



Full wwPDB EM Validation Report ⓘ

Jun 26, 2025 – 10:05 PM JST

PDB ID : 7W5B / pdb_00007w5b
EMDB ID : EMD-32321
Title : The cryo-EM structure of human C* complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2021-11-29
Resolution : 4.30 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:

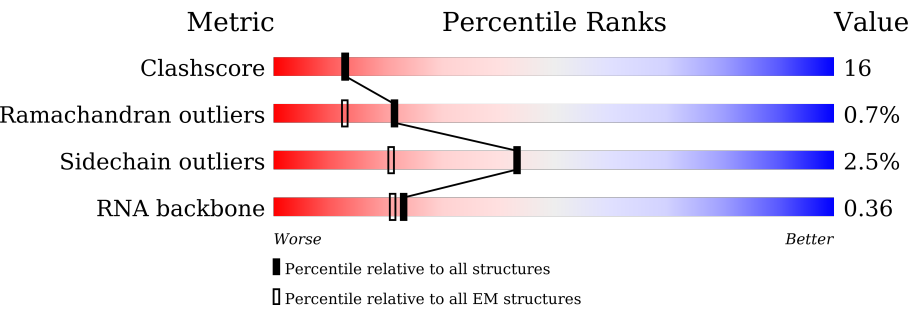
EMDB validation analysis : 0.0.1.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

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 4.30 Å.

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




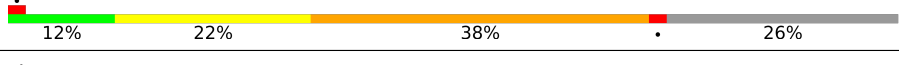
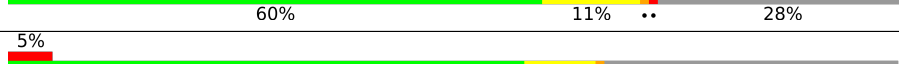
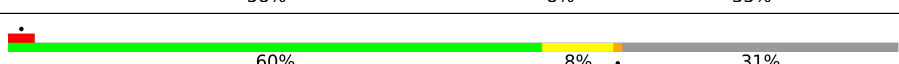
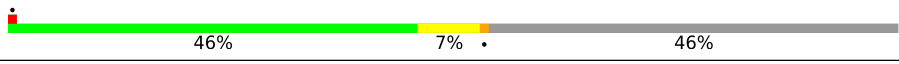
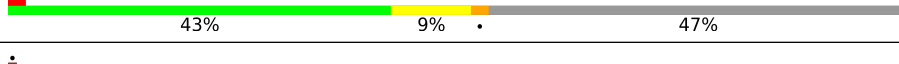


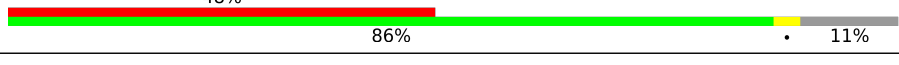

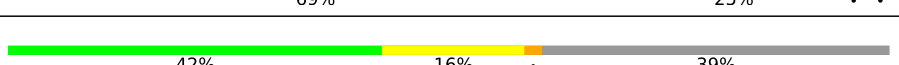
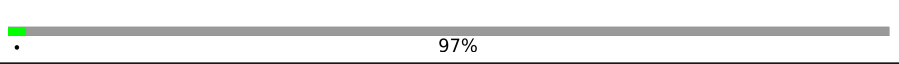


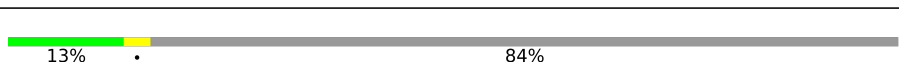
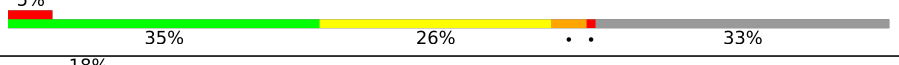
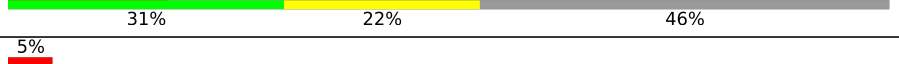


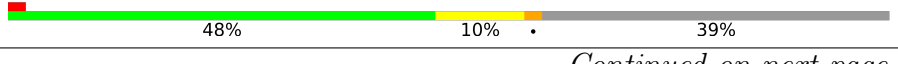



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2335	<div><div>6%</div><div>69%</div><div>24%</div><div>...</div></div>
2	B	117	<div><div>36%</div><div>22%</div><div>10%</div><div>28%</div></div>
3	C	972	<div><div>71%</div><div>17%</div><div>11%</div></div>
4	D	2136	<div><div>59%</div><div>79%</div><div>19%</div></div>
5	E	357	<div><div>61%</div><div>22%</div><div>16%</div></div>
6	F	107	<div><div>31%</div><div>23%</div><div>35%</div><div>9%</div></div>
7	4	46	<div><div>7%</div><div>11%</div><div>7%</div><div>72%</div></div>

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Mol	Chain	Length	Quality of chain
8	G	174	
9	H	188	
10	I	855	
11	J	848	
12	K	225	
13	L	802	
14	M	243	
15	N	144	
16	O	420	
17	P	229	
18	Q	1485	
19	R	536	
20	S	166	
21	T	514	
22	U	2752	
23	V	908	
24	W	579	
25	Y	1220	
26	Z	758	
27	2	184	
28	z	112	
29	b	240	
29	i	240	
30	y	301	
31	a	126	

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Mol	Chain	Length	Quality of chain
31	h	126	
32	c	119	
32	j	119	
33	d	118	
33	k	118	
34	f	86	
34	m	86	
35	e	92	
35	l	92	
36	g	76	
36	n	76	
37	q	504	
37	r	504	
37	s	504	
37	t	504	
38	o	255	
39	p	225	
40	1	586	
41	v	146	
42	w	174	
43	u	411	
44	x	703	
45	3	415	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
46	IHP	A	3000	-	-	X	-

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 106538 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-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2253	Total	C	N	O	S	0	0
			17748	11367	3144	3167	70		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	862	Total	C	N	O	S	0	0
			6787	4339	1136	1281	31		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	1722	Total	C	N	O	0	0
			8530	5086	1722	1722		

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 7 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	4	13	Total	C	N	O	P	0	0
			276	123	50	90	13		

- Molecule 8 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	82	Total	C	N	O	P	0	0
			1510	666	210	552	82		

- Molecule 9 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	140	Total	C	N	O	P	0	0
			2966	1326	510	990	140		

- Molecule 10 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	618	Total	C	N	O	S	0	0
			3857	2389	722	735	11		

- Molecule 11 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	569	Total	C	N	O	S	0	0
			3819	2379	718	716	6		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	155	Total	C	N	O		0	0
			772	462	155	155			

- Molecule 13 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	437	Total	C	N	O	S	0	0
			3015	1859	584	565	7		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	130	Total	C	N	O	S	0	0
			1098	684	204	208	2		

- Molecule 15 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 16 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	285	Total	C	N	O	S	0	0
			2296	1442	408	426	20		

- Molecule 17 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	113	Total	C	N	O	S	0	0
			953	583	189	179	2		

- Molecule 18 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	1322	Total	C	N	O		4	0
			6562	3918	1322	1322			

- Molecule 19 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	280	Total	C	N	O	P S	0	0
			2243	1401	411	416	2 13		

- Molecule 20 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 21 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	312	Total	C	N	O	S	0	0
			2454	1550	446	450	8		

- Molecule 22 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	72	Total	C	N	O	S	0	0
			422	257	82	82	1		

- Molecule 23 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	452	Total	C	N	O	S	0	0
			2632	1639	492	495	6		

- Molecule 24 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	509	Total	C	N	O	S	0	0
			4129	2628	715	762	24		

- Molecule 25 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	667	Total	C	N	O	S	4	0
			3431	2057	680	693	1		

- Molecule 26 is a protein called Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	122	Total	C	N	O	S	0	0
			1084	712	197	173	2		

- Molecule 27 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	123	Total	C	N	O	S	0	0
			1013	635	193	180	5		

- Molecule 28 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	z	60	Total	C	N	O	S	0	0
			496	306	96	92	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	102	Total	C	N	O	S	0	0
			786	492	148	139	7		
29	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		

- Molecule 30 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	y	79	Total	C	N	O	0	0
			390	232	79	79		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	77	Total	C	N	O	S	0	0
			609	381	108	115	5		
31	h	81	Total	C	N	O	S	0	0
			633	397	112	118	6		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	82	Total	C	N	O	S	0	0
			649	413	113	119	4		
32	j	82	Total	C	N	O	S	0	0
			649	413	113	119	4		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	97	Total	C	N	O	S	0	0
			776	488	143	140	5		
33	k	85	Total	C	N	O	S	0	0
			688	432	125	126	5		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
34	m	73	Total	C	N	O	S	0	0
			566	367	93	101	5		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	79	Total	C	N	O	S	0	0
			652	412	116	119	5		
35	l	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
36	n	69	Total	C	N	O	S	0	0
			542	345	97	94	6		

- Molecule 37 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	q	132	Total	C	N	O	0	0
			659	395	132	132		
37	r	131	Total	C	N	O	0	0
			654	392	131	131		
37	s	132	Total	C	N	O	0	0
			659	395	132	132		
37	t	131	Total	C	N	O	0	0
			654	392	131	131		

- Molecule 38 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	162	Total	C	N	O	S	0	0
			1282	820	219	240	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	94	Total	C	N	O	S	0	0
			760	488	135	132	5		

- Molecule 40 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1	269	Total	C	N	O	S	0	0
			2209	1389	394	418	8		

- Molecule 41 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	v	144	Total	C	N	O	0	0
			711	423	144	144		

- Molecule 42 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	w	91	Total	C	N	O	0	0
			445	263	91	91		

- Molecule 43 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	u	386	Total	C	N	O	0	0
			1907	1135	386	386		

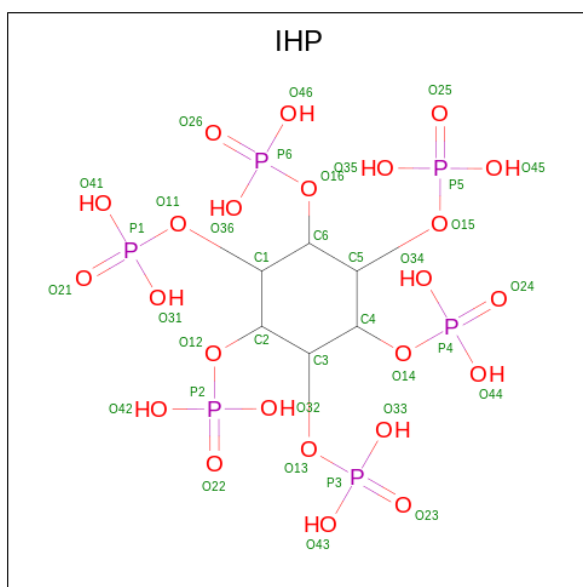
- Molecule 44 is a protein called Protein CASC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	x	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 45 is a protein called NF-kappa-B-activating protein.

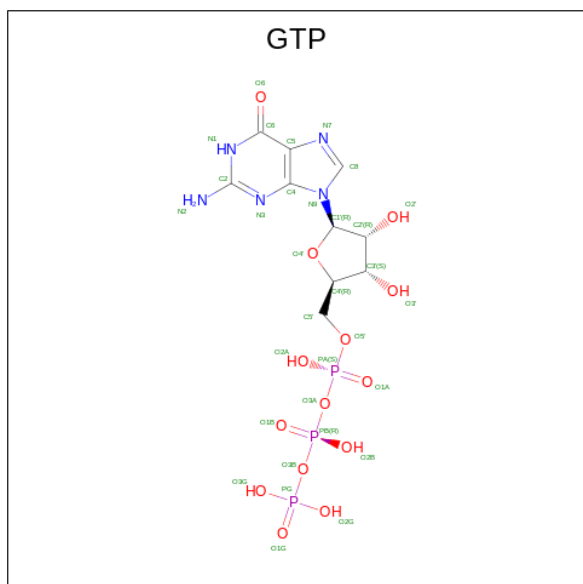
Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	30	Total	C	N	O	S	0	0
			230	140	43	45	2		

- Molecule 46 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
46	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 47 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

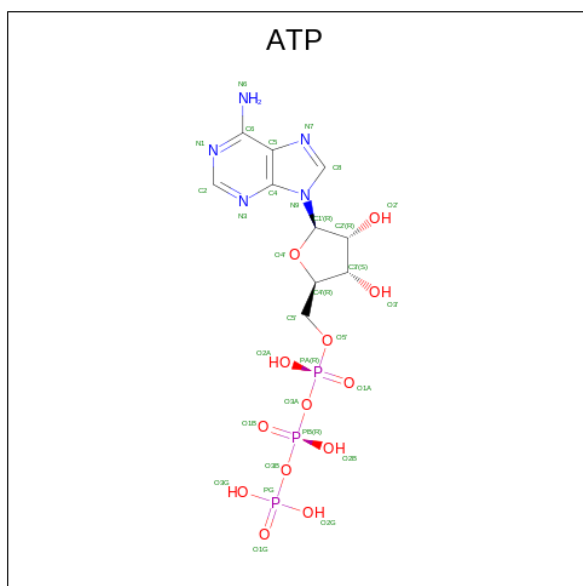
- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	C	1	Total	Mg	0
			1	1	
48	F	6	Total	Mg	0
			6	6	
48	Q	2	Total	Mg	0
			2	2	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
49	N	3	Total	Zn	0
			3	3	
49	O	3	Total	Zn	0
			3	3	
49	1	1	Total	Zn	0
			1	1	

- Molecule 50 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

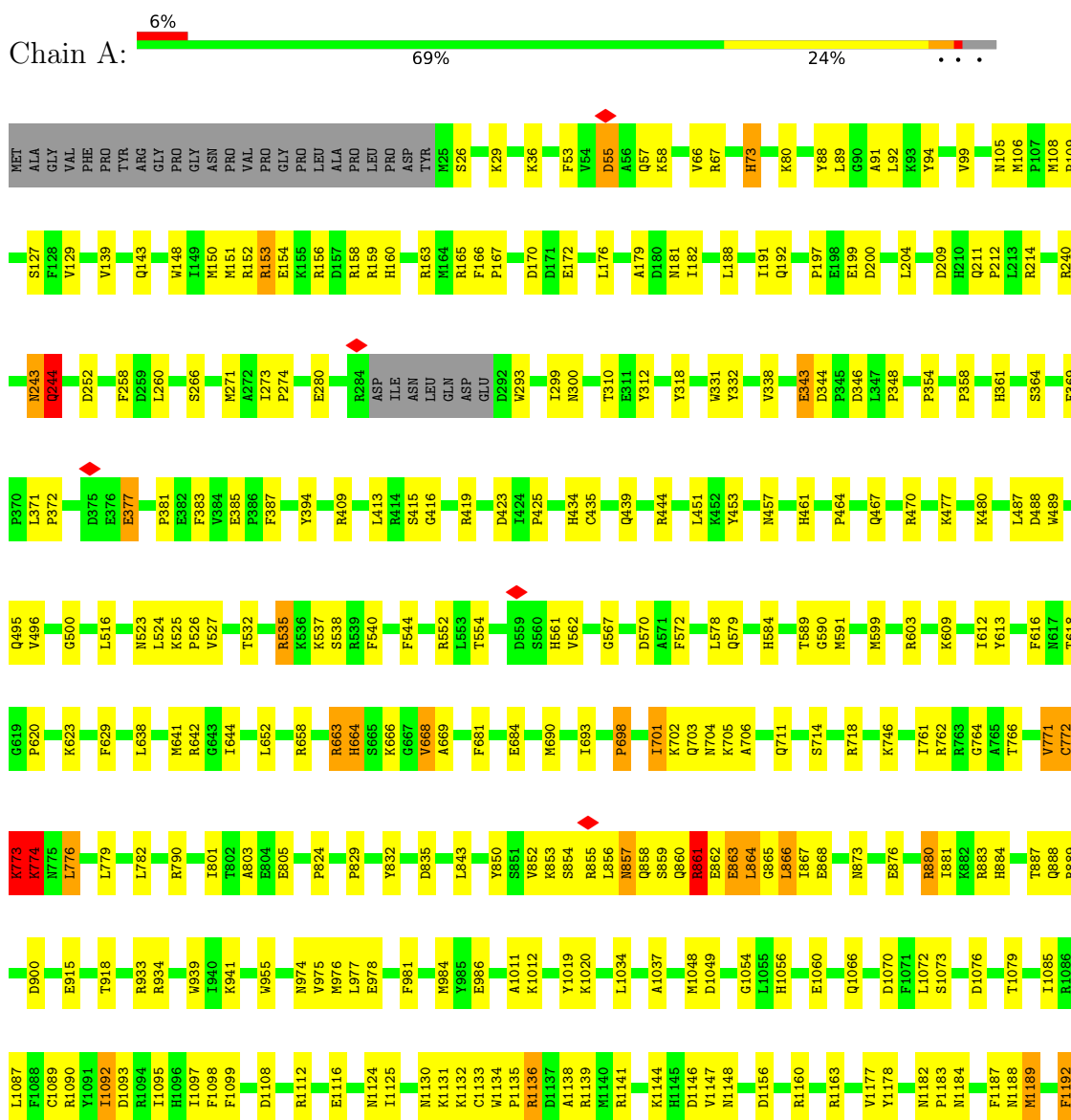


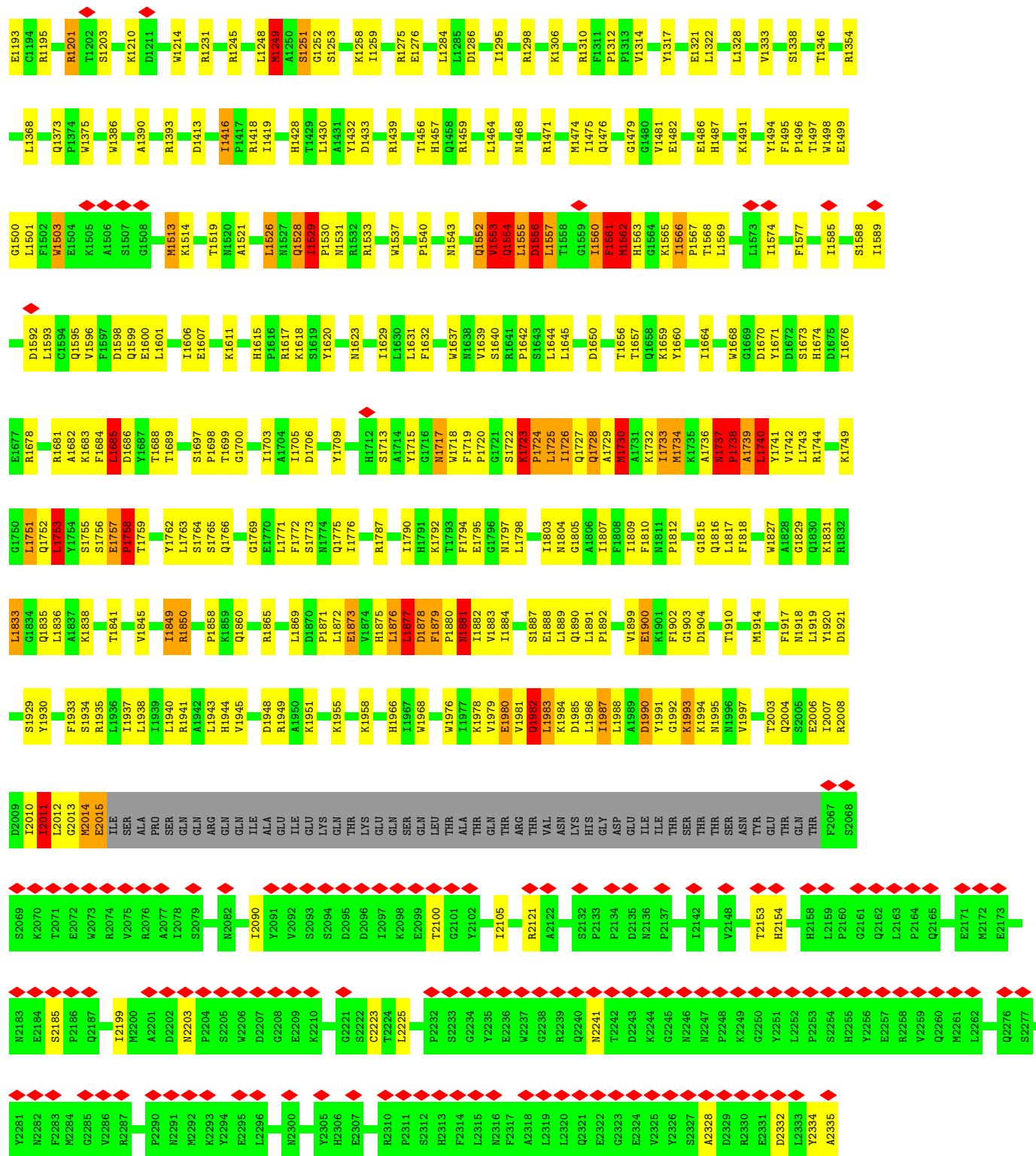
Mol	Chain	Residues	Atoms					AltConf
50	Q	1	Total	C	N	O	P	0
			31	10	5	13	3	

3 Residue-property plots

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

- Molecule 1: Pre-mRNA-processing-splicing factor 8





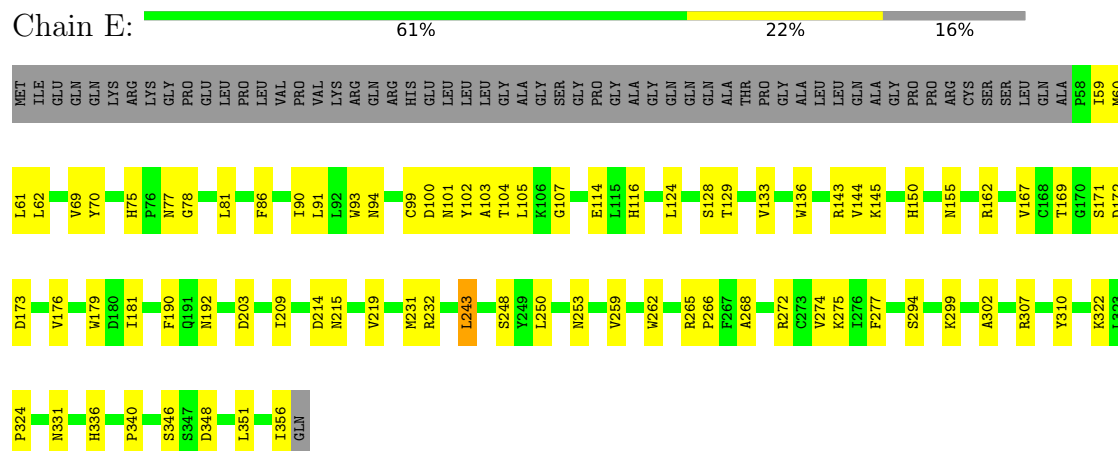
• Molecule 2: U5 snRNA



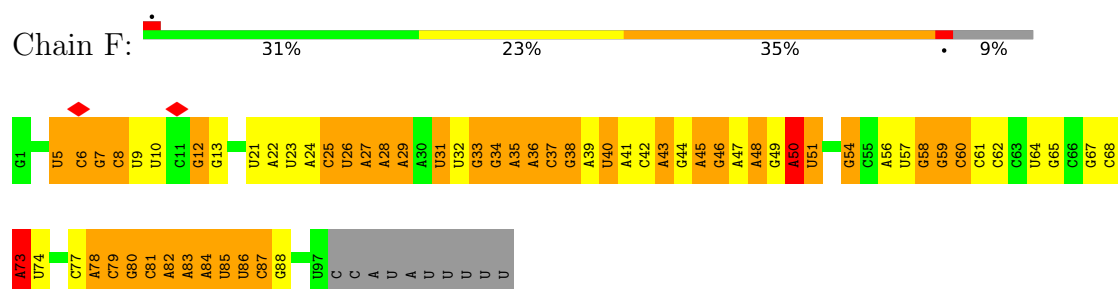
L2019	Y1959	A1897	F1832	V1752	I1641	R1570	R1475	E1395	P1306	E1212	R1133	E1054
S2020	L1960	H1898	S1833	D1753	V1645	L1571	Y1476	K1396	L1307	K1213	R1134	P1055
Y2021	K1961	L1899	M1834			T1572	I1477	F1397	P1308	G1216	K1135	S1056
E2022	Q1962	S1900	L1835		D1665	T1578	S1478	Q1398	V1309		L1136	A1057
V2023	L1963	R1901	L1836		T1666	T1579	Q1479	R1400	S1310	W1222	E1137	K1058
D2025	H1965	M1902	A1838		M1670	C1580	Q1480	L1401	A1311		E1138	I1059
K2026	F1966	Q1903	K1839		A1675	A1581	I1481	N1402	L1312	E1226	V1139	N1060
D2027	P1967	L1904	T1840		A1676	D1583	R1482	K1403	R1313	D1227	V1140	W1061
S2028	S1968	A1906	K1841		Y1676	A1582	R1483	K1404	R1314	V1228	K1141	L1062
L2029	E1969	E1907	V1842		Y1679	Q1585	P1484	V1405	S1315	D1229	K1142	F1066
R2030	H1970	L1908	R1843		P1680	R1586	S1491	F1317	A1316	S1230	I1143	L1070
S2031	I1971	S1910	L1845		T1681	Q1587	K1498	E1410	F1318	E1231	E1144	K1071
G2032	K1972	D1911	I1846		Y1682	Q1587		E1411	S1319	EL237	K1145	L1072
G2033	R1973	T1912	E1847		Q1686	L1590	A1501	S1413	L1320	K1242	N1147	E1073
P2034	C1974	E1913	I1848		A1691	H1591	H1502	T1412	Y1321		F1148	G1074
V2035	D1975	E1914	E1787		A1692	C1592	W1503	T1414	Q1322	E1249	P1149	F1075
V2036	L1976	L1915	L1788		N1692	T1593	L1504	D1415	D1323	H1250	F1150	A1076
V2037	K1977	L1916	V1789		R1693	E1594	G1505	L1416	K1324	I1251	E1151	L1077
L2038	G1978	S1917	N1694		P1694	K1595	C1506	L1417	F1325	I1252	R1152	M1078
V2039	V1979	K1918	L1695		L1696	D1596	S1507	L1418	P1326	T1253	L1153	A1079
Q2040	E1980	A1919	Q1791		Q1696	L1597	A1508	L1419	F1327		Y1154	D1080
L2041	S1981	L1920	D1697		D1698	I1598	T1509	G1420	F1328	F1259	L1155	M1081
E2042	V1982	R1921	S1794		C1702	P1599	S1510	G1422	K1421	E1260	L1156	V1082
R2043	F1983	I1922	D1795		G1708	L1600	M1517	N1423	N1329	P1261	N1157	W1084
D2044	D1984	I1923	L1796		S1709	E1602	V1518	S1427	I1331	L1262	H1158	T1085
E2045	I1985	Q1924	E1797		K1710	K1603	P1520	E1430	Q1332	P1263	N1159	Q1086
E2046	M1986	A1925	Q1798		K1711	L1604	V1521		Q1333	R1269	I1161	S1087
V2047	E1987	C1926	S1799		E1716	D1606	L1522		F1336	V1270	E1163	M1092
T2048	M1988	L1927	K1800		E1720	S1607	L1523	R1437	R1438		L1164	R1093
G2049	E1989	D1928	N1866		P1721	T1608	E1524	W1439	T1338	C1278	I1165	A1094
P2050	D1990	L1929	L1867		K1712	L1609	L1525	K1440	V1339	E1279	R1166	I1095
V2051	E1991	S1931	R1868		E1722	K1610	H1526	R1441	M1341	T1280	M1167	F1096
T2052	E1992	S1932	I1804		L1722	E1611	G1529	R1442	Q1342	Q1281	P1168	E1097
A2053	R1993	G1934	D1806		H1727	L1613	H1534	K1443	S1342	L1282	K1169	T1098
P2054	M1994	N1935	E1807		L1728	L1614	T1535	N1444	D1343	P1283	M1170	V1099
L2055	A1995	W1936	M1808		D1729	N1615	Q1536	N1445	D1344	G1171	K1172	L1100
P2057	L1996	L1937	D1809		H1730	N1616	T1537	Q1446	M1345	S1285	T1173	W1104
Q2058	L1997	P1938	V1810		C1731	G1616		I1447	G1349	L1289	Y1177	A1105
R2059	Q1998	P1938	A1811		F1736	G1623	T1551	N1448	G1353	L1290	K1183	D1109
D2060	T2000	H1877	P1812		M1737	L1624	K1552	N1449	P1292	L1291	L1184	K1110
E2061	D2001	K1878	N1814		T1742	S1625	H1553	L1450	P1293	P1292	E1185	T1111
E2062	S2002	L1879	L1815		K1743	P1626	S1554	V1452	K1294	K1294	L1186	L1112
G2063	Q2003	M1880	G1816		T1744	M1627	P1555	V1456	Y1295	P1296	S1187	N1113
W2064	I2004	M1817	M1818		K1744	E1628	K1556	Q1370	P1297	P1297	L1190	L1114
A2065	A2005	I1819	I1745		E1746	R1630	K1557	S1371	P1298	P1298	R1195	K1115
V2066	D2006	A1820	E1746		K1748	L1631	V1559	S1372	T1299	E1300	S1196	K1116
V2067	V2007	Y1821	M1747		Q1749	I1634	I1560	G1374	T1299	L1301	T1197	D1119
T2068	A2008	T1824	K1748		D1750	F1635	P1561	V1377	E1302	L1302	L1202	W1123
G2069	R2009	N1825	Q1749		A1751	F1636	S1565	E1383	D1303	D1303	T1203	Q1124
D2070	F2010	T1826	D1750		E1830	S1637	R1566	A1384	L1304	L1304		S1125
A2071	C2011	T1827	A1751		L1831	G1639			Q1305			M1126
D2072	N2012	E1830										C1127
S2073	R2013											
N2074	Y2014											
S2075	P2015											
L2076	N2016											
T2077	I2017											
S2078	E2018											



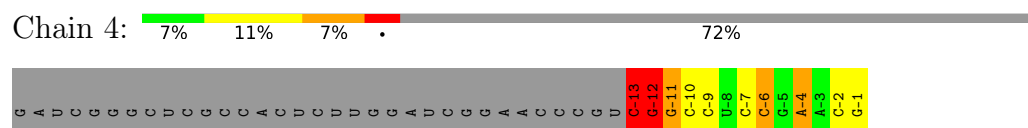
- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



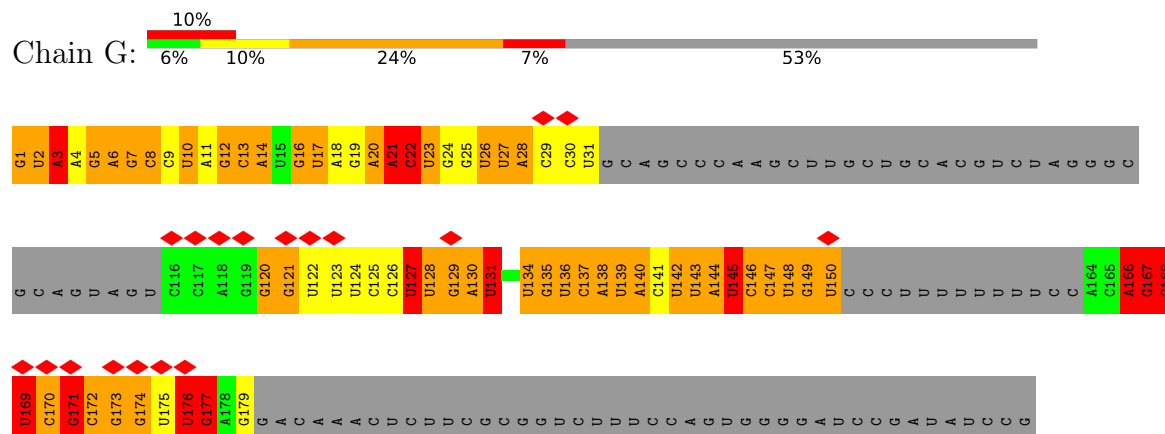
- Molecule 6: U6 snRNA



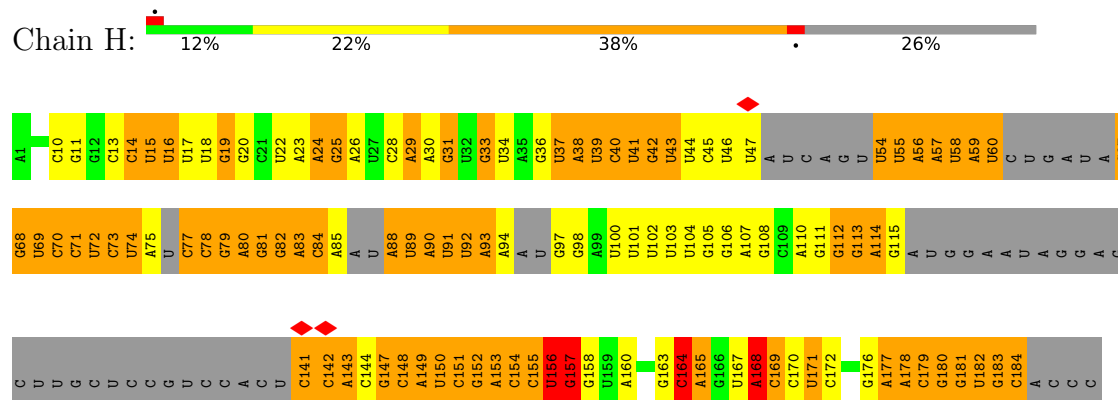
- Molecule 7: Pre-mRNA



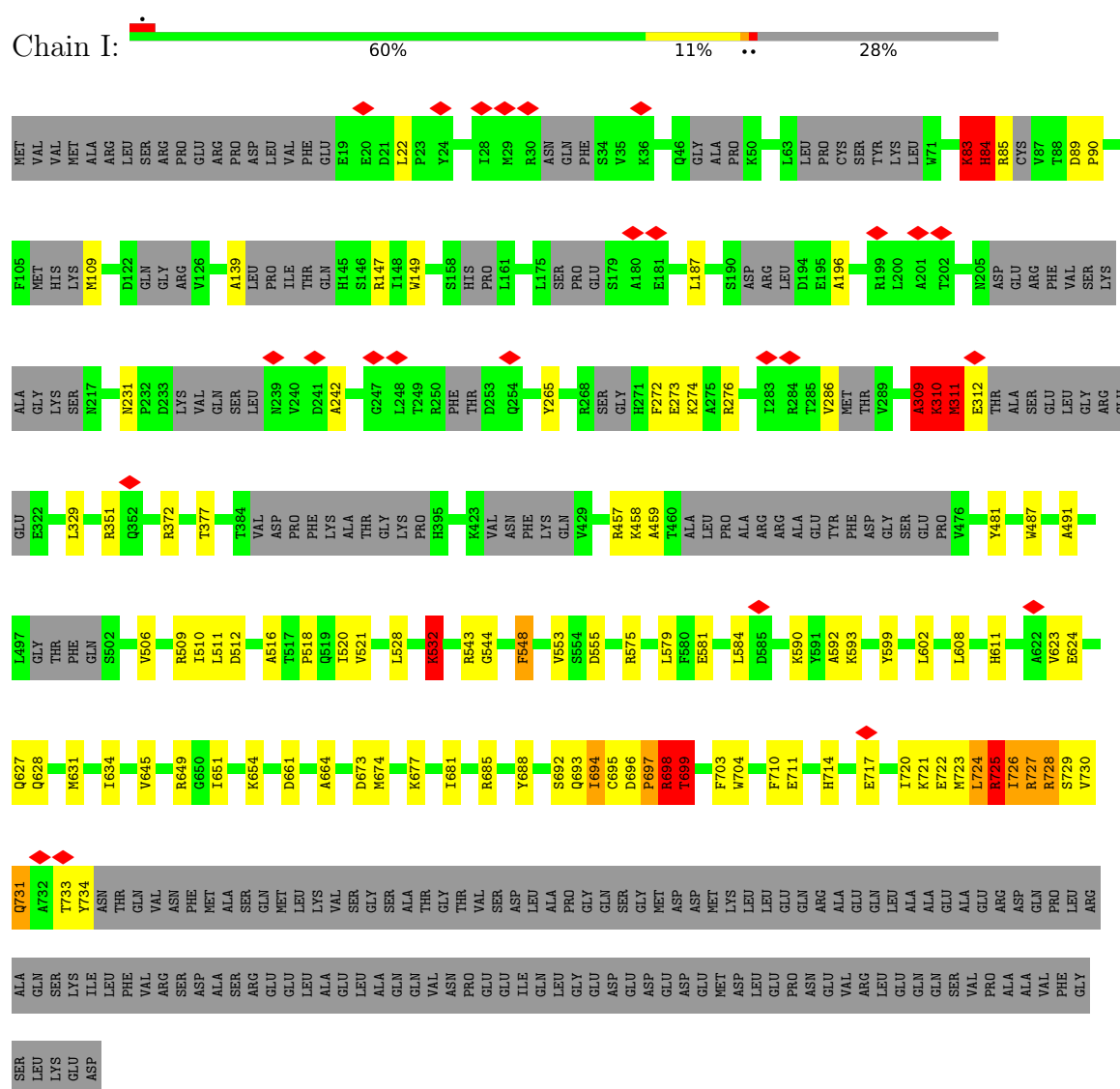
- Molecule 8: Pre-mRNA



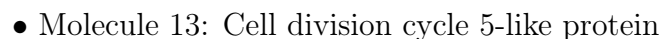
- Molecule 9: U2 snRNA

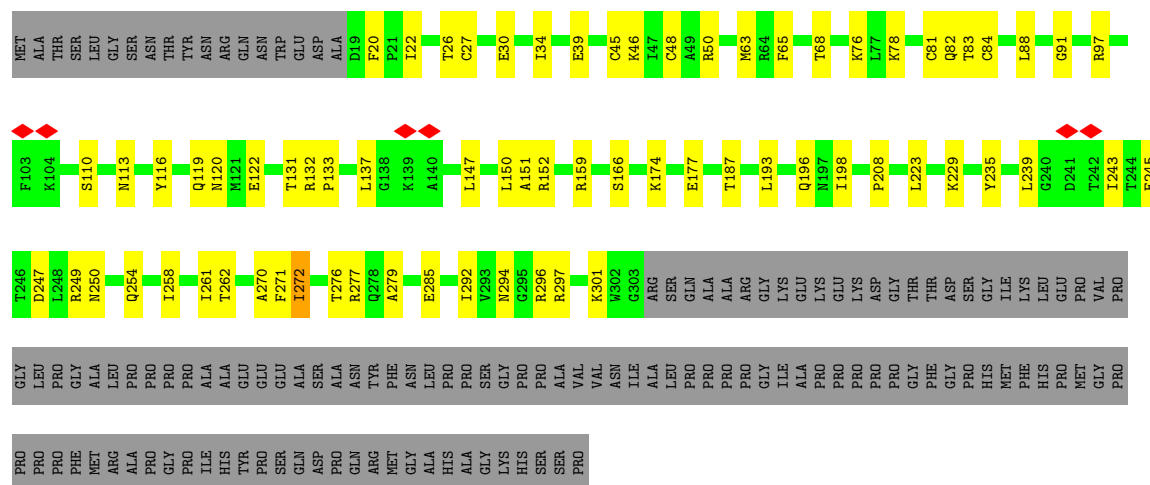


- Molecule 10: Pre-mRNA-splicing factor SYF1

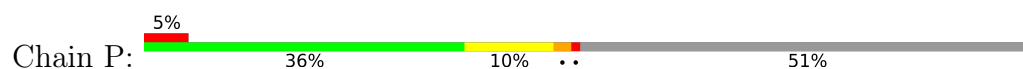


- Molecule 11: Crooked neck-like protein 1

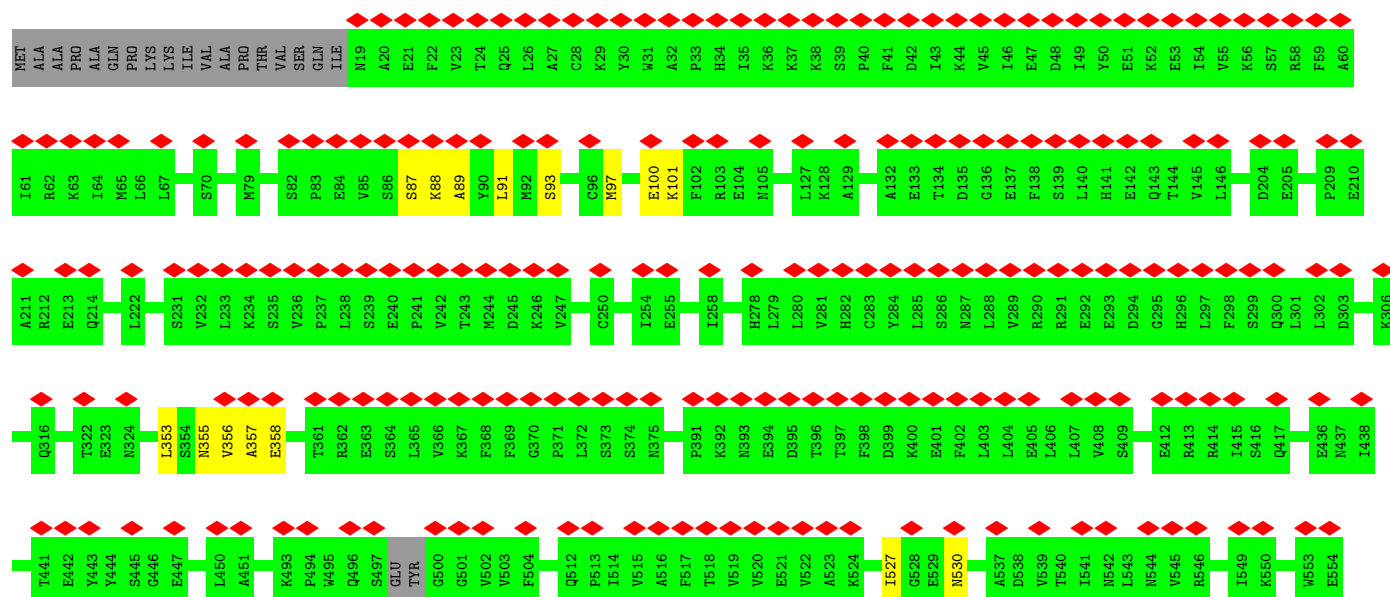
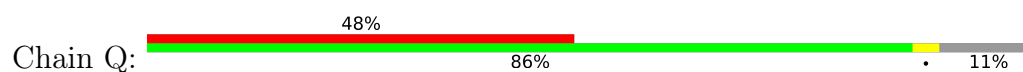


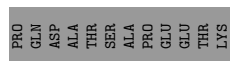


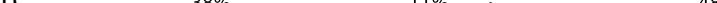
• Molecule 17: Spliceosome-associated protein CWC15 homolog



• Molecule 18: RNA helicase aquarius





Chain R: 



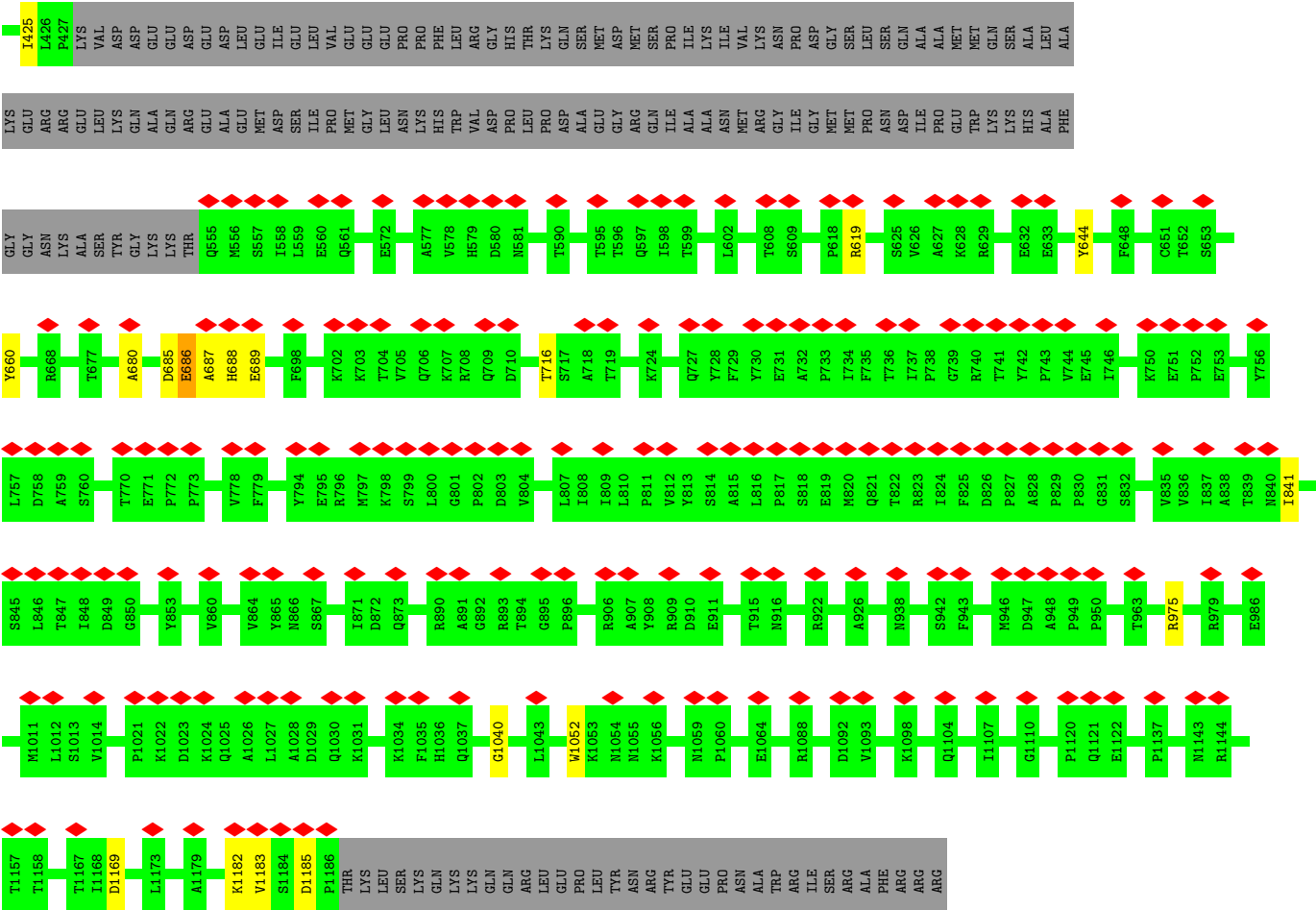


[illegible]

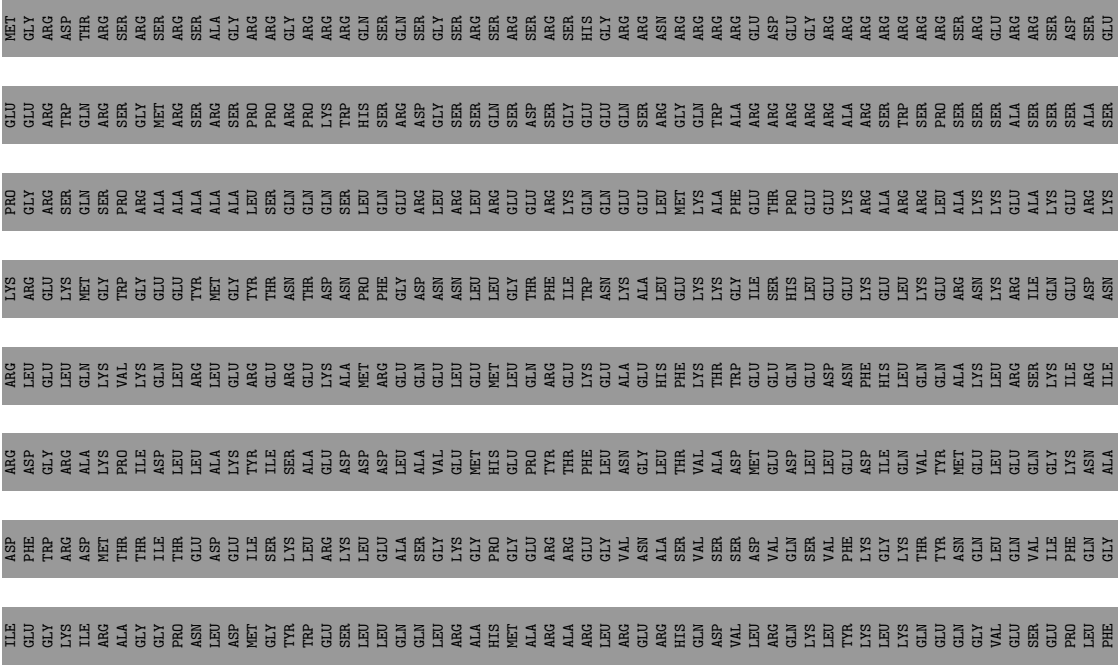
- Molecule 23: Pre-mRNA-splicing factor CWC22 homolog

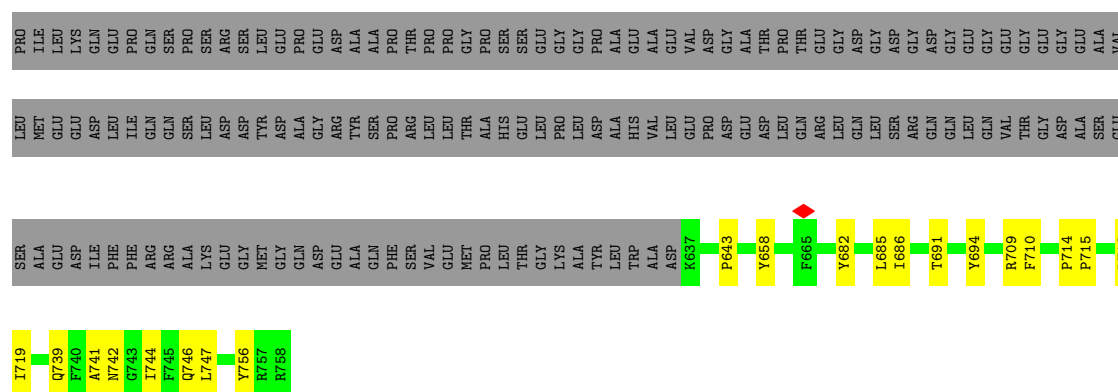
Chain V:  46% 50%

[illegible]

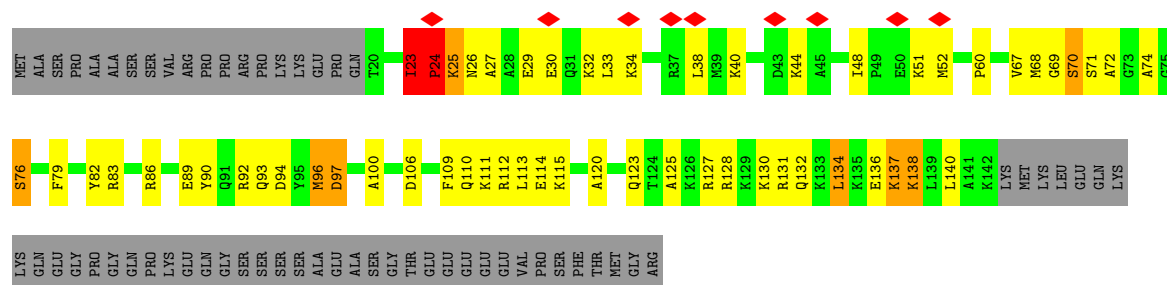


● Molecule 26: Cactin

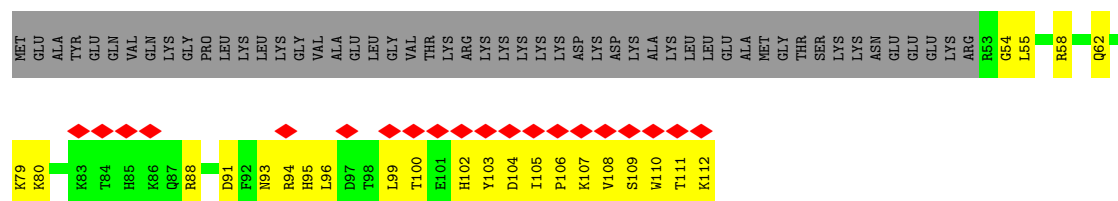
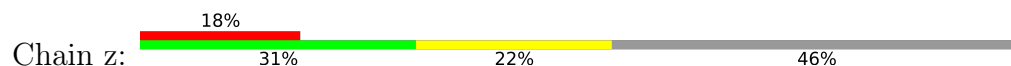




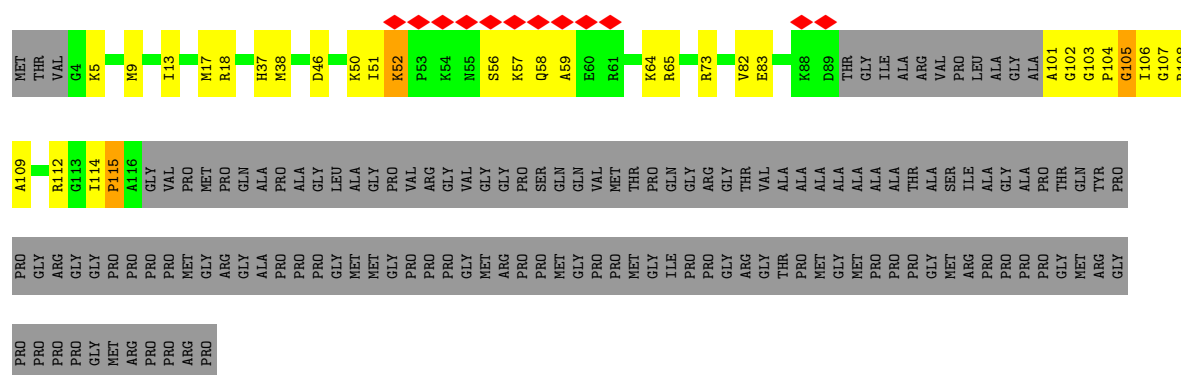
- Molecule 27: PRKR-interacting protein 1



- Molecule 28: Protein FAM32A




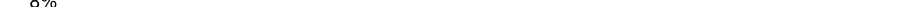
- Molecule 29: Small nuclear ribonucleoprotein-associated proteins B and B'



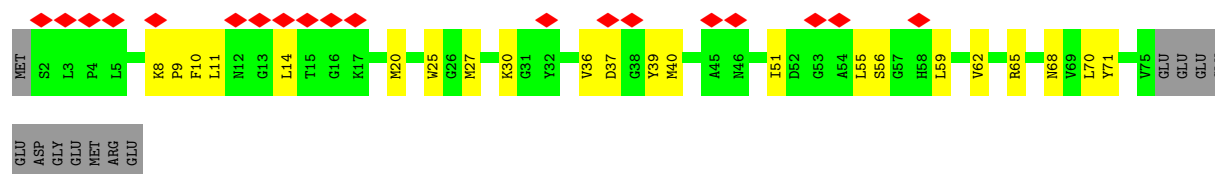
- Chain i:

- Chain y:
-
- 25% 74%
- Residues in Chain y (ordered/disordered):
- | Residue | State |
|---------|------------|
| MET | ordered |
| ALA | ordered |
| THR | ordered |
| THR | ordered |
| K5 | ordered |
| L13 | ordered |
| D18 | ordered |
| D19 | ordered |
| K20 | ordered |
| D31 | ordered |
| I32 | ordered |
| T33 | ordered |
| D34 | ordered |
| I35 | ordered |
| Y41 | ordered |
| E42 | ordered |
| T43 | ordered |
| R47 | ordered |
| G48 | ordered |
| N66 | ordered |
| G74 | ordered |
| K83 | ordered |
| PRO | ordered |
| MET | disordered |
| ARG | disordered |
| ILE | disordered |
| GLY | disordered |
| LYS | disordered |
| GLY | disordered |
| GLY | disordered |
| GLY | disordered |
| SER | disordered |
| SER | disordered |
| ARG | disordered |
| PRO | disordered |
| VAL | disordered |
| TRP | disordered |
| SER | disordered |
| SER | disordered |
| ASP | disordered |
| ASP | disordered |
| ASP | disordered |
| TRP | disordered |
| LEU | disordered |
| LYS | disordered |
| LYS | disordered |
| PHE | disordered |
| SER | disordered |
| GLY | disordered |
| LYS | disordered |
| THR | disordered |
| GLY | disordered |
| THR | disordered |
| LEU | disordered |
| GLU | disordered |
| GLU | disordered |
| ARG | disordered |

- Chain a: 

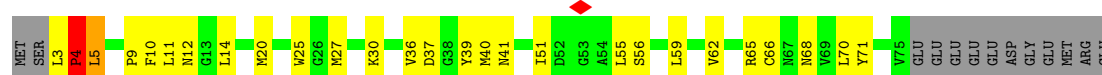
- Chain h: 

Chain f: 



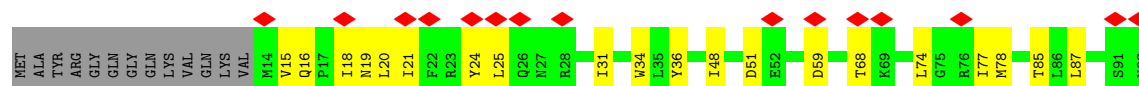
- Molecule 34: Small nuclear ribonucleoprotein F

Chain m: 53% 29% .. 15%



- Molecule 35: Small nuclear ribonucleoprotein E

Chain e: 16% 64% 22% 14%



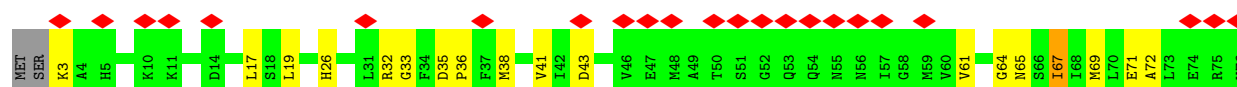
- Molecule 35: Small nuclear ribonucleoprotein E

Chain l: 18% 61% 25% 14%



- Molecule 36: Small nuclear ribonucleoprotein G

Chain g: 30% 74% 22% ..

