



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 07:07 AM UTC

PDB ID : 5Y88 / pdb_00005y88
EMDB ID : EMD-6817
Title : Cryo-EM structure of the intron-lariat spliceosome ready for disassembly from *S.cerevisiae* at 3.5 angstrom
Authors : Wan, R.; Yan, C.; Bai, R.; Lei, J.; Shi, Y.
Deposited on : 2017-08-20
Resolution : 3.46 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

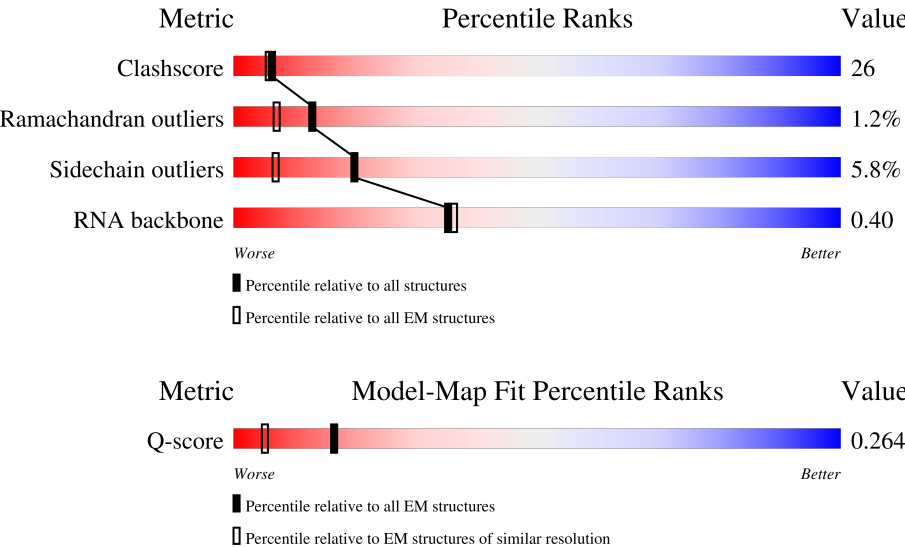
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13788 (2.96 - 3.96)

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

Mol	Chain	Length	Quality of chain
1	A	2413	
2	B	214	
3	C	1008	

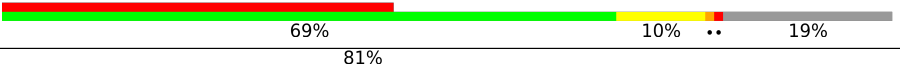
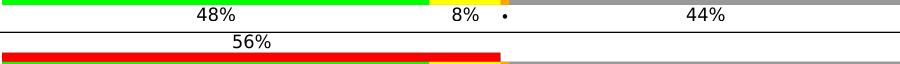
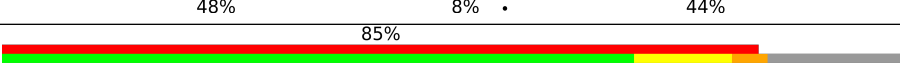
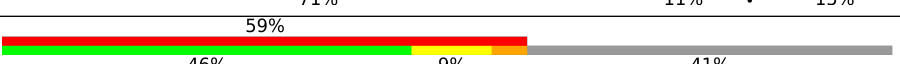
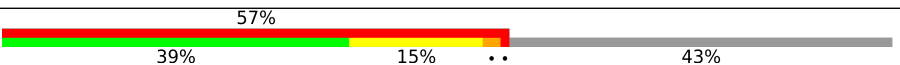
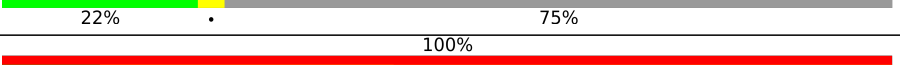
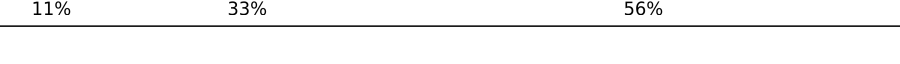
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Mol	Chain	Length	Quality of chain
4	D	112	
5	E	38	
6	F	1175	
7	G	175	
8	H	859	
9	I	687	
10	J	590	
11	K	215	
12	L	157	
13	M	364	
14	N	339	
15	O	451	
16	P	175	
17	Q	379	
18	R	278	
19	S	455	
20	T	283	
21	U	708	
22	V	322	
23	W	767	
24	a	196	
24	h	196	
25	b	94	
25	i	94	
26	c	86	

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Mol	Chain	Length	Quality of chain
26	j	86	
27	d	77	
27	k	77	
28	e	101	
28	l	101	
29	f	146	
29	m	146	
30	g	110	
30	n	110	
31	o	238	
32	p	111	
33	q	503	
33	r	503	
33	s	503	
33	t	503	
34	x	9	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 72347 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1903	Total	C	N	O	S	0	0
			15715	10107	2697	2854	57		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	913	Total	C	N	O	S	0	0
			7278	4696	1205	1347	30		

- Molecule 4 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	101	Total	C	N	O	P	0	0
			2150	963	384	702	101		

- Molecule 5 is a RNA chain called Intron lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	28	Total	C	N	O	P	0	0
			587	264	95	200	28		

- Molecule 6 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	P	0	0
			1727	772	286	587	82		

- Molecule 7 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			921	582	159	179	1		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	601	Total	C	N	O	S	0	0
			3204	1958	611	634	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	541	Total	C	N	O	S	0	0
			3542	2200	667	667	8		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	431	Total	C	N	O	S	0	0
			2944	1824	544	568	8		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 12 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	157	Total	C	N	O	S	0	0
			1290	808	240	231	11		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	182	Total	C	N	O	S	0	0
			1298	805	235	243	15		

- Molecule 14 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 15 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	68	Total	C	N	O	S	0	0
			554	348	111	94	1		

- Molecule 17 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 18 is a protein called Protein CWC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	46	Total	C	N	O	S	0	0
			379	225	73	79	2		

- Molecule 19 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	23	Total	C	N	O	0	0
			195	122	41	32		

- Molecule 20 is a protein called Pre-mRNA-splicing factor CWC23.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	107	Total	C	N	O	0	0
			816	523	144	149		

- Molecule 21 is a protein called Pre-mRNA-splicing factor SPP382.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	488	Total	C	N	O	S	0	0
			2690	1644	514	529	3		

- Molecule 22 is a protein called Pre-mRNA-splicing factor NTR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	91	Total	C	N	O	S	0	0
			619	381	112	124	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	708	Total	C	N	O	S	0	0
			3505	2089	708	708			

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
24	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
25	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
26	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
27	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	e	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
28	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	f	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
29	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
30	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

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

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

- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	p	81	Total	C	N	O	0	0
			513	332	89	92		

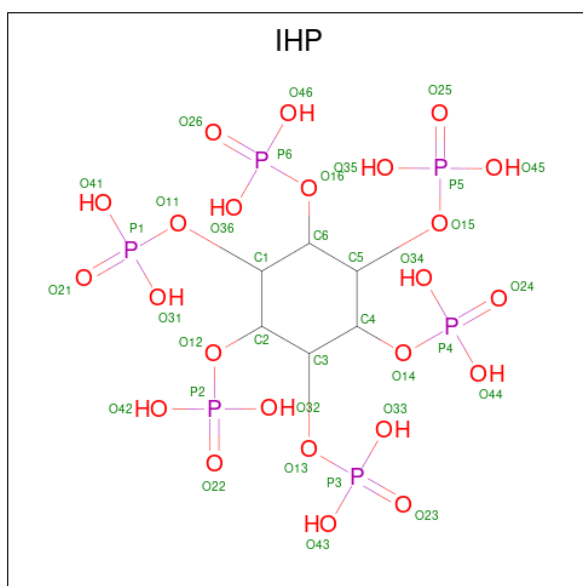
- Molecule 33 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	q	126	Total	C	N	O	S	0	0
			831	526	134	169	2		
33	r	129	Total	C	N	O	S	0	0
			849	536	137	174	2		
33	s	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
33	t	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 34 is a RNA chain called RNA (intron or U6 snRNA).

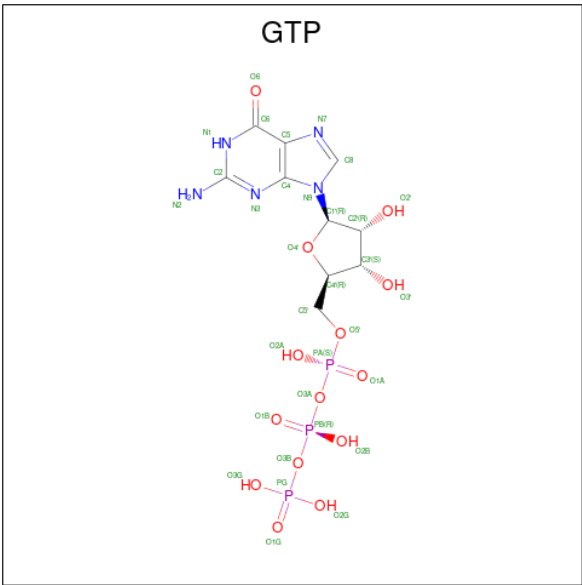
Mol	Chain	Residues	Atoms					AltConf	Trace
34	x	9	Total	C	N	O	P	0	0
			177	81	18	70	8		

- Molecule 35 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



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

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

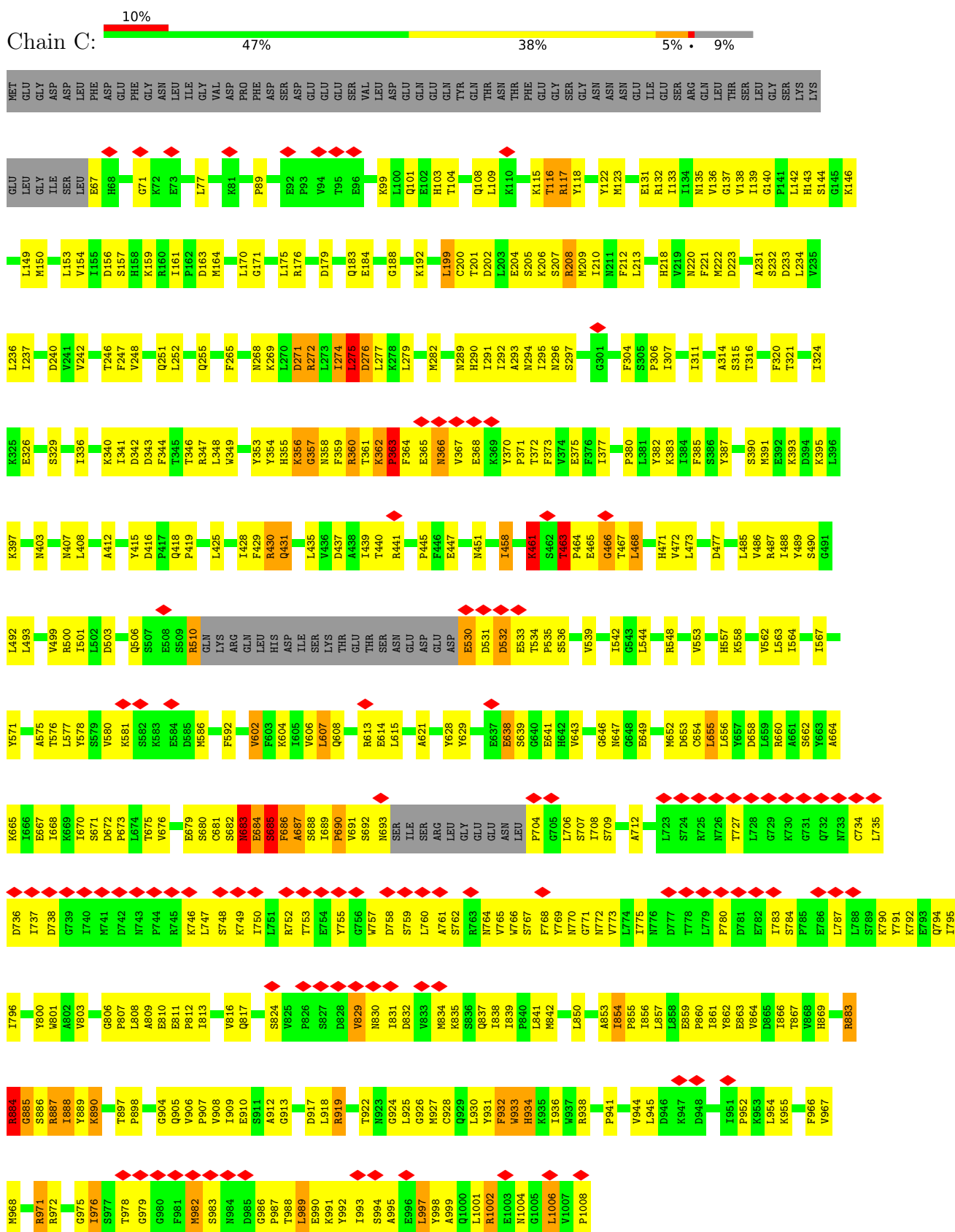
Mol	Chain	Residues	Atoms		AltConf
37	C	1	Total	Mg	0
			1	1	
37	D	5	Total	Mg	0
			5	5	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

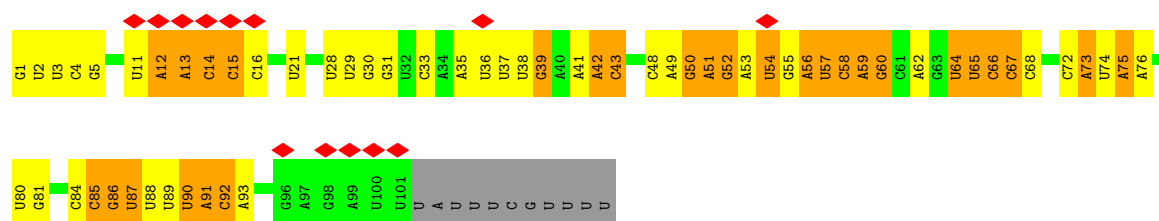
Mol	Chain	Residues	Atoms		AltConf
38	L	3	Total	Zn	0
			3	3	
38	M	2	Total	Zn	0
			2	2	
38	N	1	Total	Zn	0
			1	1	

D1747	H1687	F1567	B1498	H1431	V1371	E1307	A1246	I1168	L1072	V885
I1748	P1688	N1568	R1499	E1432	K1372	E1308	F1247	Y1169	I1073	M886
S1749	R1689	S1569	H1500	D1433	L1373	K1309	V1248	L1170	D1075	R893
R1750	K1690	V1570	T1501	E1434	G1374	K1310	S1249	D985	P899	F900
Y1751	S1691	O1571	A1503	K1435	L1375	R1315	Y1251	H1173	I1078	P901
Y1752	V1692	G1572	Y1504	K1436	N1376	R1316	S1252	F1174	A1079	F900
R1753	K1693	L1573	R1509	I1437	S1377	R1317	K1253	E1175	D1080	P902
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K1755	M1695	W1575	R1511	F1441	L1379	G1316	N1255	G1179	N1086	T904
F1756	S1696	E1576	R1512	R1442	P1380	L1319	P1257	E1180	N1087	Y905
L1757	S1697	LYS	F1514	Y1443	T1381	L1320	N1257	E1181	D1094	K906
D1758	A1698	ALA	R1521	I1444	F1382	M1321	L1258	E1182	D1096	N907
Y1759	A1699	SER	M1522	T1445	F1383	A1322	L1259	L1182	S1096	D908
T1760	D1700	PHE	F1525	T1446	S1323	S1323	F1260	E1183	H1097	P909
T1761	I1701	GLU	W1528	E1447	G1324	G1324	S1261	D1184	V1098	K910
D1762	T1702	ASP	W1527	E1448	S1325	C1263	M1262	E1185	I099	L911
M1763	M1703	MET	W1529	N1449	T1326	G1264	G1264	Y1186	K1100	L912
V1764	E1704	GLN	F1530	E1450	F1387	F1265	F1265	L1187	Y1101	D918
S1765	S1705	PHE	H1531	D1452	Y1389	F1328	R1268	A1188	S1111	
M1766	V1706	LYS	H1532	D1453	P1391	V1331	I1269	D1192	W1012	Y923
Y1767	H1707	LEU	H1533	S1454	K1392	K1334	L1270	P1193	I1013	A924
P1768	E1708	THR	D1538	W1458	E1393	W1335	P1271	M1194	K1014	S925
W1709	W1709	HIS	A1459	A1459	L1394	M1336	R1272	F1195	P1015	K926
P1770	E1710	ALA	K1460	E1460	G1395	T1337	Q1273	E1196	S1016	V927
T1771	V1711	GLN	Y1461	Y1461	G1396	S1338	R1275	M1197	D1017	R928
G1772	H1712	ARG	K1464	K1464	L1397	I1340	M1276	E1198	E1129	L929
V1773	K1713	THR	R1465	R1465	G1398	E1277	E1277	S1199	R1130	N930
M1774	P1714	GLY	A1468	A1468	M1399	V1278	V1278	T1132	N1033	A931
I1775	S1715	LEU	I1469	I1469	L1400	F1343	V1279	D1133	E936	S932
G1776	L1716	ILE	I1472	I1472	S1401	T1344	S1280	L1035	R934	E935
I1777	L1717	PRO	N1472	N1472	A1402	Y1345	S1281	A1135	E936	E935
H1778	R1718	M1603	R1473	R1473	H1404	R1346	N1281	D1040	D1040	L937
D1779	E1719	R1604	R1474	R1474	I1405	E1348	E1282	V1041	V1041	A938
L1779	F1605	R1605	R1475	R1475	L1406	A1349	E1283	S1042	R1043	L939
A1780	F1606	F1606	L1476	L1476	L1407	I1350	G1284	G1044	G1044	E941
Y1781	T1607	T1607	A1476	A1476	P1408	V1351	W1285	Q1045	Q1045	E942
M1782	D1722	L1608	F1477	F1477	A1409	T1353	D1287	S1046	S1046	A943
M1783	S1723	W1609	E1478	E1478	A1409	T1353	D1288	A1047	A1047	Y944
Y1784	F1724	W1610	E1479	E1479	S1410	E1354	V1289	V1048	V1048	D945
D1785	K1725	S1611	I1553	I1553	D1411	P1355	D1290	L1049	L1049	N946
A1786	G1726	F1554	F1554	F1554	L1412	L1357	E1291	L1050	L1050	P947
Y1787	L1727	T1555	T1555	T1555	S1413	D1358	E1292	E1051	E1051	H948
G1788	L1728	I1556	I1556	I1556	W1414	I1359	T1293	M1057	M1057	D949
M1789	T1729	L1557	L1557	L1557	S1415	L1360	K1294	K1060	K1060	T950
W1790	K1730	E1558	E1558	E1558	S1416	K1362	R1296	I1061	I1061	L951
F1791	M1731	H1559	H1559	H1559	Q1417	G1363	A1298	T1062	T1062	N952
M1792	W1732	L1560	L1560	L1560	T1418	E1364	K1299	M1067	M1067	K955
G1793	W1733	F1562	F1562	F1562	T1419	T1365	A1300	R1068	R1068	L959
L1794	F1734	K1563	K1563	K1563	D1420	R1366	A1300	R1069	R1069	M971
K1795	D1735	G1564	G1564	G1564	T1421	I1367	Y1301	L1070	L1070	E972
P1796	W1736	V1621	V1621	V1621	G1421	Q1368	L1302	R1071	R1071	
L1797	L1737	F1623	F1623	F1623	I1422	N1369	V1304			
I1798	L1738	L1624	L1624	L1624	T1423	V1305	E1306			
Q1799	R1739	V1625	V1625	V1625	H1424	S1305	E1306			
M1800	Y1740	S1626	S1626	S1626	F1425	E1244				
S1801	G1741	V1681	V1681	V1681	R1426	M1245				
D1802	D1742	T1682	T1682	T1682	A1427					
M1803	Y1743	K1683	K1683	K1683	G1428					
T1804	D1744	E1684	E1684	E1684	M1429					
I1805	S1745	V1685	V1685	V1685	T1430					
M1806	H1746									

- Molecule 2: U5 snRNA



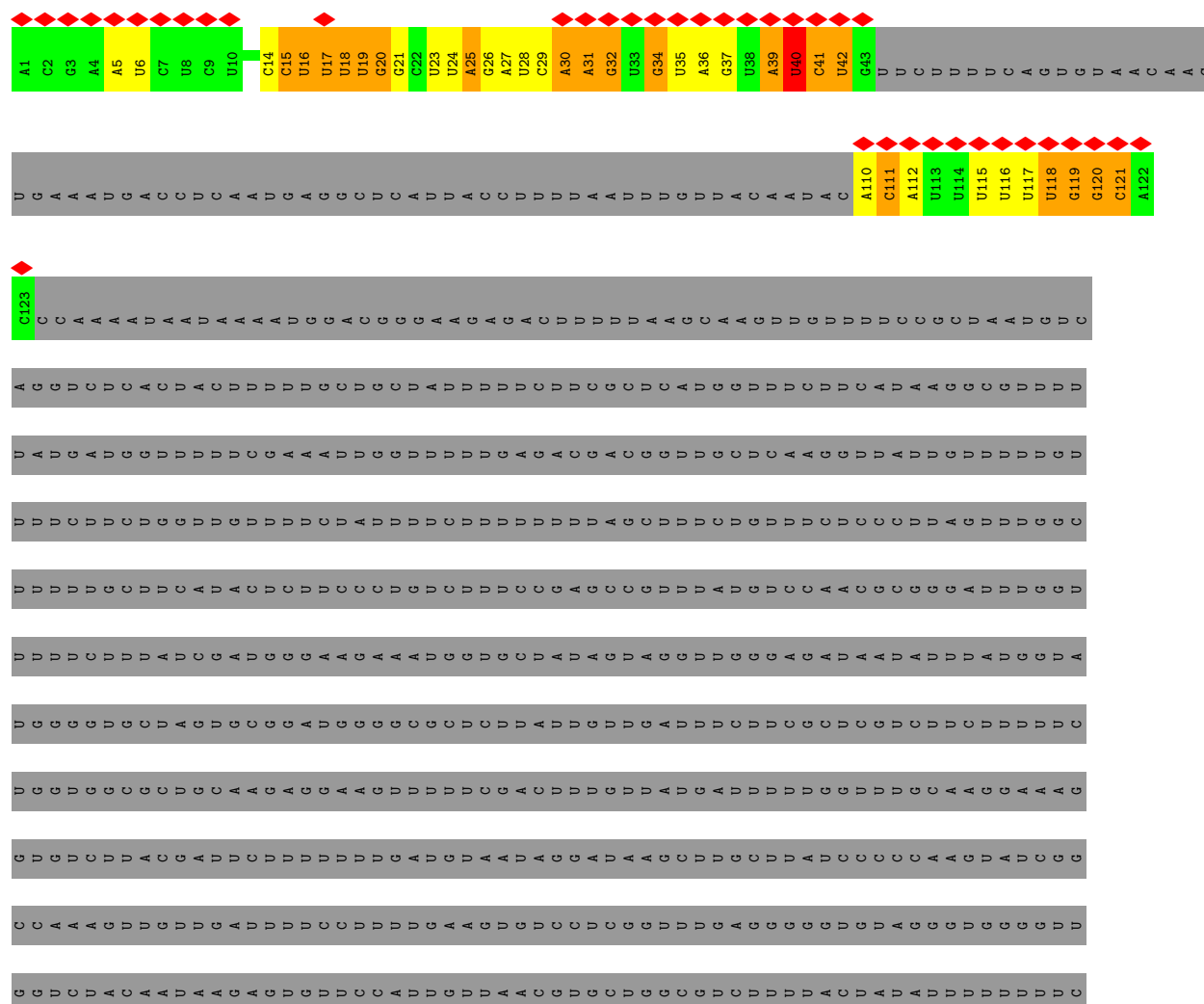
- Molecule 4: U6 snRNA

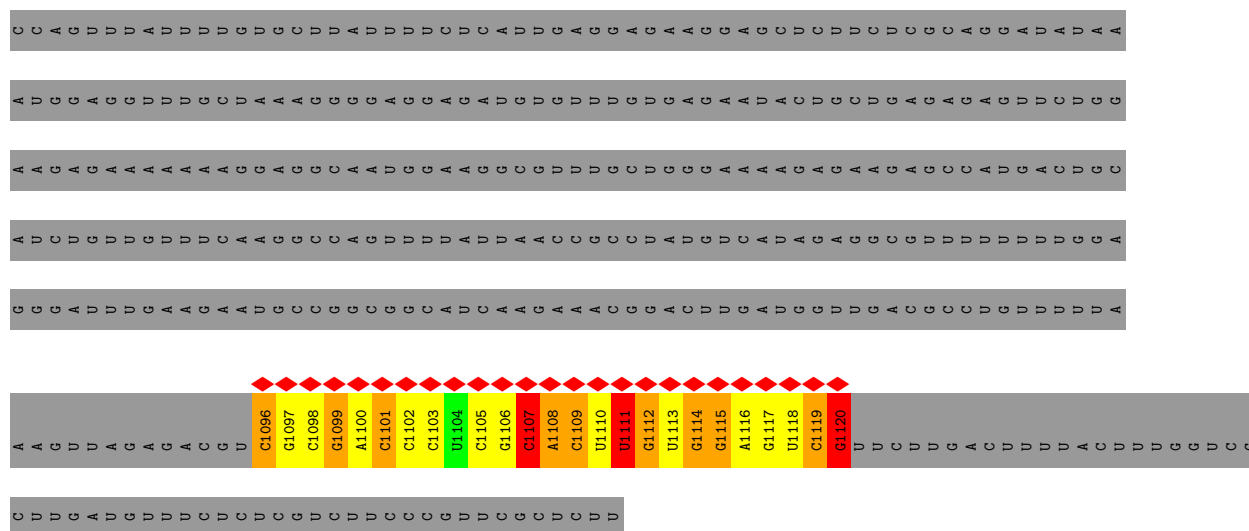


• Molecule 5: Intron lariat

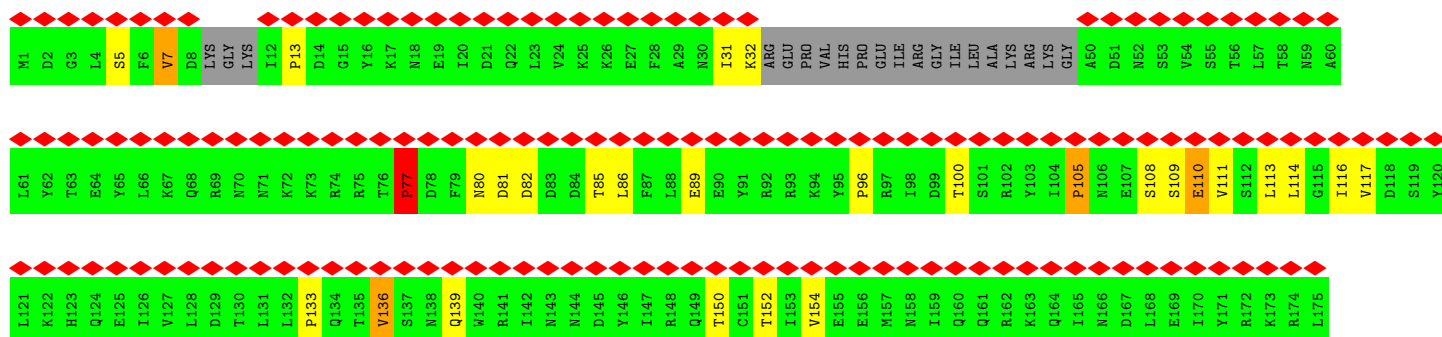
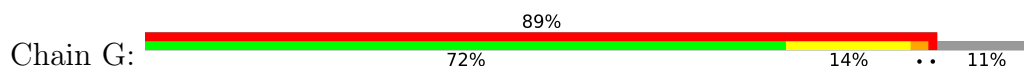


• Molecule 6: U2 snRNA

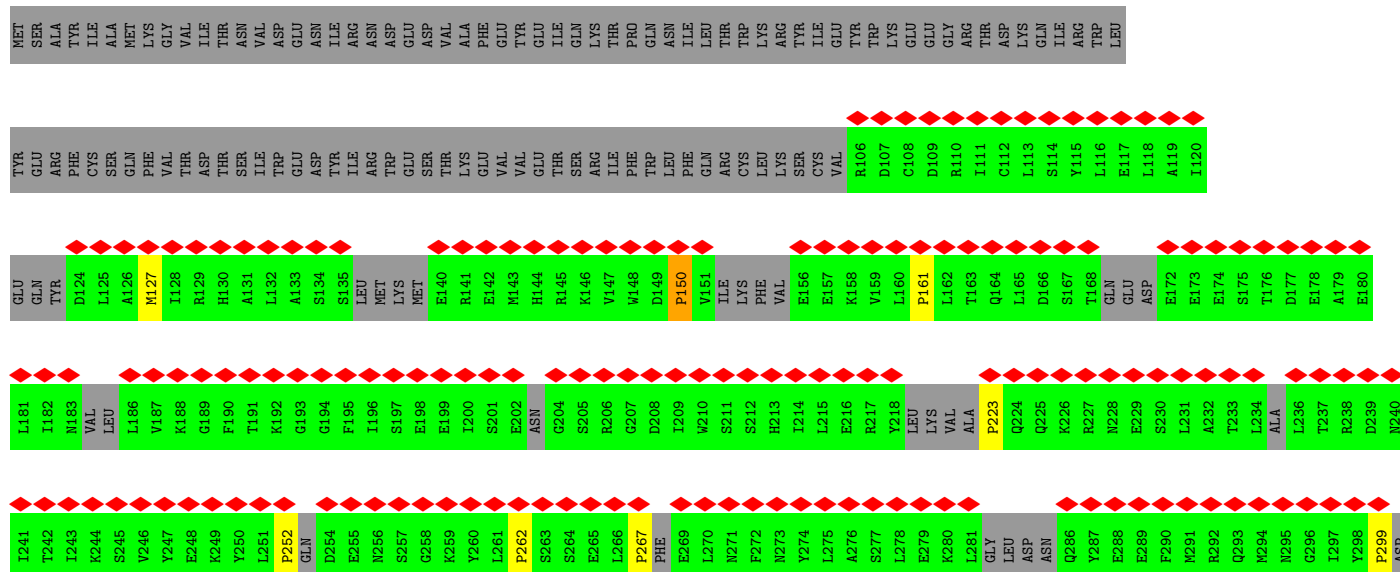


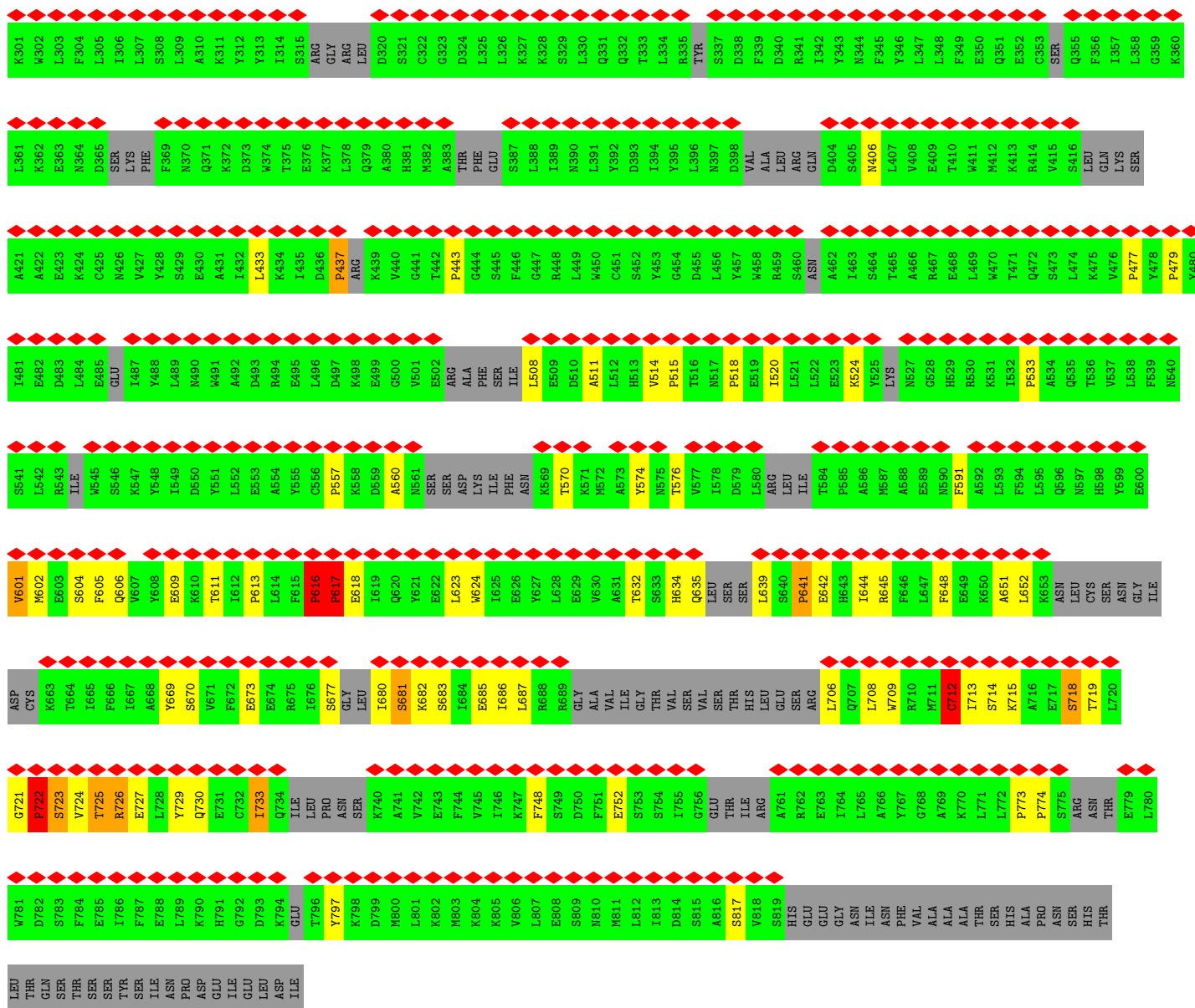


• Molecule 7: Pre-mRNA-splicing factor SNT309

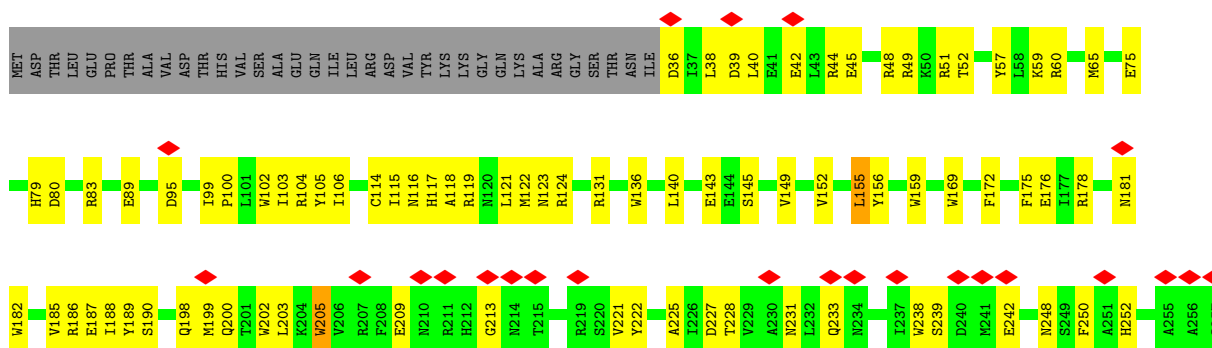


• Molecule 8: Pre-mRNA-splicing factor SYF1



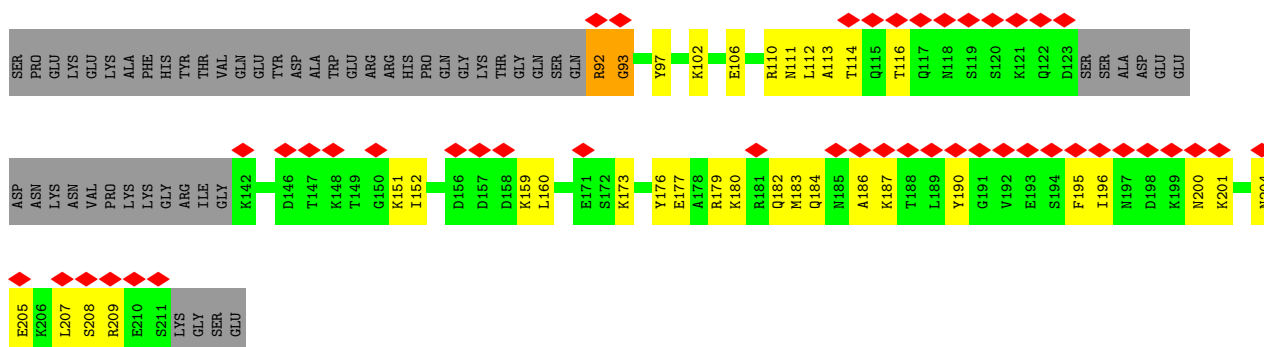
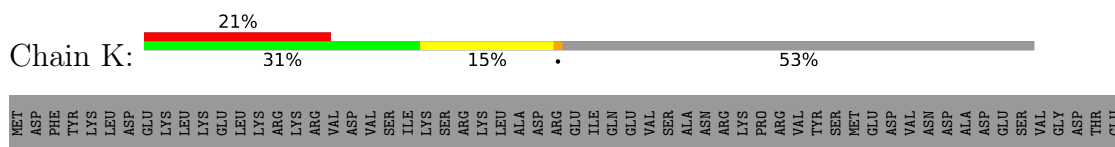


• Molecule 9: Pre-mRNA-splicing factor CLF1

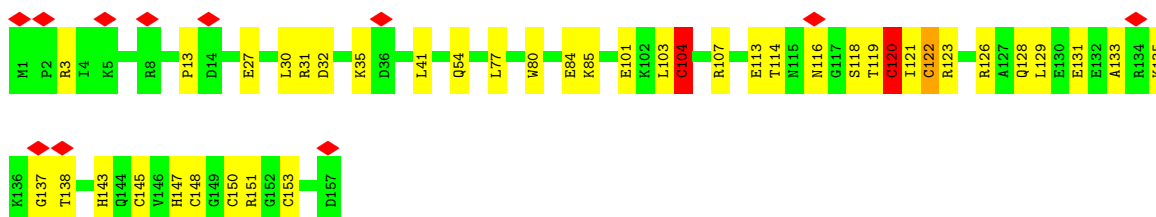
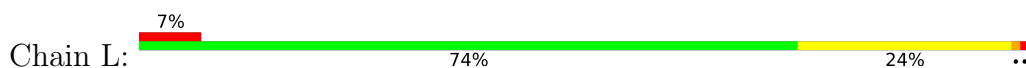




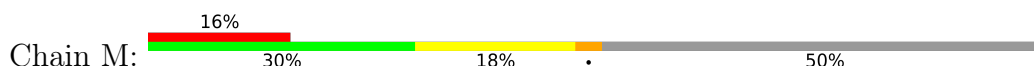
• Molecule 11: Pre-mRNA-splicing factor SYF2

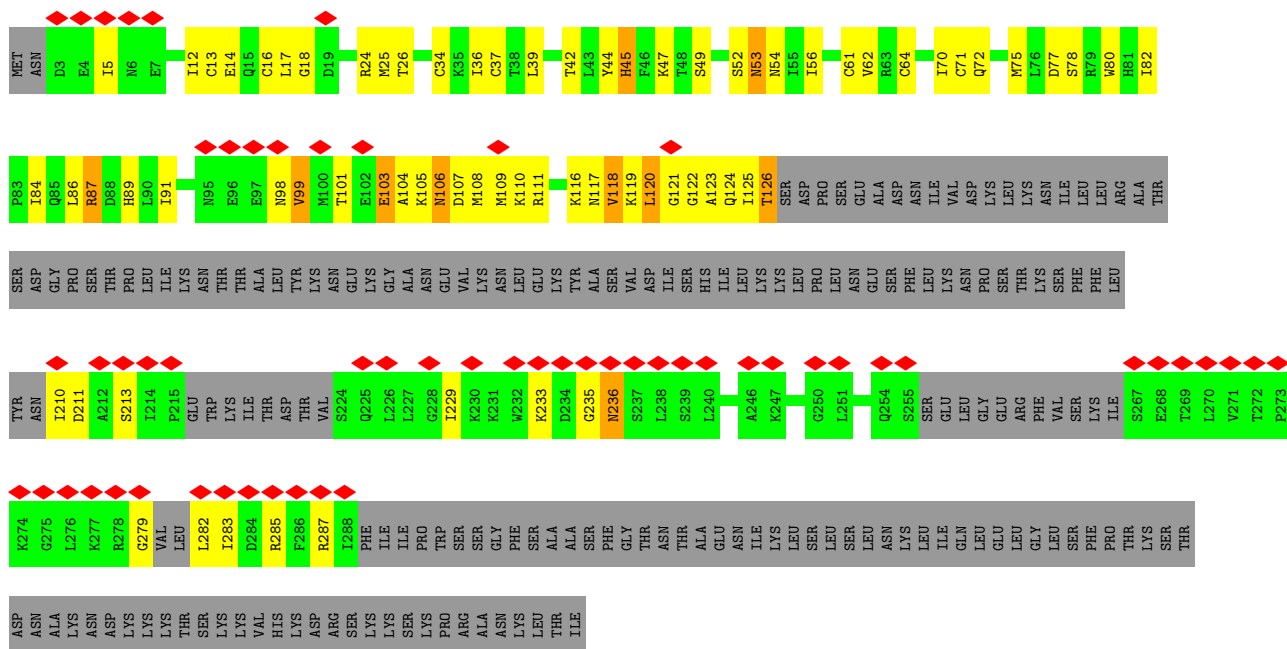


• Molecule 12: Pre-mRNA-splicing factor BUD31

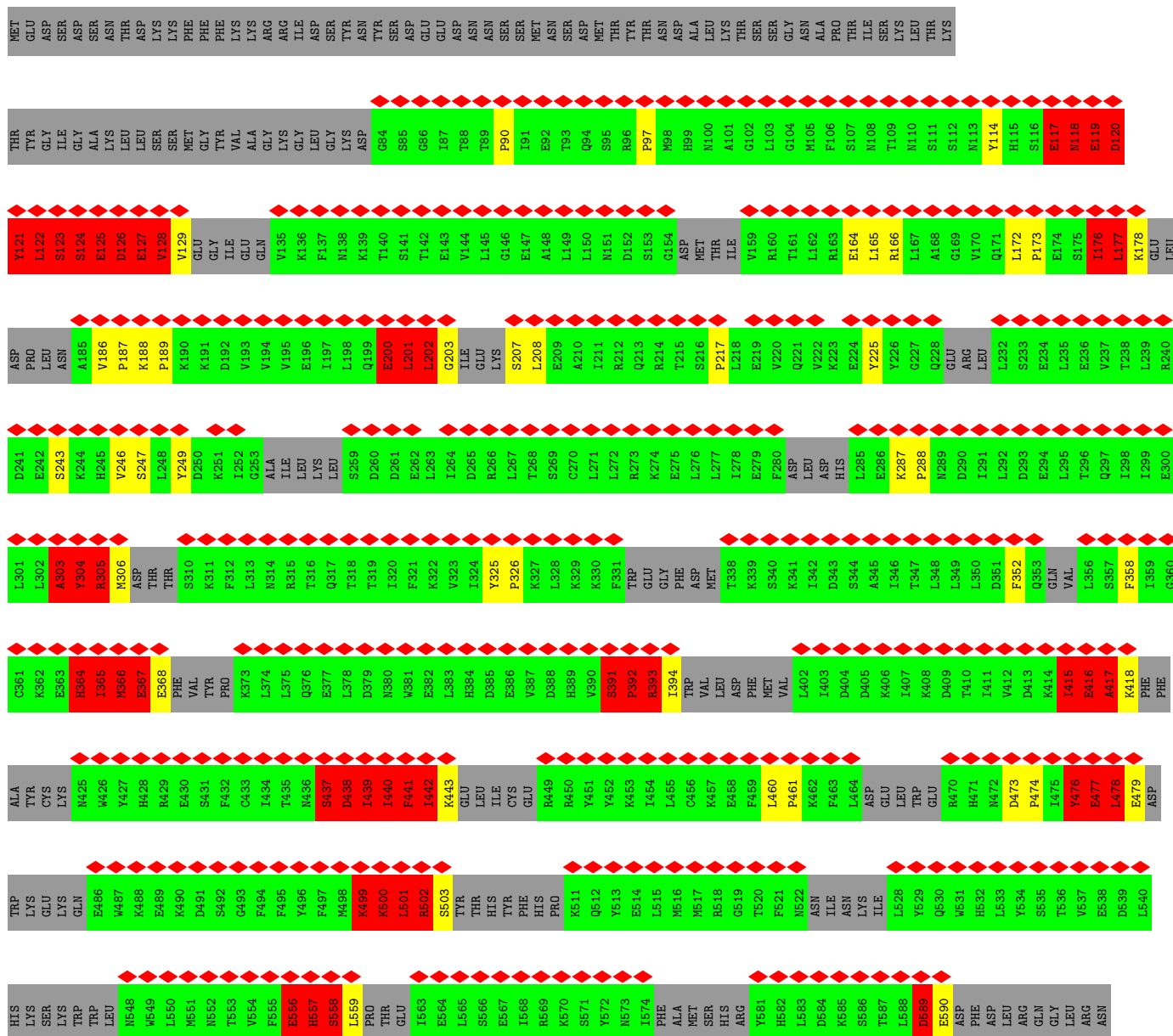


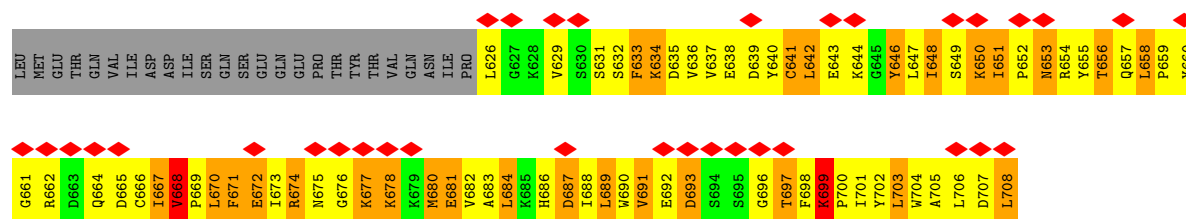
• Molecule 13: Pre-mRNA-splicing factor SLT11



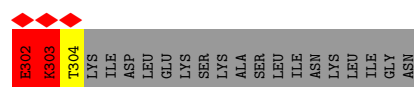
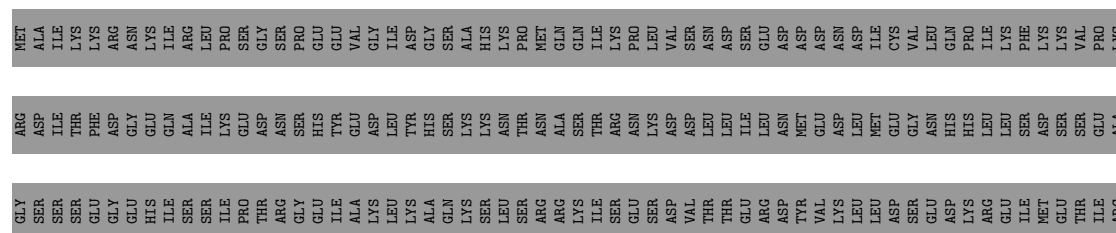


- Molecule 21: Pre-mRNA-splicing factor SPP382

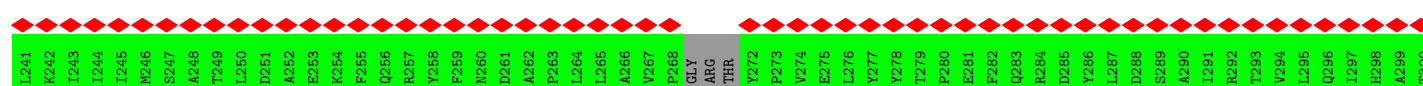
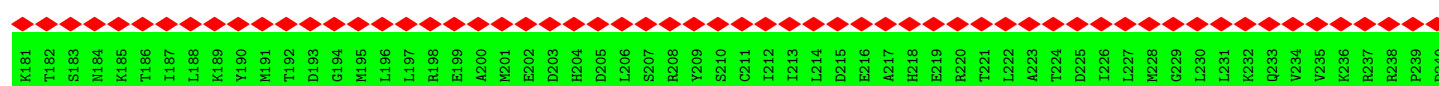
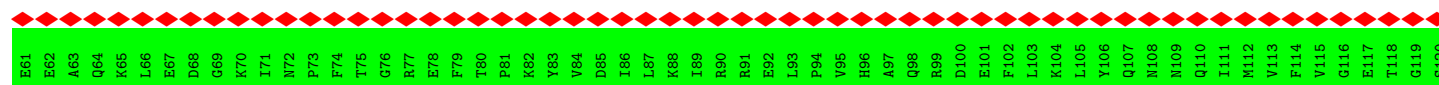
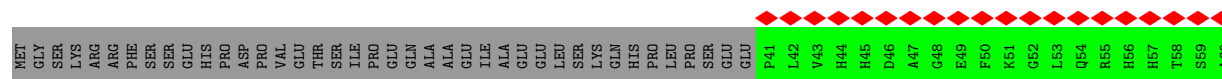
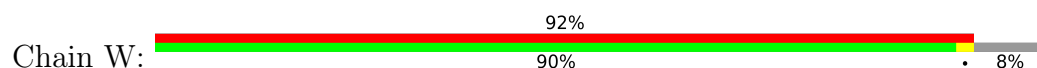


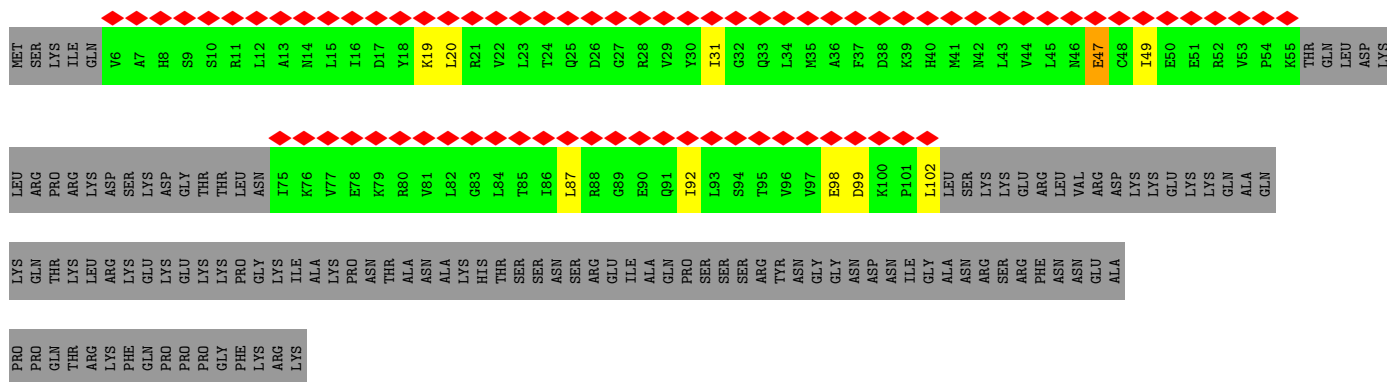


• Molecule 22: Pre-mRNA-splicing factor NTR2

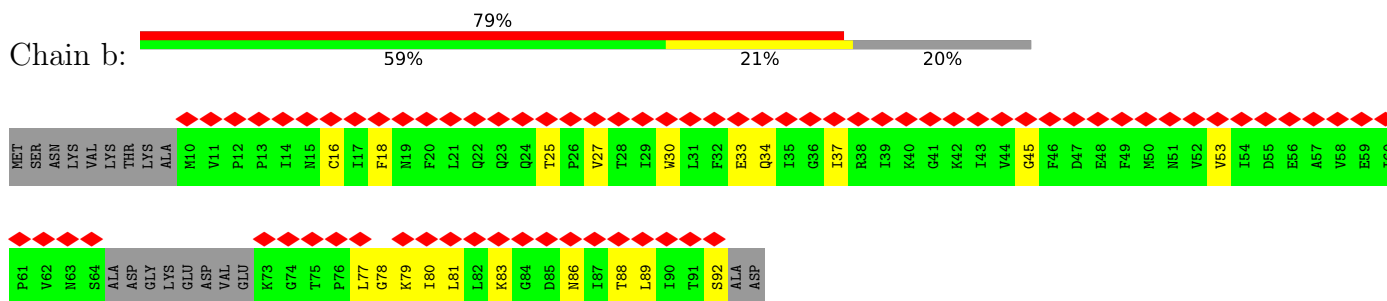


• Molecule 23: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43

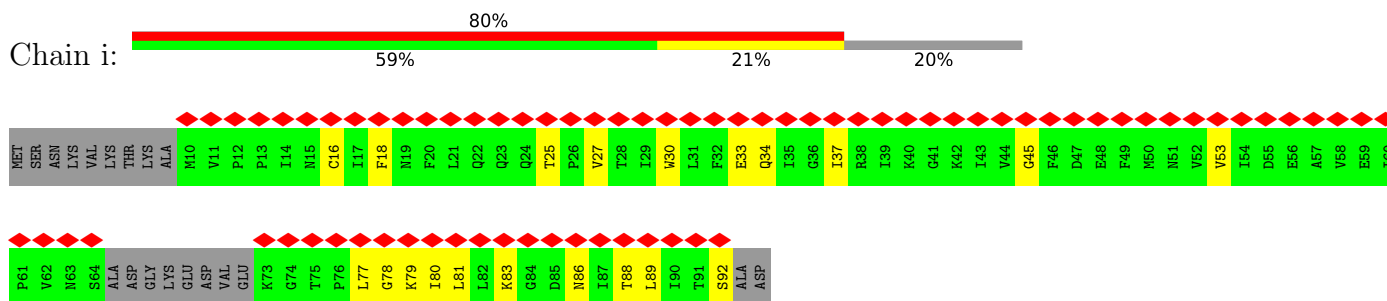




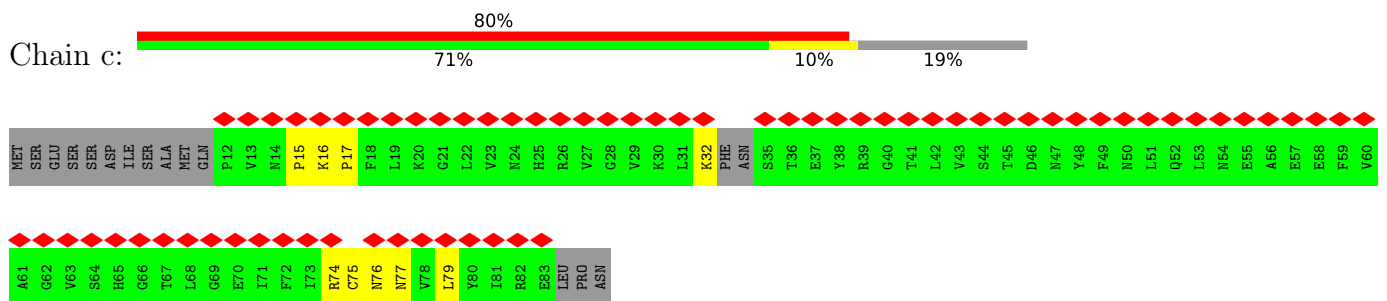
- Molecule 25: Small nuclear ribonucleoprotein E



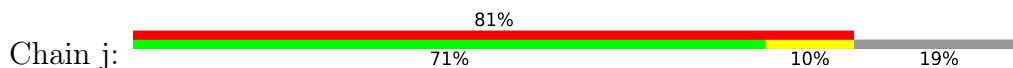
- Molecule 25: Small nuclear ribonucleoprotein E

