



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 11:44 AM UTC

PDB ID : 5ZWM / pdb_00005zwm
EMDB ID : EMD-6972
Title : Cryo-EM structure of the yeast pre-B complex at an average resolution of 3.4 4.6 angstrom (tri-snRNP and U2 snRNP Part)
Authors : Bai, R.; Wan, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2018-05-16
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

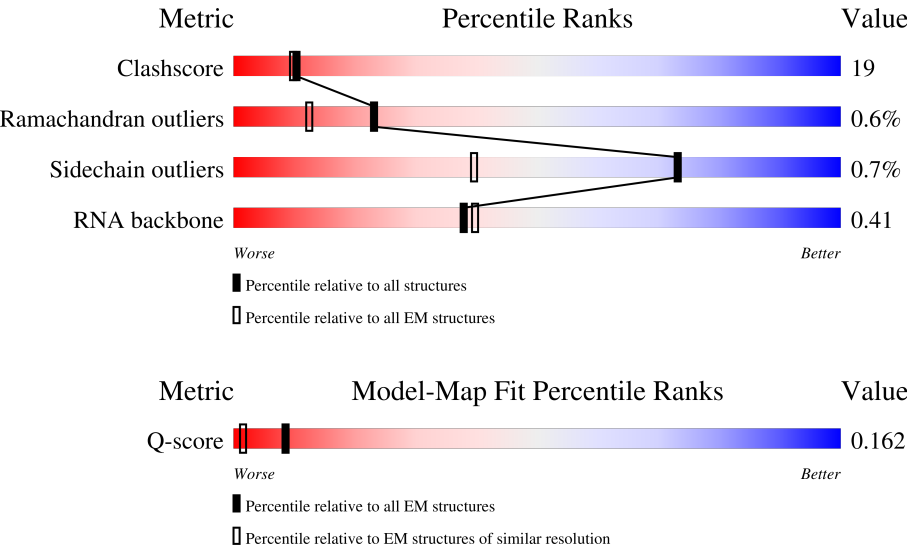
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2413	8% 60% 30% 10%
2	K	465	52% 38% 8%
3	L	494	57% 27% 16%

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Mol	Chain	Length	Quality of chain
4	N	899	
5	J	469	
6	E	143	
7	M	126	
8	C	1008	
9	z	109	
10	q	95	
11	r	89	
12	x	86	
13	t	93	
14	y	115	
15	s	187	
16	F	112	
17	I	160	
18	B	214	
19	O	587	
20	S	101	
20	d	101	
20	l	101	
21	P	196	
21	a	196	
21	h	196	
22	Q	146	
22	b	146	
22	m	146	

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Mol	Chain	Length	Quality of chain
23	R	110	
23	c	110	
23	n	110	
24	T	94	
24	e	94	
24	i	94	
25	U	86	
25	f	86	
25	j	86	
26	V	77	
26	g	77	
26	k	77	
27	D	2163	
28	G	44	
29	H	1175	
30	o	238	
31	p	111	
32	1	971	
33	2	436	
34	3	1361	
35	4	213	
36	5	107	
37	6	85	
38	X	148	
39	Y	266	

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Mol	Chain	Length	Quality of chain
40	Z	204	11%5%5%•89%
41	u	530	86%53%33%•13%
42	w	280	45%26%17%•55%
43	v	266	59%42%23%•35%

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 111041 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	2177	Total	C	N	O	S	0	0
			17877	11496	3054	3263	64		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	728	Total	C	N	O	S	0	0
			4897	3045	905	933	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	304	Total	C	N	O	S	0	0
			2439	1545	445	435	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 16 is a RNA chain called U6 snRNA.

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

- Molecule 17 is a RNA chain called U4 snRNA.

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

- Molecule 18 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	B	175	Total	C	N	O	P	0	0
			3715	1663	651	1227	174		

- Molecule 19 is a protein called 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	74	Total	C	N	O	S	0	0
			574	350	103	120	1		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	79	Total	C	N	O		0	0
			316	158	79	79			
20	S	82	Total	C	N	O	S	0	0
			632	402	109	119	2		
20	l	81	Total	C	N	O	S	0	0
			611	390	106	113	2		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	73	Total	C	N	O		0	0
			292	146	73	73			
21	P	70	Total	C	N	O	S	0	0
			563	360	98	102	3		
21	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	77	Total	C	N	O		0	0
			308	154	77	77			
22	Q	99	Total	C	N	O	S	0	0
			751	475	137	137	2		
22	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	c	90	Total	C	N	O		0	0
			360	180	90	90			
23	R	92	Total	C	N	O	S	0	0
			752	481	136	131	4		
23	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	72	Total	C	N	O		0	0
			288	144	72	72			
24	T	77	Total	C	N	O	S	0	0
			602	396	95	108	3		
24	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	70	Total	C	N	O		0	0
			280	140	70	70			
25	U	73	Total	C	N	O	S	0	0
			585	376	102	106	1		
25	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	70	Total	C	N	O		0	0
			280	140	70	70			
26	V	75	Total	C	N	O	S	0	0
			577	363	100	112	2		
26	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	1699	Total	C	N	O	S	1	0
			13601	8717	2266	2564	54		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	44	Total	C	N	O	P	0	0
			928	419	161	304	44		

- Molecule 29 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	206	Total	C	N	O	P	0	0
			4345	1940	722	1477	206		

- Molecule 30 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	o	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	p	73	Total	C	N	O	0	0
			466	304	81	81		

- Molecule 32 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1	816	Total	C	N	O	S	0	0
			6472	4165	1101	1166	40		

- Molecule 33 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	211	Total	C	N	O	S	0	0
			1726	1121	292	304	9		

- Molecule 34 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3	1180	Total	C	N	O	S	0	0
			9380	5996	1580	1753	51		

- Molecule 35 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	173	Total	C	N	O	S	0	0
			1429	930	239	258	2		

- Molecule 36 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

- Molecule 37 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 38 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	X	128	Total	C	N	O	0	0
			1051	662	181	208		

- Molecule 39 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	89	Total	C	N	O	S	0	0
			730	458	130	140	2		

- Molecule 40 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	22	Total	C	N	O	S	0	0
			173	110	25	37	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	u	461	Total	C	N	O	S	0	0
			3895	2475	675	730	15		

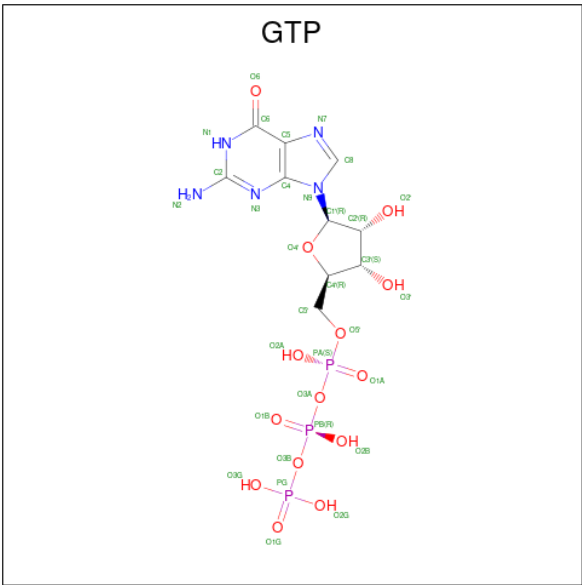
- Molecule 42 is a protein called Pre-mRNA-splicing factor PRP21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	127	Total	C	N	O	S	0	0
			1084	689	193	196	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	174	Total	C	N	O	S	0	0
			1372	862	235	269	6		

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

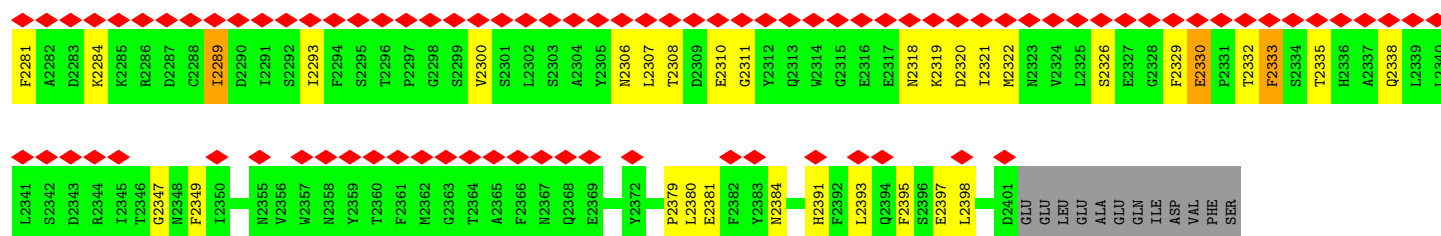
- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

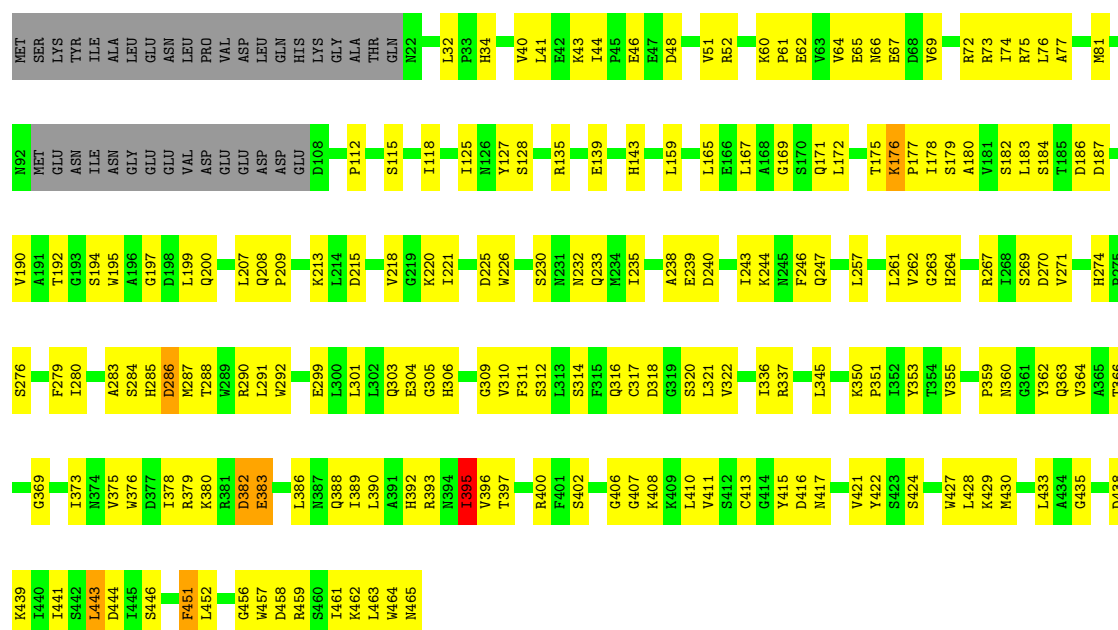
Mol	Chain	Residues	Atoms		AltConf
46	5	3	Total	Zn	0
			3	3	
46	u	2	Total	Zn	0
			2	2	
46	v	1	Total	Zn	0
			1	1	

E2220	T2160	GLU	L1891	M1802	T1702	Q1586	L1488	M1369	M1275	Y1161	L1054	T960
I2221	L2161	LEU	K1892	R1803	M1703	R1595	P1489	R1370	E1276	I1188	M1057	Y963
K2222	L2162	GLU	W1899	T1805	S1705	L1598	P1489	V1371	E1277	Y1169	A1058	
T2223	Y2163	ALA	L1905	M1809	W1709	L1598	L1494	L1375	V1279	M1170	K1060	P966
Y2224	L2164	ARG	K1910	P1810	V1711	T1601	L1376	S1377	V1285	L1171	I1061	Y967
V2225	R2165	SER	T1913	A1811	S1712	P1602	S1377		L1286	F1172	D1062	
L2226	L2166	GLU	L1920	W1814	K1713	M1603	F1383	F1383	D1287	F1174	F1063	M971
V2227	K2167	GLN	L1925	L1815	P1714	T1607	H1500	L1375	L1288	E1175	L1066	M972
P2228	R2168	ASN	Q1929	E1817	L1716	R1616	T1501	Y1389	A1298	N1197	L1070	E973
Q2229	S2169	ASP	S1923	R1816	S1715	A1617	R1509	T1390	Y1301	S1198	L1070	Y974
L2230	V2170	GLU	L1924	E1817	L1716	M1618	I1510	P1391	L1302	I1199	L1070	Q976
G2231	V2171	GLU	P1925	L1819	L1717	N1618	R1511	E1392	K1303	G1200	I1073	M977
H2232	E2172	ALA	Q1929	I1819	L1717	V1621	R1512	E1393	K1303	Y1201	V1074	Y978
V2233	S2172	GLY	Q1929	S1829	K1731	W1624	Y1517	L1394	E1306	N1202	I1078	Y981
G2234	A2173	ALA	Q1929	E1832	M1732	L1624	R1521	M1399	E1307	C1206	I1078	Y982
S2235	D2174	SER	V1935	P1833	P1734	L1624	R1521	I1400	E1308	W1207	K1085	S983
G2236	D2175	THR	T1936	F1833	D1735	I1632	R1521	I1401	E1308	P1207	M1086	Y984
V2236	F2176	VAL	R1937	P1834	R1739	F1633	P1524	S1401	K1309	W1207	N1087	D985
Q2237	V2177	MET	M1940	L1835	F1756	L1634	F1525	A1409	K1310	K1209	V1088	P986
L2238	E2178	LYS	L1941	M1836	S1745	H1635	W1526	W1414	K1311	D1210	P986	L987
S2239	E2179	THR	D1942	N1839	I1748	L1645	W1527	W1414	F1312	S1211	V1089	
M2240	Q2180	THR	P1943	M1839	I1748	I1645	T1528	Q1417	K1314	R1212	I1090	
I2241	N2180	ILE	P1943	L1843	Y1751	I1646	M1529	Q1417	M1095	R1214		D992
P2242	L2181	ASN	P1952	L1843	Y1751	P1647	D1533	G1428	S1096	N1221	M1097	L995
D2243	V2182	ALA	P1952	L1843	Y1751	P1647	G1534	G1428	H1097	N1221	V1098	R1006
Y2183	G2183	GLN	P1958	L1860	K1755	F1649	K1535	M1321	N1099	I1230	M1099	
V2184	L2184	GLY	P1958	F1861	F1756	R1650	L1536	A1322	K1100	Q1231	K1100	M1011
L2185	L2185	GLU	R1962	T1855	Y1759	Q1655	Y1542	W1335	S1232	S1232	Y1101	
L2186	L2186	ILE	L1963	N1856	D1762	K1656	R1543	R1234	R1233	R1233	R1105	K1014
P2186	P2186	VAL	P1965	N1857	N1763	T1657	T1544	M1336	G1106	P1235	G1106	S1016
K2187	K2187	VAL	F1965	N1858	N1763	H1658	T1544	L1339	L1107	P1235	L1107	
N2188	N2188	VAL	Q1985	R1859	G1772	E1659	D1545	L1340	K1103	T1239	I1020	
L2189	L2189	ALA	Q1985	V1860	G1772	S1660	Q1548	S1341	P1021	S1240	P1021	
SER	SER	SER	L1988	T1861	V1773	Q1667	Q1548	S1341	P1022	I1241	P1022	
ASP	ASP	ASP	F1989	V1862	M1774	I1668	E1448	L1342	D1122	L1241	D1122	
TYR	TYR	TYR	D1993	H1863	I1775	I1668	N1449	F1343	L1125	A1246	L1125	
GLU	GLU	GLU	D1993	T1864	G1776	G1776	E1450	F1345	L1126	F1247	L1126	
SER	SER	SER	L1996	T1865	I1777	D1674	E1558	F1451	Q1127	S1249	Q1127	
GLN	L2083	THR	L1996	F1866	L1777	D1674	F1662	S1454	N1033	S1252	L1134	N1033
THR	L2084	THR	L1996	N1869	M1782	I1678	F1662	W1458	I1350	K1253	E1143	I1038
PHE	G2085	GLN	I1999	M1870	M1783	I1678	K1563	W1458	E1348	S1252	F1144	R1043
SER	ASN	ASN	T2003	A1871	D1784	V1681	G1564	Q1466	M1145	K1253	Q1146	G1044
SER	ILE	SER	T2003		A1786	T1682	G1566	Q1466	F1147	L1259	F1147	Q1045
LYS	LYS	LYS	S2006		Y1787	T1682	G1566	Q1466	I1359	M1262	E1153	S1046
N2150	V2199	ALA	S2006	I1879	G1788	P1688	W1570	Q1470	T1353	N1257	M1145	A1047
F2151	K2200	PRO	T2009	F1880	M1789	R1689	W1575	Q1470	L1356	L1258	M1145	V1048
W2152	K2200	SER	T2010	T1881	N1789	K1690	W1575	R1473	L1356	L1258	F1147	A1047
R2153	L2201	VAL	L2010	L1882	F1791	K1690	W1575	R1473	L1356	L1258	F1147	V1048
K2154	Q2202	LYS	L2011	M1883	L1794	M1694	A1578	R1474	I1359	M1262	E1153	L1049
S2155	V2203	ARG	L2012	T1886	L1794	N1695	S1578	F1477	E1364	V1267	H1156	L1049
A2204	G2203	GLN	R2013	G1887	I1798	S1696	G1580	F1477	T1365	R1268	P1157	L1049
A2205	A2205	LYS	A2014	H1888	I1798	S1696	F1581	E1481	R1366	I1269	P1157	L1050
M2269	F2206	MET	L2015	L1889	S1801	A1699	M1585	W1484	I1367	L1160	E1051	
A2270	F2206	ALA	K2016	F1890	S1801	A1699	M1585	W1484	Q1368	L1160	E1051	
A2271	T2207	ALA	K2016	F1890	S1801	A1699	M1585	W1484	Q1368	L1160	E1051	
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L2276	V2211	ALA	K2016	F1890	S1801	A1699	M1585	W1484	Q1368	L1160	E1051	
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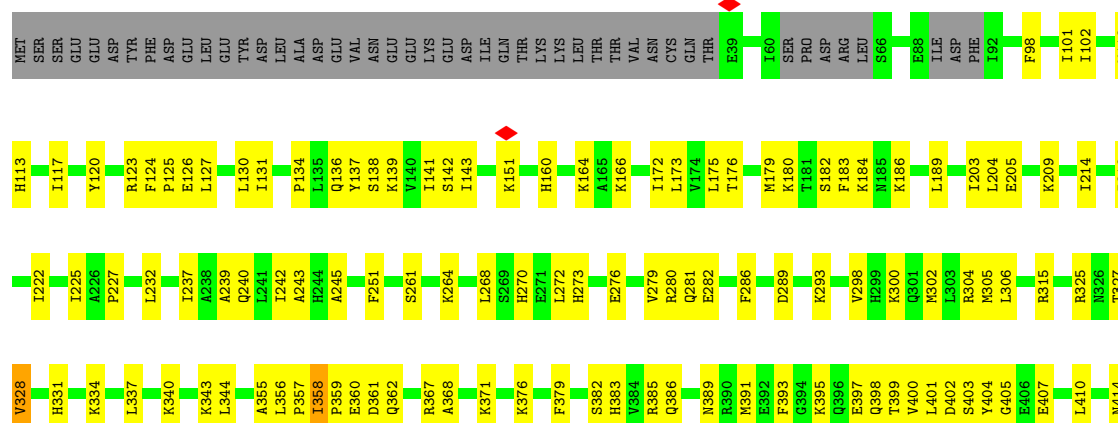
• Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

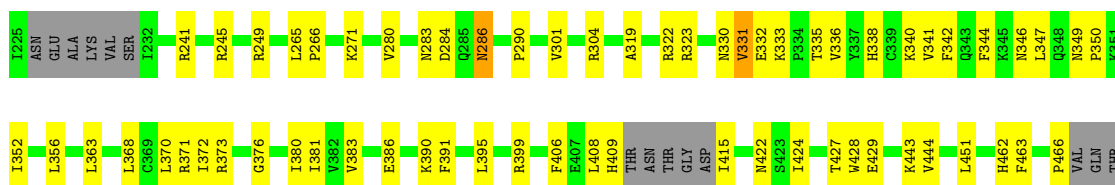
Chain K: 52% 38% 8%



• Molecule 3: Pre-mRNA-processing factor 31

Chain L: 57% 27% 16%





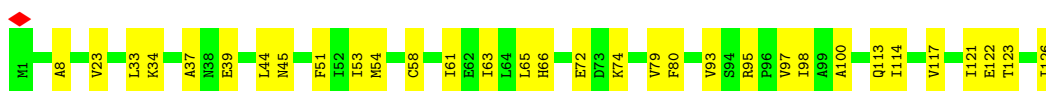
• Molecule 6: Spliceosomal protein DIB1

Chain E: 69% 29%



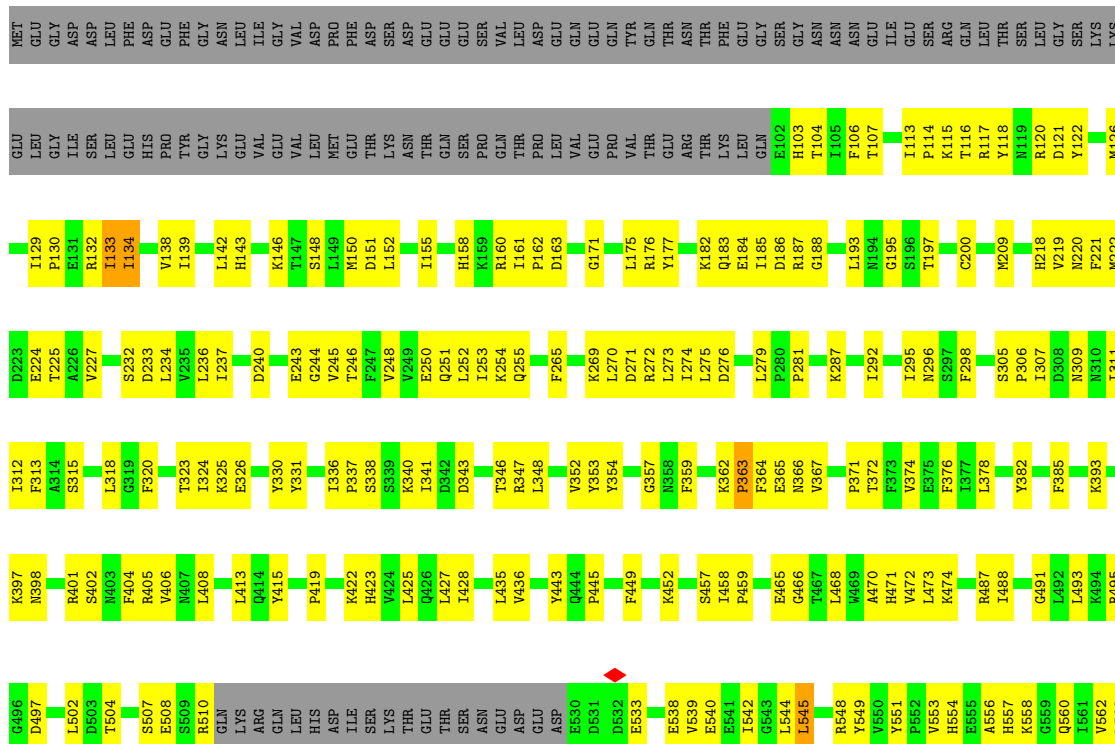
• Molecule 7: 13 kDa ribonucleoprotein-associated protein

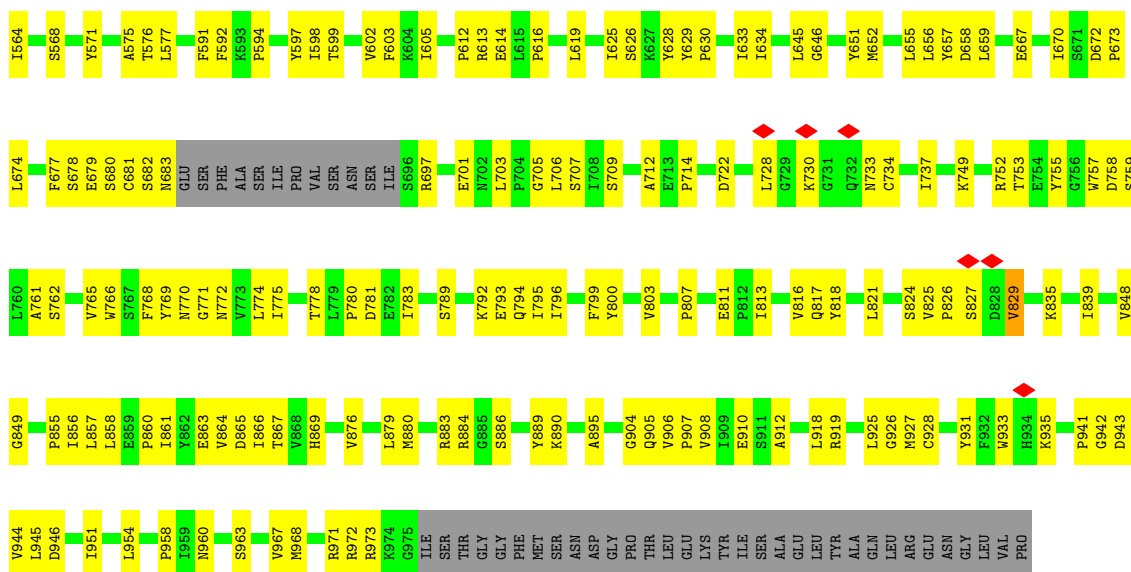
Chain M: 75% 25%



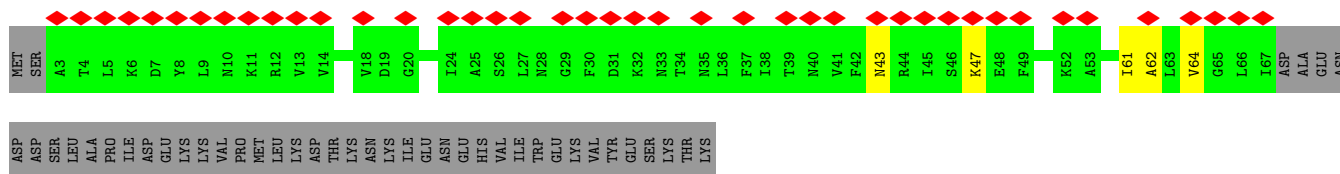
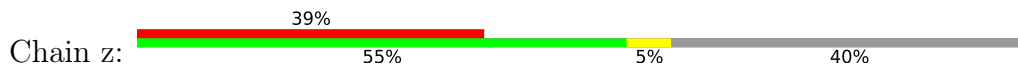
• Molecule 8: Pre-mRNA-splicing factor SNU114

Chain C: 48% 35% 16%

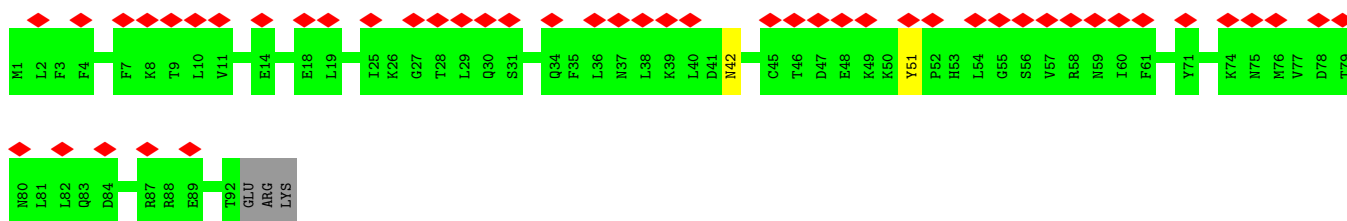




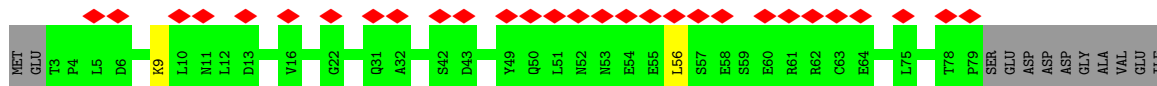
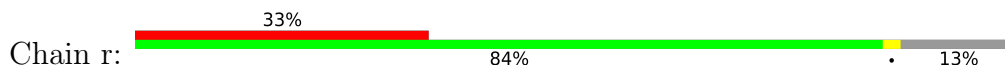
• Molecule 9: U6 snRNA-associated Sm-like protein LSm8



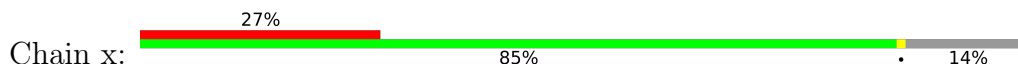
• Molecule 10: U6 snRNA-associated Sm-like protein LSm2

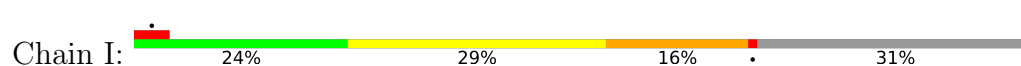


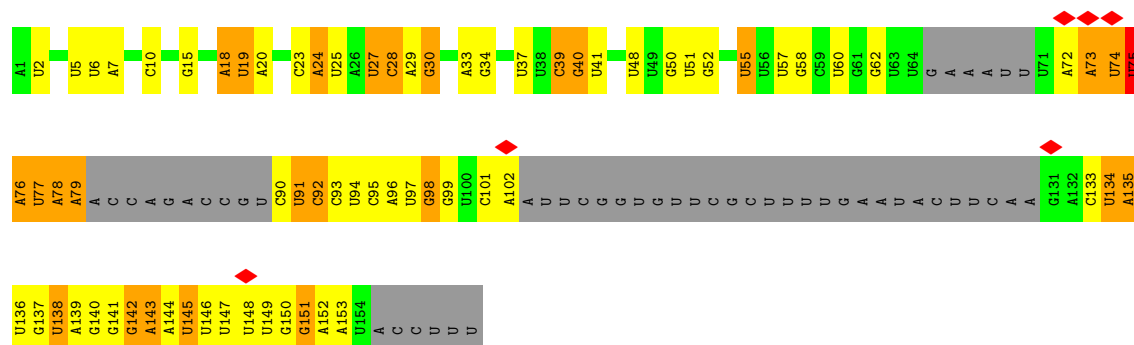
• Molecule 11: U6 snRNA-associated Sm-like protein LSm3



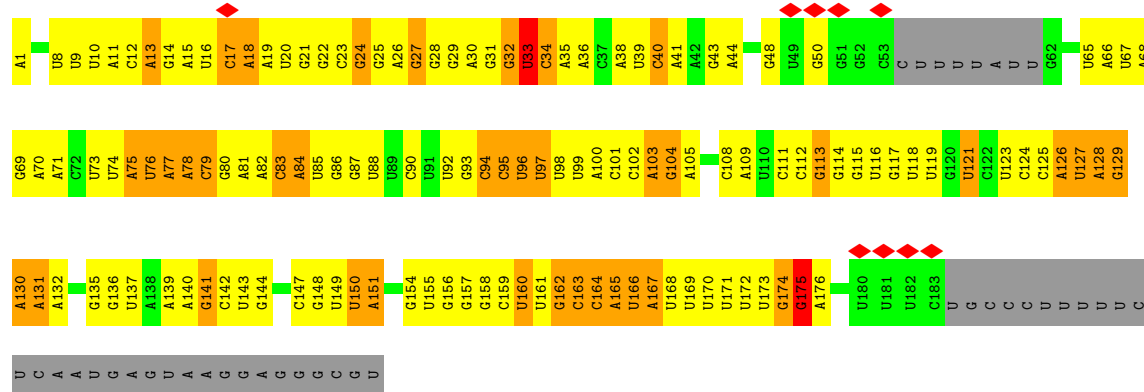
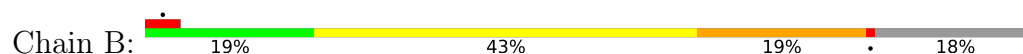
• Molecule 12: U6 snRNA-associated Sm-like protein LSm6



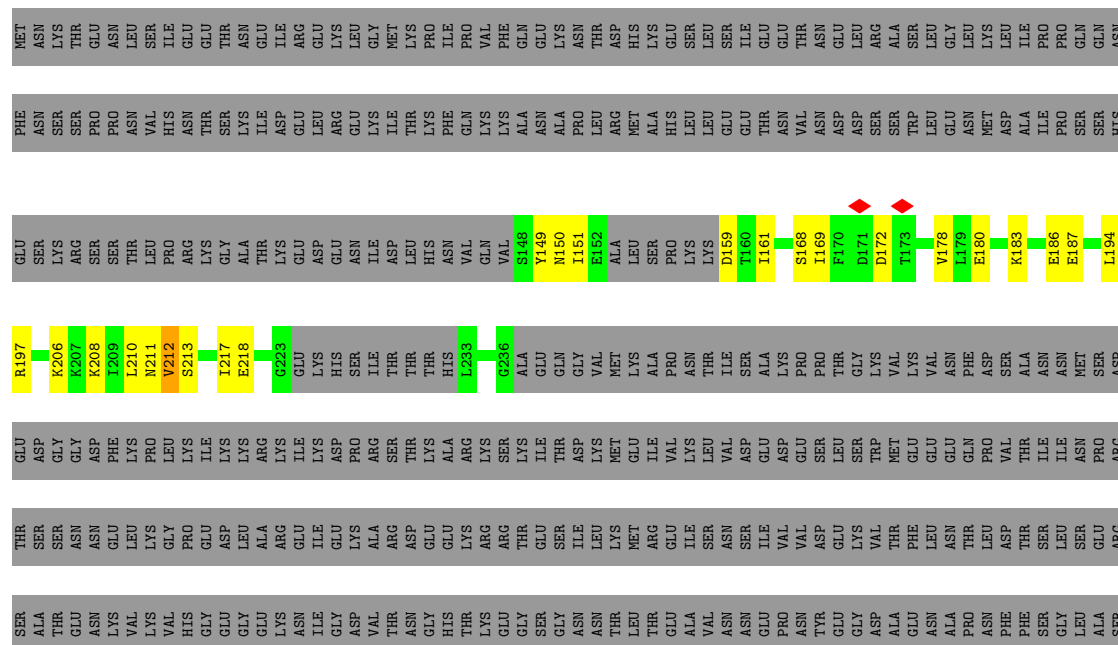


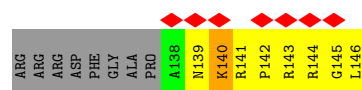


• Molecule 18: U5 snRNA

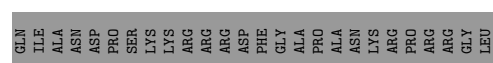
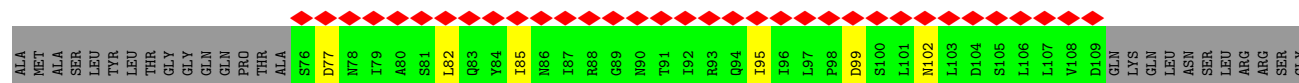
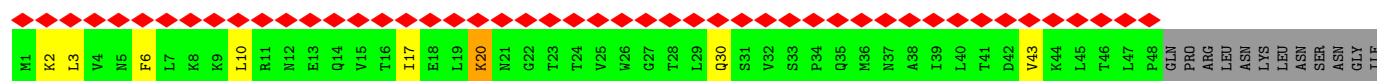


• Molecule 19: 66 kDa U4/U6.U5 small nuclear ribonucleoprotein component

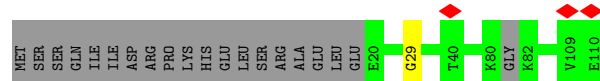
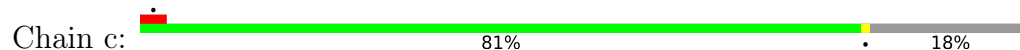




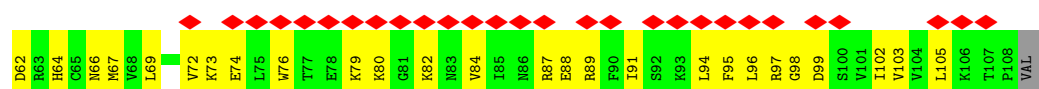
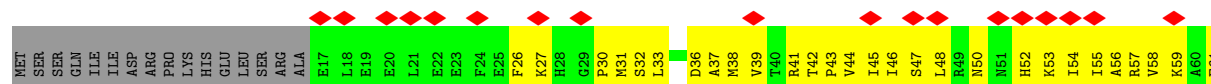
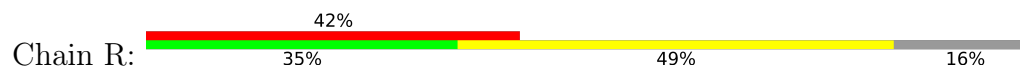
• Molecule 22: Small nuclear ribonucleoprotein Sm D1



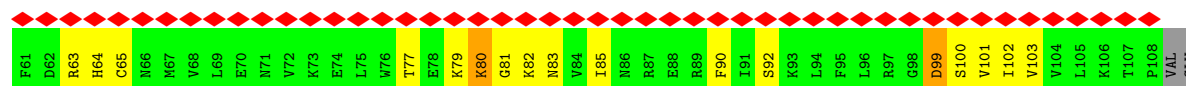
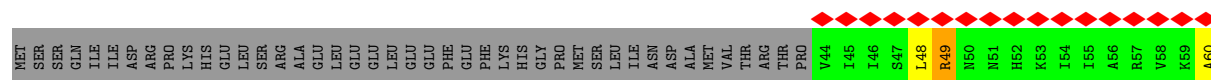
• Molecule 23: Small nuclear ribonucleoprotein Sm D2



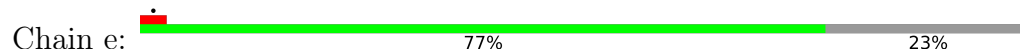
• Molecule 23: Small nuclear ribonucleoprotein Sm D2

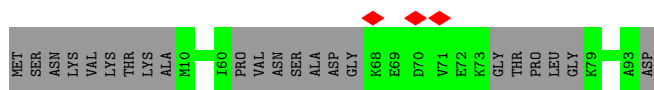


• Molecule 23: Small nuclear ribonucleoprotein Sm D2

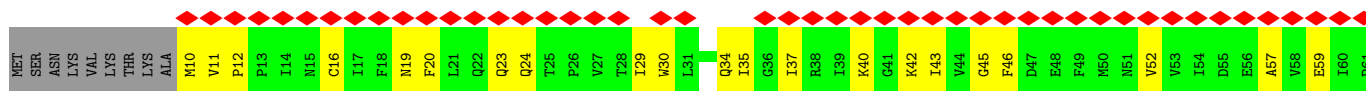
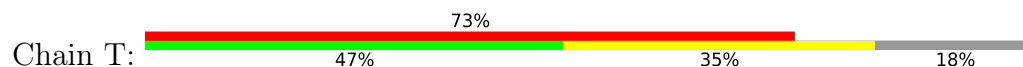


• Molecule 24: Small nuclear ribonucleoprotein E

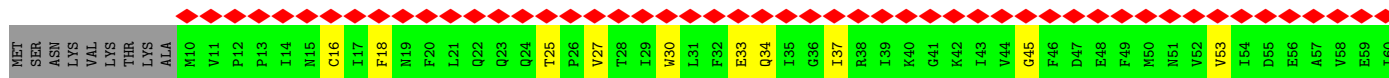
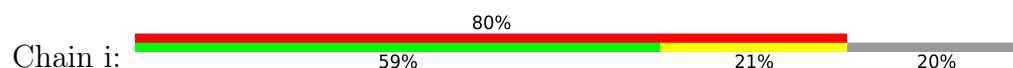




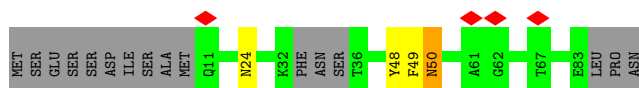
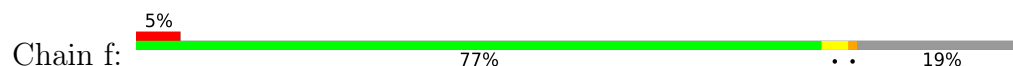
- Molecule 24: Small nuclear ribonucleoprotein E



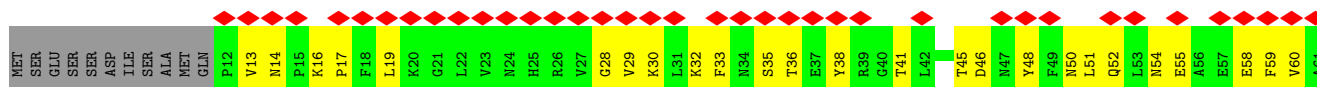
- Molecule 24: Small nuclear ribonucleoprotein E



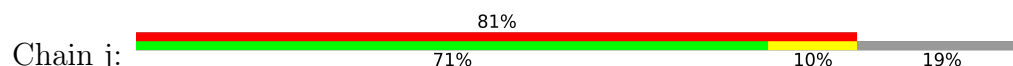
- Molecule 25: Small nuclear ribonucleoprotein F

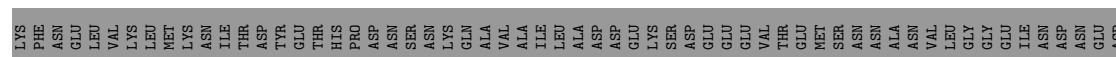


- Molecule 25: Small nuclear ribonucleoprotein F



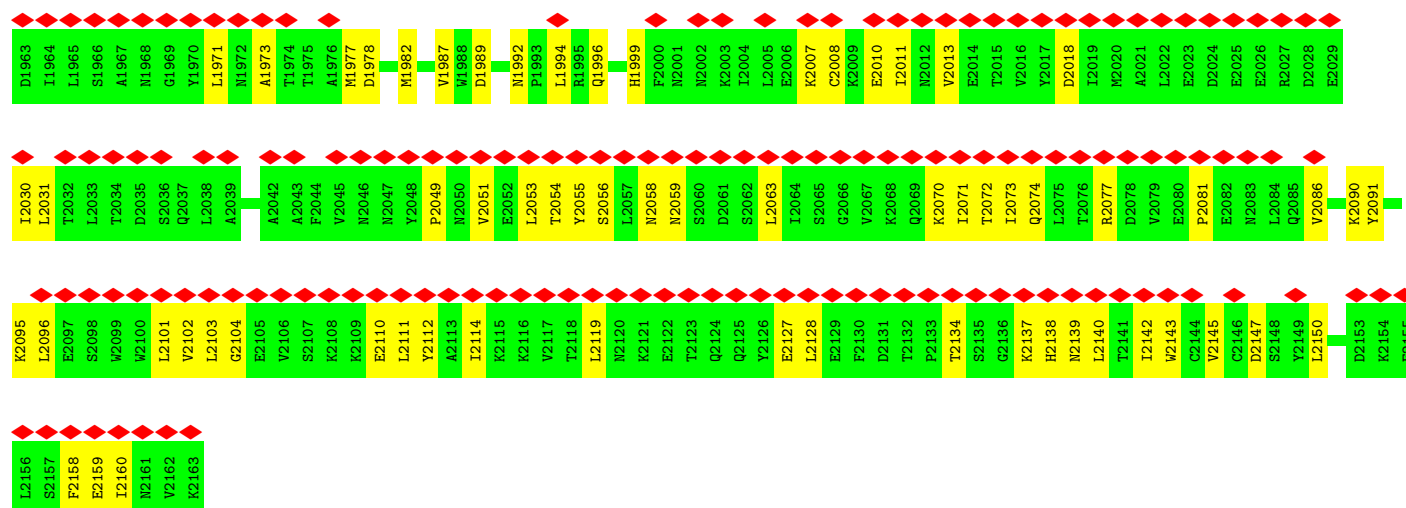
- Molecule 25: Small nuclear ribonucleoprotein F



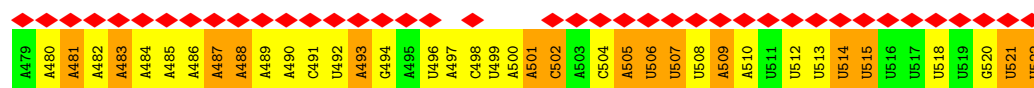
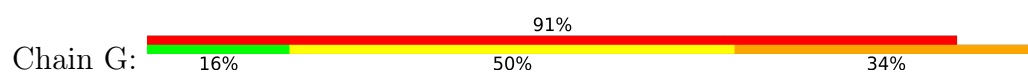




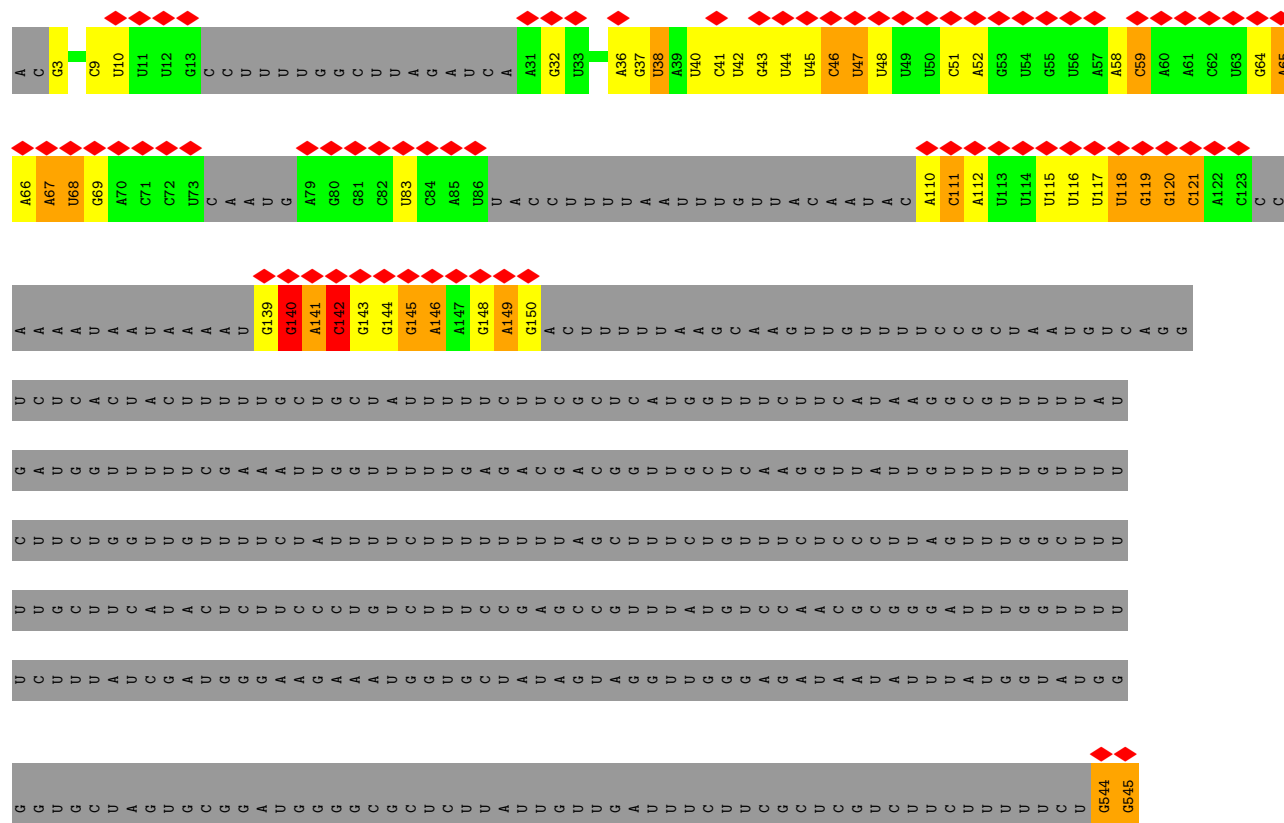
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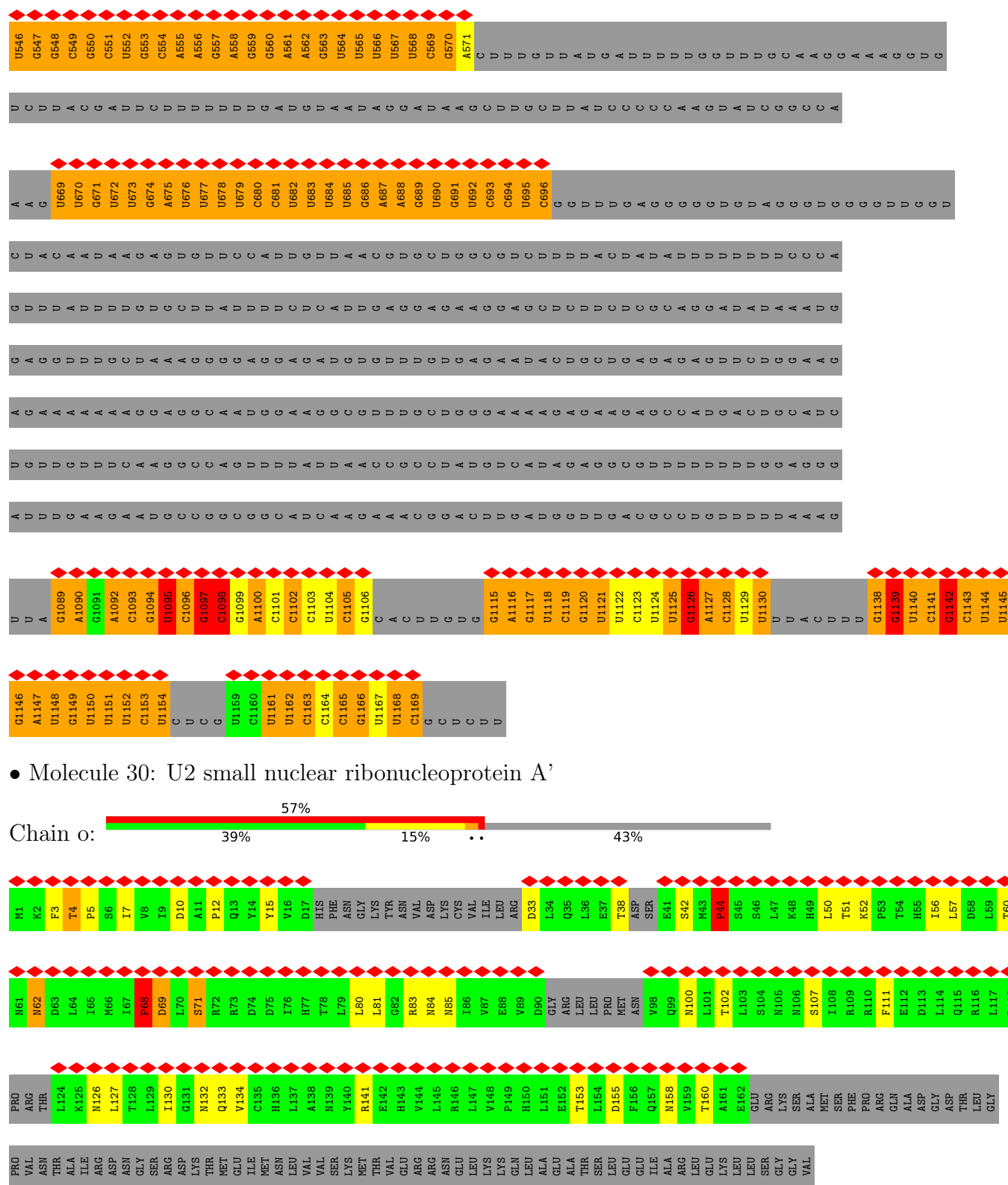


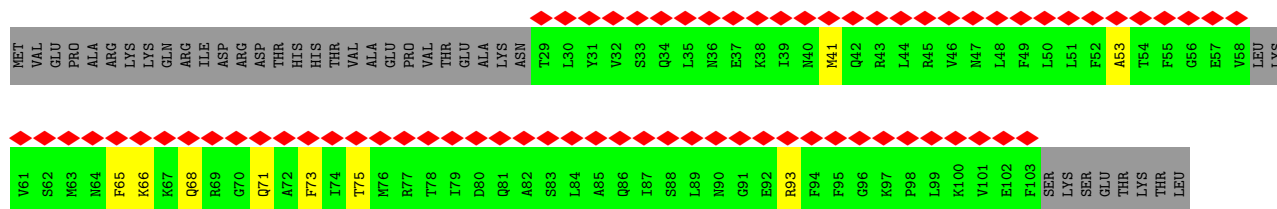
• Molecule 28: Pre-mRNA-BPS



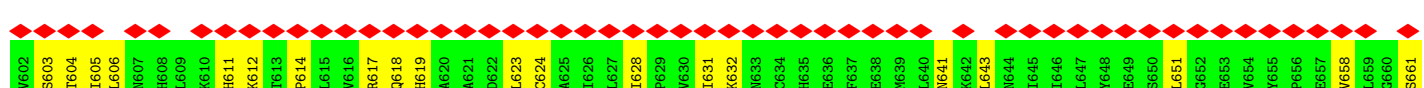
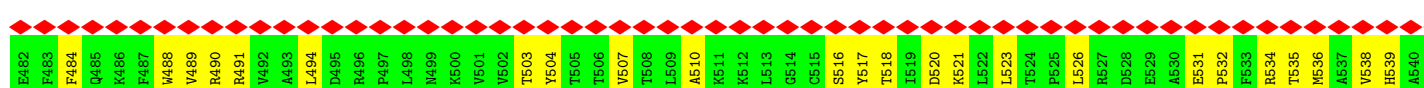
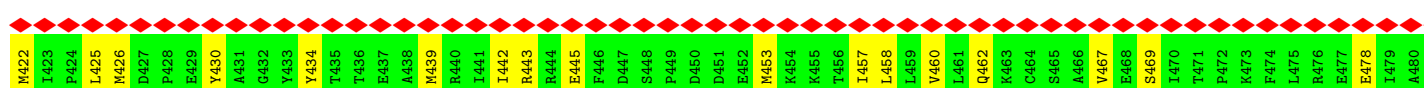
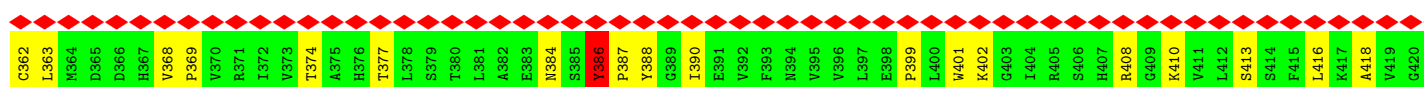
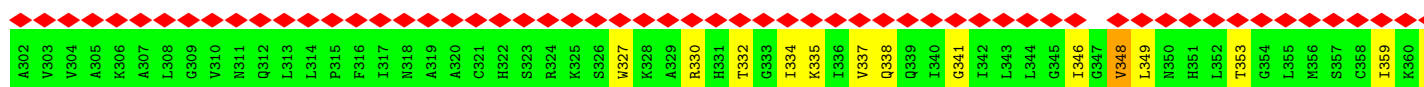
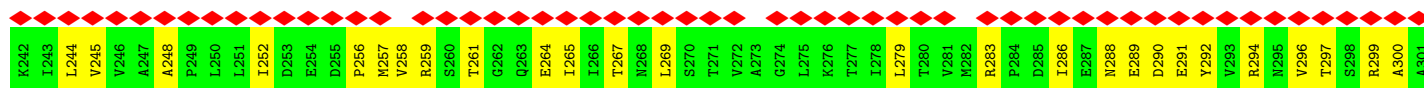
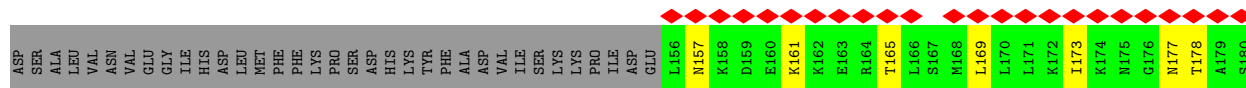
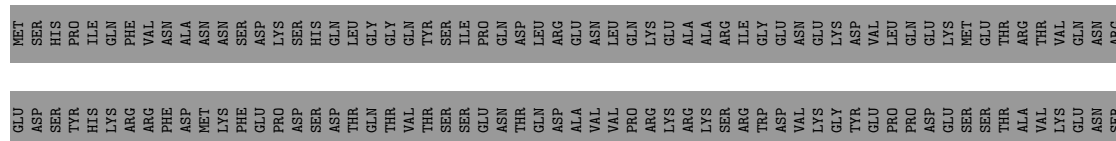
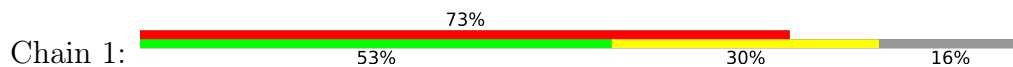
• Molecule 29: U2 snRNA

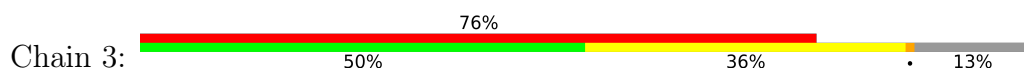




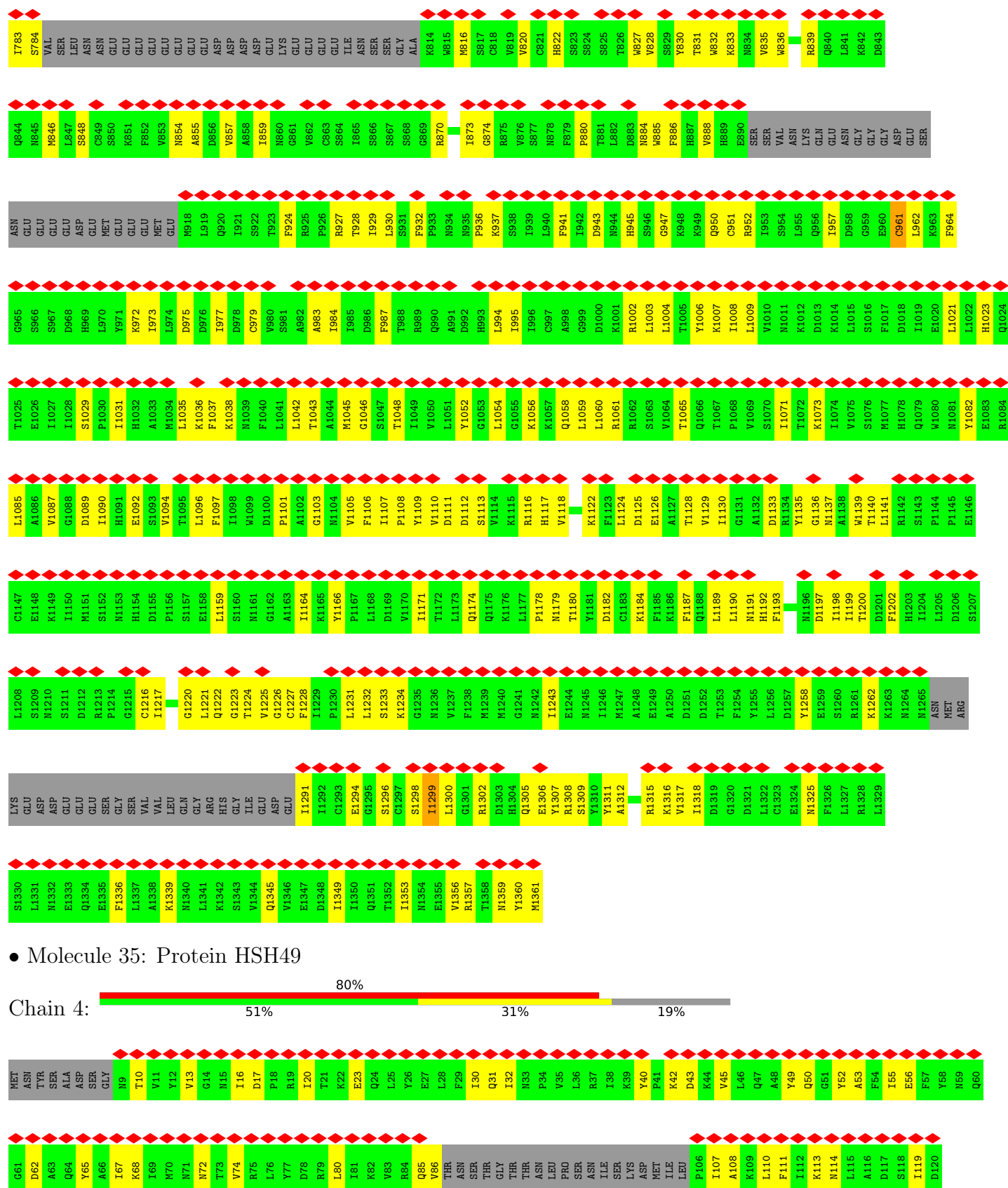


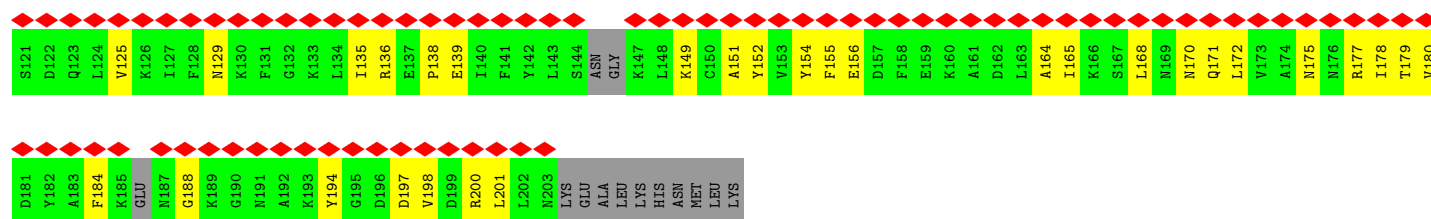
• Molecule 32: U2 snRNP component HSH155