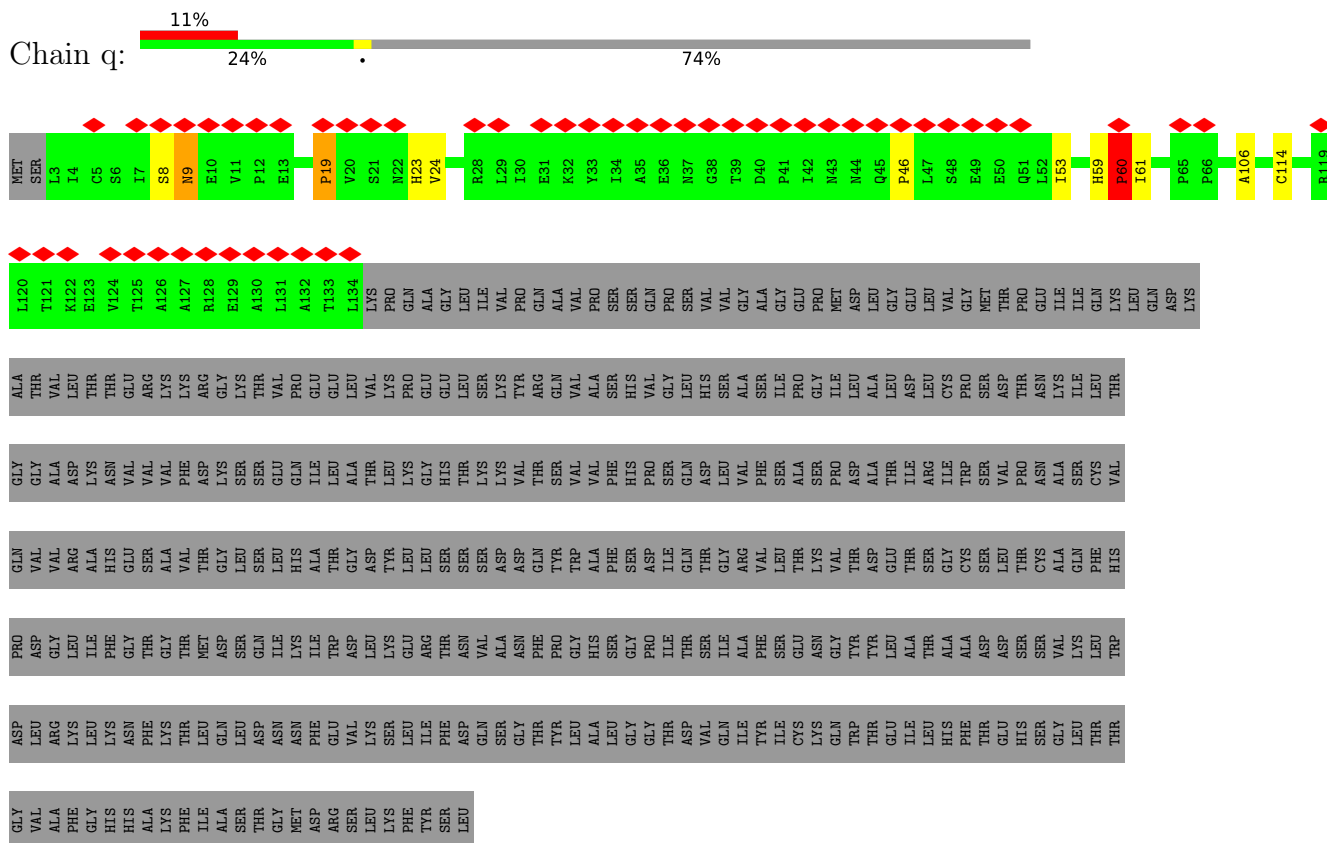


- Molecule 36: Small nuclear ribonucleoprotein G

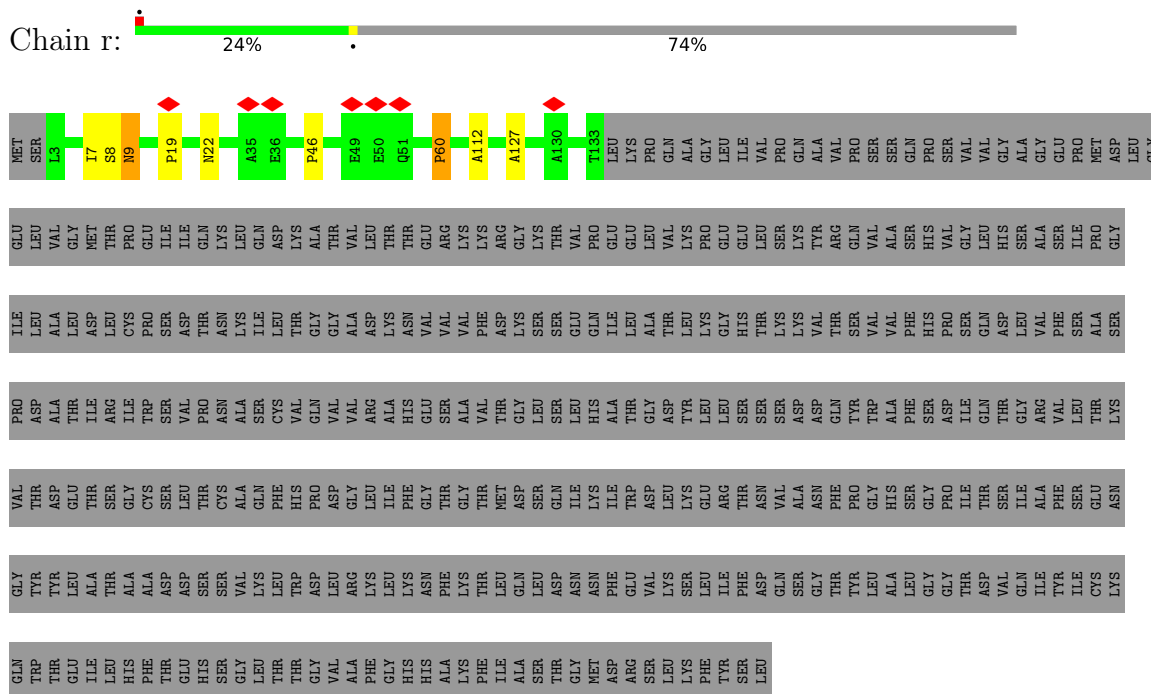
Chain n: 9% 62% 26% .. 9%



- Molecule 37: Pre-mRNA-processing factor 19

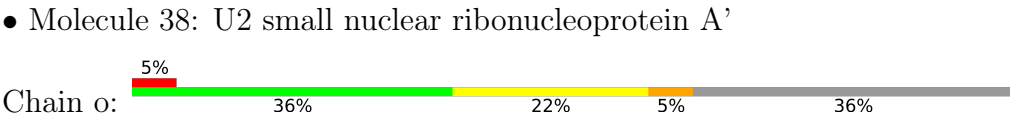
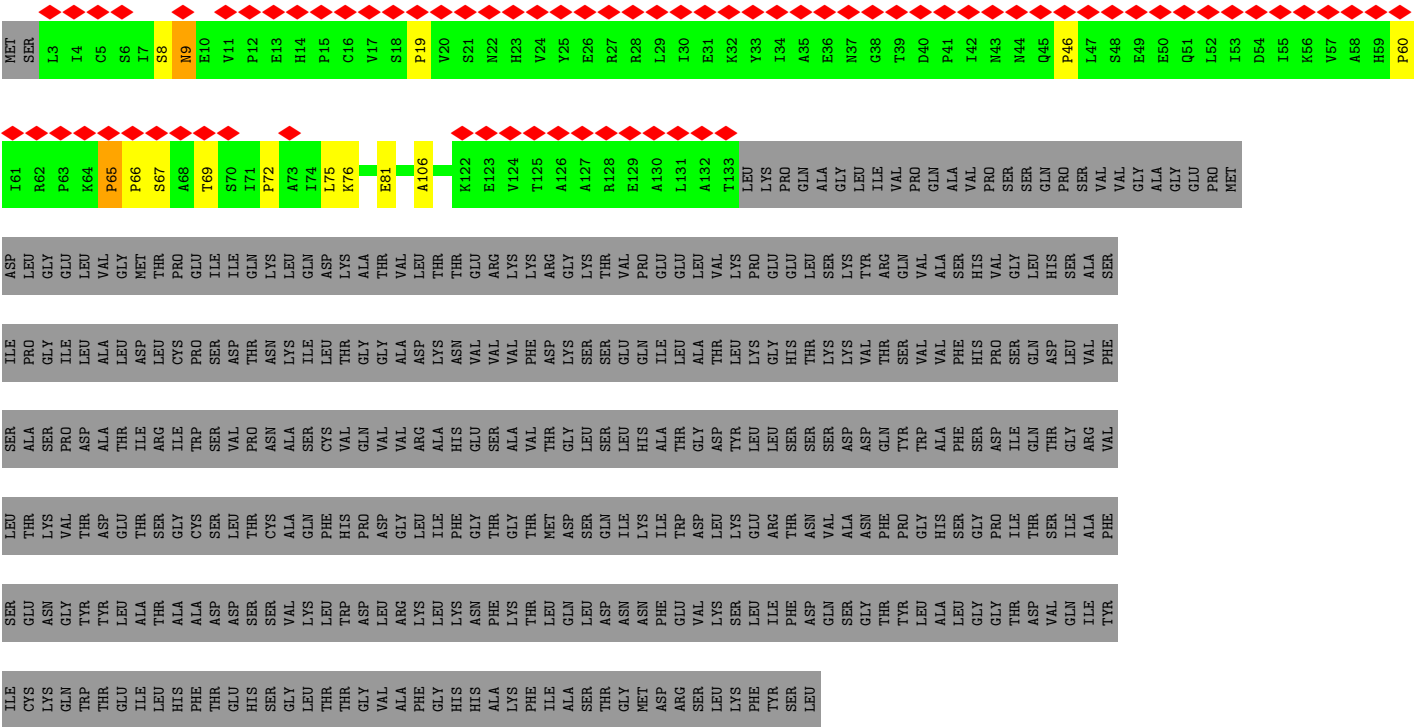
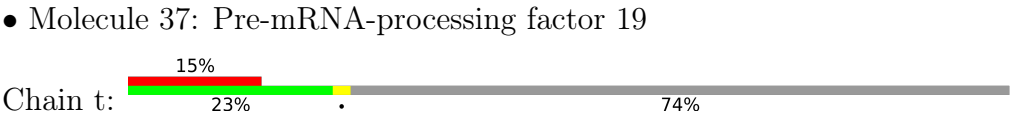
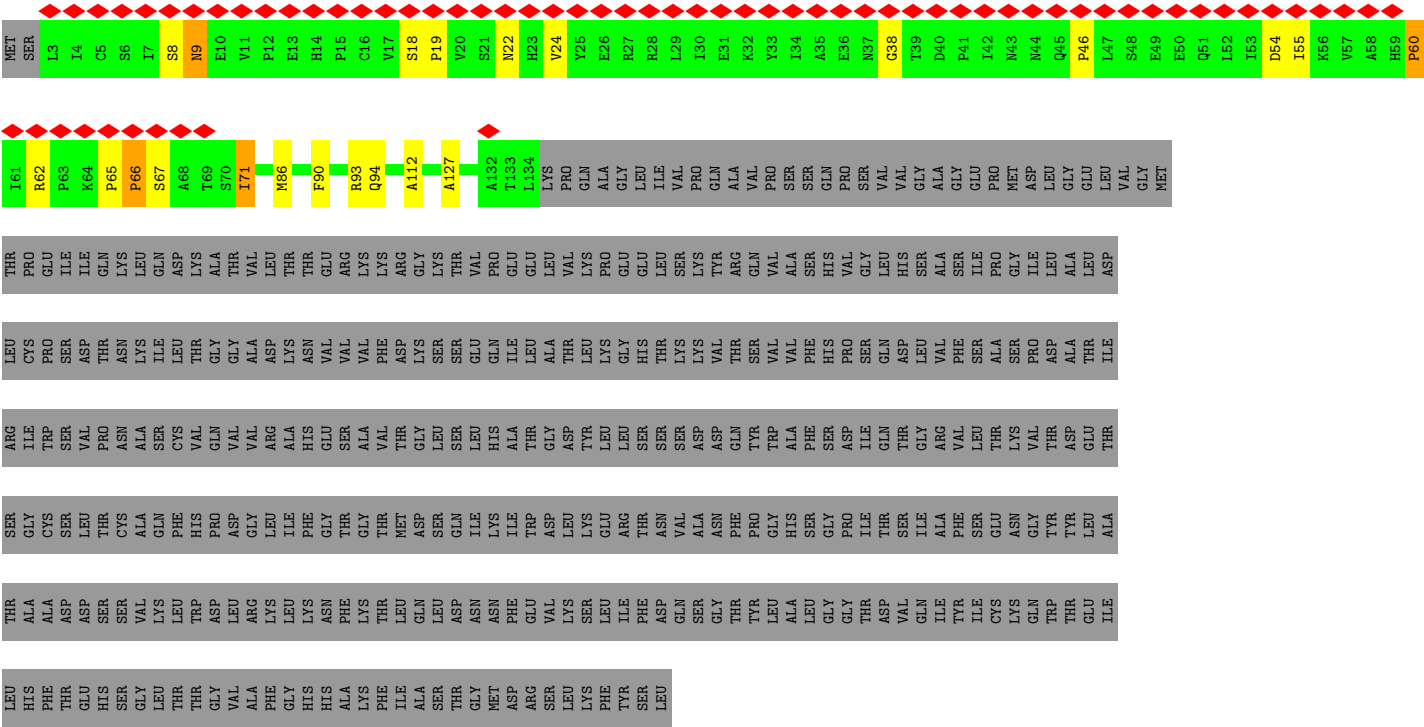


- Molecule 37: Pre-mRNA-processing factor 19

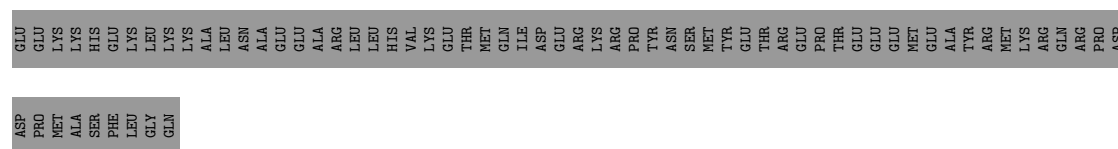


- Molecule 37: Pre-mRNA-processing factor 19

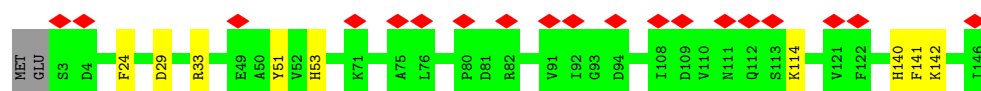
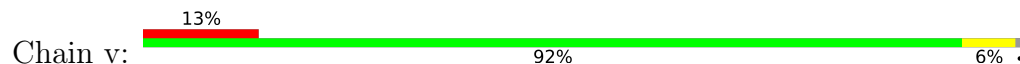




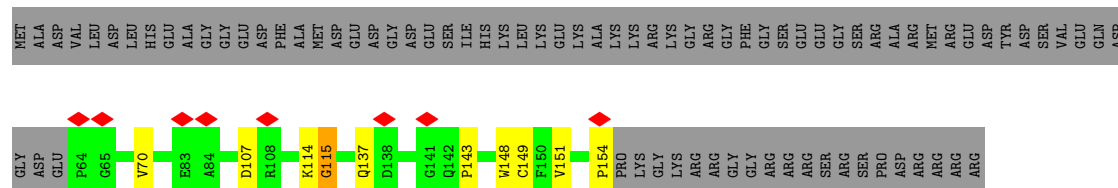




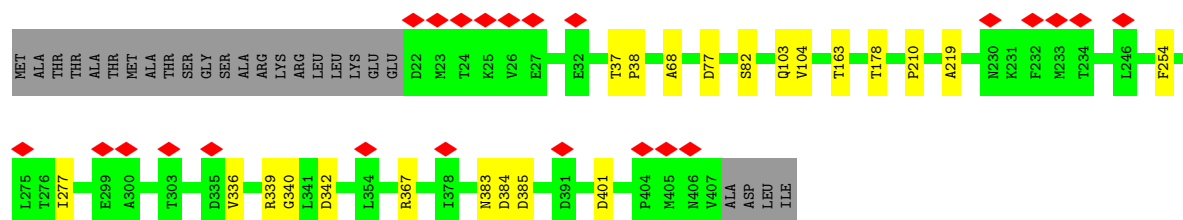
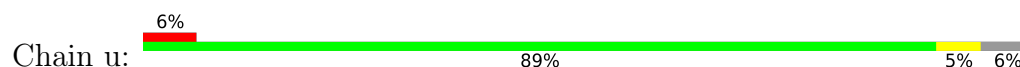
• Molecule 41: Protein mago nashi homolog



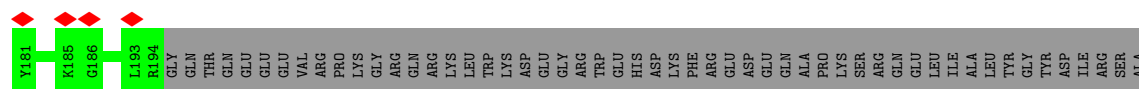
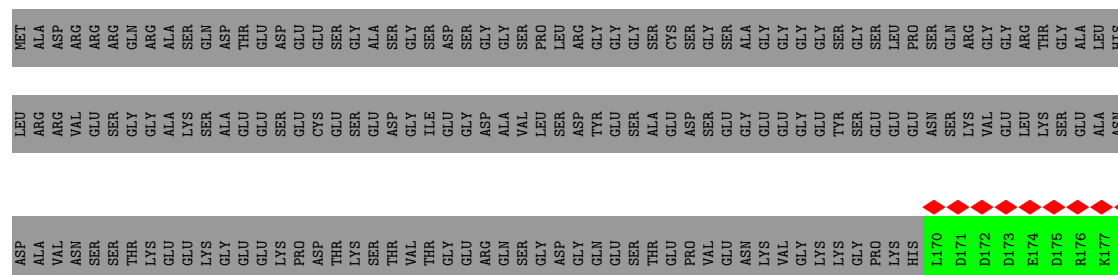
• Molecule 42: RNA-binding protein 8A



• Molecule 43: Eukaryotic initiation factor 4A-III



• Molecule 44: Protein CASC3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58374	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)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.144	Depositor
Minimum map value	-1.098	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.37	Depositor
Map size (\AA)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GTP, MG, SEP, ATP, IHP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.78	31/18191 (0.2%)	1.03	94/24720 (0.4%)
2	B	0.60	2/1970 (0.1%)	0.82	6/3060 (0.2%)
3	C	0.53	0/6938	0.83	13/9428 (0.1%)
4	D	0.55	0/8529	1.12	29/11891 (0.2%)
5	E	0.53	0/2392	0.73	0/3242
6	F	0.48	0/2323	0.82	3/3619 (0.1%)
7	4	0.72	0/307	1.00	3/476 (0.6%)
8	G	0.62	2/1674 (0.1%)	1.41	35/2594 (1.3%)
9	H	0.85	26/3305 (0.8%)	1.41	60/5130 (1.2%)
10	I	0.61	0/3884	1.42	24/5301 (0.5%)
11	J	0.54	0/3861	0.85	16/5241 (0.3%)
12	K	0.67	1/768 (0.1%)	1.08	3/1067 (0.3%)
13	L	0.50	0/3046	0.81	10/4115 (0.2%)
14	M	0.54	0/1119	0.90	6/1497 (0.4%)
15	N	0.66	0/1210	0.80	2/1622 (0.1%)
16	O	0.54	0/2344	0.83	4/3163 (0.1%)
17	P	0.74	1/967 (0.1%)	1.18	13/1285 (1.0%)
18	Q	0.41	0/6565	0.91	4/9143 (0.0%)
19	R	0.78	4/2262 (0.2%)	1.21	13/3031 (0.4%)
20	S	0.48	0/1268	0.75	1/1714 (0.1%)
21	T	0.78	0/2519	0.95	9/3433 (0.3%)
22	U	0.50	0/424	0.85	2/582 (0.3%)
23	V	0.43	0/2642	0.82	0/3602
24	W	0.43	0/4237	0.87	5/5723 (0.1%)
25	Y	0.98	0/3436	1.49	20/4774 (0.4%)
26	Z	0.31	1/1129 (0.1%)	0.55	0/1525
27	2	0.59	0/1030	1.02	6/1371 (0.4%)
28	z	0.24	0/505	0.58	0/672
29	b	0.77	0/797	1.05	4/1062 (0.4%)
29	i	0.73	0/700	1.03	4/933 (0.4%)
30	y	0.60	0/389	1.22	3/540 (0.6%)
31	a	0.67	0/616	0.97	2/830 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	h	0.66	0/639	0.86	0/857
32	c	0.74	0/657	0.98	0/888
32	j	0.74	0/657	0.98	0/888
33	d	0.94	1/786 (0.1%)	1.10	2/1053 (0.2%)
33	k	0.95	0/696	1.07	1/935 (0.1%)
34	f	1.04	1/588 (0.2%)	1.08	0/795
34	m	1.05	1/578 (0.2%)	1.15	1/783 (0.1%)
35	e	0.84	0/660	1.06	1/886 (0.1%)
35	l	0.85	0/660	1.06	1/886 (0.1%)
36	g	0.71	0/584	0.95	1/779 (0.1%)
36	n	0.70	0/548	1.00	2/729 (0.3%)
37	q	0.62	0/658	1.04	3/919 (0.3%)
37	r	0.57	0/653	1.00	3/912 (0.3%)
37	s	0.60	0/658	1.08	4/919 (0.4%)
37	t	0.62	0/653	0.94	3/912 (0.3%)
38	o	0.81	0/1299	2.06	54/1761 (3.1%)
39	p	0.78	0/774	1.71	12/1035 (1.2%)
40	l	0.34	0/2262	0.67	1/3045 (0.0%)
41	v	0.47	0/710	1.03	3/987 (0.3%)
42	w	0.47	0/444	1.21	4/614 (0.7%)
43	u	0.51	0/1906	1.20	13/2653 (0.5%)
44	x	0.53	0/123	1.12	0/170
45	3	0.25	0/232	0.60	0/307
All	All	0.65	71/108772 (0.1%)	1.05	503/150099 (0.3%)

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	19
3	C	0	9
4	D	0	1
5	E	0	1
10	I	0	6
11	J	0	5
15	N	0	4
16	O	0	1
17	P	0	3
19	R	0	7
21	T	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	W	0	2
33	d	0	1
33	k	0	1
All	All	0	63

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1724	PRO	N-CA	16.49	1.68	1.47
19	R	219	PRO	C-O	-10.51	1.11	1.23
19	R	222	PRO	N-CA	10.35	1.68	1.46
1	A	771	VAL	C-O	-9.56	1.12	1.24
19	R	221	GLY	C-N	9.29	1.44	1.33
1	A	776	LEU	C-O	-9.08	1.12	1.24
1	A	773	LYS	C-O	-8.70	1.14	1.24
1	A	854	SER	C-O	-8.39	1.14	1.23
9	H	142	C	C1'-N1	7.68	1.59	1.48
9	H	77	C	C1'-N1	7.66	1.59	1.48
1	A	1553	VAL	C-O	-7.61	1.15	1.24
1	A	663	ARG	C-O	-7.45	1.14	1.23
1	A	1163	ARG	C-O	-7.42	1.15	1.24
2	B	103	G	C1'-N9	-7.25	1.37	1.48
9	H	72	U	C1'-N1	7.21	1.59	1.48
9	H	55	U	C1'-N1	7.20	1.59	1.48
9	H	74	U	C1'-N1	7.15	1.59	1.48
9	H	54	U	C1'-N1	7.14	1.59	1.48
9	H	89	U	C1'-N1	7.13	1.59	1.48
9	H	92	U	C1'-N1	7.13	1.59	1.48
9	H	69	U	C1'-N1	7.12	1.59	1.48
9	H	60	U	C1'-N1	7.10	1.59	1.48
9	H	58	U	C1'-N1	7.07	1.59	1.48
9	H	91	U	C1'-N1	7.05	1.59	1.48
9	H	150	U	C1'-N1	6.98	1.58	1.48
9	H	182	U	C1'-N1	6.95	1.58	1.48
1	A	1459	ARG	C-O	-6.72	1.15	1.24
8	G	21	A	O3'-P	-6.69	1.51	1.61
17	P	11	PRO	C-O	-6.67	1.16	1.23
1	A	772	CYS	C-O	-6.66	1.16	1.24
9	H	73	C	C1'-N1	6.66	1.58	1.48
9	H	151	C	C1'-N1	6.66	1.58	1.48
9	H	97	G	C1'-N9	-6.65	1.38	1.48
9	H	67	C	C1'-N1	6.64	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	H	141	C	C1'-N1	6.63	1.58	1.48
9	H	184	C	C1'-N1	6.59	1.58	1.48
9	H	71	C	C1'-N1	6.53	1.58	1.48
9	H	70	C	C1'-N1	6.52	1.58	1.48
9	H	148	C	C1'-N1	6.52	1.58	1.48
1	A	864	LEU	C-O	-6.48	1.16	1.24
1	A	1529	ILE	C-N	6.47	1.49	1.33
9	H	84	C	C1'-N1	6.46	1.58	1.48
9	H	78	C	C1'-N1	6.46	1.58	1.48
1	A	1730	MET	C-O	-6.39	1.16	1.24
1	A	860	GLN	C-O	-6.33	1.16	1.24
26	Z	714	PRO	C-N	6.31	1.39	1.33
1	A	863	GLU	C-O	-6.15	1.17	1.24
1	A	859	SER	C-O	-6.05	1.17	1.24
1	A	861	ARG	C-O	-5.92	1.17	1.24
8	G	145	U	O3'-P	-5.83	1.52	1.61
1	A	1562	MET	C-O	-5.79	1.17	1.24
1	A	669	ALA	C-O	-5.69	1.16	1.24
1	A	1726	ILE	C-O	-5.64	1.17	1.24
1	A	1753	LEU	C-O	-5.63	1.17	1.24
9	H	110	A	C1'-N9	-5.50	1.39	1.48
1	A	862	GLU	C-O	-5.47	1.17	1.24
1	A	1738	PRO	C-O	-5.43	1.17	1.24
1	A	1554	GLN	C-O	-5.40	1.17	1.23
1	A	668	VAL	C-O	-5.38	1.17	1.24
12	K	162	ASP	CA-CB	-5.32	1.44	1.53
1	A	866	LEU	C-O	-5.30	1.17	1.24
19	R	220	ARG	C-O	-5.25	1.17	1.23
1	A	859	SER	CA-CB	-5.23	1.45	1.53
1	A	1557	LEU	C-O	-5.19	1.17	1.24
34	f	14	LEU	CA-C	5.13	1.59	1.52
1	A	2105	ILE	CA-CB	-5.12	1.48	1.54
1	A	774	LYS	C-O	-5.12	1.18	1.24
1	A	1561	PHE	C-O	-5.06	1.17	1.23
34	m	14	LEU	CA-C	5.04	1.59	1.52
2	B	96	A	C1'-N9	-5.02	1.40	1.48
33	d	73	MET	CA-C	-5.00	1.46	1.52

All (503) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	221	GLY	CA-C-N	18.39	139.32	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	221	GLY	C-N-CA	18.39	139.32	120.38
1	A	535	ARG	CB-CA-C	18.06	139.35	109.56
8	G	1	G	C1'-C2'-O2'	-16.53	87.00	111.80
38	o	55	ARG	CD-NE-CZ	13.18	142.85	124.40
1	A	1723	LYS	CA-C-N	13.12	136.24	119.84
1	A	1723	LYS	C-N-CA	13.12	136.24	119.84
8	G	177	G	C4'-C3'-O3'	12.58	131.87	113.00
8	G	131	U	C2'-C3'-O3'	-12.13	95.51	113.70
10	I	84	HIS	O-C-N	-12.06	109.65	122.07
10	I	83	LYS	O-C-N	-12.04	109.66	122.07
10	I	311	MET	O-C-N	-12.02	109.69	122.07
10	I	310	LYS	O-C-N	-11.99	109.72	122.07
10	I	309	ALA	O-C-N	-11.88	109.84	122.07
1	A	1877	LEU	N-CA-C	-11.66	98.56	111.28
38	o	49	PHE	CA-CB-CG	11.38	125.18	113.80
19	R	222	PRO	N-CA-C	-11.13	97.12	110.70
1	A	772	CYS	CA-CB-SG	-11.01	89.09	114.40
43	u	37	THR	CA-C-N	10.67	130.44	119.56
43	u	37	THR	C-N-CA	10.67	130.44	119.56
42	w	114	LYS	N-CA-C	-10.46	93.67	110.20
1	A	1529	ILE	CA-C-N	10.18	132.57	119.84
1	A	1529	ILE	C-N-CA	10.18	132.57	119.84
8	G	145	U	C3'-C2'-O2'	10.00	125.69	110.70
2	B	104	C	C2'-C3'-O3'	-9.94	94.58	109.50
1	A	1850	ARG	N-CA-CB	9.80	124.28	110.07
10	I	458	LYS	O-C-N	9.75	132.11	122.07
10	I	459	ALA	O-C-N	9.69	132.05	122.07
10	I	457	ARG	O-C-N	9.59	131.94	122.07
8	G	171	G	C2'-C3'-O3'	9.56	123.84	109.50
1	A	1724	PRO	N-CA-C	-9.47	92.97	112.47
37	s	46	PRO	N-CA-CB	9.44	111.19	103.36
8	G	145	U	C2'-C3'-O3'	-9.32	99.72	113.70
8	G	174	G	C4'-C3'-O3'	9.28	126.92	113.00
38	o	58	ASP	CA-CB-CG	9.13	121.73	112.60
1	A	383	PHE	N-CA-C	-9.00	102.88	114.04
13	L	124	LYS	N-CA-C	8.90	124.28	112.35
8	G	172	C	C4'-C3'-O3'	8.81	122.62	109.40
3	C	855	GLY	N-CA-C	8.78	123.27	112.73
2	B	12	U	C4'-C3'-O3'	8.77	122.56	109.40
25	Y	687	ALA	CA-C-N	8.73	133.91	120.82
25	Y	687	ALA	C-N-CA	8.73	133.91	120.82
37	r	46	PRO	N-CA-CB	8.72	111.12	103.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	458	LYS	CA-C-O	-8.71	111.67	120.82
9	H	82	G	O3'-P-O5'	-8.69	90.97	104.00
9	H	183	G	O3'-P-O5'	-8.68	90.99	104.00
9	H	77	C	O3'-P-O5'	-8.64	91.03	104.00
10	I	459	ALA	CA-C-O	-8.64	111.75	120.82
9	H	68	G	O3'-P-O5'	-8.63	91.05	104.00
9	H	78	C	O3'-P-O5'	-8.63	91.05	104.00
9	H	141	C	O3'-P-O5'	-8.63	91.06	104.00
9	H	56	A	O3'-P-O5'	-8.63	91.06	104.00
9	H	113	G	O3'-P-O5'	-8.62	91.06	104.00
9	H	148	C	O3'-P-O5'	-8.62	91.07	104.00
9	H	59	A	O3'-P-O5'	-8.62	91.07	104.00
10	I	457	ARG	CA-C-O	-8.62	111.77	120.82
9	H	180	G	O3'-P-O5'	-8.61	91.09	104.00
9	H	54	U	O3'-P-O5'	-8.61	91.09	104.00
9	H	57	A	O3'-P-O5'	-8.60	91.10	104.00
9	H	182	U	O3'-P-O5'	-8.60	91.10	104.00
9	H	74	U	O3'-P-O5'	-8.60	91.11	104.00
9	H	72	U	O3'-P-O5'	-8.59	91.11	104.00
9	H	73	C	O3'-P-O5'	-8.59	91.11	104.00
8	G	177	G	N9-C1'-C2'	-8.59	99.12	112.00
9	H	91	U	O3'-P-O5'	-8.59	91.12	104.00
9	H	93	A	O3'-P-O5'	-8.59	91.12	104.00
9	H	150	U	O3'-P-O5'	-8.59	91.12	104.00
9	H	149	A	O3'-P-O5'	-8.58	91.13	104.00
9	H	81	G	O3'-P-O5'	-8.57	91.14	104.00
9	H	79	G	O3'-P-O5'	-8.57	91.14	104.00
9	H	90	A	O3'-P-O5'	-8.57	91.14	104.00
9	H	181	G	O3'-P-O5'	-8.57	91.14	104.00
9	H	55	U	O3'-P-O5'	-8.57	91.15	104.00
9	H	84	C	O3'-P-O5'	-8.57	91.15	104.00
9	H	80	A	O3'-P-O5'	-8.56	91.15	104.00
9	H	89	U	O3'-P-O5'	-8.56	91.16	104.00
9	H	92	U	O3'-P-O5'	-8.56	91.16	104.00
9	H	69	U	O3'-P-O5'	-8.54	91.18	104.00
9	H	67	C	O3'-P-O5'	-8.54	91.19	104.00
9	H	58	U	O3'-P-O5'	-8.54	91.19	104.00
9	H	71	C	O3'-P-O5'	-8.54	91.19	104.00
9	H	114	A	O3'-P-O5'	-8.54	91.19	104.00
38	o	5	THR	N-CA-CB	-8.54	98.25	111.05
9	H	83	A	O3'-P-O5'	-8.53	91.20	104.00
9	H	88	A	O3'-P-O5'	-8.52	91.21	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	L	9	GLY	CA-C-N	8.51	137.29	121.97
13	L	9	GLY	C-N-CA	8.51	137.29	121.97
9	H	70	C	O3'-P-O5'	-8.51	91.23	104.00
8	G	171	G	C3'-C2'-O2'	8.47	127.31	114.60
37	q	46	PRO	N-CA-CB	8.47	111.22	103.34
1	A	1980	GLU	N-CA-C	-8.45	101.76	110.97
10	I	725	ARG	N-CA-C	-8.36	102.17	111.28
39	p	80	ARG	CD-NE-CZ	8.30	136.02	124.40
8	G	1	G	C4'-C3'-O3'	8.29	121.83	109.40
1	A	1689	THR	CA-C-N	8.24	133.59	121.31
1	A	1689	THR	C-N-CA	8.24	133.59	121.31
7	4	-12	G	N9-C1'-C2'	-8.24	99.64	112.00
25	Y	1040	GLY	N-CA-C	8.17	122.85	111.25
37	s	60	PRO	N-CA-CB	8.16	111.81	103.25
8	G	1	G	N9-C1'-C2'	-8.11	101.83	114.00
38	o	16	THR	CA-C-O	-8.06	111.73	120.36
3	C	754	VAL	N-CA-C	-7.93	104.85	111.91
38	o	47	ILE	N-CA-CB	7.92	123.08	111.52
1	A	861	ARG	CG-CD-NE	-7.91	94.59	112.00
38	o	99	SER	N-CA-C	7.90	122.69	112.26
13	L	54	LEU	N-CA-C	7.87	119.86	111.28
17	P	7	PRO	CA-C-N	7.86	136.55	121.54
17	P	7	PRO	C-N-CA	7.86	136.55	121.54
21	T	187	LYS	CA-C-N	7.85	129.66	119.84
21	T	187	LYS	C-N-CA	7.85	129.66	119.84
16	O	119	GLN	CB-CA-C	7.83	124.17	110.85
1	A	1561	PHE	CB-CA-C	-7.77	93.14	109.38
8	G	21	A	O3'-P-O5'	7.77	115.66	104.00
38	o	117	TYR	CA-C-O	7.72	128.51	120.40
18	Q	1379	TYR	N-CA-C	7.68	122.75	112.30
19	R	222	PRO	CA-N-CD	-7.68	101.25	112.00
14	M	120	PRO	CB-CA-C	-7.66	99.41	110.75
8	G	177	G	C1'-C2'-O2'	-7.64	96.94	108.40
9	H	168	A	P-O5'-C5'	-7.61	109.48	120.90
1	A	343	GLU	N-CA-CB	-7.54	98.78	110.39
7	4	-12	G	C4'-C3'-O3'	7.52	124.28	113.00
1	A	866	LEU	CA-C-N	7.47	132.50	120.55
1	A	866	LEU	C-N-CA	7.47	132.50	120.55
37	q	60	PRO	N-CA-CB	7.43	111.05	103.25
1	A	664	HIS	CA-CB-CG	-7.43	106.37	113.80
3	C	823	ALA	N-CA-C	7.41	120.49	108.34
2	B	20	G	N9-C1'-C2'	7.36	125.05	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	863	GLU	CB-CG-CD	-7.35	100.11	112.60
12	K	90	PRO	N-CA-CB	7.33	111.06	103.00
1	A	1560	ILE	CA-C-N	-7.31	111.22	122.62
1	A	1560	ILE	C-N-CA	-7.31	111.22	122.62
8	G	171	G	C1'-C2'-O2'	7.29	122.74	111.80
1	A	1740	LEU	CA-C-O	-7.27	113.07	121.07
9	H	22	U	C2'-C3'-O3'	-7.27	102.80	113.70
8	G	166	A	C2'-C3'-O3'	-7.26	98.61	109.50
9	H	167	U	O3'-P-O5'	-7.25	93.12	104.00
4	D	1666	THR	N-CA-C	7.22	121.54	112.87
12	K	78	PRO	N-CA-CB	7.22	110.83	103.25
38	o	71	VAL	CA-C-N	7.22	131.65	120.75
38	o	71	VAL	C-N-CA	7.22	131.65	120.75
4	D	1044	VAL	CA-C-N	7.21	126.71	118.85
4	D	1044	VAL	C-N-CA	7.21	126.71	118.85
9	H	31	G	N9-C1'-C2'	-7.20	101.21	112.00
37	t	60	PRO	N-CA-CB	7.16	111.32	103.30
8	G	176	U	C3'-C2'-O2'	7.16	121.43	110.70
18	Q	93	SER	N-CA-C	-7.15	103.57	111.36
1	A	663	ARG	CG-CD-NE	-7.14	96.29	112.00
1	A	1556	ASP	CB-CA-C	-7.13	99.69	110.88
38	o	21	ASP	CA-CB-CG	7.07	119.67	112.60
43	u	77	ASP	N-CA-C	-7.06	99.83	110.28
8	G	167	G	C2'-C3'-O3'	7.06	120.09	109.50
12	K	195	ILE	N-CA-C	-7.06	102.95	110.36
17	P	8	THR	CA-CB-OG1	-7.03	99.05	109.60
19	R	301	ALA	N-CA-C	-7.02	104.34	113.12
9	H	170	C	C3'-C2'-O2'	-7.01	104.08	114.60
38	o	72	ASN	OD1-CG-ND2	7.00	129.60	122.60
4	D	533	VAL	N-CA-C	6.97	118.85	112.29
38	o	107	ASP	CA-CB-CG	6.95	119.55	112.60
1	A	1982	GLN	CB-CA-C	-6.93	99.91	110.92
8	G	167	G	O4'-C1'-N9	-6.92	97.83	108.20
38	o	4	LEU	N-CA-C	-6.92	97.95	108.67
25	Y	685	ASP	CA-C-N	6.91	134.74	121.54
25	Y	685	ASP	C-N-CA	6.91	134.74	121.54
38	o	121	LEU	CA-C-O	6.88	128.87	121.44
37	t	46	PRO	N-CA-CB	6.85	110.44	103.25
8	G	177	G	C2'-C3'-O3'	-6.84	103.44	113.70
38	o	75	ARG	NE-CZ-NH1	-6.82	114.68	121.50
1	A	1881	ASN	CA-CB-CG	-6.80	105.80	112.60
8	G	168	C	C1'-C2'-O2'	-6.78	98.22	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	686	GLU	CA-C-N	6.78	134.49	121.54
25	Y	686	GLU	C-N-CA	6.78	134.49	121.54
21	T	309	ASP	O-C-N	6.77	131.12	122.39
10	I	697	PRO	CA-C-N	6.76	134.45	121.54
10	I	697	PRO	C-N-CA	6.76	134.45	121.54
11	J	675	PRO	N-CA-CB	6.76	110.34	103.25
17	P	10	GLU	CB-CA-C	6.75	121.67	111.14
11	J	604	PRO	N-CA-CB	6.74	110.33	103.25
37	r	19	PRO	N-CA-CB	6.73	110.30	102.76
38	o	58	ASP	N-CA-CB	-6.72	100.61	111.24
39	p	53	PHE	CA-C-O	-6.72	112.93	120.32
8	G	174	G	C1'-C2'-O2'	-6.71	98.33	108.40
31	a	76	MET	CA-C-N	-6.70	113.55	123.00
31	a	76	MET	C-N-CA	-6.70	113.55	123.00
37	q	19	PRO	N-CA-CB	6.67	110.26	103.25
9	H	164	C	C5'-C4'-O4'	-6.67	99.09	109.10
13	L	214	ILE	N-CA-C	-6.62	102.46	108.95
25	Y	689	GLU	N-CA-C	-6.62	97.28	108.26
30	y	47	ARG	CB-CA-C	-6.61	99.81	110.79
8	G	127	U	C2'-C3'-O3'	-6.60	103.81	113.70
43	u	38	PRO	N-CA-C	6.54	122.35	113.84
1	A	663	ARG	CB-CA-C	-6.53	98.49	109.65
37	t	19	PRO	N-CA-CB	6.52	110.10	103.25
11	J	239	ARG	CA-C-N	6.51	133.98	121.54
11	J	239	ARG	C-N-CA	6.51	133.98	121.54
1	A	1740	LEU	N-CA-C	-6.50	103.09	111.02
11	J	637	PRO	N-CA-CB	6.49	110.40	103.52
38	o	87	LEU	CA-C-N	6.49	126.25	119.05
38	o	87	LEU	C-N-CA	6.49	126.25	119.05
8	G	22	C	C4'-C3'-O3'	-6.47	103.30	113.00
2	B	12	U	C2'-C3'-O3'	-6.46	99.80	109.50
8	G	166	A	C3'-C2'-O2'	6.46	124.28	114.60
1	A	1556	ASP	N-CA-C	6.44	117.96	111.07
14	M	121	ASP	CA-CB-CG	-6.40	106.20	112.60
37	s	19	PRO	N-CA-CB	6.39	109.95	103.25
1	A	776	LEU	N-CA-C	-6.38	104.97	112.89
11	J	187	VAL	CA-C-N	6.37	133.71	121.54
11	J	187	VAL	C-N-CA	6.37	133.71	121.54
1	A	1753	LEU	N-CA-CB	-6.36	99.92	110.47
38	o	55	ARG	NE-CZ-NH1	6.36	127.86	121.50
38	o	40	THR	CA-C-N	6.32	131.57	122.40
38	o	40	THR	C-N-CA	6.32	131.57	122.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	774	LYS	CB-CA-C	-6.32	100.92	110.90
43	u	68	ALA	N-CA-C	6.30	119.44	111.69
19	R	124	VAL	CA-C-N	6.30	133.56	121.54
19	R	124	VAL	C-N-CA	6.30	133.56	121.54
17	P	7	PRO	CB-CA-C	-6.28	101.20	111.56
37	r	60	PRO	N-CA-CB	6.27	109.84	103.25
8	G	168	C	C3'-C2'-O2'	6.26	120.09	110.70
11	J	670	PRO	N-CA-CB	6.26	110.45	103.44
9	H	168	A	C5'-C4'-C3'	-6.25	106.62	116.00
8	G	144	A	C2'-C3'-O3'	6.25	118.88	109.50
8	G	1	G	C2'-C3'-O3'	6.25	118.87	109.50
9	H	169	C	P-O3'-C3'	6.25	129.57	120.20
2	B	26	A	P-O5'-C5'	-6.24	111.53	120.90
9	H	31	G	C4'-C3'-O3'	6.21	122.32	113.00
1	A	2011	ILE	N-CA-C	-6.21	104.46	110.42
17	P	9	PHE	CA-C-N	-6.20	115.64	123.15
17	P	9	PHE	C-N-CA	-6.20	115.64	123.15
1	A	1249	MET	N-CA-C	-6.17	103.71	111.11
27	2	70	SER	N-CA-C	-6.16	104.48	112.68
15	N	40	LYS	CA-C-N	6.15	133.29	121.54
15	N	40	LYS	C-N-CA	6.15	133.29	121.54
1	A	1849	ILE	CA-C-N	-6.15	112.08	120.44
1	A	1849	ILE	C-N-CA	-6.15	112.08	120.44
38	o	73	ASN	N-CA-C	6.13	119.82	111.17
11	J	412	ASP	CA-C-N	6.13	128.82	120.54
11	J	412	ASP	C-N-CA	6.13	128.82	120.54
30	y	48	GLY	CA-C-N	-6.12	112.09	123.05
30	y	48	GLY	C-N-CA	-6.12	112.09	123.05
43	u	339	ARG	N-CA-C	6.12	119.67	109.95
8	G	3	A	N9-C1'-C2'	-6.10	102.85	112.00
41	v	142	LYS	N-CA-C	6.10	118.58	109.25
1	A	1192	PHE	N-CA-C	6.08	119.07	110.50
10	I	377	THR	CB-CA-C	-6.08	101.34	110.88
4	D	1006	LYS	CA-C-N	6.07	126.24	119.32
4	D	1006	LYS	C-N-CA	6.07	126.24	119.32
38	o	52	ASN	CA-CB-CG	6.05	118.65	112.60
1	A	1736	ALA	CA-C-O	-6.05	112.73	119.08
11	J	566	PRO	N-CA-CB	6.04	110.21	103.44
17	P	5	ALA	N-CA-C	-6.01	104.64	111.14
1	A	1877	LEU	O-C-N	6.01	128.49	122.12
13	L	134	THR	N-CA-C	5.98	117.88	111.36
43	u	178	THR	N-CA-C	5.98	120.70	113.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1568	THR	CA-CB-OG1	-5.98	100.63	109.60
1	A	771	VAL	CA-C-O	-5.98	114.73	120.95
27	2	96	MET	O-C-N	5.97	130.69	122.46
1	A	1556	ASP	CA-C-O	-5.96	114.57	120.82
38	o	79	ILE	CA-C-N	5.95	125.75	120.10
38	o	79	ILE	C-N-CA	5.95	125.75	120.10
39	p	89	ASP	CA-CB-CG	5.95	118.55	112.60
38	o	75	ARG	N-CA-CB	-5.94	102.72	111.51
36	n	67	ILE	CB-CA-C	-5.93	104.82	111.23
8	G	172	C	P-O3'-C3'	5.93	129.10	120.20
19	R	217	LYS	CB-CA-C	-5.93	98.97	109.70
10	I	481	TYR	N-CA-C	5.93	118.69	111.82
9	H	163	G	O3'-P-O5'	-5.92	95.12	104.00
38	o	27	ARG	CB-CA-C	-5.92	98.65	109.54
36	g	67	ILE	CB-CA-C	-5.92	104.84	111.23
22	U	83	GLU	CA-C-N	5.91	132.83	121.54
22	U	83	GLU	C-N-CA	5.91	132.83	121.54
39	p	46	MET	N-CA-C	-5.91	104.75	111.07
11	J	413	GLU	N-CA-C	5.89	118.18	111.11
21	T	401	PRO	CA-C-N	5.89	136.58	126.32
21	T	401	PRO	C-N-CA	5.89	136.58	126.32
38	o	123	ASN	OD1-CG-ND2	5.88	128.48	122.60
1	A	1683	LYS	CA-C-N	5.87	132.75	121.54
1	A	1683	LYS	C-N-CA	5.87	132.75	121.54
1	A	1949	ARG	N-CA-C	-5.87	105.62	112.89
38	o	50	SER	CA-C-O	5.86	127.76	121.55
18	Q	100	GLU	N-CA-C	-5.85	105.64	112.89
1	A	1739	ALA	N-CA-C	-5.84	104.29	112.12
1	A	2199	ILE	CB-CA-C	-5.80	104.42	112.02
1	A	1982	GLN	CB-CG-CD	-5.79	102.76	112.60
1	A	773	LYS	CA-C-O	-5.78	114.42	120.55
1	A	1739	ALA	O-C-N	5.76	128.69	121.95
6	F	73	A	C2'-C3'-O3'	-5.75	100.87	109.50
4	D	1135	LEU	CA-C-N	5.73	125.67	119.76
4	D	1135	LEU	C-N-CA	5.73	125.67	119.76
43	u	336	VAL	N-CA-C	-5.73	104.02	112.04
1	A	1920	TYR	CA-C-N	5.73	130.30	121.19
1	A	1920	TYR	C-N-CA	5.73	130.30	121.19
38	o	27	ARG	CA-C-N	5.72	128.74	120.11
38	o	27	ARG	C-N-CA	5.72	128.74	120.11
1	A	1980	GLU	CB-CG-CD	5.71	122.31	112.60
1	A	1733	ILE	CB-CA-C	-5.71	104.43	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	782	PHE	N-CA-C	5.70	118.08	109.41
6	F	50	A	C1'-C2'-O2'	5.70	116.95	108.40
16	O	119	GLN	CB-CG-CD	-5.70	102.91	112.60
1	A	2153	THR	N-CA-C	-5.70	101.75	109.95
9	H	164	C	P-O3'-C3'	5.68	128.73	120.20
14	M	121	ASP	CA-C-N	5.68	132.12	122.12
14	M	121	ASP	C-N-CA	5.68	132.12	122.12
1	A	1732	LYS	CB-CA-C	-5.67	101.97	110.88
10	I	457	ARG	N-CA-C	5.67	117.14	111.07
29	i	52	LYS	CA-C-N	-5.65	114.11	119.76
29	i	52	LYS	C-N-CA	-5.65	114.11	119.76
4	D	1291	LEU	CA-C-N	5.64	125.96	119.92
4	D	1291	LEU	C-N-CA	5.64	125.96	119.92
1	A	1519	THR	CB-CA-C	-5.64	108.30	116.54
8	G	174	G	C2'-C3'-O3'	-5.63	105.25	113.70
38	o	71	VAL	O-C-N	-5.63	115.53	122.57
34	m	4	PRO	N-CA-C	5.63	124.06	112.47
38	o	149	LYS	CB-CA-C	-5.62	102.06	110.16
41	v	114	LYS	N-CA-C	-5.62	100.51	109.96
27	2	23	ILE	CA-C-N	5.62	126.86	119.84
27	2	23	ILE	C-N-CA	5.62	126.86	119.84
6	F	73	A	C3'-C2'-O2'	5.61	123.01	114.60
4	D	1048	VAL	N-CA-C	-5.60	106.33	113.22
19	R	219	PRO	CA-C-O	-5.60	114.96	121.34
38	o	16	THR	O-C-N	5.59	129.59	123.22
1	A	1683	LYS	O-C-N	5.59	130.49	122.28
9	H	157	G	P-O5'-C5'	-5.58	112.53	120.90
1	A	1553	VAL	CA-C-O	-5.58	114.58	120.39
1	A	2225	LEU	N-CA-C	5.58	117.88	109.23
13	L	9	GLY	O-C-N	5.58	129.36	122.78
13	L	7	LYS	CA-C-N	5.57	130.42	121.17
13	L	7	LYS	C-N-CA	5.57	130.42	121.17
43	u	384	ASP	N-CA-C	5.57	117.80	111.11
1	A	1758	PRO	N-CA-CB	-5.56	97.41	103.25
1	A	2241	ASN	N-CA-C	5.56	118.38	110.10
38	o	159	GLU	N-CA-C	-5.55	104.86	111.69
40	1	267	ILE	N-CA-C	-5.55	105.78	113.00
3	C	755	ASP	N-CA-C	-5.55	106.30	112.57
9	H	168	A	O4'-C1'-C2'	-5.55	102.05	107.60
1	A	1054	GLY	N-CA-C	-5.55	106.08	112.29
3	C	560	VAL	CA-C-N	5.55	130.01	121.19
3	C	560	VAL	C-N-CA	5.55	130.01	121.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	P	5	ALA	CA-C-O	-5.55	114.99	120.70
18	Q	88	LYS	O-C-N	5.54	127.80	122.03
9	H	165	A	N9-C1'-C2'	5.54	120.31	112.00
29	b	5	LYS	N-CA-C	5.53	118.23	111.82
38	o	32	PRO	CA-C-N	5.52	130.67	122.99
38	o	32	PRO	C-N-CA	5.52	130.67	122.99
38	o	40	THR	N-CA-C	-5.52	106.04	112.89
17	P	12	ALA	CA-C-O	-5.51	115.71	121.55
38	o	34	ILE	CA-C-O	-5.51	114.24	120.74
1	A	1092	ILE	N-CA-C	5.50	120.78	109.34
25	Y	688	HIS	CA-C-N	5.50	130.53	122.39
25	Y	688	HIS	C-N-CA	5.50	130.53	122.39
1	A	663	ARG	CA-C-O	-5.49	115.01	121.16
29	i	5	LYS	N-CA-C	5.49	118.18	111.82
25	Y	680	ALA	N-CA-C	-5.48	104.83	112.45
4	D	2053	ALA	CA-C-N	5.48	125.15	119.56
4	D	2053	ALA	C-N-CA	5.48	125.15	119.56
25	Y	1183	VAL	N-CA-C	5.48	114.25	106.53
3	C	800	PRO	CA-C-N	5.48	132.00	121.54
3	C	800	PRO	C-N-CA	5.48	132.00	121.54
1	A	1736	ALA	CA-C-N	-5.47	113.16	121.92
1	A	1736	ALA	C-N-CA	-5.47	113.16	121.92
1	A	2203	ASN	N-CA-C	5.47	120.77	109.11
21	T	190	TRP	N-CA-C	5.47	122.45	110.80
1	A	1552	GLN	CA-C-N	-5.47	115.83	123.10
1	A	1552	GLN	C-N-CA	-5.47	115.83	123.10
29	b	52	LYS	CA-C-N	-5.46	114.30	119.76
29	b	52	LYS	C-N-CA	-5.46	114.30	119.76
21	T	389	SER	CA-C-N	-5.46	118.41	122.18
21	T	389	SER	C-N-CA	-5.46	118.41	122.18
10	I	698	ARG	N-CA-CB	5.45	119.71	110.49
9	H	160	A	P-O5'-C5'	-5.45	112.72	120.90
1	A	1740	LEU	O-C-N	5.45	127.91	122.08
4	D	1228	VAL	CB-CA-C	-5.45	104.90	112.04
38	o	132	ARG	CD-NE-CZ	5.44	132.02	124.40
42	w	115	GLY	N-CA-C	5.44	126.08	113.18
3	C	534	VAL	N-CA-C	-5.43	101.90	109.45
17	P	4	ALA	N-CA-C	-5.40	106.28	112.92
1	A	1529	ILE	N-CA-CB	5.40	118.76	111.21
1	A	244	GLN	N-CA-C	-5.39	105.49	111.36
24	W	204	ASP	CA-C-N	5.38	130.18	121.95
24	W	204	ASP	C-N-CA	5.38	130.18	121.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1556	ASP	CA-C-N	-5.37	114.10	122.37
1	A	1556	ASP	C-N-CA	-5.37	114.10	122.37
27	2	24	PRO	N-CA-C	5.37	123.53	112.47
11	J	356	TYR	CA-C-N	-5.36	111.30	121.54
11	J	356	TYR	C-N-CA	-5.36	111.30	121.54
24	W	266	ARG	CA-C-N	5.35	128.45	120.90
24	W	266	ARG	C-N-CA	5.35	128.45	120.90
4	D	1127	CYS	CA-C-N	5.35	125.68	119.47
4	D	1127	CYS	C-N-CA	5.35	125.68	119.47
1	A	2100	THR	N-CA-C	-5.35	106.75	113.28
25	Y	975	ARG	CA-C-N	5.35	127.39	120.44
25	Y	975	ARG	C-N-CA	5.35	127.39	120.44
7	4	-13	C	C4'-C3'-O3'	5.34	117.42	109.40
1	A	1737	ASN	CB-CA-C	5.34	121.61	110.50
39	p	25	ARG	CD-NE-CZ	5.34	131.88	124.40
1	A	1685	LEU	CA-C-O	-5.34	114.89	120.55
1	A	1514	LYS	CB-CA-C	5.34	118.21	110.79
29	b	65	ARG	CB-CG-CD	5.34	123.57	111.30
25	Y	841	ILE	N-CA-CB	5.33	117.78	110.54
38	o	146	ASP	CA-C-N	5.33	130.12	122.40
38	o	146	ASP	C-N-CA	5.33	130.12	122.40
3	C	824	THR	N-CA-C	5.33	123.42	112.40
8	G	169	U	N1-C1'-C2'	-5.32	104.01	112.00
25	Y	1169	ASP	N-CA-C	-5.32	100.96	109.04
29	i	65	ARG	CB-CG-CD	5.32	123.53	111.30
1	A	1723	LYS	N-CA-C	-5.31	105.53	112.75
3	C	515	THR	CA-C-N	5.31	127.71	120.54
3	C	515	THR	C-N-CA	5.31	127.71	120.54
20	S	130	GLY	N-CA-C	5.31	118.87	110.96
38	o	33	VAL	N-CA-CB	-5.31	103.77	111.52
39	p	6	ASN	N-CA-CB	-5.31	101.66	111.53
38	o	125	VAL	CA-C-N	5.30	127.91	120.28
38	o	125	VAL	C-N-CA	5.30	127.91	120.28
4	D	811	SER	N-CA-C	5.30	115.12	108.45
4	D	1228	VAL	N-CA-C	5.29	116.66	110.62
16	O	30	GLU	CA-C-N	-5.29	114.25	121.61
16	O	30	GLU	C-N-CA	-5.29	114.25	121.61
4	D	749	GLY	N-CA-C	-5.29	108.40	114.69
1	A	862	GLU	O-C-N	5.29	127.72	122.12
37	s	54	ASP	N-CA-CB	-5.29	102.27	110.46
1	A	1730	MET	CA-C-O	-5.28	114.95	120.55
4	D	2096	ALA	CA-C-N	5.28	125.48	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2096	ALA	C-N-CA	5.28	125.48	120.31
1	A	862	GLU	CA-C-O	-5.27	114.96	120.55
4	D	1693	ARG	CA-C-N	5.27	125.08	119.28
4	D	1693	ARG	C-N-CA	5.27	125.08	119.28
38	o	113	LYS	N-CA-C	5.25	118.48	111.75
1	A	1724	PRO	CA-N-CD	-5.25	104.65	112.00
1	A	1514	LYS	CA-C-N	5.25	127.31	120.28
1	A	1514	LYS	C-N-CA	5.25	127.31	120.28
9	H	171	U	C2'-C3'-O3'	-5.24	105.84	113.70
39	p	20	LYS	N-CA-C	5.23	117.38	111.11
17	P	5	ALA	O-C-N	5.22	127.73	122.09
17	P	11	PRO	CB-CA-C	-5.22	104.73	111.46
36	n	10	LYS	CB-CA-C	5.22	120.28	110.63
9	H	156	U	C4'-C3'-C2'	5.21	107.81	102.60
38	o	88	PRO	CB-CA-C	-5.21	104.03	112.62
4	D	488	LEU	N-CA-C	5.20	119.72	113.17
19	R	310	ARG	CB-CA-C	-5.19	102.73	110.88
13	L	52	GLU	N-CA-C	5.18	117.01	111.36
39	p	51	GLN	N-CA-C	5.18	117.55	109.52
39	p	68	GLN	OE1-CD-NE2	5.18	127.78	122.60
39	p	36	HIS	CA-CB-CG	-5.18	108.62	113.80
25	Y	1052	TRP	CA-C-N	5.17	127.16	120.44
25	Y	1052	TRP	C-N-CA	5.17	127.16	120.44
38	o	83	LEU	N-CA-C	5.17	117.58	111.33
10	I	231	ASN	O-C-N	5.16	125.08	120.48
3	C	359	LYS	CA-CB-CG	5.16	124.42	114.10
43	u	163	THR	N-CA-C	-5.16	103.68	110.39
10	I	22	LEU	O-C-N	5.15	125.07	120.48
25	Y	619	ARG	CA-C-N	5.15	127.50	120.54
25	Y	619	ARG	C-N-CA	5.15	127.50	120.54
4	D	572	ASP	N-CA-C	-5.15	103.34	110.35
42	w	148	TRP	N-CA-C	-5.14	103.25	110.50
10	I	487	TRP	N-CA-C	5.14	116.96	111.36
43	u	342	ASP	N-CA-C	5.14	117.08	107.99
27	2	97	ASP	O-C-N	5.13	129.42	122.59
39	p	48	MET	N-CA-C	5.13	119.54	113.28
43	u	367	ARG	N-CA-C	-5.13	106.28	112.54
2	B	21	A	C2'-C3'-O3'	-5.12	106.02	113.70
42	w	107	ASP	N-CA-C	-5.12	102.06	109.59
4	D	574	GLN	N-CA-C	5.11	117.98	111.69
33	k	99	MET	N-CA-C	5.11	116.84	108.76
9	H	22	U	C1'-C2'-O2'	-5.11	100.74	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	o	55	ARG	NE-CZ-NH2	-5.10	114.61	119.20
4	D	1875	VAL	CA-C-N	5.10	124.55	119.24
4	D	1875	VAL	C-N-CA	5.10	124.55	119.24
43	u	210	PRO	N-CA-C	5.10	121.35	113.75
33	d	99	MET	N-CA-C	5.10	116.82	108.76
33	d	88	LYS	CG-CD-CE	-5.10	99.57	111.30
38	o	90	LEU	CA-C-O	-5.10	113.22	120.51
8	G	172	C	C3'-C2'-O2'	5.09	122.24	114.60
39	p	83	TYR	CA-C-O	-5.09	115.25	121.05
14	M	124	PHE	CA-C-N	5.09	129.28	121.19
14	M	124	PHE	C-N-CA	5.09	129.28	121.19
41	v	141	PHE	N-CA-C	5.09	120.14	113.88
24	W	79	VAL	N-CA-C	5.08	114.10	106.42
1	A	1560	ILE	CA-C-O	-5.08	114.74	120.74
35	e	85	THR	N-CA-C	-5.08	105.93	112.68
10	I	149	TRP	O-C-N	5.08	125.00	120.48
9	H	155	C	P-O3'-C3'	5.08	127.81	120.20
19	R	181	PRO	N-CA-C	5.07	120.43	113.84
9	H	160	A	C4'-C3'-C2'	-5.06	97.54	102.60
38	o	90	LEU	O-C-N	5.05	129.31	122.59
10	I	728	ARG	CB-CG-CD	-5.05	99.68	111.30
8	G	1	G	C3'-C2'-O2'	5.05	122.17	114.60
11	J	201	ARG	CA-C-N	5.05	129.53	122.36
11	J	201	ARG	C-N-CA	5.05	129.53	122.36
1	A	243	ASN	CA-C-N	-5.04	113.13	120.29
1	A	243	ASN	C-N-CA	-5.04	113.13	120.29
9	H	170	C	O4'-C1'-C2'	-5.04	100.76	105.80
10	I	89	ASP	O-C-N	5.04	124.97	120.48
21	T	495	ALA	N-CA-C	5.04	117.55	111.40
1	A	2185	SER	CA-C-N	-5.03	116.57	121.65
1	A	2185	SER	C-N-CA	-5.03	116.57	121.65
19	R	70	ALA	CA-C-N	5.03	128.80	121.31
19	R	70	ALA	C-N-CA	5.03	128.80	121.31
9	H	160	A	N9-C1'-C2'	5.03	119.54	112.00
1	A	1738	PRO	N-CA-CB	-5.02	97.97	103.25
38	o	81	GLU	N-CA-C	5.02	118.55	112.23
35	l	85	THR	N-CA-C	-5.02	106.01	112.68
38	o	99	SER	N-CA-CB	-5.01	102.94	111.17
8	G	21	A	P-O3'-C3'	-5.01	112.69	120.20
1	A	772	CYS	CA-C-O	-5.00	115.12	120.42

