



Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 09:10 AM JST

PDB ID : 5Z58
EMDB ID : EMD-6891
Title : Cryo-EM structure of a human activated spliceosome (early Bact) at 4.9 angstrom.
Authors : Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on : 2018-01-17
Resolution : 4.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

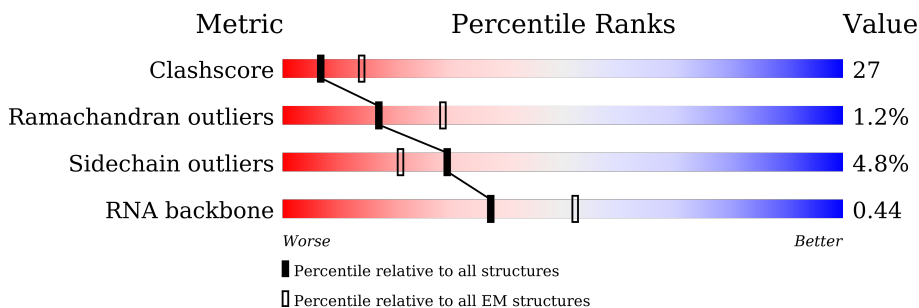
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	
4	D	2136	
5	E	357	
6	a	126	
6	h	126	

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Mol	Chain	Length	Quality of chain
7	b	231	35% 35% 65%
7	i	231	37% 37% 63%
8	c	119	68% 69% 31%
8	j	119	69% 69% 31%
9	d	118	77% 81% 18%
9	k	118	72% 71% 28%
10	f	86	85% 86% 14%
10	m	86	86% 86% 14%
11	e	92	86% 86% 14%
11	l	92	86% 86% 14%
12	g	76	97% 97%
12	n	76	89% 89% 11%
13	F	107	29% 28% 29% 30% 13%
14	G	274	9% 13% 12% 72%
15	H	188	43% 13% 40% 17% 28%
16	o	255	64% 62% 36%
17	p	225	73% 66% 7% 27%
18	w	501	78% 83% 13%
19	u	793	13% 13% 87%
20	v	464	21% 19% 79%
21	1	1304	6% 51% 28% 20%
22	2	895	13% 14% 6% 80%
23	3	1217	22% 51% 46%
24	4	424	17% 9% 8% 82%
25	5	125	5% 57% 30% 14%

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Mol	Chain	Length	Quality of chain
26	6	110	
27	7	86	
28	J	848	
29	L	802	
30	M	343	
31	P	229	
32	R	540	
33	T	514	
34	V	908	
35	X	396	
36	Y	322	
37	Z	619	
38	z	472	
39	x	1041	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
41	GTP	C	1500	-	-	X	-

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 94673 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2211	18165	11706	3163	3220	76	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	860	6716	4294	1120	1270	32	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	1722	8528	5084	1722	1722	0	0

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

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

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	81	399	237	81	81	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	h	80	393	233	80	80	0	0

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	b	82	405	241	82	82	0	0
7	i	86	422	250	86	86	0	0

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	c	82	406	242	82	82	0	0
8	j	82	406	242	82	82	0	0

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	d	97	480	286	97	97	0	0
9	k	85	422	252	85	85	0	0

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	f	74	361	213	74	74	0	0
10	m	74	361	213	74	74	0	0

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	e	79	391	233	79	79	0	0
11	l	79	391	233	79	79	0	0

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total	C	N	O	P	0	0
			1988	889	363	643	93		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total	C	N	O	P	0	0
			1545	689	240	539	77		

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total	C	N	O	P	0	0
			2886	1289	499	962	136		

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total	C	N	O	0	0
			804	480	162	162		

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total	C	N	O	0	0
			813	483	165	165		

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	437	Total	C	N	O	S	0	0
			2369	1448	460	458	3		

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	u	105	525	315	105	105	0	0

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	v	98	486	290	98	98	0	0

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	1	1038	7702	4900	1347	1415	40	0	0

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	2	183	1252	809	213	226	4	0	0

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	3	1177	9220	5854	1566	1755	45	0	0

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	4	78	527	345	83	99	0	0

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	5	108	807	512	142	150	3	0	0

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	6	89	670	410	119	128	13	0	0

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	7	66	540	343	94	98	5	0	0

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	J	522	3463	2156	653	648	6	0	0

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	L	132	1077	691	188	194	4	0	0

- Molecule 30 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	M	36	267	167	45	52	3	0	0

- Molecule 31 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	P	96	829	508	162	157	2	0	0

- Molecule 32 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	R	309	2314	1454	413	435	12	0	0

- Molecule 33 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 34 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	V	451	Total	C	N	O	0	0
			2238	1336	451	451		

- Molecule 35 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 36 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	104	Total	C	N	O	S	0	0
			737	466	126	143	2		

- Molecule 37 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	Z	113	Total	C	N	O	0	0
			755	474	147	134		

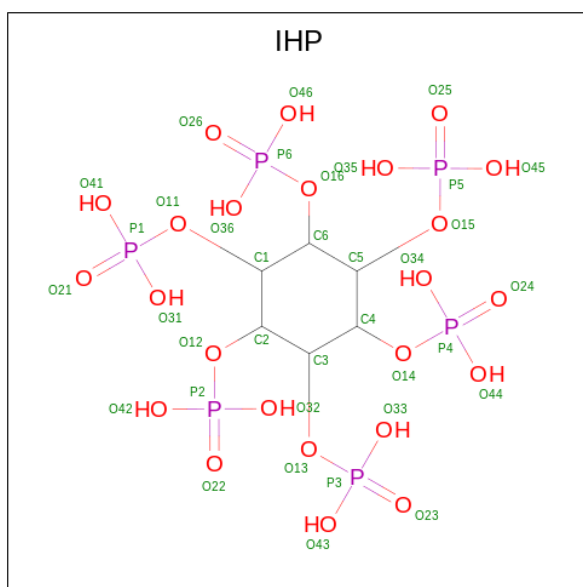
- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	z	177	Total	C	N	O	S	1	0
			1381	869	241	266	5		

- Molecule 39 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

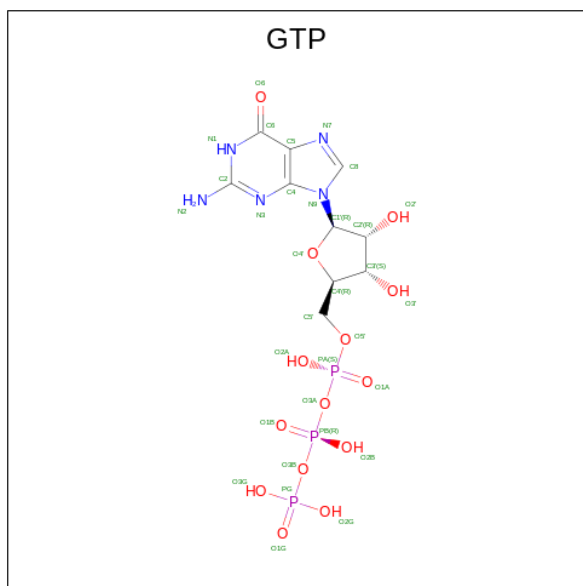
Mol	Chain	Residues	Atoms				AltConf	Trace
39	x	583	Total	C	N	O	0	0
			2882	1715	583	584		

- Molecule 40 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: C₆H₁₈O₂₄P₆).



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

- Molecule 41 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 42 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
42	C	1	Total 1	Mg 1	0
42	F	5	Total 5	Mg 5	0

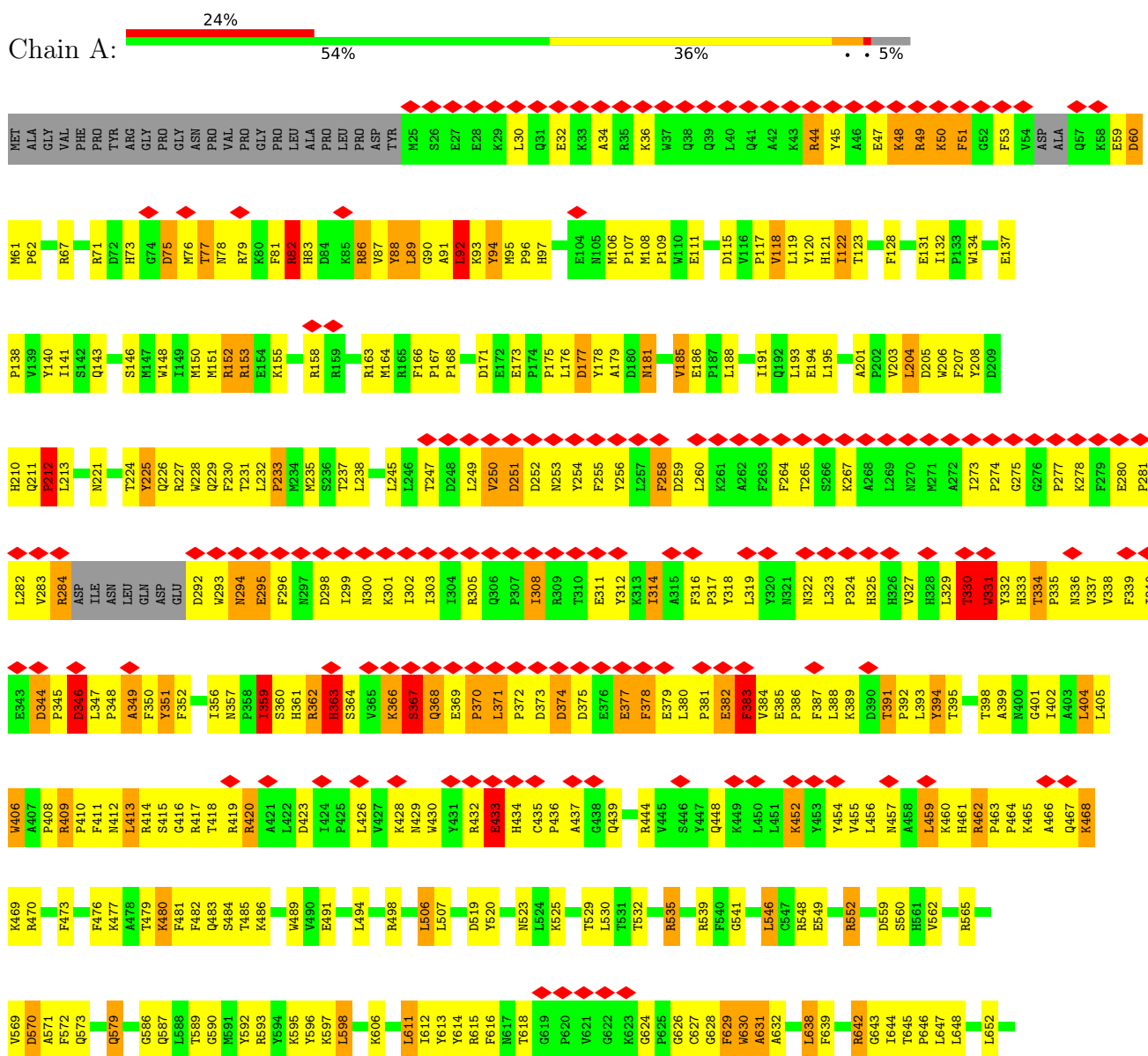
- Molecule 43 is ZINC ION (three-letter code: ZN) (formula: Zn).

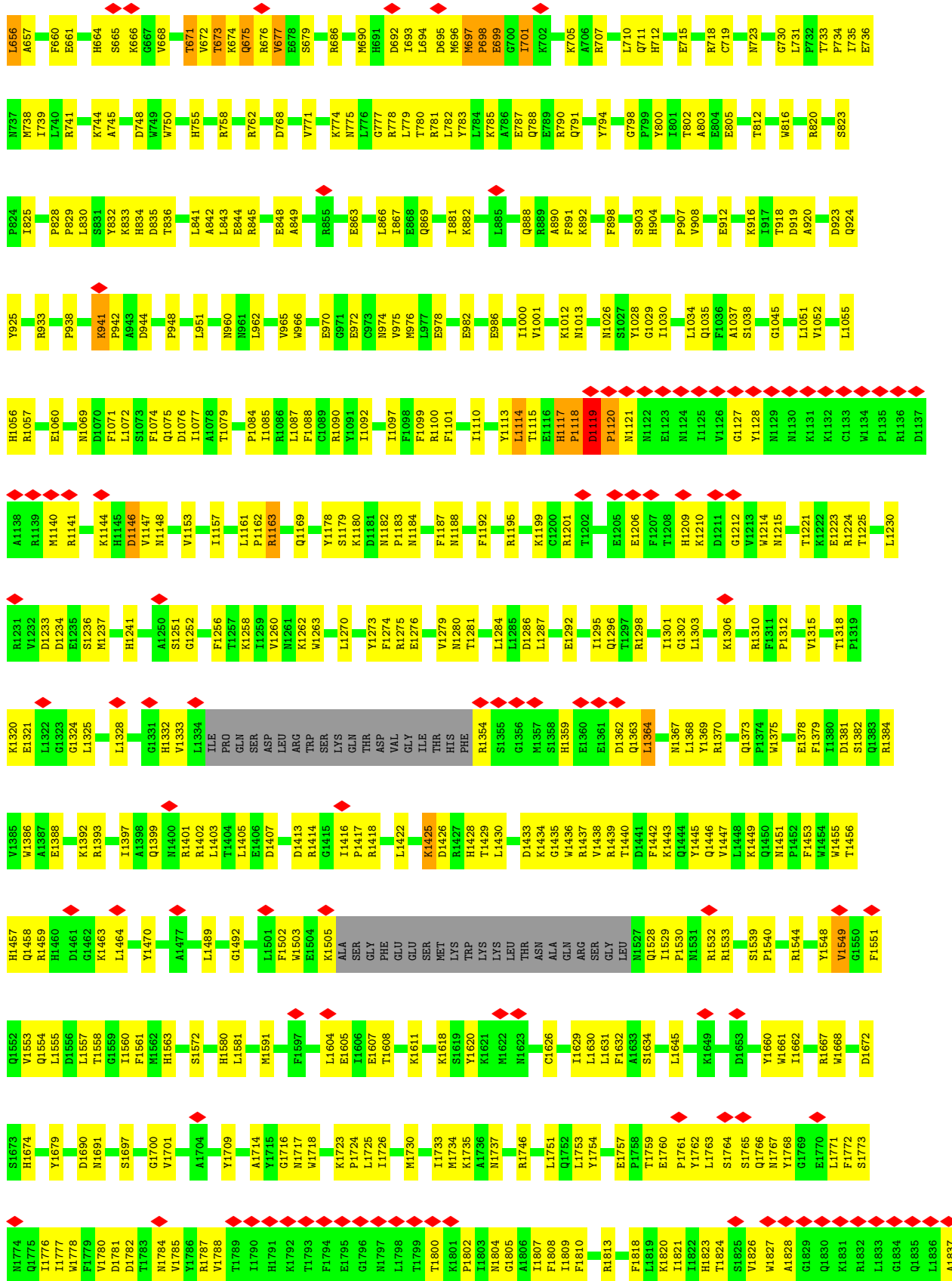
Mol	Chain	Residues	Atoms		AltConf
43	6	3	Total 3	Zn 3	0
43	M	1	Total 1	Zn 1	0

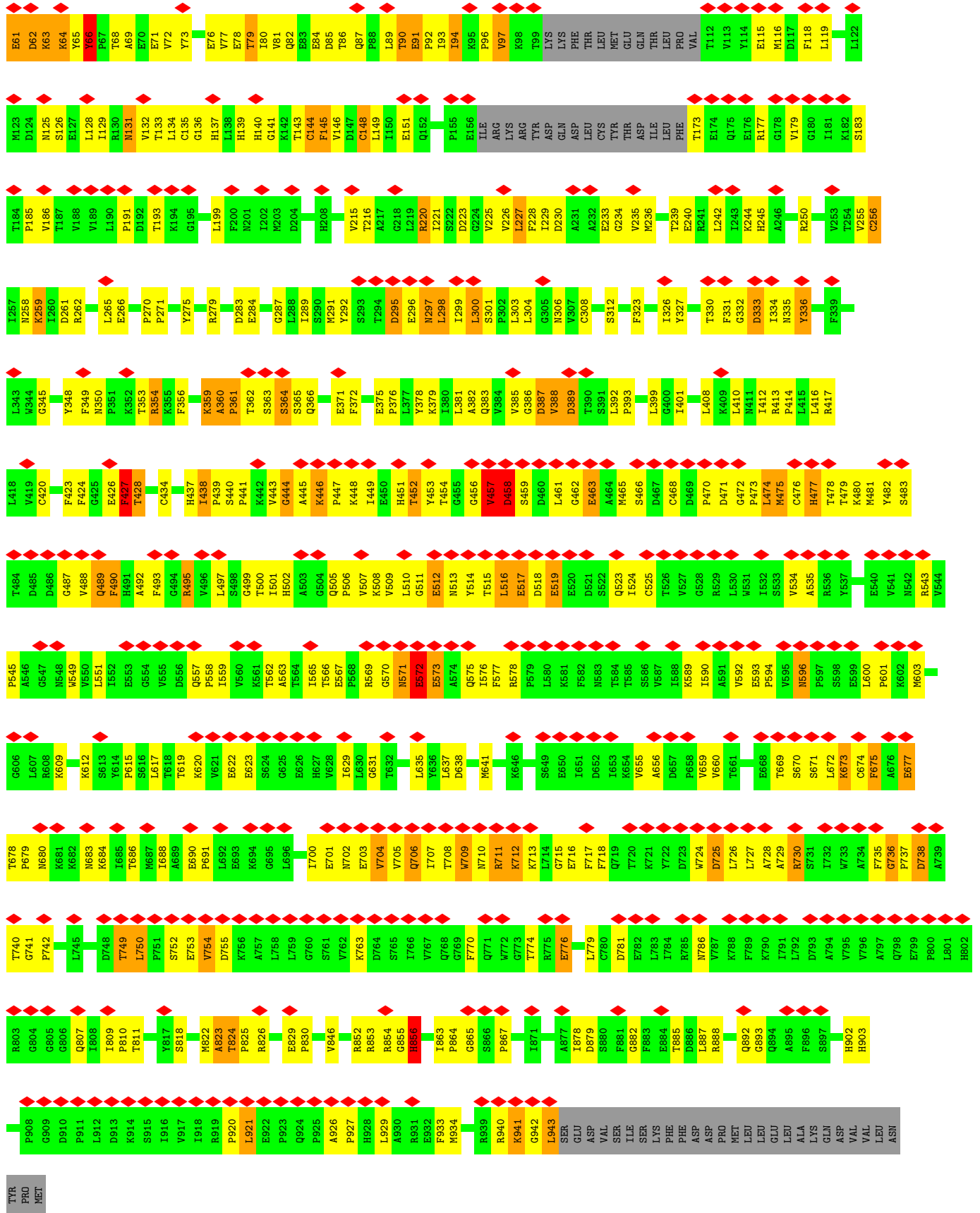
3 Residue-property plots

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

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



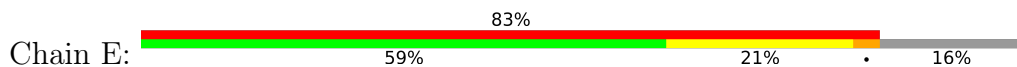




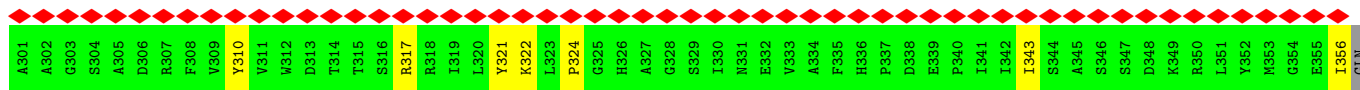
P947	L948	L949	P950	Q951	R952	P955	L956	Y957	H958	T959	A960	L962	R963	L964	R965	R966	R967	V970	R971	Y972	D973	R974	T976	G977	R978	F979	Q980	Y981	T982	E983	L984	G985	R986	H990	Y991	Y992	Y993	T994	D996	D996	T997	Y998	Q999	T1000	M1002	Q1003	L1004	L1005	K1006	P1007	T1008	L1009	S1010						
E1011	I1012	E1013	L1014	F1015	R1016	V1017	F1018	S1019	L1020	S1021	S1022	E1023	F1024	K1025	N1026	I1027	T1028	V1029	R1030	E1031	E1032	K1034	L1035	E1036	Q1038	K1039	L1040	L1041	F1042	R1043	Y1044	P1045	I1046	P1047	V1048	K1049	E1050	S1051	I1052	E1053	E1054	K1058	I1059	I1067	S1068	Q1069	T1000	M1002	Q1003	L1004	L1005	K1006	P1007	T1008	L1009	S1010			
M1081	V1082	Y1083	V1084	T1085	Q1086	S1087	G1088	R1089	R1090	L1091	M1092	R1093	A1094	I1095	F1096	E1097	I1098	V1099	L1100	M1101	R1102	G1103	M1104	A1105	Q1106	L1107	T1108	D1109	K1110	T1111	L1112	K1116	M1117	I1118	D1119	K1120	R1121	M1122	W1123	S1125	M1126	C1127	P1128	L1129	R1130	Q1131	F1132	R1133	K1134	L1135	P1136	E1137	L1138	E1139	V1139	V1140	K1141	D1080	
E1144	K1145	K1146	M1147	F1150	E1151	R1152	L1153	Y1154	D1155	L1156	M1157	H1158	M1159	E1160	I1161	G1162	E1163	L1164	I1165	R1166	M1167	P1168	K1169	M1170	G1171	K1172	T1173	I1174	H1175	K1176	Y1177	V1178	H1179	L1180	F1181	P1182	K1183	L1184	E1185	L1186	S1187	V1188	H1189	L1190	Q1191	P1192	I1193	F1193	T1194	R1195	S1196	T1197	L1198	K1199	V1200	E1201	L1202	T1203	L1204
T1205	P1206	D1207	F1208	Q1209	W1210	D1211	E1212	K1213	W1214	H1215	G1216	S1217	H1218	E1219	A1220	F1221	W1222	E1223	L1224	V1225	E1226	D1227	V1228	D1229	S1230	E1231	V1232	I1233	L1234	H1235	H1236	E1237	Y1238	F1239	L1240	L1241	K1242	A1243	K1244	Y1245	A1246	Q1247	D1248	E1249	H1250	L1251	L1252	T1253	F1254	F1255	V1256	T1257	V1258	F1259	E1260	P1261	L1262	P1263	P1264
Q1265	Y1266	F1267	I1268	R1269	D1273	R1274	W1275	L1276	S1277	C1278	E1279	L1280	Q1281	L1282	P1283	V1284	S1285	F1286	H1288	L1289	I1290	L1291	P1292	E1293	K1294	Y1295	P1296	P1297	P1298	T1299	E1300	L1301	L1302	D1303	L1304	Q1305	P1306	L1307	P1308	V1309	S1310	A1311	R1313	M1314	S1315	A1316	F1317	S1318	S1319	Y1321	D1322	K1323	K1324	F1325	P1326				
F1327	F1328	M1329	P1330	I1331	Q1332	T1333	Q1334	V1335	F1336	M1337	T1338	V1339	L1340	M1341	S1342	D1343	M1345	V1346	F1347	V1348	G1349	A1350	P1351	T1352	G1353	S1354	G1355	P1356	T1357	I1358	C1359	A1360	E1361	F1362	A1363	L1364	L1365	L1366	M1367	L1368	L1369	Q1370	A1371	S1372	E1373	G1374	S1375	C1376	V1377	V1378	W1379	T1380	P1381	M1382	E1383	A1384	L1385	A1386	
E1387	Q1388	V1389	Y1390	M1391	D1392	W1393	Y1394	E1395	K1396	F1397	Q1398	D1399	R1400	L1401	M1402	K1403	K1404	V1405	V1406	L1407	L1408	T1409	G1410	E1411	T1412	S1413	T1414	D1415	L1416	K1417	L1418	L1419	G1420	K1421	G1422	M1423	I1424	I1425	I1426	S1427	T1428	P1429	E1430	K1431	V1432	D1433	I1434	L1435	S1436	R1437	R1438	W1439	K1440	Q1441	R1442	K1443	L1444	V1445	Q1446
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S1507	A1508	T1509	S1510	L1511	F1512	M1513	F1514	H1515	P1516	M1517	V1518	R1519	P1520	V1521	P1522	L1523	E1524	L1525	H1526	I1527	Q1528	G1529	F1530	M1531	C1532	S1533	H1534	V1535	Q1536	T1537	R1538	L1539	L1540	S1541	M1542	A1543	K1544	P1545	V1546	Y1547	H1548	A1549	I1550	T1551	K1552	H1553	S1554	P1555	K1556	L1557	P1558	V1559	I1560	V1561	F1562	P1563	V1564	S1565	R1566
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V1927	D1928	V1929	L1930	S1931	S1932	M1933	G1934	M1935	L1936	S1937	P1938	A1939	L1940	A1941	A1942	M1943	E1944	L1945	A1946	Q1947	H1948	M1949	T1950	Q1951	A1952	M1953	M1954	S1955	Q1956	D1957	S1958	Y1959	L1960	K1961	Q1962	L1963	P1964	H1965	F1966	T1967	S1968	E1969	H1970	I1971	K1972	R1973	C1974	I1975	T1976	K1977	G1978	V1979	I1980	S1981	L1982	F1983	D1984	I1985	M1986
E1987	M1988	E1989	D1990	L1991	E1992	R1993	M1994	A1995	L1996	L1997	Q1998	L1999	T2000	D2001	S2002	Q2003	I2004	A2005	D2006	V2007	A2008	R2009	F2010	C2011	N2012	R2013	Y2014	N2015	N2016	I2017	E2018	L2019	S2020	Y2021	E2022	V2023	V2024	D2025	K2026	D2027	S2028	I2029	R2030	S2031	G2032	G2033	P2034	V2035	V2036	V2037	L2038	V2039	Q2040	L2041	E2042	R2043	E2044	E2045	E2046
V2047	T2048	G2049	P2050	V2051	Z2052	A2053	P2054	L2055	F2056	P2057	Q2058	R2059	K2060	E2061	E2062	G2063	W2064	W2065	V2066	V2067	I2068	G2069	D2070	A2071	K2072	S2073	N2074	S2075	L2076	I2077	S2078	L2079	K2080	R2081	L2082	L2083	L2084	Q2085	Q2086	K2087	A2088	K2089	V2090	K2091	L2092	D2093	F2094	V2095	P2097	A2098	T2099	G2100	A2101	H2102	W2103	Y2104	T2105	L2106	
Y2107	F2108	M2109	S2110	D2111	A2112	Y2113	M2114	G2115	C2116	D2117	Q2118	E2119	Y2120	K2121	F2122	S2123	W2124	D2125	VAL	LVS	GLU	ALA	GLY	THR	ASP	ASP	SER	ASP	GLN	GLN	THR	PRO	GLY	ALA	LEU	LEU	GLN	PRO	PRO	CYS	SER	LEU	GLN	ALA	P58	I59	M60												

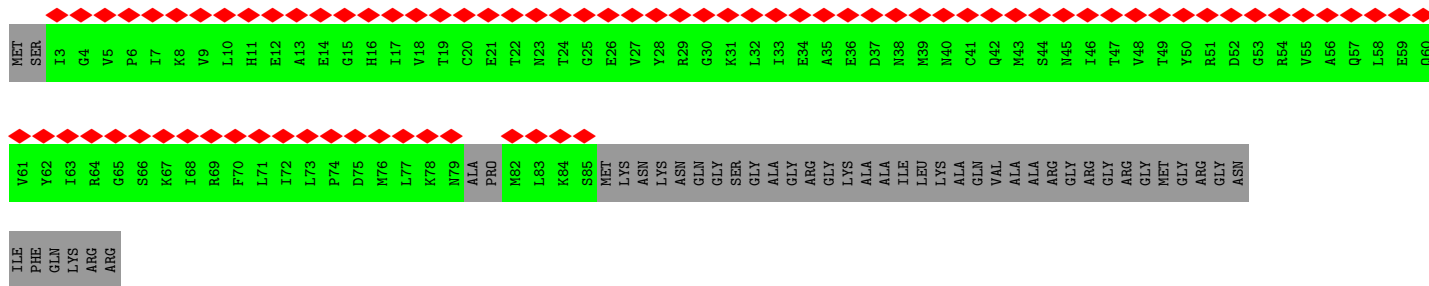
• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



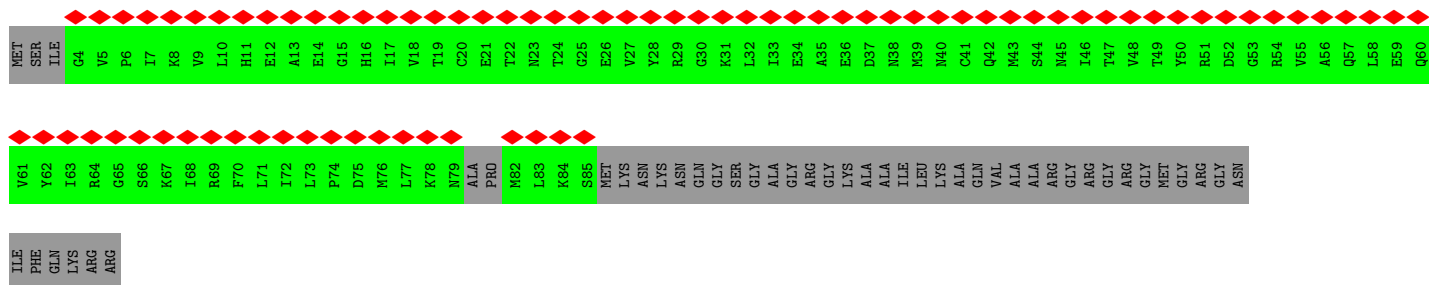
MET	ILE	GLU	GLN	LVS	ARG	LVS	GLY	PRO	PRO	LEU	VAL	PRO	VAL	ARG	GLN	HIS	GLU	LEU	LEU	LEU	GLY	ALA	GLY	ALA	GLN	GLN	ALA	THR	PRO	GLY	ALA	LEU	LEU	GLN	PRO	PRO	ARG	SER	SER	LEU	GLN	ALA	P58	I59	M60														
L61	L62	S63	G64	H65	E66	G67	E68	V69	Y70	C71	C72	F73	F74	H75	P76	M77	G78	S79	T80	L81	A82	S83	A84	G85	F86	D87	R88	L89	I90	L91	L92	W93	N94	Y95	Y96	G97	D98	C99	D100	N101	I102	A103	L104	L105	K106	G107	H108	S109	G110	A111	V112	M113	E114	L115	H116	Y117	L118	T119	D120
G121	S122	M123	L124	F125	S126	A127	S128	T129	D130	K131	T132	V133	A134	V135	W136	D137	S138	E139	T140	G141	E142	R143	V144	K145	R146	L147	K148	G149	H150	T151	S152	F153	V154	N155	S156	C157	Y158	P159	A160	R161	R162	G163	P164	Q165	L166	V167	C168	T169	G170	S171	D172	D173	G174	T175	V176	K177	L178	W179	D180
I181	R182	K183	K184	A185	A186	I187	Q188	T189	F190	Q191	N192	T193	Y194	Q195	V196	L197	A198	V199	T200	F201	N202	D203	T204	S205	D206	Q207	L208	L209	S210	G211	G212	L213	D214	N215	D216	L217	L218	V219	W220	D221	L222	R223	Q224	N225	K226	L227	T228	Y229	T230	M231	R232	G233	H234	A235	D236	G237	V238	T239	G240
L241	S242	L243	S244	S245	E246	G247	S248	Y249	L250	L251	S252	M253	M255	D256	N257	T258	V259	R260	V261	W262	D263	V264	R265	F267	A268	P269	K270	E271	R272	C273	V274	V275	L276	F277	Q278	G279	N280	V281	H282	M283	F284	E285	K286	N287	L288	L289	R290	C291	S292	W293	S294	P295	D296	G297	S298	F299	I300		



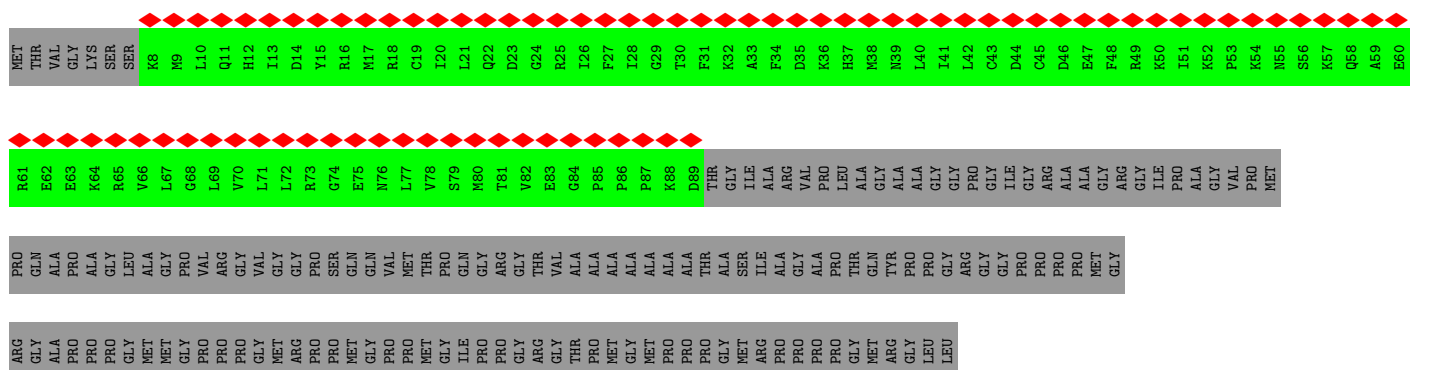
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



