3	1:A:951:LEU:HD11	1.94	0.49
1:A:912:LEU:CG	1:A:951:LEU:HD21	2.43	0.49
1:A:1014:LYS:HD3	1:A:1024:LEU:HD13	1.95	0.49
1:A:1074:VAL:HG12	1:A:1075:ASP:H	1.77	0.49
1:A:1365:THR:C	1:A:1369:ASN:ND2	2.63	0.49
1:A:1385:PRO:HG3	1:A:1407:ILE:HA	1.95	0.49
1:A:1590:LEU:HB2	1:A:1595:ARG:HH21	1.76	0.49
1:A:1922:ARG:NE	1:A:1951:PHE:HZ	2.06	0.49
2:B:276:SER:OG	2:B:277:GLY:N	2.46	0.49
3:I:98:PHE:O	3:I:102:ILE:HG12	2.12	0.49
5:K:331:VAL:O	5:K:332:GLU:HG2	2.13	0.49
8:H:160:ARG:HG3	8:H:160:ARG:HH11	1.77	0.49
8:H:191:ILE:HG23	8:H:221:PHE:CZ	2.48	0.49
8:H:539:VAL:HG13	8:H:564:ILE:HG23	1.93	0.49
27:F:31:G:N3	27:F:32:G:C1'	2.74	0.49
27:F:48:G:H2'	27:F:49:U:H6	1.77	0.49
27:F:73:U:H2'	27:F:74:U:H6	1.78	0.49
1:A:165:LEU:HD21	1:A:726:ILE:CG2	2.42	0.49
1:A:218:SER:HB2	1:A:317:PRO:HG2	1.95	0.49
1:A:272:ASP:CB	1:A:273:ASP:OD1	2.61	0.49
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.12	0.49
2:B:264:HIS:CE1	2:B:290:ARG:HD2	2.47	0.49
6:L:119:THR:HG22	6:L:131:VAL:HG11	1.94	0.49
8:H:470:ALA:HB3	8:H:577:LEU:CB	2.38	0.49
8:H:492:LEU:CD2	8:H:557:HIS:CE1	2.95	0.49
27:F:92:U:C4	27:F:93:G:N7	2.80	0.49
1:A:201:PHE:CE2	1:A:551:LEU:CD2	2.96	0.49
1:A:1204:ARG:HD2	1:A:1259:LEU:HB3	1.93	0.49
1:A:1373:LEU:CD1	6:L:139:HIS:CE1	2.80	0.49
4:G:672:LEU:HD22	4:G:703:LEU:HD12	1.93	0.49
4:G:712:ASP:OD2	4:G:721:ARG:HD2	2.13	0.49
4:G:843:VAL:CG2	4:G:895:LEU:CD1	2.88	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:571:TYR:HD2	8:H:573:LYS:O	1.96	0.49
8:H:864:VAL:HG12	8:H:866:ILE:HG13	1.94	0.49
24:C:11:A:N1	24:C:12:U:C4	2.81	0.49
25:D:83:A:HO2'	25:D:84:C:P	2.27	0.49
27:F:77:A:H1'	27:F:78:A:C5'	2.41	0.49
1:A:749:ARG:O	1:A:750:LEU:CB	2.61	0.49
3:I:93:LYS:HA	3:I:93:LYS:CE	2.43	0.49
8:H:268:ASN:ND2	8:H:316:THR:HG23	2.28	0.49
8:H:369:LYS:NZ	8:H:369:LYS:N	2.60	0.49
8:H:492:LEU:CD2	8:H:557:HIS:HA	2.39	0.49
1:A:165:LEU:CD2	1:A:726:ILE:CG2	2.90	0.49
1:A:277:LYS:HG3	1:A:278:ASP:N	2.28	0.49
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.34	0.49
1:A:2071:ILE:HD13	1:A:2071:ILE:C	2.33	0.49
2:B:117:LEU:HD22	2:B:117:LEU:O	2.13	0.49
3:I:217:TYR:CE1	3:I:221:LYS:HE2	2.48	0.49
3:I:400:VAL:HB	4:G:214:SER:HB2	1.94	0.49
4:G:101:LYS:O	4:G:105:ALA:CB	2.61	0.49
4:G:276:ASP:OD1	4:G:276:ASP:N	2.38	0.49
6:L:105:PHE:CE1	6:L:137:TYR:HE2	2.01	0.49
8:H:589:LEU:HD11	8:H:591:PHE:HE1	1.78	0.49
27:F:63:C:H2'	27:F:64:C:H6	1.78	0.49
1:A:302:SER:HA	1:A:489:THR:O	2.13	0.49
1:A:1067:ASN:OD1	3:I:270:HIS:HB3	2.11	0.49
4:G:170:LEU:HD22	4:G:170:LEU:O	2.12	0.49
5:K:159:TYR:CG	5:K:163:ASN:ND2	2.77	0.49
8:H:383:LYS:O	8:H:387:TYR:CB	2.51	0.49
1:A:175:LEU:CD1	1:A:564:TRP:CZ2	2.96	0.48
1:A:276:VAL:CG1	1:A:310:ASN:CB	2.89	0.48
1:A:1038:ILE:HG13	1:A:1039:TRP:N	2.28	0.48
1:A:1629:LEU:H	1:A:1629:LEU:CD2	2.26	0.48
2:B:197:GLY:CA	2:B:221:ILE:CD1	2.87	0.48
5:K:265:LEU:HD12	5:K:266:PRO:HD2	1.94	0.48
5:K:354:PHE:CE1	5:K:358:MET:CG	2.96	0.48
5:K:448:GLN:HE21	5:K:464:TYR:HE2	1.61	0.48
8:H:165:SER:H	8:H:168:VAL:CG2	2.26	0.48
8:H:578:TYR:CD1	8:H:578:TYR:C	2.86	0.48
24:C:-4:A:H1'	24:C:-3:A:P	2.52	0.48
1:A:140:ARG:NH2	1:A:252:GLU:HB3	2.28	0.48
2:B:282:SER:O	2:B:290:ARG:N	2.40	0.48
4:G:136:ARG:NH1	26:E:51:U:OP2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:306:PRO:O	8:H:324:ILE:CD1	2.60	0.48
8:H:677:PHE:CZ	8:H:966:PHE:CE2	3.00	0.48
8:H:791:TYR:O	8:H:795:ILE:HG13	2.13	0.48
1:A:192:LEU:HG	1:A:557:PHE:CD2	2.48	0.48
1:A:839:HIS:CE1	27:F:96:U:C5	3.02	0.48
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.48	0.48
1:A:1461:TYR:CZ	1:A:1494:LEU:HD13	2.48	0.48
1:A:1594:GLN:N	1:A:1594:GLN:HE21	2.11	0.48
3:I:376:LYS:O	3:I:377:GLU:C	2.51	0.48
4:G:99:ASN:H	4:G:99:ASN:HD22	1.61	0.48
4:G:780:LEU:O	4:G:784:GLY:N	2.45	0.48
8:H:177:TYR:O	8:H:178:LEU:HG	2.13	0.48
8:H:353:TYR:N	8:H:353:TYR:CD1	2.81	0.48
8:H:945:LEU:HD12	8:H:945:LEU:N	2.29	0.48
9:N:1198:ARG:CA	9:N:1227:ILE:N	2.71	0.48
27:F:45:A:H2'	27:F:45:A:N3	2.28	0.48
1:A:140:ARG:HH21	1:A:252:GLU:HB3	1.77	0.48
1:A:770:MET:HE1	1:A:778:LYS:C	2.33	0.48
1:A:1336:ASN:OD1	1:A:1400:ILE:HG13	2.13	0.48
1:A:1557:LEU:O	1:A:1560:THR:OG1	2.27	0.48
8:H:161:ILE:HB	8:H:164:MET:SD	2.54	0.48
8:H:161:ILE:CG2	8:H:162:PRO:HD2	2.41	0.48
8:H:489:TYR:O	8:H:558:LYS:HG3	2.13	0.48
8:H:674:LEU:HD11	8:H:973:ARG:HH22	1.77	0.48
8:H:936:ILE:HD13	8:H:936:ILE:N	2.27	0.48
24:C:8:U:H2'	24:C:9:G:C5'	2.42	0.48
27:F:46:C:H2'	27:F:47:U:H6	1.79	0.48
27:F:74:U:C2'	27:F:75:A:H5'	2.44	0.48
1:A:1183:THR:HG22	1:A:1184:ASP:N	2.29	0.48
1:A:1353:THR:O	1:A:1357:LEU:CD1	2.56	0.48
2:B:60:LYS:HG3	2:B:79:ILE:HD13	1.96	0.48
3:I:462:ASN:OD1	4:G:830:ARG:NE	2.47	0.48
8:H:881:LYS:HA	8:H:886:SER:HB3	1.95	0.48
8:H:884:ARG:CB	8:H:910:GLU:HG3	2.44	0.48
8:H:947:LYS:CD	8:H:947:LYS:N	2.73	0.48
24:C:8:U:C5	25:D:51:A:N1	2.81	0.48
1:A:1335:TRP:CZ2	1:A:1339:LEU:CD1	2.97	0.48
1:A:1650:ARG:HD2	25:D:52:G:P	2.53	0.48
1:A:1705:SER:HB3	1:A:1709:TRP:CD1	2.49	0.48
2:B:158:GLU:O	2:B:162:MET:HE3	2.14	0.48
2:B:177:PRO:HG2	2:B:195:TRP:HE1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:350:PRO:C	5:K:353:ARG:CG	2.81	0.48
6:L:76:LEU:N	6:L:76:LEU:CD1	2.77	0.48
8:H:490:SER:HA	8:H:558:LYS:HG3	1.96	0.48
27:F:48:G:C4	27:F:49:U:C5	3.02	0.48
1:A:228:LYS:HD2	1:A:691:PHE:HE1	1.78	0.48
1:A:290:SER:HG	1:A:291:LYS:NZ	2.05	0.48
1:A:774:ILE:HG23	1:A:777:LYS:NZ	2.28	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CE3	2.48	0.48
2:B:357:TRP:CD1	2:B:358:SER:N	2.82	0.48
2:B:359:PRO:CD	2:B:407:GLY:HA3	2.41	0.48
3:I:130:LEU:HD22	3:I:174:VAL:HG11	1.96	0.48
5:K:146:GLU:C	5:K:148:LYS:N	2.66	0.48
6:L:81:THR:CG2	6:L:102:LYS:NZ	2.66	0.48
8:H:858:LEU:HB3	8:H:937:TRP:HB2	1.96	0.48
8:H:950:PHE:CZ	8:H:952:PRO:O	2.66	0.48
25:D:64:U:H5'	25:D:64:U:C6	2.49	0.48
27:F:46:C:C2	27:F:47:U:C5	3.01	0.48
1:A:305:LEU:C	1:A:305:LEU:HD23	2.34	0.48
1:A:553:ASN:C	1:A:554:THR:HG23	2.33	0.48
1:A:1657:ILE:O	1:A:1661:ILE:CD1	2.62	0.48
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.18	0.48
2:B:173:VAL:CG1	2:B:200:GLN:OE1	2.54	0.48
2:B:350:LYS:HE3	5:K:431:TYR:CG	2.49	0.48
2:B:386:LEU:C	2:B:386:LEU:HD12	2.34	0.48
5:K:159:TYR:CD2	5:K:163:ASN:ND2	2.82	0.48
7:M:42:LYS:NZ	26:E:44:G:O6	2.47	0.48
8:H:449:PHE:CD1	8:H:453:THR:HG21	2.45	0.48
8:H:491:GLY:O	8:H:492:LEU:HD23	2.14	0.48
27:F:52:G:C4	27:F:53:C:C5	3.01	0.48
27:F:71:A:H2'	27:F:72:C:H6	1.79	0.48
1:A:754:TYR:CE2	1:A:758:LEU:HD21	2.49	0.48
1:A:1061:ILE:HG12	1:A:1117:TYR:CE2	2.49	0.48
2:B:177:PRO:CB	2:B:195:TRP:HE1	2.27	0.48
2:B:293:ASP:OD1	2:B:294:ALA:N	2.46	0.48
2:B:320:SER:HB2	2:B:337:ARG:HH12	1.79	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CG	2.49	0.48
2:B:395:ILE:HG22	2:B:396:VAL:N	2.18	0.48
4:G:886:CYS:CB	4:G:888:PRO:HD2	2.44	0.48
8:H:538:GLU:H	8:H:538:GLU:HG2	1.47	0.48
1:A:292:LYS:NZ	1:A:307:GLU:OE2	2.35	0.48
1:A:1908:LEU:HD12	1:A:1908:LEU:C	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:312:SER:HB2	2:B:353:TYR:O	2.14	0.48
3:I:248:VAL:O	3:I:252:SER:OG	2.30	0.48
4:G:284:LEU:CD2	4:G:284:LEU:N	2.77	0.48
5:K:141:ASN:C	5:K:142:LEU:HD22	2.33	0.48
26:E:1:A:OP2	29:E:201:M7M:HBI	2.13	0.48
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.49	0.47
2:B:60:LYS:HB3	2:B:61:PRO:HD2	1.95	0.47
2:B:404:GLU:O	2:B:405:ASP:HB3	2.13	0.47
3:I:79:ASP:O	3:I:83:ILE:N	2.31	0.47
4:G:286:GLU:OE2	4:G:292:CYS:SG	2.69	0.47
4:G:721:ARG:O	4:G:725:ILE:HD12	2.14	0.47
8:H:888:ILE:HA	8:H:904:GLY:HA2	1.96	0.47
26:E:24:A:O2'	26:E:25:U:OP1	2.28	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.96	0.47
1:A:874:ILE:O	1:A:874:ILE:HG22	2.15	0.47
1:A:1009:PHE:CE1	1:A:1115:GLN:HB3	2.49	0.47
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.39	0.47
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.30	0.47
1:A:1593:ALA:CB	6:L:118:GLU:OE1	2.63	0.47
3:I:95:LEU:HD23	3:I:98:PHE:CD2	2.49	0.47
4:G:809:LEU:HD12	4:G:841:THR:HG22	1.96	0.47
6:L:78:ASP:CG	6:L:79:PRO:HD3	2.34	0.47
6:L:118:GLU:OE2	6:L:122:ARG:NH2	2.26	0.47
8:H:132:ARG:HE	8:H:206:LYS:HD2	1.80	0.47
8:H:265:PHE:CE2	8:H:295:ILE:HB	2.49	0.47
8:H:577:LEU:HD23	8:H:577:LEU:O	2.13	0.47
9:N:1203:SER:N	9:N:1223:ILE:O	2.39	0.47
27:F:73:U:O2'	27:F:74:U:H5'	2.02	0.47
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.50	0.47
1:A:1731:LYS:O	1:A:1771:THR:OG1	2.32	0.47
1:A:1877:GLY:O	1:A:1894:ILE:CA	2.62	0.47
2:B:77:ALA:O	2:B:81:MET:HG2	2.14	0.47
4:G:702:PRO:CA	4:G:739:PHE:CE2	2.98	0.47
6:L:18:ALA:HB1	6:L:60:TYR:CE2	2.49	0.47
8:H:444:GLN:NE2	8:H:444:GLN:CA	2.73	0.47
9:N:990:ASP:O	9:N:994:ASP:N	2.45	0.47
27:F:36:A:H61	27:F:118:U:H3	1.61	0.47
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.80	0.47
1:A:1586:GLN:CG	1:A:1595:ARG:NH1	2.77	0.47
1:A:2046:GLU:HG2	1:A:2049:ILE:HD12	1.96	0.47
2:B:446:SER:CB	2:B:451:PHE:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:209:LYS:HG3	3:I:210:LEU:N	2.29	0.47
4:G:740:TYR:OH	4:G:766:LYS:NZ	2.42	0.47
4:G:852:LEU:CD1	4:G:852:LEU:N	2.76	0.47
8:H:233:ASP:HA	8:H:452:LYS:NZ	2.29	0.47
8:H:373:PHE:CE1	8:H:377:ILE:CD1	2.97	0.47
8:H:889:TYR:N	8:H:903:ARG:O	2.47	0.47
27:F:32:G:HO2'	27:F:33:U:P	2.37	0.47
1:A:719:ILE:N	1:A:720:PRO:HD2	2.28	0.47
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.37	0.47
1:A:1607:THR:O	1:A:1611:SER:N	2.47	0.47
4:G:120:MET:O	4:G:122:ILE:N	2.44	0.47
4:G:291:TYR:O	4:G:291:TYR:HD1	1.97	0.47
5:K:350:PRO:CA	5:K:353:ARG:CD	2.85	0.47
8:H:118:TYR:O	8:H:119:ASN:HB3	2.14	0.47
8:H:247:PHE:CD1	8:H:903:ARG:NH1	2.83	0.47
8:H:769:TYR:CD1	8:H:799:PHE:CD2	3.02	0.47
8:H:860:PRO:HB3	8:H:937:TRP:CE3	2.48	0.47
8:H:941:PRO:HG2	8:H:962:LEU:HD12	1.97	0.47
25:D:86:G:H8	25:D:86:G:C5'	2.19	0.47
1:A:320:ASP:C	1:A:321:GLU:HG3	2.34	0.47
1:A:454:LEU:HD22	8:H:336:ILE:HB	1.96	0.47
1:A:495:ARG:NH1	1:A:497:GLN:HE21	2.12	0.47
1:A:790:TRP:CD2	1:A:819:LYS:HD3	2.49	0.47
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.50	0.47
5:K:282:GLU:C	5:K:284:ASP:H	2.16	0.47
8:H:104:THR:O	8:H:108:GLN:HG3	2.14	0.47
8:H:175:LEU:HD23	8:H:175:LEU:C	2.34	0.47
25:D:62:A:N3	26:E:58:G:N2	2.62	0.47
27:F:52:G:H2'	27:F:53:C:H6	1.79	0.47
27:F:71:A:C4	27:F:72:C:C5	3.02	0.47
1:A:301:TRP:CZ2	1:A:491:GLY:HA3	2.50	0.47
1:A:553:ASN:O	1:A:554:THR:HG23	2.15	0.47
1:A:1262:MET:O	1:A:1263:CYS:CB	2.61	0.47
1:A:1508:HIS:HA	1:A:1511:ARG:NH2	2.29	0.47
1:A:1730:ASN:C	1:A:1731:LYS:HG3	2.35	0.47
2:B:321:LEU:HD22	2:B:335:ASP:HA	1.97	0.47
2:B:362:TYR:CD2	2:B:379:ARG:HD2	2.49	0.47
2:B:413:CYS:SG	2:B:440:ILE:HG21	2.55	0.47
4:G:15:TYR:CE1	6:L:13:TRP:HD1	2.32	0.47
4:G:368:SER:O	4:G:372:LEU:N	2.47	0.47
4:G:672:LEU:HD13	4:G:703:LEU:HD12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:853:GLY:O	4:G:854:LYS:HB2	2.14	0.47
8:H:492:LEU:HD22	8:H:557:HIS:ND1	2.24	0.47
8:H:581:LYS:NZ	8:H:581:LYS:CB	2.73	0.47
8:H:964:ARG:O	8:H:968:MET:HG2	2.15	0.47
1:A:174:LYS:O	1:A:178:ASN:ND2	2.39	0.47
1:A:239:PHE:CB	1:A:240:PRO:CD	2.92	0.47
1:A:767:LEU:HA	1:A:770:MET:HG3	1.96	0.47
1:A:1217:ARG:HD3	1:A:1217:ARG:HA	1.75	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.50	0.47
1:A:1591:THR:CG2	1:A:1592:HIS:N	2.78	0.47
2:B:120:ALA:HB1	2:B:279:PHE:CE2	2.50	0.47
2:B:187:ASP:OD2	2:B:447:ASN:CB	2.63	0.47
2:B:225:ASP:OD1	2:B:226:TRP:N	2.48	0.47
2:B:275:PRO:HG3	2:B:319:GLY:N	2.30	0.47
4:G:144:LYS:O	4:G:145:THR:OG1	2.18	0.47
6:L:105:PHE:CB	6:L:141:ARG:CD	2.92	0.47
8:H:307:ILE:HD13	8:H:345:THR:O	2.15	0.47
8:H:336:ILE:HD11	8:H:341:ILE:CG2	2.38	0.47
27:F:66:A:C4	27:F:67:U:C5	3.02	0.47
1:A:175:LEU:HD11	1:A:564:TRP:CE2	2.50	0.47
1:A:470:LEU:H	1:A:473:THR:CG2	2.27	0.47
1:A:470:LEU:H	1:A:473:THR:HG21	1.80	0.47
1:A:691:PHE:HZ	1:A:701:CYS:CA	2.26	0.47
1:A:1115:GLN:NE2	1:A:1115:GLN:CA	2.78	0.47
1:A:1369:ASN:O	1:A:1373:LEU:HG	2.15	0.47
1:A:1623:PHE:CZ	24:C:5:G:C5	3.02	0.47
1:A:1651:ALA:C	1:A:1652:HIS:HD2	2.16	0.47
2:B:181:VAL:HA	2:B:191:ALA:O	2.15	0.47
2:B:243:ILE:HD12	2:B:292:TRP:HZ3	1.78	0.47
2:B:261:LEU:HD13	2:B:292:TRP:CE3	2.50	0.47
3:I:277:SER:HB3	3:I:279:VAL:HG23	1.97	0.47
4:G:288:ASP:O	4:G:292:CYS:SG	2.72	0.47
4:G:490:GLU:O	4:G:494:HIS:N	2.48	0.47
4:G:672:LEU:HD22	4:G:703:LEU:CD1	2.45	0.47
5:K:340:LYS:HE2	5:K:389:CYS:HB3	1.97	0.47
5:K:370:LEU:HD21	5:K:454:THR:HG21	1.95	0.47
1:A:840:VAL:C	1:A:841:GLU:HG3	2.34	0.47
1:A:845:VAL:HG21	1:A:1321:MET:CE	2.44	0.47
1:A:853:THR:OG1	1:A:971:MET:HG2	2.14	0.47
1:A:1145:MET:CE	1:A:1160:LEU:HD13	2.44	0.47
2:B:161:ARG:O	2:B:165:LEU:CD2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:275:PRO:O	2:B:276:SER:O	2.33	0.47
4:G:698:VAL:N	4:G:699:PRO:CD	2.78	0.47
4:G:861:ASN:ND2	4:G:862:MET:SD	2.88	0.47
6:L:13:TRP:CH2	6:L:17:GLN:NE2	2.83	0.47
1:A:251:TYR:HA	1:A:255:ILE:CD1	2.37	0.46
1:A:289:ASP:HB3	1:A:292:LYS:HB2	1.97	0.46
2:B:206:THR:HB	2:B:208:GLN:CD	2.35	0.46
3:I:214:ILE:O	3:I:218:ILE:HG12	2.15	0.46
3:I:401:LEU:HD12	3:I:401:LEU:H	1.79	0.46
4:G:101:LYS:O	4:G:105:ALA:HB2	2.15	0.46
6:L:108:ASP:N	6:L:108:ASP:OD1	2.48	0.46
8:H:375:GLU:CG	8:H:376:PHE:CE1	2.99	0.46
8:H:500:ARG:CD	8:H:534:THR:HG23	2.10	0.46
8:H:564:ILE:HG22	8:H:567:ILE:HG12	1.95	0.46
8:H:855:PRO:CD	8:H:944:VAL:HG21	2.44	0.46
8:H:897:THR:HB	8:H:898:PRO:HD2	1.97	0.46
8:H:967:VAL:HB	8:H:968:MET:HE3	1.97	0.46
27:F:35:A:C4	27:F:120:G:N2	2.82	0.46
27:F:43:G:C2	27:F:44:A:C5	3.02	0.46
1:A:315:SER:C	1:A:317:PRO:CD	2.82	0.46
1:A:815:TYR:CD1	1:A:815:TYR:C	2.88	0.46
1:A:1115:GLN:N	1:A:1115:GLN:HE21	2.12	0.46
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.29	0.46
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.97	0.46
2:B:350:LYS:HB3	2:B:351:PRO:HD2	1.98	0.46
4:G:298:THR:O	4:G:302:PHE:CD2	2.67	0.46
5:K:395:LEU:HD13	5:K:399:ARG:CZ	2.45	0.46
8:H:941:PRO:HD2	8:H:962:LEU:HB2	1.98	0.46
25:D:48:C:H2'	25:D:49:A:C8	2.50	0.46
1:A:170:HIS:C	1:A:170:HIS:CD2	2.88	0.46
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.80	0.46
2:B:362:TYR:HD2	2:B:379:ARG:HD2	1.81	0.46
2:B:387:ASN:CA	2:B:388:GLN:OE1	2.64	0.46
4:G:325:ARG:O	4:G:329:LYS:N	2.37	0.46
5:K:334:PRO:HG2	5:K:337:TYR:HE1	1.79	0.46
8:H:488:ILE:HD11	8:H:556:ALA:HB1	1.97	0.46
8:H:500:ARG:HE	8:H:534:THR:HB	1.75	0.46
27:F:165:A:O2'	27:F:166:U:OP2	2.27	0.46
1:A:505:TRP:HZ3	1:A:690:LYS:HG3	1.78	0.46
1:A:1275:MET:CE	1:A:1299:LYS:CD	2.93	0.46
1:A:1284:GLY:HA2	1:A:1348:GLU:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1899:TRP:CH2	1:A:1909:ALA:CB	2.98	0.46
2:B:184:SER:OG	2:B:186:ASP:OD1	2.18	0.46
4:G:122:ILE:CG1	4:G:123:PRO:HD2	2.36	0.46
4:G:691:TYR:CE2	4:G:711:ILE:HD12	2.49	0.46
8:H:167:ASN:ND2	8:H:167:ASN:C	2.69	0.46
8:H:296:ASN:OD1	8:H:303:VAL:HA	2.15	0.46
8:H:387:TYR:O	8:H:391:MET:CB	2.50	0.46
1:A:1402:ALA:O	1:A:1403:SER:CB	2.63	0.46
1:A:1878:CYS:O	1:A:1878:CYS:SG	2.73	0.46
1:A:2075:THR:HG22	1:A:2076:GLN:N	2.30	0.46
2:B:177:PRO:CG	2:B:195:TRP:HE1	2.27	0.46
2:B:279:PHE:HD1	2:B:279:PHE:N	2.12	0.46
2:B:307:ASP:OD1	5:K:225:ILE:HA	2.16	0.46
2:B:313:LEU:HD11	2:B:322:VAL:HG21	1.98	0.46
2:B:408:LYS:O	2:B:424:SER:HB3	2.15	0.46
3:I:281:GLN:NE2	26:E:37:U:O4	2.48	0.46
3:I:433:ASN:ND2	3:I:433:ASN:N	2.61	0.46
4:G:13:ALA:O	4:G:15:TYR:N	2.48	0.46
6:L:45:LEU:HD11	6:L:110:LYS:HA	1.97	0.46
8:H:449:PHE:CD1	8:H:449:PHE:C	2.88	0.46
1:A:286:LEU:HD22	1:A:292:LYS:HB3	1.96	0.46
1:A:514:TYR:N	1:A:514:TYR:CD1	2.84	0.46
1:A:1065:LEU:HG	3:I:177:MET:HE1	1.98	0.46
1:A:1216:ILE:HD12	1:A:1254:ASN:CB	2.44	0.46
1:A:1593:ALA:HB3	6:L:118:GLU:OE1	2.16	0.46
1:A:1756:PHE:CD1	1:A:1756:PHE:C	2.89	0.46
1:A:1995:TRP:CE3	1:A:2007:ARG:HD2	2.50	0.46
8:H:544:LEU:HG	8:H:553:VAL:HG21	1.97	0.46
8:H:801:TRP:O	8:H:801:TRP:HD1	1.98	0.46
1:A:247:PRO:HB2	1:A:248:PRO:HD2	1.98	0.46
1:A:810:LYS:HA	1:A:810:LYS:HE3	1.98	0.46
1:A:901:PRO:HD3	1:A:1078:ILE:HD11	1.98	0.46
1:A:1125:LEU:HD21	1:A:1234:VAL:CG2	2.46	0.46
1:A:1417:GLN:OE1	1:A:1422:ILE:CG1	2.64	0.46
2:B:290:ARG:CZ	2:B:302:LEU:HD13	2.45	0.46
4:G:703:LEU:HD13	4:G:703:LEU:O	2.16	0.46
8:H:247:PHE:HB3	8:H:931:TYR:OH	2.15	0.46
24:C:-4:A:C1'	24:C:-3:A:P	3.04	0.46
1:A:318:LEU:HD12	1:A:318:LEU:N	2.31	0.46
1:A:656:ILE:O	1:A:660:ILE:HG13	2.16	0.46
1:A:1038:ILE:HD12	1:A:1039:TRP:CE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1204:ARG:CD	1:A:1259:LEU:HB3	2.46	0.46
1:A:1287:ASP:OD2	1:A:1296:ARG:NH1	2.49	0.46
2:B:321:LEU:HD13	2:B:333:LEU:HD23	1.98	0.46
2:B:422:TYR:HD1	2:B:429:LYS:HA	1.81	0.46
3:I:136:GLN:NE2	3:I:166:LYS:O	2.49	0.46
3:I:226:ALA:CB	3:I:317:ASP:OD2	2.62	0.46
4:G:144:LYS:HE3	26:E:19:U:OP1	2.16	0.46
4:G:851:ARG:C	4:G:852:LEU:HD12	2.36	0.46
5:K:453:ARG:O	5:K:457:GLN:CD	2.54	0.46
7:M:51:PHE:CE2	7:M:53:ILE:HD11	2.50	0.46
8:H:571:TYR:CD2	8:H:573:LYS:O	2.69	0.46
8:H:967:VAL:HG12	8:H:971:ARG:HG3	1.97	0.46
1:A:141:LYS:HA	1:A:144:ASN:CG	2.19	0.46
1:A:665:GLY:O	1:A:668:ARG:HG2	2.15	0.46
2:B:171:GLN:OE1	2:B:172:LEU:O	2.34	0.46
3:I:143:ILE:HG23	3:I:149:TYR:HE2	1.81	0.46
4:G:16:VAL:HG13	4:G:17:PRO:HD2	1.98	0.46
4:G:103:GLN:O	4:G:106:ASP:OD1	2.34	0.46
8:H:362:LYS:HE2	8:H:365:GLU:CB	2.45	0.46
24:C:10:U:H2'	24:C:11:A:C8	2.50	0.46
26:E:2:U:C6	26:E:3:C:C5	3.03	0.46
27:F:89:U:C4	27:F:90:C:C5	3.04	0.46
1:A:175:LEU:HD12	1:A:564:TRP:NE1	2.31	0.46
1:A:275:TYR:O	1:A:279:TRP:CE2	2.69	0.46
1:A:532:ASN:ND2	27:F:83:C:O3'	2.49	0.46
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.79	0.46
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.97	0.46
1:A:1521:ARG:CZ	3:I:404:TYR:CD2	2.99	0.46
1:A:1625:VAL:O	1:A:1633:PHE:HA	2.15	0.46
1:A:1790:TRP:CE3	1:A:1795:LYS:HG3	2.51	0.46
3:I:268:LEU:CD1	3:I:271:GLU:CG	2.83	0.46
4:G:223:LEU:HD23	4:G:223:LEU:C	2.36	0.46
4:G:692:LEU:O	4:G:696:ARG:HG3	2.15	0.46
4:G:769:SER:O	4:G:801:THR:HG22	2.15	0.46
6:L:78:ASP:CG	6:L:79:PRO:CD	2.85	0.46