There are no chirality outliers.

All (63) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1019	TYR	Peptide
1	A	1201	ARG	Peptide
1	A	1210	LYS	Peptide
1	A	1338	SER	Peptide
1	A	1503	TRP	Peptide
1	A	1513	MET	Mainchain
1	A	1561	PHE	Mainchain
1	A	166	PHE	Peptide
1	A	1717	ASN	Mainchain
1	A	1749	LYS	Mainchain
1	A	1753	LEU	Mainchain
1	A	2010	ILE	Mainchain
1	A	346	ASP	Peptide
1	A	377	GLU	Peptide
1	A	385	GLU	Peptide
1	A	55	ASP	Peptide
1	A	698	PRO	Peptide
1	A	73	HIS	Peptide
1	A	941	LYS	Peptide
3	C	308	CYS	Peptide
3	C	358	LYS	Peptide
3	C	360	ALA	Peptide
3	C	534	VAL	Peptide
3	C	799	GLU	Peptide
3	C	800	PRO	Peptide
3	C	902	HIS	Peptide
3	C	92	PRO	Peptide
3	C	93	ILE	Peptide
4	D	430	LEU	Peptide
5	E	192	ASN	Peptide
10	I	309	ALA	Mainchain
10	I	310	LYS	Mainchain
10	I	311	MET	Mainchain
10	I	693	GLN	Mainchain
10	I	83	LYS	Mainchain
10	I	84	HIS	Mainchain
11	J	205	LEU	Peptide
11	J	215	THR	Peptide
11	J	216	ASP	Peptide
11	J	240	THR	Peptide
11	J	241	VAL	Peptide
15	N	136	HIS	Peptide

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Mol	Chain	Res	Type	Group
15	N	3	LYS	Peptide
15	N	36	PRO	Peptide
15	N	4	VAL	Peptide
16	O	63	MET	Peptide
17	P	204	GLN	Peptide
17	P	30	TYR	Peptide
17	P	48	GLN	Peptide
19	R	125	MET	Peptide
19	R	126	ASN	Peptide
19	R	183	GLN	Peptide
19	R	185	GLY	Peptide
19	R	212	PHE	Peptide
19	R	66	GLU	Peptide
19	R	94	GLY	Peptide
21	T	342	GLU	Peptide
21	T	400	PHE	Peptide
21	T	405	PHE	Peptide
24	W	257	ILE	Peptide
24	W	518	PRO	Peptide
33	d	112	ASN	Peptide
33	k	112	ASN	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	17748	0	16907	1068	0
2	B	1768	0	897	65	0
3	C	6787	0	6794	123	0
4	D	8530	0	3747	18	0
5	E	2338	0	2275	72	0
6	F	2075	0	1048	174	0
7	4	276	0	142	23	0
8	G	1510	0	760	205	0
9	H	2966	0	1505	289	0
10	I	3857	0	2738	166	0
11	J	3819	0	2904	54	0
12	K	772	0	342	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	L	3015	0	2570	81	0
14	M	1098	0	1082	39	0
15	N	1184	0	1190	27	0
16	O	2296	0	2284	78	0
17	P	953	0	939	37	0
18	Q	6562	0	2836	49	0
19	R	2243	0	2298	93	0
20	S	1236	0	1210	55	0
21	T	2454	0	2413	81	0
22	U	422	0	291	10	0
23	V	2632	0	1734	56	0
24	W	4129	0	4040	166	0
25	Y	3431	0	1662	35	0
26	Z	1084	0	1019	28	0
27	2	1013	0	1058	168	0
28	z	496	0	484	83	0
29	b	786	0	811	48	0
29	i	690	0	712	15	0
30	y	390	0	190	3	0
31	a	609	0	620	26	0
31	h	633	0	645	14	0
32	c	649	0	693	10	0
32	j	649	0	693	11	0
33	d	776	0	819	32	0
33	k	688	0	709	30	0
34	f	576	0	589	21	0
34	m	566	0	573	53	0
35	e	652	0	668	20	0
35	l	652	0	668	45	0
36	g	577	0	603	15	0
36	n	542	0	568	29	0
37	q	659	0	296	19	0
37	r	654	0	294	8	0
37	s	659	0	296	21	0
37	t	654	0	294	18	0
38	o	1282	0	1305	31	0
39	p	760	0	783	12	0
40	1	2209	0	2157	328	0
41	v	711	0	299	6	0
42	w	445	0	203	6	0
43	u	1907	0	845	5	0
44	x	124	0	51	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	3	230	0	229	48	0
46	A	36	0	6	9	0
47	C	32	0	12	2	0
48	C	1	0	0	0	0
48	F	6	0	0	0	0
48	Q	2	0	0	0	0
49	1	1	0	0	0	0
49	N	3	0	0	0	0
49	O	3	0	0	0	0
50	Q	31	0	12	5	0
All	All	106538	0	83812	3113	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 16.