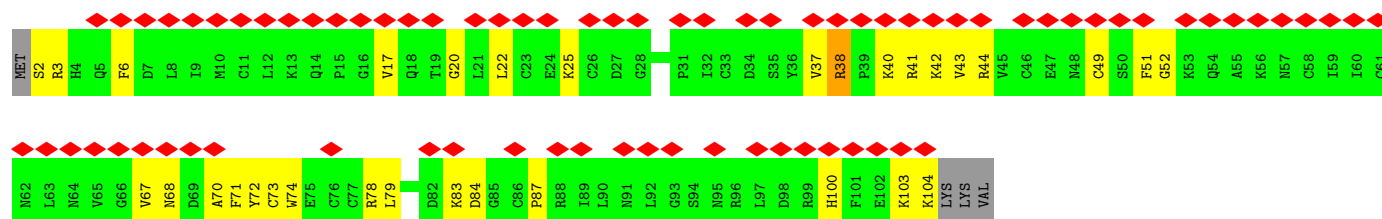


MET	TRP	GLY	GLY	LYS	MET	ALA	VAL	VAL	SER	LEU	SER	SER	PRO	HIS	THR	ALA	LYS	LEU	PHE	GLY	GLN	ALA	SER	THR	THR	MET	ALA	TYR	ASP	GLY	LEU	LYS	ARG	GLU	ALA	GLU	ARG	THR	V95	ARG	SER	ASP	HIS	ASN	ILE	THR	MET	VAL	ALA	LYS	ASP	D56	E57	L58	Y59	L60				
Y61	H62	L63	T64	L65	K66	K67	Q68	T69	N70	F71	V72	H73	S74	C75	I76	G77	H78	F79	V80	D81	L82	E83	A84	G85	S86	K87	R88	E89	Q90	S91	Q92	N93	C94	V95	A96	T97	E98	T99	H100	L101	E102	L103	Y104	D105	T106	A107	D108	G109	E110	L111	K112	L113	I114	A115	K116	F117	Q118	N119	L120	
F121	I124	T125	M127	K128	S129	L130	D131	L132	P133	H134	SER	GLY	SER	ARG	ALA	LYS	ALA	SER	ASN	W144	P145	T146	F147	L148	A149	L150	T151	S152	D153	S154	G155	N156	L157	S158	I159	V160	Q161	I162	I163	M164	H165	A166	G167	A168	L169	R170	E171	K172	T173	L174	V175	N176	Q177	P178	L179	T180	R181			
T182	T183	L184	R185	R186	V187	S188	P189	I190	S191	Y192	M193	E194	I195	D196	P197	N198	G199	R200	C201	L202	L203	L204	S205	S206	V207	E208	Q209	N210	K211	L212	C213	F214	L215	V216	D217	Y218	A219	Q220	K221	L222	R223	I224	S225	S226	P227	L228	E229	I230	L231	R232	P233	H234	M235	V236	T237	L238	D239	M240	A241	
V242	V243	D244	V245	M246	F247	M248	N249	P250	C251	F252	V253	T254	L255	E256	I257	D258	N259	A260	A261	T262	L263	L264	S265	V266	H267	L268	I269	F270	Y271	V272	L273	E274	L275	Q276	L277	N278	F279	K221	L222	V281	K282	K283	A284	D285	Y286	L287	V288	N289	P290	S291	A292	N293	F294	V295	L296	L298	P299	D300	L301	
S302	ARG	TYR	ASN	ILE	THR	SER	LEU	SER	ASP	ASN	ASN	TYR	ASP	ALA	ASP	TYR	LEU	PHE	N324	P325	F326	V327	V328	L329	G330	F331	E332	N333	H334	I335	L336	K338	D339	M340	N341	G342	F343	F344	S345	L346	K347	V348	E349	I350	P351	K352	R353	S354	I355	T356	N357	S358	R359	H360	K361					
N362	V363	T364	I365	I366	S367	G368	V369	V370	Q371	K372	L373	K374	N375	D376	F377	F378	V379	L380	L381	Q382	S383	N384	H385	G386	D387	L388	F389	K390	L391	T392	V393	S394	P395	D396	T397	N398	D399	R400	M401	R402	P403	L404	V405	Q406	E407	P408	S409	F410	D411	T412	T413	Q414	M415	S416	H417	Q418	L419	H420	I421	
F422	K423	M424	G425	Y426	L427	F428	A429	L430	S431	E432	M433	N434	N435	N436	F437	L438	F439	Q440	F441	E442	K443	L444	O445	V446	E447	K448	M449	D450	F451	S452	N453	V454	L455	T456	S457	K458	D459	P460	M461	K462	S463	L464	V465	P466	E467	P468	S469	T470	K471	L472	Q473	M474	L475	S476	I477	L478	S479	Q480	Q481	
L482	M483	L484	N485	P486	S487	L488	K489	L492	V493	S494	D495	S496	P497	L498	S499	I500	A501	T502	K503	H504	F505	T506	N507	N508	K509	I510	I511	T512	L513	T514	N515	A516	V517	N518	Y519	S520	N521	L522	S523	S524	T525	S526	L527	P528	P529	N530	A531	T532	K533	L534	M535	L536	I537	P538	D539	A541	T542			
T543	G544	D545	N546	M547	L548	L549	L550	F551	I552	T553	F554	P555	K556	K557	T558	M559	I560	L561	Q562	I563	D564	M565	E566	S567	M568	E569	E570	L571	THR	PRO	ASP	GLU	ALA	THR	ARG	SER	ALA	PHE	K582	L583	S584	Q585	D586	T587	T588	I589	H590	T591	C592	L593	M594	G595	L596	H597	S598	I599	T600	Q601	V602	
G603	T604	A605	E606	L607	H608	H609	I610	V611	P612	T613	G614	K615	S616	R617	Y618	S619	N620	K621	L622	T623	W624	V625	P626	P627	A628	G629	I630	R631	I632	V633	G634	A635	T636	S637	S638	K639	T640	Q641	L642	I643	F644	S645	L646	V647	S648	N649	L650	L651	V652	Y653	S596	F654	K655	I656	D657	V658	S659	S660	D661	S662
L663	I664	E665	L666	T667	T668	H669	P670	E671	L672	D673	T674	M675	P676	S677	K678	V679	A680	I681	V682	Q683	D684	T685	Q686	H687	A688	D689	L690	L691	A692	I693	A694	D695	N696	E697	M698	I700	K701	I702	M703	S704	L705	LYS	ASP	GLN	LYS	GLU	D711	F712	L713	T714	K715	P716	I717	S717	L718	Q719	L720	V721	S722	
E723	K724	I725	S726	D727	T728	H729	M730	V731	R732	D733	S734	S735	I736	G737	Q738	L739	N740	L741	H742	V743	G744	L745	E746	N747	G748	V749	Y750	M751	K752	F753	H754	I755	G756	D757	V758	D759	G760	K761	Q762	L763	S764	I765	K766	R767	N768	F769	L770	G771	L772	K773	P774	V775	S776	L777	Y778	L779	V780	R781	E782	

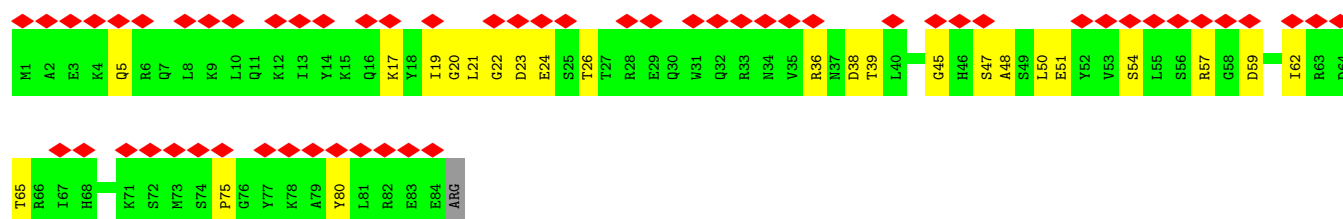




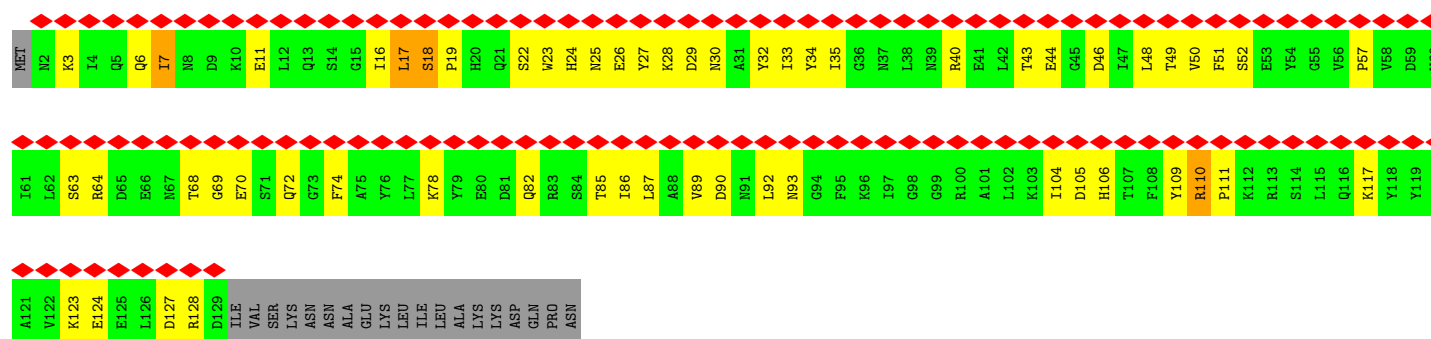
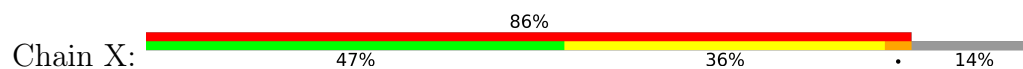
• Molecule 36: Pre-mRNA-splicing factor RDS3



• Molecule 37: RDS3 complex subunit 10

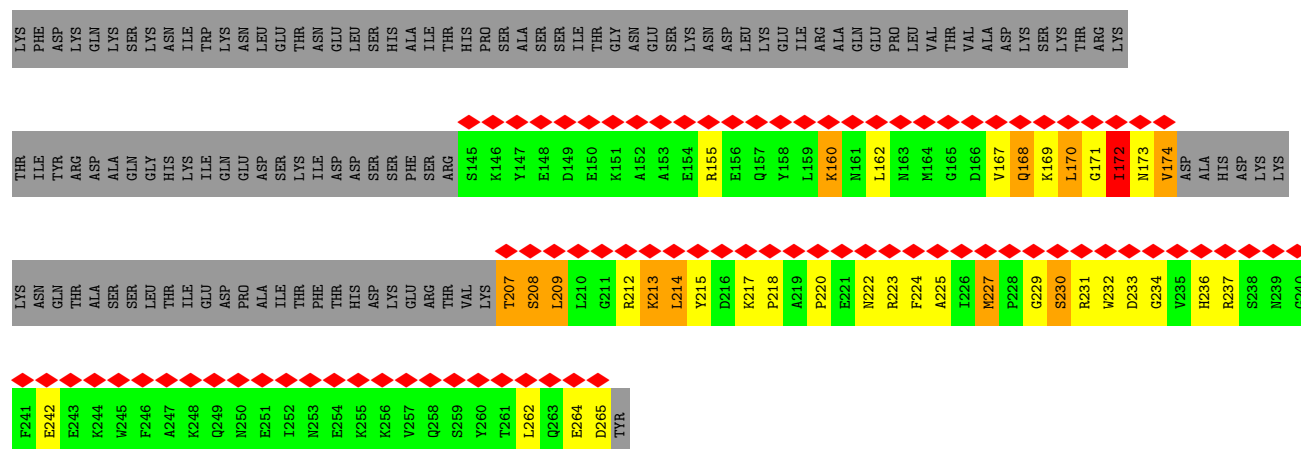


• Molecule 38: U2 snRNP component IST3

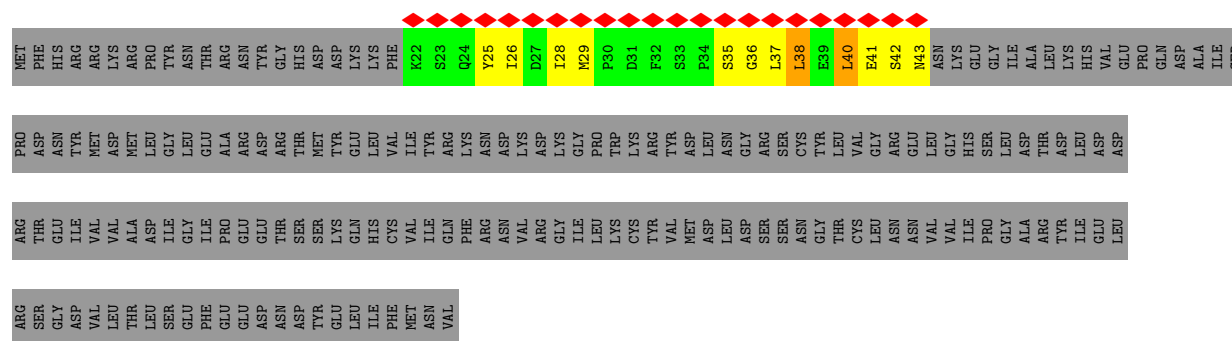


• Molecule 39: Pre-mRNA-splicing factor CWC26

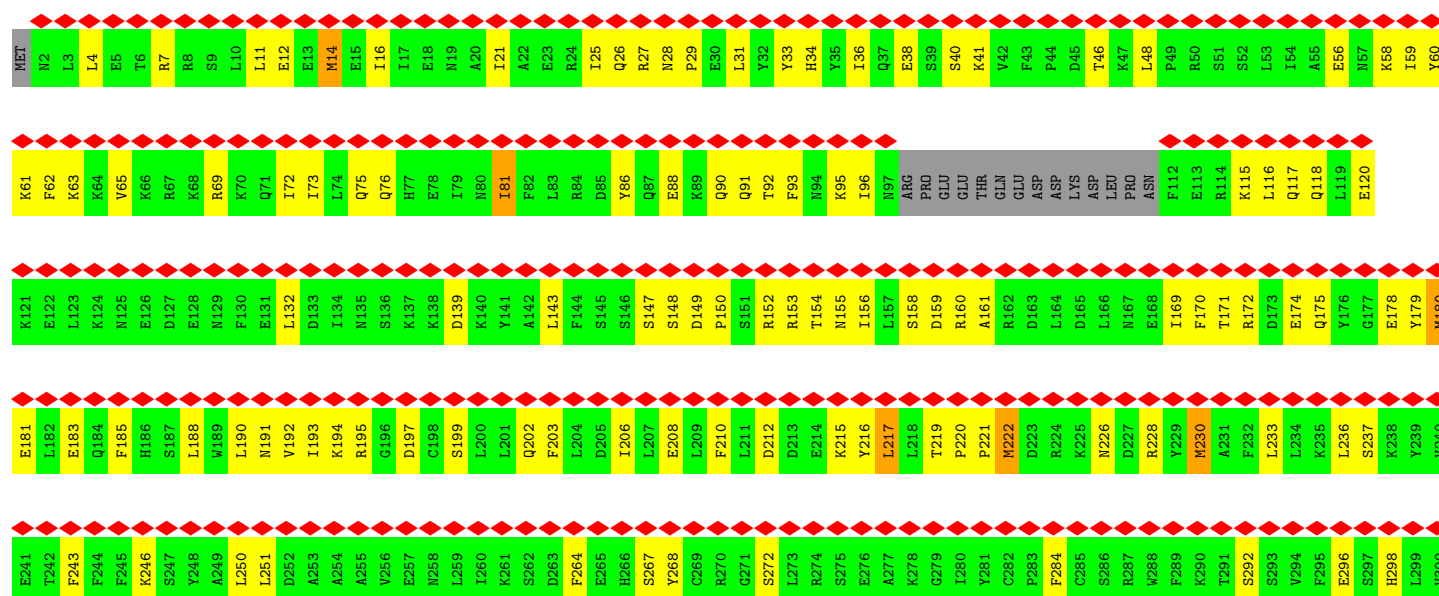
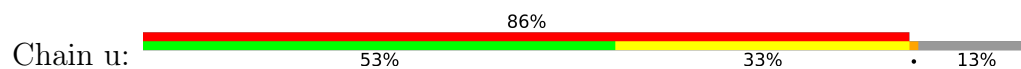


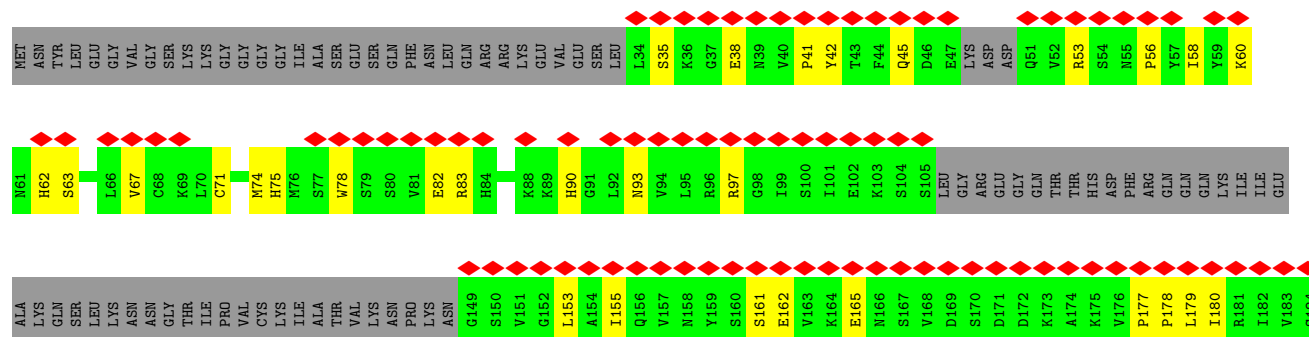


• Molecule 40: Pre-mRNA leakage protein 1



• Molecule 41: Pre-mRNA-splicing factor PRP9







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	500657	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.386	Depositor
Minimum map value	-0.170	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.023	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	0.26	1/18332 (0.0%)	0.54	7/24851 (0.0%)
2	K	0.30	0/3431	0.65	4/4631 (0.1%)
3	L	0.24	0/3219	0.53	0/4332
4	N	0.21	0/4937	0.54	2/6704 (0.0%)
5	J	0.22	0/2485	0.52	2/3333 (0.1%)
6	E	0.25	0/1167	0.52	0/1571
7	M	0.27	0/963	0.55	0/1310
8	C	0.24	0/6874	0.55	0/9305
9	z	0.78	0/259	1.35	4/322 (1.2%)
10	q	0.83	0/367	1.31	2/457 (0.4%)
11	r	0.99	0/307	1.47	2/382 (0.5%)
12	x	0.83	0/295	1.41	2/367 (0.5%)
13	t	0.81	0/306	1.26	0/379
14	y	0.83	0/262	1.22	2/324 (0.6%)
15	s	0.79	0/306	1.39	2/379 (0.5%)
16	F	0.20	0/2277	0.39	0/3534
17	I	0.32	3/2604 (0.1%)	0.43	0/4046
18	B	0.25	1/4151 (0.0%)	0.47	1/6462 (0.0%)
19	O	0.19	0/573	0.53	0/763
20	S	0.33	0/641	0.56	0/868
20	d	0.47	0/315	0.92	0/392
20	l	0.59	1/620 (0.2%)	0.95	1/841 (0.1%)
21	P	0.33	0/567	0.56	0/762
21	a	0.51	0/290	0.87	0/359
21	h	0.55	0/615	0.77	0/829
22	Q	0.35	0/756	0.72	1/1023 (0.1%)
22	b	0.51	0/305	0.89	0/376
22	m	0.59	0/649	0.81	0/880
23	R	0.29	0/764	0.55	0/1026
23	c	0.49	0/358	0.94	2/444 (0.5%)
23	n	0.60	0/535	0.80	0/717
24	T	0.46	1/612 (0.2%)	0.65	1/830 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
24	e	0.53	0/285	0.85	0/351
24	i	0.64	0/585	0.86	0/795
25	U	0.28	0/597	0.62	0/807
25	f	0.53	0/278	0.80	0/344
25	j	0.61	0/564	0.88	0/761
26	V	0.43	2/582 (0.3%)	0.80	2/785 (0.3%)
26	g	0.44	0/277	0.83	0/341
26	k	0.52	0/532	0.82	0/715
27	D	0.32	0/13899	0.67	10/18845 (0.1%)
28	G	0.14	0/1038	0.36	0/1611
29	H	0.99	57/4835 (1.2%)	1.63	141/7502 (1.9%)
30	o	1.24	6/839 (0.7%)	2.35	44/1127 (3.9%)
31	p	0.98	1/467 (0.2%)	1.88	7/623 (1.1%)
32	1	0.19	0/6600	0.49	2/8962 (0.0%)
33	2	0.16	0/1775	0.41	0/2402
34	3	0.22	0/9564	0.56	0/12963
35	4	0.13	0/1453	0.35	0/1954
36	5	0.21	0/827	0.47	0/1105
37	6	0.20	0/702	0.45	0/939
38	X	0.64	0/1071	0.81	0/1445
39	Y	0.67	0/743	1.01	2/994 (0.2%)
40	Z	0.60	0/176	0.72	0/237
41	u	0.41	10/3972 (0.3%)	0.65	2/5322 (0.0%)
42	w	0.58	8/1105 (0.7%)	0.64	0/1475
43	v	0.33	2/1396 (0.1%)	0.63	1/1881 (0.1%)
All	All	0.40	93/114304 (0.1%)	0.73	246/157085 (0.2%)

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	1
2	K	0	2
3	L	0	1
4	N	0	2
8	C	0	2
27	D	0	4
32	1	0	4
34	3	0	1
41	u	0	2
All	All	0	19

All (93) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	1161	U	O3'-P	-12.47	1.42	1.61
29	H	1092	A	O3'-P	-11.86	1.43	1.61
29	H	1163	C	O5'-C5'	11.04	1.59	1.42
30	o	69	ASP	CA-CB	-10.73	1.38	1.53
29	H	1116	A	O3'-P	-9.22	1.47	1.61
29	H	1116	A	C3'-O3'	-8.39	1.29	1.42
29	H	1162	U	O5'-C5'	7.83	1.54	1.42
29	H	1165	C	O5'-C5'	7.71	1.54	1.42
24	T	12	PRO	CA-C	7.41	1.55	1.51
29	H	1154	U	C1'-N1	7.24	1.59	1.48
29	H	546	U	C1'-N1	7.13	1.59	1.48
29	H	1140	U	C1'-N1	7.11	1.59	1.48
29	H	564	U	C1'-N1	7.08	1.59	1.48
29	H	684	U	C1'-N1	7.06	1.59	1.48
29	H	679	U	C1'-N1	7.05	1.59	1.48
29	H	673	U	C1'-N1	7.04	1.59	1.48
29	H	566	U	C1'-N1	7.03	1.58	1.48
29	H	682	U	C1'-N1	7.02	1.58	1.48
29	H	685	U	C1'-N1	7.02	1.58	1.48
29	H	669	U	C1'-N1	7.01	1.58	1.48
29	H	567	U	C1'-N1	7.01	1.58	1.48
29	H	552	U	C1'-N1	7.01	1.58	1.48
29	H	678	U	C1'-N1	7.01	1.58	1.48
29	H	565	U	C1'-N1	7.00	1.58	1.48
29	H	672	U	C1'-N1	6.98	1.58	1.48
29	H	568	U	C1'-N1	6.98	1.58	1.48
29	H	676	U	C1'-N1	6.96	1.58	1.48
29	H	1127	A	O3'-P	-6.94	1.50	1.61
30	o	102	THR	CB-OG1	6.92	1.54	1.43
29	H	1167	U	O3'-P	6.87	1.71	1.61
1	A	266	LEU	C-N	6.79	1.49	1.33
29	H	1169	C	C1'-N1	6.71	1.58	1.48
30	o	51	THR	CB-OG1	6.58	1.54	1.43
29	H	696	C	C1'-N1	6.57	1.58	1.48
18	B	175	G	C1'-N9	-6.56	1.37	1.47
29	H	693	C	C1'-N1	6.54	1.58	1.48
29	H	554	C	C1'-N1	6.50	1.58	1.48
29	H	1164	C	O3'-P	-6.50	1.51	1.61
29	H	694	C	C1'-N1	6.50	1.58	1.48
29	H	680	C	C1'-N1	6.49	1.58	1.48
29	H	549	C	C1'-N1	6.49	1.58	1.48
29	H	551	C	C1'-N1	6.47	1.58	1.48

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	681	C	C1'-N1	6.47	1.58	1.48
42	w	224	MET	SD-CE	6.46	1.95	1.79
29	H	569	C	C1'-N1	6.44	1.58	1.48
41	u	230	MET	SD-CE	6.43	1.95	1.79
41	u	180	MET	CG-SD	6.41	1.96	1.80
42	w	93	MET	SD-CE	6.35	1.95	1.79
42	w	125	MET	SD-CE	6.33	1.95	1.79
43	v	226	MET	SD-CE	6.29	1.95	1.79
41	u	14	MET	SD-CE	6.28	1.95	1.79
41	u	351	MET	SD-CE	6.23	1.95	1.79
31	p	75	THR	CB-OG1	6.19	1.53	1.43
41	u	180	MET	SD-CE	6.17	1.95	1.79
42	w	113	MET	SD-CE	6.16	1.95	1.79
41	u	222	MET	SD-CE	6.14	1.95	1.79
29	H	1116	A	O5'-C5'	6.13	1.51	1.42
42	w	113	MET	CG-SD	6.08	1.96	1.80
30	o	153	THR	CB-OG1	6.05	1.53	1.43
29	H	1151	U	O5'-C5'	-6.03	1.33	1.42
29	H	1096	C	O5'-C5'	6.01	1.51	1.42
29	H	690	U	C1'-N1	5.95	1.57	1.48
29	H	695	U	C1'-N1	5.94	1.57	1.48
41	u	14	MET	CG-SD	5.94	1.95	1.80
43	v	226	MET	CG-SD	5.94	1.95	1.80
29	H	692	U	C1'-N1	5.91	1.57	1.48
29	H	683	U	C1'-N1	5.90	1.57	1.48
42	w	224	MET	CG-SD	5.89	1.95	1.80
29	H	121	C	C1'-N1	5.87	1.57	1.48
42	w	93	MET	CG-SD	5.84	1.95	1.80
30	o	38	THR	CB-OG1	5.84	1.53	1.43
41	u	230	MET	CG-SD	5.83	1.95	1.80
29	H	677	U	C1'-N1	5.82	1.57	1.48
29	H	670	U	C1'-N1	5.82	1.57	1.48
41	u	351	MET	CG-SD	5.80	1.95	1.80
17	I	74	U	C1'-N1	5.79	1.57	1.48
42	w	125	MET	CG-SD	5.78	1.95	1.80
30	o	160	THR	CB-OG1	5.71	1.52	1.43
26	V	50	ASP	C-N	5.66	1.41	1.33
17	I	73	A	C1'-N9	-5.65	1.38	1.47
17	I	75	U	C1'-N1	5.63	1.55	1.47
29	H	1096	C	O3'-P	5.60	1.69	1.61
29	H	1128	C	C5'-C4'	-5.55	1.43	1.51
41	u	222	MET	CG-SD	5.54	1.94	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	H	146	A	O5'-C5'	5.47	1.50	1.42
29	H	1161	U	C3'-O3'	-5.36	1.34	1.42
29	H	1095	U	O3'-P	5.21	1.69	1.61
20	l	82	PRO	N-CD	5.16	1.55	1.47
29	H	1127	A	O5'-C5'	5.12	1.50	1.42
29	H	1117	G	C5'-C4'	5.10	1.58	1.51
29	H	1162	U	P-O5'	5.05	1.67	1.59
26	V	51	PRO	N-CD	5.03	1.54	1.47
29	H	1163	C	P-O5'	5.03	1.67	1.59

All (246) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1151	U	C4'-C3'-O3'	-19.99	83.02	113.00
29	H	1092	A	C2'-C3'-O3'	17.86	140.49	113.70
29	H	1097	G	C3'-C2'-O2'	16.45	135.38	110.70
30	o	44	PRO	N-CA-CB	15.88	113.87	103.23
29	H	1093	C	P-O5'-C5'	15.75	144.53	120.90
29	H	1147	A	C5'-C4'-C3'	-15.11	93.34	116.00
29	H	1168	U	C4'-C3'-O3'	-15.00	90.50	113.00
29	H	1148	U	C4'-C3'-O3'	-14.34	91.50	113.00
29	H	1092	A	C4'-C3'-O3'	-13.40	92.90	113.00
29	H	1151	U	P-O5'-C5'	12.43	139.54	120.90
30	o	81	LEU	CA-C-N	12.12	131.62	120.10
30	o	81	LEU	C-N-CA	12.12	131.62	120.10
29	H	1096	C	C1'-C2'-O2'	-11.91	90.53	108.40
29	H	1117	G	C5'-C4'-C3'	-11.64	98.54	116.00
29	H	1162	U	C5'-C4'-O4'	11.41	126.92	109.80
29	H	1162	U	C2'-C3'-O3'	-11.21	96.88	113.70
29	H	1097	G	C2'-C3'-O3'	-10.94	97.30	113.70
29	H	1163	C	C5'-C4'-C3'	-10.37	100.44	116.00
29	H	1147	A	C4'-C3'-O3'	10.34	128.51	113.00
29	H	1147	A	P-O5'-C5'	10.26	136.28	120.90
29	H	1098	C	N1-C1'-C2'	-10.24	96.64	112.00
29	H	1165	C	C4'-C3'-O3'	10.08	128.12	113.00
29	H	1162	U	C5'-C4'-C3'	-9.77	101.34	116.00
29	H	1089	G	C4'-C3'-O3'	9.66	127.49	113.00
29	H	1115	G	C4'-C3'-O3'	9.40	127.10	113.00
29	H	1152	U	P-O5'-C5'	9.29	134.83	120.90
29	H	1092	A	P-O5'-C5'	9.13	134.60	120.90
30	o	12	PRO	N-CA-CB	9.11	111.39	103.19
29	H	148	G	C5'-C4'-C3'	-8.82	102.76	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1165	C	C5'-C4'-C3'	-8.81	102.78	116.00
29	H	1167	U	C2'-C3'-O3'	8.77	126.85	113.70
29	H	1117	G	C5'-C4'-O4'	8.71	122.87	109.80
29	H	674	G	O3'-P-O5'	-8.64	91.04	104.00
29	H	558	A	O3'-P-O5'	-8.63	91.06	104.00
29	H	570	G	O3'-P-O5'	-8.63	91.06	104.00
29	H	683	U	O3'-P-O5'	-8.63	91.06	104.00
29	H	559	G	O3'-P-O5'	-8.61	91.08	104.00
29	H	547	G	O3'-P-O5'	-8.61	91.09	104.00
29	H	567	U	O3'-P-O5'	-8.61	91.09	104.00
29	H	679	U	O3'-P-O5'	-8.61	91.09	104.00
29	H	688	A	O3'-P-O5'	-8.60	91.10	104.00
29	H	545	G	O3'-P-O5'	-8.60	91.10	104.00
29	H	565	U	O3'-P-O5'	-8.60	91.10	104.00
29	H	684	U	O3'-P-O5'	-8.60	91.10	104.00
29	H	686	G	O3'-P-O5'	-8.60	91.10	104.00
29	H	671	G	O3'-P-O5'	-8.60	91.10	104.00
29	H	552	U	O3'-P-O5'	-8.60	91.11	104.00
29	H	563	G	O3'-P-O5'	-8.59	91.11	104.00
29	H	681	C	O3'-P-O5'	-8.59	91.11	104.00
29	H	693	C	O3'-P-O5'	-8.59	91.11	104.00
29	H	554	C	O3'-P-O5'	-8.59	91.12	104.00
29	H	560	G	O3'-P-O5'	-8.59	91.12	104.00
29	H	676	U	O3'-P-O5'	-8.59	91.12	104.00
29	H	678	U	O3'-P-O5'	-8.59	91.12	104.00
29	H	569	C	O3'-P-O5'	-8.59	91.12	104.00
29	H	675	A	O3'-P-O5'	-8.58	91.12	104.00
29	H	548	G	O3'-P-O5'	-8.58	91.13	104.00
29	H	551	C	O3'-P-O5'	-8.58	91.13	104.00
29	H	553	G	O3'-P-O5'	-8.58	91.13	104.00
29	H	670	U	O3'-P-O5'	-8.58	91.13	104.00
29	H	682	U	O3'-P-O5'	-8.58	91.13	104.00
29	H	550	G	O3'-P-O5'	-8.57	91.14	104.00
29	H	556	A	O3'-P-O5'	-8.57	91.14	104.00
29	H	672	U	O3'-P-O5'	-8.57	91.14	104.00
29	H	677	U	O3'-P-O5'	-8.57	91.14	104.00
29	H	546	U	O3'-P-O5'	-8.57	91.14	104.00
29	H	692	U	O3'-P-O5'	-8.57	91.14	104.00
29	H	564	U	O3'-P-O5'	-8.57	91.15	104.00
29	H	557	G	O3'-P-O5'	-8.57	91.15	104.00
29	H	561	A	O3'-P-O5'	-8.57	91.15	104.00
29	H	669	U	O3'-P-O5'	-8.57	91.15	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	691	G	O3'-P-O5'	-8.57	91.15	104.00
29	H	544	G	O3'-P-O5'	-8.56	91.15	104.00
29	H	566	U	O3'-P-O5'	-8.56	91.16	104.00
29	H	673	U	O3'-P-O5'	-8.56	91.16	104.00
29	H	562	A	O3'-P-O5'	-8.56	91.16	104.00
29	H	685	U	O3'-P-O5'	-8.56	91.16	104.00
29	H	694	C	O3'-P-O5'	-8.56	91.16	104.00
29	H	1096	C	C2'-C3'-O3'	-8.56	100.86	113.70
29	H	549	C	O3'-P-O5'	-8.55	91.17	104.00
29	H	689	G	O3'-P-O5'	-8.55	91.17	104.00
29	H	690	U	O3'-P-O5'	-8.55	91.17	104.00
29	H	695	U	O3'-P-O5'	-8.55	91.17	104.00
29	H	568	U	O3'-P-O5'	-8.55	91.18	104.00
29	H	680	C	O3'-P-O5'	-8.54	91.18	104.00
29	H	555	A	O3'-P-O5'	-8.54	91.19	104.00
29	H	687	A	O3'-P-O5'	-8.53	91.20	104.00
20	l	81	ALA	C-N-CD	8.51	139.31	120.60
29	H	1168	U	P-O5'-C5'	-8.47	108.19	120.90
29	H	1161	U	C5'-C4'-C3'	-8.27	103.60	116.00
29	H	1093	C	C5'-C4'-C3'	-8.25	103.63	116.00
30	o	5	PRO	N-CA-CB	8.19	112.00	103.23
29	H	1096	C	C4'-C3'-O3'	8.18	125.27	113.00
29	H	1169	C	P-O5'-C5'	-8.16	108.67	120.90
30	o	107	SER	N-CA-C	8.03	122.86	112.26
29	H	1096	C	C3'-C2'-O2'	8.02	122.72	110.70
30	o	15	TYR	CA-C-O	-7.99	111.81	120.36
29	H	1163	C	C5'-C4'-O4'	7.98	121.77	109.80
29	H	1162	U	C4'-C3'-O3'	7.91	124.87	113.00
29	H	1168	U	C2'-C3'-O3'	7.88	125.53	113.70
29	H	1168	U	C1'-C2'-O2'	-7.70	96.85	108.40
29	H	1105	C	C4'-C3'-O3'	-7.67	97.90	109.40
29	H	1151	U	O3'-P-O5'	-7.59	92.61	104.00
30	o	126	ASN	CA-C-O	7.52	128.30	120.40
29	H	1128	C	C4'-C3'-O3'	-7.40	101.91	113.00
29	H	1126	G	N9-C1'-C2'	-7.33	101.00	112.00
30	o	57	LEU	N-CA-CB	7.32	123.10	110.81
31	p	65	PHE	CA-CB-CG	-7.31	106.49	113.80
29	H	1139	G	N9-C1'-C2'	-7.15	101.27	112.00
24	T	12	PRO	O-C-N	7.11	124.58	121.31
30	o	33	ASP	CA-CB-CG	7.07	119.67	112.60
30	o	42	SER	N-CA-CB	-7.05	99.64	110.42
30	o	10	ASP	CA-CB-CG	7.04	119.64	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	o	7	ILE	CA-CB-CG1	6.97	122.25	110.40
29	H	1165	C	C2'-C3'-O3'	-6.96	103.26	113.70
29	H	1151	U	C1'-C2'-O2'	-6.91	98.03	108.40
27	D	1370	SER	N-CA-C	6.86	119.58	110.53
31	p	73	PHE	CA-C-O	-6.85	112.78	120.32
29	H	1163	C	C4'-C3'-O3'	6.85	123.27	113.00
30	o	3	PHE	N-CA-C	-6.83	98.09	108.67
29	H	1168	U	O3'-P-O5'	-6.79	93.81	104.00
29	H	1092	A	N9-C1'-C2'	6.78	122.18	112.00
30	o	4	THR	N-CA-CB	-6.78	98.30	110.37
11	r	9	LYS	N-CA-C	-6.69	103.80	112.23
30	o	130	ILE	CA-C-O	6.57	128.99	120.78
10	q	51	TYR	CA-C-N	6.56	128.04	119.84
10	q	51	TYR	C-N-CA	6.56	128.04	119.84
30	o	68	PRO	N-CA-CB	6.56	110.14	103.25
29	H	1147	A	O5'-C5'-C4'	6.53	121.29	111.50
29	H	1152	U	C5'-C4'-C3'	-6.50	106.24	116.00
26	V	50	ASP	CA-C-N	-6.49	113.30	119.85
26	V	50	ASP	C-N-CA	-6.49	113.30	119.85
29	H	142	C	N1-C1'-C2'	-6.47	102.30	112.00
22	Q	93	ARG	CG-CD-NE	-6.41	97.89	112.00
29	H	1129	U	C1'-C2'-O2'	6.39	117.98	108.40
29	H	1167	U	C4'-C3'-O3'	-6.35	103.48	113.00
27	D	683	PHE	CA-C-N	-6.34	109.43	121.54
27	D	683	PHE	C-N-CA	-6.34	109.43	121.54
29	H	1152	U	O4'-C4'-C3'	6.33	110.33	104.00
5	J	165	GLY	N-CA-C	6.29	123.35	114.85
29	H	1169	C	O5'-C5'-C4'	-6.27	102.09	111.50
29	H	1097	G	C4'-C3'-O3'	6.22	122.33	113.00
30	o	50	LEU	CA-C-N	6.18	131.36	122.40
30	o	50	LEU	C-N-CA	6.18	131.36	122.40
30	o	83	ARG	N-CA-C	6.17	119.87	111.17
29	H	1117	G	C2'-C3'-O3'	-6.14	104.50	113.70
30	o	111	PHE	CA-CB-CG	6.12	119.92	113.80
29	H	1153	C	C4'-C3'-O3'	-6.09	103.87	113.00
23	c	29	GLY	CA-C-N	6.08	125.56	119.24
23	c	29	GLY	C-N-CA	6.08	125.56	119.24
29	H	1093	C	O5'-C5'-C4'	-6.05	102.42	111.50
29	H	1151	U	N1-C1'-C2'	6.02	121.03	112.00
30	o	127	LEU	CA-C-N	-5.99	114.32	122.77
30	o	127	LEU	C-N-CA	-5.99	114.32	122.77
29	H	1151	U	C5'-C4'-O4'	5.98	118.77	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	o	85	ASN	N-CA-CB	-5.97	102.67	111.51
30	o	62	ASN	CA-CB-CG	5.96	118.56	112.60
29	H	1167	U	C5'-C4'-C3'	5.95	124.93	116.00
30	o	132	ASN	OD1-CG-ND2	5.95	128.55	122.60
31	p	66	LYS	N-CA-C	-5.90	104.75	111.07
15	s	85	ILE	N-CA-C	5.90	116.55	110.36
29	H	1118	U	O5'-C5'-C4'	5.85	120.27	111.50
1	A	511	ASP	CB-CA-C	-5.84	109.28	117.23
29	H	1165	C	C5'-C4'-O4'	5.79	118.48	109.80
29	H	1102	C	C3'-C2'-O2'	5.78	119.38	110.70
18	B	33	U	P-O3'-C3'	5.77	128.86	120.20
29	H	1151	U	O5'-C5'-C4'	-5.77	102.84	111.50
29	H	1117	G	C4'-C3'-O3'	5.73	121.59	113.00
30	o	44	PRO	CB-CA-C	-5.71	106.21	111.40
32	l	680	PRO	N-CA-C	5.70	117.66	110.70
9	z	64	VAL	CA-C-N	-5.69	118.25	122.18
9	z	64	VAL	C-N-CA	-5.69	118.25	122.18
30	o	60	THR	CA-C-O	5.68	127.58	121.55
27	D	944	LEU	CD1-CG-CD2	-5.68	98.31	110.80
1	A	2330	GLU	CA-C-N	5.61	125.28	119.05
1	A	2330	GLU	C-N-CA	5.61	125.28	119.05
30	o	158	ASN	CB-CA-C	-5.57	102.14	110.16
27	D	1213	ARG	NE-CZ-NH2	-5.52	114.23	119.20
12	x	30	SER	CA-C-N	-5.50	117.47	123.30
12	x	30	SER	C-N-CA	-5.50	117.47	123.30
29	H	1148	U	P-O5'-C5'	5.49	129.13	120.90
29	H	1162	U	C4'-C3'-C2'	5.48	108.08	102.60
41	u	28	ASN	CA-C-N	5.48	125.83	119.47
41	u	28	ASN	C-N-CA	5.48	125.83	119.47
30	o	141	ARG	CD-NE-CZ	5.46	132.05	124.40
29	H	1168	U	C4'-C3'-C2'	-5.46	97.14	102.60
39	Y	227	MET	CA-C-N	-5.46	114.16	119.78
39	Y	227	MET	C-N-CA	-5.46	114.16	119.78
30	o	15	TYR	O-C-N	5.45	129.44	123.22
30	o	71	SER	N-CA-CB	-5.44	102.61	110.45
29	H	148	G	C2'-C3'-O3'	-5.43	105.55	113.70
29	H	1139	G	C4'-C3'-O3'	5.42	121.14	113.00
30	o	50	LEU	N-CA-C	-5.42	106.17	112.89
29	H	149	A	O5'-C5'-C4'	5.38	119.56	111.50
29	H	146	A	C5'-C4'-C3'	-5.37	107.95	116.00
29	H	1092	A	O3'-P-O5'	-5.36	95.96	104.00
31	p	93	ARG	CA-CB-CG	-5.36	103.38	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	H	1126	G	C4'-C3'-O3'	5.34	121.01	113.00
4	N	415	ASP	CA-C-N	5.33	123.60	120.24
4	N	415	ASP	C-N-CA	5.33	123.60	120.24
29	H	1128	C	C5'-C4'-O4'	5.33	117.79	109.80
43	v	229	ASN	N-CA-C	5.31	117.29	107.73
9	z	62	ALA	N-CA-C	-5.31	107.46	114.04
31	p	41	MET	N-CA-C	5.30	117.48	111.11
30	o	133	GLN	CA-CB-CG	-5.30	103.50	114.10
2	K	382	ASP	CA-C-N	-5.30	115.07	123.23
2	K	382	ASP	C-N-CA	-5.30	115.07	123.23
29	H	1095	U	C3'-C2'-O2'	5.29	118.64	110.70
29	H	1089	G	C2'-C3'-O3'	-5.29	105.77	113.70
27	D	1774	THR	CA-C-N	-5.26	114.68	122.41
27	D	1774	THR	C-N-CA	-5.26	114.68	122.41
30	o	38	THR	CA-CB-OG1	5.25	117.48	109.60
30	o	155	ASP	CA-C-N	5.24	130.00	122.40
30	o	155	ASP	C-N-CA	5.24	130.00	122.40
27	D	1935	SER	CA-C-N	-5.23	114.72	122.41
27	D	1935	SER	C-N-CA	-5.23	114.72	122.41
29	H	1142	G	C1'-C2'-O2'	-5.22	100.57	108.40
30	o	134	VAL	CA-C-N	5.22	127.79	120.28
30	o	134	VAL	C-N-CA	5.22	127.79	120.28
29	H	140	G	C3'-C2'-O2'	5.21	118.52	110.70
29	H	148	G	C4'-C3'-O3'	5.20	120.80	113.00
31	p	71	GLN	N-CA-C	5.20	117.58	109.52
29	H	1167	U	C5'-C4'-O4'	-5.20	102.00	109.80
32	l	885	ILE	CB-CA-C	-5.18	108.78	113.70
14	y	44	GLY	N-CA-C	-5.16	107.94	115.63
29	H	1167	U	P-O3'-C3'	-5.15	112.47	120.20
30	o	100	ASN	CA-CB-CG	5.15	117.75	112.60
2	K	395	ILE	CA-C-N	5.14	129.82	121.95
2	K	395	ILE	C-N-CA	5.14	129.82	121.95
31	p	68	GLN	N-CA-C	5.13	119.54	113.28
5	J	373	ARG	CB-CA-C	-5.12	110.69	116.63
29	H	1129	U	O4'-C4'-C3'	5.12	109.11	104.00
30	o	44	PRO	CA-C-O	-5.11	114.51	120.85
9	z	61	ILE	N-CA-C	5.11	116.17	109.58
30	o	107	SER	N-CA-CB	-5.08	102.83	111.17
15	s	64	VAL	N-CA-C	5.08	115.89	108.58
27	D	1202	MET	CB-CG-SD	-5.08	97.47	112.70
11	r	56	LEU	N-CA-C	5.07	116.99	108.73
1	A	1014	LYS	N-CA-C	5.05	120.97	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	o	56	ILE	CA-C-O	-5.04	115.21	120.76
14	y	94	ILE	N-CA-C	5.04	115.54	108.89
1	A	265	ASN	CB-CA-C	-5.02	109.81	115.79
29	H	1163	C	C2'-C3'-O3'	-5.02	106.17	113.70
30	o	132	ASN	N-CA-C	-5.01	100.88	109.24
1	A	554	THR	CB-CA-C	-5.00	109.33	116.34
1	A	2159	ASN	N-CA-C	5.00	117.46	111.71

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	1	386	TYR	Peptide
32	1	830	MET	Peptide
32	1	835	ILE	Peptide
32	1	926	PRO	Peptide
34	3	208	GLU	Peptide
1	A	239	PHE	Peptide
8	C	363	PRO	Peptide
8	C	770	ASN	Peptide
27	D	1369	GLY	Peptide
27	D	684	LEU	Peptide
27	D	685	ARG	Peptide
27	D	790	ASP	Peptide
2	K	208	GLN	Peptide
2	K	383	GLU	Peptide
3	L	397	GLU	Peptide
4	N	11	PRO	Peptide
4	N	802	GLN	Peptide
41	u	462	LYS	Peptide
41	u	463	GLY	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17877	0	17800	653	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	3375	0	3343	181	0
3	L	3171	0	3140	130	0
4	N	4897	0	3994	121	0
5	J	2439	0	2341	65	0
6	E	1146	0	1133	34	0
7	M	950	0	1004	23	0
8	C	6732	0	6904	298	0
9	z	260	0	72	1	0
10	q	368	0	99	2	0
11	r	308	0	80	0	0
12	x	296	0	83	0	0
13	t	308	0	85	3	0
14	y	264	0	76	0	0
15	s	308	0	85	0	0
16	F	2043	0	1033	49	0
17	I	2334	0	1173	108	0
18	B	3715	0	1878	153	0
19	O	574	0	552	32	0
20	S	632	0	653	26	0
20	d	316	0	86	14	0
20	l	611	0	627	34	0
21	P	563	0	600	40	0
21	a	292	0	78	5	0
21	h	610	0	640	8	0
22	Q	751	0	776	64	0
22	b	308	0	78	0	0
22	m	644	0	686	22	0
23	R	752	0	786	52	0
23	c	360	0	89	0	0
23	n	528	0	573	45	0
24	T	602	0	631	38	0
24	e	288	0	74	0	0
24	i	575	0	597	21	0
25	U	585	0	587	41	0
25	f	280	0	77	1	0
25	j	554	0	556	18	0
26	V	577	0	595	37	0
26	g	280	0	79	0	0
26	k	529	0	557	7	0
27	D	13601	0	13596	650	0
28	G	928	0	468	51	0
29	H	4345	0	2199	277	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	o	841	0	614	5	0
31	p	466	0	373	2	0
32	1	6472	0	6702	260	0
33	2	1726	0	1734	67	0
34	3	9380	0	9482	412	0
35	4	1429	0	1458	48	0
36	5	814	0	811	30	0
37	6	693	0	705	25	0
38	X	1051	0	1015	105	0
39	Y	730	0	710	55	0
40	Z	173	0	165	8	0
41	u	3895	0	3824	191	0
42	w	1084	0	1081	53	0
43	v	1372	0	1345	58	0
44	C	32	0	12	6	0
45	C	1	0	0	0	0
46	5	3	0	0	2	0
46	u	2	0	0	0	0
46	v	1	0	0	0	0
All	All	111041	0	100594	4006	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 19.