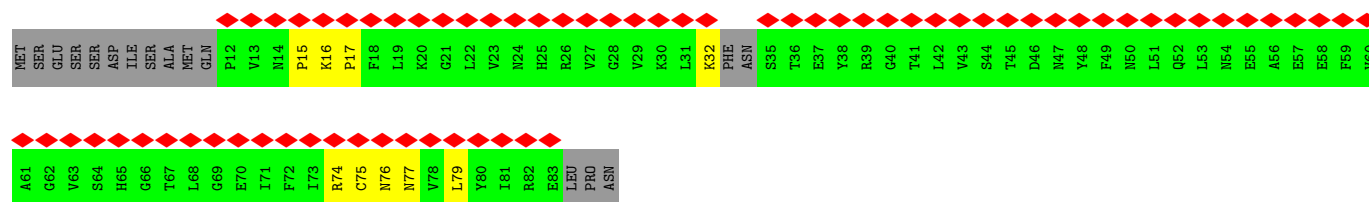


- Molecule 26: Small nuclear ribonucleoprotein F

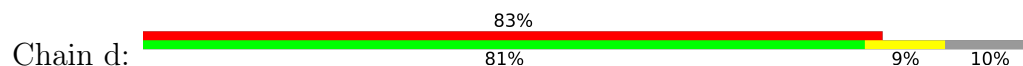


- Molecule 26: Small nuclear ribonucleoprotein F

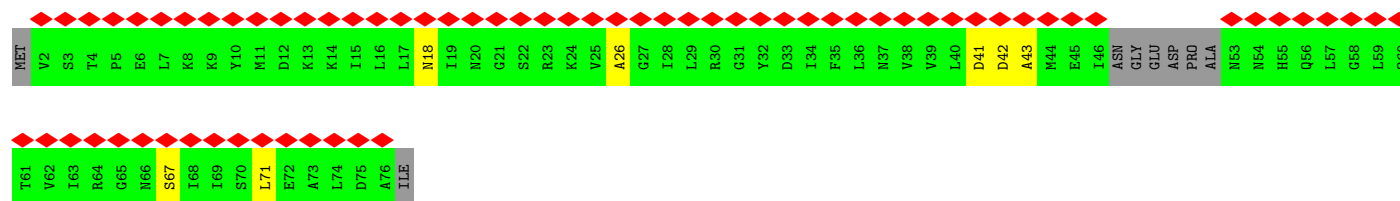
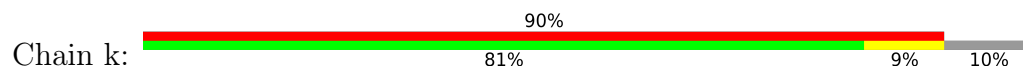




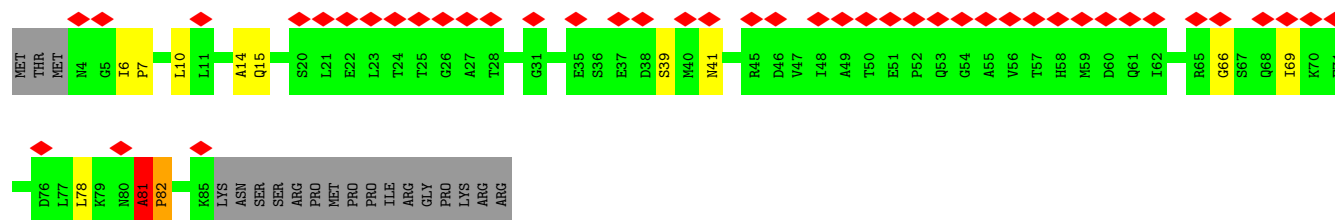
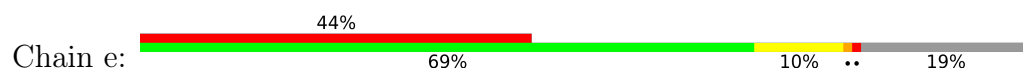
• Molecule 27: Small nuclear ribonucleoprotein G



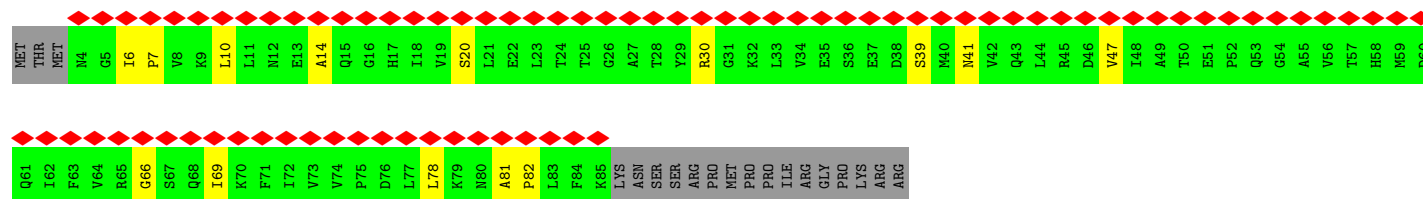
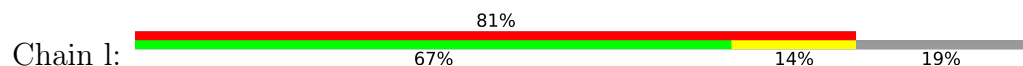
• Molecule 27: Small nuclear ribonucleoprotein G



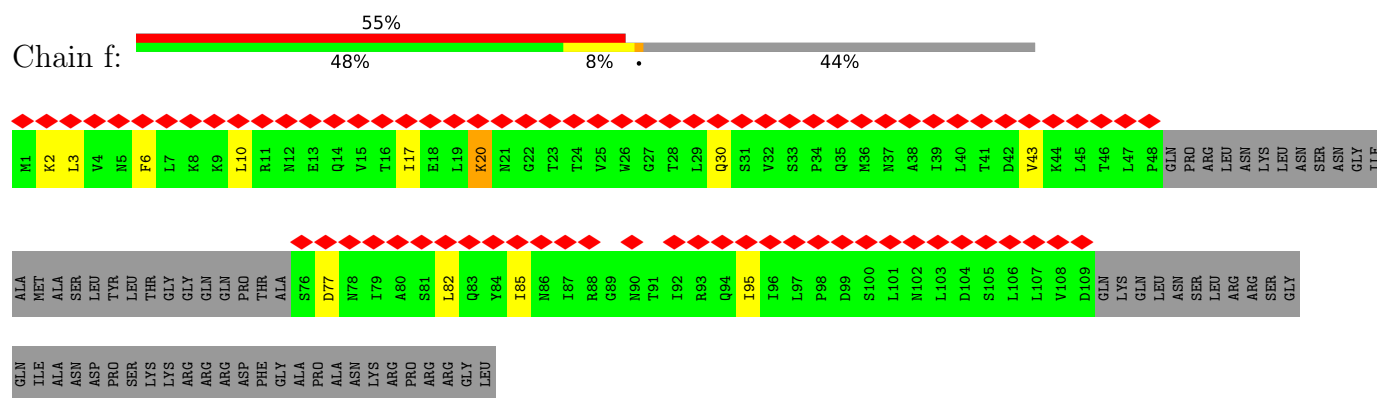
• Molecule 28: Small nuclear ribonucleoprotein Sm D3



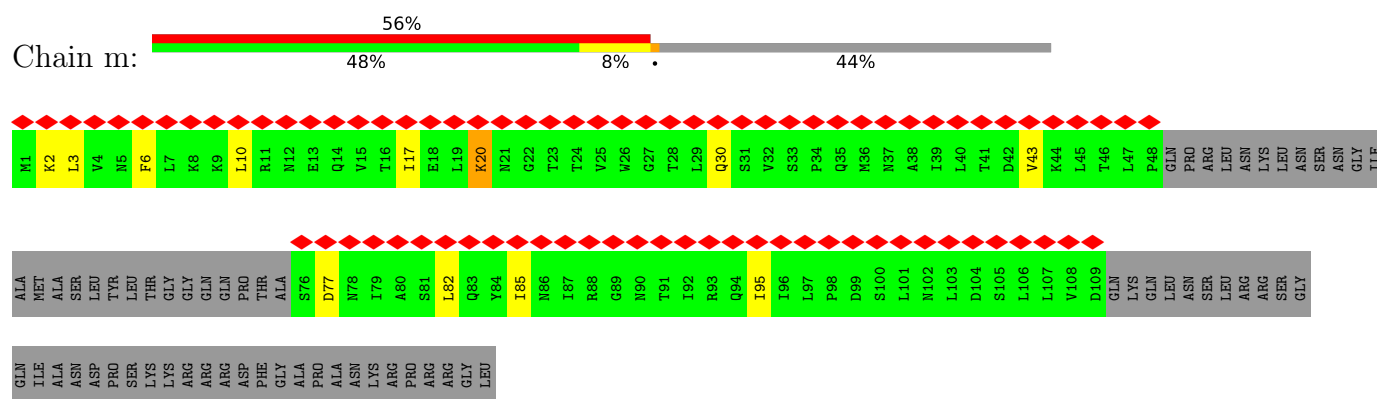
• Molecule 28: Small nuclear ribonucleoprotein Sm D3



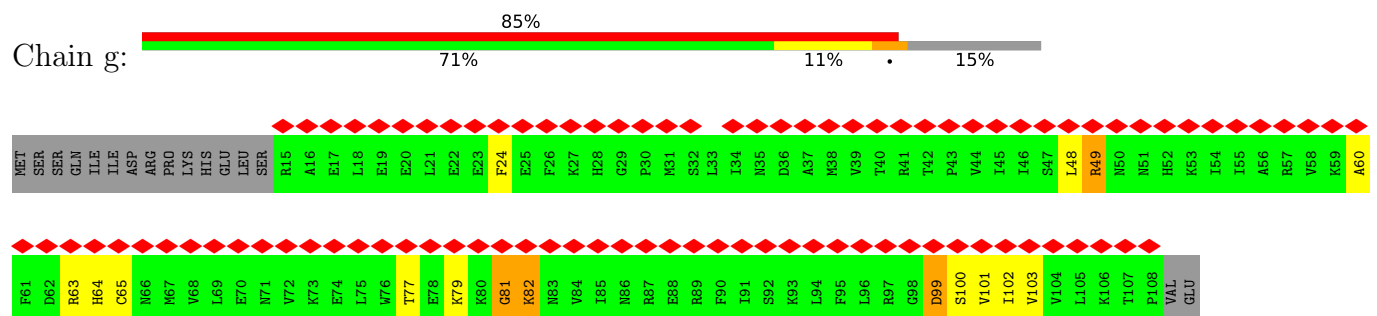
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



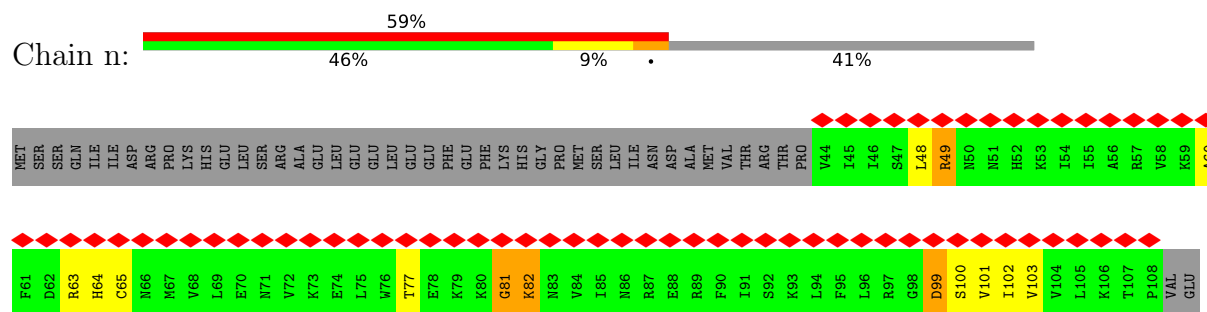
- Molecule 29: Small nuclear ribonucleoprotein Sm D1



- Molecule 30: Small nuclear ribonucleoprotein Sm D2



- Molecule 30: Small nuclear ribonucleoprotein Sm D2



- Molecule 31: U2 small nuclear ribonucleoprotein A'

[illegible]

- Molecule 33: Pre-mRNA-processing factor 19



M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	I12	P13	V14	L15	S16	P17	K18	S19	R20	T21	L22	F23	E24	K25	S26	L27	L28	E29	Q30	Y31	V32	K33	D34	T35	G36	N37	D38	P39	I40	T41	N42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	VAL	PRO	S56	A57	Q58	Q59	A60
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S61	L62	T63	E64	S65	THR	ASN	ASN	SER	ALA	ALA	THR	LEU	LYS	ALA	ALA	ASN	TYR	SER	I77	P78	M79	L80	L81	T82	S83	S84	L84	L84	Q85	M86	E87	M88	D89	A90	I91	M92	M92	L93	E94	N95	P96	K97	L98	R99	I00	T01	L02	D03	S04	L05	T06	K07	K08	L09	S10	T11	V12	M13	Y14	E15	R16	D17	A18	A19	K20
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L121	V122	A123	A124	Q125	L126	L127	L128	E129	K130	M131	M132	D133	S134	K135	D136	L137	P138	K139	S140	S141	Q142	GLN	ALA	VAL	ALA	ALA	ILE	THR	ARG	GLU	GLU	PHE	LEU	GLN	GLY	LEU	LEU	LEU	GLN	SER	SER	ARG	ASP	PHE	VAL	ALA	ALA	ARG	GLY	LYS	PRO	PRO	ILE	LEU	LYS	ASN
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GLU LEU LEU GLN GLN ALA ALA ASN TYR SER ARG ASN LYS THR PHE PRO TYR PRO LYS GLU LEU LEU ASN LYS MET MET TYR TYR ASP ASP LYS TRP VAL CYS CYS MET CYS ARG CYS GLU ASP GLY ALA LEU LEU HIS PHE THR GLN LEU LYS LYS ASP SER LYS THR ILE THR THR ILE THR THR ASN PRO PRO

THR	GLY	GLU	HIS	PRO	ALA	ILE	ILE	SER	ARG	GLY	PRO	CYS	ASN	ARG	LEU	LEU	LEU	PRO	GLY	ASN	GLN	ILE	THR	THR	SER	LYS	ASN	LYS	VAL	LEU	ARG	GLU	ILE	ILE	VAL	ASP	SER	ALA	ASN	GLU	ILE	ILE	TYR	MET	THR	GLY	HIS	ASN	GLU	VAL	ASN	THR	GLU
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TYR	PHE	ILE	TRP	ALA	ASP	ASN	ARG	GLY	THR	ILE	ILE	GLY	PHE	GLN	SER	TYR	GLU	ASP	ASP	SER	GLN	TYR	ILE	VAL	HIS	SER	ALA	LYS	SER	SER	ASP	VAL	GLU	TYR	SER	SER	GLY	VAL	LEU	HIS	LYS	ASP	ASP	LEU	LEU	ALA	LEU	LEU	TYR	SER	PRO	ASP	GLY	ILE	LEU	LEU	ASP	VAL	TYR	ASN	LEU	SER
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SER ASP PRO GLN ALA SER SER ARG PHE PRO PRO VAL ASP GLU GLU VAL LYS LYS VAL VAL LYS PHE ASP ASN GLY TRP MET VAL VAL VAL GLU CYS ASP GLN THR VAL VAL CYS PHE ASP LEU ARG LYS ASP VAL VAL THR TYR THR THR TYR THR THR TYR THR TYR

THR	GLY	THR	VAL	THR	THR	TYR	ASP	ILE	ASP	ASP	GLY	LYS	ASN	MET	ILE	ALA	ALA	TYR	THR	ASN	GLU	GLY	ASN	ASN	LEU	THR	ILE	TYR	LYS	PHE	ASP	LYS	LYS	THR	THR	LYS	ASN	TRP	THR	LYS	GLU	ASP	GLY	GLU	GLY	SER	ALA	LEU	CYS	LEU	GLN	SER	ASP	THR	THR	ASP	ASP	ASP	VAL	VAL
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CYS GLY ASP GLY GLY ILE ALA ALA ILE LEU LYS THR ASN ASP SER PHE ASN ILE VAL ALA LEU THR PRO

- Molecule 33: Pre-mRNA-processing factor 19



M1	L2	C3	A4	I5	S6	G7	K8	V9	P10	R11	I12	P13	V14	L15	S16	P17	K18	S19	R20	T21	T22	F23	E24	K25	S26	L27	L28	E29	Q30	V31	V32	K33	D34	T35	C36	N37	D38	P39	I40	T41	N42	E43	P44	L45	S46	I47	E48	E49	I50	V51	E52	I53	V54	P55	S56	A57	Q58	Q59	A60
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S61	LEU	THR	GLU	SER	THR	ASN	SER	SER	ALA	THR	LEU	LYS	ALA	ASN	TYR	S76	S77	P78	M79	L80	L81	T82	S83	L84	Q85	N86	E87	W88	D89	A90	I91	M92	L93	E94	N95	P96	K97	L98	R99	S100	T101	L102	D103	S104	L105	T106	K107	L108	L109	S110	T111	V112	M113	Y114	E115	R116	D117	A118	A119	K120
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L121	V122	A123	A124	Q125	L126	L127	M128	E129	K130	M131	E132	D133	S134	K135	D136	L137	P138	K139	S140	S141	Q142	Q143	ALA	VAL	ALA	ALA	ILE	THR	ARG	GLU	GLU	PHI	LEU	LEU	GLN	GLY	GLY	LEU	LEU	GLN	SER	SER	SER	ASP	ASP	PHE	VAL	VAL	ALA	ALA	ARG	GLY	LYS	LEU	LEU	LYS	LYS	ALA	PRO	LYS	LYS	TRP	PRO	PRO	ILE	ILE	LYS	LYS	ASN	ASN
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GLU LEU LEU LEU GLN GLN ALA ALA ASN ASN ARG ARG ILE ILE LYS THR THR PHE THR PRO PRO LYS LYS GLU GLU LEU LEU ASN ASN LYS LYS SER SER MET MET TYR TYR TYR ASP ASP LYS LYS TRP TRP VAL VAL CYS CYS MET MET CYS CYS ARG ARG CYS CYS ASP ASP GLU GLU GLY GLY ALA ALA HIS HIS PHE PHE THR THR GLN GLN LEU LEU LYS LYS ASN ASN SER SER LYS LYS THR THR ILE ILE THR THR THR THR ILE ILE THR THR PRO PRO ASN ASN PRO PRO PC

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	150363	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.282	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3060001, 1.3060001, 1.3060001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, GTP, 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	0.80	16/16117 (0.1%)	0.84	33/21848 (0.2%)
2	B	0.48	0/2747	0.66	1/4267 (0.0%)
3	C	0.91	10/7434 (0.1%)	0.92	17/10070 (0.2%)
4	D	0.48	0/2405	0.66	0/3744
5	E	0.39	0/653	0.64	0/1010
6	F	0.73	11/1922 (0.6%)	0.95	13/2984 (0.4%)
7	G	0.58	0/919	1.06	2/1237 (0.2%)
8	H	0.65	9/3180 (0.3%)	0.97	27/4331 (0.6%)
9	I	0.68	0/3574	0.82	7/4863 (0.1%)
10	J	0.56	1/2962 (0.0%)	0.92	11/3987 (0.3%)
11	K	0.60	0/826	0.75	1/1097 (0.1%)
12	L	0.87	0/1314	0.90	1/1759 (0.1%)
13	M	0.85	1/1308 (0.1%)	0.85	1/1758 (0.1%)
14	N	0.77	0/2135	0.77	1/2871 (0.0%)
15	O	1.06	1/2704 (0.0%)	0.93	2/3676 (0.1%)
16	P	0.73	0/568	1.30	8/758 (1.1%)
17	Q	0.68	0/1604	0.83	1/2160 (0.0%)
18	R	0.36	0/378	0.75	0/498
19	S	0.73	0/200	1.15	1/264 (0.4%)
20	T	0.87	5/825 (0.6%)	1.44	17/1100 (1.5%)
21	U	0.92	1/2684 (0.0%)	1.98	70/3680 (1.9%)
22	V	0.69	1/622 (0.2%)	2.02	22/843 (2.6%)
23	W	0.36	1/3502 (0.0%)	0.95	2/4877 (0.0%)
24	a	0.55	0/636	0.76	0/856
24	h	0.55	0/615	0.76	0/829
25	b	0.64	0/585	0.86	0/795
25	i	0.64	0/585	0.86	0/795
26	c	0.61	0/564	0.87	0/761
26	j	0.61	0/564	0.87	0/761
27	d	0.53	0/532	0.82	1/715 (0.1%)
27	k	0.53	0/532	0.82	1/715 (0.1%)
28	e	0.55	0/634	0.96	2/859 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	l	0.54	0/634	0.96	0/859
29	f	0.58	0/649	0.81	0/880
29	m	0.58	0/649	0.81	0/880
30	g	0.65	0/753	0.96	2/1013 (0.2%)
30	n	0.65	0/535	0.86	2/717 (0.3%)
31	o	1.24	6/839 (0.7%)	2.35	43/1127 (3.8%)
32	p	1.00	2/514 (0.4%)	1.86	8/686 (1.2%)
33	q	0.54	0/837	0.84	0/1129
33	r	0.54	0/854	0.91	0/1151
33	s	0.57	0/856	0.92	0/1155
33	t	0.54	0/828	0.86	0/1117
34	x	0.29	0/194	0.54	0/298
All	All	0.74	65/73972 (0.1%)	0.99	297/101780 (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	7
3	C	0	2
11	K	0	1
13	M	0	2
15	O	0	6
16	P	0	2
17	Q	0	1
19	S	0	2
20	T	0	9
21	U	0	47
22	V	0	14
23	W	0	1
27	d	0	1
27	k	0	1
28	e	0	2
28	l	0	2
30	g	0	2
30	n	0	2
All	All	0	104

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	934	HIS	N-CA	-10.65	1.32	1.46
31	o	69	ASP	CA-CB	-10.65	1.38	1.53
3	C	933	TRP	CA-C	-10.48	1.38	1.52
8	H	712	CYS	CB-SG	-8.52	1.53	1.81
1	A	1497	ARG	CA-C	8.12	1.63	1.52
6	F	1096	C	O3'-P	-8.07	1.49	1.61
1	A	716	ARG	NE-CZ	-7.73	1.24	1.33
22	V	227	ILE	C-O	7.68	1.32	1.24
6	F	1096	C	C1'-N1	7.65	1.59	1.48
6	F	1120	G	C1'-N9	-7.63	1.36	1.48
6	F	1118	U	C1'-N1	7.50	1.59	1.48
23	W	462	LEU	C-N	-7.30	1.23	1.33
15	O	330	ASP	C-O	-7.28	1.15	1.24
21	U	186	VAL	CA-CB	-6.98	1.50	1.54
6	F	1111	U	C1'-N1	6.97	1.58	1.48
6	F	1101	C	C1'-N1	6.96	1.58	1.48
6	F	1109	C	C1'-N1	6.95	1.57	1.47
6	F	1119	C	C1'-N1	6.95	1.58	1.48
6	F	1115	G	C1'-N9	-6.89	1.37	1.48
31	o	102	THR	CB-OG1	6.89	1.54	1.43
20	T	75	THR	C-N	-6.74	1.24	1.33
31	o	51	THR	CB-OG1	6.66	1.54	1.43
13	M	117	ASN	C-N	6.46	1.42	1.34
3	C	976	ILE	N-CA	-6.35	1.39	1.46
3	C	607	LEU	C-O	6.22	1.31	1.23
32	p	110	THR	CB-OG1	6.19	1.53	1.43
32	p	75	THR	CB-OG1	6.17	1.53	1.43
1	A	1383	PHE	C-N	6.15	1.40	1.33
31	o	153	THR	CB-OG1	6.11	1.53	1.43
6	F	1112	G	C1'-N9	-6.01	1.39	1.48
3	C	534	THR	C-N	6.00	1.41	1.33
1	A	1390	THR	C-N	5.95	1.40	1.33
31	o	38	THR	CB-OG1	5.93	1.53	1.43
1	A	1379	MET	C-N	5.88	1.41	1.34
1	A	494	VAL	C-O	-5.84	1.18	1.24
6	F	121	C	C1'-N1	5.83	1.57	1.48
31	o	160	THR	CB-OG1	5.71	1.52	1.43
8	H	718	SER	CB-OG	5.68	1.53	1.42
1	A	165	LEU	C-O	-5.67	1.17	1.24
20	T	44	THR	CB-OG1	5.65	1.52	1.43
1	A	871	GLY	C-N	5.64	1.41	1.33
20	T	141	LEU	C-N	5.63	1.41	1.33
3	C	687	ALA	CA-C	5.58	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	723	SER	CB-OG	5.57	1.53	1.42
3	C	913	GLY	C-O	5.45	1.28	1.24
3	C	535	PRO	N-CD	5.33	1.55	1.47
1	A	872	PRO	N-CD	5.32	1.55	1.47
3	C	363	PRO	N-CD	5.25	1.55	1.47
1	A	483	PRO	C-O	-5.24	1.17	1.24
1	A	901	PRO	C-N	5.24	1.40	1.33
8	H	576	THR	CB-OG1	5.24	1.52	1.43
10	J	202	LYS	C-N	-5.21	1.21	1.33
8	H	719	THR	CB-OG1	5.21	1.52	1.43
1	A	902	PRO	N-CD	5.19	1.55	1.47
1	A	1391	PRO	N-CD	5.19	1.55	1.47
8	H	714	SER	CB-OG	5.18	1.52	1.42
1	A	1380	PRO	N-CD	5.16	1.54	1.47
1	A	947	PRO	N-CD	5.15	1.54	1.47
20	T	71	THR	CB-OG1	5.13	1.51	1.43
3	C	602	VAL	C-O	-5.12	1.19	1.24
20	T	142	PRO	N-CD	5.11	1.54	1.47
8	H	681	SER	CB-OG	5.10	1.52	1.42
1	A	946	ASN	C-N	5.07	1.40	1.34
8	H	644	ILE	CB-CG1	-5.06	1.43	1.53
8	H	632	THR	CB-OG1	5.01	1.51	1.43

All (297) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	o	44	PRO	N-CA-CB	15.99	113.94	103.23
16	P	6	ARG	CA-C-N	15.58	139.31	119.84
16	P	6	ARG	C-N-CA	15.58	139.31	119.84
23	W	462	LEU	CA-C-N	-14.27	94.29	121.54
23	W	462	LEU	C-N-CA	-14.27	94.29	121.54
21	U	440	ILE	O-C-N	-12.47	109.69	121.91
21	U	365	ILE	O-C-N	-12.45	109.71	121.91
21	U	442	ILE	O-C-N	-12.43	109.73	121.91
21	U	415	ILE	O-C-N	-12.41	109.75	121.91
21	U	439	ILE	O-C-N	-12.40	109.76	121.91
21	U	128	VAL	O-C-N	-12.40	109.76	121.91
21	U	176	ILE	O-C-N	-12.39	109.76	121.91
22	V	294	VAL	O-C-N	-12.37	109.78	121.91
31	o	81	LEU	CA-C-N	12.10	131.59	120.10
31	o	81	LEU	C-N-CA	12.10	131.59	120.10
21	U	303	ALA	O-C-N	-12.06	109.65	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	113	THR	O-C-N	-12.05	109.66	122.07
21	U	119	GLU	O-C-N	-12.04	109.67	122.07
21	U	123	SER	O-C-N	-12.04	109.67	122.07
21	U	201	LEU	O-C-N	-12.04	109.67	122.07
21	U	126	ASP	O-C-N	-12.03	109.68	122.07
21	U	499	LYS	O-C-N	-12.03	109.68	122.07
21	U	393	ARG	O-C-N	-12.03	109.68	122.07
21	U	391	SER	O-C-N	-12.03	109.78	120.48
21	U	478	LEU	O-C-N	-12.02	109.69	122.07
22	V	300	ALA	O-C-N	-12.02	109.69	122.07
21	U	304	TYR	O-C-N	-12.01	109.70	122.07
20	T	123	LEU	O-C-N	-12.01	109.70	122.07
21	U	437	SER	O-C-N	-12.01	109.70	122.07
22	V	298	LEU	O-C-N	-12.01	109.70	122.07
22	V	299	GLN	O-C-N	-12.01	109.70	122.07
21	U	589	ASP	O-C-N	-12.00	109.71	122.07
22	V	290	GLN	O-C-N	-12.00	109.71	122.07
21	U	121	TYR	O-C-N	-12.00	109.71	122.07
22	V	302	GLU	O-C-N	-12.00	109.71	122.07
22	V	295	GLU	O-C-N	-11.99	109.72	122.07
21	U	558	SER	O-C-N	-11.99	109.72	122.07
21	U	117	GLU	O-C-N	-11.99	109.72	122.07
21	U	364	HIS	O-C-N	-11.99	109.72	122.07
21	U	367	GLU	O-C-N	-11.98	109.73	122.07
21	U	118	ASN	O-C-N	-11.98	109.73	122.07
22	V	301	LEU	O-C-N	-11.98	109.73	122.07
20	T	111	SER	O-C-N	-11.97	109.74	122.07
20	T	112	SER	O-C-N	-11.97	109.74	122.07
20	T	125	GLN	O-C-N	-11.97	109.74	122.07
21	U	366	MET	O-C-N	-11.97	109.74	122.07
20	T	124	LEU	O-C-N	-11.97	109.74	122.07
21	U	502	ARG	O-C-N	-11.97	109.74	122.07
22	V	292	LYS	O-C-N	-11.97	109.74	122.07
22	V	293	LYS	O-C-N	-11.97	109.74	122.07
21	U	177	LEU	O-C-N	-11.97	109.74	122.07
21	U	417	ALA	O-C-N	-11.97	109.74	122.07
21	U	556	GLU	O-C-N	-11.97	109.74	122.07
22	V	303	LYS	O-C-N	-11.97	109.74	122.07
21	U	122	LEU	O-C-N	-11.96	109.75	122.07
21	U	125	GLU	O-C-N	-11.96	109.75	122.07
21	U	441	PHE	O-C-N	-11.96	109.75	122.07
22	V	291	ARG	O-C-N	-11.96	109.75	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	V	297	ARG	O-C-N	-11.96	109.75	122.07
21	U	127	GLU	O-C-N	-11.96	109.75	122.07
21	U	501	LEU	O-C-N	-11.96	109.75	122.07
21	U	557	HIS	O-C-N	-11.96	109.75	122.07
22	V	296	MET	O-C-N	-11.96	109.75	122.07
21	U	438	ASP	O-C-N	-11.95	109.76	122.07
21	U	124	SER	O-C-N	-11.95	109.77	122.07
21	U	476	TYR	O-C-N	-11.95	109.77	122.07
21	U	202	LEU	O-C-N	-11.94	109.77	122.07
21	U	200	GLU	O-C-N	-11.94	109.77	122.07
21	U	305	ARG	O-C-N	-11.94	109.78	122.07
21	U	120	ASP	O-C-N	-11.93	109.78	122.07
21	U	416	GLU	O-C-N	-11.93	109.78	122.07
21	U	500	LYS	O-C-N	-11.92	109.79	122.07
21	U	477	GLU	O-C-N	-11.92	109.79	122.07
22	V	239	ASN	N-CA-C	11.72	135.76	110.80
3	C	976	ILE	N-CA-C	-11.69	102.30	112.12
22	V	240	GLU	N-CA-CB	11.59	130.08	110.49
21	U	392	PRO	O-C-N	-10.96	109.79	122.17
20	T	110	GLU	O-C-N	-10.31	109.70	122.17
1	A	240	PRO	N-CA-C	9.62	122.44	110.70
11	K	93	GLY	N-CA-C	9.17	121.34	112.08
31	o	12	PRO	N-CA-CB	9.06	111.34	103.19
3	C	363	PRO	CA-N-CD	-8.92	99.51	112.00
16	P	6	ARG	N-CA-C	-8.75	100.28	108.07
10	J	334	PRO	N-CA-CB	8.20	110.98	103.19
31	o	5	PRO	N-CA-CB	8.19	112.00	103.23
16	P	8	GLN	N-CA-C	8.12	120.13	111.28
1	A	488	ARG	N-CA-C	8.09	119.73	111.07
6	F	40	U	C4'-C3'-O3'	8.03	121.44	109.40
31	o	15	TYR	CA-C-O	-8.00	111.80	120.36
31	o	107	SER	N-CA-C	7.98	122.80	112.26
1	A	1536	LEU	N-CA-C	7.94	120.01	111.36
8	H	613	PRO	N-CA-CB	7.93	111.12	103.51
8	H	477	PRO	N-CA-CB	7.64	110.46	103.20
8	H	616	PRO	N-CA-CB	7.60	110.45	103.08
6	F	1111	U	P-O5'-C5'	-7.59	109.51	120.90
3	C	534	THR	CA-C-N	-7.55	112.96	120.21
3	C	534	THR	C-N-CA	-7.55	112.96	120.21
31	o	126	ASN	CA-C-O	7.54	128.31	120.40
1	A	486	PHE	N-CA-C	7.41	119.44	111.36
6	F	1110	U	O3'-P-O5'	-7.36	92.97	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	773	PRO	N-CA-CB	7.34	110.20	103.08
3	C	976	ILE	N-CA-CB	-7.31	101.88	111.90
32	p	65	PHE	CA-CB-CG	-7.30	106.50	113.80
31	o	57	LEU	N-CA-CB	7.29	123.05	110.81
3	C	461	LYS	N-CA-C	-7.29	99.67	110.23
3	C	275	LEU	N-CA-C	7.19	119.20	111.36
21	U	186	VAL	O-C-N	7.19	125.02	120.42
31	o	33	ASP	CA-CB-CG	7.16	119.76	112.60
1	A	1253	LYS	N-CA-C	-7.14	103.50	111.28
9	I	421	PRO	N-CA-CB	7.12	110.08	103.46
31	o	10	ASP	CA-CB-CG	7.08	119.69	112.60
6	F	1113	U	C3'-C2'-O2'	-7.05	104.03	114.60
8	H	722	PRO	N-CA-CB	7.04	111.07	103.33
31	o	42	SER	N-CA-CB	-7.00	99.71	110.42
1	A	1390	THR	CA-C-N	-6.96	113.14	120.03
1	A	1390	THR	C-N-CA	-6.96	113.14	120.03
31	o	7	ILE	CA-CB-CG1	6.95	122.21	110.40
8	H	223	PRO	N-CA-CB	6.89	110.58	103.00
1	A	901	PRO	CA-C-N	-6.86	112.71	119.78
1	A	901	PRO	C-N-CA	-6.86	112.71	119.78
10	J	418	PRO	N-CA-CB	6.86	110.45	103.25
31	o	3	PHE	N-CA-C	-6.85	98.05	108.67
8	H	479	PRO	N-CA-CB	6.83	110.75	103.52
32	p	73	PHE	CA-C-O	-6.82	112.82	120.32
31	o	4	THR	N-CA-CB	-6.79	98.28	110.37
8	H	617	PRO	CA-CB-CG	6.78	117.39	104.50
8	H	267	PRO	N-CA-CB	6.77	110.44	103.00
8	H	299	PRO	N-CA-CB	6.76	110.44	103.00
20	T	141	LEU	CA-C-N	-6.75	112.81	119.76
20	T	141	LEU	C-N-CA	-6.75	112.81	119.76
8	H	437	PRO	N-CA-CB	6.74	110.41	103.00
3	C	684	GLU	N-CA-C	6.71	125.10	110.80
6	F	1107	C	C5'-C4'-O4'	-6.66	99.11	109.10
6	F	23	U	C2'-C3'-O3'	-6.65	103.73	113.70
8	H	252	PRO	N-CA-CB	6.64	110.31	103.00
9	I	468	PRO	N-CA-CB	6.63	110.29	103.00
1	A	485	PRO	N-CA-C	-6.61	104.73	113.65
31	o	68	PRO	N-CA-CB	6.59	110.17	103.25
1	A	1383	PHE	CA-C-N	-6.59	113.59	120.38
1	A	1383	PHE	C-N-CA	-6.59	113.59	120.38
9	I	559	PRO	N-CA-CB	6.57	110.23	103.00
8	H	150	PRO	N-CA-CB	6.55	110.47	103.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	515	PRO	N-CA-CB	6.55	110.47	103.52
8	H	774	PRO	N-CA-CB	6.55	110.46	103.52
20	T	23	PRO	N-CA-CB	6.55	110.25	102.85
30	n	82	LYS	N-CA-C	6.53	124.71	110.80
3	C	854	ILE	CA-C-N	-6.53	114.06	120.52
3	C	854	ILE	C-N-CA	-6.53	114.06	120.52
9	I	397	PRO	N-CA-CB	6.52	110.43	103.52
16	P	6	ARG	CA-C-O	-6.51	114.63	120.56
30	g	82	LYS	N-CA-C	6.50	124.65	110.80
8	H	533	PRO	N-CA-CB	6.50	110.41	103.39
31	o	130	ILE	CA-C-O	6.50	128.90	120.78
8	H	557	PRO	N-CA-CB	6.47	110.38	103.39
21	U	97	PRO	N-CA-CB	6.44	110.41	103.33
9	I	435	PRO	N-CA-CB	6.43	110.33	103.52
1	A	484	PHE	N-CA-C	6.40	123.95	109.81
1	A	871	GLY	CA-C-N	-6.38	113.19	119.76
1	A	871	GLY	C-N-CA	-6.38	113.19	119.76
8	H	443	PRO	N-CA-CB	6.38	110.59	103.44
21	U	217	PRO	N-CA-CB	6.37	110.34	103.33
21	U	461	PRO	N-CA-CB	6.37	110.05	103.23
6	F	1112	G	P-O3'-C3'	6.36	129.75	120.20
21	U	668	VAL	CA-C-N	-6.36	114.08	120.31
21	U	668	VAL	C-N-CA	-6.36	114.08	120.31
21	U	187	PRO	N-CA-CB	6.35	110.03	103.23
21	U	173	PRO	N-CA-CB	6.34	110.02	103.23
9	I	545	PRO	N-CA-CB	6.33	110.22	103.52
21	U	288	PRO	N-CA-CB	6.32	110.00	103.23
20	T	75	THR	O-C-N	-6.31	114.51	122.27
21	U	189	PRO	N-CA-CB	6.30	109.97	103.23
8	H	518	PRO	N-CA-CB	6.30	110.20	103.52
3	C	933	TRP	CA-C-N	-6.30	110.74	120.31
3	C	933	TRP	C-N-CA	-6.30	110.74	120.31
8	H	161	PRO	N-CA-CB	6.29	110.49	103.44
21	U	326	PRO	N-CA-CB	6.29	109.96	103.23
22	V	212	THR	N-CA-C	6.26	117.77	111.07
21	U	474	PRO	N-CA-CB	6.24	109.90	103.23
31	o	50	LEU	CA-C-N	6.24	131.44	122.40
31	o	50	LEU	C-N-CA	6.24	131.44	122.40
8	H	262	PRO	N-CA-CB	6.23	110.42	103.44
6	F	1111	U	C5'-C4'-C3'	-6.22	106.67	116.00
31	o	83	ARG	N-CA-C	6.20	119.92	111.17
1	A	539	PRO	CB-CA-C	-6.19	104.81	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	467	PRO	N-CA-CB	6.17	109.73	103.25
10	J	447	PRO	N-CA-CB	6.15	109.71	103.25
1	A	1041	VAL	N-CA-C	-6.15	106.51	112.29
10	J	424	PRO	N-CA-CB	6.14	109.75	103.00
1	A	873	GLU	N-CA-C	6.13	117.96	111.28
8	H	641	PRO	CA-CB-CG	6.12	116.14	104.50
17	Q	59	THR	CB-CA-C	-6.11	108.52	115.79
31	o	62	ASN	CA-CB-CG	6.06	118.66	112.60
9	I	351	PRO	N-CA-CB	6.05	110.22	103.44
31	o	132	ASN	OD1-CG-ND2	6.04	128.65	122.60
31	o	85	ASN	N-CA-CB	-6.03	102.58	111.51
10	J	376	PRO	N-CA-CB	6.03	110.19	103.44
31	o	111	PHE	CA-CB-CG	6.02	119.82	113.80
14	N	34	TYR	N-CA-C	-6.00	102.04	110.50
31	o	127	LEU	CA-C-N	-5.98	114.34	122.77
31	o	127	LEU	C-N-CA	-5.98	114.34	122.77
8	H	617	PRO	N-CA-CB	5.95	109.50	103.25
7	G	105	PRO	CA-CB-CG	5.94	115.78	104.50
32	p	66	LYS	N-CA-C	-5.91	104.74	111.07
6	F	1106	G	O3'-P-O5'	-5.91	95.14	104.00
1	A	1443	TYR	N-CA-C	5.89	117.71	111.28
10	J	417	PRO	N-CA-CB	5.87	108.77	103.08
10	J	229	ASP	N-CA-C	5.86	119.47	111.39
10	J	432	PRO	N-CA-CB	5.83	109.70	103.52
21	U	90	PRO	N-CA-CB	5.82	109.46	103.23
16	P	7	PRO	N-CA-C	5.81	124.44	112.47
1	A	1379	MET	N-CA-C	5.81	117.84	109.48
1	A	539	PRO	N-CA-C	5.80	119.61	110.50
1	A	622	MET	CB-CG-SD	-5.80	95.30	112.70
31	o	60	THR	CA-C-O	5.80	127.70	121.55
31	o	44	PRO	CB-CA-C	-5.77	106.15	111.40
22	V	268	PRO	N-CA-CB	5.73	109.36	103.23
21	U	392	PRO	N-CA-CB	5.73	109.36	103.23
6	F	1107	C	P-O3'-C3'	5.72	128.78	120.20
1	A	1068	ARG	N-CA-C	5.66	117.52	111.36
6	F	1111	U	O4'-C1'-C2'	-5.65	101.95	107.60
2	B	81	A	C4'-C3'-O3'	-5.65	100.93	109.40
3	C	463	THR	CA-C-N	-5.62	112.81	119.84
3	C	463	THR	C-N-CA	-5.62	112.81	119.84
10	J	374	PRO	N-CA-CB	5.61	109.47	103.52
10	J	339	PRO	N-CA-CB	5.61	109.72	103.44
12	L	103	LEU	N-CA-C	5.60	118.14	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	1108	A	N9-C1'-C2'	5.60	120.40	112.00
1	A	483	PRO	O-C-N	-5.59	115.09	122.64
31	o	158	ASN	CB-CA-C	-5.59	102.11	110.16
3	C	271	ASP	N-CA-C	-5.57	105.22	111.28
20	T	23	PRO	CA-CB-CG	5.56	115.07	104.50
16	P	6	ARG	C-N-CD	-5.54	102.30	125.00
1	A	946	ASN	CA-C-N	-5.53	112.91	119.05
1	A	946	ASN	C-N-CA	-5.53	112.91	119.05
1	A	870	ASN	N-CA-C	5.52	117.38	111.36
15	O	155	PHE	CB-CA-C	-5.50	99.82	109.71
20	T	36	PRO	N-CA-CB	5.49	109.58	103.44
7	G	77	PRO	CA-CB-CG	5.45	114.86	104.50
31	o	15	TYR	O-C-N	5.45	129.43	123.22
30	g	81	GLY	N-CA-C	5.44	119.54	112.25
1	A	381	SER	N-CA-C	5.42	117.19	111.28
30	n	81	GLY	N-CA-C	5.42	119.52	112.25
31	o	71	SER	N-CA-CB	-5.40	102.68	110.45
1	A	1356	LEU	N-CA-C	-5.40	105.48	111.36
20	T	81	PRO	CA-CB-CG	5.40	114.75	104.50
31	o	50	LEU	N-CA-C	-5.39	106.20	112.89
32	p	93	ARG	CA-CB-CG	-5.39	103.31	114.10
15	O	154	TRP	N-CA-C	5.37	116.45	108.60
1	A	1384	PRO	CA-N-CD	-5.35	104.51	112.00
31	o	141	ARG	CD-NE-CZ	5.34	131.88	124.40
31	o	133	GLN	CA-CB-CG	-5.33	103.44	114.10
6	F	1113	U	O4'-C1'-C2'	-5.31	100.49	105.80
3	C	171	GLY	N-CA-C	5.31	125.76	113.18
19	S	68	PRO	N-CA-C	5.28	120.95	114.35
32	p	41	MET	N-CA-C	5.26	117.43	111.11
1	A	831	ARG	NE-CZ-NH2	-5.26	114.47	119.20
20	T	109	SER	N-CA-C	5.25	117.08	111.36
21	U	699	LYS	CA-C-N	-5.24	114.56	119.85
21	U	699	LYS	C-N-CA	-5.24	114.56	119.85
31	o	44	PRO	CA-C-O	-5.24	114.35	120.85
31	o	155	ASP	CA-C-N	5.24	130.00	122.40
31	o	155	ASP	C-N-CA	5.24	130.00	122.40
21	U	287	LYS	O-C-N	5.24	125.14	120.48
31	o	38	THR	CA-CB-OG1	5.23	117.44	109.60
3	C	363	PRO	CB-CA-C	5.22	120.17	111.56
8	H	514	VAL	O-C-N	5.21	123.77	120.07
21	U	225	TYR	N-CA-C	-5.21	105.60	111.28
32	p	71	GLN	N-CA-C	5.19	117.57	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	o	100	ASN	CA-CB-CG	5.19	117.79	112.60
8	H	641	PRO	N-CA-CB	5.18	108.69	103.25
31	o	134	VAL	CA-C-N	5.18	127.74	120.28
31	o	134	VAL	C-N-CA	5.18	127.74	120.28
22	V	216	ILE	N-CA-C	-5.14	105.38	110.62
1	A	1384	PRO	C-N-CD	-5.13	103.95	125.00
20	T	81	PRO	N-CA-CB	5.13	108.63	103.25
22	V	241	GLU	N-CA-C	5.12	116.95	111.36
20	T	126	ILE	O-C-N	-5.11	116.19	122.57
21	U	460	LEU	O-C-N	5.10	125.02	120.48
16	P	134	GLY	N-CA-C	5.09	122.35	115.32
31	o	107	SER	N-CA-CB	-5.06	102.87	111.17
13	M	106	ASN	CB-CA-C	-5.05	109.78	115.79
21	U	172	LEU	O-C-N	5.05	124.98	120.48
21	U	188	LYS	O-C-N	5.05	124.98	120.48
32	p	68	GLN	N-CA-C	5.05	119.44	113.28
27	k	42	ASP	N-CA-C	5.04	117.18	110.53
22	V	234	VAL	CA-C-N	-5.04	113.54	119.84
22	V	234	VAL	C-N-CA	-5.04	113.54	119.84
27	d	42	ASP	N-CA-C	5.03	117.17	110.53
32	p	103	PHE	CA-C-O	-5.03	115.32	121.05
21	U	325	TYR	O-C-N	5.03	124.95	120.48
21	U	473	ASP	O-C-N	5.02	124.95	120.48
1	A	262	ASP	N-CA-C	5.02	120.90	109.81
28	e	81	ALA	CA-C-N	5.01	126.11	119.84
28	e	81	ALA	C-N-CA	5.01	126.11	119.84
8	H	721	GLY	CA-C-N	5.01	124.61	119.05
8	H	721	GLY	C-N-CA	5.01	124.61	119.05
31	o	56	ILE	CA-C-O	-5.01	115.25	120.76

There are no chirality outliers.

All (104) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1375	LEU	Peptide
1	A	1377	SER	Peptide
1	A	239	PHE	Mainchain,Peptide
1	A	539	PRO	Peptide
1	A	772	GLU	Peptide
3	C	170	LEU	Peptide
3	C	885	GLY	Peptide

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Mol	Chain	Res	Type	Group
11	K	92	ARG	Peptide
13	M	103	GLU	Peptide
13	M	45	HIS	Peptide
15	O	123	PRO	Peptide
15	O	278	ASP	Peptide
15	O	351	GLY	Mainchain,Peptide
15	O	436	SER	Peptide
15	O	437	GLU	Peptide
16	P	6	ARG	Mainchain,Peptide
17	Q	85	SER	Peptide
19	S	67	GLY	Mainchain,Peptide
20	T	110	GLU	Mainchain
20	T	111	SER	Mainchain
20	T	112	SER	Mainchain
20	T	113	THR	Mainchain
20	T	123	LEU	Mainchain
20	T	124	LEU	Mainchain
20	T	125	GLN	Mainchain
20	T	126	ILE	Mainchain
20	T	75	THR	Mainchain
21	U	117	GLU	Mainchain
21	U	118	ASN	Mainchain
21	U	119	GLU	Mainchain
21	U	120	ASP	Mainchain
21	U	121	TYR	Mainchain
21	U	122	LEU	Mainchain
21	U	123	SER	Mainchain
21	U	124	SER	Mainchain
21	U	125	GLU	Mainchain
21	U	126	ASP	Mainchain
21	U	127	GLU	Mainchain
21	U	128	VAL	Mainchain
21	U	176	ILE	Mainchain
21	U	177	LEU	Mainchain
21	U	200	GLU	Mainchain
21	U	201	LEU	Mainchain
21	U	202	LEU	Mainchain
21	U	303	ALA	Mainchain
21	U	304	TYR	Mainchain
21	U	305	ARG	Mainchain
21	U	364	HIS	Mainchain
21	U	365	ILE	Mainchain

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Mol	Chain	Res	Type	Group
21	U	366	MET	Mainchain
21	U	367	GLU	Mainchain
21	U	391	SER	Mainchain
21	U	392	PRO	Mainchain
21	U	393	ARG	Mainchain
21	U	415	ILE	Mainchain
21	U	416	GLU	Mainchain
21	U	417	ALA	Mainchain
21	U	437	SER	Mainchain
21	U	438	ASP	Mainchain
21	U	439	ILE	Mainchain
21	U	440	ILE	Mainchain
21	U	441	PHE	Mainchain
21	U	442	ILE	Mainchain
21	U	476	TYR	Mainchain
21	U	477	GLU	Mainchain
21	U	478	LEU	Mainchain
21	U	499	LYS	Mainchain
21	U	500	LYS	Mainchain
21	U	501	LEU	Mainchain
21	U	502	ARG	Mainchain
21	U	556	GLU	Mainchain
21	U	557	HIS	Mainchain
21	U	558	SER	Mainchain
21	U	589	ASP	Mainchain
22	V	290	GLN	Mainchain
22	V	291	ARG	Mainchain
22	V	292	LYS	Mainchain
22	V	293	LYS	Mainchain
22	V	294	VAL	Mainchain
22	V	295	GLU	Mainchain
22	V	296	MET	Mainchain
22	V	297	ARG	Mainchain
22	V	298	LEU	Mainchain
22	V	299	GLN	Mainchain
22	V	300	ALA	Mainchain
22	V	301	LEU	Mainchain
22	V	302	GLU	Mainchain
22	V	303	LYS	Mainchain
23	W	462	LEU	Mainchain
27	d	41	ASP	Peptide
28	e	81	ALA	Mainchain,Peptide

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Mol	Chain	Res	Type	Group
30	g	81	GLY	Mainchain,Peptide
27	k	41	ASP	Peptide
28	l	81	ALA	Mainchain,Peptide
30	n	81	GLY	Mainchain,Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	15715	0	15685	1134	0
2	B	2465	0	1251	66	0
3	C	7278	0	7450	659	0
4	D	2150	0	1085	120	0
5	E	587	0	295	58	0
6	F	1727	0	877	176	0
7	G	921	0	604	11	0
8	H	3204	0	1664	59	0
9	I	3542	0	2625	129	0
10	J	2944	0	2434	194	0
11	K	822	0	845	54	0
12	L	1290	0	1312	36	0
13	M	1298	0	1176	100	0
14	N	2089	0	2053	80	0
15	O	2646	0	2639	115	0
16	P	554	0	540	50	0
17	Q	1583	0	1608	123	0
18	R	379	0	375	60	0
19	S	195	0	198	29	0
20	T	816	0	737	127	0
21	U	2690	0	1500	258	0
22	V	619	0	506	133	0
23	W	3505	0	1553	14	0
24	a	631	0	670	3	0
24	h	610	0	640	17	0
25	b	575	0	597	21	0
25	i	575	0	597	21	0
26	c	554	0	556	18	0
26	j	554	0	556	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	d	529	0	557	2	0
27	k	529	0	557	2	0
28	e	625	0	647	8	0
28	l	625	0	647	8	0
29	f	644	0	686	14	0
29	m	644	0	686	15	0
30	g	741	0	778	18	0
30	n	528	0	573	17	0
31	o	841	0	614	17	0
32	p	513	0	402	13	0
33	q	831	0	667	11	0
33	r	849	0	677	12	0
33	s	850	0	682	11	0
33	t	823	0	654	7	0
34	x	177	0	91	13	0
35	A	36	0	6	7	0
36	C	32	0	12	4	0
37	C	1	0	0	0	0
37	D	5	0	0	0	0
38	L	3	0	0	0	0
38	M	2	0	0	0	0
38	N	1	0	0	0	0
All	All	72347	0	61564	3431	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 26.