All (3113) 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:1685:LEU:HD21	40:1:173:TYR:CZ	1.30	1.66
1:A:1496:PRO:HG2	45:3:338:GLY:CA	1.29	1.61
1:A:1498:TRP:CZ3	40:1:63:ILE:HG23	1.08	1.58
1:A:1698:PRO:CB	40:1:182:VAL:HG22	1.17	1.57
1:A:1496:PRO:CG	45:3:338:GLY:HA3	1.30	1.56
1:A:1955:LYS:CD	27:2:92:ARG:HH22	1.06	1.56
1:A:526:PRO:HG3	28:z:106:PRO:CD	1.11	1.54
10:I:723:MET:HA	10:I:726:ILE:CG2	1.30	1.54
1:A:1698:PRO:HB2	40:1:182:VAL:CG2	1.32	1.54
1:A:1498:TRP:CH2	40:1:63:ILE:CG2	1.88	1.53
10:I:265:TYR:CB	10:I:274:LYS:CB	1.84	1.52
34:m:5:LEU:CD2	35:l:57:VAL:HG11	1.38	1.51
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.35	1.50
1:A:1499:GLU:HG2	40:1:63:ILE:CG1	1.40	1.50
1:A:1685:LEU:HD11	40:1:173:TYR:CD2	1.48	1.47
1:A:1498:TRP:CH2	40:1:63:ILE:HG23	1.42	1.47
1:A:1495:PHE:CD1	45:3:337:ILE:CD1	1.94	1.46
1:A:1495:PHE:CD1	45:3:337:ILE:HD11	1.46	1.45
1:A:526:PRO:CG	28:z:106:PRO:HD3	1.47	1.44
34:m:3:LEU:CD1	34:m:4:PRO:HD2	1.45	1.44
1:A:1698:PRO:HG2	40:1:182:VAL:CA	1.43	1.44
1:A:2328:ALA:HB3	4:D:788:GLY:CA	1.49	1.42
1:A:1499:GLU:CD	40:1:63:ILE:CD1	1.90	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:129:G:H4'	24:W:541:LYS:NZ	1.27	1.41
1:A:1499:GLU:CG	40:1:63:ILE:HD11	1.48	1.41
1:A:1698:PRO:CB	40:1:182:VAL:CG2	1.90	1.40
1:A:1983:LEU:CD2	1:A:1987:ILE:HG12	1.50	1.40
1:A:1849:ILE:HG22	1:A:1879:PHE:CE1	1.56	1.39
1:A:240:ARG:NH1	40:1:139:ARG:HB3	1.33	1.38
1:A:1499:GLU:CD	40:1:63:ILE:HD11	0.95	1.37
10:I:723:MET:CA	10:I:726:ILE:CG2	2.02	1.36
1:A:1498:TRP:CZ3	40:1:63:ILE:CG2	2.03	1.35
1:A:1615:HIS:CE1	28:z:96:LEU:CB	2.08	1.35
1:A:1499:GLU:HG2	40:1:63:ILE:CD1	1.55	1.34
1:A:1644:LEU:HD21	1:A:1681:ARG:CD	1.57	1.34
1:A:1499:GLU:OE2	40:1:63:ILE:HD11	1.25	1.33
1:A:1499:GLU:CG	40:1:63:ILE:CD1	2.04	1.33
1:A:1945:VAL:HG11	1:A:1990:ASP:OD2	1.16	1.32
1:A:525:LYS:HD3	28:z:102:HIS:O	1.20	1.32
19:R:222:PRO:N	19:R:222:PRO:CA	1.67	1.31
21:T:188:PRO:HB3	21:T:440:ASP:OD2	1.13	1.31
1:A:1724:PRO:N	1:A:1724:PRO:CA	1.68	1.31
1:A:526:PRO:CG	28:z:106:PRO:CD	2.06	1.31
1:A:1685:LEU:HD21	40:1:173:TYR:CE2	1.67	1.30
1:A:1698:PRO:CG	40:1:182:VAL:HG22	1.59	1.30
1:A:1130:ASN:ND2	1:A:1139:ARG:HD3	1.43	1.29
19:R:319:LYS:O	19:R:323:LYS:HD2	1.26	1.29
1:A:1615:HIS:HE1	28:z:96:LEU:CB	1.45	1.29
10:I:273:GLU:HA	18:Q:357:ALA:CB	1.63	1.28
1:A:1499:GLU:CG	40:1:63:ILE:CG1	2.11	1.27
1:A:1685:LEU:CD2	40:1:173:TYR:CZ	2.19	1.26
1:A:1938:LEU:O	1:A:1983:LEU:HD11	1.11	1.25
8:G:120:G:O2'	8:G:121:G:O4'	1.54	1.25
24:W:72:LEU:HD11	24:W:83:PRO:CG	1.64	1.25
10:I:704:TRP:CZ3	10:I:727:ARG:HG3	1.71	1.25
1:A:1955:LYS:HD2	27:2:92:ARG:NH2	0.93	1.25
8:G:129:G:C4'	24:W:541:LYS:HZ3	1.47	1.25
10:I:722:GLU:O	10:I:726:ILE:HG22	1.19	1.25
18:Q:801:GLN:O	50:Q:1501:ATP:N6	1.66	1.25
34:m:3:LEU:HD12	34:m:4:PRO:CD	1.66	1.25
23:V:499:GLN:OE1	40:1:72:TRP:CE3	1.92	1.23
8:G:129:G:C4'	24:W:541:LYS:NZ	2.01	1.23
24:W:73:ASP:CB	24:W:74:PRO:HD3	1.66	1.23
24:W:83:PRO:HB3	24:W:87:THR:OG1	1.34	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:852:ARG:NH2	7:4:-13:C:H2'	1.50	1.22
11:J:535:TYR:CB	11:J:541:ALA:HB2	1.70	1.21
24:W:73:ASP:HB3	24:W:74:PRO:CD	1.69	1.21
34:m:5:LEU:HD21	35:l:57:VAL:CG1	1.68	1.21
5:E:266:PRO:HG2	13:L:785:GLN:CB	1.71	1.21
21:T:185:MET:HG3	21:T:186:PRO:CD	1.69	1.21
1:A:584:HIS:HE1	46:A:3000:IHP:O26	1.21	1.20
1:A:537:LYS:HD2	6:F:37:C:N4	1.54	1.20
1:A:1737:ASN:OD1	1:A:1738:PRO:HD2	1.42	1.20
21:T:185:MET:CG	21:T:186:PRO:HD3	1.72	1.20
12:K:83:SER:HA	37:t:75:LEU:CB	1.72	1.18
1:A:1758:PRO:HB2	45:3:352:TYR:HB3	1.25	1.18
1:A:1495:PHE:CG	45:3:337:ILE:HD11	1.79	1.17
1:A:1596:VAL:HG13	40:1:278:LEU:CD1	1.74	1.17
24:W:72:LEU:CD1	24:W:83:PRO:HG3	1.72	1.17
1:A:1321:GLU:HB2	40:1:66:TYR:OH	1.42	1.17
1:A:1698:PRO:CG	40:1:182:VAL:HA	1.73	1.17
1:A:199:GLU:CD	40:1:139:ARG:HG2	1.70	1.17
6:F:79:C:OP2	11:J:237:LYS:NZ	1.76	1.16
6:F:80:G:OP1	13:L:174:LYS:NZ	1.77	1.16
10:I:722:GLU:O	10:I:726:ILE:CG2	1.93	1.16
1:A:1705:ILE:HG21	1:A:1734:MET:CE	1.74	1.16
23:V:499:GLN:OE1	40:1:72:TRP:CZ3	1.98	1.16
20:S:72:ARG:NE	24:W:92:GLU:OE2	1.79	1.16
20:S:72:ARG:HB3	24:W:92:GLU:OE1	1.45	1.16
1:A:1495:PHE:CD1	45:3:337:ILE:HD13	1.74	1.15
18:Q:801:GLN:C	50:Q:1501:ATP:HN62	1.53	1.15
8:G:21:A:O2'	8:G:22:C:O5'	1.64	1.15
10:I:273:GLU:CA	18:Q:357:ALA:HB2	1.77	1.15
24:W:264:ASN:ND2	35:l:16:GLN:OE1	1.78	1.15
1:A:1705:ILE:HD13	1:A:1734:MET:HE2	1.23	1.14
1:A:1719:PHE:HB2	1:A:1720:PRO:HD2	1.26	1.14
1:A:199:GLU:OE1	40:1:139:ARG:HG2	1.48	1.14
1:A:1495:PHE:CG	45:3:337:ILE:CD1	2.30	1.14
1:A:1705:ILE:HG21	1:A:1734:MET:HE3	1.16	1.14
10:I:286:VAL:O	10:I:351:ARG:CB	1.96	1.14
34:m:3:LEU:CG	34:m:4:PRO:HD2	1.76	1.14
6:F:54:G:OP1	8:G:169:U:OP2	1.65	1.14
8:G:21:A:Cl'	16:O:152:ARG:NH2	2.11	1.14
10:I:661:ASP:HB2	10:I:694:ILE:HG21	1.30	1.13
35:l:14:MET:HE1	36:n:10:LYS:CE	1.77	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:PRO:HD2	45:3:337:ILE:HG13	1.31	1.13
1:A:2004:GLN:HE22	40:1:335:TYR:HB2	1.03	1.13
1:A:172:GLU:OE1	28:z:99:LEU:HA	1.49	1.13
21:T:188:PRO:CB	21:T:440:ASP:OD2	1.97	1.12
1:A:1498:TRP:CH2	40:1:63:ILE:HG21	1.69	1.11
10:I:273:GLU:HA	18:Q:357:ALA:HB2	1.11	1.11
21:T:188:PRO:HG3	21:T:443:THR:OG1	1.47	1.11
24:W:73:ASP:HB3	24:W:74:PRO:HD3	1.17	1.11
1:A:1596:VAL:HG13	40:1:278:LEU:HD11	1.28	1.11
9:H:36:G:H2'	9:H:37:U:H5'	1.31	1.11
1:A:584:HIS:CE1	46:A:3000:IHP:O26	2.02	1.10
1:A:1471:ARG:HD3	40:1:66:TYR:CD1	1.86	1.10
1:A:1698:PRO:HG2	40:1:182:VAL:CB	1.79	1.10
9:H:47:U:OP1	27:2:40:LYS:NZ	1.84	1.10
13:L:129:ASP:OD2	13:L:130:PRO:HD2	1.51	1.10
9:H:168:A:H1'	36:n:48:MET:HE1	1.19	1.10
1:A:526:PRO:HD3	28:z:105:ILE:CA	1.80	1.10
5:E:93:TRP:HZ3	29:b:105:GLY:O	1.33	1.10
10:I:721:LYS:NZ	13:L:65:ARG:NH2	2.00	1.10
1:A:1499:GLU:OE2	40:1:63:ILE:CD1	1.92	1.10
10:I:84:HIS:CB	10:I:90:PRO:HA	1.82	1.10
1:A:2004:GLN:NE2	40:1:335:TYR:HB2	1.66	1.09
1:A:1481:VAL:HG23	40:1:85:GLN:NE2	1.66	1.09
18:Q:801:GLN:C	50:Q:1501:ATP:N6	2.08	1.09
21:T:455:GLN:HG2	21:T:456:PRO:HD2	1.15	1.09
6:F:45:A:N6	8:G:2:U:O2	1.85	1.09
17:P:212:ASN:HB3	21:T:458:SER:N	1.67	1.09
23:V:499:GLN:CD	40:1:72:TRP:CE3	2.30	1.09
35:l:14:MET:CE	36:n:10:LYS:HE3	1.83	1.09
1:A:526:PRO:HG3	28:z:106:PRO:HD2	1.24	1.09
1:A:1471:ARG:HD3	40:1:66:TYR:CE1	1.88	1.09
9:H:36:G:C2'	9:H:37:U:H5'	1.83	1.09
1:A:525:LYS:HE2	28:z:103:TYR:HA	1.27	1.08
34:m:5:LEU:CD2	35:l:57:VAL:CG1	2.26	1.08
1:A:1955:LYS:HD2	27:2:92:ARG:CZ	1.83	1.08
9:H:154:C:OP2	39:p:19:LYS:HG2	1.49	1.08
10:I:681:ILE:HG23	10:I:710:PHE:CZ	1.88	1.08
6:F:39:A:C2'	6:F:40:U:H5'	1.82	1.08
8:G:21:A:H1'	16:O:152:ARG:HH21	1.05	1.08
6:F:34:G:H2'	6:F:35:A:H5''	1.29	1.07
27:2:120:ALA:HB1	36:n:55:ASN:OD1	1.52	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1499:GLU:CG	40:1:63:ILE:HG12	1.77	1.07
1:A:1938:LEU:HB3	1:A:1983:LEU:HD13	1.12	1.07
9:H:156:U:H6	9:H:156:U:H5''	1.09	1.07
1:A:1938:LEU:O	1:A:1983:LEU:CD1	2.03	1.07
8:G:21:A:OP2	16:O:193:LEU:HD21	1.51	1.07
1:A:1739:ALA:O	1:A:1742:VAL:HB	1.55	1.07
27:2:138:LYS:HE2	27:2:138:LYS:HA	1.34	1.07
24:W:73:ASP:CG	24:W:74:PRO:HD3	1.79	1.06
1:A:1495:PHE:HB3	45:3:337:ILE:CD1	1.85	1.06
1:A:1499:GLU:HB3	40:1:60:ASN:HB3	1.30	1.06
8:G:129:G:C5'	24:W:541:LYS:HZ1	1.68	1.06
14:M:118:LYS:H	14:M:118:LYS:HD3	1.18	1.06
9:H:105:G:H2'	9:H:106:G:H5''	1.37	1.06
23:V:457:ARG:HH12	40:1:88:GLN:HG2	1.14	1.06
1:A:1495:PHE:CB	45:3:337:ILE:HD11	1.86	1.06
1:A:1849:ILE:CG2	1:A:1879:PHE:CE1	2.39	1.05
1:A:1945:VAL:CG1	1:A:1990:ASP:OD2	2.03	1.05
1:A:1983:LEU:CD2	1:A:1987:ILE:CG1	2.33	1.05
5:E:59:ILE:HD11	24:W:82:ASN:HD21	1.10	1.05
9:H:177:A:OP2	27:2:137:LYS:HG3	1.55	1.05
10:I:722:GLU:C	10:I:726:ILE:HG22	1.81	1.04
1:A:199:GLU:HB3	40:1:139:ARG:HD2	1.39	1.04
1:A:1644:LEU:HD21	1:A:1681:ARG:HD3	1.07	1.04
1:A:1979:VAL:HA	1:A:1982:GLN:HB2	1.33	1.04
11:J:535:TYR:O	11:J:538:ILE:N	1.90	1.04
1:A:1501:LEU:HD21	45:3:337:ILE:HD13	1.35	1.04
19:R:319:LYS:O	19:R:323:LYS:CD	2.03	1.04
24:W:79:VAL:HG21	29:b:114:ILE:HD11	1.05	1.04
1:A:1644:LEU:CD2	1:A:1681:ARG:HD3	1.87	1.04
1:A:1685:LEU:CD1	40:1:173:TYR:CD2	2.41	1.04
37:q:60:PRO:CB	37:s:93:ARG:C	2.30	1.04
23:V:499:GLN:NE2	40:1:72:TRP:CE3	2.26	1.03
37:s:71:ILE:CB	37:t:81:GLU:CB	2.35	1.03
35:l:14:MET:HE1	36:n:10:LYS:HE3	1.04	1.03
1:A:1698:PRO:CG	40:1:182:VAL:CG2	2.28	1.03
10:I:723:MET:O	10:I:726:ILE:HG23	1.55	1.03
8:G:129:G:C5'	24:W:541:LYS:NZ	2.21	1.03
9:H:40:C:H4'	9:H:41:U:OP1	1.56	1.03
1:A:1739:ALA:O	1:A:1742:VAL:CB	2.08	1.02
8:G:147:C:H2'	8:G:148:U:C6	1.93	1.02
1:A:1495:PHE:HB3	45:3:337:ILE:HD12	1.39	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:m:3:LEU:HD12	34:m:4:PRO:HD2	1.12	1.02
10:I:698:ARG:HA	10:I:698:ARG:HE	1.23	1.02
23:V:499:GLN:NE2	40:1:72:TRP:CD2	2.27	1.02
23:V:499:GLN:NE2	40:1:72:TRP:HB2	1.74	1.02
9:H:39:U:H6	9:H:39:U:H5''	1.23	1.01
10:I:187:LEU:HA	10:I:196:ALA:HB1	1.38	1.01
6:F:86:U:O2'	6:F:87:C:O5'	1.78	1.01
13:L:124:LYS:CE	13:L:129:ASP:OD2	2.08	1.01
1:A:1698:PRO:CG	40:1:182:VAL:CA	2.32	1.01
1:A:1955:LYS:NZ	27:2:89:GLU:OE2	1.94	1.01
1:A:526:PRO:CD	28:z:105:ILE:HA	1.90	1.01
12:K:15:ALA:HB1	37:s:112:ALA:O	1.60	1.01
34:m:3:LEU:CD1	34:m:4:PRO:CD	2.31	1.01
1:A:1589:ILE:CG2	1:A:1730:MET:HE1	1.91	1.00
1:A:1698:PRO:HG2	40:1:182:VAL:CG2	1.90	1.00
1:A:526:PRO:HD2	28:z:104:ASP:O	1.61	1.00
27:2:51:LYS:HZ3	35:l:28:ARG:HD3	1.27	1.00
8:G:20:A:HO2'	16:O:193:LEU:HD21	1.20	1.00
40:1:46:GLY:HA2	45:3:331:ILE:CG2	1.92	1.00
6:F:8:C:H6	6:F:8:C:H5''	1.23	1.00
1:A:106:MET:HE3	1:A:561:HIS:NE2	1.76	1.00
1:A:887:THR:HB	13:L:122:LYS:HE2	1.43	1.00
1:A:1596:VAL:CG1	40:1:278:LEU:CD1	2.39	1.00
21:T:455:GLN:HG2	21:T:456:PRO:CD	1.91	1.00
1:A:1910:THR:HG22	24:W:412:GLN:OE1	1.62	1.00
1:A:2014:MET:N	1:A:2014:MET:SD	2.31	1.00
8:G:138:A:C2	9:H:39:U:O2	2.14	1.00
27:2:52:MET:HB2	35:l:28:ARG:NH2	1.75	1.00
1:A:148:TRP:O	1:A:152:ARG:HG3	1.62	1.00
1:A:1596:VAL:CG1	40:1:278:LEU:HD11	1.90	0.99
1:A:1759:THR:HG21	40:1:288:LYS:HD3	1.41	0.99
40:1:46:GLY:HA2	45:3:331:ILE:HG21	1.39	0.99
24:W:79:VAL:CG2	29:b:114:ILE:HD11	1.92	0.99
1:A:1955:LYS:HZ2	27:2:89:GLU:CD	1.71	0.99
1:A:1258:LYS:CE	8:G:173:G:H4'	1.91	0.99
1:A:1495:PHE:CB	45:3:337:ILE:CD1	2.40	0.99
10:I:704:TRP:CE3	10:I:727:ARG:HG3	1.97	0.99
1:A:1386:TRP:HB3	25:Y:410:VAL:CG2	1.92	0.99
1:A:1593:LEU:HD21	1:A:1729:ALA:HB1	1.44	0.99
1:A:1938:LEU:C	1:A:1983:LEU:HD11	1.88	0.99
24:W:83:PRO:HB3	24:W:87:THR:HG1	1.20	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1794:PHE:HB2	24:W:459:PRO:HD3	1.45	0.98
27:2:29:GLU:O	27:2:33:LEU:HD12	1.63	0.98
11:J:535:TYR:C	11:J:538:ILE:HA	1.88	0.98
24:W:79:VAL:HG21	29:b:114:ILE:CD1	1.93	0.98
10:I:723:MET:C	10:I:726:ILE:CG2	2.35	0.98
1:A:526:PRO:HD3	28:z:105:ILE:HA	0.99	0.98
9:H:168:A:H5''	9:H:168:A:C8	1.98	0.98
11:J:535:TYR:C	11:J:538:ILE:CA	2.37	0.98
11:J:535:TYR:CB	11:J:541:ALA:CB	2.41	0.98
1:A:1130:ASN:HD22	1:A:1139:ARG:HD3	1.16	0.98
6:F:41:A:N1	8:G:6:A:N1	2.11	0.98
23:V:496:CYS:SG	40:1:72:TRP:HH2	1.85	0.98
10:I:721:LYS:HZ2	13:L:65:ARG:NH2	1.58	0.98
41:v:29:ASP:CB	42:w:154:PRO:CB	2.42	0.98
1:A:1739:ALA:O	1:A:1742:VAL:N	1.96	0.98
6:F:34:G:C2'	6:F:35:A:H5''	1.94	0.98
1:A:525:LYS:CD	28:z:102:HIS:O	2.11	0.97
8:G:21:A:H1'	16:O:152:ARG:NH2	1.73	0.97
8:G:21:A:H4'	8:G:22:C:OP1	1.60	0.97
1:A:1890:GLN:HB3	27:2:70:SER:OG	1.62	0.97
8:G:129:G:H4'	24:W:541:LYS:CE	1.93	0.97
9:H:40:C:O2'	9:H:41:U:H5''	1.64	0.97
1:A:1499:GLU:HG2	40:1:63:ILE:HG12	1.01	0.97
1:A:1955:LYS:CD	27:2:92:ARG:NH2	1.81	0.97
8:G:21:A:N9	16:O:152:ARG:NH2	2.11	0.97
1:A:1698:PRO:HG2	40:1:182:VAL:HA	1.00	0.97
10:I:723:MET:C	10:I:726:ILE:HG23	1.89	0.97
1:A:1983:LEU:HD23	1:A:1987:ILE:HG12	1.00	0.97
27:2:48:ILE:HG23	34:m:5:LEU:HD12	1.43	0.97
1:A:1955:LYS:NZ	27:2:89:GLU:CD	2.22	0.96
3:C:673:LYS:NZ	22:U:56:ASP:CB	2.28	0.96
3:C:852:ARG:NH2	7:4:-13:C:C6	2.32	0.96
1:A:240:ARG:NH1	40:1:139:ARG:CB	2.28	0.96
1:A:1833:LEU:HD22	1:A:1833:LEU:H	1.27	0.96
6:F:39:A:H2'	6:F:40:U:H5'	1.45	0.96
8:G:142:U:O2'	8:G:143:U:H5'	1.64	0.96
27:2:38:LEU:HD23	34:m:12:ASN:HD22	1.31	0.96
1:A:1498:TRP:HH2	40:1:63:ILE:HG21	1.12	0.96
1:A:1617:ARG:HG2	1:A:1620:TYR:OH	1.64	0.96
1:A:1499:GLU:OE1	40:1:60:ASN:HB2	1.66	0.95
23:V:450:ILE:CG1	40:1:89:PRO:HG2	1.96	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1678:ARG:NH2	40:1:96:SER:O	1.99	0.95
1:A:1684:PHE:CB	1:A:1715:TYR:CD2	2.49	0.95
23:V:457:ARG:HG3	40:1:73:TYR:CD2	2.01	0.95
1:A:525:LYS:HG2	28:z:103:TYR:C	1.91	0.95
37:q:60:PRO:C	37:s:93:ARG:CB	2.39	0.95
1:A:1685:LEU:HD11	40:1:173:TYR:CG	2.01	0.95
1:A:1386:TRP:HB3	25:Y:410:VAL:HG21	1.47	0.95
1:A:1955:LYS:NZ	27:2:93:GLN:NE2	2.15	0.95
10:I:723:MET:HA	10:I:726:ILE:HG21	0.97	0.95
10:I:723:MET:HA	10:I:726:ILE:HG23	1.48	0.94
9:H:156:U:H5''	9:H:156:U:C6	2.02	0.94
23:V:499:GLN:NE2	40:1:72:TRP:CG	2.35	0.94
31:a:74:PRO:HB2	31:a:77:LEU:HD11	1.49	0.94
10:I:721:LYS:HZ2	13:L:65:ARG:HH21	1.05	0.94
27:2:120:ALA:CB	36:n:55:ASN:OD1	2.14	0.94
1:A:160:HIS:HE1	40:1:170:TRP:HA	1.31	0.94
1:A:1883:VAL:HG22	40:1:290:ARG:O	1.66	0.94
1:A:1498:TRP:HH2	40:1:63:ILE:CG2	1.53	0.94
5:E:93:TRP:CZ3	29:b:105:GLY:O	2.20	0.94
8:G:167:G:H8	8:G:167:G:H5'	1.33	0.94
2:B:95:G:H5'	34:f:25:TRP:HH2	1.28	0.94
10:I:723:MET:CA	10:I:726:ILE:HG22	1.85	0.94
13:L:124:LYS:HE2	13:L:129:ASP:OD2	1.68	0.94
1:A:1258:LYS:HE2	8:G:173:G:H4'	1.49	0.93
1:A:1554:GLN:HA	1:A:1561:PHE:HB3	1.50	0.93
1:A:1644:LEU:CD2	1:A:1681:ARG:CD	2.44	0.93
24:W:83:PRO:CB	24:W:87:THR:OG1	2.16	0.93
1:A:537:LYS:CD	6:F:37:C:N4	2.30	0.93
1:A:1983:LEU:HD21	1:A:1987:ILE:HG12	1.49	0.93
8:G:20:A:O2'	16:O:193:LEU:HD21	1.68	0.93
1:A:1471:ARG:CD	40:1:66:TYR:CD1	2.52	0.93
9:H:40:C:O2'	9:H:41:U:C5'	2.16	0.93
1:A:1698:PRO:CB	40:1:182:VAL:HG23	1.97	0.93
1:A:1849:ILE:HG22	1:A:1879:PHE:HE1	1.29	0.93
8:G:27:U:O2'	8:G:28:A:O5'	1.84	0.93
1:A:158:ARG:HH12	28:z:62:GLN:CG	1.82	0.93
1:A:1719:PHE:CB	1:A:1720:PRO:HD2	1.99	0.93
12:K:83:SER:CA	37:t:75:LEU:CB	2.47	0.93
1:A:1769:GLY:CA	40:1:324:MET:SD	2.57	0.92
1:A:1955:LYS:HE3	27:2:89:GLU:OE2	1.68	0.92
1:A:1955:LYS:CE	27:2:89:GLU:OE2	2.16	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1994:LYS:NZ	27:2:67:VAL:HG22	1.85	0.92
8:G:147:C:H2'	8:G:148:U:H6	1.29	0.92
1:A:1684:PHE:CB	1:A:1715:TYR:HD2	1.81	0.92
27:2:137:LYS:HE2	27:2:137:LYS:HA	1.49	0.92
1:A:1615:HIS:HD2	28:z:93:ASN:OD1	1.52	0.92
8:G:27:U:C2'	8:G:28:A:O5'	2.15	0.92
27:2:127:ARG:HB3	27:2:131:ARG:HH22	1.33	0.92
1:A:1719:PHE:HB2	1:A:1720:PRO:CD	1.98	0.92
1:A:1865:ARG:NH1	8:G:147:C:OP1	2.03	0.92
1:A:172:GLU:CD	28:z:99:LEU:HA	1.94	0.92
3:C:667:VAL:H	3:C:824:THR:HG23	1.35	0.91
1:A:1944:HIS:CE1	27:2:69:GLY:O	2.24	0.91
1:A:2008:ARG:O	1:A:2011:ILE:HB	1.70	0.91
12:K:15:ALA:CB	37:s:112:ALA:O	2.18	0.91
9:H:40:C:O2'	9:H:41:U:O4'	1.87	0.91
27:2:127:ARG:HB3	27:2:131:ARG:NH2	1.85	0.91
3:C:666:VAL:HG13	3:C:823:ALA:O	1.70	0.91
10:I:698:ARG:HA	10:I:698:ARG:NE	1.79	0.91
23:V:457:ARG:HH12	40:1:88:GLN:CG	1.84	0.91
9:H:168:A:C1'	36:n:48:MET:HE1	2.00	0.91
1:A:1705:ILE:CG2	1:A:1734:MET:HE3	2.01	0.91
1:A:1889:LEU:HD11	1:A:2012:LEU:HB3	1.48	0.91
1:A:1997:VAL:HG22	26:Z:658:TYR:CD2	2.06	0.91
1:A:153:ARG:HG2	1:A:153:ARG:HH21	1.33	0.90
1:A:1130:ASN:ND2	1:A:1139:ARG:CD	2.31	0.90
18:Q:878:ARG:HA	18:Q:1036:ALA:O	1.70	0.90
1:A:1903:GLY:C	27:2:82:TYR:OH	2.14	0.90
1:A:1983:LEU:HD21	1:A:1987:ILE:CG1	2.01	0.90
1:A:525:LYS:CE	28:z:103:TYR:HA	2.00	0.90
1:A:2004:GLN:NE2	40:1:335:TYR:CB	2.35	0.90
9:H:39:U:O2'	9:H:40:C:OP1	1.87	0.90
1:A:1499:GLU:OE1	40:1:60:ASN:CB	2.20	0.90
1:A:613:TYR:HE2	46:A:3000:IHP:O45	1.52	0.90
1:A:1685:LEU:HD21	40:1:173:TYR:CE1	2.04	0.90
23:V:499:GLN:CD	40:1:72:TRP:CD2	2.49	0.90
13:L:5:MET:N	13:L:5:MET:SD	2.45	0.90
1:A:1685:LEU:CD2	40:1:173:TYR:CE1	2.54	0.90
1:A:1938:LEU:CB	1:A:1983:LEU:HD13	2.00	0.90
1:A:1501:LEU:HD21	45:3:337:ILE:CD1	2.01	0.90
1:A:1997:VAL:HG21	26:Z:658:TYR:CG	2.06	0.90
3:C:852:ARG:NH2	7:4:-13:C:C2'	2.34	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:168:A:H1'	36:n:48:MET:CE	2.01	0.90
17:P:16:ARG:HH12	19:R:220:ARG:HA	1.37	0.89
1:A:158:ARG:NH1	28:z:62:GLN:CG	2.34	0.89
10:I:187:LEU:HA	10:I:196:ALA:CB	2.02	0.89
1:A:1938:LEU:HB3	1:A:1983:LEU:CD1	2.01	0.89
9:H:20:G:O4'	17:P:7:PRO:HB3	1.72	0.89
17:P:212:ASN:HB3	21:T:458:SER:H	1.31	0.89
8:G:21:A:C1'	16:O:152:ARG:HH21	1.75	0.89
8:G:142:U:H2'	8:G:143:U:C5	2.07	0.89
3:C:852:ARG:HH22	7:4:-13:C:H6	1.13	0.89
6:F:88:G:H5''	14:M:133:ARG:HH22	1.37	0.89
8:G:20:A:O2'	8:G:21:A:OP2	1.91	0.88
8:G:147:C:C2	8:G:148:U:C5	2.61	0.88
9:H:39:U:H5''	9:H:39:U:C6	2.07	0.88
9:H:77:C:P	24:W:242:HIS:CE1	2.65	0.88
9:H:168:A:H5''	9:H:168:A:H8	1.37	0.88
8:G:171:G:N3	8:G:171:G:O2'	2.05	0.88
1:A:354:PRO:O	23:V:344:LYS:CB	2.21	0.88
1:A:537:LYS:HD2	6:F:37:C:H42	1.39	0.88
3:C:852:ARG:CZ	7:4:-13:C:H2'	2.02	0.88
1:A:1737:ASN:OD1	1:A:1738:PRO:CD	2.20	0.88
1:A:1991:TYR:HE2	1:A:1997:VAL:HB	1.38	0.88
6:F:88:G:C5'	14:M:133:ARG:HH22	1.86	0.88
18:Q:849:THR:HA	18:Q:1058:ASN:O	1.73	0.88
1:A:1471:ARG:HD3	40:1:66:TYR:CG	2.08	0.88
1:A:1528:GLN:O	1:A:1528:GLN:NE2	2.06	0.88
10:I:688:TYR:O	10:I:703:PHE:HZ	1.56	0.88
10:I:731:GLN:O	10:I:731:GLN:NE2	2.07	0.88
1:A:1136:ARG:HG2	1:A:1136:ARG:HH11	1.35	0.88
6:F:45:A:O2'	6:F:73:A:N3	2.05	0.88
1:A:1997:VAL:HG21	26:Z:658:TYR:CD1	2.09	0.87
1:A:1876:LEU:HD21	1:A:1882:ILE:HD12	1.57	0.87
2:B:95:G:H5''	33:d:47:ARG:HH22	1.38	0.87
34:m:3:LEU:HG	34:m:4:PRO:HD2	1.54	0.87
1:A:857:ASN:N	1:A:857:ASN:OD1	2.06	0.87
1:A:1471:ARG:HD3	40:1:66:TYR:CZ	2.09	0.87
1:A:1985:ASP:HA	1:A:1988:LEU:HD12	1.55	0.87
29:b:46:ASP:OD2	29:b:64:LYS:HE3	1.75	0.87
1:A:240:ARG:HH11	40:1:139:ARG:HB3	1.36	0.87
1:A:1475:ILE:HD11	40:1:66:TYR:HE2	1.38	0.87
9:H:156:U:H6	9:H:156:U:C5'	1.88	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:276:ARG:CB	18:Q:357:ALA:HB3	2.04	0.87
1:A:1471:ARG:CD	40:1:66:TYR:CG	2.58	0.86
8:G:167:G:H5'	8:G:167:G:C8	2.09	0.86
9:H:154:C:O2	9:H:176:G:N2	2.07	0.86
1:A:1498:TRP:CH2	40:1:67:ILE:CG2	2.58	0.86
8:G:22:C:O2'	8:G:23:U:OP1	1.91	0.86
1:A:1130:ASN:HD22	1:A:1139:ARG:CD	1.87	0.86
29:i:46:ASP:OD2	29:i:64:LYS:HE3	1.75	0.86
1:A:165:ARG:NH1	1:A:1623:ASN:OD1	2.07	0.86
1:A:2004:GLN:NE2	40:1:335:TYR:CG	2.44	0.86
23:V:499:GLN:NE2	40:1:72:TRP:CB	2.37	0.86
5:E:59:ILE:HD11	24:W:82:ASN:ND2	1.89	0.86
12:K:83:SER:O	37:t:76:LYS:HA	1.75	0.86
1:A:1560:ILE:HD11	1:A:1577:PHE:CE2	2.09	0.86
1:A:1849:ILE:HG22	1:A:1879:PHE:CD1	2.09	0.86
27:2:52:MET:HB2	35:l:28:ARG:HH21	1.35	0.86
1:A:1644:LEU:CD2	1:A:1681:ARG:CG	2.53	0.86
1:A:1725:LEU:O	1:A:1725:LEU:HD12	1.74	0.86
20:S:85:GLU:O	20:S:127:THR:HG23	1.74	0.86
40:1:178:HIS:HE1	40:1:181:ILE:HD11	1.41	0.86
10:I:692:SER:HA	10:I:695:CYS:HB2	1.57	0.86
1:A:199:GLU:CD	40:1:139:ARG:CG	2.49	0.86
1:A:158:ARG:NH1	28:z:62:GLN:HG3	1.91	0.85
11:J:198:ALA:O	11:J:201:ARG:HB2	1.76	0.85
6:F:33:G:H5''	6:F:33:G:H8	1.41	0.85
1:A:1724:PRO:N	1:A:1724:PRO:C	2.32	0.85
8:G:146:C:H2'	8:G:147:C:H5''	1.57	0.85
1:A:1499:GLU:CB	40:1:60:ASN:HB3	2.06	0.85
1:A:1499:GLU:CB	40:1:63:ILE:CG1	2.55	0.85
1:A:1955:LYS:HZ1	27:2:93:GLN:NE2	1.72	0.85
18:Q:851:ILE:HA	18:Q:1060:LEU:O	1.76	0.85
1:A:1481:VAL:HG21	40:1:67:ILE:HG23	1.57	0.85
1:A:1596:VAL:HG22	40:1:278:LEU:HD11	1.58	0.85
1:A:1769:GLY:HA3	40:1:324:MET:SD	2.17	0.85
1:A:1958:LYS:HD3	27:2:96:MET:O	1.77	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.77	0.85
9:H:98:G:N2	34:m:66:CYS:SG	2.50	0.85
1:A:526:PRO:CG	28:z:106:PRO:HD2	1.90	0.84
19:R:324:LEU:O	19:R:324:LEU:HD12	1.77	0.84
1:A:524:LEU:O	28:z:105:ILE:N	2.10	0.84
10:I:726:ILE:O	10:I:726:ILE:HD12	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:820:MET:O	18:Q:1130:THR:HA	1.76	0.84
31:a:74:PRO:CB	31:a:77:LEU:HD11	2.07	0.84
20:S:37:LYS:NZ	20:S:37:LYS:HB2	1.92	0.84
1:A:1498:TRP:HZ3	40:1:63:ILE:HG23	1.02	0.84
1:A:1797:ASN:OD1	8:G:143:U:H5''	1.78	0.84
10:I:273:GLU:CA	18:Q:357:ALA:CB	2.45	0.84
1:A:1983:LEU:HD23	1:A:1987:ILE:CG1	1.96	0.84
1:A:1758:PRO:HB2	45:3:352:TYR:CB	2.08	0.84
10:I:187:LEU:CA	10:I:196:ALA:HB1	2.08	0.84
21:T:455:GLN:CG	21:T:456:PRO:HD2	2.05	0.84
1:A:1495:PHE:HD1	45:3:337:ILE:HD11	1.04	0.84
1:A:1935:ARG:HH21	40:1:348:THR:HG21	1.42	0.84
9:H:18:U:OP2	14:M:221:LYS:NZ	2.10	0.84
1:A:243:ASN:O	40:1:131:LYS:NZ	2.11	0.84
3:C:750:LEU:CB	22:U:67:GLU:CB	2.56	0.84
10:I:272:PHE:CB	18:Q:356:VAL:H	1.91	0.84
9:H:154:C:OP2	39:p:19:LYS:CG	2.24	0.84
27:2:48:ILE:HG23	34:m:5:LEU:CD1	2.07	0.84
1:A:1803:ILE:HG22	24:W:451:VAL:HG22	1.60	0.83
18:Q:877:LEU:O	18:Q:1036:ALA:N	2.09	0.83
1:A:293:TRP:NE1	1:A:1136:ARG:NH1	2.26	0.83
2:B:18:C:O2'	2:B:19:A:O5'	1.96	0.83
1:A:1792:LYS:HZ1	9:H:37:U:C1'	1.91	0.83
1:A:172:GLU:OE1	28:z:99:LEU:CA	2.26	0.83
1:A:1875:HIS:O	1:A:1878:ASP:OD1	1.96	0.83
1:A:1258:LYS:HE2	8:G:173:G:C4'	2.09	0.83
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.28	0.83
5:E:266:PRO:CG	13:L:785:GLN:CB	2.54	0.83
6:F:8:C:H5''	6:F:8:C:C6	2.11	0.83
1:A:1792:LYS:HZ1	9:H:37:U:H1'	1.42	0.83
3:C:852:ARG:HH22	7:4:-13:C:H2'	1.18	0.83
3:C:855:GLY:O	3:C:874:PHE:O	1.96	0.83
14:M:118:LYS:HD3	14:M:118:LYS:N	1.86	0.83
1:A:1904:ASP:OD2	27:2:90:TYR:OH	1.95	0.83
9:H:154:C:P	39:p:19:LYS:HD3	2.19	0.83
17:P:16:ARG:NH1	19:R:220:ARG:HA	1.94	0.83
1:A:526:PRO:CD	28:z:104:ASP:O	2.26	0.83
40:1:178:HIS:CE1	40:1:181:ILE:HD11	2.13	0.82
1:A:1321:GLU:CB	40:1:66:TYR:OH	2.26	0.82
1:A:2007:ILE:O	1:A:2011:ILE:HD13	1.77	0.82
1:A:861:ARG:HB3	1:A:861:ARG:NH1	1.93	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2328:ALA:HB1	4:D:788:GLY:HA2	1.56	0.82
21:T:197:TYR:CD2	21:T:488:VAL:HG12	2.13	0.82
5:E:93:TRP:CH2	29:b:105:GLY:CA	2.63	0.82
13:L:124:LYS:HE2	13:L:129:ASP:CG	2.04	0.82
1:A:158:ARG:HH12	28:z:62:GLN:HG3	1.42	0.82
9:H:40:C:O2'	9:H:41:U:C6	2.33	0.82
9:H:105:G:C2'	9:H:106:G:H5''	2.10	0.82
9:H:152:G:N2	9:H:153:A:N7	2.27	0.82
10:I:727:ARG:HH21	10:I:727:ARG:CB	1.92	0.82
20:S:72:ARG:HB3	24:W:92:GLU:CD	2.04	0.82
1:A:1673:SER:HB2	40:1:164:ASP:OD2	1.80	0.82
1:A:1769:GLY:HA2	40:1:324:MET:SD	2.19	0.82
3:C:668:GLU:N	3:C:824:THR:HG21	1.94	0.82
10:I:725:ARG:O	10:I:725:ARG:HD2	1.79	0.82
40:1:46:GLY:O	45:3:331:ILE:HB	1.80	0.82
6:F:22:A:N7	24:W:130:ARG:HD3	1.94	0.82
9:H:152:G:H5''	9:H:153:A:OP2	1.80	0.82
9:H:152:G:OP2	27:2:127:ARG:HD3	1.79	0.82
10:I:728:ARG:NH2	13:L:62:GLU:OE2	2.12	0.82
1:A:1589:ILE:HG21	1:A:1730:MET:HE1	1.62	0.81
1:A:1698:PRO:HB2	40:1:182:VAL:HG21	1.60	0.81
1:A:1938:LEU:C	1:A:1983:LEU:CD1	2.50	0.81
1:A:1955:LYS:HZ3	27:2:93:GLN:HG3	1.45	0.81
10:I:84:HIS:CB	10:I:90:PRO:CA	2.56	0.81
10:I:704:TRP:CZ3	10:I:727:ARG:CG	2.62	0.81
1:A:532:THR:OG1	8:G:3:A:O5'	1.98	0.81
1:A:1881:ASN:ND2	40:1:270:ASP:HB3	1.94	0.81
10:I:728:ARG:HH21	10:I:728:ARG:HG2	1.43	0.81
12:K:36:VAL:O	37:r:112:ALA:HB1	1.79	0.81
1:A:1596:VAL:CG2	40:1:278:LEU:HD11	2.10	0.81
27:2:106:ASP:O	27:2:110:GLN:HG3	1.81	0.81
8:G:173:G:N3	8:G:173:G:H2'	1.96	0.81
6:F:80:G:H5''	6:F:81:C:OP2	1.81	0.81
1:A:1958:LYS:CD	27:2:96:MET:O	2.29	0.81
8:G:167:G:H3'	8:G:167:G:OP2	1.81	0.81
8:G:20:A:C2	16:O:187:THR:OG1	2.33	0.81
9:H:40:C:C4'	9:H:41:U:OP1	2.27	0.81
1:A:1481:VAL:CG2	40:1:85:GLN:NE2	2.44	0.81
1:A:1498:TRP:CH2	40:1:67:ILE:HG22	2.16	0.80
1:A:1775:GLN:HE21	40:1:315:VAL:HB	1.45	0.80
1:A:1889:LEU:CD1	1:A:2013:GLY:H	1.94	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1955:LYS:HZ2	27:2:89:GLU:CG	1.94	0.80
1:A:1994:LYS:HZ3	27:2:67:VAL:HG22	1.44	0.80
27:2:48:ILE:CG2	34:m:5:LEU:HD12	2.11	0.80
9:H:39:U:H3'	9:H:40:C:C5	2.16	0.80
24:W:84:THR:HG22	24:W:86:GLU:H	1.46	0.80
1:A:1685:LEU:CD1	40:1:173:TYR:CG	2.61	0.80
6:F:83:A:OP2	11:J:247:LYS:HD2	1.81	0.80
6:F:45:A:N3	6:F:73:A:H1'	1.97	0.80
8:G:130:A:O2'	8:G:131:U:OP2	1.99	0.80
10:I:276:ARG:CB	18:Q:358:GLU:N	2.44	0.80
27:2:51:LYS:NZ	35:l:28:ARG:HD3	1.96	0.80
6:F:45:A:N6	8:G:167:G:C5	2.49	0.80
1:A:1955:LYS:CE	27:2:92:ARG:NH2	2.45	0.80
10:I:681:ILE:HD13	10:I:714:HIS:HB3	1.63	0.80
1:A:1955:LYS:CE	27:2:93:GLN:HE21	1.94	0.79
1:A:152:ARG:NH1	40:1:133:CYS:O	2.15	0.79
19:R:305:ARG:NH1	19:R:305:ARG:HG2	1.96	0.79
3:C:673:LYS:HZ2	22:U:56:ASP:CB	1.92	0.79
9:H:40:C:H2'	9:H:41:U:C6	2.17	0.79
9:H:46:U:OP1	27:2:44:LYS:HE2	1.83	0.79
6:F:86:U:HO2'	6:F:87:C:P	2.03	0.79
18:Q:87:SER:O	18:Q:91:LEU:CB	2.30	0.79
19:R:222:PRO:N	19:R:222:PRO:C	2.40	0.79
1:A:1644:LEU:HD21	1:A:1681:ARG:CG	2.10	0.79
1:A:1850:ARG:NH1	40:1:265:LEU:HD11	1.98	0.79
35:e:20:LEU:HD22	35:e:24:TYR:CE2	2.18	0.79
1:A:240:ARG:HH12	40:1:139:ARG:HB3	1.41	0.79
6:F:43:A:H2	8:G:4:A:H61	1.31	0.79
21:T:197:TYR:CE2	21:T:488:VAL:HG11	2.18	0.79
8:G:21:A:OP2	16:O:193:LEU:CD2	2.30	0.79
13:L:124:LYS:HE3	13:L:129:ASP:OD2	1.83	0.79
1:A:1556:ASP:N	1:A:1556:ASP:OD1	2.14	0.79
10:I:692:SER:HB2	10:I:703:PHE:CE2	2.17	0.79
34:m:3:LEU:HD12	34:m:4:PRO:HD3	1.62	0.79
1:A:613:TYR:CE2	46:A:3000:IHP:O45	2.35	0.78
1:A:1615:HIS:H	1:A:1618:LYS:HE3	1.46	0.78
9:H:101:U:H5''	9:H:102:U:H5'	1.64	0.78
1:A:1495:PHE:HE1	1:A:1755:SER:CB	1.96	0.78
1:A:1955:LYS:HE2	27:2:93:GLN:HE21	1.48	0.78
9:H:153:A:H2'	9:H:154:C:H5'	1.65	0.78
17:P:212:ASN:HB3	21:T:458:SER:CA	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:z:55:LEU:CD2	40:1:180:LYS:NZ	2.47	0.78
1:A:156:ARG:NH1	40:1:134:PHE:CD2	2.52	0.78
1:A:1792:LYS:NZ	9:H:37:U:H1'	1.98	0.78
1:A:620:PRO:HD2	40:1:134:PHE:CZ	2.19	0.78
1:A:1499:GLU:HB3	40:1:63:ILE:HG13	1.64	0.78
1:A:1593:LEU:CD2	1:A:1729:ALA:HB1	2.13	0.78
6:F:29:A:N6	8:G:16:G:O2'	2.16	0.78
35:l:20:LEU:HD22	35:l:24:TYR:CE2	2.18	0.78
9:H:177:A:H5''	9:H:178:A:OP1	1.84	0.78
31:h:47:THR:CB	38:o:65:ARG:NH2	2.47	0.78
17:P:16:ARG:HH21	17:P:16:ARG:HG3	1.49	0.78
27:2:25:LYS:HZ3	27:2:25:LYS:HA	1.48	0.78
27:2:138:LYS:HA	27:2:138:LYS:CE	2.13	0.78
37:q:60:PRO:CB	37:s:93:ARG:O	2.32	0.78
1:A:2328:ALA:HB3	4:D:788:GLY:HA3	1.65	0.78
6:F:36:A:H2'	6:F:37:C:O5'	1.84	0.78
12:K:83:SER:CB	37:t:75:LEU:CB	2.62	0.78
37:q:106:ALA:HB1	37:t:106:ALA:CB	2.14	0.78
37:t:8:SER:O	37:t:9:ASN:CB	2.32	0.78
1:A:106:MET:CE	1:A:561:HIS:NE2	2.47	0.77
1:A:158:ARG:NH1	28:z:62:GLN:CD	2.42	0.77
40:1:34:ARG:CB	40:1:34:ARG:HH11	1.96	0.77
1:A:1495:PHE:CE2	1:A:1753:LEU:HD13	2.20	0.77
10:I:109:MET:N	30:y:66:ASN:CB	2.47	0.77
27:2:51:LYS:NZ	35:l:28:ARG:CD	2.48	0.77
34:f:70:LEU:HD22	34:f:71:TYR:HD2	1.50	0.77
34:m:5:LEU:O	34:m:5:LEU:HD23	1.85	0.77
1:A:525:LYS:HG2	28:z:103:TYR:CA	2.13	0.77
1:A:1997:VAL:CG2	26:Z:658:TYR:CG	2.66	0.77
3:C:121:ASP:OD2	31:a:76:MET:HB3	1.85	0.77
7:4:-2:C:P	28:z:107:LYS:HE2	2.25	0.77
23:V:499:GLN:HE22	40:1:72:TRP:HB2	1.48	0.77
37:q:60:PRO:O	37:s:93:ARG:CB	2.32	0.77
8:G:129:G:H4'	24:W:541:LYS:HZ3	0.66	0.77
9:H:33:G:O2'	27:2:68:MET:HE3	1.85	0.77
23:V:460:TYR:CE1	40:1:72:TRP:HZ2	2.02	0.77
27:2:27:ALA:O	27:2:30:GLU:HG3	1.84	0.77
1:A:165:ARG:HH11	1:A:1623:ASN:CG	1.93	0.76
2:B:90:U:H5''	2:B:91:U:H5'	1.65	0.76
6:F:45:A:O2'	6:F:73:A:C2	2.38	0.76
27:2:131:ARG:O	27:2:134:LEU:HB3	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:48:ILE:HD11	35:e:59:ASP:HB2	1.66	0.76
1:A:160:HIS:CE1	40:1:170:TRP:HA	2.19	0.76
9:H:39:U:H2'	9:H:40:C:C6	2.21	0.76
31:h:45:ASN:OD1	38:o:16:THR:CB	2.34	0.76
1:A:1615:HIS:NE2	28:z:96:LEU:CB	2.48	0.76
1:A:159:ARG:HG2	40:1:104:ARG:HB2	1.67	0.76
1:A:199:GLU:HG2	40:1:139:ARG:HD3	1.66	0.76
1:A:1499:GLU:CB	40:1:63:ILE:HG12	2.16	0.76
5:E:266:PRO:HG2	13:L:785:GLN:CA	2.15	0.76
37:q:106:ALA:HB1	37:t:106:ALA:HB1	1.64	0.76
1:A:1595:GLN:NE2	40:1:268:ARG:O	2.19	0.76
1:A:1955:LYS:HZ3	27:2:93:GLN:CG	1.98	0.76
6:F:22:A:C8	24:W:130:ARG:NE	2.53	0.76
1:A:1499:GLU:OE1	40:1:60:ASN:N	2.18	0.76
1:A:1685:LEU:CD2	40:1:173:TYR:CE2	2.57	0.76
13:L:49:ARG:NH1	13:L:133:GLU:O	2.19	0.76
27:2:68:MET:HG3	27:2:68:MET:O	1.85	0.76
28:z:54:GLY:O	40:1:174:ASN:ND2	2.18	0.76
9:H:98:G:H1	34:m:41:ASN:HD21	1.33	0.76
34:m:70:LEU:HD22	34:m:71:TYR:HD2	1.49	0.76
9:H:143:A:H3'	9:H:143:A:N3	2.00	0.76
33:d:50:LYS:HG2	33:d:74:TRP:HB3	1.68	0.76
37:q:8:SER:O	37:q:9:ASN:CB	2.34	0.76
1:A:1876:LEU:O	1:A:1876:LEU:HD22	1.86	0.76
3:C:670:SER:HA	3:C:823:ALA:HB2	1.66	0.76
11:J:535:TYR:O	11:J:538:ILE:CA	2.31	0.76
35:l:48:ILE:HD11	35:l:59:ASP:HB2	1.66	0.76
1:A:2328:ALA:HB3	4:D:788:GLY:HA2	0.76	0.75
31:a:74:PRO:O	31:a:77:LEU:CD1	2.34	0.75
1:A:1878:ASP:OD1	1:A:1878:ASP:N	2.15	0.75
8:G:21:A:C1'	16:O:152:ARG:HH22	1.97	0.75
27:2:52:MET:HE2	34:m:3:LEU:HD22	1.68	0.75
36:g:35:ASP:HB2	36:g:36:PRO:HD2	1.68	0.75
8:G:147:C:C2'	8:G:148:U:H6	1.98	0.75
1:A:165:ARG:NH1	1:A:1623:ASN:CG	2.44	0.75
1:A:1741:TYR:CG	40:1:287:PRO:HG2	2.21	0.75
3:C:670:SER:HA	3:C:823:ALA:CB	2.16	0.75
1:A:470:ARG:HH21	1:A:470:ARG:HG2	1.52	0.75
27:2:132:GLN:O	27:2:136:GLU:HG3	1.85	0.75
40:1:178:HIS:CE1	40:1:181:ILE:CD1	2.68	0.75
1:A:1495:PHE:CE1	1:A:1755:SER:CB	2.70	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:CYS:CB	7:4:-11:G:H22	1.99	0.75
6:F:5:U:H3'	6:F:7:G:H5''	1.68	0.75
1:A:354:PRO:O	23:V:344:LYS:HA	1.86	0.75
40:1:46:GLY:O	45:3:331:ILE:HD13	1.87	0.75
1:A:1685:LEU:HD11	40:1:173:TYR:CE2	2.18	0.75
8:G:27:U:H2'	8:G:28:A:O5'	1.86	0.75
12:K:90:PRO:CB	12:K:109:ASN:CB	2.64	0.75
1:A:1498:TRP:CH2	40:1:67:ILE:HG21	2.21	0.74
1:A:1739:ALA:O	1:A:1742:VAL:CA	2.35	0.74
10:I:273:GLU:HA	18:Q:357:ALA:HB3	1.67	0.74
33:d:110:LEU:HD11	34:f:59:LEU:HB3	1.69	0.74
37:s:8:SER:O	37:s:9:ASN:CB	2.34	0.74
1:A:705:LYS:HG2	9:H:15:U:C5	2.22	0.74
1:A:1685:LEU:HD22	40:1:173:TYR:CE1	2.23	0.74
10:I:329:LEU:CB	18:Q:353:LEU:HA	2.16	0.74
23:V:457:ARG:HG3	40:1:73:TYR:HD2	1.52	0.74
1:A:1501:LEU:HD23	45:3:337:ILE:HG21	1.69	0.74
34:m:70:LEU:HD22	34:m:71:TYR:CD2	2.23	0.74
1:A:106:MET:HE1	1:A:578:LEU:HD13	1.69	0.74
1:A:1991:TYR:CZ	1:A:1995:ASN:HB2	2.23	0.74
9:H:152:G:P	27:2:127:ARG:HD3	2.28	0.74
1:A:1997:VAL:CG2	26:Z:658:TYR:CD2	2.70	0.74
33:k:107:ILE:HG22	33:k:108:VAL:HG23	1.69	0.74
1:A:1792:LYS:HD3	9:H:36:G:H21	1.51	0.74
10:I:721:LYS:HZ1	13:L:65:ARG:NH2	1.84	0.74
12:K:83:SER:O	37:t:76:LYS:CA	2.35	0.74
36:n:35:ASP:HB2	36:n:36:PRO:HD2	1.68	0.74
8:G:26:U:H2'	8:G:27:U:H5''	1.69	0.74
20:S:85:GLU:O	20:S:127:THR:CG2	2.36	0.74
2:B:19:A:O2'	2:B:20:G:OP1	2.04	0.74
9:H:40:C:C2'	9:H:41:U:C6	2.71	0.74
9:H:106:G:H4'	9:H:107:A:O4'	1.88	0.74
1:A:1496:PRO:HD2	45:3:337:ILE:CG1	2.16	0.74
1:A:1644:LEU:CD2	1:A:1681:ARG:HG2	2.18	0.73
33:k:50:LYS:HG2	33:k:74:TRP:HB3	1.68	0.73
1:A:1560:ILE:CD1	1:A:1577:PHE:CE2	2.70	0.73
1:A:1872:LEU:O	1:A:1876:LEU:HB2	1.89	0.73
5:E:93:TRP:CH2	29:b:105:GLY:HA3	2.23	0.73
10:I:728:ARG:O	10:I:731:GLN:HB3	1.88	0.73
1:A:1491:LYS:HD2	1:A:1709:TYR:HD1	1.52	0.73
10:I:723:MET:CA	10:I:726:ILE:HG21	1.91	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1698:PRO:HB2	40:1:182:VAL:HG22	0.76	0.73
1:A:1798:LEU:O	8:G:143:U:H4'	1.87	0.73
8:G:146:C:C2'	8:G:147:C:H5''	2.19	0.73
33:d:107:ILE:HG22	33:d:108:VAL:HG23	1.69	0.73
33:k:110:LEU:HD11	34:m:59:LEU:HB3	1.70	0.73
1:A:1495:PHE:CE1	1:A:1755:SER:HB3	2.23	0.73
2:B:46:U:O2	22:U:11:ARG:NH2	2.20	0.73
10:I:276:ARG:CB	18:Q:357:ALA:C	2.61	0.73
19:R:317:LYS:HE3	19:R:321:GLU:OE2	1.89	0.73
1:A:1566:ILE:HD11	1:A:1569:LEU:H	1.54	0.73
1:A:1642:PRO:HB2	40:1:175:PRO:HB3	1.71	0.73
1:A:1979:VAL:CA	1:A:1982:GLN:HB2	2.16	0.73
1:A:1994:LYS:NZ	27:2:67:VAL:CG2	2.52	0.73
10:I:661:ASP:HB2	10:I:694:ILE:CG2	2.13	0.73
1:A:1719:PHE:CD2	1:A:1720:PRO:HD2	2.24	0.73
1:A:1810:PHE:CE1	1:A:1919:LEU:HD12	2.23	0.73
1:A:1910:THR:CG2	24:W:412:GLN:OE1	2.36	0.73
6:F:57:U:O2'	17:P:8:THR:OG1	2.02	0.73
10:I:276:ARG:CB	18:Q:357:ALA:CB	2.67	0.73
1:A:1526:LEU:HB3	8:G:171:G:O6	1.88	0.73
8:G:13:C:H2'	8:G:14:A:C8	2.24	0.73
9:H:179:C:H2'	9:H:180:G:H8	1.53	0.73
35:l:14:MET:HE1	36:n:10:LYS:CD	2.19	0.73
1:A:1833:LEU:HD22	1:A:1833:LEU:N	2.01	0.73
1:A:1986:LEU:HD23	1:A:1986:LEU:C	2.13	0.73
8:G:149:G:H2'	8:G:150:U:H5'	1.70	0.73
31:h:47:THR:CB	38:o:65:ARG:HH22	2.02	0.73
8:G:147:C:H5'	8:G:147:C:H6	1.53	0.72
8:G:149:G:C2'	8:G:150:U:H5'	2.19	0.72
9:H:11:G:N7	14:M:198:ARG:NH2	2.36	0.72
9:H:153:A:C2'	9:H:154:C:H5'	2.17	0.72
10:I:685:ARG:NE	10:I:711:GLU:OE2	2.19	0.72
10:I:725:ARG:HD2	10:I:725:ARG:C	2.12	0.72
27:2:111:LYS:HA	27:2:114:GLU:HG2	1.70	0.72
1:A:620:PRO:HD2	40:1:134:PHE:HZ	1.54	0.72
1:A:1521:ALA:CB	8:G:166:A:H1'	2.18	0.72
1:A:1955:LYS:NZ	27:2:93:GLN:HE21	1.86	0.72
1:A:1991:TYR:OH	1:A:1995:ASN:HB2	1.88	0.72
1:A:1495:PHE:HD1	45:3:337:ILE:CD1	1.62	0.72
6:F:28:A:O2'	15:N:39:GLY:CA	2.37	0.72
30:y:13:LEU:CB	30:y:48:GLY:O	2.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:f:70:LEU:HD22	34:f:71:TYR:CD2	2.23	0.72
1:A:1849:ILE:CG2	1:A:1879:PHE:CD1	2.70	0.72
1:A:1944:HIS:HE1	27:2:69:GLY:O	1.73	0.72
7:4:-12:G:O2'	7:4:-11:G:O5'	2.07	0.72
10:I:575:ARG:O	10:I:579:LEU:HB2	1.90	0.72
21:T:455:GLN:CG	21:T:456:PRO:CD	2.64	0.72
1:A:1698:PRO:HB3	40:1:182:VAL:CG2	2.17	0.72
20:S:72:ARG:HD3	24:W:90:ALA:O	1.87	0.72
21:T:197:TYR:HD2	21:T:488:VAL:HG12	1.53	0.72
27:2:51:LYS:HZ3	35:l:28:ARG:CD	2.03	0.72
1:A:1758:PRO:HA	45:3:353:VAL:O	1.90	0.72
6:F:41:A:C2	8:G:6:A:C2	2.78	0.72
8:G:138:A:H2	9:H:39:U:O2	1.71	0.72
6:F:59:G:O2'	6:F:60:C:OP1	2.07	0.72
9:H:153:A:H2'	9:H:154:C:C5'	2.19	0.72
24:W:82:ASN:N	24:W:83:PRO:HD2	2.05	0.72
1:A:609:LYS:NZ	46:A:3000:IHP:O31	2.23	0.72
9:H:40:C:O2'	9:H:41:U:H6	1.73	0.72
8:G:7:G:O2'	8:G:8:C:H5'	1.90	0.72
8:G:137:C:C5	8:G:137:C:OP2	2.43	0.72
10:I:723:MET:O	10:I:727:ARG:N	2.23	0.72
39:p:66:LEU:HD12	39:p:81:ILE:HG22	1.70	0.72
6:F:31:U:C2'	6:F:32:U:H5'	2.19	0.71
13:L:6:ILE:HD13	13:L:6:ILE:C	2.15	0.71
21:T:282:ARG:HB2	21:T:320:LYS:HD3	1.72	0.71
1:A:1496:PRO:CB	45:3:338:GLY:CA	2.68	0.71
6:F:36:A:C2'	6:F:37:C:O5'	2.38	0.71
19:R:315:LYS:HA	19:R:315:LYS:HZ2	1.54	0.71
19:R:332:ARG:NH1	19:R:332:ARG:HB2	2.04	0.71
8:G:20:A:H2	16:O:187:THR:HG1	1.30	0.71
9:H:106:G:H21	9:H:107:A:N6	1.87	0.71
1:A:1740:LEU:O	1:A:1743:LEU:N	2.23	0.71
8:G:21:A:C4	16:O:152:ARG:NH2	2.59	0.71
13:L:7:LYS:HB3	13:L:40:ARG:C	2.15	0.71
8:G:20:A:HO2'	8:G:21:A:P	2.12	0.71
28:z:55:LEU:HD21	40:1:180:LYS:HG3	1.71	0.71
1:A:1705:ILE:CD1	1:A:1734:MET:HE2	2.14	0.71
6:F:34:G:C5'	6:F:34:G:H8	2.03	0.71
6:F:35:A:C5'	6:F:35:A:H8	2.03	0.71
6:F:45:A:H2	6:F:73:A:O4'	1.72	0.71
25:Y:413:LYS:H	25:Y:413:LYS:HD2	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:PHE:CE2	1:A:1095:ILE:HD11	2.26	0.71
1:A:1555:LEU:HD21	1:A:1574:ILE:HG13	1.72	0.71
6:F:84:A:N3	11:J:277:THR:HG21	2.06	0.71
10:I:727:ARG:HH21	10:I:727:ARG:CG	2.04	0.71
20:S:98:LEU:HB3	20:S:130:GLY:CA	2.20	0.71
21:T:437:HIS:HD2	21:T:446:ASN:HD21	1.37	0.71
6:F:45:A:C2	6:F:73:A:H1'	2.26	0.71
40:1:34:ARG:HH11	40:1:34:ARG:CA	2.04	0.71
1:A:526:PRO:CB	28:z:106:PRO:HD2	2.21	0.70
13:L:4:ILE:O	13:L:4:ILE:HD13	1.90	0.70
19:R:310:ARG:HA	19:R:310:ARG:NE	2.06	0.70
1:A:1499:GLU:CB	40:1:63:ILE:HG13	2.21	0.70
8:G:145:U:O2'	8:G:146:C:H6	1.73	0.70
10:I:723:MET:C	10:I:726:ILE:HG22	2.08	0.70
1:A:1958:LYS:HG2	27:2:100:ALA:HB2	1.73	0.70
7:4:-2:C:OP2	28:z:107:LYS:CE	2.39	0.70
20:S:72:ARG:CZ	24:W:92:GLU:OE2	2.39	0.70
27:2:113:LEU:HD13	27:2:113:LEU:C	2.16	0.70
1:A:358:PRO:HG3	23:V:340:PHE:CB	2.21	0.70
1:A:1471:ARG:HD3	40:1:66:TYR:CD2	2.26	0.70
1:A:1997:VAL:HG22	26:Z:658:TYR:CE2	2.27	0.70
6:F:41:A:H2	8:G:6:A:H2	1.38	0.70
27:2:38:LEU:HD23	34:m:12:ASN:ND2	2.05	0.70
1:A:163:ARG:NH2	46:A:3000:IHP:O35	2.22	0.70
10:I:272:PHE:CA	18:Q:355:ASN:CB	2.69	0.70
1:A:1475:ILE:HD11	40:1:66:TYR:CE2	2.25	0.70
9:H:154:C:H2'	9:H:155:C:C6	2.27	0.70
13:L:7:LYS:CG	13:L:40:ARG:HA	2.22	0.70
31:a:77:LEU:HD12	31:a:77:LEU:N	2.07	0.70
34:m:5:LEU:HD21	35:l:57:VAL:HG11	0.72	0.70
1:A:172:GLU:OE2	28:z:100:THR:HG23	1.92	0.70
1:A:1958:LYS:HE2	27:2:97:ASP:HA	1.74	0.70
8:G:137:C:O2'	8:G:138:A:OP1	2.10	0.70
19:R:332:ARG:HB2	19:R:332:ARG:HH11	1.56	0.70
28:z:55:LEU:CD2	40:1:180:LYS:HZ2	2.04	0.70
1:A:684:GLU:HG2	21:T:308:ARG:HH12	1.56	0.70
1:A:354:PRO:O	23:V:344:LYS:CA	2.40	0.70
1:A:1428:HIS:HB2	25:Y:396:ASP:HB3	1.73	0.70
1:A:1684:PHE:CB	1:A:1715:TYR:CE2	2.74	0.70
6:F:21:U:O2	24:W:168:PHE:CE1	2.44	0.70
9:H:106:G:C5'	33:k:47:ARG:HH22	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:7:LYS:HB3	13:L:40:ARG:O	1.92	0.70
1:A:1673:SER:HB2	40:1:164:ASP:CG	2.17	0.69
8:G:145:U:O2'	8:G:146:C:C6	2.44	0.69
9:H:153:A:N6	9:H:177:A:C2	2.60	0.69
3:C:666:VAL:CG1	3:C:823:ALA:O	2.39	0.69
3:C:850:LEU:HB3	3:C:855:GLY:HA3	1.74	0.69
10:I:187:LEU:CB	10:I:196:ALA:HB1	2.22	0.69
10:I:272:PHE:HA	18:Q:355:ASN:CB	2.23	0.69
16:O:262:THR:HB	16:O:271:PHE:HB2	1.74	0.69
20:S:98:LEU:HD23	20:S:130:GLY:HA3	1.75	0.69
24:W:83:PRO:CB	24:W:87:THR:HG1	1.98	0.69
6:F:31:U:O2'	6:F:32:U:H5'	1.92	0.69
6:F:42:C:H3'	6:F:43:A:C8	2.28	0.69
1:A:1615:HIS:CD2	28:z:93:ASN:OD1	2.41	0.69
1:A:1705:ILE:HD13	1:A:1734:MET:CE	2.14	0.69
1:A:1725:LEU:HD12	1:A:1725:LEU:C	2.15	0.69
9:H:150:U:H3	9:H:181:G:H1	1.41	0.69
8:G:137:C:O2'	8:G:138:A:P	2.50	0.69
8:G:137:C:H6	8:G:137:C:C5'	2.04	0.69
9:H:10:C:N4	14:M:198:ARG:HH12	1.91	0.69
17:P:16:ARG:HG3	17:P:16:ARG:NH2	2.02	0.69
19:R:305:ARG:HG2	19:R:305:ARG:HH11	1.57	0.69
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	1.75	0.69
2:B:21:A:O3'	2:B:22:U:H4'	1.93	0.69
6:F:85:U:H3'	6:F:86:U:H5'	1.75	0.69
20:S:72:ARG:HG3	24:W:71:HIS:CE1	2.27	0.69
27:2:137:LYS:HE2	27:2:137:LYS:CA	2.22	0.69
1:A:1589:ILE:HG21	1:A:1730:MET:CE	2.22	0.69
1:A:1698:PRO:HG3	40:1:181:ILE:HG13	1.75	0.69
1:A:1958:LYS:HD3	27:2:96:MET:C	2.17	0.69
1:A:1991:TYR:OH	1:A:1995:ASN:CB	2.41	0.69
2:B:90:U:O4'	31:a:66:SER:HB3	1.92	0.69
6:F:7:G:H5'	6:F:7:G:H8	1.58	0.69
13:L:6:ILE:HD13	13:L:6:ILE:O	1.93	0.69
20:S:37:LYS:HB2	20:S:37:LYS:HZ2	1.54	0.69
1:A:1889:LEU:HD11	1:A:2013:GLY:H	1.58	0.69
9:H:10:C:N4	14:M:198:ARG:NH1	2.40	0.69
19:R:332:ARG:HH11	19:R:332:ARG:CB	2.06	0.69
27:2:25:LYS:HA	27:2:25:LYS:NZ	2.07	0.69
3:C:852:ARG:HH22	7:4:-13:C:C2'	2.01	0.69
9:H:101:U:O4'	31:h:66:SER:HB3	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:723:MET:N	10:I:726:ILE:HG22	2.07	0.69
10:I:724:LEU:HA	10:I:727:ARG:HB2	1.73	0.69
21:T:197:TYR:CE2	21:T:488:VAL:CG1	2.76	0.69
31:a:77:LEU:HD12	31:a:77:LEU:H	1.57	0.69
6:F:45:A:C6	8:G:167:G:C6	2.82	0.68
1:A:880:ARG:O	1:A:883:ARG:HB2	1.93	0.68
1:A:1645:LEU:HD22	1:A:1713:SER:HA	1.74	0.68
1:A:1130:ASN:CG	1:A:1139:ARG:HD3	2.18	0.68
6:F:24:A:C6	16:O:65:PHE:HE2	2.11	0.68
1:A:1496:PRO:CG	45:3:338:GLY:CA	2.17	0.68
6:F:39:A:O2'	6:F:40:U:H5'	1.93	0.68
1:A:663:ARG:NH2	1:A:663:ARG:HG3	2.08	0.68
1:A:1471:ARG:HD3	40:1:66:TYR:CE2	2.28	0.68
1:A:1751:LEU:N	1:A:1751:LEU:HD23	2.08	0.68
12:K:83:SER:O	37:t:75:LEU:C	2.37	0.68
20:S:71:GLY:C	20:S:111:GLN:HE22	2.00	0.68
1:A:156:ARG:NH1	40:1:153:GLU:OE2	2.27	0.68
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.76	0.68
25:Y:402:ILE:HG23	25:Y:411:LEU:HD11	1.74	0.68
1:A:1599:GLN:NE2	40:1:271:ILE:HD13	2.09	0.68
1:A:1739:ALA:C	1:A:1742:VAL:H	2.01	0.68
9:H:143:A:H2'	9:H:144:C:H6	1.58	0.68
10:I:722:GLU:O	10:I:726:ILE:CB	2.41	0.68
10:I:727:ARG:HH21	10:I:727:ARG:HB3	1.58	0.68
1:A:1890:GLN:H	1:A:2013:GLY:HA3	1.58	0.68
6:F:88:G:C5'	14:M:133:ARG:NH2	2.56	0.68
1:A:526:PRO:O	28:z:102:HIS:CD2	2.47	0.68
1:A:1958:LYS:HG2	27:2:100:ALA:CB	2.24	0.68
1:A:1997:VAL:HG11	26:Z:658:TYR:CE1	2.28	0.68
6:F:45:A:C2	6:F:73:A:C1'	2.76	0.68
9:H:40:C:H2'	9:H:41:U:C5	2.29	0.68
19:R:218:ILE:HG13	19:R:218:ILE:O	1.92	0.68
20:S:72:ARG:CB	24:W:92:GLU:OE1	2.34	0.68
1:A:105:ASN:HD22	1:A:129:VAL:HG11	1.59	0.68
11:J:201:ARG:HG2	11:J:201:ARG:HH21	1.57	0.68
1:A:1600:GLU:HG3	1:A:1725:LEU:CD2	2.24	0.67
8:G:16:G:O2'	8:G:17:U:OP2	2.10	0.67
9:H:152:G:O3'	9:H:153:A:O4'	2.11	0.67
9:H:178:A:OP1	27:2:138:LYS:NZ	2.23	0.67
10:I:721:LYS:NZ	13:L:65:ARG:HH21	1.77	0.67
23:V:499:GLN:HE21	40:1:72:TRP:HB2	1.56	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:GLU:CB	40:1:139:ARG:HD2	2.19	0.67
1:A:1482:GLU:OE1	40:1:87:PRO:HD3	1.93	0.67
8:G:20:A:C2	16:O:187:THR:HG21	2.29	0.67
9:H:168:A:C8	9:H:168:A:C5'	2.76	0.67
10:I:728:ARG:NH2	10:I:728:ARG:HG2	2.06	0.67
27:2:132:GLN:O	27:2:136:GLU:CG	2.42	0.67
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.59	0.67
3:C:673:LYS:HZ3	22:U:56:ASP:CB	2.05	0.67
27:2:25:LYS:HA	27:2:25:LYS:CE	2.24	0.67
37:q:53:ILE:CB	37:r:22:ASN:CB	2.73	0.67
33:k:33:THR:HG22	33:k:37:LYS:HE2	1.76	0.67
18:Q:1002:LYS:O	18:Q:1006:THR:N	2.26	0.67
1:A:1141:ARG:NH1	1:A:1183:PRO:HD2	2.09	0.67
1:A:1883:VAL:CG2	40:1:290:ARG:O	2.41	0.67
1:A:1889:LEU:HD12	1:A:2013:GLY:H	1.59	0.67
6:F:79:C:C2	17:P:3:THR:HG23	2.28	0.67
20:S:98:LEU:HB3	20:S:130:GLY:HA3	1.76	0.67
29:b:18:ARG:NH1	29:b:52:LYS:HB2	2.09	0.67
37:q:60:PRO:CB	37:s:94:GLN:N	2.57	0.67
1:A:1585:ILE:HG21	1:A:1740:LEU:HD21	1.77	0.67
11:J:535:TYR:C	11:J:538:ILE:CB	2.67	0.67
19:R:324:LEU:HD12	19:R:324:LEU:C	2.20	0.67
1:A:1737:ASN:CG	1:A:1738:PRO:HD2	2.20	0.67
1:A:1934:SER:HB3	40:1:347:PRO:HB3	1.74	0.67
8:G:17:U:H1'	16:O:46:LYS:NZ	2.10	0.67
8:G:26:U:H2'	8:G:27:U:C5'	2.24	0.67
9:H:151:C:O2	9:H:152:G:C8	2.48	0.67
9:H:151:C:H2'	9:H:152:G:H8	1.60	0.67
11:J:535:TYR:C	11:J:538:ILE:N	2.53	0.67
21:T:261:LEU:HB2	21:T:273:TRP:HB2	1.77	0.67
22:U:23:LEU:H	23:V:474:HIS:HD2	1.42	0.67
35:e:20:LEU:HD12	36:g:41:VAL:HG13	1.77	0.67
1:A:1991:TYR:CE1	1:A:1995:ASN:HB2	2.30	0.67
9:H:151:C:C2	9:H:152:G:C8	2.83	0.67
10:I:726:ILE:HD12	10:I:726:ILE:C	2.19	0.67
16:O:243:ILE:HG12	16:O:294:ASN:HD22	1.60	0.67
1:A:2004:GLN:NE2	40:1:335:TYR:CD1	2.63	0.67
24:W:73:ASP:OD2	24:W:74:PRO:HD3	1.94	0.67
1:A:1471:ARG:HG2	40:1:66:TYR:CD2	2.30	0.66
1:A:1872:LEU:O	1:A:1876:LEU:CB	2.42	0.66
6:F:21:U:O2	24:W:168:PHE:HE1	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:138:A:N1	9:H:39:U:O2	2.27	0.66
21:T:188:PRO:CG	21:T:443:THR:OG1	2.35	0.66
23:V:496:CYS:HG	40:1:72:TRP:HH2	0.74	0.66
27:2:134:LEU:C	27:2:134:LEU:HD12	2.20	0.66
38:o:5:THR:HG22	38:o:8:LEU:H	1.60	0.66
1:A:698:PRO:HG2	1:A:701:ILE:HD13	1.75	0.66
1:A:934:ARG:NH1	25:Y:425:ILE:HG21	2.09	0.66
1:A:1676:ILE:HD13	1:A:1706:ASP:HB2	1.77	0.66
1:A:1833:LEU:H	1:A:1833:LEU:CD2	2.02	0.66
6:F:33:G:H5''	6:F:33:G:C8	2.28	0.66
6:F:45:A:N6	8:G:167:G:N7	2.43	0.66
8:G:142:U:H2'	8:G:143:U:C6	2.30	0.66
25:Y:402:ILE:HG23	25:Y:411:LEU:CD1	2.25	0.66
29:i:18:ARG:NH1	29:i:52:LYS:HB2	2.09	0.66
6:F:85:U:H3'	6:F:86:U:C5'	2.26	0.66
8:G:17:U:O2'	16:O:46:LYS:NZ	2.27	0.66
10:I:681:ILE:HG23	10:I:710:PHE:CE2	2.30	0.66
1:A:1486:GLU:OE1	1:A:1674:HIS:NE2	2.29	0.66
1:A:1596:VAL:HG13	40:1:278:LEU:HD12	1.71	0.66
35:l:20:LEU:HD12	36:m:41:VAL:HG13	1.77	0.66
1:A:1875:HIS:O	1:A:1878:ASP:CG	2.38	0.66
9:H:67:C:H42	9:H:85:A:H61	1.44	0.66
29:i:18:ARG:NH1	29:i:52:LYS:CB	2.58	0.66
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.60	0.66
9:H:75:A:H61	9:H:77:C:H42	1.44	0.66
9:H:153:A:C3'	9:H:154:C:H5'	2.25	0.66
40:1:47:ASN:HA	45:3:331:ILE:HD13	1.77	0.66
1:A:658:ARG:NH2	6:F:65:G:OP2	2.29	0.66
1:A:1552:GLN:CD	1:A:1563:HIS:NE2	2.54	0.66
1:A:1596:VAL:HG22	40:1:278:LEU:HD21	1.78	0.66
8:G:138:A:N1	9:H:39:U:C2	2.64	0.66
27:2:109:PHE:HA	27:2:112:ARG:NH1	2.11	0.66
1:A:109:PRO:HB2	1:A:191:ILE:HD12	1.77	0.66
1:A:381:PRO:HD2	3:C:334:ILE:HG22	1.78	0.66
10:I:273:GLU:O	18:Q:357:ALA:CB	2.44	0.66
16:O:223:LEU:HD22	16:O:285:GLU:HG2	1.78	0.66
29:b:18:ARG:NH1	29:b:52:LYS:CB	2.58	0.66
1:A:1135:PRO:O	1:A:1138:ALA:N	2.26	0.65
6:F:45:A:C6	8:G:167:G:C5	2.85	0.65
7:4:-2:C:P	28:z:107:LYS:CE	2.84	0.65
8:G:17:U:H1'	16:O:46:LYS:HZ3	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:40:C:O2'	9:H:41:U:C4'	2.44	0.65
9:H:41:U:H5''	9:H:41:U:H6	1.60	0.65
10:I:721:LYS:HZ1	13:L:65:ARG:HH22	1.44	0.65
1:A:1585:ILE:CG2	1:A:1740:LEU:HD21	2.27	0.65
2:B:95:G:H5'	34:f:25:TRP:CH2	2.21	0.65
12:K:83:SER:O	37:t:76:LYS:N	2.29	0.65
33:d:33:THR:HG22	33:d:37:LYS:HE2	1.76	0.65
1:A:1487:HIS:CE1	1:A:1671:TYR:CZ	2.85	0.65
6:F:6:C:OP2	6:F:6:C:H4'	1.95	0.65
19:R:64:PHE:O	19:R:71:GLN:NE2	2.29	0.65
1:A:170:ASP:OD2	28:z:95:HIS:CE1	2.49	0.65
1:A:1193:GLU:HB3	1:A:1231:ARG:HB3	1.78	0.65
1:A:1816:GLN:HG3	1:A:1917:PHE:O	1.96	0.65
3:C:121:ASP:CG	31:a:76:MET:SD	2.79	0.65
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.77	0.65
8:G:137:C:OP2	8:G:137:C:H5	1.78	0.65
9:H:114:A:H61	9:H:142:C:H42	1.44	0.65
10:I:532:LYS:HD2	10:I:532:LYS:C	2.20	0.65
19:R:136:ASP:HB3	19:R:138:GLU:H	1.60	0.65
1:A:1501:LEU:CD2	45:3:337:ILE:HD13	2.20	0.65
21:T:314:ILE:HD12	21:T:324:HIS:HB2	1.78	0.65
1:A:1883:VAL:HA	40:l:289:THR:O	1.96	0.65
3:C:333:ASP:OD1	36:g:3:LYS:HB2	1.96	0.65
16:O:250:ASN:OD1	20:S:91:LYS:NZ	2.26	0.65
20:S:72:ARG:HG3	24:W:71:HIS:ND1	2.10	0.65
1:A:1258:LYS:HE3	8:G:173:G:H4'	1.79	0.65
1:A:419:ARG:NH2	1:A:423:ASP:O	2.30	0.65
1:A:690:MET:HE1	17:P:9:PHE:HB3	1.79	0.65
1:A:1600:GLU:HG3	1:A:1725:LEU:HD21	1.78	0.65
3:C:667:VAL:N	3:C:824:THR:HG23	2.09	0.65
24:W:341:ASN:OD1	24:W:388:GLN:NE2	2.29	0.65
9:H:33:G:H1'	27:2:68:MET:HE1	1.79	0.65
20:S:125:LYS:CB	20:S:126:HIS:CD2	2.80	0.65
25:Y:413:LYS:HA	25:Y:416:PHE:CD2	2.32	0.65
9:H:147:G:H2'	9:H:148:C:H6	1.62	0.64
1:A:537:LYS:HB2	6:F:37:C:H41	1.60	0.64
5:E:307:ARG:HH22	29:b:115:PRO:HB3	1.61	0.64
6:F:45:A:C2	6:F:73:A:O4'	2.51	0.64
8:G:148:U:O2	8:G:148:U:H2'	1.95	0.64
1:A:1141:ARG:HB2	1:A:1182:ASN:OD1	1.98	0.64
1:A:1494:TYR:CB	1:A:1744:ARG:HE	2.09	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1521:ALA:HB3	8:G:166:A:H1'	1.78	0.64
8:G:129:G:C4'	24:W:541:LYS:CE	2.66	0.64
9:H:153:A:H3'	9:H:154:C:H5'	1.79	0.64
34:m:5:LEU:HD22	35:l:48:ILE:HB	1.80	0.64
6:F:28:A:H1'	15:N:39:GLY:O	1.97	0.64
33:d:32:LEU:HD22	33:d:65:MET:HE3	1.80	0.64
1:A:1877:LEU:O	1:A:1880:PRO:HD3	1.98	0.64
1:A:1880:PRO:C	1:A:1882:ILE:H	2.06	0.64
1:A:1994:LYS:HB3	26:Z:756:TYR:HB2	1.79	0.64
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.79	0.64
5:E:93:TRP:HH2	29:b:105:GLY:CA	2.10	0.64
9:H:154:C:H2'	9:H:155:C:H6	1.62	0.64
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.31	0.64
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.30	0.64
1:A:1835:GLN:OE1	1:A:1835:GLN:HA	1.97	0.64
1:A:1869:LEU:O	1:A:1873:GLU:HB3	1.97	0.64
3:C:137:HIS:HD2	3:C:238:ASN:H	1.44	0.64
6:F:22:A:H2'	24:W:130:ARG:HH21	1.62	0.64
9:H:41:U:H2'	9:H:42:G:C8	2.33	0.64
16:O:133:PRO:HG2	16:O:137:LEU:HB2	1.80	0.64
20:S:102:ASN:ND2	20:S:108:ASN:OD1	2.30	0.64
24:W:534:ILE:HD12	24:W:544:SER:HB3	1.79	0.64
2:B:23:C:O2'	2:B:24:G:O5'	2.15	0.64
9:H:164:C:H6	9:H:164:C:H5'	1.63	0.64
10:I:704:TRP:CH2	10:I:727:ARG:HG3	2.32	0.64
23:V:544:LEU:HD11	23:V:578:SER:HB3	1.79	0.64
6:F:88:G:H5'	14:M:133:ARG:NH2	2.13	0.64
8:G:147:C:C2	8:G:148:U:C6	2.86	0.64
10:I:681:ILE:HG23	10:I:710:PHE:HZ	1.56	0.64
33:k:32:LEU:HD22	33:k:65:MET:HE3	1.79	0.64
1:A:1773:SER:HB3	40:l:321:THR:OG1	1.98	0.64
9:H:39:U:H2'	9:H:40:C:C5	2.32	0.64
6:F:42:C:H5''	6:F:43:A:OP2	1.97	0.63
8:G:21:A:OP2	16:O:193:LEU:HD11	1.98	0.63
23:V:499:GLN:HE22	40:l:72:TRP:HE3	1.40	0.63
1:A:1644:LEU:HD21	1:A:1681:ARG:HD2	1.74	0.63
5:E:93:TRP:HH2	29:b:105:GLY:HA2	1.63	0.63
5:E:307:ARG:NH2	29:b:115:PRO:HB3	2.12	0.63
37:r:8:SER:CB	37:s:86:MET:CB	2.77	0.63
1:A:1803:ILE:HG22	24:W:451:VAL:CG2	2.28	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:250:ARG:NH1	21:T:266:GLU:OE2	2.30	0.63
1:A:1471:ARG:HD2	40:1:66:TYR:CG	2.33	0.63
1:A:1955:LYS:HZ1	27:2:89:GLU:CD	2.04	0.63
9:H:77:C:H5'	24:W:242:HIS:CE1	2.34	0.63
28:z:107:LYS:NZ	28:z:109:SER:OG	2.29	0.63
1:A:1934:SER:OG	40:1:344:GLN:HA	1.98	0.63
21:T:197:TYR:CD2	21:T:488:VAL:CG1	2.81	0.63
1:A:159:ARG:HA	40:1:104:ARG:HG3	1.80	0.63
1:A:1948:ASP:HB3	27:2:60:PRO:HB3	1.81	0.63
6:F:29:A:N3	16:O:166:SER:OG	2.29	0.63
8:G:18:A:C2	16:O:196:GLN:O	2.52	0.63
1:A:1955:LYS:HZ2	27:2:89:GLU:HG2	1.61	0.63
9:H:152:G:C2	9:H:153:A:C5	2.87	0.63
24:W:70:VAL:HG22	24:W:71:HIS:CD2	2.34	0.63
1:A:526:PRO:HG3	28:z:106:PRO:HD3	0.63	0.63
1:A:1020:LYS:NZ	9:H:26:A:OP1	2.32	0.63
24:W:72:LEU:HD11	24:W:83:PRO:HG3	0.76	0.63
1:A:1615:HIS:HE2	28:z:93:ASN:HA	1.64	0.63
6:F:41:A:H2	8:G:6:A:C2	2.16	0.63
25:Y:413:LYS:HA	25:Y:416:PHE:HD2	1.64	0.63
1:A:199:GLU:CG	40:1:139:ARG:CD	2.77	0.62
1:A:1792:LYS:NZ	9:H:37:U:C1'	2.60	0.62
2:B:95:G:C5'	33:d:47:ARG:HH22	2.12	0.62
3:C:531:TRP:HB2	3:C:551:LEU:HB2	1.80	0.62
8:G:142:U:H4'	8:G:143:U:OP1	1.98	0.62
16:O:27:CYS:SG	16:O:83:THR:OG1	2.57	0.62
20:S:125:LYS:HB3	20:S:126:HIS:CD2	2.33	0.62
21:T:307:SER:OG	21:T:308:ARG:N	2.29	0.62
1:A:1798:LEU:HB2	8:G:143:U:O4'	1.98	0.62
11:J:242:ILE:HA	11:J:245:TRP:HD1	1.64	0.62
15:N:139:CYS:SG	15:N:140:ARG:N	2.72	0.62
1:A:1589:ILE:HG12	1:A:1733:ILE:HG21	1.80	0.62
1:A:2004:GLN:C	40:1:342:HIS:HE2	2.07	0.62
3:C:668:GLU:H	3:C:824:THR:HG21	1.64	0.62
6:F:27:A:O2'	6:F:28:A:C8	2.51	0.62
8:G:5:G:O5'	8:G:5:G:H8	1.81	0.62
9:H:33:G:O2'	27:2:68:MET:CE	2.46	0.62
8:G:20:A:H2	16:O:187:THR:HG21	1.64	0.62
8:G:120:G:C2'	8:G:121:G:O4'	2.46	0.62
8:G:147:C:H6	8:G:147:C:C5'	2.12	0.62
9:H:143:A:H2'	9:H:144:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:156:U:C6	9:H:156:U:C5'	2.72	0.62
3:C:177:ARG:NH2	3:C:638:ASP:OD2	2.32	0.62
9:H:157:G:H5''	9:H:157:G:H8	1.65	0.62
11:J:535:TYR:O	11:J:537:TRP:C	2.43	0.62
13:L:123:LEU:HD22	13:L:125:PRO:HD2	1.81	0.62
40:1:51:GLU:HB2	40:1:59:ILE:HB	1.81	0.62
40:1:269:GLU:OE2	40:1:269:GLU:HA	1.98	0.62
1:A:934:ARG:HH12	25:Y:425:ILE:HG21	1.64	0.62
1:A:1984:LYS:HD2	40:1:345:ALA:HB1	1.81	0.62
8:G:18:A:N1	16:O:196:GLN:O	2.32	0.62
21:T:187:LYS:N	21:T:188:PRO:CD	2.63	0.62
37:r:8:SER:O	37:r:9:ASN:CB	2.47	0.62
38:o:123:ASN:O	38:o:126:THR:HB	1.99	0.62
1:A:525:LYS:CD	28:z:103:TYR:HA	2.28	0.62
1:A:1495:PHE:HE2	1:A:1753:LEU:HD13	1.64	0.62
1:A:1997:VAL:HG13	26:Z:658:TYR:CZ	2.34	0.62
19:R:310:ARG:HA	19:R:310:ARG:CZ	2.30	0.62
1:A:1589:ILE:CG2	1:A:1730:MET:CE	2.73	0.62
9:H:15:U:C2'	9:H:16:U:OP2	2.48	0.62
10:I:273:GLU:CB	18:Q:357:ALA:HB2	2.29	0.62
1:A:1809:ILE:HD11	1:A:1845:VAL:HG22	1.82	0.62
2:B:19:A:H2'	2:B:20:G:H5''	1.82	0.62
3:C:506:PRO:HA	3:C:526:THR:HA	1.82	0.62
25:Y:413:LYS:HB3	25:Y:425:ILE:HD11	1.80	0.62
1:A:1130:ASN:HD22	1:A:1139:ARG:HH11	1.46	0.62
1:A:1499:GLU:HB3	40:1:60:ASN:CB	2.20	0.62
5:E:274:VAL:HG12	5:E:275:LYS:HG3	1.82	0.62
20:S:61:MET:HE2	20:S:63:GLN:HB2	1.82	0.62
24:W:253:SER:HB3	24:W:256:HIS:HB2	1.80	0.62
1:A:1552:GLN:CG	1:A:1563:HIS:CD2	2.83	0.61
1:A:1739:ALA:HA	1:A:1742:VAL:HG23	1.82	0.61
3:C:711:ARG:NH2	3:C:730:ARG:O	2.33	0.61
6:F:35:A:H5''	6:F:35:A:H8	1.64	0.61
28:z:55:LEU:HD22	40:1:180:LYS:NZ	2.14	0.61
1:A:1433:ASP:OD1	1:A:1439:ARG:NH2	2.33	0.61
1:A:1566:ILE:C	1:A:1566:ILE:HD12	2.25	0.61
24:W:70:VAL:HG13	24:W:71:HIS:HD2	1.63	0.61
1:A:525:LYS:HE2	28:z:103:TYR:CA	2.17	0.61
1:A:1903:GLY:HA3	27:2:82:TYR:CZ	2.35	0.61
1:A:1983:LEU:HD21	1:A:1987:ILE:HG13	1.81	0.61
6:F:43:A:O5'	6:F:43:A:H8	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:78:LYS:O	16:O:97:ARG:NH2	2.32	0.61
25:Y:401:GLU:O	25:Y:405:MET:HG2	2.00	0.61
1:A:1475:ILE:CD1	40:1:66:TYR:HE2	2.12	0.61
1:A:1496:PRO:CB	45:3:338:GLY:HA2	2.30	0.61
16:O:26:THR:OG1	16:O:159:ARG:NH2	2.34	0.61
24:W:73:ASP:CB	24:W:74:PRO:CD	2.38	0.61
1:A:153:ARG:HB3	40:1:134:PHE:HB3	1.82	0.61
1:A:1258:LYS:CE	8:G:173:G:C4'	2.72	0.61
1:A:1639:VAL:H	1:A:1656:THR:HA	1.65	0.61
1:A:1757:GLU:OE1	1:A:1757:GLU:N	2.33	0.61
2:B:12:U:O2'	2:B:13:C:O5'	2.19	0.61
9:H:39:U:H6	9:H:39:U:C5'	2.07	0.61
1:A:1615:HIS:NE2	28:z:93:ASN:HA	2.14	0.61
1:A:1698:PRO:HG2	40:1:182:VAL:N	2.12	0.61
1:A:1698:PRO:HB3	40:1:182:VAL:HG23	1.76	0.61
3:C:853:ARG:NH1	3:C:879:ASP:O	2.33	0.61
5:E:104:THR:OG1	29:b:103:GLY:HA3	2.00	0.61
5:E:307:ARG:HH22	29:b:115:PRO:HG3	1.65	0.61
13:L:4:ILE:O	13:L:4:ILE:HG23	1.99	0.61
13:L:6:ILE:O	13:L:6:ILE:HG23	2.00	0.61
1:A:1719:PHE:HD2	1:A:1720:PRO:HD2	1.64	0.61
1:A:1775:GLN:NE2	40:1:315:VAL:HB	2.15	0.61
3:C:853:ARG:NH2	3:C:886:ASP:OD2	2.33	0.61
9:H:33:G:H2'	9:H:34:U:C6	2.35	0.61
8:G:13:C:H2'	8:G:14:A:H8	1.65	0.61
9:H:106:G:H5'	33:k:47:ARG:HH22	1.66	0.61
17:P:13:ARG:HG3	17:P:13:ARG:NH1	2.14	0.61
18:Q:823:GLY:O	18:Q:1096:ASP:CB	2.48	0.61
1:A:1475:ILE:CD1	40:1:66:TYR:CE2	2.83	0.61
1:A:1566:ILE:HG13	1:A:1566:ILE:O	1.99	0.61
9:H:142:C:C2'	9:H:143:A:H5'	2.30	0.61
24:W:247:TYR:HB3	24:W:251:GLY:HA2	1.83	0.61
24:W:384:ASP:OD2	24:W:430:ASN:ND2	2.34	0.61
1:A:1698:PRO:CG	40:1:182:VAL:N	2.63	0.61
3:C:779:LEU:HB3	3:C:934:MET:HE1	1.83	0.61
5:E:162:ARG:HH21	5:E:203:ASP:HB3	1.66	0.61
9:H:112:G:H2'	9:H:113:G:H8	1.65	0.61
9:H:153:A:N6	9:H:177:A:H2	1.98	0.61
10:I:721:LYS:NZ	13:L:65:ARG:HH22	1.93	0.61
21:T:187:LYS:N	21:T:188:PRO:HD2	2.16	0.61
1:A:1955:LYS:NZ	27:2:93:GLN:CD	2.58	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2004:GLN:O	40:1:342:HIS:NE2	2.31	0.60
21:T:312:ALA:HB3	21:T:326:LEU:HB2	1.83	0.60
24:W:565:LYS:HD2	24:W:577:LEU:HD21	1.83	0.60
35:e:74:LEU:HB3	35:e:77:ILE:HD11	1.81	0.60
35:l:74:LEU:HB3	35:l:77:ILE:HD11	1.81	0.60
1:A:526:PRO:O	28:z:102:HIS:CG	2.53	0.60
1:A:532:THR:HG1	8:G:3:A:P	2.24	0.60
1:A:1471:ARG:CD	40:1:66:TYR:CD2	2.84	0.60
1:A:1521:ALA:HB1	8:G:166:A:HI'	1.83	0.60
1:A:1882:ILE:O	40:1:290:ARG:HB2	2.01	0.60
3:C:693:GLU:H	3:C:696:LEU:HD12	1.65	0.60
8:G:21:A:O2'	8:G:22:C:P	2.59	0.60
20:S:98:LEU:HB3	20:S:130:GLY:C	2.26	0.60
3:C:668:GLU:H	3:C:824:THR:CG2	2.14	0.60
3:C:829:GLU:HB2	3:C:907:VAL:HG22	1.84	0.60
5:E:81:LEU:HB2	5:E:93:TRP:HB2	1.83	0.60
10:I:608:LEU:HB2	10:I:611:HIS:HB2	1.83	0.60
10:I:692:SER:HB2	10:I:703:PHE:HE2	1.65	0.60
1:A:172:GLU:OE2	28:z:99:LEU:HA	2.00	0.60
19:R:314:GLN:OE1	19:R:314:GLN:HA	2.01	0.60
23:V:457:ARG:HG3	40:1:73:TYR:CE2	2.36	0.60
40:1:34:ARG:HH11	40:1:34:ARG:CG	2.14	0.60
1:A:1136:ARG:HH11	1:A:1136:ARG:CG	2.10	0.60
1:A:1471:ARG:HD2	40:1:66:TYR:CD1	2.37	0.60
1:A:1593:LEU:HD21	1:A:1729:ALA:CB	2.27	0.60
1:A:1876:LEU:HD12	1:A:1884:ILE:CD1	2.31	0.60
1:A:1890:GLN:CD	27:2:71:SER:OG	2.45	0.60
3:C:221:ILE:HG23	3:C:495:ARG:HB2	1.82	0.60
8:G:137:C:H6	8:G:137:C:O5'	1.85	0.60
21:T:188:PRO:HG3	21:T:443:THR:HG1	1.63	0.60
23:V:460:TYR:CE1	40:1:72:TRP:CZ2	2.88	0.60
24:W:354:ARG:NH1	24:W:373:ARG:O	2.35	0.60
1:A:252:ASP:O	1:A:332:TYR:OH	2.19	0.60
1:A:1787:ARG:HH21	1:A:1805:GLY:HA2	1.67	0.60
8:G:130:A:O2'	8:G:131:U:P	2.60	0.60
3:C:277:LYS:NZ	3:C:864:PRO:O	2.35	0.60
6:F:34:G:C5'	6:F:34:G:C8	2.85	0.60
21:T:197:TYR:HE2	21:T:488:VAL:HG11	1.64	0.60
24:W:82:ASN:N	24:W:83:PRO:CD	2.65	0.60
40:1:46:GLY:CA	45:3:331:ILE:HG21	2.23	0.60
1:A:435:CYS:HB3	7:4:-11:G:H22	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1772:PHE:HZ	1:A:1933:PHE:HB2	1.67	0.60
10:I:272:PHE:CB	18:Q:356:VAL:N	2.64	0.60
10:I:725:ARG:HD3	13:L:62:GLU:OE1	2.01	0.60
21:T:339:GLN:NE2	21:T:342:GLU:O	2.35	0.60
6:F:85:U:O2'	6:F:86:U:H5''	2.02	0.59
8:G:23:U:C6	8:G:23:U:H5''	2.37	0.59
19:R:326:GLU:HB3	19:R:330:LYS:HE3	1.83	0.59
40:1:67:ILE:HG23	40:1:85:GLN:HE21	1.66	0.59
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.83	0.59
1:A:1765:SER:H	1:A:2014:MET:CE	2.15	0.59
8:G:6:A:H2'	8:G:7:G:C8	2.37	0.59
1:A:880:ARG:HA	1:A:883:ARG:HB2	1.84	0.59
1:A:1876:LEU:CD1	1:A:1884:ILE:HD11	2.32	0.59
1:A:1980:GLU:OE2	40:1:347:PRO:HD2	2.02	0.59
11:J:182:LYS:HB2	26:Z:741:ALA:HA	1.82	0.59
12:K:82:LEU:O	37:t:72:PRO:O	2.20	0.59
19:R:126:ASN:ND2	19:R:128:ASP:O	2.36	0.59
19:R:309:GLU:HA	19:R:309:GLU:OE2	2.01	0.59
21:T:438:LEU:HD12	21:T:448:GLN:HB3	1.83	0.59
1:A:293:TRP:CD1	1:A:1136:ARG:CZ	2.85	0.59
1:A:915:GLU:OE1	1:A:1012:LYS:NZ	2.36	0.59
1:A:1481:VAL:CG2	40:1:85:GLN:HE21	2.14	0.59
1:A:1498:TRP:CZ3	40:1:67:ILE:HG21	2.38	0.59
3:C:667:VAL:H	3:C:824:THR:CG2	2.12	0.59
5:E:248:SER:HB3	5:E:265:ARG:HE	1.67	0.59
6:F:58:G:O2'	6:F:59:G:OP1	2.20	0.59
10:I:688:TYR:O	10:I:703:PHE:CZ	2.47	0.59
11:J:535:TYR:O	11:J:538:ILE:CB	2.49	0.59
1:A:58:LYS:NZ	1:A:477:LYS:O	2.35	0.59
1:A:761:ILE:CD1	1:A:772:CYS:SG	2.90	0.59
21:T:345:ILE:HB	21:T:357:TRP:HB2	1.82	0.59
37:r:7:ILE:O	37:s:90:PHE:CB	2.50	0.59
1:A:293:TRP:NE1	1:A:1136:ARG:HH12	2.01	0.59
3:C:121:ASP:OD1	31:a:76:MET:SD	2.60	0.59
6:F:35:A:C5'	6:F:35:A:C8	2.85	0.59
6:F:85:U:O2'	6:F:86:U:OP1	2.20	0.59
9:H:106:G:N2	9:H:107:A:C6	2.68	0.59
9:H:154:C:OP1	39:p:19:LYS:HD3	2.03	0.59
19:R:315:LYS:HA	19:R:315:LYS:NZ	2.17	0.59
21:T:399:LYS:HB3	21:T:404:SER:HB3	1.84	0.59
1:A:977:LEU:HB3	1:A:1097:ILE:HB	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1552:GLN:CB	1:A:1563:HIS:HD2	2.14	0.59
1:A:1772:PHE:CD2	1:A:1930:TYR:HB3	2.38	0.59
6:F:27:A:O2'	6:F:28:A:N7	2.35	0.59
26:Z:682:TYR:HB3	26:Z:685:LEU:HD11	1.85	0.59
1:A:343:GLU:HB3	40:1:144:PHE:CZ	2.38	0.59
1:A:1829:GLY:HA3	6:F:40:U:OP1	2.02	0.59
8:G:19:G:H21	16:O:196:GLN:HG3	1.67	0.59
8:G:20:A:O2'	8:G:21:A:P	2.59	0.59
10:I:696:ASP:HB3	10:I:699:THR:HB	1.85	0.59
11:J:344:GLN:HG2	14:M:132:LEU:HD21	1.83	0.59
14:M:120:PRO:O	14:M:120:PRO:HG2	2.03	0.59
23:V:457:ARG:NH1	40:1:88:GLN:CG	2.62	0.59
24:W:347:PHE:HD2	24:W:359:TRP:HB2	1.68	0.59
31:a:74:PRO:HB2	31:a:77:LEU:CD1	2.28	0.59
31:a:74:PRO:C	31:a:77:LEU:CD1	2.75	0.59
1:A:154:GLU:HG2	1:A:572:PHE:CD1	2.38	0.59
1:A:1797:ASN:OD1	8:G:143:U:C5'	2.51	0.59
8:G:134:U:C5'	8:G:135:G:OP2	2.51	0.59
10:I:731:GLN:NE2	10:I:731:GLN:HA	2.18	0.59
34:m:5:LEU:HB3	35:l:48:ILE:HG22	1.85	0.59
5:E:102:TYR:O	29:b:102:GLY:HA2	2.03	0.59
21:T:244:GLY:O	21:T:271:LYS:NZ	2.34	0.59
23:V:503:TYR:HB2	23:V:546:ASN:HA	1.84	0.59
3:C:824:THR:HG23	3:C:824:THR:O	2.02	0.58
17:P:2:THR:O	17:P:2:THR:HG22	2.02	0.58
34:f:70:LEU:CD2	34:f:71:TYR:HD2	2.16	0.58
8:G:12:G:H2'	8:G:13:C:C5	2.38	0.58
1:A:864:LEU:C	1:A:864:LEU:HD23	2.28	0.58
1:A:934:ARG:NH1	25:Y:425:ILE:CG2	2.66	0.58
3:C:196:LYS:HD2	31:a:14:GLU:OE1	2.02	0.58
8:G:22:C:O2	8:G:22:C:H2'	2.02	0.58
10:I:272:PHE:CB	18:Q:355:ASN:CB	2.81	0.58
19:R:320:HIS:HA	19:R:323:LYS:HD3	1.85	0.58
20:S:72:ARG:CB	24:W:92:GLU:CD	2.77	0.58
1:A:1393:ARG:HH11	25:Y:405:MET:HE2	1.68	0.58
8:G:134:U:C5	8:G:135:G:N2	2.71	0.58
1:A:526:PRO:HB3	28:z:106:PRO:HD2	1.84	0.58
1:A:864:LEU:HD23	1:A:864:LEU:O	2.04	0.58
1:A:1496:PRO:HB2	45:3:338:GLY:HA2	1.85	0.58
3:C:224:GLY:HA3	3:C:438:ILE:HD12	1.84	0.58
8:G:22:C:HO2'	8:G:23:U:P	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:40:C:HO2'	9:H:41:U:C1'	2.17	0.58
9:H:152:G:OP1	27:2:127:ARG:CD	2.52	0.58
13:L:135:LYS:HD2	13:L:135:LYS:N	2.17	0.58
16:O:276:THR:HG23	16:O:279:ALA:H	1.67	0.58
18:Q:828:GLY:HA2	50:Q:1501:ATP:O1B	2.04	0.58
34:m:5:LEU:HD23	35:l:57:VAL:HG11	1.69	0.58
1:A:1471:ARG:CD	40:1:66:TYR:CE1	2.78	0.58
1:A:1705:ILE:HG21	1:A:1734:MET:HE2	1.78	0.58
1:A:1879:PHE:CD2	1:A:1879:PHE:N	2.72	0.58
7:4:-2:C:OP1	28:z:107:LYS:HE2	2.04	0.58
19:R:315:LYS:HZ3	19:R:315:LYS:HB2	1.68	0.58
21:T:185:MET:HG3	21:T:186:PRO:HD3	0.77	0.58
21:T:186:PRO:HG2	21:T:188:PRO:HD3	1.84	0.58
34:m:70:LEU:CD2	34:m:71:TYR:HD2	2.16	0.58
1:A:955:TRP:CD1	1:A:1189:MET:HE1	2.39	0.58
1:A:1494:TYR:HB2	1:A:1744:ARG:HE	1.67	0.58
3:C:776:GLU:OE1	3:C:813:ARG:NH2	2.37	0.58
5:E:93:TRP:CH2	29:b:105:GLY:HA2	2.38	0.58
25:Y:405:MET:HB3	25:Y:411:LEU:HG	1.84	0.58
1:A:1601:LEU:HA	1:A:1606:ILE:HD12	1.86	0.58
6:F:77:C:H2'	6:F:78:A:H5'	1.86	0.58
9:H:10:C:C4	14:M:198:ARG:NH2	2.72	0.58
11:J:266:GLU:OE2	11:J:301:ARG:NH1	2.31	0.58
13:L:5:MET:HE2	13:L:39:HIS:ND1	2.19	0.58
16:O:239:LEU:O	16:O:296:ARG:NH1	2.34	0.58
20:S:83:GLU:HA	20:S:106:ASP:HB2	1.84	0.58
1:A:300:ASN:HB3	3:C:939:ARG:HH22	1.69	0.58
1:A:1596:VAL:CB	40:1:278:LEU:HD11	2.34	0.58
1:A:1615:HIS:CD2	28:z:93:ASN:HA	2.39	0.58
1:A:1883:VAL:HG13	40:1:289:THR:O	2.03	0.58
5:E:209:ILE:HG12	5:E:219:VAL:HG22	1.85	0.58
9:H:24:A:H3'	9:H:25:G:H5''	1.86	0.58
11:J:285:MET:O	11:J:289:ASN:ND2	2.37	0.58
12:K:110:SER:CB	13:L:699:ASN:CB	2.81	0.58
18:Q:828:GLY:CA	50:Q:1501:ATP:O1B	2.52	0.58
1:A:73:HIS:ND1	1:A:88:TYR:OH	2.34	0.57
16:O:84:CYS:SG	16:O:159:ARG:NH2	2.77	0.57
23:V:608:LEU:HB3	23:V:611:PHE:HB3	1.86	0.57
38:o:133:LEU:HD12	38:o:158:ALA:HB2	1.84	0.57
1:A:344:ASP:OD1	1:A:344:ASP:N	2.37	0.57
1:A:873:ASN:ND2	1:A:876:GLU:OE1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1253:SER:O	1:A:1253:SER:OG	2.07	0.57
1:A:1739:ALA:O	1:A:1742:VAL:CG2	2.52	0.57
1:A:1955:LYS:HE2	27:2:93:GLN:NE2	2.16	0.57
6:F:39:A:C3'	6:F:40:U:H5'	2.34	0.57
31:h:45:ASN:HB3	38:o:22:ARG:NH1	2.18	0.57
34:m:3:LEU:HG	34:m:4:PRO:CD	2.28	0.57
1:A:1553:VAL:HG13	1:A:1553:VAL:O	2.04	0.57
10:I:272:PHE:O	18:Q:355:ASN:CB	2.52	0.57
24:W:72:LEU:CD1	24:W:83:PRO:CG	2.55	0.57
1:A:1322:LEU:HD21	40:1:67:ILE:CD1	2.34	0.57
24:W:404:ASP:OD2	24:W:406:ARG:NH1	2.38	0.57
1:A:1955:LYS:CE	27:2:93:GLN:NE2	2.59	0.57
8:G:127:U:H4'	24:W:545:ARG:HH22	1.68	0.57
16:O:76:LYS:HG2	24:W:111:LEU:HD22	1.85	0.57
19:R:316:GLU:HA	19:R:319:LYS:HG2	1.87	0.57
21:T:223:SER:OG	21:T:224:ALA:N	2.37	0.57
23:V:457:ARG:NH1	40:1:88:GLN:CD	2.62	0.57
1:A:861:ARG:HB3	1:A:861:ARG:HH11	1.70	0.57
1:A:1981:VAL:O	1:A:1984:LYS:HB3	2.04	0.57
6:F:28:A:HO2'	15:N:39:GLY:CA	2.17	0.57
6:F:39:A:H2'	6:F:40:U:C5'	2.29	0.57
1:A:415:SER:OG	1:A:416:GLY:N	2.37	0.57
9:H:71:C:H2'	9:H:72:U:H6	1.70	0.57
9:H:179:C:H2'	9:H:180:G:C8	2.38	0.57
12:K:181:MET:O	12:K:185:TRP:N	2.37	0.57
28:z:55:LEU:CD2	40:1:180:LYS:HZ3	2.17	0.57
38:o:2:VAL:HG11	38:o:29:TYR:O	2.05	0.57
38:o:101:VAL:HG23	38:o:102:GLU:HG3	1.86	0.57
1:A:1596:VAL:HG11	40:1:278:LEU:CD1	2.34	0.57
1:A:1815:GLY:O	1:A:1919:LEU:N	2.31	0.57
6:F:45:A:C5	8:G:167:G:C6	2.93	0.57
8:G:136:U:OP2	8:G:136:U:H6	1.88	0.57
9:H:36:G:O2'	9:H:37:U:H5'	2.04	0.57
13:L:256:GLU:OE2	13:L:260:ARG:NH2	2.38	0.57
1:A:1900:GLU:OE2	27:2:86:ARG:HA	2.05	0.57
1:A:1875:HIS:C	1:A:1878:ASP:OD1	2.48	0.57
9:H:141:C:C2	9:H:142:C:C5	2.93	0.57
9:H:152:G:P	27:2:127:ARG:CD	2.93	0.57
11:J:180:LYS:HE3	13:L:145:ASP:HB3	1.86	0.57
1:A:480:LYS:NZ	15:N:112:ASN:OD1	2.37	0.56
9:H:39:U:C3'	9:H:40:C:C5	2.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:73:C:H2'	9:H:74:U:H6	1.70	0.56
9:H:154:C:O2'	9:H:155:C:H5'	2.04	0.56
20:S:11:PRO:O	20:S:29:TRP:NE1	2.36	0.56
21:T:343:PRO:HD3	21:T:401:PRO:HB3	1.86	0.56
27:2:127:ARG:HB2	27:2:131:ARG:HH12	1.69	0.56
1:A:153:ARG:HG2	1:A:153:ARG:NH2	2.11	0.56
1:A:761:ILE:HD13	1:A:772:CYS:SG	2.45	0.56
6:F:38:G:H2'	6:F:39:A:C8	2.40	0.56
8:G:130:A:HO2'	8:G:131:U:P	2.28	0.56
9:H:152:G:N2	9:H:153:A:C5	2.73	0.56
19:R:317:LYS:CE	19:R:321:GLU:OE2	2.52	0.56
31:a:79:ASN:OD1	31:a:79:ASN:N	2.36	0.56
34:m:11:LEU:CD1	34:m:40:MET:HE2	2.35	0.56
1:A:158:ARG:HH11	28:z:62:GLN:NE2	2.03	0.56
1:A:199:GLU:HG2	40:1:139:ARG:CD	2.36	0.56
1:A:535:ARG:CB	28:z:108:VAL:HA	2.35	0.56
1:A:623:LYS:HB3	46:A:3000:IHP:P4	2.45	0.56
1:A:852:VAL:O	1:A:852:VAL:HG12	2.05	0.56
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.56
1:A:1499:GLU:CB	40:1:60:ASN:CB	2.80	0.56
1:A:1499:GLU:HA	40:1:63:ILE:HG12	1.88	0.56
1:A:1552:GLN:HG3	1:A:1563:HIS:CD2	2.41	0.56
1:A:1719:PHE:CB	1:A:1720:PRO:CD	2.65	0.56
1:A:1994:LYS:HZ1	27:2:67:VAL:HG22	1.68	0.56
1:A:1997:VAL:CG1	26:Z:658:TYR:CZ	2.89	0.56
2:B:47:A:O2'	2:B:48:A:H5''	2.06	0.56
5:E:307:ARG:HH22	29:b:115:PRO:CB	2.17	0.56
5:E:324:PRO:O	29:b:112:ARG:NH1	2.38	0.56
8:G:171:G:N3	8:G:171:G:C2'	2.68	0.56
9:H:68:G:H2'	9:H:69:U:H6	1.70	0.56
9:H:72:U:H2'	9:H:73:C:H6	1.71	0.56
9:H:77:C:P	24:W:242:HIS:HE1	2.27	0.56
23:V:457:ARG:NH1	40:1:88:GLN:HG2	2.00	0.56
27:2:127:ARG:CB	27:2:131:ARG:HH22	2.11	0.56
34:f:11:LEU:CD1	34:f:40:MET:HE2	2.35	0.56
36:n:10:LYS:HG3	36:n:13:MET:HG3	1.86	0.56
36:n:19:LEU:O	36:n:26:HIS:HD2	1.88	0.56
1:A:1496:PRO:HG2	45:3:338:GLY:N	2.10	0.56
5:E:91:LEU:HD22	5:E:101:ASN:HD21	1.70	0.56
9:H:40:C:H5''	9:H:41:U:OP1	2.05	0.56
9:H:54:U:H2'	9:H:55:U:H6	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:69:U:H2'	9:H:70:C:H6	1.71	0.56
9:H:149:A:H2'	9:H:150:U:H6	1.70	0.56
20:S:66:ASP:CG	20:S:73:GLY:O	2.48	0.56
35:l:20:LEU:HD22	35:l:24:TYR:CZ	2.40	0.56
9:H:77:C:C2	9:H:78:C:C5	2.93	0.56
29:i:52:LYS:HE3	32:j:53:VAL:HG21	1.88	0.56
1:A:153:ARG:HH21	1:A:153:ARG:CG	2.10	0.56
6:F:45:A:H5'	6:F:46:G:OP2	2.05	0.56
9:H:57:A:H2'	9:H:58:U:H6	1.71	0.56
9:H:181:G:H2'	9:H:182:U:H6	1.71	0.56
17:P:16:ARG:HH12	19:R:220:ARG:CA	2.16	0.56
24:W:532:LEU:HD11	24:W:568:THR:HG21	1.87	0.56
1:A:1501:LEU:CD2	45:3:337:ILE:HG21	2.36	0.56
1:A:1595:GLN:HA	1:A:1598:ASP:HB2	1.86	0.56
1:A:1903:GLY:CA	27:2:82:TYR:OH	2.54	0.56
1:A:1934:SER:C	40:1:347:PRO:HG3	2.30	0.56
3:C:196:LYS:HE3	31:a:14:GLU:HB2	1.87	0.56
7:4:-2:C:OP2	28:z:107:LYS:HE3	2.05	0.56
11:J:213:LYS:HZ1	24:W:529:ASN:HA	1.70	0.56
34:m:3:LEU:CG	34:m:4:PRO:CD	2.69	0.56
1:A:537:LYS:CB	6:F:37:C:H41	2.19	0.56
1:A:1328:LEU:HB3	1:A:1368:LEU:HD11	1.88	0.56
5:E:268:ALA:HB2	5:E:272:ARG:HH21	1.69	0.56
8:G:20:A:H2	16:O:187:THR:CB	2.19	0.56
9:H:70:C:C2	9:H:71:C:C5	2.93	0.56
9:H:77:C:H2'	9:H:78:C:H6	1.70	0.56
9:H:88:A:H2'	9:H:89:U:H6	1.70	0.56
29:b:52:LYS:HE3	32:c:53:VAL:HG21	1.88	0.56
36:g:19:LEU:O	36:g:26:HIS:HD2	1.88	0.56
1:A:425:PRO:HD3	2:B:26:A:H5'	1.86	0.56
1:A:1130:ASN:ND2	1:A:1139:ARG:NH1	2.54	0.56
6:F:34:G:H8	6:F:34:G:O5'	1.89	0.56
23:V:496:CYS:SG	40:1:72:TRP:CH2	2.75	0.56
27:2:137:LYS:HZ3	27:2:140:LEU:HB3	1.69	0.56
35:e:20:LEU:HD22	35:e:24:TYR:CZ	2.40	0.56
35:l:14:MET:CE	36:n:10:LYS:CE	2.58	0.56
1:A:1555:LEU:CD2	1:A:1574:ILE:HG13	2.36	0.56
5:E:307:ARG:HH22	29:b:115:PRO:CG	2.18	0.56
9:H:70:C:H2'	9:H:71:C:H6	1.71	0.56
9:H:91:U:H2'	9:H:92:U:H6	1.70	0.56
9:H:141:C:H2'	9:H:142:C:H6	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:152:G:N2	9:H:153:A:C8	2.73	0.56
9:H:183:G:C4	9:H:184:C:C5	2.94	0.56
9:H:183:G:H2'	9:H:184:C:H6	1.71	0.56
23:V:499:GLN:HE21	40:1:72:TRP:CB	2.15	0.56
24:W:70:VAL:HG13	24:W:71:HIS:CD2	2.41	0.56
25:Y:686:GLU:HA	25:Y:716:THR:O	2.05	0.56
40:1:189:ASP:HA	40:1:192:LYS:HB2	1.88	0.56
1:A:293:TRP:CD1	1:A:1136:ARG:NH1	2.74	0.55
1:A:1790:ILE:CB	27:2:76:SER:HB3	2.35	0.55
1:A:1983:LEU:HD23	1:A:1983:LEU:C	2.31	0.55
9:H:69:U:C2	9:H:70:C:C5	2.94	0.55
9:H:71:C:C2	9:H:72:U:C5	2.94	0.55
9:H:72:U:C2	9:H:73:C:C5	2.94	0.55
9:H:147:G:C4	9:H:148:C:C5	2.94	0.55
20:S:54:HIS:CD2	20:S:71:GLY:HA3	2.41	0.55
37:r:127:ALA:HB1	37:s:127:ALA:HB3	1.87	0.55
33:k:50:LYS:HG2	33:k:74:TRP:CB	2.36	0.55
5:E:101:ASN:ND2	29:b:104:PRO:O	2.39	0.55
5:E:101:ASN:HD22	29:b:104:PRO:C	2.13	0.55
9:H:54:U:C2	9:H:55:U:C5	2.94	0.55
9:H:68:G:C4	9:H:69:U:C5	2.94	0.55
9:H:90:A:H2'	9:H:91:U:H6	1.71	0.55
1:A:774:LYS:HD2	9:H:23:A:N7	2.21	0.55
1:A:865:GLY:O	1:A:868:GLU:N	2.38	0.55
1:A:1685:LEU:HD13	40:1:173:TYR:CG	2.41	0.55
3:C:62:ASP:OD1	3:C:62:ASP:N	2.35	0.55
3:C:233:GLU:OE1	3:C:837:GLN:NE2	2.39	0.55
8:G:129:G:C4'	24:W:541:LYS:HE2	2.36	0.55
1:A:1540:PRO:HB3	1:A:1670:ASP:HA	1.88	0.55
1:A:1881:ASN:HD22	40:1:270:ASP:HB3	1.66	0.55
2:B:94:U:H2'	2:B:95:G:H5''	1.89	0.55
6:F:25:C:H4'	6:F:26:U:O5'	2.05	0.55
9:H:73:C:C2	9:H:74:U:C5	2.94	0.55
16:O:45:CYS:SG	16:O:48:CYS:N	2.76	0.55
29:b:56:SER:HB2	29:b:59:ALA:O	2.07	0.55
33:d:94:ARG:HE	33:d:96:ILE:HD11	1.72	0.55
40:1:34:ARG:HH11	40:1:34:ARG:HA	1.70	0.55
1:A:377:GLU:O	3:C:342:ARG:NH2	2.38	0.55
1:A:525:LYS:HG2	28:z:103:TYR:HA	1.87	0.55
6:F:41:A:N1	8:G:6:A:C2	2.75	0.55
9:H:83:A:C4	9:H:84:C:C5	2.95	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:34:ILE:HB	19:R:197:ILE:HG12	1.89	0.55
20:S:84:ASP:OD1	20:S:108:ASN:ND2	2.38	0.55
28:z:80:LYS:HA	28:z:88:ARG:HH22	1.72	0.55
33:d:50:LYS:HG2	33:d:74:TRP:CB	2.36	0.55
33:k:94:ARG:HE	33:k:96:ILE:HD11	1.72	0.55
1:A:537:LYS:CD	6:F:37:C:H41	2.17	0.55
1:A:1787:ARG:HG2	27:2:74:ALA:CB	2.37	0.55
9:H:59:A:C4	9:H:60:U:C5	2.95	0.55
11:J:222:ASP:O	11:J:226:ARG:NH1	2.39	0.55
11:J:502:GLU:O	11:J:506:GLU:N	2.39	0.55
38:o:14:GLN:HG2	38:o:22:ARG:NH2	2.21	0.55
1:A:152:ARG:NH2	40:1:132:ASP:O	2.40	0.55
1:A:603:ARG:NH2	7:4:-6:C:O2	2.38	0.55
1:A:762:ARG:HH22	17:P:226:LYS:HZ3	1.55	0.55
1:A:861:ARG:CB	1:A:861:ARG:CZ	2.84	0.55
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.40	0.55
1:A:1482:GLU:HB2	40:1:85:GLN:O	2.07	0.55
1:A:1596:VAL:CG2	40:1:278:LEU:CD1	2.85	0.55
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.55
6:F:45:A:N3	6:F:73:A:C1'	2.68	0.55
8:G:167:G:C8	8:G:167:G:C5'	2.87	0.55
12:K:193:TYR:O	12:K:197:ARG:N	2.35	0.55
13:L:124:LYS:N	13:L:125:PRO:HD2	2.21	0.55
23:V:450:ILE:CB	40:1:89:PRO:HG2	2.36	0.55
1:A:1719:PHE:CG	1:A:1720:PRO:HD2	2.41	0.55
6:F:81:C:H4'	6:F:82:A:OP2	2.07	0.55
19:R:97:LYS:NZ	20:S:146:GLU:OE1	2.40	0.55
27:2:25:LYS:HA	27:2:25:LYS:HE2	1.89	0.55
1:A:36:LYS:NZ	24:W:163:GLN:O	2.40	0.55
1:A:470:ARG:HG2	1:A:470:ARG:NH2	2.20	0.55
1:A:981:PHE:CZ	1:A:1095:ILE:HD11	2.41	0.55
1:A:1553:VAL:O	1:A:1553:VAL:HG22	2.07	0.55
1:A:1685:LEU:HD21	40:1:173:TYR:OH	1.96	0.55
1:A:1798:LEU:HD13	8:G:142:U:O2'	2.06	0.55
3:C:561:LYS:NZ	3:C:614:TYR:O	2.40	0.55
9:H:59:A:H2'	9:H:60:U:H6	1.71	0.55
9:H:91:U:C2	9:H:92:U:C5	2.95	0.55
21:T:188:PRO:HG3	21:T:443:THR:CB	2.34	0.55
21:T:354:ILE:HB	21:T:368:LEU:HB2	1.89	0.55
27:2:120:ALA:HB2	36:n:55:ASN:OD1	2.06	0.55
34:f:70:LEU:HD23	34:f:70:LEU:C	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:776:LEU:HD12	1:A:776:LEU:O	2.07	0.55
1:A:1552:GLN:CG	1:A:1563:HIS:HD2	2.20	0.55
1:A:1838:LYS:HG2	1:A:1871:PRO:HG2	1.88	0.55
1:A:1934:SER:HB3	40:1:347:PRO:CB	2.36	0.55
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.88	0.55
8:G:22:C:O2'	8:G:23:U:P	2.66	0.55
9:H:57:A:C4	9:H:58:U:C5	2.95	0.55
9:H:150:U:H2'	9:H:151:C:H6	1.71	0.55
27:2:51:LYS:HZ2	35:l:28:ARG:CD	2.18	0.55
1:A:1883:VAL:HG22	40:1:290:ARG:C	2.31	0.54
6:F:34:G:H8	6:F:34:G:H5''	1.70	0.54
9:H:105:G:C6	32:j:20:LYS:HD3	2.42	0.54
9:H:150:U:C2	9:H:151:C:C5	2.94	0.54
24:W:71:HIS:H	24:W:87:THR:HG22	1.72	0.54
34:m:70:LEU:HD23	34:m:70:LEU:C	2.31	0.54
1:A:461:HIS:NE2	2:B:26:A:N6	2.55	0.54
1:A:1275:ARG:NH2	1:A:1464:LEU:O	2.39	0.54
1:A:1555:LEU:HD21	1:A:1574:ILE:CG1	2.37	0.54
1:A:1596:VAL:HG22	40:1:278:LEU:CD1	2.34	0.54
6:F:22:A:C2	15:N:126:LEU:CD2	2.90	0.54
21:T:210:ILE:HG12	21:T:221:THR:HG22	1.89	0.54
29:i:56:SER:HB2	29:i:59:ALA:O	2.07	0.54
1:A:105:ASN:HD22	1:A:129:VAL:CG1	2.20	0.54
1:A:579:GLN:HG3	1:A:629:PHE:H	1.73	0.54
1:A:939:TRP:NE1	1:A:1049:ASP:OD2	2.39	0.54
1:A:1479:GLY:C	40:1:88:GLN:NE2	2.66	0.54
9:H:90:A:C4	9:H:91:U:C5	2.95	0.54
11:J:201:ARG:HG2	11:J:201:ARG:NH2	2.21	0.54
1:A:453:TYR:O	1:A:457:ASN:ND2	2.40	0.54
1:A:714:SER:O	1:A:718:ARG:NH1	2.40	0.54
1:A:1533:ARG:HG3	1:A:1751:LEU:HA	1.90	0.54
6:F:88:G:H5'	14:M:133:ARG:NH1	2.23	0.54
9:H:149:A:C4	9:H:150:U:C5	2.95	0.54
10:I:704:TRP:CH2	10:I:727:ARG:CG	2.90	0.54
10:I:722:GLU:C	10:I:726:ILE:CG2	2.59	0.54
21:T:353:THR:HG22	21:T:369:THR:HG22	1.90	0.54
27:2:25:LYS:CE	27:2:25:LYS:CA	2.86	0.54
1:A:156:ARG:HH22	40:1:134:PHE:HB2	1.71	0.54
1:A:1252:GLY:HA3	8:G:169:U:O4	2.06	0.54
1:A:1787:ARG:NH2	1:A:1804:ASN:O	2.41	0.54
1:A:1827:TRP:HZ3	1:A:1836:LEU:HB3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:17:U:O2	16:O:198:ILE:HD11	2.07	0.54
9:H:83:A:H2'	9:H:84:C:H6	1.71	0.54
9:H:88:A:C4	9:H:89:U:C5	2.95	0.54
10:I:624:GLU:O	10:I:628:GLN:N	2.41	0.54
24:W:326:ARG:NH1	24:W:363:THR:O	2.40	0.54
26:Z:739:GLN:NE2	26:Z:746:GLN:OE1	2.40	0.54