• Molecule 6: Small nuclear ribonucleoprotein Sm D3

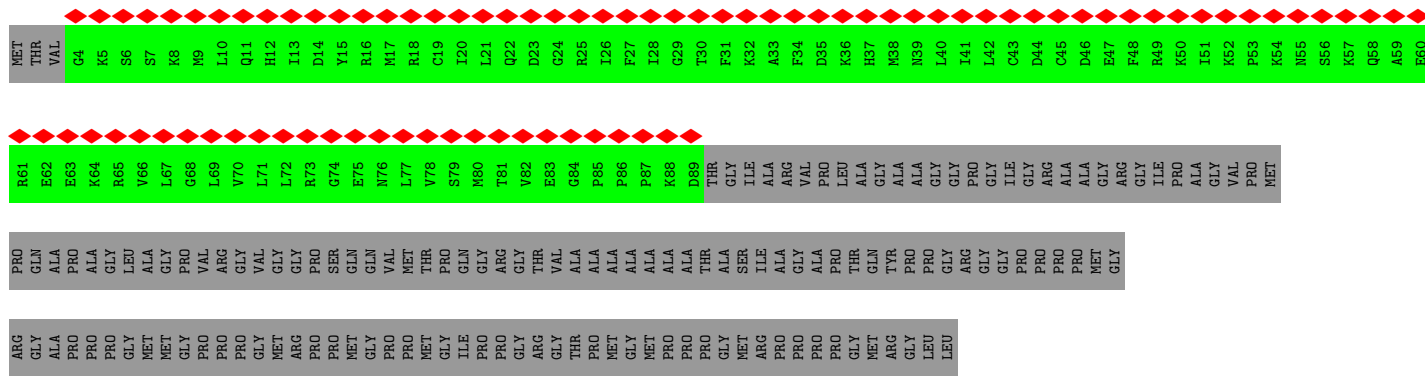


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

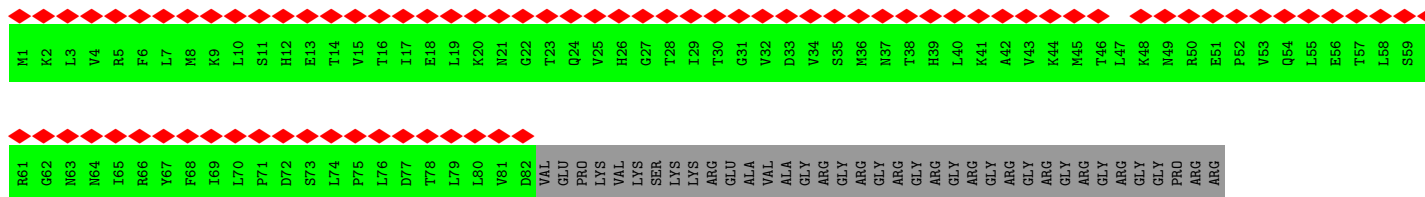


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

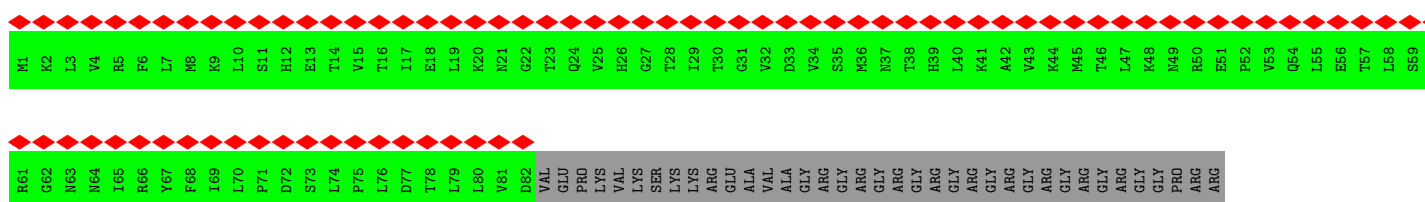




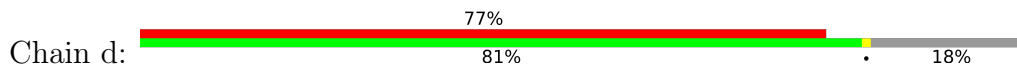
• Molecule 8: Small nuclear ribonucleoprotein Sm D1



• Molecule 8: Small nuclear ribonucleoprotein Sm D1

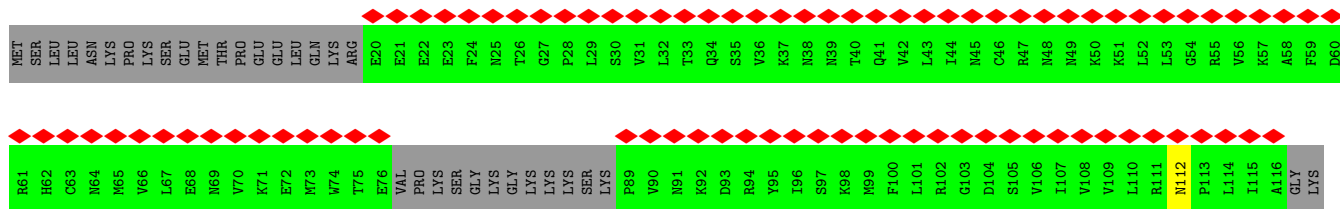


• Molecule 9: Small nuclear ribonucleoprotein Sm D2

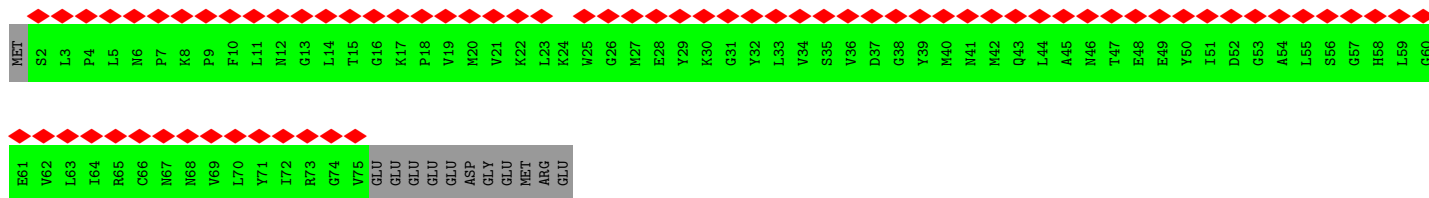
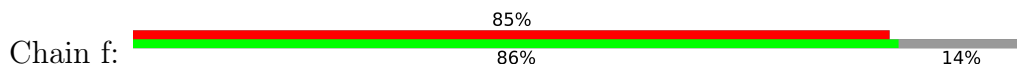


• Molecule 9: Small nuclear ribonucleoprotein Sm D2

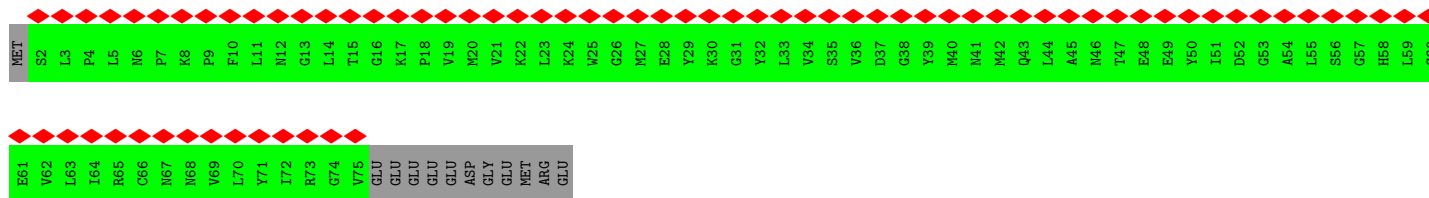
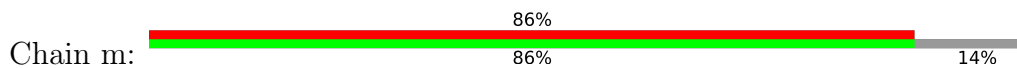




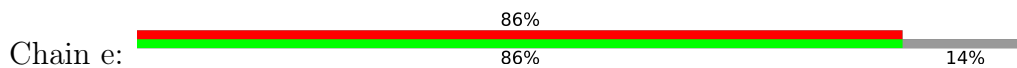
• Molecule 10: Small nuclear ribonucleoprotein F



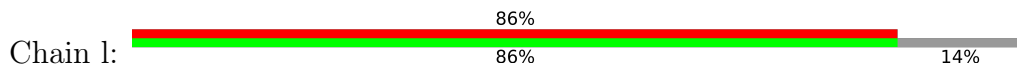
• Molecule 10: Small nuclear ribonucleoprotein F



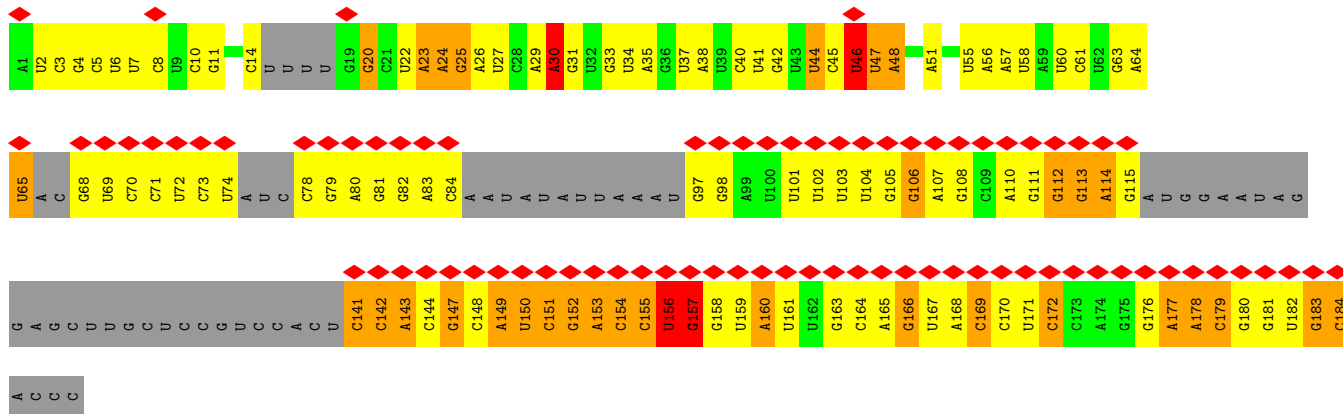
• Molecule 11: Small nuclear ribonucleoprotein E



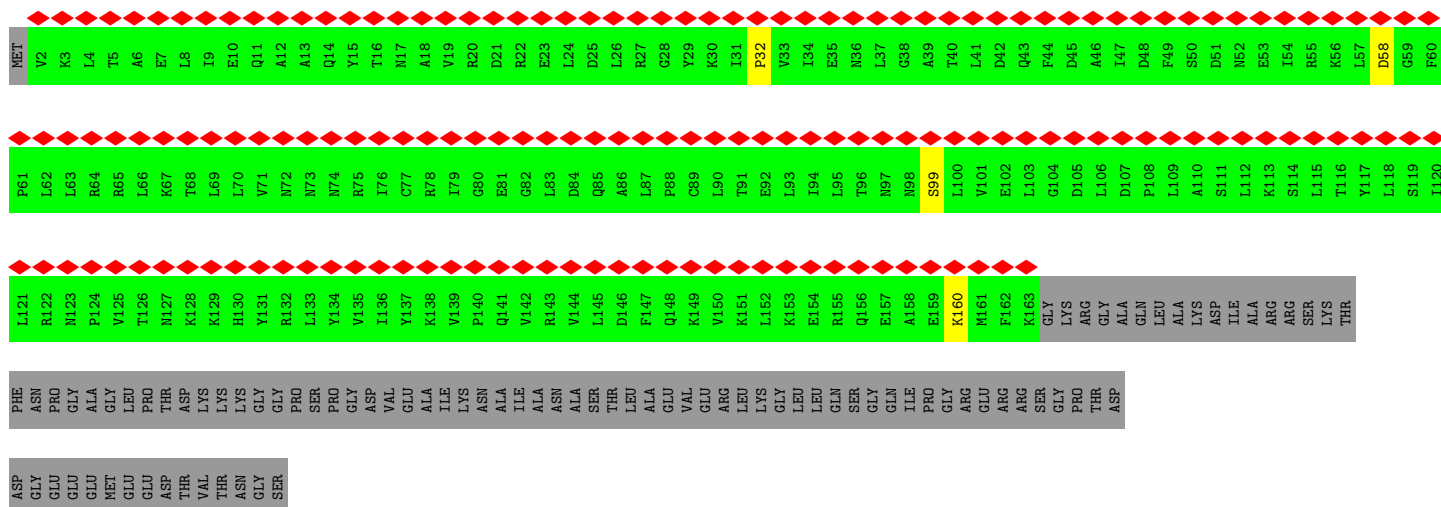
• Molecule 11: Small nuclear ribonucleoprotein E



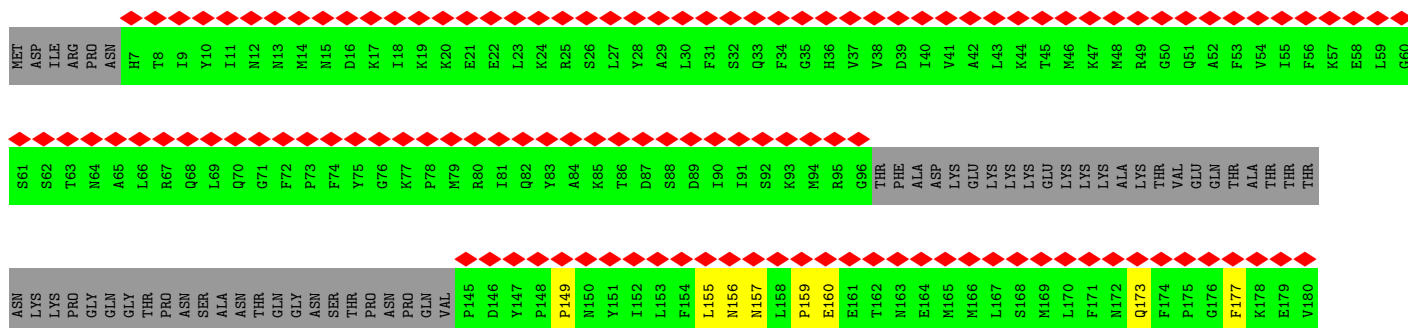
• Molecule 15: U2 snRNA

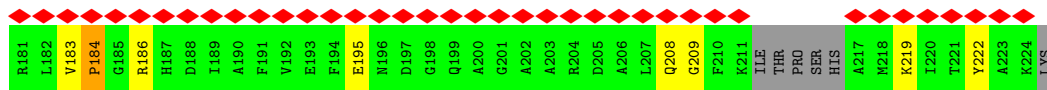


• Molecule 16: U2 small nuclear ribonucleoprotein A'

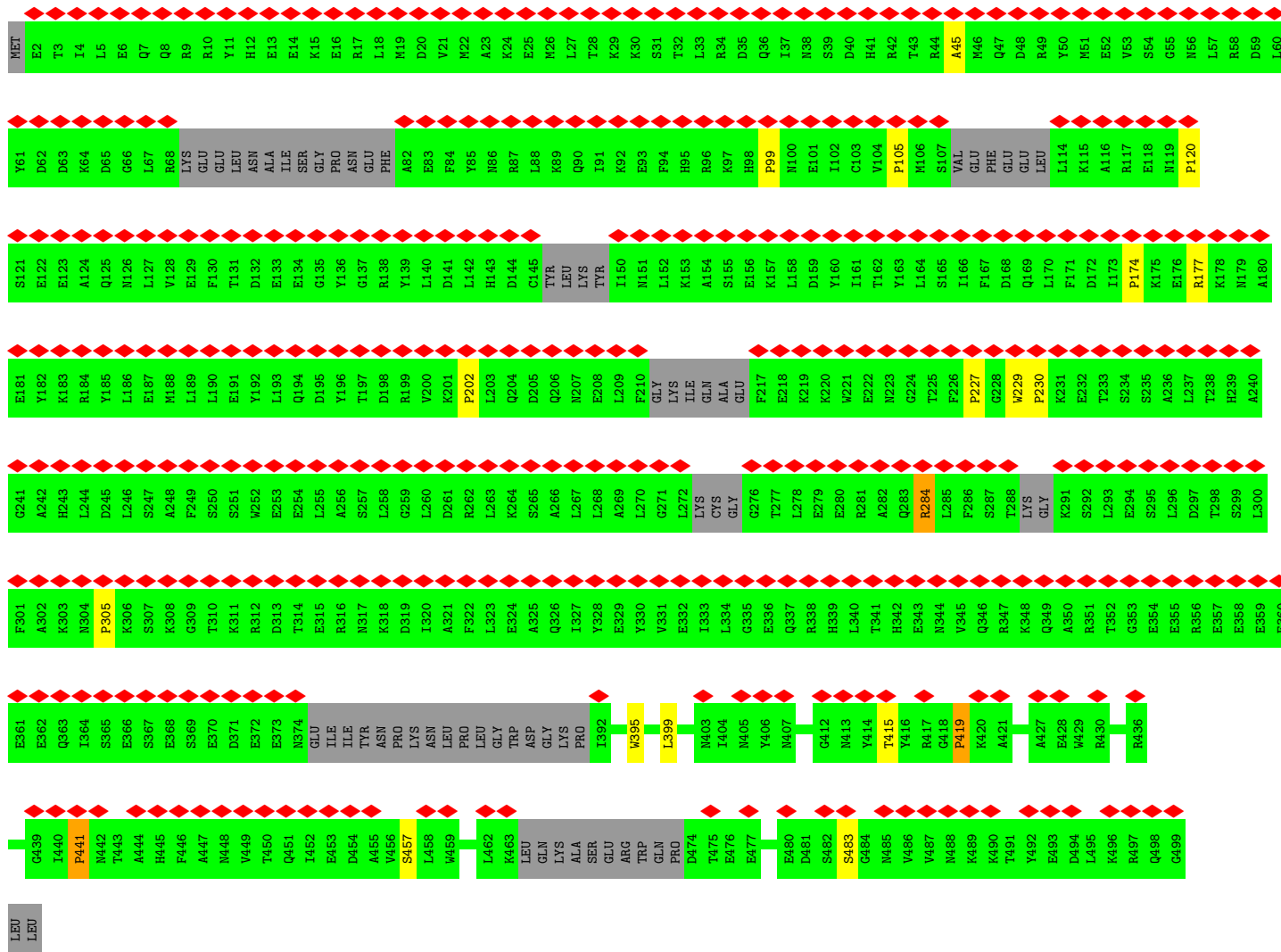
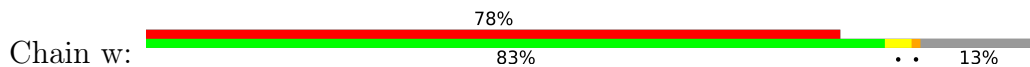


• Molecule 17: U2 small nuclear ribonucleoprotein B''

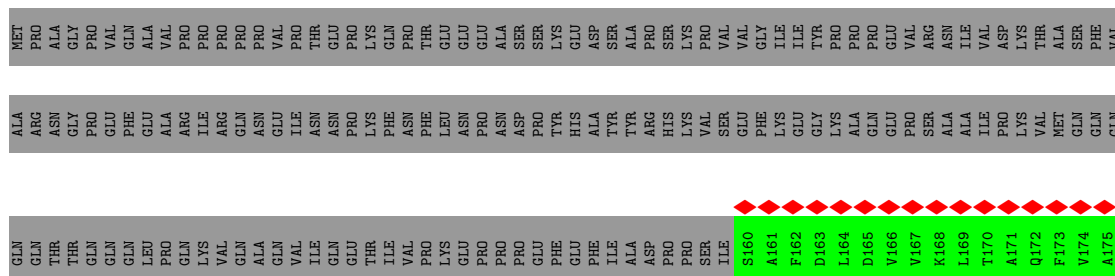


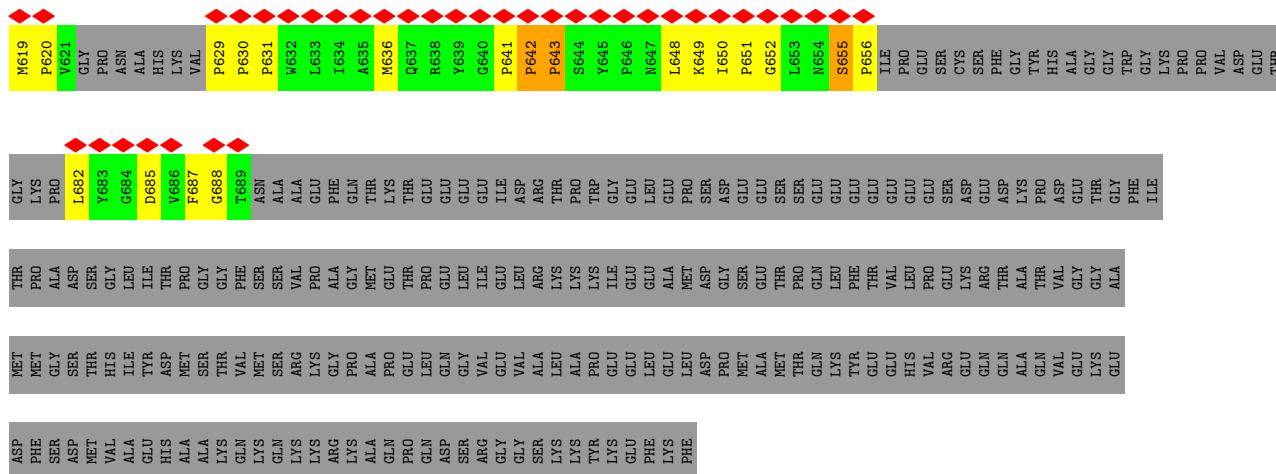


• Molecule 18: Splicing factor 3A subunit 3

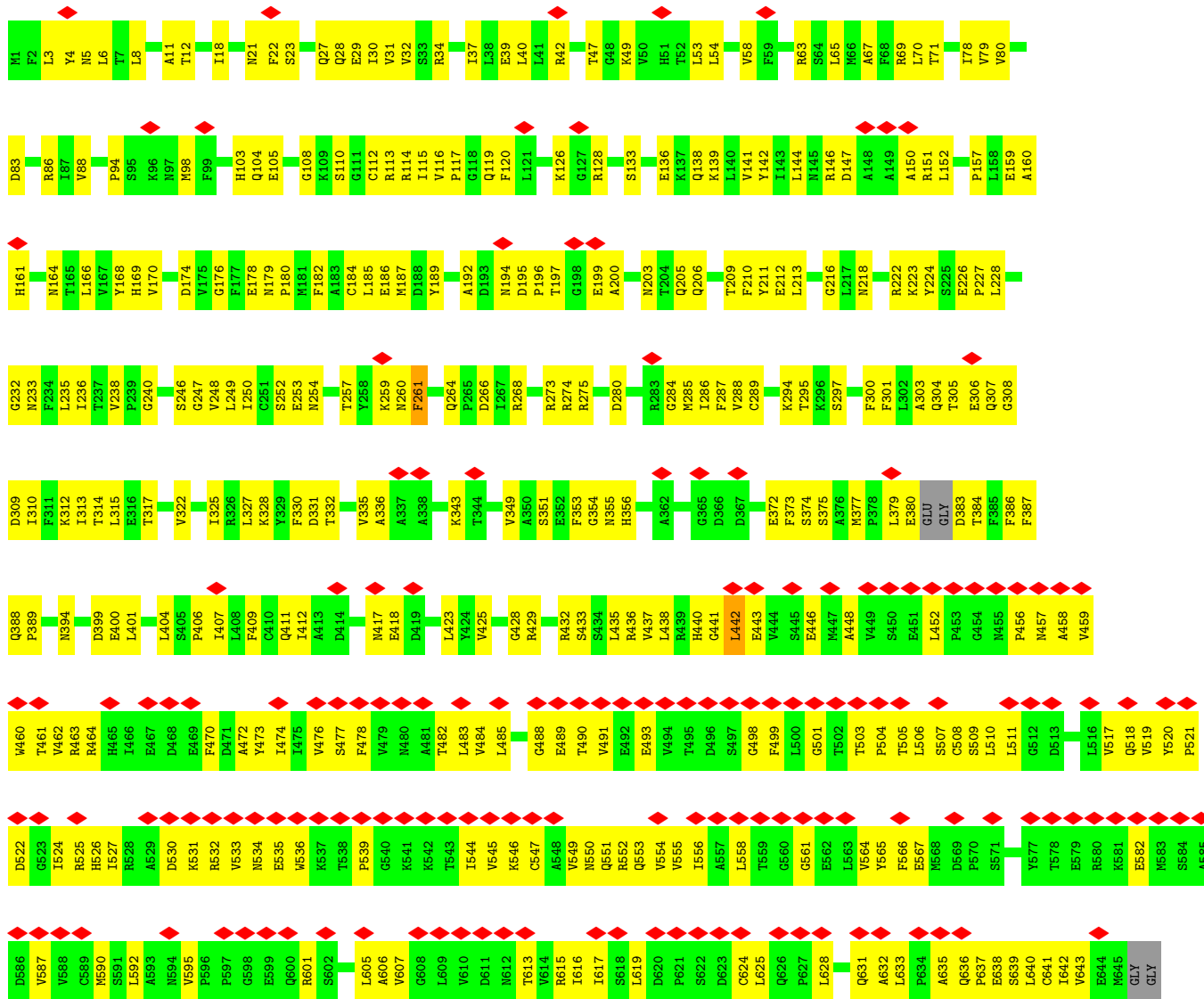


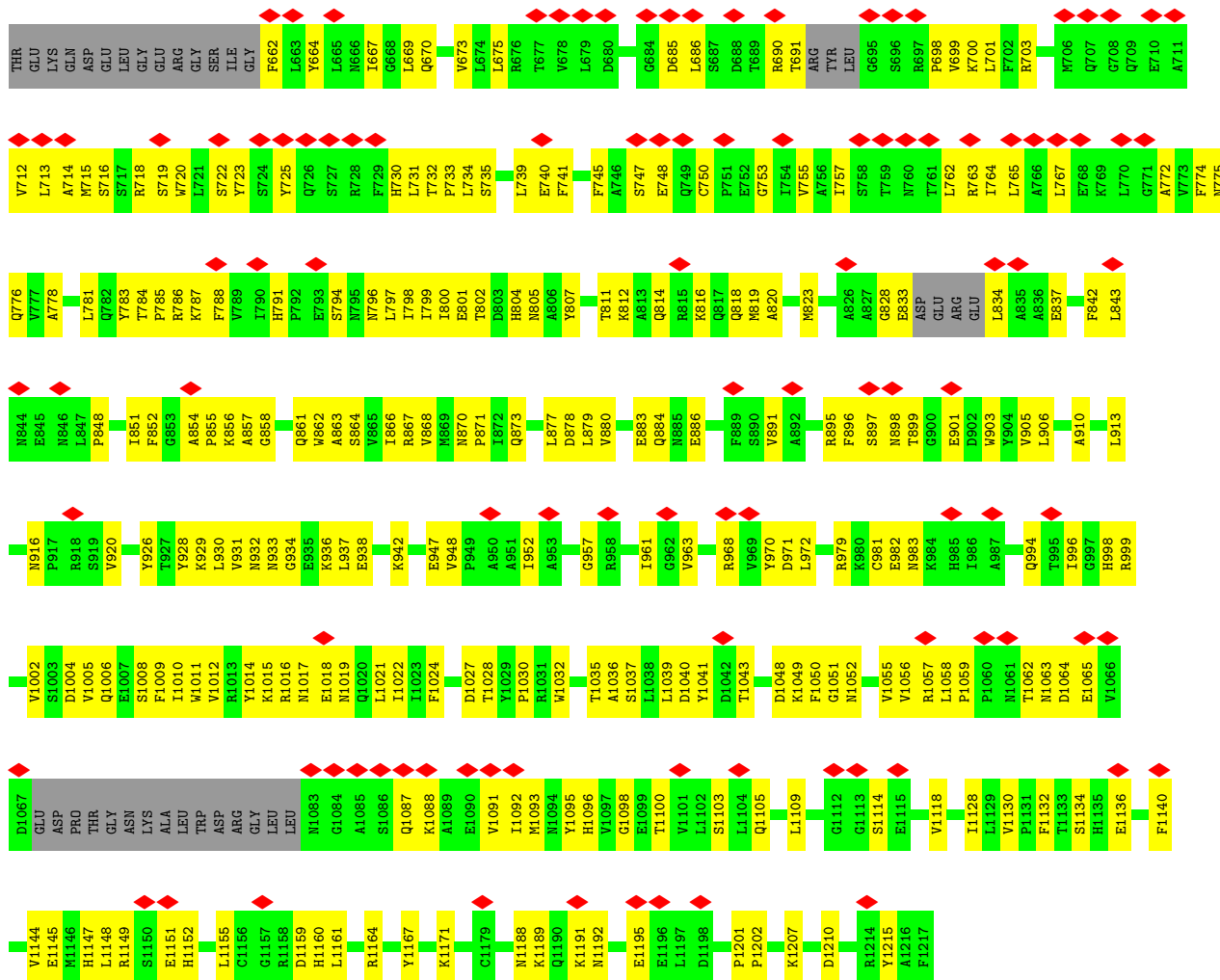
• Molecule 19: Splicing factor 3A subunit 1



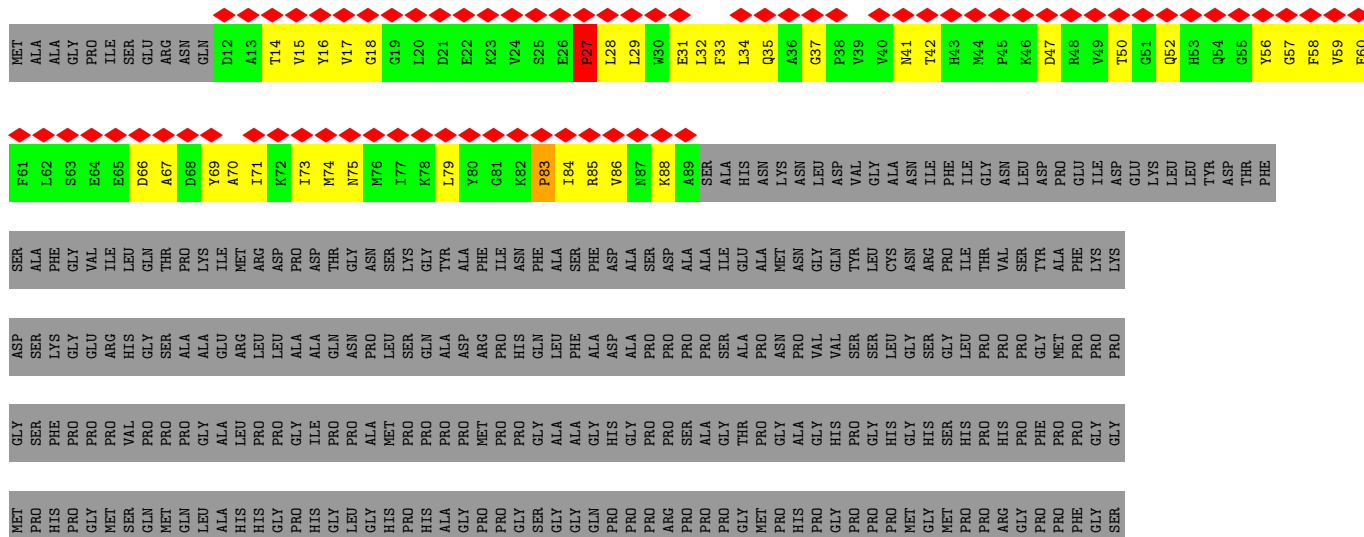


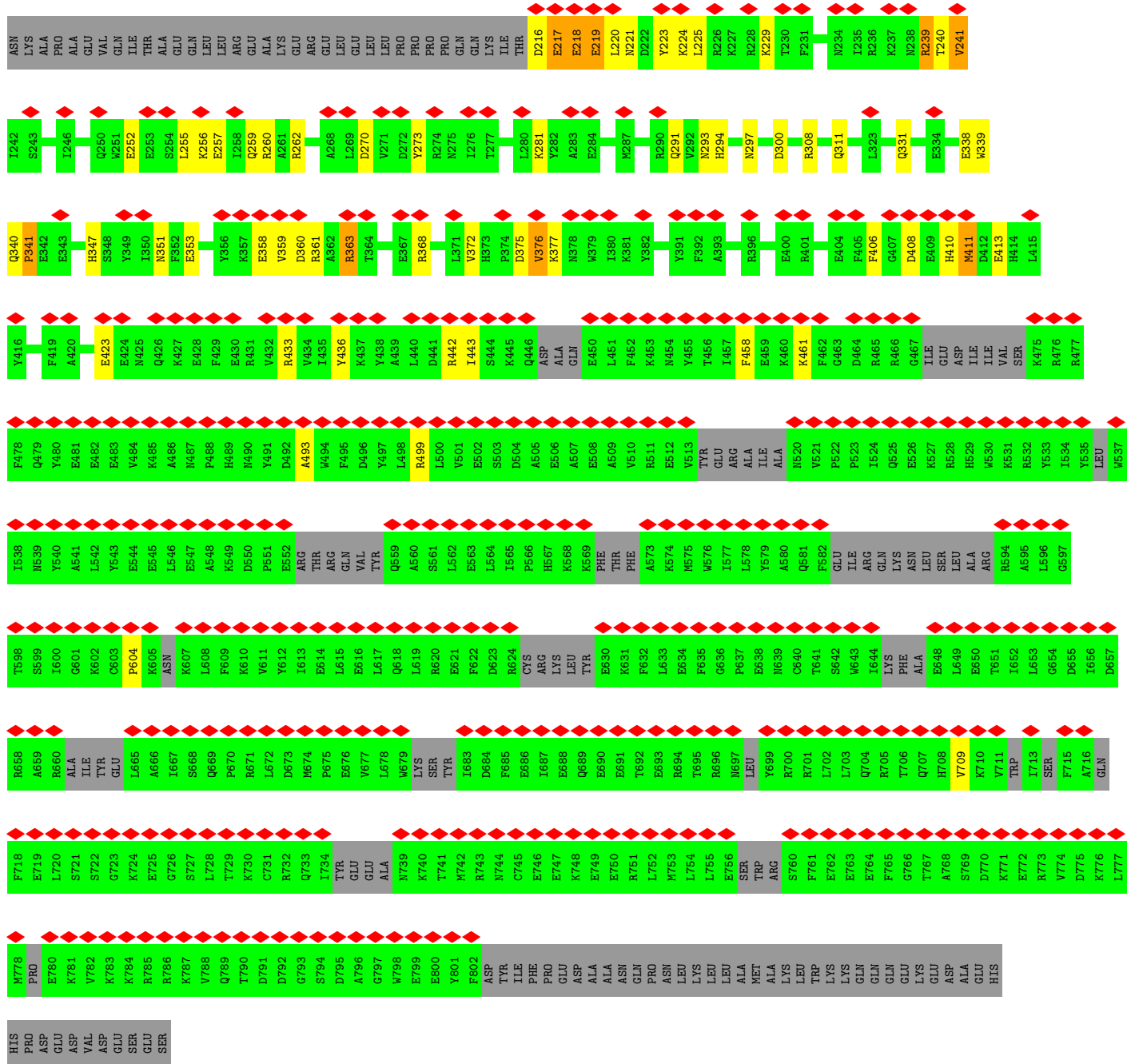
• Molecule 23: Splicing factor 3B subunit 3