All (3431) 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:1343:PHE:CD1	1:A:1350:ILE:HD13	1.33	1.60
1:A:1343:PHE:HD1	1:A:1350:ILE:CD1	1.12	1.59
3:C:274:ILE:CD1	3:C:385:PHE:HD2	1.17	1.56
3:C:681:CYS:HB3	3:C:850:LEU:CD1	1.33	1.54
1:A:1394:LEU:CD1	1:A:1556:ILE:HG21	1.37	1.49
1:A:514:TYR:CE1	1:A:689:TYR:HD2	1.30	1.47
1:A:1394:LEU:CD1	1:A:1556:ILE:CG2	1.92	1.46
3:C:989:LEU:CD1	3:C:993:ILE:HD11	1.48	1.44
1:A:1049:LEU:CD1	1:A:1260:PHE:HB3	1.46	1.42
1:A:514:TYR:CE1	1:A:689:TYR:CD2	2.06	1.42
8:H:729:TYR:CZ	8:H:748:PHE:CB	2.03	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1575:TRP:CE3	1:A:1605:ARG:NH1	1.91	1.36
23:W:462:LEU:O	23:W:464:SER:N	1.58	1.36
1:A:514:TYR:HD1	1:A:689:TYR:CE2	1.41	1.36
9:I:79:HIS:CD2	10:J:244:PHE:CD1	2.15	1.35
3:C:274:ILE:CD1	3:C:385:PHE:CD2	2.09	1.34
20:T:137:LYS:CE	21:U:639:ASP:OD2	1.73	1.34
3:C:532:ASP:CG	3:C:586:MET:HE1	1.54	1.32
1:A:1343:PHE:CD1	1:A:1350:ILE:CD1	1.94	1.31
1:A:1575:TRP:CZ3	1:A:1605:ARG:NH1	1.93	1.31
18:R:188:LYS:CG	18:R:192:GLU:OE2	1.78	1.31
8:H:729:TYR:CE1	8:H:748:PHE:CB	2.14	1.31
18:R:188:LYS:HG2	18:R:192:GLU:OE2	1.29	1.30
1:A:1343:PHE:CE1	1:A:1350:ILE:HG21	1.66	1.30
20:T:137:LYS:HE3	21:U:639:ASP:OD2	1.20	1.30
1:A:514:TYR:CD1	1:A:689:TYR:CD2	2.20	1.30
3:C:691:VAL:O	3:C:841:LEU:HD11	1.29	1.30
4:D:56:A:C2'	4:D:57:U:H5''	1.62	1.30
1:A:1553:ILE:CD1	22:V:211:LEU:HD22	1.59	1.29
10:J:109:GLU:OE1	18:R:196:ARG:CG	1.79	1.29
21:U:660:TYR:CE2	21:U:686:HIS:CD2	2.20	1.29
3:C:355:HIS:ND1	3:C:367:VAL:HG21	1.47	1.29
1:A:514:TYR:CD1	1:A:689:TYR:CE2	2.18	1.28
3:C:274:ILE:HD13	3:C:385:PHE:CD2	1.65	1.28
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	1.69	1.28
3:C:690:PRO:HA	3:C:708:ILE:O	1.28	1.28
3:C:808:LEU:CD2	3:C:987:PRO:HG3	1.63	1.27
3:C:208:ARG:NH2	3:C:440:THR:HG21	1.46	1.26
10:J:79:GLU:OE1	17:Q:202:MET:CE	1.82	1.26
1:A:1394:LEU:HD12	1:A:1556:ILE:CG2	1.55	1.25
3:C:886:SER:HB2	3:C:905:GLN:O	1.31	1.25
3:C:675:THR:HG22	3:C:909:ILE:CD1	1.66	1.25
10:J:79:GLU:OE1	17:Q:202:MET:HE1	1.29	1.24
19:S:59:ARG:O	19:S:62:THR:HG23	1.34	1.24
10:J:79:GLU:CD	17:Q:202:MET:HE1	1.62	1.23
1:A:1130:ARG:NH2	1:A:1156:HIS:HD2	1.37	1.23
5:E:500:A:O2'	5:E:501:A:OP2	1.56	1.23
21:U:651:ILE:HD11	21:U:672:GLU:CG	1.67	1.23
23:W:462:LEU:C	23:W:464:SER:N	1.89	1.23
1:A:872:PRO:HD3	17:Q:201:PHE:CD2	1.72	1.22
1:A:872:PRO:HD3	17:Q:201:PHE:CG	1.74	1.22
22:V:240:GLU:O	22:V:244:THR:CG2	1.88	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:20:LEU:HD11	20:T:67:LEU:CG	1.70	1.21
1:A:1130:ARG:NH1	1:A:1158:ILE:O	1.71	1.21
6:F:16:U:H2'	6:F:18:U:O4	1.38	1.21
21:U:638:GLU:HA	21:U:641:CYS:SG	1.83	1.19
4:D:56:A:H2'	4:D:57:U:H5''	1.21	1.19
3:C:602:VAL:CG1	3:C:908:VAL:HG21	1.73	1.18
3:C:859:GLU:OE2	3:C:909:ILE:CG2	1.89	1.18
10:J:79:GLU:OE1	17:Q:202:MET:SD	2.02	1.18
1:A:1384:PRO:O	1:A:1386:ALA:N	1.75	1.18
1:A:1047:ALA:HB3	1:A:1251:TYR:HB3	1.21	1.18
13:M:91:ILE:CD1	13:M:125:ILE:HG12	1.74	1.18
10:J:109:GLU:OE1	18:R:196:ARG:HG3	1.37	1.18
3:C:990:GLU:HB2	3:C:998:TYR:CZ	1.78	1.18
1:A:372:ARG:NH2	3:C:641:GLU:OE2	1.76	1.17
1:A:1499:ARG:NH1	22:V:234:VAL:HG22	1.57	1.17
21:U:651:ILE:CD1	21:U:672:GLU:HG2	1.72	1.17
1:A:1553:ILE:HD11	22:V:211:LEU:CD2	1.74	1.17
1:A:1355:PRO:O	1:A:1359:ILE:HG13	1.43	1.17
31:o:53:PRO:CB	24:h:98:GLU:O	1.92	1.17
3:C:604:LYS:HE2	3:C:643:VAL:CG1	1.76	1.16
3:C:971:ARG:HH21	3:C:976:ILE:CG2	1.58	1.16
23:W:462:LEU:O	23:W:463:SER:C	1.82	1.16
3:C:885:GLY:HA3	3:C:907:PRO:CD	1.76	1.16
8:H:673:GLU:OE1	8:H:677:SER:CB	1.93	1.16
1:A:1130:ARG:NH2	1:A:1156:HIS:CD2	2.13	1.15
4:D:53:A:OP1	10:J:165:LYS:HB3	1.43	1.15
1:A:1343:PHE:CE1	1:A:1350:ILE:HD13	1.80	1.15
1:A:1547:ILE:CD1	22:V:211:LEU:HD11	1.76	1.15
3:C:602:VAL:HG12	3:C:908:VAL:HG21	1.16	1.15
1:A:881:THR:OG1	16:P:133:PHE:HZ	1.26	1.15
1:A:1343:PHE:HD1	1:A:1350:ILE:HD12	1.02	1.14
9:I:79:HIS:O	10:J:241:PHE:HD1	1.27	1.14
3:C:391:MET:HE1	3:C:395:LYS:HE3	1.27	1.14
1:A:1443:TYR:CE1	1:A:1542:TYR:HA	1.82	1.14
3:C:675:THR:CG2	3:C:909:ILE:HD13	1.76	1.14
10:J:103:ASN:OD1	18:R:193:MET:CE	1.95	1.14
3:C:362:LYS:HD3	3:C:363:PRO:HG2	1.27	1.14
3:C:682:SER:O	3:C:854:ILE:HB	1.46	1.14
3:C:681:CYS:HB3	3:C:850:LEU:HD12	1.22	1.13
3:C:687:ALA:HB1	3:C:689:ILE:HD11	1.30	1.13
1:A:1394:LEU:CD1	1:A:1556:ILE:HG22	1.78	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	1.83	1.13
1:A:1049:LEU:CD1	1:A:1260:PHE:CB	2.25	1.13
3:C:859:GLU:OE2	3:C:909:ILE:HG22	0.98	1.13
4:D:56:A:O2'	4:D:57:U:C5'	1.96	1.13
6:F:31:A:H3'	6:F:32:G:H4'	1.29	1.13
20:T:137:LYS:HD3	20:T:143:TYR:OH	1.49	1.13
3:C:391:MET:HE1	3:C:395:LYS:CE	1.78	1.13
21:U:638:GLU:CA	21:U:641:CYS:SG	2.36	1.12
3:C:808:LEU:HD22	3:C:987:PRO:HG3	1.14	1.12
9:I:79:HIS:CD2	10:J:244:PHE:CE1	2.37	1.12
22:V:240:GLU:O	22:V:244:THR:HG23	0.97	1.12
1:A:863:ARG:NH1	1:A:1101:TYR:CD2	2.17	1.12
1:A:1343:PHE:HE1	1:A:1350:ILE:CG2	1.63	1.12
1:A:1547:ILE:HD12	22:V:211:LEU:HD21	1.29	1.11
3:C:681:CYS:CB	3:C:850:LEU:CD1	2.28	1.11
1:A:756:LEU:HD21	16:P:8:GLN:NE2	1.63	1.11
10:J:79:GLU:CD	17:Q:202:MET:CE	2.19	1.11
20:T:20:LEU:HD12	20:T:45:LEU:HD13	1.15	1.11
1:A:1417:GLN:NE2	1:A:1783:MET:HB3	1.63	1.11
1:A:1553:ILE:CG1	22:V:211:LEU:HD22	1.80	1.11
3:C:990:GLU:HB2	3:C:998:TYR:CE1	1.83	1.11
13:M:91:ILE:HD13	13:M:125:ILE:HG12	1.28	1.11
23:W:703:SER:N	34:x:2:U:O2	1.82	1.11
6:F:1111:U:H5''	6:F:1111:U:C6	1.86	1.11
10:J:103:ASN:OD1	18:R:193:MET:HE3	1.48	1.11
4:D:56:A:O2'	4:D:57:U:H5''	1.48	1.10
10:J:90:MET:HE2	17:Q:197:ILE:HG23	1.20	1.10
3:C:355:HIS:HB3	3:C:364:PHE:CZ	1.86	1.10
21:U:638:GLU:O	21:U:641:CYS:SG	2.08	1.10
3:C:364:PHE:HD1	3:C:365:GLU:N	1.49	1.10
6:F:1109:C:N4	32:p:109:LYS:H	1.48	1.10
17:Q:216:ARG:HA	17:Q:219:ILE:HD12	1.11	1.10
22:V:227:ILE:O	22:V:231:ILE:HD12	1.51	1.10
8:H:729:TYR:CE2	8:H:748:PHE:CB	2.33	1.10
23:W:462:LEU:C	23:W:464:SER:H	1.49	1.10
1:A:952:ASN:ND2	18:R:179:ASP:OD2	1.84	1.09
1:A:1316:ILE:HD11	1:A:1335:TRP:HZ3	1.07	1.09
1:A:1547:ILE:HA	1:A:1556:ILE:HD11	1.34	1.09
21:U:638:GLU:C	21:U:641:CYS:SG	2.34	1.09
1:A:1540:ASN:OD1	22:V:209:LEU:HB3	1.50	1.09
3:C:362:LYS:HG2	3:C:363:PRO:HD2	1.30	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:971:ARG:NH2	3:C:976:ILE:HG22	1.68	1.09
7:G:7:VAL:HG11	7:G:154:VAL:CB	1.81	1.09
1:A:1158:ILE:HG12	1:A:1172:PHE:CZ	1.89	1.08
3:C:971:ARG:HH21	3:C:976:ILE:HG22	1.01	1.08
20:T:123:LEU:CD2	21:U:700:PRO:HG3	1.83	1.08
1:A:1394:LEU:HD11	1:A:1556:ILE:HG21	1.30	1.08
9:I:79:HIS:HD2	10:J:244:PHE:CE1	1.71	1.08
21:U:660:TYR:CD2	21:U:686:HIS:CD2	2.40	1.08
1:A:1328:PHE:HD2	1:A:1371:VAL:HG22	1.11	1.08
15:O:171:THR:HG22	20:T:113:THR:CB	1.83	1.08
1:A:1547:ILE:CD1	22:V:211:LEU:HD21	1.83	1.07
20:T:139:PHE:HB3	20:T:141:LEU:CD2	1.83	1.07
22:V:212:THR:N	22:V:215:GLN:OE1	1.88	1.07
22:V:237:ARG:NH1	22:V:240:GLU:OE2	1.88	1.07
3:C:885:GLY:HA3	3:C:907:PRO:HD2	1.30	1.07
3:C:989:LEU:HD11	3:C:993:ILE:HD11	1.08	1.07
18:R:200:ILE:HG22	18:R:204:LYS:HE3	1.33	1.07
1:A:1158:ILE:CG1	1:A:1172:PHE:CE1	2.38	1.06
1:A:1049:LEU:HD12	1:A:1260:PHE:HB3	1.09	1.06
1:A:1130:ARG:HH21	1:A:1156:HIS:CD2	1.73	1.06
1:A:1233:ARG:NH2	16:P:127:TRP:HZ3	1.51	1.06
3:C:887:ARG:HH21	3:C:938:ARG:NH2	1.53	1.06
3:C:993:ILE:CG2	3:C:997:LEU:HB3	1.86	1.06
12:L:120:CYS:HB2	12:L:122:CYS:HB3	1.36	1.06
1:A:1040:ASP:O	1:A:1045:GLN:HG3	1.51	1.06
1:A:1443:TYR:HE1	1:A:1542:TYR:N	1.53	1.06
3:C:208:ARG:NH2	3:C:440:THR:CG2	2.18	1.06
5:E:2:U:H4'	5:E:3:A:OP1	1.46	1.06
1:A:1443:TYR:CE1	1:A:1542:TYR:CA	2.37	1.06
3:C:808:LEU:CD2	3:C:987:PRO:CG	2.33	1.06
6:F:1116:A:H2'	6:F:1117:G:H8	1.18	1.06
20:T:24:THR:OG1	20:T:92:ARG:NH2	1.87	1.06
1:A:756:LEU:CD2	16:P:8:GLN:HE22	1.69	1.05
4:D:56:A:C2'	4:D:57:U:C5'	2.35	1.05
1:A:871:GLY:CA	17:Q:198:ASN:HD22	1.67	1.05
6:F:1102:C:H2'	6:F:1103:C:C6	1.91	1.05
31:O:53:PRO:CB	24:h:99:ASP:CB	2.35	1.05
3:C:679:GLU:OE2	3:C:809:ALA:HB3	1.52	1.05
8:H:730:GLN:HA	8:H:733:ILE:HD11	1.37	1.05
1:A:1547:ILE:HD11	22:V:211:LEU:HD11	1.25	1.05
3:C:681:CYS:HB3	3:C:850:LEU:HD11	1.32	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:274:ILE:HD12	3:C:385:PHE:CD2	1.87	1.04
5:E:2:U:O2'	5:E:3:A:C8	2.08	1.04
21:U:633:PHE:O	21:U:635:ASP:N	1.89	1.04
20:T:20:LEU:CD1	20:T:45:LEU:HD13	1.86	1.04
3:C:692:SER:HB2	3:C:706:LEU:O	1.58	1.04
21:U:677:LYS:O	21:U:677:LYS:NZ	1.91	1.04
1:A:1174:PHE:CZ	1:A:1182:LEU:CD1	2.40	1.03
3:C:989:LEU:CD1	3:C:993:ILE:CD1	2.36	1.03
1:A:1366:ARG:HD3	2:B:95:C:P	1.97	1.03
1:A:1571:GLU:HG2	22:V:212:THR:CG2	1.86	1.03
3:C:679:GLU:OE2	3:C:809:ALA:CB	2.07	1.03
9:I:114:CYS:SG	10:J:237:ILE:HD11	1.98	1.03
33:q:51:VAL:HG21	33:r:20:ARG:CB	1.89	1.02
1:A:1366:ARG:CG	2:B:95:C:OP1	2.07	1.02
13:M:49:SER:OG	13:M:52:SER:CB	2.06	1.02
6:F:15:C:H41	11:K:209:ARG:HG2	1.21	1.02
1:A:1343:PHE:O	1:A:1347:ARG:N	1.92	1.01
3:C:353:TYR:HD2	3:C:363:PRO:O	1.42	1.01
3:C:532:ASP:OD2	3:C:586:MET:HE1	1.60	1.01
6:F:110:A:H4'	6:F:111:C:C5'	1.89	1.01
16:P:8:GLN:HG2	16:P:10:GLU:O	1.57	1.01
3:C:353:TYR:CD2	3:C:363:PRO:O	2.13	1.01
4:D:50:G:N2	5:E:2:U:H6	1.58	1.01
3:C:355:HIS:CB	3:C:364:PHE:CZ	2.43	1.01
1:A:1571:GLU:HG2	22:V:212:THR:HG21	1.38	1.01
2:B:165:A:H4'	2:B:166:U:C5'	1.89	1.01
1:A:1158:ILE:CG1	1:A:1172:PHE:HE1	1.73	1.01
1:A:1553:ILE:HD11	22:V:211:LEU:HD22	1.04	1.01
6:F:1116:A:H2'	6:F:1117:G:C8	1.95	1.01
20:T:131:GLU:OE2	21:U:626:LEU:CD2	2.09	1.01
3:C:355:HIS:HB2	3:C:364:PHE:CE2	1.96	1.00
20:T:106:LEU:HD11	20:T:110:GLU:OE2	1.59	1.00
8:H:718:SER:OG	8:H:725:THR:HG21	1.60	1.00
21:U:656:THR:OG1	21:U:698:PHE:HE2	1.43	1.00
21:U:675:ASN:HD21	21:U:678:LYS:HZ1	1.01	1.00
1:A:1443:TYR:OH	1:A:1545:ASP:HB2	1.61	1.00
3:C:604:LYS:HE2	3:C:643:VAL:HG11	1.02	1.00
22:V:215:GLN:HA	22:V:218:ILE:HB	1.43	1.00
1:A:1316:ILE:HD11	1:A:1335:TRP:CZ3	1.97	0.99
3:C:972:ARG:NH2	3:C:982:MET:HG2	1.76	0.99
3:C:355:HIS:N	3:C:364:PHE:HE2	1.60	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:165:A:C4'	2:B:166:U:H5'	1.92	0.99
3:C:355:HIS:CB	3:C:364:PHE:CE2	2.45	0.99
3:C:274:ILE:HD13	3:C:385:PHE:HD2	0.86	0.99
6:F:110:A:C4'	6:F:111:C:H5'	1.92	0.99
6:F:1114:G:O6	32:p:38:LYS:NZ	1.95	0.99
21:U:651:ILE:HD11	21:U:672:GLU:HG2	1.01	0.99
3:C:886:SER:CB	3:C:905:GLN:O	2.10	0.99
1:A:1565:THR:CG2	1:A:1823:LEU:HD12	1.91	0.98
22:V:214:ASN:O	22:V:218:ILE:N	1.96	0.98
1:A:1561:LEU:CD1	1:A:1608:LEU:O	2.10	0.98
3:C:691:VAL:C	3:C:841:LEU:HD11	1.87	0.98
1:A:329:TYR:HE1	3:C:919:ARG:NH2	1.59	0.98
3:C:274:ILE:HD12	3:C:385:PHE:HD2	1.18	0.98
20:T:106:LEU:HD11	20:T:110:GLU:CD	1.88	0.98
3:C:863:GLU:OE2	3:C:934:HIS:ND1	1.97	0.98
1:A:1499:ARG:HH12	22:V:234:VAL:CG2	1.76	0.98
1:A:1567:PHE:CE2	1:A:1825:ILE:HG21	1.99	0.98
21:U:675:ASN:HD21	21:U:678:LYS:NZ	1.62	0.98
1:A:1366:ARG:CZ	2:B:95:C:OP2	2.10	0.97
19:S:55:GLU:OE2	19:S:58:ARG:NE	1.97	0.97
1:A:1366:ARG:CD	2:B:95:C:OP1	2.11	0.97
6:F:16:U:C2'	6:F:18:U:O4	2.13	0.97
1:A:872:PRO:HD3	17:Q:201:PHE:CE2	1.99	0.97
1:A:893:ARG:NH2	1:A:1135:ALA:CB	2.26	0.97
3:C:679:GLU:OE2	3:C:809:ALA:N	1.97	0.97
21:U:675:ASN:OD1	21:U:678:LYS:HD3	1.63	0.97
3:C:887:ARG:HH21	3:C:938:ARG:CZ	1.78	0.97
21:U:637:VAL:O	21:U:641:CYS:SG	2.21	0.97
1:A:1394:LEU:HD12	1:A:1556:ILE:HG21	0.98	0.97
20:T:93:LYS:O	20:T:97:ILE:CD1	2.12	0.97
6:F:1097:G:N2	6:F:1119:C:O2	1.96	0.97
1:A:1252:SER:OG	1:A:1255:ASN:N	1.98	0.97
13:M:39:LEU:HD11	13:M:111:ARG:HG3	1.44	0.96
10:J:229:ASP:HB2	11:K:151:LYS:HB3	1.47	0.96
21:U:660:TYR:CE2	21:U:686:HIS:HD2	1.68	0.96
1:A:872:PRO:HD3	17:Q:201:PHE:CD1	1.99	0.96
1:A:1394:LEU:HD11	1:A:1556:ILE:CG2	1.86	0.96
1:A:1565:THR:HG22	1:A:1823:LEU:HD12	1.47	0.96
13:M:101:THR:HG22	13:M:120:LEU:HD11	1.46	0.96
19:S:68:PRO:HD2	19:S:69:TRP:CE3	2.01	0.96
21:U:651:ILE:HD12	21:U:671:PHE:HA	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:90:MET:HE2	17:Q:197:ILE:CG2	1.95	0.96
3:C:271:ASP:OD2	36:C:1500:GTP:N1	1.97	0.96
15:O:171:THR:HG22	20:T:113:THR:HB	1.45	0.96
3:C:690:PRO:CA	3:C:708:ILE:O	2.13	0.95
1:A:1547:ILE:HG23	1:A:1556:ILE:HD12	1.48	0.95
20:T:123:LEU:HD23	21:U:700:PRO:HG3	1.47	0.95
1:A:1499:ARG:HH12	22:V:234:VAL:HG22	1.18	0.95
1:A:1366:ARG:O	1:A:1370:ARG:HG2	1.65	0.95
5:E:495:A:H2'	5:E:496:U:C6	2.02	0.95
1:A:1366:ARG:HD3	2:B:95:C:OP1	1.63	0.95
4:D:56:A:O2'	4:D:57:U:O5'	1.84	0.95
13:M:120:LEU:HD13	13:M:121:GLY:N	1.82	0.95
21:U:682:VAL:CG1	21:U:689:LEU:HG	1.97	0.95
10:J:65:PHE:CD1	10:J:69:GLU:HB3	2.01	0.95
10:J:79:GLU:CD	17:Q:202:MET:SD	2.49	0.95
6:F:15:C:O2'	6:F:16:U:O5'	1.85	0.94
9:I:79:HIS:O	10:J:241:PHE:CD1	2.19	0.94
1:A:923:TYR:OH	1:A:936:GLU:HB3	1.67	0.94
17:Q:216:ARG:HA	17:Q:219:ILE:CD1	1.97	0.94
6:F:1116:A:C2	6:F:1117:G:C4	2.54	0.94
1:A:932:SER:O	1:A:936:GLU:HG2	1.67	0.94
1:A:1567:PHE:CE2	1:A:1825:ILE:CG2	2.50	0.94
6:F:1102:C:H2'	6:F:1103:C:C5	2.03	0.94
1:A:1343:PHE:HE1	1:A:1350:ILE:HG21	0.78	0.94
20:T:139:PHE:HB3	20:T:141:LEU:HD23	1.46	0.94
1:A:923:TYR:CZ	1:A:936:GLU:HB2	2.02	0.94
1:A:863:ARG:HH12	1:A:1101:TYR:HD2	1.01	0.94
1:A:1328:PHE:CD2	1:A:1371:VAL:HG22	2.01	0.94
1:A:1424:HIS:CE1	1:A:1747:ASP:CG	2.46	0.94
6:F:18:U:O2'	6:F:19:U:OP2	1.85	0.94
6:F:110:A:C2	29:m:2:LYS:CE	2.51	0.94
20:T:104:GLN:O	20:T:108:GLU:HG3	1.67	0.94
1:A:756:LEU:HD21	16:P:8:GLN:HE22	0.79	0.94
1:A:1411:ASP:O	1:A:1743:TYR:OH	1.84	0.94
6:F:110:A:H4'	6:F:111:C:H5'	0.95	0.94
1:A:1335:TRP:HH2	1:A:1360:LEU:HD23	1.32	0.94
3:C:354:TYR:HD1	3:C:359:PHE:CE1	1.85	0.93
3:C:355:HIS:CE1	3:C:367:VAL:HG21	2.03	0.93
6:F:31:A:C3'	6:F:32:G:H4'	1.98	0.93
10:J:65:PHE:HD1	10:J:69:GLU:CB	1.81	0.93
20:T:137:LYS:CD	20:T:143:TYR:OH	2.16	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:GLU:OE2	1:A:1447:TRP:N	2.01	0.93
6:F:1101:C:N4	32:p:38:LYS:HZ3	1.65	0.93
1:A:1263:CYS:HB3	1:A:1345:TYR:OH	1.69	0.93
3:C:430:ARG:HG3	3:C:430:ARG:HH11	1.34	0.93
8:H:729:TYR:CD1	8:H:748:PHE:CB	2.52	0.93
6:F:1111:U:O4'	28:l:30:ARG:HD3	1.67	0.93
2:B:165:A:C2	29:f:2:LYS:CE	2.51	0.93
4:D:65:U:O2'	4:D:67:C:OP2	1.85	0.93
6:F:1116:A:C6	6:F:1117:G:C6	2.57	0.93
1:A:1353:THR:O	1:A:1357:LEU:HB2	1.69	0.92
6:F:1111:U:H5''	6:F:1111:U:H6	1.25	0.92
1:A:1233:ARG:HH21	16:P:127:TRP:HZ3	1.18	0.92
1:A:1417:GLN:CB	1:A:1783:MET:HE3	1.99	0.92
3:C:734:CYS:HG	3:C:755:TYR:HH	1.03	0.92
3:C:681:CYS:CB	3:C:850:LEU:HD12	1.98	0.92
1:A:1348:GLU:HG2	1:A:1446:THR:HB	1.52	0.92
16:P:8:GLN:CG	16:P:10:GLU:O	2.18	0.92
15:O:171:THR:HG22	20:T:113:THR:CG2	1.99	0.92
33:q:20:ARG:CB	33:r:53:ILE:HA	2.00	0.92
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.34	0.92
21:U:682:VAL:HG11	21:U:689:LEU:HG	1.51	0.92
22:V:215:GLN:O	22:V:219:GLN:N	2.02	0.92
1:A:926:LYS:HE3	1:A:1521:ARG:NH2	1.85	0.91
10:J:101:ARG:NH2	10:J:105:LEU:HD13	1.85	0.91
1:A:959:LEU:HD23	18:R:186:LEU:HB3	1.52	0.91
1:A:1379:MET:HA	1:A:1379:MET:HE3	1.51	0.91
3:C:989:LEU:CG	3:C:993:ILE:HD11	2.00	0.91
6:F:19:U:O2	17:Q:178:TYR:CG	2.24	0.91
3:C:355:HIS:H	3:C:364:PHE:HE2	1.13	0.91
8:H:682:LYS:O	8:H:685:GLU:CG	2.18	0.91
1:A:854:ARG:HD2	1:A:1095:MET:HE3	1.50	0.91
1:A:1499:ARG:NH1	22:V:234:VAL:CG2	2.33	0.91
7:G:81:ASP:CB	7:G:85:THR:CB	2.49	0.91
20:T:20:LEU:CD1	20:T:67:LEU:CG	2.48	0.91
3:C:362:LYS:HD3	3:C:363:PRO:CG	2.01	0.91
3:C:989:LEU:HD11	3:C:993:ILE:CD1	1.98	0.91
21:U:681:GLU:OE1	21:U:681:GLU:N	2.04	0.91
3:C:884:ARG:NH2	3:C:941:PRO:CD	2.34	0.91
6:F:1099:G:C5	6:F:1100:A:C8	2.58	0.91
21:U:658:LEU:O	21:U:665:ASP:HA	1.71	0.91
9:I:115:ILE:N	10:J:233:GLU:OE2	2.03	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:893:ARG:HH11	1:A:893:ARG:HG3	1.36	0.91
1:A:329:TYR:CE1	3:C:919:ARG:CZ	2.55	0.90
1:A:1422:ILE:HD12	1:A:1785:ASP:OD2	1.71	0.90
3:C:602:VAL:HG12	3:C:908:VAL:CG2	2.00	0.90
4:D:53:A:OP1	10:J:165:LYS:CB	2.19	0.90
1:A:1390:THR:HG22	1:A:1394:LEU:HD12	1.52	0.90
21:U:652:PRO:HG2	21:U:653:ASN:OD1	1.71	0.90
3:C:839:ILE:HD12	21:U:647:LEU:HD11	1.52	0.90
3:C:979:GLY:N	3:C:983:SER:HB2	1.85	0.90
19:S:59:ARG:O	19:S:62:THR:CG2	2.18	0.90
1:A:514:TYR:HE1	1:A:689:TYR:CD2	1.65	0.90
1:A:849:LEU:HD12	1:A:973:GLU:HB3	1.51	0.90
1:A:893:ARG:NH2	1:A:1135:ALA:HB3	1.87	0.90
1:A:1068:ARG:HG2	1:A:1068:ARG:HH11	1.33	0.90
1:A:1394:LEU:HD13	1:A:1556:ILE:HG22	1.51	0.90
1:A:329:TYR:CE1	3:C:919:ARG:NH2	2.40	0.90
1:A:1575:TRP:HZ3	1:A:1605:ARG:HH11	1.07	0.90
1:A:1417:GLN:HB3	1:A:1783:MET:HE3	1.52	0.90
2:B:165:A:C2	29:f:2:LYS:HE2	2.07	0.90
6:F:30:A:O2'	6:F:32:G:OP2	1.88	0.90
1:A:1049:LEU:HD11	1:A:1260:PHE:HB3	1.49	0.89
22:V:229:LYS:O	22:V:233:GLU:HB2	1.70	0.89
6:F:1099:G:C6	6:F:1100:A:N7	2.41	0.89
3:C:355:HIS:CE1	3:C:367:VAL:CG2	2.55	0.89
1:A:871:GLY:HA3	17:Q:198:ASN:HD22	1.33	0.89
6:F:110:A:C2	29:m:2:LYS:HE2	2.08	0.89
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	1.88	0.89
3:C:808:LEU:HD23	3:C:987:PRO:CB	2.02	0.89
6:F:28:U:C2'	6:F:29:C:H5'	2.03	0.89
8:H:730:GLN:HA	8:H:733:ILE:CD1	2.02	0.89
10:J:109:GLU:OE1	18:R:196:ARG:HG2	1.72	0.89
1:A:1296:ARG:HH11	1:A:1296:ARG:HB2	1.38	0.89
1:A:1342:LEU:HD21	1:A:1356:LEU:CD2	2.02	0.89
3:C:856:ILE:HA	3:C:944:VAL:HG11	1.54	0.89
13:M:125:ILE:CD1	13:M:126:THR:HG23	2.02	0.89
1:A:872:PRO:CD	17:Q:201:PHE:CD2	2.55	0.89
1:A:1367:ILE:HA	1:A:1370:ARG:CG	2.03	0.88
1:A:1781:TYR:O	1:A:1783:MET:SD	2.30	0.88
3:C:391:MET:HE1	3:C:395:LYS:NZ	1.87	0.88
1:A:923:TYR:OH	1:A:936:GLU:CB	2.21	0.88
1:A:1417:GLN:HB3	1:A:1783:MET:CE	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1424:HIS:CE1	1:A:1747:ASP:OD1	2.27	0.88
3:C:355:HIS:N	3:C:364:PHE:CE2	2.41	0.88
9:I:199:MET:HB2	9:I:242:GLU:HG3	1.56	0.88
6:F:34:G:C8	6:F:34:G:OP2	2.27	0.88
6:F:16:U:O2'	11:K:179:ARG:NH2	2.04	0.88
1:A:929:LEU:HD22	1:A:933:GLU:HB3	1.55	0.88
1:A:1265:PHE:CE1	1:A:1346:PHE:HD1	1.92	0.88
1:A:1366:ARG:CD	2:B:95:C:P	2.62	0.88
3:C:391:MET:CE	3:C:395:LYS:HE3	2.04	0.88
1:A:1130:ARG:HH21	1:A:1130:ARG:HG2	1.38	0.87
2:B:165:A:H4'	2:B:166:U:H5'	0.95	0.87
1:A:1358:ASP:O	1:A:1360:LEU:N	2.08	0.87
6:F:5:A:H5'	11:K:114:THR:HG21	1.55	0.87
21:U:673:ILE:HD12	21:U:708:LEU:HD11	1.54	0.87
1:A:1174:PHE:CZ	1:A:1182:LEU:HD11	2.08	0.87
1:A:1567:PHE:CZ	1:A:1825:ILE:HG22	2.10	0.87
1:A:872:PRO:CD	17:Q:201:PHE:CG	2.56	0.87
4:D:66:C:OP2	16:P:12:ARG:NH2	2.06	0.87
1:A:1343:PHE:HA	1:A:1350:ILE:CD1	2.04	0.87
1:A:1393:GLU:O	1:A:1570:TRP:HH2	1.57	0.87
4:D:89:U:C5	11:K:176:TYR:CE1	2.63	0.87
13:M:49:SER:OG	13:M:52:SER:HB2	1.72	0.87
1:A:959:LEU:CD2	18:R:186:LEU:HB3	2.04	0.87
6:F:110:A:C2	29:m:2:LYS:HE3	2.10	0.87
6:F:1099:G:N7	6:F:1100:A:C8	2.43	0.87
21:U:649:SER:O	21:U:671:PHE:HB3	1.74	0.87
1:A:1474:ARG:NH1	22:V:232:ASN:O	2.08	0.87
3:C:365:GLU:O	3:C:367:VAL:N	2.08	0.87
3:C:274:ILE:HB	3:C:382:TYR:CE1	2.10	0.86
20:T:103:ILE:HG22	20:T:107:GLU:OE1	1.74	0.86
1:A:1393:GLU:O	1:A:1570:TRP:CH2	2.27	0.86
1:A:1561:LEU:HD12	1:A:1608:LEU:O	1.74	0.86
3:C:355:HIS:ND1	3:C:367:VAL:CG2	2.37	0.86
1:A:936:GLU:O	1:A:940:ILE:HD12	1.75	0.86
1:A:1343:PHE:O	1:A:1347:ARG:CA	2.23	0.86
3:C:681:CYS:HB3	3:C:850:LEU:HD13	1.54	0.86
18:R:188:LYS:HG3	18:R:192:GLU:OE2	1.75	0.86
1:A:312:TYR:O	1:A:319:ARG:NH2	2.08	0.86
1:A:1174:PHE:CZ	1:A:1182:LEU:HD12	2.10	0.86
20:T:93:LYS:O	20:T:97:ILE:HD13	1.73	0.86
1:A:926:LYS:CE	1:A:1521:ARG:NH2	2.39	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1547:ILE:HG22	1:A:1552:GLY:HA2	1.55	0.86
1:A:1130:ARG:CZ	1:A:1158:ILE:O	2.23	0.86
2:B:165:A:C2	29:f:2:LYS:HE3	2.10	0.86
18:R:198:GLU:O	18:R:202:ARG:HG3	1.75	0.86
18:R:198:GLU:HB3	18:R:202:ARG:NH1	1.89	0.86
20:T:99:ARG:O	20:T:103:ILE:HG13	1.76	0.86
3:C:354:TYR:CD1	3:C:359:PHE:CE1	2.64	0.86
1:A:515:PRO:HD3	1:A:689:TYR:OH	1.75	0.85
4:D:29:U:H2'	4:D:30:G:H5'	1.57	0.85
13:M:91:ILE:HD11	13:M:125:ILE:HG12	1.57	0.85
17:Q:216:ARG:CA	17:Q:219:ILE:HD12	2.01	0.85
3:C:886:SER:HB3	3:C:906:VAL:HA	1.59	0.85
18:R:205:HIS:O	18:R:209:GLU:HG3	1.75	0.85
3:C:887:ARG:HG2	3:C:887:ARG:HH11	1.41	0.85
1:A:1443:TYR:CZ	1:A:1542:TYR:HA	2.12	0.85
3:C:362:LYS:CG	3:C:363:PRO:HD2	2.07	0.85
3:C:860:PRO:HB2	3:C:908:VAL:CG1	2.06	0.85
3:C:355:HIS:HD1	3:C:367:VAL:HG21	1.41	0.85
3:C:810:GLU:OE1	3:C:976:ILE:HD11	1.76	0.85
1:A:1343:PHE:O	1:A:1347:ARG:HA	1.77	0.85
1:A:1851:PHE:O	1:A:1881:THR:HA	1.77	0.85
3:C:979:GLY:CA	3:C:983:SER:HB2	2.06	0.85
8:H:730:GLN:O	8:H:733:ILE:HD12	1.76	0.85
3:C:810:GLU:CD	3:C:976:ILE:HD11	2.02	0.84
5:E:3:A:H5''	5:E:3:A:H8	1.41	0.84
1:A:872:PRO:HB3	17:Q:201:PHE:CE1	2.12	0.84
3:C:532:ASP:CG	3:C:586:MET:CE	2.47	0.84
6:F:1099:G:C5	6:F:1100:A:N7	2.44	0.84
10:J:229:ASP:OD1	11:K:151:LYS:HE2	1.77	0.84
10:J:229:ASP:CB	11:K:151:LYS:HB3	2.06	0.84
3:C:365:GLU:O	3:C:367:VAL:HG12	1.77	0.84
5:E:499:U:O2'	5:E:500:A:OP1	1.94	0.84
6:F:1109:C:H41	32:p:109:LYS:H	1.21	0.84
1:A:926:LYS:HB3	1:A:926:LYS:NZ	1.93	0.84
5:E:500:A:C2'	5:E:501:A:OP2	2.24	0.84
6:F:30:A:O2'	6:F:31:A:H4'	1.78	0.84
1:A:893:ARG:NH2	1:A:1135:ALA:HB1	1.92	0.84
6:F:31:A:H3'	6:F:32:G:C4'	2.07	0.84
21:U:658:LEU:N	21:U:666:CYS:O	2.10	0.84
1:A:1366:ARG:HG3	2:B:95:C:OP1	1.75	0.84
3:C:860:PRO:CG	3:C:908:VAL:HG11	2.06	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:204:LEU:HD12	17:Q:204:LEU:O	1.77	0.84
1:A:329:TYR:HE1	3:C:919:ARG:CZ	1.87	0.84
1:A:948:HIS:CE1	18:R:176:GLU:HG2	2.12	0.84
10:J:103:ASN:OD1	18:R:193:MET:HE1	1.77	0.84
25:b:86:ASN:HD21	26:c:32:LYS:HD3	1.43	0.84
1:A:893:ARG:HH21	1:A:1135:ALA:HB3	1.38	0.84
1:A:1233:ARG:NH2	16:P:127:TRP:CZ3	2.43	0.84
1:A:1561:LEU:HD11	1:A:1608:LEU:O	1.78	0.84
1:A:1547:ILE:CD1	22:V:211:LEU:CD1	2.56	0.83
1:A:662:GLN:NE2	1:A:1620:TYR:CG	2.46	0.83
22:V:208:MET:O	22:V:219:GLN:NE2	2.11	0.83
22:V:229:LYS:O	22:V:233:GLU:N	2.09	0.83
3:C:692:SER:CB	3:C:706:LEU:O	2.25	0.83
3:C:808:LEU:HD23	3:C:987:PRO:CG	2.07	0.83
33:s:51:VAL:HG13	33:t:20:ARG:CB	2.09	0.83
1:A:1356:LEU:O	1:A:1360:LEU:HD12	1.78	0.83
3:C:274:ILE:HG21	3:C:385:PHE:CE2	2.13	0.83
21:U:660:TYR:O	21:U:662:ARG:N	2.11	0.83
1:A:514:TYR:HD1	1:A:689:TYR:HE2	1.25	0.83
3:C:461:LYS:HD3	3:C:461:LYS:H	1.43	0.83
17:Q:200:GLY:O	17:Q:203:LYS:HG2	1.78	0.83
3:C:604:LYS:CE	3:C:643:VAL:HG11	1.99	0.83
10:J:229:ASP:CB	11:K:151:LYS:HE3	2.09	0.83
3:C:461:LYS:HE3	3:C:461:LYS:O	1.79	0.83
3:C:687:ALA:HB1	3:C:689:ILE:CD1	2.06	0.83
20:T:106:LEU:HD12	20:T:106:LEU:O	1.78	0.83
20:T:131:GLU:OE2	21:U:626:LEU:HD21	1.78	0.83
1:A:903:LEU:HB3	18:R:180:ASP:OD1	1.79	0.83
1:A:1367:ILE:HA	1:A:1370:ARG:HG2	1.60	0.83
3:C:353:TYR:HE2	3:C:363:PRO:N	1.76	0.83
3:C:461:LYS:HB2	3:C:461:LYS:HZ2	1.44	0.83
4:D:21:U:OP2	19:S:54:SER:OG	1.96	0.83
15:O:171:THR:CG2	20:T:113:THR:HG21	2.08	0.83
1:A:864:GLN:HE22	1:A:1099:ASN:HA	1.44	0.82
1:A:1443:TYR:CE1	1:A:1542:TYR:N	2.43	0.82
22:V:209:LEU:O	22:V:209:LEU:HD13	1.79	0.82
1:A:923:TYR:O	1:A:926:LYS:HG3	1.79	0.82
7:G:114:LEU:O	7:G:117:VAL:HG12	1.78	0.82
4:D:50:G:N2	5:E:2:U:C6	2.46	0.82
10:J:70:ASP:OD2	10:J:101:ARG:NH2	2.12	0.82
1:A:923:TYR:CE2	1:A:936:GLU:HB2	2.13	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.13	0.82
1:A:1366:ARG:NE	2:B:95:C:OP2	2.13	0.82
3:C:860:PRO:O	3:C:908:VAL:HG12	1.80	0.82
13:M:49:SER:OG	13:M:52:SER:N	2.12	0.82
21:U:673:ILE:HD12	21:U:708:LEU:CD1	2.10	0.82
1:A:933:GLU:HA	1:A:936:GLU:HG3	1.61	0.82
1:A:1292:ARG:CZ	1:A:1292:ARG:HB2	2.08	0.82
4:D:84:C:O2'	4:D:85:C:OP1	1.98	0.82
15:O:223:HIS:ND1	15:O:245:ASP:OD2	2.12	0.82
1:A:1384:PRO:C	1:A:1386:ALA:H	1.87	0.82
8:H:724:VAL:O	8:H:727:GLU:CG	2.27	0.82
18:R:198:GLU:HB3	18:R:202:ARG:CZ	2.09	0.82
21:U:633:PHE:O	21:U:636:VAL:N	2.11	0.82
15:O:152:ASN:HD21	15:O:409:LYS:HB3	1.42	0.81
3:C:856:ILE:HA	3:C:944:VAL:CG1	2.08	0.81
19:S:68:PRO:HD2	19:S:69:TRP:HE3	1.43	0.81
1:A:1417:GLN:HE22	1:A:1783:MET:HB3	1.44	0.81
3:C:117:ARG:NH2	3:C:156:ASP:O	2.12	0.81
10:J:163:GLN:O	10:J:167:ALA:HB3	1.80	0.81
18:R:202:ARG:HG3	18:R:202:ARG:HH11	1.44	0.81
1:A:1290:ASP:OD1	1:A:1297:THR:HG23	1.80	0.81
13:M:104:ALA:HB1	13:M:110:LYS:HB3	1.63	0.81
1:A:1443:TYR:HE1	1:A:1542:TYR:CA	1.83	0.81
3:C:682:SER:O	3:C:854:ILE:CB	2.28	0.81
6:F:20:G:N3	16:P:6:ARG:O	2.14	0.81
21:U:644:LYS:HB3	21:U:646:TYR:CE1	2.14	0.81
25:i:86:ASN:HD21	26:j:32:LYS:HD3	1.43	0.81
3:C:602:VAL:CG1	3:C:908:VAL:CG2	2.57	0.81
20:T:94:THR:HA	20:T:97:ILE:HD13	1.62	0.81
1:A:1161:TYR:CE1	1:A:1170:MET:HE3	2.16	0.81
3:C:679:GLU:CD	3:C:809:ALA:H	1.88	0.81
6:F:1102:C:H2'	6:F:1103:C:H6	1.42	0.81
10:J:79:GLU:OE2	17:Q:202:MET:HE1	1.80	0.81
20:T:94:THR:O	20:T:97:ILE:HB	1.80	0.81
1:A:1343:PHE:HA	1:A:1350:ILE:HD11	1.62	0.80
3:C:990:GLU:CB	3:C:998:TYR:CE1	2.64	0.80
3:C:991:LYS:HG3	3:C:992:TYR:CD1	2.16	0.80
20:T:127:GLN:HB3	21:U:688:ILE:HD11	1.63	0.80
21:U:660:TYR:CD2	21:U:686:HIS:NE2	2.49	0.80
1:A:404:ASN:OD1	3:C:927:MET:HE1	1.79	0.80
3:C:274:ILE:HG21	3:C:385:PHE:HE2	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:131:GLU:OE2	21:U:626:LEU:CD1	2.30	0.80
1:A:871:GLY:HA3	17:Q:198:ASN:ND2	1.95	0.80
4:D:56:A:H2'	4:D:57:U:C5'	2.01	0.80
8:H:724:VAL:HA	8:H:727:GLU:CG	2.11	0.80
20:T:109:SER:O	20:T:113:THR:HG23	1.80	0.80
15:O:433:THR:OG1	15:O:435:GLU:OE1	1.99	0.80
1:A:1354:GLU:O	1:A:1358:ASP:N	2.14	0.80
31:o:13:GLN:HB3	24:h:102:LEU:C	2.07	0.80
1:A:1049:LEU:HD11	1:A:1260:PHE:CB	2.06	0.80
1:A:1265:PHE:CE1	1:A:1346:PHE:CD1	2.70	0.80
6:F:1100:A:H61	6:F:1116:A:H61	1.30	0.80
21:U:702:TYR:CD2	21:U:704:TRP:CZ2	2.69	0.80
31:o:34:LEU:CB	24:h:19:LYS:NZ	2.44	0.80
26:j:74:ARG:NH2	30:n:64:HIS:O	2.14	0.80
1:A:1344:THR:O	1:A:1347:ARG:HG3	1.81	0.80
1:A:1442:ARG:HB3	1:A:1442:ARG:NH1	1.96	0.80
21:U:164:GLU:CB	21:U:207:SER:CB	2.59	0.80
33:q:20:ARG:CB	33:r:53:ILE:CG1	2.59	0.80
3:C:967:VAL:O	3:C:971:ARG:HG3	1.82	0.80
13:M:120:LEU:CD1	13:M:122:GLY:H	1.95	0.80
3:C:675:THR:HG21	3:C:909:ILE:HB	1.64	0.80
9:I:124:ARG:NH1	10:J:223:PRO:O	2.13	0.80
1:A:874:ILE:O	1:A:875:THR:OG1	1.99	0.79
15:O:171:THR:HG22	20:T:113:THR:HG21	1.64	0.79
26:c:74:ARG:NH2	30:g:64:HIS:O	2.14	0.79
1:A:959:LEU:CD2	18:R:186:LEU:CB	2.60	0.79
1:A:1342:LEU:HD21	1:A:1356:LEU:HD22	1.64	0.79
1:A:930:ASN:OD1	1:A:931:ALA:N	2.15	0.79
9:I:116:ASN:CB	10:J:230:THR:HG22	2.12	0.79
21:U:673:ILE:CD1	21:U:708:LEU:HD11	2.13	0.79
1:A:905:TYR:HB3	1:A:908:ASP:CG	2.07	0.79
2:B:174:G:H5'	30:g:99:ASP:OD2	1.82	0.79
6:F:119:G:H5'	30:n:99:ASP:OD2	1.82	0.79
1:A:194:HIS:CD2	17:Q:122:LEU:HD22	2.17	0.79
3:C:364:PHE:CD1	3:C:365:GLU:N	2.34	0.79
3:C:993:ILE:HG22	3:C:997:LEU:HB3	1.63	0.79
6:F:1099:G:H5''	6:F:1099:G:N3	1.97	0.79
9:I:122:MET:HE2	9:I:122:MET:HA	1.63	0.79
15:O:171:THR:CG2	20:T:113:THR:CG2	2.60	0.79
6:F:1109:C:N4	32:p:109:LYS:N	2.30	0.79
9:I:103:ILE:HA	9:I:106:ILE:HD12	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:ILE:HD13	1:A:1101:TYR:CE1	2.17	0.79
18:R:205:HIS:HA	18:R:208:GLN:OE1	1.81	0.79
1:A:1499:ARG:HH21	22:V:239:ASN:ND2	1.80	0.79
3:C:132:ARG:O	3:C:208:ARG:HG2	1.82	0.79
3:C:859:GLU:CD	3:C:909:ILE:HG22	2.07	0.79
3:C:887:ARG:H	3:C:887:ARG:HD2	1.47	0.79
1:A:1355:PRO:O	1:A:1359:ILE:CG1	2.29	0.79
1:A:1485:ASP:O	1:A:1490:ARG:NH2	2.15	0.79
5:E:2:U:O2'	5:E:3:A:H8	1.63	0.79
1:A:1130:ARG:NH2	1:A:1158:ILE:O	2.17	0.78
2:B:43:G:O2'	2:B:45:A:H5'	1.82	0.78
6:F:1101:C:H41	32:p:38:LYS:HZ3	1.26	0.78
1:A:1509:ARG:NH1	1:A:1533:ASP:OD2	2.16	0.78
13:M:34:CYS:HB3	13:M:36:ILE:H	1.48	0.78
1:A:1547:ILE:HD12	22:V:211:LEU:CD2	2.11	0.78
1:A:488:ARG:O	3:C:416:ASP:OD1	2.01	0.78
1:A:1445:THR:HG21	1:A:1450:GLU:OE2	1.83	0.78
3:C:234:LEU:HD21	3:C:439:ILE:HG23	1.64	0.78
1:A:866:GLN:O	1:A:870:ASN:HB2	1.84	0.78
1:A:1540:ASN:OD1	22:V:209:LEU:CB	2.30	0.78
3:C:356:LYS:O	3:C:358:ASN:N	2.16	0.78
1:A:929:LEU:HD22	1:A:933:GLU:CB	2.12	0.78
22:V:243:GLU:O	22:V:247:LEU:HB2	1.84	0.78
3:C:810:GLU:CD	3:C:976:ILE:CD1	2.57	0.78
13:M:37:CYS:HB3	13:M:64:CYS:SG	2.24	0.78
21:U:644:LYS:HG3	21:U:646:TYR:CE2	2.19	0.78
21:U:648:ILE:H	21:U:648:ILE:HD12	1.49	0.78
1:A:1130:ARG:HH22	1:A:1158:ILE:HB	1.47	0.78
1:A:1424:HIS:HE1	1:A:1747:ASP:OD1	1.64	0.78
20:T:92:ARG:O	20:T:96:ASP:OD1	2.02	0.78
1:A:1879:ILE:O	1:A:1891:LEU:HA	1.84	0.77
3:C:354:TYR:CD1	3:C:359:PHE:HE1	2.00	0.77
13:M:125:ILE:HD12	13:M:126:THR:HG23	1.64	0.77
18:R:206:ALA:HA	18:R:209:GLU:OE1	1.85	0.77
20:T:35:LEU:CG	20:T:75:THR:O	2.32	0.77
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.66	0.77
9:I:250:PHE:HD2	9:I:266:LEU:HD22	1.48	0.77
10:J:228:TYR:HA	11:K:152:ILE:CG2	2.13	0.77
6:F:28:U:H2'	6:F:29:C:H5'	1.65	0.77
21:U:664:GLN:NE2	21:U:664:GLN:HA	1.99	0.77
1:A:1346:PHE:O	1:A:1348:GLU:N	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:860:PRO:CB	3:C:908:VAL:HG11	2.14	0.77
18:R:167:GLU:N	18:R:167:GLU:OE2	2.17	0.77
22:V:227:ILE:O	22:V:231:ILE:CD1	2.30	0.77
1:A:1696:SER:HA	1:A:1759:TYR:HE1	1.47	0.77
3:C:681:CYS:CB	3:C:850:LEU:HD11	2.07	0.77
9:I:79:HIS:CD2	10:J:244:PHE:CG	2.72	0.77
21:U:682:VAL:HG11	21:U:689:LEU:CG	2.14	0.77
4:D:57:U:C5'	4:D:57:U:H6	1.98	0.77
21:U:658:LEU:HD23	21:U:668:VAL:HG21	1.66	0.77
21:U:675:ASN:ND2	21:U:678:LYS:NZ	2.33	0.77
3:C:236:LEU:HD21	3:C:435:LEU:HD11	1.67	0.77
6:F:1111:U:C6	6:F:1111:U:C5'	2.65	0.77
10:J:160:LEU:O	11:K:196:ILE:CG2	2.32	0.77
10:J:160:LEU:O	11:K:196:ILE:HG23	1.85	0.77
1:A:870:ASN:C	17:Q:198:ASN:ND2	2.43	0.77
1:A:871:GLY:N	17:Q:198:ASN:HD22	1.83	0.77
1:A:1390:THR:CG2	1:A:1394:LEU:HD12	2.15	0.77
3:C:860:PRO:HB2	3:C:908:VAL:HG11	1.67	0.77
3:C:990:GLU:HG3	3:C:998:TYR:CD2	2.20	0.77
6:F:1100:A:N1	6:F:1116:A:N1	2.33	0.77
1:A:404:ASN:HA	3:C:919:ARG:HH12	1.48	0.77
3:C:945:LEU:CD1	3:C:1008:PRO:HG2	2.15	0.77
1:A:934:ARG:HH11	1:A:934:ARG:HG3	1.49	0.76
3:C:202:ASP:OD1	3:C:206:LYS:N	2.18	0.76
3:C:354:TYR:HD1	3:C:359:PHE:CD1	2.01	0.76
4:D:1:G:O2'	12:L:101:GLU:OE1	2.01	0.76
4:D:35:A:C5	12:L:41:LEU:HD21	2.20	0.76
21:U:644:LYS:HB3	21:U:646:TYR:CZ	2.19	0.76
3:C:684:GLU:O	3:C:685:SER:HB2	1.86	0.76
18:R:200:ILE:CG2	18:R:204:LYS:HE3	2.14	0.76
1:A:1304:VAL:HG11	1:A:1356:LEU:CD1	2.13	0.76
4:D:58:C:H6	4:D:58:C:H5''	1.50	0.76
21:U:633:PHE:O	21:U:634:LYS:C	2.27	0.76
1:A:905:TYR:OH	1:A:1002:GLU:OE2	2.03	0.76
3:C:675:THR:HG22	3:C:909:ILE:HD13	0.83	0.76
3:C:691:VAL:O	3:C:841:LEU:CD1	2.22	0.76
1:A:1335:TRP:CH2	1:A:1360:LEU:HD23	2.20	0.76
3:C:884:ARG:HH21	3:C:941:PRO:CD	1.99	0.76
4:D:42:A:O2'	4:D:43:C:O5'	2.01	0.76
13:M:53:ASN:HD22	13:M:54:ASN:H	1.34	0.76
22:V:246:LEU:HD23	22:V:246:LEU:C	2.10	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:ILE:CG1	1:A:1172:PHE:CZ	2.66	0.76
6:F:19:U:H3	17:Q:178:TYR:HB2	1.50	0.76
22:V:242:TRP:O	22:V:246:LEU:HB3	1.85	0.76
6:F:34:G:OP2	6:F:34:G:O4'	2.03	0.76
10:J:65:PHE:CD1	10:J:69:GLU:CB	2.62	0.76
1:A:940:ILE:O	1:A:943:ALA:HB3	1.86	0.76
1:A:1547:ILE:HD11	22:V:211:LEU:CD1	2.12	0.76
6:F:1109:C:H41	32:p:109:LYS:N	1.84	0.75
14:N:96:GLU:OE2	14:N:187:LYS:NZ	2.18	0.75
22:V:228:GLU:O	22:V:232:ASN:HB2	1.86	0.75
5:E:3:A:C8	5:E:3:A:H5''	2.21	0.75
8:H:729:TYR:CD2	8:H:748:PHE:CB	2.69	0.75
1:A:835:LYS:HD2	16:P:173:HIS:CE1	2.21	0.75
1:A:1049:LEU:HD12	1:A:1260:PHE:CB	2.04	0.75
5:E:14:U:C6	14:N:183:PHE:CE2	2.75	0.75
13:M:82:ILE:HD11	14:N:253:LEU:HD11	1.67	0.75
1:A:1017:ASP:O	1:A:1509:ARG:NH2	2.19	0.75
6:F:39:A:H2'	6:F:40:U:C5'	2.16	0.75
21:U:699:LYS:NZ	21:U:699:LYS:HB2	2.01	0.75
22:V:235:PRO:O	22:V:238:THR:OG1	2.02	0.75
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.18	0.75
4:D:89:U:O2	11:K:179:ARG:HG2	1.84	0.75
21:U:660:TYR:HE2	21:U:686:HIS:CD2	1.98	0.75
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.19	0.75
1:A:849:LEU:CD1	1:A:973:GLU:HB3	2.16	0.75
1:A:1417:GLN:CB	1:A:1783:MET:CE	2.63	0.75
20:T:137:LYS:HE2	21:U:639:ASP:OD2	1.80	0.75
1:A:770:MET:O	15:O:309:ARG:NH2	2.19	0.75
1:A:1445:THR:CG2	1:A:1450:GLU:OE2	2.35	0.75
1:A:1553:ILE:HD11	22:V:211:LEU:HB3	1.67	0.75
3:C:430:ARG:HG3	3:C:430:ARG:NH1	2.00	0.75
3:C:885:GLY:CA	3:C:907:PRO:CD	2.61	0.74
1:A:939:LEU:O	1:A:939:LEU:HD23	1.87	0.74
1:A:1328:PHE:HD2	1:A:1371:VAL:CG2	1.96	0.74
3:C:979:GLY:HA3	3:C:983:SER:HB2	1.68	0.74
14:N:161:ARG:O	14:N:165:SER:HB3	1.86	0.74
1:A:1547:ILE:CD1	22:V:211:LEU:CD2	2.61	0.74
3:C:530:GLU:OE1	3:C:531:ASP:N	2.20	0.74
3:C:972:ARG:HH21	3:C:982:MET:HG2	1.49	0.74
1:A:881:THR:OG1	16:P:133:PHE:CZ	2.11	0.74
1:A:1344:THR:O	1:A:1447:TRP:HZ2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:208:ARG:HH22	3:C:440:THR:HG21	1.49	0.74
3:C:887:ARG:HD2	3:C:887:ARG:N	2.03	0.74
1:A:1051:GLU:OE1	1:A:1204:ARG:NH2	2.20	0.74
1:A:1342:LEU:HD21	1:A:1356:LEU:HD21	1.70	0.74
4:D:91:A:C4	9:I:99:ILE:HD11	2.23	0.74
6:F:1101:C:N4	32:p:38:LYS:NZ	2.36	0.74
9:I:116:ASN:N	10:J:233:GLU:OE2	2.20	0.74
20:T:123:LEU:HD21	21:U:700:PRO:HG3	1.68	0.74
1:A:872:PRO:HD3	17:Q:201:PHE:CE1	2.22	0.74
1:A:1316:ILE:CD1	1:A:1335:TRP:HZ3	1.95	0.74
3:C:501:ILE:HD13	3:C:567:ILE:HG23	1.70	0.74
3:C:989:LEU:O	3:C:993:ILE:HD12	1.87	0.74
14:N:206:LEU:HD12	14:N:207:PRO:HD2	1.70	0.74
3:C:884:ARG:NH2	3:C:941:PRO:HD2	2.02	0.74
3:C:468:LEU:O	3:C:468:LEU:HD23	1.88	0.74
3:C:883:ARG:O	3:C:884:ARG:HB3	1.88	0.74
6:F:28:U:O2'	6:F:29:C:H5'	1.88	0.74
8:H:669:TYR:HE2	8:H:686:ILE:HG13	1.53	0.74
1:A:872:PRO:HD3	17:Q:201:PHE:CZ	2.22	0.73
3:C:679:GLU:OE2	3:C:809:ALA:CA	2.36	0.73
3:C:687:ALA:CB	3:C:689:ILE:HD11	2.15	0.73
13:M:75:MET:HE1	14:N:130:PHE:CE1	2.22	0.73
34:x:5:U:H2'	34:x:6:U:C6	2.21	0.73
1:A:929:LEU:CD2	1:A:933:GLU:HB3	2.18	0.73
1:A:1547:ILE:HD13	22:V:211:LEU:HD11	1.67	0.73
5:E:502:C:O2'	5:E:503:A:OP2	2.06	0.73
31:o:15:TYR:CB	24:h:47:GLU:HG3	2.18	0.73
1:A:487:ASN:OD1	1:A:488:ARG:HG2	1.87	0.73
1:A:835:LYS:HD2	16:P:173:HIS:HE1	1.54	0.73
1:A:926:LYS:HB3	1:A:926:LYS:HZ2	1.51	0.73
3:C:355:HIS:HB2	3:C:364:PHE:CZ	2.19	0.73
1:A:514:TYR:CD1	1:A:689:TYR:HE2	1.97	0.73
1:A:1182:LEU:HD23	16:P:128:ARG:HH22	1.51	0.73
1:A:1442:ARG:HB3	1:A:1442:ARG:CZ	2.18	0.73
3:C:808:LEU:HD23	3:C:987:PRO:HG3	1.65	0.73
3:C:989:LEU:O	3:C:989:LEU:HD12	1.88	0.73
20:T:94:THR:CA	20:T:97:ILE:HD13	2.18	0.73
1:A:1391:PRO:HD2	1:A:1394:LEU:HG	1.69	0.73
3:C:461:LYS:HB2	3:C:461:LYS:NZ	2.01	0.73
1:A:1130:ARG:NH2	1:A:1158:ILE:HB	2.04	0.73
1:A:1860:VAL:HA	1:A:1873:LYS:O	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2:U:C2'	5:E:3:A:C8	2.72	0.73
6:F:31:A:H5'	6:F:32:G:O2'	1.89	0.73
15:O:230:VAL:HG22	15:O:241:THR:HG22	1.70	0.73
20:T:42:TYR:CE1	20:T:64:PHE:CZ	2.77	0.73
3:C:860:PRO:CD	3:C:908:VAL:HG11	2.18	0.73
25:i:86:ASN:HD21	26:j:32:LYS:CD	2.02	0.73
1:A:926:LYS:HE2	1:A:1521:ARG:CZ	2.19	0.73
3:C:353:TYR:CE2	3:C:363:PRO:N	2.57	0.73
21:U:658:LEU:O	21:U:665:ASP:CA	2.35	0.73
1:A:1346:PHE:O	1:A:1347:ARG:C	2.31	0.73
1:A:1571:GLU:CG	22:V:212:THR:HG21	2.18	0.73
9:I:124:ARG:HH11	10:J:224:MET:HG2	1.54	0.72
13:M:34:CYS:SG	13:M:61:CYS:N	2.62	0.72
18:R:167:GLU:OE2	18:R:168:LYS:N	2.20	0.72
21:U:691:VAL:HG21	21:U:701:ILE:HD12	1.71	0.72
3:C:247:PHE:CE2	3:C:933:TRP:HZ3	2.06	0.72
4:D:66:C:C6	4:D:66:C:H5'	2.24	0.72
6:F:5:A:H5'	11:K:114:THR:CG2	2.20	0.72
10:J:70:ASP:CG	10:J:101:ARG:NH2	2.47	0.72
14:N:10:LYS:NZ	14:N:57:LEU:O	2.15	0.72
21:U:658:LEU:HD22	21:U:668:VAL:HG23	1.72	0.72
1:A:1460:GLU:O	1:A:1464:LYS:HD2	1.90	0.72
12:L:122:CYS:HB2	12:L:145:CYS:HB2	1.70	0.72
1:A:1344:THR:HA	1:A:1347:ARG:HG2	1.70	0.72
2:B:174:G:H4'	2:B:174:G:OP1	1.90	0.72
10:J:204:LYS:HG2	10:J:205:LYS:H	1.54	0.72
13:M:125:ILE:HD12	13:M:126:THR:N	2.05	0.72
21:U:658:LEU:CD2	21:U:668:VAL:CG2	2.66	0.72
21:U:704:TRP:CZ3	21:U:705:ALA:HB2	2.25	0.72
2:B:98:U:HO2'	4:D:75:A:H8	1.37	0.72
1:A:1390:THR:CB	1:A:1396:GLY:HA3	2.20	0.72
15:O:285:SER:OG	15:O:287:ASP:OD1	2.08	0.72
1:A:1370:ARG:CZ	1:A:1370:ARG:HB3	2.19	0.72
3:C:989:LEU:HG	3:C:993:ILE:CD1	2.20	0.72
14:N:96:GLU:HG2	14:N:188:TYR:HE2	1.53	0.72
17:Q:220:ARG:NH1	17:Q:220:ARG:HB2	2.05	0.72
20:T:105:LYS:O	20:T:109:SER:OG	2.07	0.72
25:b:86:ASN:HD21	26:c:32:LYS:CD	2.02	0.72
3:C:887:ARG:NH2	3:C:938:ARG:NH2	2.36	0.72
16:P:132:ALA:C	16:P:133:PHE:HD1	1.98	0.72
17:Q:217:GLN:CA	17:Q:217:GLN:HE21	2.03	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:247:PHE:CD2	3:C:933:TRP:HZ3	2.08	0.71
10:J:164:GLY:O	10:J:168:THR:HG23	1.89	0.71
3:C:468:LEU:HD23	3:C:468:LEU:C	2.15	0.71
13:M:16:CYS:SG	14:N:105:ARG:NH2	2.62	0.71
1:A:514:TYR:HE1	1:A:689:TYR:HD2	0.78	0.71
1:A:1296:ARG:HH11	1:A:1296:ARG:CB	2.02	0.71
1:A:1571:GLU:HG2	22:V:212:THR:HG23	1.73	0.71
3:C:356:LYS:O	3:C:358:ASN:OD1	2.07	0.71
3:C:884:ARG:NH2	3:C:941:PRO:HD3	2.05	0.71
3:C:990:GLU:HA	3:C:998:TYR:CD1	2.26	0.71
20:T:141:LEU:HD22	20:T:141:LEU:N	2.06	0.71
1:A:893:ARG:HH22	1:A:1135:ALA:HB1	1.54	0.71
1:A:1850:LEU:HD13	1:A:1930:PRO:HB3	1.71	0.71
9:I:115:ILE:H	10:J:233:GLU:CD	1.98	0.71
13:M:125:ILE:HD12	13:M:125:ILE:C	2.16	0.71
21:U:658:LEU:CD2	21:U:668:VAL:HG21	2.21	0.71
9:I:209:GLU:O	9:I:213:GLY:N	2.24	0.71
1:A:1034:ASN:HB3	1:A:1291:GLU:OE2	1.91	0.71
1:A:1263:CYS:CB	1:A:1345:TYR:OH	2.38	0.71
9:I:198:GLN:OE1	9:I:200:GLN:NE2	2.23	0.71
3:C:340:LYS:O	3:C:343:ASP:HB3	1.91	0.71
6:F:19:U:C4	17:Q:174:ASN:OD1	2.44	0.71
13:M:91:ILE:CD1	13:M:125:ILE:CG1	2.63	0.71
2:B:173:U:H4'	2:B:174:G:OP1	1.91	0.71
3:C:734:CYS:SG	3:C:755:TYR:OH	2.39	0.71
8:H:616:PRO:CG	8:H:617:PRO:N	2.53	0.71
10:J:228:TYR:HA	11:K:152:ILE:HG22	1.72	0.71
18:R:198:GLU:O	18:R:202:ARG:CG	2.39	0.71
20:T:95:ASN:O	20:T:98:GLU:HB3	1.90	0.71
1:A:925:SER:HB2	22:V:202:GLN:CD	2.16	0.71
3:C:133:ILE:HG22	3:C:209:MET:HB3	1.73	0.71
4:D:91:A:C2	9:I:99:ILE:HD11	2.26	0.71
8:H:718:SER:OG	8:H:725:THR:CG2	2.37	0.71
13:M:101:THR:CG2	13:M:120:LEU:HD11	2.20	0.71
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.22	0.70
1:A:1390:THR:OG1	1:A:1396:GLY:HA3	1.91	0.70
3:C:247:PHE:CE2	3:C:933:TRP:CZ3	2.79	0.70
1:A:1565:THR:HG21	1:A:1825:ILE:HD12	1.71	0.70
6:F:5:A:C5'	11:K:114:THR:HG21	2.21	0.70
12:L:3:ARG:NH2	12:L:85:LYS:O	2.24	0.70
13:M:91:ILE:HD11	13:M:125:ILE:CG1	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:139:PHE:CB	20:T:141:LEU:HD23	2.19	0.70
1:A:1414:TRP:HZ3	1:A:1416:LYS:HB2	1.57	0.70
1:A:1479:GLU:H	1:A:1479:GLU:CD	1.96	0.70
18:R:204:LYS:O	18:R:208:GLN:HG3	1.90	0.70
4:D:29:U:C2'	4:D:30:G:H5'	2.22	0.70
10:J:65:PHE:CE1	10:J:69:GLU:HB3	2.26	0.70
20:T:20:LEU:HD21	20:T:67:LEU:CG	2.21	0.70
21:U:637:VAL:C	21:U:641:CYS:HG	1.96	0.70
1:A:140:ARG:O	1:A:144:ASN:HB2	1.92	0.70
1:A:1050:LEU:O	1:A:1169:TYR:HA	1.91	0.70
3:C:362:LYS:CD	3:C:363:PRO:HG2	2.16	0.70
20:T:131:GLU:OE2	21:U:626:LEU:HD22	1.90	0.70
1:A:1547:ILE:HD13	22:V:211:LEU:HD21	1.72	0.70
3:C:932:PHE:O	3:C:933:TRP:CD1	2.45	0.70
6:F:1116:A:C6	6:F:1117:G:C5	2.79	0.70
21:U:660:TYR:CD2	21:U:686:HIS:HD2	1.92	0.70
1:A:662:GLN:NE2	1:A:1620:TYR:CD2	2.54	0.70
10:J:163:GLN:HB3	10:J:168:THR:HG22	1.73	0.70
20:T:34:ASP:CG	20:T:37:GLN:H	1.98	0.70
3:C:688:SER:O	3:C:709:SER:OG	2.04	0.70
6:F:119:G:OP1	6:F:119:G:H4'	1.90	0.70
15:O:156:ILE:HD13	15:O:197:LEU:HD22	1.73	0.70
21:U:644:LYS:NZ	21:U:646:TYR:OH	2.23	0.70
1:A:871:GLY:CA	17:Q:198:ASN:ND2	2.49	0.70
1:A:1348:GLU:CD	1:A:1447:TRP:HB2	2.17	0.70
1:A:1390:THR:HG22	1:A:1394:LEU:CD1	2.22	0.70
1:A:1393:GLU:HG2	1:A:1570:TRP:HZ2	1.56	0.70
3:C:385:PHE:HE1	3:C:425:LEU:HD11	1.56	0.70
1:A:1327:THR:O	1:A:1331:VAL:HG23	1.92	0.70
1:A:1710:GLU:HG2	1:A:1728:ILE:HG12	1.74	0.70
3:C:646:GLY:HA3	3:C:652:MET:HE3	1.74	0.70
5:E:10:U:C6	5:E:10:U:OP2	2.45	0.70
9:I:42:GLU:OE2	10:J:185:LEU:HD22	1.91	0.70
13:M:121:GLY:HA2	13:M:124:GLN:OE1	1.92	0.70
15:O:217:ILE:HG22	15:O:218:ARG:HG3	1.72	0.70
6:F:41:C:H4'	6:F:42:U:OP1	1.92	0.69
17:Q:212:ASP:OD1	17:Q:216:ARG:NH1	2.25	0.69
21:U:651:ILE:HD12	21:U:671:PHE:CA	2.20	0.69
1:A:609:GLU:OE2	4:D:43:C:O2'	2.04	0.69
1:A:751:ASP:OD1	1:A:752:ALA:N	2.25	0.69
10:J:209:THR:HB	13:M:108:MET:HE3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:229:ASP:CG	11:K:151:LYS:HB3	2.17	0.69
15:O:317:HIS:NE2	15:O:362:ASP:OD1	2.20	0.69
1:A:1414:TRP:HB2	1:A:1558:GLU:HG3	1.74	0.69
6:F:118:U:H4'	6:F:119:G:OP1	1.91	0.69
6:F:15:C:H41	11:K:209:ARG:CG	2.01	0.69
6:F:1116:A:C4	6:F:1117:G:C8	2.80	0.69
22:V:207:GLU:HG2	22:V:207:GLU:O	1.92	0.69
1:A:1194:ASN:O	21:U:662:ARG:NH2	2.25	0.69
1:A:1326:THR:C	1:A:1327:THR:HG23	2.17	0.69
1:A:1343:PHE:CD1	1:A:1350:ILE:HD12	1.88	0.69
3:C:993:ILE:HG21	3:C:997:LEU:HB3	1.74	0.69
1:A:934:ARG:HG3	1:A:934:ARG:NH1	2.05	0.69
1:A:1488:ILE:HG23	1:A:1489:PRO:HD3	1.73	0.69
6:F:31:A:H4'	6:F:32:G:OP2	1.93	0.69
6:F:1116:A:C2	6:F:1117:G:C5	2.80	0.69
28:l:30:ARG:O	28:l:47:VAL:HG23	1.92	0.69
1:A:870:ASN:O	17:Q:198:ASN:ND2	2.25	0.69
1:A:1204:ARG:NH1	1:A:1247:PHE:CE2	2.61	0.69
3:C:362:LYS:HG2	3:C:363:PRO:CD	2.17	0.69
6:F:119:G:N7	29:m:20:LYS:HE2	2.08	0.69
8:H:601:VAL:O	8:H:604:SER:OG	2.09	0.69
10:J:229:ASP:CA	11:K:151:LYS:HE3	2.21	0.69
20:T:139:PHE:HB3	20:T:141:LEU:HD21	1.73	0.69
21:U:667:ILE:HD12	21:U:667:ILE:N	2.08	0.69
13:M:103:GLU:OE1	14:N:131:ARG:NH1	2.26	0.69
21:U:675:ASN:ND2	21:U:678:LYS:HZ1	1.84	0.69
3:C:682:SER:HB3	3:C:854:ILE:HG22	1.73	0.69
9:I:36:ASP:O	10:J:189:ARG:NH2	2.26	0.69
19:S:55:GLU:OE2	19:S:58:ARG:CD	2.41	0.69
1:A:391:TYR:OH	3:C:912:ALA:O	2.09	0.68
3:C:510:ARG:HH11	3:C:510:ARG:HG2	1.59	0.68
6:F:120:G:C2	25:i:33:GLU:HG3	2.29	0.68
22:V:243:GLU:O	22:V:247:LEU:CB	2.41	0.68
26:c:74:ARG:NH1	30:g:65:CYS:SG	2.66	0.68
33:s:20:ARG:CB	33:t:53:ILE:HA	2.24	0.68
1:A:362:GLU:OE2	1:A:363:ASP:N	2.26	0.68
1:A:515:PRO:CD	1:A:689:TYR:OH	2.41	0.68
1:A:900:PHE:CG	1:A:901:PRO:HD2	2.28	0.68
6:F:40:U:HO2'	6:F:41:C:H5	1.41	0.68
25:b:86:ASN:HD21	26:c:32:LYS:CE	2.06	0.68
26:j:74:ARG:NH1	30:n:65:CYS:SG	2.66	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.57	0.68
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.29	0.68
2:B:43:G:H2'	2:B:43:G:N3	2.07	0.68
3:C:655:LEU:O	3:C:658:ASP:N	2.27	0.68
3:C:682:SER:C	3:C:854:ILE:HB	2.19	0.68
3:C:693:ASN:OD1	21:U:642:LEU:HG	1.94	0.68
3:C:857:LEU:CD2	3:C:966:PHE:HB2	2.24	0.68
9:I:114:CYS:SG	10:J:237:ILE:CD1	2.79	0.68
10:J:229:ASP:HB2	11:K:151:LYS:HE3	1.75	0.68
13:M:119:LYS:O	13:M:123:ALA:HB3	1.92	0.68
25:i:86:ASN:HD21	26:j:32:LYS:CE	2.05	0.68
6:F:1102:C:H6	6:F:1102:C:O5'	1.76	0.68
1:A:681:LYS:O	1:A:684:LYS:HB3	1.93	0.68
1:A:1476:ALA:O	1:A:1477:PHE:HB3	1.92	0.68
3:C:208:ARG:CZ	3:C:440:THR:HG23	2.23	0.68
15:O:354:ASN:ND2	15:O:369:ASP:OD1	2.26	0.68
1:A:1265:PHE:HE1	1:A:1346:PHE:HD1	1.40	0.68
2:B:174:G:N7	29:f:20:LYS:HE2	2.08	0.68
1:A:740:GLU:HG3	1:A:741:ILE:H	1.59	0.68
1:A:959:LEU:HD22	18:R:186:LEU:CB	2.24	0.68
4:D:64:U:O2'	4:D:65:U:OP1	2.12	0.68
21:U:658:LEU:HD23	21:U:668:VAL:CG2	2.23	0.68
21:U:660:TYR:HE2	21:U:686:HIS:HD2	1.33	0.68
1:A:161:PHE:HE1	1:A:198:ALA:HA	1.58	0.68
3:C:991:LYS:HD2	3:C:992:TYR:CE1	2.27	0.68
9:I:39:ASP:OD2	10:J:188:ARG:NH2	2.27	0.68
15:O:147:ILE:HD13	15:O:408:ASP:HA	1.76	0.68
3:C:1006:LEU:N	3:C:1006:LEU:HD23	2.08	0.68
9:I:115:ILE:N	10:J:233:GLU:CD	2.51	0.68
12:L:120:CYS:CB	12:L:122:CYS:HB3	2.21	0.68
1:A:1618:ASN:N	1:A:1744:ASP:OD2	2.25	0.67
3:C:208:ARG:HH21	3:C:440:THR:HG21	1.51	0.67
3:C:860:PRO:CB	3:C:908:VAL:CG1	2.70	0.67
6:F:19:U:O2	17:Q:178:TYR:CD1	2.46	0.67
9:I:49:ARG:NH1	10:J:181:ARG:NH2	2.41	0.67
3:C:856:ILE:CA	3:C:944:VAL:HG11	2.23	0.67
3:C:971:ARG:NH2	3:C:976:ILE:CG2	2.40	0.67
6:F:39:A:H2'	6:F:40:U:H5'	1.76	0.67
15:O:275:THR:OG1	15:O:279:PRO:O	2.12	0.67
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.76	0.67
3:C:467:THR:HG22	3:C:580:VAL:HG23	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:31:G:O6	13:M:47:LYS:NZ	2.27	0.67
8:H:602:MET:HA	8:H:605:PHE:HD2	1.57	0.67
10:J:109:GLU:OE1	18:R:196:ARG:CB	2.41	0.67
1:A:854:ARG:HD2	1:A:1095:MET:CE	2.23	0.67
1:A:872:PRO:HG3	17:Q:204:LEU:HD23	1.77	0.67
1:A:1379:MET:HE3	1:A:1379:MET:CA	2.25	0.67
3:C:604:LYS:CE	3:C:643:VAL:CG1	2.64	0.67
9:I:119:ARG:NH1	9:I:143:GLU:OE2	2.28	0.67
1:A:872:PRO:CD	17:Q:201:PHE:CE2	2.76	0.67
1:A:1087:ASN:ND2	1:A:1099:ASN:O	2.25	0.67
10:J:90:MET:CE	17:Q:197:ILE:HG23	2.13	0.67
10:J:229:ASP:OD1	11:K:151:LYS:CE	2.42	0.67
21:U:674:ARG:HB3	21:U:678:LYS:O	1.93	0.67
33:q:20:ARG:CB	33:r:53:ILE:CA	2.72	0.67
1:A:1488:ILE:CG2	1:A:1489:PRO:HD3	2.24	0.67
33:s:20:ARG:CB	33:t:52:GLU:O	2.43	0.67
1:A:1229:GLU:OE2	16:P:128:ARG:HG3	1.94	0.67
1:A:1417:GLN:NE2	1:A:1783:MET:CB	2.51	0.67
2:B:98:U:O2'	4:D:75:A:C8	2.47	0.67
3:C:532:ASP:CB	3:C:586:MET:HE1	2.24	0.67
3:C:801:TRP:CH2	21:U:648:ILE:O	2.47	0.67
15:O:111:ILE:HB	15:O:114:ARG:HH21	1.60	0.67
1:A:467:GLU:O	3:C:387:TYR:OH	2.11	0.67
2:B:174:G:C5'	30:g:99:ASP:HB2	2.24	0.67
3:C:656:LEU:HD13	3:C:670:ILE:HD13	1.77	0.67
4:D:67:C:OP2	9:I:59:LYS:HE3	1.95	0.67
9:I:250:PHE:CD2	9:I:266:LEU:HD22	2.28	0.67
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.28	0.67
1:A:1348:GLU:CD	1:A:1447:TRP:H	2.02	0.67
1:A:1494:LEU:HD21	22:V:246:LEU:HD22	1.77	0.67
3:C:122:TYR:CE2	28:e:82:PRO:HD3	2.30	0.67
3:C:531:ASP:O	3:C:532:ASP:HB3	1.95	0.67
34:x:6:U:O5'	34:x:6:U:H6	1.78	0.67
1:A:1390:THR:HG22	1:A:1394:LEU:CB	2.25	0.67
1:A:1417:GLN:OE1	1:A:1422:ILE:HD11	1.95	0.67
2:B:175:G:C2	25:b:33:GLU:HG3	2.29	0.67
3:C:860:PRO:HB3	3:C:932:PHE:CZ	2.30	0.67
10:J:16:VAL:HG13	10:J:152:LEU:HD12	1.77	0.67
12:L:128:GLN:O	12:L:131:GLU:N	2.28	0.67
6:F:119:G:C5'	30:n:99:ASP:HB2	2.25	0.66
1:A:1370:ARG:HG3	1:A:1370:ARG:HH11	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:296:ASN:OD1	3:C:304:PHE:N	2.28	0.66
3:C:972:ARG:NH2	3:C:982:MET:CG	2.57	0.66
6:F:16:U:H3'	6:F:18:U:C5	2.30	0.66
8:H:709:TRP:HA	8:H:712:CYS:SG	2.34	0.66
9:I:99:ILE:HA	9:I:102:TRP:HD1	1.60	0.66
19:S:55:GLU:OE2	19:S:55:GLU:HA	1.93	0.66
21:U:672:GLU:HA	21:U:680:MET:O	1.96	0.66
21:U:673:ILE:CD1	21:U:708:LEU:CD1	2.72	0.66
6:F:1116:A:C4	6:F:1117:G:N7	2.63	0.66
17:Q:220:ARG:NE	17:Q:220:ARG:HA	2.09	0.66
20:T:20:LEU:HD12	20:T:45:LEU:CD1	2.10	0.66
22:V:212:THR:O	22:V:213:ASP:HB2	1.93	0.66
1:A:900:PHE:O	1:A:902:PRO:HD3	1.96	0.66
1:A:1397:LEU:HD21	1:A:1606:PHE:CE1	2.30	0.66
3:C:689:ILE:N	3:C:689:ILE:HD12	2.11	0.66
3:C:971:ARG:HH21	3:C:976:ILE:HG21	1.58	0.66
3:C:780:PRO:HA	3:C:783:ILE:HB	1.76	0.66
21:U:648:ILE:HD12	21:U:648:ILE:N	2.09	0.66
1:A:768:GLU:OE2	15:O:310:SER:HB3	1.96	0.66
15:O:362:ASP:OD2	15:O:379:LYS:NZ	2.28	0.66
18:R:188:LYS:O	18:R:192:GLU:HG3	1.95	0.66
1:A:1211:SER:O	1:A:1257:ASN:ND2	2.28	0.66
1:A:1342:LEU:HD12	1:A:1342:LEU:O	1.96	0.66
1:A:1342:LEU:CD2	1:A:1356:LEU:HD21	2.26	0.66
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.26	0.66
4:D:90:U:OP2	9:I:104:ARG:NH2	2.28	0.66
8:H:729:TYR:CG	8:H:748:PHE:CB	2.79	0.66
21:U:658:LEU:O	21:U:666:CYS:N	2.28	0.66
1:A:1882:LEU:HD22	1:A:1991:ILE:HD11	1.78	0.66
3:C:831:ILE:HG13	3:C:832:ASP:H	1.61	0.66
15:O:391:GLU:HG3	15:O:392:MET:H	1.61	0.66
21:U:684:LEU:HD23	21:U:684:LEU:N	2.11	0.66
33:q:51:VAL:HG11	33:r:20:ARG:CB	2.25	0.66
1:A:1040:ASP:O	1:A:1045:GLN:CG	2.39	0.66
3:C:208:ARG:CZ	3:C:440:THR:CG2	2.74	0.66
21:U:667:ILE:HD12	21:U:667:ILE:H	1.60	0.66
1:A:1068:ARG:HG2	1:A:1068:ARG:NH1	2.01	0.66
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.78	0.66
1:A:1344:THR:HG21	1:A:1537:TRP:CE3	2.30	0.66
6:F:110:A:H2	29:m:2:LYS:HE2	1.58	0.66
13:M:70:ILE:HD13	13:M:84:ILE:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:306:HIS:CD2	17:Q:147:LEU:HD11	2.31	0.66
17:Q:204:LEU:HD12	17:Q:204:LEU:C	2.21	0.66
1:A:1366:ARG:NH1	2:B:95:C:OP2	2.28	0.65
1:A:1441:PHE:H	1:A:1441:PHE:HD2	1.44	0.65
1:A:1553:ILE:HD11	22:V:211:LEU:CB	2.26	0.65
1:A:2022:ALA:HB1	1:A:2055:MET:HE1	1.78	0.65
13:M:53:ASN:HD22	13:M:54:ASN:N	1.93	0.65
21:U:675:ASN:OD1	21:U:678:LYS:CD	2.43	0.65
29:m:82:LEU:HD12	29:m:85:ILE:HD11	1.77	0.65
1:A:1417:GLN:HB2	1:A:1783:MET:HE3	1.76	0.65
1:A:1366:ARG:CD	2:B:95:C:OP2	2.45	0.65
3:C:638:GLU:N	3:C:638:GLU:OE2	2.30	0.65
3:C:989:LEU:HG	3:C:993:ILE:HD11	1.78	0.65
13:M:49:SER:OG	13:M:52:SER:CA	2.44	0.65
18:R:198:GLU:HB3	18:R:202:ARG:NH2	2.10	0.65
22:V:236:TYR:CE1	22:V:237:ARG:HG2	2.32	0.65
3:C:355:HIS:CE1	3:C:367:VAL:HG23	2.31	0.65
3:C:1001:LEU:O	3:C:1006:LEU:HG	1.96	0.65
20:T:106:LEU:CD1	20:T:110:GLU:CD	2.67	0.65
1:A:1067:ASN:O	1:A:1071:ARG:HG2	1.96	0.65
2:B:31:G:H2'	2:B:32:G:H5'	1.78	0.65
5:E:2:U:C4'	5:E:3:A:OP1	2.36	0.65
9:I:176:GLU:OE1	9:I:181:ASN:ND2	2.25	0.65
14:N:121:ARG:HD3	14:N:125:GLY:HA3	1.78	0.65
20:T:93:LYS:O	20:T:97:ILE:HD12	1.94	0.65
3:C:307:ILE:HG12	3:C:346:THR:HA	1.79	0.65
3:C:461:LYS:H	3:C:461:LYS:CD	2.06	0.65
4:D:52:G:H4'	10:J:166:LYS:HG3	1.79	0.65
11:K:195:PHE:HE1	11:K:204:ASN:HD22	1.43	0.65
13:M:116:LYS:HG3	13:M:118:VAL:HG22	1.77	0.65
1:A:662:GLN:NE2	1:A:1620:TYR:CD1	2.64	0.65
2:B:98:U:O2'	4:D:75:A:H8	1.80	0.65
3:C:292:ILE:O	3:C:296:ASN:ND2	2.30	0.65
10:J:163:GLN:CB	10:J:168:THR:HG22	2.26	0.65
20:T:17:TYR:OH	20:T:84:ASP:OD2	2.15	0.65
21:U:633:PHE:C	21:U:635:ASP:N	2.55	0.65
22:V:241:GLU:HA	22:V:241:GLU:OE2	1.97	0.65
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.76	0.65
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.80	0.65
1:A:1366:ARG:HD3	2:B:95:C:OP2	1.96	0.65
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:117:ARG:HG2	3:C:157:SER:O	1.96	0.65
4:D:59:A:H5'	4:D:60:G:OP2	1.97	0.65
9:I:39:ASP:CG	10:J:188:ARG:HH12	2.05	0.65
12:L:32:ASP:HA	12:L:35:LYS:HD3	1.77	0.65
29:f:82:LEU:HD12	29:f:85:ILE:HD11	1.77	0.65
1:A:168:LEU:HD23	1:A:622:MET:HE2	1.78	0.65
1:A:872:PRO:CD	17:Q:201:PHE:CD1	2.76	0.65
3:C:353:TYR:HE2	3:C:363:PRO:CD	2.10	0.65
3:C:989:LEU:HD12	3:C:993:ILE:CD1	2.24	0.65
6:F:16:U:C3'	6:F:18:U:O4	2.44	0.65
6:F:19:U:O2	17:Q:178:TYR:CD2	2.49	0.65
20:T:137:LYS:CE	20:T:143:TYR:OH	2.44	0.65
21:U:660:TYR:CE2	21:U:686:HIS:NE2	2.65	0.65
31:o:53:PRO:CB	24:h:98:GLU:C	2.70	0.65
1:A:1755:LYS:HE3	1:A:1759:TYR:HE2	1.62	0.64
3:C:993:ILE:HG23	3:C:997:LEU:HD13	1.78	0.64
8:H:724:VAL:C	8:H:727:GLU:CG	2.71	0.64
12:L:121:ILE:HD11	12:L:129:LEU:HD21	1.78	0.64
21:U:647:LEU:O	21:U:673:ILE:HA	1.94	0.64
34:x:5:U:O5'	34:x:5:U:H6	1.80	0.64
1:A:1454:SER:HA	1:A:1487:GLY:HA2	1.79	0.64
5:E:2:U:H2'	5:E:3:A:C8	2.32	0.64
10:J:101:ARG:O	10:J:101:ARG:HD2	1.97	0.64
10:J:229:ASP:HA	11:K:151:LYS:HE3	1.79	0.64
25:b:77:LEU:HD21	25:b:80:ILE:HD12	1.79	0.64
1:A:1344:THR:HG23	1:A:1347:ARG:HE	1.62	0.64
1:A:1344:THR:CG2	1:A:1347:ARG:HE	2.10	0.64
3:C:320:PHE:HB2	3:C:429:PHE:HD2	1.62	0.64
6:F:19:U:N3	17:Q:174:ASN:OD1	2.30	0.64
10:J:163:GLN:OE1	10:J:168:THR:HG22	1.97	0.64
13:M:108:MET:HA	13:M:111:ARG:HB3	1.79	0.64
23:W:703:SER:CA	34:x:2:U:O2	2.38	0.64
26:c:77:ASN:OD1	30:g:49:ARG:HD3	1.97	0.64
1:A:1265:PHE:HE1	1:A:1346:PHE:CD1	2.12	0.64
6:F:18:U:HO2'	6:F:19:U:P	2.18	0.64
14:N:245:GLU:HA	14:N:248:ASN:HD22	1.62	0.64
23:W:462:LEU:O	23:W:465:THR:N	2.30	0.64
1:A:1130:ARG:CZ	1:A:1156:HIS:HB3	2.27	0.64
1:A:1161:TYR:HD1	1:A:1170:MET:HG3	1.61	0.64
1:A:1561:LEU:HD12	1:A:1608:LEU:C	2.22	0.64
3:C:430:ARG:O	3:C:431:GLN:C	2.40	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:853:ALA:O	3:C:854:ILE:HB	1.97	0.64
4:D:50:G:H21	5:E:2:U:H6	1.46	0.64
4:D:65:U:O2'	9:I:59:LYS:HE3	1.96	0.64
18:R:202:ARG:HG3	18:R:202:ARG:NH1	2.09	0.64
21:U:692:GLU:HB3	21:U:698:PHE:CE1	2.33	0.64
1:A:701:CYS:SG	1:A:702:GLY:N	2.70	0.64
1:A:948:HIS:HE1	18:R:176:GLU:HG2	1.60	0.64
1:A:959:LEU:HD23	18:R:186:LEU:CB	2.25	0.64
1:A:1417:GLN:HE21	1:A:1783:MET:HB3	1.56	0.64
20:T:134:ARG:NH1	21:U:631:SER:O	2.30	0.64
21:U:632:SER:O	21:U:635:ASP:HB2	1.98	0.64
3:C:363:PRO:O	3:C:364:PHE:HB2	1.95	0.64
13:M:120:LEU:HD13	13:M:122:GLY:H	1.63	0.64
1:A:165:LEU:HD13	1:A:578:MET:HB3	1.78	0.64
1:A:861:GLN:HE21	1:A:1097:HIS:CB	2.08	0.64
1:A:926:LYS:HE2	1:A:1521:ARG:NH2	2.11	0.64
3:C:265:PHE:HD2	3:C:295:ILE:HD12	1.62	0.64
3:C:276:ASP:OD1	3:C:276:ASP:N	2.29	0.64
6:F:1107:C:H6	6:F:1107:C:H5'	1.63	0.64
9:I:115:ILE:HG22	10:J:233:GLU:OE2	1.98	0.64
1:A:1043:ARG:HG3	1:A:1044:GLY:H	1.61	0.64
1:A:1553:ILE:HG13	22:V:211:LEU:HD22	1.75	0.64
1:A:1815:LEU:O	1:A:1818:ARG:N	2.30	0.64
1:A:1896:THR:HA	1:A:1899:TRP:HD1	1.62	0.64
1:A:893:ARG:HH22	1:A:1135:ALA:CB	2.06	0.64
3:C:829:VAL:HG12	3:C:830:ASN:H	1.61	0.64
4:D:86:G:N2	9:I:57:TYR:CD1	2.66	0.64
1:A:299:LYS:HA	1:A:493:MET:HG2	1.80	0.63
21:U:692:GLU:HA	21:U:698:PHE:HA	1.79	0.63
1:A:1842:GLU:OE1	1:A:1845:ASN:ND2	2.31	0.63
3:C:307:ILE:HA	3:C:324:ILE:HD11	1.80	0.63
4:D:51:A:O2'	4:D:52:G:OP1	2.16	0.63
3:C:922:THR:OG1	3:C:925:LEU:O	2.10	0.63
25:i:77:LEU:HD21	25:i:80:ILE:HD12	1.79	0.63
1:A:1499:ARG:NH2	22:V:239:ASN:ND2	2.45	0.63
1:A:1565:THR:CG2	1:A:1823:LEU:CD1	2.72	0.63
3:C:887:ARG:NH2	3:C:938:ARG:CZ	2.58	0.63
7:G:81:ASP:CB	7:G:85:THR:OG1	2.46	0.63
8:H:722:PRO:O	8:H:725:THR:OG1	2.15	0.63