All (4006) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2310:GLU:CB	1:A:2333:PHE:CZ	1.85	1.52
1:A:2398:LEU:HD13	27:D:1060:LYS:CD	1.36	1.51
1:A:2310:GLU:CB	1:A:2333:PHE:HZ	1.19	1.44
1:A:2398:LEU:HD13	27:D:1060:LYS:CE	1.48	1.42
1:A:2310:GLU:HB2	1:A:2333:PHE:CZ	0.89	1.41
32:1:494:LEU:HD13	38:X:7:ILE:CG2	1.49	1.41
23:n:90:PHE:CE2	41:u:194:LYS:C	1.99	1.39
1:A:2398:LEU:CD1	27:D:1060:LYS:HD2	1.53	1.38
1:A:2310:GLU:HB2	1:A:2333:PHE:CE1	1.58	1.38
8:C:129:ILE:HG12	20:d:16:GLY:CA	1.54	1.36
1:A:2152:TRP:CH2	27:D:1061:ALA:O	1.83	1.31
39:Y:207:THR:O	39:Y:214:LEU:CD1	1.79	1.28
38:X:63:SER:CB	38:X:74:PHE:CE1	2.16	1.27
41:u:172:ARG:HH22	41:u:354:MET:CE	1.49	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2395:PHE:CD1	27:D:1062:PRO:HD3	1.72	1.23
8:C:129:ILE:CG1	20:d:16:GLY:HA3	1.71	1.19
1:A:2398:LEU:CG	27:D:1060:LYS:HD2	1.72	1.17
23:n:90:PHE:CZ	41:u:195:ARG:HA	1.77	1.17
29:H:1099:G:O2'	29:H:1100:A:H5'	1.42	1.16
32:1:494:LEU:HD13	38:X:7:ILE:HG21	1.18	1.15
27:D:539:LEU:O	27:D:543:TYR:HB3	1.44	1.14
32:1:494:LEU:HD11	38:X:23:TRP:CD1	1.83	1.13
32:1:494:LEU:CD1	38:X:7:ILE:HG21	1.79	1.12
41:u:172:ARG:NH2	41:u:354:MET:HE1	1.67	1.10
20:l:81:ALA:HB1	20:l:82:PRO:HA	1.35	1.08
1:A:547:LEU:O	1:A:551:LEU:HB2	1.51	1.08
27:D:804:HIS:CE1	27:D:813:ARG:HG3	1.89	1.07
41:u:172:ARG:HH22	41:u:354:MET:HE1	1.05	1.07
1:A:2398:LEU:CD1	27:D:1060:LYS:CE	2.33	1.06
17:I:99:G:H4'	27:D:1186:GLU:HB3	1.31	1.06
8:C:867:THR:O	8:C:926:GLY:HA2	1.55	1.06
32:1:494:LEU:CD1	38:X:7:ILE:CG2	2.34	1.05
38:X:63:SER:HB2	38:X:74:PHE:CE1	1.84	1.05
17:I:75:U:C5	27:D:1100:PHE:HE1	1.73	1.05
1:A:1667:GLN:NE2	19:O:211:ASN:OD1	1.90	1.04
2:K:446:SER:OG	2:K:451:PHE:CE1	2.11	1.03
24:T:59:GLU:HG3	24:T:77:LEU:HD11	1.40	1.03
1:A:2183:TYR:HE2	1:A:2289:ILE:HG12	1.20	1.03
18:B:162:G:H3'	18:B:163:C:H4'	1.41	1.03
1:A:2398:LEU:HD13	27:D:1060:LYS:HD2	1.03	1.02
19:O:206:LYS:HD3	27:D:1051:LYS:HE3	1.39	1.02
39:Y:207:THR:O	39:Y:214:LEU:HD13	0.85	1.02
1:A:2395:PHE:CD1	27:D:1061:ALA:HA	1.95	1.01
24:T:83:LYS:NZ	25:U:75:CYS:O	1.93	1.01
29:H:110:A:H4'	29:H:111:C:C5'	1.89	1.01
17:I:91:U:O2	17:I:142:G:N2	1.95	1.00
23:n:92:SER:OG	41:u:190:LEU:HD12	1.61	1.00
27:D:757:LEU:O	27:D:761:PHE:HB3	1.62	0.99
1:A:2398:LEU:HD22	27:D:1060:LYS:HB2	1.41	0.99
1:A:2395:PHE:CE1	27:D:1061:ALA:HA	1.96	0.99
21:h:36:ALA:HB2	20:l:84:PHE:HE1	1.23	0.99
29:H:110:A:C4'	29:H:111:C:H5'	1.91	0.99
21:P:88:ARG:NH2	20:S:66:GLY:O	1.97	0.98
1:A:2395:PHE:CG	27:D:1062:PRO:HD3	1.97	0.98
1:A:1674:ASP:OD2	1:A:2200:LYS:HD3	1.62	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:n:90:PHE:HE2	41:u:194:LYS:C	1.63	0.97
1:A:2067:TYR:CB	19:O:194:LEU:HD22	1.94	0.97
23:n:90:PHE:CE2	41:u:195:ARG:N	2.33	0.96
1:A:2398:LEU:CD1	27:D:1060:LYS:NZ	2.28	0.96
1:A:2311:GLY:N	1:A:2333:PHE:HE1	1.64	0.96
32:1:494:LEU:HD13	38:X:7:ILE:HG23	1.44	0.96
2:K:187:ASP:HB3	2:K:451:PHE:HZ	1.28	0.95
29:H:1099:G:C2'	29:H:1100:A:H5'	1.97	0.95
27:D:556:LYS:NZ	27:D:602:THR:O	1.98	0.95
1:A:2152:TRP:HH2	27:D:1061:ALA:O	1.32	0.95
27:D:527:LYS:HE3	27:D:670:LEU:HB3	1.46	0.95
1:A:1962:ARG:HD3	19:O:186:GLU:OE2	1.66	0.94
23:n:90:PHE:CZ	41:u:195:ARG:CA	2.49	0.94
28:G:520:G:C6	38:X:34:TYR:CE2	2.56	0.94
1:A:2152:TRP:CZ2	27:D:1061:ALA:O	2.21	0.94
29:H:110:A:C2	22:m:2:LYS:CE	2.51	0.94
27:D:912:PHE:HB3	27:D:944:LEU:HD23	1.47	0.94
23:n:90:PHE:CD2	41:u:194:LYS:HA	2.03	0.94
41:u:63:LYS:HB2	41:u:376:GLN:HG3	1.50	0.93
27:D:869:LEU:HD13	27:D:904:GLN:HE21	1.32	0.93
24:T:87:ILE:O	26:V:64:ARG:NE	2.02	0.93
32:1:494:LEU:HB2	38:X:7:ILE:HG12	1.50	0.93
17:I:150:G:OP2	25:U:74:ARG:NH2	2.00	0.93
17:I:91:U:H3	17:I:142:G:H1	0.94	0.93
29:H:1165:C:H2'	29:H:1166:G:H8	1.32	0.93
1:A:2311:GLY:N	1:A:2333:PHE:CE1	2.36	0.93
1:A:2310:GLU:CG	1:A:2333:PHE:HZ	1.81	0.93
32:1:494:LEU:CD1	38:X:23:TRP:CD1	2.51	0.93
39:Y:208:SER:HB2	39:Y:212:ARG:O	1.68	0.93
18:B:175:G:N2	18:B:176:A:N6	2.16	0.92
16:F:102:U:H3	29:H:3:G:H1	1.17	0.92
43:v:235:GLU:O	43:v:239:LYS:HB2	1.69	0.92
18:B:175:G:N2	18:B:176:A:H62	1.65	0.92
22:Q:144:ARG:NH1	22:Q:145:GLY:O	2.03	0.92
32:1:490:ARG:NH2	38:X:25:ASN:HB3	1.86	0.91
21:P:88:ARG:NH1	20:S:67:SER:O	2.02	0.91
17:I:78:A:C2	27:D:1110:ARG:NE	2.38	0.91
27:D:781:LEU:HD21	27:D:798:GLU:HA	1.52	0.91
27:D:1086:GLN:NE2	27:D:1138:LYS:O	2.03	0.91
18:B:32:G:H1	18:B:121:U:H3	1.16	0.91
20:l:6:ILE:CG2	20:l:84:PHE:CZ	2.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:m:99:ASP:OD2	41:u:183:GLU:C	2.14	0.91
1:A:2310:GLU:C	1:A:2333:PHE:HE1	1.80	0.90
1:A:2398:LEU:HD12	27:D:1060:LYS:NZ	1.84	0.90
18:B:22:G:H1	18:B:149:U:H3	0.95	0.90
29:H:1165:C:H2'	29:H:1166:G:C8	2.06	0.90
23:n:92:SER:OG	41:u:190:LEU:CD1	2.18	0.90
16:F:30:G:H1	18:B:96:U:H3	1.15	0.90
29:H:110:A:H4'	29:H:111:C:H5'	0.95	0.90
2:K:446:SER:OG	2:K:451:PHE:CZ	2.24	0.90
2:K:232:ASN:HB3	2:K:247:GLN:HE22	1.34	0.90
2:K:395:ILE:HG22	2:K:396:VAL:H	1.35	0.90
39:Y:207:THR:C	39:Y:214:LEU:HD13	1.94	0.90
27:D:1387:HIS:HB2	27:D:1470:LEU:HD13	1.52	0.90
1:A:2398:LEU:HB2	27:D:1060:LYS:CD	2.02	0.90
18:B:1:A:H61	18:B:164:C:H42	1.11	0.89
29:H:110:A:C2	22:m:2:LYS:HE2	2.08	0.89
23:n:90:PHE:CE2	41:u:194:LYS:CA	2.55	0.89
17:I:72:A:OP2	27:D:1047:ARG:NH1	2.05	0.89
18:B:114:G:H2'	18:B:115:G:C8	2.08	0.89
39:Y:213:LYS:HB3	39:Y:230:SER:OG	1.72	0.89
1:A:1861:THR:HG22	19:O:161:ILE:HG12	1.55	0.88
1:A:2398:LEU:CD1	27:D:1060:LYS:CD	2.22	0.88
22:Q:35:GLN:OE1	22:Q:37:ASN:ND2	2.06	0.88
1:A:609:GLU:O	1:A:613:SER:HB2	1.73	0.88
1:A:2310:GLU:CB	1:A:2333:PHE:CE1	2.32	0.88
17:I:145:U:H3	26:V:35:PHE:HB3	1.39	0.88
27:D:1687:LEU:HB2	27:D:1698:TYR:HE1	1.36	0.88
17:I:75:U:C5	27:D:1100:PHE:CE1	2.62	0.87
17:I:146:U:H5''	17:I:147:U:H5'	1.56	0.87
36:5:49:CYS:HG	46:5:201:ZN:ZN	0.59	0.87
8:C:542:ILE:O	8:C:553:VAL:HB	1.72	0.87
1:A:2398:LEU:CB	27:D:1060:LYS:HD2	2.04	0.87
27:D:2049:PRO:HB2	27:D:2051:VAL:HG13	1.55	0.87
1:A:1087:ASN:HD21	3:L:272:LEU:HG	1.40	0.86
8:C:129:ILE:HG12	20:d:16:GLY:C	1.99	0.86
27:D:804:HIS:HE1	27:D:813:ARG:HG3	1.38	0.86
22:Q:36:MET:SD	23:R:97:ARG:NH1	2.48	0.86
20:l:83:LEU:HD23	20:l:84:PHE:CE2	2.10	0.86
1:A:617:ASN:ND2	18:B:99:U:O2'	2.09	0.86
8:C:132:ARG:NH2	20:d:12:ASN:O	2.09	0.85
1:A:716:ARG:HE	18:B:112:C:H1'	1.42	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:636:ILE:HG22	27:D:671:SER:HB2	1.58	0.85
1:A:2183:TYR:CE2	1:A:2289:ILE:HG12	2.11	0.85
39:Y:214:LEU:HD21	39:Y:227:MET:HB2	1.58	0.85
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.41	0.85
1:A:1565:THR:O	1:A:1820:ARG:NH2	2.10	0.85
27:D:1524:TRP:HD1	27:D:1780:ARG:CZ	1.89	0.85
27:D:1524:TRP:HB2	27:D:1780:ARG:HG3	1.58	0.85
27:D:1609:MET:HG2	27:D:1611:ASN:H	1.42	0.85
29:H:1099:G:O2'	29:H:1100:A:C5'	2.24	0.85
20:l:6:ILE:HG22	20:l:84:PHE:CZ	2.12	0.85
32:1:390:ILE:HD12	32:1:426:MET:HA	1.59	0.85
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.42	0.84
2:K:167:LEU:O	4:N:728:ARG:NH2	2.10	0.84
34:3:393:VAL:HA	34:3:404:LEU:O	1.76	0.84
5:J:409:HIS:HE1	10:q:42:ASN:CA	1.89	0.84
27:D:1213:ARG:HH22	27:D:1316:LYS:CG	1.90	0.84
1:A:2067:TYR:O	19:O:194:LEU:HD21	1.78	0.84
29:H:110:A:C2	22:m:2:LYS:HE3	2.10	0.84
38:X:63:SER:HB3	38:X:74:PHE:CE1	2.11	0.84
38:X:48:LEU:O	39:Y:231:ARG:NH1	2.11	0.84
1:A:1862:VAL:O	19:O:159:ASP:N	2.10	0.83
27:D:784:GLU:HG3	27:D:819:LEU:HD21	1.58	0.83
38:X:63:SER:OG	38:X:74:PHE:CZ	2.31	0.83
4:N:746:MET:HG2	4:N:749:ARG:HH12	1.44	0.83
8:C:603:PHE:HB3	8:C:646:GLY:O	1.78	0.83
27:D:1216:MET:HG3	27:D:1218:PHE:HE1	1.42	0.83
17:I:97:U:H3	17:I:135:A:H61	1.22	0.83
24:i:86:ASN:HD21	25:j:32:LYS:HD3	1.43	0.83
1:A:1575:TRP:HB2	3:L:391:MET:HB3	1.60	0.83
18:B:8:U:H3	18:B:157:G:H1	1.27	0.83
32:1:494:LEU:CB	38:X:7:ILE:HG12	2.09	0.83
34:3:363:VAL:HG12	34:3:364:THR:H	1.42	0.82
1:A:2152:TRP:CZ3	27:D:1064:PRO:HG3	2.14	0.82
34:3:130:LEU:HB3	34:3:195:ILE:HD13	1.61	0.82
3:L:120:TYR:HE2	3:L:141:ILE:HG12	1.45	0.82
18:B:166:U:O2'	18:B:167:A:OP1	1.97	0.82
41:u:331:GLU:O	41:u:335:THR:HG23	1.79	0.82
2:K:169:GLY:HA2	4:N:724:SER:HB3	1.59	0.82
17:I:145:U:H1'	26:V:66:ASN:HB2	1.62	0.82
28:G:520:G:N1	38:X:34:TYR:CD2	2.48	0.82
32:1:830:MET:O	32:1:832:LYS:N	2.11	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:X:63:SER:HB2	38:X:74:PHE:HE1	1.38	0.82
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.62	0.82
13:t:19:LYS:O	13:t:84:GLY:N	2.13	0.82
41:u:172:ARG:NH2	41:u:354:MET:CE	2.29	0.81
32:l:494:LEU:HB3	38:X:7:ILE:HG23	1.61	0.81
1:A:547:LEU:O	1:A:551:LEU:CB	2.27	0.81
2:K:410:LEU:HB2	2:K:422:TYR:HB2	1.62	0.81
18:B:175:G:H21	18:B:176:A:H62	1.23	0.81
27:D:462:GLU:OE1	27:D:729:LYS:NZ	2.13	0.81
27:D:2134:THR:O	27:D:2138:HIS:NE2	2.13	0.81
34:3:105:ASP:HB2	34:3:114:ILE:HD11	1.61	0.81
27:D:1213:ARG:HH22	27:D:1316:LYS:HG2	1.43	0.81
21:h:36:ALA:HB2	20:l:84:PHE:CE1	2.14	0.81
43:v:53:ARG:HE	43:v:56:PRO:HA	1.45	0.81
8:C:129:ILE:CG1	20:d:16:GLY:CA	2.45	0.81
17:I:134:U:H2'	17:I:135:A:H8	1.46	0.81
27:D:589:THR:HA	27:D:611:LYS:HG2	1.62	0.81
25:U:19:LEU:HD21	25:U:45:THR:HG21	1.63	0.81
22:m:102:ASN:HD22	41:u:350:ARG:NH2	1.78	0.81
34:3:71:PHE:HA	34:3:97:THR:HG22	1.63	0.81
38:X:63:SER:OG	38:X:74:PHE:CE1	2.32	0.81
1:A:1910:LYS:HD2	19:O:169:ILE:HG12	1.63	0.81
41:u:150:PRO:HG3	41:u:154:THR:H	1.46	0.81
8:C:133:ILE:HA	8:C:209:MET:O	1.79	0.80
1:A:2398:LEU:HD13	27:D:1060:LYS:HE3	1.61	0.80
27:D:2103:LEU:HD11	27:D:2140:LEU:HB3	1.64	0.80
29:H:1149:G:H5''	29:H:1149:G:C8	2.16	0.80
17:I:142:G:N2	21:P:39:LYS:NZ	2.29	0.80
27:D:563:LEU:HD21	27:D:836:TRP:CD1	2.16	0.80
1:A:287:GLU:HG2	1:A:288:GLU:H	1.46	0.80
1:A:690:LYS:O	1:A:694:ASN:ND2	2.15	0.80
18:B:163:C:OP2	21:a:8:HIS:C	2.25	0.80
27:D:1277:LYS:O	27:D:1281:GLN:HB2	1.81	0.80
27:D:766:ILE:O	27:D:769:LYS:NZ	2.14	0.80
23:R:74:GLU:OE2	23:R:89:ARG:NE	2.15	0.80
34:3:157:LEU:O	34:3:176:ASN:HA	1.81	0.80
2:K:177:PRO:HB3	2:K:457:TRP:HA	1.64	0.80
8:C:133:ILE:HG22	8:C:209:MET:HB3	1.62	0.80
27:D:1688:TYR:HD1	27:D:1695:TYR:CD1	2.00	0.79
25:j:74:ARG:NH2	23:n:64:HIS:O	2.14	0.79
1:A:880:THR:O	3:L:180:LYS:NZ	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1851:PHE:O	1:A:1881:THR:HA	1.83	0.79
2:K:135:ARG:NH2	5:J:167:GLU:OE2	2.15	0.79
29:H:119:G:H5'	23:n:99:ASP:OD2	1.82	0.79
18:B:162:G:H3'	18:B:163:C:C4'	2.12	0.79
32:1:294:ARG:HB3	32:1:332:THR:HG21	1.64	0.79
1:A:1962:ARG:HD3	19:O:186:GLU:CD	2.07	0.79
24:T:30:TRP:HB3	26:V:23:ARG:HH12	1.47	0.79
41:u:431:TYR:CE2	41:u:440:HIS:CD2	2.70	0.79
17:I:98:G:H1	17:I:134:U:H3	1.31	0.79
3:L:327:THR:HG22	3:L:328:VAL:H	1.47	0.79
1:A:2398:LEU:HD12	27:D:1060:LYS:HZ1	1.45	0.79
22:Q:3:LEU:HD23	23:R:95:PHE:HE1	1.48	0.79
1:A:2398:LEU:CD2	27:D:1060:LYS:HD2	2.13	0.78
18:B:126:A:H5'	18:B:127:U:OP2	1.83	0.78
27:D:1887:VAL:HG21	22:Q:140:LYS:HD2	1.65	0.78
2:K:452:LEU:HB3	2:K:464:TRP:HB2	1.64	0.78
27:D:1557:ILE:HA	27:D:1695:TYR:HE2	1.46	0.78
20:l:9:LYS:HB3	20:l:83:LEU:CD1	2.13	0.78
8:C:706:LEU:HA	8:C:824:SER:O	1.82	0.78
34:3:365:ILE:HG21	34:3:381:LEU:HG	1.63	0.78
8:C:315:SER:OG	44:C:1500:GTP:O6	2.00	0.78
1:A:1014:LYS:O	1:A:1016:SER:N	2.15	0.78
23:n:90:PHE:CE2	41:u:194:LYS:O	2.37	0.78
34:3:364:THR:OG1	34:3:384:ASN:ND2	2.16	0.78
8:C:129:ILE:HG12	20:d:16:GLY:HA3	0.82	0.78
18:B:158:G:N2	18:B:160:U:O4	2.17	0.78
33:2:285:MET:HE2	35:4:23:GLU:HG3	1.66	0.78
1:A:789:ALA:HB1	1:A:816:ILE:HD11	1.64	0.77
27:D:1895:ARG:O	27:D:1897:GLY:N	2.16	0.77
3:L:376:LYS:NZ	17:I:55:U:O2'	2.17	0.77
27:D:1515:LEU:HB2	27:D:1518:ALA:HB2	1.65	0.77
32:1:222:ILE:HG23	32:1:265:ILE:HD11	1.65	0.77
25:U:32:LYS:HA	25:U:79:LEU:HD12	1.66	0.77
1:A:2398:LEU:HB2	27:D:1060:LYS:HD3	1.62	0.77
34:3:118:GLN:HE22	34:3:171:LEU:HB3	1.49	0.77
27:D:677:TYR:HD2	27:D:691:LEU:HD21	1.47	0.77
21:P:88:ARG:HG2	21:P:90:GLU:H	1.47	0.77
3:L:112:MET:HE2	3:L:203:ILE:HD11	1.66	0.77
32:1:490:ARG:HH22	38:X:25:ASN:HD22	1.33	0.77
2:K:230:SER:HB2	2:K:232:ASN:HD22	1.50	0.77
1:A:2249:ASP:OD1	27:D:1309:ASN:ND2	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1777:TYR:OH	27:D:1781:ARG:NH1	2.17	0.76
20:l:9:LYS:CD	20:l:83:LEU:HD11	2.14	0.76
32:1:386:TYR:CD2	32:1:387:PRO:HD3	2.20	0.76
1:A:2398:LEU:HD22	27:D:1060:LYS:CB	2.15	0.76
4:N:21:ARG:NH2	6:E:74:TYR:OH	2.17	0.76
27:D:1772:TRP:HZ3	27:D:1773:PHE:CE1	2.02	0.76
41:u:150:PRO:HB3	41:u:154:THR:HB	1.64	0.76
2:K:446:SER:OG	2:K:451:PHE:CD1	2.38	0.76
4:N:15:TYR:HH	6:E:13:TRP:CG	2.04	0.76
4:N:743:LYS:O	4:N:747:GLU:HB2	1.85	0.76
17:I:76:A:N7	27:D:1107:ARG:NH2	2.33	0.76
18:B:1:A:H61	18:B:164:C:N4	1.82	0.76
18:B:32:G:H4'	18:B:33:U:OP2	1.83	0.76
27:D:708:CYS:SG	27:D:889:ILE:HA	2.25	0.76
24:T:37:ILE:HD11	24:T:59:GLU:HB3	1.66	0.76
39:Y:209:LEU:O	39:Y:209:LEU:HD12	1.85	0.76
17:I:78:A:C2	27:D:1110:ARG:NH2	2.54	0.76
41:u:172:ARG:HH22	41:u:354:MET:HE3	1.47	0.76
27:D:841:PRO:HG2	27:D:877:ARG:HG2	1.68	0.76
21:P:88:ARG:HH12	20:S:67:SER:C	1.93	0.76
28:G:520:G:C2	38:X:34:TYR:CG	2.74	0.76
20:l:9:LYS:HB3	20:l:83:LEU:HD13	1.67	0.76
1:A:261:LEU:HD22	1:A:642:GLY:HA2	1.67	0.75
17:I:142:G:N2	21:P:39:LYS:HZ3	1.82	0.75
20:l:81:ALA:CB	20:l:82:PRO:HA	2.09	0.75
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.67	0.75
32:1:835:ILE:O	32:1:837:PHE:N	2.19	0.75
1:A:796:ASN:HD21	1:A:858:LYS:HG2	1.51	0.75
1:A:181:HIS:HA	1:A:704:TRP:HZ2	1.51	0.75
32:1:348:VAL:HG13	32:1:349:LEU:H	1.52	0.75
34:3:639:LYS:HB3	34:3:686:GLN:HA	1.66	0.75
2:K:438:ASP:OD2	4:N:762:GLN:NE2	2.20	0.75
27:D:1620:TYR:HD2	27:D:1655:LEU:HD21	1.50	0.75
32:1:490:ARG:HH22	38:X:25:ASN:HB3	1.51	0.75
2:K:187:ASP:HB3	2:K:451:PHE:CZ	2.19	0.75
17:I:78:A:C2	27:D:1110:ARG:CZ	2.69	0.75
34:3:783:ILE:HG13	34:3:784:SER:H	1.51	0.75
1:A:2157:ILE:HG23	27:D:1066:ARG:HG2	1.67	0.75
8:C:769:TYR:HE1	8:C:774:LEU:HB2	1.52	0.75
1:A:1252:SER:O	1:A:1274:ARG:NH1	2.20	0.75
1:A:1320:LEU:HD21	1:A:1367:ILE:HG12	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:29:G:H2'	18:B:30:A:H8	1.52	0.75
27:D:515:SER:HB2	27:D:687:PRO:HG3	1.68	0.75
26:V:64:ARG:HH11	26:V:66:ASN:HB3	1.49	0.75
23:n:90:PHE:CE2	41:u:194:LYS:HA	2.18	0.75
18:B:48:G:H1	18:B:67:U:H3	1.32	0.74
32:1:566:LEU:HD21	32:1:601:ILE:HG12	1.69	0.74
8:C:493:LEU:HB2	8:C:556:ALA:HB3	1.67	0.74
39:Y:214:LEU:HD21	39:Y:227:MET:CB	2.17	0.74
27:D:1524:TRP:HD1	27:D:1780:ARG:NE	1.85	0.74
27:D:761:PHE:HE2	27:D:769:LYS:HD3	1.53	0.74
26:V:56:GLN:NE2	26:V:60:GLN:O	2.20	0.74
29:H:142:C:H2'	29:H:143:G:H8	1.52	0.74
34:3:239:ASP:OD2	34:3:295:VAL:N	2.20	0.74
42:w:158:ARG:HB2	42:w:158:ARG:HH11	1.53	0.74
1:A:2398:LEU:HD21	27:D:1056:GLN:O	1.88	0.74
8:C:132:ARG:HH22	20:d:13:GLU:C	1.96	0.74
27:D:1688:TYR:HD1	27:D:1695:TYR:HD1	1.34	0.74
3:L:112:MET:HB2	3:L:204:LEU:HD21	1.69	0.74
17:I:79:A:H61	27:D:593:ARG:HG3	1.50	0.74
34:3:179:LEU:HD23	34:3:189:PRO:HG2	1.69	0.74
1:A:1674:ASP:OD2	1:A:2200:LYS:CD	2.35	0.74
22:m:102:ASN:ND2	41:u:350:ARG:NH2	2.36	0.74
43:v:180:ILE:HG22	43:v:201:ILE:HG12	1.67	0.74
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.53	0.74
1:A:1673:LEU:HD12	1:A:2150:ASN:OD1	1.86	0.74
2:K:159:LEU:HD22	2:K:430:MET:HG3	1.68	0.74
17:I:134:U:H2'	17:I:135:A:C8	2.23	0.74
29:H:1138:G:P	29:H:1138:G:O4'	2.45	0.74
8:C:951:ILE:HG12	8:C:958:PRO:HD3	1.70	0.73
13:t:19:LYS:O	13:t:84:GLY:CA	2.35	0.73
40:Z:36:GLY:O	40:Z:40:LEU:HB2	1.87	0.73
1:A:923:TYR:OH	1:A:936:GLU:OE1	2.04	0.73
4:N:15:TYR:HH	6:E:13:TRP:CD1	2.06	0.73
34:3:384:ASN:O	34:3:415:ASN:ND2	2.18	0.73
37:6:57:ARG:NH1	37:6:59:ASP:OD2	2.20	0.73
1:A:1309:ILE:HG12	1:A:1356:LEU:HD12	1.70	0.73
27:D:516:ASN:HD22	27:D:685:ARG:HB3	1.53	0.73
26:k:28:ILE:CG2	26:k:41:ASP:HB2	2.18	0.73
20:l:81:ALA:HB1	20:l:82:PRO:CA	2.16	0.73
8:C:129:ILE:CG1	20:d:16:GLY:C	2.60	0.73
8:C:884:ARG:HB2	8:C:910:GLU:HG3	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:163:C:OP2	21:a:8:HIS:O	2.06	0.73
32:1:790:LYS:HD2	32:1:826:TYR:HB3	1.70	0.73
34:3:822:HIS:ND1	34:3:846:MET:O	2.21	0.73
3:L:401:LEU:H	4:N:214:SER:HB3	1.54	0.73
28:G:513:U:OP2	32:1:259:ARG:NH1	2.21	0.73
27:D:539:LEU:O	27:D:543:TYR:CB	2.31	0.73
32:1:587:THR:HG22	32:1:594:MET:HE3	1.68	0.73
1:A:1964:PRO:HA	1:A:2016:LYS:HE3	1.71	0.73
32:1:198:GLU:O	32:1:202:ASN:HB2	1.88	0.73
41:u:93:PHE:CZ	42:w:148:PHE:HE1	2.06	0.73
42:w:92:ASP:O	42:w:96:ILE:HG12	1.89	0.73
8:C:765:VAL:HA	8:C:775:ILE:HG12	1.69	0.73
24:T:20:PHE:HE1	24:T:92:SER:HB2	1.52	0.73
32:1:542:THR:HG22	32:1:582:GLY:HA3	1.68	0.73
34:3:186:ARG:NH2	37:6:38:ASP:OD1	2.22	0.73
2:K:321:LEU:HD11	5:J:169:TRP:HE1	1.52	0.73
18:B:162:G:O3'	18:B:164:C:OP1	2.07	0.73
29:H:140:G:H1	29:H:1168:U:H3	1.37	0.73
32:1:489:VAL:HG13	38:X:26:GLU:CD	2.14	0.73
34:3:927:ARG:HG3	34:3:928:THR:HG23	1.69	0.73
42:w:103:TYR:HD1	42:w:110:VAL:HG21	1.53	0.72
1:A:1943:PRO:HD3	19:O:169:ILE:CD1	2.19	0.72
17:I:76:A:OP2	27:D:590:GLY:HA3	1.89	0.72
18:B:74:U:O2'	18:B:77:A:OP2	2.07	0.72
27:D:511:PHE:CE1	27:D:537:LYS:HB2	2.23	0.72
20:l:6:ILE:HG23	20:l:83:LEU:HD21	1.71	0.72
32:1:581:LYS:O	32:1:585:ALA:N	2.20	0.72
27:D:1680:VAL:HG23	27:D:1710:ALA:HB2	1.72	0.72
32:1:778:ARG:NH1	32:1:811:ASN:OD1	2.22	0.72
32:1:213:LEU:HD13	32:1:218:ARG:HB2	1.69	0.72
8:C:160:ARG:NH1	8:C:161:ILE:O	2.23	0.72
27:D:523:THR:HG23	27:D:527:LYS:HD3	1.70	0.72
24:i:86:ASN:HD21	25:j:32:LYS:CD	2.02	0.72
34:3:157:LEU:HD12	34:3:204:LEU:HD11	1.72	0.72
34:3:732:ARG:NH1	34:3:757:ASP:OD1	2.22	0.72
27:D:1392:LYS:HD2	27:D:1469:GLU:OE1	1.90	0.72
27:D:1822:ILE:HG12	27:D:1844:ILE:HG12	1.70	0.72
29:H:119:G:H4'	29:H:119:G:OP1	1.90	0.72
41:u:150:PRO:HG3	41:u:155:ASN:H	1.55	0.72
43:v:246:ILE:HD13	43:v:246:ILE:H	1.54	0.72
27:D:535:VAL:HG13	27:D:557:ILE:HD13	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:686:LEU:HD21	32:1:727:ILE:HD11	1.72	0.72
34:3:396:ASP:HB2	34:3:404:LEU:HG	1.72	0.72
34:3:1096:LEU:HD13	34:3:1187:PHE:HZ	1.54	0.72
1:A:2067:TYR:O	19:O:194:LEU:CD2	2.38	0.71
8:C:219:VAL:HG21	8:C:931:TYR:HB3	1.70	0.71
29:H:142:C:H2'	29:H:143:G:C8	2.24	0.71
32:1:443:ARG:NH1	32:1:478:GLU:OE2	2.23	0.71
34:3:250:PRO:HG2	34:3:273:LEU:HB3	1.71	0.71
41:u:377:VAL:O	41:u:378:ASP:HB2	1.90	0.71
32:1:490:ARG:HH22	38:X:25:ASN:ND2	1.87	0.71
4:N:803:ASN:OD1	4:N:834:LYS:NZ	2.23	0.71
18:B:163:C:H4'	18:B:164:C:OP1	1.88	0.71
27:D:589:THR:HG21	27:D:608:THR:HG23	1.71	0.71
34:3:102:GLU:OE2	34:3:116:LYS:NZ	2.23	0.71
34:3:641:GLN:HE21	34:3:653:TYR:HE1	1.38	0.71
1:A:2310:GLU:C	1:A:2333:PHE:CE1	2.67	0.71
27:D:1396:VAL:HG13	27:D:1445:LEU:HD11	1.73	0.71
34:3:65:LEU:HB2	34:3:1225:VAL:HG23	1.71	0.71
1:A:975:TYR:HB2	1:A:1314:SER:HB3	1.70	0.71
1:A:1015:PRO:HB2	1:A:1510:ILE:HG12	1.72	0.71
1:A:1020:ILE:HG22	1:A:1022:PRO:HD2	1.72	0.71
34:3:369:ILE:HD13	34:3:421:ILE:HD11	1.72	0.71
1:A:244:ASP:OD1	1:A:596:ASN:ND2	2.22	0.71
5:J:340:LYS:NZ	5:J:429:GLU:OE1	2.22	0.71
1:A:2398:LEU:HB2	27:D:1060:LYS:HD2	1.67	0.71
17:I:91:U:O2'	17:I:92:C:OP1	2.08	0.71
41:u:431:TYR:HE2	41:u:440:HIS:CD2	2.09	0.71
8:C:968:MET:HB3	8:C:972:ARG:HH12	1.54	0.71
27:D:1367:PHE:HD2	27:D:1532:ILE:HG23	1.53	0.71
32:1:805:TYR:HB2	32:1:816:VAL:HG11	1.73	0.71
34:3:153:ASP:OD2	34:3:1302:ARG:NH1	2.24	0.71
1:A:1201:TYR:OH	1:A:1248:VAL:O	2.08	0.70
42:w:192:PHE:HB2	43:v:179:LEU:HD13	1.72	0.70
1:A:341:ALA:HA	1:A:355:LEU:HD23	1.72	0.70
2:K:44:ILE:HG12	2:K:76:LEU:HD13	1.73	0.70
27:D:454:LYS:HG3	27:D:463:ILE:HG22	1.73	0.70
27:D:2051:VAL:HG12	27:D:2077:ARG:HA	1.71	0.70
29:H:1093:C:H2'	29:H:1094:G:O4'	1.90	0.70
32:1:835:ILE:HG12	32:1:864:LEU:HD11	1.73	0.70
41:u:516:MET:HE2	41:u:521:TYR:HA	1.72	0.70
1:A:956:LYS:O	1:A:960:THR:OG1	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2398:LEU:CD1	27:D:1060:LYS:HZ1	2.01	0.70
2:K:411:VAL:HG11	2:K:452:LEU:HD11	1.73	0.70
17:I:97:U:H2'	17:I:98:G:C8	2.26	0.70
34:3:291:SER:OG	37:6:80:TYR:OH	2.09	0.70
34:3:886:PHE:HE2	34:3:1225:VAL:HG21	1.56	0.70
1:A:2395:PHE:HD1	27:D:1060:LYS:O	1.74	0.70
18:B:29:G:H2'	18:B:30:A:C8	2.26	0.70
32:1:618:GLN:HG3	32:1:658:VAL:HG22	1.73	0.70
3:L:441:MET:SD	3:L:444:ARG:NH2	2.64	0.70
34:3:611:VAL:HG21	34:3:621:LYS:HE2	1.74	0.70
18:B:147:C:H2'	18:B:148:G:H8	1.54	0.70
39:Y:215:TYR:CE2	39:Y:232:TRP:CE3	2.79	0.70
1:A:2152:TRP:CE3	27:D:1064:PRO:HG3	2.26	0.70
8:C:232:SER:OG	8:C:234:LEU:O	2.08	0.70
32:1:489:VAL:HG11	38:X:26:GLU:HG2	1.74	0.70
41:u:506:LEU:HD23	41:u:521:TYR:HB3	1.73	0.70
27:D:1456:SER:HA	27:D:1465:ILE:HD13	1.73	0.70
27:D:1629:LEU:HD13	27:D:1639:ILE:HB	1.73	0.70
20:l:6:ILE:HG23	20:l:83:LEU:CD2	2.20	0.70
20:l:6:ILE:HG21	20:l:84:PHE:CZ	2.26	0.70
20:l:30:ARG:O	20:l:47:VAL:HG23	1.92	0.70
41:u:33:TYR:O	41:u:36:ILE:HG22	1.91	0.70
41:u:350:ARG:CZ	41:u:350:ARG:HB2	2.20	0.70
27:D:639:LEU:HA	27:D:644:GLY:HA3	1.74	0.70
29:H:1149:G:H5''	29:H:1149:G:H8	1.56	0.70
34:3:638:SER:HB3	34:3:641:GLN:HB3	1.74	0.70
38:X:63:SER:CB	38:X:74:PHE:CD1	2.75	0.70
1:A:864:GLN:NE2	1:A:1099:ASN:OD1	2.24	0.70
8:C:129:ILE:CG2	20:d:16:GLY:HA3	2.22	0.70
8:C:857:LEU:HD22	8:C:967:VAL:HG23	1.71	0.70
34:3:104:TYR:OH	34:3:481:GLN:NE2	2.25	0.70
41:u:516:MET:HE1	41:u:524:LEU:HD22	1.72	0.70
24:T:59:GLU:OE2	25:U:30:LYS:NZ	2.20	0.69
22:m:99:ASP:OD2	41:u:183:GLU:O	2.10	0.69
2:K:171:GLN:HG2	2:K:172:LEU:H	1.57	0.69
17:I:145:U:N3	26:V:35:PHE:HB3	2.05	0.69
24:i:86:ASN:HD21	25:j:32:LYS:CE	2.05	0.69
27:D:626:GLU:OE2	27:D:658:SER:OG	2.06	0.69
27:D:1101:ILE:O	27:D:1105:ALA:HB2	1.92	0.69
27:D:1517:ASN:HB3	27:D:1781:ARG:HH12	1.55	0.69
38:X:46:ASP:OD1	40:Z:38:LEU:HD22	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1347:ARG:NH1	1:A:1450:GLU:OE2	2.26	0.69
18:B:116:U:H2'	18:B:117:G:H8	1.56	0.69
34:3:181:ARG:NH1	36:5:84:ASP:OD1	2.25	0.69
39:Y:215:TYR:CE2	39:Y:232:TRP:HE3	2.09	0.69
40:Z:26:ILE:HB	40:Z:29:MET:HE3	1.73	0.69
22:m:99:ASP:OD2	41:u:183:GLU:CB	2.40	0.69
34:3:1198:ILE:HG13	37:6:48:ALA:HB1	1.72	0.69
1:A:1624:LEU:HD22	1:A:1633:PHE:HB3	1.74	0.69
27:D:450:GLU:O	27:D:466:PRO:HD2	1.93	0.69
27:D:667:ILE:HG21	27:D:684:LEU:HD11	1.73	0.69
38:X:57:PRO:HG2	39:Y:231:ARG:HH21	1.58	0.69
24:T:40:LYS:O	24:T:57:ALA:HA	1.93	0.69
1:A:1777:ILE:HD11	1:A:1802:MET:HE1	1.74	0.69
1:A:1952:PRO:HB2	3:L:426:GLY:H	1.58	0.69
2:K:400:ARG:NH2	2:K:444:ASP:OD1	2.25	0.69
5:J:159:TYR:O	5:J:163:ASN:ND2	2.26	0.69
8:C:126:MET:SD	8:C:132:ARG:NH1	2.66	0.69
16:F:30:G:N2	18:B:96:U:O2	2.22	0.69
29:H:557:G:H1	29:H:683:U:H3	1.41	0.69
23:n:90:PHE:CZ	41:u:194:LYS:C	2.68	0.69
35:4:17:ASP:HB3	35:4:20:ILE:HG12	1.74	0.69
41:u:93:PHE:HZ	42:w:148:PHE:HE1	1.38	0.69
6:E:95:PHE:HB3	6:E:137:TYR:CE2	2.28	0.69
8:C:397:LYS:HE3	8:C:413:LEU:HD11	1.74	0.69
27:D:578:LEU:HB3	27:D:583:ILE:HD12	1.74	0.69
23:R:72:VAL:HB	23:R:91:ILE:O	1.93	0.69
43:v:203:TYR:HD1	43:v:205:PRO:HD2	1.57	0.69
1:A:2152:TRP:CZ3	27:D:1062:PRO:O	2.46	0.69
2:K:395:ILE:HD11	7:M:123:THR:HA	1.75	0.69
22:m:99:ASP:CG	41:u:183:GLU:CB	2.66	0.69
39:Y:170:LEU:O	39:Y:172:ILE:HG12	1.92	0.68
39:Y:171:GLY:C	39:Y:172:ILE:HG12	2.16	0.68
42:w:97:LYS:O	42:w:101:ARG:HG3	1.93	0.68
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.29	0.68
17:I:150:G:C8	23:R:99:ASP:HB3	2.29	0.68
27:D:589:THR:OG1	27:D:608:THR:OG1	2.06	0.68
29:H:110:A:H2	22:m:2:LYS:HE2	1.58	0.68
29:H:120:G:C2	24:i:33:GLU:HG3	2.29	0.68
3:L:124:PHE:CE2	3:L:127:LEU:HB2	2.28	0.68
3:L:261:SER:OG	3:L:281:GLN:OE1	2.10	0.68
8:C:393:LYS:HB3	8:C:413:LEU:HD22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:765:ASN:HB3	27:D:768:HIS:HD2	1.57	0.68
21:P:39:LYS:HE3	22:Q:35:GLN:HE21	1.59	0.68
20:S:65:ARG:HE	20:S:67:SER:HB3	1.58	0.68
41:u:148:SER:HB2	41:u:159:ASP:H	1.58	0.68
5:J:409:HIS:CE1	10:q:42:ASN:CA	2.74	0.68
17:I:77:U:C2	27:D:1107:ARG:HA	2.29	0.68
29:H:119:G:N7	22:m:20:LYS:HE2	2.08	0.68
29:H:545:G:H1	29:H:695:U:H3	1.41	0.68
29:H:118:U:H4'	29:H:119:G:OP1	1.92	0.68
32:1:458:LEU:O	32:1:462:GLN:HB2	1.93	0.68
1:A:216:GLN:NE2	1:A:280:LEU:O	2.24	0.68
8:C:398:ASN:OD1	8:C:401:ARG:NH2	2.26	0.68
18:B:27:G:C2	18:B:131:A:N3	2.61	0.68
23:n:90:PHE:CZ	41:u:195:ARG:N	2.60	0.68
43:v:153:LEU:H	43:v:219:LEU:HD23	1.58	0.68
22:Q:7:LEU:HB3	22:Q:32:VAL:HG11	1.76	0.68
33:2:371:GLU:H	34:3:1234:LYS:HB3	1.56	0.68
42:w:132:HIS:O	42:w:135:PHE:HB3	1.94	0.68
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.26	0.68
8:C:867:THR:O	8:C:926:GLY:CA	2.38	0.68
23:R:33:LEU:HD12	25:U:72:PHE:HB2	1.75	0.68
24:T:30:TRP:HB3	26:V:23:ARG:NH1	2.09	0.68
34:3:594:MET:O	34:3:598:SER:OG	2.11	0.68
37:6:54:SER:HA	37:6:65:THR:HG21	1.76	0.68
34:3:704:SER:OG	34:3:712:PHE:O	2.10	0.68
1:A:956:LYS:HD3	3:L:452:ALA:HA	1.74	0.68
27:D:1213:ARG:NH2	27:D:1316:LYS:HG2	2.08	0.68
29:H:550:G:H1	29:H:690:U:H3	1.41	0.68
34:3:126:SER:HB2	34:3:151:THR:HG22	1.75	0.68
34:3:630:ILE:HG21	34:3:646:LEU:HB2	1.76	0.68
34:3:1124:LEU:HB2	34:3:1130:ILE:HD12	1.76	0.68
41:u:116:LEU:HD13	42:w:102:TYR:CD2	2.29	0.68
8:C:269:LYS:HG2	44:C:1500:GTP:C5	2.28	0.67
8:C:445:PRO:O	8:C:449:PHE:HB3	1.94	0.67
27:D:1640:LEU:HD23	27:D:1666:ILE:HG12	1.76	0.67
29:H:563:G:H1	29:H:677:U:H3	1.41	0.67
25:j:74:ARG:NH1	23:n:65:CYS:SG	2.66	0.67
1:A:2380:LEU:HB3	1:A:2384:ASN:HD22	1.59	0.67
2:K:369:GLY:HA2	2:K:395:ILE:HG23	1.76	0.67
17:I:141:G:C2'	17:I:142:G:H5'	2.25	0.67
29:H:1092:A:H3'	29:H:1093:C:H6	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:963:VAL:HG21	3:L:280:ARG:HH12	1.59	0.67
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.27	0.67
8:C:307:ILE:HA	8:C:324:ILE:HD11	1.76	0.67
27:D:1890:GLU:HB3	22:Q:143:ARG:HE	1.59	0.67
24:T:24:GLN:HB3	24:T:42:LYS:HD2	1.75	0.67
20:l:6:ILE:HG22	20:l:84:PHE:HZ	1.56	0.67
1:A:1063:PHE:HE1	1:A:1086:ASN:HD22	1.40	0.67
8:C:633:ILE:HB	8:C:645:LEU:HB2	1.77	0.67
16:F:28:U:H3	18:B:98:U:H3	1.42	0.67
18:B:147:C:H2'	18:B:148:G:C8	2.29	0.67
29:H:1149:G:H2'	29:H:1150:U:H6	1.58	0.67
40:Z:40:LEU:O	40:Z:43:ASN:O	2.12	0.67
5:J:395:LEU:HA	5:J:399:ARG:HD3	1.77	0.67
8:C:598:ILE:HG23	8:C:933:TRP:CZ2	2.29	0.67
18:B:40:C:O2	18:B:115:G:N2	2.27	0.67
29:H:566:U:H3	29:H:674:G:H1	1.40	0.67
23:n:90:PHE:HD2	41:u:194:LYS:HA	1.57	0.67
26:k:28:ILE:HG22	26:k:41:ASP:HB2	1.76	0.67
32:l:494:LEU:CD1	38:X:7:ILE:HG23	2.14	0.67
33:2:176:TRP:O	33:2:177:GLN:HG2	1.93	0.67
34:3:369:ILE:HD11	34:3:380:LEU:HB2	1.77	0.67
1:A:1943:PRO:HD3	19:O:169:ILE:HD11	1.77	0.67
2:K:446:SER:CB	2:K:451:PHE:CE1	2.76	0.67
27:D:556:LYS:HB2	27:D:628:VAL:HA	1.77	0.67
27:D:1756:ASN:HA	27:D:1854:SER:OG	1.94	0.67
29:H:570:G:H1	29:H:670:U:H3	1.41	0.67
33:2:293:ARG:HG2	33:2:344:VAL:HG22	1.76	0.67
34:3:211:LYS:HD2	34:3:230:ILE:HD11	1.76	0.67
1:A:2018:ASN:HD22	1:A:2058:LEU:HD22	1.58	0.67
2:K:439:LYS:NZ	7:M:122:GLU:OE1	2.23	0.67
3:L:424:THR:HG22	3:L:425:SER:H	1.59	0.67
17:I:75:U:H5	27:D:1100:PHE:CE1	2.12	0.67
29:H:119:G:C5'	23:n:99:ASP:HB2	2.25	0.67
27:D:677:TYR:CD2	27:D:691:LEU:HD21	2.30	0.67
27:D:1971:LEU:HA	27:D:2111:LEU:HB2	1.77	0.67
42:w:221:LEU:O	42:w:225:ARG:HG3	1.95	0.67
43:v:212:GLU:HG2	43:v:214:PRO:HD3	1.76	0.67
8:C:865:ASP:HB2	8:C:931:TYR:HE2	1.60	0.66
2:K:292:TRP:CD1	2:K:299:GLU:HA	2.30	0.66
27:D:1890:GLU:O	22:Q:143:ARG:NE	2.28	0.66
34:3:363:VAL:O	34:3:364:THR:HG23	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:886:PHE:CE2	34:3:1225:VAL:HG21	2.30	0.66
36:5:73:CYS:SG	46:5:203:ZN:ZN	1.84	0.66
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.77	0.66
17:I:143:A:C6	25:U:48:TYR:HD2	2.13	0.66
27:D:2077:ARG:NH1	27:D:2119:LEU:O	2.28	0.66
29:H:548:G:H1	29:H:692:U:H3	1.41	0.66
34:3:153:ASP:OD1	34:3:154:SER:N	2.28	0.66
37:6:50:LEU:HD21	37:6:62:ILE:HG23	1.77	0.66
4:N:304:PRO:O	4:N:308:LEU:N	2.28	0.66
33:2:200:ILE:O	33:2:203:THR:OG1	2.12	0.66
34:3:380:LEU:HD23	34:3:388:LEU:HD21	1.76	0.66
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.27	0.66
8:C:274:ILE:HD13	8:C:385:PHE:HD2	1.60	0.66
8:C:354:TYR:HA	8:C:359:PHE:HA	1.76	0.66
18:B:127:U:H1'	18:B:128:A:C8	2.31	0.66
27:D:542:HIS:CD2	27:D:555:PHE:HB3	2.31	0.66
27:D:757:LEU:O	27:D:761:PHE:CB	2.41	0.66
23:R:102:ILE:HG22	23:R:103:VAL:HG23	1.77	0.66
35:4:184:PHE:HA	35:4:188:GLY:HA2	1.77	0.66
38:X:63:SER:HB3	38:X:74:PHE:CD1	2.30	0.66
43:v:53:ARG:NH2	43:v:58:ILE:O	2.28	0.66
1:A:920:LYS:HD3	1:A:940:ILE:HG21	1.78	0.66
2:K:171:GLN:HA	4:N:723:ARG:HH21	1.58	0.66
8:C:942:GLY:HA3	8:C:963:SER:H	1.61	0.66
19:O:149:TYR:HD2	19:O:178:VAL:HG12	1.60	0.66
27:D:1077:ASN:O	27:D:1081:GLN:HG3	1.96	0.66
27:D:1620:TYR:CD2	27:D:1655:LEU:HD21	2.30	0.66
27:D:2137:LYS:HB2	27:D:2159:GLU:OE2	1.94	0.66
1:A:928:ARG:NH1	1:A:1586:GLN:OE1	2.29	0.66
22:Q:107:LEU:HD11	23:R:59:LYS:HG3	1.77	0.66
32:1:198:GLU:O	32:1:202:ASN:CB	2.43	0.66
32:1:386:TYR:O	32:1:388:TYR:N	2.29	0.66
33:2:146:ILE:HD11	34:3:1178:PRO:HG2	1.78	0.66
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.77	0.66
13:t:19:LYS:O	13:t:84:GLY:HA2	1.95	0.66
28:G:522:U:H3	39:Y:155:ARG:NH2	1.94	0.66
22:m:82:LEU:HD12	22:m:85:ILE:HD11	1.77	0.66
27:D:1493:SER:HA	27:D:1524:TRP:HH2	1.60	0.66
34:3:493:VAL:HA	34:3:937:LYS:HG2	1.77	0.66
1:A:1756:PHE:HD1	1:A:1774:MET:HG2	1.60	0.66
24:i:77:LEU:HD21	24:i:80:ILE:HD12	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:77:GLY:HA3	34:3:146:THR:HG21	1.77	0.66
1:A:2259:ILE:HD11	1:A:2293:ILE:HD11	1.77	0.65
27:D:571:VAL:HG21	27:D:587:GLU:HG2	1.78	0.65
32:1:491:ARG:NH1	38:X:27:TYR:OH	2.29	0.65
32:1:695:ASN:HD22	32:1:700:VAL:HG11	1.60	0.65
32:1:966:GLU:HA	32:1:969:LEU:HD13	1.78	0.65
34:3:527:LEU:HD12	34:3:528:PRO:HD2	1.78	0.65
27:D:1550:SER:C	27:D:1551:PHE:HD1	2.03	0.65
32:1:678:LEU:HD12	32:1:682:ILE:HD11	1.78	0.65
32:1:489:VAL:CG1	38:X:26:GLU:HG2	2.26	0.65
43:v:178:PRO:HD3	43:v:203:TYR:HE2	1.61	0.65
28:G:520:G:N2	38:X:34:TYR:CG	2.65	0.65
33:2:336:ASP:OD2	33:2:338:THR:OG1	2.14	0.65
16:F:92:C:H2'	16:F:93:A:H8	1.61	0.65
21:P:21:ARG:HH11	21:P:29:VAL:HG11	1.62	0.65
21:P:21:ARG:NH1	21:P:51:GLU:OE2	2.30	0.65
22:Q:26:TRP:CE3	22:Q:44:LYS:HG2	2.31	0.65
33:2:323:THR:OG1	35:4:62:ASP:OD1	2.14	0.65
18:B:50:G:H1	18:B:65:U:H3	1.45	0.65
29:H:1115:G:H1	29:H:1130:U:H3	1.43	0.65
32:1:337:VAL:HG11	32:1:359:ILE:HD11	1.79	0.65
32:1:494:LEU:CB	38:X:7:ILE:HG23	2.26	0.65
1:A:404:ASN:ND2	8:C:142:LEU:HD13	2.11	0.65
1:A:2018:ASN:HB3	1:A:2021:SER:OG	1.97	0.65
1:A:2067:TYR:CB	19:O:194:LEU:CD2	2.73	0.65
18:B:95:C:H1'	18:B:96:U:H4'	1.79	0.65
19:O:194:LEU:HD13	19:O:197:ARG:NH1	2.12	0.65
32:1:507:VAL:HG21	32:1:543:ARG:HD2	1.77	0.65
32:1:590:LEU:HD11	32:1:594:MET:HE2	1.78	0.65
32:1:848:ASP:OD1	43:v:62:HIS:NE2	2.28	0.65
1:A:394:ARG:HB2	8:C:667:GLU:OE2	1.97	0.65
1:A:2398:LEU:CB	27:D:1060:LYS:CD	2.69	0.65
27:D:1585:LEU:HD21	27:D:1683:LEU:HD23	1.79	0.65
41:u:132:LEU:HD23	41:u:132:LEU:H	1.61	0.65
8:C:222:MET:O	8:C:225:THR:OG1	2.13	0.65
18:B:1:A:N6	18:B:164:C:H42	1.90	0.65
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.77	0.64
1:A:1832:GLU:OE1	3:L:428:ARG:NH1	2.26	0.64
2:K:415:TYR:CD1	2:K:439:LYS:HB3	2.32	0.64
8:C:318:LEU:HA	8:C:422:LYS:HG2	1.80	0.64
8:C:860:PRO:HG2	8:C:908:VAL:HG11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1487:VAL:O	27:D:1490:THR:OG1	2.13	0.64
27:D:1489:GLU:OE2	27:D:1744:SER:OG	2.11	0.64
28:G:520:G:N1	38:X:34:TYR:CE2	2.65	0.64
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.77	0.64
8:C:510:ARG:NH2	8:C:533:GLU:OE1	2.30	0.64
17:I:151:G:H4'	17:I:152:A:O4'	1.97	0.64
18:B:36:A:H61	18:B:118:U:H3	1.45	0.64
23:R:54:ILE:HG23	23:R:72:VAL:HG13	1.78	0.64
29:H:1098:C:H2'	29:H:1099:G:H8	1.63	0.64
32:1:651:LEU:HD21	32:1:692:ILE:HD11	1.79	0.64
32:1:881:MET:HG2	32:1:885:ILE:HD11	1.77	0.64
34:3:994:LEU:HB3	34:3:1006:TYR:HB2	1.79	0.64
41:u:139:ASP:O	41:u:143:LEU:HB2	1.96	0.64
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.63	0.64
1:A:1563:LYS:O	1:A:1782:ASN:ND2	2.30	0.64
1:A:2310:GLU:OE1	1:A:2333:PHE:CZ	2.49	0.64
7:M:113:GLN:HE21	16:F:77:G:H4'	1.62	0.64
8:C:705:GLY:HA3	8:C:826:PRO:HG3	1.79	0.64
27:D:453:PHE:HE2	27:D:455:ARG:HE	1.45	0.64
27:D:490:ALA:C	27:D:491:PHE:HD1	2.05	0.64
27:D:1216:MET:HG3	27:D:1218:PHE:CE1	2.30	0.64
25:j:77:ASN:OD1	23:n:49:ARG:HD3	1.97	0.64
3:L:136:GLN:NE2	3:L:166:LYS:O	2.31	0.64
8:C:539:VAL:HG13	8:C:564:ILE:HG23	1.79	0.64
8:C:780:PRO:HA	8:C:783:ILE:HB	1.78	0.64
27:D:747:ARG:NH1	27:D:1047:ARG:HG3	2.12	0.64
27:D:804:HIS:CD2	27:D:834:LEU:HD11	2.33	0.64
23:n:90:PHE:CE1	41:u:195:ARG:HA	2.30	0.64
41:u:180:MET:H	41:u:335:THR:HG21	1.62	0.64
1:A:140:ARG:HH21	1:A:252:GLU:HB2	1.61	0.64
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.62	0.64
18:B:95:C:H4'	18:B:96:U:OP1	1.96	0.64
18:B:162:G:C3'	18:B:163:C:H4'	2.22	0.64
29:H:1138:G:O2'	29:H:1139:G:C8	2.50	0.64
27:D:1688:TYR:HD2	27:D:1895:ARG:HA	1.63	0.64
21:P:86:ILE:HG22	20:S:72:ILE:HG22	1.77	0.64
24:T:85:ASP:OD2	25:U:32:LYS:NZ	2.27	0.64
29:H:37:G:OP1	32:1:186:ARG:NH2	2.31	0.64
29:H:1097:G:C2	29:H:1146:G:C4	2.86	0.64
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.32	0.64
3:L:98:PHE:HA	3:L:101:ILE:HG22	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:124:PHE:HB2	3:L:183:PHE:HD1	1.63	0.64
27:D:1524:TRP:CD1	27:D:1780:ARG:CZ	2.79	0.64
29:H:1099:G:H2'	29:H:1100:A:H5'	1.80	0.64
29:H:1138:G:O2'	29:H:1139:G:H8	1.79	0.64
2:K:179:SER:H	2:K:194:SER:HA	1.63	0.64
3:L:298:VAL:HG12	3:L:302:MET:HG2	1.80	0.64
27:D:677:TYR:HB2	27:D:691:LEU:HD11	1.78	0.64
29:H:1120:G:H2'	29:H:1121:U:H6	1.62	0.64
32:1:494:LEU:HD11	38:X:23:TRP:CG	2.31	0.64
33:2:145:GLN:HE21	34:3:1178:PRO:HG3	1.62	0.64
34:3:130:LEU:HD23	34:3:149:ALA:HB2	1.77	0.64
1:A:243:ASP:HB3	1:A:246:GLU:HB2	1.79	0.64
1:A:1258:LEU:HD22	1:A:1269:ILE:HD12	1.79	0.64
3:L:120:TYR:HD1	3:L:123:ARG:HB3	1.61	0.64
3:L:227:PRO:HG3	3:L:325:ARG:HB3	1.80	0.64
21:P:39:LYS:HE3	22:Q:35:GLN:NE2	2.13	0.64
33:2:336:ASP:HB3	33:2:339:ASN:HD22	1.62	0.64
34:3:156:ASN:HD22	34:3:178:PRO:HA	1.63	0.64
8:C:182:LYS:NZ	8:C:186:ASP:OD2	2.24	0.64
8:C:236:LEU:HD21	8:C:435:LEU:HD11	1.80	0.64
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.31	0.63
2:K:316:GLN:OE1	2:K:320:SER:OG	2.17	0.63
3:L:328:VAL:HA	3:L:331:HIS:HD2	1.62	0.63
5:J:344:PHE:CE1	5:J:347:LEU:HB2	2.33	0.63
41:u:441:PHE:CD2	41:u:462:LYS:HG3	2.32	0.63
27:D:1700:ILE:O	27:D:1704:LEU:HG	1.98	0.63
34:3:1036:LYS:NZ	34:3:1082:TYR:OH	2.31	0.63
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.30	0.63
1:A:1267:VAL:HG22	1:A:1302:LEU:HD23	1.81	0.63
34:3:884:ASN:OD1	34:3:885:TRP:N	2.23	0.63
35:4:114:ASN:ND2	35:4:177:ARG:O	2.32	0.63
1:A:976:GLN:NE2	1:A:1310:LYS:HB3	2.12	0.63
8:C:757:TRP:HD1	8:C:762:SER:HB3	1.64	0.63
27:D:610:GLU:HG2	27:D:643:ARG:NH2	2.14	0.63
1:A:681:LYS:O	1:A:684:LYS:HB3	1.99	0.63
8:C:445:PRO:O	8:C:449:PHE:CB	2.47	0.63
18:B:27:G:H8	18:B:27:G:OP2	1.81	0.63
27:D:1372:LYS:HD3	27:D:1708:GLY:HA3	1.80	0.63
41:u:81:ILE:HD11	41:u:160:ARG:HG3	1.79	0.63
1:A:408:SER:HB3	1:A:410:ILE:HD12	1.80	0.63
8:C:405:ARG:HH22	18:B:1:A:H8	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1471:MET:HE2	27:D:1473:TYR:CE1	2.33	0.63
27:D:1688:TYR:CD1	27:D:1695:TYR:CD1	2.85	0.63
27:D:1917:THR:HG22	27:D:1918:SER:H	1.64	0.63
32:1:945:TYR:HB3	32:1:948:ALA:HB3	1.81	0.63
35:4:43:ASP:HB2	35:4:50:GLN:HE21	1.63	0.63
1:A:1632:ILE:HG21	1:A:1645:LEU:HD13	1.81	0.63
8:C:603:PHE:CB	8:C:646:GLY:O	2.46	0.63
17:I:141:G:O2'	17:I:142:G:H5'	1.99	0.63
27:D:520:CYS:HB3	27:D:673:THR:HA	1.78	0.63
27:D:568:GLN:HA	27:D:587:GLU:OE2	1.99	0.63
34:3:128:LYS:NZ	34:3:193:MET:O	2.32	0.63
1:A:456:GLU:HG3	8:C:357:GLY:HA3	1.80	0.63
1:A:1058:ALA:HB3	1:A:1105:ARG:HH21	1.63	0.63
3:L:357:PRO:O	3:L:358:ILE:HG13	1.99	0.63
28:G:520:G:C2	38:X:34:TYR:CD1	2.86	0.63
32:1:510:ALA:HA	32:1:518:THR:HG21	1.80	0.63
17:I:142:G:H5''	17:I:143:A:OP2	1.99	0.63
22:Q:44:LYS:HB2	22:Q:79:ILE:HG21	1.81	0.63
32:1:484:PHE:HA	32:1:488:TRP:HD1	1.64	0.63
34:3:961:CYS:O	34:3:962:LEU:HD12	1.99	0.63
1:A:1790:TRP:HZ3	1:A:1798:ILE:HD12	1.63	0.62
8:C:274:ILE:HD12	8:C:382:TYR:CD1	2.34	0.62
32:1:542:THR:O	32:1:546:ASN:ND2	2.31	0.62
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.14	0.62
35:4:201:LEU:HA	41:u:452:CYS:HB3	1.81	0.62
1:A:656:ILE:O	1:A:660:ILE:HG13	2.00	0.62
8:C:652:MET:HG3	8:C:655:LEU:HD12	1.80	0.62
27:D:1668:LYS:HE3	27:D:1702:GLU:HG3	1.80	0.62
22:Q:3:LEU:HD13	23:R:62:ASP:HB2	1.81	0.62
32:1:334:ILE:HD11	32:1:362:CYS:HB3	1.80	0.62
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.79	0.62
1:A:1208:PRO:O	1:A:1212:ARG:HG3	1.98	0.62
1:A:1376:ASN:OD1	1:A:1377:SER:N	2.32	0.62
1:A:2398:LEU:HD22	27:D:1060:LYS:HD2	1.81	0.62
16:F:43:C:O2'	16:F:44:A:O5'	2.14	0.62
32:1:494:LEU:HD12	38:X:7:ILE:HG21	1.77	0.62
1:A:1172:PHE:HZ	1:A:1230:ILE:HD11	1.64	0.62
32:1:810:THR:HG22	43:v:63:SER:OG	2.00	0.62
34:3:394:SER:HB3	34:3:404:LEU:HB2	1.80	0.62
34:3:1124:LEU:HB3	34:3:1128:THR:HG23	1.82	0.62
3:L:401:LEU:N	4:N:214:SER:HB3	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:130:PRO:HB3	8:C:558:LYS:NZ	2.15	0.62
8:C:703:LEU:O	8:C:705:GLY:N	2.33	0.62
23:n:90:PHE:HE2	41:u:194:LYS:O	1.78	0.62
38:X:72:GLN:HA	38:X:72:GLN:OE1	1.98	0.62
3:L:175:LEU:O	3:L:179:MET:HB2	2.00	0.62
27:D:781:LEU:HD21	27:D:798:GLU:HG2	1.80	0.62
27:D:1541:ILE:HD12	27:D:1542:GLU:HG2	1.82	0.62
27:D:1996:GLN:NE2	27:D:2150:LEU:H	1.97	0.62
24:T:35:ILE:HA	26:V:23:ARG:HH21	1.64	0.62
32:1:494:LEU:HB3	38:X:7:ILE:CG2	2.29	0.62
34:3:629:GLY:O	34:3:630:ILE:HG13	1.99	0.62
34:3:987:PHE:CD2	34:3:1054:LEU:HB2	2.34	0.62
4:N:849:TYR:O	4:N:853:GLY:N	2.20	0.62
27:D:1148:GLN:HE22	27:D:1297:TRP:HA	1.64	0.62
1:A:2189:LEU:HD13	1:A:2224:VAL:HG23	1.81	0.62
2:K:285:HIS:C	2:K:287:MET:H	2.06	0.62
27:D:1772:TRP:CZ3	27:D:1773:PHE:CE1	2.86	0.62
29:H:1098:C:O5'	29:H:1098:C:H6	1.82	0.62
34:3:253:VAL:HG21	34:3:327:VAL:HG11	1.82	0.62
37:6:23:ASP:OD1	37:6:24:GLU:N	2.29	0.62
43:v:218:ILE:O	43:v:219:LEU:HG	2.00	0.62
1:A:1014:LYS:HE2	1:A:1024:LEU:HD13	1.82	0.62
3:L:239:ALA:O	3:L:243:ALA:HB2	2.00	0.62
24:T:90:ILE:HB	26:V:62:VAL:HG13	1.81	0.62
28:G:488:A:H1'	41:u:414:LEU:HD22	1.82	0.62
29:H:143:G:H2'	29:H:144:G:H8	1.65	0.62
34:3:379:VAL:O	34:3:390:LYS:HA	1.99	0.62
34:3:699:MET:HA	34:3:719:GLN:O	1.99	0.62
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.40	0.61
1:A:2349:PHE:CD2	1:A:2379:PRO:HG3	2.35	0.61
1:A:2395:PHE:CD1	27:D:1062:PRO:CD	2.67	0.61
2:K:392:HIS:HD2	2:K:396:VAL:HG22	1.65	0.61
8:C:220:ASN:HB3	8:C:651:TYR:HB2	1.80	0.61
1:A:1501:THR:HG21	4:N:163:THR:HG21	1.82	0.61
8:C:468:LEU:HD11	8:C:493:LEU:HD23	1.81	0.61
16:F:74:U:H2'	16:F:75:A:C8	2.35	0.61
26:V:30:ARG:HE	26:V:41:ASP:HB3	1.65	0.61
29:H:119:G:O5'	25:j:76:ASN:ND2	2.33	0.61
32:1:531:GLU:OE1	32:1:534:ARG:NH2	2.33	0.61
32:1:763:LEU:HD11	32:1:797:VAL:HG22	1.81	0.61
43:v:71:CYS:SG	43:v:93:ASN:ND2	2.73	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:222:ILE:HA	3:L:225:ILE:HG12	1.82	0.61
27:D:1731:TYR:OH	22:Q:146:LEU:O	2.15	0.61
27:D:1925:LYS:NZ	27:D:1946:ASP:OD2	2.25	0.61
20:l:20:SER:OG	20:l:30:ARG:HD2	2.00	0.61
1:A:304:ASP:OD1	1:A:305:LEU:N	2.32	0.61
6:E:42:MET:HG2	6:E:80:MET:HE1	1.82	0.61
27:D:1220:ILE:HD11	27:D:1272:PHE:HE2	1.65	0.61
29:H:120:G:N7	25:j:32:LYS:HD2	2.15	0.61
32:1:820:MET:HA	32:1:823:MET:HG2	1.81	0.61
34:3:768:ARG:NH2	34:3:1359:ASN:O	2.32	0.61
2:K:179:SER:HA	2:K:441:ILE:HG21	1.83	0.61
8:C:271:ASP:O	8:C:275:LEU:HB2	1.99	0.61
8:C:605:ILE:HG13	8:C:652:MET:HE1	1.81	0.61
27:D:1370:SER:OG	27:D:1535:PHE:HB2	2.00	0.61
23:n:90:PHE:CD2	41:u:194:LYS:CA	2.78	0.61
34:3:128:LYS:NZ	34:3:194:GLU:OE1	2.29	0.61
34:3:154:SER:HB3	34:3:1302:ARG:HD2	1.83	0.61
41:u:419:ARG:HE	41:u:434:ARG:HH21	1.47	0.61
1:A:2310:GLU:CD	1:A:2333:PHE:HZ	2.08	0.61
2:K:395:ILE:HG22	2:K:396:VAL:N	2.12	0.61
4:N:261:LYS:HB3	4:N:285:HIS:CD2	2.35	0.61
5:J:443:LYS:HG2	5:J:444:VAL:H	1.65	0.61
27:D:571:VAL:HG21	27:D:587:GLU:CG	2.31	0.61
21:P:49:ILE:HG22	21:P:81:VAL:HA	1.82	0.61
29:H:1161:U:O2'	29:H:1162:U:H5'	2.01	0.61
32:1:739:ASN:OD1	32:1:740:LYS:N	2.32	0.61
1:A:1562:PHE:O	1:A:1565:THR:OG1	2.17	0.61
2:K:286:ASP:O	2:K:287:MET:HG2	1.99	0.61
2:K:397:THR:OG1	2:K:413:CYS:O	2.07	0.61
18:B:136:G:O2'	18:B:137:U:O4'	2.19	0.61
27:D:1367:PHE:HE2	27:D:1518:ALA:HB1	1.64	0.61
34:3:638:SER:HA	34:3:683:GLN:HA	1.83	0.61
34:3:642:LEU:HD21	34:3:644:ILE:HG23	1.81	0.61
43:v:178:PRO:HD3	43:v:203:TYR:CE2	2.36	0.61
8:C:598:ILE:HG22	8:C:599:THR:HG23	1.82	0.61
18:B:19:A:N6	18:B:151:A:N1	2.47	0.61
27:D:960:ILE:HG23	27:D:961:SER:H	1.65	0.61
29:H:1149:G:H2'	29:H:1150:U:C6	2.34	0.61
30:o:80:LEU:HD13	31:p:53:ALA:HB1	1.83	0.61
33:2:167:LYS:NZ	34:3:1111:ASP:OD2	2.21	0.61
34:3:205:SER:HB2	34:3:211:LYS:HG2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:X:78:LYS:NZ	39:Y:162:LEU:O	2.34	0.61
41:u:26:GLN:HB2	42:w:168:THR:HG23	1.83	0.61
1:A:406:PRO:HG2	44:C:1500:GTP:O2'	2.01	0.61
1:A:609:GLU:O	1:A:613:SER:CB	2.47	0.61
1:A:2157:ILE:CG2	27:D:1066:ARG:HG2	2.31	0.61
4:N:101:LYS:O	4:N:105:ALA:HB2	2.00	0.61
7:M:93:VAL:HG12	7:M:95:ARG:H	1.64	0.61
8:C:176:ARG:NH1	8:C:184:GLU:O	2.34	0.61
8:C:415:TYR:HB3	8:C:419:PRO:HG2	1.83	0.61
22:Q:7:LEU:HD11	23:R:95:PHE:CE2	2.36	0.61
32:1:494:LEU:HB3	38:X:7:ILE:CG1	2.31	0.61
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	2.01	0.60
2:K:292:TRP:HE1	2:K:299:GLU:HG3	1.66	0.60
2:K:312:SER:HB2	2:K:353:TYR:O	2.01	0.60
17:I:146:U:O4'	20:S:67:SER:HB2	2.01	0.60
28:G:520:G:C5	38:X:34:TYR:CZ	2.88	0.60
29:H:119:G:OP2	25:j:76:ASN:CB	2.49	0.60
24:i:86:ASN:ND2	25:j:32:LYS:HD3	2.13	0.60
34:3:640:THR:OG1	34:3:686:GLN:O	2.20	0.60
34:3:1216:CYS:SG	34:3:1228:PHE:HB2	2.41	0.60
41:u:63:LYS:HE3	41:u:378:ASP:HB2	1.82	0.60
7:M:51:PHE:HE2	7:M:114:ILE:HG23	1.66	0.60
8:C:504:THR:O	8:C:507:SER:OG	2.15	0.60
8:C:918:LEU:HD23	8:C:928:CYS:HB2	1.83	0.60
27:D:1524:TRP:CD1	27:D:1780:ARG:NE	2.69	0.60
27:D:1688:TYR:CZ	27:D:1896:LYS:HE2	2.36	0.60
34:3:994:LEU:HB2	34:3:1008:ILE:HD11	1.83	0.60
42:w:185:VAL:HG13	43:v:232:GLY:HA2	1.83	0.60
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.67	0.60
2:K:261:LEU:HB3	2:K:292:TRP:CZ3	2.37	0.60
29:H:1139:G:H2'	29:H:1140:U:C6	2.36	0.60
20:l:6:ILE:HG21	20:l:84:PHE:CE1	2.37	0.60
22:m:3:LEU:HD11	23:n:60:ALA:HB1	1.82	0.60
32:1:516:SER:O	32:1:520:ASP:HB2	2.01	0.60
32:1:767:LEU:HD22	32:1:804:GLU:HG2	1.82	0.60
1:A:683:LEU:HD13	1:A:706:PRO:HB2	1.82	0.60
16:F:2:U:H2'	16:F:3:U:C6	2.36	0.60
17:I:77:U:H1'	27:D:1107:ARG:HG3	1.84	0.60
28:G:514:U:H4'	28:G:515:U:H5'	1.83	0.60
32:1:177:ASN:OD1	32:1:178:THR:N	2.34	0.60
34:3:493:VAL:O	34:3:499:SER:OG	2.13	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1037:PHE:HB2	34:3:1042:LEU:HB2	1.82	0.60
18:B:27:G:OP1	18:B:141:G:O5'	2.19	0.60
21:h:36:ALA:CB	20:l:84:PHE:HE1	2.07	0.60
18:B:27:G:N2	18:B:131:A:N3	2.48	0.60
24:i:83:LYS:NZ	25:j:75:CYS:O	2.35	0.60
34:3:184:LEU:HD21	37:6:45:GLY:HA3	1.83	0.60
34:3:379:VAL:HG22	34:3:391:LEU:HB2	1.83	0.60
39:Y:173:ASN:O	39:Y:174:VAL:HG12	2.02	0.60
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.37	0.60
1:A:1682:THR:OG1	1:A:1702:THR:OG1	2.20	0.60
1:A:2310:GLU:CA	1:A:2333:PHE:CE1	2.85	0.60
5:J:167:GLU:HB3	5:J:169:TRP:HE3	1.66	0.60
8:C:737:ILE:HG12	8:C:768:PHE:HB3	1.83	0.60
17:I:62:G:OP1	27:D:714:ASN:HB3	2.02	0.60
27:D:1409:LEU:HD22	27:D:1427:LYS:HB2	1.84	0.60
27:D:2104:GLY:HA2	27:D:2112:TYR:HD2	1.66	0.60
34:3:335:ILE:HD12	34:3:407:LEU:HD11	1.83	0.60
34:3:547:ASN:HA	34:3:563:ILE:O	2.00	0.60
41:u:179:TYR:HA	41:u:335:THR:HG22	1.83	0.60
1:A:1213:MET:HG2	1:A:1259:LEU:HD12	1.82	0.60
1:A:1777:ILE:HG12	1:A:1784:TYR:HB3	1.82	0.60
1:A:1910:LYS:CD	19:O:169:ILE:HG12	2.30	0.60
2:K:65:GLU:HG3	2:K:66:ASN:H	1.66	0.60
8:C:116:THR:OG1	8:C:120:ARG:NH1	2.34	0.60
27:D:707:PHE:HD2	27:D:895:VAL:HG13	1.67	0.60
42:w:225:ARG:HG2	43:v:242:PHE:HD1	1.66	0.60
1:A:902:PRO:HG2	1:A:905:TYR:HB2	1.82	0.60
18:B:162:G:O3'	21:a:8:HIS:N	2.35	0.60
27:D:1154:VAL:O	27:D:1157:ILE:HG13	2.02	0.60
27:D:1772:TRP:HZ3	27:D:1773:PHE:CZ	2.20	0.60
27:D:2013:VAL:HG13	27:D:2018:ASP:HB2	1.83	0.60
29:H:119:G:H5''	23:n:99:ASP:HB2	1.82	0.60
1:A:431:ILE:HA	8:C:895:ALA:HB1	1.84	0.60
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.82	0.60
1:A:2310:GLU:CG	1:A:2333:PHE:CZ	2.66	0.60
7:M:34:LYS:HB3	7:M:39:GLU:HG2	1.83	0.60
27:D:683:PHE:HA	27:D:946:VAL:HG21	1.83	0.60
32:1:494:LEU:CB	38:X:7:ILE:CG1	2.78	0.60
34:3:854:ASN:OD1	34:3:855:ALA:N	2.35	0.60
41:u:148:SER:HB2	41:u:159:ASP:N	2.17	0.60
1:A:939:LEU:HD11	3:L:441:MET:HE2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:GLN:HE22	1:A:1310:LYS:CB	2.13	0.59
2:K:135:ARG:NH1	2:K:360:ASN:O	2.33	0.59
2:K:177:PRO:O	2:K:194:SER:OG	2.15	0.59
4:N:842:TRP:HA	4:N:845:LEU:HD12	1.82	0.59
16:F:36:U:H3	16:F:45:A:H61	1.50	0.59
17:I:96:A:H2'	17:I:97:U:O4'	2.02	0.59
27:D:781:LEU:CD2	27:D:798:GLU:HA	2.29	0.59
27:D:2008:CYS:SG	27:D:2013:VAL:HB	2.42	0.59
25:U:28:GLY:HA2	25:U:38:TYR:O	2.02	0.59
29:H:1149:G:H8	29:H:1149:G:C5'	2.15	0.59
34:3:236:VAL:HG13	34:3:257:ILE:HG23	1.84	0.59
34:3:1056:LYS:O	41:u:514:ASN:ND2	2.21	0.59
5:J:346:ASN:O	5:J:422:ASN:ND2	2.35	0.59
23:n:83:ASN:OD1	23:n:85:ILE:HG13	2.02	0.59
34:3:412:THR:O	34:3:413:ILE:HG23	2.03	0.59
34:3:831:THR:HA	34:3:836:TRP:HA	1.83	0.59
34:3:924:PHE:CD2	34:3:952:ARG:HD2	2.37	0.59
38:X:90:ASP:OD2	39:Y:223:ARG:NH2	2.35	0.59
1:A:161:PHE:O	1:A:165:LEU:HB2	2.02	0.59
1:A:430:PRO:O	1:A:431:ILE:HG22	2.03	0.59
2:K:355:VAL:HG22	2:K:366:THR:HG22	1.84	0.59
3:L:225:ILE:O	3:L:325:ARG:NH1	2.35	0.59
20:S:65:ARG:NH1	26:V:65:GLY:O	2.35	0.59
41:u:29:PRO:HG3	41:u:59:ILE:HG13	1.84	0.59
1:A:675:HIS:NE2	18:B:102:C:OP1	2.36	0.59
2:K:165:LEU:HD22	2:K:465:ASN:HB3	1.83	0.59
27:D:1428:LEU:HD11	27:D:1445:LEU:HB2	1.85	0.59
27:D:1779:TYR:CE1	27:D:1783:HIS:HE1	2.21	0.59
33:2:296:GLN:NE2	33:2:306:GLU:OE2	2.35	0.59
38:X:48:LEU:O	39:Y:231:ARG:CZ	2.49	0.59
38:X:89:VAL:HG22	38:X:104:ILE:HG22	1.85	0.59
1:A:794:LYS:HB3	1:A:854:ARG:NH1	2.16	0.59
1:A:2189:LEU:HD21	1:A:2347:GLY:C	2.28	0.59
2:K:285:HIS:O	2:K:309:GLY:HA2	2.03	0.59
4:N:241:PRO:HB3	4:N:277:ILE:HD11	1.84	0.59
17:I:90:C:N3	22:Q:34:PRO:HD2	2.17	0.59
27:D:563:LEU:HD11	27:D:836:TRP:CE2	2.38	0.59
29:H:40:U:O2'	43:v:74:MET:O	2.15	0.59
29:H:1149:G:C8	29:H:1149:G:C5'	2.85	0.59
29:H:1152:U:H2'	29:H:1153:C:C6	2.38	0.59
34:3:433:MET:O	34:3:485:ASN:HB3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:1090:ILE:O	34:3:1117:HIS:HA	2.01	0.59
1:A:1202:ASN:ND2	1:A:1246:ALA:O	2.34	0.59
1:A:1308:GLU:HG2	1:A:1311:LYS:HD2	1.84	0.59
2:K:66:ASN:ND2	16:F:74:U:O2	2.35	0.59
8:C:803:VAL:HG13	8:C:813:ILE:HB	1.84	0.59
28:G:521:U:OP2	32:1:408:ARG:NH2	2.34	0.59
28:G:522:U:H3	39:Y:155:ARG:CZ	2.16	0.59
35:4:200:ARG:HB3	41:u:453:LEU:HA	1.84	0.59
38:X:11:GLU:HG2	38:X:16:ILE:HG21	1.84	0.59
1:A:1414:TRP:CD1	1:A:1555:THR:HG22	2.37	0.59
1:A:2310:GLU:CA	1:A:2333:PHE:CZ	2.82	0.59
4:N:809:LEU:HD12	4:N:841:THR:HG22	1.85	0.59
27:D:568:GLN:NE2	27:D:587:GLU:OE1	2.36	0.59
32:1:696:LYS:HG2	32:1:697:HIS:H	1.68	0.59
38:X:123:LYS:O	38:X:127:ASP:N	2.34	0.59
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.36	0.59
5:J:265:LEU:HD12	5:J:266:PRO:HD2	1.85	0.59
19:O:183:LYS:O	19:O:187:GLU:HB2	2.02	0.59
32:1:698:ARG:HE	32:1:739:ASN:HD22	1.51	0.59
34:3:1199:ILE:HA	34:3:1220:GLY:HA2	1.84	0.59
41:u:243:PHE:HA	41:u:246:LYS:HE2	1.83	0.59
8:C:968:MET:HB3	8:C:972:ARG:NH1	2.18	0.59
18:B:161:U:H2'	18:B:162:G:C8	2.38	0.59
29:H:112:A:N7	23:n:63:ARG:NE	2.51	0.59
29:H:1140:U:C2	29:H:1141:C:C5	2.91	0.59
29:H:1146:G:O2'	29:H:1147:A:O5'	2.15	0.59
32:1:327:TRP:HZ2	32:1:369:PRO:HG2	1.68	0.59
34:3:599:ILE:HB	34:3:610:ILE:HB	1.85	0.59
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.38	0.59
18:B:43:G:H2'	18:B:44:A:C8	2.38	0.59
27:D:765:ASN:CB	27:D:768:HIS:HD2	2.16	0.59
23:R:27:LYS:O	23:R:32:SER:OG	2.20	0.59
29:H:120:G:N1	24:i:33:GLU:O	2.36	0.59
34:3:180:THR:O	36:5:83:LYS:HB3	2.03	0.59
34:3:736:ILE:HG23	34:3:738:GLN:H	1.68	0.59
41:u:31:LEU:HD11	41:u:75:GLN:OE1	2.02	0.59
41:u:508:GLU:H	41:u:513:GLY:HA3	1.68	0.59
42:w:140:ALA:HA	42:w:143:LYS:HD2	1.85	0.59
1:A:1674:ASP:OD2	1:A:2200:LYS:NZ	2.33	0.58
27:D:1372:LYS:HA	27:D:1376:LYS:NZ	2.18	0.58
21:P:18:TYR:HD1	21:P:101:PRO:HG3	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:416:LEU:HD12	32:1:453:MET:HE1	1.84	0.58
32:1:442:ILE:HG23	32:1:457:ILE:HG23	1.83	0.58
32:1:632:LYS:HD2	32:1:672:VAL:HG13	1.85	0.58
34:3:208:GLU:HG3	34:3:209:GLN:H	1.67	0.58
38:X:40:ARG:NH1	38:X:72:GLN:O	2.36	0.58
1:A:867:ILE:HD13	1:A:1101:TYR:CG	2.38	0.58
1:A:927:VAL:HG13	3:L:385:ARG:HD2	1.83	0.58
27:D:1489:GLU:CD	27:D:1746:LEU:HG	2.28	0.58
27:D:1779:TYR:CE1	27:D:1783:HIS:CE1	2.91	0.58
27:D:1781:ARG:HG3	27:D:1789:TYR:HE2	1.66	0.58
33:2:292:GLY:N	35:4:31:GLN:OE1	2.30	0.58
34:3:382:GLN:NE2	34:3:416:SER:OG	2.36	0.58
1:A:365:ASN:OD1	1:A:366:GLU:N	2.36	0.58
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.03	0.58
1:A:1391:PRO:HD2	1:A:1394:LEU:HD12	1.85	0.58
4:N:401:ILE:O	4:N:405:SER:N	2.34	0.58
8:C:597:TYR:CE1	8:C:630:PRO:HB2	2.38	0.58
8:C:794:GLN:HG2	8:C:835:LYS:HG2	1.84	0.58
18:B:67:U:H2'	18:B:68:A:H8	1.68	0.58
32:1:538:VAL:O	32:1:542:THR:HG23	2.03	0.58
1:A:551:LEU:HG	1:A:557:PHE:HE2	1.69	0.58
8:C:348:LEU:HD12	8:C:372:THR:HG22	1.84	0.58
27:D:789:LEU:O	27:D:794:ARG:NE	2.32	0.58
29:H:119:G:C5	22:m:20:LYS:HE2	2.39	0.58
26:k:28:ILE:HG22	26:k:41:ASP:CB	2.32	0.58
34:3:232:ARG:HE	34:3:235:MET:HG3	1.68	0.58
34:3:387:ASP:HA	34:3:412:THR:HG22	1.84	0.58
34:3:1191:ASN:ND2	34:3:1316:LYS:HB2	2.18	0.58
2:K:197:GLY:HA2	2:K:221:ILE:HG13	1.85	0.58
6:E:137:TYR:O	6:E:139:HIS:N	2.37	0.58
8:C:706:LEU:HD23	8:C:825:VAL:HA	1.85	0.58
27:D:645:PRO:HA	27:D:648:GLU:OE2	2.03	0.58
27:D:1367:PHE:CE2	27:D:1518:ALA:HB1	2.39	0.58
23:R:72:VAL:HG21	23:R:94:LEU:HB3	1.85	0.58
1:A:325:LYS:HB2	1:A:405:ASN:HD22	1.68	0.58
2:K:171:GLN:NE2	2:K:209:PRO:O	2.36	0.58
8:C:138:VAL:HG12	8:C:146:LYS:HG2	1.85	0.58
18:B:32:G:O2'	18:B:34:C:H5''	2.03	0.58
27:D:1898:ASP:O	27:D:1902:LEU:HG	2.03	0.58
34:3:328:VAL:HG22	34:3:337:VAL:HG12	1.86	0.58
34:3:515:ASN:HB2	34:3:886:PHE:HE1	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:w:225:ARG:HG2	43:v:242:PHE:CD1	2.38	0.58
1:A:874:ILE:O	1:A:875:THR:OG1	2.21	0.58
1:A:956:LYS:NZ	3:L:451:GLN:HG3	2.19	0.58
8:C:130:PRO:HB3	8:C:558:LYS:HZ1	1.68	0.58
27:D:794:ARG:O	27:D:798:GLU:HG3	2.04	0.58
27:D:1748:TYR:CE2	22:Q:142:PRO:HD2	2.39	0.58
26:V:8:LYS:HA	26:V:11:MET:HG2	1.86	0.58
34:3:1116:ARG:HH22	34:3:1141:LEU:HD21	1.69	0.58
36:5:74:TRP:HZ2	36:5:78:ARG:HH21	1.50	0.58
41:u:170:PHE:CZ	41:u:246:LYS:HG2	2.39	0.58
1:A:377:VAL:HG12	1:A:379:ILE:H	1.68	0.58
1:A:2310:GLU:CD	1:A:2333:PHE:CZ	2.82	0.58
5:J:319:ALA:O	5:J:323:ARG:HG2	2.03	0.58
16:F:38:U:O2'	16:F:39:G:OP2	2.20	0.58
27:D:2053:LEU:HD21	27:D:2142:ILE:HG22	1.86	0.58
25:U:46:ASP:OD1	25:U:50:ASN:N	2.33	0.58
1:A:987:LEU:HG	3:L:441:MET:HE1	1.86	0.58
1:A:1417:GLN:HB2	1:A:1783:MET:HE1	1.85	0.58
1:A:2159:ASN:HA	1:A:2162:LEU:HD13	1.86	0.58
27:D:978:LEU:HD23	27:D:981:LEU:HD12	1.86	0.58
27:D:1700:ILE:HD11	27:D:1740:LEU:HD13	1.84	0.58
41:u:14:MET:HE3	41:u:86:TYR:CZ	2.39	0.58
27:D:706:GLN:C	27:D:707:PHE:HD1	2.10	0.58
22:Q:3:LEU:HD23	23:R:95:PHE:CE1	2.35	0.58
30:o:80:LEU:HD13	31:p:53:ALA:CB	2.34	0.58
32:1:601:ILE:O	32:1:604:THR:OG1	2.16	0.58
34:3:766:LYS:HD3	34:3:836:TRP:CE2	2.38	0.58
41:u:377:VAL:HG12	41:u:378:ASP:N	2.19	0.58
2:K:175:THR:O	2:K:176:LYS:HG2	2.04	0.57
4:N:286:GLU:HG3	4:N:287:SER:H	1.68	0.57
4:N:760:VAL:O	4:N:764:LEU:CB	2.52	0.57
18:B:77:A:H4'	18:B:78:A:OP1	2.03	0.57
27:D:1488:TYR:O	27:D:1492:ILE:HG12	2.03	0.57
20:l:66:GLY:HA2	20:l:69:ILE:HD12	1.85	0.57
34:3:1222:GLN:HE22	37:6:48:ALA:HB2	1.68	0.57
1:A:585:ARG:HD3	1:A:733:GLN:HG2	1.86	0.57
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.36	0.57
1:A:1694:MET:O	1:A:1759:TYR:OH	2.22	0.57
8:C:869:HIS:HD2	8:C:925:LEU:HB3	1.69	0.57
17:I:149:U:O4	23:R:66:ASN:ND2	2.32	0.57
18:B:159:C:O2'	18:B:161:U:OP2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:848:LYS:HA	27:D:889:ILE:HB	1.86	0.57
27:D:1246:THR:O	27:D:1289:PHE:HE2	1.87	0.57
27:D:1434:LEU:HB2	27:D:2096:LEU:HG	1.84	0.57
29:H:41:C:H4'	43:v:75:HIS:CE1	2.39	0.57
29:H:1141:C:H2'	29:H:1142:G:H8	1.68	0.57
22:m:43:VAL:HG11	22:m:85:ILE:HD12	1.87	0.57
32:1:257:MET:HG3	36:5:100:HIS:ND1	2.18	0.57
34:3:367:SER:HB2	34:3:382:GLN:HG2	1.84	0.57
1:A:181:HIS:HA	1:A:704:TRP:CZ2	2.36	0.57
1:A:194:HIS:HB3	1:A:198:ALA:H	1.68	0.57
1:A:1275:MET:HE1	1:A:1279:VAL:HG11	1.86	0.57
3:L:184:LYS:HE2	3:L:186:LYS:HB2	1.86	0.57
3:L:462:ASN:HA	4:N:830:ARG:HD2	1.87	0.57
8:C:625:ILE:HD11	8:C:659:LEU:HD13	1.86	0.57
20:l:9:LYS:HD3	20:l:83:LEU:HD11	1.85	0.57
32:1:882:ASN:ND2	33:2:268:ASP:O	2.37	0.57
34:3:432:GLU:O	34:3:485:ASN:ND2	2.37	0.57
35:4:136:ARG:HB2	35:4:154:TYR:HD2	1.69	0.57
41:u:516:MET:HE3	41:u:520:VAL:HG12	1.86	0.57
42:w:192:PHE:CD2	43:v:233:VAL:HG11	2.39	0.57
43:v:214:PRO:N	43:v:215:PRO:HD2	2.19	0.57
1:A:884:SER:HB3	3:L:180:LYS:HZ3	1.69	0.57
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.86	0.57
8:C:709:SER:O	8:C:821:LEU:N	2.37	0.57
8:C:752:ARG:HA	8:C:757:TRP:H	1.70	0.57
28:G:505:A:H1'	28:G:506:U:H6	1.68	0.57
29:H:1097:G:H1'	29:H:1146:G:N2	2.20	0.57
34:3:189:PRO:HA	34:3:206:SER:HB3	1.86	0.57
34:3:783:ILE:HG13	34:3:784:SER:N	2.18	0.57
42:w:134:THR:O	42:w:137:ASP:HB2	2.04	0.57
1:A:662:GLN:NE2	16:F:1:G:N3	2.52	0.57
8:C:562:VAL:HG23	8:C:564:ILE:HD11	1.86	0.57
27:D:1216:MET:CG	27:D:1218:PHE:HE1	2.14	0.57
27:D:1396:VAL:HG11	27:D:1452:PHE:CE2	2.38	0.57
29:H:36:A:N7	32:1:182:ARG:NH2	2.52	0.57
34:3:365:ILE:HD13	34:3:381:LEU:HG	1.87	0.57
41:u:377:VAL:HG12	41:u:378:ASP:H	1.69	0.57
1:A:2064:GLY:O	1:A:2068:ASN:N	2.37	0.57
18:B:10:U:H2'	18:B:11:A:N7	2.20	0.57
27:D:505:LYS:HA	27:D:508:HIS:NE2	2.19	0.57
27:D:1217:ARG:NH2	27:D:1788:TYR:OH	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:2102:VAL:O	27:D:2142:ILE:HA	2.03	0.57
21:P:21:ARG:NH1	21:P:29:VAL:HG11	2.19	0.57
25:U:74:ARG:HB3	25:U:77:ASN:HD22	1.70	0.57
33:2:183:LEU:HD22	33:2:188:LEU:HD11	1.87	0.57
40:Z:37:LEU:O	40:Z:41:GLU:HG2	2.05	0.57
41:u:199:SER:H	41:u:202:GLN:HE21	1.52	0.57
1:A:1277:GLU:O	1:A:1279:VAL:HG23	2.05	0.57
2:K:451:PHE:CD1	2:K:451:PHE:N	2.73	0.57
8:C:143:HIS:HA	44:C:1500:GTP:O3B	2.04	0.57
8:C:245:VAL:HG11	8:C:295:ILE:HG22	1.86	0.57
34:3:159:ILE:HD12	34:3:224:ILE:HD11	1.87	0.57
34:3:390:LYS:HD2	34:3:410:PHE:CZ	2.39	0.57
43:v:58:ILE:HA	43:v:67:VAL:O	2.05	0.57
27:D:648:GLU:OE1	27:D:943:TYR:HB3	2.04	0.57
27:D:801:ILE:HG22	27:D:827:VAL:HB	1.86	0.57
22:Q:43:VAL:HG11	22:Q:85:ILE:HD12	1.87	0.57
20:S:68:GLN:HG3	26:V:69:ILE:HA	1.86	0.57
24:T:10:MET:HG3	26:V:30:ARG:O	2.04	0.57
33:2:265:CYS:SG	33:2:266:PHE:N	2.78	0.57
35:4:139:GLU:O	35:4:151:ALA:HA	2.04	0.57
2:K:32:LEU:HD23	2:K:34:HIS:H	1.70	0.57
27:D:1415:ARG:HA	27:D:1418:HIS:CE1	2.40	0.57
22:Q:30:GLN:HE22	22:Q:84:TYR:HE1	1.53	0.57
1:A:778:LYS:O	1:A:781:THR:OG1	2.22	0.57
1:A:1865:THR:HG22	1:A:1866:PHE:H	1.69	0.57
4:N:285:HIS:ND1	4:N:285:HIS:O	2.38	0.57
8:C:240:ASP:HB2	8:C:243:GLU:HB3	1.87	0.57
8:C:472:VAL:HB	8:C:575:ALA:HB3	1.87	0.57
8:C:883:ARG:NH2	8:C:912:ALA:O	2.36	0.57
27:D:1008:PHE:N	27:D:1008:PHE:HD1	2.02	0.57
27:D:1370:SER:HB2	27:D:1514:CYS:SG	2.45	0.57
27:D:1513:ASN:OD1	27:D:1514:CYS:N	2.31	0.57
29:H:677:U:H2'	29:H:678:U:H6	1.70	0.57
29:H:678:U:H2'	29:H:679:U:H6	1.70	0.57
32:1:256:PRO:HA	32:1:259:ARG:HD2	1.86	0.57
34:3:190:ILE:O	34:3:191:SER:OG	2.20	0.57
34:3:269:ILE:HD11	34:3:282:LYS:HG3	1.86	0.57
34:3:540:PRO:HB2	34:3:612:PRO:HG3	1.86	0.57
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.70	0.56
8:C:701:GLU:HB2	8:C:706:LEU:HB2	1.87	0.56
16:F:72:C:H2'	16:F:73:A:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1101:ILE:O	27:D:1105:ALA:CB	2.53	0.56
27:D:1139:MET:HE1	27:D:1148:GLN:HB3	1.86	0.56
29:H:669:U:H2'	29:H:670:U:H6	1.70	0.56
29:H:671:G:H2'	29:H:672:U:H6	1.70	0.56
29:H:689:G:H2'	29:H:690:U:H6	1.71	0.56
32:1:675:LEU:HD11	32:1:714:LEU:HB3	1.86	0.56
32:1:874:GLU:HB3	34:3:1315:ARG:HH22	1.70	0.56
33:2:329:LYS:HG3	33:2:349:ILE:HD12	1.86	0.56
34:3:162:ILE:HG22	34:3:171:LEU:HD12	1.87	0.56
34:3:600:ILE:HD13	34:3:642:LEU:HD13	1.86	0.56
1:A:358:ARG:NE	1:A:361:GLU:OE2	2.34	0.56
1:A:1231:GLN:NE2	1:A:1241:ILE:O	2.35	0.56
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	1.85	0.56
1:A:1883:ASN:ND2	1:A:1886:THR:OG1	2.35	0.56
3:L:367:ARG:NH1	17:I:58:G:N7	2.53	0.56
8:C:933:TRP:C	8:C:935:LYS:H	2.13	0.56
21:P:40:HIS:O	21:P:89:GLY:HA3	2.05	0.56
25:U:16:LYS:HB2	25:U:17:PRO:HD3	1.87	0.56
29:H:682:U:H2'	29:H:683:U:H6	1.70	0.56
34:3:147:PHE:CD1	34:3:147:PHE:N	2.73	0.56
1:A:535:HIS:HE2	18:B:105:A:P	2.28	0.56
1:A:1498:ASP:HB2	4:N:159:LEU:HD12	1.86	0.56
1:A:1512:ARG:NH1	1:A:1529:ASN:OD1	2.38	0.56
2:K:410:LEU:O	2:K:421:VAL:HA	2.04	0.56
2:K:439:LYS:HB2	2:K:457:TRP:CD1	2.39	0.56
3:L:400:VAL:HG21	4:N:154:PRO:HG2	1.85	0.56
5:J:330:ASN:OD1	5:J:331:VAL:HG23	2.04	0.56
8:C:106:PHE:HE2	8:C:554:HIS:CE1	2.23	0.56
8:C:133:ILE:CA	8:C:209:MET:O	2.52	0.56
27:D:1688:TYR:CD1	27:D:1695:TYR:CE1	2.93	0.56
29:H:565:U:H2'	29:H:566:U:H6	1.70	0.56
29:H:672:U:H2'	29:H:673:U:H6	1.70	0.56
29:H:684:U:H2'	29:H:685:U:H6	1.70	0.56
29:H:691:G:H2'	29:H:692:U:H6	1.71	0.56
29:H:694:C:H2'	29:H:695:U:H6	1.70	0.56
32:1:598:LEU:HD11	32:1:631:ILE:HG12	1.87	0.56
36:5:22:LEU:HG	36:5:70:ALA:HB2	1.87	0.56
39:Y:229:GLY:O	39:Y:231:ARG:N	2.38	0.56
41:u:148:SER:HB2	41:u:158:SER:HA	1.87	0.56
1:A:579:LEU:HD22	1:A:619:PHE:CE1	2.40	0.56
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:192:THR:O	2:K:199:LEU:HA	2.05	0.56
2:K:230:SER:OG	2:K:233:GLN:OE1	2.22	0.56
18:B:114:G:H2'	18:B:115:G:H8	1.68	0.56
18:B:149:U:H2'	18:B:150:U:O4'	2.06	0.56
27:D:562:PRO:HG3	27:D:635:GLU:OE1	2.05	0.56
27:D:790:ASP:OD1	27:D:794:ARG:NH2	2.38	0.56
29:H:680:C:H2'	29:H:681:C:H6	1.71	0.56
29:H:683:U:H2'	29:H:684:U:H6	1.71	0.56
29:H:693:C:H2'	29:H:694:C:H6	1.71	0.56
29:H:693:C:C2	29:H:694:C:C5	2.93	0.56
34:3:1122:LYS:NZ	34:3:1202:PHE:O	2.38	0.56
41:u:506:LEU:HD22	41:u:518:LYS:HD2	1.88	0.56
1:A:1810:PRO:O	1:A:1814:VAL:HG23	2.05	0.56
3:L:359:PRO:HB3	6:E:118:GLU:HG2	1.88	0.56
5:J:363:LEU:HD11	5:J:391:PHE:HD2	1.70	0.56
8:C:884:ARG:HB3	8:C:907:PRO:HG2	1.85	0.56
27:D:1008:PHE:N	27:D:1008:PHE:CD1	2.72	0.56
29:H:143:G:H2'	29:H:144:G:C8	2.41	0.56
29:H:568:U:H2'	29:H:569:C:H6	1.71	0.56
34:3:207:VAL:HB	34:3:236:VAL:HG23	1.88	0.56
34:3:517:VAL:HG21	34:3:828:VAL:HG21	1.87	0.56
1:A:1060:LYS:HA	1:A:1101:TYR:CE2	2.41	0.56
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.41	0.56
1:A:1473:ARG:HH11	1:A:1474:ARG:H	1.52	0.56
4:N:144:LYS:NZ	17:I:55:U:O5'	2.39	0.56
4:N:668:HIS:CE1	4:N:669:LYS:HG3	2.41	0.56
6:E:74:TYR:CD1	6:E:83:MET:HE1	2.40	0.56
27:D:1213:ARG:HE	27:D:1281:GLN:NE2	2.03	0.56
27:D:1779:TYR:O	27:D:1782:ILE:HG22	2.06	0.56
27:D:2058:ASN:ND2	27:D:2070:LYS:O	2.38	0.56
20:S:23:LEU:HD21	26:V:69:ILE:HG23	1.87	0.56
29:H:551:C:H2'	29:H:552:U:H6	1.70	0.56
29:H:694:C:C2	29:H:695:U:C5	2.94	0.56
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.39	0.56
1:A:2177:VAL:HG12	1:A:2179:GLU:H	1.70	0.56
2:K:314:SER:OG	2:K:355:VAL:O	2.23	0.56
2:K:441:ILE:H	2:K:456:GLY:HA2	1.71	0.56
27:D:478:LYS:HB2	27:D:504:SER:HB2	1.88	0.56
27:D:901:VAL:HA	27:D:906:LEU:HD13	1.87	0.56
29:H:681:C:H2'	29:H:682:U:H6	1.70	0.56
30:o:44:PRO:O	30:o:69:ASP:CB	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:187:VAL:HG23	34:3:209:GLN:HG2	1.86	0.56
3:L:123:ARG:NH1	3:L:184:LYS:O	2.39	0.56
17:I:77:U:H2'	17:I:78:A:C8	2.41	0.56
18:B:14:G:C2	18:B:15:A:C8	2.93	0.56
27:D:1125:THR:HG21	27:D:1251:ILE:HD11	1.87	0.56
28:G:509:A:H2	32:1:503:THR:HG21	1.71	0.56
29:H:681:C:C2	29:H:682:U:C5	2.94	0.56
29:H:695:U:C2	29:H:696:C:C5	2.94	0.56
29:H:695:U:H2'	29:H:696:C:H6	1.71	0.56
29:H:1126:G:O2'	29:H:1127:A:C5'	2.54	0.56
33:2:194:PHE:HE2	33:2:196:LEU:HD23	1.71	0.56
34:3:545:ASP:OD1	34:3:546:ASN:N	2.37	0.56
38:X:27:TYR:HD2	38:X:30:ASN:HD22	1.54	0.56
3:L:124:PHE:CD1	3:L:183:PHE:HB2	2.41	0.56
8:C:626:SER:HB2	8:C:634:ILE:HD13	1.88	0.56
17:I:5:U:H2'	17:I:6:U:H6	1.71	0.56
27:D:617:ARG:HH12	27:D:1009:TYR:HD1	1.53	0.56
27:D:1217:ARG:C	27:D:1218:PHE:HD1	2.14	0.56
29:H:551:C:C2	29:H:552:U:C5	2.94	0.56
29:H:676:U:H2'	29:H:677:U:H6	1.70	0.56
29:H:684:U:C2	29:H:685:U:C5	2.94	0.56
29:H:1139:G:C5	29:H:1140:U:C5	2.94	0.56
26:k:40:LEU:HD12	26:k:41:ASP:O	2.06	0.56
34:3:699:MET:HB3	34:3:720:LEU:HD23	1.88	0.56
35:4:40:TYR:HD1	35:4:53:ALA:HB2	1.71	0.56
1:A:520:VAL:O	1:A:524:LYS:HG2	2.06	0.56
1:A:551:LEU:HG	1:A:557:PHE:CE2	2.41	0.56
1:A:1899:TRP:HE3	1:A:1905:LEU:HD22	1.71	0.56
4:N:237:ASP:OD2	4:N:240:ASN:ND2	2.35	0.56
4:N:832:LEU:HD21	4:N:845:LEU:HD11	1.87	0.56
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.87	0.56
27:D:1497:PHE:HD1	27:D:1775:TYR:CD2	2.24	0.56
27:D:1740:LEU:HD11	22:Q:146:LEU:HD12	1.88	0.56
27:D:1996:GLN:HE22	27:D:2150:LEU:N	2.03	0.56
29:H:565:U:C2	29:H:566:U:C5	2.94	0.56
29:H:680:C:C2	29:H:681:C:C5	2.94	0.56
29:H:1126:G:O2'	29:H:1127:A:O5'	2.24	0.56
29:H:1139:G:C4	29:H:1140:U:C5	2.94	0.56
29:H:1139:G:HO2'	29:H:1140:U:H6	1.53	0.56
3:L:139:LYS:O	3:L:142:SER:OG	2.17	0.55
27:D:898:TYR:HA	27:D:901:VAL:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1579:ASN:OD1	27:D:1678:ASP:HB3	2.06	0.55
29:H:567:U:H2'	29:H:568:U:H6	1.70	0.55
29:H:567:U:C2	29:H:568:U:C5	2.94	0.55
29:H:682:U:C2	29:H:683:U:C5	2.94	0.55
29:H:692:U:H2'	29:H:693:C:H6	1.71	0.55
41:u:150:PRO:CB	41:u:154:THR:HB	2.36	0.55
41:u:447:ILE:HG23	41:u:457:PRO:HG2	1.87	0.55
1:A:1125:LEU:HD22	1:A:1230:ILE:HG23	1.88	0.55
2:K:389:ILE:HD11	2:K:427:TRP:HB3	1.86	0.55
3:L:402:ASP:OD1	3:L:403:SER:N	2.40	0.55
16:F:2:U:H2'	16:F:3:U:H6	1.70	0.55
27:D:1165:VAL:HG11	27:D:1170:TYR:CE1	2.40	0.55
27:D:1213:ARG:HH22	27:D:1316:LYS:HG3	1.71	0.55
27:D:1902:LEU:HD22	27:D:1928:LEU:HD12	1.87	0.55
29:H:119:G:O6	22:m:20:LYS:HB3	2.05	0.55
29:H:672:U:C2	29:H:673:U:C5	2.94	0.55
29:H:692:U:C2	29:H:693:C:C5	2.94	0.55
29:H:1125:U:O2'	29:H:1126:G:C8	2.57	0.55
32:1:445:GLU:HG3	32:1:453:MET:HE2	1.87	0.55
32:1:494:LEU:CG	38:X:7:ILE:HG23	2.36	0.55
34:3:975:ASP:O	34:3:977:ILE:HD12	2.07	0.55
34:3:1097:PHE:HE1	34:3:1108:PRO:HB3	1.70	0.55
2:K:316:GLN:HG2	2:K:318:ASP:H	1.70	0.55
2:K:458:ASP:OD2	2:K:462:LYS:NZ	2.39	0.55
3:L:160:HIS:O	3:L:164:LYS:HB3	2.06	0.55
8:C:129:ILE:HG21	20:d:16:GLY:HA3	1.88	0.55
17:I:147:U:H3	21:P:42:ASN:HD21	1.54	0.55
18:B:116:U:H2'	18:B:117:G:C8	2.39	0.55