8:H:831:ILE:O	8:H:831:ILE:HG22	2.16	0.46
26:E:32:G:N2	26:E:44:G:N3	2.64	0.46
1:A:853:THR:OG1	1:A:971:MET:CG	2.64	0.45
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.31	0.45
5:K:159:TYR:CE1	5:K:163:ASN:ND2	2.83	0.45
6:L:36:ASP:HB2	6:L:39:CYS:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:139:HIS:NE2	27:F:96:U:O5'	2.49	0.45
8:H:328:VAL:HG21	8:H:345:THR:CG2	2.45	0.45
27:F:73:U:C2	27:F:74:U:C5	3.03	0.45
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.99	0.45
2:B:162:MET:N	2:B:162:MET:CE	2.79	0.45
2:B:244:LYS:HG2	2:B:257:LEU:HD23	1.97	0.45
2:B:261:LEU:HB3	2:B:292:TRP:CZ3	2.51	0.45
2:B:267:ARG:NH1	2:B:285:HIS:NE2	2.64	0.45
3:I:123:ARG:HB2	3:I:189:LEU:CD1	2.46	0.45
3:I:359:PRO:O	6:L:122:ARG:NH1	2.50	0.45
8:H:204:GLU:OE1	8:H:204:GLU:HA	2.17	0.45
8:H:963:SER:O	8:H:967:VAL:HG23	2.17	0.45
26:E:21:C:H2'	26:E:22:G:O4'	2.15	0.45
27:F:75:A:C4	27:F:77:A:H5''	2.50	0.45
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.98	0.45
1:A:495:ARG:CZ	1:A:497:GLN:NE2	2.78	0.45
1:A:1839:ASN:ND2	1:A:1842:GLU:OE1	2.50	0.45
3:I:98:PHE:CZ	3:I:217:TYR:CD2	2.98	0.45
3:I:424:THR:HG22	3:I:425:SER:N	2.30	0.45
4:G:487:GLN:O	4:G:491:LYS:N	2.43	0.45
5:K:337:TYR:CE2	5:K:434:ASP:HA	2.51	0.45
1:A:362:GLU:CB	1:A:1209:LYS:HG2	2.45	0.45
1:A:770:MET:HE1	1:A:778:LYS:CB	2.45	0.45
1:A:883:PHE:HB2	3:I:177:MET:SD	2.56	0.45
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.52	0.45
1:A:1589:LYS:O	1:A:1590:LEU:HD13	2.16	0.45
1:A:2066:LYS:HB2	1:A:2067:TYR:HD1	1.80	0.45
2:B:135:ARG:HD3	2:B:360:ASN:O	2.16	0.45
2:B:443:LEU:CD1	2:B:452:LEU:HD11	2.47	0.45
4:G:219:THR:HG22	4:G:221:GLU:H	1.81	0.45
4:G:238:PRO:CD	4:G:239:THR:N	2.79	0.45
4:G:255:ARG:HH11	4:G:255:ARG:HG3	1.80	0.45
4:G:285:HIS:HE1	4:G:291:TYR:HE2	1.56	0.45
4:G:668:HIS:HB2	4:G:698:VAL:HG11	1.95	0.45
4:G:691:TYR:HE2	4:G:711:ILE:CD1	2.14	0.45
5:K:144:LEU:CD2	5:K:144:LEU:H	2.29	0.45
5:K:273:LYS:O	5:K:277:MET:HB2	2.16	0.45
7:M:67:LEU:HB2	7:M:68:PRO:HD3	1.98	0.45
8:H:247:PHE:CD1	8:H:250:GLU:OE1	2.70	0.45
8:H:379:ILE:HG23	8:H:383:LYS:HE2	1.98	0.45
1:A:162:LEU:CD2	1:A:730:ILE:HD13	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:874:ILE:O	1:A:875:THR:O	2.34	0.45
1:A:1453:ASP:O	1:A:1457:VAL:HG23	2.16	0.45
2:B:155:ARG:CD	2:B:155:ARG:N	2.79	0.45
3:I:237:ILE:O	3:I:240:GLN:N	2.49	0.45
4:G:733:ASN:HB2	4:G:734:PRO:HA	1.99	0.45
6:L:102:LYS:CG	6:L:103:LEU:N	2.78	0.45
8:H:968:MET:HE2	8:H:971:ARG:HG3	1.98	0.45
9:N:1105:ALA:O	9:N:1106:GLY:C	2.54	0.45
27:F:77:A:C1'	27:F:78:A:C5'	2.95	0.45
1:A:251:TYR:O	1:A:255:ILE:HB	2.16	0.45
1:A:366:GLU:O	1:A:372:ARG:HD2	2.16	0.45
1:A:795:ALA:O	1:A:796:ASN:HB2	2.17	0.45
1:A:820:ALA:O	1:A:824:VAL:HG23	2.16	0.45
2:B:428:LEU:HD11	5:K:466:PRO:HD2	1.97	0.45
3:I:245:ALA:CB	3:I:250:GLU:HB3	2.40	0.45
4:G:252:GLU:CG	4:G:256:LYS:HE3	2.47	0.45
8:H:113:ILE:CG2	8:H:549:TYR:CD1	2.99	0.45
8:H:121:ASP:O	8:H:125:SER:N	2.49	0.45
8:H:270:LEU:CD1	8:H:313:PHE:HB3	2.45	0.45
8:H:306:PRO:HD2	8:H:349:TRP:CE2	2.51	0.45
1:A:205:THR:HG23	1:A:205:THR:O	2.16	0.45
1:A:373:VAL:CG1	1:A:374:ILE:N	2.80	0.45
1:A:1974:LEU:O	1:A:1978:VAL:HG23	2.17	0.45
2:B:88:GLU:HA	2:B:91:ASN:HB3	1.98	0.45
2:B:192:THR:CG2	2:B:200:GLN:HG3	2.47	0.45
2:B:202:LEU:N	2:B:202:LEU:CD1	2.80	0.45
3:I:92:ILE:O	3:I:96:PRO:HD3	2.16	0.45
6:L:74:TYR:CG	6:L:83:MET:CE	3.00	0.45
8:H:272:ARG:O	8:H:276:ASP:HB2	2.16	0.45
8:H:274:ILE:HD13	8:H:274:ILE:C	2.37	0.45
8:H:675:THR:HG22	8:H:909:ILE:HD13	1.98	0.45
27:F:66:A:H2'	27:F:67:U:H6	1.81	0.45
27:F:102:C:H2'	27:F:103:A:H5'	1.99	0.45
1:A:176:LEU:CD2	1:A:176:LEU:C	2.85	0.45
1:A:776:GLN:HG2	1:A:777:LYS:N	2.32	0.45
1:A:1611:SER:N	1:A:1612:PRO:HD2	2.32	0.45
2:B:447:ASN:ND2	2:B:447:ASN:C	2.70	0.45
2:B:454:SER:OG	2:B:464:TRP:NE1	2.29	0.45
3:I:66:SER:O	3:I:70:THR:N	2.50	0.45
5:K:409:HIS:ND1	5:K:414:ASP:OD1	2.44	0.45
8:H:500:ARG:HG2	8:H:534:THR:HG21	1.87	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:578:TYR:CD1	8:H:578:TYR:O	2.70	0.45
9:N:1343:PHE:O	9:N:1345:PHE:N	2.49	0.45
25:D:49:A:H2'	25:D:50:G:O5'	2.16	0.45
27:F:84:A:C2	27:F:111:C:C2	3.05	0.45
1:A:151:SER:H	1:A:577:ASN:ND2	2.14	0.45
1:A:505:TRP:HD1	1:A:505:TRP:H	1.64	0.45
1:A:505:TRP:CE3	1:A:690:LYS:HG3	2.50	0.45
1:A:956:LYS:C	1:A:956:LYS:CD	2.83	0.45
2:B:419:ILE:CG2	2:B:433:LEU:HB2	2.47	0.45
3:I:46:ILE:O	3:I:97:PHE:CE1	2.69	0.45
3:I:358:ILE:CG2	3:I:359:PRO:CD	2.94	0.45
4:G:890:GLU:OE1	4:G:890:GLU:HA	2.17	0.45
8:H:167:ASN:ND2	8:H:173:LYS:CG	2.76	0.45
8:H:471:HIS:O	8:H:486:VAL:HA	2.17	0.45
8:H:950:PHE:CE1	8:H:951:ILE:O	2.70	0.45
29:E:201:M7M:NBN	29:E:201:M7M:HBX	2.32	0.45
27:F:107:C:H2'	27:F:108:C:O4'	2.16	0.45
1:A:298:TYR:O	1:A:298:TYR:CD1	2.70	0.45
5:K:141:ASN:CG	5:K:144:LEU:HD23	2.37	0.45
24:C:11:A:C2	25:D:47:A:C6	3.05	0.45
1:A:484:PHE:CD1	27:F:81:A:C6	3.05	0.44
1:A:770:MET:HE3	1:A:775:ARG:O	2.17	0.44
1:A:860:GLU:OE2	1:A:863:ARG:NH1	2.51	0.44
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.44
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	1.98	0.44
2:B:357:TRP:HD1	2:B:358:SER:N	2.15	0.44
2:B:393:ARG:CG	2:B:393:ARG:NH2	2.74	0.44
8:H:133:ILE:HG13	8:H:134:ILE:N	2.32	0.44
8:H:234:LEU:HD23	8:H:234:LEU:H	1.82	0.44
8:H:470:ALA:HB3	8:H:577:LEU:CD2	2.46	0.44
8:H:481:ALA:HB2	8:H:565:LYS:HZ3	1.77	0.44
8:H:539:VAL:HG22	8:H:567:ILE:HD11	1.99	0.44
27:F:79:C:O2	27:F:79:C:H3'	2.17	0.44
1:A:176:LEU:HD21	1:A:708:TRP:NE1	2.31	0.44
1:A:874:ILE:C	1:A:875:THR:OG1	2.55	0.44
2:B:116:GLU:CD	2:B:117:LEU:N	2.70	0.44
3:I:113:HIS:HD2	3:I:134:PRO:CA	2.30	0.44
3:I:400:VAL:CG2	4:G:154:PRO:HG2	2.47	0.44
3:I:401:LEU:HA	3:I:407:GLU:HA	1.97	0.44
4:G:688:ARG:HH11	4:G:712:ASP:CG	2.20	0.44
5:K:341:VAL:HG21	5:K:428:TRP:CD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:110:LYS:HA	8:H:110:LYS:HD3	1.79	0.44
8:H:354:TYR:CD1	8:H:354:TYR:O	2.70	0.44
8:H:599:THR:HG23	8:H:933:TRP:HZ3	1.80	0.44
8:H:942:GLY:HA2	8:H:960:ASN:O	2.17	0.44
24:C:-3:A:HI'	24:C:-2:A:C8	2.52	0.44
25:D:83:A:O2'	25:D:84:C:P	2.75	0.44
27:F:103:A:C4	27:F:104:G:N7	2.86	0.44
1:A:165:LEU:HD23	1:A:726:ILE:HG21	1.99	0.44
1:A:1020:ILE:HD12	1:A:1020:ILE:N	2.32	0.44
1:A:1364:GLU:OE1	1:A:1405:ILE:HD11	2.17	0.44
1:A:1378:LYS:O	1:A:1379:MET:HB2	2.16	0.44
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.17	0.44
1:A:2076:GLN:HA	1:A:2079:ILE:HD12	1.98	0.44
2:B:154:SER:HG	2:B:155:ARG:HD3	1.79	0.44
3:I:429:ARG:HH11	3:I:429:ARG:HA	1.82	0.44
5:K:143:GLU:O	5:K:145:HIS:CE1	2.70	0.44
6:L:133:SER:HA	6:L:134:PRO:HD2	1.84	0.44
6:L:140:LYS:CB	6:L:141:ARG:HH11	2.30	0.44
8:H:449:PHE:O	8:H:449:PHE:CD1	2.70	0.44
27:F:50:G:H2'	27:F:51:G:H8	1.82	0.44
27:F:95:C:O3'	27:F:96:U:H4'	2.17	0.44
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.53	0.44
1:A:1373:LEU:HD11	27:F:96:U:OP1	2.17	0.44
1:A:1417:GLN:HE22	1:A:1783:MET:HA	1.83	0.44
1:A:1474:ARG:HG2	1:A:1475:LEU:N	2.33	0.44
1:A:1851:PHE:O	1:A:1881:THR:HA	2.17	0.44
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.47	0.44
1:A:1880:PHE:CD2	1:A:1889:LEU:CD2	3.00	0.44
2:B:32:LEU:HD23	2:B:34:HIS:H	1.82	0.44
2:B:359:PRO:HG2	2:B:407:GLY:CA	2.47	0.44
2:B:390:LEU:CD1	5:K:428:TRP:CD1	3.01	0.44
2:B:393:ARG:HG2	2:B:393:ARG:NH2	2.17	0.44
3:I:456:LEU:HD23	3:I:456:LEU:O	2.18	0.44
8:H:120:ARG:HA	8:H:120:ARG:HD3	1.67	0.44
8:H:354:TYR:HB2	8:H:359:PHE:CB	2.28	0.44
8:H:472:VAL:CG1	8:H:571:TYR:HE2	2.29	0.44
8:H:595:LEU:HD13	8:H:595:LEU:HA	1.83	0.44
24:C:7:A:N6	25:D:51:A:C8	2.85	0.44
1:A:162:LEU:CG	1:A:734:PHE:CE2	2.96	0.44
1:A:275:TYR:CD1	1:A:275:TYR:N	2.72	0.44
1:A:325:LYS:CE	1:A:325:LYS:CA	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:ASN:HD22	1:A:543:ASN:C	2.21	0.44
1:A:807:PRO:O	1:A:811:ILE:HG13	2.18	0.44
1:A:1073:ILE:HD12	1:A:1116:TYR:HE1	1.77	0.44
1:A:1275:MET:HE1	1:A:1299:LYS:CD	2.47	0.44
4:G:98:SER:HG	4:G:99:ASN:ND2	2.14	0.44
8:H:375:GLU:HB3	8:H:376:PHE:CD1	2.52	0.44
8:H:950:PHE:CZ	8:H:951:ILE:O	2.70	0.44
27:F:102:C:C2'	27:F:103:A:H5'	2.47	0.44
1:A:170:HIS:CD2	1:A:170:HIS:O	2.70	0.44
1:A:358:ARG:CB	1:A:358:ARG:NH1	2.80	0.44
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.98	0.44
2:B:293:ASP:HB2	2:B:300:LEU:HD11	1.99	0.44
3:I:137:TYR:O	3:I:141:ILE:HG13	2.17	0.44
3:I:398:GLN:OE1	3:I:414:ASN:ND2	2.49	0.44
4:G:111:LEU:O	4:G:113:ALA:N	2.51	0.44
6:L:25:ARG:CG	6:L:25:ARG:NH1	2.75	0.44
8:H:229:LEU:CD2	8:H:235:VAL:HG11	2.48	0.44
8:H:230:ALA:HB3	8:H:473:LEU:CD1	2.48	0.44
8:H:769:TYR:CZ	8:H:799:PHE:CE2	2.92	0.44
9:N:1382:LEU:O	9:N:1385:LEU:N	2.50	0.44
26:E:151:G:C2	26:E:152:A:N6	2.84	0.44
1:A:164:ALA:HB2	1:A:194:HIS:CD2	2.53	0.44
1:A:807:PRO:HB2	4:G:111:LEU:HD23	1.99	0.44
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.98	0.44
1:A:1661:ILE:HB	1:A:1736:VAL:HG11	2.00	0.44
2:B:154:SER:O	2:B:158:GLU:HG3	2.18	0.44
2:B:416:ASP:O	2:B:417:ASN:HB2	2.18	0.44
3:I:277:SER:CB	3:I:279:VAL:HG23	2.48	0.44
4:G:867:GLU:OE2	4:G:888:PRO:HG2	2.17	0.44
5:K:345:LYS:HB2	5:K:422:ASN:HA	2.00	0.44
8:H:123:MET:SD	8:H:209:MET:HE3	2.58	0.44
8:H:132:ARG:O	8:H:133:ILE:HG23	2.17	0.44
8:H:304:PHE:N	8:H:304:PHE:CD1	2.86	0.44
8:H:460:GLY:HA3	8:H:461:LYS:HA	1.67	0.44
1:A:171:ALA:HB2	1:A:201:PHE:CE1	2.51	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.17	0.44
1:A:613:SER:O	1:A:614:ARG:C	2.55	0.44
2:B:171:GLN:NE2	2:B:172:LEU:H	2.15	0.44
2:B:448:ASN:O	2:B:449:SER:CB	2.65	0.44
3:I:263:GLY:C	3:I:283:GLY:HA2	2.38	0.44
4:G:6:PHE:CE1	4:G:7:LEU:CD1	2.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:166:ARG:O	4:G:167:GLU:C	2.56	0.44
8:H:484:SER:O	8:H:564:ILE:HD12	2.17	0.44
26:E:6:U:H2'	26:E:7:A:H8	1.83	0.44
27:F:99:U:O2'	27:F:100:A:P	2.73	0.44
1:A:413:ASN:ND2	1:A:413:ASN:N	2.66	0.44
1:A:1276:GLU:N	1:A:1276:GLU:OE2	2.50	0.44
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.83	0.44
3:I:282:GLU:CG	3:I:286:PHE:CD2	3.00	0.44
3:I:400:VAL:HG21	4:G:154:PRO:CG	2.46	0.44
4:G:161:LYS:HA	4:G:161:LYS:CE	2.48	0.44
4:G:212:VAL:HG22	4:G:214:SER:H	1.83	0.44
4:G:272:PRO:CB	4:G:302:PHE:CD1	2.77	0.44
6:L:25:ARG:HH11	6:L:25:ARG:HG3	1.82	0.44
8:H:185:ILE:CD1	27:F:75:A:OP2	2.55	0.44
8:H:306:PRO:HG2	8:H:349:TRP:CD2	2.52	0.44
8:H:354:TYR:CD1	8:H:376:PHE:HZ	2.36	0.44
27:F:175:G:H4'	27:F:176:A:O4'	2.18	0.44
1:A:379:ILE:HG22	1:A:379:ILE:O	2.17	0.43
1:A:689:TYR:O	1:A:689:TYR:CD1	2.71	0.43
1:A:900:PHE:CZ	1:A:959:LEU:HD12	2.52	0.43
1:A:1285:VAL:HA	1:A:1300:ALA:O	2.18	0.43
1:A:1393:GLU:HG2	3:I:395:LYS:O	2.18	0.43
2:B:316:GLN:O	2:B:319:GLY:N	2.45	0.43
2:B:447:ASN:C	2:B:447:ASN:HD22	2.22	0.43
3:I:267:HIS:CE1	3:I:273:HIS:CE1	3.05	0.43
4:G:702:PRO:HB3	4:G:739:PHE:CD1	2.52	0.43
6:L:95:PHE:CE2	6:L:103:LEU:HD13	2.53	0.43
25:D:84:C:O2	25:D:84:C:C2'	2.66	0.43
27:F:175:G:C2	27:F:176:A:N6	2.84	0.43
1:A:1276:GLU:H	1:A:1276:GLU:CD	2.21	0.43
1:A:1501:THR:HG21	4:G:163:THR:HG21	1.99	0.43
1:A:1894:ILE:HG21	1:A:1899:TRP:CZ2	2.52	0.43
1:A:2067:TYR:N	1:A:2067:TYR:HD1	2.15	0.43
2:B:316:GLN:CG	2:B:357:TRP:CZ2	2.97	0.43
5:K:144:LEU:HB3	5:K:146:GLU:OE2	2.18	0.43
5:K:341:VAL:CG2	5:K:428:TRP:CD1	3.01	0.43
6:L:74:TYR:CD1	6:L:83:MET:HE1	2.52	0.43
8:H:347:ARG:HG3	8:H:359:PHE:HZ	1.81	0.43
8:H:488:ILE:HD11	8:H:560:GLN:CG	2.42	0.43
1:A:505:TRP:CD1	1:A:505:TRP:N	2.86	0.43
1:A:750:LEU:HG	1:A:751:ASP:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:357:TRP:O	2:B:401:PHE:CD2	2.72	0.43
2:B:395:ILE:CG2	2:B:396:VAL:H	2.16	0.43
2:B:409:LYS:HA	2:B:422:TYR:O	2.18	0.43
3:I:298:VAL:O	3:I:298:VAL:HG12	2.18	0.43
3:I:327:THR:O	3:I:328:VAL:CB	2.67	0.43
3:I:391:MET:SD	3:I:397:GLU:HG3	2.58	0.43
5:K:333:LYS:HD2	5:K:333:LYS:O	2.17	0.43
27:F:44:A:H61	27:F:71:A:H61	1.66	0.43
1:A:415:GLU:OE1	1:A:416:GLU:HB2	2.18	0.43
1:A:1019:GLU:HA	1:A:1023:LEU:HD23	2.00	0.43
1:A:1335:TRP:CD1	1:A:1367:ILE:CD1	3.01	0.43
1:A:1342:LEU:HD23	1:A:1350:ILE:CD1	2.49	0.43
2:B:127:TYR:HE2	2:B:276:SER:CA	2.31	0.43
3:I:450:GLN:HG3	3:I:451:GLN:H	1.83	0.43
4:G:231:LYS:HA	4:G:234:ARG:HD3	2.00	0.43
8:H:144:SER:HA	8:H:240:ASP:OD2	2.18	0.43
8:H:330:TYR:HE1	8:H:430:ARG:HH21	1.25	0.43
8:H:373:PHE:O	8:H:377:ILE:HB	2.17	0.43
8:H:566:GLY:C	8:H:567:ILE:HD13	2.39	0.43
24:C:-4:A:H4'	24:C:-3:A:OP2	2.18	0.43
27:F:47:U:H2'	27:F:48:G:H8	1.83	0.43
27:F:67:U:H2'	27:F:68:A:H8	1.82	0.43
1:A:162:LEU:HD11	1:A:730:ILE:HG22	2.01	0.43
1:A:1381:THR:OG1	1:A:1382:ARG:HG3	2.19	0.43
1:A:1664:ASP:O	1:A:1668:ILE:CG1	2.66	0.43
1:A:1739:ARG:HD2	1:A:1751:TYR:CD2	2.53	0.43
2:B:192:THR:HG23	2:B:200:GLN:CG	2.48	0.43
2:B:337:ARG:HD3	5:K:173:TYR:OH	2.18	0.43
3:I:137:TYR:CE2	3:I:141:ILE:HD11	2.54	0.43
3:I:183:PHE:CD2	3:I:185:ASN:ND2	2.86	0.43
6:L:33:ARG:HD3	6:L:65:ASP:H	1.84	0.43
8:H:349:TRP:CZ3	8:H:373:PHE:HE2	2.31	0.43
8:H:360:ARG:HG2	8:H:362:LYS:H	1.82	0.43
1:A:1168:ILE:O	1:A:1169:TYR:CD1	2.72	0.43
1:A:1580:GLY:HA3	3:I:389:ASN:ND2	2.33	0.43
2:B:222:GLY:N	2:B:237:CYS:O	2.44	0.43
3:I:143:ILE:HG23	3:I:149:TYR:CE2	2.52	0.43
3:I:380:ARG:CZ	3:I:380:ARG:CB	2.96	0.43
4:G:127:ASP:C	4:G:127:ASP:OD1	2.57	0.43
5:K:146:GLU:C	5:K:148:LYS:H	2.21	0.43
8:H:769:TYR:HE1	8:H:774:LEU:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:109:U:H3'	25:D:110:U:C5'	2.47	0.43
26:E:151:G:H4'	26:E:152:A:O4'	2.18	0.43
27:F:31:G:C6	27:F:32:G:C5	3.06	0.43
27:F:83:C:H4'	27:F:84:A:OP1	2.18	0.43
27:F:102:C:N4	27:F:103:A:H62	2.16	0.43
1:A:484:PHE:HB3	1:A:485:PRO:HD3	2.00	0.43
1:A:839:HIS:CE1	27:F:96:U:C6	3.07	0.43
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.76	0.43
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.34	0.43
1:A:2076:GLN:OE1	5:K:283:ASN:O	2.37	0.43
2:B:382:ASP:OD1	2:B:382:ASP:N	2.50	0.43
3:I:93:LYS:CE	3:I:93:LYS:CA	2.95	0.43
3:I:416:SER:HA	3:I:419:GLN:OE1	2.19	0.43
4:G:153:ILE:HG23	4:G:154:PRO:HD2	1.99	0.43
4:G:529:ILE:O	4:G:533:LEU:N	2.52	0.43
4:G:666:ILE:N	4:G:668:HIS:CD2	2.86	0.43
4:G:697:LEU:C	4:G:699:PRO:HD3	2.39	0.43
5:K:382:VAL:HG11	5:K:392:TYR:CE2	2.53	0.43
8:H:132:ARG:NH1	8:H:132:ARG:CG	2.73	0.43
8:H:364:PHE:CG	8:H:369:LYS:CD	2.94	0.43
8:H:571:TYR:CB	8:H:575:ALA:HB2	2.49	0.43
8:H:964:ARG:NH1	8:H:968:MET:CE	2.82	0.43
26:E:150:G:C2	26:E:152:A:H4'	2.54	0.43
29:E:201:M7M:HBX	29:E:201:M7M:HNBN	1.82	0.43
1:A:222:ILE:HB	1:A:266:LEU:HD11	2.01	0.43
1:A:287:GLU:HB2	1:A:288:GLU:H	1.64	0.43
1:A:755:ASP:CG	1:A:819:LYS:HE3	2.39	0.43
1:A:960:THR:HG21	3:I:455:PHE:CZ	2.54	0.43
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	2.01	0.43
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	2.01	0.43
2:B:73:ARG:O	2:B:76:LEU:HB2	2.19	0.43
2:B:202:LEU:HD12	2:B:202:LEU:N	2.33	0.43
5:K:337:TYR:HE2	5:K:434:ASP:HA	1.82	0.43
6:L:25:ARG:NH1	6:L:25:ARG:HG3	2.34	0.43
8:H:355:HIS:C	8:H:356:LYS:CG	2.86	0.43
8:H:379:ILE:O	8:H:383:LYS:CG	2.65	0.43
27:F:174:G:C2	27:F:176:A:H4'	2.54	0.43
1:A:207:ARG:NH1	1:A:299:LYS:HG3	2.34	0.43
1:A:883:PHE:O	1:A:887:VAL:HG23	2.19	0.43
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.19	0.43
1:A:1451:PHE:O	1:A:1455:GLN:OE1	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1647:GLN:O	1:A:1650:ARG:HG3	2.17	0.43
1:A:1657:ILE:O	1:A:1661:ILE:CG1	2.64	0.43
1:A:1992:TYR:HD2	1:A:2004:ALA:HB1	1.83	0.43
2:B:208:GLN:HA	2:B:209:PRO:HA	1.66	0.43
5:K:142:LEU:HD13	5:K:142:LEU:HA	1.74	0.43
5:K:146:GLU:O	5:K:149:PHE:HD2	2.01	0.43
6:L:33:ARG:HD3	6:L:65:ASP:CB	2.49	0.43
8:H:488:ILE:HD11	8:H:560:GLN:HG3	1.99	0.43
8:H:858:LEU:HB3	8:H:937:TRP:CB	2.48	0.43
27:F:62:G:H2'	27:F:63:C:C6	2.54	0.43
27:F:98:U:O2'	27:F:99:U:P	2.76	0.43
1:A:410:ILE:N	1:A:410:ILE:CD1	2.82	0.43
1:A:617:ASN:ND2	27:F:99:U:O2'	2.46	0.43
1:A:1087:ASN:ND2	3:I:274:THR:OG1	2.45	0.43
1:A:1511:ARG:HG3	1:A:1511:ARG:HH21	1.81	0.43
2:B:458:ASP:OD2	2:B:462:LYS:NZ	2.52	0.43
3:I:321:LYS:O	3:I:324:ASP:O	2.35	0.43
3:I:429:ARG:HH11	3:I:429:ARG:CG	2.32	0.43
4:G:127:ASP:OD1	4:G:128:PHE:N	2.52	0.43
8:H:114:PRO:O	8:H:115:LYS:HG3	2.18	0.43
8:H:373:PHE:HE1	8:H:377:ILE:HG21	1.84	0.43
8:H:598:ILE:CG2	8:H:933:TRP:CH2	3.01	0.43
24:C:6:U:O2	24:C:6:U:O2'	2.28	0.43
26:E:6:U:H2'	26:E:7:A:C8	2.53	0.43
1:A:291:LYS:H	1:A:291:LYS:HZ2	1.67	0.42
1:A:294:ASN:HB2	1:A:300:LYS:HB2	2.01	0.42
1:A:1020:ILE:HD12	1:A:1020:ILE:H	1.84	0.42
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.19	0.42
1:A:1468:ALA:C	1:A:1473:ARG:O	2.57	0.42
2:B:446:SER:OG	2:B:451:PHE:CG	2.69	0.42
3:I:120:TYR:OH	3:I:141:ILE:HG23	2.19	0.42
3:I:417:LEU:HB3	4:G:226:MET:HE3	2.00	0.42
4:G:702:PRO:HA	4:G:739:PHE:CZ	2.54	0.42
5:K:155:LYS:HA	5:K:158:ILE:HG12	1.99	0.42
6:L:8:GLN:HG2	6:L:61:LEU:HB2	2.01	0.42
8:H:862:TYR:N	8:H:862:TYR:CD1	2.87	0.42
8:H:884:ARG:HD3	8:H:884:ARG:O	2.19	0.42
8:H:940:VAL:HA	8:H:941:PRO:HD3	1.89	0.42
1:A:268:LEU:HD12	1:A:268:LEU:O	2.19	0.42
1:A:689:TYR:CD1	1:A:689:TYR:C	2.93	0.42
1:A:770:MET:SD	4:G:119:TRP:HZ3	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:883:PHE:CD1	3:I:177:MET:SD	3.13	0.42
1:A:940:ILE:O	1:A:943:ALA:HB3	2.18	0.42
1:A:1615:ASN:ND2	1:A:1634:LEU:HD23	2.31	0.42
2:B:247:GLN:HB2	2:B:258:LEU:HD21	1.99	0.42
2:B:349:SER:O	2:B:350:LYS:HG3	2.19	0.42
2:B:353:TYR:HE2	2:B:395:ILE:HG21	1.84	0.42
2:B:422:TYR:CD1	2:B:429:LYS:HA	2.54	0.42
4:G:245:ILE:HG23	4:G:280:GLU:HG2	2.01	0.42
8:H:129:ILE:N	8:H:129:ILE:CD1	2.73	0.42
8:H:160:ARG:HA	8:H:160:ARG:HD2	1.70	0.42
8:H:189:LEU:CD1	8:H:190:SER:O	2.66	0.42
8:H:236:LEU:HD23	8:H:266:VAL:HG21	2.00	0.42
8:H:305:SER:C	8:H:307:ILE:N	2.72	0.42
8:H:408:LEU:HD21	8:H:427:LEU:HD22	2.01	0.42
8:H:801:TRP:CD1	8:H:801:TRP:C	2.92	0.42
8:H:828:ASP:O	8:H:829:VAL:C	2.57	0.42
25:D:62:A:C2	26:E:58:G:N1	2.87	0.42
27:F:73:U:H2'	27:F:74:U:C6	2.54	0.42
1:A:396:ARG:O	1:A:398:VAL:HG23	2.19	0.42
1:A:901:PRO:HG3	1:A:998:TYR:CD2	2.54	0.42