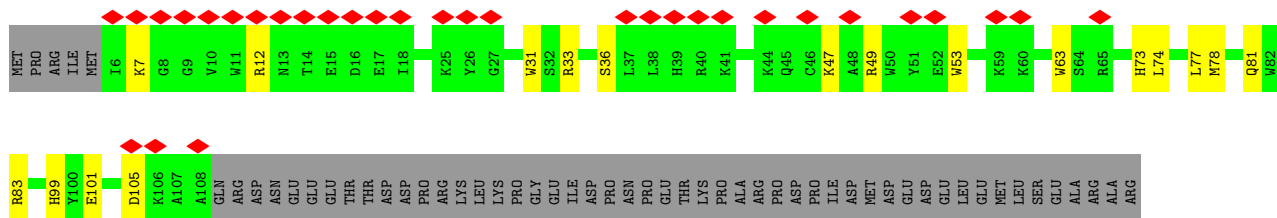


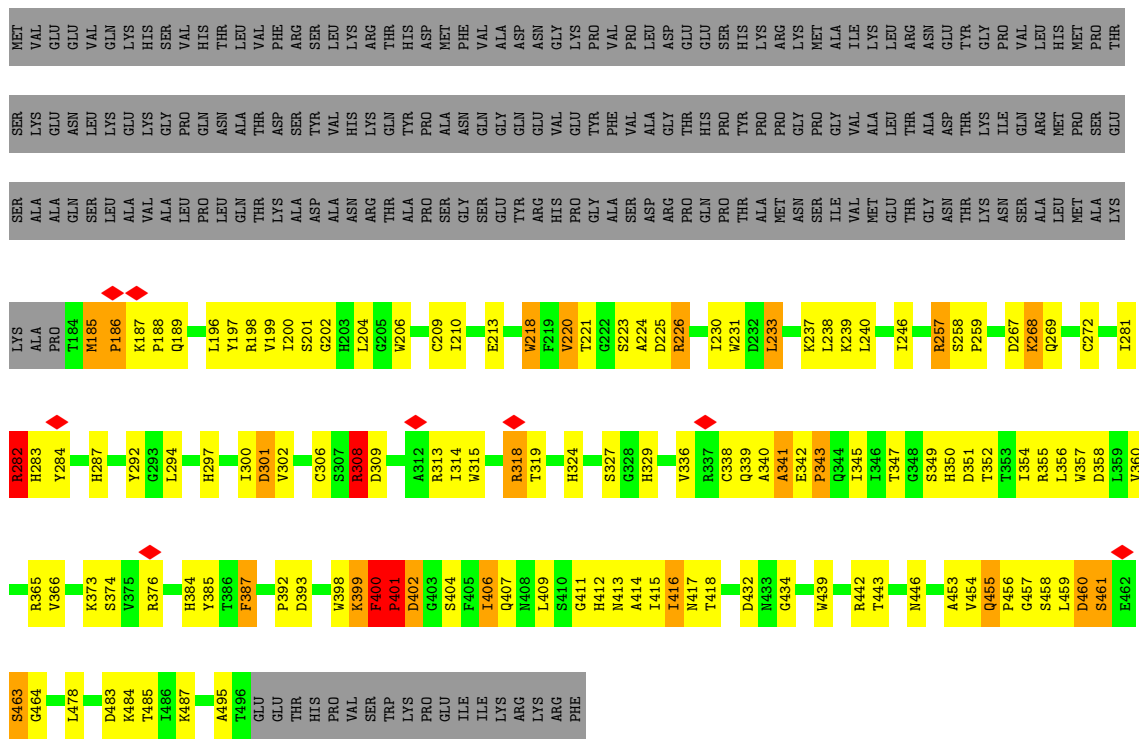
• Molecule 24: Splicing factor 3B subunit 4



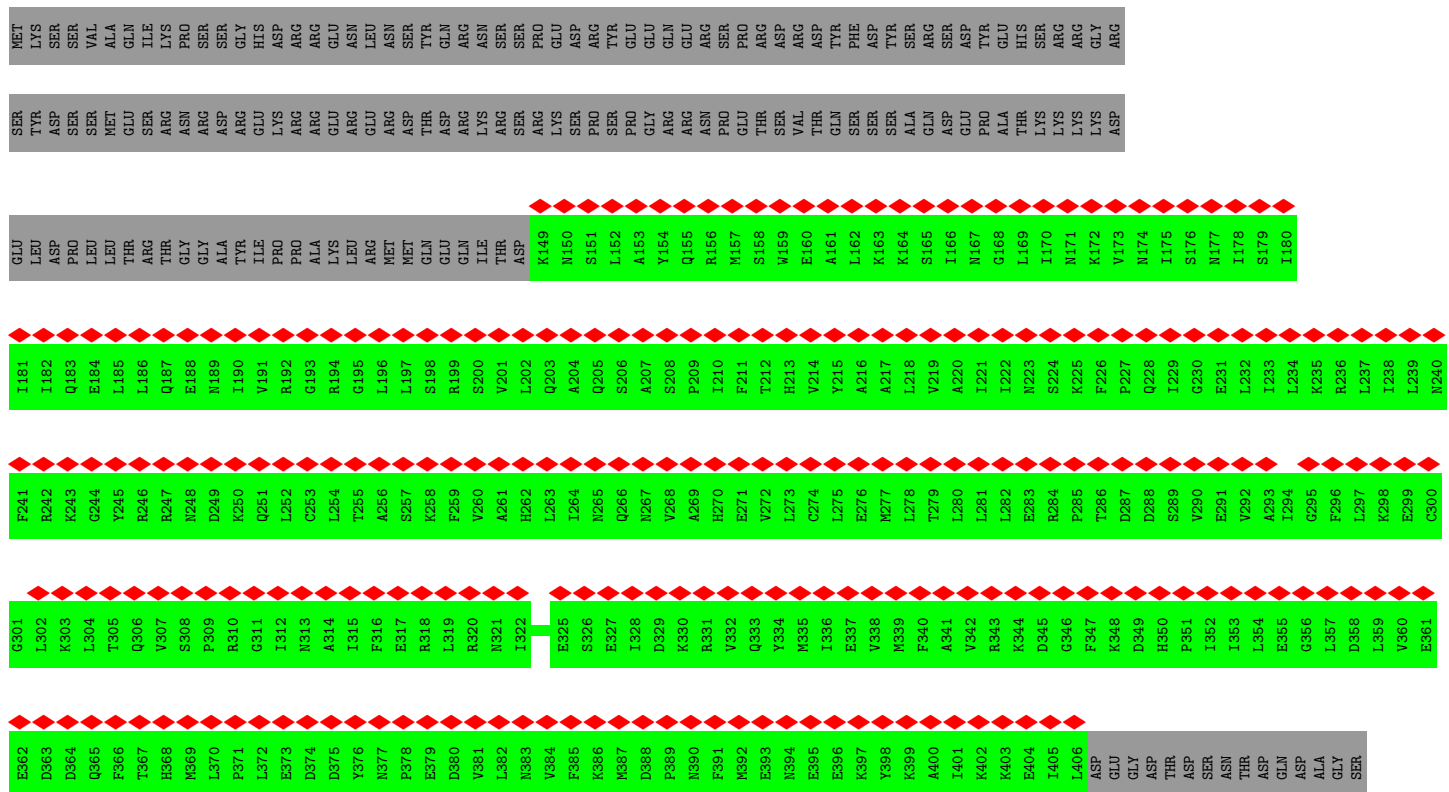


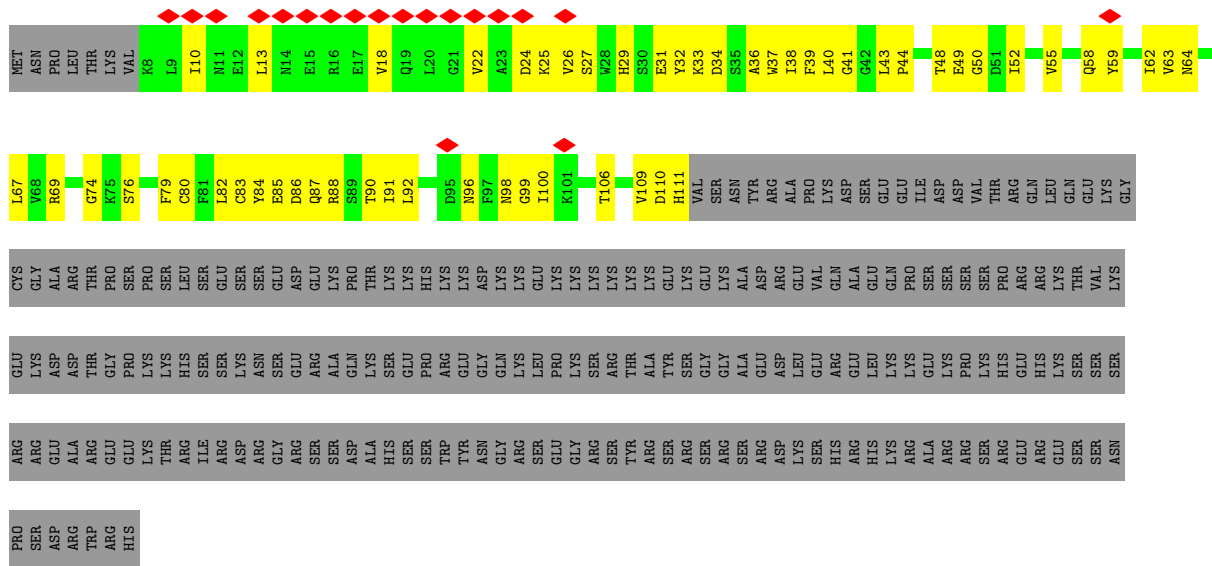
● Molecule 29: Cell division cycle 5-like protein



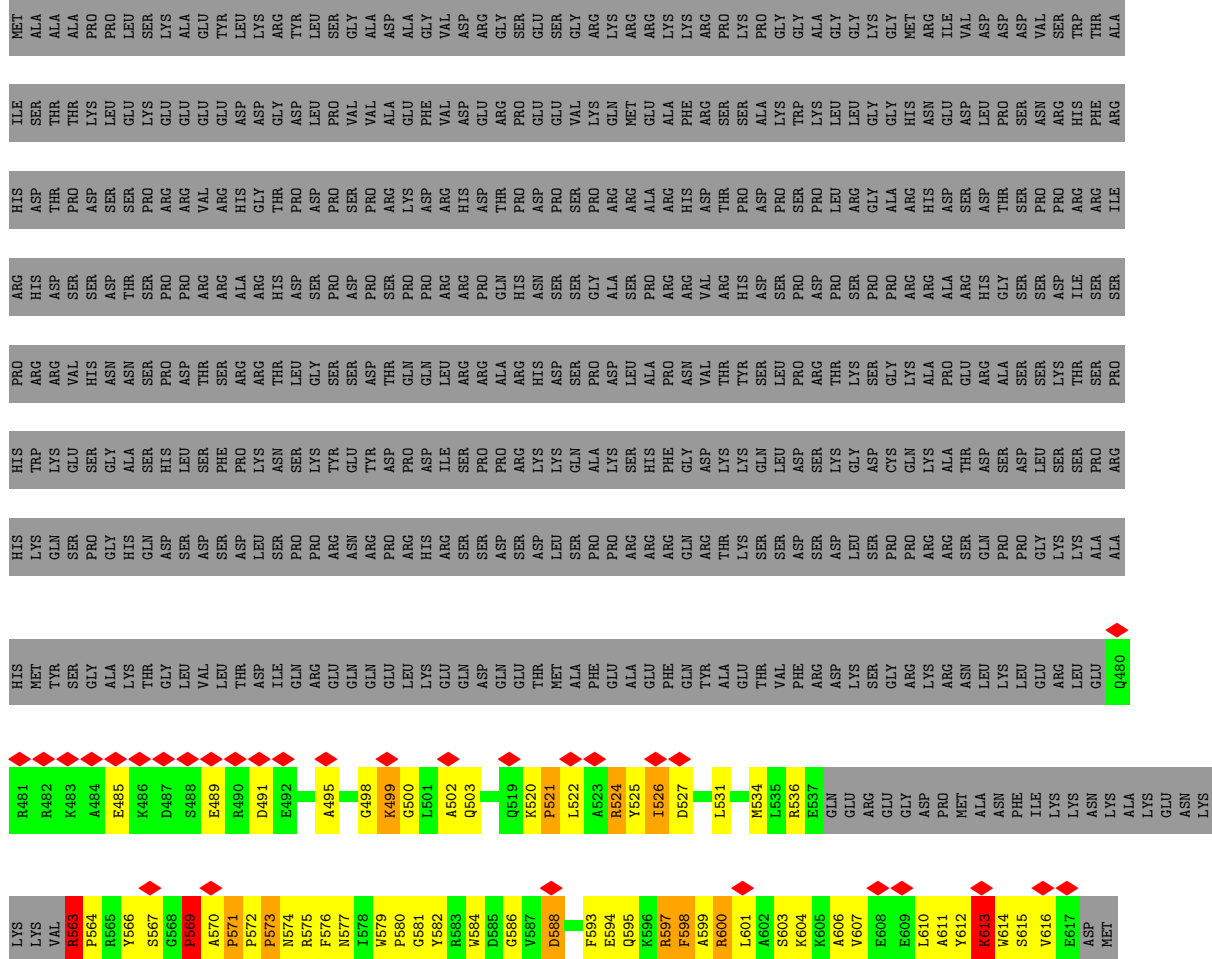


● Molecule 34: Pre-mRNA-splicing factor CWC22 homolog





• Molecule 37: BUD13 homolog



• Molecule 38: Peptidyl-prolyl cis-trans isomerase CWC27 homolog

R541	F642	R543	P644	E545	L546	K547	V648	L549	V650	A551	S552	A553	T554	M555	D556	T557	A558	R559	F560	S561	T562	F563	F564	D565	D566	A567	P568	V569	F570	R571	I572	P573	G574	R575	R576	F577	P578	V579	D580	I581	F582	Y583	T584	K585	A586	P587	E588	A589	D590	Y591	L592	E593	A594	C595	V596	V597	S598	V599	L600
Q601	I602	H603	V604	T605	Q606	PRO	PRO	G609	D610	I611	L612	V613	F614	L615	T616	G617	Q618	E619	E620	I621	E622	A623	A624	C625	E626	M627	L628	Q629	D630	R631	C632	R633	R634	L635	G636	SER	LYS	I639	R640	E641	L642	L643	V644	L645	P646	I647	Y648	A649	N650	L651	P652	S653	D654	M655	Q656	A657	R658	I659	F660
Q661	P662	T663	P664	PRO	GLY	A667	R668	K669	V670	V671	V672	A673	T674	N675	I676	E677	E678	T679	S680	L681	E682	I683	E684	C685	I686	I687	Y688	V689	L690	D691	P692	G693	F694	C695	K696	Q697	K698	S699	Y700	N701	P702	R703	T704	G705	M706	E707	S708	L709	T710	V711	T712	P713	C714	S715	K716	A717	S718	A719	N720
Q721	R722	A723	G724	R725	A726	G727	R728	V729	A730	A731	G732	K733	C734	F735	R736	L737	A740	W741	A742	Y743	Q744	H745	E746	L747	E748	E749	T750	T751	V752	F753	E754	I755	Q756	A757	T758	S759	L760	G761	N762	V763	V764	L765	L766	L767	K768	S769	L770	G771	I772	H773	L774	L775	M776	H777	F778	D779	F780	L781	
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T842	V843	A844	A845	M846	L847	S848	VAL	ASN	ASN	SER	ILE	PHE	TYR	ARG	PRO	LYS	ASP	LYS	VAL	HIS	ALA	D865	M866	A867	R868	V869	N870	F871	F872	L873	P874	G875	G876	D877	H878	L879	V880	L881	L882	N883	V884	Y885	T886	Q887	W888	A889	E890	SER	GLY	TYR	SER	SER	GLN	TRP	C898	Y899	E900	N901	
F902	V903	Q904	F905	R906	S907	M908	R909	R910	A911	R912	D913	V914	R915	E916	Q917	L918	E919	G920	L921	L922	E923	R924	V925	E926	V927	G928	L929	S930	S931	C932	Q933	G934	D935	Y936	I937	R938	V939	R940	K941	A942	I943	T944	A945	G946	Y947	F948	Y949	H950	T951	A952	R953	LEU	THR	ARG	SER	G958	Y959	R960	T961
V962	LYS	GLN	GLN	THR	V968	F969	I970	H971	P972	N973	S974	SER	ARG	LEU	PHE	GLU	Q979	Q980	Y981	R982	W983	L984	L985	Y986	E987	E988	V989	L991	T992	T993	K994	E995	F996	M997	R998	Q999	V1000	L1001	E1002	I1003	E1004	S1005	S1006	W1007	L1008	L1009	E1010	V1011	A1012	P1013	H1014	Y1015	Y1016	K1017	ALA	LYS	GLU	LEU	
GLU	ASP	PRO	HIS	ALA	LYS	LYS	MET	PRO	LYS	LYS	ILE	GLY	LYS	THR	ARG	GLU	LEU	GLY	Q981	R982	W983	L984	L985	Y986	E987	E988	V989	L991	T992	T993	K994	E995	F996	M997	R998	Q999	V1000	L1001	E1002	I1003	E1004	S1005	S1006	W1007	L1008	L1009	E1010	V1011	A1012	P1013	H1014	Y1015	Y1016	K1017	ALA	LYS	GLU	LEU	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96523	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	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	0.184	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0346	Depositor
Map size (\AA)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.338, 1.338, 1.338	Depositor

5 Model quality i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.69	10/18665 (0.1%)	0.77	26/25340 (0.1%)
2	B	0.73	2/1970 (0.1%)	0.91	7/3060 (0.2%)
3	C	0.79	1/6864 (0.0%)	0.96	10/9334 (0.1%)
4	D	0.33	0/8527	0.59	0/11887
5	E	0.64	0/2392	0.79	0/3242
6	a	0.47	0/397	0.61	0/549
6	h	0.46	0/391	0.61	0/540
7	b	0.49	0/404	0.72	0/561
7	i	0.50	0/421	0.73	0/583
8	c	0.57	0/405	0.73	0/563
8	j	0.57	0/405	0.73	0/563
9	d	0.68	0/479	0.84	0/666
9	k	0.70	0/420	0.85	0/583
10	f	0.75	0/360	0.81	0/497
10	m	0.75	0/360	0.81	0/497
11	e	0.65	0/390	0.80	0/542
11	l	0.64	0/390	0.80	0/542
12	g	0.54	0/362	0.71	0/501
12	n	0.54	0/332	0.72	0/458
13	F	0.39	0/2224	0.86	0/3462
14	G	0.35	0/1717	0.95	1/2664 (0.0%)
15	H	0.59	7/3217 (0.2%)	1.06	18/4997 (0.4%)
16	o	0.61	0/803	1.41	2/1119 (0.2%)
17	p	1.01	1/810 (0.1%)	1.46	4/1122 (0.4%)
18	w	0.53	5/2376 (0.2%)	0.67	13/3269 (0.4%)
19	u	0.23	0/519	0.62	4/717 (0.6%)
20	v	0.36	0/482	0.81	7/666 (1.1%)
21	1	0.33	0/7826	0.51	0/10617
22	2	0.52	3/1277 (0.2%)	0.73	7/1724 (0.4%)
23	3	0.32	0/9408	0.53	0/12767
24	4	0.83	2/535 (0.4%)	0.98	4/724 (0.6%)
25	5	0.29	0/823	0.48	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	6	0.29	0/678	0.51	0/909
27	7	0.31	0/556	0.45	0/751
28	J	0.62	0/3500	0.73	0/4750
29	L	0.41	0/1103	0.57	0/1487
30	M	0.29	0/272	0.49	0/363
31	P	0.83	1/841 (0.1%)	1.01	2/1117 (0.2%)
32	R	0.66	5/2351 (0.2%)	0.86	7/3163 (0.2%)
33	T	1.05	1/2522 (0.0%)	1.11	4/3438 (0.1%)
34	V	0.55	0/2234	0.67	1/3111 (0.0%)
35	X	0.27	0/1011	0.48	0/1348
36	Y	0.31	0/747	0.48	0/1006
37	Z	0.57	2/772 (0.3%)	0.79	7/1056 (0.7%)
38	z	0.29	0/1414	0.51	0/1916
39	x	0.35	0/2871	0.53	3/3981 (0.1%)
All	All	0.57	40/96823 (0.0%)	0.76	127/133875 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1
30	M	0	1
32	R	0	1
33	T	0	2
35	X	0	1
All	All	0	33

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	w	457	SER	CB-OG	8.21	1.52	1.42
18	w	483	SER	CB-OG	7.46	1.51	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	H	142	C	C1'-N1	7.35	1.59	1.48
22	2	655	SER	CB-OG	7.35	1.51	1.42
1	A	406	TRP	CB-CG	-7.08	1.37	1.50
2	B	103	G	C1'-N9	-6.95	1.37	1.46
15	H	150	U	C1'-N1	6.76	1.58	1.48
1	A	2223	CYS	CB-SG	-6.76	1.70	1.82
31	P	227	TYR	CG-CD2	-6.70	1.30	1.39
1	A	476	PHE	CG-CD2	6.63	1.48	1.38
15	H	97	G	C1'-N9	-6.48	1.37	1.46
15	H	151	C	C1'-N1	6.44	1.58	1.48
15	H	184	C	C1'-N1	6.37	1.58	1.48
15	H	141	C	C1'-N1	6.31	1.58	1.48
24	4	50	THR	CB-OG1	5.94	1.55	1.43
18	w	395	TRP	CZ3-CH2	5.86	1.49	1.40
24	4	42	THR	CB-OG1	5.85	1.54	1.43
33	T	218	TRP	CB-CG	-5.71	1.40	1.50
1	A	212	PRO	N-CA	-5.44	1.38	1.47
37	Z	569	PRO	N-CD	5.43	1.55	1.47
2	B	56	C	O3'-P	-5.41	1.54	1.61
22	2	620	PRO	N-CD	5.41	1.55	1.47
18	w	284	ARG	CA-CB	-5.37	1.42	1.53
1	A	94	TYR	CB-CG	-5.34	1.43	1.51
1	A	1120	PRO	N-CD	5.29	1.55	1.47
22	2	643	PRO	N-CD	5.24	1.55	1.47
17	p	156	ASN	C-N	-5.21	1.22	1.34
18	w	415	THR	CB-OG1	5.21	1.53	1.43
1	A	140	TYR	CG-CD2	-5.19	1.32	1.39
32	R	130	PRO	N-CD	5.18	1.55	1.47
37	Z	521	PRO	N-CD	5.15	1.55	1.47
15	H	110	A	C1'-N9	-5.13	1.39	1.46
32	R	222	PRO	N-CD	5.13	1.55	1.47
1	A	351	TYR	CB-CG	-5.10	1.44	1.51
1	A	225	TYR	CB-CG	-5.06	1.44	1.51
32	R	253	PRO	N-CD	5.05	1.54	1.47
3	C	145	PHE	CB-CG	-5.04	1.42	1.51
32	R	252	PRO	N-CD	5.04	1.54	1.47
32	R	227	PRO	N-CD	5.03	1.54	1.47
1	A	406	TRP	CG-CD2	-5.03	1.35	1.43

All (127) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	4	83	PRO	CA-CB-CG	10.19	124.17	104.80
22	2	636	MET	CG-SD-CE	9.28	115.05	100.20
37	Z	569	PRO	CA-N-CD	-8.56	99.52	111.50
37	Z	573	PRO	CA-N-CD	-8.45	99.67	111.50
1	A	404	LEU	CB-CG-CD1	8.13	124.82	111.00
1	A	552	ARG	NE-CZ-NH1	7.48	124.04	120.30
1	A	153	ARG	NE-CZ-NH2	-7.36	116.62	120.30
2	B	20	G	N9-C1'-C2'	7.28	123.46	114.00
15	H	113	G	OP2-P-O3'	7.25	121.15	105.20
15	H	141	C	OP2-P-O3'	7.24	121.14	105.20
15	H	114	A	OP2-P-O3'	7.22	121.09	105.20
3	C	144	CYS	N-CA-CB	7.20	123.56	110.60
15	H	150	U	OP2-P-O3'	7.19	121.01	105.20
32	R	180	THR	C-N-CD	-7.16	104.85	120.60
18	w	441	PRO	N-CA-CB	7.16	111.89	103.30
19	u	222	PRO	N-CA-CB	7.14	111.87	103.30
1	A	611	LEU	CB-CG-CD1	-7.13	98.88	111.00
22	2	656	PRO	N-CA-CB	6.88	111.56	103.30
1	A	565	ARG	NE-CZ-NH2	-6.81	116.90	120.30
15	H	155	C	P-O3'-C3'	6.78	127.84	119.70
2	B	26	A	O5'-P-OP2	6.77	118.83	110.70
15	H	141	C	O3'-P-O5'	-6.77	91.14	104.00
15	H	150	U	O3'-P-O5'	-6.77	91.14	104.00
2	B	104	C	C2'-C3'-O3'	-6.77	94.61	109.50
15	H	113	G	O3'-P-O5'	-6.73	91.21	104.00
15	H	114	A	O3'-P-O5'	-6.72	91.23	104.00
15	H	30	A	O5'-P-OP1	-6.71	99.66	105.70
2	B	12	U	N1-C1'-C2'	-6.66	104.67	112.00
20	v	115	PRO	N-CA-CB	6.65	111.28	103.30
3	C	420	CYS	CA-CB-SG	-6.63	102.07	114.00
31	P	215	LEU	CB-CG-CD1	-6.61	99.76	111.00
20	v	139	PRO	N-CA-CB	6.54	111.15	103.30
24	4	27	PRO	N-CA-CB	6.50	111.10	103.30
1	A	598	LEU	CB-CG-CD2	-6.48	99.98	111.00
31	P	215	LEU	CB-CG-CD2	6.47	122.00	111.00
18	w	120	PRO	N-CA-CB	6.47	111.06	103.30
18	w	227	PRO	N-CA-CB	6.47	111.06	103.30
3	C	921	LEU	CB-CG-CD1	6.41	121.89	111.00
39	x	403	PRO	N-CA-CB	6.35	110.92	103.30
19	u	200	PRO	N-CA-CB	6.31	110.87	103.30
32	R	205	ASP	CB-CG-OD2	6.30	123.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	v	218	PRO	N-CA-CB	6.28	110.83	103.30
37	Z	570	ALA	C-N-CD	6.25	141.52	128.40
1	A	476	PHE	CB-CG-CD1	6.24	125.17	120.80
18	w	105	PRO	N-CA-CB	6.24	110.79	103.30
18	w	305	PRO	N-CA-CB	6.23	110.77	103.30
22	2	641	PRO	N-CA-CB	6.21	110.76	103.30
18	w	174	PRO	N-CA-CB	6.21	110.75	103.30
1	A	153	ARG	NE-CZ-NH1	6.20	123.40	120.30
33	T	220	VAL	CB-CA-C	-6.18	99.65	111.40
33	T	282	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	506	LEU	CB-CG-CD1	-6.17	100.51	111.00
19	u	221	PRO	N-CA-CB	6.17	110.70	103.30
39	x	509	PRO	N-CA-CB	6.14	110.66	103.30
17	p	184	PRO	N-CA-CB	6.10	110.62	103.30
1	A	1117	HIS	C-N-CD	6.05	141.11	128.40
18	w	202	PRO	N-CA-CB	6.04	110.55	103.30
20	v	221	PRO	N-CA-CB	6.04	110.55	103.30
17	p	155	LEU	N-CA-CB	5.99	122.37	110.40
14	G	156	U	C2-N1-C1'	5.97	124.87	117.70
20	v	162	PRO	N-CA-CB	5.96	110.45	103.30
18	w	99	PRO	N-CA-CB	5.96	110.45	103.30
32	R	252	PRO	C-N-CD	5.93	140.85	128.40
18	w	230	PRO	N-CA-CB	5.86	110.33	103.30
17	p	219	LYS	O-C-N	5.86	132.07	122.70
20	v	220	PRO	N-CA-CB	5.86	110.33	103.30
18	w	419	PRO	N-CA-CB	5.85	110.32	103.30
20	v	217	PRO	N-CA-CB	5.84	110.31	103.30
15	H	172	C	P-O3'-C3'	5.84	126.71	119.70
3	C	148	CYS	CB-CA-C	5.82	122.04	110.40
3	C	446	LYS	C-N-CD	5.81	140.61	128.40
15	H	156	U	P-O3'-C3'	-5.77	112.78	119.70
22	2	629	PRO	N-CA-CB	5.77	110.22	103.30
37	Z	563	ARG	C-N-CD	5.76	140.49	128.40
32	R	221	GLY	C-N-CD	5.66	140.29	128.40
22	2	642	PRO	C-N-CD	5.65	140.27	128.40
24	4	27	PRO	CA-CB-CG	5.64	115.51	104.80
1	A	1364	LEU	CA-CB-CG	5.63	128.25	115.30
37	Z	520	LYS	C-N-CD	5.61	140.18	128.40
1	A	565	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	1119	ASP	C-N-CD	5.58	140.12	128.40
15	H	46	U	P-O3'-C3'	5.57	126.39	119.70
39	x	785	PRO	N-CA-CB	5.56	109.97	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	o	58	ASP	N-CA-CB	-5.52	100.66	110.60
1	A	656	LEU	CB-CG-CD1	-5.48	101.68	111.00
1	A	118	VAL	CB-CA-C	-5.47	101.01	111.40
15	H	157	G	O4'-C1'-N9	-5.47	103.83	108.20
3	C	146	VAL	CA-CB-CG2	-5.46	102.70	110.90
1	A	420	ARG	NE-CZ-NH2	-5.46	117.57	120.30
18	w	399	LEU	CB-CG-CD1	-5.42	101.78	111.00
3	C	91	GLU	C-N-CD	-5.42	108.68	120.60
1	A	2310	ARG	CG-CD-NE	5.41	123.16	111.80
22	2	651	PRO	N-CA-CB	5.39	109.77	103.30
1	A	251	ASP	CB-CG-OD1	5.38	123.14	118.30
33	T	308	ARG	NE-CZ-NH2	-5.36	117.62	120.30
22	2	619	MET	C-N-CD	5.36	139.66	128.40
15	H	106	G	O5'-P-OP1	5.34	117.10	110.70
15	H	156	U	OP2-P-O3'	5.33	116.93	105.20
1	A	92	LEU	CB-CG-CD1	-5.30	101.99	111.00
32	R	178	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	656	LEU	CA-CB-CG	-5.30	103.12	115.30
1	A	314	ILE	CA-CB-CG1	-5.29	100.95	111.00
2	B	40	U	N1-C1'-C2'	5.28	120.86	114.00
2	B	37	G	O5'-P-OP2	-5.27	100.96	105.70
24	4	50	THR	CA-CB-OG1	5.25	120.02	109.00
3	C	921	LEU	CB-CG-CD2	-5.24	102.09	111.00
17	p	149	PRO	N-CA-CB	5.23	109.58	103.30
1	A	656	LEU	CB-CG-CD2	5.21	119.85	111.00
37	Z	588	ASP	CB-CG-OD2	5.20	122.98	118.30
3	C	776	GLU	N-CA-C	5.19	125.02	111.00
32	R	178	ARG	NE-CZ-NH1	5.19	122.90	120.30
37	Z	527	ASP	CB-CG-OD2	5.19	122.97	118.30
19	u	203	SER	N-CA-CB	-5.18	102.73	110.50
1	A	330	THR	CA-CB-CG2	-5.15	105.19	112.40
15	H	157	G	P-O5'-C5'	-5.13	112.69	120.90
34	V	467	LEU	CB-CA-C	-5.12	100.47	110.20
1	A	647	LEU	CB-CG-CD1	-5.12	102.31	111.00
1	A	638	LEU	CA-CB-CG	-5.11	103.55	115.30
2	B	20	G	O4'-C1'-N9	5.09	112.28	108.20
18	w	399	LEU	CD1-CG-CD2	5.09	125.76	110.50
15	H	156	U	C4'-C3'-C2'	5.08	107.68	102.60
1	A	677	VAL	CB-CA-C	-5.07	101.78	111.40
33	T	233	LEU	CB-CG-CD1	-5.06	102.40	111.00
18	w	45	ALA	N-CA-CB	-5.04	103.04	110.10
32	R	101	ILE	CB-CA-C	-5.04	101.53	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	o	99	SER	N-CA-CB	-5.03	102.96	110.50
3	C	220	ARG	NE-CZ-NH2	-5.01	117.79	120.30

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1	1028	HIS	Peptide
21	1	1105	GLU	Peptide
21	1	1107	GLN	Peptide
21	1	220	GLN	Peptide
21	1	415	LEU	Peptide
21	1	418	PRO	Peptide
21	1	460	PRO	Peptide
21	1	717	THR	Peptide
21	1	943	LYS	Peptide
22	2	558	ARG	Peptide
23	3	261	PHE	Peptide
23	3	530	ASP	Peptide
23	3	552	ARG	Peptide
23	3	916	ASN	Peptide
27	7	74	GLN	Peptide
1	A	1119	ASP	Peptide
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	736	GLY	Peptide
3	C	823	ALA	Peptide
4	D	430	LEU	Peptide
30	M	196	ASP	Peptide
32	R	94	GLY	Peptide
33	T	400	PHE	Mainchain,Peptide
35	X	193	ASN	Peptide
9	d	112	ASN	Peptide
9	k	112	ASN	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	18165	0	17930	1529	0
2	B	1768	0	897	123	0
3	C	6716	0	6691	968	0
4	D	8528	0	3745	69	0
5	E	2338	0	2272	136	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	0	0
9	k	422	0	175	0	0
10	f	361	0	158	0	0
10	m	361	0	158	0	0
11	e	391	0	163	0	0
11	l	391	0	163	0	0
12	g	363	0	160	0	0
12	n	334	0	143	0	0
13	F	1988	0	1005	133	0
14	G	1545	0	786	121	0
15	H	2886	0	1463	239	0
16	o	804	0	350	0	0
17	p	813	0	365	0	0
18	w	2369	0	1298	0	0
19	u	525	0	216	0	0
20	v	486	0	206	0	0
21	1	7702	0	7389	291	0
22	2	1252	0	1040	56	0
23	3	9220	0	9139	481	0
24	4	527	0	438	40	0
25	5	807	0	729	27	0
26	6	670	0	654	21	0
27	7	540	0	509	25	0
28	J	3463	0	2544	106	0
29	L	1077	0	1067	54	0
30	M	267	0	225	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	P	829	0	814	187	0
32	R	2314	0	2189	405	0
33	T	2457	0	2416	251	0
34	V	2238	0	969	49	0
35	X	1012	0	731	18	0
36	Y	737	0	608	67	0
37	Z	755	0	591	155	0
38	z	1381	0	1298	0	0
39	x	2882	0	1308	0	0
40	A	36	0	6	0	0
41	C	32	0	12	11	0
42	C	1	0	0	0	0
42	F	5	0	0	0	0
43	6	3	0	0	0	0
43	M	1	0	0	0	0
All	All	94673	0	74250	4461	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 27.