29:H:545:G:H2'	29:H:546:U:H6	1.70	0.55
29:H:553:G:C4	29:H:554:C:C5	2.94	0.55
29:H:564:U:H2'	29:H:565:U:H6	1.70	0.55
29:H:1098:C:H2'	29:H:1099:G:C8	2.41	0.55
20:l:9:LYS:HD2	20:l:83:LEU:HD11	1.87	0.55
30:o:68:PRO:O	30:o:69:ASP:CB	2.54	0.55
34:3:1298:SER:C	34:3:1300:LEU:H	2.14	0.55
1:A:363:ASP:O	1:A:368:ASN:ND2	2.39	0.55
4:N:695:THR:HG22	4:N:704:LEU:HB3	1.89	0.55
5:J:301:VAL:HG22	5:J:304:ARG:HH21	1.70	0.55
17:I:73:A:H3'	27:D:833:THR:HG22	1.88	0.55
27:D:809:THR:HA	27:D:1092:PHE:CD1	2.41	0.55
27:D:1208:ALA:O	27:D:1209:GLN:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:545:G:C4	29:H:546:U:C5	2.95	0.55
29:H:564:U:C2	29:H:565:U:C5	2.94	0.55
29:H:679:U:C2	29:H:680:C:C5	2.94	0.55
29:H:683:U:C2	29:H:684:U:C5	2.95	0.55
34:3:351:PRO:HD3	34:3:407:LEU:HD13	1.89	0.55
34:3:839:ARG:HG3	34:3:880:PRO:HG2	1.87	0.55
1:A:2308:THR:OG1	1:A:2333:PHE:CE2	2.60	0.55
2:K:167:LEU:HA	2:K:464:TRP:HA	1.89	0.55
2:K:395:ILE:CG2	2:K:396:VAL:H	2.12	0.55
2:K:413:CYS:SG	2:K:443:LEU:HD13	2.47	0.55
4:N:721:ARG:O	4:N:724:SER:OG	2.18	0.55
27:D:1458:ARG:HH22	27:D:1462:ARG:NH1	2.03	0.55
27:D:1781:ARG:HG3	27:D:1789:TYR:CE2	2.40	0.55
29:H:691:G:C4	29:H:692:U:C5	2.95	0.55
1:A:342:LEU:HD22	1:A:392:ASN:ND2	2.21	0.55
4:N:720:VAL:HG12	4:N:722:ALA:H	1.72	0.55
8:C:889:TYR:CD2	8:C:890:LYS:HG2	2.41	0.55
29:H:548:G:C4	29:H:549:C:C5	2.94	0.55
29:H:550:G:H2'	29:H:551:C:H6	1.71	0.55
29:H:566:U:C2	29:H:567:U:C5	2.94	0.55
29:H:675:A:H2'	29:H:676:U:H6	1.70	0.55
1:A:1303:LYS:HG3	1:A:1353:THR:HG22	1.89	0.55
2:K:239:GLU:HA	2:K:267:ARG:HB2	1.89	0.55
8:C:185:ILE:HG21	18:B:75:A:OP2	2.07	0.55
9:z:43:ASN:O	9:z:47:LYS:N	2.37	0.55
27:D:2056:SER:HG	27:D:2072:THR:HG1	1.51	0.55
26:V:64:ARG:NH1	26:V:66:ASN:HB3	2.21	0.55
29:H:553:G:H2'	29:H:554:C:H6	1.71	0.55
29:H:563:G:H2'	29:H:564:U:H6	1.70	0.55
29:H:568:U:C2	29:H:569:C:C5	2.94	0.55
29:H:671:G:C4	29:H:672:U:C5	2.95	0.55
29:H:676:U:C2	29:H:677:U:C5	2.94	0.55
32:1:386:TYR:CG	32:1:387:PRO:HD3	2.42	0.55
32:1:916:MET:HB3	32:1:920:TRP:NE1	2.21	0.55
34:3:182:THR:O	34:3:183:THR:HG23	2.06	0.55
1:A:963:VAL:HG21	3:L:280:ARG:NH1	2.20	0.55
1:A:1393:GLU:HG2	3:L:395:LYS:O	2.06	0.55
2:K:115:SER:HA	2:K:118:ILE:HD12	1.89	0.55
4:N:105:ALA:HA	4:N:108:LYS:HG2	1.89	0.55
8:C:292:ILE:O	8:C:296:ASN:ND2	2.38	0.55
27:D:535:VAL:HG13	27:D:557:ILE:CD1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:766:ILE:HG23	27:D:767:THR:HG23	1.89	0.55
27:D:1628:HIS:O	27:D:1632:PRO:HD2	2.06	0.55
24:i:77:LEU:HD21	24:i:80:ILE:CD1	2.35	0.55
23:n:90:PHE:HE2	41:u:194:LYS:CA	2.05	0.55
32:1:864:LEU:O	32:1:868:CYS:HB2	2.07	0.55
34:3:416:SER:HA	34:3:431:SER:HA	1.89	0.55
34:3:432:GLU:HB2	37:6:62:ILE:HD12	1.88	0.55
34:3:650:GLU:HA	34:3:671:GLU:HA	1.87	0.55
39:Y:264:GLU:HG3	39:Y:265:ASP:H	1.72	0.55
1:A:1586:GLN:HE21	1:A:1595:ARG:HD2	1.72	0.55
3:L:218:ILE:O	3:L:222:ILE:HB	2.07	0.55
8:C:133:ILE:O	8:C:134:ILE:HG23	2.07	0.55
8:C:158:HIS:CE1	8:C:549:TYR:HE2	2.25	0.55
27:D:516:ASN:HD22	27:D:685:ARG:CB	2.18	0.55
27:D:1431:ASP:HB2	27:D:1434:LEU:HB3	1.89	0.55
27:D:1583:VAL:HG22	27:D:1681:ILE:HB	1.89	0.55
27:D:1609:MET:SD	27:D:1611:ASN:ND2	2.79	0.55
29:H:566:U:H2'	29:H:567:U:H6	1.70	0.55
32:1:252:ILE:HD13	32:1:296:VAL:HG22	1.89	0.55
32:1:490:ARG:HH22	38:X:25:ASN:CB	2.19	0.55
34:3:770:LEU:HB2	34:3:827:TRP:NE1	2.22	0.55
34:3:957:ILE:HG22	34:3:962:LEU:HD11	1.89	0.55
1:A:794:LYS:HB3	1:A:854:ARG:HH12	1.70	0.55
1:A:1509:ARG:NH2	1:A:1533:ASP:OD1	2.40	0.55
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.42	0.55
1:A:1790:TRP:CZ3	1:A:1798:ILE:HD12	2.42	0.55
1:A:1889:LEU:HD12	1:A:1989:PHE:HB2	1.89	0.55
27:D:1220:ILE:HG22	27:D:1222:ILE:HG13	1.88	0.55
27:D:1245:ASP:HA	27:D:1288:PHE:HD1	1.71	0.55
27:D:1779:TYR:CZ	27:D:1783:HIS:CE1	2.95	0.55
29:H:679:U:H2'	29:H:680:C:H6	1.70	0.55
23:n:90:PHE:CE1	41:u:195:ARG:CA	2.89	0.55
32:1:824:PHE:HZ	32:1:838:ILE:HD13	1.72	0.55
33:2:329:LYS:HB3	33:2:335:TRP:HB2	1.88	0.55
34:3:1096:LEU:HD13	34:3:1187:PHE:CZ	2.39	0.55
34:3:1117:HIS:O	34:3:1133:ASP:HA	2.07	0.55
34:3:1243:ILE:HG21	34:3:1353:ILE:HD11	1.87	0.55
38:X:63:SER:HB2	38:X:74:PHE:CD1	2.40	0.55
41:u:21:ILE:HD11	42:w:164:CYS:SG	2.47	0.55
3:L:268:LEU:HD13	3:L:270:HIS:CE1	2.41	0.54
8:C:656:LEU:HD13	8:C:670:ILE:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:114:G:N2	18:B:115:G:C2	2.75	0.54
27:D:465:ILE:HB	27:D:705:GLN:HB2	1.89	0.54
27:D:1489:GLU:OE2	27:D:1746:LEU:HG	2.06	0.54
20:S:49:ALA:O	20:S:56:VAL:HA	2.07	0.54
29:H:669:U:C2	29:H:670:U:C5	2.94	0.54
29:H:689:G:C4	29:H:690:U:C5	2.95	0.54
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.40	0.54
8:C:273:LEU:HD11	8:C:279:LEU:HD22	1.88	0.54
27:D:639:LEU:HD23	27:D:943:TYR:CD2	2.42	0.54
27:D:1194:ASP:HB3	27:D:1198:ARG:HH12	1.72	0.54
27:D:2138:HIS:O	27:D:2159:GLU:HG3	2.08	0.54
24:T:43:ILE:HD12	24:T:52:VAL:HG11	1.90	0.54
28:G:513:U:O3'	32:1:299:ARG:NH2	2.40	0.54
29:H:675:A:C4	29:H:676:U:C5	2.95	0.54
29:H:678:U:C2	29:H:679:U:C5	2.94	0.54
32:1:927:ALA:C	32:1:929:ASN:H	2.14	0.54
34:3:125:THR:HG22	34:3:191:SER:HA	1.89	0.54
39:Y:213:LYS:HB3	39:Y:230:SER:CB	2.38	0.54
1:A:570:GLN:O	1:A:574:GLN:HG2	2.08	0.54
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.71	0.54
1:A:2157:ILE:CG1	27:D:1064:PRO:HB2	2.37	0.54
1:A:2398:LEU:HD22	27:D:1060:LYS:CG	2.38	0.54
2:K:125:ILE:HG12	2:K:337:ARG:HD3	1.90	0.54
27:D:642:ASP:O	27:D:645:PRO:HG2	2.06	0.54
27:D:1368:VAL:HB	27:D:1511:LEU:HD23	1.90	0.54
29:H:548:G:H2'	29:H:549:C:H6	1.71	0.54
29:H:550:G:C4	29:H:551:C:C5	2.94	0.54
29:H:677:U:C2	29:H:678:U:C5	2.95	0.54
29:H:1097:G:C5	29:H:1146:G:C6	2.96	0.54
34:3:165:HIS:HB3	34:3:170:ARG:HD3	1.89	0.54
27:D:1629:LEU:HD23	27:D:1648:ASP:CG	2.32	0.54
27:D:1757:GLU:HB3	27:D:1763:ILE:HD12	1.90	0.54
29:H:563:G:C4	29:H:564:U:C5	2.95	0.54
21:h:31:ILE:HD11	21:h:49:ILE:HD12	1.90	0.54
41:u:62:PHE:HB3	41:u:375:GLU:HB2	1.89	0.54
41:u:93:PHE:HZ	42:w:148:PHE:CE1	2.24	0.54
41:u:148:SER:CB	41:u:159:ASP:H	2.20	0.54
2:K:139:GLU:OE1	2:K:379:ARG:NH2	2.35	0.54
3:L:279:VAL:HG21	3:L:286:PHE:CE1	2.43	0.54
3:L:417:LEU:HD21	4:N:229:ILE:HD12	1.90	0.54
27:D:614:ILE:HD11	27:D:1009:TYR:CG	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:T:30:TRP:CE2	24:T:89:LEU:HD22	2.42	0.54
34:3:381:LEU:O	34:3:389:PHE:HB2	2.08	0.54
27:D:789:LEU:HD11	27:D:797:ILE:HG13	1.88	0.54
27:D:1624:LEU:HD12	27:D:1630:ARG:HD2	1.88	0.54
23:R:80:LYS:HE3	23:R:82:LYS:HG3	1.90	0.54
29:H:1126:G:HO2'	29:H:1127:A:H8	1.56	0.54
34:3:96:ALA:HB2	34:3:101:LEU:HD13	1.90	0.54
1:A:1268:ARG:HD3	1:A:1301:TYR:HD2	1.73	0.54
2:K:317:CYS:SG	2:K:359:PRO:HA	2.48	0.54
3:L:113:HIS:CD2	3:L:134:PRO:HA	2.42	0.54
27:D:1629:LEU:HD23	27:D:1648:ASP:OD2	2.08	0.54
29:H:67:A:O2'	29:H:68:U:OP2	2.25	0.54
29:H:1127:A:O2'	29:H:1128:C:H5'	2.08	0.54
29:H:1148:U:H2'	29:H:1149:G:C8	2.43	0.54
22:m:99:ASP:OD2	41:u:183:GLU:CA	2.55	0.54
32:1:605:ILE:HG21	32:1:624:CYS:SG	2.47	0.54
32:1:897:MET:HE1	36:5:6:PHE:CZ	2.43	0.54
34:3:632:ILE:HA	34:3:646:LEU:HA	1.88	0.54
34:3:839:ARG:NH1	34:3:1357:ARG:O	2.41	0.54
42:w:205:LYS:HB3	43:v:212:GLU:HB3	1.90	0.54
1:A:579:LEU:HD11	1:A:626:LEU:HD12	1.90	0.54
1:A:2189:LEU:HD22	1:A:2349:PHE:CE1	2.42	0.54
3:L:175:LEU:O	3:L:179:MET:CB	2.55	0.54
3:L:371:LYS:HD3	17:I:18:A:H61	1.72	0.54
3:L:398:GLN:OE1	3:L:414:ASN:ND2	2.34	0.54
4:N:140:GLN:NE2	17:I:19:U:O2	2.41	0.54
4:N:286:GLU:HB2	4:N:292:CYS:SG	2.47	0.54
8:C:769:TYR:CE1	8:C:774:LEU:HB2	2.37	0.54
17:I:18:A:H5''	17:I:19:U:O5'	2.08	0.54
18:B:163:C:P	21:a:8:HIS:N	2.80	0.54
27:D:491:PHE:HE1	27:D:533:LEU:HD21	1.73	0.54
27:D:516:ASN:O	27:D:687:PRO:HD2	2.08	0.54
27:D:793:LEU:HD13	27:D:808:LEU:HD13	1.88	0.54
28:G:520:G:H4'	38:X:74:PHE:CE2	2.43	0.54
29:H:46:C:H4'	29:H:47:U:H5''	1.89	0.54
34:3:76:ILE:HD11	34:3:422:PHE:CE1	2.43	0.54
41:u:147:SER:HA	41:u:155:ASN:O	2.08	0.54
41:u:319:TYR:O	41:u:322:HIS:HB3	2.08	0.54
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.43	0.54
8:C:132:ARG:HH22	20:d:13:GLU:CA	2.21	0.54
18:B:111:C:H2'	18:B:112:C:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:455:ARG:HB2	27:D:462:GLU:HG3	1.90	0.54
27:D:1814:LEU:HB3	27:D:1820:ILE:HG12	1.90	0.54
24:T:59:GLU:O	24:T:74:GLY:HA2	2.08	0.54
43:v:41:PRO:HD2	43:v:53:ARG:NH1	2.23	0.54
1:A:480:TYR:CE2	8:C:275:LEU:HD23	2.43	0.54
1:A:933:GLU:OE1	1:A:933:GLU:N	2.38	0.54
1:A:1696:SER:HA	1:A:1759:TYR:HE1	1.73	0.54
1:A:1732:MET:HG3	1:A:1791:PHE:HE2	1.72	0.54
2:K:220:LYS:HB3	2:K:239:GLU:HB3	1.90	0.54
3:L:125:PRO:HD2	3:L:182:SER:HB2	1.89	0.54
4:N:708:LEU:HD22	4:N:725:ILE:HG21	1.90	0.54
5:J:406:PHE:HE1	5:J:408:LEU:HB2	1.73	0.54
17:I:6:U:H2'	17:I:7:A:H8	1.71	0.54
18:B:127:U:O2'	18:B:128:A:N7	2.23	0.54
23:n:90:PHE:HB2	41:u:191:ASN:HA	1.88	0.54
34:3:208:GLU:H	34:3:236:VAL:HA	1.72	0.54
2:K:207:LEU:HD11	2:K:463:LEU:HB2	1.88	0.53
4:N:706:VAL:HA	4:N:746:MET:HE1	1.89	0.53
5:J:341:VAL:HG22	5:J:381:ILE:HG12	1.91	0.53
8:C:161:ILE:HD12	8:C:162:PRO:HD2	1.90	0.53
8:C:338:SER:O	8:C:341:ILE:HG12	2.08	0.53
27:D:1748:TYR:HB3	22:Q:140:LYS:N	2.23	0.53
20:l:9:LYS:HB3	20:l:83:LEU:HD11	1.88	0.53
33:2:248:HIS:CE1	33:2:375:PHE:HB2	2.43	0.53
33:2:367:LEU:HB2	33:2:370:PHE:HE1	1.71	0.53
34:3:97:THR:O	34:3:97:THR:OG1	2.17	0.53
34:3:764:ASP:OD2	34:3:766:LYS:HE2	2.08	0.53
38:X:64:ARG:NH2	38:X:69:GLY:O	2.41	0.53
41:u:251:LEU:HD12	41:u:251:LEU:O	2.08	0.53
1:A:2189:LEU:HD22	1:A:2349:PHE:HE1	1.73	0.53
8:C:347:ARG:O	8:C:352:VAL:HG11	2.08	0.53
18:B:130:A:H4'	18:B:131:A:O5'	2.08	0.53
19:O:151:ILE:HB	19:O:180:GLU:HG2	1.90	0.53
27:D:614:ILE:HD11	27:D:1009:TYR:CD1	2.43	0.53
27:D:945:TYR:CE2	27:D:949:LEU:HD11	2.43	0.53
27:D:1312:LYS:N	27:D:1787:SER:OG	2.39	0.53
23:R:56:ALA:HB2	23:R:72:VAL:HA	1.90	0.53
20:S:34:VAL:CG2	20:S:45:ARG:HG3	2.39	0.53
34:3:943:ASP:HB2	34:3:952:ARG:HG2	1.91	0.53
34:3:1060:LEU:HB2	41:u:505:GLU:HB2	1.89	0.53
43:v:204:GLU:HB3	43:v:205:PRO:HD3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1888:HIS:HE1	1:A:1988:LEU:HD22	1.74	0.53
1:A:2165:ARG:HB3	1:A:2300:VAL:HG13	1.89	0.53
2:K:270:ASP:OD1	2:K:271:VAL:N	2.40	0.53
3:L:102:ILE:HD11	3:L:214:ILE:HG21	1.89	0.53
18:B:128:A:H2'	18:B:129:G:H2'	1.90	0.53
22:Q:7:LEU:HD11	23:R:95:PHE:CZ	2.44	0.53
23:n:92:SER:OG	41:u:190:LEU:HD11	2.06	0.53
32:1:689:LEU:HA	32:1:692:ILE:HD12	1.89	0.53
34:3:299:PRO:HD2	34:3:377:PHE:CE1	2.44	0.53
34:3:547:ASN:ND2	34:3:564:ASP:HB2	2.24	0.53
34:3:655:LYS:HE2	34:3:664:ILE:HD11	1.89	0.53
42:w:129:HIS:ND1	42:w:130:PRO:HD2	2.23	0.53
1:A:1350:ILE:HG23	1:A:1356:LEU:HD22	1.90	0.53
8:C:292:ILE:HG12	8:C:311:ILE:HD13	1.91	0.53
8:C:855:PRO:O	8:C:944:VAL:HG11	2.09	0.53
18:B:84:A:H2'	18:B:85:U:H6	1.73	0.53
18:B:111:C:H2'	18:B:112:C:H6	1.73	0.53
34:3:712:PHE:CE2	34:3:713:LEU:HD23	2.43	0.53
1:A:259:GLU:HG3	1:A:260:PRO:HD2	1.89	0.53
1:A:768:GLU:OE1	4:N:108:LYS:NZ	2.34	0.53
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.24	0.53
16:F:74:U:H2'	16:F:75:A:H8	1.72	0.53
27:D:563:LEU:HD11	27:D:836:TRP:NE1	2.24	0.53
27:D:1380:ALA:HB2	27:D:1511:LEU:HD11	1.90	0.53
20:l:9:LYS:CB	20:l:83:LEU:HD11	2.39	0.53
33:2:162:SER:O	33:2:166:THR:OG1	2.24	0.53
34:3:211:LYS:HB2	34:3:230:ILE:HG13	1.91	0.53
34:3:441:PHE:HB3	34:3:475:LEU:HD23	1.88	0.53
36:5:41:ARG:HH12	36:5:83:LYS:NZ	2.05	0.53
42:w:202:GLN:HB3	43:v:210:ALA:HB3	1.91	0.53
1:A:1257:ASN:OD1	1:A:1268:ARG:NH2	2.41	0.53
1:A:1943:PRO:HD3	19:O:169:ILE:HD12	1.91	0.53
1:A:2070:ASN:HB3	27:D:858:GLY:O	2.08	0.53
1:A:2183:TYR:CD1	1:A:2219:LYS:HB2	2.44	0.53
3:L:434:GLN:HA	4:N:149:PRO:HB3	1.90	0.53
4:N:757:GLU:HG2	4:N:780:LEU:HD11	1.90	0.53
27:D:675:PRO:HG3	27:D:905:GLN:C	2.34	0.53
27:D:759:ASN:O	27:D:763:GLU:HG3	2.09	0.53
27:D:1213:ARG:NH2	27:D:1316:LYS:CG	2.67	0.53
27:D:1476:ALA:HB3	27:D:1512:SER:HB2	1.91	0.53
25:U:33:PHE:C	25:U:35:SER:H	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:366:ALA:O	34:3:1232:LEU:HD22	2.09	0.53
33:2:367:LEU:C	33:2:369:SER:H	2.16	0.53
39:Y:214:LEU:N	39:Y:230:SER:OG	2.42	0.53
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.44	0.53
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.43	0.53
2:K:171:GLN:HG2	2:K:172:LEU:N	2.22	0.53
5:J:370:LEU:HD13	5:J:451:LEU:HG	1.89	0.53
8:C:163:ASP:OD2	8:C:548:ARG:NH1	2.41	0.53
27:D:1436:LEU:HD22	27:D:1462:ARG:CZ	2.37	0.53
1:A:1674:ASP:OD2	1:A:2200:LYS:CE	2.56	0.53
17:I:72:A:OP2	27:D:1047:ARG:CZ	2.56	0.53
27:D:924:VAL:HG12	27:D:998:ALA:HB2	1.90	0.53
27:D:1679:GLU:HG2	27:D:1719:LYS:HB3	1.91	0.53
24:i:27:VAL:HG22	24:i:92:SER:HB2	1.91	0.53
32:1:536:MET:HA	32:1:539:HIS:HD2	1.74	0.53
34:3:65:LEU:HD11	34:3:1227:CYS:SG	2.48	0.53
34:3:612:PRO:HA	34:3:618:TYR:HD1	1.74	0.53
38:X:35:ILE:HD13	38:X:51:PHE:CE2	2.43	0.53
1:A:1268:ARG:CG	1:A:1301:TYR:HB2	2.39	0.53
4:N:742:ALA:O	4:N:746:MET:HB2	2.09	0.53
27:D:567:VAL:HG13	27:D:606:VAL:HG12	1.89	0.53
27:D:781:LEU:HD21	27:D:798:GLU:CA	2.33	0.53
27:D:1457:ARG:NH1	27:D:1854:SER:O	2.42	0.53
24:T:20:PHE:CE1	24:T:92:SER:HB2	2.40	0.53
29:H:1089:G:H2'	29:H:1090:A:O5'	2.09	0.53
32:1:361:ASP:OD1	32:1:362:CYS:N	2.42	0.53
32:1:614:PRO:HA	32:1:617:ARG:HE	1.74	0.53
34:3:1023:HIS:HB3	34:3:1058:GLN:HA	1.91	0.53
41:u:90:GLN:HG3	42:w:153:ILE:HG13	1.90	0.53
1:A:297:SER:HB3	18:B:32:G:OP1	2.09	0.53
1:A:1804:THR:HG21	19:O:218:GLU:OE1	2.10	0.53
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	1.91	0.53
1:A:2208:TYR:HE1	1:A:2255:LEU:HD13	1.74	0.53
2:K:376:TRP:CH2	2:K:386:LEU:HD23	2.44	0.53
2:K:390:LEU:HD13	5:J:428:TRP:CD1	2.43	0.53
2:K:459:ARG:NH2	7:M:72:GLU:O	2.42	0.53
3:L:239:ALA:O	3:L:243:ALA:CB	2.57	0.53
5:J:372:ILE:O	5:J:376:GLY:HA3	2.08	0.53
8:C:274:ILE:HD12	8:C:382:TYR:HD1	1.73	0.53
27:D:1399:ASN:O	27:D:1405:ILE:HD11	2.09	0.53
22:Q:95:ILE:HG23	23:R:95:PHE:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:580:PHE:HZ	32:1:619:HIS:HD1	1.57	0.53
39:Y:208:SER:HA	39:Y:214:LEU:CD1	2.39	0.53
1:A:1335:TRP:CZ2	1:A:1339:LEU:HD13	2.44	0.52
8:C:880:MET:HB3	8:C:886:SER:HA	1.91	0.52
27:D:1982:MET:HE2	27:D:1989:ASP:H	1.73	0.52
32:1:208:LEU:HD21	32:1:221:MET:HB2	1.91	0.52
32:1:539:HIS:O	32:1:542:THR:OG1	2.23	0.52
1:A:298:TYR:CE2	1:A:493:MET:HE2	2.44	0.52
1:A:701:CYS:SG	1:A:702:GLY:N	2.81	0.52
1:A:1633:PHE:HZ	1:A:1694:MET:HG3	1.74	0.52
4:N:760:VAL:O	4:N:764:LEU:HB2	2.08	0.52
8:C:682:SER:HA	8:C:714:PRO:HG3	1.92	0.52
17:I:140:G:H2'	17:I:141:G:O4'	2.09	0.52
27:D:781:LEU:HD11	27:D:798:GLU:HA	1.90	0.52
27:D:1898:ASP:HA	27:D:1943:PHE:CZ	2.45	0.52
26:V:30:ARG:HE	26:V:41:ASP:CB	2.21	0.52
32:1:569:PHE:HD1	32:1:579:ILE:HG21	1.72	0.52
34:3:257:ILE:HD11	34:3:264:LEU:HD11	1.91	0.52
34:3:1112:ASP:OD1	34:3:1113:SER:N	2.41	0.52
42:w:103:TYR:CD1	42:w:110:VAL:HG21	2.40	0.52
1:A:394:ARG:HE	1:A:396:ARG:HH12	1.57	0.52
1:A:1775:ILE:HG12	1:A:1786:ALA:HB2	1.91	0.52
2:K:288:THR:HA	2:K:303:GLN:O	2.09	0.52
4:N:746:MET:HG2	4:N:749:ARG:NH1	2.20	0.52
8:C:458:ILE:HG23	8:C:459:PRO:HD2	1.91	0.52
17:I:143:A:N7	25:U:48:TYR:HE2	2.08	0.52
27:D:1783:HIS:CE1	27:D:1799:ILE:HG21	2.44	0.52
23:R:37:ALA:HA	23:R:42:THR:HG22	1.92	0.52
25:U:58:GLU:C	25:U:59:PHE:HD1	2.17	0.52
28:G:498:C:H2'	28:G:499:U:H6	1.75	0.52
36:5:67:VAL:HG23	36:5:68:ASN:H	1.74	0.52
1:A:770:MET:HE1	1:A:778:LYS:HB2	1.92	0.52
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	2.25	0.52
1:A:2174:ASP:OD1	1:A:2175:ASP:N	2.42	0.52
4:N:849:TYR:CD1	4:N:855:ASP:HB2	2.45	0.52
28:G:500:A:OP1	32:1:818:LYS:NZ	2.28	0.52
28:G:520:G:C2	38:X:34:TYR:CD2	2.95	0.52
32:1:532:PRO:O	32:1:535:THR:OG1	2.26	0.52
36:5:42:LYS:HG2	36:5:71:PHE:HE1	1.75	0.52
1:A:921:ASP:HB3	3:L:403:SER:HB2	1.91	0.52
1:A:1161:TYR:CD1	1:A:1170:MET:HG2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:379:PHE:CZ	4:N:144:LYS:HD3	2.43	0.52
4:N:269:GLN:O	4:N:272:PRO:HG3	2.10	0.52
4:N:691:TYR:HB3	4:N:708:LEU:HD12	1.90	0.52
18:B:75:A:O2'	18:B:76:U:H3'	2.09	0.52
27:D:645:PRO:HG3	27:D:911:GLN:O	2.10	0.52
27:D:851:ASP:HA	27:D:861:GLU:O	2.10	0.52
27:D:2077:ARG:HH12	27:D:2081:PRO:HG3	1.73	0.52
34:3:1178:PRO:O	34:3:1182:ASP:HB2	2.10	0.52
6:E:98:GLY:HA3	16:F:30:G:H4'	1.92	0.52
8:C:474:LYS:HZ3	8:C:630:PRO:HD3	1.75	0.52
8:C:942:GLY:HA2	8:C:960:ASN:O	2.09	0.52
27:D:1763:ILE:HG21	27:D:1769:CYS:HB3	1.91	0.52
23:R:26:PHE:CE1	23:R:31:MET:HB3	2.45	0.52
20:S:10:LEU:HB2	20:S:83:LEU:HD11	1.90	0.52
25:U:14:ASN:HB2	25:U:17:PRO:HD2	1.92	0.52
32:1:338:GLN:HG3	32:1:377:THR:HG22	1.91	0.52
41:u:350:ARG:CZ	41:u:350:ARG:CB	2.88	0.52
43:v:42:TYR:HB2	43:v:45:GLN:HG3	1.91	0.52
1:A:1817:GLU:HA	1:A:1820:ARG:HG2	1.91	0.52
3:L:120:TYR:CE2	3:L:141:ILE:HG12	2.34	0.52
3:L:343:LYS:HD3	17:I:27:U:O2'	2.09	0.52
32:1:410:LYS:O	32:1:413:SER:OG	2.27	0.52
34:3:104:TYR:HD1	34:3:113:LEU:HA	1.75	0.52
34:3:691:LEU:HB3	34:3:703:MET:HB2	1.92	0.52
1:A:185:GLN:HG2	1:A:263:PRO:HD3	1.91	0.52
3:L:98:PHE:O	3:L:102:ILE:HG12	2.09	0.52
8:C:616:PRO:O	8:C:619:LEU:HB2	2.10	0.52
16:F:17:U:H2'	16:F:18:U:C6	2.44	0.52
17:I:6:U:H2'	17:I:7:A:C8	2.44	0.52
17:I:91:U:H2'	17:I:92:C:C6	2.45	0.52
18:B:27:G:N3	18:B:131:A:N3	2.58	0.52
27:D:656:TRP:HH2	27:D:929:ILE:HG13	1.73	0.52
27:D:1557:ILE:HA	27:D:1695:TYR:CE2	2.36	0.52
27:D:1924:PHE:CZ	27:D:1928:LEU:HD11	2.45	0.52
27:D:1933:TYR:HE1	27:D:2090:LYS:O	1.93	0.52
29:H:119:G:H8	23:n:99:ASP:OD2	1.91	0.52
34:3:332:GLU:HG2	34:3:333:ASN:N	2.24	0.52
34:3:511:ILE:HG23	34:3:888:VAL:HG13	1.92	0.52
34:3:1006:TYR:HD1	34:3:1021:LEU:HA	1.73	0.52
34:3:1159:LEU:HD23	34:3:1164:ILE:HD13	1.92	0.52
1:A:1320:LEU:HD22	1:A:1370:ARG:HD2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1494:LEU:O	1:A:1499:ARG:NH2	2.43	0.52
2:K:172:LEU:HD23	4:N:752:ASN:HD22	1.75	0.52
2:K:213:LYS:NZ	2:K:215:ASP:OD1	2.41	0.52
4:N:256:LYS:HG2	4:N:257:PHE:H	1.75	0.52
16:F:96:G:H2'	16:F:97:A:H8	1.75	0.52
17:I:75:U:O2	27:D:643:ARG:NH1	2.42	0.52
18:B:164:C:O2	18:B:164:C:H2'	2.09	0.52
27:D:765:ASN:CB	27:D:768:HIS:CD2	2.93	0.52
27:D:781:LEU:HD23	27:D:781:LEU:C	2.35	0.52
27:D:1513:ASN:ND2	27:D:1704:LEU:HD13	2.25	0.52
27:D:1938:GLU:OE1	27:D:1938:GLU:N	2.40	0.52
34:3:125:THR:H	34:3:152:SER:HA	1.75	0.52
36:5:40:LYS:HG3	36:5:41:ARG:HG3	1.91	0.52
4:N:212:VAL:HG12	4:N:215:LEU:HD23	1.92	0.52
18:B:127:U:H1'	18:B:128:A:N7	2.25	0.52
27:D:1426:ASN:HD22	27:D:1442:SER:HB2	1.73	0.52
24:T:35:ILE:HG22	26:V:23:ARG:HE	1.74	0.52
26:V:10:TYR:CE2	26:V:71:LEU:HD11	2.45	0.52
34:3:294:PHE:HZ	34:3:381:LEU:HD11	1.74	0.52
34:3:983:ALA:O	34:3:995:ILE:HB	2.10	0.52
4:N:850:ALA:HB2	4:N:896:MET:HE1	1.91	0.51
8:C:423:HIS:O	8:C:427:LEU:HB2	2.09	0.51
8:C:616:PRO:HA	8:C:619:LEU:HD12	1.92	0.51
8:C:869:HIS:NE2	8:C:925:LEU:HD22	2.24	0.51
19:O:210:LEU:HB3	19:O:212:VAL:HG13	1.92	0.51
27:D:804:HIS:HE1	27:D:813:ARG:CG	2.18	0.51
27:D:1387:HIS:CE1	27:D:1392:LYS:HB3	2.46	0.51
23:R:50:ASN:ND2	23:R:52:HIS:CD2	2.78	0.51
23:R:50:ASN:ND2	23:R:52:HIS:HD2	2.09	0.51
29:H:1097:G:C2	29:H:1146:G:C5	2.98	0.51
32:1:244:LEU:O	32:1:248:ALA:CB	2.58	0.51
32:1:580:PHE:CZ	32:1:619:HIS:HA	2.46	0.51
34:3:486:PRO:HG2	34:3:505:PHE:HB2	1.91	0.51
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.93	0.51
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	1.92	0.51
3:L:359:PRO:O	6:E:122:ARG:NH2	2.43	0.51
5:J:283:ASN:OD1	5:J:284:ASP:N	2.43	0.51
8:C:697:ARG:HH21	8:C:849:GLY:HA2	1.75	0.51
16:F:10:A:H61	16:F:16:C:H42	1.57	0.51
18:B:16:U:O2'	18:B:18:A:N7	2.43	0.51
27:D:1115:ILE:O	27:D:1119:ARG:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1853:ALA:HB1	27:D:1863:ILE:HG13	1.93	0.51
29:H:139:G:H2'	29:H:140:G:O5'	2.09	0.51
29:H:1140:U:H2'	29:H:1141:C:H6	1.75	0.51
32:1:927:ALA:O	32:1:929:ASN:N	2.43	0.51
34:3:607:LEU:HB2	34:3:624:TRP:HB3	1.92	0.51
39:Y:224:PHE:O	39:Y:225:ALA:HB3	2.11	0.51
41:u:292:SER:O	41:u:296:GLU:HG2	2.10	0.51
1:A:1045:GLN:HG2	1:A:1175:GLU:HG2	1.92	0.51
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.25	0.51
2:K:46:GLU:HB2	2:K:73:ARG:NH1	2.26	0.51
2:K:177:PRO:HB2	2:K:195:TRP:NE1	2.25	0.51
3:L:358:ILE:HG22	3:L:360:GLU:H	1.74	0.51
8:C:269:LYS:HG2	44:C:1500:GTP:C4	2.46	0.51
8:C:465:GLU:CD	8:C:466:GLY:H	2.19	0.51
27:D:1751:HIS:HA	27:D:1810:CYS:SG	2.50	0.51
29:H:1139:G:HO2'	29:H:1140:U:C5'	2.24	0.51
32:1:539:HIS:ND1	32:1:578:ILE:HG12	2.25	0.51
33:2:131:LYS:NZ	33:2:153:ASP:OD1	2.44	0.51
34:3:102:GLU:HG2	34:3:116:LYS:HG2	1.92	0.51
34:3:294:PHE:HE2	34:3:365:ILE:HB	1.76	0.51
35:4:45:VAL:HG13	43:v:97:ARG:HH12	1.75	0.51
41:u:81:ILE:HD13	41:u:161:ALA:HB2	1.92	0.51
41:u:185:PHE:CE2	41:u:236:LEU:HA	2.46	0.51
41:u:220:PRO:HB2	41:u:222:MET:O	2.10	0.51
41:u:409:TYR:OH	41:u:413:LYS:NZ	2.27	0.51
1:A:165:LEU:HG	1:A:578:MET:SD	2.50	0.51
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.09	0.51
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.92	0.51
8:C:883:ARG:NH2	8:C:910:GLU:O	2.41	0.51
8:C:889:TYR:H	8:C:904:GLY:HA2	1.76	0.51
16:F:61:C:H2'	16:F:62:A:O4'	2.10	0.51
18:B:114:G:N2	18:B:115:G:N3	2.58	0.51
27:D:505:LYS:HA	27:D:508:HIS:CD2	2.45	0.51
27:D:724:ASP:HA	27:D:760:LYS:NZ	2.25	0.51
27:D:1936:ARG:HD3	27:D:2090:LYS:HE3	1.92	0.51
22:Q:34:PRO:C	22:Q:36:MET:H	2.17	0.51
22:Q:141:ARG:HB2	22:Q:142:PRO:HD3	1.92	0.51
34:3:217:ASP:OD1	34:3:218:TYR:N	2.43	0.51
34:3:242:VAL:HG22	34:3:252:PHE:HB2	1.92	0.51
1:A:849:LEU:HD12	1:A:973:GLU:HB3	1.91	0.51
2:K:287:MET:HA	2:K:310:VAL:HG23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:789:LEU:HD11	7:M:45:ASN:HB3	1.91	0.51
8:C:176:ARG:HH22	8:C:188:GLY:HA2	1.75	0.51
8:C:253:ILE:HD11	8:C:298:PHE:HB2	1.93	0.51
8:C:470:ALA:HB3	8:C:577:LEU:HD22	1.93	0.51
27:D:648:GLU:OE2	27:D:912:PHE:HD1	1.93	0.51
27:D:1395:ALA:HB3	27:D:1444:VAL:HG22	1.91	0.51
26:V:56:GLN:HG3	26:V:61:THR:HB	1.93	0.51
33:2:325:TYR:HB3	33:2:328:LEU:HB2	1.92	0.51
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.92	0.51
2:K:184:SER:OG	2:K:186:ASP:OD1	2.28	0.51
5:J:381:ILE:HD13	5:J:463:PHE:HD2	1.75	0.51
8:C:701:GLU:HG2	8:C:703:LEU:H	1.75	0.51
32:1:955:VAL:HA	32:1:959:ASN:HD22	1.75	0.51
34:3:59:TYR:CE1	34:3:1316:LYS:HD2	2.46	0.51
34:3:105:ASP:OD1	34:3:106:THR:N	2.41	0.51
34:3:292:ALA:HA	34:3:331:PHE:CD1	2.45	0.51
34:3:1073:LYS:HD2	34:3:1090:ILE:HD11	1.92	0.51
35:4:164:ALA:O	35:4:168:LEU:HB2	2.11	0.51
38:X:49:THR:HG23	39:Y:233:ASP:HB2	1.92	0.51
41:u:56:GLU:OE1	41:u:63:LYS:HE2	2.11	0.51
42:w:195:ILE:HD11	42:w:197:TRP:CZ2	2.45	0.51
1:A:287:GLU:HG2	1:A:288:GLU:N	2.22	0.51
1:A:1835:LEU:HD21	1:A:1843:LEU:HD21	1.93	0.51
8:C:326:GLU:HG2	8:C:330:TYR:HE2	1.75	0.51
18:B:27:G:OP1	18:B:141:G:C5'	2.58	0.51
27:D:683:PHE:CD1	27:D:943:TYR:HA	2.46	0.51
27:D:1032:PHE:HB3	27:D:1077:ASN:HB2	1.92	0.51
27:D:1890:GLU:HB3	22:Q:143:ARG:NE	2.26	0.51
27:D:1913:PHE:HE2	27:D:1917:THR:HB	1.76	0.51
28:G:487:A:H2'	28:G:488:A:H5'	1.92	0.51
21:h:46:ASN:OD1	20:l:79:LYS:HE2	2.09	0.51
32:1:579:ILE:O	32:1:583:PHE:N	2.38	0.51
33:2:329:LYS:O	33:2:346:GLY:HA2	2.10	0.51
38:X:105:ASP:OD1	38:X:106:HIS:N	2.43	0.51
2:K:64:VAL:HG12	2:K:65:GLU:H	1.76	0.51
2:K:177:PRO:HB2	2:K:195:TRP:CD1	2.44	0.51
3:L:356:LEU:HD13	6:E:52:ARG:HB3	1.91	0.51
4:N:148:ALA:HB1	4:N:152:LEU:HD12	1.92	0.51
8:C:270:LEU:HD11	8:C:313:PHE:HB3	1.93	0.51
8:C:326:GLU:HG2	8:C:330:TYR:CE2	2.45	0.51
16:F:79:A:H2'	16:F:80:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1213:ARG:HE	27:D:1281:GLN:HE21	1.58	0.51
27:D:1748:TYR:CE2	22:Q:142:PRO:CD	2.94	0.51
27:D:2071:ILE:O	27:D:2127:GLU:HA	2.11	0.51
27:D:2071:ILE:HG22	27:D:2128:LEU:HB2	1.92	0.51
29:H:1139:G:H2'	29:H:1140:U:H6	1.76	0.51
32:1:363:LEU:HA	32:1:374:THR:HG21	1.93	0.51
32:1:399:PRO:HA	32:1:402:LYS:HG2	1.93	0.51
33:2:203:THR:HG22	33:2:250:VAL:HG21	1.91	0.51
34:3:293:ASN:HD22	34:3:364:THR:HB	1.76	0.51
1:A:1791:PHE:H	1:A:1794:LEU:HD12	1.76	0.51
1:A:2207:ILE:HD12	1:A:2256:LEU:HB2	1.93	0.51
8:C:542:ILE:HA	8:C:563:LEU:O	2.11	0.51
8:C:680:SER:HB2	8:C:858:LEU:HD11	1.92	0.51
27:D:536:LEU:HD21	27:D:578:LEU:CD2	2.41	0.51
27:D:1457:ARG:O	27:D:1760:ASN:ND2	2.44	0.51
27:D:1687:LEU:HB2	27:D:1698:TYR:CE1	2.29	0.51
27:D:1750:ILE:HD13	27:D:1806:LEU:HG	1.93	0.51
27:D:1996:GLN:HE22	27:D:2150:LEU:H	1.59	0.51
32:1:685:ILE:O	32:1:688:THR:OG1	2.25	0.51
32:1:689:LEU:HD21	32:1:707:PHE:CD2	2.45	0.51
32:1:887:ASN:HB3	32:1:899:ILE:HD13	1.92	0.51
34:3:410:PHE:HE1	34:3:445:GLY:HA3	1.76	0.51
34:3:496:SER:HB3	34:3:497:PRO:HD3	1.92	0.51
34:3:1048:THR:OG1	34:3:1065:THR:O	2.26	0.51
41:u:302:LYS:O	41:u:306:LYS:HG2	2.11	0.51
1:A:2183:TYR:HE1	1:A:2219:LYS:HG3	1.76	0.51
3:L:315:ARG:HD3	7:M:66:HIS:CE1	2.46	0.51
8:C:353:TYR:HD1	8:C:371:PRO:HA	1.74	0.51
27:D:789:LEU:HB2	27:D:794:ARG:HG2	1.93	0.51
27:D:1424:ILE:H	27:D:1443:HIS:CD2	2.29	0.51
20:S:10:LEU:HD12	20:S:83:LEU:HD12	1.93	0.51
32:1:264:GLU:HA	32:1:267:THR:HG22	1.93	0.51
32:1:418:ALA:O	32:1:422:MET:HG2	2.11	0.51
34:3:332:GLU:HG2	34:3:333:ASN:H	1.76	0.51
35:4:67:ILE:HD13	35:4:85:GLN:HB3	1.92	0.51
1:A:487:ASN:OD1	1:A:488:ARG:HG3	2.11	0.50
2:K:218:VAL:HG21	2:K:238:ALA:HB3	1.92	0.50
3:L:355:ALA:HB2	6:E:54:ARG:NH1	2.27	0.50
5:J:338:HIS:O	5:J:383:VAL:HA	2.11	0.50
8:C:115:LYS:O	8:C:116:THR:OG1	2.24	0.50
8:C:121:ASP:OD1	8:C:122:TYR:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:94:C:H5'	18:B:95:C:OP2	2.11	0.50
27:D:682:ARG:NH2	27:D:946:VAL:HG13	2.26	0.50
29:H:1120:G:H2'	29:H:1121:U:C6	2.45	0.50
32:1:832:LYS:HB2	32:1:871:THR:HG21	1.93	0.50
34:3:832:TRP:CG	34:3:833:LYS:H	2.29	0.50
34:3:1002:ARG:NH2	34:3:1004:LEU:HD11	2.26	0.50
34:3:1166:TYR:CZ	34:3:1184:LYS:HE3	2.46	0.50
35:4:170:ASN:ND2	35:4:179:THR:HG22	2.25	0.50
1:A:138:HIS:O	1:A:142:ILE:HG12	2.11	0.50
1:A:301:TRP:HD1	1:A:493:MET:SD	2.34	0.50
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.44	0.50
1:A:2051:ILE:O	1:A:2055:MET:HG2	2.11	0.50
2:K:177:PRO:HB2	2:K:195:TRP:HE1	1.75	0.50
5:J:245:ARG:O	5:J:249:ARG:HG2	2.11	0.50
8:C:281:PRO:HG3	8:C:382:TYR:CD2	2.46	0.50
18:B:123:U:H2'	18:B:124:C:C6	2.46	0.50
27:D:639:LEU:HD23	27:D:943:TYR:CE2	2.46	0.50
27:D:810:ARG:HH11	27:D:813:ARG:HE	1.57	0.50
28:G:520:G:N2	38:X:34:TYR:CB	2.73	0.50
32:1:288:ASN:OD1	32:1:289:GLU:N	2.43	0.50
37:6:22:GLY:HA2	37:6:26:THR:HG21	1.94	0.50
39:Y:209:LEU:HD12	39:Y:209:LEU:C	2.36	0.50
41:u:91:GLN:HG2	41:u:95:LYS:HE2	1.94	0.50
1:A:1888:HIS:CE1	1:A:1988:LEU:HD22	2.46	0.50
3:L:399:THR:HB	3:L:407:GLU:HB3	1.93	0.50
27:D:1493:SER:HA	27:D:1524:TRP:CH2	2.43	0.50
27:D:1861:PHE:CD2	22:Q:140:LYS:HD3	2.46	0.50
21:P:86:ILE:O	20:S:71:PHE:HB2	2.12	0.50
22:Q:139:ASN:O	22:Q:140:LYS:HB3	2.10	0.50
23:R:76:TRP:NE1	23:R:87:ARG:HB2	2.27	0.50
24:T:59:GLU:O	24:T:74:GLY:CA	2.59	0.50
33:2:159:LEU:O	33:2:162:SER:OG	2.29	0.50
34:3:63:LEU:HB2	34:3:1227:CYS:SG	2.51	0.50
1:A:863:ARG:HH12	1:A:1059:GLU:HB3	1.76	0.50
2:K:60:LYS:HB3	2:K:61:PRO:HD2	1.94	0.50
8:C:129:ILE:CB	20:d:16:GLY:HA3	2.37	0.50
8:C:605:ILE:HG13	8:C:652:MET:CE	2.42	0.50
27:D:2073:ILE:HD11	27:D:2142:ILE:HD13	1.92	0.50
29:H:64:G:H2'	29:H:65:A:C8	2.46	0.50
32:1:739:ASN:HB3	32:1:742:ILE:HD12	1.94	0.50
34:3:936:PRO:O	34:3:937:LYS:HD2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:994:LEU:HD22	34:3:1006:TYR:HD2	1.77	0.50
34:3:1087:VAL:O	34:3:1094:VAL:HA	2.12	0.50
1:A:175:LEU:HD22	1:A:571:LEU:HD23	1.93	0.50
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.47	0.50
2:K:69:VAL:HB	5:J:322:ARG:NH1	2.26	0.50
2:K:243:ILE:HB	2:K:261:LEU:HB2	1.93	0.50
4:N:678:TYR:O	4:N:682:GLY:N	2.26	0.50
6:E:85:PHE:HD1	6:E:90:HIS:HA	1.76	0.50
17:I:151:G:N7	25:U:32:LYS:HD3	2.27	0.50
18:B:166:U:O2'	18:B:167:A:P	2.70	0.50
19:O:206:LYS:HB2	19:O:208:LYS:HZ3	1.75	0.50
25:f:48:TYR:O	25:f:50:ASN:N	2.45	0.50
27:D:1387:HIS:CB	27:D:1470:LEU:HD13	2.32	0.50
25:U:41:THR:HG23	25:U:55:GLU:OE2	2.12	0.50
28:G:505:A:H1'	28:G:506:U:C6	2.46	0.50
24:i:86:ASN:HD21	25:j:32:LYS:NZ	2.09	0.50
25:j:74:ARG:HD3	23:n:101:VAL:O	2.12	0.50
34:3:432:GLU:OE1	37:6:62:ILE:HB	2.11	0.50
36:5:51:PHE:HD1	36:5:52:GLY:H	1.59	0.50
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.93	0.50
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.45	0.50
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.12	0.50
1:A:1863:HIS:HA	19:O:159:ASP:N	2.26	0.50
2:K:283:ALA:HB1	2:K:310:VAL:HG12	1.93	0.50
3:L:361:ASP:OD1	3:L:362:GLN:N	2.45	0.50
6:E:97:THR:HG23	6:E:99:ASN:H	1.77	0.50
17:I:92:C:H2'	17:I:93:C:H6	1.75	0.50
27:D:453:PHE:CE2	27:D:455:ARG:HG3	2.46	0.50
27:D:1168:GLY:O	27:D:1172:GLN:HG3	2.11	0.50
27:D:1913:PHE:CE2	27:D:1917:THR:HB	2.47	0.50
24:T:40:LYS:NZ	24:T:93:ALA:HB3	2.26	0.50
29:H:44:U:C2	29:H:45:U:C5	3.00	0.50
29:H:145:G:H2'	29:H:146:A:H8	1.77	0.50
32:1:580:PHE:HZ	32:1:619:HIS:HA	1.76	0.50
33:2:367:LEU:O	33:2:368:ILE:HG22	2.12	0.50
34:3:766:LYS:HD3	34:3:836:TRP:CZ2	2.47	0.50
34:3:1097:PHE:HB3	34:3:1106:PHE:HB3	1.93	0.50
41:u:14:MET:HE3	41:u:86:TYR:OH	2.11	0.50
1:A:2206:PHE:HE2	1:A:2241:ILE:HA	1.76	0.50
27:D:1252:LEU:HD11	27:D:1288:PHE:CE1	2.46	0.50
26:V:20:ASN:ND2	26:V:69:ILE:HD11	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:492:U:H2'	28:G:493:A:C8	2.47	0.50
32:1:252:ILE:HD11	32:1:296:VAL:HA	1.93	0.50
34:3:493:VAL:HG13	34:3:499:SER:OG	2.11	0.50
34:3:503:LYS:HD3	34:3:941:PHE:CD1	2.46	0.50
34:3:1223:GLY:O	34:3:1224:THR:OG1	2.24	0.50
41:u:75:GLN:HE21	41:u:156:ILE:HG21	1.76	0.50
41:u:115:LYS:HA	41:u:118:GLN:HB3	1.93	0.50
4:N:161:LYS:O	4:N:165:GLU:CB	2.60	0.50
8:C:789:SER:HA	8:C:792:LYS:HG2	1.92	0.50
27:D:464:HIS:CE1	27:D:706:GLN:NE2	2.80	0.50
27:D:985:GLU:HG3	27:D:1001:LEU:HD22	1.93	0.50
27:D:1320:PRO:HB2	27:D:1534:ASN:O	2.12	0.50
21:P:19:LYS:HD2	21:P:99:ASP:HB2	1.93	0.50
34:3:630:ILE:HD13	34:3:646:LEU:HD13	1.94	0.50
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.47	0.50
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.25	0.50
1:A:1667:GLN:CD	19:O:211:ASN:OD1	2.52	0.50
1:A:1705:SER:HB3	1:A:1709:TRP:NE1	2.27	0.50
1:A:2255:LEU:HD11	1:A:2281:PHE:HE1	1.77	0.50
2:K:178:ILE:HD13	2:K:461:ILE:HG13	1.94	0.50
4:N:251:GLU:OE2	4:N:255:ARG:HB3	2.12	0.50
4:N:890:GLU:O	4:N:894:ARG:HG2	2.12	0.50
27:D:1209:GLN:NE2	27:D:1788:TYR:O	2.45	0.50
27:D:1387:HIS:CE1	27:D:1470:LEU:HB2	2.47	0.50
27:D:1624:LEU:O	27:D:1624:LEU:HD23	2.12	0.50
28:G:491:C:H2'	28:G:492:U:C6	2.47	0.50
34:3:643:ILE:HG21	34:3:691:LEU:HD11	1.94	0.50
39:Y:170:LEU:HD22	39:Y:170:LEU:N	2.27	0.50
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.30	0.49
5:J:335:THR:HG23	5:J:336:VAL:HG22	1.94	0.49
18:B:113:G:C2	18:B:114:G:C8	3.00	0.49
27:D:1461:GLN:OE1	27:D:1461:GLN:N	2.44	0.49
29:H:42:U:H1'	43:v:83:ARG:NH2	2.27	0.49
29:H:142:C:O2'	29:H:143:G:O4'	2.29	0.49
32:1:743:ARG:HD2	32:1:780:CYS:SG	2.52	0.49
33:2:294:ILE:HG23	33:2:298:LEU:HD23	1.93	0.49
34:3:215:LEU:HB3	34:3:225:SER:HB3	1.94	0.49
34:3:673:ASP:OD1	34:3:674:THR:N	2.45	0.49
41:u:206:ILE:HG23	41:u:221:PRO:HG3	1.94	0.49
41:u:342:LYS:HA	41:u:345:PHE:CD2	2.47	0.49
1:A:653:ILE:HA	1:A:656:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1285:VAL:HG22	1:A:1301:TYR:CE1	2.47	0.49
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.47	0.49
1:A:1578:ALA:HA	1:A:1581:PHE:HB3	1.94	0.49
1:A:1751:TYR:O	1:A:1755:LYS:HG2	2.11	0.49
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.12	0.49
2:K:159:LEU:HD13	2:K:430:MET:HE2	1.94	0.49
5:J:331:VAL:HG12	5:J:333:LYS:N	2.27	0.49
27:D:656:TRP:CH2	27:D:929:ILE:HG13	2.47	0.49
27:D:1035:PHE:CD2	27:D:1080:LEU:HD22	2.47	0.49
34:3:106:THR:HG21	34:3:422:PHE:CE2	2.47	0.49
34:3:339:ASP:OD1	34:3:340:MET:N	2.45	0.49
35:4:165:ILE:HG12	35:4:180:VAL:HG12	1.94	0.49
39:Y:213:LYS:C	39:Y:230:SER:OG	2.55	0.49
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.12	0.49
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	1.94	0.49
1:A:1089:VAL:HG22	1:A:1098:VAL:HG22	1.94	0.49
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.93	0.49
1:A:2381:GLU:HB3	1:A:2384:ASN:HB2	1.94	0.49
2:K:233:GLN:HA	2:K:246:PHE:O	2.13	0.49
27:D:467:ALA:HB1	27:D:702:PRO:HB2	1.95	0.49
27:D:747:ARG:HH12	27:D:1047:ARG:HG3	1.77	0.49
27:D:1584:PHE:HZ	27:D:1709:LEU:HD22	1.77	0.49
24:T:43:ILE:HG23	24:T:52:VAL:HG13	1.94	0.49
32:1:931:ARG:NE	37:6:24:GLU:OE2	2.44	0.49
34:3:59:TYR:HE1	34:3:1316:LYS:HD2	1.76	0.49
34:3:353:ARG:NH2	34:3:387:ASP:OD1	2.44	0.49
34:3:712:PHE:HE2	34:3:713:LEU:HD23	1.76	0.49
34:3:1192:HIS:CE1	34:3:1312:ALA:HB3	2.47	0.49
41:u:171:THR:HG21	41:u:181:GLU:OE2	2.11	0.49
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.12	0.49
1:A:1586:GLN:HG2	1:A:1595:ARG:HH11	1.77	0.49
1:A:2157:ILE:HG13	27:D:1064:PRO:HB2	1.94	0.49
1:A:2306:ASN:HB2	1:A:2335:THR:OG1	2.12	0.49
2:K:225:ASP:OD1	2:K:226:TRP:N	2.45	0.49
2:K:285:HIS:O	2:K:287:MET:N	2.45	0.49
3:L:398:GLN:NE2	3:L:419:GLN:HG3	2.28	0.49
4:N:846:PHE:HE1	4:N:859:LEU:HD23	1.77	0.49
8:C:183:GLN:HE21	8:C:657:TYR:HD2	1.60	0.49
16:F:38:U:H4'	16:F:39:G:O5'	2.12	0.49
27:D:820:PHE:CD2	27:D:828:LEU:HD22	2.48	0.49
27:D:2007:LYS:HB3	27:D:2030:ILE:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:G:520:G:C6	38:X:34:TYR:CZ	3.00	0.49
29:H:1151:U:H2'	29:H:1152:U:C6	2.46	0.49
32:1:517:TYR:OH	32:1:521:LYS:NZ	2.42	0.49
32:1:872:GLY:HA2	34:3:1315:ARG:HG3	1.95	0.49
33:2:299:ARG:NH2	33:2:343:ASP:O	2.40	0.49
34:3:379:VAL:CG2	34:3:391:LEU:HB2	2.41	0.49
36:5:20:GLY:H	36:5:43:VAL:HG23	1.77	0.49
41:u:11:LEU:HD11	42:w:148:PHE:HZ	1.77	0.49
41:u:26:GLN:CB	42:w:168:THR:HG23	2.42	0.49
1:A:1717:LEU:HG	1:A:1786:ALA:HB3	1.93	0.49
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.47	0.49
1:A:1962:ARG:CD	19:O:186:GLU:CD	2.82	0.49
1:A:2177:VAL:H	1:A:2338:GLN:HE22	1.58	0.49
3:L:273:HIS:ND1	3:L:273:HIS:O	2.45	0.49
4:N:161:LYS:O	4:N:165:GLU:HB2	2.11	0.49
8:C:343:ASP:O	8:C:346:THR:OG1	2.28	0.49
8:C:544:LEU:HG	8:C:553:VAL:HG21	1.94	0.49
8:C:864:VAL:HG12	8:C:866:ILE:HG13	1.95	0.49
17:I:78:A:H2	27:D:1110:ARG:NH2	2.08	0.49
27:D:510:ALA:HB2	27:D:517:MET:HE1	1.93	0.49
27:D:835:ALA:HA	27:D:874:ARG:HD3	1.94	0.49
27:D:1431:ASP:OD2	27:D:2095:LYS:HD2	2.13	0.49
21:P:96:VAL:HG12	22:Q:85:ILE:HG12	1.95	0.49
22:Q:96:ILE:HG13	23:R:94:LEU:HD13	1.94	0.49
29:H:1089:G:C2'	29:H:1090:A:O5'	2.60	0.49
32:1:925:HIS:CG	32:1:926:PRO:HD2	2.48	0.49
41:u:237:SER:HA	41:u:321:LEU:HD13	1.93	0.49
42:w:141:GLN:O	42:w:144:ARG:HB2	2.13	0.49
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.94	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
1:A:2395:PHE:HD1	27:D:1060:LYS:C	2.20	0.49
2:K:77:ALA:O	2:K:81:MET:HG2	2.13	0.49
3:L:127:LEU:HD11	3:L:131:ILE:HD12	1.93	0.49
6:E:53:VAL:HG12	6:E:57:ALA:HB3	1.93	0.49
17:I:150:G:N2	17:I:152:A:H5'	2.28	0.49
27:D:588:LEU:HD11	27:D:599:ILE:HD11	1.94	0.49
27:D:1095:ASN:O	27:D:1099:VAL:HG23	2.12	0.49
27:D:1852:ILE:O	27:D:1856:TYR:HD2	1.96	0.49
29:H:1097:G:C2	29:H:1098:C:C4	3.00	0.49
32:1:715:ALA:HB1	32:1:718:TYR:CD2	2.47	0.49
32:1:827:ILE:HG13	32:1:827:ILE:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:266:VAL:HG12	34:3:290:PRO:HA	1.94	0.49
34:3:455:LEU:HD11	34:3:464:LEU:HB3	1.93	0.49
34:3:636:THR:HB	34:3:679:VAL:HG23	1.93	0.49
42:w:139:VAL:O	42:w:143:LYS:HG3	2.12	0.49
1:A:139:LEU:HD13	1:A:193:TYR:CG	2.48	0.49
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.94	0.49
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.43	0.49
2:K:435:GLY:N	2:K:464:TRP:HH2	2.11	0.49
2:K:438:ASP:HB3	2:K:457:TRP:HB2	1.95	0.49
6:E:38:GLN:HA	6:E:106:ILE:HD11	1.93	0.49
8:C:775:ILE:HD12	8:C:817:GLN:HE21	1.76	0.49
18:B:8:U:O4	18:B:157:G:O6	2.31	0.49
18:B:74:U:H3'	18:B:75:A:H5''	1.94	0.49
27:D:1524:TRP:CD1	27:D:1780:ARG:NH2	2.80	0.49
27:D:2051:VAL:CG1	27:D:2077:ARG:HG2	2.43	0.49
26:V:65:GLY:HA2	26:V:68:ILE:HD12	1.95	0.49
34:3:324:ASN:OD1	34:3:341:ASN:ND2	2.43	0.49
41:u:117:GLN:HB3	42:w:113:MET:HE3	1.94	0.49
41:u:377:VAL:O	41:u:378:ASP:CB	2.60	0.49
1:A:286:LEU:HD21	1:A:289:ASP:HB2	1.93	0.49
1:A:852:LEU:HD23	1:A:855:LEU:HD12	1.94	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:HE1	1.75	0.49
4:N:13:ALA:HB3	4:N:15:TYR:CE2	2.47	0.49
4:N:772:LEU:O	4:N:775:VAL:N	2.46	0.49
5:J:349:ASN:HB3	5:J:352:ILE:HD12	1.95	0.49
17:I:101:C:H2'	17:I:102:A:H8	1.77	0.49
17:I:151:G:H21	17:I:152:A:N6	2.10	0.49
18:B:78:A:H3'	18:B:78:A:OP2	2.13	0.49
19:O:150:ASN:OD1	19:O:151:ILE:N	2.45	0.49
21:P:29:VAL:HB	21:P:51:GLU:HG3	1.95	0.49
23:R:67:MET:HE2	23:R:69:LEU:HD21	1.94	0.49
25:U:51:LEU:HB2	25:U:73:ILE:HB	1.94	0.49
28:G:481:A:H5'	35:4:52:TYR:CD2	2.48	0.49
21:h:36:ALA:CB	20:l:84:PHE:CE1	2.90	0.49
32:1:494:LEU:CD1	38:X:23:TRP:CG	2.93	0.49
32:1:583:PHE:O	32:1:587:THR:HG23	2.12	0.49
33:2:262:HIS:HB2	33:2:280:THR:HG22	1.95	0.49
38:X:19:PRO:HA	38:X:22:SER:OG	2.13	0.49
1:A:481:HIS:NE2	8:C:276:ASP:OD1	2.46	0.49
7:M:44:LEU:O	7:M:74:LYS:NZ	2.43	0.49
8:C:967:VAL:O	8:C:971:ARG:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:91:U:C2	17:I:142:G:N2	2.78	0.49
27:D:1740:LEU:HD11	22:Q:146:LEU:CD1	2.42	0.49
27:D:1950:ILE:O	27:D:1954:VAL:HG13	2.12	0.49
42:w:119:GLU:C	42:w:121:ARG:H	2.21	0.49
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.95	0.49
1:A:2183:TYR:HE2	1:A:2289:ILE:CG1	2.08	0.49
2:K:382:ASP:OD1	2:K:383:GLU:N	2.46	0.49
8:C:129:ILE:CG2	20:d:16:GLY:CA	2.89	0.49
8:C:353:TYR:CD1	8:C:371:PRO:HA	2.48	0.49
18:B:10:U:O2	18:B:156:G:N1	2.46	0.49
27:D:945:TYR:O	27:D:949:LEU:HG	2.13	0.49
27:D:1016:ASP:OD1	27:D:1017:VAL:N	2.46	0.49
27:D:1095:ASN:O	27:D:1098:ILE:HG22	2.12	0.49
22:Q:4:VAL:HG11	22:Q:34:PRO:HA	1.95	0.49
24:T:10:MET:HA	26:V:30:ARG:C	2.38	0.49
34:3:118:GLN:HE21	34:3:1299:ILE:HD13	1.78	0.49
42:w:191:GLN:O	42:w:195:ILE:HG23	2.12	0.49
1:A:255:ILE:HD11	1:A:637:VAL:HG13	1.94	0.48
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.47	0.48
1:A:688:TYR:HA	1:A:691:PHE:CE2	2.47	0.48
1:A:794:LYS:O	1:A:1095:MET:HE3	2.13	0.48
1:A:884:SER:HB3	3:L:180:LYS:NZ	2.27	0.48
1:A:1952:PRO:HB2	3:L:426:GLY:N	2.26	0.48
4:N:9:GLN:HB3	4:N:11:PRO:HD3	1.95	0.48
4:N:464:ILE:O	4:N:467:ALA:HB3	2.14	0.48
8:C:793:GLU:HA	8:C:796:ILE:HG22	1.95	0.48
27:D:1228:TRP:CE2	27:D:1261:PRO:HG3	2.48	0.48
27:D:1241:LEU:HA	27:D:1292:LEU:HD23	1.95	0.48
23:R:47:SER:OG	23:R:103:VAL:HB	2.12	0.48
25:U:60:VAL:HG12	25:U:65:HIS:HB2	1.95	0.48
26:V:47:ASN:HD21	26:V:51:PRO:HB2	1.78	0.48
32:1:341:GLY:O	32:1:384:ASN:ND2	2.46	0.48
32:1:950:VAL:HG13	37:6:39:THR:HG22	1.95	0.48
34:3:607:LEU:HD13	34:3:624:TRP:HD1	1.78	0.48
39:Y:167:VAL:O	39:Y:171:GLY:N	2.45	0.48
1:A:209:ILE:HG21	1:A:303:PHE:HE2	1.78	0.48
1:A:219:ALA:HB1	1:A:266:LEU:HD13	1.94	0.48
1:A:1525:PHE:HD2	3:L:405:GLY:HA3	1.78	0.48
2:K:73:ARG:O	2:K:76:LEU:HB2	2.13	0.48
8:C:406:VAL:HG11	8:C:427:LEU:HD21	1.95	0.48
27:D:1320:PRO:HB2	27:D:1535:PHE:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1:161:LYS:O	32:1:165:THR:HG23	2.12	0.48
32:1:491:ARG:HD2	38:X:27:TYR:OH	2.13	0.48
32:1:960:ASN:HD21	32:1:963:TYR:HA	1.78	0.48
34:3:1133:ASP:OD2	34:3:1137:ASN:HB2	2.13	0.48
1:A:220:THR:O	1:A:224:MET:HG2	2.12	0.48
1:A:400:ILE:HB	8:C:186:ASP:HB3	1.95	0.48
1:A:972:MET:HG2	1:A:981:VAL:HG21	1.95	0.48
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.78	0.48
1:A:1087:ASN:ND2	3:L:272:LEU:HG	2.19	0.48
1:A:1963:LEU:HD13	1:A:1965:PHE:HE2	1.77	0.48
2:K:378:ILE:HG22	5:J:168:TRP:HE1	1.78	0.48
3:L:280:ARG:NH2	17:I:37:U:OP2	2.46	0.48
4:N:721:ARG:O	4:N:725:ILE:HD12	2.12	0.48
8:C:856:ILE:HA	8:C:944:VAL:HG11	1.94	0.48
16:F:47:A:H3'	16:F:48:C:H5'	1.94	0.48
18:B:86:G:H2'	18:B:87:G:H8	1.76	0.48
27:D:1908:ARG:HD3	23:R:39:VAL:HG23	1.95	0.48
22:Q:88:ARG:NH1	22:Q:90:ASN:HB3	2.28	0.48
29:H:119:G:OP2	25:j:76:ASN:HB2	2.12	0.48
32:1:494:LEU:CB	38:X:7:ILE:CG2	2.89	0.48
32:1:801:ILE:HG22	32:1:816:VAL:HG13	1.95	0.48
39:Y:217:LYS:HB3	39:Y:218:PRO:HD2	1.95	0.48
41:u:192:VAL:HG12	41:u:222:MET:HE1	1.95	0.48
43:v:42:TYR:HD1	43:v:60:LYS:HB2	1.77	0.48
1:A:645:ASP:OD1	1:A:646:ALA:N	2.46	0.48
1:A:842:LYS:HE2	1:A:1322:ALA:HA	1.94	0.48
1:A:1090:ILE:O	1:A:1096:SER:HA	2.13	0.48
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.28	0.48
1:A:2152:TRP:HZ3	27:D:1064:PRO:HG3	1.75	0.48
4:N:655:PHE:O	4:N:659:ARG:CB	2.62	0.48
7:M:33:LEU:HD11	7:M:100:ALA:HB1	1.95	0.48
8:C:143:HIS:HA	44:C:1500:GTP:PB	2.54	0.48
8:C:362:LYS:CG	8:C:363:PRO:HD2	2.43	0.48
8:C:652:MET:HA	8:C:655:LEU:HD12	1.96	0.48
8:C:678:SER:HB2	8:C:858:LEU:HB2	1.94	0.48
17:I:136:U:O2'	27:D:1194:ASP:OD2	2.26	0.48
27:D:1459:TRP:NE1	27:D:1762:ILE:HD11	2.28	0.48
21:P:50:GLU:O	21:P:79:LYS:HA	2.14	0.48
1:A:299:LYS:HA	1:A:493:MET:HG3	1.95	0.48
1:A:930:ASN:HB3	1:A:933:GLU:OE1	2.14	0.48
1:A:995:LEU:HD11	1:A:1078:ILE:HG23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2166:LEU:HD11	1:A:2194:ILE:HG13	1.95	0.48
1:A:2395:PHE:CG	27:D:1062:PRO:CD	2.82	0.48
3:L:282:GLU:HG3	3:L:286:PHE:CD2	2.49	0.48
8:C:707:SER:HB3	8:C:824:SER:HB3	1.96	0.48
18:B:76:U:O2'	18:B:78:A:OP1	2.30	0.48
18:B:143:U:H2'	18:B:144:G:H8	1.78	0.48
27:D:828:LEU:HG	27:D:830:CYS:SG	2.53	0.48
27:D:1563:MET:HE1	27:D:1684:GLY:HA2	1.95	0.48
27:D:1804:SER:HA	27:D:1807:VAL:HG22	1.96	0.48
22:Q:29:LEU:HD23	22:Q:40:LEU:HG	1.94	0.48
28:G:504:C:OP1	36:5:25:LYS:NZ	2.21	0.48
29:H:1116:A:O2'	29:H:1117:G:H5'	2.13	0.48
24:i:34:GLN:HE21	24:i:37:ILE:HD12	1.78	0.48
32:1:327:TRP:HD1	32:1:330:ARG:HH21	1.61	0.48
32:1:830:MET:O	32:1:832:LYS:HG2	2.13	0.48
34:3:74:SER:OG	34:3:95:VAL:HG22	2.13	0.48
34:3:586:ASP:OD1	34:3:587:THR:N	2.47	0.48
34:3:1136:GLY:HA2	34:3:1197:ASP:O	2.14	0.48
35:4:136:ARG:HB2	35:4:154:TYR:CD2	2.49	0.48
41:u:31:LEU:HD23	41:u:72:ILE:HG23	1.96	0.48
41:u:178:GLU:HA	41:u:334:ARG:HH11	1.78	0.48
41:u:350:ARG:CB	41:u:350:ARG:NH1	2.76	0.48
41:u:461:PHE:CZ	41:u:474:TRP:HE3	2.32	0.48
1:A:772:GLU:HA	1:A:775:ARG:HB2	1.96	0.48
1:A:1964:PRO:HB3	1:A:2013:ARG:HD2	1.95	0.48
2:K:195:TRP:CZ3	2:K:220:LYS:HE3	2.49	0.48
4:N:212:VAL:HG13	4:N:215:LEU:H	1.78	0.48
4:N:704:LEU:O	4:N:707:SER:OG	2.28	0.48
8:C:222:MET:HE1	8:C:252:LEU:HD21	1.95	0.48
27:D:2011:ILE:HD12	27:D:2030:ILE:HD11	1.96	0.48
22:Q:31:SER:HB2	22:Q:39:ILE:HD11	1.95	0.48
23:R:38:MET:SD	23:R:61:PHE:HE2	2.36	0.48
28:G:499:U:H2'	28:G:500:A:C8	2.49	0.48
29:H:45:U:H2'	29:H:46:C:C6	2.49	0.48
33:2:322:PRO:HA	35:4:65:TYR:CE2	2.49	0.48
34:3:414:GLN:NE2	34:3:434:ASN:O	2.47	0.48
34:3:533:LYS:HA	34:3:848:SER:OG	2.14	0.48
34:3:1043:THR:HG21	34:3:1052:TYR:HE2	1.79	0.48
35:4:110:LEU:HD12	35:4:155:PHE:HE2	1.77	0.48
37:6:50:LEU:CD2	37:6:62:ILE:HG23	2.43	0.48
41:u:62:PHE:HA	41:u:376:GLN:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1169:TYR:OH	1:A:1262:MET:HA	2.14	0.48
1:A:1414:TRP:HB2	1:A:1558:GLU:HG3	1.94	0.48
1:A:1748:ILE:HG22	1:A:1785:ASP:HB2	1.94	0.48
2:K:218:VAL:HG23	2:K:240:ASP:CG	2.39	0.48
3:L:205:GLU:O	3:L:209:LYS:HG2	2.13	0.48
4:N:787:SER:O	17:I:40:G:O2'	2.31	0.48
5:J:163:ASN:C	5:J:165:GLY:H	2.22	0.48
8:C:152:LEU:O	8:C:155:ILE:HG13	2.13	0.48
8:C:227:VAL:HG11	8:C:474:LYS:HB2	1.94	0.48
27:D:1688:TYR:CD2	27:D:1895:ARG:HA	2.44	0.48
27:D:1847:LEU:O	27:D:1851:LEU:HD13	2.13	0.48
23:R:79:LYS:HD3	23:R:84:VAL:HG22	1.95	0.48
32:1:401:TRP:CZ2	32:1:434:TYR:HD1	2.31	0.48
32:1:550:THR:HG23	32:1:553:LEU:HD22	1.96	0.48
33:2:134:LEU:HD13	33:2:138:LYS:HE2	1.96	0.48
34:3:1037:PHE:CE2	34:3:1038:LYS:HG2	2.49	0.48
35:4:108:ALA:HA	35:4:194:TYR:OH	2.14	0.48
37:6:23:ASP:CG	37:6:24:GLU:H	2.21	0.48
1:A:717:GLY:HA3	18:B:84:A:O2'	2.14	0.48
2:K:200:GLN:HB3	2:K:213:LYS:HG3	1.96	0.48
2:K:267:ARG:HG3	2:K:285:HIS:CD2	2.49	0.48
3:L:120:TYR:CD1	3:L:123:ARG:HB3	2.46	0.48
3:L:367:ARG:NH2	17:I:57:U:C4	2.81	0.48
4:N:261:LYS:HE2	4:N:285:HIS:HA	1.94	0.48
8:C:250:GLU:HG2	8:C:298:PHE:CE2	2.48	0.48
8:C:766:TRP:CZ2	8:C:792:LYS:HB3	2.49	0.48
27:D:836:TRP:HE3	27:D:870:GLN:HE22	1.62	0.48
27:D:1515:LEU:O	27:D:1534:ASN:ND2	2.44	0.48
27:D:1682:ILE:HD12	27:D:1722:ILE:HG12	1.95	0.48
27:D:2103:LEU:HD13	27:D:2142:ILE:HG13	1.96	0.48
20:I:80:ASN:O	20:I:81:ALA:HB2	2.14	0.48
34:3:71:PHE:O	34:3:430:LEU:HD21	2.13	0.48
43:v:190:ASP:HB2	43:v:192:LYS:HE3	1.94	0.48
1:A:644:VAL:O	1:A:645:ASP:HB2	2.14	0.48
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.78	0.48
1:A:1673:LEU:HD21	1:A:1681:VAL:HG23	1.96	0.48
4:N:864:ASP:CG	4:N:889:ARG:HH21	2.22	0.48
8:C:237:ILE:HD12	8:C:265:PHE:HE1	1.78	0.48
8:C:769:TYR:N	8:C:772:ASN:O	2.45	0.48
21:P:15:LEU:HB3	21:P:20:LEU:HD11	1.95	0.48
22:Q:8:LYS:HE3	22:Q:34:PRO:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:42:U:C2	29:H:43:G:C8	3.02	0.48
29:H:1093:C:C2	29:H:1094:G:C8	3.02	0.48
29:H:1162:U:O2'	29:H:1163:C:H5'	2.14	0.48
29:H:1166:G:H8	29:H:1166:G:O5'	1.96	0.48
32:1:606:LEU:HD21	32:1:643:LEU:HD23	1.96	0.48
32:1:928:LYS:HD2	37:6:24:GLU:OE2	2.14	0.48
34:3:551:PHE:HD2	34:3:591:THR:HG21	1.79	0.48
34:3:1193:PHE:CE1	34:3:1308:ARG:HD2	2.49	0.48
41:u:150:PRO:CG	41:u:154:THR:H	2.24	0.48
41:u:210:PHE:CE1	41:u:216:TYR:HB2	2.49	0.48
41:u:267:SER:O	41:u:272:SER:HB2	2.13	0.48
41:u:431:TYR:OH	41:u:440:HIS:CE1	2.67	0.48
43:v:244:ASP:OD2	43:v:247:SER:HB3	2.14	0.48
1:A:543:ASN:OD1	1:A:544:LYS:N	2.47	0.48
1:A:635:THR:HG21	1:A:656:ILE:HD11	1.96	0.48
1:A:966:PRO:HA	1:A:1088:VAL:HG12	1.95	0.48
4:N:692:LEU:HD23	4:N:708:LEU:HD11	1.96	0.48
8:C:292:ILE:HD13	8:C:306:PRO:HD3	1.95	0.48
27:D:1032:PHE:HE2	27:D:1081:GLN:HG2	1.79	0.48
27:D:1255:ASP:N	27:D:1255:ASP:OD1	2.47	0.48
21:P:53:VAL:HB	21:P:54:PRO:HD3	1.96	0.48
29:H:1097:G:H2'	29:H:1098:C:H5	1.78	0.48
34:3:60:LEU:HB2	34:3:1317:VAL:HG22	1.94	0.48
1:A:863:ARG:NH1	1:A:1059:GLU:HB3	2.29	0.47
2:K:290:ARG:HA	2:K:301:LEU:O	2.13	0.47
5:J:342:PHE:HB2	5:J:380:ILE:HB	1.95	0.47
17:I:143:A:C5	25:U:48:TYR:HD2	2.31	0.47
27:D:542:HIS:O	27:D:551:ASN:HB3	2.14	0.47
27:D:1621:ILE:HD12	27:D:1630:ARG:HG3	1.96	0.47
21:P:28:ARG:HD3	21:P:50:GLU:OE2	2.14	0.47
29:H:142:C:C2'	29:H:143:G:H8	2.23	0.47
29:H:679:U:H2'	29:H:680:C:C6	2.49	0.47
23:n:90:PHE:HZ	41:u:195:ARG:HA	1.63	0.47
32:1:954:PRO:O	32:1:959:ASN:ND2	2.47	0.47
34:3:294:PHE:CE2	34:3:330:GLY:HA3	2.49	0.47
41:u:195:ARG:HD3	41:u:197:ASP:OD2	2.14	0.47
43:v:155:ILE:HB	43:v:252:VAL:CG2	2.44	0.47
1:A:460:PRO:HG3	8:C:376:PHE:CD1	2.49	0.47
1:A:691:PHE:CZ	1:A:701:CYS:HB2	2.49	0.47
1:A:1451:PHE:O	1:A:1454:SER:N	2.45	0.47
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:53:VAL:HG13	6:E:56:PHE:CZ	2.49	0.47
8:C:835:LYS:HB3	8:C:839:ILE:HD12	1.95	0.47
8:C:879:LEU:O	8:C:883:ARG:HG2	2.14	0.47
27:D:843:HIS:HA	27:D:876:GLY:HA2	1.96	0.47
27:D:1987:VAL:HG23	27:D:2150:LEU:HD22	1.95	0.47
24:T:46:PHE:O	25:U:14:ASN:ND2	2.47	0.47
29:H:1094:G:C6	29:H:1149:G:C6	3.03	0.47
34:3:208:GLU:HG3	34:3:209:GLN:N	2.29	0.47
34:3:380:LEU:HB3	34:3:388:LEU:HD11	1.96	0.47
38:X:49:THR:CG2	39:Y:233:ASP:HB2	2.45	0.47
41:u:267:SER:C	41:u:272:SER:HB2	2.39	0.47
1:A:1268:ARG:HG2	1:A:1301:TYR:HB2	1.95	0.47
1:A:2398:LEU:HD12	27:D:1060:LYS:HZ2	1.72	0.47
2:K:446:SER:OG	2:K:451:PHE:CE2	2.60	0.47
17:I:143:A:C5	25:U:48:TYR:CD2	3.02	0.47
27:D:585:VAL:HG22	27:D:604:VAL:HB	1.97	0.47
27:D:1771:ASP:O	27:D:1774:THR:OG1	2.18	0.47
24:T:85:ASP:OD1	24:T:86:ASN:N	2.48	0.47
34:3:94:CYS:SG	34:3:101:LEU:HD11	2.54	0.47
34:3:211:LYS:NZ	34:3:256:GLU:OE2	2.38	0.47
34:3:750:TYR:HE1	34:3:777:LEU:HD21	1.79	0.47
34:3:1107:ILE:HD12	34:3:1108:PRO:HD2	1.96	0.47
35:4:138:PRO:HA	35:4:152:TYR:O	2.14	0.47
43:v:161:SER:C	43:v:162:GLU:HG3	2.39	0.47
1:A:713:ASN:HB3	18:B:84:A:H5'	1.96	0.47
1:A:796:ASN:OD1	1:A:858:LYS:HE2	2.14	0.47
2:K:382:ASP:CG	2:K:383:GLU:H	2.22	0.47
2:K:428:LEU:HD11	5:J:466:PRO:HD2	1.96	0.47
18:B:67:U:H2'	18:B:68:A:C8	2.47	0.47
21:P:76:LYS:HD3	21:P:79:LYS:HD3	1.96	0.47
24:T:90:ILE:HB	26:V:62:VAL:CG1	2.44	0.47
32:1:850:ASP:OD1	32:1:853:HIS:HD2	1.98	0.47
33:2:363:TYR:HA	34:3:1125:ASP:OD2	2.14	0.47
34:3:503:LYS:HG2	34:3:929:ILE:HD11	1.97	0.47
41:u:208:GLU:HG3	41:u:332:PHE:CE2	2.49	0.47
1:A:228:LYS:HD2	1:A:701:CYS:H	1.77	0.47
1:A:374:ILE:HD12	8:C:674:LEU:HD22	1.97	0.47
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.95	0.47
3:L:113:HIS:HD2	3:L:134:PRO:HA	1.80	0.47
8:C:835:LYS:O	8:C:839:ILE:HB	2.15	0.47
17:I:141:G:H2'	17:I:142:G:H5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:587:GLU:O	27:D:594:LEU:HG	2.15	0.47
27:D:1252:LEU:HD11	27:D:1288:PHE:CD1	2.49	0.47
23:R:46:ILE:HD11	23:R:67:MET:HE1	1.97	0.47
29:H:1143:C:H4'	29:H:1144:U:H2'	1.96	0.47
32:1:169:LEU:O	32:1:173:ILE:HD12	2.13	0.47
32:1:935:TRP:CE3	37:6:22:GLY:HA3	2.49	0.47
38:X:33:ILE:HG22	38:X:85:THR:HG23	1.95	0.47
41:u:172:ARG:NH2	41:u:354:MET:HE3	2.16	0.47
41:u:219:THR:N	41:u:220:PRO:HD3	2.30	0.47
1:A:984:VAL:HG12	1:A:985:ASP:N	2.30	0.47
1:A:1169:TYR:CZ	1:A:1262:MET:HG2	2.50	0.47
1:A:1616:ARG:HH21	1:A:1618:ASN:HD22	1.63	0.47
1:A:2017:THR:HB	1:A:2062:GLU:OE1	2.13	0.47
1:A:2177:VAL:N	1:A:2338:GLN:HE22	2.12	0.47
2:K:353:TYR:CE1	7:M:126:ILE:HG12	2.48	0.47
2:K:362:TYR:HB2	2:K:379:ARG:HG3	1.95	0.47
16:F:50:G:H4'	16:F:51:A:OP2	2.15	0.47
17:I:138:U:H5	27:D:1227:ILE:HG12	1.79	0.47
27:D:491:PHE:N	27:D:491:PHE:CD1	2.82	0.47
27:D:574:PHE:HB2	27:D:585:VAL:HG11	1.97	0.47
27:D:1685:THR:O	27:D:1697:PRO:HA	2.15	0.47
27:D:1724:THR:HG22	27:D:1725:SER:N	2.30	0.47
27:D:2051:VAL:HG12	27:D:2077:ARG:HG2	1.97	0.47
22:Q:23:THR:HA	22:Q:48:PRO:HD3	1.96	0.47
26:V:31:GLY:H	26:V:39:VAL:HB	1.78	0.47
28:G:506:U:O2	28:G:507:U:H5''	2.14	0.47
38:X:52:SER:HB3	39:Y:231:ARG:CZ	2.44	0.47
1:A:364:TYR:CE2	1:A:1209:LYS:HB3	2.50	0.47
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.96	0.47
1:A:688:TYR:HD1	1:A:691:PHE:CZ	2.32	0.47
1:A:876:PRO:HB3	3:L:172:ILE:HG22	1.95	0.47
1:A:1054:LEU:O	1:A:1239:THR:HB	2.14	0.47
1:A:1126:LEU:HD11	1:A:1161:TYR:CD2	2.50	0.47
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.50	0.47
1:A:1562:PHE:CZ	1:A:1570:TRP:HB3	2.50	0.47
1:A:1777:ILE:HG12	1:A:1784:TYR:CB	2.45	0.47
1:A:2398:LEU:HD22	27:D:1060:LYS:CD	2.43	0.47
2:K:244:LYS:HE3	2:K:257:LEU:HD22	1.96	0.47
3:L:137:TYR:O	3:L:141:ILE:HG13	2.15	0.47
3:L:222:ILE:HD11	3:L:242:ILE:HD12	1.97	0.47
3:L:410:LEU:O	3:L:410:LEU:HD12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:335:THR:HG23	5:J:336:VAL:H	1.79	0.47
6:E:9:LEU:HD13	6:E:15:VAL:HA	1.97	0.47
8:C:116:THR:HG22	8:C:118:TYR:H	1.80	0.47
8:C:233:ASP:OD1	8:C:487:ARG:NH2	2.47	0.47
8:C:423:HIS:O	8:C:427:LEU:CB	2.63	0.47
17:I:137:G:H5''	27:D:1198:ARG:NH2	2.29	0.47
18:B:166:U:H4'	18:B:167:A:OP1	2.14	0.47
27:D:686:VAL:HG12	27:D:687:PRO:O	2.14	0.47
27:D:1640:LEU:HB2	27:D:1664:LEU:HD11	1.97	0.47
23:R:53:LYS:O	23:R:74:GLU:HA	2.15	0.47
24:T:24:GLN:CB	24:T:42:LYS:HD2	2.44	0.47
28:G:501:A:C6	32:1:783:VAL:HG11	2.49	0.47
29:H:119:G:N7	22:m:20:LYS:CE	2.77	0.47
29:H:565:U:H2'	29:H:566:U:C6	2.50	0.47
29:H:566:U:H2'	29:H:567:U:C6	2.50	0.47
29:H:689:G:H2'	29:H:690:U:C6	2.50	0.47
29:H:1126:G:O2'	29:H:1127:A:H8	1.97	0.47
23:n:90:PHE:CE1	41:u:195:ARG:C	2.93	0.47
32:1:611:HIS:CD2	32:1:612:LYS:H	2.31	0.47
32:1:683:ASN:OD1	32:1:684:GLN:N	2.46	0.47
33:2:311:PRO:HG2	35:4:74:VAL:HG22	1.96	0.47
33:2:322:PRO:HB3	35:4:32:ILE:O	2.14	0.47
34:3:832:TRP:HB3	34:3:835:VAL:HG23	1.97	0.47
34:3:1003:LEU:HD23	34:3:1059:LEU:HD11	1.97	0.47
34:3:1193:PHE:CZ	34:3:1308:ARG:HD2	2.49	0.47
41:u:156:ILE:HG12	41:u:366:TYR:HB2	1.97	0.47
42:w:127:SER:HA	42:w:132:HIS:CG	2.50	0.47
1:A:404:ASN:OD1	8:C:927:MET:HE3	2.14	0.47
2:K:171:GLN:O	2:K:172:LEU:HD12	2.15	0.47
7:M:61:ILE:O	7:M:65:LEU:HG	2.15	0.47
8:C:132:ARG:O	8:C:133:ILE:HG12	2.14	0.47
27:D:635:GLU:N	27:D:670:LEU:O	2.47	0.47
29:H:139:G:C2'	29:H:140:G:O5'	2.62	0.47
29:H:551:C:H2'	29:H:552:U:C6	2.50	0.47
29:H:678:U:H2'	29:H:679:U:C6	2.50	0.47
29:H:693:C:H2'	29:H:694:C:C6	2.50	0.47
29:H:1140:U:H2'	29:H:1141:C:C6	2.50	0.47
34:3:337:VAL:HG22	34:3:346:LEU:HB2	1.97	0.47
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.28	0.47
1:A:325:LYS:HB2	1:A:405:ASN:ND2	2.28	0.47
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2393:LEU:O	1:A:2397:GLU:CB	2.63	0.47
4:N:887:THR:HB	4:N:890:GLU:HB3	1.96	0.47
8:C:943:ASP:OD2	8:C:946:ASP:HB2	2.15	0.47
16:F:29:U:H2'	16:F:30:G:C8	2.50	0.47
28:G:494:G:H21	43:v:83:ARG:HH12	1.62	0.47
28:G:514:U:C4'	28:G:515:U:H5'	2.45	0.47
29:H:671:G:H2'	29:H:672:U:C6	2.50	0.47
29:H:682:U:H2'	29:H:683:U:C6	2.50	0.47
29:H:695:U:H2'	29:H:696:C:C6	2.50	0.47
29:H:1097:G:C6	29:H:1146:G:C6	3.02	0.47
32:1:258:VAL:HA	32:1:261:THR:HG22	1.97	0.47
32:1:963:TYR:CG	32:1:964:ILE:N	2.83	0.47
35:4:108:ALA:HB3	35:4:155:PHE:O	2.15	0.47
41:u:7:ARG:HD2	41:u:96:ILE:HG22	1.97	0.47
1:A:2395:PHE:CD1	27:D:1061:ALA:CA	2.84	0.47
2:K:388:GLN:HE21	5:J:462:HIS:CE1	2.32	0.47
2:K:408:LYS:O	2:K:424:SER:HB3	2.15	0.47
2:K:443:LEU:HG	2:K:444:ASP:N	2.30	0.47
5:J:280:VAL:O	5:J:286:ASN:ND2	2.48	0.47
8:C:148:SER:O	8:C:151:ASP:HB3	2.15	0.47
8:C:697:ARG:HG3	8:C:709:SER:HA	1.97	0.47
17:I:150:G:O2'	17:I:152:A:OP1	2.32	0.47
18:B:21:G:H2'	18:B:22:G:C8	2.50	0.47
24:T:11:VAL:O	26:V:31:GLY:HA3	2.15	0.47
33:2:185:GLY:O	33:2:189:LEU:HG	2.14	0.47
34:3:259:ASN:O	37:6:75:PRO:HD3	2.14	0.47
41:u:193:ILE:HG22	41:u:222:MET:HE2	1.96	0.47
42:w:139:VAL:HG23	42:w:140:ALA:H	1.80	0.47
43:v:155:ILE:N	43:v:155:ILE:HD12	2.29	0.47
1:A:300:LYS:H	1:A:493:MET:HG2	1.80	0.46
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	2.15	0.46
1:A:1498:ASP:HB2	4:N:159:LEU:HB2	1.96	0.46
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.49	0.46
1:A:2395:PHE:CD1	27:D:1060:LYS:O	2.63	0.46
4:N:13:ALA:HB3	4:N:15:TYR:CD2	2.50	0.46
4:N:652:ALA:O	4:N:656:LEU:CB	2.63	0.46
16:F:5:G:H2'	16:F:6:C:C6	2.49	0.46
17:I:5:U:H2'	17:I:6:U:C6	2.50	0.46
17:I:150:G:H2'	17:I:151:G:H5''	1.97	0.46
27:D:783:THR:O	27:D:787:ASN:ND2	2.48	0.46
27:D:1372:LYS:CD	27:D:1708:GLY:HA3	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:23:LEU:HD23	20:S:24:THR:H	1.80	0.46
32:1:746:ALA:O	32:1:749:THR:OG1	2.32	0.46
32:1:823:MET:O	32:1:827:ILE:HG12	2.15	0.46
34:3:370:VAL:HG23	34:3:379:VAL:HG12	1.98	0.46
34:3:964:PHE:CZ	34:3:972:LYS:HD3	2.50	0.46
1:A:364:TYR:CB	1:A:1214:ARG:HG2	2.45	0.46
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.97	0.46
2:K:366:THR:O	2:K:373:ILE:HA	2.16	0.46
5:J:406:PHE:CE1	5:J:408:LEU:HB2	2.50	0.46
6:E:53:VAL:CG1	6:E:57:ALA:HB3	2.46	0.46
8:C:139:ILE:HD12	8:C:252:LEU:HD22	1.96	0.46
27:D:699:ARG:HH21	27:D:875:ALA:HB3	1.81	0.46
27:D:1213:ARG:HG3	27:D:1313:LEU:HB3	1.96	0.46
27:D:1629:LEU:HD21	27:D:1652:VAL:CG2	2.45	0.46
22:Q:43:VAL:CG1	22:Q:85:ILE:HD12	2.44	0.46
29:H:677:U:H2'	29:H:678:U:C6	2.50	0.46
32:1:523:LEU:HD23	32:1:526:LEU:HD12	1.97	0.46
34:3:411:ASP:OD2	34:3:472:LEU:HG	2.14	0.46
34:3:952:ARG:HA	34:3:972:LYS:O	2.14	0.46
34:3:1306:GLU:HG3	36:5:78:ARG:NH1	2.30	0.46
39:Y:160:LYS:HB2	39:Y:160:LYS:NZ	2.30	0.46
3:L:232:LEU:HD23	3:L:334:LYS:HG3	1.97	0.46
8:C:195:GLY:C	8:C:545:LEU:HD13	2.39	0.46
8:C:197:THR:HG23	8:C:545:LEU:HD12	1.97	0.46
8:C:468:LEU:HA	8:C:491:GLY:HA3	1.97	0.46
8:C:576:THR:HG21	8:C:591:PHE:HB3	1.96	0.46
28:G:494:G:H21	43:v:83:ARG:NH1	2.13	0.46
32:1:232:LEU:HD12	32:1:233:GLY:N	2.30	0.46
38:X:124:GLU:O	38:X:128:ARG:HG2	2.16	0.46
42:w:158:ARG:HB2	42:w:158:ARG:NH1	2.25	0.46
43:v:35:SER:O	43:v:38:GLU:HG2	2.16	0.46
1:A:1545:ASP:HA	1:A:1548:GLN:HG2	1.97	0.46
2:K:180:ALA:O	2:K:192:THR:HA	2.14	0.46
4:N:219:THR:HG22	4:N:221:GLU:HG2	1.97	0.46
6:E:85:PHE:CD1	6:E:90:HIS:HA	2.50	0.46
16:F:83:A:H1'	16:F:84:C:H5'	1.97	0.46
27:D:766:ILE:HD12	27:D:769:LYS:HZ1	1.80	0.46
27:D:986:LEU:HD21	27:D:1015:MET:HG2	1.97	0.46
20:S:23:LEU:HD23	20:S:24:THR:N	2.30	0.46
32:1:894:HIS:HA	32:1:897:MET:HE3	1.97	0.46
33:2:252:PHE:O	33:2:256:ALA:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:88:ARG:HH12	34:3:144:TRP:N	2.14	0.46
34:3:1046:GLY:O	34:3:1073:LYS:HA	2.16	0.46
34:3:1171:ILE:O	34:3:1174:GLN:N	2.48	0.46
36:5:41:ARG:HH12	36:5:83:LYS:HZ2	1.62	0.46
1:A:774:ILE:HG23	1:A:777:LYS:HD3	1.97	0.46
2:K:290:ARG:HB3	2:K:292:TRP:NE1	2.29	0.46
18:B:114:G:C2	18:B:115:G:C4	3.03	0.46
27:D:633:ILE:HG21	27:D:636:ILE:HD13	1.98	0.46
27:D:1351:ILE:HB	27:D:1374:THR:HG21	1.97	0.46
27:D:1459:TRP:HE1	27:D:1762:ILE:HD11	1.81	0.46
27:D:1471:MET:HE1	27:D:1495:MET:HG3	1.96	0.46
27:D:1902:LEU:HB3	27:D:1928:LEU:HD12	1.98	0.46
28:G:490:A:H2'	28:G:491:C:C6	2.51	0.46
29:H:112:A:N7	23:n:63:ARG:CZ	2.78	0.46
29:H:120:G:H4'	29:H:121:C:O4'	2.15	0.46
29:H:680:C:H2'	29:H:681:C:C6	2.49	0.46
29:H:690:U:H2'	29:H:691:G:H8	1.81	0.46
20:l:30:ARG:C	20:l:47:VAL:HG23	2.40	0.46
32:1:565:LEU:O	32:1:569:PHE:CB	2.63	0.46
32:1:624:CYS:O	32:1:628:ILE:HG12	2.15	0.46
32:1:935:TRP:CZ3	37:6:22:GLY:HA3	2.51	0.46
33:2:163:ILE:O	33:2:169:VAL:HG21	2.14	0.46
34:3:186:ARG:HB2	34:3:207:VAL:HG23	1.97	0.46
34:3:678:LYS:H	34:3:694:ALA:HB3	1.80	0.46
34:3:1116:ARG:HH12	34:3:1189:LEU:HD13	1.79	0.46
1:A:354:PRO:O	1:A:355:LEU:HB3	2.16	0.46
1:A:1014:LYS:HD3	1:A:1144:PHE:CE1	2.51	0.46
3:L:131:ILE:HD11	3:L:175:LEU:HD11	1.98	0.46
5:J:408:LEU:O	5:J:415:ILE:N	2.48	0.46
17:I:90:C:N3	22:Q:34:PRO:CD	2.78	0.46
27:D:809:THR:HA	27:D:1092:PHE:CG	2.50	0.46
27:D:1194:ASP:HB3	27:D:1198:ARG:NH1	2.30	0.46
27:D:1496:ILE:HD12	27:D:1524:TRP:CZ3	2.50	0.46
21:P:33:GLN:O	21:P:45:LEU:HA	2.16	0.46
22:Q:18:GLU:O	22:Q:93:ARG:HB3	2.15	0.46
28:G:488:A:H2'	28:G:489:A:H8	1.80	0.46
29:H:544:G:H2'	29:H:545:G:H8	1.81	0.46
29:H:559:G:H2'	29:H:560:G:H8	1.81	0.46
29:H:567:U:H2'	29:H:568:U:C6	2.50	0.46
29:H:669:U:H2'	29:H:670:U:C6	2.49	0.46
29:H:691:G:H2'	29:H:692:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:1098:C:HO2'	29:H:1099:G:C5'	2.28	0.46
34:3:68:GLN:HE21	34:3:1222:GLN:HG2	1.79	0.46
34:3:1118:VAL:HG12	34:3:1139:TRP:HZ2	1.81	0.46
34:3:1124:LEU:HB2	34:3:1130:ILE:CD1	2.45	0.46
38:X:32:TYR:CE1	38:X:78:LYS:HD3	2.50	0.46
41:u:169:ILE:O	41:u:246:LYS:HD2	2.15	0.46
41:u:171:THR:HG22	41:u:174:GLU:CD	2.40	0.46
42:w:99:THR:HG21	42:w:122:LEU:HD22	1.97	0.46
1:A:563:ASP:OD1	1:A:564:TRP:N	2.49	0.46
1:A:928:ARG:NH2	4:N:145:THR:OG1	2.44	0.46
1:A:2319:LYS:HG3	1:A:2320:ASP:H	1.79	0.46
7:M:51:PHE:CE1	7:M:53:ILE:HD11	2.51	0.46
8:C:287:LYS:NZ	8:C:895:ALA:O	2.39	0.46
8:C:292:ILE:HA	8:C:295:ILE:HG12	1.97	0.46
8:C:331:TYR:CE1	8:C:404:PHE:HD1	2.34	0.46
16:F:15:A:H2'	16:F:16:C:H6	1.81	0.46
27:D:1085:SER:OG	27:D:1140:TRP:NE1	2.30	0.46
27:D:1631:ALA:HB3	27:D:1632:PRO:HD3	1.98	0.46
29:H:562:A:H2'	29:H:563:G:H8	1.81	0.46
29:H:688:A:H2'	29:H:689:G:H8	1.81	0.46
29:H:1152:U:H2'	29:H:1153:C:H6	1.80	0.46
32:1:327:TRP:CZ2	32:1:369:PRO:HG2	2.49	0.46
32:1:565:LEU:O	32:1:569:PHE:HB2	2.16	0.46
32:1:806:THR:HB	33:2:211:THR:HG21	1.98	0.46
33:2:271:TYR:CZ	33:2:274:ARG:HB2	2.51	0.46
34:3:71:PHE:HD1	34:3:97:THR:CG2	2.28	0.46
1:A:318:LEU:HD23	1:A:501:LEU:HD23	1.98	0.46
1:A:616:GLY:O	1:A:619:PHE:HB3	2.15	0.46
2:K:322:VAL:HB	2:K:336:ILE:HD11	1.98	0.46
4:N:778:ILE:HG23	4:N:794:PHE:HE1	1.81	0.46
8:C:605:ILE:HD11	8:C:673:PRO:HA	1.98	0.46
28:G:481:A:H61	35:4:86:VAL:HB	1.80	0.46
24:i:86:ASN:ND2	25:j:32:LYS:NZ	2.64	0.46
32:1:195:PHE:HB2	32:1:200:ILE:HD11	1.98	0.46
32:1:286:ILE:HG23	32:1:332:THR:OG1	2.16	0.46
32:1:439:MET:HA	32:1:442:ILE:HD12	1.98	0.46
32:1:698:ARG:HG3	32:1:699:LYS:N	2.31	0.46
34:3:78:HIS:O	34:3:146:THR:HG22	2.16	0.46
38:X:82:GLN:HB3	39:Y:168:GLN:NE2	2.31	0.46
39:Y:223:ARG:HG3	39:Y:242:GLU:OE2	2.16	0.46
42:w:108:SER:O	42:w:112:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:64:VAL:HG12	2:K:65:GLU:N	2.31	0.46
2:K:395:ILE:HD11	7:M:123:THR:HG23	1.98	0.46
8:C:272:ARG:HG3	8:C:276:ASP:OD2	2.16	0.46
8:C:471:HIS:HB2	8:C:592:PHE:CE2	2.51	0.46
8:C:772:ASN:ND2	8:C:816:VAL:H	2.14	0.46
19:O:212:VAL:HG23	19:O:213:SER:H	1.80	0.46
27:D:648:GLU:CD	27:D:912:PHE:CD1	2.94	0.46
27:D:673:THR:OG1	27:D:694:PHE:O	2.28	0.46
27:D:1217:ARG:HH12	22:Q:146:LEU:HD23	1.80	0.46
27:D:1564:LEU:HD21	27:D:1597:ALA:HB1	1.98	0.46
27:D:1587:SER:HB3	27:D:1895:ARG:CZ	2.45	0.46
26:V:15:ILE:HG22	26:V:73:ALA:HA	1.97	0.46
29:H:1139:G:C6	29:H:1140:U:C4	3.04	0.46
25:j:16:LYS:N	25:j:17:PRO:CD	2.79	0.46
32:1:484:PHE:HA	32:1:488:TRP:CD1	2.48	0.46
32:1:641:ASN:HD21	32:1:673:MET:HE1	1.81	0.46
34:3:732:ARG:NH2	34:3:737:GLY:O	2.49	0.46
41:u:12:GLU:O	41:u:16:ILE:HG13	2.15	0.46
42:w:106:ASP:O	42:w:107:LYS:HB2	2.16	0.46
1:A:248:PRO:HD3	1:A:595:TYR:CE1	2.50	0.46
1:A:460:PRO:HD3	8:C:354:TYR:OH	2.16	0.46
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.30	0.46
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.49	0.46
1:A:2050:THR:O	1:A:2053:SER:OG	2.31	0.46
2:K:291:LEU:HB3	2:K:301:LEU:HB3	1.97	0.46
3:L:289:ASP:HB3	3:L:293:LYS:HE3	1.98	0.46
3:L:398:GLN:CD	3:L:419:GLN:HG3	2.41	0.46
8:C:315:SER:HB3	8:C:320:PHE:CE2	2.51	0.46
16:F:26:A:H2'	16:F:27:U:H6	1.80	0.46
17:I:99:G:H4'	27:D:1186:GLU:CB	2.23	0.46
27:D:1890:GLU:C	22:Q:143:ARG:HE	2.23	0.46
27:D:1999:HIS:ND1	27:D:1999:HIS:O	2.49	0.46
27:D:2055:TYR:CE2	27:D:2158:PHE:CD2	3.04	0.46
22:Q:46:THR:OG1	22:Q:79:ILE:HG12	2.16	0.46
29:H:545:G:H2'	29:H:546:U:C6	2.50	0.46
29:H:553:G:H2'	29:H:554:C:C6	2.50	0.46
29:H:673:U:H2'	29:H:674:G:H8	1.81	0.46
29:H:1165:C:C2	29:H:1166:G:N7	2.83	0.46
22:m:6:PHE:CZ	22:m:10:LEU:HD11	2.51	0.46
23:n:90:PHE:CD2	41:u:194:LYS:C	2.81	0.46
32:1:430:TYR:HB3	32:1:434:TYR:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:156:ASN:ND2	34:3:178:PRO:HA	2.29	0.46
34:3:369:ILE:HG23	34:3:419:LEU:HB2	1.98	0.46
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.51	0.45
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.51	0.45
1:A:1050:LEU:CD2	1:A:1248:VAL:HG22	2.44	0.45
1:A:1733:TRP:CZ2	1:A:1772:GLY:HA3	2.51	0.45
2:K:393:ARG:HB2	5:J:429:GLU:HG2	1.98	0.45
7:M:113:GLN:NE2	16:F:77:G:H4'	2.29	0.45
8:C:331:TYR:OH	8:C:428:ILE:O	2.34	0.45
8:C:613:ARG:NH1	8:C:614:GLU:OE2	2.49	0.45
16:F:15:A:H2'	16:F:16:C:C6	2.51	0.45
16:F:92:C:H2'	16:F:93:A:C8	2.45	0.45
17:I:78:A:N1	27:D:1110:ARG:NE	2.64	0.45
18:B:22:G:O6	18:B:149:U:O4	2.34	0.45
18:B:75:A:N6	18:B:77:A:N1	2.65	0.45
18:B:135:G:N1	18:B:136:G:N2	2.64	0.45
27:D:929:ILE:HD13	27:D:935:ALA:HA	1.99	0.45
27:D:1371:GLY:O	27:D:1376:LYS:NZ	2.40	0.45
27:D:1888:GLU:HB3	27:D:1953:LYS:HG2	1.97	0.45
28:G:502:C:OP2	32:1:775:ARG:NH1	2.31	0.45
29:H:555:A:H2'	29:H:556:A:H8	1.82	0.45
32:1:760:HIS:HB3	33:2:240:LEU:HD12	1.97	0.45
32:1:866:LEU:HD21	36:5:79:LEU:HD21	1.98	0.45
34:3:1097:PHE:CE1	34:3:1108:PRO:HB3	2.48	0.45
34:3:1356:VAL:HA	34:3:1360:TYR:CD2	2.51	0.45