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.18	0.42
2:B:123:PHE:CD1	2:B:123:PHE:C	2.93	0.42
2:B:321:LEU:CD2	2:B:335:ASP:HA	2.49	0.42
3:I:376:LYS:HE2	26:E:56:U:OP2	2.20	0.42
3:I:400:VAL:O	3:I:400:VAL:HG23	2.19	0.42
4:G:264:ILE:HG22	4:G:281:ASN:OD1	2.19	0.42
4:G:364:PHE:O	4:G:368:SER:N	2.38	0.42
5:K:323:ARG:O	5:K:326:ALA:HB3	2.19	0.42
5:K:333:LYS:O	5:K:333:LYS:CE	2.67	0.42
8:H:124:LEU:HD12	8:H:124:LEU:O	2.18	0.42
8:H:470:ALA:N	8:H:577:LEU:O	2.48	0.42
8:H:483:TRP:CH2	8:H:565:LYS:CG	3.01	0.42
8:H:933:TRP:HB2	8:H:934:HIS:CE1	2.55	0.42
1:A:703:PHE:CD1	1:A:703:PHE:C	2.93	0.42
1:A:1206:CYS:HB2	1:A:1266:GLU:OE1	2.19	0.42
1:A:1846:ASN:CA	1:A:1885:LYS:NZ	2.79	0.42
2:B:119:PHE:CD1	2:B:119:PHE:C	2.93	0.42
2:B:315:PHE:CE1	2:B:322:VAL:HB	2.54	0.42
3:I:135:LEU:HD21	3:I:136:GLN:HG3	2.01	0.42
3:I:168:THR:O	3:I:172:ILE:HD12	2.19	0.42
3:I:385:ARG:CZ	4:G:153:ILE:HD11	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:134:ARG:CZ	4:G:134:ARG:CB	2.96	0.42
4:G:275:SER:O	4:G:279:LEU:HG	2.19	0.42
5:K:443:LYS:HG2	5:K:444:VAL:H	1.84	0.42
8:H:167:ASN:HD22	8:H:168:VAL:N	2.16	0.42
1:A:1559:HIS:ND1	1:A:1613:THR:HG21	2.34	0.42
1:A:1697:SER:CB	1:A:1759:TYR:CE1	3.02	0.42
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.40	0.42
2:B:112:PRO:O	2:B:113:ALA:HB3	2.19	0.42
2:B:125:ILE:HA	2:B:128:SER:OG	2.20	0.42
4:G:846:PHE:CD1	4:G:859:LEU:CD2	2.88	0.42
5:K:164:HIS:O	5:K:164:HIS:CG	2.71	0.42
5:K:309:LEU:HD23	5:K:309:LEU:HA	1.79	0.42
8:H:234:LEU:HD23	8:H:234:LEU:N	2.34	0.42
8:H:510:ARG:HD3	8:H:591:PHE:CZ	2.54	0.42
8:H:652:MET:HA	8:H:655:LEU:HD12	2.01	0.42
8:H:957:ALA:HB2	8:H:965:ASP:OD2	2.19	0.42
27:F:95:C:C1'	27:F:96:U:OP1	2.67	0.42
1:A:294:ASN:C	1:A:294:ASN:ND2	2.73	0.42
1:A:410:ILE:CG1	8:H:276:ASP:OD1	2.65	0.42
1:A:779:ALA:CA	1:A:782:ILE:HD12	2.23	0.42
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.53	0.42
2:B:124:LEU:HD22	2:B:274:HIS:HE1	1.84	0.42
2:B:320:SER:O	2:B:321:LEU:HD23	2.20	0.42
3:I:95:LEU:O	3:I:98:PHE:HB2	2.20	0.42
3:I:227:PRO:HG3	3:I:325:ARG:HG2	2.02	0.42
8:H:968:MET:CE	8:H:971:ARG:HG3	2.49	0.42
1:A:173:LEU:CD1	1:A:712:LEU:HD12	2.50	0.42
1:A:939:LEU:HA	1:A:939:LEU:HD23	1.85	0.42
1:A:1335:TRP:HZ3	1:A:1400:ILE:O	2.03	0.42
1:A:1344:THR:HG22	1:A:1347:ARG:HH21	1.83	0.42
1:A:1586:GLN:HB3	1:A:1595:ARG:HH12	1.84	0.42
4:G:251:GLU:CD	4:G:260:ALA:HB2	2.37	0.42
5:K:143:GLU:HA	5:K:145:HIS:HE1	1.84	0.42
6:L:33:ARG:HD3	6:L:65:ASP:OD1	2.17	0.42
8:H:500:ARG:HD3	8:H:534:THR:OG1	2.19	0.42
8:H:964:ARG:HA	8:H:964:ARG:HD2	1.77	0.42
24:C:-1:A:O2'	24:C:0:U:C6	2.73	0.42
26:E:26:A:O2'	26:E:27:U:P	2.78	0.42
1:A:193:TYR:CZ	1:A:558:GLN:HB3	2.55	0.42
1:A:370:ILE:HD12	8:H:953:LYS:HD2	2.00	0.42
1:A:908:ASP:HB3	1:A:951:LEU:CD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:ASN:C	1:A:976:GLN:H	2.23	0.42
1:A:1274:ARG:O	1:A:1277:GLU:OE1	2.37	0.42
1:A:1629:LEU:CD2	1:A:1629:LEU:N	2.82	0.42
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	2.00	0.42
1:A:2066:LYS:HB2	1:A:2067:TYR:CD1	2.54	0.42
2:B:159:LEU:N	2:B:159:LEU:HD23	2.34	0.42
2:B:275:PRO:O	2:B:276:SER:C	2.57	0.42
2:B:418:LEU:CD2	2:B:434:ALA:HB2	2.50	0.42
3:I:93:LYS:HD2	3:I:93:LYS:N	2.34	0.42
3:I:102:ILE:HB	3:I:103:PRO:CD	2.48	0.42
4:G:15:TYR:O	4:G:15:TYR:CD1	2.72	0.42
4:G:508:TRP:O	4:G:512:ASP:N	2.52	0.42
4:G:678:TYR:HD1	4:G:678:TYR:HA	1.74	0.42
8:H:271:ASP:OD2	8:H:318:LEU:HG	2.20	0.42
1:A:1629:LEU:HD23	1:A:1630:THR:HG22	1.98	0.42
1:A:1652:HIS:CD2	1:A:1652:HIS:N	2.87	0.42
1:A:1715:SER:HB2	1:A:1719:GLU:OE1	2.19	0.42
1:A:2075:THR:CG2	1:A:2076:GLN:N	2.82	0.42
1:A:2079:ILE:HG22	1:A:2083:ILE:CD1	2.44	0.42
1:A:2388:ARG:O	1:A:2389:PRO:C	2.57	0.42
2:B:345:LEU:HB3	2:B:376:TRP:CH2	2.54	0.42
3:I:123:ARG:HB2	3:I:189:LEU:HD11	2.02	0.42
3:I:424:THR:CG2	3:I:425:SER:N	2.83	0.42
4:G:282:ILE:HG12	4:G:295:LEU:HB3	2.01	0.42
4:G:349:ALA:O	4:G:353:GLN:N	2.48	0.42
4:G:671:PHE:CZ	4:G:693:SER:OG	2.64	0.42
5:K:280:VAL:HG12	5:K:282:GLU:H	1.85	0.42
5:K:350:PRO:CB	5:K:353:ARG:HD2	2.48	0.42
8:H:449:PHE:O	8:H:449:PHE:HD1	2.02	0.42
8:H:483:TRP:CZ3	8:H:565:LYS:HG3	2.54	0.42
8:H:572:ILE:HD12	8:H:572:ILE:C	2.40	0.42
1:A:276:VAL:CG1	1:A:310:ASN:HB2	2.49	0.42
1:A:465:GLU:HG3	8:H:387:TYR:OH	2.20	0.42
1:A:843:THR:HG21	6:L:108:ASP:CB	2.49	0.42
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.78	0.42
1:A:1453:ASP:O	1:A:1456:ARG:CG	2.58	0.42
1:A:1851:PHE:HB2	1:A:1882:LEU:HD13	2.01	0.42
1:A:2026:LEU:HD11	1:A:2040:TRP:HZ3	1.85	0.42
4:G:19:ILE:HD12	4:G:20:GLY:HA2	2.02	0.42
4:G:252:GLU:HG3	4:G:284:LEU:CD1	2.50	0.42
4:G:281:ASN:HD22	4:G:281:ASN:C	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:78:ASP:OD2	6:L:79:PRO:HD2	2.20	0.42
8:H:475:THR:HG22	8:H:483:TRP:O	2.20	0.42
8:H:798:GLY:O	8:H:802:ALA:N	2.53	0.42
8:H:968:MET:CE	8:H:968:MET:N	2.82	0.42
1:A:358:ARG:HD3	1:A:360:GLU:HB2	2.00	0.41
1:A:1390:THR:HA	1:A:1391:PRO:HD3	1.75	0.41
2:B:171:GLN:CD	2:B:172:LEU:H	2.23	0.41
2:B:280:ILE:N	2:B:292:TRP:O	2.45	0.41
2:B:445:ILE:HG12	2:B:446:SER:N	2.35	0.41
3:I:429:ARG:HH11	3:I:429:ARG:CA	2.33	0.41
4:G:83:LYS:C	4:G:85:ARG:N	2.73	0.41
5:K:146:GLU:CA	5:K:149:PHE:CD2	2.91	0.41
7:M:95:ARG:NH1	7:M:95:ARG:CG	2.73	0.41
9:N:1610:LEU:O	9:N:1660:ALA:O	2.38	0.41
27:F:48:G:H2'	27:F:49:U:C6	2.55	0.41
1:A:474:LYS:C	1:A:474:LYS:CD	2.89	0.41
1:A:703:PHE:HD1	1:A:703:PHE:C	2.23	0.41
1:A:774:ILE:CG2	1:A:777:LYS:NZ	2.83	0.41
1:A:958:LEU:HD22	1:A:1081:TYR:CD2	2.56	0.41
2:B:218:VAL:HG23	2:B:240:ASP:CG	2.40	0.41
2:B:335:ASP:OD1	2:B:337:ARG:CD	2.58	0.41
3:I:390:ARG:O	3:I:412:MET:HG2	2.20	0.41
4:G:397:GLN:O	4:G:401:ILE:N	2.38	0.41
5:K:300:GLN:OE1	5:K:300:GLN:CA	2.68	0.41
6:L:39:CYS:SG	6:L:79:PRO:O	2.78	0.41
6:L:59:ILE:HG22	6:L:60:TYR:N	2.33	0.41
6:L:74:TYR:CG	6:L:83:MET:HE1	2.55	0.41
8:H:159:LYS:H	8:H:159:LYS:HG2	1.53	0.41
8:H:191:ILE:O	8:H:224:GLU:OE1	2.38	0.41
8:H:372:THR:O	8:H:373:PHE:C	2.58	0.41
8:H:656:LEU:HD13	8:H:670:ILE:HD13	2.02	0.41
8:H:933:TRP:C	8:H:934:HIS:CG	2.92	0.41
27:F:77:A:C4'	27:F:78:A:C5'	2.93	0.41
1:A:217:TRP:NE1	1:A:703:PHE:CE1	2.89	0.41
1:A:276:VAL:HG11	1:A:310:ASN:HB2	2.01	0.41
1:A:286:LEU:HD22	1:A:292:LYS:CB	2.47	0.41
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.55	0.41
1:A:594:ASP:C	1:A:594:ASP:OD1	2.59	0.41
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.20	0.41
1:A:1626:GLN:HE22	1:A:1694:MET:HG2	1.84	0.41
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:TRP:HB2	2:B:313:LEU:HD23	2.01	0.41
2:B:316:GLN:OE1	2:B:321:LEU:HB2	2.20	0.41
3:I:92:ILE:HB	3:I:93:LYS:HD2	2.01	0.41
3:I:441:MET:SD	3:I:444:ARG:NH2	2.93	0.41
4:G:115:THR:O	4:G:119:TRP:HD1	2.03	0.41
8:H:108:GLN:OE1	8:H:109:LEU:HD23	2.19	0.41
8:H:507:SER:C	8:H:509:SER:N	2.71	0.41
8:H:571:TYR:H	8:H:571:TYR:HD1	1.69	0.41
8:H:879:LEU:O	8:H:883:ARG:HG2	2.20	0.41
27:F:32:G:O2'	27:F:33:U:P	2.79	0.41
27:F:45:A:N3	27:F:46:C:C5	2.87	0.41
1:A:672:LYS:C	1:A:674:MET:N	2.72	0.41
1:A:1115:GLN:CA	1:A:1115:GLN:HE21	2.33	0.41
1:A:1216:ILE:HG21	1:A:1254:ASN:ND2	2.36	0.41
1:A:1697:SER:OG	1:A:1759:TYR:CE1	2.64	0.41
1:A:1738:LEU:HD23	1:A:1777:ILE:HB	2.01	0.41
1:A:2020:GLU:HA	1:A:2023:LYS:HB2	2.01	0.41
3:I:329:LEU:HD12	3:I:333:TRP:CH2	2.55	0.41
5:K:354:PHE:CZ	5:K:358:MET:SD	3.14	0.41
5:K:362:GLU:HG2	29:E:201:M7M:NBN	2.35	0.41
7:M:126:ILE:HG22	7:M:126:ILE:O	2.21	0.41
8:H:177:TYR:O	8:H:178:LEU:CB	2.69	0.41
8:H:482:GLU:HG2	8:H:482:GLU:O	2.20	0.41
8:H:608:GLN:NE2	8:H:641:GLU:CG	2.61	0.41
1:A:458:PHE:O	1:A:458:PHE:CD1	2.74	0.41
1:A:484:PHE:N	1:A:485:PRO:CD	2.83	0.41
1:A:1204:ARG:HG3	1:A:1259:LEU:HD13	2.00	0.41
1:A:1417:GLN:OE1	1:A:1422:ILE:CD1	2.65	0.41
1:A:1678:ILE:HD13	1:A:1703:MET:CE	2.50	0.41
2:B:174:SER:OG	2:B:175:THR:N	2.54	0.41
2:B:316:GLN:HE21	2:B:318:ASP:H	1.67	0.41
2:B:362:TYR:CB	2:B:379:ARG:HD2	2.48	0.41
3:I:141:ILE:HG21	3:I:197:ILE:HG23	2.03	0.41
5:K:159:TYR:CE2	5:K:163:ASN:ND2	2.89	0.41
5:K:386:GLU:HG2	5:K:390:LYS:HE2	2.01	0.41
8:H:193:LEU:CB	8:H:214:ASP:O	2.67	0.41
8:H:325:LYS:HD2	8:H:325:LYS:HA	1.92	0.41
8:H:327:PHE:HE1	8:H:331:TYR:CD2	2.39	0.41
8:H:467:THR:HG23	8:H:579:SER:O	2.21	0.41
8:H:578:TYR:C	8:H:578:TYR:HD1	2.24	0.41
8:H:950:PHE:CD1	8:H:951:ILE:N	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:63:C:H2'	27:F:64:C:C6	2.55	0.41
1:A:294:ASN:ND2	27:F:32:G:OP1	2.53	0.41
1:A:1054:LEU:HD23	1:A:1054:LEU:HA	1.86	0.41
1:A:1175:GLU:O	1:A:1179:GLY:N	2.49	0.41
1:A:1312:PHE:CD1	1:A:1342:LEU:HD12	2.55	0.41
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.56	0.41
1:A:1405:ILE:HB	1:A:1437:ILE:HD12	2.03	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:O	2.74	0.41
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.48	0.41
1:A:1582:GLU:OE2	1:A:1586:GLN:NE2	2.53	0.41
1:A:1594:GLN:NE2	1:A:1594:GLN:CA	2.83	0.41
2:B:405:ASP:OD2	2:B:408:LYS:HD2	2.21	0.41
2:B:456:GLY:C	2:B:458:ASP:N	2.71	0.41
4:G:255:ARG:O	4:G:256:LYS:CB	2.68	0.41
5:K:159:TYR:CZ	5:K:163:ASN:ND2	2.88	0.41
7:M:5:ASN:HD21	7:M:61:ILE:HG21	1.85	0.41
7:M:58:CYS:SG	7:M:98:ILE:HG21	2.60	0.41
8:H:362:LYS:CG	8:H:363:PRO:HD2	2.50	0.41
8:H:461:LYS:HZ2	8:H:464:PRO:CB	2.34	0.41
8:H:475:THR:CG2	8:H:483:TRP:O	2.68	0.41
25:D:87:U:O5'	25:D:87:U:H6	2.04	0.41
27:F:49:U:H2'	27:F:50:G:H8	1.84	0.41
1:A:166:LYS:C	1:A:169:PRO:HD2	2.39	0.41
1:A:473:THR:HG23	1:A:474:LYS:N	2.35	0.41
1:A:778:LYS:HE2	1:A:778:LYS:CA	2.50	0.41
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.21	0.41
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.36	0.41
1:A:1308:GLU:OE1	1:A:1346:PHE:CZ	2.70	0.41
2:B:177:PRO:N	2:B:195:TRP:HD1	2.18	0.41
2:B:408:LYS:O	2:B:424:SER:CB	2.68	0.41
4:G:677:ILE:O	4:G:681:MET:HG2	2.20	0.41
5:K:158:ILE:HG13	5:K:159:TYR:N	2.34	0.41
5:K:159:TYR:CD1	5:K:163:ASN:ND2	2.76	0.41
8:H:352:VAL:HG13	8:H:352:VAL:O	2.21	0.41
8:H:365:GLU:O	8:H:366:ASN:HB2	2.20	0.41
8:H:792:LYS:O	8:H:796:ILE:N	2.43	0.41
25:D:49:A:N6	25:D:50:G:C6	2.88	0.41
1:A:258:ILE:HG21	1:A:640:ARG:HG3	2.03	0.41
1:A:691:PHE:CD1	1:A:691:PHE:O	2.73	0.41
1:A:750:LEU:HD23	1:A:752:ALA:HB3	2.03	0.41
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1144:PHE:HZ	1:A:1162:THR:HG21	1.85	0.41
1:A:1195:PHE:HB3	1:A:1217:ARG:HH11	1.82	0.41
1:A:1795:LYS:N	1:A:1796:PRO:HD2	2.36	0.41
2:B:196:ALA:C	2:B:219:GLY:O	2.58	0.41
3:I:259:ILE:HD13	3:I:259:ILE:HG21	1.76	0.41
3:I:321:LYS:HG3	3:I:324:ASP:O	2.21	0.41
3:I:358:ILE:CG2	3:I:359:PRO:N	2.84	0.41
4:G:19:ILE:CD1	4:G:20:GLY:N	2.81	0.41
4:G:669:LYS:O	4:G:673:GLN:HG3	2.21	0.41
4:G:804:ASP:OD1	4:G:805:HIS:N	2.53	0.41
4:G:851:ARG:C	4:G:852:LEU:CD1	2.89	0.41
5:K:303:LEU:C	5:K:303:LEU:CD2	2.84	0.41
5:K:330:ASN:HD22	5:K:331:VAL:HG23	1.85	0.41
6:L:95:PHE:HD1	6:L:133:SER:CB	2.33	0.41
8:H:132:ARG:O	8:H:133:ILE:CG1	2.66	0.41
8:H:178:LEU:N	8:H:178:LEU:CD2	2.83	0.41
8:H:386:SER:O	8:H:390:SER:CB	2.69	0.41
24:C:9:G:O5'	24:C:9:G:H8	2.04	0.41
25:D:48:C:H2'	25:D:48:C:O2	2.20	0.41
27:F:46:C:H2'	27:F:47:U:C6	2.55	0.41
1:A:331:PHE:CD2	1:A:509:HIS:CE1	3.09	0.41
1:A:767:LEU:HD21	1:A:779:ALA:HB1	2.00	0.41
1:A:882:ILE:HD13	1:A:1238:LEU:HD21	2.03	0.41
1:A:1067:ASN:HD22	1:A:1067:ASN:HA	1.62	0.41
1:A:1174:PHE:HD2	1:A:1222:LEU:HD11	1.85	0.41
1:A:1183:THR:CG2	1:A:1184:ASP:N	2.83	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:C	2.94	0.41
1:A:1464:LYS:HZ2	1:A:1479:GLU:HB3	1.86	0.41
1:A:1594:GLN:HE21	1:A:1594:GLN:CA	2.33	0.41
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.56	0.41
2:B:68:ASP:OD1	2:B:69:VAL:N	2.53	0.41
2:B:267:ARG:HG3	2:B:285:HIS:HD2	1.82	0.41
2:B:275:PRO:HG3	2:B:319:GLY:HA2	2.02	0.41
2:B:383:GLU:OE1	2:B:383:GLU:HA	2.21	0.41
2:B:419:ILE:HG21	2:B:419:ILE:HD13	1.89	0.41
3:I:40:LYS:O	3:I:44:PHE:N	2.44	0.41
3:I:271:GLU:O	3:I:272:LEU:HB3	2.19	0.41
4:G:284:LEU:HD22	4:G:284:LEU:N	2.36	0.41
6:L:33:ARG:CD	6:L:65:ASP:OD2	2.54	0.41
7:M:36:GLY:CA	26:E:30:G:O2'	2.69	0.41
8:H:449:PHE:CD1	8:H:453:THR:HG23	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:578:TYR:CE2	8:H:589:LEU:CD1	3.04	0.41
8:H:586:MET:O	8:H:586:MET:SD	2.79	0.41
8:H:615:LEU:HB3	8:H:616:PRO:HD3	2.02	0.41
8:H:808:LEU:HD11	8:H:855:PRO:HB2	2.01	0.41
8:H:906:VAL:HA	8:H:907:PRO:HD3	1.97	0.41
8:H:908:VAL:HG13	8:H:909:ILE:N	2.34	0.41
8:H:950:PHE:CG	8:H:951:ILE:N	2.89	0.41
25:D:49:A:C2'	25:D:50:G:O5'	2.69	0.41
26:E:2:U:C5	26:E:3:C:H5	2.32	0.41
27:F:96:U:P	27:F:96:U:O4'	2.79	0.41
1:A:160:ALA:HB1	1:A:194:HIS:HE1	1.79	0.41
1:A:294:ASN:OD1	1:A:300:LYS:HE3	2.18	0.41
1:A:795:ALA:HA	1:A:1095:MET:HE2	1.94	0.41
1:A:863:ARG:NH2	1:A:1059:GLU:HB3	2.36	0.41
2:B:235:ILE:CD1	2:B:280:ILE:HG21	2.51	0.41
2:B:418:LEU:HD23	2:B:434:ALA:HB2	2.02	0.41
5:K:158:ILE:HG13	5:K:159:TYR:H	1.86	0.41
5:K:427:THR:OG1	5:K:428:TRP:N	2.54	0.41
8:H:116:THR:CG2	8:H:158:HIS:HD2	2.16	0.41
8:H:117:ARG:NE	8:H:156:ASP:O	2.54	0.41
8:H:486:VAL:HG22	8:H:487:ARG:N	2.36	0.41
8:H:576:THR:CG2	8:H:592:PHE:H	2.14	0.41
25:D:87:U:H3'	25:D:87:U:H6	1.86	0.41
1:A:543:ASN:ND2	1:A:544:LYS:HB2	2.36	0.40
1:A:867:ILE:HG22	1:A:867:ILE:O	2.21	0.40
1:A:1481:GLU:OE2	4:G:256:LYS:HD3	2.20	0.40
1:A:1623:PHE:CZ	24:C:5:G:C4	3.09	0.40
6:L:9:LEU:HD11	6:L:60:TYR:CB	2.51	0.40
6:L:97:THR:HG23	6:L:99:ASN:H	1.86	0.40
8:H:122:TYR:HD1	8:H:122:TYR:O	2.05	0.40
8:H:123:MET:SD	8:H:209:MET:SD	3.19	0.40
8:H:164:MET:HG2	8:H:175:LEU:CD1	2.50	0.40
8:H:305:SER:O	8:H:307:ILE:N	2.55	0.40
1:A:175:LEU:HD12	1:A:564:TRP:HE1	1.86	0.40
1:A:574:GLN:HA	1:A:574:GLN:OE1	2.21	0.40
1:A:1029:THR:HG22	1:A:1260:PHE:HZ	1.85	0.40
1:A:1049:LEU:HD11	1:A:1258:LEU:HD21	2.04	0.40
1:A:1203:ASN:N	1:A:1203:ASN:OD1	2.54	0.40
2:B:162:MET:HG3	2:B:421:VAL:HG11	2.03	0.40
2:B:366:THR:O	2:B:373:ILE:HA	2.22	0.40
4:G:302:PHE:O	4:G:303:ASN:OD1	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:178:LEU:HD13	8:H:194:ASN:O	2.20	0.40
8:H:187:ARG:HD3	8:H:650:LEU:HD11	2.02	0.40
8:H:589:LEU:O	8:H:589:LEU:HG	2.20	0.40
8:H:737:ILE:HG12	8:H:768:PHE:HB3	2.03	0.40
26:E:1:A:C6	29:E:201:M7M:HBZB	2.56	0.40
1:A:141:LYS:CA	1:A:144:ASN:CG	2.89	0.40
1:A:1182:LEU:HD23	1:A:1182:LEU:HA	1.91	0.40
1:A:1653:LEU:CD2	1:A:1815:LEU:HD23	2.48	0.40
3:I:161:LEU:HB3	3:I:167:LEU:HD12	2.03	0.40
3:I:222:ILE:HD13	3:I:222:ILE:HA	1.89	0.40
4:G:278:TRP:CE2	4:G:298:THR:HB	2.52	0.40
6:L:25:ARG:HB2	6:L:25:ARG:NH1	2.27	0.40
6:L:34:LYS:HD2	6:L:34:LYS:N	2.35	0.40
8:H:500:ARG:CD	8:H:534:THR:CB	2.88	0.40
8:H:796:ILE:HD12	8:H:796:ILE:HA	1.87	0.40
8:H:951:ILE:CB	8:H:952:PRO:HD2	2.30	0.40
25:D:62:A:C2'	25:D:63:G:C5'	2.98	0.40
27:F:103:A:C4	27:F:104:G:C8	3.10	0.40
1:A:287:GLU:H	1:A:287:GLU:HG3	1.47	0.40
1:A:297:SER:HB2	27:F:32:G:P	2.59	0.40
1:A:510:PRO:O	1:A:514:TYR:CE1	2.74	0.40
1:A:766:ILE:HG21	1:A:782:ILE:HG21	2.03	0.40
1:A:1790:TRP:CD1	1:A:1795:LYS:HE3	2.56	0.40
1:A:1887:GLY:O	1:A:1990:ASN:HA	2.21	0.40
2:B:173:VAL:HA	2:B:200:GLN:OE1	2.20	0.40
2:B:311:PHE:HE2	7:M:126:ILE:HD13	1.84	0.40
3:I:248:VAL:HG11	3:I:317:ASP:HB3	2.03	0.40
3:I:415:THR:O	3:I:418:GLN:N	2.52	0.40
5:K:339:CYS:SG	5:K:340:LYS:N	2.94	0.40
8:H:135:ASN:ND2	8:H:487:ARG:HH21	2.18	0.40
8:H:189:LEU:HD12	8:H:190:SER:O	2.22	0.40
8:H:247:PHE:HD1	8:H:903:ARG:NH1	2.18	0.40
8:H:586:MET:C	8:H:586:MET:SD	3.00	0.40
27:F:43:G:N3	27:F:44:A:N7	2.69	0.40
27:F:77:A:C1'	27:F:78:A:H5'	2.45	0.40
1:A:143:ILE:HA	1:A:146:HIS:HB3	2.03	0.40
1:A:168:LEU:N	1:A:169:PRO:HD2	2.36	0.40
1:A:298:TYR:CE1	1:A:493:MET:CE	3.00	0.40
1:A:305:LEU:N	1:A:306:PRO:HD2	2.36	0.40
1:A:770:MET:CE	1:A:778:LYS:HB3	2.51	0.40
3:I:402:ASP:O	3:I:403:SER:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:256:LYS:O	4:G:257:PHE:HB3	2.21	0.40
5:K:244:LEU:HD23	5:K:244:LEU:HA	1.69	0.40
8:H:375:GLU:HG2	8:H:376:PHE:CE1	2.57	0.40
8:H:942:GLY:CA	8:H:960:ASN:O	2.70	0.40
25:D:49:A:C3'	25:D:50:G:C5'	2.99	0.40
27:F:94:C:H5''	27:F:94:C:C6	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2166/2413 (90%)	2019 (93%)	110 (5%)	37 (2%)	9	43
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	7	40
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	10	46
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	6	38
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	8	42
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	10	46
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	9	44
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	6	37
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	25	62
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5	36
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5	36
11	O	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
11	S	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
12	P	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11	46
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Q	85/110 (77%)	82 (96%)	3 (4%)	0	100	100
13	U	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
14	V	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
14	Y	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
15	W	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	25
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	2	25
16	X	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
16	a	65/77 (84%)	59 (91%)	6 (9%)	0	100	100
17	b	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
18	c	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
19	d	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
20	e	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
21	f	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	11	46
22	g	62/115 (54%)	62 (100%)	0	0	100	100
23	h	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
All	All	8236/10574 (78%)	7611 (92%)	505 (6%)	120 (2%)	14	46