34:f:8:LYS:HB3	34:f:9:PRO:HD3	1.88	0.54
6:F:28:A:HO2'	15:N:39:GLY:C	2.16	0.54
9:H:181:G:C4	9:H:182:U:C5	2.95	0.54
10:I:273:GLU:C	18:Q:357:ALA:CB	2.80	0.54
10:I:704:TRP:CE3	10:I:727:ARG:CG	2.83	0.54
11:J:181:ASN:HB3	26:Z:691:THR:HG22	1.90	0.54
13:L:782:LYS:O	13:L:786:HIS:N	2.39	0.54
24:W:341:ASN:ND2	24:W:345:THR:OG1	2.37	0.54
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.89	0.54
1:A:108:MET:HB3	1:A:109:PRO:HD2	1.90	0.54
1:A:1560:ILE:HG12	1:A:1668:TRP:HB2	1.90	0.54
1:A:2004:GLN:HE22	40:1:335:TYR:CB	1.91	0.54
5:E:155:ASN:ND2	5:E:172:ASP:OD1	2.40	0.54
8:G:21:A:O2'	8:G:22:C:C5'	2.55	0.54
9:H:10:C:H41	14:M:198:ARG:HH12	1.54	0.54
10:I:723:MET:O	10:I:727:ARG:HB2	2.07	0.54
10:I:727:ARG:HB3	10:I:727:ARG:NH2	2.21	0.54
15:N:2:PRO:HG2	15:N:4:VAL:HA	1.90	0.54
1:A:425:PRO:CD	2:B:26:A:H5'	2.38	0.54
1:A:1499:GLU:CA	40:1:63:ILE:HG12	2.38	0.54
2:B:16:U:OP1	19:R:170:LYS:HE3	2.08	0.54
24:W:73:ASP:CG	24:W:74:PRO:CD	2.69	0.54
25:Y:402:ILE:O	25:Y:406:ILE:HD12	2.07	0.54
37:q:106:ALA:HB1	37:t:106:ALA:HB3	1.89	0.54
1:A:526:PRO:HD2	28:z:104:ASP:C	2.32	0.54
1:A:955:TRP:HE1	1:A:976:MET:HE1	1.73	0.54
1:A:1144:LYS:O	1:A:1148:ASN:ND2	2.41	0.54
1:A:1390:ALA:HB2	25:Y:410:VAL:CG1	2.38	0.54
5:E:62:LEU:HD23	29:b:107:GLY:HA2	1.88	0.54
33:d:88:LYS:HG3	33:d:89:PRO:HD2	1.89	0.54
1:A:176:LEU:HB3	1:A:181:ASN:HD22	1.73	0.54
5:E:128:SER:OG	5:E:129:THR:N	2.41	0.54
8:G:5:G:H2'	8:G:6:A:C8	2.43	0.54
10:I:723:MET:N	10:I:726:ILE:CG2	2.68	0.54
13:L:264:LYS:O	13:L:268:LYS:N	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:310:ARG:NE	19:R:310:ARG:CA	2.71	0.54
20:S:70:THR:HG22	24:W:73:ASP:HA	1.90	0.54
24:W:443:ARG:NH1	24:W:452:ASP:OD2	2.41	0.54
1:A:1481:VAL:HG21	40:1:67:ILE:CG2	2.35	0.53
1:A:1495:PHE:HE1	1:A:1755:SER:OG	1.91	0.53
1:A:1991:TYR:C	1:A:1991:TYR:CD2	2.83	0.53
3:C:259:LYS:HG2	47:C:1500:GTP:C6	2.43	0.53
3:C:704:VAL:HG23	3:C:705:VAL:HG13	1.89	0.53
6:F:80:G:H5''	6:F:81:C:P	2.48	0.53
8:G:129:G:H5'	24:W:541:LYS:NZ	2.18	0.53
9:H:40:C:C5'	9:H:41:U:OP1	2.56	0.53
34:m:3:LEU:O	34:m:5:LEU:N	2.41	0.53
1:A:156:ARG:NH2	40:1:134:PHE:CB	2.71	0.53
8:G:147:C:N1	8:G:148:U:C5	2.77	0.53
22:U:77:MET:O	22:U:81:GLY:N	2.40	0.53
24:W:103:GLN:O	24:W:108:ARG:NH2	2.39	0.53
24:W:465:PRO:HG2	24:W:481:MET:HE3	1.89	0.53
27:2:29:GLU:OE1	27:2:29:GLU:HA	2.07	0.53
27:2:30:GLU:O	27:2:34:LYS:HD2	2.08	0.53
27:2:113:LEU:HD13	27:2:113:LEU:O	2.09	0.53
1:A:1632:PHE:HE1	1:A:1659:LYS:HG2	1.73	0.53
1:A:1881:ASN:HD21	40:1:270:ASP:HB3	1.73	0.53
3:C:343:LEU:HD13	3:C:373:ILE:HD11	1.91	0.53
9:H:153:A:C3'	9:H:154:C:C5'	2.86	0.53
10:I:273:GLU:O	18:Q:357:ALA:HB3	2.07	0.53
24:W:453:PHE:HA	27:2:79:PHE:HE2	1.72	0.53
1:A:188:LEU:HD22	1:A:567:GLY:HA2	1.88	0.53
1:A:1322:LEU:HD21	40:1:67:ILE:HD11	1.90	0.53
1:A:1884:ILE:O	40:1:289:THR:HG22	2.08	0.53
1:A:1983:LEU:HD23	1:A:1983:LEU:O	2.08	0.53
3:C:137:HIS:HB2	3:C:239:THR:HG23	1.91	0.53
20:S:126:HIS:CD2	20:S:126:HIS:N	2.76	0.53
27:2:111:LYS:CA	27:2:114:GLU:HG2	2.36	0.53
1:A:1552:GLN:HB2	1:A:1563:HIS:HD2	1.74	0.53
1:A:2011:ILE:HG22	1:A:2012:LEU:HD23	1.88	0.53
5:E:133:VAL:HG21	5:E:169:THR:HG21	1.90	0.53
9:H:39:U:C2'	9:H:40:C:C6	2.92	0.53
10:I:310:LYS:O	10:I:311:MET:C	2.51	0.53
10:I:721:LYS:CE	13:L:65:ARG:NH2	2.70	0.53
21:T:185:MET:N	21:T:186:PRO:CD	2.71	0.53
24:W:449:ILE:HG22	24:W:451:VAL:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:z:91:ASP:OD1	28:z:94:ARG:NH2	2.41	0.53
31:a:74:PRO:CA	31:a:77:LEU:HD11	2.37	0.53
1:A:526:PRO:CD	28:z:104:ASP:C	2.81	0.53
9:H:15:U:H2'	9:H:16:U:OP2	2.08	0.53
13:L:569:GLN:HA	37:q:114:CYS:O	2.07	0.53
16:O:81:CYS:HB3	16:O:84:CYS:HB2	1.90	0.53
17:P:13:ARG:HG3	17:P:13:ARG:HH11	1.72	0.53
27:2:24:PRO:HA	27:2:29:GLU:HB2	1.91	0.53
32:j:68:PHE:HB2	33:k:100:PHE:HB3	1.91	0.53
1:A:158:ARG:HH11	28:z:62:GLN:CD	2.16	0.53
1:A:762:ARG:NH2	17:P:227:TYR:OH	2.42	0.53
1:A:1087:LEU:HB2	1:A:1098:PHE:HB3	1.89	0.53
1:A:1491:LYS:HD2	1:A:1709:TYR:CD1	2.37	0.53
1:A:1664:ILE:HD13	1:A:1703:ILE:HB	1.90	0.53
1:A:1803:ILE:CG2	24:W:451:VAL:CG2	2.87	0.53
20:S:70:THR:HA	24:W:73:ASP:OD1	2.09	0.53
1:A:1258:LYS:HE2	8:G:173:G:C3'	2.38	0.53
1:A:1592:ASP:O	1:A:1596:VAL:N	2.39	0.53
1:A:1976:TRP:O	1:A:1980:GLU:N	2.30	0.53
8:G:142:U:O2'	8:G:143:U:C5'	2.49	0.53
8:G:177:G:C2'	8:G:177:G:N3	2.72	0.53
21:T:270:VAL:HG21	21:T:305:THR:HG21	1.89	0.53
36:n:17:LEU:HD23	36:n:72:ALA:HA	1.91	0.53
1:A:974:ASN:HD22	1:A:1178:TYR:HD2	1.57	0.53
3:C:677:GLU:OE1	3:C:681:LYS:NZ	2.38	0.53
5:E:243:LEU:HD23	5:E:250:LEU:HD12	1.91	0.53
6:F:58:G:O2'	6:F:59:G:P	2.66	0.53
9:H:39:U:C4	9:H:40:C:N4	2.77	0.53
9:H:153:A:H3'	9:H:154:C:C5'	2.38	0.53
11:J:497:TYR:HA	11:J:537:TRP:N	2.24	0.53
24:W:209:SER:O	24:W:213:GLN:N	2.41	0.53
1:A:199:GLU:CG	40:1:139:ARG:HD3	2.35	0.53
1:A:1130:ASN:ND2	1:A:1139:ARG:HH11	2.07	0.53
1:A:1958:LYS:CG	27:2:96:MET:O	2.57	0.53
3:C:757:ALA:O	3:C:761:SER:OG	2.26	0.53
6:F:42:C:H2'	6:F:43:A:C1'	2.39	0.53
9:H:154:C:OP2	39:p:19:LYS:CD	2.56	0.53
9:H:154:C:OP2	39:p:19:LYS:HD3	2.09	0.53
9:H:177:A:C8	27:2:134:LEU:HD13	2.43	0.53
10:I:727:ARG:CG	10:I:727:ARG:NH2	2.70	0.53
19:R:60:ASP:N	19:R:60:ASP:OD1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:125:LYS:C	20:S:126:HIS:CD2	2.87	0.53
6:F:40:U:H2'	6:F:41:A:C8	2.44	0.52
1:A:1703:ILE:HG21	1:A:1730:MET:HE2	1.91	0.52
10:I:84:HIS:O	10:I:85:ARG:C	2.51	0.52
20:S:72:ARG:CG	24:W:71:HIS:ND1	2.72	0.52
40:1:122:ASN:ND2	40:1:133:CYS:SG	2.71	0.52
1:A:158:ARG:HH12	28:z:62:GLN:HG2	1.73	0.52
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.41	0.52
1:A:1994:LYS:CD	26:Z:756:TYR:HD1	2.22	0.52
6:F:26:U:O2'	6:F:27:A:P	2.67	0.52
10:I:592:ALA:HB3	10:I:623:VAL:HG12	1.91	0.52
27:2:123:GLN:O	27:2:127:ARG:NH1	2.42	0.52
1:A:94:TYR:HB2	19:R:207:MET:HE1	1.91	0.52
1:A:300:ASN:HB3	3:C:939:ARG:HH12	1.74	0.52
1:A:526:PRO:HD3	28:z:105:ILE:N	2.24	0.52
1:A:623:LYS:O	46:A:3000:IHP:O24	2.26	0.52
1:A:1593:LEU:HA	1:A:1596:VAL:HB	1.91	0.52
5:E:171:SER:OG	5:E:173:ASP:OD1	2.26	0.52
6:F:58:G:H2'	6:F:59:G:C8	2.44	0.52
9:H:39:U:H3'	9:H:40:C:H5	1.72	0.52
19:R:315:LYS:NZ	19:R:315:LYS:CA	2.73	0.52
23:V:584:LYS:HG3	23:V:634:ILE:HG12	1.91	0.52
9:H:164:C:H5'	9:H:164:C:C6	2.44	0.52
10:I:696:ASP:OD1	10:I:697:PRO:HD2	2.09	0.52
19:R:303:GLU:OE1	19:R:303:GLU:HA	2.08	0.52
27:2:52:MET:HB2	35:l:28:ARG:HH22	1.71	0.52
40:1:34:ARG:CG	40:1:34:ARG:NH1	2.73	0.52
1:A:1903:GLY:HA3	27:2:82:TYR:OH	2.10	0.52
2:B:27:U:O2'	2:B:28:A:O5'	2.25	0.52
3:C:938:ARG:O	3:C:942:GLY:N	2.42	0.52
8:G:20:A:H2	16:O:187:THR:CG2	2.21	0.52
9:H:33:G:H3'	9:H:33:G:OP2	2.10	0.52
10:I:309:ALA:O	10:I:310:LYS:C	2.52	0.52
27:2:90:TYR:O	27:2:94:ASP:N	2.42	0.52
32:c:68:PHE:HB2	33:d:100:PHE:HB3	1.90	0.52
35:l:14:MET:HE1	36:n:10:LYS:HD2	1.92	0.52
40:1:46:GLY:CA	45:3:331:ILE:CG2	2.79	0.52
40:1:282:SER:OG	40:1:283:ALA:N	2.42	0.52
1:A:1481:VAL:HG23	40:1:85:GLN:HE21	1.65	0.52
1:A:1890:GLN:HB3	27:2:70:SER:HG	1.70	0.52
6:F:79:C:O2	17:P:3:THR:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:20:A:O2'	16:O:193:LEU:CD2	2.50	0.52
8:G:128:U:O2'	8:G:129:G:OP2	2.24	0.52
13:L:7:LYS:CB	13:L:40:ARG:HA	2.39	0.52
20:S:15:TYR:HB3	20:S:163:TYR:HB2	1.91	0.52
1:A:527:VAL:O	28:z:102:HIS:CD2	2.62	0.52
1:A:863:GLU:C	1:A:863:GLU:CD	2.78	0.52
1:A:1471:ARG:CG	40:1:66:TYR:CD2	2.92	0.52
1:A:1723:LYS:N	1:A:1724:PRO:CD	2.73	0.52
8:G:21:A:HO2'	8:G:22:C:P	2.32	0.52
10:I:681:ILE:HD11	10:I:714:HIS:ND1	2.25	0.52
21:T:185:MET:N	21:T:186:PRO:HD2	2.25	0.52
21:T:294:LEU:HD12	21:T:303:LEU:HD11	1.92	0.52
24:W:243:VAL:HG13	24:W:245:GLU:H	1.74	0.52
35:l:87:LEU:HB2	36:n:61:VAL:HB	1.92	0.52
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.43	0.52
1:A:1354:ARG:HG3	22:U:19:VAL:HG22	1.92	0.52
2:B:18:C:C2'	2:B:19:A:O5'	2.58	0.52
3:C:207:GLY:O	3:C:238:ASN:ND2	2.42	0.52
6:F:5:U:H5'	6:F:6:C:OP2	2.10	0.52
19:R:315:LYS:NZ	19:R:315:LYS:CB	2.72	0.52
24:W:305:LEU:HD21	24:W:313:ILE:HG23	1.92	0.52
35:e:87:LEU:HB2	36:g:61:VAL:HB	1.92	0.52
36:g:17:LEU:HD23	36:g:72:ALA:HA	1.91	0.52
1:A:1938:LEU:HD22	1:A:1983:LEU:HD22	1.92	0.52
1:A:2011:ILE:N	1:A:2011:ILE:CD1	2.72	0.52
2:B:22:U:O2	2:B:22:U:H2'	2.09	0.52
2:B:89:U:O2'	31:a:64:ARG:NH2	2.43	0.52
6:F:88:G:H5'	14:M:133:ARG:CZ	2.40	0.52
8:G:147:C:C6	8:G:148:U:H5	2.28	0.52
9:H:147:G:H2'	9:H:148:C:C6	2.43	0.52
14:M:236:ASN:ND2	14:M:242:ALA:O	2.43	0.52
17:P:10:GLU:HG2	17:P:10:GLU:O	2.09	0.52
23:V:620:ASN:HB3	23:V:623:ASN:HB2	1.92	0.52
27:2:27:ALA:HA	27:2:30:GLU:CG	2.40	0.52
40:1:46:GLY:HA2	45:3:331:ILE:HG22	1.85	0.52
1:A:776:LEU:HD22	1:A:900:ASP:HB2	1.92	0.51
1:A:1501:LEU:HD13	1:A:1753:LEU:HD11	1.91	0.51
1:A:1983:LEU:CD2	1:A:1983:LEU:C	2.83	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:114:TYR:CE2	31:a:78:LYS:HB2	2.45	0.51
6:F:77:C:C2'	6:F:78:A:H5'	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:512:ASP:OD2	11:J:427:LYS:HE2	2.10	0.51
17:P:66:ARG:O	17:P:69:ALA:N	2.43	0.51
23:V:590:LEU:HD22	23:V:599:LEU:HD13	1.90	0.51
33:d:85:LYS:HG2	33:d:85:LYS:O	2.09	0.51
1:A:525:LYS:CG	28:z:103:TYR:HA	2.41	0.51
1:A:620:PRO:HD2	40:1:134:PHE:CE2	2.46	0.51
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.92	0.51
5:E:93:TRP:CZ3	29:b:105:GLY:C	2.87	0.51
6:F:43:A:C6	6:F:44:G:O6	2.64	0.51
23:V:549:LYS:O	23:V:553:HIS:ND1	2.44	0.51
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.42	0.51
8:G:136:U:OP2	8:G:136:U:C6	2.62	0.51
9:H:14:C:N4	14:M:224:ARG:HD2	2.24	0.51
13:L:222:LEU:HD12	19:R:84:ASN:HB3	1.93	0.51
18:Q:809:ALA:HB2	18:Q:1131:VAL:CB	2.40	0.51
20:S:25:LEU:HD23	20:S:98:LEU:HD22	1.93	0.51
23:V:460:TYR:CD1	40:1:72:TRP:CZ2	2.98	0.51
1:A:312:TYR:OH	3:C:886:ASP:OD2	2.27	0.51
1:A:934:ARG:HH12	25:Y:425:ILE:CG2	2.23	0.51
1:A:977:LEU:HD23	1:A:1097:ILE:HD12	1.92	0.51
1:A:1070:ASP:OD1	1:A:1073:SER:OG	2.24	0.51
10:I:731:GLN:NE2	10:I:731:GLN:CA	2.71	0.51
21:T:418:THR:HG21	21:T:468:CYS:H	1.75	0.51
31:h:55:VAL:HG21	38:o:67:LYS:NZ	2.25	0.51
34:m:5:LEU:HB3	35:l:48:ILE:CG2	2.40	0.51
38:o:5:THR:CG2	38:o:8:LEU:H	2.23	0.51
38:o:102:GLU:HG2	38:o:128:LYS:HZ1	1.76	0.51
1:A:1321:GLU:HG3	40:1:66:TYR:HE1	1.76	0.51
1:A:1592:ASP:OD1	40:1:275:LEU:HD21	2.11	0.51
12:K:36:VAL:O	37:r:112:ALA:CB	2.55	0.51
1:A:461:HIS:CD2	2:B:26:A:N6	2.78	0.51
9:H:152:G:OP2	27:2:131:ARG:NH2	2.42	0.51
10:I:83:LYS:O	10:I:84:HIS:C	2.51	0.51
12:K:15:ALA:CB	37:s:112:ALA:C	2.82	0.51
1:A:1479:GLY:HA2	40:1:88:GLN:NE2	2.25	0.51
8:G:147:C:C2'	8:G:148:U:C6	2.77	0.51
12:K:90:PRO:CB	12:K:109:ASN:C	2.83	0.51
23:V:570:LEU:HD13	23:V:611:PHE:HA	1.93	0.51
37:q:106:ALA:CB	37:t:106:ALA:CB	2.87	0.51
1:A:888:GLN:O	1:A:889:ARG:NH1	2.39	0.51
1:A:1134:TRP:HB3	1:A:1138:ALA:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1589:ILE:HG23	1:A:1730:MET:HE1	1.87	0.51
3:C:476:CYS:SG	3:C:477:HIS:N	2.83	0.51
6:F:28:A:O2'	15:N:39:GLY:C	2.53	0.51
8:G:177:G:N3	8:G:177:G:H2'	2.22	0.51
40:1:267:ILE:HD13	40:1:267:ILE:N	2.25	0.51
1:A:1688:THR:HB	40:1:178:HIS:NE2	2.26	0.51
3:C:136:GLY:O	3:C:142:LYS:NZ	2.38	0.51
23:V:457:ARG:HH12	40:1:88:GLN:CD	2.19	0.51
24:W:446:GLU:OE2	27:2:83:ARG:HD2	2.11	0.51
24:W:453:PHE:CB	27:2:79:PHE:HE2	2.23	0.51
33:k:41:GLN:H	33:k:115:ILE:HB	1.76	0.51
1:A:152:ARG:NH1	40:1:133:CYS:C	2.69	0.51
1:A:641:MET:HA	1:A:644:ILE:HG22	1.93	0.51
1:A:1312:PRO:HG2	1:A:1314:VAL:HG12	1.93	0.51
1:A:1528:GLN:HB2	1:A:1531:ASN:HD22	1.74	0.51
2:B:94:U:H5	33:d:104:ASP:O	1.94	0.51
10:I:727:ARG:HH21	10:I:727:ARG:C	2.18	0.51
16:O:235:TYR:HB3	16:O:301:LYS:HB2	1.93	0.51
17:P:16:ARG:NH1	19:R:220:ARG:CA	2.72	0.51
23:V:535:THR:HA	23:V:538:ARG:HB2	1.92	0.51
28:z:58:ARG:HH21	40:1:180:LYS:HE2	1.76	0.51
45:3:329:LYS:HE3	45:3:342:GLU:HG3	1.93	0.51
1:A:864:LEU:C	1:A:864:LEU:CD2	2.84	0.50
1:A:1090:ARG:HG3	1:A:1090:ARG:O	2.11	0.50
1:A:1739:ALA:HA	1:A:1742:VAL:CG2	2.41	0.50
5:E:124:LEU:HB3	5:E:136:TRP:HB2	1.94	0.50
16:O:50:ARG:NH1	16:O:122:GLU:OE1	2.44	0.50
17:P:38:HIS:HB3	21:T:282:ARG:HH21	1.75	0.50
1:A:861:ARG:NH1	1:A:861:ARG:CB	2.71	0.50
1:A:1740:LEU:C	1:A:1742:VAL:N	2.68	0.50
9:H:100:U:O2'	31:h:64:ARG:NH2	2.43	0.50
25:Y:413:LYS:H	25:Y:413:LYS:CD	2.18	0.50
34:m:5:LEU:O	35:l:49:GLY:HA3	2.10	0.50
1:A:766:THR:HG1	2:B:39:C:N4	2.09	0.50
1:A:1585:ILE:HD13	1:A:1740:LEU:CD2	2.40	0.50
1:A:1818:PHE:HB3	1:A:1914:MET:HE1	1.93	0.50
1:A:1994:LYS:HD2	26:Z:756:TYR:HD1	1.76	0.50
3:C:300:LEU:HA	3:C:306:ASN:HD22	1.76	0.50
6:F:50:A:O2'	6:F:51:U:P	2.69	0.50
8:G:7:G:H2'	8:G:8:C:C6	2.46	0.50
8:G:145:U:H2'	8:G:146:C:C6	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:51:ARG:NH2	24:W:192:PHE:O	2.45	0.50
20:S:55:ARG:HH21	20:S:57:ILE:HD11	1.77	0.50
28:z:107:LYS:O	28:z:110:TRP:HB3	2.11	0.50
29:b:50:LYS:HG2	29:b:51:ILE:HG13	1.93	0.50
40:1:34:ARG:HA	40:1:34:ARG:NH1	2.27	0.50
40:1:185:TYR:O	40:1:188:VAL:N	2.45	0.50
41:v:53:HIS:CB	42:w:149:CYS:O	2.58	0.50
1:A:92:LEU:HG	1:A:652:LEU:HD13	1.93	0.50
1:A:266:SER:OG	1:A:271:MET:O	2.28	0.50
1:A:618:THR:HG21	40:1:132:ASP:OD2	2.12	0.50
1:A:1700:GLY:H	1:A:1717:ASN:HB2	1.77	0.50
5:E:93:TRP:CZ3	29:b:105:GLY:HA3	2.46	0.50
6:F:22:A:N7	24:W:130:ARG:CD	2.72	0.50
6:F:41:A:C2	8:G:6:A:H2	2.16	0.50
6:F:45:A:C6	8:G:2:U:O2	2.61	0.50
6:F:85:U:C3'	6:F:86:U:C5'	2.90	0.50
8:G:20:A:C2	16:O:187:THR:CG2	2.94	0.50
9:H:111:G:O3'	9:H:112:G:O4'	2.29	0.50
12:K:18:TYR:CB	12:K:171:GLN:CB	2.90	0.50
25:Y:405:MET:HE1	25:Y:410:VAL:HG11	1.93	0.50
1:A:159:ARG:HG2	40:1:104:ARG:CB	2.39	0.50
1:A:705:LYS:HG2	9:H:15:U:C4	2.46	0.50
1:A:1955:LYS:HZ1	27:2:93:GLN:CD	2.18	0.50
1:A:2008:ARG:HB2	40:1:342:HIS:CE1	2.46	0.50
9:H:33:G:O2'	9:H:34:U:O4'	2.23	0.50
9:H:107:A:C6	9:H:108:G:C5	2.98	0.50
21:T:289:SER:OG	21:T:308:ARG:NH2	2.44	0.50
21:T:347:THR:HG21	21:T:357:TRP:HE1	1.76	0.50
24:W:70:VAL:HG22	24:W:71:HIS:HD2	1.74	0.50
1:A:139:VAL:O	1:A:143:GLN:N	2.40	0.50
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.45	0.50
1:A:1878:ASP:HB2	1:A:1879:PHE:CD2	2.46	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
3:C:210:ASN:HB3	3:C:636:TYR:HB2	1.93	0.50
3:C:607:LEU:O	3:C:611:ASN:ND2	2.45	0.50
8:G:21:A:OP2	16:O:193:LEU:CG	2.58	0.50
10:I:511:LEU:HD12	10:I:543:ARG:HD2	1.92	0.50
34:f:20:MET:HE2	34:f:30:LYS:HB2	1.94	0.50
40:1:266:ARG:C	40:1:268:ARG:N	2.68	0.50
1:A:658:ARG:HD3	6:F:67:G:OP1	2.12	0.50
1:A:880:ARG:C	1:A:883:ARG:HB2	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:700:ILE:O	3:C:740:THR:OG1	2.28	0.50
35:l:15:VAL:O	36:n:33:GLY:HA3	2.12	0.50
1:A:1475:ILE:HD12	40:1:66:TYR:CD2	2.46	0.50
1:A:1476:GLN:NE2	40:1:85:GLN:OE1	2.44	0.50
1:A:1958:LYS:CE	27:2:97:ASP:HA	2.41	0.50
3:C:183:SER:OG	3:C:480:LYS:NZ	2.44	0.50
6:F:22:A:C5	24:W:130:ARG:HD3	2.46	0.50
6:F:43:A:N6	6:F:44:G:O6	2.44	0.50
6:F:45:A:H1'	6:F:73:A:C2	2.47	0.50
11:J:440:LEU:HG	11:J:445:LYS:HD2	1.93	0.50
13:L:145:ASP:OD1	13:L:145:ASP:N	2.40	0.50
16:O:116:TYR:O	16:O:120:ASN:ND2	2.45	0.50
1:A:1991:TYR:OH	1:A:1995:ASN:HB3	2.12	0.50
1:A:1997:VAL:CG1	26:Z:658:TYR:CE1	2.95	0.50
8:G:8:C:H2'	8:G:9:C:C6	2.46	0.50
8:G:168:C:H3'	8:G:168:C:OP2	2.12	0.50
10:I:265:TYR:CA	10:I:274:LYS:CB	2.80	0.50
10:I:311:MET:O	10:I:312:GLU:C	2.51	0.50
19:R:319:LYS:HG3	19:R:320:HIS:ND1	2.27	0.50
24:W:392:VAL:HG12	24:W:424:ILE:HD13	1.92	0.50
24:W:445:TRP:HE1	24:W:452:ASP:HB3	1.77	0.50
28:z:111:THR:O	28:z:112:LYS:OXT	2.30	0.50
40:1:31:GLU:O	40:1:34:ARG:HG3	2.12	0.50
1:A:148:TRP:CD1	1:A:152:ARG:HD2	2.47	0.49
1:A:1386:TRP:CB	25:Y:410:VAL:CG2	2.80	0.49
1:A:1479:GLY:HA2	40:1:88:GLN:HE22	1.77	0.49
1:A:1561:PHE:O	1:A:1561:PHE:HD2	1.95	0.49
1:A:1903:GLY:HA3	27:2:82:TYR:CE1	2.47	0.49
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.49
2:B:23:C:O2'	2:B:24:G:H3'	2.11	0.49
8:G:147:C:N1	8:G:148:U:H5	2.10	0.49
9:H:106:G:H5'	34:m:25:TRP:HH2	1.76	0.49
24:W:73:ASP:HB3	24:W:74:PRO:HD2	1.81	0.49
24:W:527:ASP:OD1	24:W:531:LYS:N	2.44	0.49
27:2:111:LYS:HA	27:2:114:GLU:CG	2.39	0.49
27:2:123:GLN:HB3	27:2:127:ARG:HH12	1.77	0.49
31:a:74:PRO:O	31:a:77:LEU:HD12	2.12	0.49
34:f:51:ILE:HG22	34:f:56:SER:HB2	1.93	0.49
1:A:435:CYS:HB3	7:4:-11:G:N2	2.27	0.49
1:A:855:ARG:NH2	9:H:29:A:H5''	2.27	0.49
1:A:880:ARG:HG3	1:A:884:HIS:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1719:PHE:CD2	1:A:1720:PRO:CD	2.95	0.49
5:E:107:GLY:O	5:E:143:ARG:NH1	2.45	0.49
5:E:253:ASN:HD21	5:E:302:ALA:HB1	1.76	0.49
5:E:340:PRO:HB2	5:E:356:ILE:HB	1.93	0.49
8:G:21:A:OP2	16:O:193:LEU:CD1	2.60	0.49
26:Z:694:TYR:HA	26:Z:709:ARG:O	2.12	0.49
27:2:111:LYS:HA	27:2:114:GLU:OE2	2.13	0.49
35:e:20:LEU:HD13	36:g:61:VAL:CG2	2.43	0.49
31:h:75:ASP:O	31:h:78:LYS:HG2	2.12	0.49
29:i:50:LYS:HG2	29:i:51:ILE:HG13	1.93	0.49
1:A:409:ARG:NH1	2:B:25:C:C6	2.81	0.49
1:A:467:GLN:CG	2:B:19:A:C5	2.95	0.49
1:A:790:ARG:NH1	1:A:986:GLU:O	2.44	0.49
1:A:1599:GLN:NE2	40:1:271:ILE:CD1	2.75	0.49
1:A:1880:PRO:C	1:A:1882:ILE:N	2.70	0.49
1:A:1980:GLU:OE2	40:1:347:PRO:CD	2.59	0.49
3:C:673:LYS:HG3	3:C:686:THR:HG23	1.95	0.49
6:F:83:A:OP2	11:J:247:LYS:CD	2.58	0.49
9:H:98:G:H2'	34:m:39:TYR:CE2	2.47	0.49
10:I:272:PHE:CB	18:Q:355:ASN:CA	2.90	0.49
16:O:22:ILE:HD13	24:W:111:LEU:HD23	1.94	0.49
27:2:113:LEU:C	27:2:113:LEU:CD1	2.86	0.49
40:1:125:ALA:HB2	40:1:150:ALA:HB3	1.94	0.49
1:A:1555:LEU:HD23	1:A:1556:ASP:H	1.76	0.49
6:F:45:A:H2	6:F:73:A:C1'	2.19	0.49
8:G:137:C:C5'	8:G:137:C:C6	2.90	0.49
9:H:104:U:O2'	34:m:65:ARG:NH2	2.45	0.49
9:H:153:A:C2'	9:H:154:C:C5'	2.86	0.49
10:I:696:ASP:HB3	10:I:699:THR:CG2	2.43	0.49
13:L:176:LEU:HD22	24:W:440:LYS:HE3	1.95	0.49
16:O:132:ARG:HD3	16:O:133:PRO:HD2	1.95	0.49
21:T:392:PRO:HG3	21:T:415:ILE:HA	1.93	0.49
25:Y:397:PRO:O	25:Y:400:TRP:HB3	2.13	0.49
33:d:41:GLN:H	33:d:115:ILE:HB	1.76	0.49
35:e:15:VAL:O	36:g:33:GLY:HA3	2.12	0.49
40:1:102:TYR:HB3	40:1:156:GLN:HE21	1.77	0.49
1:A:209:ASP:HB3	1:A:212:PRO:HA	1.93	0.49
1:A:425:PRO:HG3	2:B:26:A:H5''	1.94	0.49
1:A:1136:ARG:NH1	1:A:1136:ARG:CG	2.72	0.49
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.45	0.49
1:A:1765:SER:HB2	1:A:2014:MET:HE1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1955:LYS:HB2	27:2:92:ARG:HH12	1.78	0.49
3:C:682:LYS:HB3	3:C:797:ALA:HB2	1.95	0.49
8:G:20:A:HO2'	16:O:193:LEU:CD2	2.09	0.49
27:2:89:GLU:O	27:2:93:GLN:N	2.40	0.49
2:B:93:U:O2'	34:f:65:ARG:NH2	2.45	0.49
6:F:8:C:C6	6:F:8:C:C5'	2.91	0.49
8:G:7:G:OP2	8:G:7:G:H8	1.94	0.49
10:I:681:ILE:CD1	10:I:714:HIS:ND1	2.76	0.49
11:J:263:SER:O	11:J:267:ARG:N	2.45	0.49
16:O:68:THR:HA	16:O:83:THR:HG22	1.93	0.49
24:W:103:GLN:NE2	24:W:111:LEU:O	2.46	0.49
24:W:547:LYS:HE2	24:W:547:LYS:O	2.13	0.49
37:q:60:PRO:CB	37:s:93:ARG:CB	2.91	0.49
38:o:66:LEU:HD21	38:o:69:LEU:HG	1.94	0.49
1:A:66:VAL:HG11	1:A:487:LEU:HD11	1.94	0.49
1:A:609:LYS:CE	46:A:3000:IHP:O31	2.60	0.49
1:A:1685:LEU:HD22	40:1:170:TRP:CZ3	2.47	0.49
1:A:1728:GLN:HE21	1:A:1728:GLN:C	2.20	0.49
1:A:1935:ARG:N	40:1:347:PRO:HG3	2.26	0.49
1:A:1935:ARG:NH2	40:1:348:THR:HG21	2.21	0.49
1:A:1994:LYS:HZ1	27:2:67:VAL:CG2	2.24	0.49
2:B:87:A:H2'	34:f:39:TYR:CE2	2.47	0.49
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.49
6:F:34:G:C8	6:F:34:G:H5''	2.47	0.49
6:F:39:A:H61	8:G:8:C:H42	1.59	0.49
6:F:42:C:H2'	6:F:43:A:H1'	1.94	0.49
17:P:3:THR:O	17:P:3:THR:OG1	2.23	0.49
1:A:435:CYS:SG	7:4:-11:G:N2	2.78	0.49
1:A:1252:GLY:O	8:G:170:C:N4	2.46	0.49
1:A:1497:THR:HG23	1:A:1499:GLU:H	1.77	0.49
2:B:57:G:H2'	2:B:58:U:H5'	1.95	0.49
6:F:37:C:H3'	6:F:37:C:H6	1.77	0.49
6:F:79:C:P	11:J:237:LYS:NZ	2.84	0.49
10:I:273:GLU:C	18:Q:357:ALA:HB2	2.38	0.49
13:L:569:GLN:CB	37:q:114:CYS:C	2.86	0.49
23:V:528:ILE:HA	23:V:531:GLU:HB2	1.93	0.49
23:V:620:ASN:O	23:V:624:THR:N	2.43	0.49
27:2:137:LYS:HA	27:2:137:LYS:CE	2.32	0.49
1:A:1011:ALA:HB2	13:L:80:THR:HB	1.94	0.49
1:A:1321:GLU:HG3	40:1:66:TYR:CE1	2.48	0.49
1:A:1588:SER:O	1:A:1592:ASP:N	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1865:ARG:CZ	8:G:147:C:OP1	2.60	0.49
1:A:1891:LEU:HD22	1:A:1937:ILE:HD12	1.94	0.49
3:C:857:VAL:HG22	3:C:873:ALA:HB2	1.95	0.49
5:E:214:ASP:OD1	5:E:214:ASP:N	2.46	0.49
6:F:45:A:N6	8:G:167:G:C6	2.80	0.49
8:G:147:C:C2	8:G:148:U:H5	2.22	0.49
9:H:77:C:C5'	24:W:242:HIS:CE1	2.95	0.49
12:K:81:LEU:CB	37:t:72:PRO:CB	2.90	0.49
13:L:51:TYR:O	13:L:58:ILE:HD11	2.12	0.49
24:W:82:ASN:H	24:W:83:PRO:HD2	1.76	0.49
27:2:137:LYS:CE	27:2:140:LEU:HD23	2.43	0.49
33:d:107:ILE:HG22	33:d:108:VAL:CG2	2.39	0.49
40:1:267:ILE:HG22	40:1:267:ILE:O	2.12	0.49
1:A:156:ARG:HH22	40:1:134:PHE:CB	2.25	0.49
1:A:1201:ARG:O	1:A:1203:SER:N	2.45	0.49
1:A:1456:THR:OG1	1:A:1457:HIS:N	2.46	0.49
1:A:1552:GLN:CD	1:A:1563:HIS:CD2	2.91	0.49
1:A:1876:LEU:CG	1:A:1884:ILE:HD11	2.42	0.49
1:A:1903:GLY:CA	27:2:82:TYR:CZ	2.96	0.49
3:C:259:LYS:HD2	3:C:262:ARG:HD2	1.93	0.49
5:E:215:ASN:O	5:E:232:ARG:NH1	2.46	0.49
9:H:77:C:O5'	24:W:242:HIS:HE1	1.95	0.49
25:Y:412:SER:OG	25:Y:415:GLU:HG3	2.13	0.49
34:m:51:ILE:HG22	34:m:56:SER:HB2	1.93	0.49
40:1:169:ARG:HG3	40:1:170:TRP:CD1	2.47	0.49
1:A:1275:ARG:HD2	1:A:1375:TRP:CE2	2.47	0.48
1:A:1275:ARG:NH1	1:A:1373:GLN:O	2.40	0.48
1:A:2335:ALA:O	4:D:570:THR:CB	2.60	0.48
17:P:212:ASN:CB	21:T:458:SER:H	2.13	0.48
20:S:20:MET:HE2	20:S:141:ARG:HB3	1.95	0.48
26:Z:742:ASN:HB2	26:Z:744:ILE:HD12	1.94	0.48
35:l:20:LEU:HD13	36:n:61:VAL:CG2	2.42	0.48
1:A:1921:ASP:OD2	1:A:1968:TRP:N	2.46	0.48
3:C:440:SER:HB2	3:C:443:VAL:H	1.77	0.48
16:O:229:LYS:HD3	16:O:277:ARG:HH12	1.78	0.48
1:A:244:GLN:CD	1:A:244:GLN:N	2.70	0.48
1:A:642:ARG:NE	2:B:55:C:O2	2.31	0.48
1:A:1876:LEU:HG	1:A:1884:ILE:HD11	1.95	0.48
1:A:1986:LEU:HD23	1:A:1986:LEU:O	2.12	0.48
5:E:60:MET:HA	29:b:109:ALA:HA	1.94	0.48
6:F:50:A:O2'	6:F:51:U:OP1	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:192:ARG:NH2	13:L:198:ILE:O	2.46	0.48
21:T:427:LEU:HB3	21:T:439:TRP:HB2	1.95	0.48
9:H:24:A:H2	13:L:29:ASN:HB3	1.79	0.48
10:I:723:MET:CA	10:I:726:ILE:HG23	2.02	0.48
21:T:247:SER:OG	21:T:248:THR:N	2.46	0.48
34:m:20:MET:HE2	34:m:30:LYS:HB2	1.94	0.48
1:A:1699:THR:HA	1:A:1717:ASN:HD22	1.78	0.48
3:C:560:VAL:HG12	3:C:561:LYS:H	1.79	0.48
6:F:22:A:C2	15:N:126:LEU:HD23	2.48	0.48
6:F:41:A:C2	8:G:6:A:N1	2.79	0.48
10:I:681:ILE:CG2	10:I:710:PHE:CZ	2.80	0.48
13:L:55:ASP:HB3	13:L:58:ILE:HG13	1.95	0.48
40:1:135:GLU:OE1	40:1:138:ARG:NH1	2.46	0.48
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.96	0.48
1:A:1728:GLN:C	1:A:1728:GLN:NE2	2.71	0.48
1:A:1765:SER:HB2	1:A:2014:MET:CE	2.44	0.48
5:E:78:GLY:O	5:E:336:HIS:NE2	2.45	0.48
5:E:93:TRP:CZ3	29:b:105:GLY:CA	2.97	0.48
6:F:31:U:H2'	6:F:32:U:H5'	1.95	0.48
8:G:12:G:H2'	8:G:13:C:C6	2.49	0.48
9:H:143:A:N3	9:H:143:A:C3'	2.73	0.48
10:I:242:ALA:HA	18:Q:527:ILE:CB	2.43	0.48
10:I:727:ARG:NH2	10:I:727:ARG:C	2.71	0.48
13:L:18:ILE:O	13:L:22:ALA:N	2.47	0.48
17:P:13:ARG:HH11	17:P:13:ARG:CG	2.26	0.48
27:2:114:GLU:HG3	27:2:115:LYS:N	2.29	0.48
27:2:138:LYS:CE	27:2:138:LYS:CA	2.87	0.48
1:A:532:THR:CB	8:G:3:A:O5'	2.61	0.48
2:B:92:U:O4	29:b:38:MET:HG3	2.14	0.48
8:G:137:C:OP2	8:G:137:C:C6	2.66	0.48
10:I:728:ARG:O	10:I:731:GLN:CB	2.61	0.48
27:2:134:LEU:HD12	27:2:134:LEU:O	2.14	0.48
1:A:668:VAL:O	1:A:668:VAL:HG12	2.14	0.48
1:A:702:LYS:NZ	14:M:127:TYR:OH	2.47	0.48
1:A:1476:GLN:HG3	40:1:73:TYR:OH	2.14	0.48
1:A:1501:LEU:HB3	1:A:1753:LEU:HD21	1.95	0.48
9:H:44:U:H2'	9:H:45:C:C6	2.48	0.48
9:H:107:A:C2	9:H:108:G:C4	3.01	0.48
10:I:725:ARG:C	10:I:725:ARG:CD	2.85	0.48
13:L:6:ILE:C	13:L:6:ILE:CD1	2.82	0.48
16:O:245:GLU:OE1	16:O:249:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:457:ARG:CG	40:1:73:TYR:HD2	2.24	0.48
27:2:25:LYS:HE2	27:2:25:LYS:CA	2.44	0.48
1:A:199:GLU:CB	40:1:139:ARG:CD	2.90	0.48
1:A:681:PHE:HE2	1:A:746:LYS:HG3	1.78	0.48
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.43	0.48
5:E:75:HIS:ND1	5:E:77:ASN:OD1	2.46	0.48
8:G:19:G:H21	16:O:196:GLN:CG	2.27	0.48
9:H:39:U:C2'	9:H:40:C:C5	2.97	0.48
27:2:38:LEU:CD2	34:m:12:ASN:HD22	2.13	0.48
37:q:60:PRO:CB	37:s:94:GLN:HA	2.43	0.48
37:r:127:ALA:HB1	37:s:127:ALA:CB	2.44	0.48
1:A:1131:LYS:HZ1	1:A:1188:ASN:HB2	1.78	0.48
1:A:1644:LEU:HD22	1:A:1681:ARG:CG	2.40	0.48
1:A:1890:GLN:CB	27:2:70:SER:OG	2.50	0.48
1:A:1958:LYS:HD3	27:2:96:MET:HB3	1.96	0.48
6:F:43:A:C6	6:F:44:G:C6	3.02	0.48
10:I:661:ASP:CB	10:I:694:ILE:HG21	2.20	0.48
11:J:183:ALA:HB3	13:L:142:ILE:HG12	1.96	0.48
11:J:201:ARG:NH2	11:J:201:ARG:CG	2.73	0.48
16:O:147:LEU:O	16:O:151:ALA:N	2.47	0.48
18:Q:936:PHE:CB	18:Q:1005:PHE:CB	2.92	0.48
36:g:35:ASP:HB2	36:g:36:PRO:CD	2.42	0.48
33:k:107:ILE:HG22	33:k:108:VAL:CG2	2.39	0.48
34:m:10:PHE:CE2	35:l:78:MET:HB2	2.49	0.48
1:A:151:MET:HA	1:A:154:GLU:HB3	1.95	0.47
10:I:661:ASP:HA	10:I:664:ALA:HB3	1.95	0.47
11:J:535:TYR:C	11:J:537:TRP:C	2.82	0.47
19:R:265:ASP:N	19:R:265:ASP:OD1	2.45	0.47
21:T:267:ASP:OD2	21:T:269:GLN:NE2	2.47	0.47
24:W:256:HIS:HB3	24:W:257:ILE:HD12	1.96	0.47
24:W:453:PHE:CB	27:2:79:PHE:CE2	2.97	0.47
41:v:140:HIS:O	42:w:70:VAL:CB	2.62	0.47
1:A:1495:PHE:CE1	1:A:1755:SER:OG	2.67	0.47
1:A:1537:TRP:HE3	1:A:1751:LEU:HD13	1.79	0.47
5:E:294:SER:HB3	5:E:299:LYS:HB2	1.96	0.47
6:F:50:A:HO2'	6:F:51:U:P	2.36	0.47
9:H:77:C:H2'	9:H:78:C:C6	2.49	0.47
9:H:151:C:C2	9:H:152:G:N7	2.82	0.47
10:I:555:ASP:OD1	10:I:555:ASP:N	2.46	0.47
37:q:61:ILE:N	37:s:93:ARG:CB	2.75	0.47
1:A:200:ASP:OD1	1:A:240:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:HIS:CE1	23:V:324:HIS:HA	2.48	0.47
1:A:467:GLN:HG2	2:B:19:A:C5	2.49	0.47
1:A:824:PRO:O	1:A:933:ARG:NH1	2.45	0.47
1:A:1248:LEU:HD21	1:A:1295:ILE:HG22	1.95	0.47
1:A:1386:TRP:HB3	25:Y:410:VAL:HG23	1.88	0.47
1:A:1615:HIS:HD2	28:z:93:ASN:CG	2.20	0.47
1:A:1995:ASN:ND2	26:Z:756:TYR:CD2	2.82	0.47
9:H:42:G:H8	9:H:42:G:O5'	1.98	0.47
10:I:329:LEU:CB	18:Q:353:LEU:CA	2.90	0.47
15:N:51:ARG:HH21	24:W:193:LEU:HD23	1.78	0.47
16:O:88:LEU:O	19:R:183:GLN:NE2	2.47	0.47
19:R:314:GLN:CD	19:R:314:GLN:N	2.72	0.47
21:T:471:ASP:OD1	21:T:471:ASP:N	2.46	0.47
27:2:24:PRO:HA	27:2:29:GLU:CB	2.44	0.47
1:A:80:LYS:HD3	15:N:37:HIS:HE2	1.79	0.47
1:A:280:GLU:HG2	2:B:48:A:O4'	2.14	0.47
1:A:1482:GLU:OE1	40:1:86:ARG:HA	2.14	0.47
2:B:20:G:H1'	2:B:21:A:OP1	2.14	0.47
6:F:22:A:N1	15:N:126:LEU:HD23	2.29	0.47
9:H:69:U:H2'	9:H:70:C:C6	2.49	0.47
10:I:593:LYS:HE2	10:I:631:MET:HG3	1.95	0.47
19:R:318:GLU:O	19:R:322:GLU:HG3	2.14	0.47
19:R:326:GLU:HB3	19:R:330:LYS:CE	2.44	0.47
34:f:10:PHE:CE2	35:e:78:MET:HB2	2.49	0.47
41:v:24:PHE:HA	41:v:33:ARG:O	2.14	0.47
1:A:53:PHE:HE2	1:A:55:ASP:HB3	1.79	0.47
1:A:589:THR:OG1	1:A:590:GLY:N	2.46	0.47
1:A:761:ILE:HD11	1:A:772:CYS:SG	2.54	0.47
1:A:1657:THR:OG1	1:A:1659:LYS:O	2.28	0.47
5:E:176:VAL:HB	5:E:190:PHE:HB2	1.95	0.47
6:F:8:C:H6	6:F:8:C:C5'	2.09	0.47
10:I:272:PHE:C	18:Q:355:ASN:CB	2.88	0.47
10:I:727:ARG:HH21	10:I:727:ARG:HG2	1.76	0.47
25:Y:644:TYR:HA	25:Y:660:TYR:O	2.14	0.47
1:A:154:GLU:HG2	1:A:572:PHE:CE1	2.50	0.47
1:A:2011:ILE:HG22	1:A:2012:LEU:CD2	2.44	0.47
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.49	0.47
5:E:69:VAL:O	5:E:331:ASN:ND2	2.38	0.47
8:G:17:U:O2	16:O:198:ILE:CD1	2.63	0.47
9:H:39:U:C3'	9:H:40:C:C6	2.97	0.47
9:H:60:U:O2'	9:H:67:C:N4	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:153:A:C8	9:H:154:C:H5'	2.50	0.47
13:L:15:GLU:HG2	13:L:151:MET:HE1	1.96	0.47
14:M:211:ILE:HD12	14:M:212:ASN:HB2	1.95	0.47
19:R:316:GLU:HA	19:R:319:LYS:HE3	1.95	0.47
24:W:523:VAL:HB	24:W:535:TRP:HB2	1.96	0.47
34:m:36:VAL:HG12	34:m:37:ASP:N	2.29	0.47
1:A:127:SER:OG	1:A:495:GLN:NE2	2.45	0.47
1:A:244:GLN:OE1	1:A:244:GLN:HA	2.13	0.47
1:A:525:LYS:HE2	28:z:103:TYR:CD1	2.49	0.47
1:A:704:ASN:ND2	9:H:16:U:OP2	2.48	0.47
1:A:711:GLN:HE22	9:H:18:U:H3'	1.79	0.47
1:A:1108:ASP:OD2	1:A:1112:ARG:NH1	2.48	0.47
1:A:1596:VAL:HG11	40:1:278:LEU:HD13	1.96	0.47
1:A:1615:HIS:HB3	1:A:1618:LYS:HB2	1.96	0.47
1:A:1759:THR:HG22	40:1:286:ASP:OD2	2.15	0.47
1:A:1879:PHE:HB2	1:A:1882:ILE:HD12	1.96	0.47
6:F:28:A:O2'	15:N:39:GLY:HA2	2.13	0.47
9:H:103:U:O4	29:i:38:MET:HG3	2.14	0.47
9:H:141:C:H2'	9:H:142:C:C6	2.50	0.47
23:V:457:ARG:CG	40:1:73:TYR:CD2	2.88	0.47
32:c:20:LYS:HE2	32:c:63:ASN:O	2.15	0.47
33:d:108:VAL:CG1	34:f:62:VAL:HG13	2.44	0.47
31:h:45:ASN:HB3	38:o:22:ARG:HH11	1.79	0.47
38:o:153:LYS:O	38:o:157:GLU:HG3	2.14	0.47
1:A:150:MET:O	1:A:153:ARG:HG3	2.15	0.47
1:A:152:ARG:NH1	40:1:132:ASP:O	2.48	0.47
1:A:439:GLN:O	1:A:444:ARG:NH1	2.48	0.47
1:A:1555:LEU:CD2	1:A:1574:ILE:CG1	2.91	0.47
6:F:24:A:C6	16:O:65:PHE:CE2	2.97	0.47
6:F:25:C:O4'	6:F:26:U:OP2	2.33	0.47
9:H:57:A:H2'	9:H:58:U:C6	2.50	0.47
9:H:59:A:H2'	9:H:60:U:C6	2.50	0.47
9:H:71:C:H2'	9:H:72:U:C6	2.50	0.47
9:H:149:A:H2'	9:H:150:U:C6	2.50	0.47
10:I:139:ALA:HB2	10:I:147:ARG:CB	2.45	0.47
10:I:722:GLU:O	10:I:726:ILE:HB	2.15	0.47
10:I:722:GLU:O	10:I:726:ILE:N	2.43	0.47
16:O:196:GLN:HE21	16:O:208:PRO:HG2	1.80	0.47
21:T:335:THR:OG1	21:T:336:VAL:N	2.47	0.47
36:g:64:GLY:HA2	36:g:67:ILE:HD12	1.97	0.47
32:j:6:PHE:CD1	32:j:6:PHE:C	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:j:61:ARG:HB3	32:j:64:ASN:HD22	1.80	0.47
35:l:68:THR:HG22	35:l:68:THR:O	2.15	0.47
9:H:54:U:H2'	9:H:55:U:C6	2.50	0.47
13:L:135:LYS:N	13:L:135:LYS:CD	2.78	0.47
20:S:97:ILE:CG2	20:S:128:ILE:HG23	2.45	0.47
27:2:137:LYS:HE2	27:2:140:LEU:HB3	1.96	0.47
31:a:24:THR:O	31:a:51:ARG:NH1	2.46	0.47
38:o:2:VAL:O	38:o:2:VAL:HG13	2.13	0.47
38:o:14:GLN:HG3	38:o:44:PHE:HE1	1.80	0.47
1:A:153:ARG:NH2	1:A:153:ARG:CG	2.72	0.47
1:A:702:LYS:HD2	14:M:124:PHE:HE2	1.80	0.47
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.97	0.47
3:C:852:ARG:NH1	7:4:-13:C:H2'	2.27	0.47
5:E:145:LYS:NZ	5:E:181:ILE:O	2.39	0.47
8:G:27:U:HO2'	8:G:28:A:C4'	2.27	0.47
9:H:70:C:H2'	9:H:71:C:C6	2.50	0.47
9:H:72:U:H2'	9:H:73:C:C6	2.49	0.47
9:H:90:A:H2'	9:H:91:U:C6	2.50	0.47
9:H:150:U:H2'	9:H:151:C:C6	2.50	0.47
13:L:7:LYS:HG3	13:L:40:ARG:HA	1.96	0.47
13:L:54:LEU:O	13:L:55:ASP:C	2.58	0.47
13:L:123:LEU:HD22	13:L:125:PRO:CD	2.44	0.47
31:a:43:MET:HB3	31:a:46:ILE:HD11	1.97	0.47
34:f:36:VAL:HG12	34:f:37:ASP:N	2.29	0.47
32:j:20:LYS:HE2	32:j:63:ASN:O	2.15	0.47
36:n:64:GLY:HA2	36:n:67:ILE:HD12	1.97	0.47
40:1:178:HIS:CE1	40:1:181:ILE:HG12	2.50	0.47
1:A:1070:ASP:OD1	1:A:1070:ASP:N	2.39	0.46
1:A:1498:TRP:HZ3	40:1:63:ILE:CG2	1.82	0.46
1:A:1640:SER:CB	1:A:1718:TRP:O	2.63	0.46
1:A:1724:PRO:N	1:A:1725:LEU:N	2.63	0.46
1:A:2335:ALA:HA	4:D:570:THR:O	2.15	0.46
9:H:73:C:H2'	9:H:74:U:C6	2.50	0.46
19:R:324:LEU:HA	19:R:327:MET:CE	2.45	0.46
20:S:72:ARG:HD3	24:W:90:ALA:HB3	1.97	0.46
20:S:72:ARG:NH2	24:W:92:GLU:OE2	2.48	0.46
20:S:125:LYS:HB2	20:S:126:HIS:CD2	2.48	0.46
31:a:74:PRO:O	31:a:77:LEU:HD13	2.14	0.46
32:c:6:PHE:CD1	32:c:6:PHE:C	2.93	0.46
33:k:108:VAL:CG1	34:m:62:VAL:HG13	2.45	0.46
36:n:10:LYS:HD2	36:n:34:PHE:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:o:61:PRO:O	38:o:86:ALA:HB1	2.15	0.46
1:A:832:TYR:HD2	1:A:835:ASP:HB3	1.79	0.46
1:A:1494:TYR:CG	1:A:1744:ARG:NE	2.84	0.46
1:A:1739:ALA:CA	1:A:1742:VAL:HG23	2.44	0.46
1:A:1872:LEU:O	1:A:1876:LEU:HB3	2.13	0.46
5:E:266:PRO:CB	13:L:788:TYR:CB	2.92	0.46
8:G:145:U:C2'	8:G:146:C:C6	2.98	0.46
9:H:83:A:H2'	9:H:84:C:C6	2.49	0.46
11:J:224:LYS:HE2	11:J:255:LEU:HD13	1.96	0.46
19:R:123:GLU:HG3	19:R:124:VAL:HG12	1.96	0.46
20:S:66:ASP:OD1	20:S:73:GLY:O	2.32	0.46
35:e:18:ILE:HA	35:e:21:ILE:HD12	1.98	0.46
37:s:65:PRO:O	37:s:66:PRO:C	2.59	0.46
38:o:56:LYS:HG2	38:o:58:ASP:HB2	1.97	0.46
1:A:58:LYS:HB2	1:A:477:LYS:HE2	1.97	0.46
1:A:663:ARG:NH1	6:F:64:U:OP2	2.49	0.46
1:A:1136:ARG:HG2	1:A:1136:ARG:NH1	2.13	0.46
1:A:1860:GLN:HG2	1:A:1883:VAL:HB	1.97	0.46
3:C:785:ARG:HG2	3:C:786:ASN:HB2	1.97	0.46
3:C:843:VAL:HG13	3:C:871:ILE:HD11	1.97	0.46
3:C:905:GLN:HE22	43:u:104:VAL:HA	1.80	0.46
10:I:728:ARG:NH2	10:I:728:ARG:CG	2.72	0.46
11:J:523:PRO:O	11:J:527:LYS:N	2.46	0.46
19:R:147:THR:HG23	21:T:360:VAL:HG12	1.96	0.46
19:R:318:GLU:CD	19:R:318:GLU:N	2.72	0.46
40:1:34:ARG:CA	40:1:34:ARG:NH1	2.76	0.46
1:A:53:PHE:CE1	2:B:65:G:C5'	2.98	0.46
1:A:372:PRO:HG2	3:C:342:ARG:HG2	1.97	0.46
1:A:435:CYS:CB	7:4:-11:G:N2	2.74	0.46
1:A:467:GLN:NE2	2:B:19:A:C6	2.84	0.46
3:C:221:ILE:O	3:C:495:ARG:NH1	2.48	0.46
6:F:36:A:O2'	6:F:37:C:P	2.74	0.46
8:G:7:G:H2'	8:G:8:C:H6	1.80	0.46
10:I:624:GLU:HB3	10:I:627:GLN:HB2	1.97	0.46
10:I:725:ARG:NH1	10:I:729:SER:HB2	2.30	0.46
11:J:195:LEU:HD22	13:L:24:MET:HE1	1.96	0.46
11:J:196:ARG:HA	14:M:208:ILE:HD11	1.98	0.46
11:J:454:ASN:O	11:J:458:PHE:N	2.46	0.46
13:L:216:PHE:CE1	19:R:219:PRO:HG3	2.51	0.46
19:R:315:LYS:HG3	19:R:319:LYS:HE2	1.98	0.46
19:R:332:ARG:HA	19:R:335:ARG:CD	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1543:ASN:HB2	1:A:1569:LEU:CD2	2.46	0.46
3:C:174:GLU:OE2	3:C:182:LYS:N	2.44	0.46
5:E:114:GLU:OE2	5:E:116:HIS:NE2	2.43	0.46
19:R:309:GLU:CD	19:R:309:GLU:N	2.71	0.46
32:c:61:ARG:HB3	32:c:64:ASN:HD22	1.80	0.46
1:A:182:ILE:HD11	1:A:562:VAL:HG13	1.97	0.46
1:A:880:ARG:O	1:A:883:ARG:CB	2.64	0.46
1:A:1698:PRO:CG	40:1:181:ILE:HG13	2.44	0.46
1:A:1771:LEU:HD22	1:A:1812:PRO:HG2	1.97	0.46
1:A:1816:GLN:HA	1:A:1918:ASN:HA	1.97	0.46
1:A:1889:LEU:CD1	1:A:2013:GLY:N	2.72	0.46
1:A:1940:LEU:HD23	1:A:1943:LEU:HD12	1.97	0.46
1:A:1955:LYS:HZ3	27:2:93:GLN:CD	2.22	0.46
9:H:68:G:H2'	9:H:69:U:C6	2.50	0.46
9:H:183:G:H2'	9:H:184:C:C6	2.50	0.46
23:V:498:ALA:HB1	23:V:543:LYS:HB3	1.97	0.46
27:2:48:ILE:HG12	34:m:5:LEU:HD12	1.98	0.46
27:2:97:ASP:O	27:2:100:ALA:N	2.48	0.46
33:k:46:CYS:HB3	33:k:48:ASN:OD1	2.15	0.46
35:l:18:ILE:HA	35:l:21:ILE:HD12	1.98	0.46
1:A:1066:GLN:OE1	1:A:1066:GLN:HA	2.15	0.46
1:A:1739:ALA:O	1:A:1742:VAL:HG23	2.14	0.46
1:A:1958:LYS:HG2	27:2:96:MET:O	2.15	0.46
6:F:88:G:H5'	14:M:133:ARG:HH12	1.81	0.46
9:H:182:U:H2'	9:H:183:G:H8	1.81	0.46
13:L:77:LEU:HD22	19:R:285:ALA:HA	1.98	0.46
20:S:125:LYS:HB2	20:S:126:HIS:HD2	1.80	0.46
35:e:16:GLN:HB3	35:e:19:ASN:OD1	2.16	0.46
31:h:24:THR:O	31:h:51:ARG:NH1	2.46	0.46
1:A:464:PRO:HD2	2:B:20:G:O2'	2.16	0.46
1:A:1552:GLN:HB2	1:A:1563:HIS:CD2	2.51	0.46
1:A:1700:GLY:O	1:A:1717:ASN:N	2.49	0.46
1:A:1849:ILE:HG21	1:A:1879:PHE:CD1	2.48	0.46
1:A:1883:VAL:CG2	40:1:291:ALA:HB2	2.46	0.46
3:C:508:LYS:HA	3:C:524:ILE:HG22	1.98	0.46
9:H:10:C:H41	14:M:198:ARG:NH1	2.10	0.46
9:H:39:U:N3	9:H:40:C:N4	2.63	0.46
9:H:107:A:C6	9:H:108:G:C6	3.04	0.46
9:H:152:G:O2'	9:H:153:A:H1'	2.16	0.46
10:I:516:ALA:HA	10:I:520:ILE:HD11	1.98	0.46
13:L:5:MET:HE2	13:L:39:HIS:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:210:ILE:HG13	21:T:480:ALA:HB2	1.97	0.46
24:W:420:ALA:O	24:W:438:ASP:N	2.48	0.46
27:2:27:ALA:HA	27:2:30:GLU:HG2	1.97	0.46
27:2:137:LYS:NZ	27:2:140:LEU:HB3	2.31	0.46
35:e:68:THR:O	35:e:68:THR:HG22	2.15	0.46
31:h:43:MET:HB3	31:h:46:ILE:HD11	1.97	0.46
40:1:124:GLY:HA3	40:1:149:ILE:HG23	1.97	0.46
1:A:1827:TRP:CE3	1:A:1833:LEU:HD12	2.51	0.46
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.81	0.46
2:B:93:U:O4	33:d:64:ASN:ND2	2.42	0.46
17:P:77:ASP:O	17:P:78:ARG:NE	2.47	0.46
19:R:329:GLN:CD	19:R:329:GLN:C	2.84	0.46
21:T:193:PRO:HD2	21:T:495:ALA:HB1	1.98	0.46
29:b:17:MET:HE1	29:b:82:VAL:HG22	1.98	0.46
1:A:843:LEU:HD22	1:A:867:ILE:HG23	1.97	0.46
1:A:1640:SER:HB2	1:A:1650:ASP:HB3	1.98	0.46
1:A:2015:GLU:C	1:A:2015:GLU:CD	2.84	0.46
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.16	0.46
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.46
5:E:90:ILE:HB	5:E:105:LEU:HB2	1.98	0.46
9:H:114:A:H2'	9:H:115:G:H8	1.81	0.46
24:W:155:SER:OG	24:W:158:GLU:OE1	2.25	0.46
40:1:102:TYR:HD1	40:1:156:GLN:HB3	1.81	0.46
1:A:773:LYS:HB3	9:H:23:A:N3	2.31	0.45
1:A:829:PRO:HG2	1:A:832:TYR:HB2	1.96	0.45
1:A:1251:SER:OG	1:A:1259:ILE:HD11	2.16	0.45
1:A:1705:ILE:HD11	1:A:1730:MET:CE	2.46	0.45
1:A:1705:ILE:HD11	1:A:1730:MET:HE3	1.97	0.45
1:A:1772:PHE:CZ	1:A:1933:PHE:HB2	2.49	0.45
8:G:134:U:H5''	8:G:135:G:OP2	2.15	0.45
9:H:113:G:H2'	9:H:114:A:H8	1.81	0.45
20:S:142:VAL:HG13	20:S:157:VAL:HG11	1.98	0.45
21:T:404:SER:OG	21:T:405:PHE:N	2.48	0.45
33:d:46:CYS:HB3	33:d:48:ASN:OD1	2.15	0.45
37:t:65:PRO:O	37:t:66:PRO:C	2.58	0.45
38:o:120:ILE:HG22	38:o:120:ILE:O	2.16	0.45
1:A:803:ALA:HB2	19:R:287:LEU:HA	1.98	0.45
1:A:1697:SER:OG	1:A:1699:THR:O	2.31	0.45
1:A:1882:ILE:O	40:1:290:ARG:CB	2.65	0.45
2:B:23:C:HO2'	2:B:24:G:P	2.38	0.45
9:H:78:C:H2'	9:H:79:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:79:G:H2'	9:H:80:A:H8	1.82	0.45
9:H:181:G:H2'	9:H:182:U:C6	2.50	0.45
16:O:131:THR:HG23	24:W:111:LEU:H	1.81	0.45
27:2:127:ARG:CB	27:2:131:ARG:NH2	2.68	0.45
36:n:38:MET:HE2	36:n:67:ILE:HG21	1.98	0.45
40:1:293:ARG:HB2	45:3:352:TYR:CZ	2.51	0.45
1:A:80:LYS:NZ	15:N:38:GLU:O	2.49	0.45
1:A:1116:GLU:OE2	17:P:196:ASN:ND2	2.48	0.45
1:A:1479:GLY:HA2	40:1:88:GLN:OE1	2.16	0.45
1:A:1876:LEU:CD2	1:A:1882:ILE:HD12	2.38	0.45
6:F:36:A:HO2'	6:F:37:C:P	2.40	0.45
9:H:180:G:H2'	9:H:181:G:H8	1.81	0.45
14:M:125:SER:HB3	19:R:239:VAL:HG22	1.97	0.45
19:R:233:PRO:HB2	19:R:234:SER:H	1.62	0.45
29:i:17:MET:HE1	29:i:82:VAL:HG22	1.98	0.45
33:k:72:GLU:HG2	33:k:74:TRP:CE3	2.52	0.45
1:A:53:PHE:CE1	2:B:65:G:H5''	2.52	0.45
1:A:537:LYS:HB2	6:F:37:C:N4	2.30	0.45
1:A:880:ARG:CA	1:A:883:ARG:HB2	2.47	0.45
1:A:1562:MET:HE2	1:A:1562:MET:HB2	1.54	0.45
3:C:121:ASP:OD2	31:a:76:MET:CB	2.61	0.45
9:H:58:U:H2'	9:H:59:A:H8	1.82	0.45
9:H:89:U:H2'	9:H:90:A:H8	1.82	0.45
10:I:599:TYR:HA	10:I:602:LEU:HG	1.99	0.45
11:J:197:GLU:O	11:J:201:ARG:HG2	2.17	0.45
11:J:267:ARG:HH11	13:L:216:PHE:HB2	1.82	0.45
13:L:699:ASN:O	13:L:703:MET:N	2.50	0.45
21:T:339:GLN:NE2	21:T:343:PRO:O	2.42	0.45
24:W:79:VAL:CG2	29:b:114:ILE:CD1	2.72	0.45
24:W:453:PHE:CA	27:2:79:PHE:HE2	2.30	0.45
33:d:72:GLU:HG2	33:d:74:TRP:CE3	2.51	0.45
1:A:26:SER:H	1:A:29:LYS:HD2	1.81	0.45
1:A:540:PHE:HB3	1:A:544:PHE:HB3	1.98	0.45
1:A:1430:LEU:HB2	25:Y:400:TRP:CZ3	2.52	0.45
1:A:1487:HIS:NE2	1:A:1671:TYR:CZ	2.84	0.45
3:C:725:ASP:HB3	3:C:728:ALA:HB3	1.98	0.45
8:G:137:C:O2'	8:G:138:A:O5'	2.35	0.45
9:H:81:G:H2'	9:H:82:G:H8	1.81	0.45
23:V:460:TYR:CD1	40:1:72:TRP:HZ2	2.33	0.45
24:W:70:VAL:CG1	24:W:71:HIS:HD2	2.29	0.45
24:W:436:THR:HG21	24:W:464:MET:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:525:SER:OG	24:W:526:GLY:N	2.49	0.45
33:d:22:GLU:OE1	33:d:22:GLU:HA	2.17	0.45
37:s:65:PRO:O	37:s:67:SER:N	2.49	0.45
35:l:16:GLN:HB3	35:l:19:ASN:OD1	2.16	0.45
38:o:92:GLU:OE1	39:p:25:ARG:NE	2.39	0.45
1:A:1475:ILE:HD12	40:1:66:TYR:HD2	1.82	0.45
1:A:1495:PHE:CG	45:3:337:ILE:HD13	2.23	0.45
8:G:141:C:H2'	8:G:142:U:C6	2.51	0.45
9:H:14:C:N4	14:M:224:ARG:CD	2.79	0.45
9:H:80:A:H2'	9:H:81:G:H8	1.81	0.45
9:H:82:G:H2'	9:H:83:A:H8	1.81	0.45
9:H:93:A:H2'	9:H:94:A:H8	1.82	0.45
9:H:168:A:C2'	36:n:48:MET:HE1	2.46	0.45
11:J:308:ARG:HH21	11:J:339:TRP:HE3	1.64	0.45
16:O:258:ILE:HD13	16:O:261:ILE:HD11	1.99	0.45
19:R:62:GLY:N	20:S:132:VAL:O	2.41	0.45
36:n:32:ARG:HG3	36:n:43:ASP:HB2	1.99	0.45
43:u:82:SER:O	43:u:219:ALA:HA	2.17	0.45
1:A:240:ARG:HH12	40:1:139:ARG:CB	2.16	0.45
1:A:299:ILE:HG12	1:A:1346:THR:HG21	1.99	0.45
1:A:1321:GLU:CG	40:1:66:TYR:OH	2.65	0.45
1:A:1495:PHE:CA	45:3:337:ILE:HD11	2.42	0.45
8:G:23:U:H5''	8:G:23:U:H6	1.82	0.45
8:G:27:U:HO2'	8:G:28:A:C5'	2.26	0.45
9:H:142:C:H2'	9:H:143:A:H5'	1.97	0.45
19:R:224:SEP:O3P	21:T:355:ARG:NH1	2.38	0.45
19:R:318:GLU:HA	19:R:318:GLU:OE2	2.16	0.45
21:T:477:LEU:HB3	21:T:489:TYR:HB2	1.98	0.45
27:2:26:ASN:OD1	27:2:26:ASN:N	2.47	0.45
36:g:38:MET:HE2	36:g:67:ILE:HG21	1.98	0.45
33:k:48:ASN:O	33:k:49:ASN:HB2	2.17	0.45
1:A:53:PHE:HE1	2:B:65:G:H5''	1.81	0.45
1:A:73:HIS:HD1	1:A:88:TYR:HH	1.53	0.45
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	2.50	0.45
1:A:1955:LYS:HD3	27:2:96:MET:HE1	1.98	0.45
6:F:12:G:H2'	6:F:13:G:O4'	2.17	0.45
6:F:28:A:HO2'	15:N:39:GLY:HA3	1.82	0.45
10:I:272:PHE:CB	18:Q:355:ASN:HA	2.46	0.45
14:M:148:THR:HA	14:M:151:ARG:HB2	1.99	0.45
17:P:41:ILE:HD11	21:T:318:ARG:HB3	1.99	0.45
21:T:190:TRP:CE3	21:T:190:TRP:O	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:74:PRO:C	31:a:77:LEU:HD11	2.42	0.45
1:A:1756:SER:HB3	45:3:335:GLY:C	2.42	0.45
1:A:1955:LYS:NZ	27:2:93:GLN:HG3	2.25	0.45
3:C:348:TYR:HE1	3:C:367:ARG:HG2	1.82	0.45
3:C:663:CYS:HB2	3:C:828:MET:HB2	1.98	0.45
5:E:62:LEU:HB2	5:E:351:LEU:HB2	1.97	0.45
9:H:74:U:H2'	9:H:75:A:H8	1.81	0.45
9:H:78:C:H1'	30:y:41:TYR:CB	2.47	0.45
19:R:316:GLU:C	19:R:316:GLU:CD	2.85	0.45
26:Z:643:PRO:HD2	26:Z:719:ILE:HD11	1.99	0.45
33:d:48:ASN:O	33:d:49:ASN:HB2	2.17	0.45
1:A:211:GLN:OE1	1:A:214:ARG:NH1	2.48	0.45
1:A:984:MET:HG3	1:A:1048:MET:HE1	1.99	0.45
1:A:1495:PHE:HD1	45:3:337:ILE:CG1	2.26	0.45
1:A:1719:PHE:HD2	1:A:1720:PRO:CD	2.28	0.45
1:A:1921:ASP:HB3	1:A:1966:HIS:HB3	1.99	0.45
1:A:1934:SER:HG	40:1:344:GLN:HA	1.81	0.45
9:H:56:A:H2'	9:H:57:A:H8	1.82	0.45
9:H:67:C:H2'	9:H:68:G:H8	1.81	0.45
9:H:84:C:H2'	9:H:85:A:H8	1.82	0.45
9:H:148:C:H2'	9:H:149:A:H8	1.82	0.45
9:H:152:G:OP2	27:2:127:ARG:CD	2.58	0.45
20:S:41:GLU:OE2	20:S:44:ARG:NH2	2.38	0.45
21:T:197:TYR:O	21:T:197:TYR:CD1	2.70	0.45
24:W:84:THR:O	24:W:87:THR:N	2.50	0.45
24:W:313:ILE:HB	24:W:328:PHE:HB2	1.99	0.45
27:2:137:LYS:HE3	27:2:140:LEU:HD23	1.99	0.45
29:b:37:HIS:O	29:b:38:MET:HB2	2.17	0.45
36:n:35:ASP:HB2	36:n:36:PRO:CD	2.42	0.45
1:A:53:PHE:CE2	1:A:55:ASP:HB3	2.52	0.44
1:A:1499:GLU:OE1	40:1:60:ASN:CA	2.65	0.44
1:A:1890:GLN:CG	27:2:71:SER:OG	2.65	0.44
2:B:12:U:H3	2:B:65:G:H1	1.63	0.44
3:C:323:PHE:CD2	3:C:373:ILE:HG12	2.52	0.44
3:C:682:LYS:HG3	3:C:803:ARG:HD3	1.99	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
5:E:70:TYR:HE2	5:E:86:PHE:HB2	1.81	0.44
9:H:88:A:H2'	9:H:89:U:C6	2.50	0.44
10:I:692:SER:HA	10:I:695:CYS:H	1.82	0.44
18:Q:929:CYS:CB	18:Q:1012:ARG:HA	2.47	0.44
19:R:299:ARG:O	19:R:303:GLU:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:341:ASN:HB3	24:W:345:THR:H	1.81	0.44
24:W:547:LYS:O	24:W:547:LYS:HD2	2.17	0.44
33:d:43:LEU:HD11	33:d:51:LYS:HB3	1.99	0.44
40:1:46:GLY:O	45:3:331:ILE:CD1	2.60	0.44
1:A:172:GLU:OE1	28:z:99:LEU:CB	2.65	0.44
1:A:1757:GLU:HB2	1:A:1758:PRO:CD	2.47	0.44
1:A:1772:PHE:CD1	1:A:1929:SER:HB2	2.51	0.44
1:A:1883:VAL:HG22	40:1:291:ALA:HB2	1.98	0.44
1:A:1991:TYR:CE2	1:A:1997:VAL:HB	2.31	0.44
3:C:834:VAL:HG11	3:C:883:PHE:HE2	1.82	0.44
9:H:92:U:H2'	9:H:93:A:H8	1.82	0.44
16:O:229:LYS:HA	16:O:277:ARG:HH12	1.82	0.44
20:S:35:THR:HG22	20:S:82:PHE:HE2	1.82	0.44
24:W:453:PHE:CD2	27:2:83:ARG:CD	3.00	0.44
25:Y:413:LYS:HD2	25:Y:413:LYS:N	2.27	0.44
35:e:25:LEU:C	35:e:25:LEU:HD23	2.42	0.44
31:h:5:VAL:HB	31:h:6:PRO:HD3	2.00	0.44
33:k:33:THR:CG2	33:k:37:LYS:HE2	2.45	0.44
1:A:526:PRO:HD3	28:z:104:ASP:C	2.42	0.44
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.34	0.44
1:A:1306:LYS:NZ	2:B:38:C:O2'	2.49	0.44
1:A:1416:ILE:HD13	1:A:1416:ILE:HA	1.76	0.44
1:A:1557:LEU:HA	1:A:1557:LEU:HD23	1.80	0.44
1:A:1698:PRO:HB3	40:1:178:HIS:HD1	1.81	0.44
6:F:28:A:O2'	15:N:39:GLY:O	2.32	0.44
6:F:34:G:C3'	6:F:35:A:H5''	2.46	0.44
8:G:145:U:H2'	8:G:146:C:C5	2.52	0.44
19:R:185:GLY:O	19:R:187:ALA:N	2.51	0.44
35:l:25:LEU:HD23	35:l:25:LEU:C	2.42	0.44
1:A:1125:ILE:HG22	1:A:1147:VAL:HG21	1.99	0.44
1:A:1130:ASN:HD22	1:A:1139:ARG:NH1	2.10	0.44
1:A:1317:TYR:HB3	1:A:1474:MET:HE3	1.98	0.44
1:A:1526:LEU:HD23	1:A:1526:LEU:HA	1.75	0.44
3:C:605:ASP:OD1	3:C:608:ARG:NH1	2.41	0.44
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.44
6:F:35:A:H5''	6:F:35:A:C8	2.50	0.44
9:H:19:G:H21	17:P:8:THR:HA	1.82	0.44
9:H:112:G:H2'	9:H:113:G:C8	2.50	0.44
9:H:153:A:H2'	9:H:154:C:H5''	1.99	0.44
10:I:697:PRO:HD2	10:I:734:TYR:HD2	1.82	0.44
14:M:218:PHE:HE2	19:R:262:ILE:HD11	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:82:ASN:N	24:W:82:ASN:HD22	2.15	0.44
26:Z:686:ILE:HG12	26:Z:715:PRO:HB3	1.99	0.44
29:b:18:ARG:NH1	29:b:52:LYS:HB3	2.31	0.44
31:h:77:LEU:N	31:h:77:LEU:HD12	2.32	0.44
33:k:22:GLU:OE1	33:k:22:GLU:HA	2.16	0.44
40:1:346:ASP:N	40:1:346:ASP:OD1	2.50	0.44
1:A:318:TYR:O	3:C:645:ARG:NH1	2.49	0.44
1:A:1585:ILE:HG23	1:A:1740:LEU:HD21	2.00	0.44
1:A:1607:GLU:HB3	1:A:1632:PHE:HB3	1.99	0.44
3:C:130:ARG:HE	3:C:435:VAL:HA	1.83	0.44
6:F:58:G:O3'	17:P:12:ALA:HB2	2.17	0.44
8:G:120:G:O2'	8:G:121:G:C1'	2.59	0.44
10:I:649:ARG:HG2	10:I:674:MET:HE1	2.00	0.44
19:R:74:LEU:HD12	20:S:136:ILE:HG23	1.99	0.44
23:V:499:GLN:HE22	40:1:72:TRP:CB	2.16	0.44
28:z:79:LYS:O	28:z:88:ARG:NH2	2.50	0.44
29:b:52:LYS:HG3	29:b:52:LYS:O	2.18	0.44
35:e:20:LEU:CD2	35:e:24:TYR:CZ	3.00	0.44
1:A:197:PRO:HA	1:A:204:LEU:HD13	1.99	0.44
1:A:488:ASP:OD1	1:A:489:TRP:N	2.51	0.44
5:E:266:PRO:CD	13:L:785:GLN:CB	2.96	0.44
8:G:26:U:C2'	8:G:27:U:H5''	2.43	0.44
9:H:106:G:H5''	33:k:47:ARG:HH22	1.82	0.44
19:R:315:LYS:HZ3	19:R:315:LYS:CB	2.30	0.44
20:S:37:LYS:HB2	20:S:37:LYS:HZ3	1.78	0.44
21:T:399:LYS:HB2	21:T:406:ILE:HD11	1.99	0.44
24:W:79:VAL:HG23	29:b:114:ILE:HG12	2.00	0.44
31:a:5:VAL:HB	31:a:6:PRO:HD3	1.99	0.44
33:k:43:LEU:HD11	33:k:51:LYS:HB3	2.00	0.44
1:A:57:GLN:NE2	2:B:13:C:O2'	2.51	0.44
1:A:80:LYS:HD3	15:N:37:HIS:NE2	2.33	0.44
1:A:701:ILE:O	1:A:703:GLN:NE2	2.50	0.44
1:A:1776:ILE:HB	1:A:1858:PRO:HA	1.98	0.44
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.44
6:F:22:A:O4'	15:N:121:VAL:HG21	2.18	0.44
6:F:58:G:HO2'	6:F:59:G:P	2.35	0.44
10:I:651:ILE:HD12	10:I:654:LYS:HE2	2.00	0.44
13:L:56:PRO:HG2	19:R:268:LEU:HD11	1.98	0.44
24:W:79:VAL:CG2	29:b:114:ILE:CG1	2.96	0.44
24:W:475:TRP:HA	24:W:490:ALA:H	1.82	0.44
29:i:18:ARG:NH1	29:i:52:LYS:HB3	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1955:LYS:NZ	27:2:92:ARG:NH2	2.64	0.44
3:C:115:GLU:O	3:C:119:LEU:N	2.50	0.44
3:C:756:LYS:HA	3:C:759:LEU:HB3	1.99	0.44
5:E:150:HIS:CG	5:E:171:SER:HG	2.34	0.44
6:F:40:U:O4	6:F:41:A:N6	2.50	0.44
10:I:548:PHE:HD1	10:I:553:VAL:HG22	1.82	0.44
11:J:506:GLU:O	11:J:510:VAL:N	2.47	0.44
15:N:115:THR:OG1	15:N:116:ASN:N	2.51	0.44
16:O:261:ILE:HG23	16:O:272:ILE:HG13	1.99	0.44
21:T:248:THR:HB	21:T:266:GLU:HG3	2.00	0.44
24:W:453:PHE:CD2	27:2:83:ARG:NE	2.86	0.44
24:W:497:ASN:OD1	24:W:497:ASN:N	2.49	0.44
40:1:266:ARG:C	40:1:268:ARG:H	2.23	0.44
1:A:1561:PHE:O	1:A:1561:PHE:CD2	2.70	0.44
1:A:1764:SER:OG	1:A:1766:GLN:NE2	2.49	0.44
1:A:1792:LYS:HG2	1:A:1798:LEU:HG	1.99	0.44
3:C:532:ILE:HD13	3:C:532:ILE:HA	1.87	0.44
6:F:26:U:H4'	6:F:27:A:OP2	2.18	0.44
6:F:87:C:OP1	14:M:137:ARG:NH2	2.42	0.44
8:G:5:G:C5'	8:G:5:G:C8	3.01	0.44
21:T:270:VAL:HB	21:T:284:TYR:HB2	1.98	0.44
24:W:338:ILE:HG22	24:W:349:SER:HA	1.99	0.44
24:W:391:PHE:HB2	24:W:403:TRP:HB2	1.99	0.44
29:i:37:HIS:O	29:i:38:MET:HB2	2.17	0.44
40:1:46:GLY:C	45:3:331:ILE:HB	2.41	0.44
1:A:644:ILE:HD12	1:A:644:ILE:HA	1.90	0.43
1:A:1192:PHE:CD2	1:A:1192:PHE:N	2.86	0.43
1:A:1529:ILE:HA	1:A:1529:ILE:HD13	1.40	0.43
1:A:1640:SER:OG	1:A:1718:TRP:O	2.31	0.43
1:A:1686:ASP:HA	40:1:170:TRP:CZ2	2.53	0.43
1:A:1738:PRO:HA	40:1:287:PRO:HB2	2.00	0.43
1:A:1986:LEU:C	1:A:1986:LEU:CD2	2.84	0.43
5:E:94:ASN:HB3	5:E:100:ASP:H	1.83	0.43
6:F:25:C:C4'	6:F:26:U:OP2	2.65	0.43
8:G:7:G:C8	8:G:7:G:OP2	2.71	0.43
19:R:95:LYS:H	19:R:95:LYS:HD2	1.83	0.43
19:R:158:LYS:NZ	21:T:322:SER:O	2.51	0.43
29:b:18:ARG:HB2	29:b:83:GLU:HG2	1.99	0.43
35:l:34:TRP:CD1	35:l:34:TRP:N	2.86	0.43
2:B:27:U:HO2'	2:B:28:A:P	2.41	0.43
9:H:55:U:H2'	9:H:56:A:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:143:A:OP2	9:H:143:A:C2	2.71	0.43
10:I:509:ARG:HD3	10:I:509:ARG:HA	1.79	0.43
19:R:302:VAL:HA	19:R:305:ARG:HD2	2.00	0.43
19:R:332:ARG:HA	19:R:335:ARG:HD2	1.99	0.43
1:A:293:TRP:HE1	1:A:1136:ARG:NH1	2.11	0.43
1:A:766:THR:OG1	2:B:39:C:N4	2.51	0.43
3:C:94:ILE:H	3:C:94:ILE:HG13	1.59	0.43
6:F:7:G:H5'	6:F:7:G:C8	2.45	0.43
6:F:35:A:H8	6:F:35:A:H5'	1.82	0.43
9:H:142:C:O2'	9:H:143:A:H5'	2.18	0.43
9:H:157:G:H2'	9:H:158:G:O4'	2.19	0.43
10:I:518:PRO:HA	10:I:521:VAL:HG12	2.00	0.43
16:O:254:GLN:NE2	20:S:120:GLN:OE1	2.51	0.43
19:R:123:GLU:HG3	19:R:124:VAL:H	1.84	0.43
19:R:222:PRO:O	19:R:222:PRO:HG2	2.18	0.43
21:T:407:GLN:HE22	21:T:443:THR:HA	1.83	0.43
35:e:20:LEU:HD13	36:g:61:VAL:HG22	2.00	0.43
29:i:18:ARG:HB2	29:i:83:GLU:HG2	1.99	0.43
38:o:37:LEU:HB2	38:o:61:PRO:HD3	2.00	0.43
41:v:51:TYR:CB	42:w:151:VAL:O	2.66	0.43
1:A:1187:PHE:CD2	1:A:1189:MET:HE3	2.53	0.43
1:A:1498:TRP:HZ3	40:1:64:PRO:HD2	1.81	0.43
1:A:1751:LEU:N	1:A:1751:LEU:CD2	2.73	0.43
1:A:1792:LYS:NZ	9:H:37:U:O4'	2.52	0.43
5:E:99:CYS:O	29:b:107:GLY:HA3	2.18	0.43
6:F:42:C:C5'	6:F:43:A:OP2	2.65	0.43
13:L:646:GLY:O	13:L:650:GLY:N	2.52	0.43
21:T:216:ASN:HD21	21:T:473:SER:H	1.67	0.43
27:2:48:ILE:CG1	34:m:5:LEU:HD12	2.48	0.43
27:2:130:LYS:HB2	27:2:130:LYS:HE2	1.83	0.43
32:c:67:TYR:HB2	33:d:100:PHE:O	2.19	0.43
36:g:32:ARG:HG3	36:g:43:ASP:HB2	1.99	0.43
1:A:693:ILE:HD12	1:A:706:ALA:HA	2.01	0.43
1:A:1890:GLN:HG2	27:2:71:SER:OG	2.18	0.43
1:A:1958:LYS:CE	27:2:96:MET:O	2.67	0.43
5:E:259:VAL:HB	5:E:277:PHE:HB2	1.99	0.43
6:F:39:A:H2'	6:F:40:U:O4'	2.18	0.43
13:L:7:LYS:HB3	13:L:40:ARG:HA	2.00	0.43
24:W:417:HIS:ND1	24:W:437:SER:HB3	2.34	0.43
41:v:53:HIS:N	42:w:149:CYS:O	2.34	0.43
43:u:254:PHE:HA	43:u:401:ASP:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1596:VAL:HG22	40:1:278:LEU:CD2	2.48	0.43
1:A:1685:LEU:HD13	40:1:170:TRP:CE3	2.53	0.43
1:A:1728:GLN:NE2	40:1:278:LEU:O	2.52	0.43
2:B:40:U:H6	2:B:40:U:O5'	2.01	0.43
6:F:45:A:C2'	6:F:73:A:C2	3.02	0.43
9:H:85:A:H2'	9:H:88:A:N6	2.33	0.43
9:H:154:C:O2'	9:H:155:C:C5'	2.66	0.43
10:I:692:SER:C	10:I:694:ILE:N	2.75	0.43
16:O:239:LEU:HD22	16:O:270:ALA:HB2	2.00	0.43
19:R:332:ARG:HA	19:R:335:ARG:HG3	2.00	0.43
26:Z:709:ARG:NH2	26:Z:718:ASP:OD2	2.51	0.43
32:j:67:TYR:HB2	33:k:100:PHE:O	2.19	0.43
34:m:5:LEU:HD22	35:l:57:VAL:CG1	2.40	0.43
1:A:856:LEU:N	9:H:29:A:N7	2.61	0.43
1:A:1873:GLU:HG3	40:1:290:ARG:HH22	1.84	0.43
5:E:266:PRO:HB3	13:L:788:TYR:CB	2.49	0.43
8:G:127:U:H4'	24:W:545:ARG:NH2	2.32	0.43
8:G:139:U:H2'	8:G:140:A:O4'	2.18	0.43
24:W:84:THR:N	24:W:87:THR:OG1	2.52	0.43
25:Y:412:SER:HG	25:Y:415:GLU:HG3	1.84	0.43
34:f:65:ARG:HH11	34:f:65:ARG:HG3	1.83	0.43
37:q:106:ALA:CB	37:t:106:ALA:HB1	2.43	0.43
35:l:20:LEU:CD2	35:l:24:TYR:CZ	3.00	0.43
40:1:46:GLY:O	45:3:331:ILE:CB	2.60	0.43
40:1:106:VAL:HB	40:1:151:PRO:HB2	2.00	0.43
1:A:1093:ASP:OD1	1:A:1093:ASP:N	2.51	0.43
1:A:1817:LEU:HD12	1:A:1817:LEU:HA	1.87	0.43
3:C:501:ILE:HG22	3:C:530:LEU:HD11	2.00	0.43
5:E:346:SER:OG	5:E:348:ASP:OD1	2.31	0.43
10:I:673:ASP:OD1	10:I:677:LYS:HE3	2.19	0.43
19:R:317:LYS:HB3	19:R:321:GLU:OE1	2.19	0.43
19:R:326:GLU:HB3	19:R:330:LYS:NZ	2.34	0.43
28:z:58:ARG:HD2	28:z:62:GLN:HB3	2.00	0.43
38:o:161:MET:O	38:o:162:PHE:HB2	2.19	0.43
45:3:330:ARG:HH11	45:3:332:PRO:HA	1.84	0.43
1:A:1393:ARG:NH1	25:Y:405:MET:HG3	2.33	0.43
1:A:1526:LEU:CD1	8:G:171:G:O6	2.67	0.43
1:A:1526:LEU:HD12	8:G:171:G:O6	2.18	0.43
8:G:21:A:N6	16:O:91:GLY:O	2.51	0.43
9:H:91:U:H2'	9:H:92:U:C6	2.50	0.43
9:H:178:A:N3	9:H:178:A:H2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:273:GLU:CA	18:Q:357:ALA:HB3	2.37	0.43
10:I:685:ARG:HH21	10:I:711:GLU:CD	2.26	0.43
19:R:305:ARG:HH11	19:R:305:ARG:CG	2.25	0.43
19:R:315:LYS:HG3	19:R:319:LYS:CE	2.48	0.43
23:V:450:ILE:CG1	40:1:89:PRO:CG	2.82	0.43
24:W:551:LYS:HB3	24:W:572:ASP:HB3	2.00	0.43
27:2:125:ALA:HA	27:2:128:ARG:HB2	2.01	0.43
37:q:106:ALA:CB	37:t:106:ALA:HB3	2.48	0.43
1:A:1543:ASN:HB2	1:A:1569:LEU:HD21	2.00	0.43
1:A:1995:ASN:ND2	26:Z:756:TYR:HB3	2.33	0.43
8:G:171:G:N3	8:G:171:G:H2'	2.32	0.43
9:H:98:G:H5'	9:H:104:U:OP2	2.19	0.43
18:Q:826:GLY:O	18:Q:1136:GLN:HA	2.18	0.43
27:2:71:SER:OG	27:2:71:SER:O	2.31	0.43
38:o:132:ARG:NE	38:o:154:GLU:OE1	2.43	0.43
42:w:137:GLN:O	42:w:143:PRO:HA	2.19	0.43
1:A:331:TRP:HZ3	3:C:179:VAL:HG11	1.83	0.42
1:A:369:GLU:O	1:A:371:LEU:N	2.51	0.42
1:A:1124:ASN:ND2	1:A:1148:ASN:OD1	2.52	0.42
1:A:1482:GLU:OE1	40:1:86:ARG:HD3	2.19	0.42
1:A:1500:GLY:HA2	40:1:62:HIS:HB2	2.00	0.42
1:A:1566:ILE:HD12	1:A:1567:PRO:N	2.34	0.42
1:A:1642:PRO:CB	40:1:175:PRO:HB3	2.46	0.42
1:A:1817:LEU:HB3	1:A:1917:PHE:HB2	2.01	0.42
1:A:1889:LEU:HD12	1:A:2013:GLY:N	2.28	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:769:GLY:O	3:C:773:GLY:N	2.52	0.42
5:E:307:ARG:HH12	29:b:115:PRO:CG	2.32	0.42
9:H:43:U:H2'	9:H:44:U:C6	2.54	0.42
24:W:266:ARG:HD3	35:l:14:MET:N	2.34	0.42
24:W:416:ARG:HB3	24:W:443:ARG:HH12	1.84	0.42
24:W:552:VAL:HG13	24:W:571:TRP:CD1	2.54	0.42
28:z:58:ARG:NH2	40:1:180:LYS:HE2	2.34	0.42
29:i:52:LYS:HG3	29:i:52:LYS:O	2.18	0.42
1:A:99:VAL:HG13	1:A:554:THR:HG21	2.00	0.42
1:A:1468:ASN:OD1	8:G:177:G:H5'	2.19	0.42
1:A:1560:ILE:CD1	1:A:1577:PHE:HE2	2.25	0.42
1:A:1611:LYS:HA	1:A:1629:ILE:HG12	2.01	0.42
1:A:1807:ILE:HG23	1:A:1841:THR:HG23	2.00	0.42
1:A:1976:TRP:HA	1:A:1979:VAL:HG22	2.00	0.42
3:C:874:PHE:CE2	43:u:103:GLN:CB	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1583:ASP:C	4:D:1585:GLN:H	2.26	0.42
9:H:33:G:OP2	9:H:33:G:H8	2.01	0.42
9:H:77:C:H5'	24:W:242:HIS:ND1	2.33	0.42
11:J:206:LEU:HD23	11:J:206:LEU:HA	1.92	0.42
11:J:486:ALA:O	11:J:490:ASN:N	2.52	0.42
11:J:526:GLU:O	11:J:530:TRP:N	2.48	0.42
14:M:118:LYS:O	14:M:118:LYS:HE3	2.18	0.42
20:S:72:ARG:CD	24:W:90:ALA:O	2.62	0.42
24:W:248:ASP:HB2	24:W:252:ARG:HG2	2.00	0.42
24:W:341:ASN:HB2	24:W:346:GLN:H	1.84	0.42
24:W:398:LYS:HG2	24:W:419:GLY:H	1.84	0.42
37:s:18:SER:O	37:s:22:ASN:CB	2.67	0.42
40:1:305:ASP:OD1	40:1:305:ASP:N	2.52	0.42
1:A:934:ARG:CZ	25:Y:425:ILE:HG21	2.49	0.42
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	2.01	0.42
1:A:1698:PRO:HG3	40:1:181:ILE:C	2.44	0.42
3:C:566:THR:OG1	3:C:567:GLU:N	2.51	0.42
5:E:103:ALA:HA	29:b:101:ALA:O	2.20	0.42
8:G:134:U:H3'	8:G:135:G:H21	1.84	0.42
17:P:13:ARG:HA	21:T:309:ASP:O	2.19	0.42
33:d:33:THR:CG2	33:d:37:LYS:HE2	2.46	0.42
38:o:160:LYS:O	38:o:161:MET:C	2.63	0.42
1:A:199:GLU:CD	40:1:139:ARG:CD	2.92	0.42
1:A:772:CYS:SG	1:A:1249:MET:HE1	2.60	0.42
1:A:1934:SER:CB	40:1:347:PRO:HB3	2.46	0.42
9:H:155:C:H2'	9:H:156:U:H5''	2.02	0.42
10:I:491:ALA:HB2	10:I:510:ILE:HD11	2.00	0.42
11:J:216:ASP:O	11:J:218:GLU:N	2.53	0.42
17:P:9:PHE:CD2	17:P:9:PHE:N	2.88	0.42
21:T:465:ILE:HG12	21:T:481:GLU:HG2	2.02	0.42
29:b:9:MET:HE2	32:c:39:HIS:HE1	1.85	0.42
34:m:65:ARG:HG3	34:m:65:ARG:HH11	1.83	0.42
1:A:331:TRP:CZ3	3:C:179:VAL:HG21	2.54	0.42
1:A:1631:LEU:HB3	1:A:1637:TRP:HZ3	1.84	0.42
1:A:1955:LYS:HZ3	27:2:93:GLN:NE2	2.11	0.42
3:C:261:ASP:OD2	47:C:1500:GTP:N1	2.46	0.42
8:G:14:A:C8	8:G:14:A:OP2	2.72	0.42
9:H:101:U:H4'	29:i:73:ARG:NH2	2.35	0.42
9:H:107:A:N1	9:H:108:G:C5	2.88	0.42
10:I:84:HIS:CB	10:I:90:PRO:CB	2.97	0.42
10:I:696:ASP:HB3	10:I:699:THR:CB	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:212:ASN:HB3	14:M:215:ASN:H	1.84	0.42
27:2:48:ILE:CG2	34:m:5:LEU:CD1	2.83	0.42
35:e:51:ASP:C	35:e:51:ASP:OD1	2.61	0.42
33:k:68:GLU:HA	33:k:97:SER:O	2.19	0.42
35:l:51:ASP:C	35:l:51:ASP:OD1	2.61	0.42
38:o:56:LYS:HE2	38:o:58:ASP:CG	2.44	0.42
1:A:451:LEU:HD23	1:A:451:LEU:HA	1.84	0.42
1:A:663:ARG:HG3	1:A:663:ARG:HH21	1.81	0.42
1:A:1333:VAL:HG11	23:V:467:LEU:HD12	2.01	0.42
1:A:1737:ASN:OD1	1:A:1738:PRO:N	2.51	0.42
2:B:57:G:C2'	2:B:58:U:H5'	2.49	0.42
2:B:95:G:C6	35:e:36:TYR:O	2.71	0.42
8:G:147:C:N3	8:G:148:U:C5	2.88	0.42
10:I:590:LYS:HA	10:I:590:LYS:HD3	1.84	0.42
16:O:247:ASP:HA	16:O:250:ASN:HD22	1.84	0.42
19:R:324:LEU:HA	19:R:327:MET:HE2	2.01	0.42
19:R:329:GLN:HA	19:R:332:ARG:NH1	2.34	0.42
29:b:50:LYS:C	29:b:51:ILE:HG13	2.45	0.42
32:c:63:ASN:HA	33:d:102:ARG:CZ	2.50	0.42
1:A:310:THR:OG1	22:U:2:TYR:O	2.37	0.42
1:A:881:ILE:HG23	1:A:918:THR:HG23	2.02	0.42
1:A:1560:ILE:HD11	1:A:1577:PHE:HE2	1.74	0.42
2:B:87:A:H5'	2:B:93:U:OP2	2.18	0.42
3:C:264:ILE:HG12	3:C:378:TYR:CE1	2.55	0.42
3:C:534:VAL:HB	3:C:537:TYR:HB2	2.00	0.42
3:C:667:VAL:N	3:C:824:THR:CG2	2.78	0.42
6:F:43:A:O2'	6:F:44:G:H5'	2.19	0.42
10:I:727:ARG:NH2	10:I:727:ARG:HG2	2.33	0.42
13:L:5:MET:SD	13:L:5:MET:O	2.78	0.42
14:M:182:MET:HE2	14:M:182:MET:HB3	1.97	0.42
15:N:117:CYS:SG	15:N:119:CYS:HB3	2.60	0.42
24:W:84:THR:C	24:W:86:GLU:N	2.74	0.42
24:W:265:LEU:HD12	24:W:300:SER:HB2	2.02	0.42
24:W:504:GLY:H	24:W:535:TRP:HZ2	1.65	0.42
26:Z:710:PHE:HE1	26:Z:747:LEU:HD13	1.84	0.42
27:2:111:LYS:HG2	27:2:114:GLU:OE2	2.19	0.42
32:c:66:ARG:CZ	33:d:48:ASN:HB3	2.49	0.42
32:j:63:ASN:HA	33:k:102:ARG:CZ	2.49	0.42
34:m:65:ARG:HG3	34:m:65:ARG:NH1	2.35	0.42
1:A:258:PHE:CE2	1:A:434:HIS:HA	2.55	0.42
1:A:773:LYS:HA	1:A:773:LYS:HD2	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1160:ARG:HD3	17:P:192:VAL:HG11	2.01	0.42
1:A:1479:GLY:HA2	40:1:88:GLN:CD	2.44	0.42
1:A:1552:GLN:CB	1:A:1563:HIS:CD2	3.01	0.42
1:A:1994:LYS:HD2	26:Z:756:TYR:CD1	2.55	0.42
6:F:88:G:C4'	14:M:121:ASP:HB2	2.50	0.42
8:G:129:G:O4'	24:W:541:LYS:HE2	2.19	0.42
8:G:173:G:N3	8:G:173:G:C2'	2.72	0.42
9:H:43:U:OP2	9:H:43:U:C6	2.73	0.42
9:H:77:C:C5'	24:W:242:HIS:HE1	2.33	0.42
10:I:731:GLN:NE2	10:I:731:GLN:C	2.74	0.42
13:L:7:LYS:HB3	13:L:40:ARG:CA	2.49	0.42
21:T:418:THR:OG1	21:T:466:PHE:O	2.38	0.42
24:W:553:CYS:HA	24:W:570:GLY:HA2	2.01	0.42
1:A:1757:GLU:CB	1:A:1758:PRO:CD	2.98	0.42
3:C:589:LYS:HG3	3:C:628:VAL:HG13	2.02	0.42
5:E:266:PRO:HG2	13:L:785:GLN:HA	1.96	0.42
8:G:7:G:C2'	8:G:8:C:H5'	2.50	0.42
9:H:157:G:H5''	9:H:157:G:C8	2.50	0.42
11:J:313:TRP:CE3	11:J:336:TRP:HB2	2.55	0.42
24:W:462:HIS:ND1	24:W:482:ASP:HB3	2.35	0.42
33:d:28:PRO:HD2	34:f:37:ASP:HB3	2.02	0.42
33:k:28:PRO:HD2	34:m:37:ASP:HB3	2.02	0.42
33:k:103:GLY:O	33:k:106:VAL:HG23	2.20	0.42
35:l:20:LEU:HD13	36:n:61:VAL:HG22	2.00	0.42
1:A:612:ILE:O	1:A:616:PHE:N	2.46	0.42
1:A:975:VAL:HG22	1:A:1177:VAL:HG22	2.01	0.42
1:A:1430:LEU:CB	25:Y:400:TRP:CZ3	3.03	0.42
1:A:1615:HIS:HE2	28:z:96:LEU:CB	2.32	0.42
1:A:1631:LEU:HD23	1:A:1631:LEU:HA	1.85	0.42
1:A:2003:THR:H	1:A:2006:GLU:HB2	1.85	0.42
1:A:2014:MET:SD	1:A:2014:MET:C	3.01	0.42
1:A:2014:MET:SD	1:A:2014:MET:O	2.78	0.42
13:L:633:GLN:O	13:L:637:VAL:N	2.50	0.42
27:2:23:ILE:O	27:2:23:ILE:HG13	2.16	0.42
28:z:55:LEU:HD22	40:1:180:LYS:HZ2	1.76	0.42
35:e:34:TRP:N	35:e:34:TRP:CD1	2.86	0.42
31:h:58:LEU:HD22	36:n:71:GLU:CD	2.45	0.42
29:i:50:LYS:C	29:i:51:ILE:HG13	2.44	0.42
32:j:66:ARG:CZ	33:k:48:ASN:HB3	2.49	0.42
40:1:178:HIS:CE1	40:1:181:ILE:CG1	3.02	0.42
1:A:152:ARG:CZ	40:1:132:ASP:O	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:764:GLY:HA2	1:A:1245:ARG:NH1	2.35	0.41
1:A:1764:SER:HB2	1:A:1888:GLU:HB3	2.02	0.41
1:A:1995:ASN:HD21	26:Z:756:TYR:HB3	1.85	0.41
6:F:23:U:C6	15:N:118:ILE:HG23	2.55	0.41
6:F:37:C:C3'	6:F:37:C:C6	3.02	0.41
10:I:581:GLU:HA	10:I:584:LEU:HD12	2.01	0.41
14:M:138:LEU:HD23	14:M:138:LEU:HA	1.89	0.41
15:N:102:CYS:HB3	15:N:104:ARG:H	1.84	0.41
24:W:315:LEU:O	24:W:325:LEU:N	2.47	0.41
33:d:68:GLU:HA	33:d:97:SER:O	2.19	0.41
1:A:470:ARG:NH2	1:A:470:ARG:CG	2.81	0.41
1:A:1501:LEU:HD21	45:3:337:ILE:HD12	1.97	0.41
1:A:1660:TYR:OH	1:A:1717:ASN:O	2.30	0.41
1:A:2332:ASP:C	1:A:2334:TYR:H	2.28	0.41
2:B:90:U:H4'	29:b:73:ARG:NH2	2.35	0.41
6:F:22:A:C8	24:W:130:ARG:CD	3.03	0.41
6:F:25:C:N4	16:O:39:GLU:OE1	2.53	0.41
19:R:310:ARG:CZ	19:R:310:ARG:CA	2.97	0.41
29:i:9:MET:HE2	32:j:39:HIS:HE1	1.84	0.41
38:o:52:ASN:HB2	38:o:74:ASN:OD1	2.20	0.41
1:A:526:PRO:CB	28:z:106:PRO:CD	2.81	0.41
1:A:1251:SER:OG	1:A:1259:ILE:HG12	2.20	0.41
1:A:1850:ARG:NH1	40:1:265:LEU:CD1	2.75	0.41
3:C:140:HIS:CD2	3:C:230:ASP:HB2	2.56	0.41
5:E:61:LEU:O	29:b:108:ARG:O	2.38	0.41
5:E:266:PRO:HB3	13:L:788:TYR:C	2.46	0.41
6:F:48:A:H61	13:L:30:GLN:HE22	1.68	0.41
10:I:273:GLU:HA	18:Q:357:ALA:H	1.85	0.41
10:I:511:LEU:HD11	10:I:521:VAL:HG23	2.01	0.41
10:I:699:THR:CG2	10:I:699:THR:O	2.68	0.41
14:M:165:ASN:HB2	19:R:95:LYS:HA	2.02	0.41
24:W:304:LEU:HD11	24:W:567:ILE:HG21	2.02	0.41
37:q:60:PRO:CB	37:s:94:GLN:CA	2.97	0.41
2:B:20:G:C1'	2:B:21:A:OP1	2.68	0.41
8:G:129:G:C5'	24:W:541:LYS:HZ3	2.02	0.41
9:H:24:A:C2	13:L:29:ASN:HB3	2.53	0.41
11:J:527:LYS:O	11:J:531:LYS:N	2.48	0.41
15:N:124:SER:OG	15:N:125:LYS:NZ	2.47	0.41
15:N:132:ILE:HD13	15:N:132:ILE:HA	1.88	0.41
19:R:99:ASP:OD2	19:R:103:ARG:NE	2.42	0.41
35:e:24:TYR:CD1	35:e:31:ILE:HD11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:j:3:LEU:O	32:j:6:PHE:HB3	2.21	0.41
1:A:274:PRO:HB3	7:4:-11:G:C8	2.56	0.41
1:A:599:MET:HE3	1:A:599:MET:HB3	1.89	0.41
1:A:858:GLN:C	1:A:858:GLN:CD	2.85	0.41
1:A:1156:ASP:OD2	1:A:1160:ARG:NH2	2.54	0.41
1:A:1682:ALA:O	40:1:170:TRP:CD1	2.74	0.41
1:A:1985:ASP:N	1:A:1985:ASP:OD1	2.52	0.41
5:E:310:TYR:CE1	5:E:322:LYS:HE2	2.55	0.41
6:F:43:A:N1	6:F:44:G:C6	2.89	0.41
8:G:21:A:C8	16:O:152:ARG:NH2	2.86	0.41
9:H:103:U:C3'	9:H:104:U:H5'	2.51	0.41
10:I:329:LEU:CB	18:Q:353:LEU:CB	2.98	0.41
10:I:729:SER:C	10:I:731:GLN:N	2.77	0.41
11:J:529:HIS:O	11:J:533:TYR:N	2.42	0.41
18:Q:97:MET:O	18:Q:101:LYS:N	2.53	0.41
34:f:65:ARG:HB3	34:f:68:ASN:HD22	1.85	0.41
34:m:65:ARG:HB3	34:m:68:ASN:HD22	1.85	0.41
1:A:591:MET:HE2	1:A:591:MET:HB3	1.84	0.41
1:A:1803:ILE:CG2	24:W:451:VAL:HG21	2.50	0.41
1:A:1930:TYR:HA	1:A:1933:PHE:HB3	2.02	0.41
1:A:1951:LYS:O	1:A:1955:LYS:N	2.52	0.41
1:A:1978:LYS:O	1:A:1982:GLN:N	2.53	0.41
1:A:2332:ASP:O	1:A:2334:TYR:N	2.54	0.41
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.41
8:G:147:C:C5'	8:G:147:C:C6	3.00	0.41
9:H:39:U:C6	9:H:39:U:C5'	2.90	0.41
10:I:717:GLU:HA	10:I:720:ILE:HB	2.02	0.41
17:P:72:ARG:O	17:P:76:ARG:N	2.54	0.41
24:W:82:ASN:ND2	24:W:82:ASN:N	2.69	0.41
28:z:107:LYS:O	28:z:110:TRP:CB	2.69	0.41
33:d:39:ASN:OD1	33:d:55:ARG:HD3	2.20	0.41
39:p:74:PHE:CG	39:p:79:MET:HE3	2.55	0.41
1:A:467:GLN:HG2	2:B:19:A:C4	2.55	0.41
1:A:1611:LYS:HA	1:A:1629:ILE:HA	2.03	0.41
1:A:1981:VAL:HA	1:A:1984:LYS:HB3	2.03	0.41
3:C:307:VAL:HG12	3:C:308:CYS:O	2.20	0.41
3:C:366:GLN:HB3	3:C:370:VAL:HB	2.02	0.41
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.55	0.41
9:H:24:A:H3'	9:H:25:G:C5'	2.50	0.41
9:H:152:G:H2'	9:H:153:A:C1'	2.51	0.41
10:I:699:THR:O	10:I:699:THR:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:258:ILE:O	11:J:262:ARG:N	2.51	0.41
23:V:171:ASN:CB	43:u:277:ILE:HA	2.51	0.41
40:1:183:GLU:O	40:1:187:LYS:NZ	2.43	0.41
1:A:526:PRO:O	28:z:102:HIS:HB2	2.21	0.41
1:A:779:LEU:HD23	1:A:782:LEU:HD12	2.02	0.41
8:G:176:U:O2	8:G:176:U:C2'	2.67	0.41
10:I:681:ILE:HA	10:I:710:PHE:HZ	1.86	0.41
18:Q:875:HIS:O	18:Q:1034:ILE:N	2.49	0.41
33:d:103:GLY:O	33:d:106:VAL:HG23	2.20	0.41
1:A:273:ILE:H	1:A:273:ILE:HG13	1.56	0.41
1:A:461:HIS:CD2	2:B:26:A:H61	2.39	0.41
1:A:516:LEU:HD11	1:A:538:SER:HB2	2.03	0.41
1:A:1883:VAL:CA	40:1:289:THR:O	2.68	0.41
1:A:1955:LYS:CB	27:2:92:ARG:HH12	2.33	0.41
1:A:1991:TYR:O	1:A:1993:LYS:N	2.54	0.41
3:C:131:ASN:HA	3:C:201:ASN:HB2	2.03	0.41
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.53	0.41
3:C:604:LEU:HD21	3:C:627:HIS:CE1	2.56	0.41
3:C:666:VAL:CG1	3:C:824:THR:HG22	2.49	0.41
3:C:755:ASP:O	3:C:759:LEU:N	2.44	0.41
6:F:7:G:H4'	6:F:7:G:OP1	2.20	0.41
6:F:26:U:HO2'	6:F:27:A:P	2.42	0.41
8:G:20:A:OP2	16:O:159:ARG:HG3	2.21	0.41
8:G:139:U:H3	9:H:38:A:H61	1.69	0.41
9:H:20:G:N7	17:P:5:ALA:HB1	2.36	0.41
9:H:106:G:H5'	33:k:47:ARG:NH2	2.34	0.41
9:H:152:G:H2'	9:H:152:G:N3	2.36	0.41
11:J:238:ASN:C	11:J:240:THR:H	2.28	0.41
14:M:165:ASN:OD1	14:M:166:SER:N	2.54	0.41
16:O:81:CYS:SG	16:O:82:GLN:N	2.94	0.41
16:O:292:ILE:HG12	16:O:297:ARG:HA	2.03	0.41
19:R:318:GLU:OE2	19:R:318:GLU:CA	2.69	0.41
20:S:11:PRO:HA	20:S:12:PRO:HD3	1.89	0.41
20:S:70:THR:HG21	24:W:71:HIS:HB3	2.03	0.41
21:T:349:SER:OG	21:T:351:ASP:OD1	2.30	0.41
23:V:623:ASN:HA	23:V:626:PHE:HB3	2.03	0.41
24:W:79:VAL:HG21	29:b:114:ILE:CG1	2.49	0.41
24:W:458:GLU:HB3	24:W:460:SER:H	1.86	0.41
27:2:137:LYS:CE	27:2:140:LEU:HB3	2.50	0.41
31:a:58:LEU:HD22	36:g:71:GLU:CD	2.46	0.41
34:f:65:ARG:HG3	34:f:65:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:21:ILE:HA	35:e:24:TYR:HD2	1.86	0.41
35:l:18:ILE:H	35:l:18:ILE:HG13	1.70	0.41
35:l:24:TYR:CD1	35:l:31:ILE:HD11	2.56	0.41
38:o:140:PRO:O	38:o:155:ARG:NH1	2.48	0.41
39:p:13:ASN:HB2	39:p:80:ARG:HH21	1.86	0.41
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.89	0.41
1:A:158:ARG:NH1	28:z:62:GLN:NE2	2.63	0.41
1:A:260:LEU:HA	1:A:260:LEU:HD23	1.91	0.41
1:A:274:PRO:HG3	22:U:1:MET:HB3	2.02	0.41
1:A:801:ILE:O	1:A:805:GLU:HB3	2.20	0.41
1:A:1555:LEU:HB2	1:A:1560:ILE:O	2.21	0.41
1:A:1565:LYS:HB3	7:4:-4:A:P	2.61	0.41
1:A:1758:PRO:HB3	45:3:354:MET:SD	2.61	0.41
1:A:1795:GLU:OE1	13:L:172:ARG:NH2	2.54	0.41
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.86	0.41
10:I:631:MET:HA	10:I:634:ILE:HB	2.03	0.41
14:M:118:LYS:O	14:M:118:LYS:CE	2.69	0.41
16:O:120:ASN:OD1	19:R:222:PRO:HD2	2.21	0.41
19:R:132:LEU:HB3	21:T:399:LYS:HE3	2.02	0.41
27:2:38:LEU:CD2	34:m:9:PRO:HA	2.51	0.41
33:k:62:HIS:O	33:k:103:GLY:HA3	2.21	0.41
39:p:3:ILE:HG22	39:p:83:TYR:HB2	2.02	0.41
1:A:1728:GLN:NE2	1:A:1728:GLN:O	2.53	0.40
3:C:458:ASP:OD1	3:C:458:ASP:N	2.54	0.40
4:D:577:LYS:O	4:D:581:SER:N	2.54	0.40
5:E:144:VAL:HG12	5:E:145:LYS:HG3	2.02	0.40
14:M:118:LYS:O	14:M:118:LYS:CG	2.70	0.40
15:N:131:ILE:HG21	16:O:177:GLU:HG2	2.04	0.40
17:P:10:GLU:O	17:P:10:GLU:CG	2.69	0.40
21:T:427:LEU:O	21:T:439:TRP:N	2.50	0.40
33:d:110:LEU:CD1	34:f:59:LEU:HB3	2.46	0.40
33:k:110:LEU:CD1	34:m:59:LEU:HB3	2.46	0.40
38:o:107:ASP:OD1	38:o:134:TYR:OH	2.27	0.40
40:1:130:LYS:HB3	40:1:130:LYS:HE2	1.80	0.40
1:A:156:ARG:NH1	40:1:134:PHE:CE2	2.87	0.40
1:A:496:VAL:O	1:A:500:GLY:N	2.52	0.40
2:B:12:U:O2'	2:B:13:C:P	2.79	0.40
3:C:935:ILE:HG22	3:C:939:ARG:HE	1.87	0.40
4:D:538:ILE:O	4:D:585:ILE:HA	2.21	0.40
9:H:39:U:HO2'	9:H:40:C:P	2.28	0.40
9:H:40:C:C2'	9:H:41:U:H5''	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:168:A:C2	36:n:54:GLN:CB	3.04	0.40
9:H:171:U:H2'	9:H:172:C:O4'	2.21	0.40
11:J:215:THR:OG1	11:J:216:ASP:N	2.47	0.40
17:P:10:GLU:HA	17:P:11:PRO:HD2	1.88	0.40
20:S:71:GLY:O	20:S:111:GLN:NE2	2.50	0.40
24:W:368:SER:OG	24:W:369:ARG:N	2.55	0.40
27:2:111:LYS:HA	27:2:114:GLU:CD	2.47	0.40
32:c:20:LYS:O	32:c:66:ARG:NH2	2.55	0.40
33:k:39:ASN:OD1	33:k:55:ARG:HD3	2.21	0.40
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.77	0.40
1:A:1386:TRP:CD1	25:Y:408:ALA:HB1	2.56	0.40
3:C:134:LEU:O	3:C:205:THR:OG1	2.29	0.40
6:F:28:A:C2	16:O:174:LYS:HB2	2.55	0.40
6:F:33:G:O2'	6:F:34:G:P	2.79	0.40
7:4:-12:G:HO2'	7:4:-11:G:C5'	2.32	0.40
8:G:9:C:H2'	8:G:10:U:O4'	2.22	0.40
8:G:176:U:O2	8:G:176:U:O2'	2.30	0.40
9:H:88:A:C6	9:H:89:U:C4	3.09	0.40
9:H:183:G:C6	9:H:184:C:N4	2.89	0.40
10:I:521:VAL:HG21	10:I:544:GLY:HA3	2.03	0.40
24:W:348:LEU:HD11	24:W:356:LEU:HD21	2.03	0.40
24:W:357:LYS:HE2	24:W:369:ARG:HD3	2.04	0.40
24:W:401:VAL:HG13	24:W:410:ILE:HG23	2.03	0.40
25:Y:418:ASP:OD1	25:Y:418:ASP:N	2.55	0.40
33:d:62:HIS:O	33:d:103:GLY:HA3	2.21	0.40
38:o:37:LEU:HB2	38:o:61:PRO:CD	2.51	0.40
1:A:91:ALA:HA	19:R:207:MET:HE3	2.04	0.40
1:A:192:GLN:H	1:A:192:GLN:HG2	1.73	0.40
1:A:641:MET:HE3	1:A:641:MET:HB3	1.94	0.40
1:A:1284:LEU:HA	1:A:1284:LEU:HD23	1.89	0.40
1:A:1432:TYR:OH	25:Y:399:LYS:NZ	2.49	0.40
1:A:1685:LEU:CG	40:1:173:TYR:CE2	3.05	0.40
1:A:1762:TYR:HB3	1:A:1887:SER:HA	2.04	0.40
1:A:1877:LEU:HA	1:A:1877:LEU:HD12	1.86	0.40
1:A:1997:VAL:CG2	26:Z:658:TYR:CD1	2.93	0.40
3:C:304:LEU:HD23	3:C:304:LEU:HA	1.90	0.40
4:D:1481:ILE:C	4:D:1483:ARG:H	2.28	0.40
5:E:167:VAL:HB	5:E:179:TRP:HB2	2.03	0.40
9:H:33:G:OP2	9:H:33:G:C8	2.73	0.40
14:M:118:LYS:O	14:M:118:LYS:CD	2.70	0.40
19:R:303:GLU:OE1	19:R:303:GLU:CA	2.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:318:GLU:O	19:R:322:GLU:CG	2.69	0.40
21:T:331:ASN:HB3	21:T:332:ALA:H	1.77	0.40
24:W:101:THR:HG23	24:W:104:MET:H	1.86	0.40
24:W:207:LYS:HE2	24:W:207:LYS:HB2	1.93	0.40
31:a:63:ILE:HG12	36:g:69:MET:HG3	2.03	0.40
39:p:72:PHE:HA	39:p:73:PRO:HD3	1.83	0.40
1:A:348:PRO:HB3	1:A:394:TYR:CZ	2.56	0.40
6:F:37:C:H3'	6:F:37:C:C6	2.56	0.40
6:F:45:A:H5'	13:L:169:ARG:HH22	1.85	0.40
9:H:36:G:C3'	9:H:37:U:H5'	2.48	0.40
10:I:491:ALA:HA	10:I:506:VAL:HG11	2.03	0.40
13:L:710:ALA:O	13:L:714:GLU:N	2.55	0.40
13:L:721:LEU:O	13:L:725:GLN:N	2.39	0.40
16:O:110:SER:OG	16:O:113:ASN:ND2	2.53	0.40
18:Q:876:LEU:HA	18:Q:1034:ILE:O	2.22	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	2247/2335 (96%)	2044 (91%)	191 (8%)	12 (0%)	25	63
3	C	856/972 (88%)	781 (91%)	71 (8%)	4 (0%)	25	63
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	44	78
5	E	297/357 (83%)	275 (93%)	22 (7%)	0	100	100
10	I	576/855 (67%)	558 (97%)	14 (2%)	4 (1%)	19	56
11	J	530/848 (62%)	489 (92%)	33 (6%)	8 (2%)	8	39
12	K	147/225 (65%)	136 (92%)	8 (5%)	3 (2%)	6	32
13	L	425/802 (53%)	408 (96%)	15 (4%)	2 (0%)	25	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	128/243 (53%)	117 (91%)	11 (9%)	0	100	100
15	N	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	19	56
16	O	283/420 (67%)	259 (92%)	23 (8%)	1 (0%)	30	67
17	P	107/229 (47%)	89 (83%)	15 (14%)	3 (3%)	4	25
18	Q	1308/1485 (88%)	1280 (98%)	26 (2%)	2 (0%)	44	78
19	R	274/536 (51%)	247 (90%)	23 (8%)	4 (2%)	8	39
20	S	157/166 (95%)	148 (94%)	9 (6%)	0	100	100
21	T	310/514 (60%)	275 (89%)	29 (9%)	6 (2%)	6	33
22	U	68/2752 (2%)	60 (88%)	8 (12%)	0	100	100
23	V	444/908 (49%)	431 (97%)	12 (3%)	1 (0%)	44	78
24	W	507/579 (88%)	432 (85%)	69 (14%)	6 (1%)	11	43
25	Y	667/1220 (55%)	642 (96%)	23 (3%)	2 (0%)	37	72
26	Z	120/758 (16%)	107 (89%)	13 (11%)	0	100	100
27	2	121/184 (66%)	110 (91%)	7 (6%)	4 (3%)	3	22
28	z	58/112 (52%)	56 (97%)	2 (3%)	0	100	100
29	b	98/240 (41%)	93 (95%)	2 (2%)	3 (3%)	3	23
29	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
30	y	77/301 (26%)	75 (97%)	2 (3%)	0	100	100
31	a	75/126 (60%)	74 (99%)	1 (1%)	0	100	100
31	h	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
32	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
32	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
33	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
33	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
34	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
34	m	71/86 (83%)	67 (94%)	3 (4%)	1 (1%)	9	40
35	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
35	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
36	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
36	n	65/76 (86%)	63 (97%)	2 (3%)	0	100	100
37	q	130/504 (26%)	117 (90%)	7 (5%)	6 (5%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	8	37
37	s	130/504 (26%)	116 (89%)	6 (5%)	8 (6%)	1	14
37	t	129/504 (26%)	116 (90%)	9 (7%)	4 (3%)	3	23
38	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	10	42
39	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
40	1	265/586 (45%)	246 (93%)	19 (7%)	0	100	100
41	v	142/146 (97%)	138 (97%)	4 (3%)	0	100	100
42	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	12	46
43	u	384/411 (93%)	372 (97%)	9 (2%)	3 (1%)	16	53
44	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
45	3	28/415 (7%)	27 (96%)	1 (4%)	0	100	100
All	All	14373/25726 (56%)	13438 (94%)	839 (6%)	96 (1%)	21	56