39:Y:208:SER:CB	39:Y:214:LEU:HD12	2.45	0.45
1:A:2199:VAL:HG23	1:A:2200:LYS:HG3	1.98	0.45
8:C:866:ILE:HG23	8:C:918:LEU:HD21	1.98	0.45
27:D:610:GLU:OE2	27:D:646:VAL:HG21	2.17	0.45
27:D:765:ASN:HB2	27:D:768:HIS:CD2	2.51	0.45
27:D:1482:GLY:HA3	22:Q:143:ARG:O	2.15	0.45
27:D:1677:THR:O	27:D:1710:ALA:HA	2.15	0.45
27:D:1722:ILE:HG22	27:D:1724:THR:OG1	2.16	0.45
27:D:1757:GLU:CB	27:D:1763:ILE:HD12	2.46	0.45
27:D:1772:TRP:CZ3	27:D:1773:PHE:CZ	3.03	0.45
23:R:66:ASN:OD1	23:R:98:GLY:N	2.50	0.45
20:S:22:GLU:HG2	20:S:70:LYS:HD2	1.97	0.45
29:H:548:G:H2'	29:H:549:C:C6	2.50	0.45
29:H:564:U:H2'	29:H:565:U:C6	2.50	0.45
29:H:570:G:H2'	29:H:571:A:H8	1.82	0.45
29:H:670:U:H2'	29:H:671:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:685:U:H2'	29:H:686:G:H8	1.81	0.45
20:l:9:LYS:CB	20:l:83:LEU:CD1	2.90	0.45
32:1:221:MET:O	32:1:224:THR:OG1	2.24	0.45
32:1:843:GLU:OE1	32:1:879:HIS:NE2	2.49	0.45
34:3:153:ASP:O	34:3:154:SER:OG	2.21	0.45
34:3:333:ASN:O	34:3:350:ILE:HG22	2.17	0.45
38:X:11:GLU:HG2	38:X:16:ILE:CG2	2.46	0.45
41:u:233:LEU:HD12	41:u:233:LEU:HA	1.82	0.45
43:v:165:GLU:O	43:v:165:GLU:HG2	2.16	0.45
1:A:2162:LEU:HD23	1:A:2194:ILE:O	2.16	0.45
4:N:771:ALA:HB3	4:N:806:ARG:HH21	1.81	0.45
5:J:443:LYS:HG2	5:J:444:VAL:N	2.30	0.45
6:E:112:GLU:HG2	6:E:135:TYR:CE2	2.51	0.45
8:C:869:HIS:CD2	8:C:925:LEU:HB3	2.51	0.45
18:B:94:C:H3'	18:B:95:C:H4'	1.98	0.45
27:D:1165:VAL:HG13	27:D:1166:PRO:HD2	1.98	0.45
27:D:1625:THR:OG1	27:D:1648:ASP:HB2	2.17	0.45
27:D:2011:ILE:CD1	27:D:2030:ILE:HD11	2.46	0.45
21:P:21:ARG:HB2	21:P:98:GLU:OE1	2.16	0.45
20:S:20:SER:OG	20:S:73:VAL:HB	2.16	0.45
29:H:554:C:H2'	29:H:555:A:H8	1.82	0.45
29:H:672:U:H2'	29:H:673:U:C6	2.50	0.45
29:H:694:C:H2'	29:H:695:U:C6	2.50	0.45
32:1:489:VAL:CG1	38:X:26:GLU:CG	2.94	0.45
34:3:294:PHE:CE2	34:3:365:ILE:HB	2.51	0.45
34:3:932:PHE:HA	34:3:984:ILE:HD11	1.98	0.45
34:3:977:ILE:HG12	34:3:1004:LEU:HD22	1.99	0.45
36:5:37:VAL:C	36:5:38:ARG:HG2	2.42	0.45
41:u:264:PHE:CE1	41:u:268:TYR:CD2	3.04	0.45
42:w:205:LYS:CB	43:v:212:GLU:HB3	2.46	0.45
1:A:620:HIS:HB3	1:A:669:TYR:CD2	2.51	0.45
1:A:1014:LYS:HD2	1:A:1014:LYS:HA	1.58	0.45
1:A:1049:LEU:HB2	1:A:1249:SER:OG	2.16	0.45
1:A:1105:ARG:HD2	1:A:1517:TYR:CE1	2.51	0.45
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.52	0.45
1:A:2014:ALA:HB3	1:A:2055:MET:HE3	1.99	0.45
8:C:251:GLN:HE22	8:C:254:LYS:HD3	1.81	0.45
8:C:769:TYR:HA	8:C:800:TYR:HE1	1.80	0.45
16:F:16:C:O2'	16:F:17:U:O5'	2.35	0.45
23:R:38:MET:HG3	23:R:39:VAL:N	2.30	0.45
29:H:568:U:H2'	29:H:569:C:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:683:U:H2'	29:H:684:U:C6	2.50	0.45
29:H:692:U:H2'	29:H:693:C:C6	2.50	0.45
32:1:591:ASP:OD1	32:1:592:ILE:HD12	2.17	0.45
32:1:835:ILE:C	32:1:837:PHE:H	2.24	0.45
33:2:166:THR:HG22	33:2:167:LYS:H	1.82	0.45
41:u:60:TYR:CE2	41:u:61:LYS:HG2	2.51	0.45
41:u:175:GLN:HB2	41:u:178:GLU:HB3	1.99	0.45
41:u:504:LEU:HB2	41:u:518:LYS:HG2	1.97	0.45
1:A:234:PHE:HD2	1:A:699:PRO:HB2	1.81	0.45
1:A:454:LEU:HD11	8:C:340:LYS:HG3	1.98	0.45
1:A:537:THR:HG21	18:B:84:A:H62	1.82	0.45
1:A:1317:ARG:HE	1:A:1366:ARG:NH1	2.15	0.45
18:B:75:A:N6	18:B:77:A:C6	2.85	0.45
27:D:1436:LEU:HD22	27:D:1462:ARG:NH2	2.31	0.45
27:D:1453:GLU:OE2	27:D:1494:ARG:NH2	2.42	0.45
21:P:28:ARG:NH1	20:S:22:GLU:OE2	2.48	0.45
26:V:47:ASN:OD1	26:V:51:PRO:HD2	2.17	0.45
26:V:59:LEU:O	26:V:60:GLN:HG2	2.16	0.45
28:G:520:G:C4	38:X:34:TYR:CZ	3.03	0.45
29:H:1139:G:H2'	29:H:1140:U:C5	2.51	0.45
24:i:30:TRP:CE2	24:i:89:LEU:HD22	2.51	0.45
32:1:835:ILE:O	32:1:838:ILE:N	2.32	0.45
34:3:641:GLN:NE2	34:3:705:LEU:HD23	2.31	0.45
34:3:1198:ILE:O	34:3:1221:LEU:N	2.50	0.45
35:4:171:GLN:O	35:4:178:ILE:HG12	2.17	0.45
42:w:99:THR:O	42:w:103:TYR:HB2	2.17	0.45
1:A:221:TRP:CB	1:A:318:LEU:HD11	2.46	0.45
1:A:283:SER:O	1:A:285:PRO:HD3	2.17	0.45
1:A:2183:TYR:CE1	1:A:2219:LYS:HG3	2.51	0.45
1:A:2189:LEU:HD11	1:A:2347:GLY:HA3	1.99	0.45
4:N:256:LYS:HG2	4:N:257:PHE:N	2.32	0.45
4:N:760:VAL:O	4:N:764:LEU:HB3	2.16	0.45
8:C:183:GLN:HE21	8:C:657:TYR:HB3	1.80	0.45
27:D:486:TRP:NE1	27:D:487:CYS:SG	2.90	0.45
27:D:1880:LEU:HD21	27:D:1931:GLN:HE21	1.81	0.45
27:D:2101:LEU:O	27:D:2114:ILE:HA	2.16	0.45
24:T:80:ILE:HG23	25:U:80:TYR:HB2	1.98	0.45
29:H:119:G:C8	23:n:99:ASP:OD2	2.69	0.45
34:3:487:SER:O	34:3:1200:THR:HG21	2.16	0.45
34:3:600:ILE:HG13	34:3:608:ARG:O	2.16	0.45
34:3:1302:ARG:NH2	34:3:1307:TYR:HA	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:4:13:VAL:HG21	35:4:55:ILE:HD12	1.98	0.45
37:6:47:SER:O	37:6:51:GLU:HG2	2.17	0.45
38:X:89:VAL:HG21	38:X:106:HIS:CD2	2.51	0.45
1:A:140:ARG:NH2	1:A:252:GLU:HB2	2.29	0.45
1:A:364:TYR:HB2	1:A:1214:ARG:HG2	1.99	0.45
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.99	0.45
1:A:660:ILE:HD12	1:A:711:TRP:CE2	2.52	0.45
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.45
1:A:2003:THR:HA	1:A:2006:SER:OG	2.16	0.45
4:N:124:ASP:OD1	4:N:125:ALA:N	2.48	0.45
8:C:193:LEU:HD23	8:C:224:GLU:HB3	1.98	0.45
16:F:96:G:H2'	16:F:97:A:C8	2.51	0.45
18:B:73:U:H2'	18:B:74:U:C6	2.51	0.45
27:D:452:SER:HB2	27:D:466:PRO:HG3	1.99	0.45
27:D:766:ILE:HD12	27:D:769:LYS:NZ	2.31	0.45
27:D:1933:TYR:OH	27:D:2091:TYR:HB2	2.16	0.45
22:Q:107:LEU:HD12	23:R:59:LYS:HE3	1.99	0.45
29:H:112:A:N7	23:n:63:ARG:NH1	2.64	0.45
29:H:546:U:H2'	29:H:547:G:H8	1.81	0.45
29:H:549:C:H2'	29:H:550:G:H8	1.81	0.45
29:H:681:C:H2'	29:H:682:U:C6	2.50	0.45
32:1:830:MET:C	32:1:832:LYS:H	2.15	0.45
32:1:835:ILE:HG23	32:1:864:LEU:HD21	1.99	0.45
41:u:4:LEU:HD21	42:w:146:TYR:OH	2.16	0.45
1:A:796:ASN:ND2	1:A:858:LYS:HG2	2.26	0.45
1:A:1575:TRP:N	3:L:391:MET:O	2.28	0.45
1:A:2192:LYS:HE3	1:A:2379:PRO:HG2	1.97	0.45
4:N:277:ILE:H	4:N:277:ILE:HD12	1.82	0.45
4:N:815:PHE:HB2	4:N:824:SER:HB3	1.99	0.45
6:E:87:HIS:C	6:E:89:LYS:H	2.24	0.45
8:C:452:LYS:HZ2	8:C:487:ARG:HH12	1.65	0.45
8:C:778:THR:OG1	8:C:780:PRO:HD2	2.16	0.45
17:I:33:A:H2'	17:I:34:G:O4'	2.17	0.45
18:B:65:U:H2'	18:B:66:A:H8	1.81	0.45
18:B:83:C:H4'	18:B:84:A:OP1	2.16	0.45
18:B:164:C:OP2	18:B:165:A:OP1	2.34	0.45
27:D:820:PHE:HB2	27:D:825:LEU:HD12	1.99	0.45
27:D:1163:SER:HB2	27:D:1184:ARG:HH22	1.82	0.45
22:Q:9:LYS:HD3	22:Q:106:LEU:HD22	1.99	0.45
22:Q:16:THR:HA	22:Q:25:VAL:O	2.16	0.45
29:H:563:G:H2'	29:H:564:U:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:569:C:H2'	29:H:570:G:H8	1.81	0.45
29:H:674:G:H2'	29:H:675:A:H8	1.81	0.45
32:1:346:ILE:O	32:1:349:LEU:HG	2.16	0.45
32:1:462:GLN:HE21	32:1:504:TYR:HE2	1.63	0.45
34:3:1299:ILE:C	34:3:1300:LEU:HD12	2.42	0.45
39:Y:167:VAL:O	39:Y:171:GLY:HA2	2.17	0.45
39:Y:220:PRO:HG3	39:Y:236:HIS:CE1	2.51	0.45
41:u:188:LEU:O	41:u:192:VAL:HG23	2.16	0.45
1:A:218:SER:HA	1:A:318:LEU:HD13	1.99	0.45
1:A:700:GLY:O	1:A:701:CYS:HB3	2.17	0.45
1:A:984:VAL:HG12	1:A:985:ASP:H	1.82	0.45
1:A:1126:LEU:HD13	1:A:1134:LEU:HD12	1.98	0.45
1:A:1345:TYR:HD2	1:A:1346:PHE:CE1	2.34	0.45
1:A:1699:ALA:HB1	1:A:1733:TRP:HB2	1.98	0.45
1:A:1715:SER:O	1:A:1787:TYR:HA	2.16	0.45
2:K:128:SER:CB	2:K:337:ARG:HH21	2.29	0.45
2:K:373:ILE:HB	2:K:389:ILE:HB	1.99	0.45
4:N:789:LEU:O	4:N:792:THR:OG1	2.35	0.45
5:J:347:LEU:HD23	5:J:371:ARG:NH2	2.31	0.45
8:C:171:GLY:HA3	8:C:422:LYS:NZ	2.32	0.45
8:C:866:ILE:HA	8:C:927:MET:O	2.16	0.45
8:C:876:VAL:HA	8:C:879:LEU:HD12	1.99	0.45
18:B:10:U:H1'	18:B:156:G:H22	1.82	0.45
27:D:508:HIS:O	27:D:512:GLU:HG3	2.17	0.45
27:D:1014:SER:OG	27:D:1039:GLU:HB3	2.16	0.45
22:Q:44:LYS:HB2	22:Q:79:ILE:CG2	2.46	0.45
29:H:558:A:H2'	29:H:559:G:H8	1.81	0.45
29:H:675:A:H2'	29:H:676:U:C6	2.50	0.45
24:i:30:TRP:CD2	24:i:89:LEU:HD22	2.52	0.45
34:3:162:ILE:HG22	34:3:171:LEU:CD1	2.46	0.45
34:3:582:LYS:N	34:3:601:GLN:OE1	2.50	0.45
41:u:219:THR:HG22	41:u:219:THR:O	2.17	0.45
1:A:416:GLU:HG2	1:A:418:ASP:H	1.82	0.45
1:A:535:HIS:NE2	18:B:105:A:OP1	2.43	0.45
1:A:1098:VAL:HG23	3:L:276:GLU:OE1	2.17	0.45
1:A:1833:PRO:HD3	3:L:383:HIS:CE1	2.52	0.45
1:A:2310:GLU:OE1	1:A:2333:PHE:HZ	1.94	0.45
1:A:2398:LEU:CD2	27:D:1060:LYS:HB2	2.28	0.45
3:L:124:PHE:CD2	3:L:127:LEU:HB2	2.51	0.45
4:N:244:TRP:CE3	4:N:267:GLY:HA3	2.52	0.45
4:N:762:GLN:O	4:N:765:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:95:PHE:HB3	6:E:137:TYR:HE2	1.80	0.45
6:E:103:LEU:HD11	6:E:105:PHE:CE2	2.52	0.45
8:C:681:CYS:HA	8:C:855:PRO:HA	1.99	0.45
8:C:856:ILE:HA	8:C:944:VAL:CG1	2.47	0.45
17:I:143:A:N7	25:U:48:TYR:CE2	2.85	0.45
18:B:93:G:H5'	18:B:94:C:OP2	2.17	0.45
27:D:1403:GLU:HG2	27:D:1642:LYS:NZ	2.32	0.45
27:D:1411:ASP:O	27:D:1415:ARG:HG2	2.17	0.45
27:D:2063:LEU:HD13	27:D:2160:ILE:HB	1.99	0.45
23:R:48:LEU:HD11	23:R:54:ILE:HD12	1.98	0.45
29:H:547:G:H2'	29:H:548:G:H8	1.81	0.45
29:H:550:G:H2'	29:H:551:C:C6	2.50	0.45
29:H:556:A:H2'	29:H:557:G:H8	1.81	0.45
29:H:1150:U:C6	29:H:1150:U:OP2	2.70	0.45
34:3:119:ASN:HB2	34:3:1325:ASN:HD21	1.82	0.45
34:3:854:ASN:HB3	34:3:857:VAL:H	1.82	0.45
34:3:1294:GLU:HG3	36:5:41:ARG:HG2	1.98	0.45
38:X:16:ILE:CG2	38:X:17:LEU:N	2.80	0.45
38:X:57:PRO:HG2	39:Y:231:ARG:NH2	2.27	0.45
41:u:34:HIS:CD2	41:u:76:GLN:HE22	2.35	0.45
41:u:440:HIS:CE1	41:u:446:HIS:HB2	2.52	0.45
43:v:178:PRO:HG2	43:v:250:TYR:CD1	2.52	0.45
43:v:240:CYS:HB2	43:v:253:GLN:C	2.42	0.45
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.22	0.44
1:A:1657:ILE:HG12	1:A:1811:ALA:HB1	1.99	0.44
3:L:447:GLU:O	3:L:450:GLN:HG2	2.17	0.44
4:N:241:PRO:HA	4:N:244:TRP:HD1	1.81	0.44
5:J:249:ARG:HD3	17:I:10:C:OP1	2.17	0.44
7:M:54:MET:HB2	7:M:80:PHE:CD1	2.52	0.44
8:C:402:SER:O	8:C:405:ARG:NH1	2.50	0.44
18:B:79:C:N4	18:B:114:G:O6	2.50	0.44
18:B:162:G:OP1	18:B:163:C:C6	2.70	0.44
18:B:166:U:C6	18:B:166:U:OP1	2.70	0.44
27:D:981:LEU:HD23	27:D:986:LEU:HD12	1.99	0.44
21:P:39:LYS:HD2	21:P:39:LYS:HA	1.48	0.44
23:R:44:VAL:O	23:R:55:ILE:HD12	2.17	0.44
24:T:29:ILE:HD11	24:T:87:ILE:HA	1.98	0.44
29:H:676:U:H2'	29:H:677:U:C6	2.50	0.44
20:l:39:SER:O	20:l:41:ASN:N	2.48	0.44
32:1:244:LEU:O	32:1:248:ALA:HB2	2.18	0.44
32:1:873:HIS:C	32:1:875:ASP:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:508:ASN:ND2	34:3:924:PHE:O	2.48	0.44
34:3:528:PRO:HG2	34:3:554:PHE:CZ	2.51	0.44
41:u:169:ILE:HG22	41:u:246:LYS:CD	2.47	0.44
1:A:208:VAL:HB	1:A:213:TYR:HB2	1.99	0.44
1:A:209:ILE:HG21	1:A:303:PHE:CE2	2.53	0.44
1:A:1774:MET:O	1:A:1786:ALA:HA	2.16	0.44
1:A:1794:LEU:O	1:A:1798:ILE:N	2.36	0.44
1:A:2010:LEU:HD21	1:A:2083:ILE:HD13	1.98	0.44
2:K:393:ARG:O	2:K:416:ASP:HB2	2.16	0.44
3:L:343:LYS:NZ	17:I:28:C:OP1	2.50	0.44
8:C:861:ILE:HG23	8:C:906:VAL:O	2.17	0.44
17:I:76:A:C8	27:D:1107:ARG:CZ	3.00	0.44
27:D:491:PHE:HD1	27:D:491:PHE:N	2.16	0.44
27:D:529:ASN:O	27:D:533:LEU:HG	2.17	0.44
27:D:676:ASN:HD22	27:D:907:PRO:HB3	1.82	0.44
27:D:1218:PHE:N	27:D:1218:PHE:CD1	2.85	0.44
27:D:1610:LEU:HD23	27:D:1612:VAL:HB	1.99	0.44
24:T:34:GLN:O	26:V:23:ARG:NH2	2.51	0.44
28:G:489:A:H2'	28:G:490:A:C8	2.52	0.44
32:1:567:ILE:O	32:1:570:GLN:HG2	2.17	0.44
34:3:61:TYR:CE2	34:3:63:LEU:HD11	2.52	0.44
34:3:177:GLN:HE22	36:5:44:ARG:HD3	1.83	0.44
34:3:523:ILE:HD11	34:3:873:ILE:HG13	1.98	0.44
34:3:564:ASP:OD1	34:3:565:ASN:N	2.48	0.44
41:u:172:ARG:HG3	41:u:361:TYR:HB2	1.99	0.44
41:u:178:GLU:O	41:u:334:ARG:HD2	2.17	0.44
43:v:177:PRO:HB3	43:v:243:TRP:CD1	2.53	0.44
1:A:326:ASN:ND2	1:A:407:VAL:HG22	2.32	0.44
1:A:802:PRO:O	1:A:804:MET:HG2	2.17	0.44
1:A:1336:ASN:HD21	1:A:1399:MET:HA	1.82	0.44
1:A:1859:ARG:NH2	19:O:161:ILE:HD13	2.32	0.44
1:A:2241:ILE:HD12	1:A:2284:LYS:HD3	1.98	0.44
1:A:2398:LEU:CD1	27:D:1060:LYS:HZ2	2.26	0.44
2:K:182:SER:HA	2:K:444:ASP:OD2	2.18	0.44
2:K:220:LYS:O	2:K:239:GLU:N	2.51	0.44
2:K:393:ARG:NH1	5:J:427:THR:O	2.50	0.44
3:L:120:TYR:OH	3:L:141:ILE:HG23	2.18	0.44
3:L:143:ILE:HD11	3:L:164:LYS:HD2	1.99	0.44
4:N:286:GLU:CG	4:N:287:SER:H	2.30	0.44
8:C:507:SER:HB2	8:C:591:PHE:HB2	2.00	0.44
8:C:697:ARG:HH22	8:C:848:VAL:HG12	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:B:97:U:H2'	18:B:98:U:H6	1.82	0.44
27:D:602:THR:HG22	27:D:603:GLN:N	2.33	0.44
27:D:1120:GLY:HA2	27:D:1251:ILE:HB	1.98	0.44
27:D:1537:PRO:O	27:D:1540:ARG:NH1	2.50	0.44
23:R:30:PRO:HA	25:U:52:GLN:HB2	1.99	0.44
29:H:51:C:H2'	29:H:52:A:H8	1.83	0.44
29:H:149:A:H2'	29:H:150:G:H8	1.82	0.44
29:H:557:G:H2'	29:H:558:A:H8	1.82	0.44
29:H:560:G:H2'	29:H:561:A:H8	1.82	0.44
29:H:561:A:H2'	29:H:562:A:H8	1.81	0.44
29:H:687:A:H2'	29:H:688:A:H8	1.82	0.44
21:h:20:LEU:O	21:h:31:ILE:HA	2.16	0.44
34:3:839:ARG:HH22	34:3:1361:MET:C	2.25	0.44
34:3:1085:LEU:HB2	34:3:1097:PHE:HB2	1.99	0.44
41:u:117:GLN:HB3	42:w:113:MET:CE	2.47	0.44
42:w:139:VAL:HG23	42:w:140:ALA:N	2.33	0.44
1:A:372:ARG:O	8:C:973:ARG:NH2	2.50	0.44
1:A:553:ASN:OD1	1:A:554:THR:N	2.47	0.44
1:A:632:ILE:O	1:A:635:THR:OG1	2.26	0.44
1:A:1393:GLU:HG3	3:L:391:MET:SD	2.57	0.44
4:N:290:HIS:O	4:N:294:THR:HG23	2.18	0.44
8:C:318:LEU:HB3	8:C:425:LEU:HD12	1.98	0.44
8:C:508:GLU:OE2	8:C:594:PRO:HG2	2.18	0.44
18:B:10:U:H1'	18:B:156:G:N2	2.33	0.44
19:O:194:LEU:HD13	19:O:197:ARG:HH11	1.78	0.44
27:D:499:LEU:HD23	27:D:503:GLN:HB3	2.00	0.44
27:D:644:GLY:N	27:D:645:PRO:HD2	2.33	0.44
27:D:845:VAL:HG21	27:D:874:ARG:O	2.16	0.44
27:D:1377:THR:O	27:D:1381:GLU:HG3	2.17	0.44
21:P:89:GLY:O	21:P:92:ILE:HG22	2.17	0.44
34:3:75:CYS:SG	34:3:94:CYS:HB3	2.57	0.44
34:3:704:SER:HB3	34:3:716:ILE:HD11	2.00	0.44
35:4:119:ILE:O	35:4:149:LYS:NZ	2.38	0.44
38:X:110:ARG:HE	38:X:110:ARG:HB3	1.61	0.44
1:A:342:LEU:HD22	1:A:392:ASN:HD21	1.83	0.44
1:A:2318:ASN:HB3	1:A:2322:MET:HG3	1.99	0.44
3:L:113:HIS:CE1	3:L:117:ILE:HD11	2.52	0.44
8:C:218:HIS:HB3	8:C:221:PHE:HD2	1.83	0.44
8:C:251:GLN:NE2	8:C:254:LYS:HD3	2.32	0.44
8:C:474:LYS:NZ	8:C:628:TYR:O	2.40	0.44
18:B:17:C:O2'	18:B:18:A:OP2	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:536:LEU:HD23	27:D:536:LEU:HA	1.69	0.44
27:D:617:ARG:HD3	27:D:1006:SER:OG	2.18	0.44
27:D:723:ASN:HB3	27:D:756:TRP:NE1	2.33	0.44
27:D:1000:ASP:OD1	27:D:1000:ASP:N	2.50	0.44
27:D:1541:ILE:H	27:D:1541:ILE:HG13	1.65	0.44
28:G:506:U:P	32:1:698:ARG:HD3	2.58	0.44
29:H:141:A:H2'	29:H:142:C:C6	2.52	0.44
32:1:489:VAL:HG13	38:X:26:GLU:CG	2.48	0.44
32:1:531:GLU:HA	32:1:534:ARG:HE	1.82	0.44
34:3:75:CYS:HB2	34:3:129:SER:OG	2.18	0.44
34:3:175:VAL:HG11	34:3:224:ILE:HD12	1.99	0.44
41:u:355:ASP:O	41:u:359:GLN:HG2	2.17	0.44
42:w:181:HIS:O	42:w:185:VAL:HG23	2.18	0.44
1:A:591:LEU:HB3	1:A:599:LEU:HD11	2.00	0.44
1:A:953:ARG:HG2	1:A:957:TYR:CE2	2.52	0.44
1:A:1414:TRP:CB	1:A:1558:GLU:HG3	2.48	0.44
1:A:1490:ARG:HA	1:A:1490:ARG:HD3	1.83	0.44
2:K:304:GLU:HG2	2:K:305:GLY:H	1.83	0.44
8:C:683:ASN:ND2	8:C:712:ALA:O	2.39	0.44
17:I:23:C:H2'	17:I:24:A:C8	2.53	0.44
27:D:883:PHE:CD1	27:D:883:PHE:C	2.95	0.44
27:D:1751:HIS:NE2	27:D:1813:ASP:OD2	2.50	0.44
27:D:2054:THR:OG1	27:D:2074:GLN:HB3	2.16	0.44
28:G:488:A:H2'	28:G:489:A:C8	2.52	0.44
29:H:42:U:H1'	43:v:83:ARG:HH21	1.81	0.44
32:1:198:GLU:HG2	32:1:239:TYR:OH	2.18	0.44
32:1:600:PRO:O	32:1:603:SER:OG	2.19	0.44
32:1:728:CYS:SG	32:1:753:ILE:HG21	2.57	0.44
34:3:477:ILE:O	34:3:479:SER:N	2.50	0.44
1:A:670:LYS:O	1:A:673:VAL:HG12	2.18	0.44
1:A:1317:ARG:HE	1:A:1366:ARG:HH12	1.65	0.44
1:A:1440:ILE:O	1:A:1443:TYR:N	2.45	0.44
1:A:1477:PHE:O	1:A:1481:GLU:N	2.51	0.44
1:A:1603:ASN:O	1:A:1607:THR:HG23	2.17	0.44
1:A:2349:PHE:CE2	1:A:2379:PRO:HG3	2.52	0.44
2:K:433:LEU:HB3	2:K:464:TRP:CZ3	2.52	0.44
8:C:385:PHE:HE1	8:C:425:LEU:HD11	1.83	0.44
8:C:497:ASP:O	8:C:538:GLU:HA	2.18	0.44
18:B:84:A:H2'	18:B:85:U:C6	2.51	0.44
27:D:758:LYS:O	27:D:762:ALA:HB3	2.18	0.44
27:D:1163:SER:HB3	27:D:1184:ARG:HH12	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:1912:ARG:HA	27:D:1912:ARG:HD2	1.67	0.44
28:G:514:U:H4'	28:G:515:U:OP2	2.18	0.44
29:H:9:C:H2'	29:H:10:U:H6	1.83	0.44
32:1:442:ILE:HD11	32:1:460:VAL:CG1	2.48	0.44
32:1:641:ASN:ND2	32:1:673:MET:HE1	2.33	0.44
32:1:873:HIS:O	32:1:875:ASP:N	2.46	0.44
32:1:889:PHE:CE2	33:2:176:TRP:HB3	2.53	0.44
32:1:962:GLU:HG3	37:6:36:ARG:HD2	1.99	0.44
35:4:171:GLN:HA	35:4:177:ARG:HH11	1.83	0.44
38:X:48:LEU:C	39:Y:231:ARG:NH1	2.76	0.44
39:Y:229:GLY:C	39:Y:231:ARG:H	2.25	0.44
41:u:21:ILE:O	41:u:25:ILE:HG13	2.18	0.44
1:A:770:MET:HG2	4:N:119:TRP:CZ3	2.53	0.44
1:A:889:TRP:HA	1:A:1128:GLN:HE22	1.83	0.44
1:A:1678:ILE:HG23	1:A:1704:GLU:O	2.17	0.44
2:K:48:ASP:OD1	2:K:69:VAL:HG21	2.18	0.44
2:K:167:LEU:HD23	2:K:435:GLY:HA3	1.99	0.44
2:K:345:LEU:HD13	2:K:376:TRP:CG	2.53	0.44
5:J:368:LEU:HD13	5:J:370:LEU:HG	1.99	0.44
6:E:43:ASP:O	6:E:47:SER:HB3	2.18	0.44
8:C:312:ILE:HG12	8:C:323:THR:HG22	1.99	0.44
8:C:336:ILE:HB	8:C:337:PRO:HD2	2.00	0.44
16:F:43:C:O2'	16:F:44:A:H8	2.00	0.44
16:F:79:A:H2'	16:F:80:U:H6	1.82	0.44
27:D:1008:PHE:HE2	27:D:1110:ARG:HG3	1.83	0.44
27:D:1473:TYR:CE2	27:D:1492:ILE:HD12	2.52	0.44
27:D:1763:ILE:HD13	27:D:1769:CYS:HA	2.00	0.44
27:D:2007:LYS:O	27:D:2010:GLU:HB3	2.18	0.44
29:H:1099:G:H2'	29:H:1100:A:H8	1.83	0.44
23:n:80:LYS:O	23:n:83:ASN:HB3	2.18	0.44
32:1:904:GLU:O	32:1:907:SER:OG	2.22	0.44
33:2:361:ARG:C	33:2:363:TYR:H	2.25	0.44
34:3:1258:TYR:CZ	34:3:1262:LYS:HD2	2.53	0.44
41:u:203:PHE:O	41:u:206:ILE:HB	2.18	0.44
43:v:53:ARG:NE	43:v:56:PRO:HA	2.22	0.44
1:A:628:MET:SD	1:A:660:ILE:HD13	2.58	0.44
1:A:1023:LEU:HD13	1:A:1451:PHE:CE1	2.53	0.44
1:A:1655:GLN:NE2	1:A:1688:PRO:O	2.50	0.44
1:A:1857:VAL:HG21	1:A:1913:THR:HG21	1.99	0.44
2:K:41:LEU:HD11	2:K:74:ILE:HG12	2.00	0.44
2:K:345:LEU:HD22	2:K:376:TRP:CE3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:359:PRO:HB2	2:K:406:GLY:C	2.42	0.44
3:L:382:SER:O	3:L:386:GLN:HG3	2.18	0.44
8:C:246:THR:HG23	8:C:248:VAL:HG12	1.99	0.44
8:C:799:PHE:HZ	8:C:818:TYR:HD2	1.66	0.44
18:B:43:G:H2'	18:B:44:A:H8	1.81	0.44
27:D:1263:ILE:HD11	27:D:1693:HIS:O	2.18	0.44
27:D:1431:ASP:OD2	27:D:2096:LEU:N	2.37	0.44
22:Q:26:TRP:HE3	22:Q:44:LYS:HG2	1.82	0.44
24:T:45:GLY:HA3	25:U:13:VAL:O	2.18	0.44
29:H:684:U:H2'	29:H:685:U:C6	2.50	0.44
29:H:1146:G:HO2'	29:H:1147:A:P	2.37	0.44
34:3:331:PHE:HD2	34:3:334:HIS:NE2	2.15	0.44
34:3:387:ASP:HA	34:3:412:THR:CG2	2.48	0.44
1:A:850:GLY:O	1:A:854:ARG:HG2	2.19	0.43
1:A:909:THR:HG21	4:N:167:GLU:HB3	1.99	0.43
1:A:2398:LEU:HA	27:D:1060:LYS:HZ2	1.82	0.43
2:K:52:ARG:HG3	2:K:62:GLU:HG3	2.00	0.43
3:L:237:ILE:O	3:L:240:GLN:N	2.51	0.43
18:B:14:G:N3	18:B:14:G:H2'	2.33	0.43
18:B:34:C:OP1	18:B:34:C:H4'	2.18	0.43
27:D:578:LEU:HD23	27:D:578:LEU:HA	1.71	0.43
27:D:1220:ILE:HD13	27:D:1241:LEU:HD11	2.00	0.43
27:D:1224:ALA:HB1	27:D:1226:TRP:CZ3	2.53	0.43
27:D:1459:TRP:CZ3	27:D:1502:LEU:HD11	2.53	0.43
27:D:1887:VAL:HG21	22:Q:140:LYS:CD	2.43	0.43
27:D:1897:GLY:O	27:D:1901:LEU:HB2	2.18	0.43
22:Q:30:GLN:NE2	22:Q:84:TYR:HE1	2.16	0.43
20:S:64:VAL:HG23	26:V:70:SER:HB2	2.00	0.43
24:T:81:LEU:HB3	25:U:81:ILE:HG22	1.99	0.43
28:G:483:A:N1	35:4:10:THR:HG21	2.32	0.43
28:G:489:A:H2'	28:G:490:A:H8	1.82	0.43
29:H:68:U:H2'	29:H:69:G:H8	1.82	0.43
23:n:90:PHE:CD2	41:u:195:ARG:N	2.85	0.43
34:3:1071:ILE:HG12	34:3:1089:ASP:OD2	2.18	0.43
38:X:33:ILE:CG2	38:X:85:THR:HG23	2.48	0.43
38:X:46:ASP:OD2	40:Z:35:SER:OG	2.34	0.43
38:X:51:PHE:CE1	38:X:92:LEU:HD23	2.53	0.43
38:X:87:LEU:HD21	39:Y:222:ASN:HD21	1.82	0.43
1:A:807:PRO:HB2	4:N:111:LEU:HD23	2.00	0.43
1:A:1791:PHE:HD2	1:A:1794:LEU:HD11	1.82	0.43
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:445:ILE:O	3:L:449:ASN:ND2	2.51	0.43
4:N:251:GLU:OE1	4:N:260:ALA:HB2	2.17	0.43
6:E:46:LEU:HD21	6:E:113:MET:HE2	2.00	0.43
8:C:722:ASP:OD2	8:C:755:TYR:OH	2.32	0.43
18:B:16:U:H2'	18:B:17:C:O4'	2.18	0.43
27:D:457:LYS:HE3	27:D:462:GLU:OE2	2.17	0.43
29:H:552:U:H2'	29:H:553:G:H8	1.81	0.43
32:1:157:ASN:O	32:1:161:LYS:HG3	2.18	0.43
33:2:141:VAL:HG12	33:2:143:TYR:H	1.83	0.43
34:3:180:THR:HG21	34:3:188:SER:HB2	2.00	0.43
34:3:365:ILE:HG23	34:3:382:GLN:O	2.18	0.43
34:3:770:LEU:HD12	34:3:770:LEU:O	2.18	0.43
34:3:816:MET:HE2	34:3:830:TYR:HB2	2.00	0.43
39:Y:232:TRP:CZ3	39:Y:234:GLY:HA2	2.53	0.43
2:K:364:VAL:O	2:K:375:VAL:HA	2.19	0.43
5:J:335:THR:HG23	5:J:336:VAL:N	2.33	0.43
8:C:495:ARG:HG3	8:C:540:GLU:O	2.19	0.43
8:C:677:PHE:HB2	8:C:811:GLU:OE1	2.18	0.43
17:I:51:U:H2'	17:I:52:G:H8	1.83	0.43
18:B:10:U:H2'	18:B:11:A:C8	2.53	0.43
27:D:683:PHE:CA	27:D:946:VAL:HG21	2.48	0.43
27:D:707:PHE:CD2	27:D:895:VAL:HG13	2.50	0.43
27:D:1396:VAL:HG12	27:D:1398:ILE:HG13	2.00	0.43
27:D:1917:THR:HG22	27:D:1918:SER:N	2.32	0.43
27:D:1951:LEU:HA	27:D:1954:VAL:HG22	1.99	0.43
20:l:14:ALA:HA	20:l:78:LEU:HD21	2.01	0.43
20:l:81:ALA:CB	20:l:82:PRO:CA	2.85	0.43
32:1:181:ARG:O	32:1:185:MET:HG2	2.19	0.43
32:1:241:HIS:O	32:1:245:VAL:HG23	2.18	0.43
32:1:786:GLY:HA2	32:1:823:MET:HB3	2.00	0.43
34:3:434:ASN:HD21	34:3:504:HIS:CE1	2.36	0.43
41:u:217:LEU:HD12	41:u:217:LEU:HA	1.82	0.43
41:u:431:TYR:HH	41:u:440:HIS:CE1	2.36	0.43
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.58	0.43
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	2.00	0.43
1:A:1962:ARG:HG3	1:A:2013:ARG:HH12	1.83	0.43
2:K:40:VAL:O	2:K:43:LYS:HG2	2.18	0.43
8:C:240:ASP:O	8:C:244:GLY:N	2.45	0.43
18:B:10:U:O2	18:B:11:A:N6	2.51	0.43
18:B:118:U:H2'	18:B:119:U:C6	2.53	0.43
27:D:521:ALA:O	27:D:672:ALA:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:703:LEU:HD21	27:D:872:LEU:HD23	2.00	0.43
27:D:758:LYS:O	27:D:762:ALA:CB	2.67	0.43
27:D:766:ILE:CD1	27:D:769:LYS:HZ1	2.32	0.43
27:D:1204:VAL:O	27:D:1304:ILE:HG21	2.18	0.43
27:D:1621:ILE:HG21	27:D:1633:LEU:HD22	2.01	0.43
27:D:1675:CYS:O	27:D:1677:THR:HG23	2.18	0.43
25:U:33:PHE:N	25:U:33:PHE:CD1	2.86	0.43
29:H:1094:G:H2'	29:H:1095:U:C6	2.54	0.43
24:i:88:THR:HG23	26:k:67:SER:CB	2.48	0.43
32:1:279:LEU:O	32:1:283:ARG:HG3	2.18	0.43
32:1:292:TYR:O	32:1:296:VAL:HG23	2.18	0.43
32:1:698:ARG:HG3	32:1:699:LYS:H	1.82	0.43
32:1:881:MET:O	32:1:884:LEU:N	2.50	0.43
34:3:192:TYR:HB2	34:3:205:SER:OG	2.18	0.43
34:3:542:THR:OG1	34:3:547:ASN:HB2	2.18	0.43
34:3:551:PHE:CD1	34:3:560:ILE:HG12	2.54	0.43
35:4:72:ASN:C	35:4:80:LEU:HD11	2.43	0.43
39:Y:222:ASN:OD1	39:Y:223:ARG:N	2.51	0.43
1:A:1343:PHE:HD1	1:A:1350:ILE:HD13	1.82	0.43
2:K:171:GLN:C	2:K:172:LEU:HD12	2.43	0.43
3:L:113:HIS:O	3:L:117:ILE:HD12	2.18	0.43
4:N:803:ASN:O	4:N:834:LYS:NZ	2.45	0.43
6:E:42:MET:HE1	6:E:107:VAL:H	1.82	0.43
8:C:227:VAL:HG13	8:C:473:LEU:HB3	1.99	0.43
8:C:471:HIS:HB2	8:C:592:PHE:CZ	2.54	0.43
8:C:504:THR:HB	8:C:594:PRO:HG3	2.01	0.43
8:C:672:ASP:OD1	8:C:673:PRO:HD2	2.18	0.43
18:B:175:G:H4'	18:B:176:A:O4'	2.18	0.43
27:D:1392:LYS:HB3	27:D:1469:GLU:OE1	2.19	0.43
27:D:1519:ARG:O	27:D:1523:GLU:HG3	2.18	0.43
27:D:1633:LEU:CD1	27:D:1652:VAL:HG22	2.48	0.43
27:D:1694:LYS:HG2	27:D:1695:TYR:N	2.33	0.43
27:D:1992:ASN:HD21	27:D:1994:LEU:HB2	1.82	0.43
26:V:18:ASN:O	26:V:69:ILE:HB	2.19	0.43
29:H:120:G:C2	24:i:33:GLU:O	2.71	0.43
29:H:1138:G:C6	29:H:1139:G:O6	2.71	0.43
32:1:191:LYS:HE3	32:1:194:THR:HG21	2.00	0.43
32:1:793:GLY:HA2	32:1:794:PRO:HD3	1.88	0.43
41:u:264:PHE:CE1	41:u:268:TYR:HD2	2.36	0.43
1:A:1063:PHE:O	1:A:1066:LEU:N	2.51	0.43
1:A:1993:ASP:CG	1:A:2038:HIS:HB3	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2006:SER:O	1:A:2009:THR:OG1	2.35	0.43
4:N:826:LYS:O	4:N:830:ARG:HB2	2.19	0.43
8:C:103:HIS:O	8:C:107:THR:HG23	2.19	0.43
8:C:769:TYR:HB2	8:C:771:GLY:C	2.42	0.43
8:C:861:ILE:HG21	8:C:905:GLN:HB3	1.99	0.43
18:B:9:U:H2'	18:B:10:U:O4'	2.19	0.43
18:B:13:A:C2	18:B:14:G:H1'	2.53	0.43
18:B:175:G:C2	18:B:176:A:N6	2.84	0.43
27:D:468:PRO:HD2	27:D:702:PRO:HB2	2.01	0.43
27:D:682:ARG:CZ	27:D:946:VAL:HG13	2.49	0.43
27:D:1402:GLY:HA2	27:D:1405:ILE:HD12	2.00	0.43
27:D:1497:PHE:HD1	27:D:1775:TYR:CE2	2.36	0.43
27:D:2077:ARG:NH1	27:D:2081:PRO:HG3	2.34	0.43
20:S:34:VAL:HG23	20:S:45:ARG:HG3	2.01	0.43
29:H:1094:G:H2'	29:H:1095:U:H6	1.83	0.43
33:2:364:PHE:CE2	34:3:1124:LEU:HD11	2.54	0.43
34:3:519:TYR:CE1	34:3:874:GLY:HA3	2.53	0.43
34:3:945:HIS:CE1	34:3:947:GLY:HA3	2.54	0.43
34:3:1125:ASP:HB3	34:3:1128:THR:HG22	2.00	0.43
38:X:24:HIS:HB3	38:X:86:ILE:HG12	2.00	0.43
43:v:200:VAL:HA	43:v:209:ILE:O	2.18	0.43
1:A:936:GLU:HG2	1:A:986:PRO:HB3	2.00	0.43
3:L:123:ARG:HD3	3:L:189:LEU:HD11	2.00	0.43
3:L:302:MET:O	3:L:306:LEU:N	2.41	0.43
6:E:31:PHE:O	6:E:80:MET:HA	2.18	0.43
7:M:37:ALA:HB2	7:M:98:ILE:HD11	2.00	0.43
7:M:58:CYS:SG	7:M:63:ILE:HD11	2.59	0.43
8:C:679:GLU:OE1	8:C:807:PRO:HD2	2.17	0.43
8:C:884:ARG:NH2	8:C:941:PRO:HD2	2.34	0.43
27:D:539:LEU:HG	27:D:555:PHE:CZ	2.54	0.43
27:D:1584:PHE:CD2	27:D:1706:MET:HG2	2.54	0.43
27:D:1668:LYS:HD3	27:D:1687:LEU:HD13	2.01	0.43
27:D:2143:TRP:HB3	27:D:2145:VAL:HG23	2.01	0.43
29:H:142:C:C2'	29:H:143:G:C8	3.00	0.43
32:1:733:GLU:HG2	32:1:736:LYS:HZ1	1.84	0.43
33:2:367:LEU:O	33:2:369:SER:N	2.50	0.43
34:3:693:ILE:HG23	34:3:701:LYS:HB2	2.01	0.43
34:3:1125:ASP:CG	34:3:1126:GLU:H	2.26	0.43
35:4:172:LEU:HD21	35:4:175:ASN:HA	2.01	0.43
38:X:117:LYS:HG2	40:Z:25:TYR:HB3	2.01	0.43
39:Y:167:VAL:HG11	39:Y:209:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:u:212:ASP:HB3	41:u:215:LYS:HB2	2.00	0.43
1:A:1014:LYS:HE2	1:A:1024:LEU:CD1	2.47	0.43
3:L:367:ARG:NH2	17:I:58:G:O6	2.52	0.43
5:J:331:VAL:HG12	5:J:332:GLU:N	2.33	0.43
8:C:863:GLU:HB3	8:C:931:TYR:CE1	2.54	0.43
17:I:143:A:C6	25:U:48:TYR:CD2	3.01	0.43
27:D:617:ARG:NH1	27:D:1009:TYR:HD1	2.16	0.43
27:D:1557:ILE:CA	27:D:1695:TYR:HE2	2.24	0.43
27:D:1748:TYR:HE2	22:Q:142:PRO:CD	2.32	0.43
29:H:43:G:C4	29:H:44:U:C5	3.06	0.43
24:i:45:GLY:HA3	24:i:53:VAL:HG12	2.00	0.43
32:1:658:VAL:O	32:1:661:SER:OG	2.32	0.43
38:X:28:LYS:HA	38:X:82:GLN:HE22	1.82	0.43
38:X:50:VAL:HG12	39:Y:237:ARG:CD	2.49	0.43
39:Y:229:GLY:C	39:Y:231:ARG:N	2.76	0.43
41:u:152:ARG:C	41:u:153:ARG:HG3	2.44	0.43
41:u:180:MET:H	41:u:335:THR:CG2	2.28	0.43
1:A:569:LEU:HD21	1:A:637:VAL:HG21	2.00	0.43
1:A:681:LYS:NZ	16:F:1:G:O6	2.41	0.43
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.29	0.43
1:A:1575:TRP:NE1	3:L:393:PHE:HD1	2.17	0.43
1:A:2333:PHE:HD2	1:A:2333:PHE:HA	1.72	0.43
2:K:69:VAL:HG22	2:K:72:ARG:HH12	1.84	0.43
8:C:374:VAL:HG22	8:C:378:LEU:HD12	2.00	0.43
8:C:488:ILE:CD1	8:C:556:ALA:HB1	2.49	0.43
8:C:869:HIS:CD2	8:C:925:LEU:HD13	2.54	0.43
16:F:1:G:C2	16:F:2:U:C5	3.06	0.43
17:I:77:U:C2	17:I:78:A:N7	2.87	0.43
17:I:148:U:O4	21:P:41:MET:HG3	2.19	0.43
18:B:174:G:C2	18:B:176:A:H4'	2.54	0.43
27:D:804:HIS:CG	27:D:834:LEU:HD11	2.54	0.43
27:D:1224:ALA:HB3	27:D:1264:VAL:HA	2.00	0.43
27:D:1355:VAL:HG11	27:D:1368:VAL:HG13	2.00	0.43
27:D:1458:ARG:HB3	27:D:1461:GLN:HB2	2.01	0.43
27:D:1550:SER:HA	27:D:1724:THR:O	2.18	0.43
21:P:88:ARG:HH22	20:S:69:ILE:H	1.66	0.43
29:H:112:A:N7	23:n:63:ARG:HB3	2.34	0.43
29:H:1148:U:H2'	29:H:1149:G:H8	1.83	0.43
22:m:17:ILE:HG12	22:m:95:ILE:HG23	2.00	0.43
32:1:534:ARG:O	32:1:538:VAL:HG23	2.18	0.43
32:1:925:HIS:ND1	32:1:926:PRO:HD2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:173:PRO:O	33:2:176:TRP:HD1	2.00	0.43
34:3:61:TYR:HB2	34:3:1231:LEU:HD11	2.00	0.43
34:3:770:LEU:HB2	34:3:827:TRP:CD1	2.54	0.43
34:3:1058:GLN:NE2	41:u:514:ASN:HB3	2.33	0.43
34:3:1109:TYR:CD1	34:3:1110:VAL:HG23	2.54	0.43
34:3:1299:ILE:O	34:3:1300:LEU:HD12	2.19	0.43
38:X:35:ILE:O	38:X:74:PHE:HA	2.18	0.43
43:v:222:GLU:HG3	43:v:222:GLU:O	2.18	0.43
1:A:880:THR:HG23	3:L:180:LYS:HE3	2.00	0.43
1:A:1393:GLU:CD	1:A:1543:ARG:HH12	2.27	0.43
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.54	0.43
3:L:300:LYS:NZ	3:L:304:ARG:HH22	2.17	0.43
4:N:25:GLY:O	4:N:26:PHE:HB2	2.18	0.43
4:N:264:ILE:O	4:N:268:CYS:HB2	2.19	0.43
18:B:23:C:N4	18:B:24:G:O6	2.52	0.43
18:B:154:G:H2'	18:B:155:U:C6	2.54	0.43
27:D:1688:TYR:CD1	27:D:1695:TYR:HD1	2.23	0.43
25:U:50:ASN:HB3	25:U:72:PHE:CE1	2.54	0.43
29:H:52:A:N6	29:H:64:G:O6	2.52	0.43
20:l:6:ILE:HG23	20:l:83:LEU:HD23	1.99	0.43
32:1:698:ARG:O	32:1:701:GLU:N	2.52	0.43
32:1:839:THR:HG21	32:1:876:ALA:HB1	2.00	0.43
32:1:912:PRO:HG2	32:1:952:PHE:HE2	1.84	0.43
33:2:319:ILE:HD13	35:4:68:LYS:HE2	2.00	0.43
34:3:649:TYR:O	34:3:672:LEU:N	2.51	0.43
34:3:950:GLN:HE21	34:3:973:ILE:CG2	2.32	0.43
35:4:111:PHE:HE2	35:4:113:LYS:HE3	1.84	0.43
36:5:103:LYS:HG3	36:5:104:LYS:H	1.84	0.43
38:X:17:LEU:O	38:X:18:SER:OG	2.30	0.43
38:X:19:PRO:O	38:X:25:ASN:HB2	2.19	0.43
43:v:155:ILE:HD13	43:v:252:VAL:HG23	2.00	0.43
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.54	0.42
1:A:1865:THR:HG22	1:A:1866:PHE:N	2.33	0.42
1:A:1880:PHE:HD1	1:A:1891:LEU:HD21	1.84	0.42
1:A:1920:LEU:O	1:A:1923:SER:OG	2.27	0.42
2:K:402:SER:OG	2:K:407:GLY:HA2	2.19	0.42
2:K:415:TYR:HB3	2:K:439:LYS:HD3	2.00	0.42
2:K:416:ASP:O	2:K:417:ASN:HB2	2.19	0.42
8:C:827:SER:C	8:C:829:VAL:H	2.27	0.42
18:B:124:C:H2'	18:B:125:C:O4'	2.18	0.42
23:R:58:VAL:HA	23:R:69:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:1153:C:H2'	29:H:1154:U:H6	1.84	0.42
34:3:930:LEU:HD13	34:3:984:ILE:HG23	2.01	0.42
39:Y:223:ARG:CG	39:Y:242:GLU:OE2	2.67	0.42
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.54	0.42
2:K:143:HIS:HA	5:J:151:LEU:HD13	2.01	0.42
3:L:245:ALA:HB3	3:L:251:PHE:HB2	2.01	0.42
3:L:447:GLU:O	3:L:451:GLN:HG2	2.19	0.42
8:C:138:VAL:HG21	8:C:150:MET:HE3	2.00	0.42
8:C:457:SER:O	8:C:458:ILE:HB	2.19	0.42
17:I:92:C:H1'	21:P:39:LYS:HD3	2.01	0.42
27:D:558:VAL:HB	27:D:631:LEU:HD12	2.01	0.42
27:D:1700:ILE:CD1	27:D:1740:LEU:HD13	2.49	0.42
29:H:121:C:O2'	22:m:20:LYS:HE3	2.19	0.42
20:l:6:ILE:N	20:l:7:PRO:CD	2.82	0.42
32:1:550:THR:HG21	32:1:590:LEU:HD23	2.01	0.42
34:3:60:LEU:HD12	34:3:1317:VAL:HG22	2.01	0.42
38:X:27:TYR:C	38:X:29:ASP:H	2.27	0.42
41:u:38:GLU:O	41:u:41:LYS:HG2	2.18	0.42
41:u:425:ILE:HB	41:u:465:THR:O	2.19	0.42
1:A:400:ILE:HG23	8:C:187:ARG:HE	1.85	0.42
1:A:850:GLY:HA2	1:A:853:THR:HG22	2.01	0.42
1:A:1342:LEU:HD21	1:A:1356:LEU:HD21	2.01	0.42
1:A:1566:GLY:HA3	1:A:1816:ARG:HD3	2.02	0.42
1:A:1633:PHE:CZ	1:A:1694:MET:HG3	2.54	0.42
2:K:390:LEU:HD13	5:J:428:TRP:HD1	1.82	0.42
8:C:919:ARG:NH1	8:C:927:MET:HE1	2.34	0.42
17:I:92:C:C1'	21:P:39:LYS:HD3	2.50	0.42
18:B:22:G:N2	18:B:149:U:O2	2.34	0.42
18:B:26:A:N6	18:B:141:G:H8	2.16	0.42
23:R:73:LYS:HE3	23:R:88:GLU:HG3	2.01	0.42
20:S:24:THR:HA	20:S:70:LYS:HE3	2.00	0.42
24:i:88:THR:HG22	24:i:89:LEU:HD12	2.01	0.42
32:1:213:LEU:HD12	32:1:213:LEU:O	2.19	0.42
32:1:240:VAL:HG13	32:1:269:LEU:HD21	2.01	0.42
32:1:353:THR:HG23	34:3:277:LEU:HD21	2.01	0.42
32:1:916:MET:HB3	32:1:920:TRP:HE1	1.82	0.42
32:1:956:THR:H	32:1:959:ASN:HB3	1.84	0.42
34:3:61:TYR:HB2	34:3:1231:LEU:CD1	2.49	0.42
34:3:228:LEU:HD12	34:3:273:LEU:HD11	2.01	0.42
34:3:1061:ARG:NH1	41:u:503:GLU:HG2	2.34	0.42
34:3:1305:GLN:O	34:3:1309:SER:CB	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:170:LEU:N	39:Y:170:LEU:CD2	2.82	0.42
39:Y:215:TYR:CE2	39:Y:232:TRP:CZ3	3.08	0.42
41:u:319:TYR:CZ	41:u:323:ARG:HD2	2.54	0.42
1:A:299:LYS:HA	1:A:493:MET:CG	2.49	0.42
1:A:1030:GLN:HG3	1:A:1034:ASN:ND2	2.34	0.42
1:A:2043:PHE:HB2	1:A:2048:TRP:CD1	2.54	0.42
2:K:127:TYR:CE2	2:K:276:SER:HB2	2.54	0.42
2:K:262:VAL:HG12	2:K:263:GLY:N	2.34	0.42
4:N:770:ASN:ND2	4:N:772:LEU:HB2	2.34	0.42
17:I:145:U:O4	26:V:37:ASN:ND2	2.47	0.42
19:O:149:TYR:CD2	19:O:178:VAL:HG12	2.47	0.42
27:D:561:ALA:HB1	27:D:566:LEU:HD22	2.01	0.42
27:D:1095:ASN:HA	27:D:1098:ILE:HG22	2.01	0.42
27:D:1875:THR:O	27:D:1879:MET:HG3	2.20	0.42
27:D:2095:LYS:NZ	27:D:2147:ASP:OD2	2.46	0.42
23:R:41:ARG:O	23:R:57:ARG:HD2	2.20	0.42
20:S:41:ASN:HB3	20:S:63:PHE:CZ	2.55	0.42
21:h:87:LEU:HG	21:h:92:ILE:HD11	2.00	0.42
23:n:102:ILE:HG22	23:n:103:VAL:HG23	2.01	0.42
34:3:927:ARG:HG2	34:3:979:CYS:SG	2.60	0.42
41:u:40:SER:HA	41:u:46:THR:OG1	2.20	0.42
1:A:149:MET:HG2	1:A:154:TYR:CZ	2.54	0.42
1:A:919:LEU:HD21	1:A:1108:LYS:HE3	2.01	0.42
1:A:1656:LYS:O	1:A:1660:SER:HB2	2.20	0.42
1:A:1714:PRO:HA	1:A:1788:GLY:O	2.20	0.42
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	2.01	0.42
1:A:2395:PHE:HB2	27:D:1062:PRO:HG3	2.01	0.42
2:K:451:PHE:N	2:K:451:PHE:HD1	2.15	0.42
5:J:167:GLU:HB3	5:J:169:TRP:CE3	2.51	0.42
5:J:301:VAL:HG22	5:J:304:ARG:NH2	2.32	0.42
8:C:116:THR:HG22	8:C:117:ARG:N	2.35	0.42
8:C:129:ILE:HG13	20:d:16:GLY:C	2.40	0.42
18:B:166:U:C6	18:B:166:U:C3'	3.02	0.42
19:O:168:SER:O	19:O:172:ASP:CB	2.67	0.42
27:D:580:PHE:CE2	27:D:581:LEU:HG	2.54	0.42
27:D:907:PRO:HG2	27:D:947:ARG:NH2	2.34	0.42
27:D:2030:ILE:HG22	27:D:2031:LEU:HD12	2.02	0.42
27:D:2137:LYS:HE3	27:D:2159:GLU:OE2	2.20	0.42
22:Q:33:SER:HB3	22:Q:37:ASN:HB2	2.02	0.42
29:H:38:U:H4'	32:1:892:SER:OG	2.20	0.42
34:3:154:SER:HB3	34:3:1302:ARG:CD	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:3:155:GLY:O	34:3:179:LEU:N	2.44	0.42
34:3:419:LEU:HD23	34:3:429:ALA:HA	2.01	0.42
34:3:455:LEU:HD11	34:3:464:LEU:CB	2.49	0.42
34:3:779:TYR:C	34:3:780:LEU:HD12	2.44	0.42
38:X:109:TYR:CD1	38:X:109:TYR:C	2.97	0.42
41:u:250:LEU:HD23	41:u:250:LEU:HA	1.88	0.42
1:A:805:PRO:HG2	1:A:808:ILE:HD12	2.00	0.42
1:A:1014:LYS:C	1:A:1016:SER:N	2.77	0.42
1:A:1345:TYR:CD2	1:A:1346:PHE:CE1	3.07	0.42
1:A:1466:GLN:O	1:A:1470:GLN:HB2	2.20	0.42
4:N:257:PHE:CD2	4:N:258:SER:N	2.88	0.42
4:N:770:ASN:HD21	4:N:772:LEU:HB2	1.83	0.42
8:C:219:VAL:HA	8:C:222:MET:HG2	2.00	0.42
27:D:695:ASP:OD1	27:D:696:SER:N	2.45	0.42
27:D:956:LYS:O	27:D:958:PRO:HD3	2.20	0.42
27:D:1113:PHE:HZ	27:D:1240:LEU:HD13	1.84	0.42
27:D:1381:GLU:HG2	27:D:1416:PHE:CZ	2.54	0.42
27:D:1938:GLU:HG2	27:D:1938:GLU:O	2.20	0.42
28:G:496:U:H2'	28:G:497:A:H8	1.83	0.42
32:1:605:ILE:HD11	32:1:623:LEU:HD22	2.01	0.42
34:3:542:THR:HB	34:3:545:ASP:HB3	2.01	0.42
34:3:642:LEU:HD22	34:3:654:PHE:HD2	1.84	0.42
34:3:738:GLN:NE2	34:3:740:ASN:OD1	2.53	0.42
39:Y:231:ARG:HG3	39:Y:231:ARG:HH11	1.85	0.42
41:u:423:CYS:SG	41:u:425:ILE:HG22	2.59	0.42
42:w:195:ILE:HD11	42:w:197:TRP:CH2	2.54	0.42
1:A:939:LEU:HD21	3:L:445:ILE:HD11	2.01	0.42
1:A:1199:ILE:HD11	8:C:612:PRO:HG2	2.01	0.42
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	2.03	0.42
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.19	0.42
1:A:1964:PRO:O	1:A:2012:LEU:HB3	2.20	0.42
2:K:395:ILE:HD12	2:K:415:TYR:CD2	2.55	0.42
6:E:109:ASP:OD1	6:E:110:LYS:N	2.52	0.42
8:C:568:SER:HA	8:C:571:TYR:CE2	2.55	0.42
19:O:206:LYS:HB2	19:O:208:LYS:NZ	2.34	0.42
27:D:524:GLY:O	27:D:525:SER:HB3	2.19	0.42
27:D:557:ILE:HD12	27:D:604:VAL:HG22	2.00	0.42
27:D:708:CYS:SG	27:D:889:ILE:HG12	2.60	0.42
27:D:981:LEU:HB3	27:D:987:VAL:HG22	2.01	0.42
27:D:1412:TRP:CE2	27:D:1416:PHE:HE2	2.38	0.42
29:H:1097:G:C4	29:H:1146:G:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:j:16:LYS:CG	25:j:17:PRO:HD3	2.49	0.42
33:2:191:LYS:HD3	43:v:62:HIS:CE1	2.55	0.42
34:3:486:PRO:HG2	34:3:505:PHE:CB	2.50	0.42
34:3:542:THR:HG22	34:3:615:LYS:NZ	2.35	0.42
34:3:1065:THR:HG22	34:3:1105:VAL:HA	2.01	0.42
35:4:108:ALA:O	35:4:154:TYR:HA	2.19	0.42
35:4:125:VAL:HG12	35:4:129:ASN:HD21	1.84	0.42
41:u:69:ARG:O	41:u:73:ILE:HG12	2.20	0.42
41:u:202:GLN:O	41:u:206:ILE:HG13	2.20	0.42
41:u:449:HIS:O	41:u:453:LEU:HB2	2.19	0.42
1:A:2152:TRP:CZ3	27:D:1064:PRO:CG	2.95	0.42
2:K:261:LEU:HD13	2:K:292:TRP:HE3	1.84	0.42
8:C:251:GLN:HG2	8:C:933:TRP:CE2	2.55	0.42
16:F:46:U:C4	16:F:47:A:C2	3.07	0.42
17:I:142:G:N2	21:P:39:LYS:CE	2.82	0.42
18:B:118:U:H2'	18:B:119:U:H6	1.84	0.42
27:D:830:CYS:SG	27:D:834:LEU:HD22	2.59	0.42
27:D:929:ILE:CD1	27:D:935:ALA:HA	2.50	0.42
27:D:1415:ARG:HA	27:D:1418:HIS:HE1	1.83	0.42
27:D:2059:ASN:OD1	27:D:2059:ASN:N	2.53	0.42
28:G:520:G:N2	38:X:34:TYR:HB2	2.34	0.42
29:H:1098:C:O5'	29:H:1098:C:C6	2.69	0.42
24:i:34:GLN:NE2	24:i:37:ILE:HD12	2.34	0.42
23:n:90:PHE:CZ	41:u:194:LYS:O	2.71	0.42
32:1:368:VAL:N	32:1:369:PRO:HD2	2.35	0.42
32:1:889:PHE:CZ	32:1:930:VAL:HG22	2.54	0.42
32:1:955:VAL:HG12	32:1:963:TYR:HD1	1.83	0.42
34:3:61:TYR:HD1	34:3:1318:ILE:HD11	1.83	0.42
34:3:337:VAL:CG2	34:3:346:LEU:HB2	2.50	0.42
34:3:421:ILE:HG22	34:3:422:PHE:O	2.20	0.42
34:3:561:LEU:HG	34:3:569:GLU:O	2.20	0.42
34:3:929:ILE:HG12	34:3:941:PHE:CD1	2.55	0.42
41:u:450:LEU:HB2	41:u:457:PRO:HG3	2.02	0.42
1:A:1814:VAL:CG1	1:A:1818:ARG:HE	2.32	0.42
1:A:1892:LYS:HD2	1:A:1985:GLN:O	2.20	0.42
3:L:368:ALA:O	16:F:60:G:C8	2.73	0.42
6:E:86:TYR:CE2	6:E:87:HIS:HD2	2.38	0.42
7:M:23:VAL:HG21	7:M:117:VAL:HG21	2.01	0.42
8:C:200:CYS:HB3	8:C:436:VAL:HG21	2.02	0.42
8:C:251:GLN:HE21	8:C:255:GLN:HE21	1.67	0.42
8:C:305:SER:OG	8:C:307:ILE:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:135:A:C6	17:I:136:U:C4	3.07	0.42
18:B:163:C:OP2	21:a:8:HIS:N	2.52	0.42
27:D:1137:THR:HB	27:D:1139:MET:HE3	2.00	0.42
27:D:1183:ILE:O	27:D:1183:ILE:HG22	2.19	0.42
27:D:1587:SER:HB3	27:D:1895:ARG:NE	2.35	0.42
27:D:1699:THR:HG22	22:Q:144:ARG:HD2	2.01	0.42
27:D:1781:ARG:HG2	27:D:1789:TYR:OH	2.20	0.42
27:D:1971:LEU:HB2	27:D:2110:GLU:C	2.45	0.42
27:D:1978:ASP:O	27:D:1982:MET:HG3	2.20	0.42
25:U:30:LYS:HE2	25:U:80:TYR:CE2	2.55	0.42
26:k:28:ILE:HG23	26:k:41:ASP:HB2	2.00	0.42
32:1:387:PRO:HA	32:1:425:LEU:HB3	2.02	0.42
32:1:900:LEU:O	32:1:904:GLU:HG2	2.20	0.42
33:2:340:LEU:HD13	33:2:345:TYR:HA	2.02	0.42
34:3:832:TRP:CD1	34:3:833:LYS:H	2.37	0.42
34:3:1043:THR:HG21	34:3:1052:TYR:CE2	2.55	0.42
34:3:1345:GLN:O	34:3:1349:ILE:HG12	2.20	0.42
38:X:89:VAL:O	38:X:93:ASN:HB2	2.20	0.42
41:u:81:ILE:CD1	41:u:161:ALA:HB2	2.50	0.42
41:u:192:VAL:HG13	41:u:228:ARG:HB3	2.02	0.42
41:u:359:GLN:OE1	41:u:359:GLN:HA	2.20	0.42
43:v:71:CYS:SG	43:v:90:HIS:HA	2.60	0.42
43:v:178:PRO:O	43:v:179:LEU:HD23	2.19	0.42
1:A:617:ASN:HD21	18:B:99:U:HO2'	1.65	0.42
1:A:1033:ASN:HD22	1:A:1288:LEU:HB3	1.85	0.42
1:A:1057:MET:O	1:A:1061:ILE:HG13	2.19	0.42
1:A:1925:PRO:O	1:A:1929:GLN:HG3	2.19	0.42
1:A:1941:LEU:HD23	1:A:1941:LEU:HA	1.91	0.42
2:K:65:GLU:OE1	5:J:241:ARG:NH2	2.53	0.42
2:K:112:PRO:HA	5:J:217:VAL:N	2.34	0.42
2:K:232:ASN:O	2:K:247:GLN:NE2	2.53	0.42
2:K:390:LEU:HB2	5:J:428:TRP:CD1	2.55	0.42
4:N:150:ASP:O	4:N:153:ILE:HG12	2.19	0.42
5:J:342:PHE:HB3	5:J:424:ILE:HD11	2.01	0.42
8:C:234:LEU:HD23	8:C:443:TYR:HB2	2.00	0.42
16:F:5:G:H2'	16:F:6:C:H6	1.85	0.42
17:I:91:U:O2	21:P:39:LYS:NZ	2.37	0.42
17:I:135:A:C4	17:I:136:U:C5	3.08	0.42
17:I:152:A:H2'	17:I:153:A:C8	2.54	0.42
18:B:150:U:H4'	18:B:151:A:OP1	2.19	0.42
27:D:589:THR:HB	27:D:608:THR:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:648:GLU:CD	27:D:912:PHE:HD1	2.27	0.42
27:D:730:VAL:HG22	27:D:740:ILE:HD13	2.01	0.42
27:D:912:PHE:CD2	27:D:944:LEU:HD23	2.55	0.42
27:D:1412:TRP:CD1	27:D:1416:PHE:CE2	3.07	0.42
23:R:55:ILE:HG23	23:R:73:LYS:HB3	2.01	0.42
29:H:51:C:H2'	29:H:52:A:C8	2.55	0.42
32:1:290:ASP:OD1	32:1:291:GLU:N	2.53	0.42
34:3:493:VAL:HG23	34:3:937:LYS:HB3	2.02	0.42
34:3:1116:ARG:NH2	34:3:1141:LEU:HD21	2.35	0.42
34:3:1190:LEU:O	34:3:1315:ARG:HD3	2.19	0.42
34:3:1217:ILE:HA	34:3:1226:GLY:O	2.19	0.42
38:X:43:THR:OG1	38:X:44:GLU:OE1	2.38	0.42
40:Z:26:ILE:HG22	40:Z:28:ILE:H	1.84	0.42
41:u:152:ARG:HG3	41:u:153:ARG:HG3	2.02	0.42
43:v:205:PRO:HG2	43:v:206:PHE:CD1	2.55	0.42
1:A:266:LEU:HG	1:A:267:PRO:HD2	2.02	0.41
1:A:1372:LYS:HE2	1:A:1383:PHE:CB	2.50	0.41
2:K:350:LYS:HB3	2:K:351:PRO:HD2	2.01	0.41
3:L:138:SER:HA	3:L:141:ILE:HD12	2.01	0.41
3:L:173:LEU:O	3:L:176:THR:OG1	2.26	0.41
3:L:204:LEU:HD23	3:L:204:LEU:HA	1.82	0.41
4:N:144:LYS:O	4:N:145:THR:OG1	2.30	0.41
5:J:346:ASN:N	5:J:422:ASN:OD1	2.46	0.41
5:J:386:GLU:HG2	5:J:390:LYS:HE2	2.01	0.41
8:C:120:ARG:NH2	8:C:549:TYR:OH	2.53	0.41
8:C:408:LEU:HD21	8:C:427:LEU:HD22	2.01	0.41
8:C:749:LYS:O	8:C:753:THR:OG1	2.25	0.41
27:D:484:PRO:O	27:D:488:GLN:HG3	2.20	0.41
27:D:945:TYR:CE1	27:D:970:ARG:HD3	2.55	0.41
27:D:1183:ILE:O	27:D:1184:ARG:HG2	2.20	0.41
21:P:39:LYS:CE	22:Q:35:GLN:NE2	2.83	0.41
24:T:83:LYS:NZ	25:U:75:CYS:C	2.74	0.41
28:G:509:A:O3'	32:1:543:ARG:NH2	2.53	0.41
28:G:520:G:C4	38:X:34:TYR:CE1	3.07	0.41
29:H:68:U:H2'	29:H:69:G:C8	2.54	0.41
32:1:807:THR:HG22	33:2:211:THR:HG23	2.02	0.41
34:3:188:SER:O	34:3:190:ILE:N	2.49	0.41
34:3:197:PRO:HG2	34:3:244:ASP:HB3	2.02	0.41
34:3:411:ASP:OD1	34:3:472:LEU:HA	2.19	0.41
34:3:1073:LYS:HD2	34:3:1090:ILE:CD1	2.48	0.41
35:4:197:ASP:OD1	35:4:198:VAL:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:u:58:LYS:HB3	41:u:63:LYS:HA	2.02	0.41
41:u:226:ASN:O	41:u:230:MET:HG3	2.20	0.41
1:A:660:ILE:O	1:A:664:THR:OG1	2.27	0.41
4:N:741:ILE:O	4:N:745:GLN:HB3	2.20	0.41
7:M:97:VAL:HG22	17:I:30:G:H2'	2.02	0.41
8:C:557:HIS:O	8:C:560:GLN:HG2	2.20	0.41
17:I:149:U:C2	23:R:64:HIS:HB3	2.55	0.41
18:B:87:G:H2'	18:B:88:U:H6	1.85	0.41
27:D:1493:SER:CA	27:D:1524:TRP:HH2	2.28	0.41
21:P:18:TYR:CD1	21:P:101:PRO:HG3	2.53	0.41
21:P:31:ILE:O	21:P:48:CYS:HA	2.20	0.41
23:R:76:TRP:CZ3	23:R:89:ARG:HG2	2.56	0.41
25:U:36:THR:HG21	25:U:38:TYR:CZ	2.55	0.41
32:1:689:LEU:HD21	32:1:707:PHE:HD2	1.85	0.41
32:1:925:HIS:HA	33:2:160:LEU:HD11	2.02	0.41
34:3:82:LEU:C	34:3:84:ALA:H	2.28	0.41
41:u:116:LEU:HD11	41:u:120:GLU:OE2	2.21	0.41
1:A:644:VAL:HG12	1:A:648:GLN:HB2	2.03	0.41
1:A:939:LEU:HD23	1:A:939:LEU:HA	1.81	0.41
1:A:1341:SER:HB3	1:A:1524:PRO:HB2	2.02	0.41
5:J:271:LYS:HD3	16:F:62:A:H5''	2.02	0.41
8:C:769:TYR:C	8:C:771:GLY:H	2.28	0.41
18:B:103:A:O2'	18:B:104:G:O5'	2.30	0.41
18:B:114:G:C2	18:B:115:G:C5	3.08	0.41
27:D:1141:PRO:HG3	27:D:1298:TRP:CZ3	2.55	0.41
27:D:1486:ALA:HA	27:D:1489:GLU:HG2	2.02	0.41
27:D:1583:VAL:C	27:D:1584:PHE:HD1	2.28	0.41
27:D:1933:TYR:CE1	27:D:2090:LYS:O	2.73	0.41
23:R:36:ASP:HA	23:R:39:VAL:HG12	2.02	0.41
29:H:1139:G:C2'	29:H:1140:U:H6	2.34	0.41
29:H:1146:G:H2'	29:H:1147:A:H8	1.84	0.41
29:H:1149:G:C4	29:H:1150:U:C5	3.08	0.41
30:o:62:ASN:HB2	30:o:84:ASN:OD1	2.20	0.41
32:1:828:GLY:HA3	36:5:38:ARG:NH2	2.36	0.41
33:2:246:LYS:O	33:2:250:VAL:HG23	2.21	0.41
34:3:118:GLN:HB2	34:3:1325:ASN:OD1	2.20	0.41
34:3:224:ILE:O	36:5:17:VAL:HG11	2.20	0.41
34:3:327:VAL:O	34:3:337:VAL:HA	2.21	0.41
34:3:759:ASP:OD1	34:3:760:GLY:N	2.53	0.41
34:3:1308:ARG:HD3	34:3:1308:ARG:HA	1.87	0.41
43:v:213:LEU:C	43:v:215:PRO:HD2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:HA	1:A:199:ILE:HD11	2.03	0.41
1:A:268:LEU:HD13	1:A:273:ASP:HB2	2.01	0.41
1:A:297:SER:HB2	18:B:32:G:H5'	2.03	0.41
1:A:659:HIS:O	1:A:662:GLN:N	2.54	0.41
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.56	0.41
1:A:1144:PHE:CZ	1:A:1145:MET:HE2	2.55	0.41
1:A:1375:LEU:CD2	1:A:1607:THR:HG22	2.50	0.41
1:A:1477:PHE:O	1:A:1481:GLU:HG3	2.21	0.41
1:A:2152:TRP:HZ3	27:D:1064:PRO:CG	2.32	0.41
1:A:2307:LEU:HD11	1:A:2311:GLY:HA3	2.02	0.41
2:K:167:LEU:HD13	4:N:724:SER:HB2	2.01	0.41
2:K:235:ILE:HA	2:K:244:LYS:O	2.20	0.41
2:K:264:HIS:CE1	2:K:290:ARG:HH11	2.38	0.41
2:K:269:SER:OG	2:K:311:PHE:HA	2.20	0.41
2:K:279:PHE:HB3	2:K:291:LEU:HD11	2.02	0.41
4:N:98:SER:OG	4:N:99:ASN:N	2.48	0.41
4:N:144:LYS:HE3	17:I:19:U:OP1	2.20	0.41
4:N:726:LEU:HD21	4:N:746:MET:HE1	2.02	0.41
4:N:863:PHE:CE2	4:N:888:PRO:HB2	2.55	0.41
5:J:350:PRO:HB2	16:F:83:A:N7	2.35	0.41
8:C:113:ILE:HD13	8:C:551:TYR:HD1	1.85	0.41
8:C:274:ILE:HD13	8:C:385:PHE:CD2	2.48	0.41
8:C:385:PHE:CE1	8:C:425:LEU:HD11	2.55	0.41
18:B:69:G:H2'	18:B:70:A:C8	2.55	0.41
18:B:70:A:H2'	18:B:71:A:C8	2.56	0.41
27:D:1439:LEU:HD21	27:D:1465:ILE:HG13	2.01	0.41
25:U:54:ASN:OD1	25:U:55:GLU:N	2.51	0.41
33:2:144:PRO:HG2	41:u:460:VAL:CG2	2.50	0.41
33:2:293:ARG:O	35:4:31:GLN:NE2	2.53	0.41
34:3:326:PHE:CD1	34:3:339:ASP:HA	2.55	0.41
34:3:453:ASN:HA	34:3:464:LEU:HD11	2.03	0.41
34:3:488:ILE:HG22	34:3:489:LYS:HG2	2.02	0.41
34:3:526:SER:HA	34:3:870:ARG:HG3	2.02	0.41
34:3:1101:PRO:C	34:3:1103:GLY:H	2.28	0.41
41:u:172:ARG:HH12	41:u:354:MET:HE3	1.85	0.41
1:A:1814:VAL:HG12	1:A:1818:ARG:HE	1.85	0.41
1:A:2032:ILE:HG22	1:A:2041:PRO:HB2	2.02	0.41
2:K:306:HIS:CD2	2:K:310:VAL:HG22	2.55	0.41
2:K:337:ARG:HD2	5:J:173:TYR:CE2	2.55	0.41
8:C:309:ASN:HD21	8:C:325:LYS:HG3	1.85	0.41
8:C:502:LEU:HB3	8:C:576:THR:OG1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:758:ASP:HB3	8:C:761:ALA:HB3	2.02	0.41
27:D:593:ARG:O	27:D:593:ARG:HG2	2.20	0.41
27:D:1668:LYS:CE	27:D:1702:GLU:HG3	2.47	0.41
27:D:1862:THR:OG1	27:D:1887:VAL:HG12	2.20	0.41
27:D:1905:LEU:HD11	27:D:1937:LEU:HD13	2.03	0.41
23:R:76:TRP:HZ3	23:R:89:ARG:HG2	1.85	0.41
24:T:85:ASP:CG	25:U:32:LYS:NZ	2.79	0.41
29:H:58:A:H2'	29:H:59:C:O4'	2.19	0.41
32:1:230:TYR:HE2	37:6:5:GLN:HG3	1.85	0.41
32:1:430:TYR:HB3	32:1:434:TYR:HE2	1.85	0.41
33:2:134:LEU:HA	33:2:137:LEU:HB3	2.02	0.41
33:2:275:ASN:HD21	33:2:278:GLU:CD	2.29	0.41
34:3:157:LEU:HD11	34:3:202:ILE:HG21	2.01	0.41
34:3:180:THR:HG21	34:3:188:SER:CB	2.51	0.41
34:3:676:PRO:CB	34:3:693:ILE:HD11	2.50	0.41
34:3:1089:ASP:HB2	34:3:1092:GLU:O	2.20	0.41
34:3:1291:ILE:HA	34:3:1296:SER:HB2	2.03	0.41
36:5:72:TYR:OH	36:5:87:PRO:HG3	2.20	0.41
41:u:48:LEU:HD12	41:u:48:LEU:O	2.20	0.41
41:u:88:GLU:O	41:u:92:THR:HG23	2.20	0.41
41:u:149:ASP:N	41:u:150:PRO:HD2	2.36	0.41
1:A:370:ILE:HB	1:A:375:PHE:HZ	1.85	0.41
1:A:375:PHE:CE2	8:C:954:LEU:HD23	2.56	0.41
1:A:1409:ALA:HB1	1:A:1428:GLY:HA3	2.03	0.41
1:A:1658:HIS:HE1	1:A:1690:LYS:NZ	2.19	0.41
2:K:51:VAL:HG13	2:K:76:LEU:HD11	2.01	0.41
3:L:358:ILE:CG2	3:L:360:GLU:H	2.33	0.41
4:N:273:ARG:O	4:N:303:ASN:ND2	2.47	0.41
4:N:666:ILE:HG22	4:N:667:CYS:N	2.36	0.41
4:N:674:LEU:O	4:N:678:TYR:HD2	2.03	0.41
6:E:105:PHE:CE2	6:E:137:TYR:CZ	3.09	0.41
8:C:366:ASN:OD1	8:C:367:VAL:HG23	2.20	0.41
8:C:778:THR:HG23	8:C:781:ASP:H	1.85	0.41
18:B:27:G:OP1	18:B:141:G:H5''	2.19	0.41
27:D:453:PHE:HE2	27:D:455:ARG:NE	2.14	0.41
27:D:587:GLU:O	27:D:592:SER:HB3	2.21	0.41
22:Q:4:VAL:HG11	22:Q:34:PRO:O	2.21	0.41
22:Q:4:VAL:CG1	22:Q:34:PRO:HA	2.50	0.41
25:U:59:PHE:N	25:U:59:PHE:CD1	2.88	0.41
29:H:1097:G:N1	29:H:1146:G:C5	2.88	0.41
29:H:1143:C:H4'	29:H:1144:U:H3'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:i:77:LEU:HD23	24:i:78:GLY:N	2.35	0.41
32:1:843:GLU:OE1	32:1:883:LEU:HD11	2.21	0.41
33:2:248:HIS:ND1	33:2:375:PHE:HB2	2.35	0.41
34:3:187:VAL:HG21	37:6:17:LYS:O	2.20	0.41
34:3:333:ASN:OD1	34:3:334:HIS:ND1	2.44	0.41
34:3:951:CYS:SG	34:3:952:ARG:N	2.93	0.41
35:4:43:ASP:HB2	35:4:50:GLN:NE2	2.32	0.41
36:5:67:VAL:HG23	36:5:68:ASN:N	2.35	0.41
38:X:27:TYR:O	38:X:29:ASP:N	2.48	0.41
1:A:929:LEU:HG	4:N:148:ALA:HB2	2.03	0.41
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.21	0.41
1:A:1580:GLY:HA3	3:L:389:ASN:CG	2.46	0.41
2:K:285:HIS:C	2:K:287:MET:N	2.75	0.41
2:K:350:LYS:HB3	2:K:351:PRO:CD	2.49	0.41
2:K:390:LEU:HD22	5:J:428:TRP:NE1	2.35	0.41
3:L:328:VAL:HA	3:L:331:HIS:CD2	2.48	0.41
5:J:352:ILE:O	5:J:356:LEU:HG	2.20	0.41
8:C:114:PRO:C	8:C:115:LYS:HG2	2.45	0.41
8:C:175:LEU:HD23	8:C:176:ARG:N	2.35	0.41
8:C:629:TYR:OH	8:C:658:ASP:OD2	2.37	0.41
8:C:733:ASN:OD1	8:C:734:CYS:N	2.54	0.41
18:B:163:C:P	18:B:164:C:OP1	2.79	0.41
27:D:491:PHE:CE1	27:D:533:LEU:HD21	2.54	0.41
27:D:727:TYR:CD2	27:D:760:LYS:HE2	2.55	0.41
27:D:1821:GLU:CG	27:D:1845:SER:HB2	2.51	0.41
22:Q:26:TRP:O	22:Q:43:VAL:HA	2.21	0.41
29:H:142:C:HO2'	29:H:143:G:H8	1.66	0.41
32:1:874:GLU:HB3	34:3:1315:ARG:NH2	2.35	0.41
34:3:527:LEU:HD21	34:3:552:ILE:HG21	2.03	0.41
35:4:42:LYS:HB2	35:4:49:TYR:CE1	2.56	0.41
43:v:178:PRO:HB3	43:v:203:TYR:HD2	1.85	0.41
1:A:576:HIS:HE1	1:A:593:LEU:O	2.04	0.41
1:A:631:LEU:HD21	1:A:663:LEU:HD13	2.03	0.41
1:A:766:ILE:O	1:A:770:MET:HG3	2.20	0.41
1:A:1521:ARG:HD3	3:L:404:TYR:CE2	2.55	0.41
1:A:2152:TRP:HZ3	27:D:1064:PRO:CD	2.33	0.41
1:A:2326:SER:O	1:A:2329:PHE:HB3	2.21	0.41
2:K:422:TYR:HD1	2:K:429:LYS:HA	1.85	0.41
3:L:264:LYS:NZ	17:I:39:C:O2	2.53	0.41
18:B:30:A:H2'	18:B:31:G:H8	1.86	0.41
18:B:38:A:N1	18:B:117:G:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:912:PHE:CB	27:D:944:LEU:HD23	2.33	0.41
27:D:1583:VAL:HB	27:D:1665:LEU:HD23	2.03	0.41
27:D:1640:LEU:CD1	27:D:1649:GLU:HG3	2.51	0.41
23:R:80:LYS:HE3	23:R:82:LYS:CG	2.50	0.41
25:U:29:VAL:HG22	25:U:81:ILE:HG13	2.02	0.41
25:U:45:THR:HG23	25:U:50:ASN:O	2.20	0.41
25:j:32:LYS:HG3	25:j:77:ASN:HA	2.03	0.41
32:1:173:ILE:HG12	32:1:185:MET:SD	2.61	0.41
32:1:490:ARG:HH22	38:X:25:ASN:CG	2.29	0.41
32:1:927:ALA:C	32:1:929:ASN:N	2.78	0.41
34:3:97:THR:OG1	34:3:100:HIS:HB3	2.21	0.41
34:3:426:TYR:HA	34:3:439:PHE:O	2.20	0.41
34:3:690:LEU:HA	34:3:703:MET:O	2.21	0.41
38:X:3:LYS:O	38:X:7:ILE:HD12	2.21	0.41
38:X:68:THR:HG23	38:X:70:GLU:HG2	2.03	0.41
41:u:33:TYR:O	41:u:34:HIS:C	2.62	0.41
41:u:412:TYR:O	41:u:417:LEU:N	2.54	0.41
41:u:431:TYR:CZ	41:u:440:HIS:CD2	3.08	0.41
42:w:199:LYS:O	43:v:208:ASN:HB2	2.20	0.41
42:w:226:LEU:O	42:w:227:ARG:HD3	2.20	0.41
1:A:167:TYR:CD1	1:A:547:LEU:HD21	2.56	0.41
1:A:380:ARG:HB3	1:A:382:GLU:OE1	2.21	0.41
1:A:408:SER:HA	8:C:272:ARG:NH2	2.36	0.41
1:A:522:TYR:CE1	1:A:686:ILE:HD12	2.55	0.41
1:A:687:ILE:O	1:A:688:TYR:C	2.62	0.41
1:A:1043:ARG:O	1:A:1045:GLN:HG3	2.21	0.41
1:A:1048:VAL:HA	1:A:1249:SER:O	2.20	0.41
1:A:2193:PHE:HA	1:A:2196:ILE:HG12	2.03	0.41
1:A:2249:ASP:OD1	27:D:1307:SER:OG	2.34	0.41
1:A:2319:LYS:HG3	1:A:2320:ASP:N	2.36	0.41
2:K:235:ILE:HD13	2:K:280:ILE:HG21	2.03	0.41
2:K:235:ILE:CD1	2:K:280:ILE:HD13	2.51	0.41
2:K:390:LEU:HD12	2:K:390:LEU:O	2.21	0.41
3:L:359:PRO:HD3	6:E:56:PHE:CD2	2.56	0.41
5:J:163:ASN:HB3	5:J:167:GLU:O	2.20	0.41
5:J:271:LYS:HE3	5:J:304:ARG:HH11	1.85	0.41
8:C:161:ILE:HG12	8:C:177:TYR:OH	2.21	0.41
8:C:365:GLU:HG3	8:C:366:ASN:H	1.86	0.41
8:C:625:ILE:HG23	8:C:629:TYR:HD2	1.85	0.41
8:C:728:LEU:HD12	8:C:730:LYS:HE3	2.02	0.41
8:C:752:ARG:HD3	8:C:759:SER:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:884:ARG:CB	8:C:910:GLU:HG3	2.44	0.41
16:F:47:A:C3'	16:F:48:C:H5'	2.50	0.41
18:B:26:A:O4'	18:B:131:A:H5'	2.21	0.41
27:D:594:LEU:HD22	27:D:598:GLN:OE1	2.21	0.41
27:D:707:PHE:N	27:D:707:PHE:CD1	2.89	0.41
27:D:778:LYS:O	27:D:782:LYS:HG2	2.21	0.41
27:D:944:LEU:O	27:D:948:MET:HG2	2.20	0.41
27:D:1647:ASN:O	27:D:1651:ILE:HG12	2.21	0.41
27:D:1898:ASP:HA	27:D:1943:PHE:HZ	1.86	0.41
27:D:1973:ALA:O	27:D:1977:MET:HG3	2.21	0.41
27:D:2139:ASN:ND2	27:D:2159:GLU:OE1	2.53	0.41
22:Q:4:VAL:HG12	22:Q:8:LYS:HZ1	1.86	0.41
23:R:45:ILE:HG23	23:R:105:LEU:HB3	2.02	0.41
23:R:48:LEU:HD21	23:R:96:LEU:HD21	2.02	0.41
23:R:105:LEU:HD12	25:U:70:GLU:O	2.21	0.41
20:S:77:LEU:HD23	20:S:77:LEU:O	2.20	0.41
28:G:522:U:H5	38:X:111:PRO:O	2.04	0.41
29:H:548:G:C6	29:H:549:C:N4	2.89	0.41
29:H:1118:U:H2'	29:H:1119:C:H6	1.86	0.41
29:H:1139:G:O2'	29:H:1140:U:O5'	2.33	0.41
29:H:1144:U:O2	29:H:1144:U:C2'	2.69	0.41
22:m:99:ASP:CB	41:u:183:GLU:CB	2.99	0.41
23:n:80:LYS:HD2	23:n:81:GLY:H	1.85	0.41
23:n:80:LYS:HD3	23:n:80:LYS:HA	1.96	0.41
32:1:198:GLU:O	32:1:202:ASN:HB3	2.20	0.41
32:1:467:VAL:HG12	32:1:469:SER:H	1.86	0.41
34:3:380:LEU:HA	34:3:389:PHE:O	2.21	0.41
34:3:390:LYS:O	34:3:407:LEU:HA	2.20	0.41
34:3:626:PRO:HB3	34:3:630:ILE:HB	2.02	0.41
34:3:643:ILE:HG23	34:3:651:LEU:HD21	2.02	0.41
34:3:643:ILE:HD11	34:3:653:TYR:HD1	1.85	0.41
34:3:693:ILE:CG2	34:3:701:LYS:HB2	2.51	0.41
34:3:832:TRP:CG	34:3:833:LYS:N	2.89	0.41
34:3:1129:VAL:O	34:3:1140:THR:HA	2.20	0.41
34:3:1135:TYR:HB3	34:3:1311:TYR:CE2	2.56	0.41
34:3:1189:LEU:HD21	34:3:1192:HIS:HB2	2.03	0.41
35:4:10:THR:HA	35:4:56:GLU:HA	2.03	0.41
36:5:41:ARG:NH1	36:5:83:LYS:HZ2	2.18	0.41
38:X:32:TYR:OH	39:Y:162:LEU:HD11	2.20	0.41
39:Y:208:SER:HB3	39:Y:212:ARG:N	2.36	0.41
41:u:132:LEU:H	41:u:132:LEU:CD2	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:w:221:LEU:HA	42:w:224:MET:HB3	2.02	0.41
43:v:78:TRP:NE1	43:v:82:GLU:OE2	2.54	0.41
1:A:293:VAL:HG22	1:A:294:ASN:N	2.36	0.41
1:A:499:VAL:HG12	1:A:501:LEU:HD12	2.02	0.41
1:A:507:LEU:O	1:A:508:GLN:HB2	2.21	0.41
1:A:615:LEU:HD21	1:A:619:PHE:CE2	2.56	0.41
1:A:1996:LEU:HA	1:A:1999:ILE:O	2.21	0.41
2:K:274:HIS:HD2	2:K:276:SER:HB3	1.86	0.41
4:N:771:ALA:O	4:N:775:VAL:HG23	2.21	0.41
8:C:133:ILE:HG13	8:C:134:ILE:N	2.36	0.41
8:C:652:MET:HB3	8:C:652:MET:HE2	1.79	0.41
17:I:149:U:H1'	23:R:99:ASP:CG	2.46	0.41
18:B:24:G:H2'	18:B:25:G:C8	2.56	0.41
18:B:65:U:H2'	18:B:66:A:C8	2.57	0.41
27:D:777:SER:O	27:D:781:LEU:HB2	2.21	0.41
27:D:1699:THR:HG22	22:Q:144:ARG:CZ	2.50	0.41
24:T:86:ASN:HD21	25:U:79:LEU:HA	1.86	0.41
29:H:1092:A:H3'	29:H:1093:C:C6	2.47	0.41
32:1:297:THR:HA	32:1:300:ALA:HB3	2.03	0.41
32:1:348:VAL:HG13	32:1:349:LEU:N	2.29	0.41
34:3:76:ILE:HD11	34:3:422:PHE:CD1	2.56	0.41
34:3:242:VAL:HG22	34:3:252:PHE:CB	2.51	0.41
34:3:270:PHE:HD2	34:3:284:ALA:HB3	1.85	0.41
34:3:555:PRO:O	34:3:587:THR:HB	2.21	0.41
34:3:612:PRO:HA	34:3:618:TYR:CD1	2.54	0.41
34:3:1007:LYS:HE3	34:3:1009:LEU:HD21	2.03	0.41
41:u:171:THR:HG21	41:u:181:GLU:CD	2.46	0.41
42:w:140:ALA:O	42:w:143:LYS:HB2	2.21	0.41
1:A:974:ASN:C	1:A:976:GLN:H	2.29	0.40
1:A:1054:LEU:HD21	1:A:1168:ILE:HD11	2.03	0.40
1:A:1234:VAL:HG12	1:A:1235:PRO:O	2.21	0.40
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	2.02	0.40
2:K:67:GLU:OE1	2:K:75:ARG:NE	2.45	0.40
2:K:183:LEU:HD23	2:K:190:VAL:HG22	2.02	0.40
4:N:793:ILE:HA	4:N:796:ASP:HB3	2.02	0.40
5:J:141:ASN:HD22	5:J:144:LEU:HG	1.85	0.40
8:C:795:ILE:O	8:C:799:PHE:HB2	2.21	0.40
18:B:117:G:H2'	18:B:118:U:C6	2.56	0.40
18:B:148:G:H2'	18:B:149:U:C6	2.56	0.40
27:D:1326:ASN:OD1	27:D:1326:ASN:N	2.54	0.40
27:D:1651:ILE:O	27:D:1655:LEU:HG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:2104:GLY:HA2	27:D:2112:TYR:CD2	2.53	0.40
24:T:16:CYS:HA	24:T:19:ASN:ND2	2.36	0.40
28:G:499:U:H2'	28:G:500:A:H8	1.85	0.40
29:H:43:G:H2'	29:H:44:U:C6	2.56	0.40
32:1:335:LYS:O	32:1:338:GLN:HB2	2.21	0.40
34:3:542:THR:HG21	34:3:547:ASN:OD1	2.21	0.40
34:3:742:HIS:HE2	34:3:752:LYS:HE2	1.85	0.40
34:3:1179:ASN:OD1	34:3:1180:THR:N	2.54	0.40
36:5:43:VAL:HA	36:5:72:TYR:CE2	2.56	0.40
41:u:59:ILE:HD12	42:w:168:THR:HG21	2.04	0.40
41:u:181:GLU:O	41:u:181:GLU:HG3	2.21	0.40
42:w:195:ILE:HA	42:w:196:PRO:HD3	1.92	0.40
43:v:219:LEU:O	43:v:219:LEU:HD12	2.20	0.40
1:A:457:ASP:OD1	1:A:458:PHE:N	2.54	0.40
1:A:697:LYS:HA	1:A:697:LYS:HD2	1.90	0.40
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.54	0.40
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.36	0.40
1:A:1673:LEU:HA	1:A:1678:ILE:HB	2.02	0.40
1:A:1879:ILE:HG12	1:A:1913:THR:HG22	2.03	0.40
1:A:2052:GLU:CD	5:J:290:PRO:HG2	2.46	0.40
1:A:2395:PHE:HE1	27:D:1061:ALA:HA	1.74	0.40
3:L:340:LYS:O	3:L:344:LEU:HG	2.21	0.40
8:C:104:THR:O	8:C:107:THR:N	2.55	0.40
8:C:114:PRO:HB2	8:C:160:ARG:O	2.20	0.40
8:C:362:LYS:HG3	8:C:363:PRO:HD2	2.03	0.40
8:C:405:ARG:NH2	18:B:1:A:C8	2.86	0.40
8:C:869:HIS:CD2	8:C:925:LEU:HD22	2.56	0.40
8:C:945:LEU:HD12	8:C:945:LEU:O	2.22	0.40
16:F:80:U:H2'	16:F:81:G:H8	1.86	0.40
17:I:94:U:C4	17:I:95:C:C4	3.09	0.40
17:I:133:C:H2'	17:I:134:U:C6	2.56	0.40
27:D:502:ILE:HD11	27:D:522:PRO:HD2	2.02	0.40
27:D:610:GLU:OE1	27:D:1009:TYR:CE2	2.73	0.40
27:D:1092:PHE:CD1	27:D:1095:ASN:HB3	2.56	0.40
27:D:1331:THR:HG23	27:D:1346:LYS:O	2.21	0.40
27:D:1367:PHE:HB2	27:D:1527:MET:SD	2.62	0.40
27:D:1689:ASP:OD1	27:D:1692:GLU:HB3	2.21	0.40
27:D:1853:ALA:CB	27:D:1863:ILE:HG13	2.52	0.40
21:P:88:ARG:HG2	21:P:90:GLU:N	2.24	0.40
32:1:488:TRP:CE3	32:1:536:MET:HE3	2.57	0.40
32:1:854:ARG:NH1	33:2:183:LEU:HD12	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:363:TYR:C	33:2:365:GLY:H	2.29	0.40
34:3:270:PHE:CD2	34:3:284:ALA:HB3	2.56	0.40
34:3:565:ASN:C	34:3:567:SER:H	2.28	0.40
34:3:820:VAL:HG12	34:3:828:VAL:HG12	2.03	0.40
34:3:1336:PHE:O	34:3:1339:LYS:HG2	2.21	0.40
1:A:156:THR:OG1	1:A:157:ASP:N	2.54	0.40
1:A:913:VAL:HG21	4:N:163:THR:HG22	2.03	0.40
1:A:1087:ASN:HA	1:A:1099:ASN:O	2.22	0.40
1:A:2177:VAL:HB	1:A:2338:GLN:HE22	1.87	0.40
1:A:2264:GLU:HG2	1:A:2266:LEU:HG	2.03	0.40
2:K:51:VAL:HG13	2:K:76:LEU:CD1	2.51	0.40
2:K:269:SER:H	2:K:284:SER:HA	1.85	0.40
3:L:172:ILE:O	3:L:176:THR:HG23	2.21	0.40
3:L:305:MET:HG2	3:L:337:LEU:CD2	2.52	0.40
4:N:832:LEU:HD11	4:N:845:LEU:HD11	2.03	0.40
17:I:96:A:C6	17:I:137:G:C6	3.09	0.40
18:B:85:U:C2	18:B:86:G:C8	3.09	0.40
27:D:619:SER:O	27:D:622:LEU:HG	2.21	0.40
27:D:1245:ASP:HA	27:D:1288:PHE:CD1	2.55	0.40
27:D:1387:HIS:CE1	27:D:1392:LYS:CB	3.04	0.40
27:D:1448:THR:HB	27:D:1449:PRO:HD2	2.02	0.40
27:D:1497:PHE:CE2	27:D:1762:ILE:HG21	2.55	0.40
27:D:1644:MET:HE2	27:D:1644:MET:HB3	1.97	0.40
22:Q:139:ASN:O	22:Q:140:LYS:CB	2.69	0.40
23:R:43:PRO:HA	23:R:56:ALA:O	2.22	0.40
34:3:97:THR:O	34:3:98:GLU:C	2.64	0.40
34:3:118:GLN:HE21	34:3:1299:ILE:CD1	2.33	0.40
34:3:361:LYS:C	34:3:363:VAL:H	2.28	0.40
34:3:507:ASN:ND2	34:3:509:LYS:HE2	2.36	0.40
35:4:135:ILE:HB	35:4:156:GLU:HG2	2.04	0.40
1:A:264:ILE:HD12	1:A:647:PHE:CE1	2.57	0.40
1:A:1364:GLU:OE2	1:A:1389:TYR:OH	2.32	0.40
1:A:2152:TRP:CD1	1:A:2391:HIS:CD2	3.09	0.40
2:K:159:LEU:HB3	2:K:430:MET:HE2	2.03	0.40
2:K:362:TYR:CD1	2:K:363:GLN:HG3	2.56	0.40
2:K:380:LYS:O	2:K:382:ASP:N	2.53	0.40
3:L:441:MET:CE	3:L:444:ARG:HH21	2.34	0.40
6:E:63:ASP:HB2	6:E:66:GLU:HB2	2.01	0.40
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.56	0.40
16:F:61:C:C2	16:F:62:A:C8	3.09	0.40
17:I:24:A:C2	17:I:50:G:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:91:U:O2'	17:I:92:C:P	2.79	0.40
27:D:502:ILE:CD1	27:D:522:PRO:HD2	2.51	0.40
27:D:557:ILE:HG23	27:D:630:LEU:HD23	2.04	0.40
27:D:725:ALA:O	27:D:729:LYS:HG2	2.21	0.40
27:D:1486:ALA:HB1	27:D:1746:LEU:HD23	2.03	0.40
27:D:1585:LEU:CD1	27:D:1591:CYS:HA	2.52	0.40
27:D:1641:TYR:CZ	27:D:1644:MET:HG2	2.57	0.40
27:D:1895:ARG:O	27:D:1895:ARG:HG3	2.21	0.40
27:D:2086:VAL:HB	27:D:2095:LYS:HB3	2.03	0.40
27:D:2138:HIS:C	27:D:2159:GLU:HG3	2.46	0.40
24:T:19:ASN:O	24:T:23:GLN:HG3	2.22	0.40
29:H:43:G:H2'	29:H:44:U:H6	1.87	0.40
29:H:1145:U:O2	29:H:1145:U:C2'	2.69	0.40
26:k:26:ALA:C	26:k:43:ALA:HB3	2.46	0.40
32:l:215:ASP:OD1	32:l:216:GLN:N	2.53	0.40
32:l:737:SER:O	32:l:743:ARG:NH1	2.54	0.40
33:2:289:LYS:HB3	35:4:30:ILE:HD13	2.02	0.40
34:3:71:PHE:CD2	34:3:95:VAL:HG11	2.57	0.40
34:3:99:THR:O	34:3:120:LEU:HD12	2.21	0.40
34:3:115:ALA:HB2	34:3:169:LEU:HD12	2.02	0.40
34:3:513:LEU:HD21	34:3:886:PHE:CD2	2.56	0.40
34:3:782:GLU:O	34:3:816:MET:N	2.54	0.40
34:3:1029:SER:OG	34:3:1045:MET:HA	2.20	0.40
35:4:107:ILE:HD13	35:4:154:TYR:HB3	2.03	0.40
35:4:110:LEU:O	35:4:152:TYR:HA	2.22	0.40
36:5:2:SER:OG	36:5:3:ARG:N	2.54	0.40
37:6:20:GLY:O	37:6:21:LEU:HD12	2.22	0.40
41:u:284:PHE:HE1	41:u:312:ARG:HA	1.86	0.40
41:u:521:TYR:O	41:u:525:LYS:HG3	2.21	0.40
42:w:89:SER:O	42:w:93:MET:HG2	2.22	0.40
42:w:157:LYS:O	42:w:158:ARG:C	2.65	0.40
1:A:837:GLY:C	1:A:1317:ARG:HH12	2.25	0.40
1:A:1046:SER:O	1:A:1173:HIS:HD2	2.04	0.40
3:L:126:GLU:O	3:L:130:LEU:HG	2.21	0.40
4:N:15:TYR:OH	6:E:13:TRP:CD1	2.69	0.40
8:C:473:LEU:HD23	8:C:473:LEU:HA	1.95	0.40
8:C:775:ILE:HD12	8:C:817:GLN:NE2	2.37	0.40
16:F:26:A:H2'	16:F:27:U:C6	2.56	0.40
16:F:42:A:O2'	16:F:43:C:H5'	2.21	0.40
27:D:464:HIS:CE1	27:D:706:GLN:HE21	2.40	0.40
27:D:562:PRO:HA	27:D:609:PRO:CD	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:D:781:LEU:HD21	27:D:798:GLU:CG	2.49	0.40
27:D:1580:SER:H	27:D:1678:ASP:HB2	1.85	0.40
27:D:1688:TYR:CE1	27:D:1896:LYS:HE2	2.57	0.40
20:S:34:VAL:HG22	20:S:45:ARG:HD2	2.02	0.40
26:V:8:LYS:HD2	26:V:11:MET:HG3	2.02	0.40
26:V:36:LEU:O	26:V:38:VAL:HG23	2.21	0.40
29:H:145:G:O2'	29:H:146:A:H5'	2.22	0.40
29:H:1161:U:H2'	29:H:1162:U:H6	1.86	0.40
29:H:1168:U:H2'	29:H:1169:C:C6	2.56	0.40
33:2:197:PRO:HB3	33:2:258:TRP:CH2	2.56	0.40
33:2:364:PHE:CD2	34:3:1124:LEU:HD21	2.57	0.40
34:3:1035:LEU:HD11	34:3:1042:LEU:HD23	2.03	0.40
35:4:13:VAL:HG12	35:4:16:ILE:HD11	2.03	0.40
36:5:37:VAL:O	36:5:38:ARG:HG2	2.22	0.40
41:u:230:MET:HA	41:u:314:PHE:CE1	2.56	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	2169/2413 (90%)	2040 (94%)	115 (5%)	14 (1%)	21	50
2	K	425/465 (91%)	388 (91%)	34 (8%)	3 (1%)	18	47
3	L	410/494 (83%)	392 (96%)	15 (4%)	3 (1%)	18	47
4	N	678/899 (75%)	626 (92%)	51 (8%)	1 (0%)	48	78
5	J	294/469 (63%)	281 (96%)	10 (3%)	3 (1%)	12	40
6	E	137/143 (96%)	128 (93%)	9 (7%)	0	100	100
7	M	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
8	C	837/1008 (83%)	779 (93%)	53 (6%)	5 (1%)	21	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	z	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
10	q	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
11	r	75/89 (84%)	70 (93%)	5 (7%)	0	100	100
12	x	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
13	t	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	9	31
14	y	62/115 (54%)	62 (100%)	0	0	100	100
15	s	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
19	O	68/587 (12%)	64 (94%)	3 (4%)	1 (2%)	8	30
20	S	80/101 (79%)	77 (96%)	3 (4%)	0	100	100
20	d	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	4	21
20	l	79/101 (78%)	70 (89%)	8 (10%)	1 (1%)	9	33
21	P	66/196 (34%)	62 (94%)	4 (6%)	0	100	100
21	a	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
21	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
22	Q	93/146 (64%)	89 (96%)	3 (3%)	1 (1%)	11	38
22	b	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	9	31
22	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
23	R	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
23	c	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
23	n	63/110 (57%)	60 (95%)	3 (5%)	0	100	100
24	T	73/94 (78%)	72 (99%)	1 (1%)	0	100	100
24	e	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
24	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	U	71/86 (83%)	68 (96%)	3 (4%)	0	100	100
25	f	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	12
25	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
26	V	73/77 (95%)	66 (90%)	6 (8%)	1 (1%)	9	31
26	g	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
26	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	D	1694/2163 (78%)	1631 (96%)	60 (4%)	3 (0%)	43	71
30	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	p	69/111 (62%)	67 (97%)	2 (3%)	0	100	100
32	1	814/971 (84%)	762 (94%)	46 (6%)	6 (1%)	18	47
33	2	205/436 (47%)	192 (94%)	11 (5%)	2 (1%)	12	40
34	3	1164/1361 (86%)	1046 (90%)	109 (9%)	9 (1%)	16	44
35	4	165/213 (78%)	164 (99%)	1 (1%)	0	100	100
36	5	101/107 (94%)	87 (86%)	13 (13%)	1 (1%)	12	40
37	6	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	10	35
38	X	126/148 (85%)	117 (93%)	7 (6%)	2 (2%)	7	29
39	Y	85/266 (32%)	80 (94%)	3 (4%)	2 (2%)	4	22
40	Z	20/204 (10%)	14 (70%)	6 (30%)	0	100	100
41	u	453/530 (86%)	415 (92%)	38 (8%)	0	100	100
42	w	123/280 (44%)	112 (91%)	11 (9%)	0	100	100
43	v	168/266 (63%)	142 (84%)	25 (15%)	1 (1%)	21	50
All	All	12585/17187 (73%)	11769 (94%)	746 (6%)	70 (1%)	23	50