All (4461) 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)
36:Y:37:TRP:CH2	37:Z:498:GLY:HA2	1.23	1.65
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.57
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
3:C:77:VAL:HG11	33:T:196:LEU:CG	1.39	1.52
36:Y:37:TRP:CH2	37:Z:498:GLY:CA	1.93	1.51
1:A:2270:PHE:CB	4:D:1264:PRO:CB	1.86	1.50
37:Z:564:PRO:HB2	37:Z:582:TYR:CG	1.45	1.49
31:P:193:VAL:HG23	31:P:194:PHE:CD2	1.46	1.47
32:R:442:ARG:HH11	32:R:443:GLY:C	1.17	1.45
1:A:844:GLU:CB	32:R:422:MET:CE	1.94	1.45
31:P:193:VAL:CG2	31:P:194:PHE:HD2	1.28	1.45
23:3:440:HIS:CE1	23:3:733:PRO:HD3	1.50	1.43
32:R:414:ARG:NH1	37:Z:598:PHE:CZ	1.86	1.43
1:A:73:HIS:HD2	1:A:81:PHE:CE2	1.37	1.42
1:A:530:LEU:H	30:M:198:GLN:NE2	1.18	1.42
1:A:2270:PHE:CD1	4:D:1264:PRO:CB	2.03	1.41
3:C:705:VAL:HG23	3:C:717:PHE:CD2	1.55	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:79:THR:CG2	33:T:199:VAL:HB	1.51	1.40
28:J:293:ASN:CB	29:L:225:TYR:CB	1.98	1.39
1:A:312:TYR:CE2	3:C:882:GLY:HA3	1.58	1.39
3:C:79:THR:HG23	33:T:199:VAL:CB	1.49	1.39
5:E:260:ARG:NH1	5:E:273:CYS:SG	1.95	1.39
1:A:530:LEU:HB2	30:M:198:GLN:NE2	1.38	1.38
28:J:339:TRP:HA	32:R:116:TYR:CE2	1.58	1.38
3:C:387:ASP:O	3:C:388:VAL:HG12	1.20	1.37
32:R:442:ARG:CD	32:R:443:GLY:H	1.37	1.37
1:A:393:LEU:HA	3:C:379:LYS:CG	1.52	1.36
3:C:77:VAL:HG12	33:T:196:LEU:C	1.46	1.36
1:A:762:ARG:HH22	31:P:226:LYS:NZ	1.19	1.35
28:J:339:TRP:HA	32:R:116:TYR:CD2	1.60	1.35
32:R:414:ARG:NH1	37:Z:598:PHE:CE2	1.93	1.35
3:C:77:VAL:CG1	33:T:196:LEU:C	1.94	1.35
1:A:393:LEU:N	3:C:379:LYS:HE2	1.42	1.34
3:C:149:LEU:CD1	3:C:427:PHE:CD2	2.08	1.34
32:R:442:ARG:HD3	32:R:443:GLY:N	1.05	1.34
1:A:121:HIS:NE2	1:A:481:PHE:HB3	1.42	1.34
32:R:414:ARG:NE	37:Z:598:PHE:CZ	1.95	1.34
3:C:452:THR:CG2	3:C:577:PHE:HD2	1.40	1.34
1:A:312:TYR:CZ	3:C:882:GLY:HA3	1.61	1.34
1:A:1962:THR:CG2	37:Z:524:ARG:HB2	1.57	1.33
1:A:384:VAL:HG12	3:C:331:PHE:CB	1.58	1.32
1:A:388:LEU:CD1	3:C:399:LEU:HD21	1.58	1.32
3:C:145:PHE:CA	3:C:312:SER:HB2	1.57	1.31
32:R:414:ARG:CZ	37:Z:598:PHE:CZ	2.14	1.31
3:C:670:SER:HA	3:C:823:ALA:CB	1.60	1.31
31:P:212:ASN:O	33:T:458:SER:HA	1.30	1.30
1:A:73:HIS:CD2	1:A:81:PHE:CE2	2.20	1.30
1:A:384:VAL:HA	3:C:331:PHE:CD2	1.67	1.30
1:A:844:GLU:CB	32:R:422:MET:HE3	1.54	1.30
1:A:305:ARG:HB3	3:C:879:ASP:OD1	1.28	1.29
1:A:73:HIS:CD2	1:A:81:PHE:CZ	2.20	1.29
31:P:211:VAL:HG13	33:T:457:GLY:CA	1.62	1.29
3:C:77:VAL:CG1	33:T:196:LEU:HG	1.63	1.28
3:C:705:VAL:CG2	3:C:717:PHE:CE2	2.15	1.28
1:A:264:PHE:CZ	1:A:459:LEU:HD13	1.66	1.27
23:3:440:HIS:CE1	23:3:733:PRO:CD	2.14	1.27
1:A:384:VAL:CG1	3:C:331:PHE:HB3	1.64	1.27
1:A:2268:LEU:HD23	4:D:1261:PRO:O	1.21	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:LEU:HD11	3:C:399:LEU:CD2	1.63	1.27
1:A:2268:LEU:HD22	4:D:1261:PRO:CB	1.65	1.26
1:A:666:LYS:CB	1:A:668:VAL:HG22	1.64	1.26
3:C:78:GLU:O	33:T:198:ARG:HA	1.35	1.26
1:A:530:LEU:CA	30:M:198:GLN:HE22	1.49	1.26
3:C:145:PHE:HA	3:C:312:SER:CB	1.65	1.26
31:P:211:VAL:CG1	33:T:457:GLY:HA3	1.65	1.26
1:A:406:TRP:HZ3	3:C:265:LEU:O	1.14	1.26
1:A:392:PRO:C	3:C:379:LYS:HE2	1.54	1.26
31:P:193:VAL:CG2	31:P:194:PHE:CD2	2.09	1.26
5:E:146:ARG:NH1	5:E:148:LYS:CE	1.98	1.25
32:R:414:ARG:CZ	37:Z:598:PHE:HZ	1.47	1.25
1:A:2113:LYS:HE3	4:D:1229:ASP:O	1.33	1.25
1:A:530:LEU:CB	30:M:198:GLN:HE22	1.47	1.24
24:4:14:THR:HA	24:4:59:VAL:O	1.32	1.24
32:R:442:ARG:HD2	32:R:444:GLY:N	1.50	1.24
3:C:679:PRO:HB2	3:C:807:GLN:OE1	1.25	1.24
3:C:84:GLU:O	33:T:238:LEU:HD23	1.34	1.24
1:A:530:LEU:N	30:M:198:GLN:NE2	1.84	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:CA	2.20	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA2	1.73	1.23
3:C:140:HIS:CG	3:C:230:ASP:HB2	1.74	1.22
1:A:121:HIS:CE1	1:A:481:PHE:HB3	1.73	1.22
23:3:440:HIS:NE2	23:3:733:PRO:CD	2.03	1.22
2:B:42:U:N3	14:G:-3:A:C2	2.07	1.22
1:A:762:ARG:HH22	31:P:226:LYS:CE	1.51	1.22
3:C:78:GLU:HG2	3:C:80:ILE:CD1	1.69	1.22
3:C:145:PHE:CA	3:C:312:SER:CB	2.18	1.22
28:J:256:LYS:O	29:L:232:TYR:CD2	1.93	1.22
1:A:530:LEU:CB	30:M:198:GLN:NE2	2.02	1.21
3:C:77:VAL:HG13	33:T:196:LEU:O	1.40	1.21
3:C:497:LEU:HD13	3:C:577:PHE:CZ	1.76	1.21
36:Y:18:VAL:CB	37:Z:600:ARG:HH21	1.53	1.21
1:A:2325:VAL:HG13	4:D:788:GLY:O	1.40	1.21
1:A:1320:LYS:HE2	32:R:434:TYR:CE1	1.76	1.21
3:C:137:HIS:CD2	3:C:236:MET:HB2	1.75	1.21
32:R:442:ARG:CD	32:R:443:GLY:N	1.95	1.20
1:A:2298:LEU:HB3	4:D:1283:PRO:CB	1.71	1.20
23:3:699:VAL:HA	23:3:715:MET:O	1.40	1.20
1:A:384:VAL:CG2	3:C:334:ILE:HG21	1.72	1.19
1:A:755:HIS:ND1	31:P:223:PHE:CG	2.10	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:705:VAL:HG23	3:C:717:PHE:CE2	1.75	1.19
1:A:227:ARG:HA	1:A:416:GLY:O	1.39	1.19
1:A:401:GLY:HA3	3:C:386:GLY:HA2	1.20	1.19
5:E:146:ARG:NH1	5:E:148:LYS:HE3	1.53	1.19
13:F:68:C:N4	31:P:33:ARG:HB3	1.55	1.18
1:A:695:ASP:HB3	33:T:374:SER:OG	1.40	1.18
1:A:2268:LEU:CD2	4:D:1261:PRO:O	1.91	1.17
3:C:149:LEU:HD13	3:C:427:PHE:CG	1.79	1.17
1:A:232:LEU:CD1	1:A:404:LEU:HD12	1.75	1.17
1:A:705:LYS:CB	32:R:251:ILE:HD12	1.72	1.17
3:C:140:HIS:CG	3:C:230:ASP:CB	2.27	1.17
1:A:151:MET:HE3	1:A:628:GLY:O	1.41	1.17
1:A:406:TRP:CZ3	3:C:265:LEU:O	1.98	1.17
1:A:696:MET:CB	33:T:415:ILE:CD1	2.22	1.17
3:C:465:MET:HE1	3:C:475:MET:HG3	1.26	1.17
3:C:77:VAL:CG1	33:T:196:LEU:O	1.89	1.16
1:A:393:LEU:HA	3:C:379:LYS:HG3	1.28	1.16
3:C:78:GLU:CG	3:C:80:ILE:HD11	1.72	1.16
3:C:221:ILE:HD11	3:C:479:THR:OG1	1.46	1.16
1:A:758:ARG:HB3	31:P:227:TYR:CE2	1.79	1.16
1:A:384:VAL:HG21	3:C:334:ILE:CG2	1.76	1.15
3:C:679:PRO:CB	3:C:807:GLN:OE1	1.95	1.15
1:A:1900:GLU:OE1	37:Z:522:LEU:HB2	1.47	1.15
1:A:755:HIS:CE1	31:P:223:PHE:CG	2.35	1.14
1:A:1262:LYS:HG2	32:R:431:ASP:CB	1.77	1.14
3:C:670:SER:HA	3:C:823:ALA:HB1	1.27	1.14
5:E:74:PHE:CE1	5:E:81:LEU:HD21	1.82	1.14
24:4:28:LEU:O	24:4:32:LEU:HB2	1.48	1.14
32:R:101:ILE:O	32:R:104:GLN:HG3	1.48	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:HD23	1.29	1.14
15:H:156:U:H6	15:H:156:U:H5 ^{''}	1.10	1.14
36:Y:18:VAL:CB	37:Z:600:ARG:NH2	2.10	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:CD2	1.78	1.14
1:A:2298:LEU:O	4:D:1283:PRO:CB	1.95	1.14
3:C:77:VAL:HG12	33:T:197:TYR:N	1.61	1.14
32:R:442:ARG:NH1	32:R:443:GLY:C	2.00	1.14
1:A:1757:GLU:OE1	32:R:451:ILE:HG12	1.49	1.13
14:G:11:A:C2	14:G:12:G:C8	2.36	1.13
3:C:452:THR:CG2	3:C:577:PHE:CD2	2.31	1.13
3:C:679:PRO:HD2	3:C:807:GLN:HB3	1.16	1.13
1:A:252:ASP:CB	1:A:334:THR:HG21	1.79	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:LYS:HB2	32:R:251:ILE:HD12	1.28	1.13
1:A:762:ARG:NH2	31:P:226:LYS:NZ	1.95	1.13
3:C:216:THR:HG22	3:C:245:HIS:HE1	0.97	1.12
23:3:440:HIS:ND1	23:3:733:PRO:HG3	1.63	1.12
1:A:299:ILE:CD1	3:C:921:LEU:HB2	1.79	1.12
3:C:81:VAL:HG13	33:T:201:SER:CB	1.77	1.12
3:C:140:HIS:CB	3:C:230:ASP:HB2	1.79	1.12
3:C:507:VAL:HG11	3:C:565:ILE:HG23	1.30	1.12
3:C:216:THR:HG22	3:C:245:HIS:CE1	1.85	1.12
13:F:68:C:C4	31:P:33:ARG:HB3	1.85	1.12
1:A:696:MET:CB	33:T:415:ILE:HD11	1.80	1.11
1:A:758:ARG:HB3	31:P:227:TYR:HE2	0.96	1.11
1:A:1548:TYR:CD2	1:A:1549:VAL:HG22	1.83	1.11
1:A:439:GLN:NE2	1:A:614:TYR:CZ	2.18	1.11
3:C:77:VAL:HG11	33:T:196:LEU:CB	1.79	1.11
1:A:762:ARG:NH2	31:P:226:LYS:CE	2.14	1.11
1:A:1548:TYR:HD2	1:A:1549:VAL:HG22	1.14	1.11
32:R:420:LYS:HE3	32:R:420:LYS:HA	1.18	1.11
37:Z:566:TYR:CE2	37:Z:584:TRP:CZ3	2.39	1.11
1:A:692:ASP:HA	33:T:376:ARG:NH2	1.65	1.10
23:3:440:HIS:HE1	23:3:720:TRP:CZ3	1.67	1.10
1:A:73:HIS:HD2	1:A:81:PHE:CD2	1.69	1.10
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.15	1.10
1:A:1505:LYS:CE	37:Z:615:SER:OG	1.99	1.10
1:A:349:ALA:HB2	1:A:399:ALA:HB2	1.27	1.10
1:A:1900:GLU:HG2	37:Z:521:PRO:HG2	1.33	1.10
1:A:2287:ARG:NH2	4:D:1147:ASN:CB	2.14	1.10
28:J:225:LEU:HD21	29:L:211:ASN:HB2	1.29	1.10
1:A:86:ARG:HH22	32:R:211:ARG:HG3	1.08	1.10
1:A:232:LEU:HD23	3:C:388:VAL:CG1	1.80	1.10
1:A:1962:THR:HG22	37:Z:524:ARG:HB2	1.18	1.10
3:C:470:PRO:HB3	3:C:500:THR:HG23	1.34	1.10
1:A:252:ASP:HB2	1:A:334:THR:CG2	1.81	1.09
1:A:73:HIS:NE2	1:A:81:PHE:CE1	2.20	1.09
1:A:299:ILE:HD11	3:C:921:LEU:HB2	1.33	1.09
1:A:762:ARG:NH2	31:P:226:LYS:HE2	1.66	1.09
1:A:232:LEU:HD23	3:C:388:VAL:HG12	1.21	1.09
1:A:312:TYR:OH	3:C:853:ARG:NH2	1.85	1.09
1:A:666:LYS:HB2	1:A:668:VAL:HG22	1.18	1.09
3:C:66:TYR:CD2	33:T:457:GLY:HA2	1.87	1.09
36:Y:85:GLU:O	37:Z:502:ALA:N	1.85	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:MET:CE	1:A:88:TYR:CD2	2.36	1.08
1:A:76:MET:HE1	1:A:88:TYR:CD2	1.89	1.08
1:A:393:LEU:N	3:C:379:LYS:CE	2.15	1.08
1:A:349:ALA:CB	1:A:399:ALA:HB2	1.82	1.08
3:C:465:MET:CE	3:C:475:MET:HG3	1.82	1.08
37:Z:566:TYR:CE2	37:Z:584:TRP:HZ3	1.71	1.08
1:A:384:VAL:HG21	3:C:334:ILE:HG21	1.21	1.08
1:A:529:THR:HG22	30:M:197:TYR:O	1.52	1.08
1:A:783:TYR:CE1	31:P:228:ILE:HG21	1.88	1.08
1:A:666:LYS:HB2	1:A:668:VAL:CG2	1.82	1.08
28:J:259:GLN:HE22	29:L:220:PRO:CD	1.66	1.08
1:A:417:ARG:NH1	2:B:58:U:O3'	1.87	1.07
3:C:497:LEU:CD1	3:C:577:PHE:CZ	2.36	1.07
1:A:395:THR:CG2	3:C:383:GLN:HE22	1.65	1.07
24:4:17:VAL:HA	24:4:85:ARG:O	1.53	1.07
3:C:670:SER:CB	3:C:823:ALA:HB3	1.85	1.07
1:A:546:LEU:HD11	1:A:595:LYS:HD2	1.12	1.06
1:A:744:LYS:CE	31:P:213:ASP:HA	1.84	1.06
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	1.89	1.06
13:F:68:C:C4	31:P:33:ARG:CB	2.38	1.06
1:A:369:GLU:O	1:A:371:LEU:N	1.88	1.06
1:A:393:LEU:HA	3:C:379:LYS:HG2	1.34	1.06
28:J:406:PHE:CD2	28:J:411:MET:HE3	1.90	1.06
1:A:91:ALA:CB	32:R:207:MET:HE2	1.85	1.05
1:A:264:PHE:CE1	1:A:455:VAL:HG13	1.90	1.05
2:B:39:C:H4'	2:B:40:U:OP1	1.23	1.05
1:A:168:PRO:HG3	1:A:559:ASP:HB3	1.39	1.05
1:A:387:PHE:HE1	3:C:327:TYR:HA	1.14	1.05
1:A:705:LYS:CG	32:R:251:ILE:HD12	1.86	1.05
3:C:452:THR:HG22	3:C:577:PHE:HD2	1.21	1.05
1:A:664:HIS:CE1	1:A:668:VAL:HG23	1.92	1.04
1:A:664:HIS:HE1	1:A:668:VAL:HG23	1.21	1.04
1:A:844:GLU:CB	32:R:422:MET:HE1	1.83	1.04
33:T:399:LYS:CG	33:T:406:ILE:HD11	1.87	1.04
1:A:692:ASP:HA	33:T:376:ARG:HH22	1.18	1.04
3:C:228:PHE:HA	3:C:256:CYS:O	1.57	1.04
32:R:178:ARG:HD3	32:R:194:GLN:HE22	1.17	1.04
1:A:1449:LYS:HE3	32:R:428:GLY:HA3	1.37	1.04
3:C:78:GLU:HG2	3:C:80:ILE:HD11	1.06	1.04
1:A:331:TRP:CE3	3:C:179:VAL:HG21	1.91	1.04
1:A:755:HIS:ND1	31:P:223:PHE:CD1	2.26	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:488:VAL:HG13	3:C:609:LYS:HE2	1.39	1.04
13:F:25:C:H4'	13:F:26:U:OP2	1.22	1.04
32:R:436:VAL:HG23	32:R:437:TYR:CD1	1.93	1.04
1:A:232:LEU:HD12	1:A:404:LEU:HD12	1.04	1.04
24:4:70:ALA:O	24:4:74:MET:CB	2.04	1.03
1:A:168:PRO:CG	1:A:559:ASP:HB3	1.87	1.03
1:A:755:HIS:CE1	31:P:223:PHE:CD2	2.46	1.03
29:L:224:PHE:CD1	32:R:86:LEU:HD12	1.93	1.03
28:J:273:TYR:CZ	32:R:228:PRO:HB3	1.94	1.03
4:D:754:GLU:CB	23:3:662:PHE:CZ	2.41	1.03
15:H:105:G:H2'	15:H:106:G:H5''	1.37	1.03
1:A:254:TYR:CZ	1:A:434:HIS:HB3	1.93	1.02
3:C:452:THR:HG22	3:C:577:PHE:CD2	1.94	1.02
28:J:331:GLN:HG2	32:R:98:TYR:OH	1.59	1.02
37:Z:564:PRO:CB	37:Z:582:TYR:CG	2.41	1.02
1:A:250:VAL:HB	1:A:337:VAL:HG11	1.41	1.02
3:C:387:ASP:O	3:C:388:VAL:CG1	2.07	1.02
32:R:420:LYS:HG3	32:R:421:GLY:H	1.20	1.02
1:A:338:VAL:HG23	3:C:867:PRO:HG3	1.39	1.02
13:F:68:C:C5	31:P:33:ARG:CB	2.42	1.02
32:R:434:TYR:O	32:R:435:ASN:ND2	1.90	1.02
36:Y:37:TRP:CD1	36:Y:83:CYS:HB2	1.92	1.02
1:A:254:TYR:CE2	1:A:434:HIS:HB2	1.94	1.02
13:F:36:A:H3'	13:F:37:C:H5''	1.39	1.02
32:R:442:ARG:HD2	32:R:444:GLY:H	0.97	1.02
1:A:299:ILE:HD11	3:C:921:LEU:CB	1.90	1.01
1:A:305:ARG:CB	3:C:879:ASP:OD1	2.07	1.01
23:3:440:HIS:CE1	23:3:720:TRP:CZ3	2.47	1.01
37:Z:525:TYR:CD1	37:Z:526:ILE:HG23	1.95	1.01
3:C:511:GLY:O	3:C:576:ILE:CD1	2.07	1.01
1:A:1457:HIS:HE1	1:A:1459:ARG:CG	1.74	1.01
1:A:1900:GLU:HG2	37:Z:521:PRO:CG	1.91	1.01
3:C:132:VAL:HG12	3:C:226:VAL:HG23	1.43	1.01
3:C:349:PHE:CD1	3:C:356:PHE:CE1	2.49	1.01
1:A:299:ILE:HD11	3:C:921:LEU:CA	1.91	1.00
1:A:1900:GLU:OE2	37:Z:521:PRO:HB2	1.59	1.00
23:3:440:HIS:O	23:3:733:PRO:HG2	1.61	1.00
3:C:261:ASP:OD2	41:C:1500:GTP:N1	1.92	1.00
3:C:703:GLU:OE2	3:C:740:THR:HG21	1.61	1.00
15:H:179:C:H2'	15:H:180:G:H8	1.25	1.00
1:A:312:TYR:CZ	3:C:882:GLY:CA	2.45	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1301:ILE:CD1	1:A:1306:LYS:HE2	1.92	1.00
2:B:42:U:N3	14:G:-3:A:H2	1.50	1.00
3:C:705:VAL:CG2	3:C:717:PHE:CD2	2.39	1.00
31:P:193:VAL:HG21	31:P:194:PHE:HD2	1.26	1.00
1:A:264:PHE:CE1	1:A:459:LEU:HD13	1.96	1.00
3:C:81:VAL:CG1	33:T:201:SER:HB3	1.90	1.00
23:3:303:ALA:O	23:3:310:ILE:HA	1.61	1.00
2:B:64:G:H5'	5:E:106:LYS:HZ3	1.26	1.00
3:C:85:ASP:HB3	33:T:238:LEU:HG	1.43	1.00
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.44	1.00
1:A:1162:PRO:HG2	31:P:194:PHE:CE2	1.97	1.00
37:Z:525:TYR:CE1	37:Z:526:ILE:HG23	1.96	1.00
1:A:779:LEU:HD21	31:P:223:PHE:CE2	1.97	0.99
23:3:440:HIS:CE1	23:3:733:PRO:CG	2.45	0.99
32:R:414:ARG:NE	37:Z:598:PHE:HZ	1.38	0.99
1:A:783:TYR:HB2	31:P:228:ILE:HG12	1.43	0.99
28:J:270:ASP:OD2	32:R:222:PRO:CG	2.10	0.99
1:A:232:LEU:HD12	1:A:404:LEU:CD1	1.91	0.99
1:A:267:LYS:NZ	2:B:49:A:OP1	1.94	0.99
1:A:1505:LYS:HE3	37:Z:615:SER:OG	1.62	0.99
1:A:696:MET:CB	33:T:415:ILE:HD13	1.89	0.99
33:T:434:GLY:HA2	33:T:464:GLY:HA2	1.41	0.99
1:A:715:GLU:OE2	32:R:258:TRP:HZ3	1.43	0.99
37:Z:600:ARG:HB3	37:Z:600:ARG:HH11	1.24	0.99
1:A:384:VAL:CG1	3:C:332:GLY:H	1.76	0.99
3:C:64:LYS:HE3	31:P:206:LYS:HE2	1.45	0.99
3:C:137:HIS:CD2	3:C:236:MET:CB	2.45	0.99
13:F:68:C:C5	31:P:33:ARG:HB2	1.97	0.99
1:A:1457:HIS:NE2	32:R:425:GLY:N	2.09	0.99
1:A:2287:ARG:HH21	4:D:1147:ASN:CB	1.72	0.99
1:A:232:LEU:CD1	1:A:404:LEU:CD1	2.41	0.99
1:A:1900:GLU:OE1	37:Z:522:LEU:CB	2.10	0.98
3:C:78:GLU:O	33:T:198:ARG:CA	2.11	0.98
1:A:1084:PRO:HG2	31:P:188:TRP:HZ2	1.26	0.98
23:3:440:HIS:CE1	23:3:733:PRO:HG3	1.99	0.98
31:P:210:PHE:CD2	33:T:455:GLN:OE1	2.16	0.98
32:R:420:LYS:HB2	37:Z:610:LEU:HD11	1.44	0.98
3:C:306:ASN:OD1	3:C:437:HIS:CE1	2.16	0.98
31:P:30:TYR:OH	32:R:162:ALA:HA	1.63	0.98
1:A:417:ARG:NH2	2:B:58:U:H5''	1.79	0.98
1:A:2074:ARG:NH2	4:D:1044:VAL:O	1.96	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:GLU:OE2	1:A:369:GLU:N	1.97	0.98
15:H:83:A:H2'	15:H:84:C:O4'	1.64	0.98
3:C:84:GLU:O	33:T:238:LEU:CD2	2.12	0.97
3:C:670:SER:CA	3:C:823:ALA:HB3	1.94	0.97
3:C:66:TYR:HB3	33:T:456:PRO:O	1.64	0.97
3:C:81:VAL:HG13	33:T:201:SER:HB3	0.99	0.97
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA3	2.00	0.97
34:V:548:ALA:CB	34:V:585:ILE:CB	2.42	0.97
37:Z:566:TYR:HE2	37:Z:584:TRP:HZ3	1.05	0.97
3:C:711:ARG:HD3	3:C:730:ARG:HH11	1.29	0.97
3:C:500:THR:HG22	3:C:545:PRO:HA	1.47	0.97
3:C:670:SER:HA	3:C:823:ALA:HB3	1.43	0.97
1:A:299:ILE:HG12	3:C:920:PRO:O	1.64	0.97
1:A:546:LEU:HD11	1:A:595:LYS:CD	1.94	0.97
1:A:1320:LYS:HE2	32:R:434:TYR:HE1	1.15	0.97
1:A:2328:ALA:HB2	4:D:788:GLY:HA2	1.43	0.97
1:A:256:TYR:CE1	3:C:888:ARG:NH1	2.33	0.96
3:C:670:SER:CA	3:C:823:ALA:CB	2.43	0.96
28:J:300:ASP:OD2	32:R:101:ILE:HG13	1.65	0.96
23:3:440:HIS:NE2	23:3:733:PRO:HD3	1.70	0.96
1:A:121:HIS:NE2	1:A:481:PHE:CB	2.29	0.96
3:C:855:GLY:O	3:C:856:HIS:HB3	1.63	0.96
33:T:352:THR:HG22	33:T:373:LYS:O	1.65	0.96
36:Y:37:TRP:HH2	37:Z:498:GLY:CA	1.70	0.96
1:A:47:GLU:O	1:A:50:LYS:HB2	1.64	0.96
3:C:135:CYS:SG	3:C:227:LEU:HD12	2.06	0.96
15:H:78:C:H2'	15:H:79:G:H8	1.27	0.96
1:A:748:ASP:OD1	31:P:214:THR:HG22	1.64	0.96
1:A:1900:GLU:CD	37:Z:522:LEU:HB2	1.85	0.96
3:C:115:GLU:O	3:C:118:PHE:N	1.98	0.95
1:A:232:LEU:CD2	3:C:388:VAL:CG1	2.43	0.95
1:A:783:TYR:CD1	31:P:228:ILE:HG21	2.01	0.95
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.44	0.95
5:E:146:ARG:HH11	5:E:148:LYS:HE2	1.27	0.95
14:G:11:A:N3	14:G:12:G:H8	1.64	0.95
36:Y:37:TRP:CH2	37:Z:498:GLY:HA3	1.96	0.95
23:3:440:HIS:NE2	23:3:733:PRO:HD2	1.77	0.95
32:R:442:ARG:HD3	32:R:443:GLY:CA	1.96	0.95
1:A:171:ASP:O	1:A:520:TYR:CD2	2.20	0.95
1:A:664:HIS:CE1	1:A:666:LYS:HB2	2.02	0.95
15:H:156:U:H5''	15:H:156:U:C6	2.02	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2335:ALA:O	4:D:570:THR:HA	1.65	0.95
3:C:145:PHE:CB	3:C:312:SER:HB3	1.97	0.95
32:R:442:ARG:HH11	32:R:444:GLY:N	1.64	0.95
1:A:86:ARG:HH22	32:R:211:ARG:CG	1.79	0.95
3:C:700:ILE:HG23	3:C:735:PHE:CD2	2.01	0.95
1:A:393:LEU:CA	3:C:379:LYS:CG	2.45	0.95
1:A:705:LYS:HG2	32:R:251:ILE:HB	1.49	0.95
1:A:221:ASN:OD1	2:B:12:U:OP1	1.83	0.95
1:A:1505:LYS:HE2	37:Z:615:SER:OG	1.65	0.95
1:A:305:ARG:HH21	3:C:854:ARG:NH1	1.65	0.94
1:A:785:LYS:CE	31:P:215:LEU:HD11	1.97	0.94
14:G:11:A:C2	14:G:12:G:N7	2.34	0.94
1:A:384:VAL:CG2	3:C:334:ILE:CG2	2.42	0.94
1:A:1162:PRO:HG3	31:P:194:PHE:CD2	2.02	0.94
1:A:1457:HIS:CE1	32:R:424:SER:HA	2.01	0.94
28:J:339:TRP:CA	32:R:116:TYR:CE2	2.48	0.94
3:C:711:ARG:NH2	3:C:730:ARG:O	2.00	0.94
13:F:49:G:N7	29:L:33:ARG:NH1	2.15	0.94
1:A:278:LYS:NZ	14:G:-9:C:OP1	1.99	0.94
1:A:386:PRO:HD3	3:C:372:PHE:HE1	1.28	0.94
5:E:119:THR:CG2	5:E:161:ARG:HB3	1.97	0.94
15:H:180:G:H2'	15:H:181:G:H8	1.30	0.94
33:T:352:THR:HG22	33:T:373:LYS:C	1.86	0.94
1:A:264:PHE:CZ	1:A:459:LEU:CD1	2.50	0.94
1:A:402:ILE:HG13	3:C:385:VAL:HG21	1.45	0.94
1:A:530:LEU:N	30:M:198:GLN:HE22	1.52	0.94
1:A:1405:LEU:CB	32:R:415:LEU:CD2	2.45	0.94
1:A:1459:ARG:HE	32:R:423:ASP:HB2	1.31	0.94
1:A:1962:THR:CG2	37:Z:524:ARG:CB	2.45	0.94
3:C:145:PHE:HA	3:C:312:SER:HB2	0.95	0.94
3:C:445:ALA:HB3	3:C:466:SER:HA	1.50	0.94
15:H:79:G:H2'	15:H:80:A:H8	1.33	0.94
24:4:69:TYR:CZ	24:4:73:ILE:HG13	2.03	0.94
3:C:349:PHE:HD1	3:C:356:PHE:CD1	1.85	0.94
1:A:2113:LYS:CE	4:D:1229:ASP:O	2.16	0.93
13:F:8:C:H6	13:F:8:C:H5''	1.31	0.93
1:A:2268:LEU:CD2	4:D:1261:PRO:CB	2.46	0.93
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.01	0.93
1:A:256:TYR:CZ	3:C:888:ARG:NH1	2.36	0.93
13:F:25:C:C4'	13:F:26:U:OP2	2.16	0.93
32:R:171:LEU:HD12	32:R:201:GLU:OE1	1.67	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:HIS:CD2	1:A:81:PHE:CE1	2.56	0.93
1:A:151:MET:CE	1:A:628:GLY:O	2.15	0.93
1:A:366:LYS:HE3	1:A:366:LYS:H	1.29	0.93
3:C:76:GLU:OE1	3:C:76:GLU:N	2.01	0.93
5:E:146:ARG:NH1	5:E:148:LYS:HE2	1.82	0.93
1:A:76:MET:HE1	1:A:88:TYR:CG	2.03	0.93
3:C:149:LEU:CD1	3:C:427:PHE:HD2	1.80	0.93
1:A:695:ASP:CB	33:T:374:SER:OG	2.15	0.93
3:C:449:ILE:HG21	3:C:457:VAL:CG1	1.99	0.93
28:J:259:GLN:NE2	29:L:220:PRO:CD	2.30	0.93
28:J:294:HIS:CE1	29:L:227:THR:HB	2.04	0.93
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.02	0.93
1:A:1900:GLU:OE2	37:Z:521:PRO:C	2.06	0.93
1:A:2314:PHE:CB	4:D:1125:SER:CA	2.47	0.93
3:C:497:LEU:HD13	3:C:577:PHE:HZ	1.17	0.93
13:F:68:C:C4	31:P:33:ARG:CG	2.52	0.93
2:B:40:U:H3	14:G:-1:G:H1	1.14	0.92
32:R:101:ILE:O	32:R:104:GLN:CG	2.16	0.92
3:C:69:ALA:HA	33:T:456:PRO:HG3	1.49	0.92
3:C:449:ILE:CG2	3:C:457:VAL:CG1	2.46	0.92
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.35	0.92
1:A:228:TRP:O	1:A:415:SER:HA	1.70	0.92
1:A:402:ILE:HG12	3:C:265:LEU:CD2	1.99	0.92
1:A:548:ARG:NH2	1:A:549:GLU:OE2	2.01	0.92
1:A:2113:LYS:HE2	4:D:1229:ASP:CB	1.98	0.92
2:B:43:U:N3	14:G:-4:A:N1	2.17	0.92