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1092	ILE
1	A	1831	LYS
1	A	1881	ASN
3	C	801	LEU
4	D	957	VAL
4	D	1584	ILE
10	I	698	ARG
11	J	217	GLU
11	J	241	VAL
12	K	78	PRO
13	L	10	VAL
13	L	125	PRO
17	P	8	THR
19	R	233	PRO
21	T	187	LYS
21	T	188	PRO
21	T	190	TRP
24	W	73	ASP
24	W	74	PRO
24	W	82	ASN
24	W	83	PRO
27	2	24	PRO

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Mol	Chain	Res	Type
27	2	76	SER
37	q	24	VAL
37	q	59	HIS
37	q	60	PRO
37	s	9	ASN
37	s	55	ILE
37	s	60	PRO
37	s	66	PRO
37	s	71	ILE
37	t	9	ASN
37	t	69	THR
34	m	4	PRO
43	u	383	ASN
1	A	1992	GLY
3	C	94	ILE
3	C	439	PRO
10	I	532	LYS
11	J	709	VAL
18	Q	530	ASN
21	T	406	ILE
25	Y	1185	ASP
37	q	9	ASN
37	q	19	PRO
38	o	160	LYS
42	w	115	GLY
43	u	340	GLY
43	u	385	ASP
1	A	167	PRO
1	A	1503	TRP
1	A	1513	MET
10	I	699	THR
11	J	188	GLN
11	J	205	LEU
17	P	6	ARG
19	R	52	PRO
23	V	597	PRO
24	W	258	PRO
27	2	32	LYS
27	2	72	ALA
37	q	23	HIS
37	r	9	ASN
37	s	24	VAL