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
1	A	157	ASP
1	A	239	PHE
1	A	240	PRO
1	A	259	GLU
1	A	264	ILE
1	A	287	GLU
1	A	546	LYS
1	A	645	ASP
1	A	699	PRO
1	A	1044	GLY
1	A	1403	SER
2	B	113	ALA
2	B	171	GLN
2	B	276	SER
2	B	395	ILE
3	I	266	LYS

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Mol	Chain	Res	Type
3	I	328	VAL
3	I	434	GLN
4	G	10	GLU
4	G	287	SER
4	G	700	ASN
5	K	147	ASP
8	H	115	LYS
8	H	133	ILE
8	H	356	LYS
8	H	364	PHE
8	H	431	GLN
8	H	704	PRO
8	H	829	VAL
8	H	884	ARG
8	H	952	PRO
9	N	766	ILE
9	N	1200	PRO
1	A	156	THR
1	A	554	THR
1	A	803	GLY
1	A	1088	VAL
2	B	449	SER
3	I	152	ASN
4	G	112	ALA
5	K	220	PRO
5	K	332	GLU
8	H	146	LYS
8	H	350	GLY
8	H	366	ASN
8	H	367	VAL
8	H	508	GLU
9	N	1693	HIS
10	R	40	MET
12	T	12	ASN
15	W	24	ASN
15	W	49	PHE
10	J	40	MET
12	P	12	ASN
15	Z	24	ASN
15	Z	49	PHE
1	A	261	LEU
1	A	539	PRO