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	PRO
2	K	395	ILE
3	L	328	VAL
8	C	364	PHE
8	C	602	VAL
30	o	68	PRO
32	1	831	SER
32	1	836	TYR
33	2	368	ILE
34	3	363	VAL
34	3	413	ILE
34	3	1299	ILE
38	X	17	LEU
1	A	156	THR
1	A	1088	VAL
5	J	167	GLU
8	C	133	ILE
8	C	134	ILE
20	d	40	MET

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Mol	Chain	Res	Type
22	b	12	ASN
25	f	24	ASN
25	f	49	PHE
22	Q	140	LYS
32	1	830	MET
32	1	835	ILE
39	Y	172	ILE
39	Y	230	SER
5	J	331	VAL
27	D	791	PRO
27	D	1896	LYS
26	V	60	GLN
34	3	364	THR
1	A	508	GLN
1	A	1621	VAL
1	A	1869	ASN
1	A	2321	ILE
3	L	151	LYS
4	N	736	ASP
5	J	286	ASN
19	O	212	VAL
27	D	960	ILE
34	3	961	CYS
34	3	1233	SER
37	6	19	ILE
1	A	239	PHE
1	A	645	ASP
25	f	50	ASN
20	l	81	ALA
33	2	167	LYS
38	X	18	SER
43	v	232	GLY
2	K	286	ASP
20	d	51	GLU
36	5	38	ARG
1	A	1870	VAL
25	j	15	PRO
30	o	52	LYS
32	1	348	VAL
8	C	829	VAL
34	3	859	ILE
1	A	407	VAL