13:M:125:ILE:HD11	13:M:126:THR:HG23	1.81	0.63
19:S:60:ARG:O	19:S:62:THR:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:126:ILE:O	20:T:127:GLN:C	2.41	0.63
22:V:227:ILE:C	22:V:231:ILE:HD12	2.24	0.63
26:j:77:ASN:OD1	30:n:49:ARG:HD3	1.97	0.63
1:A:1367:ILE:HA	1:A:1370:ARG:HG3	1.77	0.63
1:A:1553:ILE:HD11	22:V:211:LEU:CG	2.28	0.63
1:A:817:LYS:NZ	16:P:159:ASP:OD1	2.31	0.63
1:A:1417:GLN:HE22	1:A:1783:MET:CB	2.12	0.63
1:A:1478:GLU:HA	1:A:1478:GLU:OE2	1.98	0.63
3:C:693:ASN:OD1	21:U:642:LEU:CG	2.46	0.63
3:C:861:ILE:HB	3:C:936:ILE:CD1	2.28	0.63
11:K:196:ILE:HB	11:K:200:ASN:ND2	2.13	0.63
13:M:213:SER:HA	13:M:283:ILE:O	1.99	0.63
1:A:1049:LEU:HD12	1:A:1259:LEU:O	1.99	0.63
1:A:1275:MET:O	1:A:1276:GLU:HG2	1.99	0.63
1:A:1344:THR:HA	1:A:1347:ARG:CG	2.28	0.63
3:C:662:SER:O	3:C:665:LYS:NZ	2.26	0.63
8:H:602:MET:HA	8:H:605:PHE:CD2	2.33	0.63
20:T:97:ILE:HD12	20:T:97:ILE:N	2.13	0.63
21:U:658:LEU:CD2	21:U:668:VAL:HG23	2.29	0.63
1:A:1233:ARG:HH22	16:P:127:TRP:HZ3	1.46	0.63
5:E:1:G:C5'	5:E:501:A:C8	2.82	0.63
10:J:70:ASP:CG	10:J:101:ARG:HH21	2.07	0.63
10:J:163:GLN:HB3	10:J:168:THR:CG2	2.29	0.63
10:J:216:ASP:OD1	10:J:217:ILE:N	2.32	0.63
20:T:141:LEU:HD22	20:T:141:LEU:H	1.62	0.63
1:A:1319:ILE:CG2	1:A:1331:VAL:HG13	2.29	0.63
1:A:1402:ALA:O	1:A:1403:SER:HB3	1.98	0.63
6:F:14:C:O2	6:F:16:U:O4	2.17	0.63
3:C:468:LEU:HD21	3:C:577:LEU:HD23	1.81	0.62
15:O:171:THR:CG2	20:T:113:THR:HB	2.23	0.62
20:T:41:LYS:O	20:T:45:LEU:HG	1.98	0.62
1:A:1174:PHE:CE2	1:A:1182:LEU:HD12	2.33	0.62
1:A:1195:PHE:HB3	1:A:1217:ARG:HE	1.64	0.62
6:F:119:G:O5'	26:j:76:ASN:ND2	2.32	0.62
6:F:1098:C:O5'	6:F:1098:C:H6	1.82	0.62
9:I:79:HIS:HD2	10:J:244:PHE:CZ	2.16	0.62
1:A:744:THR:O	1:A:749:ARG:NH2	2.32	0.62
2:B:78:A:O2'	2:B:79:C:O5'	2.15	0.62
2:B:83:C:O2'	2:B:84:A:O5'	2.17	0.62
3:C:885:GLY:HA3	3:C:907:PRO:CG	2.28	0.62
4:D:39:G:O6	14:N:127:ILE:O	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:1120:G:H5''	6:F:1120:G:H8	1.65	0.62
1:A:342:LEU:HD13	1:A:392:ASN:HD22	1.64	0.62
1:A:1159:ARG:O	1:A:1160:LEU:HD23	2.00	0.62
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.34	0.62
2:B:174:G:O5'	26:c:76:ASN:ND2	2.32	0.62
3:C:412:ALA:HA	3:C:415:TYR:CE2	2.33	0.62
3:C:765:VAL:HG22	3:C:775:ILE:HG12	1.82	0.62
3:C:991:LYS:HD2	3:C:992:TYR:HE1	1.63	0.62
5:E:500:A:H2'	5:E:502:C:H5	1.65	0.62
8:H:611:THR:CB	8:H:623:LEU:HD13	2.29	0.62
17:Q:174:ASN:ND2	17:Q:178:TYR:O	2.25	0.62
1:A:1353:THR:O	1:A:1357:LEU:CB	2.47	0.62
1:A:1389:TYR:HE2	1:A:1401:SER:HB3	1.65	0.62
1:A:1567:PHE:CZ	1:A:1825:ILE:CG2	2.77	0.62
1:A:1991:ILE:HG21	1:A:2008:LEU:HD22	1.80	0.62
9:I:123:ASN:ND2	10:J:228:TYR:HE1	1.98	0.62
21:U:677:LYS:HZ2	21:U:677:LYS:C	1.99	0.62
1:A:137:GLU:HG3	12:L:30:LEU:HD13	1.80	0.62
1:A:1335:TRP:CZ2	1:A:1339:LEU:HD12	2.35	0.62
1:A:1553:ILE:CG1	22:V:211:LEU:CD2	2.69	0.62
1:A:864:GLN:NE2	1:A:1100:LYS:H	1.96	0.62
3:C:860:PRO:CD	3:C:908:VAL:CG1	2.77	0.62
6:F:16:U:H4'	6:F:17:U:OP2	1.99	0.62
18:R:188:LYS:CD	18:R:192:GLU:OE2	2.46	0.62
20:T:106:LEU:HD12	20:T:106:LEU:C	2.23	0.62
21:U:246:VAL:O	21:U:249:TYR:N	2.32	0.62
1:A:732:ARG:NH1	4:D:73:A:OP1	2.30	0.62
9:I:38:LEU:HD21	10:J:189:ARG:HD3	1.82	0.62
18:R:198:GLU:HB3	18:R:202:ARG:HH12	1.64	0.62
21:U:680:MET:HE1	21:U:706:LEU:HD21	1.82	0.62
1:A:926:LYS:HE3	1:A:1521:ARG:HH22	1.63	0.62
1:A:1130:ARG:NH2	1:A:1130:ARG:HG2	2.13	0.62
2:B:174:G:H5''	30:g:99:ASP:HB2	1.82	0.62
19:S:72:TRP:O	19:S:73:SER:OG	2.17	0.62
1:A:683:LEU:O	1:A:687:ILE:HG13	2.00	0.62
1:A:847:LYS:HG2	6:F:24:U:C6	2.35	0.62
1:A:900:PHE:CD1	1:A:901:PRO:HD2	2.35	0.62
1:A:1158:ILE:HA	1:A:1172:PHE:CE1	2.35	0.62
1:A:1348:GLU:OE2	1:A:1447:TRP:CA	2.47	0.62
6:F:1099:G:C8	6:F:1100:A:C8	2.87	0.62
15:O:277:VAL:HG13	17:Q:63:ILE:HG22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:24:THR:OG1	20:T:92:ARG:CZ	2.48	0.62
20:T:99:ARG:CD	20:T:103:ILE:HD11	2.30	0.62
20:T:143:TYR:CD2	20:T:146:TRP:CH2	2.88	0.62
21:U:166:ARG:HA	22:V:268:PRO:CB	2.30	0.62
29:f:3:LEU:HD11	30:g:60:ALA:HB1	1.82	0.62
1:A:1309:ILE:HG12	1:A:1356:LEU:HD12	1.82	0.61
1:A:1565:THR:O	1:A:1820:ARG:NE	2.25	0.61
6:F:120:G:N7	26:j:32:LYS:HD2	2.15	0.61
9:I:267:TYR:O	9:I:271:ILE:HD12	2.00	0.61
10:J:65:PHE:HD1	10:J:69:GLU:HB2	1.62	0.61
13:M:12:ILE:HB	17:Q:105:LEU:HD21	1.81	0.61
29:m:3:LEU:HD11	30:n:60:ALA:HB1	1.82	0.61
1:A:341:ALA:HA	1:A:355:LEU:HD23	1.82	0.61
1:A:1499:ARG:HH12	22:V:234:VAL:CG1	2.13	0.61
10:J:12:VAL:HG22	10:J:13:TRP:H	1.65	0.61
10:J:227:ILE:O	11:K:152:ILE:HG22	1.99	0.61
13:M:118:VAL:O	13:M:119:LYS:HB3	1.98	0.61
18:R:200:ILE:HG22	18:R:204:LYS:CE	2.21	0.61
1:A:903:LEU:CB	18:R:180:ASP:OD1	2.47	0.61
1:A:912:LEU:HD11	1:A:951:LEU:HG	1.83	0.61
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.18	0.61
1:A:1458:TRP:CH2	22:V:246:LEU:HD21	2.35	0.61
4:D:89:U:O2	11:K:179:ARG:CG	2.49	0.61
11:K:180:LYS:O	11:K:183:MET:HB2	2.01	0.61
17:Q:217:GLN:HE21	17:Q:217:GLN:N	1.98	0.61
17:Q:220:ARG:HG2	17:Q:220:ARG:HH11	1.65	0.61
21:U:687:ASP:C	21:U:688:ILE:HG13	2.26	0.61
3:C:274:ILE:CG2	3:C:385:PHE:HE2	2.12	0.61
20:T:131:GLU:OE2	21:U:626:LEU:HD11	2.01	0.61
3:C:200:CYS:SG	3:C:210:ILE:HD12	2.40	0.61
6:F:119:G:H5''	30:n:99:ASP:HB2	1.82	0.61
6:F:1116:A:N1	6:F:1117:G:C6	2.68	0.61
17:Q:215:ALA:O	17:Q:219:ILE:HG13	1.99	0.61
1:A:416:GLU:HG2	1:A:418:ASP:H	1.64	0.61
1:A:871:GLY:N	17:Q:198:ASN:ND2	2.49	0.61
1:A:1182:LEU:CD2	16:P:128:ARG:HH22	2.14	0.61
3:C:749:LYS:O	3:C:753:THR:OG1	2.15	0.61
4:D:57:U:H6	4:D:57:U:H5'	1.64	0.61
20:T:137:LYS:NZ	21:U:639:ASP:OD2	2.32	0.61
21:U:668:VAL:HG12	21:U:669:PRO:HD2	1.81	0.61
1:A:697:LYS:NZ	35:A:3000:IHP:P5	2.74	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1011:ASN:ND2	1:A:1012:TRP:N	2.48	0.61
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.83	0.61
2:B:165:A:H2	29:f:2:LYS:HE2	1.58	0.61
2:B:175:G:N7	26:c:32:LYS:HD2	2.15	0.61
9:I:116:ASN:HB2	10:J:230:THR:HG22	1.81	0.61
15:O:379:LYS:HD3	17:Q:47:ARG:NH2	2.15	0.61
20:T:15:ASN:CG	20:T:18:ASP:H	2.08	0.61
21:U:692:GLU:N	21:U:698:PHE:HD1	1.99	0.61
3:C:861:ILE:CD1	3:C:938:ARG:CZ	2.79	0.61
3:C:887:ARG:HG2	3:C:887:ARG:NH1	2.15	0.61
3:C:945:LEU:HD11	3:C:1008:PRO:HG2	1.83	0.61
14:N:254:ILE:O	14:N:258:THR:OG1	2.14	0.61
25:b:86:ASN:ND2	26:c:32:LYS:HD3	2.13	0.61
28:l:20:SER:OG	28:l:30:ARG:HD2	2.01	0.61
1:A:1292:ARG:HG3	1:A:1292:ARG:HH11	1.66	0.61
15:O:259:VAL:HG12	15:O:260:ILE:HG13	1.82	0.61
15:O:382:HIS:CE1	15:O:442:TRP:H	2.19	0.61
1:A:487:ASN:OD1	1:A:488:ARG:N	2.34	0.60
3:C:687:ALA:CB	3:C:689:ILE:CD1	2.75	0.60
3:C:995:ALA:O	3:C:999:ALA:N	2.32	0.60
4:D:56:A:H4'	4:D:57:U:OP1	2.01	0.60
4:D:86:G:N2	9:I:57:TYR:CE1	2.69	0.60
6:F:39:A:H2'	6:F:40:U:H5''	1.81	0.60
12:L:107:ARG:HH21	12:L:147:HIS:CE1	2.18	0.60
17:Q:220:ARG:HH11	17:Q:220:ARG:CG	2.14	0.60
20:T:42:TYR:CE1	20:T:64:PHE:HZ	2.19	0.60
21:U:644:LYS:HB3	21:U:646:TYR:CD1	2.35	0.60
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.60
3:C:769:TYR:CD1	3:C:800:TYR:CE1	2.89	0.60
13:M:18:GLY:O	17:Q:110:HIS:CE1	2.54	0.60
1:A:985:ASP:OD1	10:J:46:ARG:NH1	2.34	0.60
8:H:724:VAL:CA	8:H:727:GLU:CG	2.79	0.60
10:J:90:MET:CE	17:Q:197:ILE:CG2	2.77	0.60
1:A:460:PRO:HG3	3:C:375:GLU:HG3	1.83	0.60
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.37	0.60
3:C:132:ARG:CD	3:C:208:ARG:HG3	2.32	0.60
3:C:727:THR:H	3:C:736:ASP:HB2	1.67	0.60
3:C:761:ALA:HA	3:C:764:ASN:HB2	1.82	0.60
9:I:131:ARG:NE	17:Q:148:HIS:O	2.31	0.60
1:A:1856:ASN:ND2	1:A:1966:SER:O	2.34	0.60
1:A:1862:VAL:HG13	1:A:1870:VAL:HG13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:115:ILE:CG2	10:J:233:GLU:OE2	2.50	0.60
25:b:83:LYS:NZ	26:c:75:CYS:O	2.35	0.60
1:A:376:ARG:HH11	1:A:376:ARG:CG	2.15	0.60
1:A:379:ILE:HG22	1:A:379:ILE:O	2.01	0.60
1:A:766:ILE:HG21	1:A:782:ILE:HG12	1.83	0.60
1:A:1270:LEU:HD12	1:A:1301:TYR:HE2	1.65	0.60
1:A:1328:PHE:CE2	1:A:1371:VAL:HG13	2.36	0.60
3:C:863:GLU:OE2	3:C:934:HIS:CE1	2.54	0.60
14:N:253:LEU:O	14:N:257:ASN:HB2	2.01	0.60
1:A:645:ASP:OD1	1:A:646:ALA:N	2.34	0.60
1:A:1424:HIS:HE1	1:A:1747:ASP:CG	1.99	0.60
3:C:607:LEU:HD22	3:C:668:ILE:HD12	1.83	0.60
4:D:50:G:O2'	4:D:51:A:OP2	2.20	0.60
8:H:673:GLU:CD	8:H:677:SER:CB	2.73	0.60
9:I:155:LEU:HD13	17:Q:34:ILE:HD11	1.83	0.60
25:i:83:LYS:NZ	26:j:75:CYS:O	2.35	0.60
1:A:1367:ILE:CA	1:A:1370:ARG:HG2	2.30	0.60
1:A:1390:THR:CG2	1:A:1394:LEU:HB3	2.32	0.60
2:B:174:G:OP2	26:c:76:ASN:CB	2.49	0.60
3:C:682:SER:HB3	3:C:854:ILE:CG2	2.31	0.60
20:T:42:TYR:HE1	20:T:64:PHE:CZ	2.19	0.60
25:i:86:ASN:ND2	26:j:32:LYS:HD3	2.13	0.60
1:A:1158:ILE:CA	1:A:1172:PHE:HE1	2.15	0.60
1:A:1370:ARG:CG	1:A:1370:ARG:HH11	2.14	0.60
3:C:132:ARG:NH2	28:e:15:GLN:O	2.34	0.60
3:C:362:LYS:HD3	3:C:363:PRO:CD	2.30	0.60
3:C:807:PRO:HG3	3:C:850:LEU:HD23	1.84	0.60
5:E:495:A:C8	5:E:496:U:C5	2.90	0.60
1:A:893:ARG:HH11	1:A:893:ARG:CG	2.12	0.60
1:A:1367:ILE:O	1:A:1370:ARG:HB2	2.02	0.60
10:J:79:GLU:CG	17:Q:202:MET:SD	2.89	0.60
14:N:161:ARG:O	14:N:165:SER:CB	2.50	0.60
23:W:550:SER:O	34:x:7:U:C4	2.55	0.60
1:A:959:LEU:HD22	18:R:186:LEU:HB2	1.83	0.59
3:C:353:TYR:HE2	3:C:363:PRO:CA	2.15	0.59
3:C:501:ILE:HD11	3:C:567:ILE:HD12	1.83	0.59
4:D:28:U:H5''	12:L:118:SER:O	2.02	0.59
20:T:74:LEU:HA	20:T:80:ARG:CB	2.32	0.59
20:T:93:LYS:C	20:T:97:ILE:HD13	2.26	0.59
1:A:161:PHE:CE1	1:A:198:ALA:HA	2.37	0.59
1:A:923:TYR:CZ	1:A:936:GLU:CB	2.75	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.37	0.59
1:A:2025:ILE:HD12	1:A:2058:LEU:HD11	1.84	0.59
18:R:167:GLU:CD	18:R:168:LYS:H	2.09	0.59
1:A:910:LYS:NZ	1:A:1504:TYR:HE2	2.00	0.59
1:A:1292:ARG:HB2	1:A:1292:ARG:NH1	2.18	0.59
5:E:1:G:H5"	5:E:501:A:C8	2.38	0.59
21:U:651:ILE:HD11	21:U:672:GLU:HG3	1.79	0.59
22:V:228:GLU:O	22:V:232:ASN:N	2.28	0.59
1:A:1292:ARG:HH11	1:A:1292:ARG:CG	2.14	0.59
1:A:1335:TRP:CZ2	1:A:1339:LEU:CD1	2.86	0.59
1:A:1512:ARG:NH2	1:A:1525:PHE:O	2.35	0.59
3:C:690:PRO:HB2	3:C:707:SER:OG	2.02	0.59
6:F:119:G:OP2	26:j:76:ASN:CB	2.49	0.59
21:U:648:ILE:HG13	21:U:673:ILE:HG22	1.83	0.59
1:A:903:LEU:HD13	18:R:180:ASP:OD1	2.02	0.59
1:A:1210:ASP:CG	3:C:954:LEU:HD11	2.26	0.59
1:A:1370:ARG:HB3	1:A:1370:ARG:NH1	2.17	0.59
3:C:265:PHE:CD2	3:C:295:ILE:HD12	2.37	0.59
3:C:884:ARG:C	3:C:884:ARG:HD3	2.26	0.59
3:C:989:LEU:CG	3:C:993:ILE:CD1	2.72	0.59
15:O:206:VAL:HG21	15:O:241:THR:HG21	1.83	0.59
1:A:1407:ILE:CD1	1:A:1550:LEU:HD23	2.32	0.59
1:A:1852:VAL:HG22	1:A:1881:THR:HG22	1.84	0.59
2:B:175:G:N1	25:b:33:GLU:O	2.36	0.59
4:D:35:A:C6	12:L:41:LEU:HD21	2.37	0.59
13:M:49:SER:HG	13:M:52:SER:CB	2.13	0.59
15:O:171:THR:CG2	20:T:113:THR:CB	2.73	0.59
17:Q:101:PRO:O	17:Q:103:ASN:N	2.35	0.59
21:U:691:VAL:CG2	21:U:701:ILE:HD12	2.31	0.59
28:l:66:GLY:HA2	28:l:69:ILE:HD12	1.85	0.59
1:A:452:PHE:HZ	3:C:347:ARG:HG3	1.67	0.59
1:A:1047:ALA:N	1:A:1251:TYR:O	2.35	0.59
1:A:1158:ILE:HG13	1:A:1172:PHE:CE1	2.34	0.59
1:A:1343:PHE:CE1	1:A:1350:ILE:CD1	2.61	0.59
4:D:64:U:O2'	4:D:65:U:P	2.61	0.59
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.27	0.59
3:C:860:PRO:HD2	3:C:908:VAL:HG11	1.84	0.59
4:D:85:C:OP1	4:D:85:C:O4'	2.20	0.59
8:H:687:LEU:HD23	8:H:713:ILE:HA	1.84	0.59
14:N:255:ASN:O	14:N:259:ASN:ND2	2.36	0.59
20:T:35:LEU:HB2	20:T:77:ALA:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:GLN:HE21	1:A:709:ARG:HG3	1.68	0.59
1:A:1251:TYR:HE1	1:A:1256:PRO:O	1.84	0.59
1:A:1387:VAL:CG1	1:A:1606:PHE:HZ	2.15	0.59
2:B:167:A:N7	30:g:63:ARG:NE	2.51	0.59
3:C:353:TYR:CE2	3:C:363:PRO:CA	2.85	0.59
3:C:860:PRO:HD2	3:C:908:VAL:CG1	2.32	0.59
10:J:525:ARG:O	10:J:528:GLN:CG	2.51	0.59
28:e:66:GLY:HA2	28:e:69:ILE:HD12	1.85	0.59
1:A:1530:SER:HB3	22:V:204:PHE:CE1	2.37	0.59
1:A:1547:ILE:HA	1:A:1556:ILE:CD1	2.22	0.59
9:I:44:ARG:HD2	10:J:214:ASN:HD21	1.68	0.59
16:P:167:GLN:O	16:P:171:HIS:HB2	2.02	0.59
21:U:658:LEU:HD22	21:U:668:VAL:CG2	2.33	0.59
1:A:318:LEU:HD13	1:A:501:LEU:HD23	1.85	0.58
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.68	0.58
3:C:682:SER:N	3:C:854:ILE:O	2.34	0.58
3:C:686:PHE:HD1	3:C:687:ALA:N	2.01	0.58
5:E:500:A:C4	5:E:502:C:N4	2.71	0.58
8:H:611:THR:CB	8:H:623:LEU:CD1	2.81	0.58
9:I:79:HIS:NE2	10:J:244:PHE:CD1	2.68	0.58
15:O:229:THR:HG21	15:O:272:VAL:H	1.68	0.58
21:U:648:ILE:HG13	21:U:673:ILE:CG2	2.33	0.58
1:A:452:PHE:CE2	3:C:343:ASP:OD2	2.56	0.58
1:A:621:LEU:HD23	1:A:722:LEU:HD21	1.85	0.58
1:A:1195:PHE:HB3	1:A:1217:ARG:NE	2.19	0.58
1:A:1326:THR:O	1:A:1327:THR:HG23	2.02	0.58
1:A:1394:LEU:O	1:A:1609:TRP:NE1	2.36	0.58
1:A:1443:TYR:CD1	1:A:1542:TYR:HB2	2.38	0.58
1:A:1572:GLY:O	1:A:1827:GLN:HA	2.03	0.58
6:F:1102:C:C2'	6:F:1103:C:H6	2.15	0.58
6:F:1116:A:N1	6:F:1117:G:C5	2.71	0.58
14:N:157:GLU:OE2	14:N:161:ARG:NE	2.35	0.58
15:O:200:VAL:HG11	15:O:230:VAL:HG23	1.85	0.58
17:Q:34:ILE:HG23	17:Q:35:ALA:H	1.68	0.58
17:Q:217:GLN:HE21	17:Q:217:GLN:HA	1.67	0.58
21:U:654:ARG:HG2	21:U:654:ARG:HH11	1.67	0.58
21:U:674:ARG:HA	21:U:678:LYS:O	2.02	0.58
1:A:563:ASP:OD1	1:A:564:TRP:N	2.36	0.58
1:A:1366:ARG:NE	2:B:95:C:P	2.76	0.58
1:A:1811:ALA:O	1:A:1814:VAL:N	2.36	0.58
13:M:91:ILE:HD11	13:M:125:ILE:CD1	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:15:ASN:O	20:T:19:VAL:HG23	2.02	0.58
1:A:872:PRO:HB3	17:Q:201:PHE:CZ	2.37	0.58
3:C:277:LEU:HB3	3:C:279:LEU:HD13	1.84	0.58
3:C:510:ARG:HH11	3:C:510:ARG:CG	2.14	0.58
9:I:83:ARG:CZ	10:J:217:ILE:HD13	2.32	0.58
13:M:13:CYS:SG	13:M:16:CYS:N	2.74	0.58
22:V:210:ALA:HB1	22:V:215:GLN:CD	2.29	0.58
23:W:598:GLY:O	23:W:600:HIS:N	2.37	0.58
1:A:472:ASN:HB2	3:C:390:SER:OG	2.04	0.58
1:A:1899:TRP:HE3	1:A:1905:LEU:HD22	1.68	0.58
1:A:1915:GLU:O	1:A:1918:SER:OG	2.17	0.58
3:C:839:ILE:CD1	21:U:647:LEU:HD11	2.29	0.58
10:J:66:SER:OG	10:J:69:GLU:HG2	2.04	0.58
13:M:49:SER:HG	13:M:52:SER:N	2.01	0.58
13:M:103:GLU:OE2	14:N:131:ARG:NH2	2.37	0.58
1:A:379:ILE:HD11	3:C:672:ASP:OD1	2.03	0.58
1:A:488:ARG:C	1:A:489:THR:HG23	2.27	0.58
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.38	0.58
1:A:794:LYS:HB3	1:A:854:ARG:NH1	2.19	0.58
1:A:893:ARG:HG3	1:A:893:ARG:NH1	2.12	0.58
1:A:1390:THR:OG1	1:A:1610:TRP:CZ2	2.56	0.58
13:M:120:LEU:HD13	13:M:121:GLY:H	1.65	0.58
22:V:236:TYR:O	22:V:237:ARG:HB2	2.02	0.58
1:A:905:TYR:HB3	1:A:908:ASP:OD2	2.03	0.58
3:C:679:GLU:O	3:C:813:ILE:HA	2.03	0.58
3:C:884:ARG:HH21	3:C:941:PRO:CG	2.16	0.58
6:F:119:G:C5	29:m:20:LYS:HE2	2.39	0.58
22:V:242:TRP:O	22:V:246:LEU:CB	2.52	0.58
33:r:98:LEU:HD12	33:s:98:LEU:HD23	1.85	0.58
1:A:713:ASN:ND2	2:B:83:C:H4'	2.18	0.58
3:C:247:PHE:HE2	3:C:933:TRP:CZ3	2.22	0.58
5:E:502:C:O2'	5:E:503:A:P	2.62	0.58
8:H:642:GLU:HG3	9:I:329:LEU:CB	2.33	0.58
9:I:205:TRP:CH2	9:I:221:VAL:HG21	2.39	0.58
15:O:187:ASP:OD1	15:O:188:VAL:N	2.36	0.58
1:A:380:ARG:NH1	1:A:380:ARG:HG2	2.17	0.58
1:A:480:TYR:CD2	3:C:275:LEU:HD22	2.39	0.58
1:A:1130:ARG:HH22	1:A:1158:ILE:CB	2.16	0.58
1:A:1390:THR:HB	1:A:1396:GLY:HA3	1.85	0.58
3:C:247:PHE:HE2	3:C:933:TRP:CE3	2.21	0.58
9:I:189:TYR:HB3	9:I:205:TRP:CD1	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:227:ASP:O	9:I:231:ASN:HB2	2.04	0.58
13:M:75:MET:HE1	14:N:130:PHE:HE1	1.69	0.58
14:N:244:LEU:O	14:N:248:ASN:ND2	2.36	0.58
21:U:683:ALA:O	21:U:690:TRP:HD1	1.86	0.58
17:Q:85:SER:O	17:Q:87:ASN:N	2.35	0.58
1:A:886:MET:SD	1:A:1120:VAL:HG22	2.44	0.57
1:A:1335:TRP:CE2	1:A:1339:LEU:HD12	2.39	0.57
1:A:1499:ARG:HH12	22:V:234:VAL:HG13	1.69	0.57
6:F:120:G:N1	25:i:33:GLU:O	2.36	0.57
9:I:89:GLU:CD	10:J:223:PRO:HA	2.28	0.57
14:N:253:LEU:O	14:N:257:ASN:CB	2.52	0.57
23:W:346:GLY:HA3	34:x:5:U:OP1	2.04	0.57
1:A:1281:ASN:ND2	1:A:1285:VAL:HG21	2.19	0.57
1:A:1627:LEU:HD11	1:A:1634:LEU:HG	1.86	0.57
3:C:218:HIS:HB3	3:C:221:PHE:HD2	1.69	0.57
4:D:57:U:C5'	4:D:57:U:C6	2.85	0.57
6:F:112:A:N7	30:n:63:ARG:NE	2.51	0.57
13:M:49:SER:OG	13:M:52:SER:HB3	1.97	0.57
13:M:119:LYS:O	13:M:119:LYS:HD2	2.04	0.57
14:N:23:PRO:O	14:N:37:TRP:NE1	2.30	0.57
18:R:198:GLU:HG2	18:R:202:ARG:NH2	2.19	0.57
21:U:671:PHE:HD1	21:U:682:VAL:O	1.87	0.57
1:A:1265:PHE:CE1	1:A:1346:PHE:HA	2.39	0.57
1:A:1547:ILE:CA	1:A:1556:ILE:HD11	2.22	0.57
19:S:54:SER:O	19:S:58:ARG:HG2	2.04	0.57
1:A:903:LEU:HD23	1:A:904:THR:H	1.70	0.57
1:A:947:PRO:O	1:A:950:THR:HG22	2.04	0.57
3:C:122:TYR:CZ	28:e:82:PRO:HD3	2.39	0.57
3:C:461:LYS:HD3	3:C:461:LYS:N	2.18	0.57
3:C:532:ASP:HB2	3:C:586:MET:CE	2.34	0.57
9:I:124:ARG:HH11	10:J:224:MET:CG	2.18	0.57
14:N:170:ILE:HD13	14:N:173:ILE:HD11	1.87	0.57
20:T:139:PHE:O	20:T:140:ASN:HB2	2.05	0.57
1:A:1067:ASN:HD22	10:J:81:PRO:HB2	1.68	0.57
1:A:1880:PHE:HD1	1:A:1891:LEU:HD21	1.69	0.57
3:C:163:ASP:OD2	3:C:548:ARG:NH1	2.37	0.57
3:C:466:GLY:HA2	3:C:581:LYS:HE2	1.85	0.57
3:C:681:CYS:CA	3:C:850:LEU:HD11	2.35	0.57
3:C:808:LEU:HD23	3:C:987:PRO:HB2	1.83	0.57
5:E:1:G:H5'	5:E:501:A:C8	2.38	0.57
9:I:116:ASN:HB3	10:J:230:THR:HG22	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:TYR:HE1	1:A:701:CYS:HG	1.52	0.57
1:A:1417:GLN:HE21	1:A:1783:MET:HE3	1.69	0.57
1:A:1441:PHE:CD2	1:A:1441:PHE:N	2.73	0.57
1:A:1562:PHE:HB2	1:A:1609:TRP:CH2	2.38	0.57
2:B:174:G:C5	29:f:20:LYS:HE2	2.39	0.57
3:C:811:GLU:HB3	3:C:812:PRO:HD2	1.85	0.57
4:D:91:A:C5	9:I:99:ILE:HD11	2.39	0.57
6:F:16:U:C4'	6:F:17:U:OP2	2.53	0.57
21:U:653:ASN:OD1	21:U:653:ASN:N	2.37	0.57
2:B:174:G:O6	29:f:20:LYS:HB3	2.05	0.57
3:C:686:PHE:CD1	3:C:687:ALA:HB2	2.38	0.57
11:K:196:ILE:HB	11:K:200:ASN:HD21	1.69	0.57
17:Q:111:HIS:O	17:Q:112:ILE:HG13	2.05	0.57
20:T:15:ASN:CG	20:T:18:ASP:HB2	2.29	0.57
31:o:15:TYR:CG	24:h:47:GLU:HG3	2.38	0.57
1:A:522:TYR:CZ	1:A:686:ILE:HD12	2.39	0.57
3:C:418:GLN:HB3	3:C:419:PRO:HD3	1.85	0.57
3:C:830:ASN:HB2	3:C:834:MET:HG2	1.86	0.57
19:S:60:ARG:C	19:S:62:THR:N	2.62	0.57
21:U:246:VAL:O	21:U:247:SER:C	2.47	0.57
22:V:214:ASN:O	22:V:217:ALA:HB3	2.05	0.57
1:A:522:TYR:CE2	1:A:686:ILE:CD1	2.88	0.57
3:C:693:ASN:OD1	21:U:642:LEU:CD2	2.53	0.57
10:J:63:THR:HG22	10:J:93:ARG:HH12	1.70	0.57
21:U:671:PHE:N	21:U:671:PHE:CD1	2.73	0.57
29:m:43:VAL:HG11	29:m:85:ILE:HD12	1.87	0.57
1:A:874:ILE:HD11	1:A:1062:ASP:OD2	2.04	0.57
1:A:1547:ILE:CD1	22:V:211:LEU:CG	2.83	0.57
3:C:467:THR:CG2	3:C:580:VAL:HG23	2.34	0.57
3:C:967:VAL:O	3:C:971:ARG:CG	2.53	0.57
9:I:52:THR:HG22	10:J:213:TYR:HD2	1.70	0.57
1:A:320:ASP:HB3	1:A:483:PRO:HG2	1.86	0.56
1:A:959:LEU:CD2	18:R:186:LEU:HB2	2.32	0.56
1:A:1389:TYR:CE2	1:A:1401:SER:HB3	2.39	0.56
1:A:1560:THR:HB	1:A:1609:TRP:CE2	2.40	0.56
2:B:78:A:O2'	2:B:79:C:P	2.63	0.56
7:G:7:VAL:CG1	7:G:154:VAL:CB	2.72	0.56
9:I:123:ASN:HD21	10:J:228:TYR:HE1	1.53	0.56
15:O:392:MET:HG3	15:O:393:VAL:H	1.70	0.56
1:A:1547:ILE:O	1:A:1552:GLY:N	2.38	0.56
3:C:463:THR:HG21	3:C:490:SER:OG	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:31:A:H3'	6:F:32:G:C3'	2.35	0.56
9:I:40:LEU:HB2	10:J:249:ASN:OD1	2.04	0.56
12:L:27:GLU:OE2	12:L:31:ARG:NE	2.39	0.56
12:L:116:ASN:HD22	13:M:24:ARG:CD	2.18	0.56
18:R:198:GLU:CG	18:R:202:ARG:NH2	2.68	0.56
1:A:863:ARG:NH1	1:A:1101:TYR:CE2	2.72	0.56
1:A:1316:ILE:CD1	1:A:1335:TRP:CZ3	2.78	0.56
1:A:1344:THR:O	1:A:1447:TRP:CZ2	2.55	0.56
1:A:1748:ILE:O	1:A:1751:TYR:N	2.37	0.56
3:C:430:ARG:O	3:C:431:GLN:O	2.22	0.56
3:C:686:PHE:HD1	3:C:687:ALA:HB2	1.68	0.56
6:F:119:G:O6	29:m:20:LYS:HB3	2.05	0.56
11:K:92:ARG:N	11:K:93:GLY:HA3	2.20	0.56
31:o:15:TYR:HB2	24:h:47:GLU:HG3	1.87	0.56
3:C:639:SER:OG	3:C:641:GLU:HB2	2.05	0.56
4:D:50:G:N2	5:E:2:U:H2'	2.20	0.56
5:E:9:U:C4'	5:E:10:U:OP2	2.53	0.56
6:F:31:A:H3'	6:F:32:G:O3'	2.05	0.56
10:J:210:ASP:OD1	10:J:211:ILE:N	2.39	0.56
15:O:188:VAL:HG13	15:O:197:LEU:HD11	1.88	0.56
21:U:165:LEU:N	21:U:207:SER:CB	2.68	0.56
21:U:651:ILE:HD11	21:U:672:GLU:N	2.20	0.56
22:V:236:TYR:CE1	22:V:237:ARG:CG	2.89	0.56
1:A:881:THR:O	1:A:884:SER:OG	2.21	0.56
1:A:1204:ARG:CZ	1:A:1247:PHE:CD2	2.88	0.56
1:A:1309:ILE:HG12	1:A:1356:LEU:CD1	2.36	0.56
3:C:356:LYS:C	3:C:358:ASN:H	2.14	0.56
3:C:706:LEU:HD21	3:C:834:MET:HE1	1.87	0.56
3:C:770:ASN:OD1	3:C:771:GLY:N	2.38	0.56
9:I:265:ALA:O	9:I:269:ILE:HD12	2.05	0.56
10:J:109:GLU:HB2	18:R:196:ARG:HG2	1.86	0.56
21:U:114:TYR:CB	22:V:283:MET:CB	2.84	0.56
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.24	0.56
1:A:1711:VAL:HG11	1:A:1789:ASN:HB3	1.87	0.56
3:C:472:VAL:HB	3:C:575:ALA:O	2.05	0.56
3:C:532:ASP:OD2	3:C:586:MET:CE	2.46	0.56
3:C:979:GLY:HA3	3:C:983:SER:CA	2.34	0.56
3:C:979:GLY:HA3	3:C:983:SER:CB	2.33	0.56
6:F:1116:A:N3	6:F:1117:G:C8	2.74	0.56
1:A:1696:SER:HA	1:A:1759:TYR:CE1	2.34	0.56
2:B:43:G:OP2	3:C:99:LYS:NZ	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:758:ASP:HB3	3:C:761:ALA:HB3	1.87	0.56
4:D:1:G:H2'	4:D:2:U:C6	2.41	0.56
1:A:1130:ARG:HH21	1:A:1130:ARG:CG	2.13	0.56
3:C:775:ILE:HD12	3:C:817:GLN:HE21	1.70	0.56
31:o:34:LEU:CB	24:h:19:LYS:HZ3	2.17	0.56
1:A:1279:VAL:O	1:A:1299:LYS:NZ	2.39	0.56
3:C:108:GLN:O	3:C:109:LEU:HD12	2.05	0.56
3:C:447:GLU:O	3:C:451:ASN:ND2	2.39	0.56
3:C:693:ASN:OD1	21:U:642:LEU:HD21	2.05	0.56
3:C:791:TYR:HA	3:C:794:GLN:HG2	1.87	0.56
6:F:19:U:O4	17:Q:174:ASN:OD1	2.23	0.56
20:T:143:TYR:HD1	20:T:143:TYR:H	1.54	0.56
21:U:648:ILE:HG23	21:U:673:ILE:HG23	1.88	0.56
31:o:44:PRO:O	31:o:69:ASP:CB	2.54	0.56
25:i:77:LEU:HD21	25:i:80:ILE:CD1	2.36	0.56
1:A:653:ILE:HD11	1:A:704:TRP:CE2	2.41	0.56
3:C:829:VAL:O	3:C:830:ASN:ND2	2.39	0.56
22:V:244:THR:OG1	22:V:245:GLN:N	2.39	0.56
29:f:43:VAL:HG11	29:f:85:ILE:HD12	1.87	0.56
1:A:881:THR:CB	16:P:133:PHE:CZ	2.89	0.55
1:A:900:PHE:O	1:A:902:PRO:CD	2.53	0.55
1:A:910:LYS:HZ2	1:A:1504:TYR:HE2	1.53	0.55
4:D:84:C:H4'	9:I:60:ARG:NH1	2.20	0.55
5:E:499:U:C2'	5:E:500:A:H5'	2.37	0.55
10:J:65:PHE:CD2	10:J:101:ARG:HG2	2.41	0.55
12:L:123:ARG:HH11	12:L:153:CYS:HB3	1.71	0.55
20:T:138:HIS:CD2	21:U:629:VAL:HG13	2.41	0.55
22:V:215:GLN:CA	22:V:218:ILE:HB	2.29	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.21	0.55
1:A:1443:TYR:CE1	1:A:1542:TYR:CB	2.88	0.55
3:C:89:PRO:O	15:O:211:LEU:O	2.25	0.55
3:C:884:ARG:HH22	3:C:941:PRO:CD	2.17	0.55
13:M:49:SER:HG	13:M:52:SER:CA	2.18	0.55
13:M:49:SER:HG	13:M:52:SER:HB2	1.67	0.55
15:O:365:PHE:HZ	15:O:373:LEU:HD22	1.70	0.55
1:A:662:GLN:NE2	1:A:1620:TYR:C	2.63	0.55
6:F:1100:A:C2	6:F:1101:C:C2	2.95	0.55
21:U:649:SER:O	21:U:671:PHE:CB	2.52	0.55
1:A:1253:LYS:HG3	1:A:1254:ASN:N	2.21	0.55
1:A:1458:TRP:NE1	1:A:1489:PRO:HD2	2.22	0.55
2:B:79:C:H3'	2:B:79:C:O2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:539:VAL:HG13	3:C:564:ILE:HG23	1.89	0.55
3:C:888:ILE:HD12	3:C:888:ILE:O	2.07	0.55
3:C:986:GLY:O	3:C:988:THR:HG23	2.06	0.55
1:A:1553:ILE:CD1	22:V:211:LEU:HB3	2.35	0.55
3:C:613:ARG:NH1	3:C:614:GLU:OE2	2.40	0.55
10:J:79:GLU:OE2	17:Q:202:MET:CE	2.46	0.55
17:Q:221:SER:O	17:Q:225:LEU:HG	2.06	0.55
21:U:651:ILE:CG1	21:U:672:GLU:HG2	2.36	0.55
1:A:591:LEU:HB3	1:A:599:LEU:HD11	1.89	0.55
1:A:1397:LEU:CD2	1:A:1606:PHE:CE1	2.90	0.55
3:C:860:PRO:HB2	3:C:908:VAL:CB	2.37	0.55
10:J:159:LEU:O	11:K:196:ILE:CD1	2.54	0.55
15:O:138:HIS:CE1	15:O:159:SER:HB2	2.42	0.55
22:V:227:ILE:HG22	22:V:231:ILE:HD11	1.88	0.55
25:b:77:LEU:HD21	25:b:80:ILE:CD1	2.36	0.55
1:A:1049:LEU:CD1	1:A:1260:PHE:HB2	2.31	0.55
1:A:1049:LEU:HD13	1:A:1260:PHE:CB	2.30	0.55
1:A:1210:ASP:OD1	3:C:954:LEU:HD11	2.06	0.55
1:A:1344:THR:CG2	1:A:1347:ARG:HH21	2.20	0.55
3:C:1004:ASN:CB	3:C:1006:LEU:HD21	2.37	0.55
5:E:497:A:C5	5:E:498:C:N4	2.75	0.55
8:H:406:ASN:CB	23:W:575:PRO:CB	2.85	0.55
12:L:126:ARG:HG3	19:S:72:TRP:CE2	2.41	0.55
15:O:171:THR:HG23	20:T:113:THR:HG21	1.87	0.55
15:O:184:THR:O	15:O:201:SER:OG	2.22	0.55
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.89	0.55
1:A:932:SER:O	1:A:936:GLU:CG	2.48	0.55
1:A:934:ARG:HH11	1:A:934:ARG:CG	2.19	0.55
1:A:1293:THR:OG1	1:A:1295:GLN:OE1	2.17	0.55
1:A:1461:TYR:OH	22:V:243:GLU:OE1	2.23	0.55
1:A:1731:LYS:O	1:A:1769:SER:OG	2.20	0.55
3:C:477:ASP:HB2	3:C:628:TYR:CE1	2.42	0.55
4:D:92:C:O2'	4:D:93:A:O4'	2.24	0.55
8:H:606:GLN:HA	8:H:609:GLU:CG	2.37	0.55
8:H:718:SER:HG	8:H:725:THR:HG21	1.68	0.55
13:M:86:LEU:O	13:M:89:HIS:N	2.38	0.55
1:A:1182:LEU:HD23	16:P:128:ARG:NH2	2.18	0.55
1:A:1493:THR:CG2	1:A:1534:GLY:CA	2.85	0.55
6:F:1105:C:N4	32:p:97:LYS:NZ	2.54	0.55
8:H:817:SER:O	10:J:68:GLU:OE2	2.25	0.55
9:I:52:THR:HG22	10:J:213:TYR:CD2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:167:GLN:O	16:P:171:HIS:CB	2.55	0.55
20:T:19:VAL:HG11	20:T:66:LEU:CB	2.37	0.55
1:A:756:LEU:CD2	16:P:8:GLN:NE2	2.45	0.55
1:A:1129:GLU:O	1:A:1132:THR:OG1	2.22	0.55
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.47	0.55
1:A:1305:SER:OG	1:A:1307:GLU:OE1	2.25	0.54
1:A:1390:THR:CG2	1:A:1394:LEU:CB	2.86	0.54
1:A:2012:LEU:HD23	1:A:2015:LEU:HD12	1.89	0.54
3:C:682:SER:O	3:C:854:ILE:O	2.25	0.54
3:C:691:VAL:HG13	3:C:841:LEU:CD1	2.37	0.54
4:D:39:G:N1	14:N:120:TYR:O	2.40	0.54
6:F:1102:C:H2'	6:F:1103:C:H5	1.69	0.54
9:I:99:ILE:O	9:I:102:TRP:N	2.39	0.54
21:U:671:PHE:CD1	21:U:682:VAL:O	2.60	0.54
21:U:699:LYS:HB2	21:U:699:LYS:HZ2	1.71	0.54
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.37	0.54
1:A:1049:LEU:HD11	1:A:1260:PHE:CG	2.42	0.54
1:A:1233:ARG:HD3	16:P:131:THR:HG21	1.88	0.54
1:A:1283:GLU:OE1	1:A:1446:THR:CG2	2.55	0.54
1:A:1419:ASP:HB3	1:A:1803:ARG:CZ	2.37	0.54
1:A:1477:PHE:CD1	1:A:1477:PHE:C	2.85	0.54
3:C:532:ASP:CB	3:C:586:MET:CE	2.84	0.54
3:C:860:PRO:HB2	3:C:908:VAL:HB	1.89	0.54
3:C:886:SER:HB3	3:C:906:VAL:CA	2.33	0.54
4:D:11:U:O4	4:D:15:C:N4	2.41	0.54
10:J:101:ARG:HH21	10:J:105:LEU:HD13	1.72	0.54
10:J:163:GLN:CB	10:J:168:THR:CG2	2.86	0.54
11:K:111:ASN:O	11:K:114:THR:OG1	2.23	0.54
1:A:931:ALA:HA	1:A:934:ARG:HG3	1.88	0.54
1:A:1161:TYR:HD1	1:A:1170:MET:CG	2.20	0.54
1:A:1328:PHE:CD1	1:A:1328:PHE:N	2.73	0.54
1:A:1442:ARG:CZ	1:A:1442:ARG:CB	2.86	0.54
1:A:1443:TYR:OH	1:A:1545:ASP:CB	2.47	0.54
2:B:78:A:H4'	2:B:79:C:OP1	2.07	0.54
3:C:183:GLN:HE22	3:C:654:CYS:HA	1.72	0.54
3:C:356:LYS:C	3:C:358:ASN:N	2.64	0.54
3:C:407:ASN:OD1	3:C:408:LEU:N	2.40	0.54
3:C:952:PRO:HB2	3:C:955:LYS:HB2	1.89	0.54
4:D:53:A:H5'	4:D:54:U:OP2	2.07	0.54
10:J:218:VAL:O	13:M:109:MET:SD	2.65	0.54
11:K:207:LEU:HD22	17:Q:184:ARG:NH2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:150:CYS:SG	12:L:151:ARG:N	2.80	0.54
13:M:61:CYS:O	13:M:72:GLN:NE2	2.40	0.54
14:N:138:TYR:HD1	14:N:183:PHE:HE1	1.55	0.54
19:S:55:GLU:O	19:S:59:ARG:HB2	2.08	0.54
20:T:130:GLY:O	20:T:134:ARG:HG2	2.07	0.54
31:o:68:PRO:O	31:o:69:ASP:CB	2.54	0.54
1:A:380:ARG:HG3	1:A:383:TYR:CE2	2.43	0.54
1:A:1130:ARG:HD3	1:A:1156:HIS:CG	2.42	0.54
3:C:240:ASP:OD1	3:C:269:LYS:HD3	2.07	0.54
3:C:353:TYR:CE2	3:C:363:PRO:HA	2.42	0.54
3:C:468:LEU:HD11	3:C:493:LEU:CD2	2.37	0.54
3:C:863:GLU:CD	3:C:934:HIS:ND1	2.65	0.54
3:C:990:GLU:CA	3:C:998:TYR:CE1	2.90	0.54
6:F:40:U:O2'	6:F:41:C:H5	1.89	0.54
14:N:159:ARG:HD3	14:N:205:LEU:H	1.73	0.54
15:O:190:VAL:HG22	15:O:197:LEU:HD13	1.88	0.54
17:Q:147:LEU:HD12	17:Q:147:LEU:O	2.08	0.54
20:T:141:LEU:CD2	20:T:141:LEU:H	2.19	0.54
3:C:220:ASN:O	3:C:647:ASN:ND2	2.32	0.54
3:C:247:PHE:CD2	3:C:933:TRP:CZ3	2.95	0.54
3:C:355:HIS:CG	3:C:367:VAL:HG21	2.36	0.54
4:D:38:U:O4	14:N:222:LEU:HA	2.08	0.54
6:F:16:U:H3'	6:F:18:U:C4	2.43	0.54
9:I:39:ASP:OD2	10:J:188:ARG:NH1	2.40	0.54
15:O:412:LEU:HD11	20:T:103:ILE:HD13	1.88	0.54
22:V:235:PRO:C	22:V:238:THR:HG1	2.06	0.54
24:a:31:ILE:HD11	24:a:49:ILE:HD12	1.90	0.54
1:A:329:TYR:CE1	3:C:919:ARG:NE	2.75	0.54
1:A:412:GLN:OE1	1:A:412:GLN:N	2.41	0.54
1:A:413:ASN:ND2	1:A:419:THR:OG1	2.41	0.54
3:C:176:ARG:NH2	3:C:179:ASP:OD2	2.40	0.54
3:C:204:GLU:OE1	3:C:204:GLU:HA	2.07	0.54
3:C:463:THR:HG21	3:C:490:SER:CB	2.38	0.54
3:C:755:TYR:HB2	3:C:757:TRP:HB2	1.89	0.54
3:C:795:ILE:HG23	3:C:842:MET:HE3	1.90	0.54
3:C:991:LYS:CG	3:C:992:TYR:CD1	2.89	0.54
3:C:995:ALA:O	3:C:998:TYR:N	2.40	0.54
10:J:65:PHE:CZ	10:J:93:ARG:NE	2.76	0.54
16:P:8:GLN:O	16:P:10:GLU:N	2.41	0.54
21:U:693:ASP:OD1	21:U:699:LYS:HD2	2.08	0.54
21:U:696:GLY:C	21:U:697:THR:HG23	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1883:ASN:HD21	1:A:1886:THR:HG23	1.73	0.54
3:C:139:ILE:HD12	3:C:252:LEU:HD22	1.90	0.54
3:C:271:ASP:CG	36:C:1500:GTP:HN21	2.15	0.54
3:C:660:ARG:HH22	3:C:670:ILE:HD12	1.72	0.54
3:C:932:PHE:O	3:C:933:TRP:HD1	1.91	0.54
4:D:64:U:HO2'	4:D:65:U:P	2.31	0.54
8:H:682:LYS:O	8:H:686:ILE:HG12	2.08	0.54
10:J:209:THR:HB	13:M:108:MET:CE	2.36	0.54
22:V:214:ASN:OD1	22:V:215:GLN:N	2.41	0.54
22:V:236:TYR:CD1	22:V:236:TYR:C	2.85	0.54
22:V:241:GLU:O	22:V:245:GLN:CG	2.56	0.54
1:A:930:ASN:O	1:A:934:ARG:N	2.38	0.54
1:A:1539:LEU:HB3	1:A:1543:ARG:NH1	2.22	0.54
3:C:752:ARG:HD3	3:C:759:SER:HA	1.90	0.54
6:F:16:U:H3'	6:F:18:U:O4	2.06	0.54
8:H:726:ARG:HA	8:H:729:TYR:CD2	2.42	0.54
10:J:39:LEU:HD12	10:J:158:ARG:HH11	1.71	0.54
19:S:55:GLU:O	19:S:58:ARG:HG3	2.08	0.54
21:U:166:ARG:N	22:V:268:PRO:CB	2.71	0.54
1:A:168:LEU:HD21	1:A:626:LEU:HD21	1.90	0.54
1:A:185:GLN:HE21	1:A:263:PRO:HD3	1.72	0.54
1:A:234:PHE:HD2	1:A:699:PRO:HG2	1.72	0.54
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.42	0.54
1:A:1963:LEU:HD13	1:A:1965:PHE:HE2	1.73	0.54
3:C:437:ASP:OD1	3:C:441:ARG:NH2	2.41	0.54
5:E:499:U:O5'	5:E:499:U:H6	1.91	0.54
1:A:480:TYR:CE2	3:C:275:LEU:HD22	2.43	0.54
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.29	0.54
1:A:1161:TYR:CD1	1:A:1170:MET:HG3	2.43	0.54
3:C:137:GLY:N	3:C:232:SER:OG	2.40	0.54
3:C:675:THR:CG2	3:C:909:ILE:CD1	2.55	0.54
10:J:223:PRO:O	10:J:224:MET:HG2	2.08	0.54
21:U:123:SER:O	21:U:124:SER:C	2.51	0.54
21:U:646:TYR:CD1	21:U:646:TYR:N	2.75	0.54
1:A:420:PRO:HG2	1:A:423:PHE:HB2	1.90	0.53
1:A:1051:GLU:HB3	1:A:1167:ARG:HH21	1.72	0.53
1:A:1474:ARG:HH12	22:V:232:ASN:C	2.09	0.53
1:A:1990:ASN:ND2	1:A:1993:ASP:O	2.40	0.53
2:B:174:G:H8	30:g:99:ASP:OD2	1.91	0.53
3:C:766:TRP:CG	3:C:792:LYS:HE3	2.43	0.53
3:C:1002:ARG:NH1	3:C:1002:ARG:HG2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:41:C:O2'	6:F:42:U:O5'	2.25	0.53
20:T:19:VAL:HG11	20:T:66:LEU:CG	2.39	0.53
21:U:128:VAL:O	21:U:129:VAL:C	2.51	0.53
21:U:556:GLU:O	21:U:557:HIS:C	2.51	0.53
21:U:683:ALA:O	21:U:690:TRP:CD1	2.61	0.53
21:U:687:ASP:O	21:U:688:ILE:HG13	2.08	0.53
22:V:235:PRO:HD2	22:V:238:THR:OG1	2.08	0.53
1:A:1049:LEU:N	1:A:1249:SER:O	2.41	0.53
1:A:1268:ARG:HE	1:A:1301:TYR:HD2	1.56	0.53
1:A:1414:TRP:CZ3	1:A:1416:LYS:HB2	2.41	0.53
6:F:119:G:H8	30:n:99:ASP:OD2	1.91	0.53
6:F:1114:G:H8	6:F:1114:G:O5'	1.91	0.53
9:I:51:ARG:NE	9:I:75:GLU:OE2	2.40	0.53
10:J:202:LYS:O	10:J:204:LYS:N	2.37	0.53
15:O:365:PHE:CZ	15:O:373:LEU:HD22	2.44	0.53
20:T:124:LEU:O	20:T:125:GLN:C	2.51	0.53
21:U:119:GLU:O	21:U:120:ASP:C	2.51	0.53
21:U:201:LEU:O	21:U:202:LEU:C	2.51	0.53
21:U:501:LEU:O	21:U:502:ARG:C	2.51	0.53
22:V:236:TYR:CZ	22:V:237:ARG:HG2	2.43	0.53
1:A:805:PRO:HG2	1:A:808:ILE:HD12	1.90	0.53
1:A:1283:GLU:OE1	1:A:1446:THR:HG21	2.07	0.53
1:A:1315:ARG:O	1:A:1319:ILE:HD12	2.09	0.53
1:A:1377:SER:HB3	1:A:1379:MET:H	1.73	0.53
6:F:1114:G:H2'	6:F:1115:G:C8	2.43	0.53
19:S:55:GLU:OE2	19:S:58:ARG:HD2	2.08	0.53
21:U:126:ASP:O	21:U:127:GLU:C	2.51	0.53
21:U:441:PHE:O	21:U:442:ILE:C	2.51	0.53
21:U:655:TYR:CD1	21:U:655:TYR:C	2.87	0.53
21:U:696:GLY:O	21:U:697:THR:HG23	2.09	0.53
21:U:704:TRP:CE3	21:U:705:ALA:N	2.76	0.53
1:A:1348:GLU:OE2	1:A:1448:GLU:N	2.41	0.53
1:A:1493:THR:HG21	1:A:1534:GLY:N	2.24	0.53
3:C:689:ILE:O	3:C:709:SER:HA	2.08	0.53
6:F:1103:C:C6	6:F:1114:G:N2	2.76	0.53
13:M:16:CYS:HB2	14:N:104:LEU:HD21	1.89	0.53
17:Q:220:ARG:HB2	17:Q:220:ARG:CZ	2.38	0.53
21:U:121:TYR:O	21:U:122:LEU:C	2.51	0.53
22:V:301:LEU:O	22:V:302:GLU:C	2.51	0.53
33:r:102:LEU:O	33:r:105:LEU:CG	2.57	0.53
1:A:366:GLU:HG3	1:A:372:ARG:CZ	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:124:ARG:HD3	10:J:224:MET:HG3	1.91	0.53
21:U:439:ILE:O	21:U:440:ILE:C	2.51	0.53
21:U:440:ILE:O	21:U:441:PHE:C	2.51	0.53
21:U:442:ILE:O	21:U:443:LYS:C	2.52	0.53
21:U:478:LEU:O	21:U:479:GLU:C	2.51	0.53
21:U:500:LYS:O	21:U:501:LEU:C	2.51	0.53
21:U:688:ILE:HG22	21:U:689:LEU:N	2.24	0.53
22:V:302:GLU:O	22:V:303:LYS:C	2.51	0.53
31:o:53:PRO:CA	24:h:98:GLU:O	2.56	0.53
1:A:1392:LYS:HE2	1:A:1398:GLY:HA3	1.91	0.53
6:F:19:U:N3	17:Q:178:TYR:HB2	2.22	0.53
8:H:560:ALA:HA	8:H:570:THR:HG21	1.89	0.53
21:U:202:LEU:O	21:U:203:GLY:C	2.51	0.53
21:U:365:ILE:O	21:U:366:MET:C	2.51	0.53
1:A:878:GLU:O	1:A:881:THR:OG1	2.27	0.53
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.43	0.53
1:A:1348:GLU:OE2	1:A:1447:TRP:HB2	2.08	0.53
3:C:355:HIS:HB2	3:C:364:PHE:CD2	2.43	0.53
3:C:862:TYR:CD1	3:C:930:LEU:HB3	2.44	0.53
9:I:199:MET:O	9:I:202:TRP:N	2.41	0.53
9:I:238:TRP:HD1	9:I:242:GLU:OE2	1.91	0.53
12:L:54:GLN:HB2	19:S:69:TRP:CE2	2.44	0.53
20:T:123:LEU:O	20:T:124:LEU:C	2.52	0.53
1:A:299:LYS:HA	1:A:493:MET:CG	2.39	0.53
3:C:291:ILE:O	3:C:294:ASN:N	2.41	0.53
3:C:689:ILE:HG22	3:C:690:PRO:N	2.23	0.53
4:D:59:A:H3'	4:D:60:G:H5''	1.90	0.53
5:E:496:U:H3'	5:E:497:A:H5''	1.91	0.53
6:F:1105:C:H42	32:p:97:LYS:NZ	2.07	0.53
22:V:297:ARG:O	22:V:298:LEU:C	2.51	0.53
1:A:1304:VAL:HG11	1:A:1356:LEU:HD12	1.90	0.53
3:C:889:TYR:C	3:C:890:LYS:HG2	2.32	0.53
20:T:20:LEU:CD2	20:T:67:LEU:CG	2.87	0.53
21:U:393:ARG:O	21:U:394:ILE:C	2.51	0.53
22:V:291:ARG:O	22:V:292:LYS:C	2.51	0.53
9:I:116:ASN:C	10:J:230:THR:HG22	2.34	0.53
10:J:46:ARG:O	10:J:50:LEU:HB2	2.08	0.53
10:J:218:VAL:O	13:M:109:MET:CE	2.56	0.53
14:N:76:PHE:HB2	14:N:91:HIS:CD2	2.43	0.53
17:Q:35:ALA:O	17:Q:37:ASN:N	2.42	0.53
21:U:557:HIS:O	21:U:558:SER:C	2.51	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:294:VAL:O	22:V:295:GLU:C	2.52	0.53
22:V:295:GLU:O	22:V:296:MET:C	2.52	0.53
1:A:697:LYS:HG2	35:A:3000:IHP:O46	2.09	0.52
1:A:874:ILE:O	1:A:875:THR:CB	2.57	0.52
1:A:1282:ASP:OD1	1:A:1283:GLU:N	2.36	0.52
3:C:692:SER:OG	3:C:704:PRO:HA	2.08	0.52
3:C:860:PRO:HG2	3:C:908:VAL:HG11	1.90	0.52
6:F:39:A:C2'	6:F:40:U:C5'	2.87	0.52
6:F:41:C:H2'	6:F:42:U:C6	2.44	0.52
13:M:87:ARG:NH1	13:M:122:GLY:C	2.67	0.52
21:U:499:LYS:O	21:U:500:LYS:C	2.51	0.52
21:U:656:THR:OG1	21:U:698:PHE:CE2	2.33	0.52
21:U:677:LYS:C	21:U:678:LYS:HD2	2.34	0.52
22:V:292:LYS:O	22:V:293:LYS:C	2.51	0.52
1:A:872:PRO:CB	17:Q:201:PHE:CE1	2.89	0.52
1:A:903:LEU:C	1:A:904:THR:HG23	2.33	0.52
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.41	0.52
1:A:1144:PHE:CE2	1:A:1145:MET:HE2	2.44	0.52
1:A:1801:SER:O	1:A:1804:THR:OG1	2.19	0.52
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.44	0.52
2:B:31:G:C2'	2:B:32:G:H5'	2.40	0.52
3:C:355:HIS:CA	3:C:364:PHE:CE2	2.91	0.52
3:C:503:ASP:HB2	3:C:506:GLN:HG2	1.92	0.52
3:C:991:LYS:CG	3:C:992:TYR:CE1	2.93	0.52
5:E:495:A:N7	5:E:496:U:C4	2.77	0.52
6:F:1097:G:N1	6:F:1119:C:N3	2.50	0.52
6:F:1116:A:C5	6:F:1117:G:C5	2.97	0.52
15:O:151:ASP:HB3	15:O:153:GLU:HG2	1.91	0.52
15:O:155:PHE:CZ	15:O:415:ILE:HG12	2.44	0.52
21:U:200:GLU:O	21:U:201:LEU:C	2.51	0.52
21:U:660:TYR:C	21:U:660:TYR:CD1	2.88	0.52
22:V:298:LEU:O	22:V:299:GLN:C	2.51	0.52
1:A:923:TYR:N	1:A:923:TYR:CD1	2.73	0.52
1:A:1443:TYR:CE1	1:A:1542:TYR:HB2	2.45	0.52
1:A:1561:LEU:HD21	1:A:1612:PRO:HD3	1.91	0.52
1:A:1902:GLN:HG2	1:A:1908:LEU:HD22	1.91	0.52
3:C:242:VAL:HG21	3:C:272:ARG:HG2	1.90	0.52
3:C:857:LEU:HD22	3:C:967:VAL:HG23	1.91	0.52
5:E:499:U:H2'	5:E:500:A:H5'	1.91	0.52
20:T:111:SER:O	20:T:112:SER:C	2.51	0.52
21:U:303:ALA:O	21:U:304:TYR:C	2.51	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:367:GLU:O	21:U:368:GLU:C	2.52	0.52
21:U:476:TYR:O	21:U:477:GLU:C	2.51	0.52
21:U:692:GLU:N	21:U:698:PHE:CD1	2.78	0.52
1:A:687:ILE:HD13	1:A:703:PHE:HD2	1.74	0.52
1:A:1342:LEU:HD12	1:A:1342:LEU:C	2.34	0.52
1:A:1376:ASN:O	1:A:1377:SER:OG	2.18	0.52
4:D:2:U:H2'	4:D:3:U:H6	1.74	0.52
21:U:366:MET:O	21:U:367:GLU:C	2.51	0.52
24:h:31:ILE:HD11	24:h:49:ILE:HD12	1.90	0.52
1:A:742:VAL:HG22	15:O:221:TYR:OH	2.10	0.52
1:A:1213:MET:SD	1:A:1250:VAL:HG23	2.50	0.52
1:A:1420:THR:O	1:A:1718:HIS:CG	2.62	0.52
1:A:2007:ARG:HH12	1:A:2048:TRP:HB3	1.73	0.52
3:C:768:PHE:HB3	3:C:773:VAL:HG23	1.90	0.52
3:C:978:THR:C	3:C:983:SER:HB2	2.33	0.52
21:U:127:GLU:O	21:U:128:VAL:C	2.51	0.52
21:U:177:LEU:O	21:U:178:LYS:C	2.51	0.52
1:A:606:THR:OG1	1:A:609:GLU:HG2	2.09	0.52
1:A:1342:LEU:O	1:A:1346:PHE:HD2	1.92	0.52
3:C:362:LYS:CD	3:C:363:PRO:HD2	2.39	0.52
3:C:681:CYS:HB2	3:C:853:ALA:HB3	1.91	0.52
3:C:995:ALA:O	3:C:998:TYR:HB3	2.10	0.52
20:T:144:GLY:C	20:T:146:TRP:H	2.18	0.52
21:U:438:ASP:O	21:U:439:ILE:C	2.52	0.52
21:U:558:SER:O	21:U:559:LEU:C	2.51	0.52
21:U:678:LYS:CD	21:U:678:LYS:N	2.73	0.52
22:V:241:GLU:O	22:V:245:GLN:HG3	2.10	0.52
22:V:296:MET:O	22:V:297:ARG:C	2.51	0.52
33:r:124:ALA:O	33:r:127:LEU:CG	2.58	0.52
1:A:803:GLY:O	17:Q:166:PRO:HG2	2.09	0.52
1:A:868:GLN:O	17:Q:198:ASN:HB2	2.10	0.52
3:C:277:LEU:HB3	3:C:279:LEU:CD1	2.40	0.52
4:D:49:A:C2'	4:D:50:G:H5'	2.40	0.52
6:F:1102:C:O2'	6:F:1103:C:H5'	2.10	0.52
15:O:201:SER:OG	15:O:202:GLU:N	2.43	0.52
21:U:118:ASN:O	21:U:119:GLU:C	2.52	0.52
21:U:122:LEU:O	21:U:123:SER:C	2.52	0.52
21:U:176:ILE:O	21:U:177:LEU:C	2.52	0.52
1:A:244:ASP:OD1	1:A:596:ASN:ND2	2.42	0.52
1:A:881:THR:HB	16:P:133:PHE:CE1	2.45	0.52
3:C:1004:ASN:HB3	3:C:1006:LEU:HD21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:498:C:H6	5:E:498:C:O5'	1.93	0.52
6:F:1116:A:N6	6:F:1117:G:C6	2.77	0.52
14:N:96:GLU:HG2	14:N:188:TYR:CE2	2.39	0.52
21:U:437:SER:O	21:U:438:ASP:C	2.52	0.52
21:U:477:GLU:O	21:U:478:LEU:C	2.52	0.52
21:U:641:CYS:CB	21:U:648:ILE:HD11	2.39	0.52
1:A:1283:GLU:HB2	1:A:1446:THR:HG21	1.92	0.52
1:A:1292:ARG:NH1	1:A:1292:ARG:CB	2.73	0.52
1:A:1390:THR:HG22	1:A:1394:LEU:CG	2.39	0.52
1:A:1407:ILE:HD13	1:A:1550:LEU:HD23	1.92	0.52
3:C:532:ASP:HB2	3:C:586:MET:HE2	1.91	0.52
5:E:493:A:H2'	5:E:494:G:O4'	2.09	0.52
6:F:16:U:H3'	6:F:18:U:H5	1.74	0.52
9:I:38:LEU:HD21	10:J:189:ARG:CD	2.40	0.52
20:T:125:GLN:O	20:T:126:ILE:C	2.52	0.52
1:A:939:LEU:HD23	1:A:939:LEU:C	2.33	0.52
1:A:1122:ASP:OD2	1:A:1163:ARG:NE	2.28	0.52
1:A:1604:ARG:HA	1:A:1640:THR:HG21	1.90	0.52
1:A:1658:HIS:NE2	1:A:1700:ASP:OD2	2.42	0.52
3:C:316:THR:OG1	36:C:1500:GTP:N7	2.42	0.52
15:O:379:LYS:HD3	17:Q:47:ARG:HH22	1.75	0.52
17:Q:220:ARG:CZ	17:Q:220:ARG:CB	2.87	0.52
18:R:168:LYS:NZ	18:R:168:LYS:CB	2.73	0.52
20:T:131:GLU:O	20:T:134:ARG:HG3	2.09	0.52
21:U:675:ASN:CG	21:U:678:LYS:HZ2	2.18	0.52
31:o:53:PRO:CB	24:h:99:ASP:CA	2.88	0.52
1:A:177:GLU:HB3	1:A:712:LEU:HD11	1.91	0.51
1:A:310:ASN:OD1	1:A:313:ARG:NH2	2.43	0.51
1:A:484:PHE:O	1:A:485:PRO:C	2.52	0.51
1:A:1547:ILE:HG23	1:A:1556:ILE:CD1	2.30	0.51
3:C:292:ILE:HG12	3:C:311:ILE:HD13	1.91	0.51
3:C:461:LYS:CD	3:C:461:LYS:N	2.73	0.51
3:C:860:PRO:O	3:C:908:VAL:N	2.33	0.51
4:D:14:C:H4'	4:D:15:C:O5'	2.10	0.51
4:D:41:A:H2'	4:D:42:A:H5'	1.92	0.51
17:Q:37:ASN:ND2	17:Q:145:PRO:HD3	2.25	0.51
17:Q:101:PRO:C	17:Q:103:ASN:H	2.16	0.51
21:U:120:ASP:O	21:U:121:TYR:C	2.52	0.51
21:U:124:SER:O	21:U:125:GLU:C	2.51	0.51
1:A:376:ARG:CG	1:A:376:ARG:NH1	2.73	0.51
1:A:856:TRP:CD1	16:P:174:VAL:HG11	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1337:THR:O	1:A:1341:SER:OG	2.19	0.51
1:A:1575:TRP:HE3	1:A:1605:ARG:NH1	1.89	0.51
3:C:692:SER:HA	3:C:841:LEU:CD2	2.41	0.51
10:J:110:ASP:OD1	10:J:111:SER:N	2.42	0.51
10:J:160:LEU:C	11:K:196:ILE:HG23	2.35	0.51
13:M:25:MET:HB2	13:M:45:HIS:O	2.10	0.51
17:Q:217:GLN:CA	17:Q:217:GLN:NE2	2.73	0.51
19:S:68:PRO:HD2	19:S:69:TRP:CZ3	2.44	0.51
20:T:113:THR:O	20:T:114:ILE:C	2.51	0.51
21:U:415:ILE:O	21:U:416:GLU:C	2.51	0.51
21:U:644:LYS:HB3	21:U:646:TYR:CE2	2.45	0.51
22:V:227:ILE:CG2	22:V:231:ILE:HD11	2.41	0.51
22:V:290:GLN:O	22:V:291:ARG:C	2.51	0.51
25:b:27:VAL:HG22	25:b:92:SER:HB2	1.91	0.51
34:x:5:U:O2'	34:x:6:U:H5'	2.09	0.51
1:A:1158:ILE:HG13	1:A:1172:PHE:HE1	1.65	0.51
1:A:1265:PHE:CZ	1:A:1346:PHE:HA	2.45	0.51
3:C:629:TYR:OH	3:C:658:ASP:OD2	2.19	0.51
4:D:51:A:H4'	4:D:52:G:OP1	2.10	0.51
6:F:41:C:HO2'	6:F:42:U:C5'	2.22	0.51
20:T:99:ARG:HD3	20:T:103:ILE:HD11	1.91	0.51
21:U:304:TYR:O	21:U:305:ARG:C	2.52	0.51
21:U:417:ALA:O	21:U:418:LYS:C	2.52	0.51
1:A:1328:PHE:HE1	1:A:1603:ASN:ND2	2.08	0.51
1:A:1907:GLN:O	1:A:1911:TRP:HD1	1.94	0.51
3:C:103:HIS:CD2	3:C:104:THR:HG23	2.45	0.51
3:C:326:GLU:O	3:C:329:SER:N	2.43	0.51
4:D:66:C:C6	4:D:66:C:C3'	2.93	0.51
5:E:15:U:OP1	14:N:174:ARG:NH2	2.38	0.51
15:O:414:LEU:HB3	15:O:426:TRP:HB2	1.92	0.51
17:Q:216:ARG:HH11	17:Q:216:ARG:HB2	1.76	0.51
21:U:117:GLU:O	21:U:118:ASN:C	2.51	0.51
21:U:164:GLU:CB	21:U:208:LEU:N	2.74	0.51
3:C:854:ILE:HG22	3:C:854:ILE:O	2.10	0.51
6:F:1116:A:C5	6:F:1117:G:N7	2.79	0.51
9:I:49:ARG:NH1	10:J:181:ARG:HH21	2.09	0.51
9:I:185:VAL:HA	9:I:188:ILE:HD12	1.93	0.51
9:I:225:ALA:O	9:I:228:THR:OG1	2.25	0.51
10:J:218:VAL:O	13:M:109:MET:HE1	2.11	0.51
13:M:39:LEU:CD1	13:M:111:ARG:HG3	2.30	0.51
16:P:134:GLY:O	16:P:135:ARG:NE	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:51:PHE:HE1	19:S:55:GLU:HG3	1.74	0.51
20:T:112:SER:O	20:T:113:THR:C	2.52	0.51
21:U:502:ARG:O	21:U:503:SER:C	2.51	0.51
21:U:656:THR:CB	21:U:698:PHE:CE2	2.93	0.51
21:U:682:VAL:HG11	21:U:689:LEU:CD2	2.40	0.51
25:i:27:VAL:HG22	25:i:92:SER:HB2	1.91	0.51
1:A:590:TYR:OH	1:A:609:GLU:OE1	2.18	0.51
1:A:744:THR:HG22	4:D:75:A:OP1	2.11	0.51
1:A:859:ASN:ND2	16:P:170:LEU:HD12	2.26	0.51
1:A:903:LEU:O	1:A:904:THR:OG1	2.21	0.51
1:A:923:TYR:HE2	1:A:936:GLU:C	2.19	0.51
1:A:1130:ARG:NH2	1:A:1130:ARG:CG	2.73	0.51
1:A:1849:LYS:HG2	1:A:1932:GLN:HB2	1.93	0.51
3:C:510:ARG:CG	3:C:510:ARG:NH1	2.73	0.51
5:E:492:U:H2'	5:E:493:A:C8	2.46	0.51
6:F:14:C:C2	6:F:16:U:O4	2.64	0.51
10:J:95:ALA:O	10:J:98:CYS:N	2.42	0.51
15:O:407:PHE:CE1	15:O:414:LEU:HD13	2.46	0.51
20:T:146:TRP:HZ2	21:U:643:GLU:CD	2.19	0.51
22:V:293:LYS:O	22:V:294:VAL:C	2.51	0.51
1:A:453:THR:HB	3:C:357:GLY:O	2.11	0.51
1:A:1387:VAL:HG13	1:A:1606:PHE:CZ	2.45	0.51
1:A:1540:ASN:O	1:A:1541:ALA:C	2.53	0.51
3:C:274:ILE:HB	3:C:382:TYR:HE1	1.70	0.51
3:C:918:LEU:HD23	3:C:928:CYS:HB2	1.93	0.51
11:K:196:ILE:H	11:K:200:ASN:HD22	1.58	0.51
20:T:97:ILE:CD1	20:T:97:ILE:N	2.73	0.51
31:o:15:TYR:CG	24:h:47:GLU:CB	2.93	0.51
34:x:8:U:O2'	34:x:9:U:OP2	2.24	0.51
1:A:905:TYR:HB3	1:A:908:ASP:OD1	2.10	0.51
1:A:1130:ARG:HH22	1:A:1158:ILE:C	2.19	0.51
1:A:1161:TYR:CD1	1:A:1170:MET:HE3	2.45	0.51
1:A:1843:LEU:HD22	1:A:1851:PHE:HZ	1.76	0.51
3:C:671:SER:OG	3:C:672:ASP:N	2.44	0.51
3:C:766:TRP:CE3	3:C:792:LYS:HG3	2.45	0.51
4:D:41:A:C8	14:N:34:TYR:CE2	2.99	0.51
4:D:66:C:H6	4:D:66:C:H3'	1.75	0.51
10:J:160:LEU:HA	11:K:196:ILE:HG23	1.93	0.51
10:J:219:TYR:CZ	17:Q:135:VAL:HG21	2.46	0.51
16:P:8:GLN:C	16:P:10:GLU:H	2.18	0.51
20:T:136:LEU:O	20:T:140:ASN:N	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:143:TYR:HD2	20:T:146:TRP:CZ3	2.29	0.51
21:U:125:GLU:O	21:U:126:ASP:C	2.52	0.51
21:U:243:SER:O	21:U:247:SER:N	2.33	0.51
21:U:392:PRO:O	21:U:393:ARG:C	2.51	0.51
21:U:640:TYR:CD1	21:U:640:TYR:C	2.89	0.51
34:x:6:U:H2'	34:x:7:U:C6	2.46	0.51
1:A:515:PRO:HD3	1:A:689:TYR:HH	1.73	0.51
4:D:52:G:HO2'	4:D:53:A:C4'	2.24	0.51
20:T:141:LEU:CD2	20:T:141:LEU:N	2.73	0.51
2:B:79:C:H3'	2:B:80:G:H5'	1.93	0.51
3:C:132:ARG:HD3	3:C:208:ARG:HG3	1.93	0.51
3:C:271:ASP:O	3:C:275:LEU:HB2	2.11	0.51
6:F:21:G:N7	16:P:6:ARG:HD2	2.26	0.51
10:J:230:THR:O	10:J:232:THR:N	2.36	0.51
13:M:211:ASP:HA	13:M:285:ARG:O	2.11	0.51
15:O:410:THR:O	20:T:99:ARG:NH2	2.44	0.51
17:Q:220:ARG:NH1	17:Q:220:ARG:CB	2.73	0.51
21:U:589:ASP:O	21:U:590:GLU:C	2.51	0.51
1:A:867:ILE:CD1	1:A:1101:TYR:CD1	2.75	0.50
1:A:1567:PHE:CE1	1:A:1827:GLN:HB2	2.46	0.50
1:A:2009:THR:O	1:A:2013:ARG:HG3	2.11	0.50
20:T:110:GLU:O	20:T:111:SER:C	2.51	0.50
21:U:305:ARG:O	21:U:306:MET:C	2.51	0.50
22:V:228:GLU:O	22:V:232:ASN:CB	2.58	0.50
1:A:140:ARG:HH21	1:A:252:GLU:HB2	1.74	0.50
1:A:618:SER:OG	1:A:725:TYR:HB3	2.12	0.50
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.44	0.50
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.11	0.50
18:R:200:ILE:CG2	18:R:204:LYS:CE	2.86	0.50
21:U:391:SER:O	21:U:392:PRO:C	2.51	0.50
21:U:416:GLU:O	21:U:417:ALA:C	2.51	0.50
1:A:649:LEU:O	1:A:652:GLY:N	2.45	0.50
1:A:1011:ASN:HD22	1:A:1012:TRP:N	2.09	0.50
1:A:1292:ARG:NH1	1:A:1292:ARG:CG	2.73	0.50
1:A:1862:VAL:HA	1:A:1871:ALA:O	2.12	0.50
1:A:1899:TRP:HH2	1:A:1909:ALA:HA	1.75	0.50
3:C:576:THR:HG22	3:C:592:PHE:HD2	1.77	0.50
15:O:204:LYS:HG2	15:O:225:SER:HA	1.93	0.50
26:j:74:ARG:HD3	30:n:101:VAL:O	2.12	0.50
1:A:402:TRP:CZ3	3:C:188:GLY:HA2	2.46	0.50
1:A:462:LEU:HD12	3:C:403:ASN:ND2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:952:ASN:ND2	18:R:179:ASP:CG	2.68	0.50
3:C:223:ASP:CG	3:C:647:ASN:HD21	2.19	0.50
3:C:888:ILE:HD12	3:C:888:ILE:C	2.37	0.50
4:D:87:U:C4'	4:D:87:U:OP1	2.59	0.50
12:L:143:HIS:CD2	14:N:63:ARG:HH21	2.29	0.50
17:Q:220:ARG:NE	17:Q:220:ARG:CA	2.73	0.50
19:S:60:ARG:C	19:S:62:THR:H	2.17	0.50
20:T:94:THR:O	20:T:97:ILE:N	2.45	0.50
1:A:143:ILE:HG13	1:A:144:ASN:N	2.25	0.50
1:A:168:LEU:O	1:A:171:ALA:N	2.44	0.50
1:A:326:ASN:ND2	3:C:924:GLY:O	2.45	0.50
1:A:868:GLN:HE22	1:A:1100:LYS:HZ3	1.59	0.50
1:A:947:PRO:HA	1:A:950:THR:HG22	1.93	0.50
1:A:1265:PHE:CD1	1:A:1346:PHE:HD1	2.29	0.50
3:C:691:VAL:HG13	3:C:841:LEU:HD11	1.94	0.50
8:H:606:GLN:HA	8:H:609:GLU:HG3	1.93	0.50
10:J:13:TRP:CE2	10:J:51:ARG:HD2	2.46	0.50
25:i:86:ASN:HD21	26:j:32:LYS:NZ	2.09	0.50
33:t:124:ALA:O	33:t:127:LEU:CG	2.59	0.50
1:A:376:ARG:O	1:A:377:VAL:O	2.29	0.50
1:A:1048:VAL:CG1	1:A:1248:VAL:CG1	2.90	0.50
1:A:1275:MET:C	1:A:1277:GLU:H	2.19	0.50
1:A:1490:ARG:NH1	1:A:1536:LEU:O	2.44	0.50
3:C:251:GLN:NE2	3:C:255:GLN:HE21	2.10	0.50
3:C:689:ILE:HD12	3:C:689:ILE:H	1.74	0.50
9:I:182:TRP:O	9:I:186:ARG:NH1	2.45	0.50
10:J:14:THR:HG23	10:J:17:GLU:H	1.77	0.50
14:N:4:TRP:HZ3	14:N:5:ARG:CZ	2.25	0.50
15:O:238:LEU:HD21	17:Q:74:ILE:HD13	1.92	0.50
18:R:198:GLU:CB	18:R:202:ARG:NH2	2.73	0.50
21:U:364:HIS:O	21:U:365:ILE:C	2.51	0.50
21:U:644:LYS:CG	21:U:646:TYR:CE2	2.92	0.50
21:U:671:PHE:CE1	21:U:684:LEU:HD21	2.47	0.50
21:U:702:TYR:CD2	21:U:704:TRP:HZ2	2.27	0.50
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.46	0.50
3:C:428:ILE:HG22	3:C:429:PHE:CD1	2.47	0.50
3:C:794:GLN:HB3	3:C:838:ILE:HG21	1.94	0.50
6:F:1107:C:H5'	6:F:1107:C:C6	2.44	0.50
15:O:160:ASN:HA	15:O:184:THR:OG1	2.11	0.50
20:T:139:PHE:O	20:T:140:ASN:CB	2.60	0.50
33:q:100:SER:O	33:q:103:ASP:CG	2.55	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:LEU:HD11	1:A:987:LEU:CD2	2.42	0.50
1:A:1370:ARG:CG	1:A:1370:ARG:NH1	2.73	0.50
1:A:1424:HIS:CE1	1:A:1747:ASP:OD2	2.65	0.50
2:B:75:A:H61	3:C:101:GLN:HE21	1.59	0.50
2:B:174:G:OP2	26:c:76:ASN:HB2	2.12	0.50
3:C:164:MET:HG2	3:C:175:LEU:HD13	1.94	0.50
4:D:51:A:H62	5:E:2:U:H1'	1.77	0.50
4:D:56:A:H2'	4:D:57:U:C6	2.46	0.50
14:N:72:PHE:CE2	14:N:94:PRO:HG3	2.47	0.50
20:T:146:TRP:CZ2	21:U:643:GLU:OE1	2.65	0.50
21:U:166:ARG:CA	22:V:268:PRO:CB	2.89	0.50
21:U:637:VAL:C	21:U:641:CYS:SG	2.90	0.50
22:V:299:GLN:O	22:V:300:ALA:C	2.52	0.50
1:A:191:VAL:HA	1:A:201:PHE:O	2.12	0.50
1:A:1011:ASN:HD22	1:A:1011:ASN:C	2.19	0.50
1:A:1440:ILE:O	1:A:1441:PHE:C	2.54	0.50
3:C:867:THR:O	3:C:926:GLY:HA2	2.11	0.50
13:M:82:ILE:HG23	13:M:86:LEU:HD23	1.93	0.50
21:U:634:LYS:CE	21:U:638:GLU:OE2	2.59	0.50
25:b:86:ASN:HD21	26:c:32:LYS:NZ	2.09	0.50
1:A:470:LEU:HB3	1:A:471:PRO:HD2	1.94	0.49
1:A:1304:VAL:HG11	1:A:1356:LEU:HD11	1.94	0.49
1:A:1547:ILE:HG22	1:A:1552:GLY:CA	2.34	0.49
12:L:114:THR:OG1	12:L:118:SER:HA	2.12	0.49
13:M:87:ARG:HH11	13:M:122:GLY:C	2.20	0.49
15:O:156:ILE:HG12	15:O:166:VAL:HG22	1.94	0.49
1:A:867:ILE:CD1	1:A:1101:TYR:CE1	2.92	0.49
1:A:872:PRO:CD	17:Q:201:PHE:CE1	2.95	0.49
1:A:1048:VAL:HA	1:A:1249:SER:O	2.12	0.49
1:A:1290:ASP:CG	1:A:1297:THR:HG23	2.37	0.49
1:A:1342:LEU:HD12	1:A:1346:PHE:HD2	1.77	0.49
1:A:1422:ILE:CD1	1:A:1785:ASP:OD2	2.53	0.49
3:C:686:PHE:CD1	3:C:687:ALA:N	2.79	0.49
3:C:787:LEU:HD12	3:C:790:LYS:HD2	1.94	0.49
5:E:493:A:H2'	5:E:494:G:C1'	2.42	0.49
11:K:182:GLN:O	11:K:186:ALA:HB2	2.12	0.49
14:N:73:CYS:HB2	14:N:89:TYR:HB2	1.93	0.49
15:O:397:GLU:HG3	15:O:400:ARG:HH12	1.77	0.49
16:P:134:GLY:O	16:P:135:ARG:HB2	2.11	0.49
21:U:648:ILE:HA	21:U:673:ILE:HG22	1.94	0.49
22:V:215:GLN:HA	22:V:218:ILE:CB	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:HD11	1:A:571:LEU:HD11	1.93	0.49
1:A:380:ARG:HG2	1:A:380:ARG:HH11	1.76	0.49
1:A:570:GLN:O	1:A:574:GLN:HG2	2.12	0.49
1:A:868:GLN:NE2	1:A:1100:LYS:NZ	2.59	0.49
1:A:931:ALA:N	1:A:934:ARG:NH1	2.60	0.49
1:A:1336:ASN:ND2	1:A:1400:ILE:HG13	2.27	0.49
1:A:1393:GLU:HG2	1:A:1570:TRP:CZ2	2.43	0.49
1:A:1484:TRP:CZ3	1:A:1495:PHE:CD2	3.00	0.49
3:C:354:TYR:C	3:C:354:TYR:CD2	2.90	0.49
3:C:362:LYS:HD3	3:C:363:PRO:HD2	1.93	0.49
3:C:806:GLY:H	3:C:810:GLU:HA	1.76	0.49
10:J:513:ILE:HA	10:J:516:LYS:CG	2.43	0.49
18:R:198:GLU:CB	18:R:202:ARG:CZ	2.88	0.49
33:q:20:ARG:CB	33:r:53:ILE:CB	2.90	0.49
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.47	0.49
1:A:1252:SER:OG	1:A:1255:ASN:CB	2.60	0.49
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.47	0.49
3:C:246:THR:HG23	3:C:248:VAL:HG12	1.94	0.49
3:C:362:LYS:CG	3:C:363:PRO:CD	2.85	0.49
3:C:855:PRO:C	3:C:856:ILE:HG23	2.38	0.49
3:C:884:ARG:HH22	3:C:941:PRO:HD3	1.74	0.49
14:N:206:LEU:HD23	14:N:208:SER:O	2.12	0.49
15:O:152:ASN:ND2	15:O:409:LYS:HB3	2.20	0.49
21:U:654:ARG:HH11	21:U:654:ARG:CG	2.24	0.49
22:V:202:GLN:HA	22:V:205:GLN:OE1	2.12	0.49
22:V:300:ALA:O	22:V:301:LEU:C	2.51	0.49
1:A:376:ARG:NH1	3:C:910:GLU:OE2	2.46	0.49
1:A:380:ARG:HH11	1:A:380:ARG:CG	2.26	0.49
1:A:839:HIS:ND1	1:A:839:HIS:O	2.45	0.49
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.47	0.49
1:A:1530:SER:HB3	22:V:204:PHE:HE1	1.77	0.49
3:C:869:HIS:HD2	3:C:925:LEU:HB3	1.78	0.49
4:D:91:A:N3	9:I:99:ILE:HD11	2.25	0.49
6:F:1105:C:N4	32:p:97:LYS:HZ1	2.10	0.49
6:F:1120:G:H8	6:F:1120:G:C5'	2.25	0.49
9:I:136:TRP:CZ3	9:I:159:TRP:HB2	2.47	0.49
12:L:143:HIS:O	12:L:151:ARG:HG2	2.12	0.49
14:N:4:TRP:NE1	14:N:92:HIS:HB3	2.27	0.49
15:O:221:TYR:O	15:O:251:TRP:HH2	1.96	0.49
17:Q:43:PHE:CD1	17:Q:147:LEU:HD13	2.47	0.49
1:A:168:LEU:HB3	1:A:622:MET:CE	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1184:ASP:O	1:A:1188:ALA:HB2	2.13	0.49
1:A:1499:ARG:HH12	22:V:234:VAL:CB	2.25	0.49
9:I:38:LEU:HD22	10:J:189:ARG:NE	2.28	0.49
9:I:114:CYS:SG	10:J:237:ILE:CG1	3.00	0.49
9:I:238:TRP:HD1	9:I:242:GLU:CD	2.20	0.49
13:M:5:ILE:HG22	13:M:42:THR:HG23	1.94	0.49
13:M:17:LEU:HD13	17:Q:105:LEU:HD23	1.93	0.49
15:O:306:HIS:NE2	17:Q:147:LEU:HD11	2.27	0.49
22:V:214:ASN:O	22:V:218:ILE:HG13	2.12	0.49
1:A:831:ARG:NH2	1:A:978:ILE:HG13	2.27	0.49
1:A:1290:ASP:OD2	1:A:1297:THR:HG21	2.13	0.49
1:A:1387:VAL:HG13	1:A:1606:PHE:HZ	1.78	0.49
1:A:1695:ASN:O	1:A:1759:TYR:OH	2.16	0.49
3:C:161:ILE:HG22	3:C:163:ASP:H	1.77	0.49
3:C:738:ASP:HA	3:C:768:PHE:CZ	2.48	0.49
15:O:348:GLU:CD	15:O:349:LYS:H	2.21	0.49
3:C:463:THR:CG2	3:C:490:SER:OG	2.61	0.49
3:C:499:VAL:O	3:C:536:SER:HA	2.13	0.49
10:J:228:TYR:HA	11:K:152:ILE:HG23	1.91	0.49
22:V:303:LYS:O	22:V:304:THR:C	2.51	0.49
1:A:168:LEU:N	1:A:169:PRO:HD2	2.28	0.49
1:A:372:ARG:CZ	3:C:641:GLU:OE2	2.56	0.49
1:A:861:GLN:HG2	1:A:1097:HIS:CG	2.48	0.49
1:A:929:LEU:HD22	1:A:933:GLU:HB2	1.92	0.49
1:A:1048:VAL:CG1	1:A:1248:VAL:HG13	2.43	0.49
3:C:89:PRO:HA	15:O:212:GLU:O	2.11	0.49
3:C:416:ASP:HB2	3:C:419:PRO:HD2	1.95	0.49
3:C:861:ILE:HD11	3:C:938:ARG:HD2	1.94	0.49
7:G:86:LEU:O	7:G:89:GLU:CG	2.61	0.49
9:I:145:SER:HA	11:K:112:LEU:HD11	1.95	0.49
11:K:184:GLN:HA	11:K:187:LYS:NZ	2.26	0.49
20:T:96:ASP:OD1	20:T:96:ASP:N	2.42	0.49
21:U:164:GLU:C	21:U:207:SER:CB	2.86	0.49
26:c:74:ARG:HD3	30:g:101:VAL:O	2.12	0.49
3:C:675:THR:OG1	3:C:676:VAL:N	2.44	0.49
4:D:2:U:H2'	4:D:3:U:C6	2.48	0.49
9:I:106:ILE:HG12	9:I:122:MET:HE3	1.94	0.49
9:I:187:GLU:O	9:I:190:SER:HB3	2.13	0.49
11:K:102:LYS:NZ	11:K:106:GLU:OE2	2.40	0.49
15:O:326:ALA:HB2	15:O:356:LEU:HD11	1.95	0.49
1:A:1348:GLU:CG	1:A:1447:TRP:H	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:232:SER:OG	3:C:234:LEU:O	2.31	0.48
3:C:271:ASP:OD2	36:C:1500:GTP:C2	2.64	0.48
3:C:353:TYR:HE2	3:C:363:PRO:HD3	1.77	0.48
3:C:468:LEU:O	3:C:578:TYR:HA	2.12	0.48
15:O:437:GLU:N	15:O:438:PRO:HD3	2.27	0.48
21:U:675:ASN:ND2	21:U:678:LYS:HZ2	2.07	0.48
1:A:291:LYS:HE2	1:A:292:LYS:HD3	1.94	0.48
1:A:367:PHE:HB2	3:C:608:GLN:OE1	2.13	0.48
1:A:930:ASN:O	1:A:934:ARG:HG3	2.13	0.48