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Mol	Chain	Res	Type
37	t	67	SER
1	A	570	ASP
3	C	83	GLU
11	J	341	PRO
11	J	604	PRO
12	K	65	ILE
15	N	41	ARG
17	P	205	LYS
19	R	73	PRO
19	R	186	VAL
25	Y	1182	LYS
37	t	65	PRO
38	o	32	PRO
1	A	364	SER
1	A	1530	PRO
18	Q	89	ALA
21	T	343	PRO
21	T	462	GLU
29	b	105	GLY
29	b	106	ILE
37	s	62	ARG
1	A	1758	PRO
10	I	372	ARG
11	J	216	ASP
16	O	20	PHE
29	b	115	PRO
1	A	1419	ILE
12	K	17	PRO
24	W	271	PRO
37	s	38	GLY
4	D	585	ILE
37	r	60	PRO

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	1775/2108 (84%)	1707 (96%)	68 (4%)	28	50
3	C	758/866 (88%)	755 (100%)	3 (0%)	89	91
5	E	256/300 (85%)	255 (100%)	1 (0%)	89	91
10	I	199/749 (27%)	185 (93%)	14 (7%)	12	33
11	J	241/751 (32%)	239 (99%)	2 (1%)	79	85
13	L	218/709 (31%)	211 (97%)	7 (3%)	34	55
14	M	117/209 (56%)	115 (98%)	2 (2%)	56	73
15	N	130/130 (100%)	129 (99%)	1 (1%)	79	85
16	O	255/361 (71%)	253 (99%)	2 (1%)	79	85
17	P	101/203 (50%)	97 (96%)	4 (4%)	27	49
19	R	236/457 (52%)	224 (95%)	12 (5%)	20	43
20	S	129/134 (96%)	127 (98%)	2 (2%)	58	74
21	T	268/441 (61%)	264 (98%)	4 (2%)	60	75
22	U	21/2432 (1%)	19 (90%)	2 (10%)	7	23
23	V	98/838 (12%)	95 (97%)	3 (3%)	35	56
24	W	448/502 (89%)	441 (98%)	7 (2%)	58	74
25	Y	32/1085 (3%)	29 (91%)	3 (9%)	7	23
26	Z	110/655 (17%)	110 (100%)	0	100	100
27	2	106/157 (68%)	101 (95%)	5 (5%)	22	45
28	z	51/99 (52%)	51 (100%)	0	100	100
29	b	83/177 (47%)	80 (96%)	3 (4%)	30	52
29	i	77/177 (44%)	74 (96%)	3 (4%)	27	50
31	a	68/101 (67%)	66 (97%)	2 (3%)	37	58
31	h	70/101 (69%)	70 (100%)	0	100	100
32	c	77/101 (76%)	75 (97%)	2 (3%)	41	61
32	j	77/101 (76%)	75 (97%)	2 (3%)	41	61
33	d	90/110 (82%)	89 (99%)	1 (1%)	70	80
33	k	80/110 (73%)	79 (99%)	1 (1%)	65	77
34	f	63/74 (85%)	61 (97%)	2 (3%)	34	55
34	m	61/74 (82%)	58 (95%)	3 (5%)	21	43
35	e	74/84 (88%)	74 (100%)	0	100	100
35	l	74/84 (88%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	g	64/66 (97%)	63 (98%)	1 (2%)	58	74
36	n	60/66 (91%)	58 (97%)	2 (3%)	33	55
38	o	139/218 (64%)	133 (96%)	6 (4%)	25	48
39	p	82/195 (42%)	79 (96%)	3 (4%)	29	51
40	1	235/520 (45%)	230 (98%)	5 (2%)	48	67
45	3	25/366 (7%)	25 (100%)	0	100	100
All	All	7048/15911 (44%)	6870 (98%)	178 (2%)	43	63

All (178) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ARG
1	A	244	GLN
1	A	338	VAL
1	A	387	PHE
1	A	413	LEU
1	A	664	HIS
1	A	666	LYS
1	A	701	ILE
1	A	771	VAL
1	A	773	LYS
1	A	774	LYS
1	A	850	TYR
1	A	853	LYS
1	A	857	ASN
1	A	861	ARG
1	A	866	LEU
1	A	880	ARG
1	A	1089	CYS
1	A	1132	LYS
1	A	1133	CYS
1	A	1136	ARG
1	A	1189	MET
1	A	1249	MET
1	A	1251	SER
1	A	1416	ILE
1	A	1526	LEU
1	A	1528	GLN
1	A	1529	ILE
1	A	1553	VAL

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Mol	Chain	Res	Type
1	A	1554	GLN
1	A	1555	LEU
1	A	1556	ASP
1	A	1561	PHE
1	A	1562	MET
1	A	1566	ILE
1	A	1685	LEU
1	A	1722	SER
1	A	1723	LYS
1	A	1725	LEU
1	A	1726	ILE
1	A	1727	GLN
1	A	1728	GLN
1	A	1730	MET
1	A	1734	MET
1	A	1737	ASN
1	A	1738	PRO
1	A	1740	LEU
1	A	1751	LEU
1	A	1752	GLN
1	A	1753	LEU
1	A	1757	GLU
1	A	1758	PRO
1	A	1763	LEU
1	A	1833	LEU
1	A	1873	GLU
1	A	1876	LEU
1	A	1877	LEU
1	A	1878	ASP
1	A	1879	PHE
1	A	1900	GLU
1	A	1982	GLN
1	A	1983	LEU
1	A	1987	ILE
1	A	1990	ASP
1	A	1993	LYS
1	A	2011	ILE
1	A	2014	MET
1	A	2015	GLU
3	C	513	ASN
3	C	572	GLU
3	C	573	GLU