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Mol	Chain	Res	Type
1	A	750	LEU
1	A	875	THR
1	A	1015	PRO
2	B	384	GLY
4	G	11	PRO
4	G	105	ALA
4	G	734	PRO
6	L	75	GLU
8	H	488	ILE
9	N	492	PRO
9	N	1936	ARG
1	A	407	VAL
1	A	511	ASP
1	A	538	LEU
1	A	701	CYS
1	A	1087	ASN
1	A	1621	VAL
1	A	2019	GLU
2	B	204	SER
2	B	210	LEU
2	B	347	GLY
4	G	256	LYS
4	G	769	SER
4	G	819	ALA
5	K	283	ASN
8	H	119	ASN
9	N	1555	GLU
9	N	1968	ASN
1	A	300	LYS
1	A	377	VAL
1	A	841	GLU
1	A	1379	MET
1	A	1380	PRO
4	G	782	LYS
8	H	171	GLY
8	H	305	SER
15	W	50	ASN
15	Z	50	ASN
1	A	802	PRO
4	G	239	THR
4	G	257	PHE
4	G	887	THR

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Mol	Chain	Res	Type
6	L	78	ASP
7	M	60	PRO
8	H	134	ILE
9	N	622	LEU
9	N	1202	MET
10	R	51	GLU
10	J	51	GLU
1	A	406	PRO
4	G	698	VAL
7	M	10	PRO
9	N	791	PRO
4	G	414	PRO
1	A	644	VAL
5	K	222	PRO
21	f	41	VAL
1	A	181	HIS
3	I	132	PRO
3	I	347	ALA
8	H	319	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1749/2182 (80%)	1543 (88%)	206 (12%)	5	26
2	B	374/410 (91%)	321 (86%)	53 (14%)	3	21
3	I	327/445 (74%)	264 (81%)	63 (19%)	1	10
4	G	361/813 (44%)	295 (82%)	66 (18%)	1	11
5	K	253/436 (58%)	228 (90%)	25 (10%)	8	32
6	L	129/132 (98%)	113 (88%)	16 (12%)	4	24
7	M	104/104 (100%)	98 (94%)	6 (6%)	20	51
8	H	757/910 (83%)	639 (84%)	118 (16%)	2	17
All	All	4054/5432 (75%)	3501 (86%)	553 (14%)	7	22