1:A:1319:ILE:CG2	1:A:1331:VAL:CG1	2.91	0.48
1:A:1687:HIS:CG	1:A:1688:PRO:HD2	2.48	0.48
3:C:604:LYS:HG3	3:C:643:VAL:CG1	2.43	0.48
3:C:990:GLU:HB2	3:C:998:TYR:CE2	2.42	0.48
10:J:75:ASP:O	10:J:79:GLU:HG2	2.13	0.48
15:O:229:THR:HG21	15:O:272:VAL:N	2.28	0.48
16:P:132:ALA:C	16:P:133:PHE:CD1	2.86	0.48
1:A:416:GLU:HG2	1:A:418:ASP:N	2.27	0.48
1:A:856:TRP:CD1	16:P:174:VAL:HG21	2.49	0.48
1:A:1251:TYR:CE1	1:A:1256:PRO:O	2.65	0.48
1:A:1411:ASP:C	1:A:1743:TYR:OH	2.53	0.48
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.14	0.48
3:C:887:ARG:NH1	3:C:887:ARG:CG	2.73	0.48
4:D:66:C:H5'	4:D:66:C:H6	1.76	0.48
9:I:45:GLU:OE2	9:I:48:ARG:NH1	2.45	0.48
12:L:116:ASN:HD22	13:M:24:ARG:HD2	1.78	0.48
20:T:93:LYS:O	20:T:96:ASP:HB2	2.13	0.48
3:C:355:HIS:HB3	3:C:364:PHE:HZ	1.65	0.48
3:C:602:VAL:HG11	3:C:908:VAL:CG2	2.41	0.48
3:C:693:ASN:HD22	3:C:693:ASN:C	2.20	0.48
3:C:832:ASP:HA	3:C:835:LYS:HG2	1.95	0.48
3:C:863:GLU:OE2	3:C:934:HIS:CG	2.67	0.48
5:E:14:U:O4'	14:N:183:PHE:HE2	1.96	0.48
23:W:462:LEU:O	23:W:464:SER:CA	2.54	0.48
1:A:688:TYR:O	1:A:692:ASN:HB2	2.13	0.48
1:A:1094:ASP:OD1	6:F:25:A:N3	2.47	0.48
1:A:1468:ALA:HA	1:A:1473:ARG:HG2	1.95	0.48
1:A:1773:VAL:HA	1:A:1788:GLY:HA2	1.94	0.48
3:C:738:ASP:HA	3:C:768:PHE:HZ	1.78	0.48
3:C:758:ASP:OD1	3:C:759:SER:N	2.47	0.48
3:C:796:ILE:HG13	3:C:800:TYR:CE2	2.49	0.48
3:C:810:GLU:CD	3:C:976:ILE:HD13	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:115:ILE:CA	10:J:233:GLU:OE2	2.61	0.48
1:A:772:GLU:HG3	1:A:773:SER:H	1.78	0.48
1:A:1253:LYS:HB2	1:A:1253:LYS:HE3	1.64	0.48
1:A:1445:THR:HG23	1:A:1450:GLU:OE2	2.13	0.48
3:C:693:ASN:C	3:C:693:ASN:ND2	2.71	0.48
6:F:1116:A:N6	6:F:1117:G:O6	2.46	0.48
9:I:122:MET:HA	9:I:122:MET:CE	2.41	0.48
13:M:80:TRP:CE3	14:N:253:LEU:HD21	2.48	0.48
15:O:112:VAL:O	15:O:115:TYR:N	2.46	0.48
21:U:640:TYR:CD2	21:U:703:LEU:HD22	2.49	0.48
1:A:1343:PHE:HA	1:A:1350:ILE:HD12	1.90	0.48
3:C:468:LEU:CD1	3:C:493:LEU:HD23	2.43	0.48
3:C:991:LYS:CD	3:C:992:TYR:CE1	2.94	0.48
6:F:1109:C:N4	32:p:108:THR:HA	2.28	0.48
21:U:677:LYS:HB2	21:U:677:LYS:HZ3	1.79	0.48
21:U:701:ILE:HG22	21:U:705:ALA:HB3	1.95	0.48
1:A:468:LEU:HD12	1:A:469:ILE:HG12	1.95	0.48
1:A:484:PHE:CD1	1:A:484:PHE:C	2.91	0.48
1:A:1051:GLU:HG2	1:A:1169:TYR:CD1	2.49	0.48
1:A:1344:THR:HG23	1:A:1347:ARG:NE	2.26	0.48
1:A:1416:LYS:HG2	1:A:1417:GLN:N	2.28	0.48
3:C:231:ALA:HB2	3:C:473:LEU:HD11	1.95	0.48
3:C:681:CYS:SG	3:C:816:VAL:HG13	2.54	0.48
3:C:767:SER:OG	3:C:796:ILE:HD13	2.13	0.48
8:H:726:ARG:HA	8:H:729:TYR:CE2	2.48	0.48
12:L:133:ALA:O	12:L:137:GLY:N	2.45	0.48
14:N:22:ILE:O	14:N:22:ILE:HG13	2.12	0.48
14:N:62:THR:HG21	14:N:89:TYR:O	2.14	0.48
15:O:161:ASP:O	15:O:162:THR:OG1	2.23	0.48
22:V:246:LEU:HD23	22:V:246:LEU:O	2.14	0.48
1:A:133:GLU:OE2	1:A:561:THR:HG23	2.14	0.48
1:A:428:LEU:CD2	3:C:898:PRO:HD3	2.44	0.48
1:A:532:ASN:ND2	2:B:84:A:OP2	2.45	0.48
1:A:872:PRO:CD	17:Q:201:PHE:CZ	2.95	0.48
3:C:115:LYS:HB2	3:C:159:LYS:HG2	1.95	0.48
3:C:144:SER:HA	3:C:240:ASP:OD1	2.13	0.48
3:C:362:LYS:CD	3:C:363:PRO:CD	2.91	0.48
9:I:140:LEU:HD21	9:I:155:LEU:HG	1.95	0.48
17:Q:220:ARG:O	17:Q:224:GLU:HG2	2.14	0.48
1:A:697:LYS:HZ2	35:A:3000:IHP:P5	2.36	0.48
1:A:864:GLN:OE1	1:A:1098:VAL:O	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1047:ALA:O	1:A:1250:VAL:HA	2.14	0.48
1:A:1296:ARG:CB	1:A:1296:ARG:NH1	2.73	0.48
3:C:122:TYR:CG	28:e:81:ALA:HB3	2.49	0.48
3:C:772:ASN:HD21	3:C:803:VAL:CG2	2.27	0.48
3:C:862:TYR:HD1	3:C:931:TYR:N	2.11	0.48
3:C:990:GLU:HG3	3:C:998:TYR:CG	2.49	0.48
11:K:184:GLN:HA	11:K:187:LYS:HZ3	1.79	0.48
14:N:64:GLY:O	14:N:68:GLY:N	2.46	0.48
14:N:105:ARG:HG2	14:N:109:LEU:HD11	1.95	0.48
17:Q:220:ARG:NH1	17:Q:220:ARG:CG	2.73	0.48
21:U:164:GLU:CB	21:U:208:LEU:H	2.27	0.48
1:A:404:ASN:CG	3:C:927:MET:HE1	2.39	0.47
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.96	0.47
2:B:30:A:H2'	2:B:31:G:O4'	2.14	0.47
6:F:15:C:HO2'	6:F:16:U:P	2.31	0.47
6:F:119:G:N7	29:m:20:LYS:CE	2.77	0.47
6:F:1099:G:N3	6:F:1099:G:C5'	2.73	0.47
9:I:79:HIS:HD2	10:J:244:PHE:CD1	1.82	0.47
15:O:331:ILE:HD12	15:O:376:TYR:HE2	1.79	0.47
18:R:198:GLU:C	18:R:202:ARG:NH1	2.72	0.47
1:A:402:TRP:CG	1:A:402:TRP:O	2.67	0.47
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.49	0.47
3:C:315:SER:HB3	3:C:320:PHE:CE1	2.50	0.47
3:C:602:VAL:HG13	3:C:860:PRO:HG2	1.96	0.47
3:C:667:GLU:OE1	3:C:667:GLU:N	2.48	0.47
4:D:35:A:HO2'	14:N:75:PHE:HZ	1.57	0.47
6:F:119:G:OP2	26:j:76:ASN:HB2	2.12	0.47
9:I:200:GLN:OE1	9:I:200:GLN:N	2.40	0.47
10:J:581:GLN:O	10:J:584:LEU:CG	2.63	0.47
12:L:13:PRO:HG2	12:L:77:LEU:HA	1.96	0.47
12:L:131:GLU:OE2	12:L:135:LYS:NZ	2.46	0.47
15:O:319:LYS:O	17:Q:57:LEU:HB3	2.13	0.47
21:U:650:LYS:O	21:U:670:LEU:O	2.31	0.47
1:A:179:MET:HE1	1:A:653:ILE:HD12	1.95	0.47
1:A:581:LEU:O	1:A:585:ARG:HB2	2.13	0.47
1:A:926:LYS:CE	1:A:1521:ARG:CZ	2.85	0.47
1:A:1033:ASN:HD22	1:A:1288:LEU:HB3	1.79	0.47
1:A:1080:ASP:HB3	10:J:82:ASN:ND2	2.29	0.47
1:A:1130:ARG:O	1:A:1133:ASP:HB2	2.14	0.47
1:A:1382:ARG:HA	1:A:1616:ARG:HD3	1.96	0.47
10:J:101:ARG:HD2	10:J:101:ARG:C	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:160:LEU:CA	11:K:196:ILE:HG23	2.44	0.47
11:K:190:TYR:HE2	11:K:195:PHE:HZ	1.61	0.47
18:R:200:ILE:O	18:R:204:LYS:HG3	2.14	0.47
1:A:757:GLU:HA	1:A:757:GLU:OE2	2.14	0.47
1:A:1458:TRP:CH2	22:V:246:LEU:CD2	2.97	0.47
1:A:1566:GLY:HA3	1:A:1820:ARG:HH21	1.78	0.47
1:A:2060:LEU:HD11	1:A:2083:ILE:HD11	1.95	0.47
3:C:681:CYS:HA	3:C:855:PRO:HA	1.96	0.47
3:C:683:ASN:HB2	3:C:854:ILE:HG13	1.96	0.47
6:F:17:U:H4'	6:F:18:U:OP1	2.13	0.47
9:I:124:ARG:NH1	10:J:224:MET:HG2	2.27	0.47
10:J:39:LEU:CD1	10:J:158:ARG:HD2	2.45	0.47
1:A:376:ARG:NH1	1:A:376:ARG:HG3	2.29	0.47
1:A:1386:ALA:O	1:A:1390:THR:OG1	2.33	0.47
1:A:1404:HIS:C	1:A:1404:HIS:ND1	2.73	0.47
1:A:1677:GLN:HB3	1:A:1706:VAL:HB	1.96	0.47
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.45	0.47
1:A:1993:ASP:CG	1:A:2038:HIS:HB3	2.38	0.47
1:A:2071:ILE:HA	1:A:2074:LEU:HD12	1.96	0.47
3:C:675:THR:CG2	3:C:909:ILE:HB	2.41	0.47
3:C:968:MET:O	3:C:972:ARG:NH1	2.48	0.47
4:D:65:U:O2'	9:I:59:LYS:CE	2.63	0.47
4:D:91:A:C6	9:I:99:ILE:HD11	2.50	0.47
6:F:1100:A:C2	6:F:1101:C:N1	2.82	0.47
9:I:65:MET:HE3	9:I:95:ASP:HB3	1.95	0.47
15:O:327:CYS:SG	15:O:328:THR:N	2.87	0.47
15:O:373:LEU:HD21	15:O:402:VAL:HG21	1.96	0.47
22:V:214:ASN:O	22:V:217:ALA:N	2.47	0.47
1:A:220:THR:O	1:A:224:MET:HG2	2.15	0.47
1:A:1292:ARG:NH1	1:A:1292:ARG:C	2.73	0.47
1:A:2050:THR:O	1:A:2053:SER:OG	2.22	0.47
3:C:856:ILE:HA	3:C:944:VAL:HG13	1.93	0.47
3:C:857:LEU:HD23	3:C:966:PHE:HB2	1.96	0.47
3:C:990:GLU:CA	3:C:998:TYR:CD1	2.97	0.47
14:N:72:PHE:HE1	14:N:90:LEU:HD12	1.80	0.47
22:V:219:GLN:O	22:V:223:LYS:HG3	2.15	0.47
1:A:421:ALA:HB3	1:A:469:ILE:HD12	1.96	0.47
1:A:653:ILE:HD11	1:A:704:TRP:NE1	2.30	0.47
1:A:1182:LEU:CD2	16:P:128:ARG:NH2	2.77	0.47
1:A:1863:HIS:CD2	1:A:1873:LYS:HD2	2.49	0.47
1:A:1880:PHE:HA	1:A:1891:LEU:HD23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2041:PRO:HG2	1:A:2043:PHE:HE2	1.80	0.47
3:C:437:ASP:O	3:C:440:THR:N	2.47	0.47
3:C:857:LEU:CD2	3:C:966:PHE:CB	2.92	0.47
11:K:159:LYS:O	11:K:160:LEU:HB2	2.15	0.47
13:M:125:ILE:CD1	13:M:125:ILE:C	2.86	0.47
22:V:227:ILE:HG22	22:V:231:ILE:CD1	2.44	0.47
25:b:34:GLN:HE21	25:b:37:ILE:HD12	1.79	0.47
33:q:51:VAL:CG2	33:r:20:ARG:CB	2.77	0.47
1:A:780:ARG:NH2	16:P:9:LEU:HD21	2.30	0.47
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.96	0.47
1:A:1417:GLN:HB2	1:A:1783:MET:CE	2.38	0.47
1:A:1920:LEU:O	1:A:1923:SER:OG	2.32	0.47
3:C:116:THR:O	3:C:117:ARG:C	2.56	0.47
6:F:1115:G:H2'	6:F:1116:A:H8	1.80	0.47
10:J:65:PHE:CE1	10:J:93:ARG:NE	2.83	0.47
28:l:39:SER:O	28:l:41:ASN:N	2.48	0.47
1:A:984:VAL:HG12	1:A:985:ASP:N	2.30	0.47
1:A:1011:ASN:ND2	1:A:1011:ASN:C	2.73	0.47
1:A:1390:THR:HG21	1:A:1394:LEU:HB3	1.96	0.47
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.80	0.47
3:C:136:VAL:O	3:C:212:PHE:HA	2.15	0.47
3:C:223:ASP:OD2	3:C:647:ASN:ND2	2.39	0.47
3:C:274:ILE:CG2	3:C:385:PHE:CE2	2.90	0.47
3:C:861:ILE:CG2	3:C:905:GLN:HB3	2.45	0.47
3:C:869:HIS:CD2	3:C:925:LEU:HD13	2.50	0.47
8:H:645:ARG:NE	8:H:669:TYR:OH	2.48	0.47
10:J:148:GLU:HA	10:J:151:MET:HE3	1.97	0.47
10:J:243:GLN:O	10:J:247:LYS:HG2	2.15	0.47
21:U:678:LYS:HD2	21:U:678:LYS:N	2.30	0.47
1:A:470:LEU:O	1:A:473:THR:HG22	2.15	0.47
1:A:1050:LEU:HD23	1:A:1050:LEU:HA	1.81	0.47
2:B:175:G:H4'	2:B:176:A:O4'	2.15	0.47
3:C:282:MET:HE1	3:C:371:PRO:HD3	1.96	0.47
3:C:336:ILE:HD11	3:C:341:ILE:HG22	1.97	0.47
3:C:354:TYR:HD2	3:C:354:TYR:O	1.98	0.47
3:C:1002:ARG:HG2	3:C:1002:ARG:HH11	1.80	0.47
4:D:31:G:O6	13:M:47:LYS:CE	2.63	0.47
9:I:149:VAL:HA	9:I:152:VAL:HG22	1.97	0.47
10:J:35:LYS:O	10:J:38:SER:OG	2.23	0.47
13:M:105:LYS:O	13:M:109:MET:HB2	2.14	0.47
22:V:229:LYS:O	22:V:233:GLU:CB	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:o:34:LEU:CB	24:h:19:LYS:HZ1	2.28	0.47
25:i:34:GLN:HE21	25:i:37:ILE:HD12	1.79	0.47
1:A:515:PRO:CD	1:A:689:TYR:HH	2.28	0.46
1:A:929:LEU:CD2	1:A:933:GLU:CB	2.84	0.46
1:A:1414:TRP:HB2	1:A:1558:GLU:CG	2.43	0.46
2:B:167:A:N7	30:g:63:ARG:CZ	2.78	0.46
3:C:855:PRO:HG2	3:C:944:VAL:HG21	1.97	0.46
4:D:49:A:H2'	4:D:50:G:H5'	1.97	0.46
4:D:55:G:H5'	10:J:158:ARG:CG	2.45	0.46
6:F:112:A:N7	30:n:63:ARG:CZ	2.78	0.46
15:O:194:HIS:NE2	15:O:237:ASP:OD1	2.45	0.46
20:T:97:ILE:CD1	20:T:97:ILE:H	2.27	0.46
1:A:893:ARG:CG	1:A:893:ARG:NH1	2.73	0.46
1:A:1810:PRO:O	1:A:1814:VAL:HG23	2.15	0.46
3:C:486:VAL:HG11	3:C:564:ILE:HD11	1.97	0.46
4:D:1:G:H2'	4:D:2:U:H6	1.80	0.46
6:F:34:G:H2'	6:F:35:U:O4'	2.15	0.46
6:F:120:G:H4'	6:F:121:C:O4'	2.15	0.46
8:H:730:GLN:C	8:H:733:ILE:HD12	2.38	0.46
14:N:146:LEU:HD23	14:N:147:ASN:H	1.80	0.46
17:Q:37:ASN:HD21	17:Q:145:PRO:HD3	1.79	0.46
20:T:131:GLU:OE2	21:U:626:LEU:HD13	2.13	0.46
20:T:143:TYR:CD2	20:T:146:TRP:CZ3	3.04	0.46
21:U:641:CYS:HB2	21:U:648:ILE:HD11	1.97	0.46
21:U:671:PHE:O	21:U:681:GLU:HA	2.15	0.46
28:l:30:ARG:C	28:l:47:VAL:HG23	2.40	0.46
1:A:319:ARG:HG2	1:A:320:ASP:N	2.30	0.46
1:A:997:GLN:OE1	1:A:1511:ARG:NH2	2.48	0.46
1:A:1799:GLN:O	1:A:1803:ARG:HG3	2.15	0.46
3:C:77:LEU:HD11	15:O:135:ILE:HG12	1.97	0.46
3:C:681:CYS:SG	3:C:816:VAL:HG22	2.55	0.46
3:C:686:PHE:HD1	3:C:687:ALA:CB	2.28	0.46
3:C:737:ILE:HD12	3:C:747:LEU:HD11	1.98	0.46
5:E:500:A:C2'	5:E:502:C:H5	2.28	0.46
9:I:38:LEU:CD2	10:J:189:ARG:CD	2.93	0.46
14:N:117:PHE:O	14:N:129:SER:HA	2.15	0.46
17:Q:178:TYR:CD2	17:Q:178:TYR:N	2.82	0.46
22:V:214:ASN:C	22:V:218:ILE:HG13	2.40	0.46
25:i:86:ASN:ND2	26:j:32:LYS:NZ	2.64	0.46
1:A:1319:ILE:O	1:A:1323:SER:HB2	2.15	0.46
3:C:183:GLN:NE2	3:C:654:CYS:HA	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:160:LEU:HA	11:K:196:ILE:HG12	1.98	0.46
13:M:87:ARG:NH1	13:M:122:GLY:HA3	2.30	0.46
17:Q:217:GLN:N	17:Q:217:GLN:NE2	2.62	0.46
1:A:1495:PHE:HB3	22:V:230:ALA:HB1	1.97	0.46
1:A:1551:GLY:C	1:A:1555:THR:HG21	2.40	0.46
3:C:760:LEU:C	3:C:764:ASN:HD22	2.23	0.46
15:O:187:ASP:OD2	15:O:230:VAL:N	2.29	0.46
15:O:409:LYS:HD3	20:T:102:LEU:HD11	1.98	0.46
17:Q:178:TYR:N	17:Q:178:TYR:HD2	2.12	0.46
26:c:16:LYS:N	26:c:17:PRO:CD	2.79	0.46
1:A:1343:PHE:CD2	1:A:1440:ILE:HG21	2.51	0.46
1:A:1547:ILE:HD13	22:V:211:LEU:CD1	2.35	0.46
1:A:2063:TYR:CD1	1:A:2067:TYR:HD2	2.34	0.46
2:B:174:G:N7	29:f:20:LYS:CE	2.78	0.46
3:C:997:LEU:O	3:C:997:LEU:HD23	2.15	0.46
6:F:1115:G:H2'	6:F:1116:A:C8	2.50	0.46
8:H:606:GLN:HA	8:H:609:GLU:HG2	1.98	0.46
9:I:40:LEU:HD21	9:I:44:ARG:HH21	1.80	0.46
13:M:120:LEU:HD12	13:M:122:GLY:H	1.77	0.46
15:O:208:CYS:SG	15:O:209:TRP:N	2.89	0.46
17:Q:182:LEU:O	17:Q:186:VAL:N	2.43	0.46
20:T:131:GLU:OE2	21:U:626:LEU:CG	2.61	0.46
21:U:658:LEU:HB3	21:U:666:CYS:HB2	1.97	0.46
21:U:704:TRP:CE3	21:U:705:ALA:CA	2.98	0.46
29:f:6:PHE:CZ	29:f:10:LEU:HD11	2.51	0.46
1:A:401:PRO:O	1:A:402:TRP:HB3	2.16	0.46
1:A:918:ASP:OD2	1:A:1511:ARG:NH1	2.49	0.46
1:A:1383:PHE:N	1:A:1383:PHE:CD1	2.83	0.46
1:A:1442:ARG:NH1	1:A:1442:ARG:CB	2.75	0.46
2:B:179:U:OP1	30:g:79:LYS:HG2	2.16	0.46
3:C:365:GLU:O	3:C:366:ASN:C	2.58	0.46
3:C:746:LYS:O	3:C:750:ILE:HG12	2.16	0.46
3:C:991:LYS:HG3	3:C:992:TYR:N	2.30	0.46
5:E:494:G:O2'	5:E:495:A:OP1	2.30	0.46
14:N:121:ARG:HB3	14:N:125:GLY:H	1.81	0.46
21:U:702:TYR:O	21:U:705:ALA:HB3	2.16	0.46
1:A:333:LYS:O	1:A:336:PHE:N	2.48	0.46
1:A:845:VAL:HG12	1:A:973:GLU:OE1	2.15	0.46
1:A:1068:ARG:HA	1:A:1068:ARG:HD3	1.72	0.46
1:A:1451:PHE:O	1:A:1454:SER:OG	2.19	0.46
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:861:ILE:HB	3:C:936:ILE:HG13	1.98	0.46
3:C:885:GLY:CA	3:C:907:PRO:HG2	2.46	0.46
13:M:13:CYS:N	13:M:71:CYS:SG	2.83	0.46
18:R:172:LYS:HA	18:R:175:GLN:OE1	2.16	0.46
25:i:30:TRP:CE2	25:i:89:LEU:HD22	2.51	0.46
1:A:452:PHE:CZ	3:C:343:ASP:OD1	2.68	0.46
3:C:139:ILE:O	3:C:237:ILE:HA	2.16	0.46
3:C:682:SER:O	3:C:854:ILE:CA	2.64	0.46
4:D:55:G:H5'	10:J:158:ARG:HG3	1.97	0.46
5:E:497:A:C6	5:E:498:C:N4	2.84	0.46
6:F:1100:A:H61	6:F:1116:A:N6	2.07	0.46
8:H:712:CYS:O	8:H:713:ILE:C	2.57	0.46
8:H:712:CYS:O	8:H:715:LYS:N	2.49	0.46
9:I:38:LEU:HD13	10:J:189:ARG:NH2	2.30	0.46
10:J:65:PHE:CE2	10:J:101:ARG:HG2	2.51	0.46
14:N:221:LEU:HD12	14:N:221:LEU:O	2.16	0.46
15:O:348:GLU:CD	15:O:349:LYS:N	2.74	0.46
20:T:143:TYR:N	20:T:143:TYR:CD1	2.84	0.46
25:b:30:TRP:CE2	25:b:89:LEU:HD22	2.51	0.46
1:A:515:PRO:HD2	1:A:689:TYR:CZ	2.51	0.46
1:A:806:ALA:N	1:A:807:PRO:HD2	2.31	0.46
1:A:1047:ALA:O	1:A:1251:TYR:N	2.48	0.46
1:A:1068:ARG:HH11	1:A:1068:ARG:CG	2.14	0.46
1:A:1540:ASN:O	1:A:1543:ARG:N	2.48	0.46
3:C:471:HIS:HB2	3:C:592:PHE:CZ	2.51	0.46
3:C:683:ASN:O	3:C:684:GLU:HB3	2.16	0.46
4:D:12:A:N3	4:D:12:A:H2'	2.32	0.46
4:D:66:C:C6	4:D:66:C:C5'	2.98	0.46
4:D:66:C:C3'	4:D:66:C:H6	2.28	0.46
6:F:1098:C:H2'	6:F:1099:G:H5''	1.98	0.46
9:I:248:ASN:O	9:I:252:HIS:CB	2.64	0.46
14:N:154:ALA:O	14:N:158:SER:OG	2.29	0.46
20:T:94:THR:O	20:T:97:ILE:CB	2.57	0.46
1:A:217:TRP:CD1	1:A:703:PHE:CE1	3.04	0.45
1:A:269:ASP:OD1	1:A:270:SER:N	2.50	0.45
1:A:304:ASP:OD1	1:A:305:LEU:N	2.45	0.45
1:A:484:PHE:HE1	1:A:488:ARG:HD2	1.81	0.45
1:A:995:LEU:HD11	1:A:1078:ILE:HG23	1.98	0.45
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.97	0.45
2:B:43:G:N3	2:B:43:G:C2'	2.79	0.45
3:C:621:ALA:HB2	3:C:664:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:660:ARG:NH2	3:C:670:ILE:HD12	2.30	0.45
3:C:780:PRO:O	3:C:784:SER:N	2.25	0.45
9:I:49:ARG:HH12	10:J:181:ARG:NH2	2.14	0.45
13:M:37:CYS:SG	13:M:39:LEU:HB2	2.55	0.45
14:N:245:GLU:HG3	14:N:249:MET:HE2	1.98	0.45
26:j:16:LYS:N	26:j:17:PRO:CD	2.79	0.45
1:A:133:GLU:HG3	1:A:560:THR:HA	1.98	0.45
1:A:503:LYS:HG2	1:A:507:LEU:HD13	1.98	0.45
1:A:1335:TRP:CZ2	1:A:1339:LEU:HD11	2.51	0.45
1:A:1393:GLU:CG	1:A:1570:TRP:HZ2	2.26	0.45
1:A:1478:GLU:N	1:A:1479:GLU:OE1	2.49	0.45
1:A:1805:ILE:HA	1:A:1808:ALA:HB3	1.99	0.45
3:C:391:MET:HE1	3:C:395:LYS:HZ1	1.78	0.45
4:D:42:A:H1'	4:D:43:C:OP1	2.17	0.45
6:F:25:A:H2'	6:F:27:A:OP2	2.15	0.45
13:M:107:ASP:O	13:M:110:LYS:HG2	2.16	0.45
13:M:210:ILE:O	13:M:287:ARG:N	2.43	0.45
1:A:585:ARG:HG3	14:N:33:TRP:CD2	2.51	0.45
1:A:928:ARG:HG3	1:A:929:LEU:N	2.30	0.45
1:A:1368:GLN:O	1:A:1372:LYS:HG3	2.15	0.45
1:A:1562:PHE:HA	1:A:1609:TRP:CH2	2.52	0.45
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.51	0.45
2:B:167:A:N7	30:g:63:ARG:NH1	2.65	0.45
3:C:306:PRO:HG2	3:C:349:TRP:CE3	2.51	0.45
4:D:15:C:OP2	4:D:15:C:H6	2.00	0.45
14:N:108:VAL:HG23	14:N:109:LEU:HG	1.98	0.45
15:O:125:TRP:HE1	15:O:437:GLU:HB3	1.81	0.45
15:O:379:LYS:HA	17:Q:47:ARG:HH21	1.80	0.45
21:U:654:ARG:HB3	21:U:654:ARG:CZ	2.46	0.45
29:m:6:PHE:CZ	29:m:10:LEU:HD11	2.51	0.45
1:A:263:PRO:HG2	1:A:265:ASN:ND2	2.30	0.45
1:A:514:TYR:CE1	1:A:689:TYR:CE2	2.67	0.45
1:A:910:LYS:HD3	1:A:1504:TYR:CD2	2.52	0.45
1:A:931:ALA:O	1:A:934:ARG:HB2	2.17	0.45
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.52	0.45
3:C:67:GLU:O	3:C:71:GLY:N	2.49	0.45
3:C:857:LEU:HD21	3:C:966:PHE:CB	2.46	0.45
3:C:864:VAL:HG12	3:C:866:ILE:HG13	1.98	0.45
3:C:885:GLY:CA	3:C:907:PRO:CG	2.90	0.45
6:F:30:A:H1'	6:F:31:A:OP1	2.16	0.45
6:F:1103:C:N1	6:F:1114:G:N2	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:635:GLN:HB3	8:H:639:LEU:CG	2.47	0.45
10:J:229:ASP:HB2	11:K:151:LYS:CB	2.34	0.45
13:M:77:ASP:OD1	13:M:78:SER:N	2.49	0.45
14:N:4:TRP:CZ2	14:N:92:HIS:CD2	3.05	0.45
15:O:437:GLU:OE1	15:O:438:PRO:HA	2.15	0.45
24:h:20:LEU:O	24:h:31:ILE:HA	2.16	0.45
1:A:854:ARG:NH2	6:F:25:A:H5''	2.31	0.45
1:A:872:PRO:CG	17:Q:201:PHE:CD1	2.99	0.45
1:A:1246:ALA:C	1:A:1247:PHE:HD1	2.24	0.45
1:A:1880:PHE:CE1	1:A:1889:LEU:HD22	2.52	0.45
3:C:132:ARG:HD2	3:C:208:ARG:HG3	1.99	0.45
4:D:91:A:C2	9:I:99:ILE:CD1	2.98	0.45
11:K:110:ARG:O	11:K:114:THR:HG23	2.17	0.45
15:O:406:THR:O	15:O:414:LEU:HD12	2.17	0.45
33:t:62:LEU:O	33:t:63:THR:C	2.59	0.45
1:A:662:GLN:NE2	1:A:1620:TYR:CE2	2.80	0.45
1:A:697:LYS:O	35:A:3000:IHP:O36	2.34	0.45
1:A:1048:VAL:HG12	1:A:1248:VAL:HG13	1.99	0.45
1:A:1882:LEU:HD21	1:A:1965:PHE:CE1	2.50	0.45
1:A:1964:PRO:HG3	1:A:2013:ARG:HG3	1.98	0.45
2:B:103:A:O2'	2:B:104:G:P	2.74	0.45
3:C:140:GLY:O	3:C:146:LYS:NZ	2.45	0.45
4:D:28:U:C1'	12:L:121:ILE:HD13	2.47	0.45
4:D:39:G:C5	14:N:117:PHE:CD2	3.05	0.45
11:K:187:LYS:HA	11:K:201:LYS:NZ	2.31	0.45
15:O:392:MET:HG3	15:O:393:VAL:N	2.32	0.45
18:R:188:LYS:HE3	18:R:192:GLU:OE2	2.17	0.45
1:A:1144:PHE:CZ	1:A:1162:THR:HG21	2.52	0.45
1:A:1319:ILE:HG23	1:A:1331:VAL:HG13	1.99	0.45
1:A:1547:ILE:HD13	22:V:211:LEU:CD2	2.39	0.45
3:C:289:ASN:O	3:C:293:ALA:CB	2.65	0.45
3:C:760:LEU:O	3:C:764:ASN:ND2	2.50	0.45
8:H:673:GLU:CB	8:H:683:SER:HB3	2.47	0.45
10:J:39:LEU:HD12	10:J:158:ARG:NH1	2.32	0.45
10:J:109:GLU:CB	18:R:196:ARG:HG2	2.47	0.45
20:T:127:GLN:HG3	20:T:128:ARG:N	2.32	0.45
1:A:782:ILE:HD13	17:Q:165:ILE:HD13	1.99	0.45
1:A:939:LEU:HD11	1:A:987:LEU:HD23	1.98	0.45
1:A:971:MET:CE	16:P:174:VAL:HG13	2.47	0.45
1:A:1173:HIS:CD2	1:A:1173:HIS:C	2.95	0.45
1:A:1417:GLN:HB3	1:A:1783:MET:HE1	1.90	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1562:PHE:CA	1:A:1609:TRP:CH2	3.00	0.45
3:C:154:VAL:O	3:C:157:SER:N	2.50	0.45
3:C:989:LEU:HD12	3:C:989:LEU:C	2.41	0.45
4:D:12:A:C2	4:D:13:A:O4'	2.69	0.45
6:F:1102:C:C2'	6:F:1103:C:C6	2.80	0.45
9:I:169:TRP:O	9:I:172:PHE:N	2.49	0.45
25:b:86:ASN:ND2	26:c:32:LYS:NZ	2.64	0.45
1:A:367:PHE:CE1	3:C:606:VAL:HG12	2.52	0.45
1:A:864:GLN:NE2	1:A:1099:ASN:OD1	2.50	0.45
1:A:1319:ILE:HG12	1:A:1334:LYS:HB3	1.98	0.45
1:A:1567:PHE:CD2	1:A:1825:ILE:HG21	2.50	0.45
1:A:1716:LEU:HB2	1:A:1719:GLU:HG3	1.98	0.45
3:C:354:TYR:CD2	3:C:354:TYR:O	2.70	0.45
3:C:362:LYS:CD	3:C:363:PRO:CG	2.86	0.45
3:C:473:LEU:HD12	3:C:485:LEU:CD2	2.47	0.45
3:C:837:GLN:NE2	21:U:642:LEU:HD12	2.32	0.45
6:F:1116:A:C4	6:F:1117:G:C5	3.05	0.45
8:H:624:TRP:HE1	8:H:651:ALA:CB	2.30	0.45
8:H:708:LEU:O	8:H:712:CYS:SG	2.70	0.45
13:M:120:LEU:HD13	13:M:122:GLY:N	2.31	0.45
14:N:70:LEU:HB3	14:N:102:LEU:CD2	2.47	0.45
14:N:150:HIS:HB3	14:N:155:GLN:HG3	1.99	0.45
21:U:702:TYR:CG	21:U:704:TRP:CZ2	3.03	0.45
24:a:20:LEU:O	24:a:31:ILE:HA	2.16	0.45
30:n:49:ARG:HA	30:n:49:ARG:HD2	1.63	0.45
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.17	0.45
1:A:1219:ASP:OD2	1:A:1255:ASN:ND2	2.50	0.45
1:A:1295:GLN:H	1:A:1295:GLN:HG3	1.60	0.45
1:A:1358:ASP:CG	1:A:1359:ILE:N	2.75	0.45
1:A:1464:LYS:HG2	1:A:1479:GLU:HG3	1.98	0.45
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.32	0.45
3:C:353:TYR:HD1	3:C:371:PRO:HA	1.82	0.45
3:C:656:LEU:HD23	3:C:656:LEU:HA	1.75	0.45
11:K:205:GLU:O	11:K:208:SER:OG	2.22	0.45
15:O:121:GLN:OE1	15:O:121:GLN:N	2.50	0.45
21:U:696:GLY:O	21:U:697:THR:OG1	2.30	0.45
33:r:98:LEU:HD21	33:s:102:LEU:HD12	1.99	0.45
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.52	0.44
1:A:380:ARG:NH1	1:A:380:ARG:CG	2.80	0.44
1:A:618:SER:OG	4:D:72:C:H5'	2.17	0.44
1:A:697:LYS:NZ	35:A:3000:IHP:O45	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:910:LYS:HD3	1:A:1504:TYR:HD2	1.82	0.44
1:A:1337:THR:HG23	22:V:201:MET:HG3	1.99	0.44
1:A:1661:ILE:HG13	1:A:1809:ASN:ND2	2.31	0.44
2:B:174:G:C8	30:g:99:ASP:OD2	2.69	0.44
3:C:231:ALA:O	3:C:487:ARG:NH1	2.50	0.44
3:C:290:HIS:O	3:C:294:ASN:HB2	2.17	0.44
3:C:458:ILE:H	3:C:458:ILE:HG12	1.62	0.44
3:C:533:GLU:OE1	3:C:533:GLU:HA	2.17	0.44
3:C:861:ILE:CD1	3:C:938:ARG:NE	2.80	0.44
3:C:883:ARG:HA	3:C:883:ARG:HD2	1.66	0.44
3:C:990:GLU:CB	3:C:998:TYR:CD1	3.00	0.44
4:D:86:G:C2	9:I:57:TYR:CE1	3.06	0.44
5:E:1:G:C2	5:E:1:G:OP1	2.70	0.44
9:I:79:HIS:NE2	10:J:244:PHE:CE1	2.84	0.44
9:I:136:TRP:CE3	9:I:159:TRP:HB2	2.52	0.44
19:S:60:ARG:O	19:S:63:ARG:HG2	2.17	0.44
33:r:100:SER:O	33:r:103:ASP:CG	2.60	0.44
1:A:1012:TRP:CD1	1:A:1012:TRP:H	2.36	0.44
1:A:1171:LEU:HD12	1:A:1172:PHE:N	2.31	0.44
1:A:1185:GLU:HA	1:A:1185:GLU:OE2	2.16	0.44
1:A:1308:GLU:HG2	1:A:1311:LYS:HD2	1.99	0.44
3:C:360:ARG:NH1	3:C:360:ARG:HG2	2.32	0.44
3:C:862:TYR:N	3:C:906:VAL:O	2.49	0.44
6:F:39:A:C2'	6:F:40:U:H5''	2.47	0.44
10:J:176:LEU:O	10:J:179:SER:OG	2.26	0.44
13:M:53:ASN:ND2	13:M:54:ASN:N	2.64	0.44
13:M:279:GLY:O	13:M:282:LEU:HG	2.17	0.44
25:i:30:TRP:CD2	25:i:89:LEU:HD22	2.52	0.44
1:A:856:TRP:NE1	16:P:174:VAL:HG11	2.33	0.44
1:A:1883:ASN:OD1	1:A:1886:THR:OG1	2.25	0.44
3:C:735:LEU:HG	3:C:736:ASP:O	2.16	0.44
5:E:2:U:O2'	5:E:3:A:O4'	2.33	0.44
8:H:127:MET:HA	8:H:150:PRO:CB	2.47	0.44
8:H:574:TYR:CZ	8:H:591:PHE:HB2	2.53	0.44
15:O:345:PHE:CD2	15:O:381:GLY:HA2	2.52	0.44
20:T:99:ARG:HD2	20:T:103:ILE:HD11	1.99	0.44
29:f:17:ILE:HG12	29:f:95:ILE:HG23	2.00	0.44
1:A:390:LEU:HD13	3:C:652:MET:HB3	1.99	0.44
1:A:555:LYS:HA	12:L:113:GLU:OE1	2.17	0.44
1:A:722:LEU:HD23	1:A:722:LEU:HA	1.87	0.44
1:A:740:GLU:HG3	1:A:741:ILE:N	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:772:GLU:HG3	1:A:773:SER:N	2.32	0.44
1:A:1400:ILE:HG23	1:A:1542:TYR:CE2	2.53	0.44
1:A:1899:TRP:CE3	1:A:1905:LEU:HD22	2.52	0.44
3:C:707:SER:H	3:C:824:SER:HB3	1.82	0.44
6:F:15:C:O2	6:F:16:U:C5	2.70	0.44
8:H:680:ILE:O	8:H:683:SER:OG	2.22	0.44
13:M:14:GLU:HB2	17:Q:106:LEU:HD13	1.99	0.44
21:U:644:LYS:NZ	21:U:646:TYR:CE2	2.85	0.44
21:U:701:ILE:HG22	21:U:702:TYR:N	2.32	0.44
25:b:30:TRP:CD2	25:b:89:LEU:HD22	2.52	0.44
33:q:96:PHE:HD2	33:t:5:ILE:HG23	1.80	0.44
1:A:217:TRP:O	1:A:220:THR:OG1	2.32	0.44
1:A:391:TYR:CE1	3:C:673:PRO:HG2	2.53	0.44
1:A:428:LEU:HD22	3:C:897:THR:HA	2.00	0.44
1:A:951:LEU:HD22	1:A:955:LYS:NZ	2.33	0.44
1:A:1174:PHE:HZ	1:A:1182:LEU:CD1	2.14	0.44
1:A:1379:MET:HE3	1:A:1380:PRO:HD3	1.98	0.44
1:A:1932:GLN:HG2	1:A:1955:ALA:HB3	1.99	0.44
1:A:2081:ASP:O	1:A:2085:GLY:N	2.51	0.44
6:F:17:U:O5'	6:F:17:U:C6	2.70	0.44
6:F:112:A:N7	30:n:63:ARG:NH1	2.65	0.44
9:I:200:GLN:HA	9:I:203:LEU:HB3	1.99	0.44
20:T:133:LEU:HD11	20:T:146:TRP:CE3	2.52	0.44
21:U:656:THR:OG1	21:U:670:LEU:HD23	2.17	0.44
33:s:14:VAL:HG12	33:s:52:GLU:HA	1.98	0.44
1:A:209:ILE:HB	1:A:212:VAL:HB	1.99	0.44
1:A:1328:PHE:CE1	1:A:1603:ASN:ND2	2.86	0.44
1:A:1543:ARG:O	1:A:1547:ILE:HG13	2.18	0.44
3:C:142:LEU:HB3	3:C:143:HIS:CD2	2.53	0.44
3:C:385:PHE:CE1	3:C:425:LEU:HD11	2.45	0.44
3:C:615:LEU:HD21	21:U:667:ILE:HD11	1.99	0.44
3:C:860:PRO:N	3:C:908:VAL:HG12	2.32	0.44
5:E:9:U:H1'	5:E:10:U:OP1	2.18	0.44
15:O:304:LEU:HD13	15:O:334:TRP:CE3	2.53	0.44
31:o:15:TYR:CG	24:h:47:GLU:HB3	2.52	0.44
1:A:831:ARG:HD2	1:A:831:ARG:HA	1.74	0.44
1:A:1111:SER:HA	1:A:1514:PHE:CE2	2.52	0.44
1:A:1384:PRO:CB	1:A:1385:PRO:HD2	2.47	0.44
1:A:1414:TRP:CB	1:A:1558:GLU:HG3	2.45	0.44
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.45	0.44
4:D:14:C:C4'	4:D:15:C:OP2	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:80:ASP:HB2	10:J:241:PHE:HE1	1.83	0.44
19:S:60:ARG:O	19:S:61:LYS:C	2.60	0.44
20:T:42:TYR:CZ	20:T:64:PHE:HZ	2.35	0.44
20:T:129:HIS:ND1	20:T:129:HIS:C	2.75	0.44
28:e:39:SER:O	28:e:41:ASN:N	2.48	0.44
1:A:380:ARG:HD3	1:A:381:SER:N	2.33	0.44
1:A:864:GLN:NE2	1:A:1100:LYS:N	2.64	0.44
1:A:910:LYS:HD2	1:A:1504:TYR:CE2	2.52	0.44
1:A:1252:SER:OG	1:A:1255:ASN:HB2	2.17	0.44
1:A:1468:ALA:HA	1:A:1473:ARG:CG	2.48	0.44
1:A:2013:ARG:CZ	1:A:2085:GLY:HA2	2.48	0.44
3:C:689:ILE:HG23	3:C:690:PRO:HD2	1.99	0.44
3:C:837:GLN:NE2	21:U:642:LEU:O	2.51	0.44
3:C:990:GLU:HG3	3:C:998:TYR:CE2	2.52	0.44
16:P:159:ASP:OD1	16:P:160:MET:N	2.51	0.44
21:U:699:LYS:HG3	21:U:699:LYS:O	2.17	0.44
22:V:237:ARG:HH12	22:V:240:GLU:CD	2.20	0.44
33:s:102:LEU:O	33:s:105:LEU:CG	2.66	0.44
1:A:354:PRO:O	1:A:355:LEU:HB3	2.18	0.44
1:A:1080:ASP:HB3	10:J:82:ASN:HD22	1.83	0.44
1:A:1229:GLU:O	1:A:1232:SER:OG	2.28	0.44
1:A:1812:LEU:HB3	1:A:1816:ARG:HH12	1.83	0.44
1:A:1934:ILE:HG12	1:A:1957:ARG:HB2	2.00	0.44
3:C:500:ARG:NH1	3:C:536:SER:OG	2.51	0.44
3:C:979:GLY:HA3	3:C:983:SER:HA	1.98	0.44
3:C:1004:ASN:HB2	3:C:1006:LEU:HD21	2.00	0.44
6:F:120:G:C2	25:i:33:GLU:O	2.71	0.44
8:H:433:LEU:O	8:H:437:PRO:N	2.50	0.44
9:I:115:ILE:O	9:I:118:ALA:N	2.51	0.44
9:I:172:PHE:O	9:I:175:PHE:HB3	2.18	0.44
9:I:222:TYR:HB3	9:I:250:PHE:CD1	2.53	0.44
10:J:68:GLU:OE1	10:J:68:GLU:N	2.50	0.44
13:M:91:ILE:HD11	13:M:125:ILE:HD11	2.00	0.44
19:S:51:PHE:HE1	19:S:55:GLU:CG	2.31	0.44
20:T:139:PHE:HD1	20:T:139:PHE:HA	1.74	0.44
21:U:634:LYS:HE3	21:U:638:GLU:OE2	2.18	0.44
21:U:665:ASP:OD1	21:U:665:ASP:N	2.51	0.44
29:m:17:ILE:HG12	29:m:95:ILE:HG23	2.00	0.44
1:A:537:THR:HG21	2:B:84:A:H62	1.82	0.43
1:A:1161:TYR:CD1	1:A:1170:MET:CE	3.02	0.43
1:A:1252:SER:O	1:A:1255:ASN:O	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1292:ARG:HG3	1:A:1293:THR:N	2.33	0.43
3:C:242:VAL:HG13	3:C:897:THR:HG21	1.99	0.43
3:C:468:LEU:HD11	3:C:493:LEU:HD23	1.98	0.43
3:C:680:SER:OG	3:C:681:CYS:N	2.51	0.43
3:C:997:LEU:O	3:C:1001:LEU:HG	2.18	0.43
4:D:56:A:O2'	4:D:57:U:P	2.76	0.43
4:D:85:C:N4	10:J:166:LYS:HD2	2.32	0.43
8:H:729:TYR:O	8:H:733:ILE:HG13	2.17	0.43
10:J:44:THR:HG22	10:J:45:ALA:N	2.33	0.43
10:J:103:ASN:CG	18:R:193:MET:HE1	2.42	0.43
11:K:190:TYR:CE2	11:K:195:PHE:HZ	2.36	0.43
15:O:251:TRP:CZ3	15:O:258:PRO:HB3	2.52	0.43
15:O:443:ASN:HA	15:O:444:PRO:HD2	1.87	0.43
16:P:20:TYR:CE1	17:Q:133:LYS:HB2	2.53	0.43
19:S:72:TRP:O	19:S:73:SER:CB	2.66	0.43
21:U:656:THR:HG21	21:U:698:PHE:CE2	2.53	0.43
21:U:691:VAL:CG2	21:U:701:ILE:CD1	2.95	0.43
22:V:237:ARG:NH1	22:V:240:GLU:CD	2.73	0.43
28:I:14:ALA:HA	28:I:78:LEU:HD21	2.00	0.43
1:A:1094:ASP:OD1	6:F:25:A:C2	2.71	0.43
1:A:1419:ASP:O	1:A:1803:ARG:NH2	2.50	0.43
3:C:251:GLN:HE21	3:C:255:GLN:HG2	1.84	0.43
3:C:544:LEU:HD23	3:C:562:VAL:HG12	1.99	0.43
3:C:567:ILE:HG22	3:C:571:TYR:HE2	1.83	0.43
3:C:861:ILE:HD11	3:C:938:ARG:CD	2.49	0.43
10:J:212:ASP:H	13:M:106:ASN:ND2	2.16	0.43
13:M:120:LEU:O	13:M:124:GLN:HG3	2.18	0.43
13:M:235:GLY:O	13:M:236:ASN:CB	2.64	0.43
24:a:87:LEU:HG	24:a:92:ILE:HD11	2.00	0.43
26:c:16:LYS:CG	26:c:17:PRO:HD3	2.49	0.43
25:i:88:THR:HG23	27:k:67:SER:CB	2.49	0.43
1:A:218:SER:O	1:A:221:TRP:HB3	2.18	0.43
1:A:959:LEU:HD22	18:R:186:LEU:HB3	1.86	0.43
1:A:1286:TRP:HB2	1:A:1300:ALA:HB3	2.00	0.43
1:A:1417:GLN:OE1	1:A:1422:ILE:CG1	2.67	0.43
1:A:1617:ALA:N	1:A:1744:ASP:OD2	2.52	0.43
3:C:117:ARG:CG	3:C:157:SER:O	2.66	0.43
3:C:604:LYS:HE2	3:C:643:VAL:HG13	1.87	0.43
3:C:884:ARG:C	3:C:884:ARG:CD	2.91	0.43
3:C:945:LEU:HD12	3:C:945:LEU:O	2.18	0.43
6:F:1102:C:C2	6:F:1103:C:C5	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:140:LEU:HD13	9:I:156:TYR:CZ	2.53	0.43
10:J:212:ASP:H	13:M:106:ASN:HD21	1.66	0.43
11:K:173:LYS:O	11:K:177:GLU:HG2	2.18	0.43
13:M:229:ILE:O	13:M:233:LYS:CB	2.66	0.43
15:O:162:THR:HG22	15:O:183:MET:C	2.44	0.43
15:O:332:ARG:HD3	15:O:341:LEU:HD11	2.00	0.43
1:A:134:MET:HE1	12:L:107:ARG:HH11	1.83	0.43
1:A:1290:ASP:OD1	1:A:1290:ASP:N	2.50	0.43
1:A:1342:LEU:CD2	1:A:1356:LEU:CD2	2.83	0.43
1:A:1626:GLN:NE2	1:A:1692:TYR:O	2.49	0.43
2:B:175:G:C2	25:b:33:GLU:O	2.71	0.43
3:C:132:ARG:O	3:C:208:ARG:CG	2.59	0.43
5:E:500:A:O2'	5:E:501:A:P	2.66	0.43
9:I:38:LEU:CD2	10:J:189:ARG:HG2	2.49	0.43
10:J:33:TRP:O	10:J:36:VAL:N	2.50	0.43
15:O:405:SER:HA	15:O:415:ILE:O	2.18	0.43
20:T:50:HIS:CD2	20:T:52:ASP:HB2	2.53	0.43
21:U:688:ILE:CG2	21:U:689:LEU:N	2.81	0.43
34:x:4:U:H5''	34:x:4:U:H6	1.83	0.43
1:A:266:LEU:HD23	1:A:268:LEU:H	1.84	0.43
1:A:872:PRO:HG3	17:Q:201:PHE:CD1	2.53	0.43
1:A:1022:PRO:HB3	1:A:1265:PHE:HE2	1.84	0.43
1:A:1348:GLU:OE2	1:A:1447:TRP:CB	2.66	0.43
1:A:1348:GLU:HG3	1:A:1447:TRP:CD1	2.53	0.43
1:A:1367:ILE:O	1:A:1370:ARG:CB	2.66	0.43
1:A:1714:PRO:HB2	1:A:1787:TYR:CZ	2.53	0.43
3:C:294:ASN:O	3:C:297:SER:OG	2.28	0.43
3:C:468:LEU:C	3:C:468:LEU:CD2	2.86	0.43
3:C:885:GLY:C	3:C:907:PRO:HD3	2.44	0.43
3:C:972:ARG:HH21	3:C:982:MET:CG	2.26	0.43
4:D:55:G:N7	10:J:35:LYS:HG2	2.33	0.43
9:I:205:TRP:CZ3	9:I:221:VAL:HG21	2.54	0.43
11:K:113:ALA:O	11:K:116:THR:OG1	2.33	0.43
16:P:10:GLU:HG2	16:P:11:ALA:N	2.33	0.43
25:b:45:GLY:HA3	25:b:53:VAL:HG12	2.00	0.43
1:A:531:LEU:HD23	1:A:531:LEU:HA	1.82	0.43
1:A:676:GLN:OE1	1:A:676:GLN:N	2.45	0.43
1:A:852:LEU:HD23	1:A:852:LEU:HA	1.67	0.43
1:A:1344:THR:C	1:A:1347:ARG:HG3	2.42	0.43
2:B:103:A:O2'	2:B:104:G:OP2	2.28	0.43
3:C:861:ILE:HB	3:C:936:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:888:ILE:HA	3:C:904:GLY:HA2	2.00	0.43
4:D:52:G:O2'	4:D:53:A:O4'	2.36	0.43
5:E:9:U:H4'	5:E:10:U:OP2	2.17	0.43
6:F:1120:G:C5'	6:F:1120:G:C8	3.00	0.43
13:M:24:ARG:HH11	17:Q:115:VAL:HG21	1.84	0.43
13:M:53:ASN:ND2	13:M:53:ASN:N	2.66	0.43
14:N:163:VAL:HG11	14:N:199:MET:HE2	2.01	0.43
17:Q:203:LYS:HG3	17:Q:204:LEU:N	2.33	0.43
21:U:692:GLU:CA	21:U:698:PHE:HD1	2.32	0.43
25:b:88:THR:HG23	27:d:67:SER:CB	2.49	0.43
1:A:134:MET:CE	12:L:107:ARG:HD2	2.48	0.43
1:A:299:LYS:HE2	1:A:299:LYS:HB3	1.91	0.43
1:A:429:ASN:HB3	1:A:430:PRO:HD2	2.01	0.43
1:A:691:PHE:C	1:A:691:PHE:CD1	2.97	0.43
1:A:861:GLN:HG2	1:A:1097:HIS:CB	2.48	0.43
1:A:1049:LEU:HD13	1:A:1260:PHE:HB2	1.98	0.43
2:B:176:A:O2'	29:f:20:LYS:HE3	2.19	0.43
3:C:222:MET:HE1	3:C:252:LEU:HD21	2.00	0.43
3:C:859:GLU:CD	3:C:909:ILE:CG2	2.78	0.43
6:F:121:C:O2'	29:m:20:LYS:HE3	2.19	0.43
7:G:81:ASP:C	7:G:82:ASP:CG	2.86	0.43
9:I:105:TYR:CE2	9:I:121:LEU:HD13	2.54	0.43
10:J:45:ALA:O	10:J:48:SER:N	2.51	0.43
10:J:79:GLU:HG3	17:Q:202:MET:SD	2.59	0.43
14:N:207:PRO:O	14:N:212:TRP:NE1	2.51	0.43
22:V:230:ALA:O	22:V:234:VAL:HG23	2.18	0.43
25:i:34:GLN:NE2	25:i:37:ILE:HD12	2.34	0.43
1:A:294:ASN:HB2	1:A:299:LYS:O	2.19	0.43
1:A:594:ASP:OD1	1:A:598:ASN:N	2.50	0.43
1:A:705:GLN:HE21	1:A:709:ARG:CG	2.30	0.43
1:A:778:LYS:HD2	17:Q:165:ILE:HB	2.00	0.43
1:A:984:VAL:HG12	1:A:985:ASP:H	1.83	0.43
1:A:1282:ASP:CG	1:A:1283:GLU:H	2.23	0.43
1:A:1856:ASN:HD22	1:A:1969:MET:HG2	1.84	0.43
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.17	0.43
3:C:689:ILE:CG2	3:C:690:PRO:CD	2.97	0.43
3:C:857:LEU:HD21	3:C:966:PHE:HB3	2.00	0.43
3:C:989:LEU:HG	3:C:993:ILE:HD13	1.97	0.43
10:J:159:LEU:O	11:K:196:ILE:HD11	2.18	0.43
13:M:98:ASN:O	13:M:99:VAL:HG12	2.17	0.43
21:U:633:PHE:C	21:U:635:ASP:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:e:14:ALA:HA	28:e:78:LEU:HD21	2.01	0.43
33:q:112:VAL:O	33:q:115:GLU:CG	2.66	0.43
1:A:617:ASN:O	1:A:621:LEU:CB	2.67	0.43
1:A:1605:ARG:HD2	1:A:1823:LEU:O	2.19	0.43
3:C:268:ASN:HA	3:C:314:ALA:O	2.19	0.43
3:C:282:MET:HE2	3:C:370:TYR:CD1	2.54	0.43
3:C:689:ILE:CG2	3:C:690:PRO:N	2.82	0.43
6:F:5:A:H2'	6:F:6:U:C6	2.53	0.43
6:F:119:G:C8	30:n:99:ASP:OD2	2.69	0.43
6:F:1097:G:H2'	6:F:1098:C:C6	2.54	0.43
10:J:230:THR:C	10:J:232:THR:H	2.24	0.43
12:L:147:HIS:HB2	12:L:148:CYS:SG	2.58	0.43
13:M:125:ILE:CD1	13:M:126:THR:N	2.78	0.43
14:N:70:LEU:HB3	14:N:102:LEU:HD23	2.01	0.43
14:N:97:GLU:O	14:N:100:GLY:N	2.52	0.43
15:O:132:SER:OG	15:O:425:ILE:O	2.28	0.43
15:O:159:SER:OG	15:O:160:ASN:N	2.52	0.43
15:O:214:ASN:O	15:O:215:GLN:NE2	2.52	0.43
16:P:8:GLN:C	16:P:10:GLU:N	2.77	0.43
21:U:644:LYS:CB	21:U:646:TYR:CZ	2.96	0.43
25:i:45:GLY:HA3	25:i:53:VAL:HG12	2.00	0.43
1:A:845:VAL:CG1	1:A:973:GLU:OE1	2.67	0.43
1:A:1174:PHE:HZ	1:A:1182:LEU:HD11	1.70	0.43
1:A:1342:LEU:HD12	1:A:1346:PHE:CD2	2.53	0.43
1:A:1484:TRP:HZ3	1:A:1495:PHE:CD2	2.37	0.43
1:A:1499:ARG:HH22	22:V:234:VAL:HG11	1.84	0.43
3:C:463:THR:HG21	3:C:490:SER:HB2	2.01	0.43
9:I:99:ILE:O	9:I:100:PRO:C	2.61	0.43
13:M:53:ASN:HD22	13:M:53:ASN:N	2.17	0.43
26:j:16:LYS:CG	26:j:17:PRO:HD3	2.49	0.43
28:l:6:ILE:N	28:l:7:PRO:CD	2.82	0.43
33:s:123:ALA:O	33:s:127:LEU:CG	2.67	0.43
1:A:161:PHE:HD1	1:A:161:PHE:HA	1.73	0.42
1:A:939:LEU:C	1:A:939:LEU:CD2	2.92	0.42
1:A:1421:GLY:HA2	1:A:1718:HIS:CD2	2.54	0.42
3:C:859:GLU:CD	3:C:907:PRO:HB3	2.44	0.42
10:J:218:VAL:HA	13:M:109:MET:SD	2.59	0.42
15:O:121:GLN:NE2	17:Q:49:SER:O	2.52	0.42
19:S:65:GLY:C	19:S:66:ASP:CG	2.86	0.42
21:U:674:ARG:CB	21:U:678:LYS:O	2.63	0.42
21:U:677:LYS:O	21:U:677:LYS:HG3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:g:49:ARG:HA	30:g:49:ARG:HD2	1.64	0.42
1:A:462:LEU:HB3	3:C:383:LYS:HD3	2.02	0.42
1:A:514:TYR:HB3	1:A:518:VAL:HG21	2.01	0.42
1:A:923:TYR:HD2	1:A:937:LEU:HB2	1.83	0.42
1:A:1458:TRP:CZ2	1:A:1491:ILE:HD13	2.54	0.42
1:A:1499:ARG:HH11	22:V:234:VAL:HG22	1.68	0.42
1:A:1551:GLY:C	1:A:1555:THR:CG2	2.92	0.42
1:A:1678:ILE:HD13	1:A:1703:MET:HE1	2.01	0.42
1:A:2070:ASN:OD1	1:A:2071:ILE:N	2.52	0.42
2:B:167:A:N7	30:g:63:ARG:HB3	2.34	0.42
3:C:77:LEU:HD12	3:C:77:LEU:O	2.19	0.42
3:C:341:ILE:HG13	3:C:342:ASP:N	2.33	0.42
3:C:430:ARG:H	3:C:430:ARG:HG2	1.65	0.42
3:C:492:LEU:HD22	3:C:557:HIS:ND1	2.34	0.42
3:C:829:VAL:HG12	3:C:830:ASN:N	2.33	0.42
3:C:927:MET:HG3	3:C:928:CYS:N	2.34	0.42
3:C:987:PRO:O	3:C:987:PRO:HG2	2.18	0.42
7:G:136:VAL:O	7:G:139:GLN:CG	2.67	0.42
9:I:199:MET:HB2	9:I:242:GLU:CG	2.40	0.42
15:O:239:ILE:HB	15:O:251:TRP:HB2	2.02	0.42
17:Q:202:MET:HE3	17:Q:206:GLU:OE1	2.19	0.42
21:U:644:LYS:CG	21:U:646:TYR:CZ	3.03	0.42
1:A:363:ASP:N	1:A:363:ASP:OD1	2.53	0.42
1:A:756:LEU:CG	16:P:8:GLN:NE2	2.82	0.42
1:A:864:GLN:CD	1:A:1100:LYS:H	2.28	0.42
1:A:1033:ASN:HD22	1:A:1288:LEU:CB	2.33	0.42
1:A:1547:ILE:CG2	1:A:1553:ILE:N	2.82	0.42
1:A:1865:THR:HG21	1:A:1869:ASN:HD22	1.84	0.42
1:A:2013:ARG:NH2	1:A:2084:LEU:O	2.52	0.42
3:C:684:GLU:O	3:C:685:SER:CB	2.63	0.42
3:C:689:ILE:CG2	3:C:690:PRO:HD2	2.50	0.42
3:C:855:PRO:HG2	3:C:944:VAL:CG2	2.49	0.42
4:D:48:C:H2'	4:D:49:A:O4'	2.18	0.42
4:D:52:G:N2	4:D:53:A:C2	2.87	0.42
4:D:52:G:OP2	10:J:169:ARG:NH1	2.52	0.42
15:O:229:THR:OG1	15:O:270:ASN:O	2.36	0.42
20:T:106:LEU:CD1	20:T:110:GLU:HG3	2.49	0.42
25:b:88:THR:HG22	25:b:89:LEU:HD12	2.01	0.42
1:A:342:LEU:HD13	1:A:392:ASN:ND2	2.31	0.42
1:A:404:ASN:OD1	1:A:405:ASN:N	2.53	0.42
1:A:662:GLN:NE2	1:A:1620:TYR:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:855:LEU:HB3	16:P:170:LEU:HD11	2.01	0.42
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	2.00	0.42
1:A:1275:MET:HE1	1:A:1299:LYS:HD2	2.00	0.42
3:C:314:ALA:HB1	3:C:321:THR:HG22	2.00	0.42
3:C:488:ILE:HG22	3:C:558:LYS:HA	2.01	0.42
3:C:489:TYR:HD2	3:C:592:PHE:HZ	1.65	0.42
3:C:712:ALA:HA	3:C:817:GLN:O	2.19	0.42
3:C:735:LEU:HB3	3:C:750:ILE:HG21	2.01	0.42
3:C:749:LYS:O	3:C:753:THR:CB	2.67	0.42
3:C:995:ALA:HA	3:C:998:TYR:HB3	1.99	0.42
4:D:65:U:HO2'	9:I:59:LYS:HE3	1.82	0.42
1:A:1354:GLU:N	1:A:1355:PRO:HD2	2.35	0.42
1:A:1370:ARG:NH1	1:A:1370:ARG:CB	2.82	0.42
1:A:1417:GLN:OE1	1:A:1422:ILE:CD1	2.66	0.42
3:C:233:ASP:OD1	3:C:487:ARG:NH1	2.45	0.42
3:C:274:ILE:HG21	3:C:385:PHE:CD2	2.52	0.42
3:C:485:LEU:HA	3:C:563:LEU:HD23	2.01	0.42
3:C:687:ALA:C	3:C:689:ILE:HD12	2.45	0.42
3:C:693:ASN:N	3:C:841:LEU:HD13	2.34	0.42
3:C:794:GLN:CD	3:C:794:GLN:N	2.77	0.42
4:D:4:C:H2'	4:D:5:G:O4'	2.20	0.42
6:F:36:A:H2'	6:F:37:G:H8	1.85	0.42
8:H:508:LEU:O	8:H:511:ALA:HB3	2.19	0.42
8:H:605:PHE:O	8:H:609:GLU:HG2	2.20	0.42
15:O:376:TYR:HE1	15:O:383:LYS:HD3	1.85	0.42
15:O:418:GLU:OE2	15:O:424:LYS:HD2	2.20	0.42
21:U:680:MET:HE3	21:U:680:MET:HB3	1.75	0.42
22:V:201:MET:CG	22:V:201:MET:O	2.66	0.42
22:V:242:TRP:NE1	22:V:246:LEU:HD13	2.34	0.42
28:e:6:ILE:N	28:e:7:PRO:CD	2.82	0.42
1:A:1130:ARG:HG2	1:A:1156:HIS:CD2	2.55	0.42
3:C:883:ARG:NH1	3:C:917:ASP:OD2	2.53	0.42
5:E:496:U:C3'	5:E:497:A:H5''	2.49	0.42
9:I:38:LEU:CD2	10:J:189:ARG:NE	2.82	0.42
10:J:509:LEU:O	10:J:513:ILE:N	2.49	0.42
15:O:155:PHE:CD2	15:O:167:TRP:HB2	2.54	0.42
15:O:203:ASP:OD1	15:O:205:THR:OG1	2.29	0.42
21:U:674:ARG:H	21:U:674:ARG:HG3	1.79	0.42
25:i:77:LEU:HD23	25:i:78:GLY:N	2.35	0.42
1:A:275:TYR:HB2	1:A:310:ASN:HD22	1.85	0.42
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2048:TRP:O	1:A:2052:GLU:HG3	2.20	0.42
3:C:769:TYR:CD1	3:C:800:TYR:CD1	3.08	0.42
3:C:855:PRO:O	3:C:856:ILE:HG23	2.20	0.42
4:D:91:A:C5	11:K:97:TYR:CD1	3.08	0.42
6:F:112:A:N7	30:n:63:ARG:HB3	2.34	0.42
8:H:730:GLN:CA	8:H:733:ILE:CD1	2.86	0.42
14:N:159:ARG:O	14:N:163:VAL:HG23	2.19	0.42
15:O:265:HIS:NE2	15:O:283:SER:OG	2.43	0.42
21:U:675:ASN:CG	21:U:678:LYS:NZ	2.76	0.42
23:W:403:ASN:O	23:W:407:ARG:N	2.53	0.42
25:b:34:GLN:NE2	25:b:37:ILE:HD12	2.34	0.42
25:b:77:LEU:HD23	25:b:78:GLY:N	2.35	0.42
24:h:87:LEU:HG	24:h:92:ILE:HD11	2.00	0.42
1:A:854:ARG:CD	1:A:1095:MET:CE	2.96	0.42
1:A:1211:SER:OG	1:A:1268:ARG:NH1	2.52	0.42
1:A:1347:ARG:HB2	1:A:1447:TRP:NE1	2.34	0.42
6:F:34:G:OP2	6:F:34:G:H8	1.97	0.42
8:H:648:PHE:CD1	8:H:669:TYR:HB2	2.55	0.42
14:N:127:ILE:HG22	14:N:128:GLY:N	2.34	0.42
19:S:63:ARG:NH1	19:S:70:GLY:O	2.46	0.42
20:T:126:ILE:O	20:T:128:ARG:N	2.53	0.42
30:g:102:ILE:HG22	30:g:103:VAL:HG23	2.01	0.42
25:i:88:THR:HG22	25:i:89:LEU:HD12	2.01	0.42
1:A:288:GLU:HG2	1:A:288:GLU:O	2.20	0.42
1:A:354:PRO:C	1:A:356:TYR:H	2.28	0.42
1:A:404:ASN:CG	1:A:405:ASN:N	2.78	0.42
1:A:868:GLN:NE2	1:A:1100:LYS:HZ3	2.16	0.42
1:A:899:PRO:HD3	1:A:1006:ARG:HH12	1.85	0.42
1:A:978:ILE:O	16:P:174:VAL:HA	2.19	0.42
1:A:1014:LYS:HG3	1:A:1016:SER:OG	2.19	0.42
1:A:1021:PRO:HG2	1:A:1345:TYR:HE1	1.85	0.42
1:A:1388:PHE:HA	1:A:1397:LEU:HG	2.01	0.42
1:A:1502:LEU:HD22	1:A:1532:HIS:CE1	2.55	0.42
3:C:237:ILE:HB	3:C:265:PHE:CD1	2.55	0.42
9:I:205:TRP:CE3	9:I:221:VAL:HG11	2.55	0.42
12:L:119:THR:O	12:L:120:CYS:C	2.63	0.42
14:N:33:TRP:HD1	14:N:34:TYR:CD1	2.38	0.42
15:O:210:ASP:HB2	15:O:217:ILE:CG1	2.49	0.42
15:O:224:LEU:HD13	16:P:12:ARG:HG2	2.01	0.42
1:A:137:GLU:OE2	1:A:140:ARG:NH1	2.52	0.42
1:A:548:LEU:O	1:A:551:LEU:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:LEU:HD23	1:A:683:LEU:HA	1.90	0.42
1:A:732:ARG:NH1	4:D:73:A:P	2.93	0.42
1:A:775:ARG:O	1:A:779:ALA:N	2.44	0.42
1:A:910:LYS:CD	1:A:1504:TYR:CD2	3.02	0.42
1:A:1405:ILE:HB	1:A:1437:ILE:HD12	2.02	0.42
1:A:1458:TRP:HH2	22:V:246:LEU:HD21	1.81	0.42
1:A:1479:GLU:CD	1:A:1479:GLU:N	2.73	0.42
1:A:1562:PHE:HB2	1:A:1609:TRP:HH2	1.80	0.42
3:C:153:LEU:HD13	3:C:212:PHE:CZ	2.55	0.42
7:G:109:SER:O	7:G:110:GLU:CB	2.67	0.42
9:I:140:LEU:HD22	9:I:156:TYR:CE2	2.54	0.42
13:M:26:THR:O	13:M:44:TYR:HA	2.19	0.42
13:M:107:ASP:O	13:M:110:LYS:N	2.52	0.42
31:o:62:ASN:HB2	31:o:84:ASN:OD1	2.20	0.42
1:A:499:VAL:HG12	1:A:501:LEU:HD12	2.01	0.41
1:A:610:ARG:O	1:A:614:ARG:HG3	2.20	0.41
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.53	0.41
1:A:971:MET:HE3	1:A:978:ILE:HG22	2.02	0.41
1:A:1060:LYS:HA	1:A:1101:TYR:HE2	1.85	0.41
1:A:1174:PHE:HE2	1:A:1226:VAL:CG2	2.33	0.41
1:A:1393:GLU:HB3	1:A:1570:TRP:CZ2	2.55	0.41
1:A:1442:ARG:HH11	1:A:1442:ARG:CG	2.33	0.41
3:C:855:PRO:O	3:C:856:ILE:CG2	2.68	0.41
5:E:2:U:H2'	5:E:3:A:N7	2.34	0.41
6:F:17:U:O5'	6:F:17:U:H6	2.02	0.41
15:O:342:LEU:O	17:Q:45:PRO:CB	2.68	0.41
20:T:144:GLY:C	20:T:146:TRP:N	2.78	0.41
1:A:484:PHE:HE1	1:A:488:ARG:CD	2.34	0.41
1:A:810:LYS:NZ	15:O:397:GLU:HB3	2.35	0.41
1:A:1552:GLY:N	1:A:1555:THR:OG1	2.53	0.41
3:C:123:MET:HB2	3:C:199:LEU:HD23	2.03	0.41
4:D:42:A:HO2'	4:D:43:C:P	2.33	0.41
4:D:50:G:H22	5:E:2:U:H2'	1.82	0.41
6:F:21:G:C8	16:P:6:ARG:HB3	2.54	0.41
9:I:49:ARG:HH12	10:J:181:ARG:HH21	1.67	0.41
10:J:533:LEU:O	10:J:536:GLN:CG	2.68	0.41
12:L:138:THR:HG22	12:L:138:THR:O	2.20	0.41
14:N:75:PHE:O	14:N:80:MET:N	2.48	0.41
15:O:359:ASN:OD1	15:O:411:GLY:HA3	2.21	0.41
30:n:102:ILE:HG22	30:n:103:VAL:HG23	2.01	0.41
1:A:288:GLU:OE1	1:A:288:GLU:N	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:HIS:HB2	3:C:653:ASP:OD1	2.21	0.41
1:A:861:GLN:HE21	1:A:1097:HIS:CG	2.38	0.41
1:A:923:TYR:C	1:A:926:LYS:HG3	2.43	0.41
1:A:1057:MET:HE3	1:A:1121:ILE:HD12	2.02	0.41
1:A:1551:GLY:CA	1:A:1555:THR:HG21	2.50	0.41
3:C:135:ASN:O	3:C:233:ASP:N	2.50	0.41
5:E:495:A:C8	5:E:496:U:C4	3.09	0.41
14:N:163:VAL:CG1	14:N:199:MET:HE2	2.50	0.41
21:U:650:LYS:HE3	21:U:669:PRO:HB2	2.02	0.41
21:U:664:GLN:HA	21:U:664:GLN:HE21	1.79	0.41
21:U:675:ASN:OD1	21:U:678:LYS:NZ	2.52	0.41
23:W:550:SER:O	34:x:7:U:O4	2.39	0.41
33:s:59:GLN:O	33:s:60:ALA:HB3	2.20	0.41
33:t:112:VAL:O	33:t:115:GLU:CG	2.68	0.41
1:A:183:TRP:CD1	1:A:184:GLU:HG3	2.55	0.41
1:A:466:GLU:HG2	1:A:467:GLU:N	2.36	0.41
1:A:510:PRO:O	1:A:514:TYR:HD2	2.03	0.41
1:A:1724:PHE:HD1	1:A:1791:PHE:HA	1.86	0.41
1:A:1734:PHE:CD1	1:A:1773:VAL:HB	2.54	0.41
3:C:131:GLU:OE2	3:C:445:PRO:HG3	2.20	0.41
3:C:231:ALA:HB2	3:C:473:LEU:CD1	2.50	0.41
3:C:869:HIS:CD2	3:C:925:LEU:HD22	2.55	0.41
4:D:50:G:HO2'	4:D:51:A:P	2.43	0.41
4:D:51:A:O2'	4:D:52:G:P	2.79	0.41
9:I:175:PHE:HA	9:I:178:ARG:NH2	2.35	0.41
10:J:80:LEU:HA	10:J:81:PRO:HD2	1.93	0.41
14:N:146:LEU:HD23	14:N:147:ASN:N	2.35	0.41
15:O:329:ASP:OD2	15:O:349:LYS:HG3	2.21	0.41
18:R:167:GLU:CG	18:R:168:LYS:N	2.83	0.41
20:T:123:LEU:HD23	21:U:700:PRO:CG	2.34	0.41
21:U:691:VAL:O	21:U:699:LYS:HG2	2.20	0.41
1:A:430:PRO:O	1:A:431:ILE:HG22	2.20	0.41
1:A:1156:HIS:HD2	1:A:1158:ILE:HB	1.86	0.41
1:A:1343:PHE:HE1	1:A:1350:ILE:CB	2.29	0.41
1:A:1346:PHE:O	1:A:1349:ALA:N	2.52	0.41
1:A:1358:ASP:C	1:A:1360:LEU:N	2.77	0.41
1:A:1390:THR:OG1	1:A:1610:TRP:HZ2	2.01	0.41
3:C:348:LEU:O	3:C:372:THR:HB	2.20	0.41
3:C:861:ILE:HG21	3:C:905:GLN:HB3	2.01	0.41
3:C:1002:ARG:HH11	3:C:1002:ARG:CG	2.34	0.41
9:I:117:HIS:N	10:J:230:THR:HG22	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:65:PHE:CE1	10:J:93:ARG:CZ	3.04	0.41
10:J:146:ASP:O	10:J:149:LYS:HB2	2.21	0.41
15:O:306:HIS:CD2	17:Q:147:LEU:CD1	3.03	0.41
22:V:236:TYR:O	22:V:236:TYR:CD1	2.73	0.41
1:A:526:LEU:HD23	1:A:526:LEU:HA	1.89	0.41
1:A:831:ARG:HD3	1:A:848:ASN:HD21	1.85	0.41
1:A:912:LEU:HD11	1:A:951:LEU:CG	2.47	0.41
1:A:2013:ARG:NH1	1:A:2085:GLY:HA2	2.35	0.41
3:C:602:VAL:HG11	3:C:908:VAL:HG21	1.85	0.41
3:C:683:ASN:CB	3:C:854:ILE:HG13	2.50	0.41
5:E:495:A:C5	5:E:496:U:C4	3.08	0.41
6:F:1096:C:H2'	6:F:1097:G:H8	1.85	0.41
10:J:46:ARG:O	10:J:50:LEU:CB	2.69	0.41
20:T:146:TRP:HZ2	21:U:643:GLU:OE2	2.03	0.41
34:x:3:U:H4'	34:x:4:U:O5'	2.19	0.41
3:C:146:LYS:O	3:C:149:LEU:HB3	2.20	0.41
4:D:59:A:H3'	4:D:60:G:C5'	2.50	0.41
5:E:494:G:O2'	5:E:495:A:P	2.78	0.41
7:G:113:LEU:O	7:G:116:ILE:CG1	2.69	0.41
14:N:76:PHE:C	14:N:79:GLY:H	2.28	0.41
15:O:236:LEU:HD11	17:Q:70:THR:HG21	2.02	0.41
15:O:379:LYS:CD	17:Q:47:ARG:NH2	2.82	0.41
22:V:213:ASP:O	22:V:216:ILE:HB	2.21	0.41
1:A:260:PRO:O	1:A:261:LEU:HB3	2.20	0.41
1:A:402:TRP:CZ3	3:C:188:GLY:CA	3.03	0.41
1:A:584:HIS:HB3	14:N:31:ASN:OD1	2.20	0.41
1:A:2054:GLN:O	1:A:2058:LEU:HG	2.21	0.41
3:C:353:TYR:CD1	3:C:371:PRO:HA	2.55	0.41
6:F:5:A:H5'	11:K:114:THR:CB	2.51	0.41
9:I:49:ARG:NH1	10:J:181:ARG:CZ	2.83	0.41
10:J:224:MET:HE3	10:J:225:PRO:HD2	2.03	0.41
12:L:80:TRP:CZ2	12:L:84:GLU:HG3	2.55	0.41
14:N:46:ARG:HH22	14:N:222:LEU:HG	1.85	0.41
14:N:46:ARG:NH2	14:N:220:GLY:O	2.54	0.41
15:O:306:HIS:CG	15:O:334:TRP:HH2	2.39	0.41
19:S:59:ARG:HH11	19:S:59:ARG:CG	2.33	0.41
21:U:654:ARG:CG	21:U:654:ARG:NH1	2.83	0.41
26:j:32:LYS:HG3	26:j:77:ASN:HA	2.03	0.41
1:A:140:ARG:HH21	1:A:252:GLU:CB	2.34	0.41
1:A:236:ARG:NH1	35:A:3000:IHP:O41	2.48	0.41
1:A:680:CYS:SG	1:A:711:TRP:NE1	2.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:VAL:HG22	15:O:221:TYR:CZ	2.56	0.41
1:A:903:LEU:CD1	18:R:180:ASP:OD1	2.67	0.41
1:A:923:TYR:CD2	1:A:937:LEU:HB2	2.55	0.41
1:A:1265:PHE:HZ	1:A:1345:TYR:O	2.04	0.41
1:A:1320:LEU:HD23	1:A:1320:LEU:HA	1.92	0.41
1:A:1358:ASP:CG	1:A:1359:ILE:H	2.29	0.41
1:A:1370:ARG:CZ	1:A:1370:ARG:CB	2.91	0.41
1:A:1392:LYS:HD2	1:A:1392:LYS:H	1.86	0.41
1:A:1419:ASP:HB3	1:A:1803:ARG:NE	2.36	0.41
1:A:1711:VAL:CG1	1:A:1789:ASN:HB3	2.48	0.41
1:A:1752:VAL:HG12	1:A:1787:TYR:HB3	2.02	0.41
1:A:1843:LEU:HD23	1:A:1849:LYS:NZ	2.36	0.41
1:A:1859:ARG:O	1:A:1874:ALA:HA	2.21	0.41
1:A:1889:LEU:O	1:A:1988:LEU:HA	2.21	0.41
1:A:1891:LEU:HD12	1:A:1989:PHE:CE2	2.56	0.41
3:C:138:VAL:HG21	3:C:150:MET:HE3	2.01	0.41
3:C:184:GLU:OE2	3:C:192:LYS:N	2.51	0.41
3:C:344:PHE:CE1	3:C:359:PHE:HZ	2.39	0.41
3:C:353:TYR:CE2	3:C:363:PRO:HD3	2.56	0.41
3:C:430:ARG:C	3:C:431:GLN:O	2.64	0.41
3:C:769:TYR:HD1	3:C:800:TYR:CE1	2.33	0.41
4:D:87:U:OP1	4:D:87:U:H4'	2.21	0.41
5:E:3:A:H3'	5:E:4:U:H6	1.86	0.41
5:E:499:U:O5'	5:E:499:U:C6	2.72	0.41
8:H:652:LEU:HA	8:H:652:LEU:HD12	1.85	0.41
9:I:42:GLU:CD	10:J:185:LEU:HD22	2.45	0.41
9:I:116:ASN:HD22	10:J:230:THR:HA	1.86	0.41
10:J:162:THR:HG21	17:Q:177:GLY:HA3	2.03	0.41
10:J:517:VAL:O	10:J:521:GLU:N	2.46	0.41
13:M:101:THR:HG22	13:M:120:LEU:CD1	2.33	0.41
14:N:54:GLN:H	14:N:58:HIS:HD2	1.68	0.41
20:T:102:LEU:HD23	20:T:102:LEU:HA	1.93	0.41
27:d:26:ALA:C	27:d:43:ALA:HB3	2.46	0.41
1:A:147:SER:OG	1:A:573:ARG:NH1	2.54	0.41
1:A:177:GLU:CB	1:A:712:LEU:HD11	2.51	0.41
1:A:882:ILE:HD11	1:A:1238:LEU:HD11	2.03	0.41
1:A:1049:LEU:HD23	1:A:1049:LEU:HA	1.87	0.41
1:A:1265:PHE:HE1	1:A:1346:PHE:HA	1.84	0.41
1:A:1661:ILE:HG13	1:A:1809:ASN:HD21	1.85	0.41
1:A:1773:VAL:HG22	1:A:1788:GLY:HA3	2.03	0.41
35:A:3000:IHP:O15	35:A:3000:IHP:P6	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:542:ILE:HA	3:C:563:LEU:O	2.21	0.41
3:C:691:VAL:HG13	3:C:841:LEU:HD12	2.03	0.41
3:C:748:SER:HB2	3:C:762:SER:HB3	2.03	0.41
3:C:794:GLN:OE1	3:C:794:GLN:HA	2.21	0.41
6:F:1115:G:C6	6:F:1116:A:N6	2.89	0.41
12:L:104:CYS:HB2	12:L:153:CYS:SG	2.60	0.41
22:V:210:ALA:HB1	22:V:215:GLN:NE2	2.35	0.41
33:s:101:THR:O	33:s:105:LEU:CG	2.69	0.41
1:A:179:MET:HE2	1:A:179:MET:HB3	1.93	0.40
1:A:522:TYR:CE2	1:A:686:ILE:HD12	2.56	0.40
1:A:790:TRP:NE1	1:A:794:LYS:HE3	2.36	0.40
1:A:1494:LEU:CD2	22:V:246:LEU:HD22	2.50	0.40
1:A:1539:LEU:HD12	1:A:1539:LEU:HA	1.82	0.40
1:A:1893:ILE:HG21	1:A:1981:ALA:HB3	2.03	0.40
1:A:1951:PHE:HB3	1:A:1954:ILE:HD12	2.03	0.40
3:C:213:LEU:HD23	3:C:213:LEU:HA	1.83	0.40
3:C:373:PHE:O	3:C:377:ILE:HB	2.21	0.40
3:C:757:TRP:HD1	3:C:762:SER:OG	2.04	0.40
3:C:860:PRO:C	3:C:908:VAL:HG12	2.44	0.40
4:D:75:A:H2'	4:D:76:A:H5'	2.03	0.40
5:E:9:U:O4'	5:E:10:U:OP2	2.39	0.40
8:H:670:SER:CB	8:H:687:LEU:HD11	2.51	0.40
9:I:239:SER:O	9:I:242:GLU:HB3	2.21	0.40
10:J:15:ASN:O	10:J:19:GLN:HG2	2.21	0.40
12:L:151:ARG:NH2	19:S:69:TRP:O	2.54	0.40
14:N:72:PHE:CE1	14:N:90:LEU:HD12	2.56	0.40
20:T:139:PHE:C	20:T:141:LEU:HD22	2.46	0.40
30:g:49:ARG:HA	30:g:102:ILE:HD11	2.03	0.40
1:A:288:GLU:H	1:A:288:GLU:CD	2.30	0.40
1:A:662:GLN:NE2	1:A:1620:TYR:CE1	2.89	0.40
1:A:926:LYS:HB3	1:A:926:LYS:HZ3	1.78	0.40
1:A:1708:GLU:HG3	1:A:1730:ASN:OD1	2.21	0.40
1:A:1711:VAL:HG12	1:A:1712:SER:H	1.86	0.40
1:A:1865:THR:OG1	1:A:1869:ASN:HB2	2.21	0.40
9:I:248:ASN:O	9:I:252:HIS:HB2	2.20	0.40
14:N:55:PRO:O	14:N:59:SER:OG	2.29	0.40
17:Q:34:ILE:HG23	17:Q:35:ALA:N	2.35	0.40
17:Q:104:LEU:HG	17:Q:108:ASN:CG	2.47	0.40
20:T:139:PHE:CB	20:T:141:LEU:CD2	2.74	0.40
21:U:696:GLY:O	21:U:697:THR:CB	2.69	0.40
22:V:237:ARG:HA	22:V:237:ARG:HD2	1.81	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:HB3	1:A:622:MET:HE3	2.04	0.40
1:A:579:LEU:HD23	1:A:579:LEU:HA	1.86	0.40
1:A:910:LYS:CD	1:A:1504:TYR:CE2	3.04	0.40
3:C:252:LEU:HA	3:C:252:LEU:HD23	1.85	0.40
3:C:377:ILE:O	3:C:380:PRO:HG2	2.21	0.40
3:C:391:MET:HE2	3:C:395:LYS:HG2	2.02	0.40
4:D:57:U:C6	4:D:57:U:C4'	3.05	0.40
9:I:176:GLU:HG3	9:I:188:ILE:CD1	2.51	0.40
9:I:233:GLN:HG2	9:I:274:TRP:CZ2	2.56	0.40
10:J:39:LEU:HD11	10:J:158:ARG:HD2	2.02	0.40
14:N:92:HIS:HE1	14:N:98:ASP:OD2	2.03	0.40
14:N:210:LYS:HG3	14:N:211:GLU:N	2.36	0.40
15:O:437:GLU:N	15:O:438:PRO:CD	2.84	0.40
17:Q:105:LEU:HG	17:Q:106:LEU:HG	2.03	0.40
21:U:692:GLU:HB3	21:U:698:PHE:CD1	2.56	0.40
26:c:32:LYS:HG3	26:c:77:ASN:HA	2.02	0.40
27:k:26:ALA:C	27:k:43:ALA:HB3	2.46	0.40
1:A:847:LYS:HE2	1:A:847:LYS:HB3	1.84	0.40
1:A:1012:TRP:HZ3	1:A:1122:ASP:OD2	2.04	0.40
1:A:1204:ARG:NH1	1:A:1247:PHE:CD2	2.89	0.40
1:A:1857:VAL:HG13	1:A:1894:ILE:HD12	2.03	0.40
1:A:1879:ILE:HB	1:A:1892:LYS:HB3	2.02	0.40
3:C:118:TYR:CD1	3:C:199:LEU:HG	2.56	0.40
3:C:393:LYS:O	3:C:397:LYS:HB2	2.20	0.40
3:C:544:LEU:HG	3:C:553:VAL:HG21	2.02	0.40
3:C:861:ILE:CG2	3:C:936:ILE:HD11	2.51	0.40
3:C:885:GLY:HA3	3:C:907:PRO:HG2	2.01	0.40
5:E:15:U:C4'	14:N:231:ASP:HB3	2.52	0.40
6:F:110:A:N1	29:m:2:LYS:HE3	2.36	0.40
8:H:520:ILE:O	8:H:524:LYS:N	2.54	0.40
10:J:230:THR:OG1	10:J:231:SER:N	2.48	0.40
13:M:62:VAL:HA	13:M:72:GLN:NE2	2.36	0.40
15:O:342:LEU:O	17:Q:45:PRO:HB2	2.21	0.40
15:O:418:GLU:OE1	15:O:424:LYS:NZ	2.32	0.40
16:P:134:GLY:O	16:P:135:ARG:CB	2.70	0.40
19:S:63:ARG:NH1	19:S:68:PRO:O	2.55	0.40
21:U:165:LEU:C	22:V:268:PRO:CB	2.94	0.40
21:U:352:PHE:O	21:U:358:PHE:CB	2.70	0.40
21:U:648:ILE:HG23	21:U:673:ILE:CG2	2.50	0.40
22:V:246:LEU:C	22:V:246:LEU:CD2	2.83	0.40
1:A:183:TRP:HE3	1:A:220:THR:HG21	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:LEU:C	1:A:712:LEU:HD23	2.45	0.40
1:A:817:LYS:HG2	15:O:399:GLU:OE2	2.22	0.40
1:A:1047:ALA:CB	1:A:1251:TYR:HB3	2.16	0.40
1:A:1287:ASP:OD2	1:A:1296:ARG:NH2	2.55	0.40
1:A:1309:ILE:HG12	1:A:1356:LEU:HG	2.02	0.40
1:A:1756:PHE:CZ	1:A:1760:THR:HG21	2.56	0.40
3:C:201:THR:HA	3:C:207:SER:HA	2.03	0.40
4:D:85:C:H42	10:J:166:LYS:HD2	1.86	0.40
6:F:1105:C:H42	32:p:97:LYS:HZ1	1.67	0.40
7:G:31:ILE:O	7:G:32:LYS:CB	2.68	0.40
10:J:227:ILE:HD12	17:Q:33:GLN:OE1	2.20	0.40
14:N:111:CYS:N	14:N:193:GLU:OE1	2.46	0.40
21:U:651:ILE:CD1	21:U:672:GLU:N	2.83	0.40
21:U:699:LYS:HB2	21:U:699:LYS:HZ3	1.82	0.40
21:U:704:TRP:CE3	21:U:705:ALA:HB2	2.56	0.40
30:n:49:ARG:HA	30:n:102:ILE:HD11	2.03	0.40
33:q:78:PRO:HG3	33:s:88:TRP:CZ2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1895/2413 (78%)	1750 (92%)	125 (7%)	20 (1%)	11	42
3	C	907/1008 (90%)	820 (90%)	70 (8%)	17 (2%)	6	33
7	G	149/175 (85%)	134 (90%)	12 (8%)	3 (2%)	6	32
8	H	529/859 (62%)	505 (96%)	18 (3%)	6 (1%)	11	42
9	I	500/687 (73%)	468 (94%)	30 (6%)	2 (0%)	30	62
10	J	413/590 (70%)	384 (93%)	22 (5%)	7 (2%)	7	35
11	K	98/215 (46%)	96 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	155/157 (99%)	136 (88%)	17 (11%)	2 (1%)	9	39
13	M	172/364 (47%)	151 (88%)	19 (11%)	2 (1%)	10	41
14	N	259/339 (76%)	241 (93%)	18 (7%)	0	100	100
15	O	335/451 (74%)	295 (88%)	34 (10%)	6 (2%)	6	34
16	P	62/175 (35%)	56 (90%)	4 (6%)	2 (3%)	3	24
17	Q	193/379 (51%)	175 (91%)	13 (7%)	5 (3%)	4	27
18	R	44/278 (16%)	44 (100%)	0	0	100	100
19	S	21/455 (5%)	19 (90%)	1 (5%)	1 (5%)	2	16
20	T	97/283 (34%)	93 (96%)	4 (4%)	0	100	100
21	U	442/708 (62%)	430 (97%)	5 (1%)	7 (2%)	7	36
22	V	87/322 (27%)	82 (94%)	4 (5%)	1 (1%)	11	42
23	W	702/767 (92%)	657 (94%)	39 (6%)	6 (1%)	14	46
24	a	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
24	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
25	b	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
26	c	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
26	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
27	d	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
28	e	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
28	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
29	f	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
29	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
30	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	11	42
30	n	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	7	36
31	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	36
32	p	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
33	q	120/503 (24%)	114 (95%)	4 (3%)	2 (2%)	7	35
33	r	123/503 (24%)	117 (95%)	6 (5%)	0	100	100
33	s	125/503 (25%)	115 (92%)	6 (5%)	4 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	t	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	28
All	All	8774/14606 (60%)	8126 (93%)	544 (6%)	104 (1%)	13	41