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Mol	Chain	Res	Type
5	E	243	LEU
10	I	528	LEU
10	I	532	LYS
10	I	548	PHE
10	I	645	VAL
10	I	694	ILE
10	I	698	ARG
10	I	699	THR
10	I	724	LEU
10	I	725	ARG
10	I	726	ILE
10	I	727	ARG
10	I	730	VAL
10	I	731	GLN
10	I	733	THR
11	J	201	ARG
11	J	214	ILE
13	L	4	ILE
13	L	5	MET
13	L	6	ILE
13	L	7	LYS
13	L	10	VAL
13	L	123	LEU
13	L	133	GLU
14	M	118	LYS
14	M	152	LEU
15	N	119	CYS
16	O	150	LEU
16	O	272	ILE
17	P	3	THR
17	P	7	PRO
17	P	10	GLU
17	P	18	LYS
19	R	95	LYS
19	R	217	LYS
19	R	262	ILE
19	R	302	VAL
19	R	307	GLN
19	R	309	GLU
19	R	310	ARG
19	R	315	LYS
19	R	318	GLU

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Mol	Chain	Res	Type
19	R	324	LEU
19	R	333	GLU
19	R	334	ARG
20	S	37	LYS
20	S	126	HIS
21	T	197	TYR
21	T	412	HIS
21	T	416	ILE
21	T	454	VAL
22	U	23	LEU
22	U	25	LEU
23	V	458	THR
23	V	535	THR
23	V	597	PRO
24	W	82	ASN
24	W	200	VAL
24	W	205	VAL
24	W	243	VAL
24	W	257	ILE
24	W	294	VAL
24	W	552	VAL
25	Y	413	LYS
25	Y	418	ASP
25	Y	420	ASP
27	2	23	ILE
27	2	25	LYS
27	2	134	LEU
27	2	137	LYS
27	2	138	LYS
29	b	13	ILE
29	b	57	LYS
29	b	58	GLN
31	a	77	LEU
31	a	79	ASN
32	c	4	VAL
32	c	40	LEU
33	d	112	ASN
34	f	27	MET
34	f	55	LEU
36	g	65	ASN
29	i	13	ILE
29	i	57	LYS

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Mol	Chain	Res	Type
29	i	58	GLN
32	j	4	VAL
32	j	40	LEU
33	k	112	ASN
34	m	5	LEU
34	m	27	MET
34	m	55	LEU
36	n	10	LYS
36	n	65	ASN
38	o	5	THR
38	o	71	VAL
38	o	79	ILE
38	o	101	VAL
38	o	114	SER
38	o	126	THR
39	p	46	MET
39	p	66	LEU
39	p	87	ASP
40	1	34	ARG
40	1	181	ILE
40	1	265	LEU
40	1	267	ILE
40	1	315	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (135) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	78	ASN
1	A	105	ASN
1	A	181	ASN
1	A	270	ASN
1	A	321	ASN
1	A	361	HIS
1	A	368	GLN
1	A	457	ASN
1	A	467	GLN
1	A	542	ASN
1	A	584	HIS
1	A	703	GLN
1	A	711	GLN
1	A	834	HIS

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Mol	Chain	Res	Type
1	A	904	HIS
1	A	974	ASN
1	A	994	ASN
1	A	1013	ASN
1	A	1014	ASN
1	A	1023	ASN
1	A	1024	HIS
1	A	1096	HIS
1	A	1117	HIS
1	A	1124	ASN
1	A	1130	ASN
1	A	1359	HIS
1	A	1373	GLN
1	A	1460	HIS
1	A	1476	GLN
1	A	1487	HIS
1	A	1531	ASN
1	A	1599	GLN
1	A	1615	HIS
1	A	1710	ASN
1	A	1717	ASN
1	A	1727	GLN
1	A	1728	GLN
1	A	1766	GLN
1	A	1775	GLN
1	A	1816	GLN
1	A	1830	GLN
1	A	1881	ASN
1	A	1944	HIS
1	A	1995	ASN
1	A	2004	GLN
3	C	137	HIS
3	C	154	HIS
3	C	208	HIS
3	C	245	HIS
3	C	280	HIS
3	C	297	ASN
3	C	411	ASN
3	C	451	HIS
3	C	513	ASN
3	C	538	HIS
3	C	702	ASN

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Mol	Chain	Res	Type
3	C	892	GLN
5	E	101	ASN
5	E	188	GLN
5	E	253	ASN
10	I	531	HIS
10	I	601	GLN
10	I	705	GLN
11	J	212	GLN
11	J	221	ASN
11	J	238	ASN
11	J	250	GLN
11	J	259	GLN
11	J	373	HIS
13	L	186	GLN
13	L	245	GLN
13	L	266	HIS
14	M	212	ASN
16	O	113	ASN
16	O	196	GLN
16	O	251	HIS
16	O	294	ASN
17	P	29	GLN
19	R	133	GLN
19	R	189	ASN
19	R	279	HIS
20	S	10	GLN
20	S	38	ASN
20	S	87	HIS
20	S	126	HIS
21	T	189	GLN
21	T	278	ASN
21	T	283	HIS
21	T	407	GLN
21	T	437	HIS
21	T	455	GLN
22	U	3	ASN
22	U	20	GLN
23	V	474	HIS
23	V	499	GLN
24	W	71	HIS
24	W	82	ASN
24	W	128	GLN

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Mol	Chain	Res	Type
24	W	147	GLN
24	W	242	HIS
24	W	492	ASN
24	W	529	ASN
26	Z	656	ASN
26	Z	662	HIS
27	2	93	GLN
27	2	116	ASN
28	z	62	GLN
28	z	95	HIS
28	z	102	HIS
29	b	22	GLN
29	b	76	ASN
31	a	60	GLN
32	c	64	ASN
33	d	34	GLN
34	f	58	HIS
35	e	65	HIS
36	g	65	ASN
31	h	60	GLN
29	i	22	GLN
29	i	76	ASN
32	j	64	ASN
33	k	34	GLN
34	m	12	ASN
34	m	58	HIS
35	l	65	HIS
36	n	65	ASN
38	o	156	GLN
39	p	7	HIS
40	1	85	GLN
40	1	92	GLN
40	1	154	HIS
40	1	156	GLN
40	1	171	ASN
40	1	328	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	4 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	F	96/107 (89%)	46 (47%)	16 (16%)
7	4	13/46 (28%)	8 (61%)	3 (23%)
8	G	80/174 (45%)	63 (78%)	20 (25%)
9	H	133/188 (70%)	34 (25%)	10 (7%)
All	All	404/632 (63%)	168 (41%)	53 (13%)

All (168) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	26	A
2	B	28	A
2	B	36	C
2	B	38	C
2	B	45	C
2	B	57	G
2	B	70	A
2	B	71	C
6	F	5	U
6	F	6	C
6	F	7	G
6	F	8	C
6	F	9	U
6	F	10	U
6	F	12	G
6	F	25	C
6	F	26	U
6	F	27	A
6	F	28	A
6	F	29	A
6	F	31	U
6	F	33	G
6	F	34	G
6	F	35	A

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Mol	Chain	Res	Type
6	F	36	A
6	F	37	C
6	F	38	G
6	F	40	U
6	F	43	A
6	F	45	A
6	F	46	G
6	F	47	A
6	F	48	A
6	F	49	G
6	F	51	U
6	F	54	G
6	F	56	A
6	F	59	G
6	F	60	C
6	F	61	C
6	F	62	C
6	F	68	C
6	F	73	A
6	F	74	U
6	F	78	A
6	F	79	C
6	F	80	G
6	F	81	C
6	F	82	A
6	F	83	A
6	F	84	A
6	F	85	U
6	F	86	U
6	F	87	C
7	4	-12	G
7	4	-11	G
7	4	-10	C
7	4	-9	C
7	4	-7	C
7	4	-6	C
7	4	-4	A
7	4	-1	G
8	G	2	U
8	G	3	A
8	G	5	G
8	G	6	A

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Mol	Chain	Res	Type
8	G	7	G
8	G	8	C
8	G	10	U
8	G	11	A
8	G	12	G
8	G	13	C
8	G	14	A
8	G	17	U
8	G	21	A
8	G	22	C
8	G	23	U
8	G	24	G
8	G	25	G
8	G	26	U
8	G	27	U
8	G	28	A
8	G	29	C
8	G	30	C
8	G	31	U
8	G	120	G
8	G	121	G
8	G	122	U
8	G	123	U
8	G	124	U
8	G	125	C
8	G	126	C
8	G	127	U
8	G	128	U
8	G	129	G
8	G	130	A
8	G	131	U
8	G	134	U
8	G	135	G
8	G	136	U
8	G	137	C
8	G	138	A
8	G	139	U
8	G	140	A
8	G	143	U
8	G	144	A
8	G	145	U
8	G	146	C

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Mol	Chain	Res	Type
8	G	147	C
8	G	148	U
8	G	149	G
8	G	150	U
8	G	166	A
8	G	167	G
8	G	168	C
8	G	169	U
8	G	170	C
8	G	171	G
8	G	172	C
8	G	173	G
8	G	174	G
8	G	175	U
8	G	176	U
8	G	177	G
8	G	179	G
9	H	13	C
9	H	14	C
9	H	15	U
9	H	16	U
9	H	17	U
9	H	19	G
9	H	24	A
9	H	25	G
9	H	28	C
9	H	29	A
9	H	30	A
9	H	31	G
9	H	33	G
9	H	37	U
9	H	39	U
9	H	40	C
9	H	41	U
9	H	42	G
9	H	43	U
9	H	112	G
9	H	143	A
9	H	147	G
9	H	152	G
9	H	153	A
9	H	154	C

Continued on next page...

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Mol	Chain	Res	Type
9	H	156	U
9	H	157	G
9	H	164	C
9	H	165	A
9	H	168	A
9	H	169	C
9	H	177	A
9	H	178	A
9	H	179	C

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	18	C
2	B	19	A
2	B	20	G
2	B	27	U
6	F	5	U
6	F	7	G
6	F	25	C
6	F	26	U
6	F	33	G
6	F	34	G
6	F	35	A
6	F	36	A
6	F	45	A
6	F	50	A
6	F	58	G
6	F	59	G
6	F	73	A
6	F	81	C
6	F	84	A
6	F	86	U
7	4	-13	C
7	4	-12	G
7	4	-11	G
8	G	1	G
8	G	16	G
8	G	20	A
8	G	21	A
8	G	22	C
8	G	23	U

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Mol	Chain	Res	Type
8	G	137	C
8	G	142	U
8	G	143	U
8	G	144	A
8	G	145	U
8	G	147	C
8	G	166	A
8	G	167	G
8	G	168	C
8	G	171	G
8	G	172	C
8	G	173	G
8	G	175	U
8	G	176	U
9	H	15	U
9	H	28	C
9	H	29	A
9	H	30	A
9	H	38	A
9	H	39	U
9	H	40	C
9	H	156	U
9	H	164	C
9	H	168	A

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
19	SEP	R	224	19	8,9,10	1.00	0	8,12,14	1.53	1 (12%)
19	SEP	R	232	19	8,9,10	1.56	1 (12%)	8,12,14	1.71	2 (25%)

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
19	SEP	R	224	19	-	0/5/8/10	-
19	SEP	R	232	19	-	1/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	232	SEP	P-O1P	3.40	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	232	SEP	P-OG-CB	-4.04	107.16	118.30
19	R	224	SEP	OG-CB-CA	-2.66	105.55	108.14
19	R	232	SEP	OG-CB-CA	2.37	110.45	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	R	232	SEP	N-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	R	224	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
47	GTP	C	1500	48	26,34,34	1.50	3 (11%)	32,54,54	1.95	7 (21%)
46	IHP	A	3000	-	36,36,36	0.72	0	54,60,60	1.05	0
50	ATP	Q	1501	48	26,33,33	1.72	8 (30%)	31,52,52	1.85	10 (32%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	GTP	C	1500	48	-	1/18/38/38	0/3/3/3
46	IHP	A	3000	-	-	3/30/54/54	0/1/1/1
50	ATP	Q	1501	48	-	4/18/38/38	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	C	1500	GTP	C5-C6	-4.83	1.37	1.47
50	Q	1501	ATP	C2'-C1'	-3.59	1.48	1.53
50	Q	1501	ATP	C4-N3	3.40	1.40	1.35
50	Q	1501	ATP	C6-N6	3.34	1.46	1.34
50	Q	1501	ATP	C2'-C3'	-2.74	1.45	1.53
47	C	1500	GTP	C5-C4	-2.42	1.36	1.43
50	Q	1501	ATP	O2'-C2'	-2.25	1.37	1.43
47	C	1500	GTP	O4'-C4'	-2.25	1.40	1.45
50	Q	1501	ATP	C2-N3	2.18	1.35	1.32
50	Q	1501	ATP	C3'-C4'	-2.18	1.47	1.53
50	Q	1501	ATP	O3'-C3'	-2.16	1.37	1.43

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	C	1500	GTP	PA-O3A-PB	-5.64	113.48	132.83
50	Q	1501	ATP	PB-O3B-PG	-5.47	114.07	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	C	1500	GTP	PB-O3B-PG	-4.37	117.84	132.83
50	Q	1501	ATP	N3-C2-N1	-4.18	122.14	128.68
47	C	1500	GTP	C5-C6-N1	3.72	120.52	113.95
47	C	1500	GTP	C2-N1-C6	-3.47	118.71	125.10
47	C	1500	GTP	C3'-C2'-C1'	3.21	105.81	100.98
47	C	1500	GTP	C8-N7-C5	2.82	108.36	102.99
50	Q	1501	ATP	PA-O3A-PB	-2.62	123.85	132.83
50	Q	1501	ATP	C1'-N9-C4	-2.50	122.25	126.64
50	Q	1501	ATP	O2G-PG-O1G	-2.41	101.23	110.68
50	Q	1501	ATP	O2A-PA-O1A	-2.35	100.65	112.24
50	Q	1501	ATP	O2G-PG-O3B	2.25	112.17	104.64
47	C	1500	GTP	O6-C6-C5	-2.22	120.04	124.37
50	Q	1501	ATP	O2B-PB-O1B	-2.08	101.97	112.24
50	Q	1501	ATP	O5'-C5'-C4'	2.07	116.12	108.99
50	Q	1501	ATP	O3G-PG-O3B	2.05	111.50	104.64

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	A	3000	IHP	C3-O13-P3-O43
47	C	1500	GTP	O4'-C4'-C5'-O5'
50	Q	1501	ATP	C5'-O5'-PA-O1A
50	Q	1501	ATP	C5'-O5'-PA-O2A
46	A	3000	IHP	C3-C4-O14-P4
50	Q	1501	ATP	PB-O3A-PA-O2A
46	A	3000	IHP	C4-O14-P4-O44
50	Q	1501	ATP	C5'-O5'-PA-O3A

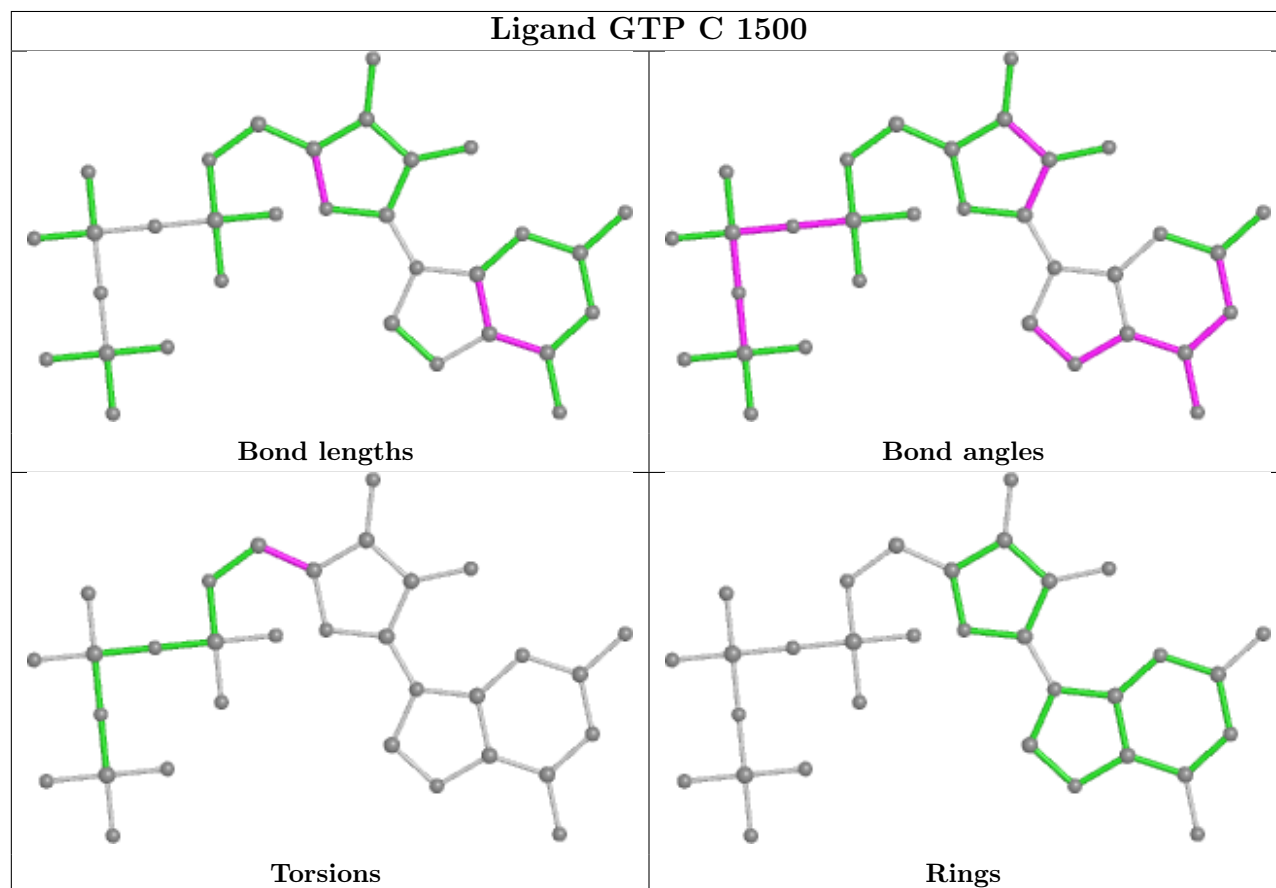
There are no ring outliers.

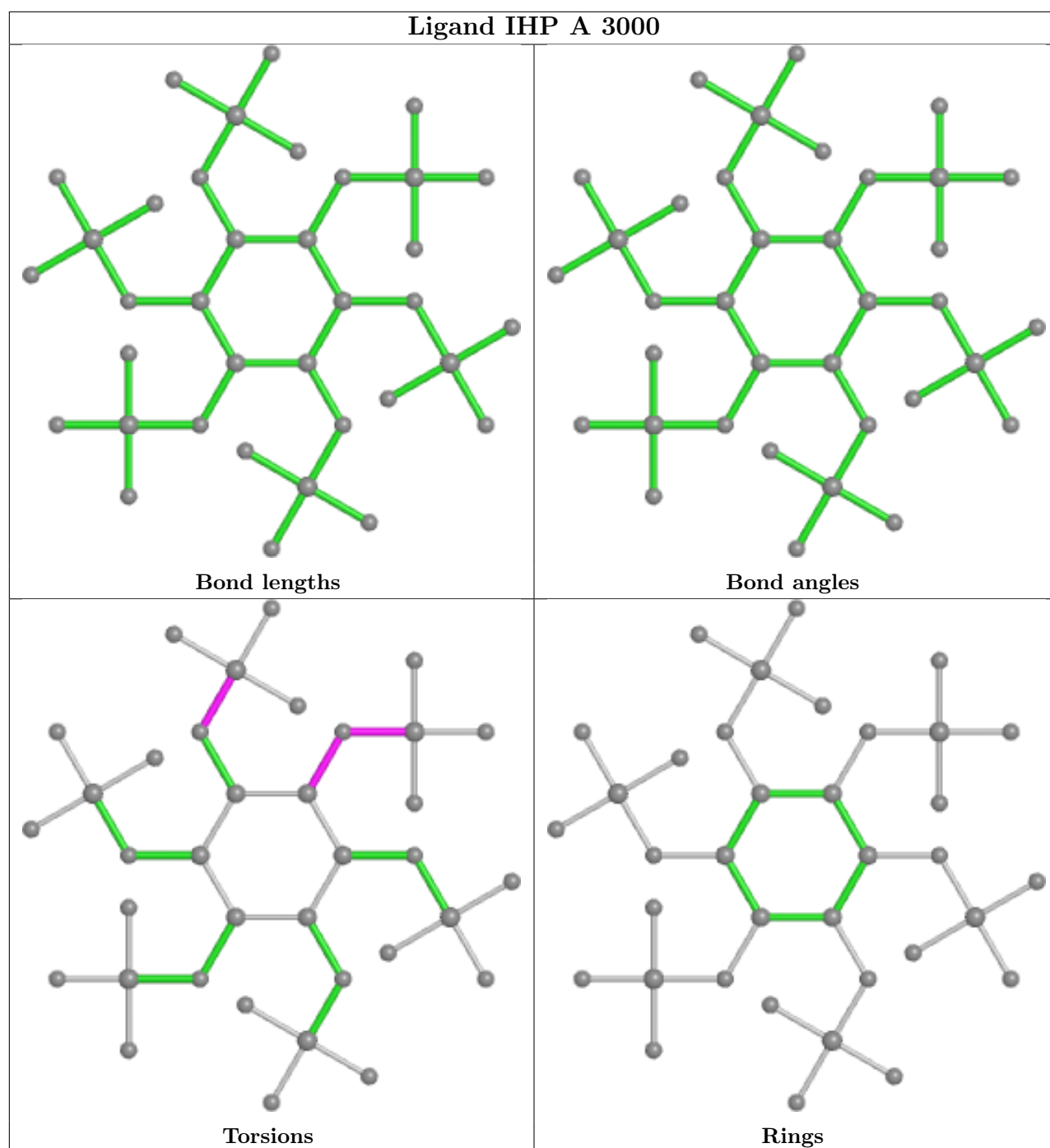
3 monomers are involved in 16 short contacts:

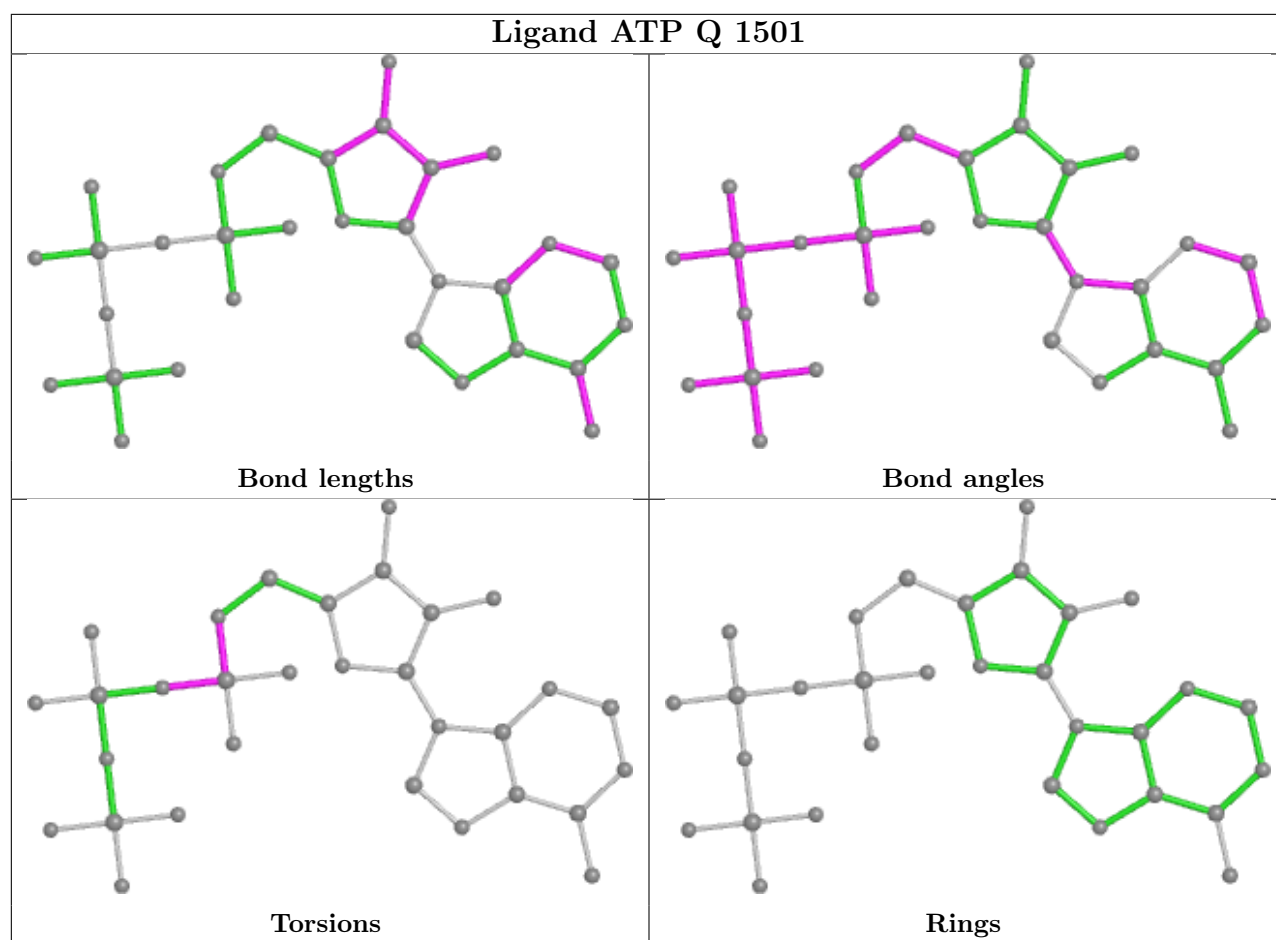
Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	C	1500	GTP	2	0
46	A	3000	IHP	9	0
50	Q	1501	ATP	5	0

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.

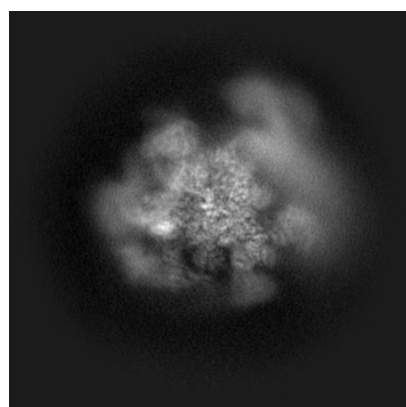
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32321. These allow visual inspection of the internal detail of the map and identification of artifacts.

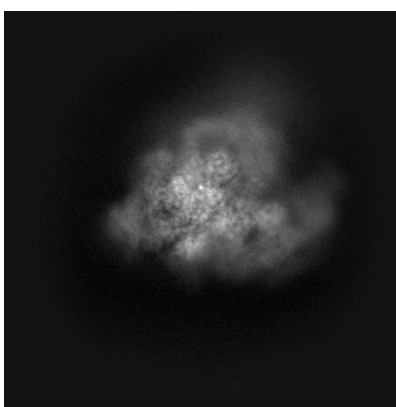
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

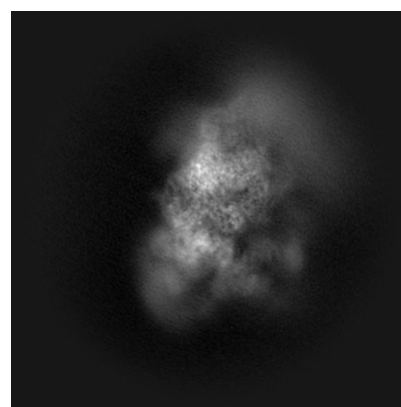
6.1.1 Primary map



X



Y

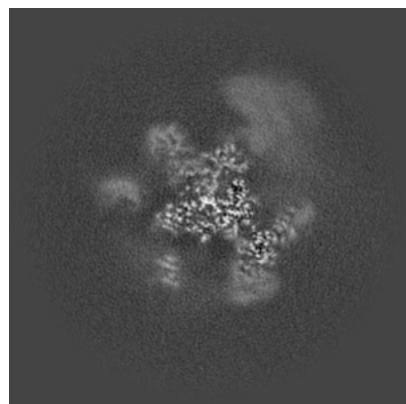


Z

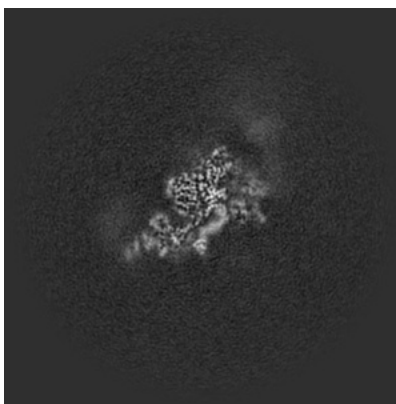
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

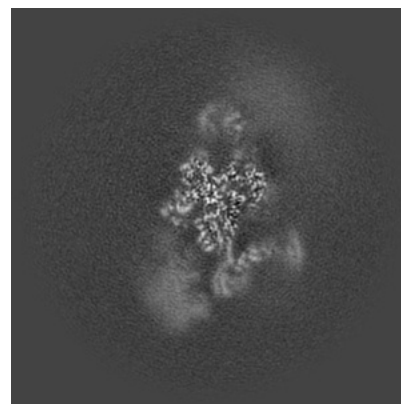
6.2.1 Primary map



X Index: 200



Y Index: 200

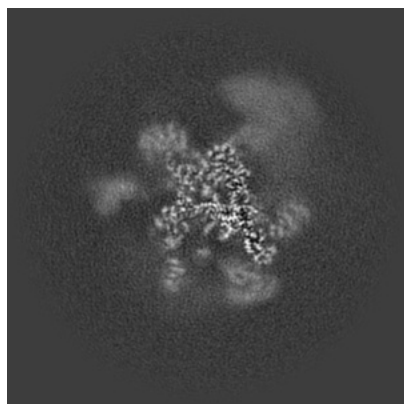


Z Index: 200

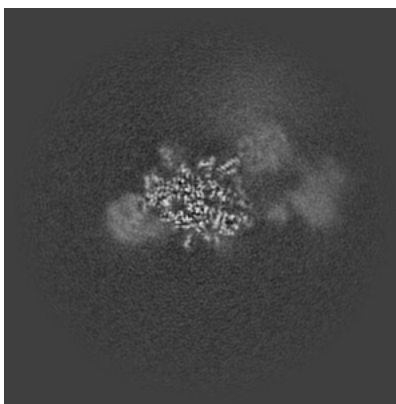
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

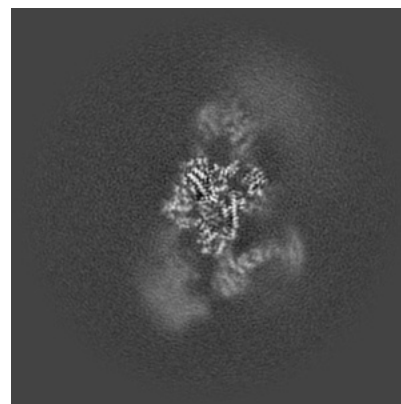
6.3.1 Primary map



X Index: 194



Y Index: 238

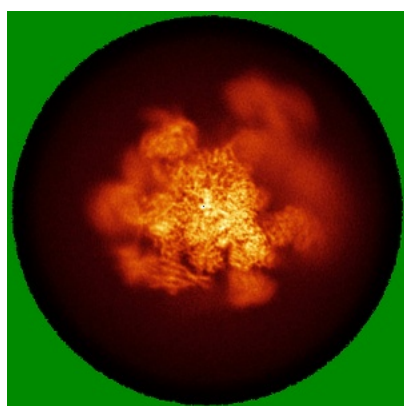


Z Index: 197

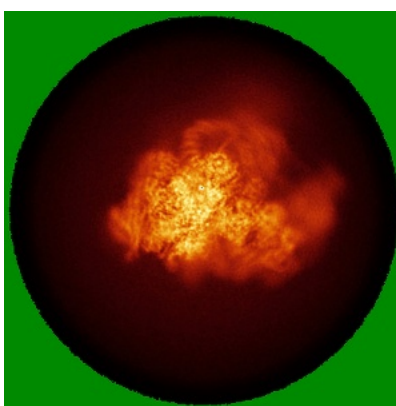
The images above show the largest variance slices of the map in three orthogonal directions.

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

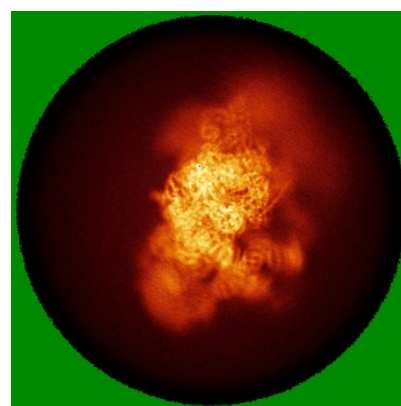
6.4.1 Primary map



X



Y

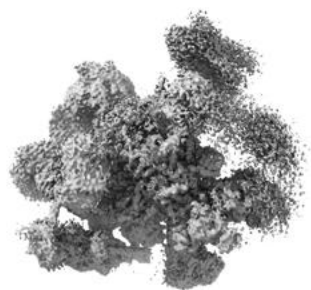


Z

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](#)

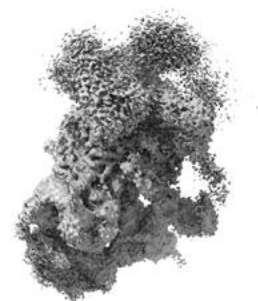
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.37. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

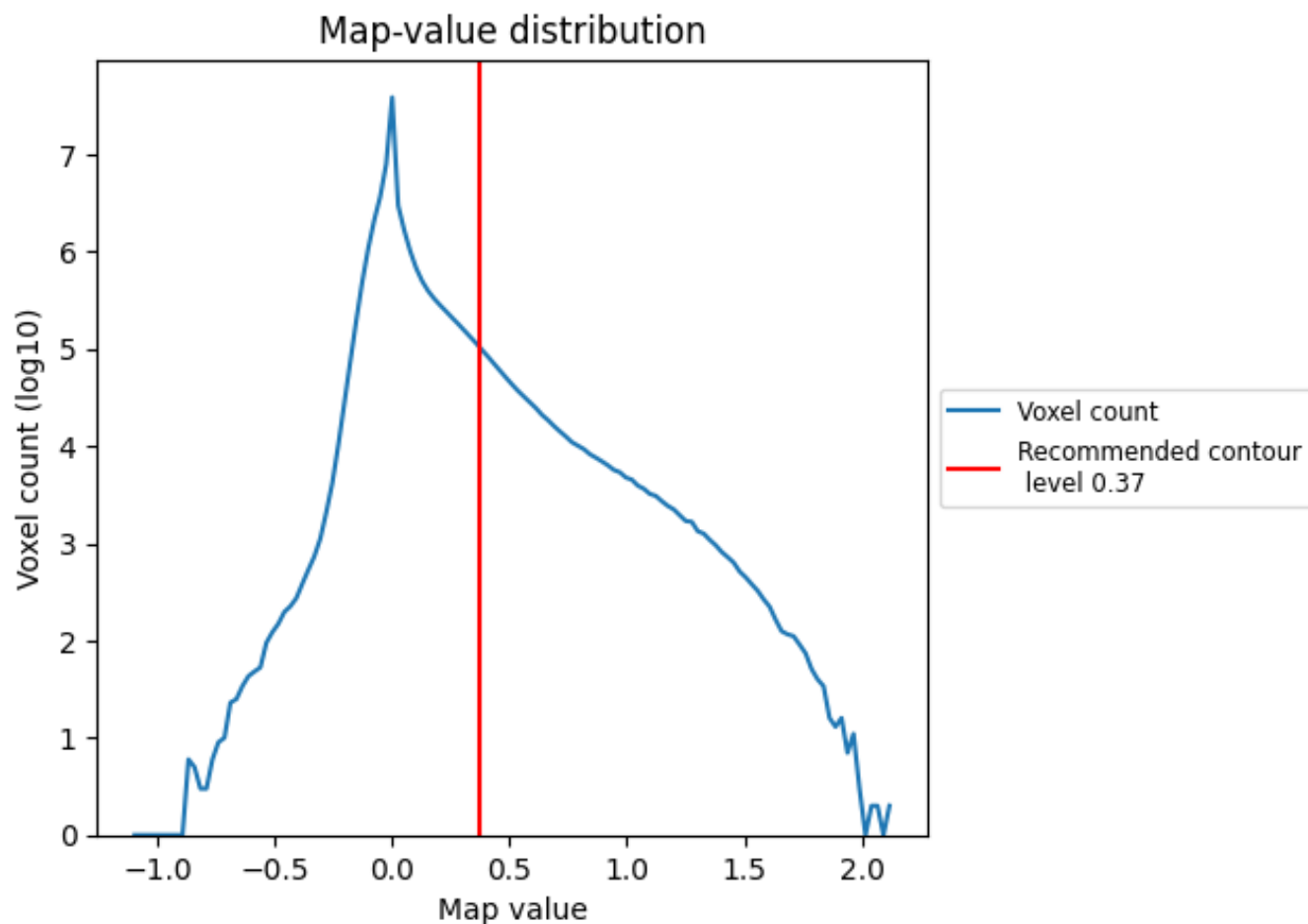
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

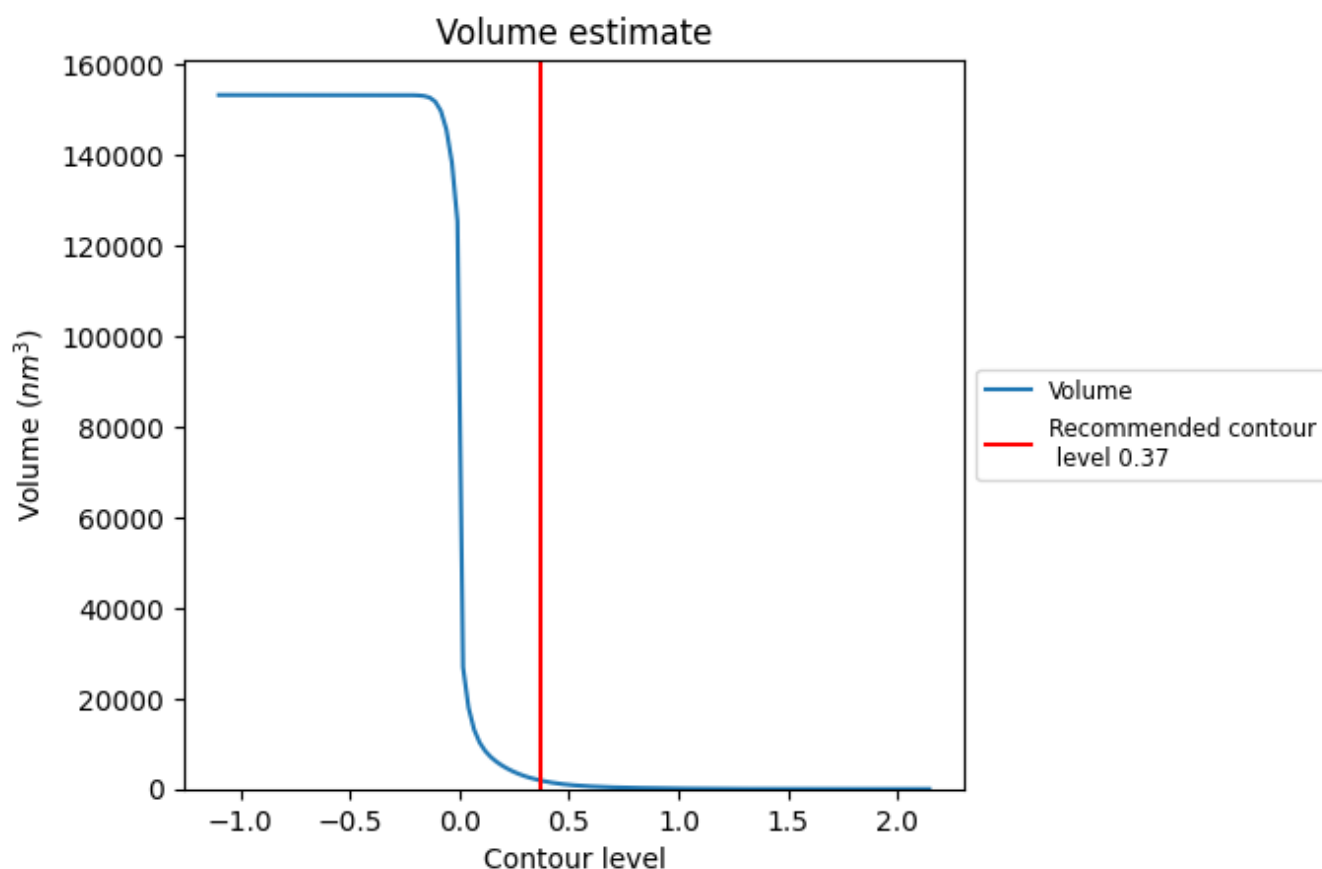
This section contains the results of statistical analysis of the map.

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.

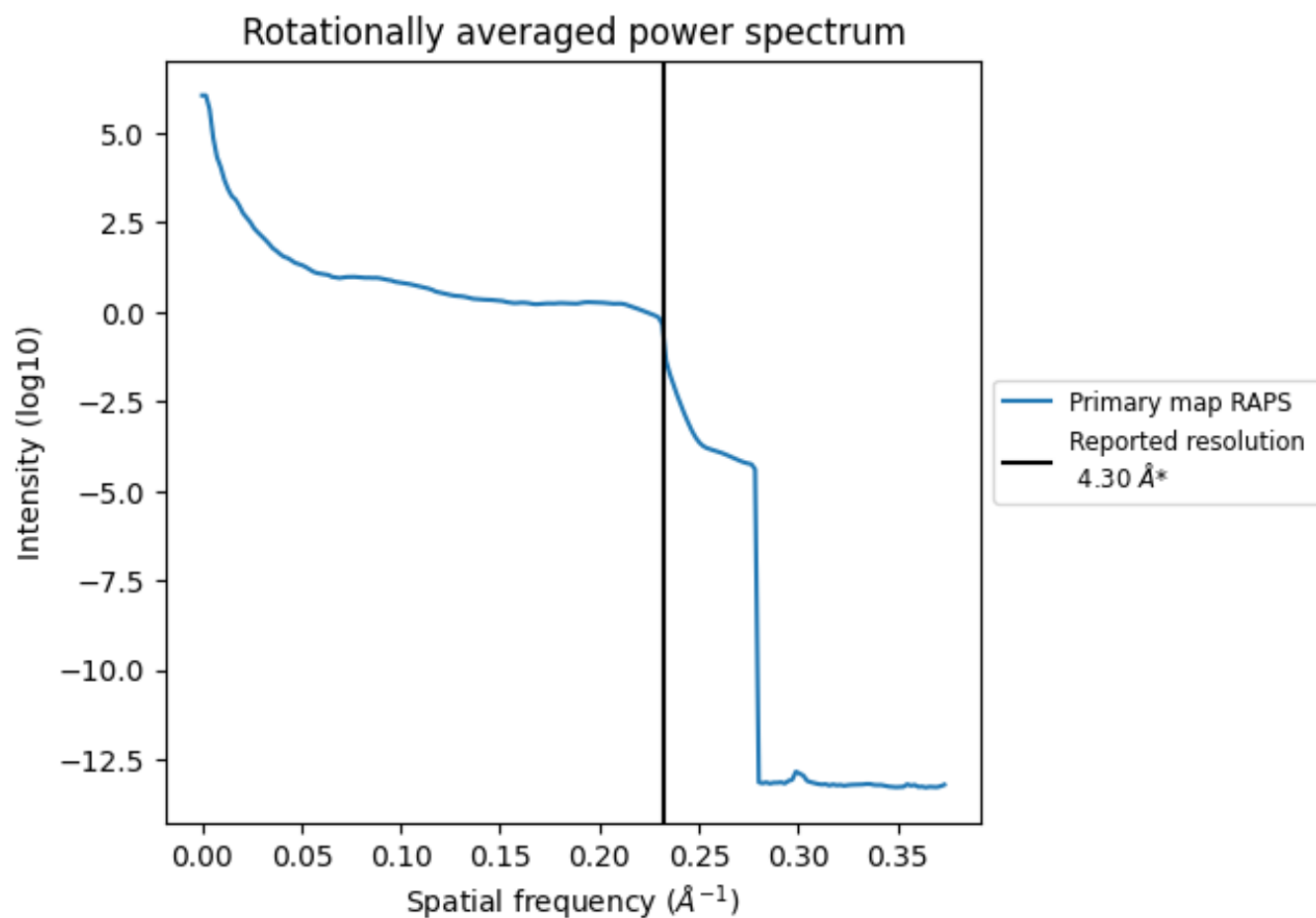
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1869 nm³; this corresponds to an approximate mass of 1688 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 0.233 Å⁻¹

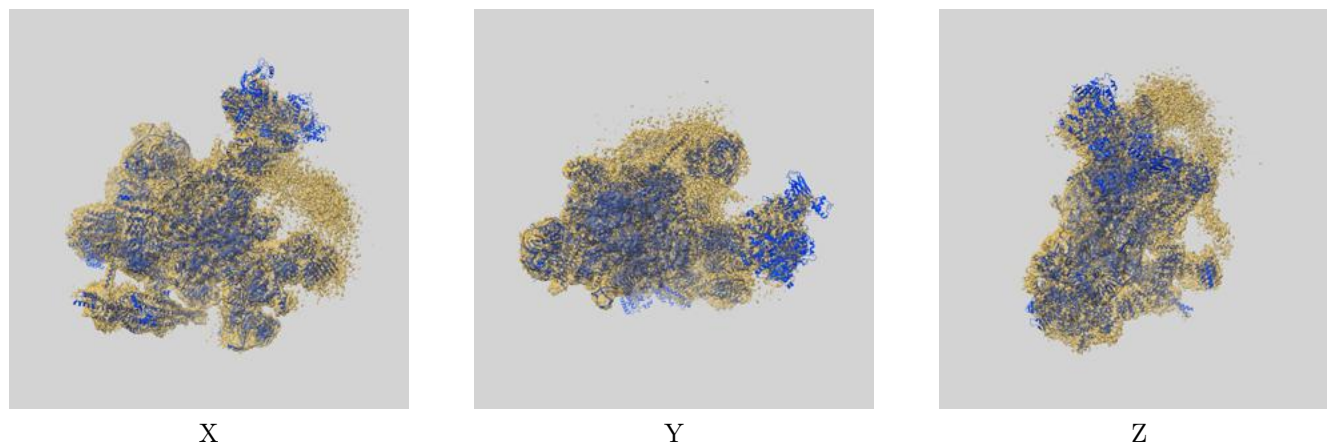
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

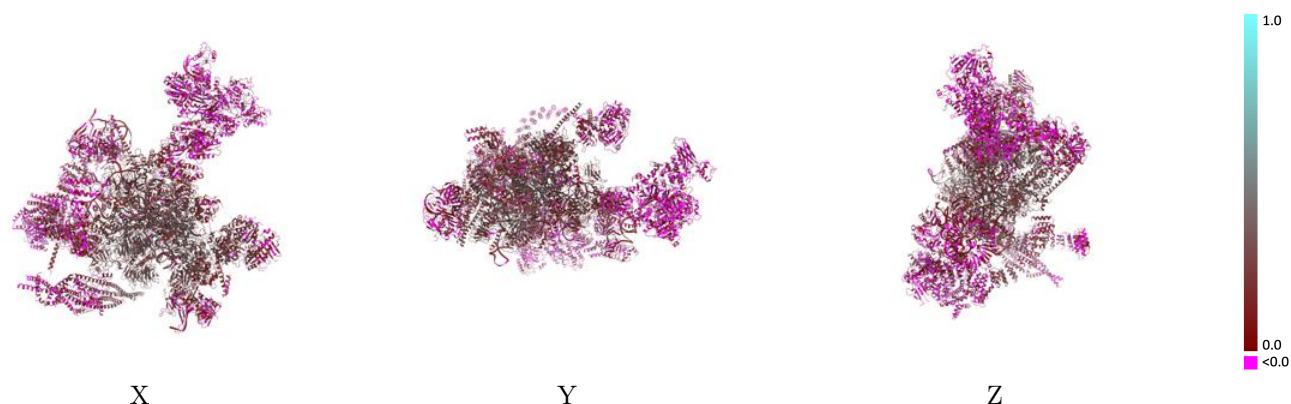
This section contains information regarding the fit between EMDB map EMD-32321 and PDB model 7W5B. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



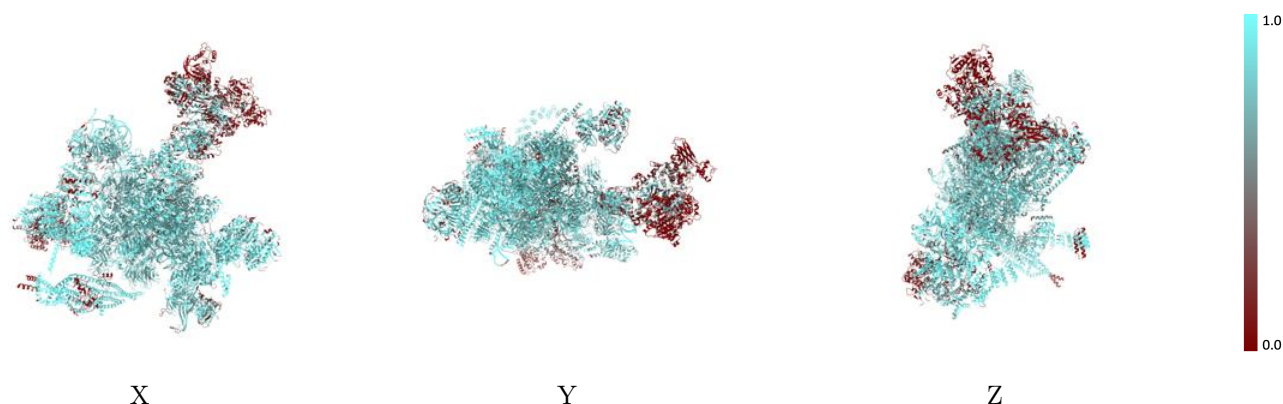
The images above show the 3D surface view of the map at the recommended contour level 0.37 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



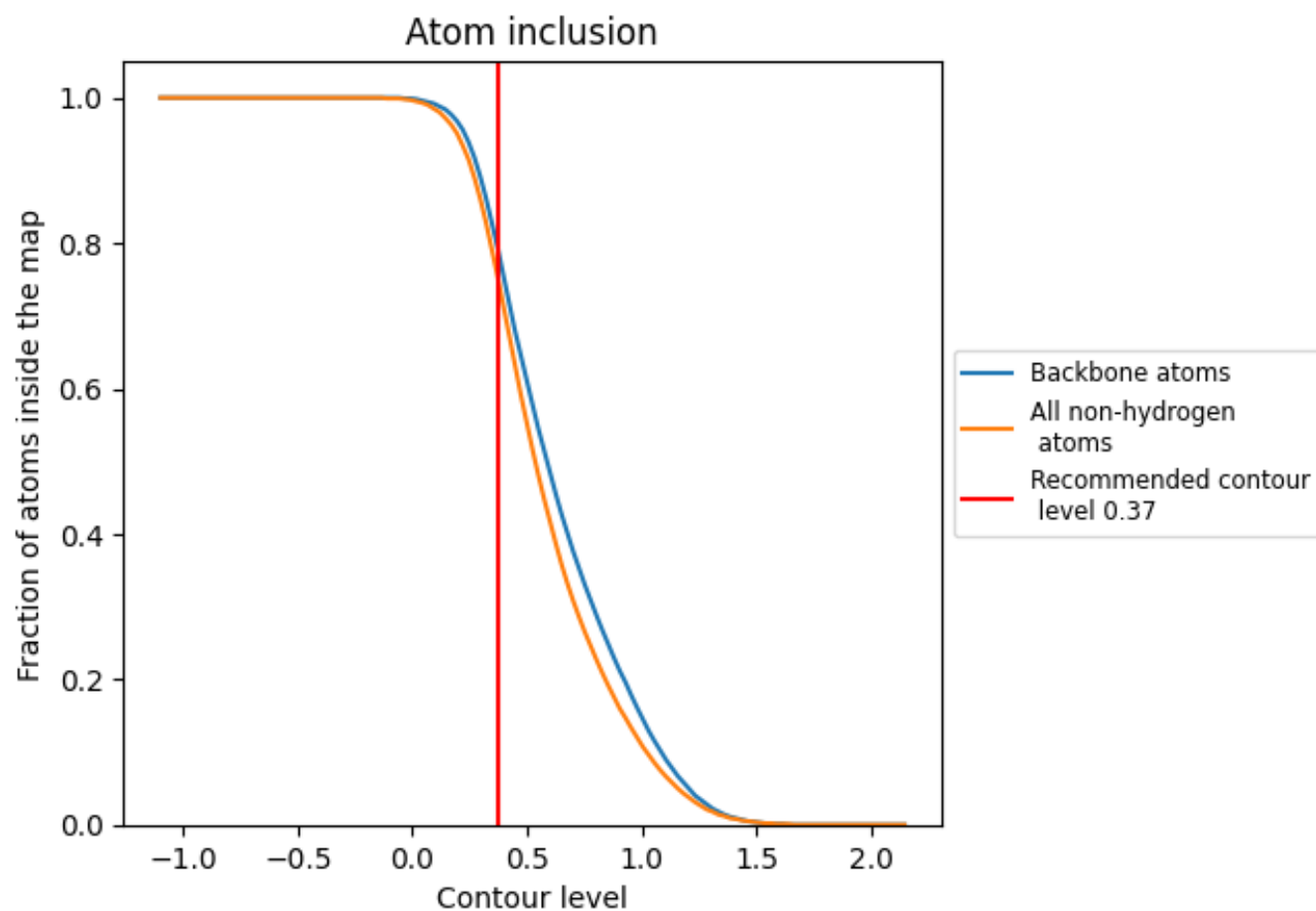
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.37).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 76% 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 (0.37) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.1920
1	 0.6780	 0.2120
2	 0.7950	 0.1810
3	 0.6740	 0.2640
4	 0.9860	 0.3870
A	 0.8190	 0.2900
B	 0.9440	 0.2580
C	 0.8620	 0.2950
D	 0.2740	 0.0240
E	 0.9100	 0.2900
F	 0.9610	 0.3000
G	 0.7620	 0.1640
H	 0.9120	 0.1490
I	 0.8920	 0.1500
J	 0.8430	 0.1950
K	 0.9520	 0.2010
L	 0.8500	 0.2470
M	 0.8040	 0.2660
N	 0.8740	 0.3000
O	 0.8590	 0.2530
P	 0.7430	 0.2680
Q	 0.4580	 0.0290
R	 0.8280	 0.3040
S	 0.8900	 0.2590
T	 0.9120	 0.3710
U	 0.9180	 0.2580
V	 0.8400	 0.2200
W	 0.8180	 0.2180
Y	 0.6650	 0.0970
Z	 0.8400	 0.2360
a	 0.7800	 0.1570
b	 0.7990	 0.1220
c	 0.8970	 0.0790
d	 0.7990	 0.0610
e	 0.7010	 0.0590



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Chain	Atom inclusion	Q-score
f	 0.7170	 0.0680
g	 0.5610	 0.0740
h	 0.7390	 0.0730
i	 0.6150	 0.0230
j	 0.8330	 0.0500
k	 0.7490	 0.0550
l	 0.6900	 0.0660
m	 0.9190	 0.1090
n	 0.7640	 0.0740
o	 0.8050	 0.0720
p	 0.8980	 0.0790
q	 0.6060	 0.0700
r	 0.9400	 0.1470
s	 0.4960	 0.1050
t	 0.4110	 0.0150
u	 0.9030	 0.2540
v	 0.7860	 0.1330
w	 0.8720	 0.1370
x	 0.4110	 0.0800
y	 0.8210	 0.0850
z	 0.5410	 0.1300