All (553) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	147	SER
1	A	148	ASP
1	A	152	LYS
1	A	153	MET
1	A	154	TYR
1	A	156	THR
1	A	158	LYS
1	A	162	LEU
1	A	165	LEU
1	A	166	LYS
1	A	168	LEU
1	A	175	LEU
1	A	177	GLU
1	A	187	LYS
1	A	224	MET
1	A	229	ARG
1	A	249	LEU
1	A	252	GLU
1	A	254	HIS
1	A	256	GLU
1	A	257	ASN
1	A	261	LEU
1	A	266	LEU
1	A	268	LEU
1	A	273	ASP
1	A	275	TYR
1	A	279	TRP
1	A	283	SER
1	A	287	GLU
1	A	288	GLU
1	A	291	LYS
1	A	294	ASN
1	A	298	TYR
1	A	299	LYS
1	A	313	ARG
1	A	321	GLU
1	A	324	ASP
1	A	325	LYS
1	A	328	TYR
1	A	331	PHE
1	A	351	LYS

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Mol	Chain	Res	Type
1	A	353	GLU
1	A	355	LEU
1	A	358	ARG
1	A	360	GLU
1	A	361	GLU
1	A	362	GLU
1	A	363	ASP
1	A	364	TYR
1	A	367	PHE
1	A	371	ASP
1	A	372	ARG
1	A	376	ARG
1	A	408	SER
1	A	409	CYS
1	A	412	GLN
1	A	413	ASN
1	A	414	ASP
1	A	416	GLU
1	A	418	ASP
1	A	425	ASP
1	A	427	SER
1	A	454	LEU
1	A	456	GLU
1	A	458	PHE
1	A	462	LEU
1	A	468	LEU
1	A	469	ILE
1	A	472	ASN
1	A	474	LYS
1	A	501	LEU
1	A	503	LYS
1	A	504	LYS
1	A	507	LEU
1	A	511	ASP
1	A	514	TYR
1	A	543	ASN
1	A	544	LYS
1	A	545	THR
1	A	546	LYS
1	A	547	LEU
1	A	549	LYS
1	A	555	LYS

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Mol	Chain	Res	Type
1	A	581	LEU
1	A	608	LYS
1	A	611	LYS
1	A	614	ARG
1	A	678	ARG
1	A	691	PHE
1	A	703	PHE
1	A	749	ARG
1	A	758	LEU
1	A	768	GLU
1	A	774	ILE
1	A	776	GLN
1	A	777	LYS
1	A	778	LYS
1	A	786	LEU
1	A	813	GLU
1	A	815	TYR
1	A	817	LYS
1	A	841	GLU
1	A	842	LYS
1	A	844	MET
1	A	849	LEU
1	A	852	LEU
1	A	858	LYS
1	A	861	GLN
1	A	862	GLU
1	A	878	GLU
1	A	880	THR
1	A	909	THR
1	A	932	SER
1	A	933	GLU
1	A	937	LEU
1	A	955	LYS
1	A	956	LYS
1	A	959	LEU
1	A	960	THR
1	A	992	ASP
1	A	995	LEU
1	A	1002	GLU
1	A	1035	LEU
1	A	1066	LEU
1	A	1067	ASN

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Mol	Chain	Res	Type
1	A	1068	ARG
1	A	1083	THR
1	A	1088	VAL
1	A	1095	MET
1	A	1105	ARG
1	A	1109	PHE
1	A	1115	GLN
1	A	1128	GLN
1	A	1170	MET
1	A	1183	THR
1	A	1202	ASN
1	A	1214	ARG
1	A	1217	ARG
1	A	1222	LEU
1	A	1262	MET
1	A	1275	MET
1	A	1276	GLU
1	A	1282	ASP
1	A	1314	SER
1	A	1317	ARG
1	A	1329	THR
1	A	1339	LEU
1	A	1344	THR
1	A	1354	GLU
1	A	1356	LEU
1	A	1358	ASP
1	A	1365	THR
1	A	1366	ARG
1	A	1382	ARG
1	A	1383	PHE
1	A	1405	ILE
1	A	1415	SER
1	A	1416	LYS
1	A	1418	THR
1	A	1460	GLU
1	A	1461	TYR
1	A	1465	ARG
1	A	1470	GLN
1	A	1473	ARG
1	A	1490	ARG
1	A	1499	ARG
1	A	1500	HIS

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Mol	Chain	Res	Type
1	A	1509	ARG
1	A	1511	ARG
1	A	1519	LEU
1	A	1590	LEU
1	A	1594	GLN
1	A	1616	ARG
1	A	1618	ASN
1	A	1627	LEU
1	A	1629	LEU
1	A	1650	ARG
1	A	1652	HIS
1	A	1661	ILE
1	A	1663	PHE
1	A	1690	LYS
1	A	1755	LYS
1	A	1762	ASP
1	A	1839	ASN
1	A	1882	LEU
1	A	1885	LYS
1	A	1888	HIS
1	A	1892	LYS
1	A	1908	LEU
1	A	1910	LYS
1	A	1912	LYS
1	A	1915	GLU
1	A	1916	GLU
1	A	1920	LEU
1	A	1951	PHE
1	A	1973	LYS
1	A	2007	ARG
1	A	2013	ARG
1	A	2023	LYS
1	A	2065	ARG
1	A	2067	TYR
1	A	2068	ASN
1	A	2071	ILE
1	A	2076	GLN
1	A	2078	GLU
2	B	47	GLU
2	B	48	ASP
2	B	66	ASN
2	B	73	ARG

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Mol	Chain	Res	Type
2	B	75	ARG
2	B	114	THR
2	B	117	LEU
2	B	119	PHE
2	B	122	ARG
2	B	123	PHE
2	B	128	SER
2	B	129	LEU
2	B	132	SER
2	B	133	ARG
2	B	136	LEU
2	B	137	GLN
2	B	140	MET
2	B	145	LYS
2	B	147	ASN
2	B	155	ARG
2	B	156	ARG
2	B	162	MET
2	B	171	GLN
2	B	172	LEU
2	B	192	THR
2	B	199	LEU
2	B	206	THR
2	B	208	GLN
2	B	244	LYS
2	B	257	LEU
2	B	267	ARG
2	B	276	SER
2	B	287	MET
2	B	313	LEU
2	B	316	GLN
2	B	323	CYS
2	B	333	LEU
2	B	337	ARG
2	B	358	SER
2	B	362	TYR
2	B	382	ASP
2	B	388	GLN
2	B	390	LEU
2	B	393	ARG
2	B	400	ARG
2	B	408	LYS

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Mol	Chain	Res	Type
2	B	409	LYS
2	B	443	LEU
2	B	444	ASP
2	B	446	SER
2	B	447	ASN
2	B	448	ASN
2	B	457	TRP
3	I	92	ILE
3	I	93	LYS
3	I	94	LEU
3	I	107	SER
3	I	118	SER
3	I	135	LEU
3	I	145	GLU
3	I	155	ASP
3	I	161	LEU
3	I	164	LYS
3	I	173	LEU
3	I	184	LYS
3	I	186	LYS
3	I	187	GLU
3	I	189	LEU
3	I	190	ASP
3	I	198	LEU
3	I	204	LEU
3	I	205	GLU
3	I	208	TRP
3	I	209	LYS
3	I	210	LEU
3	I	236	GLU
3	I	249	LEU
3	I	252	SER
3	I	253	ARG
3	I	257	CYS
3	I	264	LYS
3	I	268	LEU
3	I	271	GLU
3	I	272	LEU
3	I	273	HIS
3	I	280	ARG
3	I	281	GLN
3	I	312	LEU

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Mol	Chain	Res	Type
3	I	317	ASP
3	I	320	GLN
3	I	321	LYS
3	I	325	ARG
3	I	327	THR
3	I	342	ARG
3	I	344	LEU
3	I	346	GLU
3	I	350	ILE
3	I	353	THR
3	I	362	GLN
3	I	364	LYS
3	I	370	ARG
3	I	373	ARG
3	I	374	LYS
3	I	380	ARG
3	I	393	PHE
3	I	395	LYS
3	I	401	LEU
3	I	427	SER
3	I	428	ARG
3	I	429	ARG
3	I	433	ASN
3	I	436	LYS
3	I	447	GLU
3	I	450	GLN
3	I	454	GLU
3	I	456	LEU
4	G	5	SER
4	G	9	GLN
4	G	15	TYR
4	G	24	THR
4	G	99	ASN
4	G	100	VAL
4	G	102	ARG
4	G	107	LEU
4	G	108	LYS
4	G	126	THR
4	G	129	THR
4	G	130	ARG
4	G	134	ARG
4	G	138	GLN

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Mol	Chain	Res	Type
4	G	140	GLN
4	G	141	LEU
4	G	143	ARG
4	G	156	ASN
4	G	159	LEU
4	G	160	ASN
4	G	161	LYS
4	G	162	LEU
4	G	164	GLU
4	G	165	GLU
4	G	168	LYS
4	G	169	LEU
4	G	170	LEU
4	G	171	GLN
4	G	176	GLU
4	G	214	SER
4	G	216	SER
4	G	221	GLU
4	G	222	ASP
4	G	226	MET
4	G	227	ARG
4	G	230	LEU
4	G	232	SER
4	G	251	GLU
4	G	252	GLU
4	G	268	CYS
4	G	274	SER
4	G	275	SER
4	G	276	ASP
4	G	277	ILE
4	G	281	ASN
4	G	284	LEU
4	G	291	TYR
4	G	671	PHE
4	G	678	TYR
4	G	686	MET
4	G	687	SER
4	G	688	ARG
4	G	689	GLU
4	G	696	ARG
4	G	700	ASN
4	G	721	ARG

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Mol	Chain	Res	Type
4	G	852	LEU
4	G	854	LYS
4	G	855	ASP
4	G	859	LEU
4	G	861	ASN
4	G	862	MET
4	G	863	PHE
4	G	886	CYS
4	G	887	THR
4	G	889	ARG
5	K	142	LEU
5	K	147	ASP
5	K	166	TYR
5	K	171	THR
5	K	174	LEU
5	K	243	ARG
5	K	245	ARG
5	K	248	ARG
5	K	249	ARG
5	K	250	LYS
5	K	261	LYS
5	K	298	LYS
5	K	299	ASP
5	K	310	GLU
5	K	317	GLU
5	K	323	ARG
5	K	328	ASN
5	K	329	MET
5	K	332	GLU
5	K	333	LYS
5	K	362	GLU
5	K	399	ARG
5	K	448	GLN
5	K	457	GLN
5	K	459	ASP
6	L	25	ARG
6	L	34	LYS
6	L	63	ASP
6	L	73	MET
6	L	77	THR
6	L	78	ASP
6	L	102	LYS

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Mol	Chain	Res	Type
6	L	108	ASP
6	L	113	MET
6	L	118	GLU
6	L	125	ARG
6	L	133	SER
6	L	135	TYR
6	L	137	TYR
6	L	139	HIS
6	L	140	LYS
7	M	7	LYS
7	M	35	LYS
7	M	46	ARG
7	M	94	SER
7	M	95	ARG
7	M	96	PRO
8	H	107	THR
8	H	108	GLN
8	H	109	LEU
8	H	110	LYS
8	H	111	LYS
8	H	112	ASN
8	H	115	LYS
8	H	116	THR
8	H	117	ARG
8	H	120	ARG
8	H	122	TYR
8	H	132	ARG
8	H	133	ILE
8	H	160	ARG
8	H	166	LYS
8	H	167	ASN
8	H	168	VAL
8	H	173	LYS
8	H	177	TYR
8	H	178	LEU
8	H	187	ARG
8	H	189	LEU
8	H	193	LEU
8	H	202	ASP
8	H	203	LEU
8	H	204	GLU
8	H	205	SER

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Mol	Chain	Res	Type
8	H	206	LYS
8	H	208	ARG
8	H	222	MET
8	H	235	VAL
8	H	236	LEU
8	H	240	ASP
8	H	265	PHE
8	H	274	ILE
8	H	275	LEU
8	H	296	ASN
8	H	297	SER
8	H	300	LYS
8	H	305	SER
8	H	326	GLU
8	H	329	SER
8	H	330	TYR
8	H	336	ILE
8	H	339	SER
8	H	353	TYR
8	H	354	TYR
8	H	364	PHE
8	H	366	ASN
8	H	368	GLU
8	H	369	LYS
8	H	372	THR
8	H	373	PHE
8	H	389	LEU
8	H	391	MET
8	H	393	LYS
8	H	416	ASP
8	H	448	LEU
8	H	449	PHE
8	H	452	LYS
8	H	456	LEU
8	H	457	SER
8	H	461	LYS
8	H	465	GLU
8	H	469	TRP
8	H	474	LYS
8	H	478	TYR
8	H	487	ARG
8	H	489	TYR

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Mol	Chain	Res	Type
8	H	490	SER
8	H	503	ASP
8	H	505	SER
8	H	508	GLU
8	H	509	SER
8	H	510	ARG
8	H	536	SER
8	H	538	GLU
8	H	545	LEU
8	H	558	LYS
8	H	565	LYS
8	H	568	SER
8	H	569	SER
8	H	573	LYS
8	H	578	TYR
8	H	581	LYS
8	H	582	SER
8	H	583	LYS
8	H	584	GLU
8	H	586	MET
8	H	587	LYS
8	H	589	LEU
8	H	590	LYS
8	H	595	LEU
8	H	603	PHE
8	H	608	GLN
8	H	617	LYS
8	H	652	MET
8	H	797	GLN
8	H	799	PHE
8	H	814	TYR
8	H	884	ARG
8	H	887	ARG
8	H	888	ILE
8	H	889	TYR
8	H	919	ARG
8	H	931	TYR
8	H	932	PHE
8	H	934	HIS
8	H	936	ILE
8	H	945	LEU
8	H	947	LYS

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Mol	Chain	Res	Type
8	H	948	ASP
8	H	959	ILE
8	H	960	ASN
8	H	970	THR
8	H	971	ARG
8	H	972	ARG
8	H	974	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	254	HIS
1	A	310	ASN
1	A	326	ASN
1	A	344	ASN
1	A	392	ASN
1	A	413	ASN
1	A	429	ASN
1	A	497	GLN
1	A	543	ASN
1	A	592	HIS
1	A	868	GLN
1	A	948	HIS
1	A	976	GLN
1	A	1067	ASN
1	A	1115	GLN
1	A	1128	GLN
1	A	1156	HIS
1	A	1496	GLN
1	A	1594	GLN
1	A	1603	ASN
1	A	1615	ASN
1	A	1652	HIS
1	A	1809	ASN
1	A	1839	ASN
2	B	144	GLN
2	B	208	GLN
2	B	227	HIS
2	B	232	ASN
2	B	247	GLN
2	B	274	HIS

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Mol	Chain	Res	Type
2	B	316	GLN
2	B	374	ASN
2	B	392	HIS
2	B	420	ASN
2	B	447	ASN
2	B	448	ASN
2	B	450	HIS
3	I	113	HIS
3	I	146	ASN
3	I	148	ASN
3	I	152	ASN
3	I	196	GLN
3	I	201	ASN
3	I	211	GLN
3	I	267	HIS
3	I	281	GLN
3	I	398	GLN
3	I	414	ASN
3	I	433	ASN
3	I	449	ASN
3	I	461	HIS
4	G	99	ASN
4	G	138	GLN
4	G	140	GLN
4	G	160	ASN
4	G	281	ASN
4	G	285	HIS
4	G	668	HIS
4	G	700	ASN
4	G	805	HIS
5	K	163	ASN
5	K	316	HIS
5	K	330	ASN
6	L	14	HIS
6	L	17	GLN
6	L	87	HIS
6	L	139	HIS
7	M	45	ASN
8	H	112	ASN
8	H	135	ASN
8	H	158	HIS
8	H	167	ASN

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Mol	Chain	Res	Type
8	H	211	ASN
8	H	296	ASN
8	H	334	HIS
8	H	355	HIS
8	H	418	GLN
8	H	444	GLN
8	H	554	HIS
8	H	608	GLN
8	H	721	GLN
8	H	797	GLN
8	H	929	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	C	19/20 (95%)	17 (89%)	2 (10%)
25	D	41/112 (36%)	22 (53%)	4 (9%)
26	E	85/160 (53%)	28 (32%)	7 (8%)
27	F	111/214 (51%)	51 (45%)	14 (12%)
All	All	256/506 (50%)	118 (46%)	27 (10%)

All (118) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	C	-5	A
24	C	-4	A
24	C	-3	A
24	C	-2	A
24	C	-1	A
24	C	0	U
24	C	1	U
24	C	2	A
24	C	3	A
24	C	4	G
24	C	5	G
24	C	6	U
24	C	7	A
24	C	8	U
24	C	9	G
24	C	10	U
24	C	12	U

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Mol	Chain	Res	Type
25	D	48	C
25	D	49	A
25	D	50	G
25	D	51	A
25	D	52	G
25	D	57	U
25	D	62	A
25	D	63	G
25	D	66	C
25	D	72	C
25	D	75	A
25	D	76	A
25	D	77	G
25	D	78	G
25	D	79	A
25	D	83	A
25	D	84	C
25	D	85	C
25	D	86	G
25	D	87	U
25	D	109	U
25	D	110	U
26	E	2	U
26	E	4	C
26	E	15	G
26	E	18	A
26	E	19	U
26	E	20	A
26	E	25	U
26	E	27	U
26	E	28	C
26	E	30	G
26	E	39	C
26	E	43	C
26	E	48	U
26	E	51	U
26	E	55	U
26	E	56	U
26	E	60	U
26	E	140	G
26	E	141	G
26	E	142	G

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Mol	Chain	Res	Type
26	E	143	A
26	E	144	A
26	E	146	U
26	E	147	U
26	E	148	U
26	E	149	U
26	E	150	G
26	E	151	G
27	F	32	G
27	F	33	U
27	F	34	C
27	F	39	U
27	F	40	C
27	F	41	A
27	F	74	U
27	F	75	A
27	F	76	U
27	F	77	A
27	F	78	A
27	F	79	C
27	F	80	G
27	F	81	A
27	F	82	A
27	F	83	C
27	F	84	A
27	F	90	C
27	F	92	U
27	F	93	G
27	F	94	C
27	F	95	C
27	F	96	U
27	F	97	U
27	F	98	U
27	F	99	U
27	F	100	A
27	F	101	C
27	F	103	A
27	F	104	G
27	F	107	C
27	F	108	C
27	F	109	A
27	F	110	U