32:R:412:ASP:CG	32:R:413:GLN:H	1.69	0.92
3:C:77:VAL:CG1	33:T:196:LEU:CB	2.45	0.92
3:C:140:HIS:CG	3:C:230:ASP:HB3	2.03	0.92
32:R:414:ARG:NH1	37:Z:598:PHE:HE2	1.58	0.92
1:A:305:ARG:HA	1:A:305:ARG:HH11	1.33	0.92
2:B:44:A:C2	14:G:-5:G:N1	2.36	0.92
3:C:445:ALA:O	3:C:449:ILE:N	2.03	0.92
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.51	0.92
28:J:339:TRP:CA	32:R:116:TYR:CD2	2.51	0.92
1:A:1301:ILE:HD11	1:A:1306:LYS:HE2	1.51	0.92
23:3:440:HIS:HE1	23:3:720:TRP:HZ3	1.06	0.92
1:A:387:PHE:CE1	3:C:327:TYR:HA	2.05	0.92
1:A:539:ARG:NH2	13:F:64:U:O2'	2.02	0.92
2:B:39:C:C4'	2:B:40:U:OP1	2.16	0.92
3:C:670:SER:HB3	3:C:823:ALA:HB3	1.48	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:259:GLN:HE22	29:L:220:PRO:HD2	1.32	0.92
1:A:762:ARG:HH22	31:P:226:LYS:HZ1	1.08	0.92
1:A:779:LEU:HD21	31:P:223:PHE:CZ	2.05	0.92
3:C:244:LYS:HA	3:C:292:TYR:HD2	1.34	0.91
32:R:106:GLN:HG2	32:R:110:LYS:HE2	1.51	0.91
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.51	0.91
1:A:235:MET:CE	1:A:411:PHE:HA	1.99	0.91
3:C:483:SER:HA	3:C:490:PHE:HB3	1.52	0.91
3:C:674:CYS:SG	3:C:822:MET:SD	2.67	0.91
3:C:86:THR:O	33:T:239:LYS:O	1.88	0.91
3:C:132:VAL:CG1	3:C:226:VAL:HG23	2.00	0.91
2:B:64:G:H5'	5:E:106:LYS:NZ	1.83	0.91
2:B:41:U:O4	14:G:-2:C:N4	2.03	0.91
1:A:1761:PRO:HB2	1:A:1930:TYR:OH	1.71	0.91
1:A:1962:THR:HG22	37:Z:524:ARG:CB	2.00	0.91
1:A:417:ARG:HH12	2:B:58:U:C3'	1.84	0.91
1:A:463:PRO:HB3	2:B:20:G:O2'	1.69	0.91
1:A:1320:LYS:CE	32:R:434:TYR:CE1	2.54	0.91
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.53	0.91
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.99	0.91
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.52	0.91
29:L:224:PHE:CD1	32:R:86:LEU:CD1	2.53	0.91
1:A:384:VAL:HA	3:C:331:PHE:HD2	1.03	0.90
3:C:145:PHE:N	3:C:312:SER:HB2	1.85	0.90
13:F:35:A:C8	14:G:12:G:C6	2.59	0.90
23:3:34:ARG:HB2	23:3:37:ILE:HB	1.51	0.90
1:A:393:LEU:CA	3:C:379:LYS:CE	2.48	0.90
1:A:666:LYS:HB3	1:A:668:VAL:HG22	1.52	0.90
3:C:230:ASP:OD2	3:C:233:GLU:HG2	1.70	0.90
1:A:1457:HIS:CE1	32:R:425:GLY:H	1.88	0.90
3:C:678:THR:OG1	3:C:680:ASN:O	1.89	0.90
1:A:171:ASP:HB3	1:A:519:ASP:HB2	1.53	0.90
1:A:1320:LYS:CE	32:R:434:TYR:HE1	1.85	0.90
36:Y:37:TRP:NE1	36:Y:83:CYS:HB2	1.87	0.90
1:A:312:TYR:CE2	3:C:882:GLY:CA	2.53	0.90
1:A:1426:ASP:CG	32:R:421:GLY:HA3	1.91	0.90
1:A:254:TYR:CZ	1:A:434:HIS:CB	2.54	0.90
3:C:221:ILE:CD1	3:C:479:THR:OG1	2.19	0.90
13:F:94:C:P	28:J:351:ASN:HD22	1.95	0.90
1:A:782:LEU:HD13	31:P:220:HIS:HE1	1.34	0.90
3:C:711:ARG:HD3	3:C:730:ARG:NH1	1.86	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:228:PHE:CA	3:C:256:CYS:O	2.20	0.90
1:A:705:LYS:HG2	32:R:251:ILE:CB	2.01	0.89
33:T:399:LYS:HG3	33:T:406:ILE:HD11	1.54	0.89
1:A:419:ARG:NH2	1:A:423:ASP:O	2.06	0.89
36:Y:36:ALA:HB2	37:Z:499:LYS:O	1.72	0.89
1:A:744:LYS:HE2	31:P:213:ASP:HA	1.52	0.89
1:A:227:ARG:CA	1:A:416:GLY:O	2.20	0.89
31:P:192:VAL:HG12	31:P:194:PHE:H	1.35	0.89
1:A:748:ASP:HA	31:P:214:THR:HG21	1.54	0.89
15:H:80:A:H2'	15:H:81:G:H8	1.36	0.89
32:R:81:LYS:HA	32:R:81:LYS:CE	2.02	0.89
1:A:232:LEU:CD2	3:C:388:VAL:HG11	2.03	0.89
28:J:220:LEU:HD11	28:J:224:LYS:HE3	1.53	0.89
1:A:90:GLY:HA3	32:R:207:MET:O	1.73	0.89
1:A:175:PRO:HG2	1:A:498:ARG:NH2	1.88	0.89
1:A:333:HIS:CA	3:C:139:HIS:NE2	2.36	0.89
15:H:81:G:H2'	15:H:82:G:H8	1.35	0.89
15:H:82:G:H2'	15:H:83:A:H8	1.38	0.89
32:R:442:ARG:CD	32:R:444:GLY:H	1.85	0.89
3:C:64:LYS:HZ1	31:P:206:LYS:HG2	1.38	0.88
31:P:193:VAL:HG21	31:P:194:PHE:CD2	2.02	0.88
14:G:11:A:N3	14:G:12:G:C8	2.38	0.88
32:R:81:LYS:HA	32:R:81:LYS:NZ	1.88	0.88
1:A:785:LYS:HE2	31:P:215:LEU:HD11	1.54	0.88
3:C:78:GLU:O	33:T:199:VAL:N	2.06	0.88
3:C:140:HIS:CE1	3:C:233:GLU:HB2	2.07	0.88
3:C:679:PRO:CG	3:C:807:GLN:OE1	2.21	0.88
3:C:678:THR:CG2	3:C:683:ASN:HB2	2.04	0.88
13:F:68:C:C4	31:P:33:ARG:HG2	2.07	0.88
1:A:251:ASP:HB3	1:A:337:VAL:HG23	1.54	0.88
32:R:442:ARG:CD	32:R:444:GLY:N	2.34	0.88
1:A:715:GLU:OE2	32:R:258:TRP:CZ3	2.25	0.88
1:A:2314:PHE:HB2	4:D:1125:SER:CA	2.02	0.88
22:2:614:ARG:HH11	22:2:614:ARG:HG3	1.38	0.88
3:C:261:ASP:OD1	41:C:1500:GTP:O6	1.92	0.88
1:A:1457:HIS:CE1	32:R:425:GLY:N	2.41	0.88
1:A:1459:ARG:HG3	32:R:422:MET:O	1.74	0.88
23:3:440:HIS:O	23:3:733:PRO:CG	2.22	0.88
31:P:224:MET:CE	31:P:228:ILE:HD13	2.04	0.88
1:A:305:ARG:NH2	3:C:854:ARG:HH11	1.72	0.87
3:C:97:VAL:CG2	31:P:45:GLN:HG3	2.03	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:179:C:O2'	15:H:180:G:H5'	1.74	0.87
1:A:48:LYS:O	1:A:53:PHE:CD2	2.27	0.87
3:C:149:LEU:HD12	3:C:427:PHE:HD2	1.39	0.87
3:C:700:ILE:HG23	3:C:735:PHE:CE2	2.09	0.87
23:3:812:LYS:O	23:3:816:LYS:HB2	1.74	0.87
2:B:42:U:N3	14:G:-3:A:N1	2.16	0.87
14:G:137:C:H42	15:H:40:C:H42	1.22	0.87
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.57	0.87
24:4:75:ASN:OD1	24:4:86:VAL:HB	1.74	0.87
3:C:523:GLN:OE1	3:C:524:ILE:N	2.07	0.87
1:A:393:LEU:CA	3:C:379:LYS:HG2	2.02	0.87
1:A:1118:PRO:C	1:A:1120:PRO:HA	1.94	0.87
3:C:705:VAL:HG21	3:C:717:PHE:CE2	2.07	0.87
5:E:243:LEU:CD1	5:E:247:GLY:HA2	2.04	0.87
15:H:68:G:O2'	15:H:69:U:H5'	1.74	0.87
15:H:78:C:H2'	15:H:79:G:C8	2.10	0.87
1:A:1162:PRO:CG	31:P:194:PHE:CE2	2.57	0.87
3:C:488:VAL:HG13	3:C:609:LYS:CE	2.05	0.87
15:H:154:C:O2	15:H:176:G:N2	2.07	0.87
28:J:339:TRP:CD2	32:R:116:TYR:HD2	1.93	0.87
32:R:423:ASP:O	32:R:424:SER:OG	1.92	0.87
1:A:86:ARG:NH2	32:R:211:ARG:HG3	1.88	0.87
1:A:384:VAL:HG12	3:C:332:GLY:H	1.38	0.87
1:A:395:THR:HG21	3:C:383:GLN:HE22	1.38	0.87
15:H:180:G:H2'	15:H:181:G:C8	2.10	0.87
3:C:701:GLU:HA	3:C:740:THR:OG1	1.75	0.87
28:J:255:LEU:HD22	29:L:235:LEU:HD13	1.56	0.87
3:C:216:THR:CG2	3:C:245:HIS:HE1	1.84	0.86
32:R:442:ARG:NH1	32:R:443:GLY:O	2.07	0.86
1:A:420:ARG:NH1	2:B:56:C:O2'	2.07	0.86
1:A:91:ALA:HB1	32:R:207:MET:HE2	1.57	0.86
1:A:331:TRP:CE3	3:C:179:VAL:CG2	2.59	0.86
15:H:179:C:H2'	15:H:180:G:C8	2.09	0.86
1:A:1757:GLU:CD	32:R:451:ILE:HG12	1.96	0.86
15:H:148:C:O2'	15:H:149:A:H5'	1.75	0.86
21:1:1179:ASP:OD2	21:1:1185:ARG:NH1	2.08	0.86
33:T:399:LYS:HG2	33:T:406:ILE:HD11	1.53	0.86
1:A:401:GLY:HA3	3:C:386:GLY:CA	2.03	0.86
5:E:269:PRO:O	5:E:270:LYS:HB3	1.76	0.86
13:F:26:U:H3'	13:F:27:A:H5''	1.56	0.86
28:J:256:LYS:O	29:L:232:TYR:CE2	2.29	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:210:PHE:HD2	33:T:455:GLN:OE1	1.53	0.86
32:R:147:THR:HG23	33:T:360:VAL:HG12	1.57	0.86
23:3:442:LEU:HD12	23:3:733:PRO:O	1.76	0.86
33:T:417:ASN:OD1	33:T:432:ASP:OD1	1.94	0.86
1:A:386:PRO:HA	3:C:327:TYR:CE2	2.10	0.86
1:A:152:ARG:HB3	1:A:152:ARG:HH11	1.39	0.85
32:R:135:PRO:O	32:R:136:ASP:OD1	1.94	0.85
1:A:433:GLU:OE1	1:A:436:PRO:HB3	1.74	0.85
32:R:420:LYS:HE3	32:R:420:LYS:CA	1.98	0.85
1:A:252:ASP:HB2	1:A:334:THR:HG21	0.90	0.85
3:C:72:VAL:HG22	33:T:453:ALA:HB1	1.58	0.85
3:C:149:LEU:HD12	3:C:427:PHE:CD2	2.07	0.85
15:H:79:G:O2'	15:H:80:A:H5'	1.76	0.85
3:C:145:PHE:HB2	3:C:312:SER:HB3	1.57	0.85
21:1:672:ALA:HA	21:1:679:ILE:HD11	1.58	0.85
1:A:363:HIS:NE2	3:C:287:GLY:HA3	1.91	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.76	0.85
32:R:414:ARG:NH1	37:Z:598:PHE:HZ	1.44	0.85
5:E:162:ARG:NH2	5:E:203:ASP:O	2.10	0.85
1:A:388:LEU:HD11	3:C:399:LEU:HD21	0.86	0.85
32:R:414:ARG:HB2	32:R:414:ARG:NH2	1.92	0.85
3:C:133:THR:O	3:C:226:VAL:N	2.10	0.85
1:A:386:PRO:HA	3:C:327:TYR:CZ	2.11	0.85
2:B:42:U:H3	14:G:-3:A:H2	0.90	0.85
14:G:1:G:N2	30:M:202:CYS:SG	2.50	0.85
1:A:232:LEU:CD2	3:C:388:VAL:HG12	2.05	0.84
1:A:595:LYS:HE3	1:A:644:ILE:HD11	1.58	0.84
1:A:1900:GLU:CG	37:Z:521:PRO:CG	2.55	0.84
3:C:94:ILE:HD13	31:P:44:ARG:NH1	1.92	0.84
15:H:156:U:H6	15:H:156:U:C5'	1.88	0.84
37:Z:600:ARG:HH11	37:Z:600:ARG:CB	1.90	0.84
1:A:73:HIS:CD2	1:A:81:PHE:CD2	2.57	0.84
1:A:1370:ARG:HH11	34:V:467:LEU:CA	1.89	0.84
1:A:1900:GLU:OE2	37:Z:522:LEU:N	2.11	0.84
3:C:444:GLY:O	3:C:447:PRO:HD2	1.77	0.84
3:C:516:LEU:HD12	3:C:517:GLU:HG3	1.59	0.84
1:A:121:HIS:CG	1:A:481:PHE:O	2.30	0.84
13:F:36:A:H2'	13:F:38:G:OP2	1.78	0.84
15:H:80:A:O2'	15:H:81:G:H5'	1.78	0.84
15:H:181:G:O2'	15:H:182:U:H5'	1.77	0.84
15:H:182:U:O2'	15:H:183:G:H5'	1.75	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:356:HIS:HB2	23:3:401:LEU:HB2	1.60	0.84
3:C:80:ILE:O	33:T:200:ILE:HA	1.78	0.84
32:R:415:LEU:O	32:R:417:ASN:N	2.09	0.84
1:A:91:ALA:CB	32:R:207:MET:CE	2.56	0.84
1:A:755:HIS:CE1	31:P:223:PHE:CB	2.60	0.84
3:C:711:ARG:HD3	3:C:730:ARG:HE	1.42	0.84
1:A:232:LEU:HD11	3:C:412:ILE:HD11	1.59	0.84
1:A:1505:LYS:HE2	37:Z:615:SER:CB	2.07	0.84
3:C:244:LYS:HA	3:C:292:TYR:CD2	2.13	0.84
3:C:365:SER:OG	3:C:371:GLU:OE2	1.95	0.84
3:C:725:ASP:OD1	3:C:727:LEU:N	2.10	0.84
15:H:78:C:O2'	15:H:79:G:H5'	1.77	0.84
32:R:178:ARG:HD3	32:R:194:GLN:NE2	1.91	0.84
1:A:393:LEU:CA	3:C:379:LYS:HE3	2.07	0.84
1:A:1426:ASP:CB	32:R:421:GLY:HA3	2.08	0.84
1:A:1457:HIS:CE1	1:A:1459:ARG:CG	2.61	0.84
1:A:1457:HIS:NE2	32:R:424:SER:HA	1.93	0.83
3:C:705:VAL:HG21	3:C:717:PHE:HE2	1.40	0.83
1:A:333:HIS:O	3:C:139:HIS:CE1	2.31	0.83
3:C:79:THR:C	3:C:80:ILE:HD12	1.98	0.83
3:C:348:TYR:CD1	3:C:359:LYS:HB3	2.13	0.83
15:H:71:C:O2'	15:H:72:U:H5'	1.78	0.83
37:Z:566:TYR:CE2	37:Z:584:TRP:CE3	2.66	0.83
1:A:168:PRO:HG3	1:A:559:ASP:CB	2.07	0.83
1:A:254:TYR:CE2	1:A:434:HIS:CB	2.61	0.83
1:A:1301:ILE:HD12	2:B:39:C:H5''	1.60	0.83
3:C:488:VAL:CG1	3:C:609:LYS:HE2	2.08	0.83
14:G:22:C:O2'	14:G:23:U:OP1	1.95	0.83
15:H:152:G:N2	15:H:153:A:N7	2.27	0.83
1:A:338:VAL:CG2	3:C:867:PRO:HG3	2.07	0.83
5:E:74:PHE:CE1	5:E:81:LEU:CD2	2.62	0.83
36:Y:37:TRP:CZ2	37:Z:498:GLY:HA2	2.08	0.83
1:A:1757:GLU:CD	32:R:451:ILE:CG1	2.47	0.83
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.11	0.83
15:H:70:C:O2'	15:H:71:C:H5'	1.78	0.83
23:3:442:LEU:O	23:3:735:SER:N	2.10	0.83
32:R:117:THR:O	32:R:120:VAL:HG12	1.78	0.83
3:C:77:VAL:CG1	33:T:196:LEU:CG	2.35	0.83
1:A:1301:ILE:CD1	2:B:39:C:H5''	2.09	0.83
3:C:80:ILE:N	33:T:199:VAL:O	2.12	0.83
1:A:387:PHE:CZ	3:C:326:ILE:HG22	2.13	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:824:THR:HG23	3:C:824:THR:O	1.77	0.83
28:J:270:ASP:CG	32:R:222:PRO:HB3	1.99	0.83
32:R:134:ARG:O	32:R:136:ASP:N	2.12	0.83
1:A:1457:HIS:HE1	1:A:1459:ARG:HG2	1.43	0.83
1:A:1900:GLU:OE2	37:Z:521:PRO:CB	2.26	0.83
3:C:145:PHE:CA	3:C:312:SER:HB3	2.04	0.83
15:H:72:U:O2'	15:H:73:C:H5'	1.77	0.83
3:C:470:PRO:HB3	3:C:500:THR:CG2	2.08	0.82
21:1:1108:ASN:ND2	21:1:1111:CYS:SG	2.52	0.82
1:A:91:ALA:HB1	32:R:207:MET:CE	2.09	0.82
1:A:529:THR:CG2	30:M:197:TYR:O	2.26	0.82
1:A:615:ARG:O	1:A:618:THR:OG1	1.96	0.82
15:H:73:C:O2'	15:H:74:U:H5'	1.79	0.82
1:A:319:LEU:HD11	3:C:590:ILE:HD11	1.60	0.82
1:A:1084:PRO:HG2	31:P:188:TRP:CZ2	2.12	0.82
3:C:220:ARG:NH1	3:C:578:ARG:O	2.12	0.82
3:C:228:PHE:CB	3:C:256:CYS:O	2.27	0.82
3:C:482:TYR:HE2	3:C:493:PHE:CG	1.97	0.82
5:E:165:GLN:O	5:E:166:LEU:HD23	1.79	0.82
28:J:259:GLN:NE2	29:L:220:PRO:HD2	1.94	0.82
2:B:42:U:C2	14:G:-3:A:H2	1.97	0.82
3:C:705:VAL:CB	3:C:717:PHE:CE2	2.61	0.82
14:G:11:A:C4	14:G:12:G:C8	2.67	0.82
15:H:69:U:O2'	15:H:70:C:H5'	1.80	0.82
32:R:103:ARG:HB3	32:R:103:ARG:HH11	1.44	0.82
15:H:81:G:O2'	15:H:82:G:H5'	1.78	0.82
3:C:140:HIS:ND1	3:C:230:ASP:HB3	1.94	0.82
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.44	0.82
1:A:393:LEU:HD12	3:C:379:LYS:HG3	1.60	0.82
1:A:417:ARG:HH12	2:B:58:U:C4'	1.92	0.82
1:A:1370:ARG:HH12	34:V:468:ASP:N	1.77	0.82
3:C:489:GLN:O	3:C:489:GLN:NE2	2.13	0.82
15:H:105:G:C2'	15:H:106:G:H5''	2.10	0.82
31:P:30:TYR:OH	32:R:162:ALA:CA	2.27	0.82
1:A:1457:HIS:CE1	1:A:1459:ARG:HG2	2.15	0.82
3:C:259:LYS:HG2	3:C:262:ARG:CD	2.09	0.82
31:P:212:ASN:HB3	33:T:458:SER:HB2	1.61	0.82
2:B:18:C:O2'	2:B:19:A:O5'	1.98	0.82
1:A:331:TRP:CZ3	3:C:179:VAL:HG21	2.14	0.81
1:A:2113:LYS:HE3	4:D:1229:ASP:C	2.01	0.81
5:E:74:PHE:CE2	5:E:343:ILE:HG12	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:37:TRP:HA	36:Y:82:LEU:O	1.80	0.81
1:A:305:ARG:HG2	3:C:878:ILE:HG21	1.60	0.81
1:A:331:TRP:CZ3	3:C:179:VAL:CG2	2.64	0.81
1:A:1900:GLU:CG	37:Z:521:PRO:HG2	2.09	0.81
3:C:64:LYS:HE3	31:P:206:LYS:CE	2.10	0.81
3:C:244:LYS:HB2	3:C:292:TYR:CE2	2.15	0.81
3:C:306:ASN:OD1	3:C:437:HIS:ND1	2.14	0.81
3:C:507:VAL:CG1	3:C:565:ILE:HG23	2.10	0.81
22:2:643:PRO:HD2	24:4:69:TYR:CD2	2.16	0.81
23:3:42:ARG:HE	23:3:53:LEU:HD11	1.45	0.81
23:3:210:PHE:HB2	23:3:224:TYR:HB2	1.60	0.81
26:6:49:CYS:HB3	26:6:87:LYS:HD3	1.61	0.81
1:A:247:THR:OG1	1:A:429:ASN:HB3	1.80	0.81
31:P:193:VAL:HG23	31:P:194:PHE:CG	2.15	0.81
1:A:232:LEU:HD11	3:C:412:ILE:CD1	2.10	0.81
1:A:235:MET:HE1	1:A:411:PHE:HA	1.61	0.81
1:A:250:VAL:HG23	1:A:337:VAL:HB	1.60	0.81
23:3:772:ALA:HB1	23:3:775:ASN:HD21	1.44	0.81
33:T:213:GLU:HG3	33:T:218:TRP:CE2	2.16	0.81
1:A:1301:ILE:HD13	1:A:1306:LYS:HE2	1.63	0.81
3:C:511:GLY:O	3:C:576:ILE:HD13	1.79	0.81
32:R:443:GLY:HA2	32:R:446:ASP:HB3	1.62	0.81
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.14	0.81
1:A:1426:ASP:HB2	32:R:421:GLY:CA	2.11	0.81
3:C:452:THR:HG21	3:C:577:PHE:HD2	1.43	0.81
5:E:74:PHE:CZ	5:E:81:LEU:HD21	2.16	0.81
1:A:705:LYS:HB2	32:R:251:ILE:CD1	2.07	0.81
1:A:439:GLN:O	1:A:444:ARG:NH1	2.14	0.81
1:A:907:PRO:HD3	31:P:229:LYS:HB2	1.63	0.81
3:C:96:PRO:HA	31:P:48:GLN:HE21	1.44	0.81
3:C:140:HIS:NE2	3:C:233:GLU:HG3	1.95	0.81
1:A:660:PHE:CD2	32:R:209:PRO:HB2	2.16	0.81
3:C:140:HIS:ND1	3:C:230:ASP:N	2.28	0.81
3:C:452:THR:CB	3:C:577:PHE:HD2	1.93	0.81
3:C:507:VAL:HG11	3:C:565:ILE:CG2	2.09	0.81
3:C:711:ARG:HD3	3:C:730:ARG:NE	1.96	0.81
1:A:228:TRP:N	1:A:416:GLY:O	2.14	0.80
15:H:183:G:H2'	15:H:184:C:H6	1.44	0.80
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.46	0.80
15:H:83:A:H2'	15:H:84:C:C1'	2.10	0.80
23:3:440:HIS:CG	23:3:733:PRO:HG3	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:68:C:H41	31:P:33:ARG:HB3	1.45	0.80
28:J:273:TYR:CE1	32:R:228:PRO:HB3	2.17	0.80
14:G:134:U:H3	15:H:42:G:H1	1.24	0.80
23:3:979:ARG:HD2	23:3:982:GLU:HB2	1.63	0.80
32:R:65:PRO:HG2	32:R:66:GLU:OE2	1.79	0.80
15:H:149:A:H2'	15:H:150:U:H6	1.44	0.80
22:2:682:LEU:HD13	22:2:687:PHE:HA	1.63	0.80
1:A:357:ASN:O	3:C:865:GLY:N	2.15	0.80
1:A:417:ARG:HH22	2:B:58:U:H5''	1.42	0.80
1:A:748:ASP:CA	31:P:214:THR:HG21	2.11	0.80
3:C:705:VAL:CG2	3:C:717:PHE:HE2	1.84	0.80
15:H:82:G:O2'	15:H:83:A:H5'	1.81	0.80
1:A:121:HIS:HA	1:A:482:PHE:HA	1.62	0.80
1:A:384:VAL:CG1	3:C:332:GLY:N	2.45	0.80
3:C:87:GLN:OE1	3:C:91:GLU:HG2	1.82	0.80
3:C:140:HIS:CE1	3:C:230:ASP:HB3	2.16	0.80
3:C:776:GLU:O	3:C:781:ASP:OD1	2.00	0.80
5:E:265:ARG:H	5:E:272:ARG:NH2	1.80	0.80
13:F:68:C:N3	31:P:33:ARG:HG2	1.97	0.80
15:H:152:G:H5''	15:H:153:A:OP2	1.80	0.80
21:1:732:TRP:HE1	21:1:768:GLU:HG2	1.47	0.80
1:A:1144:LYS:O	1:A:1147:VAL:HG22	1.82	0.80
1:A:1764:SER:HB3	1:A:1766:GLN:HG2	1.64	0.80
3:C:445:ALA:HB1	3:C:449:ILE:HD11	1.63	0.80
3:C:738:ASP:HB2	3:C:740:THR:O	1.82	0.80
1:A:305:ARG:NH2	3:C:854:ARG:NH1	2.29	0.80
1:A:401:GLY:CA	3:C:386:GLY:HA2	2.08	0.80
1:A:402:ILE:HG12	3:C:265:LEU:HD23	1.61	0.80
1:A:1370:ARG:HH11	34:V:467:LEU:HA	1.43	0.80
1:A:2314:PHE:HB3	4:D:1125:SER:CA	2.11	0.80
5:E:248:SER:HB2	5:E:249:TYR:CD1	2.17	0.80
23:3:637:PRO:HA	23:3:669:LEU:HA	1.63	0.80
24:4:28:LEU:O	24:4:32:LEU:CB	2.27	0.80
2:B:90:U:H5''	2:B:91:U:H5'	1.65	0.79
5:E:209:ILE:HG21	5:E:250:LEU:CD1	2.12	0.79
23:3:442:LEU:HD12	23:3:734:LEU:HD23	1.64	0.79
23:3:477:SER:HA	23:3:482:THR:HG22	1.65	0.79
29:L:222:LEU:H	29:L:222:LEU:HD22	1.45	0.79
1:A:264:PHE:HE1	1:A:455:VAL:CG1	1.94	0.79
1:A:299:ILE:CG1	3:C:920:PRO:O	2.30	0.79
1:A:362:ARG:NH2	3:C:284:GLU:OE2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:ILE:HB	1:A:1001:VAL:HG12	1.65	0.79
3:C:145:PHE:N	3:C:312:SER:CB	2.41	0.79
33:T:292:TYR:CZ	33:T:308:ARG:HG3	2.18	0.79
1:A:168:PRO:HG2	1:A:559:ASP:HB3	1.64	0.79
1:A:232:LEU:HD13	1:A:404:LEU:CD1	2.12	0.79
1:A:318:TYR:N	3:C:638:ASP:OD1	2.14	0.79
3:C:77:VAL:HG11	33:T:196:LEU:HG	0.79	0.79
5:E:310:TYR:CE1	5:E:322:LYS:HD2	2.18	0.79
33:T:306:CYS:SG	33:T:336:VAL:HB	2.22	0.79
23:3:772:ALA:CB	23:3:775:ASN:HD21	1.95	0.79
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.16	0.79
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	1.65	0.79
3:C:244:LYS:HB2	3:C:292:TYR:HE2	1.47	0.79
1:A:283:VAL:O	1:A:284:ARG:NE	2.15	0.79
15:H:153:A:H2'	15:H:154:C:H5'	1.65	0.79
32:R:67:ILE:HG22	32:R:69:VAL:HG23	1.65	0.79
31:P:212:ASN:O	33:T:458:SER:CA	2.23	0.79
32:R:420:LYS:HG3	32:R:421:GLY:N	1.97	0.79
33:T:351:ASP:O	33:T:352:THR:OG1	1.98	0.79
3:C:515:THR:O	3:C:517:GLU:N	2.16	0.79
3:C:705:VAL:HB	3:C:717:PHE:CE2	2.18	0.79
1:A:393:LEU:HB2	3:C:379:LYS:HE3	1.65	0.79
3:C:140:HIS:ND1	3:C:230:ASP:CB	2.46	0.79
3:C:259:LYS:HE2	3:C:262:ARG:CD	2.13	0.79
15:H:68:G:H1	15:H:84:C:H42	1.29	0.79
15:H:79:G:H2'	15:H:80:A:C8	2.17	0.79
1:A:256:TYR:CD1	3:C:888:ARG:NH2	2.51	0.78
1:A:293:TRP:CZ3	1:A:295:GLU:OE1	2.35	0.78
1:A:435:CYS:HB2	3:C:892:GLN:NE2	1.98	0.78
13:F:34:G:N7	14:G:12:G:O6	2.16	0.78
15:H:101:U:H5''	15:H:102:U:H5'	1.64	0.78
37:Z:593:PHE:O	37:Z:597:ARG:HB2	1.83	0.78
1:A:1767:ASN:O	1:A:1771:LEU:HB2	1.82	0.78
1:A:48:LYS:O	1:A:53:PHE:CG	2.37	0.78
1:A:718:ARG:NH2	32:R:259:LYS:HE3	1.98	0.78
15:H:82:G:H2'	15:H:83:A:C8	2.17	0.78
23:3:1109:LEU:HD11	23:3:1128:ILE:HG21	1.65	0.78
1:A:250:VAL:CB	1:A:337:VAL:HG11	2.14	0.78
1:A:695:ASP:OD2	33:T:350:HIS:HB3	1.83	0.78
23:3:641:CYS:HB2	23:3:701:LEU:HB3	1.64	0.78
23:3:435:LEU:HD22	23:3:799:ILE:HD11	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:440:HIS:HE1	23:3:733:PRO:HD3	1.46	0.78
1:A:1370:ARG:NH1	34:V:468:ASP:N	2.32	0.78
32:R:132:LEU:HB3	33:T:399:LYS:NZ	1.99	0.78
1:A:705:LYS:HG2	32:R:251:ILE:HD12	1.65	0.78
1:A:758:ARG:CB	31:P:227:TYR:CE2	2.64	0.78
2:B:43:U:H4'	13:F:67:G:H1	1.48	0.78
33:T:387:PHE:CE1	33:T:398:TRP:CD1	2.72	0.78
1:A:152:ARG:HH11	1:A:152:ARG:CB	1.96	0.78
24:4:17:VAL:HG22	24:4:86:VAL:HG22	1.66	0.78
33:T:434:GLY:HA2	33:T:464:GLY:CA	2.14	0.78
1:A:1505:LYS:HD2	37:Z:615:SER:HB3	1.66	0.78
3:C:133:THR:HB	3:C:225:VAL:HG23	1.65	0.78
23:3:295:THR:HG22	23:3:297:SER:H	1.48	0.78
3:C:452:THR:HG21	3:C:577:PHE:CD2	2.16	0.78
22:2:649:LYS:HB3	22:2:655:SER:HB2	1.65	0.78
24:4:17:VAL:O	24:4:56:TYR:HA	1.83	0.78
31:P:224:MET:HE2	31:P:228:ILE:HD13	1.63	0.78
33:T:267:ASP:HB3	33:T:269:GLN:HG2	1.64	0.78
1:A:468:LYS:HD3	1:A:469:LYS:N	1.99	0.77
1:A:692:ASP:CA	33:T:376:ARG:HH22	1.97	0.77
1:A:919:ASP:OD2	1:A:1012:LYS:NZ	2.17	0.77
1:A:1838:LYS:HG2	1:A:1871:PRO:HG2	1.66	0.77
21:1:1053:ARG:NH1	22:2:559:PRO:O	2.17	0.77
23:3:590:MET:HG2	23:3:607:VAL:HA	1.63	0.77
23:3:805:ASN:ND2	23:3:858:GLY:O	2.14	0.77
1:A:398:THR:HG23	3:C:382:ALA:HB1	1.67	0.77
2:B:42:U:C4	14:G:-3:A:N1	2.53	0.77
1:A:329:LEU:HB3	3:C:177:ARG:NE	1.98	0.77
3:C:449:ILE:HG21	3:C:457:VAL:HG12	1.66	0.77
3:C:677:GLU:OE2	3:C:684:LYS:HG2	1.83	0.77
21:1:941:ASN:HA	21:1:948:ARG:HH22	1.48	0.77
1:A:91:ALA:HA	32:R:207:MET:CE	2.14	0.77
1:A:203:VAL:HG21	1:A:237:THR:CG2	2.14	0.77