All (104) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1347	ARG
1	A	1359	ILE
1	A	1385	PRO
1	A	1403	SER
3	C	363	PRO
3	C	366	ASN
3	C	431	GLN
3	C	464	PRO
3	C	466	GLY
3	C	683	ASN
3	C	685	SER
7	G	77	PRO
8	H	616	PRO
8	H	797	TYR
9	I	315	ASN
10	J	417	PRO
10	J	418	PRO
16	P	7	PRO
21	U	633	PHE
21	U	634	LYS
21	U	661	GLY
22	V	213	ASP
23	W	463	SER
23	W	599	ILE
31	o	68	PRO
33	s	53	ILE
33	s	77	ILE
33	t	64	GLU
1	A	483	PRO
1	A	1358	ASP
3	C	357	GLY
3	C	532	ASP
7	G	110	GLU
8	H	601	VAL
8	H	618	GLU
10	J	230	THR

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Mol	Chain	Res	Type
10	J	415	ILE
13	M	99	VAL
13	M	236	ASN
16	P	9	LEU
17	Q	36	LYS
17	Q	86	ASN
17	Q	112	ILE
23	W	734	GLY
33	q	56	SER
1	A	540	THR
1	A	645	ASP
1	A	741	ILE
3	C	116	THR
3	C	829	VAL
7	G	80	ASN
8	H	634	HIS
8	H	752	GLU
15	O	124	GLU
19	S	61	LYS
23	W	453	SER
23	W	598	GLY
33	q	17	PRO
33	t	20	ARG
1	A	377	VAL
1	A	1384	PRO
1	A	1628	ASP
3	C	994	SER
9	I	529	LYS
10	J	231	SER
12	L	104	CYS
15	O	278	ASP
15	O	279	PRO
15	O	391	GLU
21	U	697	THR
28	e	82	PRO
30	g	82	LYS
28	l	82	PRO
30	n	82	LYS
1	A	1327	THR
3	C	649	GLU
3	C	655	LEU
3	C	690	PRO