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Mol	Chain	Res	Type
27	F	113	G
27	F	120	G
27	F	121	U
27	F	126	A
27	F	127	U
27	F	164	C
27	F	165	A
27	F	166	U
27	F	167	A
27	F	168	U
27	F	169	U
27	F	170	U
27	F	171	U
27	F	172	U
27	F	173	U
27	F	174	G
27	F	175	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	C	-4	A
24	C	6	U
25	D	48	C
25	D	50	G
25	D	83	A
25	D	85	C
26	E	1	A
26	E	18	A
26	E	19	U
26	E	24	A
26	E	139	A
26	E	142	G
26	E	148	U
27	F	32	G
27	F	33	U
27	F	75	A
27	F	77	A
27	F	81	A
27	F	83	C
27	F	95	C
27	F	97	U

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Mol	Chain	Res	Type
27	F	98	U
27	F	107	C
27	F	163	C
27	F	166	U
27	F	168	U
27	F	172	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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
28	GTP	H	1500	-	26,34,34	0.93	1 (3%)	32,54,54	1.62	4 (12%)
29	M7M	E	201	26	29,33,33	1.50	5 (17%)	39,52,52	2.02	7 (17%)

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
28	GTP	H	1500	-	-	4/18/38/38	0/3/3/3
29	M7M	E	201	26	-	6/20/48/48	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	4.47	1.46	1.37
29	E	201	M7M	CBG-NBH	-3.22	1.32	1.35
29	E	201	M7M	CBF-NBE	-2.80	1.33	1.38
28	H	1500	GTP	C6-N1	-2.41	1.34	1.37
29	E	201	M7M	CBO-NBP	-2.12	1.32	1.35
29	E	201	M7M	CBO-NBN	-2.10	1.33	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	201	M7M	NBP-CBI-NBH	-5.79	95.09	103.38
29	E	201	M7M	PBK-OB-PAZ	-5.05	115.50	132.83
28	H	1500	GTP	PB-O3B-PG	-4.56	117.19	132.83
29	E	201	M7M	PBK-OB-CBT	4.44	147.72	121.68
28	H	1500	GTP	PA-O3A-PB	-4.06	118.89	132.83
29	E	201	M7M	NBN-CBM-NBV	-3.59	114.98	118.04
29	E	201	M7M	CBG-CBO-NBN	-3.56	117.72	124.00
28	H	1500	GTP	C3'-C2'-C1'	3.39	106.08	100.98
29	E	201	M7M	OB-PBK-OBL	-3.39	95.83	109.07
29	E	201	M7M	OAY-PAZ-OBA	2.93	122.13	110.68
28	H	1500	GTP	C8-N7-C5	2.50	107.75	102.99

There are no chirality outliers.

All (10) torsion outliers are listed below:

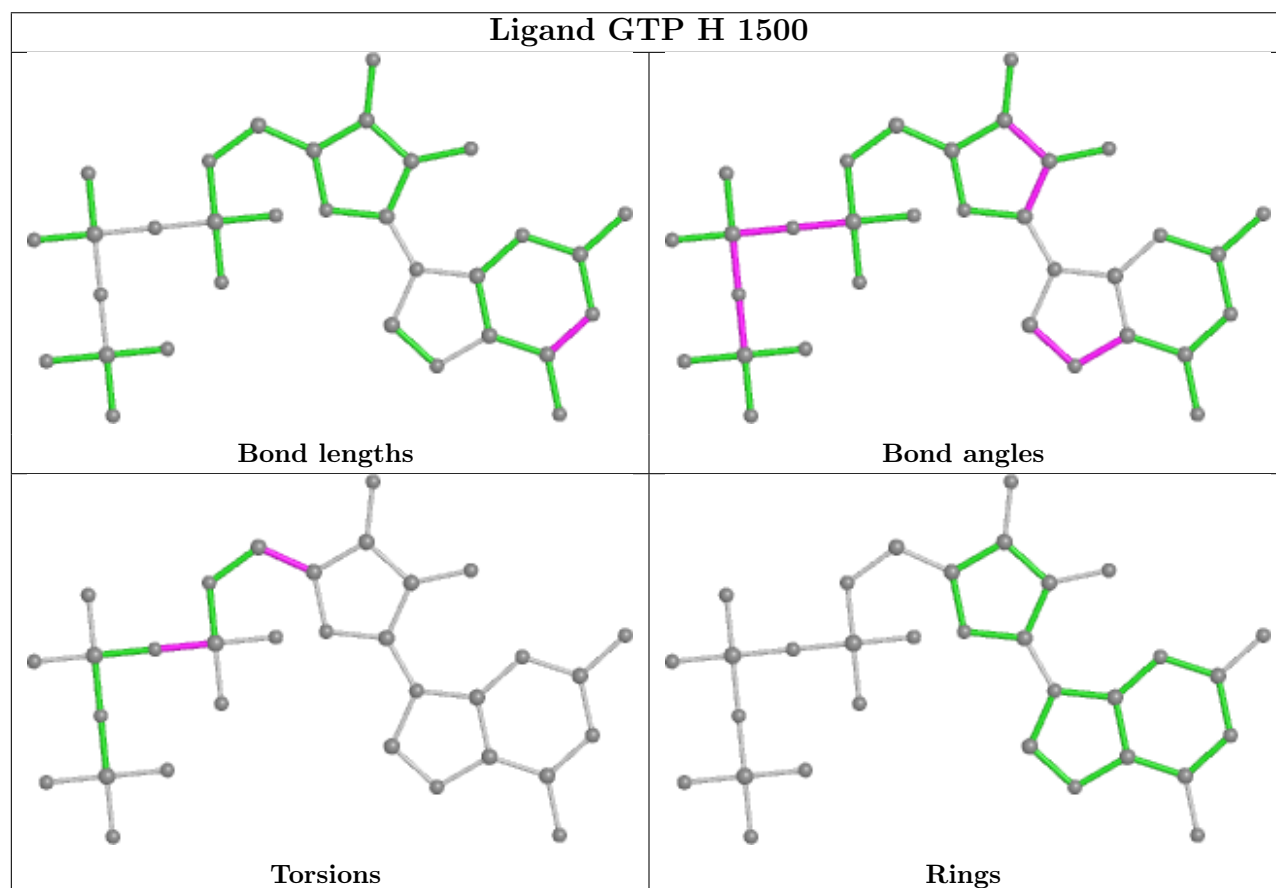
Mol	Chain	Res	Type	Atoms
29	E	201	M7M	NBE-CBM-NBV-CBW
29	E	201	M7M	NBE-CBM-NBV-CBZ
29	E	201	M7M	NBN-CBM-NBV-CBZ
29	E	201	M7M	CBS-CBT-OB-PBK
28	H	1500	GTP	O4'-C4'-C5'-O5'
28	H	1500	GTP	C3'-C4'-C5'-O5'
29	E	201	M7M	NBN-CBM-NBV-CBW
29	E	201	M7M	CBX-CBQ-NBP-CBI
28	H	1500	GTP	PB-O3A-PA-O2A
28	H	1500	GTP	PB-O3A-PA-O1A

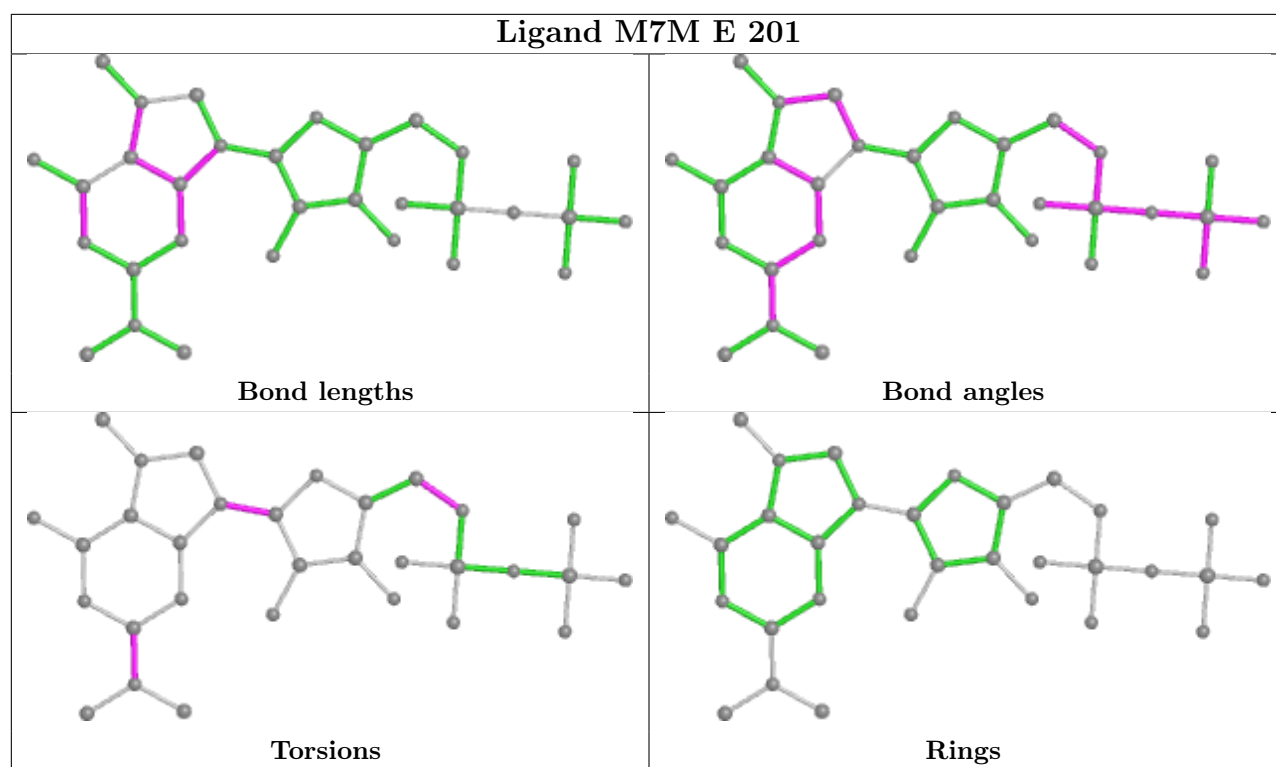
There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	H	1500	GTP	10	0
29	E	201	M7M	6	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.

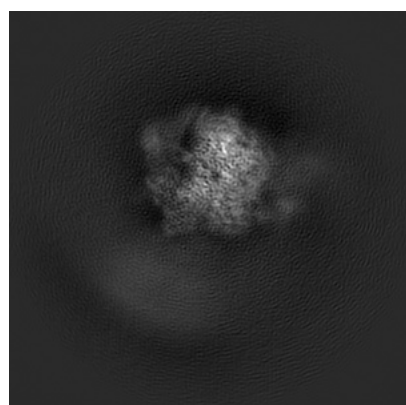
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6561. These allow visual inspection of the internal detail of the map and identification of artifacts.

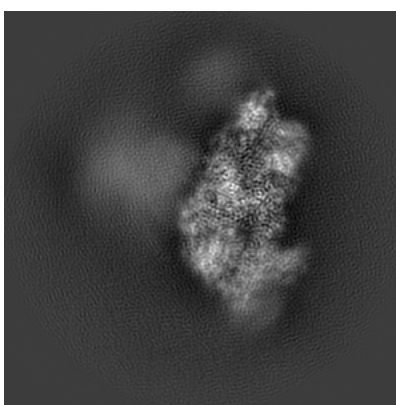
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

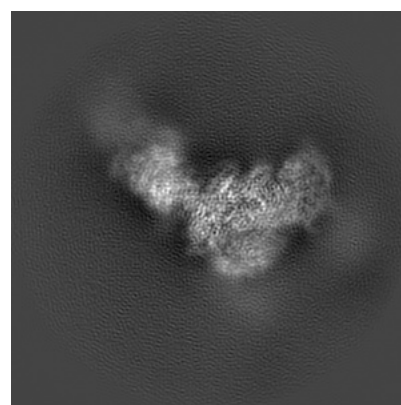
6.1.1 Primary map



X



Y

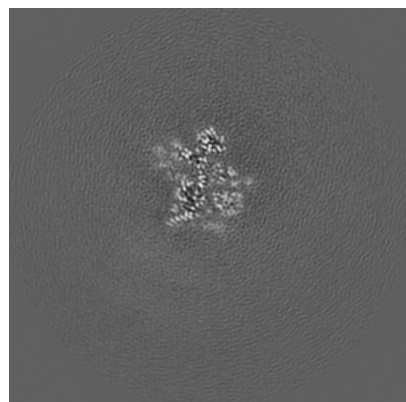


Z

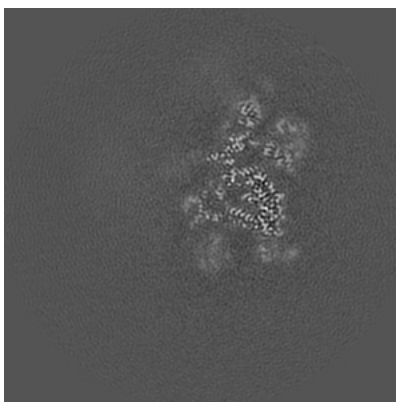
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

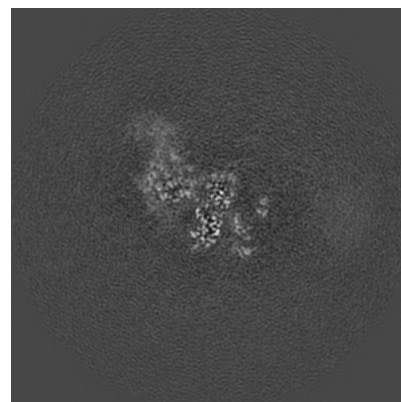
6.2.1 Primary map



X Index: 160



Y Index: 160

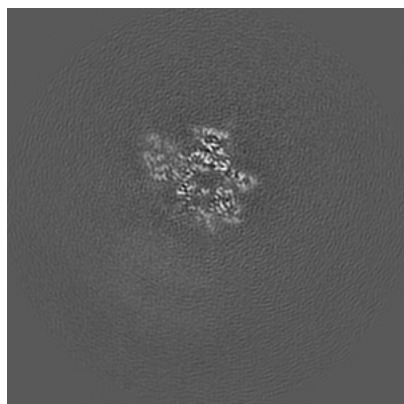


Z Index: 160

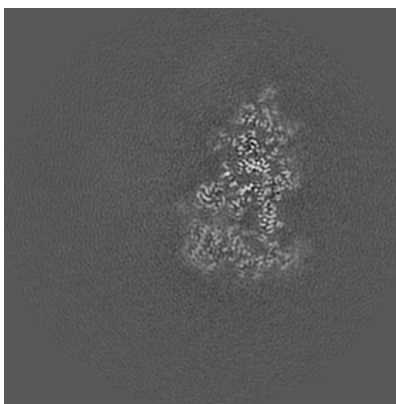
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

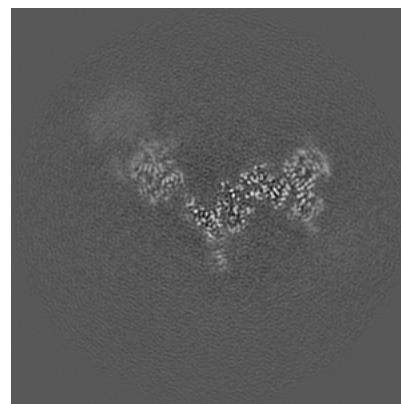
6.3.1 Primary map



X Index: 167



Y Index: 171



Z Index: 199

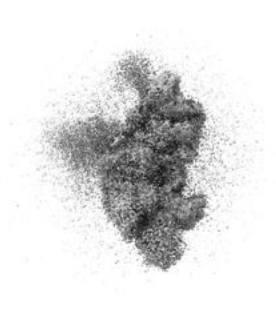
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