1:A:1405:LEU:CA	32:R:415:LEU:CD2	2.62	0.77
3:C:449:ILE:CD1	3:C:466:SER:OG	2.33	0.77
15:H:80:A:H2'	15:H:81:G:C8	2.19	0.77
24:4:69:TYR:CE1	24:4:73:ILE:HG13	2.19	0.77
37:Z:595:GLN:O	37:Z:599:ALA:N	2.14	0.77
1:A:456:LEU:O	1:A:460:LYS:HG2	1.84	0.77
3:C:140:HIS:HA	3:C:259:LYS:HZ3	1.47	0.77
3:C:349:PHE:CD1	3:C:356:PHE:CD1	2.68	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:277:PHE:HE2	5:E:300:ILE:CD1	1.98	0.77
13:F:8:C:H5''	13:F:8:C:C6	2.19	0.77
23:3:474:ILE:O	23:3:485:LEU:HB2	1.83	0.77
23:3:772:ALA:HB1	23:3:775:ASN:ND2	1.99	0.77
3:C:85:ASP:CB	33:T:238:LEU:HG	2.14	0.77
3:C:151:GLU:OE1	3:C:417:ARG:CZ	2.33	0.77
14:G:11:A:H2'	14:G:12:G:O4'	1.84	0.77
36:Y:86:ASP:HA	37:Z:502:ALA:HB3	1.65	0.77
1:A:1505:LYS:CE	37:Z:615:SER:CB	2.62	0.77
28:J:291:GLN:NE2	29:L:230:GLU:OE2	2.17	0.77
33:T:318:ARG:HG3	33:T:319:THR:HG23	1.67	0.77
1:A:664:HIS:CE1	1:A:668:VAL:CG2	2.66	0.77
1:A:1757:GLU:OE2	32:R:451:ILE:HD11	1.85	0.77
3:C:482:TYR:HE2	3:C:493:PHE:CB	1.98	0.77
37:Z:603:SER:O	37:Z:607:VAL:HG23	1.84	0.77
1:A:1426:ASP:HB2	32:R:421:GLY:HA3	1.64	0.77
3:C:145:PHE:CZ	3:C:427:PHE:CE1	2.73	0.77
3:C:471:ASP:H	3:C:499:GLY:HA2	1.47	0.77
5:E:74:PHE:CD1	5:E:81:LEU:CD2	2.67	0.77
23:3:785:PRO:HA	23:3:800:ILE:O	1.84	0.77
3:C:567:GLU:HG2	3:C:572:GLU:OE2	1.85	0.77
15:H:177:A:H5''	15:H:178:A:OP1	1.84	0.77
23:3:981:CYS:SG	23:3:982:GLU:N	2.57	0.77
1:A:232:LEU:HD21	3:C:388:VAL:HG11	1.67	0.76
1:A:630:TRP:O	1:A:632:ALA:N	2.18	0.76
1:A:782:LEU:HD13	31:P:220:HIS:CE1	2.18	0.76
3:C:82:GLN:CB	33:T:231:TRP:HZ3	1.98	0.76
3:C:711:ARG:HD3	3:C:730:ARG:CZ	2.16	0.76
5:E:146:ARG:HH12	5:E:148:LYS:HE3	1.49	0.76
1:A:232:LEU:HD13	1:A:404:LEU:HD13	1.66	0.76
21:1:473:GLN:HE22	25:5:93:ASN:H	1.33	0.76
32:R:420:LYS:HG2	32:R:423:ASP:OD2	1.84	0.76
1:A:705:LYS:CB	32:R:251:ILE:CD1	2.59	0.76
2:B:44:A:H2	14:G:-5:G:N1	1.81	0.76
3:C:449:ILE:HD11	3:C:466:SER:N	1.99	0.76
15:H:143:A:H3'	15:H:143:A:N3	2.01	0.76
1:A:362:ARG:O	1:A:362:ARG:NE	2.18	0.76
3:C:261:ASP:CG	41:C:1500:GTP:HN1	1.88	0.76
5:E:162:ARG:NH2	5:E:204:THR:HA	1.99	0.76
15:H:148:C:H2'	15:H:149:A:H8	1.48	0.76
1:A:417:ARG:CZ	2:B:58:U:H5''	2.14	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:471:ASP:OD1	3:C:472:GLY:N	2.19	0.76
22:2:611:ASP:O	22:2:614:ARG:HB3	1.86	0.76
32:R:412:ASP:CG	32:R:413:GLN:N	2.39	0.76
1:A:755:HIS:HA	31:P:223:PHE:CE1	2.20	0.76
1:A:1119:ASP:N	1:A:1120:PRO:HA	2.01	0.76
23:3:423:LEU:HB2	23:3:438:LEU:HB2	1.66	0.76
34:V:548:ALA:HB1	34:V:586:PHE:N	2.00	0.76
15:H:168:A:H5'	15:H:169:C:OP2	1.86	0.76
37:Z:566:TYR:HD2	37:Z:580:PRO:HG2	1.50	0.76
3:C:750:LEU:O	3:C:754:VAL:HG23	1.84	0.76
13:F:40:U:H2'	13:F:41:A:C8	2.20	0.76
23:3:328:LYS:HB2	23:3:372:GLU:HG3	1.68	0.76
1:A:229:GLN:HG2	1:A:415:SER:HB2	1.68	0.76
1:A:405:LEU:CD1	3:C:265:LEU:HD13	2.15	0.76
1:A:779:LEU:CD2	31:P:223:PHE:CE2	2.69	0.76
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.21	0.76
1:A:305:ARG:HH21	3:C:854:ARG:HH11	1.28	0.75
1:A:435:CYS:SG	3:C:892:GLN:NE2	2.57	0.75
1:A:1162:PRO:CG	31:P:194:PHE:CD2	2.69	0.75
23:3:11:ALA:O	23:3:34:ARG:NH1	2.17	0.75
37:Z:594:GLU:O	37:Z:598:PHE:HB2	1.86	0.75
3:C:149:LEU:CD1	3:C:427:PHE:CG	2.53	0.75
3:C:593:GLU:HG3	3:C:594:PRO:HD2	1.67	0.75
14:G:132:G:H1	15:H:44:U:H3	1.34	0.75
23:3:784:THR:O	23:3:786:ARG:NH1	2.18	0.75
32:R:66:GLU:OE2	32:R:66:GLU:N	2.19	0.75
32:R:181:PRO:O	32:R:182:SER:HB2	1.84	0.75
1:A:319:LEU:HD11	3:C:590:ILE:CD1	2.16	0.75
1:A:378:PHE:HZ	3:C:335:ASN:HB2	1.51	0.75
14:G:11:A:C4	14:G:12:G:H8	2.04	0.75
15:H:81:G:H2'	15:H:82:G:C8	2.19	0.75
23:3:905:VAL:HB	23:3:928:TYR:HB2	1.68	0.75
1:A:1951:LYS:HD3	37:Z:521:PRO:O	1.85	0.75
23:3:720:TRP:HB3	23:3:731:LEU:HD11	1.69	0.75
1:A:230:PHE:N	1:A:414:ARG:O	2.18	0.75
1:A:305:ARG:HD3	3:C:933:PHE:CZ	2.22	0.75
3:C:470:PRO:HA	3:C:499:GLY:HA2	1.67	0.75
3:C:711:ARG:CD	3:C:730:ARG:HE	1.99	0.75
15:H:10:C:H2'	15:H:11:G:H8	1.52	0.75
23:3:441:GLY:HA3	23:3:734:LEU:O	1.85	0.75
23:3:1105:GLN:O	23:3:1118:VAL:HB	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LEU:HD12	1:A:484:SER:HB2	1.67	0.75
1:A:221:ASN:CG	2:B:12:U:OP1	2.25	0.75
1:A:1762:TYR:O	1:A:1768:TYR:OH	2.05	0.75
13:F:36:A:C3'	13:F:37:C:H5''	2.16	0.75
28:J:339:TRP:CE3	32:R:116:TYR:HD2	2.04	0.75
34:V:515:CYS:HA	34:V:521:TYR:CB	2.17	0.75
3:C:82:GLN:HB2	33:T:231:TRP:HZ3	1.50	0.75
3:C:465:MET:HE1	3:C:475:MET:CG	2.13	0.75
15:H:71:C:H2'	15:H:72:U:C6	2.21	0.75
1:A:384:VAL:HG21	3:C:334:ILE:HG12	1.69	0.75
15:H:153:A:C2'	15:H:154:C:H5'	2.17	0.75
34:V:538:ARG:HA	37:Z:534:MET:CB	2.16	0.75
1:A:405:LEU:HD13	3:C:265:LEU:HD13	1.68	0.74
3:C:348:TYR:CE1	3:C:359:LYS:HB3	2.22	0.74
3:C:510:LEU:HD22	3:C:514:TYR:CE2	2.22	0.74
28:J:256:LYS:O	29:L:232:TYR:HD2	1.66	0.74
28:J:273:TYR:CG	32:R:228:PRO:HG2	2.21	0.74
1:A:231:THR:HA	3:C:389:ASP:OD2	1.86	0.74
1:A:1405:LEU:CA	32:R:415:LEU:HD21	2.15	0.74
1:A:1784:ASN:HD22	1:A:1897:LEU:HD12	1.50	0.74
1:A:2073:TRP:CD1	1:A:2074:ARG:HD2	2.22	0.74
3:C:449:ILE:CG2	3:C:457:VAL:HG12	2.17	0.74
1:A:203:VAL:CG2	1:A:237:THR:CG2	2.66	0.74
1:A:783:TYR:CB	31:P:228:ILE:HG12	2.17	0.74
37:Z:525:TYR:HD1	37:Z:526:ILE:HG23	1.52	0.74
23:3:437:VAL:O	23:3:776:GLN:HA	1.87	0.74
1:A:463:PRO:CB	2:B:20:G:O2'	2.35	0.74
1:A:1457:HIS:CD2	32:R:425:GLY:H	2.04	0.74
3:C:137:HIS:CG	3:C:236:MET:HB2	2.22	0.74
15:H:180:G:O2'	15:H:181:G:H5'	1.88	0.74
32:R:70:ALA:O	32:R:71:GLN:O	2.05	0.74
1:A:1301:ILE:HG13	2:B:39:C:OP1	1.87	0.74
1:A:1405:LEU:HA	32:R:415:LEU:CD2	2.17	0.74
23:3:294:LYS:O	23:3:343:LYS:NZ	2.21	0.74
23:3:931:VAL:HG12	23:3:932:ASN:H	1.53	0.74
28:J:270:ASP:OD2	32:R:222:PRO:HG2	1.88	0.74
1:A:168:PRO:CG	1:A:559:ASP:CB	2.64	0.74
1:A:388:LEU:CD1	3:C:399:LEU:CD2	2.41	0.74
5:E:258:THR:HG22	5:E:260:ARG:HG2	1.68	0.74
1:A:76:MET:HE3	1:A:506:LEU:HD11	1.70	0.74
1:A:744:LYS:HE3	31:P:213:ASP:HA	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:140:HIS:CA	3:C:230:ASP:HB2	2.17	0.74
13:F:34:G:H5''	13:F:34:G:N3	2.03	0.74
32:R:422:MET:O	32:R:424:SER:N	2.17	0.74
33:T:385:TYR:O	33:T:400:PHE:HB2	1.88	0.74
3:C:445:ALA:HB1	3:C:449:ILE:CD1	2.17	0.74
1:A:748:ASP:OD1	31:P:214:THR:CG2	2.36	0.73
5:E:243:LEU:HD11	5:E:247:GLY:HA2	1.68	0.73
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.70	0.73
28:J:406:PHE:CD2	28:J:411:MET:CE	2.70	0.73
1:A:546:LEU:CD1	1:A:595:LYS:HD2	2.06	0.73
5:E:119:THR:HG21	5:E:161:ARG:CB	2.17	0.73
1:A:378:PHE:CZ	3:C:335:ASN:HB2	2.22	0.73
3:C:97:VAL:HG21	31:P:45:GLN:HG3	1.69	0.73
21:1:563:LEU:HD22	21:1:566:LEU:HD22	1.70	0.73
1:A:231:THR:CB	3:C:389:ASP:OD2	2.37	0.73
1:A:253:ASN:ND2	1:A:334:THR:O	2.21	0.73
1:A:1900:GLU:CD	37:Z:522:LEU:CB	2.55	0.73
3:C:94:ILE:HD11	31:P:44:ARG:NH2	2.03	0.73
23:3:772:ALA:O	23:3:775:ASN:ND2	2.21	0.73
1:A:260:LEU:HD23	1:A:455:VAL:HG22	1.70	0.73
2:B:42:U:O4	14:G:-3:A:N1	2.21	0.73
3:C:516:LEU:CD1	3:C:517:GLU:HG3	2.18	0.73
3:C:671:SER:O	3:C:672:LEU:HD13	1.89	0.73
15:H:69:U:H2'	15:H:70:C:C6	2.23	0.73
15:H:165:A:O2'	15:H:166:G:H5'	1.88	0.73
5:E:287:ASN:O	5:E:289:LEU:HD23	1.88	0.73
26:6:51:TYR:H	26:6:54:TYR:HB2	1.53	0.73
32:R:67:ILE:HG22	32:R:69:VAL:CG2	2.18	0.73
1:A:1301:ILE:O	1:A:1303:LEU:O	2.06	0.73
1:A:2325:VAL:HG13	4:D:788:GLY:C	2.07	0.73
1:A:91:ALA:HB2	32:R:207:MET:HE2	1.71	0.73
1:A:2078:ILE:CG2	4:D:1047:PRO:CB	2.66	0.73
15:H:106:G:H4'	15:H:107:A:O4'	1.89	0.73
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.21	0.73
28:J:339:TRP:CE3	32:R:116:TYR:CD2	2.76	0.73
3:C:711:ARG:CD	3:C:730:ARG:HH11	2.01	0.73
28:J:259:GLN:NE2	29:L:220:PRO:HD3	2.02	0.73
3:C:449:ILE:HG22	3:C:457:VAL:CG1	2.18	0.72
5:E:146:ARG:HH12	5:E:148:LYS:CE	1.99	0.72
5:E:250:LEU:HD23	5:E:250:LEU:O	1.88	0.72
15:H:70:C:H2'	15:H:71:C:C6	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:HIS:ND1	1:A:435:CYS:SG	2.62	0.72
3:C:508:LYS:HE3	3:C:566:THR:HG21	1.70	0.72
23:3:547:CYS:HA	23:3:555:VAL:O	1.89	0.72
33:T:434:GLY:CA	33:T:464:GLY:HA2	2.19	0.72
3:C:93:ILE:HD13	33:T:230:ILE:HD13	1.72	0.72
15:H:106:G:H21	15:H:107:A:N6	1.87	0.72
15:H:182:U:H2'	15:H:183:G:H8	1.53	0.72
21:1:428:ALA:O	21:1:432:THR:N	2.21	0.72
1:A:368:GLN:OE1	1:A:368:GLN:HA	1.88	0.72
1:A:541:GLY:HA3	13:F:66:C:OP1	1.87	0.72
1:A:675:GLN:OE1	13:F:70:A:OP1	2.08	0.72
3:C:519:GLU:N	3:C:519:GLU:OE2	2.21	0.72
13:F:34:G:N3	13:F:34:G:H3'	2.05	0.72
1:A:1457:HIS:HE2	32:R:424:SER:CA	2.02	0.72
1:A:2324:GLU:HG2	1:A:2330:ARG:HH12	1.54	0.72
3:C:125:ASN:O	3:C:126:SER:OG	2.04	0.72
3:C:726:LEU:HD12	3:C:726:LEU:O	1.89	0.72
33:T:352:THR:CG2	33:T:373:LYS:C	2.58	0.72
1:A:712:HIS:CE1	32:R:254:CYS:HB2	2.24	0.72
3:C:77:VAL:CG1	33:T:196:LEU:CA	2.68	0.72
3:C:449:ILE:HG21	3:C:457:VAL:HG11	1.70	0.72
13:F:5:U:H3'	13:F:7:G:H5''	1.71	0.72
1:A:107:PRO:O	1:A:111:GLU:OE1	2.08	0.72
1:A:193:LEU:HD12	1:A:194:GLU:H	1.55	0.72
1:A:462:ARG:HD2	1:A:462:ARG:N	2.05	0.72
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.21	0.72
1:A:2325:VAL:CG1	4:D:789:MET:HA	2.20	0.72
3:C:250:ARG:HE	3:C:451:HIS:CD2	2.07	0.72
23:3:442:LEU:CD1	23:3:734:LEU:HD23	2.19	0.72
34:V:548:ALA:HB3	34:V:585:ILE:CB	2.19	0.72
1:A:150:MET:SD	1:A:153:ARG:NH2	2.62	0.72
1:A:335:PRO:HG3	3:C:139:HIS:HB3	1.70	0.72
13:F:39:A:H61	14:G:8:C:H42	1.36	0.72
22:2:614:ARG:HG3	22:2:614:ARG:NH1	1.98	0.72
1:A:332:TYR:CB	3:C:177:ARG:O	2.38	0.72
1:A:718:ARG:CZ	32:R:259:LYS:HE3	2.20	0.72
1:A:2078:ILE:HG21	4:D:1047:PRO:CB	2.20	0.72
5:E:264:VAL:HA	5:E:272:ARG:HH21	1.55	0.72
23:3:783:TYR:HB2	23:3:801:GLU:HB3	1.72	0.72
1:A:386:PRO:HD3	3:C:372:PHE:CE1	2.20	0.72
1:A:785:LYS:HE3	31:P:215:LEU:HD11	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:165:A:C2'	15:H:166:G:H5'	2.20	0.72
23:3:440:HIS:CE1	23:3:720:TRP:HZ3	1.96	0.72
1:A:228:TRP:O	1:A:415:SER:CA	2.38	0.71
1:A:480:LYS:HE2	32:R:203:GLN:OE1	1.90	0.71
3:C:64:LYS:NZ	31:P:206:LYS:HG2	2.05	0.71
3:C:129:ILE:HA	3:C:199:LEU:O	1.90	0.71
1:A:176:LEU:HD13	1:A:181:ASN:HD22	1.52	0.71
1:A:549:GLU:OE1	1:A:552:ARG:NH1	2.23	0.71
1:A:1301:ILE:CG1	2:B:39:C:OP1	2.38	0.71
28:J:273:TYR:CE1	32:R:228:PRO:CB	2.72	0.71
29:L:224:PHE:CE1	32:R:86:LEU:CD1	2.73	0.71
31:P:66:ARG:HB2	31:P:66:ARG:HH11	1.55	0.71
1:A:231:THR:HB	3:C:389:ASP:OD2	1.89	0.71
1:A:730:GLY:O	32:R:252:PRO:HG2	1.90	0.71
1:A:1364:LEU:HD22	34:V:465:SER:CB	2.20	0.71
1:A:1402:ARG:HH22	37:Z:572:PRO:HA	1.53	0.71
2:B:44:A:H2	14:G:-5:G:C6	2.08	0.71
21:1:1206:ASP:OD1	21:1:1207:SER:N	2.21	0.71
23:3:446:GLU:OE1	23:3:763:ARG:NH1	2.24	0.71
1:A:264:PHE:CE2	1:A:459:LEU:CD1	2.73	0.71
1:A:384:VAL:HG12	3:C:332:GLY:N	2.04	0.71
15:H:153:A:H2'	15:H:154:C:C5'	2.19	0.71
21:1:405:ASP:HA	25:5:49:ARG:HH22	1.55	0.71
1:A:529:THR:HG22	30:M:197:TYR:C	2.11	0.71
3:C:706:GLN:HE21	3:C:708:THR:H	1.38	0.71
5:E:74:PHE:CE2	5:E:343:ILE:CG1	2.73	0.71
31:P:224:MET:CE	31:P:224:MET:HA	2.21	0.71
32:R:414:ARG:CZ	32:R:414:ARG:HB2	2.18	0.71
1:A:1962:THR:HG23	37:Z:524:ARG:HB2	1.68	0.71
3:C:700:ILE:HA	3:C:705:VAL:CG1	2.21	0.71
3:C:705:VAL:HG23	3:C:717:PHE:HD2	1.48	0.71
15:H:72:U:H2'	15:H:73:C:C6	2.26	0.71
1:A:203:VAL:HG23	1:A:237:THR:HG21	1.72	0.71
1:A:393:LEU:CB	3:C:379:LYS:HE3	2.21	0.71
1:A:1529:ILE:O	1:A:1532:ARG:N	2.24	0.71
3:C:80:ILE:HD12	3:C:80:ILE:N	2.05	0.71
3:C:94:ILE:HD13	31:P:44:ARG:CZ	2.20	0.71
3:C:441:PRO:O	3:C:444:GLY:HA3	1.90	0.71
3:C:490:PHE:CZ	3:C:612:LYS:HD2	2.26	0.71
31:P:191:ASP:N	31:P:191:ASP:OD1	2.23	0.71
37:Z:612:TYR:O	37:Z:614:TRP:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:43:U:C4	14:G:-4:A:N1	2.58	0.71
1:A:81:PHE:O	1:A:83:HIS:N	2.24	0.71
1:A:171:ASP:O	1:A:520:TYR:CG	2.44	0.71
1:A:1459:ARG:CG	32:R:422:MET:O	2.39	0.71
1:A:2156:THR:OG1	1:A:2157:VAL:N	2.21	0.71
3:C:679:PRO:HG2	3:C:807:GLN:OE1	1.91	0.71
28:J:270:ASP:OD2	32:R:222:PRO:HG3	1.88	0.71
32:R:422:MET:HG2	32:R:423:ASP:N	2.05	0.71
34:V:549:LYS:O	34:V:552:ALA:HB3	1.91	0.71
1:A:76:MET:CE	1:A:88:TYR:CG	2.70	0.71
1:A:377:GLU:O	1:A:378:PHE:HB3	1.91	0.71
1:A:705:LYS:HG2	32:R:251:ILE:CD1	2.21	0.71
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.56	0.71
1:A:1306:LYS:NZ	2:B:38:C:H2'	2.05	0.71
21:1:1221:GLU:HG3	21:1:1223:SER:H	1.56	0.71
28:J:353:GLU:OE1	28:J:358:GLU:HB3	1.91	0.71
31:P:189:ASP:OD2	31:P:192:VAL:HG21	1.91	0.71
33:T:366:VAL:HG21	33:T:402:ASP:HA	1.72	0.71
1:A:73:HIS:NE2	1:A:81:PHE:CZ	2.51	0.70
1:A:181:ASN:O	1:A:185:VAL:HG22	1.90	0.70
1:A:719:CYS:SG	32:R:258:TRP:CH2	2.84	0.70
3:C:259:LYS:HG3	41:C:1500:GTP:C6	2.26	0.70
1:A:301:LYS:HG2	3:C:940:ARG:N	2.06	0.70
1:A:2328:ALA:HB3	4:D:788:GLY:N	2.05	0.70
15:H:160:A:O2'	15:H:161:U:H5'	1.90	0.70
14:G:11:A:N3	14:G:11:A:H5''	2.05	0.70
15:H:168:A:N3	15:H:168:A:H2'	2.06	0.70
13:F:24:A:H2	13:F:26:U:C2	2.09	0.70
32:R:189:ASN:HD21	32:R:195:ARG:NH2	1.90	0.70
33:T:267:ASP:O	33:T:268:LYS:HG3	1.91	0.70
1:A:251:ASP:CB	1:A:337:VAL:HG23	2.20	0.70
1:A:316:PHE:CE1	3:C:635:LEU:HA	2.27	0.70
2:B:40:U:H4'	2:B:41:U:OP2	1.89	0.70
2:B:43:U:N3	14:G:-4:A:C2	2.51	0.70
3:C:449:ILE:HD13	3:C:466:SER:OG	1.92	0.70
13:F:94:C:OP1	28:J:351:ASN:ND2	2.25	0.70
15:H:181:G:H2'	15:H:182:U:C6	2.26	0.70
21:1:901:GLN:HA	21:1:939:ARG:NH2	2.07	0.70
32:R:103:ARG:HH11	32:R:103:ARG:CB	2.04	0.70
34:V:536:ILE:O	34:V:578:SER:CB	2.39	0.70
1:A:76:MET:CE	1:A:506:LEU:HD11	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:457:VAL:CB	3:C:462:GLY:HA3	2.22	0.70
13:F:38:G:P	13:F:38:G:H8	2.14	0.70
13:F:68:C:C2	31:P:33:ARG:HG2	2.27	0.70
14:G:12:G:N3	14:G:12:G:H2'	2.07	0.70
21:1:1108:ASN:OD1	21:1:1110:VAL:N	2.25	0.70
1:A:1860:GLN:HG2	1:A:1883:VAL:HB	1.74	0.70
2:B:40:U:C4'	2:B:41:U:OP2	2.39	0.70
3:C:132:VAL:CG1	3:C:226:VAL:CG2	2.70	0.70
3:C:135:CYS:SG	3:C:227:LEU:CD1	2.80	0.70
32:R:220:ARG:NH1	32:R:220:ARG:HB2	2.06	0.70
1:A:664:HIS:NE2	1:A:666:LYS:HG2	2.06	0.70
1:A:675:GLN:O	13:F:55:C:O2'	2.10	0.70
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.73	0.70
15:H:154:C:H2'	15:H:155:C:C6	2.27	0.70
21:1:1155:PHE:HA	21:1:1158:ILE:HG12	1.73	0.70
32:R:80:LYS:O	32:R:81:LYS:NZ	2.25	0.70
1:A:231:THR:CA	3:C:389:ASP:OD2	2.40	0.70
1:A:719:CYS:SG	32:R:258:TRP:HH2	2.13	0.70
3:C:137:HIS:CE1	3:C:236:MET:SD	2.85	0.70
1:A:299:ILE:HD12	3:C:921:LEU:HB2	1.74	0.69
1:A:718:ARG:NE	32:R:259:LYS:HE3	2.06	0.69
3:C:452:THR:HB	3:C:577:PHE:CD2	2.26	0.69
23:3:722:SER:HA	23:3:730:HIS:O	1.92	0.69
1:A:76:MET:SD	1:A:88:TYR:CG	2.85	0.69
1:A:363:HIS:CE1	3:C:287:GLY:HA3	2.27	0.69
1:A:673:THR:O	1:A:677:VAL:HG23	1.91	0.69
3:C:64:LYS:NZ	31:P:206:LYS:CG	2.55	0.69
3:C:452:THR:O	3:C:577:PHE:HA	1.92	0.69
5:E:74:PHE:HE2	5:E:343:ILE:HG12	1.54	0.69
5:E:264:VAL:HA	5:E:272:ARG:NH2	2.07	0.69
1:A:232:LEU:HD23	3:C:387:ASP:O	1.92	0.69
1:A:250:VAL:CG2	1:A:337:VAL:CG1	2.70	0.69
1:A:311:GLU:HB3	3:C:885:THR:CG2	2.21	0.69
1:A:461:HIS:CD2	2:B:26:A:H61	2.10	0.69
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.73	0.69
1:A:439:GLN:NE2	1:A:614:TYR:CE2	2.49	0.69
1:A:805:GLU:CB	31:P:194:PHE:HZ	2.04	0.69
1:A:2314:PHE:HD2	4:D:1123:TRP:CB	2.05	0.69
3:C:709:TRP:HB3	3:C:713:LYS:HD2	1.73	0.69
23:3:280:ASP:H	23:3:857:ALA:HB3	1.58	0.69
31:P:30:TYR:OH	32:R:161:ALA:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:436:VAL:HG23	32:R:437:TYR:CE1	2.26	0.69
1:A:645:THR:HB	1:A:646:PRO:HD3	1.74	0.69
1:A:755:HIS:HE1	31:P:223:PHE:CD2	2.06	0.69
15:H:149:A:H2'	15:H:150:U:C6	2.27	0.69
15:H:153:A:N6	15:H:177:A:C2	2.60	0.69
15:H:183:G:H2'	15:H:184:C:C6	2.26	0.69
32:R:408:GLU:CG	32:R:409:VAL:H	2.04	0.69
1:A:71:ARG:HD2	1:A:177:ASP:OD2	1.91	0.69
1:A:1180:LYS:HA	1:A:1201:ARG:HH12	1.58	0.69
23:3:428:GLY:HA3	23:3:433:SER:HA	1.73	0.69
1:A:203:VAL:CG2	1:A:237:THR:HG21	2.23	0.69
1:A:256:TYR:CE1	3:C:888:ARG:CZ	2.76	0.69
1:A:367:SER:CB	3:C:299:ILE:HD12	2.23	0.69
1:A:384:VAL:CA	3:C:331:PHE:CD2	2.61	0.69
1:A:762:ARG:NH2	31:P:226:LYS:HZ3	1.87	0.69
1:A:1505:LYS:CD	37:Z:615:SER:HB3	2.22	0.69
3:C:89:LEU:HD23	3:C:89:LEU:C	2.14	0.69
3:C:482:TYR:CE2	3:C:493:PHE:HB2	2.28	0.69
5:E:178:LEU:CD1	5:E:222:LEU:CD2	2.71	0.69
15:H:83:A:C2'	15:H:84:C:O4'	2.39	0.69
23:3:452:LEU:HD11	23:3:762:LEU:HB2	1.74	0.69
25:5:18:ASN:OD1	25:5:19:ARG:N	2.25	0.69
35:X:185:ARG:O	35:X:189:HIS:HB2	1.93	0.69
1:A:1459:ARG:HG3	32:R:424:SER:H	1.57	0.69
1:A:2267:PHE:HA	4:D:1261:PRO:CB	2.23	0.69
3:C:93:ILE:CG2	33:T:218:TRP:CE2	2.76	0.69
3:C:736:GLY:CA	3:C:770:PHE:CE2	2.75	0.69
15:H:152:G:O3'	15:H:153:A:O4'	2.11	0.69
23:3:236:ILE:HB	23:3:249:LEU:HB2	1.75	0.69
28:J:353:GLU:OE1	28:J:358:GLU:CB	2.41	0.69
31:P:30:TYR:CZ	32:R:162:ALA:HA	2.28	0.69
31:P:224:MET:CE	31:P:228:ILE:CD1	2.71	0.69
1:A:299:ILE:HD11	3:C:921:LEU:HA	1.74	0.69
1:A:392:PRO:C	3:C:379:LYS:CE	2.48	0.69
3:C:72:VAL:HG22	33:T:453:ALA:CB	2.23	0.69
3:C:256:CYS:SG	3:C:308:CYS:HB2	2.33	0.69
5:E:74:PHE:CD1	5:E:81:LEU:HD23	2.28	0.69
1:A:229:GLN:CG	1:A:415:SER:HB2	2.21	0.68
1:A:253:ASN:OD1	1:A:334:THR:OG1	2.03	0.68
1:A:388:LEU:HD12	3:C:399:LEU:HD21	1.72	0.68
1:A:755:HIS:CE1	31:P:223:PHE:HB3	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.11	0.68
13:F:37:C:H4'	13:F:38:G:OP2	1.91	0.68
22:2:487:LEU:O	22:2:490:HIS:N	2.26	0.68
23:3:718:ARG:NH2	23:3:734:LEU:O	2.25	0.68
1:A:255:PHE:HE1	1:A:432:ARG:O	1.75	0.68
3:C:140:HIS:CD2	3:C:230:ASP:HB3	2.28	0.68
3:C:445:ALA:CB	3:C:466:SER:HA	2.20	0.68
3:C:725:ASP:OD1	3:C:728:ALA:N	2.25	0.68
32:R:434:TYR:HE2	32:R:436:VAL:HG22	1.57	0.68
1:A:73:HIS:NE2	1:A:81:PHE:CD1	2.59	0.68
1:A:1301:ILE:CD1	1:A:1306:LYS:CE	2.70	0.68
2:B:21:A:O3'	2:B:22:U:H4'	1.94	0.68
22:2:643:PRO:HD2	24:4:69:TYR:CG	2.27	0.68
31:P:72:ARG:NH1	31:P:72:ARG:HB2	2.08	0.68
32:R:106:GLN:CG	32:R:110:LYS:HE2	2.22	0.68
32:R:420:LYS:HG2	32:R:423:ASP:CG	2.13	0.68
36:Y:33:LYS:HA	36:Y:87:GLN:HE22	1.59	0.68
1:A:32:GLU:HG3	1:A:36:LYS:HE3	1.74	0.68
1:A:402:ILE:HG12	3:C:265:LEU:HD22	1.75	0.68
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.28	0.68
36:Y:86:ASP:HB2	37:Z:502:ALA:CB	2.23	0.68
1:A:44:ARG:HD2	1:A:45:TYR:CE2	2.28	0.68
1:A:1900:GLU:OE2	37:Z:522:LEU:HB2	1.93	0.68
1:A:2146:VAL:HG22	1:A:2272:MET:HB2	1.74	0.68
3:C:482:TYR:CE2	3:C:493:PHE:CB	2.77	0.68
3:C:678:THR:HG21	3:C:683:ASN:ND2	2.06	0.68
14:G:-2:C:H2'	14:G:-1:G:C8	2.28	0.68
23:3:441:GLY:O	23:3:775:ASN:CG	2.31	0.68
23:3:868:VAL:O	23:3:877:LEU:N	2.27	0.68
5:E:108:HIS:CE1	5:E:128:SER:CB	2.77	0.68
15:H:147:G:O2'	15:H:148:C:H5'	1.94	0.68
23:3:524:ILE:HD11	23:3:556:ILE:HG21	1.74	0.68
31:P:63:LEU:O	31:P:63:LEU:HD23	1.94	0.68
32:R:414:ARG:NE	37:Z:598:PHE:CE1	2.47	0.68
1:A:338:VAL:HG21	3:C:867:PRO:CD	2.24	0.68
1:A:779:LEU:CD2	31:P:223:PHE:HE2	2.06	0.68
1:A:1457:HIS:HE2	32:R:424:SER:HA	1.55	0.68
13:F:68:C:C5	31:P:33:ARG:HB3	2.20	0.68
32:R:88:ILE:CG2	32:R:96:ILE:CG2	2.71	0.68
3:C:79:THR:HG23	33:T:199:VAL:CG2	2.24	0.68
3:C:452:THR:HG22	3:C:577:PHE:CB	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:74:PHE:CD1	5:E:81:LEU:HD21	2.29	0.68
34:V:547:VAL:O	34:V:550:MET:N	2.27	0.68
37:Z:597:ARG:NH1	37:Z:601:LEU:CD1	2.57	0.68