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Mol	Chain	Res	Type
13	t	41	VAL
1	A	699	PRO
1	A	2330	GLU
2	K	176	LYS
3	L	358	ILE
32	1	386	TYR
34	3	523	ILE
34	3	1031	ILE
1	A	264	ILE

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	1964/2182 (90%)	1959 (100%)	5 (0%)	86	84
2	K	373/410 (91%)	371 (100%)	2 (0%)	81	81
3	L	327/445 (74%)	327 (100%)	0	100	100
4	N	361/813 (44%)	361 (100%)	0	100	100
5	J	248/436 (57%)	248 (100%)	0	100	100
6	E	129/132 (98%)	129 (100%)	0	100	100
7	M	104/104 (100%)	104 (100%)	0	100	100
8	C	757/910 (83%)	756 (100%)	1 (0%)	88	89
19	O	60/534 (11%)	59 (98%)	1 (2%)	53	67
20	S	71/89 (80%)	71 (100%)	0	100	100
20	l	67/89 (75%)	65 (97%)	2 (3%)	36	59
21	P	64/176 (36%)	64 (100%)	0	100	100
21	h	67/176 (38%)	66 (98%)	1 (2%)	57	69
22	Q	81/129 (63%)	80 (99%)	1 (1%)	63	72
22	m	77/129 (60%)	74 (96%)	3 (4%)	28	53
23	R	85/103 (82%)	85 (100%)	0	100	100
23	n	59/103 (57%)	51 (86%)	8 (14%)	3	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	T	69/83 (83%)	69 (100%)	0	100	100
24	i	65/83 (78%)	60 (92%)	5 (8%)	12	37
25	U	65/77 (84%)	65 (100%)	0	100	100
25	j	61/77 (79%)	60 (98%)	1 (2%)	55	68
26	V	64/66 (97%)	64 (100%)	0	100	100
26	k	58/66 (88%)	55 (95%)	3 (5%)	21	48
27	D	1524/1955 (78%)	1520 (100%)	4 (0%)	86	84
30	o	46/219 (21%)	43 (94%)	3 (6%)	15	42
31	p	23/100 (23%)	23 (100%)	0	100	100
32	1	724/867 (84%)	723 (100%)	1 (0%)	88	89
33	2	190/392 (48%)	190 (100%)	0	100	100
34	3	1088/1244 (88%)	1086 (100%)	2 (0%)	87	85
35	4	154/189 (82%)	154 (100%)	0	100	100
36	5	93/97 (96%)	93 (100%)	0	100	100
37	6	76/77 (99%)	76 (100%)	0	100	100
38	X	114/132 (86%)	111 (97%)	3 (3%)	40	61
39	Y	77/240 (32%)	65 (84%)	12 (16%)	2	10
40	Z	21/186 (11%)	18 (86%)	3 (14%)	3	13
41	u	425/492 (86%)	417 (98%)	8 (2%)	50	66
42	w	118/259 (46%)	115 (98%)	3 (2%)	42	62
43	v	156/236 (66%)	154 (99%)	2 (1%)	61	71
All	All	10105/14097 (72%)	10031 (99%)	74 (1%)	73	78