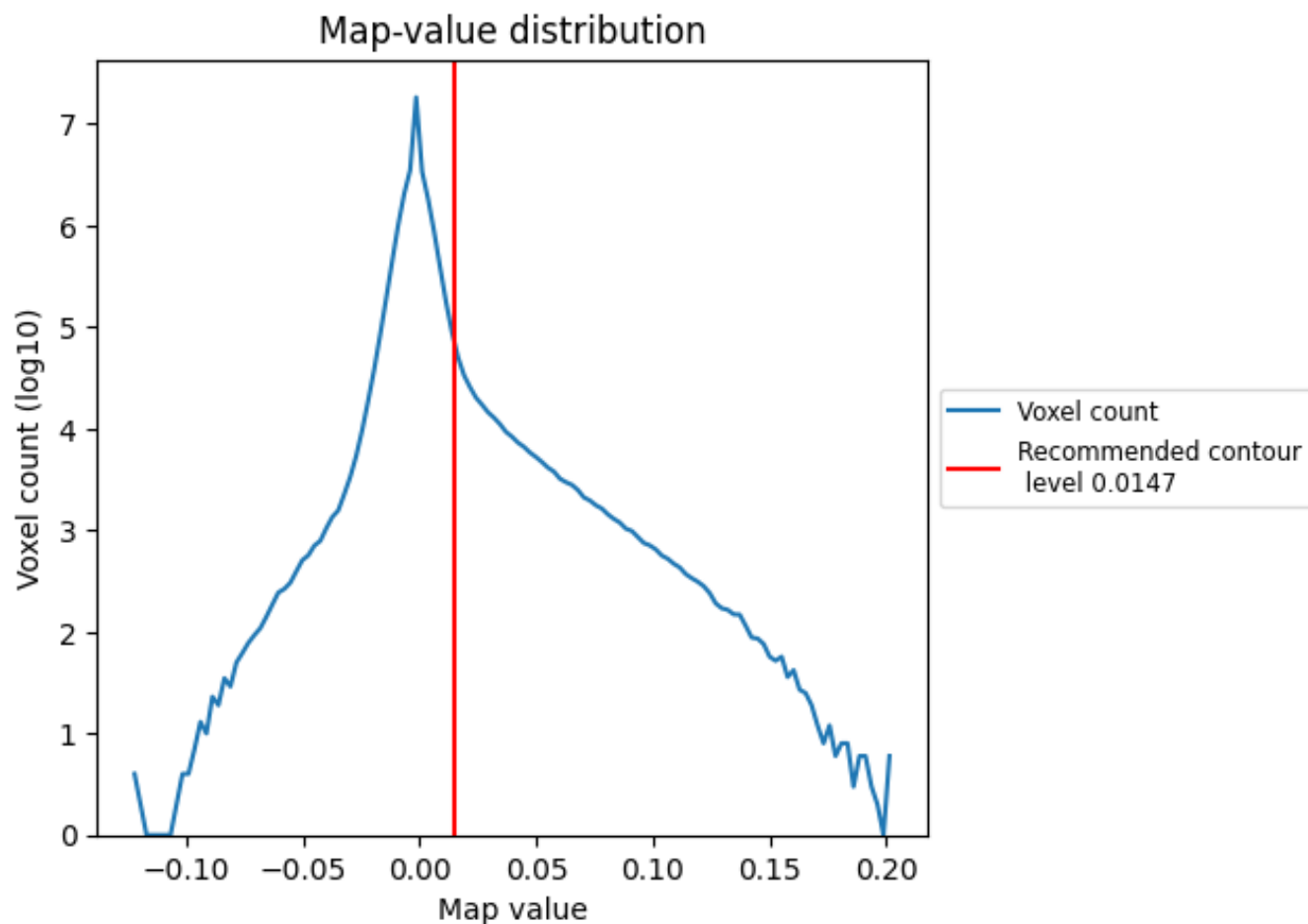
6.5 Mask visualisation

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

7 Map analysis [i](#)

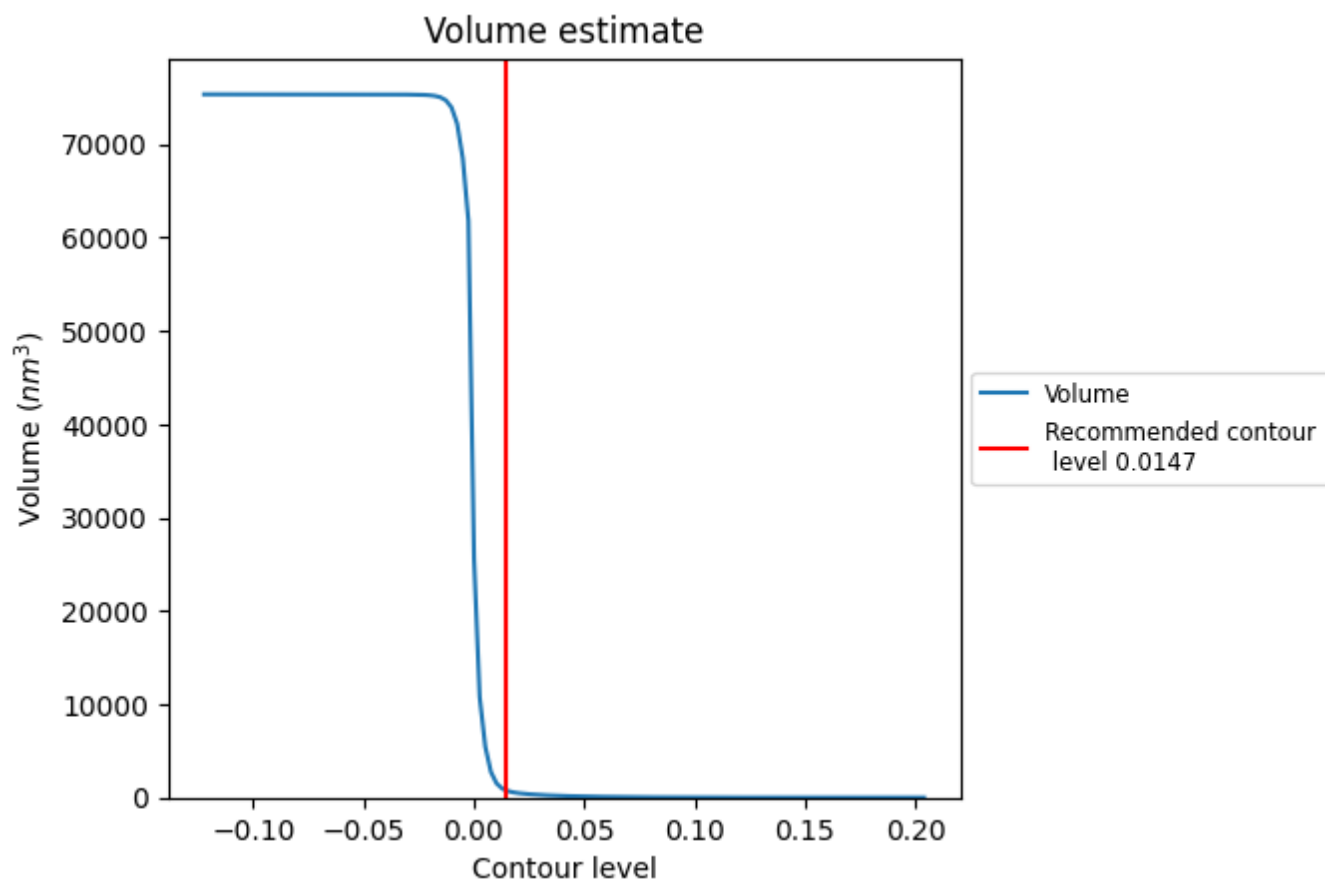
This section contains the results of statistical analysis of the map.

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.

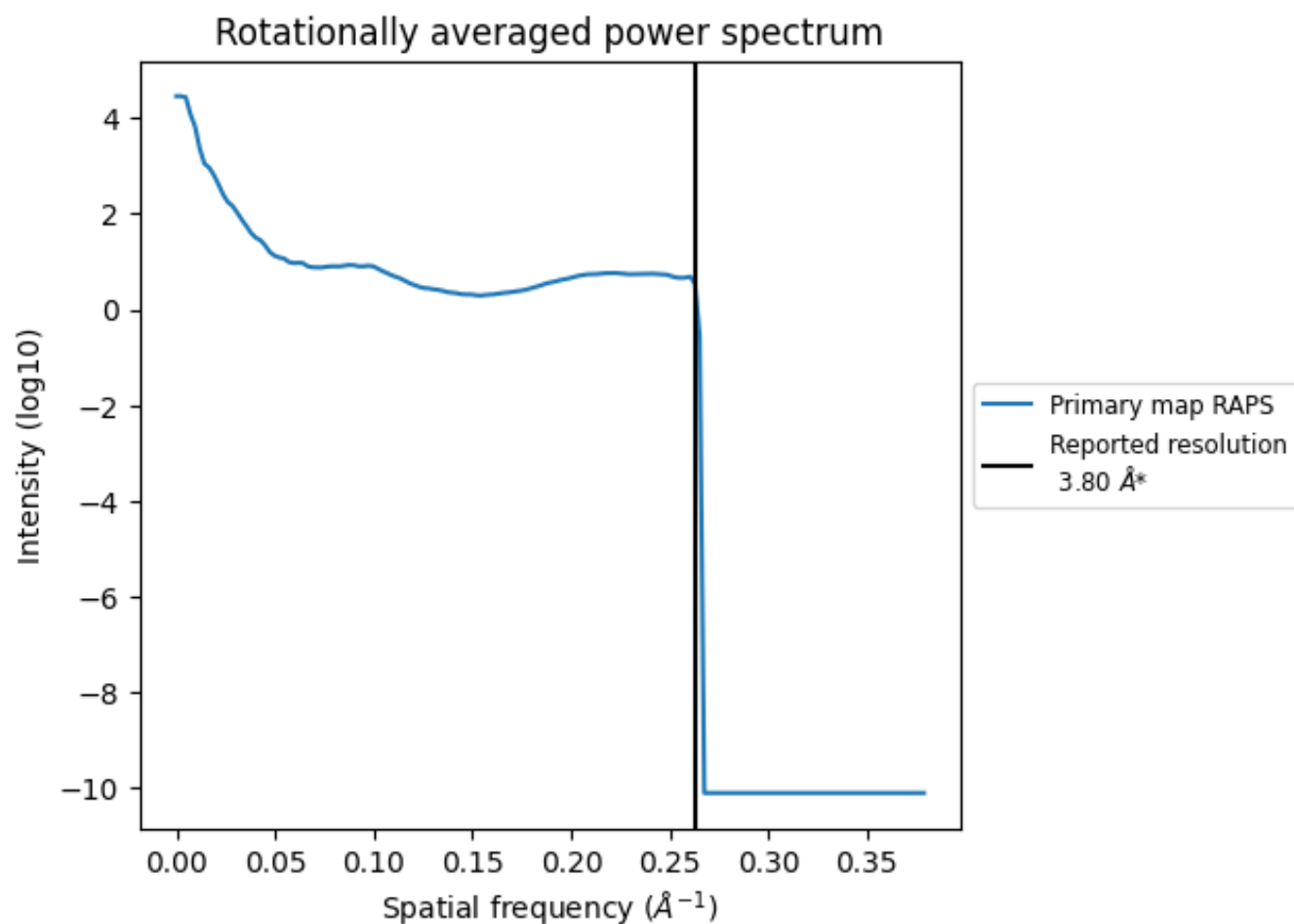
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 773 nm^3 ; this corresponds to an approximate mass of 699 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 0.263 Å⁻¹

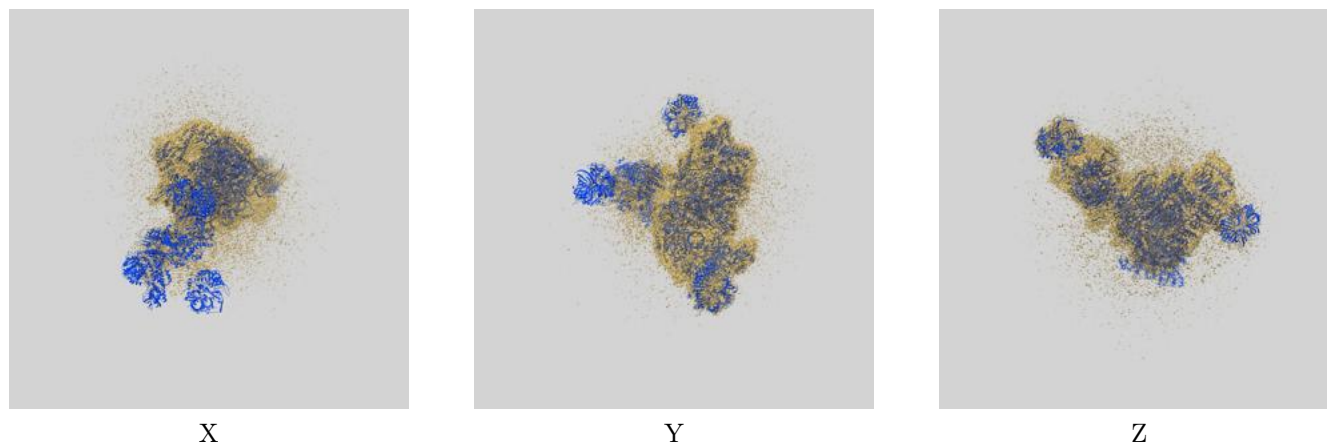
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

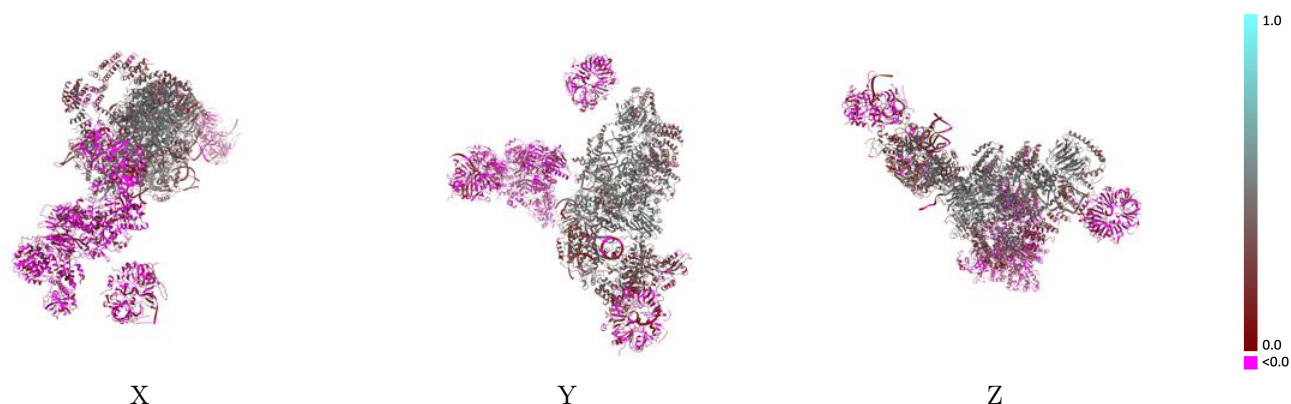
This section contains information regarding the fit between EMDB map EMD-6561 and PDB model 3JCM. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



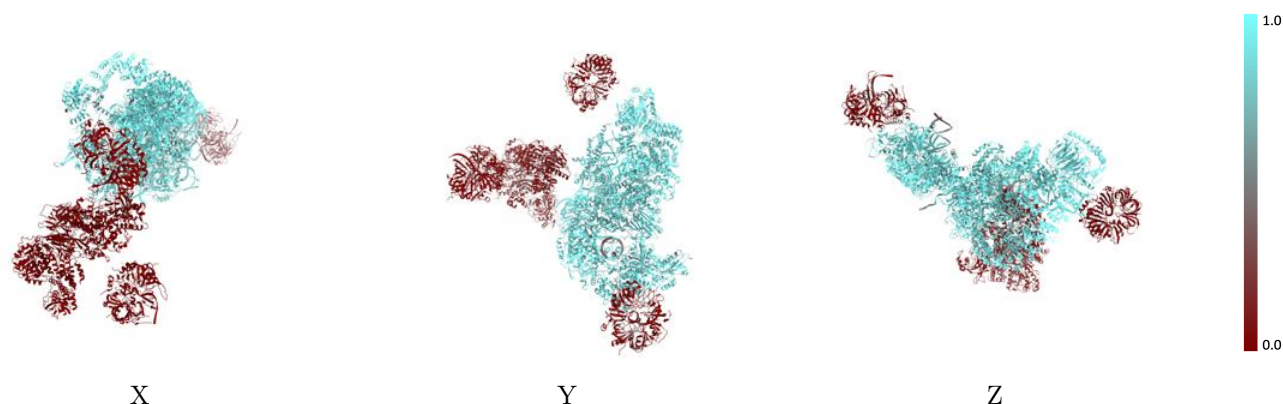
The images above show the 3D surface view of the map at the recommended contour level 0.0147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



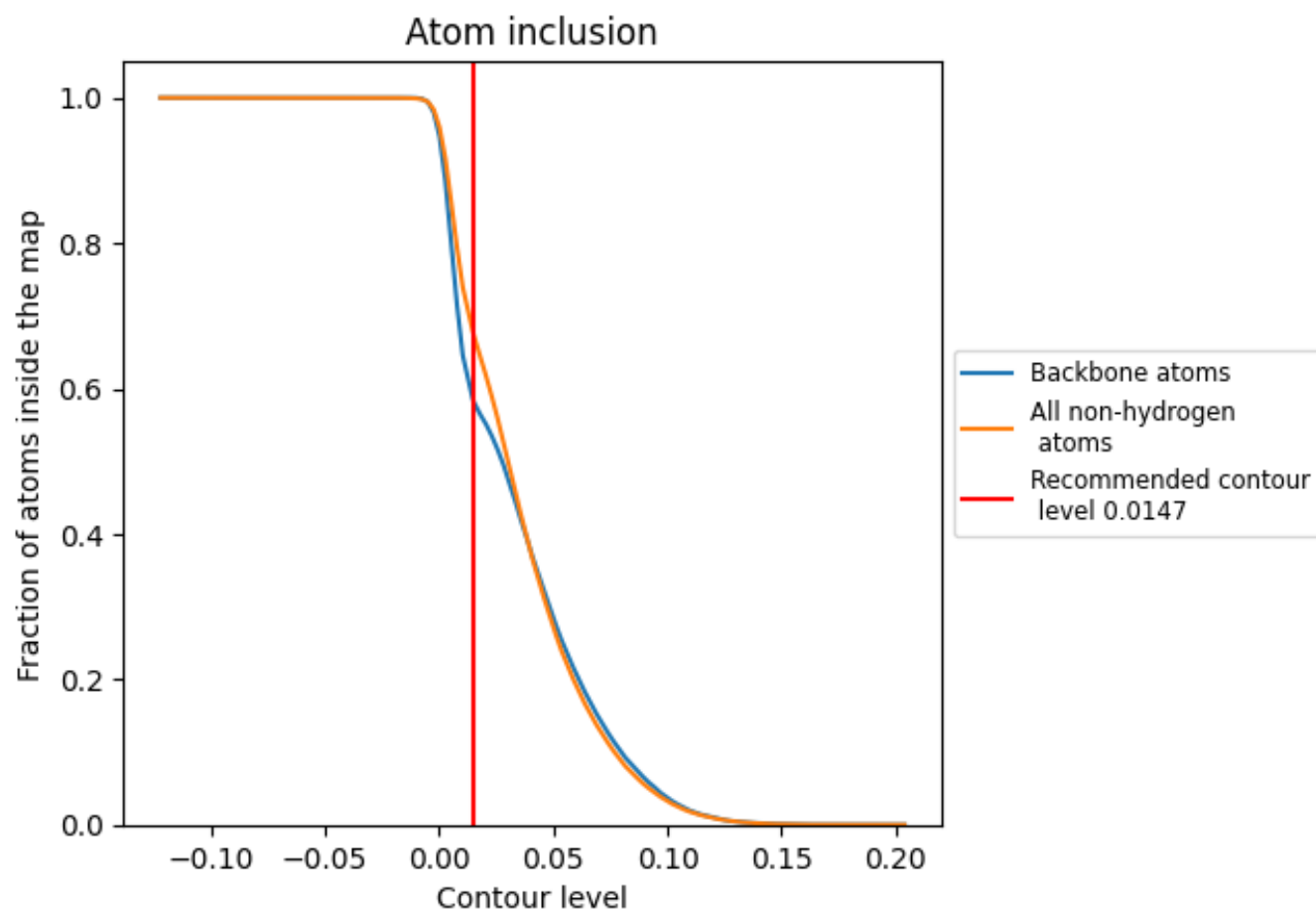
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0147).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 68% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6783	 0.2940
A	 0.8564	 0.3990
B	 0.9063	 0.4200
C	 0.8695	 0.2880
D	 0.8910	 0.3730
E	 0.7473	 0.3630
F	 0.7107	 0.2090
G	 0.9070	 0.3400
H	 0.8914	 0.3210
I	 0.9216	 0.4400
J	 0.0000	 -0.0190
K	 0.9073	 0.4070
L	 0.9241	 0.4570
M	 0.9275	 0.4890
N	 0.0233	 0.0020
O	 0.0000	 0.0160
P	 0.0032	 0.0440
Q	 0.0000	 0.0460
R	 0.1487	 0.0620
S	 0.0514	 0.0240
T	 0.0909	 0.0940
U	 0.1222	 0.0370
V	 0.0486	 -0.0010
W	 0.1321	 0.0400
X	 0.0500	 0.0310
Y	 0.0000	 -0.0070
Z	 0.0036	 0.0190
a	 0.0000	 0.0320
b	 0.0115	 0.0180
c	 0.0109	 0.0280
d	 0.0097	 0.0140
e	 0.0270	 0.0190
f	 0.0130	 0.0250
g	 0.0114	 0.0220
h	 0.0162	 -0.0580