1:A:660:PHE:CD2	32:R:209:PRO:CB	2.76	0.68
1:A:758:ARG:HG3	1:A:779:LEU:HD11	1.75	0.68
1:A:1210:LYS:NZ	1:A:1369:TYR:OH	2.27	0.68
2:B:19:A:O2'	2:B:20:G:OP1	2.12	0.68
3:C:141:GLY:O	3:C:258:ASN:ND2	2.27	0.68
22:2:614:ARG:NH2	22:2:685:ASP:OD1	2.26	0.68
23:3:301:PHE:HB2	23:3:313:ILE:HB	1.76	0.68
27:7:48:ASP:O	27:7:51:ASN:N	2.27	0.68
28:J:360:ASP:O	28:J:363:ARG:HG3	1.93	0.68
36:Y:86:ASP:CA	37:Z:502:ALA:HB3	2.23	0.68
1:A:91:ALA:O	1:A:93:LYS:N	2.27	0.68
1:A:121:HIS:HE2	1:A:481:PHE:HB3	1.51	0.68
1:A:245:LEU:HA	1:A:430:TRP:CZ2	2.28	0.68
3:C:94:ILE:CD1	31:P:44:ARG:NH1	2.57	0.68
13:F:35:A:H5''	13:F:35:A:N3	2.09	0.68
15:H:159:U:O2'	15:H:160:A:H5'	1.94	0.68
23:3:374:SER:HB3	23:3:377:MET:HG3	1.76	0.68
28:J:353:GLU:OE2	28:J:361:ARG:NH2	2.27	0.68
1:A:76:MET:HE1	1:A:88:TYR:CB	2.23	0.67
3:C:94:ILE:CD1	31:P:44:ARG:CZ	2.72	0.67
3:C:360:ALA:H	3:C:361:PRO:HD3	1.59	0.67
3:C:534:VAL:HG12	3:C:535:ALA:H	1.59	0.67
32:R:420:LYS:HB2	37:Z:610:LEU:CD1	2.22	0.67
1:A:122:ILE:CD1	1:A:483:GLN:HG3	2.24	0.67
1:A:298:ASP:O	1:A:302:ILE:HG12	1.95	0.67
1:A:305:ARG:HG3	3:C:878:ILE:HB	1.77	0.67
1:A:2270:PHE:HD1	4:D:1264:PRO:CB	1.96	0.67
3:C:140:HIS:HB3	3:C:230:ASP:HB2	1.71	0.67
23:3:18:ILE:HD12	23:3:67:ALA:HB2	1.77	0.67
32:R:147:THR:CG2	33:T:360:VAL:HG12	2.23	0.67
1:A:91:ALA:CA	32:R:207:MET:CE	2.71	0.67
3:C:140:HIS:CD2	3:C:230:ASP:CB	2.77	0.67
3:C:737:PRO:HG3	3:C:774:THR:OG1	1.93	0.67
21:1:437:PRO:O	35:X:262:TYR:HA	1.94	0.67
23:3:753:GLY:HA3	23:3:765:LEU:O	1.94	0.67
1:A:75:ASP:OD1	1:A:75:ASP:N	2.26	0.67
1:A:228:TRP:O	1:A:416:GLY:N	2.26	0.67
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:PRO:HD2	1:A:1119:ASP:H	1.59	0.67
1:A:1962:THR:HG23	37:Z:524:ARG:HG3	1.74	0.67
3:C:259:LYS:HE2	3:C:262:ARG:HD2	1.74	0.67
21:1:1097:LEU:O	21:1:1100:ASN:ND2	2.24	0.67
23:3:412:ILE:HG12	23:3:423:LEU:HG	1.76	0.67
1:A:76:MET:SD	1:A:88:TYR:CD1	2.88	0.67
1:A:89:LEU:HD22	1:A:656:LEU:HD22	1.76	0.67
1:A:1422:LEU:HD22	21:1:88:VAL:CB	2.25	0.67
1:A:2113:LYS:CE	4:D:1229:ASP:CB	2.71	0.67
3:C:389:ASP:OD1	3:C:389:ASP:N	2.26	0.67
5:E:66:GLU:HB2	5:E:87:ASP:OD2	1.94	0.67
21:1:474:TYR:OH	25:5:93:ASN:ND2	2.27	0.67
21:1:798:THR:HG22	21:1:800:GLY:H	1.60	0.67
32:R:119:LEU:CB	32:R:232:MET:HG3	2.24	0.67
32:R:285:ASN:OD1	32:R:286:GLU:N	2.27	0.67
33:T:185:MET:CB	33:T:186:PRO:HD3	2.24	0.67
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.59	0.67
3:C:94:ILE:HD11	31:P:44:ARG:HH22	1.60	0.67
3:C:132:VAL:HG12	3:C:226:VAL:CG2	2.23	0.67
5:E:246:GLU:HB2	5:E:248:SER:OG	1.94	0.67
33:T:455:GLN:HG3	33:T:485:THR:HG21	1.76	0.67
1:A:435:CYS:CB	3:C:892:GLN:NE2	2.57	0.67
1:A:1258:LYS:HE2	32:R:432:GLU:HA	1.77	0.67
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.30	0.67
1:A:2300:ASN:OD1	4:D:1228:VAL:O	2.12	0.67
3:C:736:GLY:CA	3:C:770:PHE:HE2	2.07	0.67
36:Y:62:ILE:HA	36:Y:84:TYR:HA	1.75	0.67
36:Y:100:ILE:O	36:Y:106:THR:HA	1.94	0.67
37:Z:597:ARG:NH1	37:Z:601:LEU:HD12	2.08	0.67
1:A:171:ASP:OD2	1:A:519:ASP:OD2	2.12	0.67
1:A:299:ILE:CD1	3:C:920:PRO:O	2.43	0.67
1:A:393:LEU:HA	3:C:379:LYS:CD	2.24	0.67
1:A:696:MET:C	1:A:698:PRO:HD3	2.15	0.67
2:B:40:U:C5'	2:B:41:U:OP2	2.43	0.67
3:C:572:GLU:HG3	3:C:573:GLU:H	1.60	0.67
15:H:151:C:C2	15:H:152:G:C8	2.83	0.67
32:R:81:LYS:HA	32:R:81:LYS:HZ1	1.59	0.67
32:R:119:LEU:HA	32:R:232:MET:SD	2.34	0.67
33:T:272:CYS:HB3	33:T:282:ARG:HG3	1.76	0.67
1:A:229:GLN:HA	1:A:414:ARG:O	1.94	0.67
1:A:293:TRP:HZ3	1:A:295:GLU:OE1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:452:THR:CB	3:C:577:PHE:CD2	2.73	0.67
5:E:243:LEU:HD12	5:E:247:GLY:HA2	1.76	0.67
14:G:10:U:O5'	14:G:10:U:H6	1.78	0.67
15:H:169:C:O2'	15:H:170:C:H5'	1.95	0.67
23:3:63:ARG:NH2	23:3:119:GLN:OE1	2.22	0.67
23:3:470:PHE:HB3	23:3:747:SER:HA	1.75	0.67
23:3:802:THR:HA	23:3:863:ALA:O	1.95	0.67
1:A:91:ALA:HA	32:R:207:MET:HE3	1.74	0.67
1:A:439:GLN:NE2	1:A:614:TYR:OH	2.27	0.67
3:C:149:LEU:HD13	3:C:427:PHE:CE2	2.22	0.67
3:C:510:LEU:HD22	3:C:514:TYR:CD2	2.30	0.67
15:H:153:A:C3'	15:H:154:C:H5'	2.25	0.67
21:1:1126:PHE:HA	21:1:1165:TYR:OH	1.94	0.67
32:R:135:PRO:O	32:R:136:ASP:CG	2.33	0.67
1:A:406:TRP:CZ3	3:C:265:LEU:C	2.69	0.66
1:A:417:ARG:HH22	2:B:58:U:C5'	2.07	0.66
1:A:1984:LYS:HG3	1:A:2011:ILE:HD11	1.76	0.66
1:A:2306:HIS:CD2	1:A:2308:VAL:H	2.13	0.66
3:C:77:VAL:CG1	33:T:196:LEU:HB3	2.24	0.66
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.23	0.66
23:3:1035:THR:HG21	23:3:1103:SER:HA	1.75	0.66
24:4:17:VAL:HG13	24:4:84:ILE:HG23	1.77	0.66
1:A:398:THR:CG2	3:C:382:ALA:HB1	2.23	0.66
3:C:230:ASP:OD1	3:C:259:LYS:CB	2.43	0.66
15:H:143:A:H2'	15:H:144:C:H6	1.59	0.66
15:H:151:C:O2	15:H:152:G:C8	2.48	0.66
1:A:676:ARG:NE	13:F:56:A:OP1	2.28	0.66
1:A:1768:TYR:HA	1:A:1771:LEU:HB3	1.75	0.66
3:C:62:ASP:OD1	3:C:62:ASP:N	2.28	0.66
3:C:244:LYS:CB	3:C:292:TYR:CE2	2.79	0.66
15:H:151:C:H2'	15:H:152:G:H8	1.59	0.66
23:3:147:ASP:OD1	23:3:151:ARG:N	2.25	0.66
23:3:546:LYS:O	23:3:556:ILE:HA	1.94	0.66
23:3:947:GLU:HB3	23:3:963:VAL:HG22	1.75	0.66
1:A:338:VAL:CG2	3:C:867:PRO:CG	2.73	0.66
1:A:377:GLU:O	1:A:378:PHE:CB	2.44	0.66
1:A:748:ASP:OD2	33:T:204:LEU:O	2.13	0.66
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.61	0.66
1:A:1457:HIS:CE1	1:A:1459:ARG:HB2	2.30	0.66
5:E:146:ARG:HH11	5:E:148:LYS:CE	1.83	0.66
15:H:73:C:H2'	15:H:74:U:C6	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:114:A:H61	15:H:142:C:H42	1.44	0.66
21:1:397:ARG:HD3	21:1:398:PRO:HD2	1.78	0.66
26:6:25:LYS:NZ	26:6:26:CYS:SG	2.68	0.66
1:A:480:LYS:HG2	32:R:203:GLN:OE1	1.95	0.66
2:B:19:A:H2'	2:B:20:G:H5''	1.78	0.66
2:B:47:A:HO2'	2:B:48:A:H8	1.42	0.66
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.25	0.66
3:C:473:PRO:O	3:C:474:LEU:HB3	1.96	0.66
3:C:474:LEU:HD23	3:C:474:LEU:C	2.16	0.66
15:H:47:U:H1'	15:H:48:A:H8	1.61	0.66
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.29	0.66
31:P:212:ASN:OD1	33:T:483:ASP:HA	1.96	0.66
33:T:314:ILE:HD12	33:T:324:HIS:HB2	1.75	0.66
36:Y:39:PHE:O	36:Y:109:VAL:HA	1.95	0.66
36:Y:98:ASN:OD1	36:Y:99:GLY:N	2.25	0.66
37:Z:525:TYR:HE1	37:Z:526:ILE:HG23	1.57	0.66
1:A:1370:ARG:NH1	34:V:467:LEU:C	2.49	0.66
3:C:145:PHE:CE1	3:C:427:PHE:HE1	2.14	0.66
3:C:221:ILE:CG1	3:C:479:THR:OG1	2.43	0.66
33:T:342:GLU:HB3	33:T:343:PRO:CD	2.26	0.66
34:V:548:ALA:HB1	34:V:585:ILE:CB	2.25	0.66
1:A:76:MET:HE2	1:A:88:TYR:CD2	2.30	0.66
1:A:312:TYR:CE1	3:C:882:GLY:CA	2.78	0.66
1:A:395:THR:CG2	3:C:383:GLN:NE2	2.49	0.66
1:A:718:ARG:HH21	32:R:259:LYS:HE3	1.58	0.66
1:A:785:LYS:HE3	31:P:215:LEU:CD1	2.26	0.66
3:C:140:HIS:HA	3:C:259:LYS:NZ	2.10	0.66
5:E:116:HIS:O	5:E:124:LEU:HD12	1.95	0.66
23:3:355:ASN:OD1	23:3:436:ARG:NH2	2.26	0.66
1:A:366:LYS:HE3	1:A:366:LYS:N	2.07	0.66
14:G:146:C:H41	21:1:1107:GLN:HG3	1.60	0.66
23:3:952:ILE:HG12	23:3:961:ILE:HG12	1.78	0.66
27:7:63:ARG:O	27:7:67:ASN:ND2	2.29	0.66
28:J:300:ASP:OD2	32:R:101:ILE:CG1	2.44	0.66
1:A:225:TYR:O	1:A:418:THR:OG1	2.11	0.66
1:A:755:HIS:HE1	31:P:223:PHE:HB3	1.61	0.66
1:A:829:PRO:O	1:A:882:LYS:NZ	2.27	0.66
1:A:1457:HIS:NE2	32:R:424:SER:CA	2.59	0.66
3:C:87:GLN:HE21	33:T:239:LYS:HD3	1.61	0.66
23:3:330:PHE:O	23:3:394:ASN:ND2	2.29	0.66
3:C:77:VAL:HG12	33:T:197:TYR:CA	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:GLY:HA2	3:C:239:THR:HG22	1.77	0.65
5:E:178:LEU:HD11	5:E:222:LEU:CD2	2.26	0.65
32:R:124:VAL:HG13	32:R:125:MET:H	1.60	0.65
1:A:333:HIS:O	3:C:139:HIS:NE2	2.29	0.65
1:A:344:ASP:N	1:A:344:ASP:OD1	2.28	0.65
1:A:1459:ARG:HE	32:R:423:ASP:CB	2.06	0.65
14:G:-12:G:H2'	14:G:-11:G:C8	2.30	0.65
23:3:440:HIS:CG	23:3:733:PRO:CG	2.79	0.65
33:T:439:TRP:CZ3	33:T:446:ASN:HB2	2.32	0.65
21:1:1171:PRO:O	21:1:1174:GLU:HB2	1.96	0.65
31:P:210:PHE:HB3	33:T:455:GLN:HE22	1.61	0.65
1:A:1459:ARG:CD	32:R:422:MET:O	2.45	0.65
1:A:1962:THR:O	37:Z:524:ARG:CG	2.45	0.65
21:1:713:ALA:HA	21:1:716:ALA:HB3	1.77	0.65
31:P:66:ARG:HH11	31:P:66:ARG:CB	2.09	0.65
3:C:457:VAL:HB	3:C:462:GLY:HA3	1.78	0.65
33:T:327:SER:O	33:T:357:TRP:HH2	1.79	0.65
1:A:254:TYR:OH	1:A:434:HIS:HB3	1.95	0.65
1:A:435:CYS:CB	3:C:892:GLN:HE22	2.09	0.65
3:C:700:ILE:HG21	3:C:741:GLY:O	1.97	0.65
14:G:137:C:H42	15:H:40:C:N4	1.95	0.65
21:1:584:ASP:OD1	21:1:585:GLU:N	2.29	0.65
22:2:487:LEU:HD12	27:7:28:LYS:HE3	1.78	0.65
22:2:511:LEU:HD23	22:2:593:GLU:HG3	1.79	0.65
23:3:458:ALA:HA	23:3:741:PHE:HB3	1.78	0.65
33:T:459:LEU:HD12	33:T:460:ASP:H	1.61	0.65
1:A:91:ALA:CA	32:R:207:MET:HE3	2.26	0.65
1:A:333:HIS:C	3:C:139:HIS:NE2	2.49	0.65
1:A:361:HIS:HD2	3:C:279:ARG:NH1	1.95	0.65
5:E:108:HIS:CE1	5:E:128:SER:HB3	2.31	0.65
13:F:24:A:H2	13:F:26:U:N3	1.94	0.65
1:A:134:TRP:HB3	1:A:418:THR:HG21	1.79	0.65
1:A:405:LEU:HD11	3:C:385:VAL:HG11	1.78	0.65
2:B:40:U:H5'	2:B:41:U:OP2	1.97	0.65
3:C:572:GLU:HG3	3:C:573:GLU:N	2.12	0.65
23:3:866:ILE:HB	23:3:880:VAL:HB	1.79	0.65
32:R:451:ILE:HD13	32:R:451:ILE:N	2.12	0.65
33:T:458:SER:OG	33:T:459:LEU:N	2.30	0.65
2:B:43:U:O4	14:G:-4:A:N1	2.29	0.65
23:3:791:HIS:HE1	23:3:934:GLY:HA3	1.62	0.65
24:4:75:ASN:OD1	24:4:86:VAL:CB	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:HIS:HD2	1:A:473:PHE:CZ	2.15	0.65
1:A:2314:PHE:CD2	4:D:1123:TRP:CB	2.80	0.65
3:C:749:THR:O	3:C:753:GLU:N	2.27	0.65
13:F:33:G:OP2	13:F:33:G:H8	1.80	0.65
15:H:153:A:H3'	15:H:154:C:H5'	1.79	0.65
15:H:156:U:C6	15:H:156:U:C5'	2.72	0.65
21:1:1026:ASN:HD22	21:1:1031:VAL:HG11	1.60	0.65
31:P:210:PHE:CE2	33:T:455:GLN:OE1	2.50	0.65
3:C:97:VAL:CG1	31:P:47:THR:OG1	2.45	0.64
3:C:463:GLU:OE1	3:C:463:GLU:N	2.29	0.64
3:C:488:VAL:HG13	3:C:609:LYS:NZ	2.12	0.64
5:E:277:PHE:HE2	5:E:300:ILE:HD13	1.61	0.64
21:1:912:ASN:OD1	21:1:957:ARG:NH1	2.30	0.64
32:R:171:LEU:CD1	32:R:201:GLU:OE1	2.44	0.64
1:A:664:HIS:NE2	1:A:666:LYS:HB2	2.11	0.64
3:C:72:VAL:CG2	33:T:453:ALA:HB1	2.26	0.64
14:G:11:A:N3	14:G:11:A:H3'	2.12	0.64
15:H:148:C:H2'	15:H:149:A:C8	2.30	0.64
1:A:378:PHE:CD1	1:A:379:GLU:N	2.65	0.64
3:C:141:GLY:C	3:C:258:ASN:HD22	2.01	0.64
5:E:153:PHE:O	5:E:171:SER:HB2	1.97	0.64
23:3:429:ARG:HH12	27:7:58:ASN:HA	1.62	0.64
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.79	0.64
1:A:363:HIS:CD2	3:C:283:ASP:O	2.50	0.64
1:A:779:LEU:HD21	31:P:223:PHE:HE2	1.59	0.64
1:A:1051:LEU:CD2	31:P:193:VAL:HG11	2.27	0.64
3:C:256:CYS:SG	3:C:308:CYS:CB	2.86	0.64
23:3:206:GLN:HG3	23:3:228:LEU:HD12	1.78	0.64
23:3:670:GLN:HA	23:3:698:PRO:HA	1.78	0.64
32:R:88:ILE:H	32:R:88:ILE:HD12	1.61	0.64
36:Y:24:ASP:O	36:Y:27:SER:N	2.30	0.64
37:Z:594:GLU:O	37:Z:598:PHE:N	2.25	0.64
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.78	0.64
1:A:1069:ASN:OD1	1:A:1075:GLN:NE2	2.31	0.64
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.74	0.64
3:C:97:VAL:HG22	31:P:45:GLN:HG3	1.77	0.64
3:C:482:TYR:HE2	3:C:493:PHE:CD2	2.14	0.64
1:A:305:ARG:HA	1:A:305:ARG:NH1	2.09	0.64
15:H:68:G:H1	15:H:84:C:N4	1.95	0.64
23:3:714:ALA:O	23:3:720:TRP:HB2	1.97	0.64
32:R:419:SER:O	32:R:420:LYS:O	2.16	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:ILE:CG2	3:C:933:PHE:CE1	2.81	0.64
3:C:350:ASN:ND2	3:C:353:THR:HG23	2.13	0.64
3:C:705:VAL:HB	3:C:717:PHE:CZ	2.33	0.64
14:G:149:G:C2	14:G:150:U:H2'	2.32	0.64
21:1:847:ALA:O	21:1:851:SER:CB	2.46	0.64
32:R:433:ILE:HD12	32:R:435:ASN:ND2	2.12	0.64
1:A:250:VAL:CG2	1:A:337:VAL:HG11	2.28	0.64
1:A:305:ARG:HG2	3:C:878:ILE:CG2	2.27	0.64
1:A:1118:PRO:O	1:A:1119:ASP:CB	2.44	0.64
3:C:824:THR:O	3:C:824:THR:CG2	2.45	0.64
13:F:38:G:H8	13:F:38:G:O5'	1.79	0.64
21:1:599:ASN:O	21:1:603:ALA:HB2	1.98	0.64
21:1:702:ARG:O	21:1:705:SER:OG	2.13	0.64
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.78	0.64
24:4:15:VAL:O	24:4:58:PHE:HA	1.97	0.64
29:L:224:PHE:HD1	32:R:86:LEU:HD12	1.54	0.64
1:A:406:TRP:CH2	3:C:266:GLU:HB2	2.33	0.64
1:A:1252:GLY:HA2	1:A:1298:ARG:NH2	2.13	0.64
1:A:1370:ARG:NH1	34:V:467:LEU:HA	2.12	0.64
3:C:363:SER:O	3:C:364:SER:OG	2.11	0.64
15:H:25:G:H2'	15:H:26:A:H8	1.62	0.64
28:J:294:HIS:CE1	29:L:227:THR:CB	2.80	0.64
1:A:176:LEU:HD13	1:A:181:ASN:ND2	2.13	0.64
1:A:338:VAL:HG23	3:C:867:PRO:CG	2.24	0.64
1:A:384:VAL:CG1	3:C:331:PHE:CB	2.46	0.64
1:A:393:LEU:HA	3:C:379:LYS:CE	2.18	0.64
1:A:1215:ASN:HB3	1:A:1224:ARG:HD2	1.79	0.64
1:A:1457:HIS:CE1	32:R:424:SER:CA	2.79	0.64
3:C:678:THR:HG21	3:C:683:ASN:HB2	1.76	0.64
14:G:155:U:H4'	14:G:156:U:H5'	1.79	0.64
1:A:1962:THR:HG23	37:Z:524:ARG:CG	2.27	0.63
1:A:2319:LEU:HG	1:A:2320:LEU:N	2.11	0.63
3:C:482:TYR:CE2	3:C:493:PHE:CD2	2.86	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63
23:3:673:VAL:HA	23:3:691:THR:H	1.63	0.63
1:A:175:PRO:HG2	1:A:498:ARG:CZ	2.27	0.63
1:A:366:LYS:H	1:A:366:LYS:CE	2.09	0.63
2:B:12:U:O2'	2:B:13:C:O5'	2.14	0.63
3:C:481:MET:SD	3:C:492:ALA:HB2	2.37	0.63
3:C:596:ASN:HD22	3:C:596:ASN:N	1.96	0.63
13:F:94:C:OP1	28:J:351:ASN:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:152:G:C2	15:H:153:A:C5	2.87	0.63
23:3:524:ILE:HD11	23:3:556:ILE:HD13	1.80	0.63
24:4:75:ASN:OD1	24:4:86:VAL:N	2.31	0.63
1:A:109:PRO:HD3	1:A:630:TRP:CZ2	2.33	0.63
3:C:77:VAL:HG12	33:T:196:LEU:O	1.70	0.63
5:E:119:THR:HG23	5:E:161:ARG:HB3	1.80	0.63
13:F:35:A:H2'	13:F:36:A:C5'	2.28	0.63
23:3:187:MET:HE2	23:3:206:GLN:HB3	1.80	0.63
23:3:931:VAL:N	23:3:936:LYS:O	2.29	0.63
25:5:20:ILE:HG12	25:5:63:VAL:HG22	1.78	0.63
1:A:305:ARG:HD3	3:C:933:PHE:HZ	1.64	0.63
1:A:755:HIS:CD2	31:P:219:PHE:HE2	2.15	0.63
13:F:58:G:H2'	13:F:59:G:C8	2.32	0.63
23:3:86:ARG:HA	23:3:105:GLU:O	1.98	0.63
23:3:174:ASP:OD2	23:3:240:GLY:N	2.31	0.63
23:3:489:GLU:HG2	23:3:748:GLU:HB3	1.80	0.63
35:X:241:GLY:N	35:X:262:TYR:O	2.31	0.63
1:A:44:ARG:HD2	1:A:45:TYR:CZ	2.34	0.63
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.27	0.63
3:C:295:ASP:OD1	3:C:297:ASN:N	2.32	0.63
3:C:350:ASN:CG	3:C:353:THR:HG23	2.19	0.63
3:C:456:GLY:O	3:C:457:VAL:HG22	1.99	0.63
13:F:36:A:C5'	13:F:36:A:H8	2.12	0.63
32:R:132:LEU:HD23	32:R:132:LEU:H	1.63	0.63
1:A:251:ASP:HB3	1:A:337:VAL:CG2	2.25	0.63
1:A:468:LYS:HD3	1:A:469:LYS:H	1.61	0.63
1:A:1852:LEU:HD12	1:A:1853:PRO:HD2	1.80	0.63
23:3:794:SER:OG	23:3:796:ASN:OD1	2.15	0.63
32:R:123:GLU:OE1	32:R:124:VAL:N	2.30	0.63
1:A:97:HIS:CD2	1:A:473:PHE:CZ	2.87	0.63
1:A:1260:VAL:HG21	1:A:1325:LEU:HB3	1.80	0.63
1:A:1787:ARG:NH2	1:A:1804:ASN:O	2.31	0.63
1:A:1820:LYS:HD3	1:A:1914:MET:HE2	1.78	0.63
5:E:178:LEU:HD21	5:E:208:ILE:CD1	2.28	0.63
15:H:47:U:H1'	15:H:48:A:C8	2.34	0.63
21:1:812:PRO:HB2	21:1:813:PRO:HD3	1.81	0.63
25:5:23:ILE:HD12	25:5:89:VAL:HG12	1.81	0.63
1:A:331:TRP:CZ3	3:C:179:VAL:HG22	2.33	0.63
1:A:693:ILE:HG13	1:A:738:MET:SD	2.38	0.63
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.81	0.63
3:C:93:ILE:CD1	33:T:230:ILE:HD13	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:476:CYS:CB	3:C:565:ILE:HB	2.27	0.63
21:1:698:GLN:O	21:1:702:ARG:NH1	2.32	0.63
23:3:399:ASP:OD1	23:3:400:GLU:N	2.32	0.63
23:3:521:PRO:HA	23:3:544:ILE:HG22	1.81	0.63
32:R:67:ILE:HD13	32:R:67:ILE:N	2.13	0.63
1:A:155:LYS:NZ	1:A:624:GLY:O	2.29	0.63
3:C:259:LYS:HE2	3:C:262:ARG:HD3	1.79	0.63
13:F:26:U:C3'	13:F:27:A:H5''	2.29	0.63
13:F:40:U:H2'	13:F:41:A:H8	1.61	0.63
32:R:418:GLN:O	37:Z:606:ALA:HB2	1.97	0.63
1:A:768:ASP:HB2	1:A:771:VAL:HG12	1.79	0.62
3:C:250:ARG:NE	3:C:451:HIS:NE2	2.47	0.62
5:E:265:ARG:H	5:E:272:ARG:HH21	1.47	0.62
15:H:179:C:C2	15:H:180:G:N7	2.67	0.62
32:R:250:LYS:HD3	32:R:251:ILE:N	2.13	0.62
34:V:549:LYS:O	34:V:552:ALA:N	2.32	0.62
37:Z:566:TYR:HB2	37:Z:581:GLY:O	1.98	0.62
1:A:1085:ILE:HG12	1:A:1099:PHE:CE1	2.34	0.62
5:E:251:LEU:HG	5:E:291:CYS:SG	2.39	0.62
1:A:203:VAL:HG21	1:A:237:THR:HG22	1.81	0.62
1:A:312:TYR:CE1	3:C:882:GLY:O	2.52	0.62
1:A:312:TYR:CE1	3:C:882:GLY:HA3	2.28	0.62
3:C:79:THR:HG23	33:T:199:VAL:HB	0.68	0.62
21:1:1010:THR:OG1	21:1:1011:PRO:HD3	1.98	0.62
1:A:395:THR:HG23	3:C:383:GLN:HE22	1.58	0.62
1:A:417:ARG:NH1	2:B:58:U:H5''	2.14	0.62
1:A:755:HIS:ND1	31:P:223:PHE:CD2	2.60	0.62
1:A:1301:ILE:HD11	1:A:1306:LYS:CE	2.25	0.62
3:C:360:ALA:N	3:C:361:PRO:HD3	2.14	0.62
21:1:1257:PRO:HG3	22:2:482:ALA:HB2	1.81	0.62
23:3:553:GLN:NE2	23:3:565:TYR:OH	2.31	0.62
37:Z:566:TYR:CD2	37:Z:584:TRP:CE3	2.88	0.62
1:A:386:PRO:CD	3:C:372:PHE:HE1	2.07	0.62
3:C:132:VAL:HG11	3:C:434:CYS:SG	2.39	0.62
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.32	0.62
23:3:380:GLU:O	23:3:383:ASP:N	2.32	0.62
32:R:250:LYS:HA	32:R:250:LYS:HE3	1.81	0.62
33:T:185:MET:HB3	33:T:186:PRO:HD3	1.81	0.62
1:A:755:HIS:HE1	31:P:223:PHE:CG	2.11	0.62
3:C:259:LYS:HG2	3:C:262:ARG:HD2	1.81	0.62
15:H:182:U:H2'	15:H:183:G:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:273:ARG:O	23:3:386:PHE:HA	2.00	0.62
1:A:361:HIS:CD2	3:C:279:ARG:NH1	2.68	0.62
1:A:393:LEU:HD11	3:C:378:TYR:HB2	1.81	0.62
1:A:414:ARG:HD3	3:C:410:LEU:O	1.99	0.62
1:A:800:TYR:CG	3:C:59:LEU:HD13	2.34	0.62
1:A:2105:ILE:HD13	1:A:2266:ARG:HH22	1.64	0.62
5:E:119:THR:HG21	5:E:161:ARG:HB3	1.72	0.62
23:3:440:HIS:CD2	23:3:733:PRO:CD	2.82	0.62
23:3:567:GLU:OE2	23:3:601:ARG:NE	2.29	0.62
31:P:211:VAL:HG13	33:T:457:GLY:HA3	0.75	0.62
33:T:356:LEU:N	33:T:356:LEU:HD12	2.15	0.62
1:A:282:LEU:C	1:A:282:LEU:HD23	2.20	0.62
5:E:146:ARG:CZ	5:E:148:LYS:HE3	2.27	0.62
21:1:847:ALA:O	21:1:851:SER:HB3	1.99	0.62
23:3:440:HIS:CE1	23:3:720:TRP:CH2	2.87	0.62
37:Z:600:ARG:HH11	37:Z:600:ARG:CG	2.13	0.62
1:A:155:LYS:HD2	1:A:626:GLY:O	2.00	0.62
1:A:303:ILE:HG21	3:C:933:PHE:CE1	2.34	0.62
1:A:344:ASP:OD1	1:A:347:LEU:HD12	2.00	0.62
1:A:762:ARG:NH2	31:P:226:LYS:HZ1	1.79	0.62
1:A:2328:ALA:HB3	4:D:788:GLY:CA	2.30	0.62
15:H:154:C:H2'	15:H:155:C:H6	1.63	0.62
15:H:161:U:H6	15:H:161:U:O5'	1.83	0.62
21:1:664:GLY:HA2	21:1:667:ILE:HD12	1.80	0.62
21:1:696:ASP:OD1	21:1:697:GLU:N	2.33	0.62
21:1:1052:ALA:HA	21:1:1055:TRP:HD1	1.64	0.62
22:2:612:GLU:O	22:2:615:ILE:N	2.33	0.62
23:3:642:ILE:O	23:3:703:ARG:NH2	2.32	0.62
28:J:406:PHE:CE2	28:J:411:MET:CE	2.83	0.62
37:Z:573:PRO:HD2	37:Z:573:PRO:O	1.99	0.62
1:A:141:ILE:HG12	1:A:426:LEU:CD2	2.30	0.62
3:C:230:ASP:OD1	3:C:259:LYS:HB3	2.00	0.62
4:D:754:GLU:CB	23:3:662:PHE:CE1	2.83	0.62
25:5:53:THR:OG1	25:5:56:THR:OG1	2.14	0.62
1:A:256:TYR:CD1	3:C:888:ARG:CZ	2.83	0.61
1:A:329:LEU:CD1	3:C:173:THR:HG23	2.30	0.61
1:A:835:ASP:OD1	1:A:836:THR:N	2.32	0.61
5:E:277:PHE:HE2	5:E:300:ILE:HD12	1.63	0.61
23:3:811:THR:OG1	23:3:884:GLN:OE1	2.14	0.61
23:3:1004:ASP:OD1	23:3:1005:VAL:N	2.33	0.61
31:P:194:PHE:O	31:P:196:ASN:N	4.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:CD2	1:A:455:VAL:HG22	2.30	0.61
1:A:2068:SER:HB2	1:A:2072:GLU:HB2	1.81	0.61
3:C:141:GLY:C	3:C:258:ASN:ND2	2.53	0.61
13:F:24:A:C2	13:F:26:U:C2	2.88	0.61
14:G:13:C:H2'	14:G:14:A:C8	2.36	0.61
23:3:786:ARG:NH1	23:3:802:THR:O	2.33	0.61
28:J:262:ARG:HD3	29:L:220:PRO:HG2	1.82	0.61
37:Z:597:ARG:HH12	37:Z:601:LEU:HD12	1.66	0.61
1:A:783:TYR:HB2	31:P:228:ILE:CG1	2.26	0.61
13:F:38:G:P	13:F:38:G:C8	2.94	0.61
21:1:866:LYS:HG3	21:1:909:VAL:HG11	1.82	0.61