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Mol	Chain	Res	Type
3	C	884	ARG
12	L	120	CYS
15	O	435	GLU
17	Q	102	ALA
21	U	651	ILE
33	s	60	ALA
1	A	240	PRO
1	A	261	LEU
1	A	407	VAL
1	A	875	THR
1	A	1015	PRO
21	U	659	PRO
23	W	709	THR
1	A	259	GLU
10	J	218	VAL
21	U	676	GLY
26	c	15	PRO
31	o	52	LYS
26	j	15	PRO
33	s	36	GLY
3	C	975	GLY
15	O	277	VAL
1	A	264	ILE
10	J	16	VAL
17	Q	34	ILE
33	t	36	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1727/2182 (79%)	1648 (95%)	79 (5%)	24	51
3	C	822/910 (90%)	783 (95%)	39 (5%)	23	51
7	G	40/165 (24%)	27 (68%)	13 (32%)	0	2
8	H	59/786 (8%)	48 (81%)	11 (19%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	219/633 (35%)	216 (99%)	3 (1%)	59	72
10	J	213/525 (41%)	202 (95%)	11 (5%)	21	49
11	K	92/193 (48%)	92 (100%)	0	100	100
12	L	141/141 (100%)	138 (98%)	3 (2%)	47	66
13	M	121/332 (36%)	115 (95%)	6 (5%)	22	49
14	N	224/296 (76%)	221 (99%)	3 (1%)	61	73
15	O	295/397 (74%)	295 (100%)	0	100	100
16	P	55/151 (36%)	54 (98%)	1 (2%)	51	70
17	Q	173/328 (53%)	161 (93%)	12 (7%)	14	41
18	R	40/256 (16%)	29 (72%)	11 (28%)	0	3
19	S	20/413 (5%)	13 (65%)	7 (35%)	0	1
20	T	75/272 (28%)	56 (75%)	19 (25%)	0	3
21	U	76/663 (12%)	48 (63%)	28 (37%)	0	1
22	V	47/296 (16%)	31 (66%)	16 (34%)	0	2
24	a	70/176 (40%)	69 (99%)	1 (1%)	59	72
24	h	67/176 (38%)	66 (98%)	1 (2%)	57	72
25	b	65/83 (78%)	60 (92%)	5 (8%)	12	38
25	i	65/83 (78%)	60 (92%)	5 (8%)	12	38
26	c	61/77 (79%)	60 (98%)	1 (2%)	55	71
26	j	61/77 (79%)	60 (98%)	1 (2%)	55	71
27	d	58/66 (88%)	56 (97%)	2 (3%)	32	59
27	k	58/66 (88%)	56 (97%)	2 (3%)	32	59
28	e	69/89 (78%)	68 (99%)	1 (1%)	59	72
28	l	69/89 (78%)	68 (99%)	1 (1%)	59	72
29	f	77/129 (60%)	74 (96%)	3 (4%)	28	56
29	m	77/129 (60%)	74 (96%)	3 (4%)	28	56
30	g	79/103 (77%)	73 (92%)	6 (8%)	12	38
30	n	59/103 (57%)	54 (92%)	5 (8%)	10	35
31	o	47/219 (22%)	44 (94%)	3 (6%)	16	43
32	p	25/100 (25%)	25 (100%)	0	100	100
33	q	62/451 (14%)	56 (90%)	6 (10%)	8	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	r	62/451 (14%)	54 (87%)	8 (13%)	4	21
33	s	63/451 (14%)	55 (87%)	8 (13%)	4	22
33	t	60/451 (13%)	55 (92%)	5 (8%)	10	35
All	All	5693/12508 (46%)	5364 (94%)	329 (6%)	20	45