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	940	ILE
1	A	1038	ILE
1	A	2289	ILE
1	A	2332	THR
1	A	2333	PHE
2	K	443	LEU
2	K	451	PHE
8	C	545	LEU
19	O	217	ILE

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Mol	Chain	Res	Type
27	D	491	PHE
27	D	707	PHE
27	D	1008	PHE
27	D	1551	PHE
22	Q	82	LEU
21	h	47	GLU
24	i	16	CYS
24	i	18	PHE
24	i	25	THR
24	i	79	LYS
24	i	81	LEU
25	j	79	LEU
26	k	18	ASN
26	k	41	ASP
26	k	71	LEU
20	l	10	LEU
20	l	79	LYS
22	m	20	LYS
22	m	30	GLN
22	m	77	ASP
23	n	48	LEU
23	n	49	ARG
23	n	77	THR
23	n	79	LYS
23	n	80	LYS
23	n	82	LYS
23	n	99	ASP
23	n	100	SER
30	o	4	THR
30	o	44	PRO
30	o	71	SER
32	1	757	ILE
34	3	147	PHE
34	3	523	ILE
38	X	6	GLN
38	X	7	ILE
38	X	110	ARG
39	Y	160	LYS
39	Y	168	GLN
39	Y	169	LYS
39	Y	170	LEU
39	Y	172	ILE

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Mol	Chain	Res	Type
39	Y	174	VAL
39	Y	207	THR
39	Y	208	SER
39	Y	209	LEU
39	Y	213	LYS
39	Y	214	LEU
39	Y	262	LEU
40	Z	38	LEU
40	Z	40	LEU
40	Z	42	SER
41	u	27	ARG
41	u	65	VAL
41	u	81	ILE
41	u	217	LEU
41	u	298	HIS
41	u	317	SER
41	u	357	LEU
41	u	358	THR
42	w	113	MET
42	w	153	ILE
42	w	158	ARG
43	v	226	MET
43	v	246	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (203) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	326	ASN
1	A	429	ASN
1	A	592	HIS
1	A	617	ASN
1	A	620	HIS
1	A	648	GLN
1	A	658	ASN
1	A	796	ASN
1	A	868	GLN
1	A	948	HIS
1	A	952	ASN
1	A	976	GLN
1	A	997	GLN
1	A	1033	ASN
1	A	1087	ASN

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Mol	Chain	Res	Type
1	A	1146	GLN
1	A	1369	ASN
1	A	1404	HIS
1	A	1470	GLN
1	A	1496	GLN
1	A	1508	HIS
1	A	1532	HIS
1	A	1603	ASN
1	A	1618	ASN
1	A	1635	HIS
1	A	1687	HIS
1	A	1718	HIS
1	A	1809	ASN
1	A	1839	ASN
1	A	1947	HIS
1	A	2018	ASN
1	A	2306	ASN
1	A	2336	HIS
1	A	2338	GLN
2	K	137	GLN
2	K	144	GLN
2	K	232	ASN
2	K	247	GLN
2	K	360	ASN
2	K	374	ASN
2	K	388	GLN
2	K	450	HIS
3	L	113	HIS
3	L	136	GLN
3	L	160	HIS
3	L	185	ASN
3	L	201	ASN
3	L	258	ASN
3	L	267	HIS
3	L	331	HIS
4	N	171	GLN
4	N	173	GLN
4	N	770	ASN
4	N	777	GLN
5	J	141	ASN
5	J	145	HIS
5	J	276	ASN

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Mol	Chain	Res	Type
5	J	409	HIS
6	E	14	HIS
6	E	87	HIS
6	E	111	GLN
7	M	45	ASN
7	M	66	HIS
8	C	112	ASN
8	C	158	HIS
8	C	183	GLN
8	C	251	GLN
8	C	444	GLN
8	C	554	HIS
8	C	608	GLN
8	C	721	GLN
8	C	776	ASN
8	C	837	GLN
8	C	869	HIS
27	D	516	ASN
27	D	568	GLN
27	D	621	ASN
27	D	676	ASN
27	D	706	GLN
27	D	768	HIS
27	D	804	HIS
27	D	894	ASN
27	D	904	GLN
27	D	921	ASN
27	D	1025	HIS
27	D	1028	GLN
27	D	1123	HIS
27	D	1148	GLN
27	D	1266	HIS
27	D	1281	GLN
27	D	1349	ASN
27	D	1354	GLN
27	D	1390	GLN
27	D	1418	HIS
27	D	1443	HIS
27	D	1517	ASN
27	D	1611	ASN
27	D	1726	HIS
27	D	1756	ASN

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Mol	Chain	Res	Type
27	D	1855	HIS
27	D	1931	GLN
27	D	1968	ASN
27	D	1996	GLN
27	D	2085	GLN
27	D	2139	ASN
27	D	2161	ASN
21	P	33	GLN
22	Q	30	GLN
22	Q	94	GLN
23	R	52	HIS
23	R	64	HIS
24	T	15	ASN
25	U	77	ASN
26	V	20	ASN
21	h	8	HIS
21	h	91	GLN
24	i	34	GLN
24	i	86	ASN
25	j	25	HIS
25	j	52	GLN
26	k	66	ASN
20	l	17	HIS
20	l	41	ASN
22	m	30	GLN
22	m	86	ASN
23	n	71	ASN
32	1	175	ASN
32	1	311	ASN
32	1	322	HIS
32	1	367	HIS
32	1	376	HIS
32	1	407	HIS
32	1	679	GLN
32	1	695	ASN
32	1	803	ASN
32	1	829	ASN
32	1	853	HIS
32	1	859	ASN
32	1	882	ASN
32	1	887	ASN
32	1	894	HIS

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Mol	Chain	Res	Type
32	1	959	ASN
33	2	136	GLN
33	2	145	GLN
33	2	262	HIS
33	2	273	ASN
33	2	339	ASN
34	3	68	GLN
34	3	73	HIS
34	3	92	GLN
34	3	156	ASN
34	3	165	HIS
34	3	177	GLN
34	3	209	GLN
34	3	249	ASN
34	3	382	GLN
34	3	385	HIS
34	3	398	ASN
34	3	434	ASN
34	3	474	ASN
34	3	481	GLN
34	3	507	ASN
34	3	585	GLN
34	3	590	HIS
34	3	609	HIS
34	3	641	GLN
34	3	669	HIS
34	3	687	HIS
34	3	738	GLN
34	3	920	GLN
34	3	944	ASN
34	3	950	GLN
34	3	1117	HIS
34	3	1154	HIS
34	3	1174	GLN
34	3	1188	GLN
34	3	1191	ASN
34	3	1192	HIS
34	3	1203	HIS
34	3	1359	ASN
35	4	50	GLN
35	4	129	ASN
35	4	170	ASN

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Mol	Chain	Res	Type
35	4	187	ASN
36	5	14	GLN
37	6	37	ASN
38	X	5	GLN
38	X	25	ASN
38	X	106	HIS
39	Y	168	GLN
39	Y	173	ASN
39	Y	236	HIS
39	Y	239	ASN
39	Y	249	GLN
41	u	34	HIS
41	u	91	GLN
41	u	167	ASN
41	u	175	GLN
41	u	191	ASN
41	u	202	GLN
41	u	307	ASN
41	u	440	HIS
43	v	93	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	F	95/112 (84%)	38 (40%)	1 (1%)
17	I	106/160 (66%)	31 (29%)	6 (5%)
18	B	173/214 (80%)	64 (36%)	13 (7%)
28	G	43/44 (97%)	22 (51%)	2 (4%)
29	H	196/1175 (16%)	53 (27%)	23 (11%)
All	All	613/1705 (35%)	208 (33%)	45 (7%)

All (208) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	F	2	U
16	F	12	U
16	F	13	U
16	F	14	U
16	F	17	U
16	F	25	C
16	F	26	A

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Mol	Chain	Res	Type
16	F	28	U
16	F	31	G
16	F	32	U
16	F	37	U
16	F	38	U
16	F	39	G
16	F	40	A
16	F	41	A
16	F	43	C
16	F	44	A
16	F	46	U
16	F	47	A
16	F	48	C
16	F	49	A
16	F	50	G
16	F	51	A
16	F	57	U
16	F	58	C
16	F	64	U
16	F	66	C
16	F	71	G
16	F	75	A
16	F	76	A
16	F	77	G
16	F	82	A
16	F	83	A
16	F	84	C
16	F	86	G
16	F	87	U
16	F	109	U
16	F	111	U
17	I	2	U
17	I	15	G
17	I	19	U
17	I	20	A
17	I	25	U
17	I	27	U
17	I	28	C
17	I	29	A
17	I	30	G
17	I	39	C
17	I	40	G

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Mol	Chain	Res	Type
17	I	41	U
17	I	48	U
17	I	55	U
17	I	60	U
17	I	74	U
17	I	75	U
17	I	76	A
17	I	77	U
17	I	78	A
17	I	79	A
17	I	92	C
17	I	98	G
17	I	134	U
17	I	135	A
17	I	138	U
17	I	139	A
17	I	143	A
17	I	144	A
17	I	145	U
17	I	151	G
18	B	12	C
18	B	13	A
18	B	18	A
18	B	20	U
18	B	24	G
18	B	27	G
18	B	28	G
18	B	32	G
18	B	33	U
18	B	34	C
18	B	35	A
18	B	39	U
18	B	40	C
18	B	41	A
18	B	75	A
18	B	76	U
18	B	77	A
18	B	78	A
18	B	79	C
18	B	80	G
18	B	81	A
18	B	82	A

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Mol	Chain	Res	Type
18	B	83	C
18	B	84	A
18	B	90	C
18	B	92	U
18	B	94	C
18	B	95	C
18	B	96	U
18	B	97	U
18	B	100	A
18	B	101	C
18	B	103	A
18	B	104	G
18	B	108	C
18	B	109	A
18	B	113	G
18	B	121	U
18	B	126	A
18	B	127	U
18	B	128	A
18	B	129	G
18	B	131	A
18	B	132	A
18	B	139	A
18	B	140	A
18	B	141	G
18	B	142	C
18	B	151	A
18	B	160	U
18	B	162	G
18	B	163	C
18	B	164	C
18	B	165	A
18	B	166	U
18	B	167	A
18	B	168	U
18	B	169	U
18	B	170	U
18	B	171	U
18	B	172	U
18	B	173	U
18	B	174	G
18	B	175	G

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Mol	Chain	Res	Type
28	G	481	A
28	G	482	A
28	G	483	A
28	G	484	A
28	G	485	A
28	G	486	A
28	G	487	A
28	G	488	A
28	G	493	A
28	G	501	A
28	G	502	C
28	G	505	A
28	G	506	U
28	G	507	U
28	G	508	U
28	G	509	A
28	G	510	A
28	G	512	U
28	G	515	U
28	G	518	U
28	G	521	U
28	G	522	U
29	H	32	G
29	H	38	U
29	H	47	U
29	H	48	U
29	H	59	C
29	H	65	A
29	H	66	A
29	H	67	A
29	H	68	U
29	H	83	U
29	H	111	C
29	H	115	U
29	H	116	U
29	H	117	U
29	H	118	U
29	H	119	G
29	H	120	G
29	H	140	G
29	H	141	A
29	H	142	C

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Mol	Chain	Res	Type
29	H	145	G
29	H	1090	A
29	H	1094	G
29	H	1095	U
29	H	1096	C
29	H	1097	G
29	H	1098	C
29	H	1100	A
29	H	1101	C
29	H	1102	C
29	H	1103	C
29	H	1104	U
29	H	1105	C
29	H	1106	G
29	H	1119	C
29	H	1120	G
29	H	1121	U
29	H	1122	U
29	H	1123	C
29	H	1124	U
29	H	1125	U
29	H	1126	G
29	H	1130	U
29	H	1139	G
29	H	1141	C
29	H	1142	G
29	H	1143	C
29	H	1144	U
29	H	1145	U
29	H	1146	G
29	H	1149	G
29	H	1150	U
29	H	1166	G

All (45) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	F	50	G
17	I	18	A
17	I	19	U
17	I	24	A
17	I	91	U

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Mol	Chain	Res	Type
17	I	134	U
17	I	142	G
18	B	17	C
18	B	32	G
18	B	33	U
18	B	77	A
18	B	83	C
18	B	94	C
18	B	95	C
18	B	128	A
18	B	130	A
18	B	150	U
18	B	166	U
18	B	168	U
18	B	172	U
28	G	480	A
28	G	514	U
29	H	46	C
29	H	66	A
29	H	117	U
29	H	1095	U
29	H	1096	C
29	H	1097	G
29	H	1100	A
29	H	1101	C
29	H	1102	C
29	H	1105	C
29	H	1119	C
29	H	1120	G
29	H	1121	U
29	H	1122	U
29	H	1123	C
29	H	1124	U
29	H	1125	U
29	H	1138	G
29	H	1141	C
29	H	1142	G
29	H	1144	U
29	H	1145	U
29	H	1149	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	GTP	C	1500	45	33,34,34	1.09	3 (9%)	50,54,54	1.71	7 (14%)

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
44	GTP	C	1500	45	-	4/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	C	1500	GTP	C5-C4	3.15	1.47	1.38
44	C	1500	GTP	C6-N1	-2.45	1.34	1.38
44	C	1500	GTP	C5-N7	-2.14	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C5-C4-N3	-6.09	118.70	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C2-N3-C4	4.84	120.63	112.30
44	C	1500	GTP	N9-C4-N3	4.33	134.60	125.95
44	C	1500	GTP	C6-C5-N7	3.27	136.24	130.29
44	C	1500	GTP	C4-C5-N7	-2.83	106.19	110.67
44	C	1500	GTP	C3'-C2'-C1'	2.41	106.02	101.46
44	C	1500	GTP	O6-C6-C5	-2.06	121.09	126.53

There are no chirality outliers.

All (4) torsion outliers are listed below:

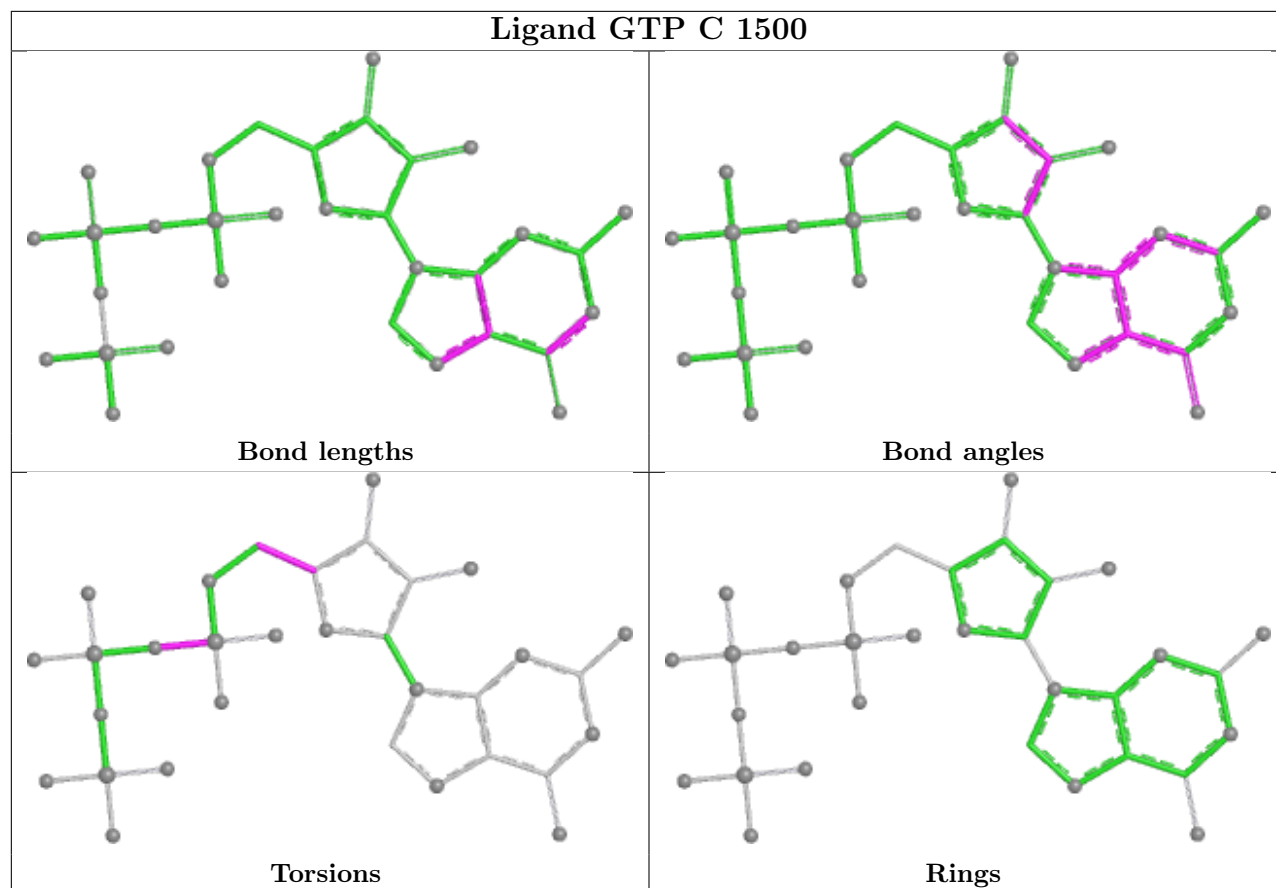
Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'
44	C	1500	GTP	PB-O3A-PA-O2A
44	C	1500	GTP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	C	1500	GTP	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.

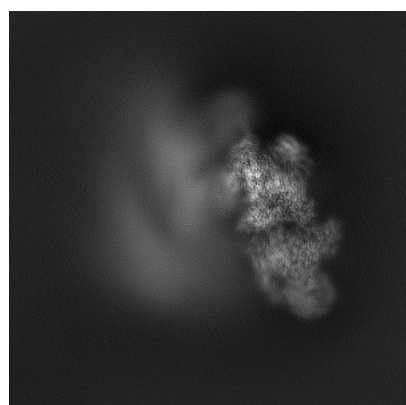
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6972. These allow visual inspection of the internal detail of the map and identification of artifacts.

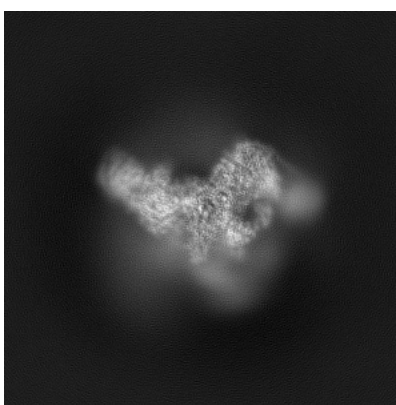
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

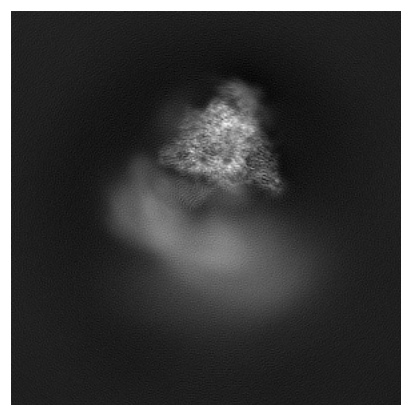
6.1.1 Primary map



X



Y

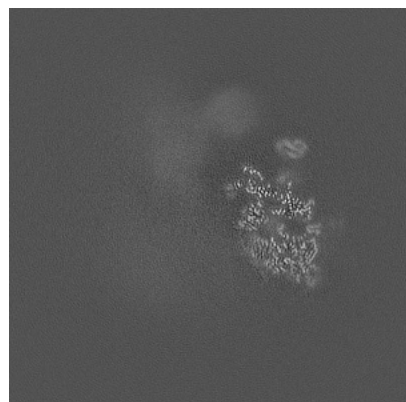


Z

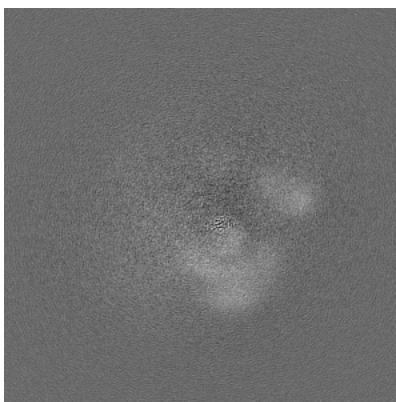
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

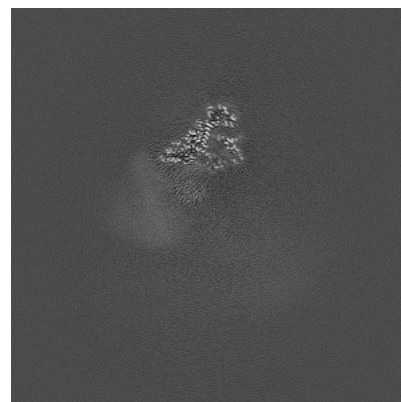
6.2.1 Primary map



X Index: 200



Y Index: 200

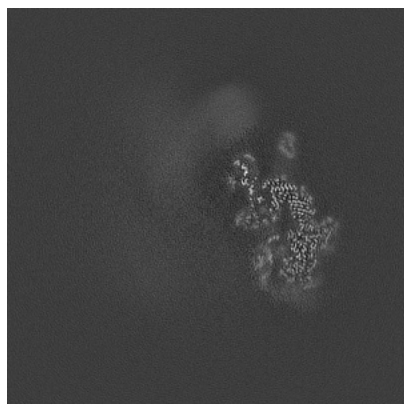


Z Index: 200

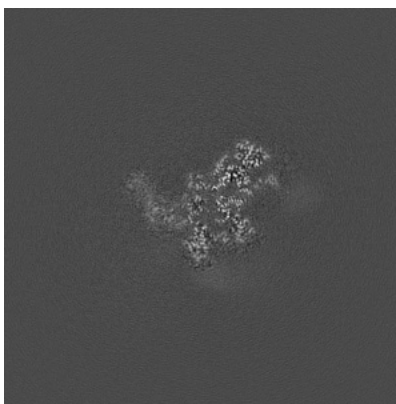
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

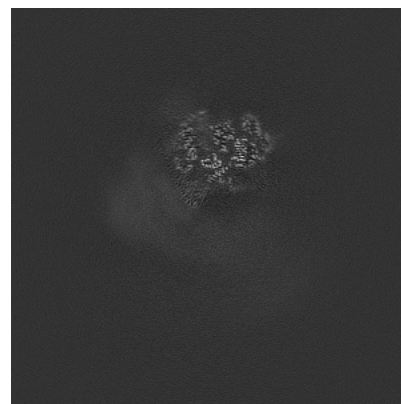
6.3.1 Primary map



X Index: 212



Y Index: 247

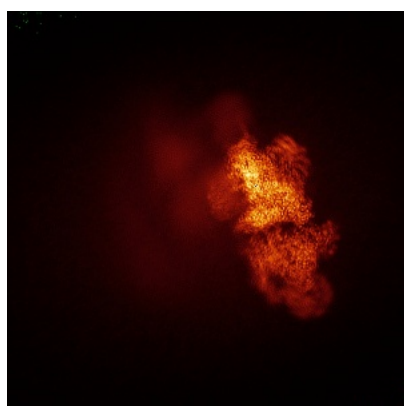


Z Index: 224

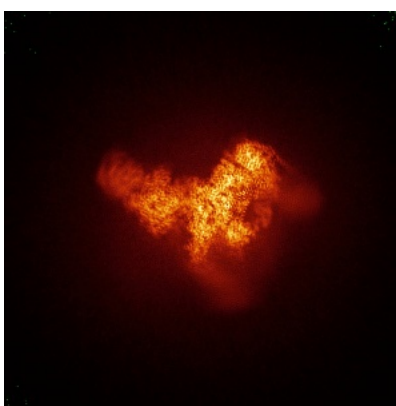
The images above show the largest variance slices of the map in three orthogonal directions.

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

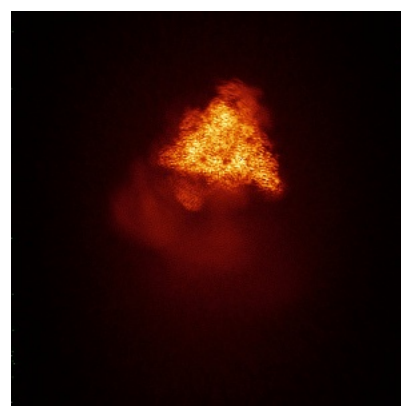
6.4.1 Primary map



X



Y



Z

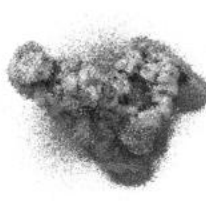
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

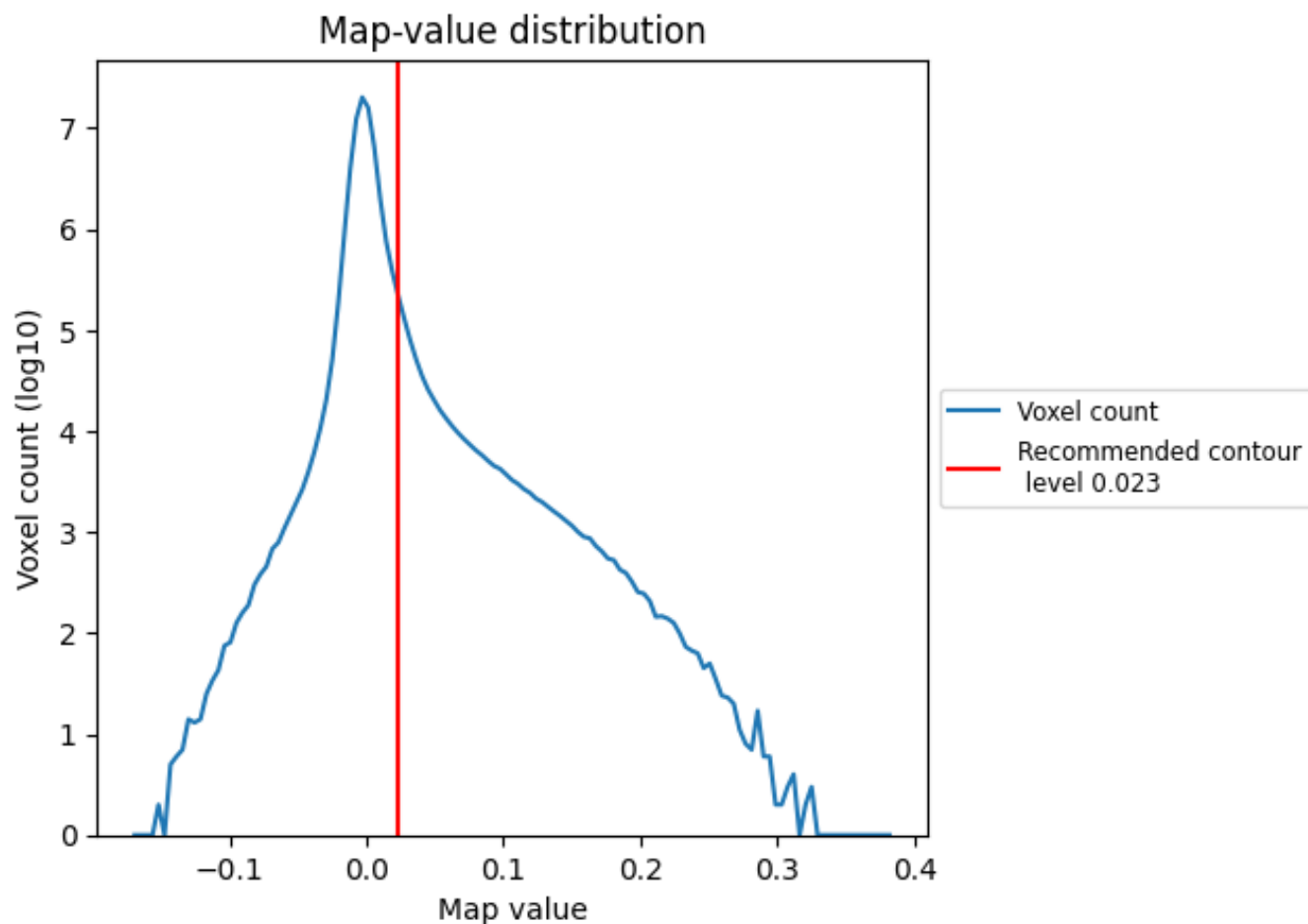
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

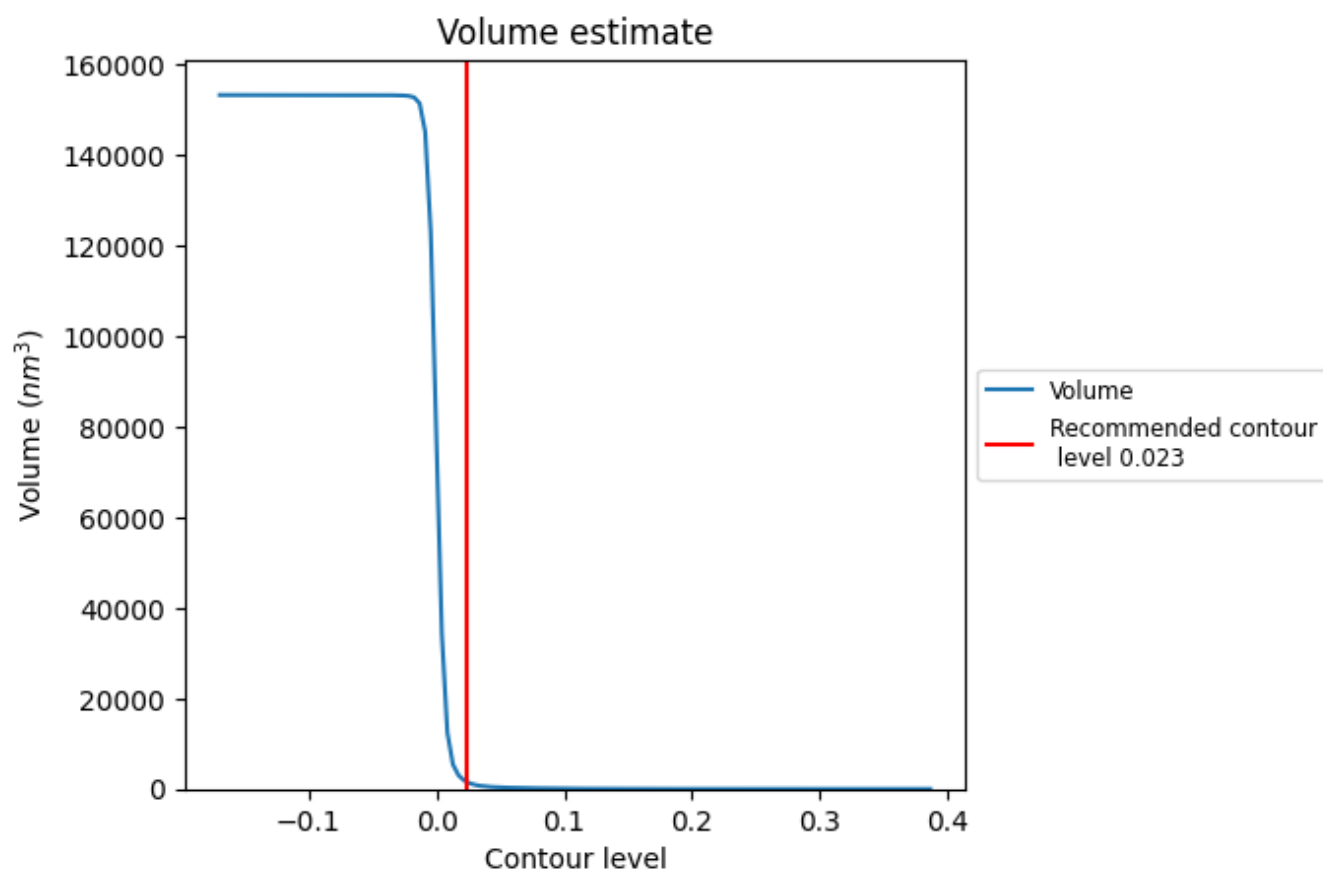
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

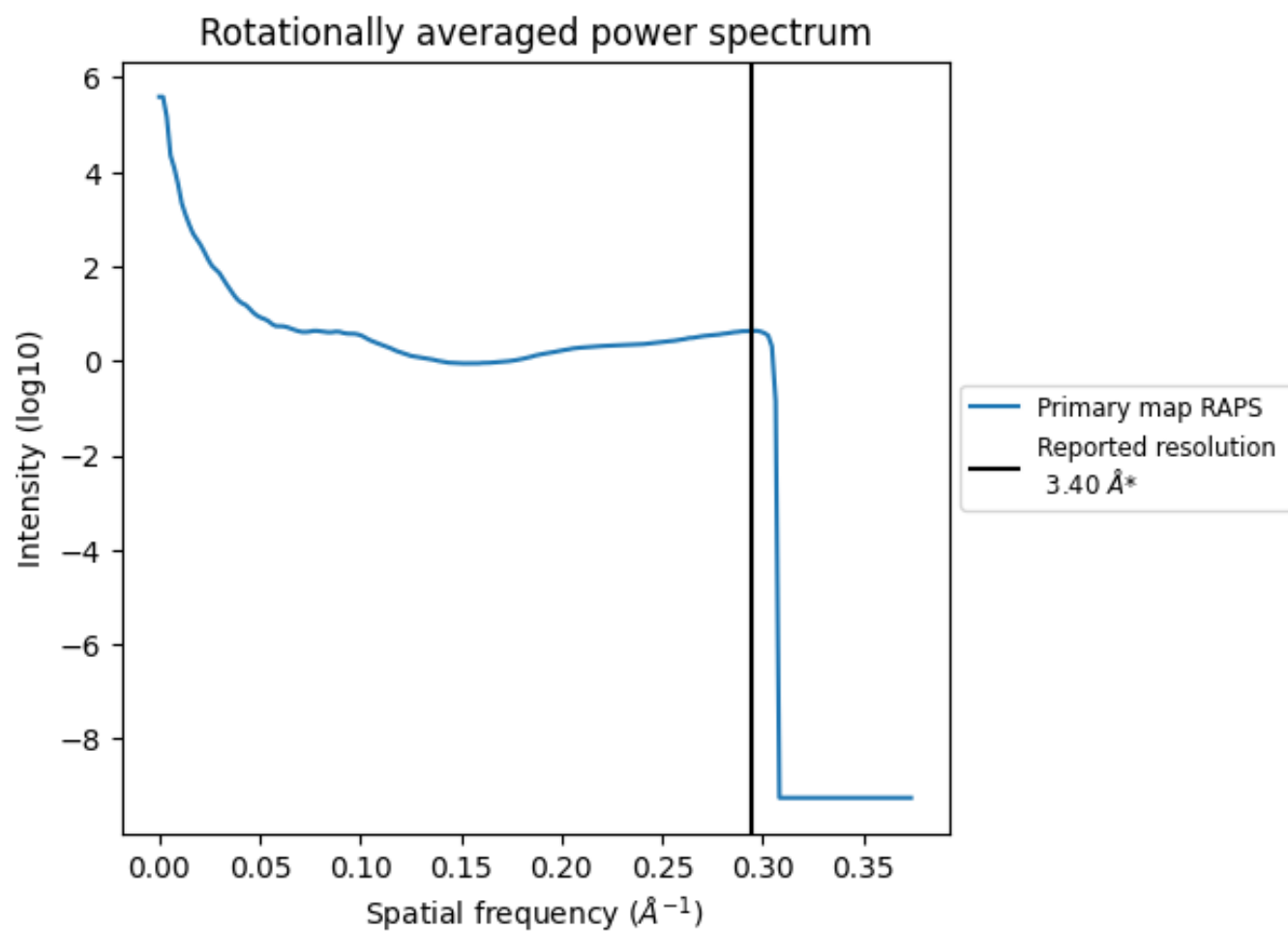
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1701 nm^3 ; this corresponds to an approximate mass of 1536 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

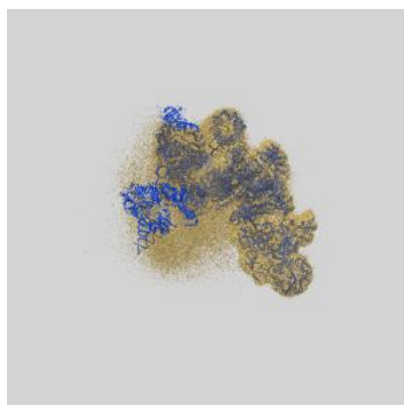
8 Fourier-Shell correlation

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

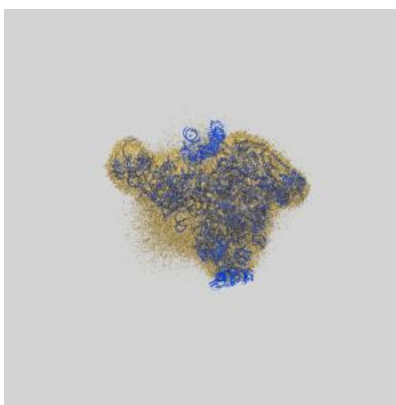
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6972 and PDB model 5ZWM. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

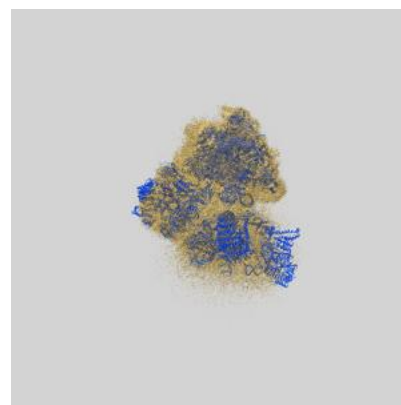
9.1 Map-model overlay [i](#)



X



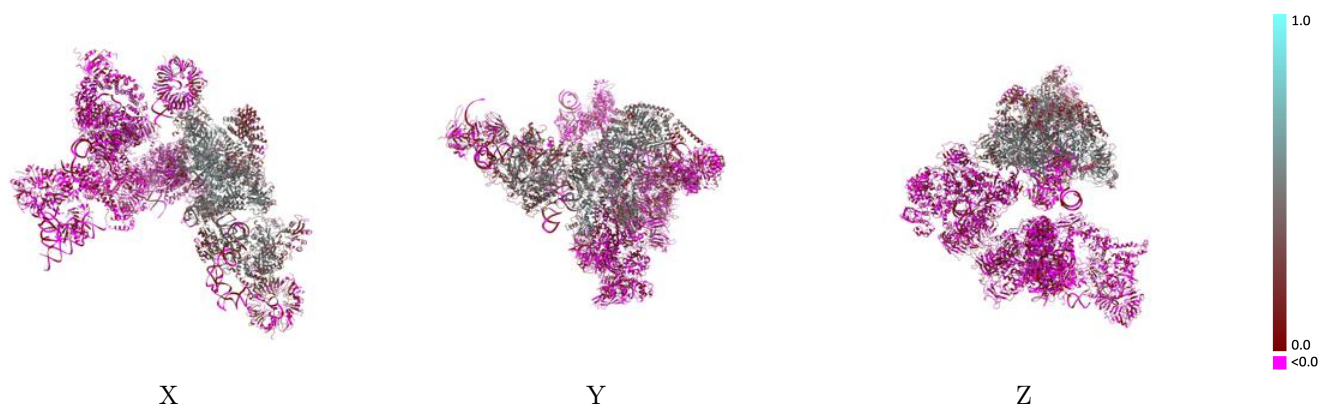
Y



Z

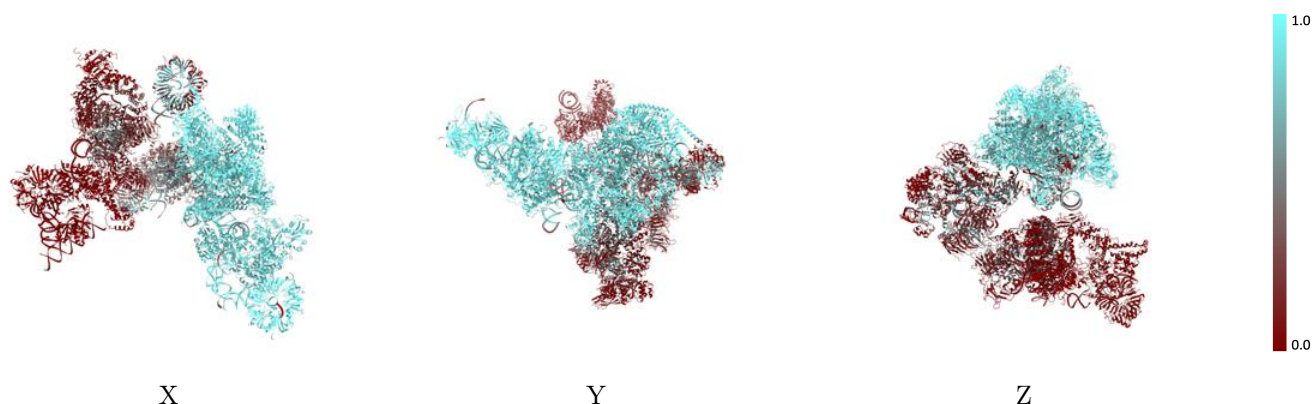
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



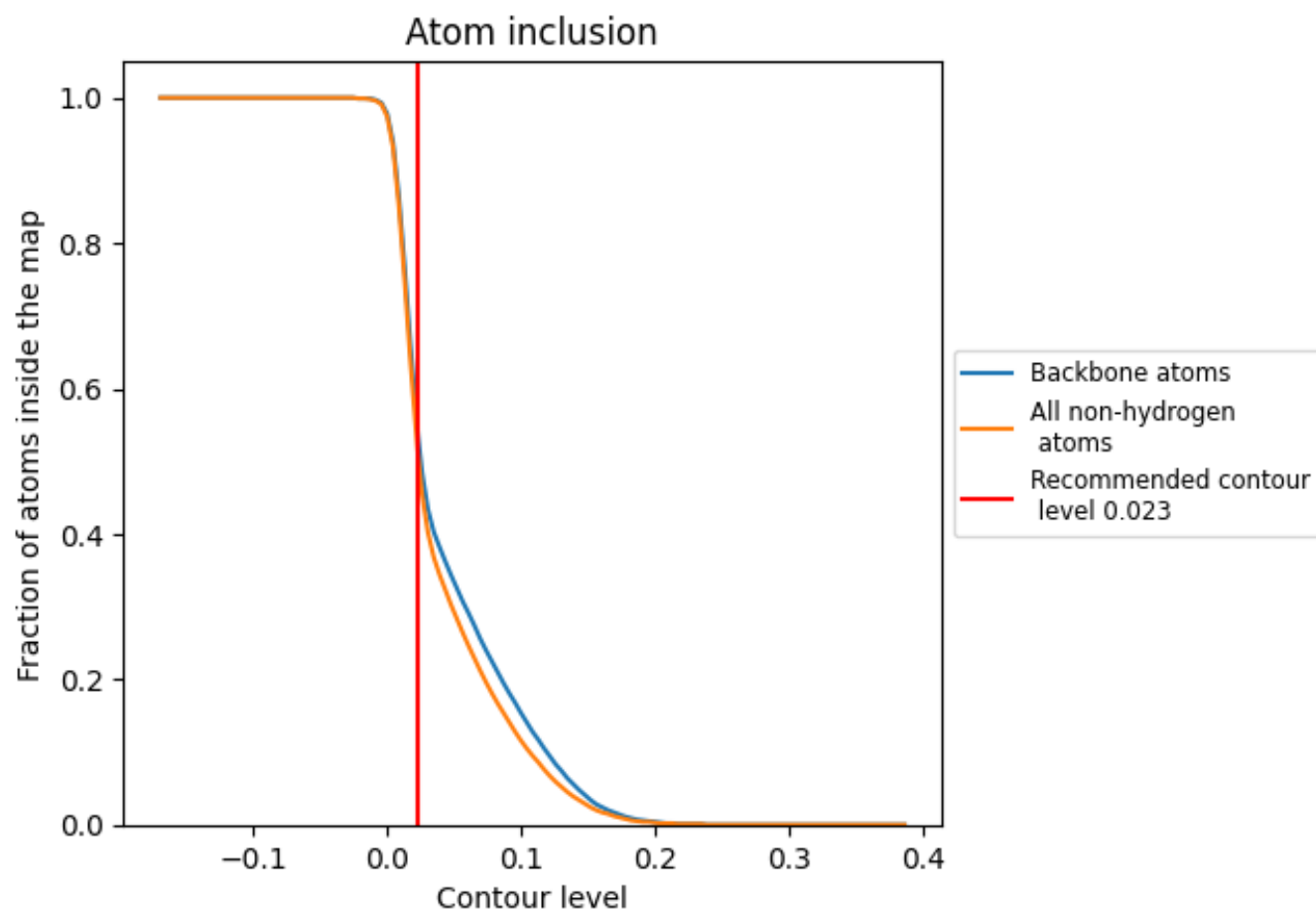
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.023).

9.4 Atom inclusion ⓘ



At the recommended contour level, 53% of all backbone atoms, 50% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5050	 0.1620
1	 0.1700	 0.0010
2	 0.1600	 0.0170
3	 0.1710	 0.0070
4	 0.0560	 -0.0180
5	 0.2770	 0.0070
6	 0.3170	 -0.0020
A	 0.8430	 0.3780
B	 0.8820	 0.1520
C	 0.9060	 0.3540
D	 0.2770	 -0.0020
E	 0.9180	 0.4420
F	 0.8230	 0.2670
G	 0.2000	 -0.0050
H	 0.0740	 0.0020
I	 0.8240	 0.3140
J	 0.9240	 0.4150
K	 0.9220	 0.4350
L	 0.9290	 0.4290
M	 0.9550	 0.5200
N	 0.9200	 0.3230
O	 0.7580	 0.2720
P	 0.5390	 -0.0080
Q	 0.3850	 -0.0020
R	 0.4290	 -0.0110
S	 0.5940	 0.0110
T	 0.1550	 -0.0060
U	 0.2720	 -0.0290
V	 0.2620	 0.0160
X	 0.0050	 0.0070
Y	 0.0010	 -0.0100
Z	 0.0060	 -0.0350
a	 0.9490	 0.2050
b	 0.9380	 0.1490
c	 0.9310	 0.0690



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Chain	Atom inclusion	Q-score
d	 0.9810	 0.2910
e	 0.9510	 0.0850
f	 0.9210	 0.1000
g	 0.8570	 0.0540
h	 0.0070	 0.0250
i	 0.0020	 0.0280
j	 0.0040	 -0.0190
k	 0.0040	 -0.0070
l	 0.0150	 0.0050
m	 0.0080	 0.0080
n	 0.0020	 0.0010
o	 0.0080	 0.0140
p	 0.0060	 0.0150
q	 0.4430	 0.0150
r	 0.5030	 0.0150
s	 0.4160	 0.0280
t	 0.6400	 0.0210
u	 0.0320	 -0.0030
v	 0.0980	 -0.0010
w	 0.0060	 -0.0230
x	 0.5510	 0.0480
y	 0.6170	 0.0200
z	 0.2920	 -0.0110