All (329) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	331	PHE
1	A	365	ASN
1	A	372	ARG
1	A	376	ARG
1	A	380	ARG
1	A	382	GLU
1	A	461	LEU
1	A	489	THR
1	A	495	ARG
1	A	588	LEU
1	A	612	LYS
1	A	689	TYR
1	A	693	LYS
1	A	742	VAL
1	A	874	ILE
1	A	893	ARG
1	A	903	LEU
1	A	906	LYS
1	A	926	LYS
1	A	927	VAL
1	A	928	ARG
1	A	934	ARG
1	A	936	GLU
1	A	937	LEU
1	A	941	GLU
1	A	1011	ASN
1	A	1045	GLN
1	A	1046	SER
1	A	1049	LEU
1	A	1050	LEU
1	A	1068	ARG
1	A	1130	ARG
1	A	1171	LEU

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Mol	Chain	Res	Type
1	A	1173	HIS
1	A	1181	GLU
1	A	1250	VAL
1	A	1292	ARG
1	A	1295	GLN
1	A	1296	ARG
1	A	1297	THR
1	A	1326	THR
1	A	1328	PHE
1	A	1331	VAL
1	A	1334	LYS
1	A	1337	THR
1	A	1339	LEU
1	A	1341	SER
1	A	1342	LEU
1	A	1356	LEU
1	A	1360	LEU
1	A	1361	VAL
1	A	1362	LYS
1	A	1370	ARG
1	A	1381	THR
1	A	1390	THR
1	A	1392	LYS
1	A	1393	GLU
1	A	1394	LEU
1	A	1405	ILE
1	A	1415	SER
1	A	1416	LYS
1	A	1418	THR
1	A	1441	PHE
1	A	1442	ARG
1	A	1443	TYR
1	A	1448	GLU
1	A	1464	LYS
1	A	1465	ARG
1	A	1474	ARG
1	A	1475	LEU
1	A	1477	PHE
1	A	1479	GLU
1	A	1480	LEU
1	A	1536	LEU
1	A	1539	LEU

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Mol	Chain	Res	Type
1	A	1545	ASP
1	A	1550	LEU
1	A	1571	GLU
1	A	1661	ILE
3	C	117	ARG
3	C	199	LEU
3	C	205	SER
3	C	208	ARG
3	C	272	ARG
3	C	274	ILE
3	C	275	LEU
3	C	276	ASP
3	C	356	LYS
3	C	360	ARG
3	C	361	THR
3	C	362	LYS
3	C	363	PRO
3	C	368	GLU
3	C	430	ARG
3	C	458	ILE
3	C	461	LYS
3	C	463	THR
3	C	465	GLU
3	C	468	LEU
3	C	510	ARG
3	C	530	GLU
3	C	638	GLU
3	C	683	ASN
3	C	685	SER
3	C	686	PHE
3	C	883	ARG
3	C	884	ARG
3	C	887	ARG
3	C	888	ILE
3	C	890	LYS
3	C	919	ARG
3	C	932	PHE
3	C	971	ARG
3	C	982	MET
3	C	989	LEU
3	C	997	LEU
3	C	1002	ARG

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Mol	Chain	Res	Type
3	C	1006	LEU
7	G	5	SER
7	G	7	VAL
7	G	13	PRO
7	G	77	PRO
7	G	96	PRO
7	G	100	THR
7	G	105	PRO
7	G	108	SER
7	G	111	VAL
7	G	133	PRO
7	G	136	VAL
7	G	150	THR
7	G	152	THR
8	H	616	PRO
8	H	617	PRO
8	H	641	PRO
8	H	681	SER
8	H	706	LEU
8	H	712	CYS
8	H	722	PRO
8	H	723	SER
8	H	725	THR
8	H	726	ARG
8	H	733	ILE
9	I	155	LEU
9	I	205	TRP
9	I	269	ILE
10	J	20	ILE
10	J	160	LEU
10	J	166	LYS
10	J	169	ARG
10	J	504	PRO
10	J	505	PRO
10	J	506	THR
10	J	517	VAL
10	J	523	LEU
10	J	532	PRO
10	J	550	PRO
12	L	104	CYS
12	L	120	CYS
12	L	122	CYS

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Mol	Chain	Res	Type
13	M	53	ASN
13	M	56	ILE
13	M	87	ARG
13	M	118	VAL
13	M	120	LEU
13	M	126	THR
14	N	8	SER
14	N	10	LYS
14	N	146	LEU
16	P	7	PRO
17	Q	112	ILE
17	Q	122	LEU
17	Q	202	MET
17	Q	204	LEU
17	Q	206	GLU
17	Q	209	GLU
17	Q	213	LYS
17	Q	216	ARG
17	Q	217	GLN
17	Q	219	ILE
17	Q	220	ARG
17	Q	222	LYS
18	R	167	GLU
18	R	168	LYS
18	R	170	LEU
18	R	172	LYS
18	R	175	GLN
18	R	177	GLN
18	R	191	LEU
18	R	193	MET
18	R	196	ARG
18	R	198	GLU
18	R	202	ARG
19	S	51	PHE
19	S	55	GLU
19	S	57	LYS
19	S	58	ARG
19	S	59	ARG
19	S	62	THR
19	S	66	ASP
20	T	23	PRO
20	T	24	THR

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Mol	Chain	Res	Type
20	T	36	PRO
20	T	81	PRO
20	T	84	ASP
20	T	96	ASP
20	T	97	ILE
20	T	99	ARG
20	T	101	LYS
20	T	106	LEU
20	T	107	GLU
20	T	109	SER
20	T	128	ARG
20	T	132	LEU
20	T	133	LEU
20	T	135	LYS
20	T	140	ASN
20	T	143	TYR
20	T	146	TRP
21	U	641	CYS
21	U	642	LEU
21	U	646	TYR
21	U	648	ILE
21	U	650	LYS
21	U	653	ASN
21	U	656	THR
21	U	657	GLN
21	U	658	LEU
21	U	667	ILE
21	U	668	VAL
21	U	670	LEU
21	U	671	PHE
21	U	672	GLU
21	U	674	ARG
21	U	677	LYS
21	U	678	LYS
21	U	680	MET
21	U	681	GLU
21	U	684	LEU
21	U	687	ASP
21	U	689	LEU
21	U	691	VAL
21	U	693	ASP
21	U	699	LYS

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Mol	Chain	Res	Type
21	U	703	LEU
21	U	707	ASP
21	U	708	LEU
22	V	205	GLN
22	V	206	ASP
22	V	207	GLU
22	V	208	MET
22	V	209	LEU
22	V	211	LEU
22	V	215	GLN
22	V	219	GLN
22	V	229	LYS
22	V	231	ILE
22	V	233	GLU
22	V	236	TYR
22	V	237	ARG
22	V	241	GLU
22	V	245	GLN
22	V	249	LYS
24	a	47	GLU
25	b	16	CYS
25	b	18	PHE
25	b	25	THR
25	b	79	LYS
25	b	81	LEU
26	c	79	LEU
27	d	18	ASN
27	d	71	LEU
28	e	10	LEU
29	f	20	LYS
29	f	30	GLN
29	f	77	ASP
30	g	24	PHE
30	g	48	LEU
30	g	49	ARG
30	g	77	THR
30	g	99	ASP
30	g	100	SER
31	o	4	THR
31	o	44	PRO
31	o	71	SER
24	h	47	GLU

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Mol	Chain	Res	Type
25	i	16	CYS
25	i	18	PHE
25	i	25	THR
25	i	79	LYS
25	i	81	LEU
26	j	79	LEU
27	k	18	ASN
27	k	71	LEU
28	l	10	LEU
29	m	20	LYS
29	m	30	GLN
29	m	77	ASP
30	n	48	LEU
30	n	49	ARG
30	n	77	THR
30	n	99	ASP
30	n	100	SER
33	q	17	PRO
33	q	26	SER
33	q	44	PRO
33	q	63	THR
33	q	109	LEU
33	q	134	SER
33	r	17	PRO
33	r	44	PRO
33	r	63	THR
33	r	80	LEU
33	r	85	GLN
33	r	93	LEU
33	r	98	LEU
33	r	109	LEU
33	s	14	VAL
33	s	17	PRO
33	s	44	PRO
33	s	55	PRO
33	s	56	SER
33	s	61	SER
33	s	102	LEU
33	s	126	LEU
33	t	17	PRO
33	t	44	PRO
33	t	63	THR

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Mol	Chain	Res	Type
33	t	93	LEU
33	t	109	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	265	ASN
1	A	365	ASN
1	A	392	ASN
1	A	405	ASN
1	A	429	ASN
1	A	542	HIS
1	A	658	ASN
1	A	659	HIS
1	A	662	GLN
1	A	705	GLN
1	A	796	ASN
1	A	848	ASN
1	A	861	GLN
1	A	864	GLN
1	A	868	GLN
1	A	948	HIS
1	A	1011	ASN
1	A	1033	ASN
1	A	1045	GLN
1	A	1097	HIS
1	A	1099	ASN
1	A	1156	HIS
1	A	1376	ASN
1	A	1417	GLN
1	A	1424	HIS
1	A	1470	GLN
1	A	1508	HIS
1	A	1635	HIS
1	A	1652	HIS
1	A	1718	HIS
1	A	1737	GLN
1	A	1863	HIS
1	A	1947	HIS
1	A	2018	ASN
3	C	82	ASN

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Mol	Chain	Res	Type
3	C	101	GLN
3	C	251	GLN
3	C	289	ASN
3	C	403	ASN
3	C	423	HIS
3	C	444	GLN
3	C	683	ASN
3	C	764	ASN
3	C	794	GLN
3	C	817	GLN
3	C	830	ASN
3	C	869	HIS
3	C	1004	ASN
9	I	79	HIS
10	J	214	ASN
11	K	200	ASN
12	L	54	GLN
12	L	56	HIS
12	L	116	ASN
12	L	143	HIS
13	M	53	ASN
13	M	81	HIS
13	M	117	ASN
14	N	58	HIS
14	N	91	HIS
14	N	92	HIS
14	N	150	HIS
14	N	191	ASN
14	N	201	ASN
14	N	227	ASN
14	N	248	ASN
15	O	126	HIS
15	O	138	HIS
15	O	215	GLN
15	O	344	ASN
15	O	382	HIS
15	O	428	GLN
16	P	8	GLN
16	P	34	HIS
16	P	173	HIS
17	Q	37	ASN
17	Q	111	HIS

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Mol	Chain	Res	Type
17	Q	198	ASN
17	Q	217	GLN
20	T	50	HIS
20	T	104	GLN
20	T	138	HIS
21	U	664	GLN
21	U	686	HIS
24	a	8	HIS
24	a	91	GLN
25	b	34	GLN
25	b	86	ASN
26	c	25	HIS
26	c	52	GLN
26	c	54	ASN
27	d	66	ASN
28	e	41	ASN
29	f	30	GLN
29	f	86	ASN
31	o	62	ASN
24	h	91	GLN
25	i	34	GLN
25	i	86	ASN
26	j	25	HIS
26	j	52	GLN
26	j	54	ASN
27	k	66	ASN
28	l	17	HIS
28	l	41	ASN
29	m	86	ASN
30	n	71	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	114/214 (53%)	30 (26%)	3 (2%)
34	x	8/9 (88%)	5 (62%)	0
4	D	100/112 (89%)	35 (35%)	8 (8%)
5	E	27/38 (71%)	15 (55%)	7 (25%)
6	F	79/1175 (6%)	30 (37%)	11 (13%)
All	All	328/1548 (21%)	115 (35%)	29 (8%)

All (115) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	29	G
2	B	31	G
2	B	32	G
2	B	33	U
2	B	42	A
2	B	44	A
2	B	74	U
2	B	75	A
2	B	76	U
2	B	77	A
2	B	79	C
2	B	80	G
2	B	81	A
2	B	82	A
2	B	84	A
2	B	90	C
2	B	92	U
2	B	94	C
2	B	101	C
2	B	104	G
2	B	127	U
2	B	164	C
2	B	165	A
2	B	166	U
2	B	170	U
2	B	171	U
2	B	172	U
2	B	173	U
2	B	174	G
2	B	175	G
4	D	12	A
4	D	13	A
4	D	14	C
4	D	15	C
4	D	16	C
4	D	33	C
4	D	36	U
4	D	37	U
4	D	39	G
4	D	43	C
4	D	50	G
4	D	51	A
4	D	52	G

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Mol	Chain	Res	Type
4	D	54	U
4	D	57	U
4	D	58	C
4	D	59	A
4	D	60	G
4	D	62	A
4	D	65	U
4	D	66	C
4	D	67	C
4	D	68	C
4	D	73	A
4	D	74	U
4	D	75	A
4	D	80	U
4	D	81	G
4	D	85	C
4	D	86	G
4	D	87	U
4	D	88	U
4	D	90	U
4	D	91	A
4	D	92	C
5	E	2	U
5	E	3	A
5	E	4	U
5	E	9	U
5	E	10	U
5	E	11	A
5	E	13	U
5	E	494	G
5	E	495	A
5	E	496	U
5	E	497	A
5	E	500	A
5	E	501	A
5	E	502	C
5	E	503	A
6	F	15	C
6	F	16	U
6	F	17	U
6	F	18	U
6	F	19	U

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Mol	Chain	Res	Type
6	F	20	G
6	F	25	A
6	F	26	G
6	F	30	A
6	F	31	A
6	F	32	G
6	F	34	G
6	F	39	A
6	F	40	U
6	F	41	C
6	F	42	U
6	F	111	C
6	F	115	U
6	F	116	U
6	F	117	U
6	F	118	U
6	F	119	G
6	F	120	G
6	F	1099	G
6	F	1107	C
6	F	1108	A
6	F	1111	U
6	F	1112	G
6	F	1114	G
6	F	1120	G
34	x	2	U
34	x	3	U
34	x	4	U
34	x	8	U
34	x	9	U

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	78	A
2	B	83	C
2	B	172	U
4	D	14	C
4	D	42	A
4	D	51	A
4	D	56	A
4	D	57	U

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Mol	Chain	Res	Type
4	D	58	C
4	D	64	U
4	D	66	C
5	E	1	G
5	E	2	U
5	E	3	A
5	E	9	U
5	E	494	G
5	E	499	U
5	E	500	A
6	F	15	C
6	F	16	U
6	F	17	U
6	F	18	U
6	F	19	U
6	F	30	A
6	F	40	U
6	F	41	C
6	F	117	U
6	F	1107	C
6	F	1111	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 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
36	GTP	C	1500	37	33,34,34	1.32	4 (12%)	50,54,54	1.96	11 (22%)
35	IHP	A	3000	-	36,36,36	0.69	0	60,60,60	0.98	0

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
36	GTP	C	1500	37	-	5/22/38/38	0/3/3/3
35	IHP	A	3000	-	-	10/30/54/54	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	C5-N7	-3.25	1.32	1.39
36	C	1500	GTP	C6-N1	-2.92	1.33	1.38
36	C	1500	GTP	PA-O3A	-2.92	1.56	1.59
36	C	1500	GTP	C4-N9	-2.07	1.32	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	N9-C4-N3	6.22	138.38	125.95
36	C	1500	GTP	C5-C4-N3	-5.98	118.87	128.39
36	C	1500	GTP	C2-N3-C4	4.89	120.72	112.30
36	C	1500	GTP	O6-C6-C5	-3.98	116.02	126.53
36	C	1500	GTP	C8-N9-C4	2.71	111.11	106.03
36	C	1500	GTP	C2-N1-C6	-2.54	120.51	125.11
36	C	1500	GTP	C5-C6-N1	2.53	119.69	113.25
36	C	1500	GTP	O6-C6-N1	2.22	124.29	120.11
36	C	1500	GTP	N9-C8-N7	-2.18	109.36	113.40
36	C	1500	GTP	C2'-C1'-N9	-2.14	107.28	113.25
36	C	1500	GTP	C2'-C3'-C4'	2.00	106.48	102.61

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	A	3000	IHP	C1-C6-O16-P6

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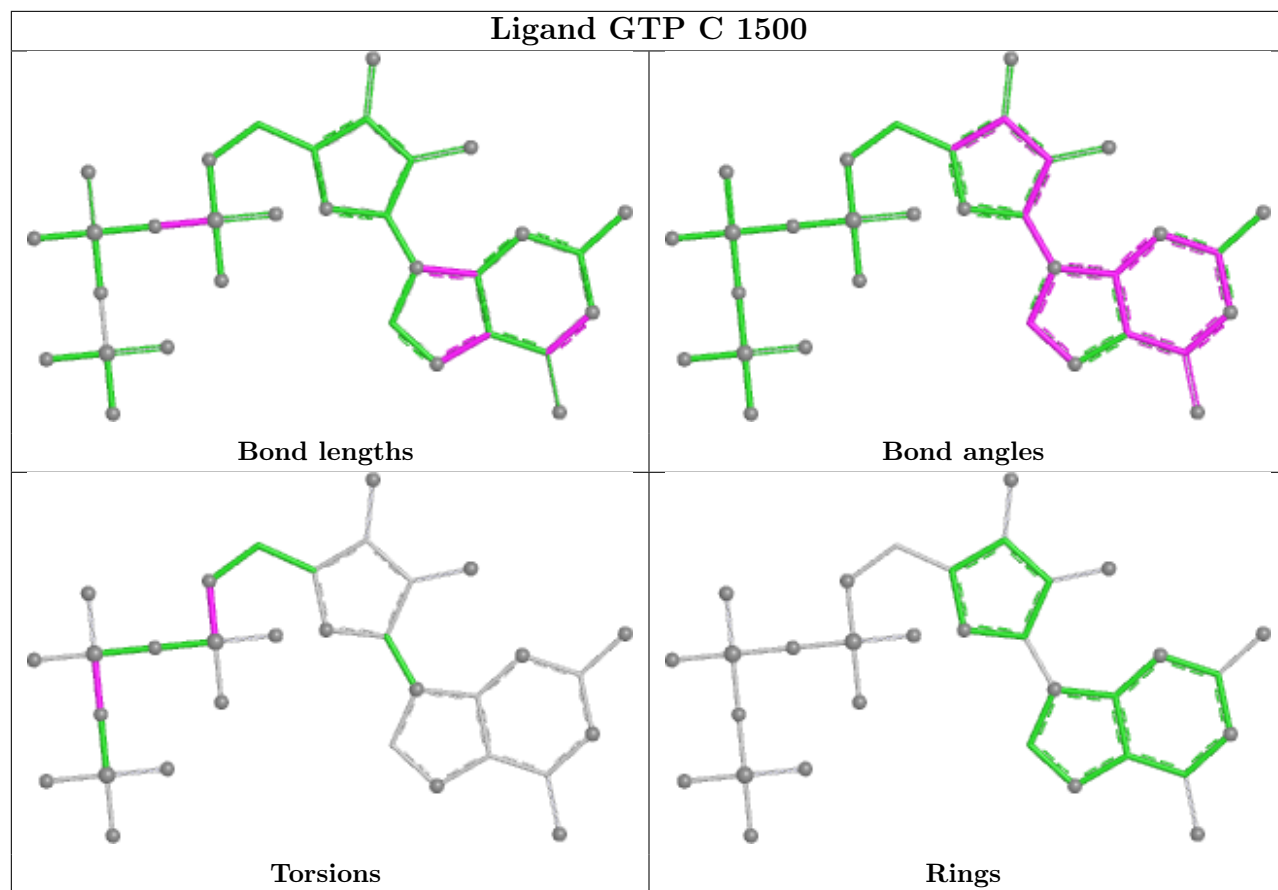
Mol	Chain	Res	Type	Atoms
35	A	3000	IHP	C5-C6-O16-P6
36	C	1500	GTP	C5'-O5'-PA-O1A
36	C	1500	GTP	C5'-O5'-PA-O2A
35	A	3000	IHP	C4-O14-P4-O24
35	A	3000	IHP	C4-C5-O15-P5
35	A	3000	IHP	C6-C5-O15-P5
36	C	1500	GTP	C5'-O5'-PA-O3A
35	A	3000	IHP	C3-C4-O14-P4
35	A	3000	IHP	C6-O16-P6-O26
36	C	1500	GTP	PG-O3B-PB-O1B
36	C	1500	GTP	PG-O3B-PB-O2B
35	A	3000	IHP	C3-O13-P3-O33
35	A	3000	IHP	C6-O16-P6-O36
35	A	3000	IHP	C6-O16-P6-O46

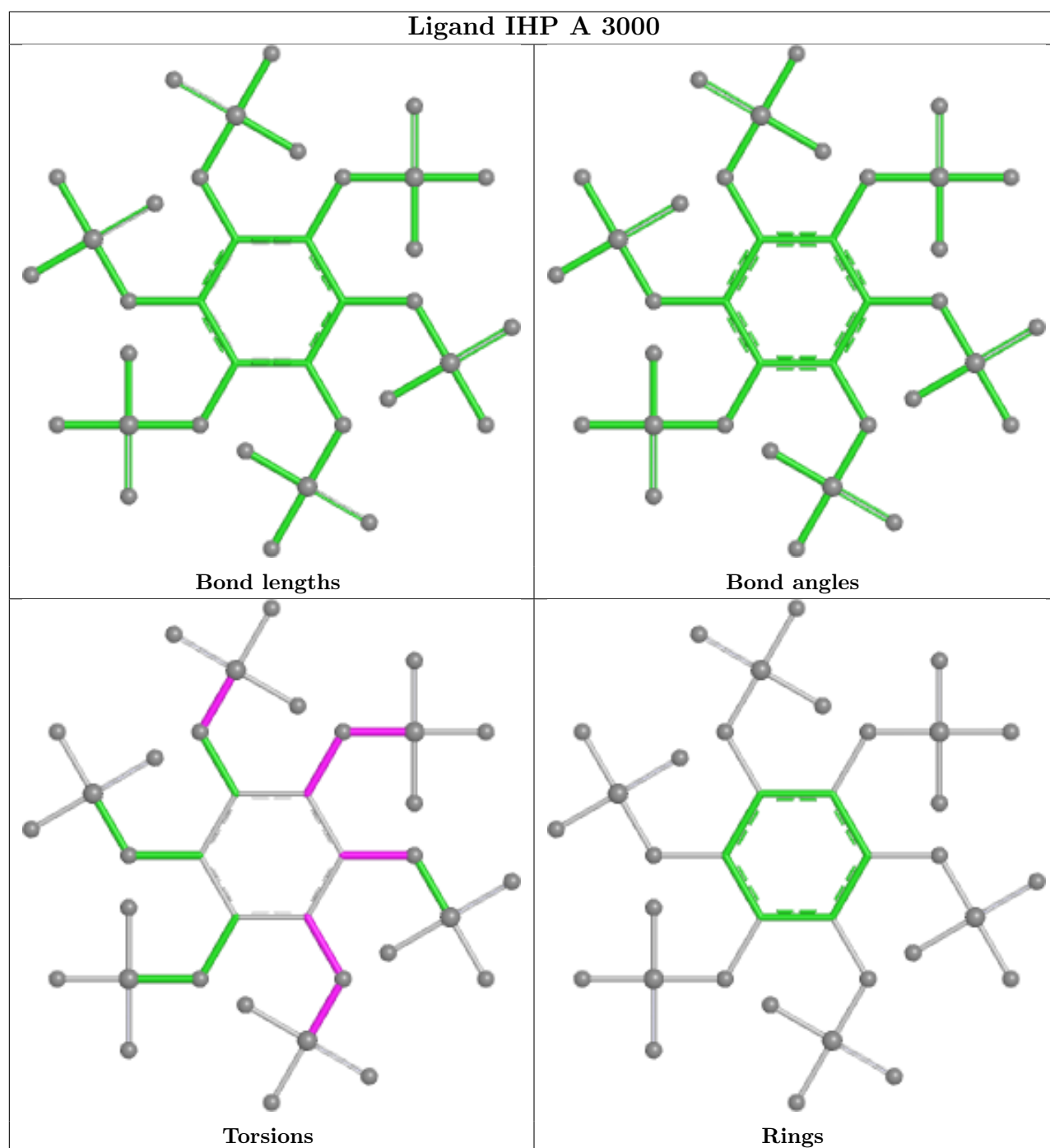
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	4	0
35	A	3000	IHP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

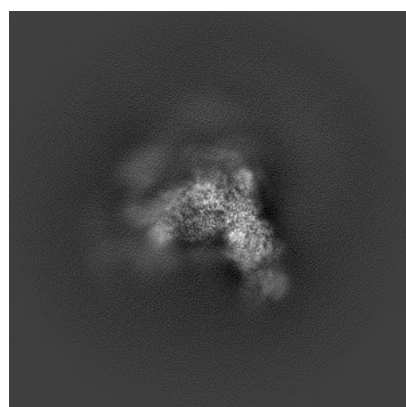
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6817. These allow visual inspection of the internal detail of the map and identification of artifacts.

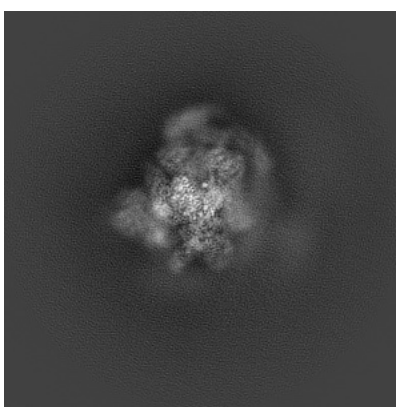
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

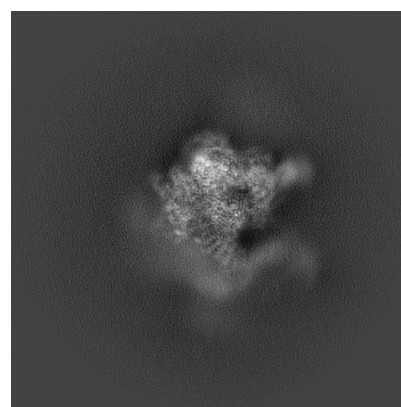
6.1.1 Primary map



X



Y

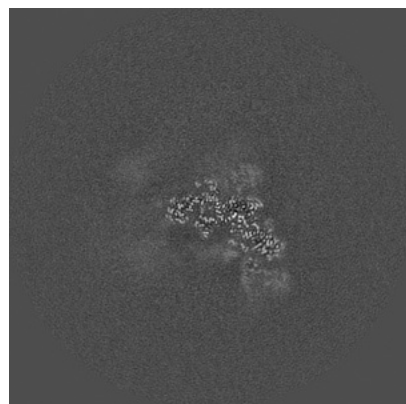


Z

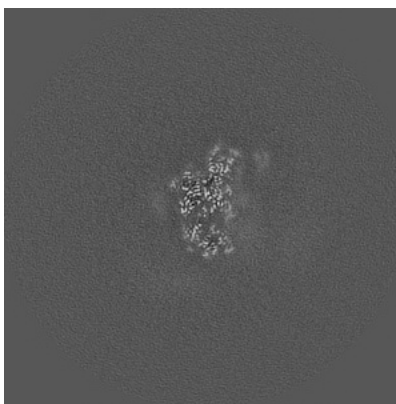
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

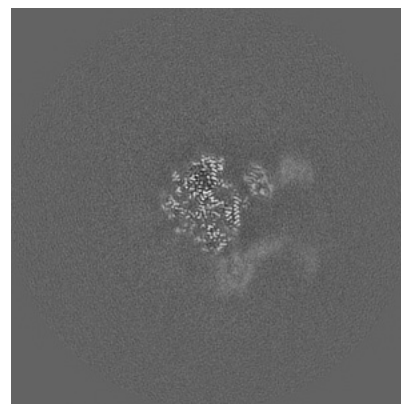
6.2.1 Primary map



X Index: 200



Y Index: 200

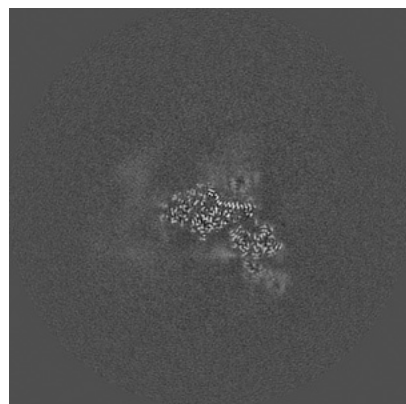


Z Index: 200

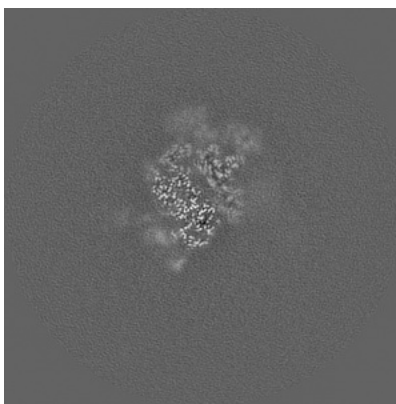
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

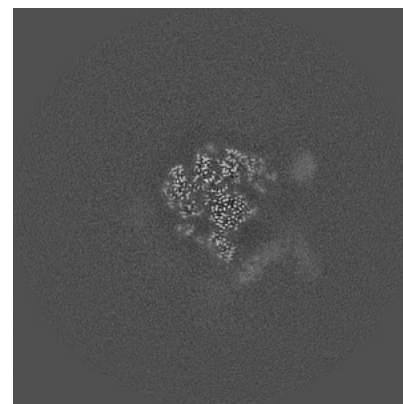
6.3.1 Primary map



X Index: 204



Y Index: 230

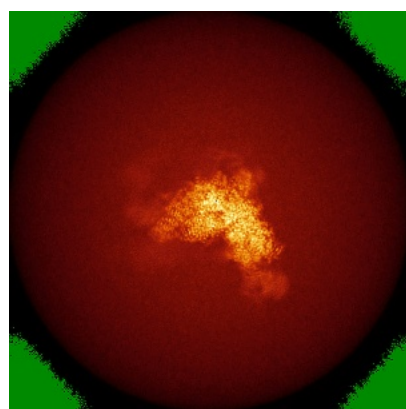


Z Index: 186

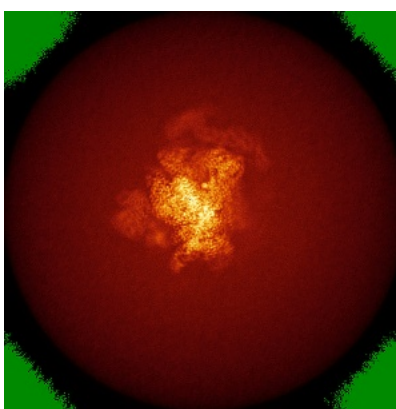
The images above show the largest variance slices of the map in three orthogonal directions.

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

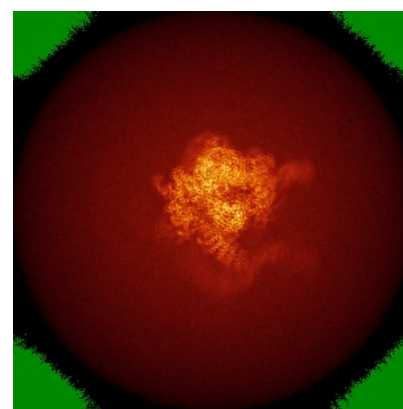
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

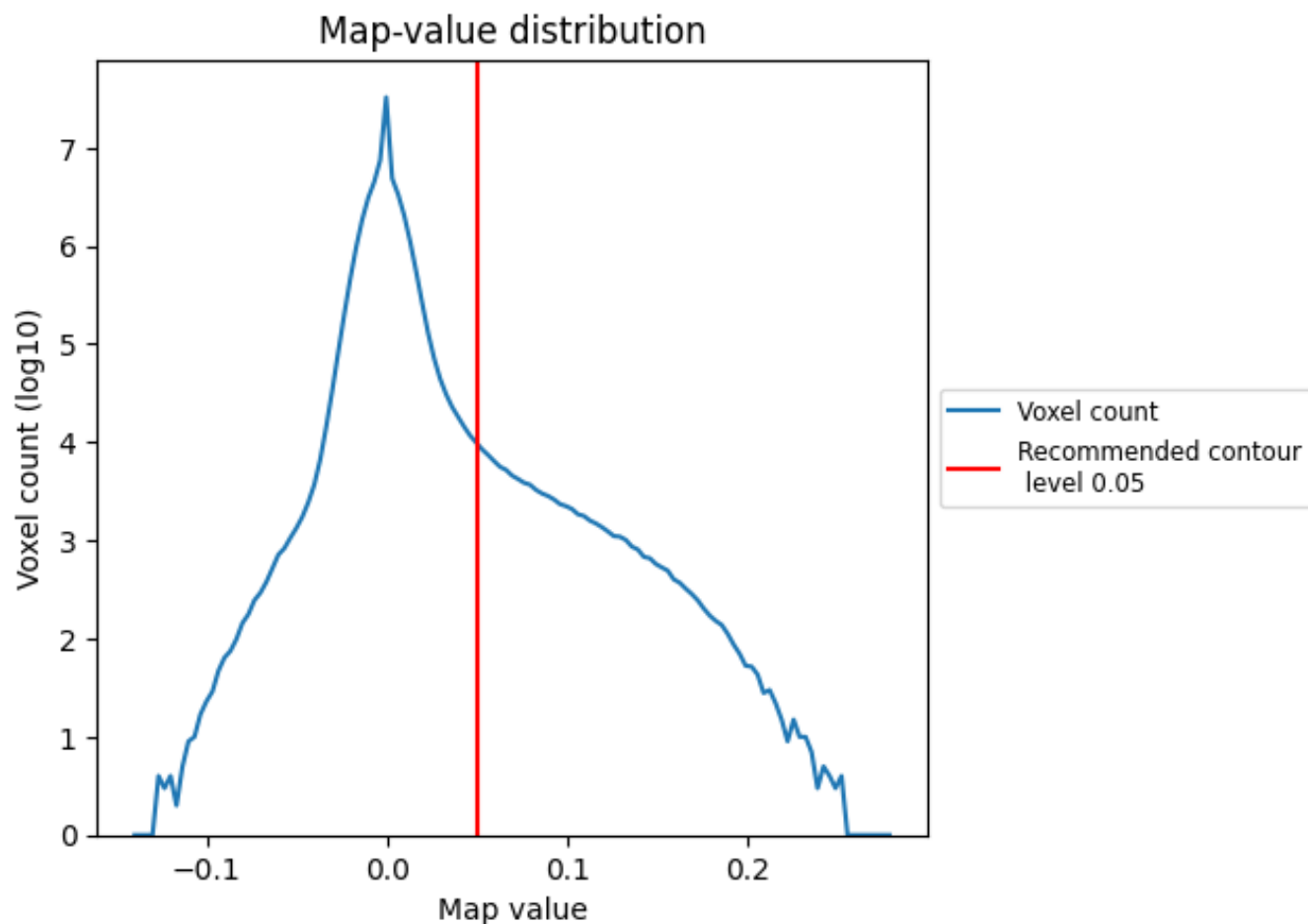
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

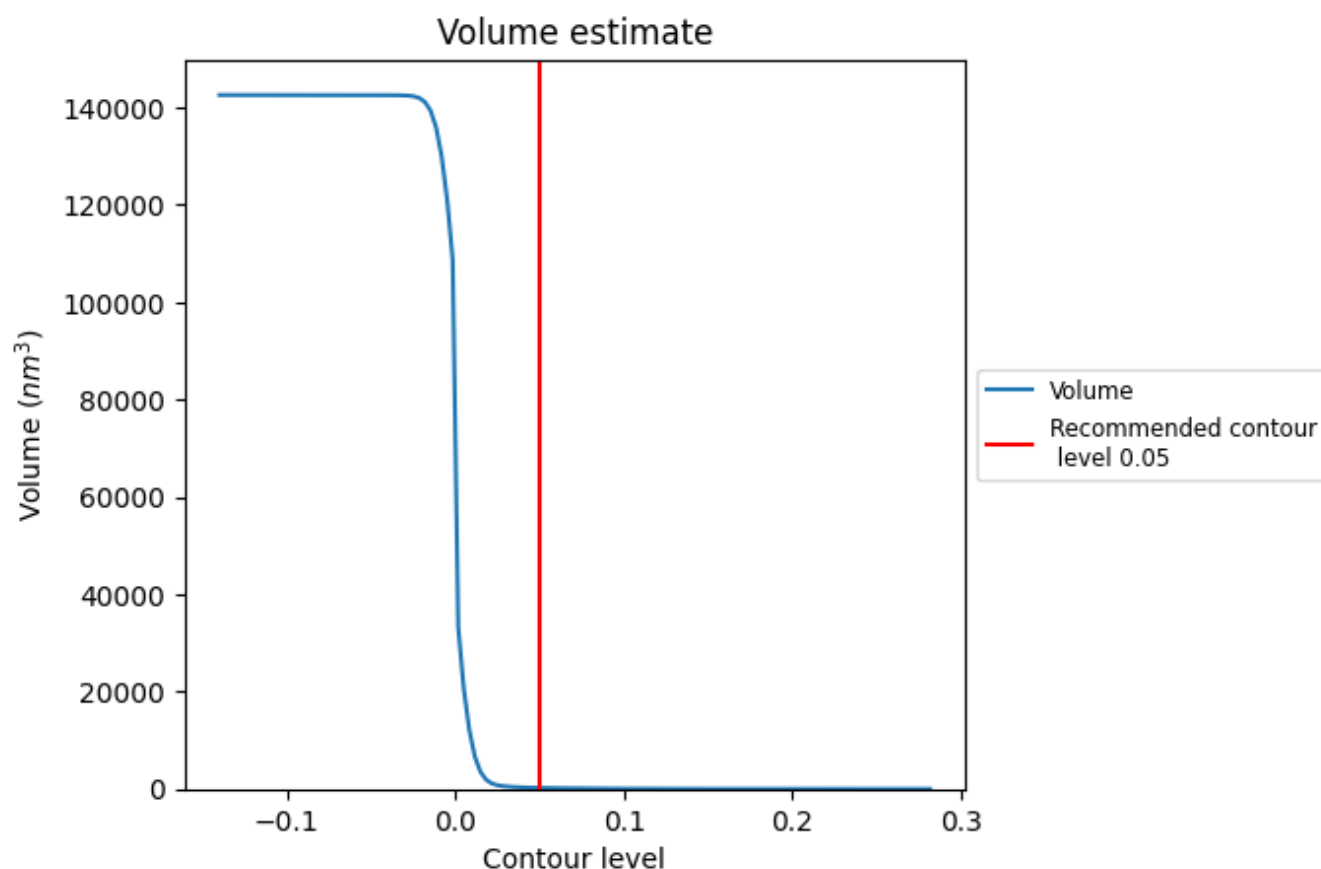
This section contains the results of statistical analysis of the map.

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.

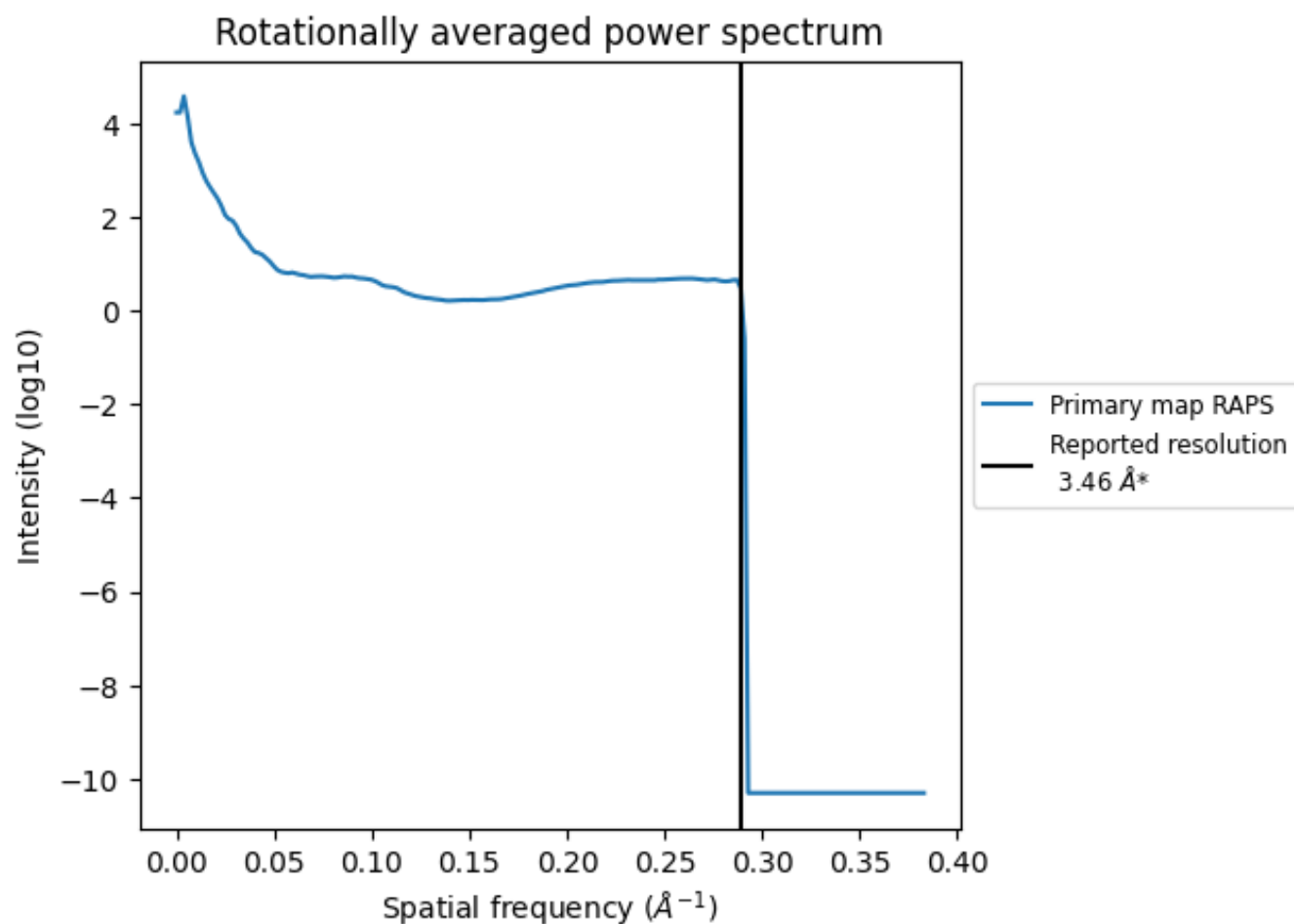
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 214 nm^3 ; this corresponds to an approximate mass of 193 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 0.289 Å⁻¹

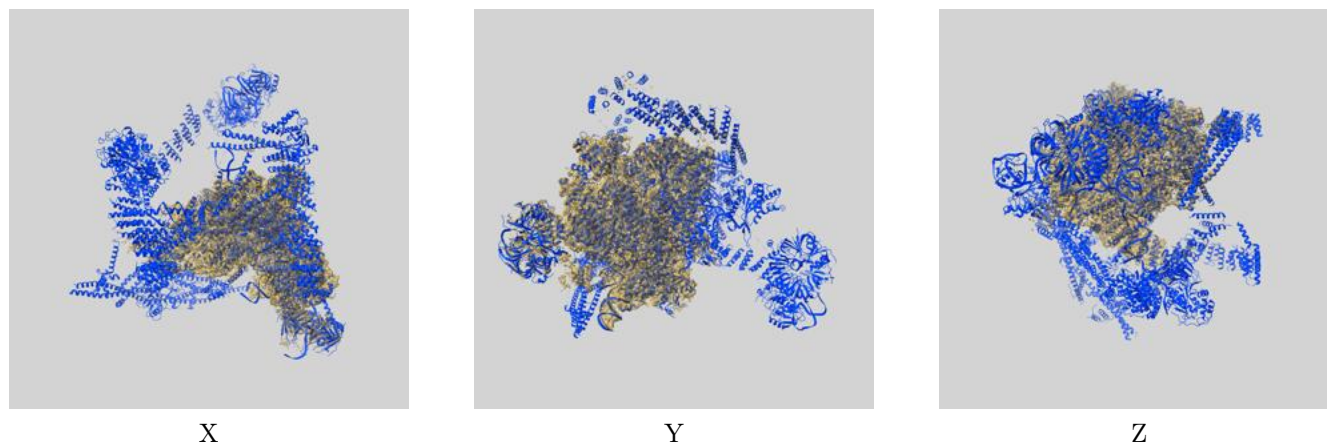
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

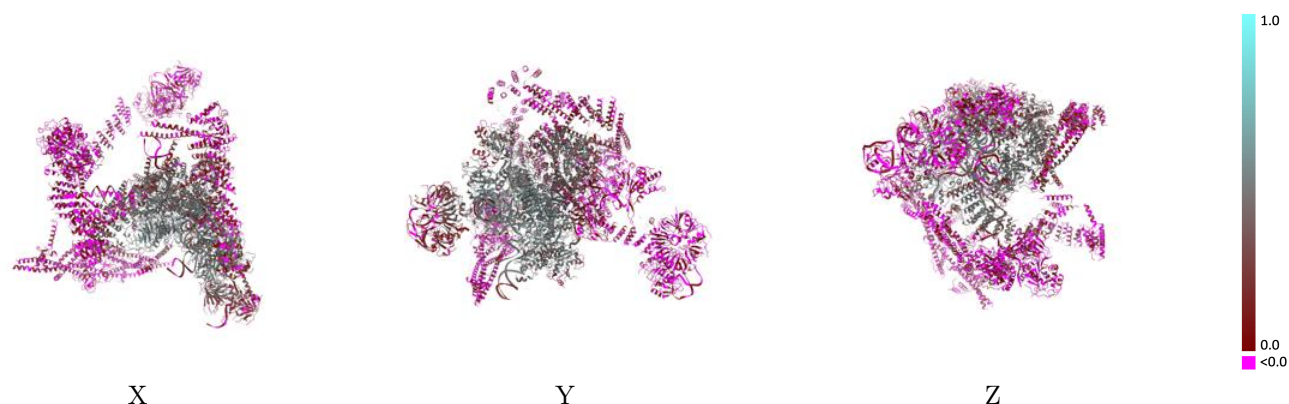
This section contains information regarding the fit between EMDB map EMD-6817 and PDB model 5Y88. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



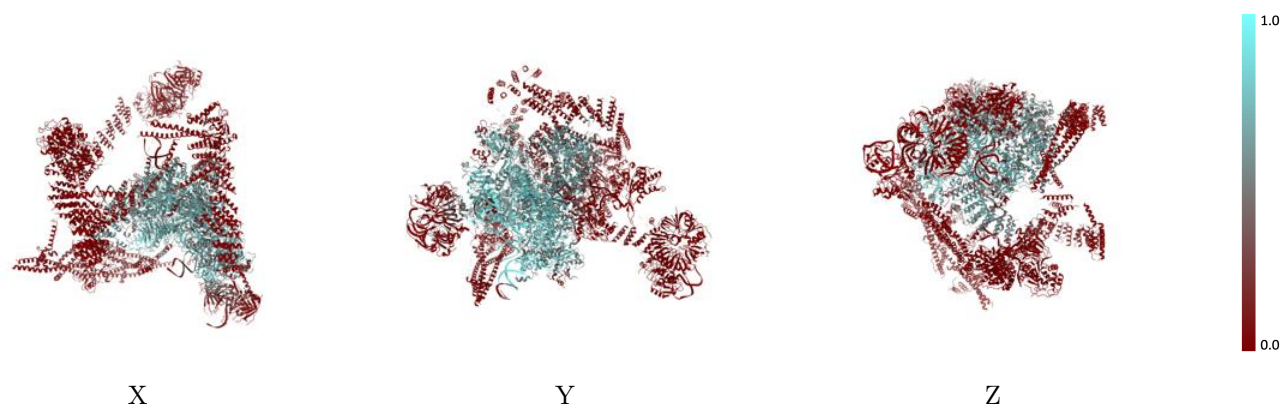
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



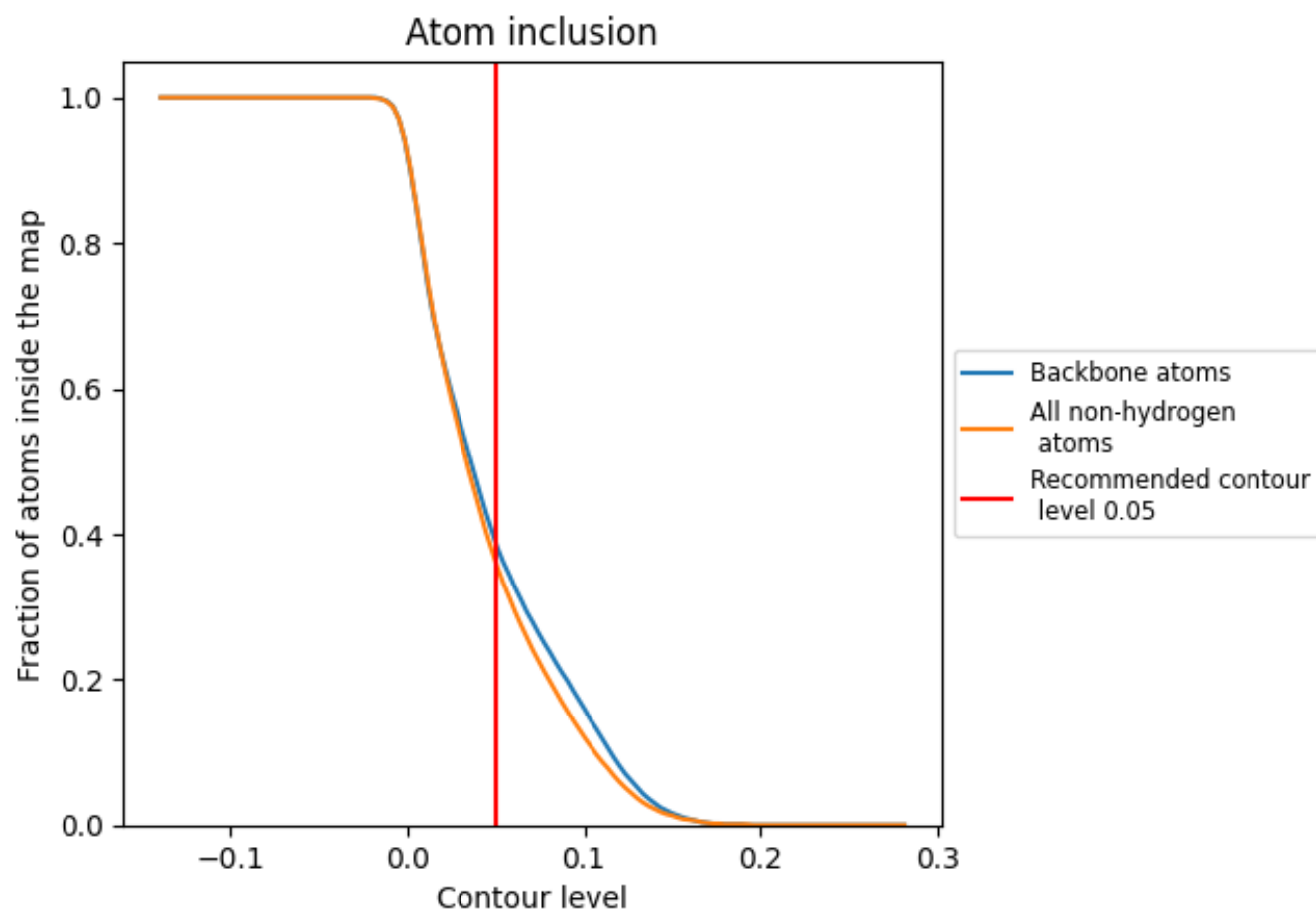
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 36% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3620	 0.2640
A	 0.4920	 0.3410
B	 0.6360	 0.3930
C	 0.6660	 0.4500
D	 0.7370	 0.4380
E	 0.2590	 0.1780
F	 0.1930	 0.1400
G	 0.0000	 0.0050
H	 0.0110	 0.0250
I	 0.3750	 0.2640
J	 0.2990	 0.2320
K	 0.3900	 0.3570
L	 0.7300	 0.4710
M	 0.5540	 0.4190
N	 0.6640	 0.4310
O	 0.7480	 0.5060
P	 0.4470	 0.4480
Q	 0.4960	 0.4030
R	 0.0920	 0.2520
S	 0.6430	 0.4470
T	 0.1840	 0.1710
U	 0.1330	 0.1710
V	 0.2630	 0.2790
W	 0.0000	 0.0080
a	 0.1670	 0.3050
b	 0.0380	 0.1550
c	 0.0370	 0.0920
d	 0.1570	 0.2530
e	 0.3560	 0.3730
f	 0.0770	 0.1570
g	 0.0500	 0.1510
h	 0.0000	 -0.0100
i	 0.0000	 -0.0110
j	 0.0000	 0.0030
k	 0.0000	 0.0180



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Chain	Atom inclusion	Q-score
l	 0.0000	 0.0080
m	 0.0000	 0.0270
n	 0.0000	 0.0050
o	 0.0000	 -0.0210
p	 0.0000	 0.0010
q	 0.0000	 0.0350
r	 0.0000	 -0.0090
s	 0.0000	 0.0000
t	 0.0000	 -0.0040
x	 0.0000	 -0.0440