23:3:317:THR:HA	23:3:322:VAL:HA	1.81	0.61
1:A:203:VAL:CG2	1:A:237:THR:HB	2.30	0.61
1:A:630:TRP:O	1:A:631:ALA:C	2.37	0.61
1:A:1900:GLU:HG2	37:Z:521:PRO:HG3	1.82	0.61
14:G:146:C:H1'	15:H:33:G:N2	2.15	0.61
15:H:165:A:H8	15:H:165:A:O5'	1.84	0.61
32:R:55:LEU:O	32:R:73:PRO:O	2.19	0.61
35:X:343:ARG:HB3	35:X:378:GLU:HG3	1.83	0.61
37:Z:566:TYR:CD1	37:Z:567:SER:N	2.69	0.61
1:A:2106:LEU:HD12	1:A:2107:PRO:HD2	1.83	0.61
3:C:679:PRO:HD3	3:C:811:THR:OG1	1.99	0.61
3:C:750:LEU:C	3:C:750:LEU:HD12	2.21	0.61
15:H:56:A:H61	22:2:505:CYS:HA	1.66	0.61
15:H:68:G:H2'	15:H:69:U:C6	2.35	0.61
21:1:648:LEU:O	21:1:651:VAL:N	2.33	0.61
23:3:288:VAL:HG23	23:3:289:CYS:H	1.65	0.61
23:3:994:GLN:NE2	23:3:1036:ALA:O	2.33	0.61
33:T:327:SER:O	33:T:357:TRP:CH2	2.53	0.61
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.48	0.61
1:A:530:LEU:H	30:M:198:GLN:CD	1.96	0.61
3:C:64:LYS:HZ2	31:P:206:LYS:HG3	1.63	0.61
3:C:97:VAL:HG13	31:P:47:THR:OG1	2.00	0.61
3:C:140:HIS:CG	3:C:230:ASP:H	2.18	0.61
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.82	0.61
23:3:1191:LYS:NZ	23:3:1195:GLU:OE2	2.33	0.61
1:A:349:ALA:HB1	1:A:399:ALA:HB2	1.78	0.61
2:B:43:U:H3	14:G:-4:A:H2	1.45	0.61
3:C:471:ASP:N	3:C:499:GLY:HA2	2.15	0.61
3:C:495:ARG:HD2	3:C:497:LEU:HD23	1.81	0.61
21:1:720:GLY:N	23:3:216:GLY:O	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:185:GLY:O	32:R:186:VAL:HG22	2.00	0.61
33:T:339:GLN:NE2	33:T:342:GLU:O	2.34	0.61
33:T:355:ARG:C	33:T:356:LEU:HD12	2.21	0.61
34:V:537:HIS:HA	34:V:578:SER:CB	2.31	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CD1	2.88	0.61
1:A:283:VAL:HG13	1:A:284:ARG:H	1.64	0.61
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.33	0.61
3:C:151:GLU:OE1	3:C:417:ARG:NH1	2.34	0.61
3:C:470:PRO:HA	3:C:499:GLY:CA	2.29	0.61
3:C:675:PHE:HD1	3:C:675:PHE:H	1.47	0.61
14:G:8:C:H2'	14:G:9:C:C6	2.35	0.61
15:H:106:G:N2	15:H:107:A:C6	2.67	0.61
15:H:142:C:C2'	15:H:143:A:H5'	2.30	0.61
15:H:157:G:H5''	15:H:157:G:H8	1.65	0.61
28:J:408:ASP:OD1	28:J:442:ARG:HG2	2.01	0.61
3:C:478:THR:OG1	3:C:563:ALA:O	2.14	0.61
3:C:705:VAL:HG22	3:C:705:VAL:O	2.00	0.61
15:H:153:A:N6	15:H:177:A:H2	1.98	0.61
23:3:452:LEU:HB3	23:3:478:PHE:HE1	1.66	0.61
29:L:74:LEU:HD23	29:L:77:LEU:HD12	1.83	0.61
36:Y:87:GLN:O	36:Y:90:THR:N	2.33	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CG	2.89	0.61
1:A:402:ILE:CG1	3:C:385:VAL:HG21	2.25	0.61
5:E:108:HIS:CE1	5:E:128:SER:HB2	2.35	0.61
13:F:6:C:OP2	13:F:6:C:H4'	1.99	0.61
21:1:1203:GLY:O	23:3:1171:LYS:NZ	2.34	0.61
23:3:226:GLU:HG3	23:3:261:PHE:HZ	1.65	0.61
24:4:71:ILE:HD11	24:4:88:LYS:HB3	1.83	0.61
33:T:349:SER:OG	33:T:351:ASP:OD1	2.18	0.61
1:A:122:ILE:N	1:A:481:PHE:O	2.34	0.60
1:A:1405:LEU:HA	32:R:415:LEU:HD21	1.78	0.60
3:C:133:THR:O	3:C:226:VAL:HB	2.01	0.60
3:C:135:CYS:O	3:C:228:PHE:N	2.28	0.60
3:C:449:ILE:HD11	3:C:466:SER:CA	2.31	0.60
3:C:710:ASN:O	3:C:713:LYS:N	2.31	0.60
15:H:143:A:H2'	15:H:144:C:C6	2.35	0.60
21:1:1293:ASN:HB3	27:7:76:CYS:HB3	1.83	0.60
28:J:406:PHE:CG	28:J:411:MET:HE3	2.36	0.60
37:Z:524:ARG:NE	37:Z:524:ARG:O	2.34	0.60
1:A:121:HIS:CE1	1:A:481:PHE:CB	2.68	0.60
1:A:800:TYR:CD2	3:C:59:LEU:HD13	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1457:HIS:CE1	1:A:1459:ARG:CB	2.83	0.60
13:F:26:U:O2'	13:F:27:A:OP1	2.18	0.60
21:1:918:VAL:HG12	21:1:961:VAL:HG21	1.83	0.60
23:3:505:THR:HG21	23:3:508:CYS:SG	2.40	0.60
28:J:338:GLU:O	32:R:116:TYR:CD1	2.54	0.60
37:Z:491:ASP:O	37:Z:495:ALA:CB	2.48	0.60
1:A:151:MET:SD	1:A:628:GLY:C	2.80	0.60
1:A:387:PHE:CZ	3:C:330:THR:HB	2.35	0.60
28:J:291:GLN:OE1	29:L:230:GLU:HG3	2.01	0.60
33:T:339:GLN:HG2	33:T:340:ALA:N	2.16	0.60
37:Z:491:ASP:O	37:Z:495:ALA:HB2	2.01	0.60
1:A:82:ARG:HB3	1:A:83:HIS:ND1	2.17	0.60
1:A:301:LYS:HG2	3:C:940:ARG:CA	2.31	0.60
14:G:13:C:H2'	14:G:14:A:H8	1.66	0.60
23:3:441:GLY:O	23:3:775:ASN:HB2	2.00	0.60
24:4:31:GLU:O	24:4:35:GLN:HG2	2.02	0.60
33:T:292:TYR:CE2	33:T:308:ARG:HG3	2.36	0.60
1:A:351:TYR:HA	3:C:270:PRO:HG3	1.84	0.60
1:A:461:HIS:CD2	2:B:26:A:N6	2.68	0.60
1:A:664:HIS:HE1	1:A:668:VAL:CG2	2.04	0.60
1:A:1827:TRP:HH2	1:A:1837:ALA:HB2	1.67	0.60
1:A:2073:TRP:CZ3	1:A:2310:ARG:HG2	2.36	0.60
5:E:178:LEU:HD21	5:E:208:ILE:HD13	1.82	0.60
23:3:833:GLU:HA	23:3:834:LEU:HB2	1.84	0.60
29:L:233:GLN:OE1	29:L:233:GLN:HA	2.01	0.60
32:R:171:LEU:CD1	32:R:201:GLU:CD	2.70	0.60
1:A:392:PRO:O	3:C:379:LYS:HG2	2.01	0.60
1:A:1447:VAL:HG11	1:A:1449:LYS:HE2	1.82	0.60
3:C:86:THR:HG22	33:T:238:LEU:O	2.01	0.60
3:C:452:THR:HG22	3:C:577:PHE:CG	2.37	0.60
3:C:706:GLN:NE2	3:C:708:THR:OG1	2.35	0.60
34:V:483:GLU:O	34:V:486:THR:CB	2.49	0.60
1:A:344:ASP:OD1	1:A:347:LEU:CD1	2.49	0.60
1:A:924:GLN:HE22	1:A:1439:ARG:CZ	2.14	0.60
3:C:221:ILE:HD11	3:C:479:THR:HG1	1.65	0.60
23:3:898:ASN:OD1	23:3:899:THR:N	2.34	0.60
1:A:384:VAL:HG12	3:C:331:PHE:HB3	0.71	0.60
1:A:705:LYS:HE2	32:R:251:ILE:HB	1.82	0.60
1:A:960:ASN:ND2	1:A:1225:THR:OG1	2.32	0.60
1:A:2298:LEU:CD1	4:D:1265:GLN:CB	2.79	0.60
3:C:77:VAL:HG21	33:T:196:LEU:HD23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:148:CYS:HA	3:C:417:ARG:NH2	2.16	0.60
23:3:325:ILE:O	23:3:375:SER:N	2.35	0.60
33:T:267:ASP:O	33:T:268:LYS:CB	2.47	0.60
33:T:455:GLN:HG2	33:T:456:PRO:HD3	1.83	0.60
1:A:661:GLU:HG3	32:R:210:PRO:CB	2.32	0.60
3:C:140:HIS:HA	3:C:230:ASP:HB2	1.83	0.60
3:C:567:GLU:OE2	3:C:570:GLY:HA3	2.02	0.60
13:F:7:G:H5'	13:F:7:G:H8	1.66	0.60
13:F:37:C:H41	14:G:5:G:P	2.24	0.60
15:H:83:A:C2	15:H:84:C:C2	2.90	0.60
29:L:77:LEU:HD22	32:R:289:ALA:HA	1.84	0.60
33:T:342:GLU:HB3	33:T:343:PRO:HD3	1.83	0.60
37:Z:563:ARG:HH21	37:Z:563:ARG:CG	2.14	0.60
1:A:1384:ARG:HH21	1:A:1414:ARG:HH12	1.50	0.60
1:A:1426:ASP:OD2	32:R:421:GLY:HA3	2.01	0.60
3:C:79:THR:CG2	33:T:199:VAL:CB	2.37	0.60
3:C:82:GLN:HB2	33:T:231:TRP:CZ3	2.36	0.60
3:C:94:ILE:CD1	31:P:44:ARG:NH2	2.65	0.60
3:C:443:VAL:O	3:C:447:PRO:HD3	2.02	0.60
3:C:678:THR:CG2	3:C:683:ASN:CB	2.79	0.60
21:1:862:GLU:OE1	21:1:904:THR:OG1	2.19	0.60
23:3:457:ASN:ND2	23:3:478:PHE:O	2.35	0.60
32:R:106:GLN:HG2	32:R:110:LYS:CE	2.28	0.60
33:T:185:MET:SD	33:T:442:ARG:NH1	2.71	0.60
23:3:968:ARG:HD3	23:3:979:ARG:HD3	1.84	0.59
1:A:329:LEU:HD13	3:C:173:THR:HG23	1.82	0.59
3:C:73:TYR:CD2	33:T:199:VAL:HG21	2.36	0.59
3:C:73:TYR:CZ	33:T:487:LYS:HE3	2.37	0.59
3:C:669:THR:HG22	3:C:690:GLU:HB3	1.84	0.59
28:J:406:PHE:CE2	28:J:411:MET:HE3	2.36	0.59
31:P:72:ARG:HB2	31:P:72:ARG:HH11	1.66	0.59
33:T:455:GLN:HG2	33:T:456:PRO:CD	2.32	0.59
1:A:718:ARG:HE	32:R:259:LYS:HE3	1.67	0.59
3:C:186:VAL:HG22	3:C:535:ALA:HA	1.85	0.59
23:3:883:GLU:HG3	23:3:884:GLN:H	1.66	0.59
32:R:104:GLN:NE2	32:R:105:GLY:N	2.50	0.59
37:Z:574:ASN:O	37:Z:575:ARG:C	2.40	0.59
5:E:233:GLY:O	5:E:260:ARG:NH2	2.35	0.59
14:G:22:C:O2'	14:G:23:U:P	2.60	0.59
28:J:493:ALA:HB1	28:J:499:ARG:CB	2.32	0.59
32:R:124:VAL:HG22	32:R:125:MET:N	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:420:LYS:HA	32:R:420:LYS:CE	2.12	0.59
1:A:398:THR:HG23	3:C:382:ALA:CB	2.32	0.59
1:A:944:ASP:OD2	1:A:1435:GLY:N	2.34	0.59
1:A:1262:LYS:CG	32:R:431:ASP:CB	2.69	0.59
1:A:1405:LEU:HA	32:R:415:LEU:HD22	1.84	0.59
1:A:1962:THR:O	37:Z:524:ARG:HG3	2.02	0.59
3:C:298:LEU:HD13	3:C:298:LEU:N	2.18	0.59
15:H:56:A:H2'	15:H:57:A:C8	2.38	0.59
23:3:895:ARG:NH2	23:3:901:GLU:OE1	2.34	0.59
23:3:1040:ASP:OD1	23:3:1043:THR:N	2.35	0.59
34:V:514:PHE:O	34:V:521:TYR:CB	2.51	0.59
1:A:181:ASN:N	1:A:181:ASN:OD1	2.35	0.59
1:A:435:CYS:HB2	3:C:892:GLN:CD	2.22	0.59
1:A:692:ASP:O	1:A:696:MET:CB	2.50	0.59
1:A:942:PRO:HB2	1:A:1438:VAL:HG12	1.84	0.59
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.35	0.59
1:A:1363:GLN:HG2	1:A:1364:LEU:H	1.66	0.59
3:C:66:TYR:HE2	31:P:211:VAL:HG11	1.67	0.59
3:C:91:GLU:OE1	3:C:91:GLU:HA	2.01	0.59
3:C:145:PHE:CB	3:C:312:SER:CB	2.65	0.59
13:F:36:A:C5'	13:F:36:A:C8	2.85	0.59
15:H:112:G:H2'	15:H:113:G:H8	1.65	0.59
21:1:936:VAL:O	21:1:940:LEU:HB2	2.03	0.59
21:1:1125:PRO:HA	21:1:1128:VAL:HG22	1.84	0.59
23:3:740:GLU:HB2	23:3:757:ILE:HD12	1.83	0.59
33:T:345:ILE:HB	33:T:357:TRP:HB2	1.85	0.59
1:A:86:ARG:HG3	1:A:87:VAL:N	2.17	0.59
1:A:132:ILE:HD13	2:B:57:G:OP1	2.02	0.59
1:A:367:SER:HB3	3:C:299:ILE:HD12	1.85	0.59
1:A:1405:LEU:CB	32:R:415:LEU:HD22	2.33	0.59
1:A:2095:ASP:OD2	1:A:2258:ARG:NE	2.36	0.59
3:C:149:LEU:CD1	3:C:427:PHE:CB	2.80	0.59
23:3:224:TYR:HB3	23:3:261:PHE:HE2	1.66	0.59
23:3:1015:LYS:HE2	23:3:1065:GLU:HG2	1.85	0.59
28:J:225:LEU:CD2	29:L:211:ASN:HB2	2.20	0.59
32:R:90:VAL:CG1	32:R:94:GLY:O	2.50	0.59
32:R:110:LYS:HD2	32:R:110:LYS:C	2.23	0.59
36:Y:88:ARG:HH11	37:Z:576:PHE:HB3	1.68	0.59
1:A:44:ARG:CG	1:A:45:TYR:CD2	2.85	0.59
1:A:417:ARG:NH1	2:B:58:U:C4'	2.65	0.59
1:A:569:VAL:O	1:A:570:ASP:CB	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:GLN:NE2	1:A:890:ALA:O	2.19	0.59
3:C:227:LEU:O	3:C:255:VAL:HA	2.03	0.59
23:3:613:THR:HG22	23:3:632:ALA:HA	1.84	0.59
23:3:784:THR:HB	23:3:786:ARG:HH12	1.67	0.59
23:3:1027:ASP:OD1	23:3:1028:THR:N	2.35	0.59
26:6:56:GLY:O	26:6:65:GLY:N	2.21	0.59
32:R:420:LYS:HG2	32:R:423:ASP:OD1	2.02	0.59
32:R:421:GLY:O	32:R:423:ASP:N	2.35	0.59
1:A:122:ILE:HD13	1:A:483:GLN:CG	2.32	0.59
1:A:303:ILE:HG21	3:C:933:PHE:CD1	2.38	0.59
2:B:44:A:C2	14:G:-5:G:C6	2.89	0.59
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.35	0.59
3:C:497:LEU:HD11	3:C:577:PHE:CZ	2.32	0.59
21:1:1223:SER:HB2	21:1:1226:VAL:HG12	1.83	0.59
3:C:145:PHE:CE1	3:C:427:PHE:CE1	2.91	0.59
3:C:465:MET:CE	3:C:475:MET:CG	2.70	0.59
3:C:736:GLY:HA2	3:C:770:PHE:CE2	2.38	0.59
13:F:45:A:H1'	13:F:73:A:C2	2.38	0.59
21:1:522:LYS:HD3	21:1:526:PHE:CZ	2.38	0.59
23:3:22:PHE:HD2	23:3:29:GLU:HB2	1.68	0.59
23:3:587:VAL:HG11	23:3:590:MET:HG3	1.85	0.59
28:J:259:GLN:HE22	29:L:220:PRO:CG	2.15	0.59
32:R:125:MET:CE	32:R:131:ASP:OD1	2.51	0.59
32:R:148:ARG:HG3	32:R:148:ARG:HH11	1.68	0.59
1:A:44:ARG:HG3	1:A:45:TYR:CD2	2.37	0.58
1:A:480:LYS:CD	32:R:203:GLN:OE1	2.50	0.58
1:A:723:ASN:HB2	1:A:785:LYS:HG2	1.83	0.58
1:A:1370:ARG:HH11	34:V:467:LEU:C	2.06	0.58
3:C:69:ALA:CA	33:T:456:PRO:HG3	2.28	0.58
3:C:359:LYS:HE3	3:C:359:LYS:O	2.02	0.58
13:F:35:A:O2'	13:F:36:A:OP1	2.21	0.58
21:1:1278:ASP:OD2	23:3:112:CYS:N	2.36	0.58
22:2:648:LEU:HD11	22:2:650:ILE:HG13	1.85	0.58
23:3:336:ALA:HA	23:3:351:SER:HA	1.85	0.58
23:3:463:ARG:HB2	23:3:510:LEU:HD22	1.85	0.58
28:J:339:TRP:CG	32:R:116:TYR:HD2	2.21	0.58
33:T:185:MET:SD	33:T:442:ARG:NH2	2.75	0.58
36:Y:52:ILE:HA	36:Y:55:VAL:HG22	1.84	0.58
1:A:695:ASP:CG	33:T:374:SER:OG	2.41	0.58
1:A:2073:TRP:CD1	1:A:2074:ARG:N	2.71	0.58
1:A:2073:TRP:HD1	1:A:2074:ARG:HD2	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2268:LEU:HD22	4:D:1261:PRO:O	1.96	0.58
3:C:78:GLU:CD	33:T:198:ARG:HE	2.07	0.58
3:C:474:LEU:HD11	3:C:501:ILE:HG12	1.85	0.58
21:1:982:LEU:HD11	21:1:997:LEU:HD11	1.83	0.58
21:1:1147:VAL:O	21:1:1150:SER:OG	2.17	0.58
23:3:417:ASN:OD1	23:3:418:GLU:N	2.36	0.58
23:3:673:VAL:HG12	23:3:690:ARG:HA	1.84	0.58
23:3:797:LEU:HG	23:3:871:PRO:HG3	1.85	0.58
23:3:903:TRP:HB3	23:3:930:LEU:HD23	1.84	0.58
32:R:433:ILE:CD1	32:R:435:ASN:ND2	2.67	0.58
36:Y:86:ASP:CB	37:Z:502:ALA:HB3	2.33	0.58
1:A:32:GLU:OE2	1:A:36:LYS:HE3	2.03	0.58
1:A:305:ARG:HD3	3:C:933:PHE:CE1	2.38	0.58
1:A:316:PHE:HE1	3:C:635:LEU:HA	1.67	0.58
3:C:133:THR:O	3:C:226:VAL:CA	2.51	0.58
5:E:87:ASP:O	5:E:88:ARG:HG3	2.04	0.58
21:1:773:LEU:HD21	21:1:792:VAL:HG22	1.84	0.58
23:3:304:GLN:NE2	23:3:335:VAL:HA	2.18	0.58
23:3:638:GLU:H	23:3:669:LEU:HA	1.68	0.58
31:P:210:PHE:HD2	33:T:455:GLN:CD	2.05	0.58
32:R:233:HIS:CD2	32:R:233:HIS:H	2.22	0.58
34:V:497:CYS:CB	34:V:507:PHE:CB	2.81	0.58
1:A:480:LYS:CE	32:R:203:GLN:OE1	2.50	0.58
1:A:657:ALA:HA	32:R:210:PRO:HG2	1.84	0.58
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.18	0.58
3:C:679:PRO:HD2	3:C:807:GLN:CB	2.10	0.58
23:3:440:HIS:O	23:3:718:ARG:NH2	2.36	0.58
28:J:338:GLU:O	32:R:116:TYR:CG	2.57	0.58
1:A:388:LEU:HD11	3:C:399:LEU:CG	2.31	0.58
1:A:1367:ASN:OD1	1:A:1368:LEU:N	2.37	0.58
1:A:1900:GLU:OE1	37:Z:522:LEU:HB3	2.00	0.58
3:C:750:LEU:O	3:C:750:LEU:HD12	2.03	0.58
5:E:263:ASP:HB3	5:E:274:VAL:HG21	1.84	0.58
37:Z:566:TYR:CD2	37:Z:584:TRP:HE3	2.20	0.58
1:A:60:ASP:OD1	1:A:60:ASP:N	2.36	0.58
1:A:229:GLN:HA	1:A:415:SER:HA	1.85	0.58
1:A:357:ASN:HB2	3:C:863:ILE:O	2.04	0.58
1:A:1863:VAL:HG11	1:A:1868:MET:HB2	1.84	0.58
1:A:2310:ARG:NH1	1:A:2314:PHE:HE1	2.02	0.58
5:E:87:ASP:O	5:E:88:ARG:CB	2.51	0.58
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4:18:GLY:H	24:4:85:ARG:HB2	1.67	0.58
31:P:35:LEU:HB3	31:P:36:PRO:HD2	1.86	0.58
34:V:609:GLN:O	34:V:612:PHE:N	2.36	0.58
1:A:303:ILE:CG2	3:C:933:PHE:CD1	2.87	0.58
1:A:329:LEU:HB3	3:C:177:ARG:CZ	2.33	0.58
1:A:798:GLY:HA2	32:R:288:PHE:CE2	2.39	0.58
1:A:1962:THR:O	37:Z:524:ARG:HG2	2.03	0.58
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.03	0.58
3:C:509:VAL:O	3:C:510:LEU:HD23	2.04	0.58
15:H:147:G:H2'	15:H:148:C:C6	2.38	0.58
30:M:196:ASP:O	30:M:198:GLN:N	2.36	0.58
1:A:76:MET:SD	1:A:88:TYR:CD2	2.95	0.58
1:A:280:GLU:OE2	1:A:281:PRO:HD2	2.03	0.58
1:A:392:PRO:CA	3:C:379:LYS:HE2	2.32	0.58
1:A:417:ARG:NH2	2:B:58:U:OP1	2.37	0.58
1:A:1757:GLU:OE1	32:R:451:ILE:CG1	2.36	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CG	2.66	0.58
15:H:80:A:C2	15:H:81:G:C5	2.92	0.58
23:3:461:THR:HA	23:3:473:TYR:O	2.03	0.58
25:5:24:ARG:HG2	25:5:59:THR:HG22	1.86	0.58
31:P:188:TRP:C	31:P:190:ASP:N	2.52	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CB	2.67	0.58
14:G:141:C:H2'	14:G:142:U:H6	1.69	0.58
21:1:415:LEU:O	25:5:36:TYR:OH	2.21	0.58
21:1:1109:ARG:NH2	21:1:1142:ASN:HB2	2.19	0.58
21:1:1165:TYR:HE1	22:2:575:PHE:CD1	2.21	0.58
23:3:878:ASP:OD1	23:3:879:LEU:N	2.37	0.58
32:R:124:VAL:HG22	32:R:126:ASN:H	1.68	0.58
37:Z:566:TYR:HE2	37:Z:584:TRP:CZ3	1.92	0.58
1:A:378:PHE:HZ	3:C:335:ASN:CB	2.16	0.58
1:A:593:ARG:HH22	1:A:1551:PHE:CB	2.17	0.58
3:C:573:GLU:N	3:C:573:GLU:OE1	2.37	0.58
23:3:8:LEU:HD23	23:3:774:PHE:HZ	1.68	0.58
23:3:753:GLY:CA	23:3:765:LEU:O	2.51	0.58
32:R:125:MET:HE3	32:R:131:ASP:OD1	2.03	0.58
32:R:171:LEU:HD23	32:R:171:LEU:O	2.03	0.58
1:A:121:HIS:ND1	1:A:481:PHE:O	2.36	0.57
1:A:301:LYS:HG2	3:C:940:ARG:HA	1.85	0.57
3:C:145:PHE:CD1	3:C:312:SER:HB3	2.39	0.57
5:E:165:GLN:HG3	5:E:181:ILE:HD11	1.85	0.57
32:R:189:ASN:HD21	32:R:195:ARG:HH22	1.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:415:LEU:C	32:R:417:ASN:H	2.05	0.57
33:T:399:LYS:HG2	33:T:406:ILE:CD1	2.31	0.57
5:E:277:PHE:CE2	5:E:300:ILE:CD1	2.85	0.57
13:F:39:A:N6	14:G:8:C:H42	2.02	0.57
14:G:12:G:N2	14:G:13:C:O4'	2.38	0.57
23:3:440:HIS:CD2	23:3:733:PRO:HD2	2.39	0.57
23:3:781:LEU:HB3	23:3:801:GLU:OE2	2.04	0.57
31:P:188:TRP:O	31:P:189:ASP:C	2.42	0.57
1:A:152:ARG:HH11	1:A:152:ARG:CG	2.16	0.57
1:A:224:THR:CG2	2:B:13:C:OP2	2.52	0.57
1:A:384:VAL:HG13	3:C:332:GLY:H	1.67	0.57
3:C:749:THR:OG1	3:C:752:SER:HB2	2.04	0.57
35:X:285:ARG:NH1	35:X:304:ALA:O	2.35	0.57
1:A:82:ARG:NH1	14:G:16:G:O6	2.37	0.57
1:A:322:ASN:OD1	3:C:655:VAL:N	2.38	0.57
1:A:535:ARG:CZ	1:A:535:ARG:HB3	2.33	0.57
1:A:800:TYR:HB3	3:C:59:LEU:CD1	2.34	0.57
3:C:617:LEU:HD11	3:C:629:ILE:HG23	1.87	0.57
23:3:306:GLU:OE2	27:7:63:ARG:HG3	2.03	0.57
23:3:1050:PHE:HB3	23:3:1167:TYR:CE2	2.38	0.57
29:L:73:HIS:O	29:L:77:LEU:HG	2.04	0.57
32:R:171:LEU:HD12	32:R:201:GLU:CD	2.25	0.57
1:A:50:LYS:O	1:A:51:PHE:C	2.43	0.57
1:A:1771:LEU:HD11	1:A:1777:ILE:HG21	1.86	0.57
3:C:79:THR:HG23	33:T:199:VAL:CG1	2.27	0.57
21:1:850:ILE:O	21:1:854:VAL:HG23	2.04	0.57
23:3:791:HIS:CE1	23:3:934:GLY:HA3	2.39	0.57
32:R:55:LEU:CB	32:R:73:PRO:O	2.53	0.57
1:A:785:LYS:CE	31:P:215:LEU:CD1	2.78	0.57
3:C:93:ILE:O	3:C:94:ILE:HB	2.04	0.57
3:C:572:GLU:O	3:C:573:GLU:HB2	2.04	0.57
3:C:669:THR:CG2	3:C:690:GLU:OE1	2.52	0.57
14:G:137:C:N4	15:H:40:C:H42	1.99	0.57
23:3:211:TYR:CE1	23:3:222:ARG:HG2	2.40	0.57
23:3:429:ARG:NH1	27:7:58:ASN:OD1	2.38	0.57
23:3:635:ALA:H	23:3:669:LEU:HD21	1.70	0.57
31:P:73:GLU:O	31:P:76:ARG:HG2	2.04	0.57
31:P:188:TRP:N	31:P:188:TRP:CE3	2.73	0.57
1:A:226:GLN:OE1	1:A:417:ARG:NE	2.31	0.57
1:A:356:ILE:HG22	1:A:357:ASN:N	2.20	0.57
1:A:461:HIS:NE2	2:B:26:A:N6	2.49	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:745:ALA:HB2	33:T:206:TRP:CZ2	2.40	0.57
1:A:783:TYR:CG	31:P:228:ILE:HG12	2.39	0.57
2:B:20:G:O6	2:B:24:G:OP1	2.21	0.57
3:C:140:HIS:HE2	3:C:233:GLU:HG3	1.68	0.57
15:H:166:G:OP2	15:H:166:G:N2	2.27	0.57
29:L:33:ARG:O	29:L:36:SER:OG	2.20	0.57
31:P:31:SER:N	31:P:34:ASP:OD2	2.37	0.57
34:V:483:GLU:O	34:V:486:THR:N	2.33	0.57
1:A:71:ARG:NH1	1:A:177:ASP:OD2	2.32	0.57
1:A:282:LEU:HD23	1:A:282:LEU:O	2.05	0.57
1:A:705:LYS:CG	32:R:251:ILE:HB	2.27	0.57
1:A:1370:ARG:NH1	34:V:467:LEU:CA	2.64	0.57
1:A:2153:THR:HG22	1:A:2154:HIS:H	1.70	0.57
3:C:140:HIS:CE1	3:C:233:GLU:CB	2.83	0.57
3:C:487:GLY:HA3	3:C:489:GLN:OE1	2.05	0.57
3:C:490:PHE:HZ	3:C:612:LYS:HD2	1.69	0.57
3:C:511:GLY:O	3:C:576:ILE:HD12	2.02	0.57
15:H:148:C:O5'	15:H:148:C:H6	1.87	0.57
21:1:1109:ARG:HH22	21:1:1142:ASN:HB2	1.69	0.57
21:1:1258:ALA:HB3	21:1:1261:VAL:HG12	1.86	0.57
23:3:184:CYS:SG	23:3:209:THR:OG1	2.56	0.57
23:3:275:ARG:HE	23:3:386:PHE:HD2	1.51	0.57
32:R:434:TYR:CD2	32:R:435:ASN:N	2.73	0.57
34:V:489:LEU:O	34:V:492:MET:CB	2.53	0.57
1:A:178:TYR:CD2	1:A:491:GLU:HB2	2.40	0.57
1:A:692:ASP:CA	33:T:376:ARG:NH2	2.53	0.57
1:A:705:LYS:CG	32:R:251:ILE:CD1	2.70	0.57
1:A:1757:GLU:HG3	32:R:451:ILE:HG13	1.87	0.57
5:E:310:TYR:CE1	5:E:322:LYS:CD	2.86	0.57
15:H:152:G:N2	15:H:153:A:C5	2.73	0.57
21:1:1098:LEU:HD13	21:1:1135:GLU:HG3	1.85	0.57
21:1:1126:PHE:CE2	22:2:572:HIS:HA	2.39	0.57
28:J:224:LYS:HE2	28:J:255:LEU:HD13	1.85	0.57
37:Z:525:TYR:CD1	37:Z:526:ILE:N	2.73	0.57
1:A:249:LEU:HD22	1:A:254:TYR:HB2	1.86	0.57
1:A:250:VAL:HG23	1:A:337:VAL:CB	2.32	0.57
1:A:299:ILE:HD11	3:C:920:PRO:C	2.25	0.57
1:A:434:HIS:CE1	1:A:435:CYS:SG	2.98	0.57
1:A:570:ASP:OD1	1:A:571:ALA:N	2.38	0.57
1:A:832:TYR:CE2	1:A:834:HIS:HB2	2.40	0.57
3:C:508:LYS:HE3	3:C:566:THR:CG2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:807:LYS:HA	21:1:811:LEU:HD12	1.87	0.57
21:1:942:ASN:HD22	21:1:947:VAL:HG11	1.70	0.57
23:3:442:LEU:CD1	23:3:733:PRO:O	2.50	0.57
33:T:347:THR:CG2	33:T:357:TRP:HE1	2.18	0.57
37:Z:611:ALA:O	37:Z:614:TRP:HB3	2.05	0.57
1:A:32:GLU:CG	1:A:36:LYS:HE3	2.35	0.56
1:A:393:LEU:CD1	3:C:375:GLU:O	2.53	0.56
1:A:464:PRO:O	1:A:465:LYS:HB3	2.05	0.56
3:C:261:ASP:OD1	41:C:1500:GTP:C6	2.57	0.56
3:C:456:GLY:C	3:C:457:VAL:HG13	2.25	0.56
28:J:270:ASP:OD2	32:R:222:PRO:CB	2.52	0.56
33:T:306:CYS:SG	33:T:336:VAL:CG1	2.93	0.56
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.41	0.56
1:A:378:PHE:C	1:A:379:GLU:HG2	2.25	0.56
1:A:385:GLU:HB3	1:A:386:PRO:HD2	1.86	0.56
1:A:790:ARG:NE	1:A:986:GLU:OE2	2.38	0.56
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.37	0.56
1:A:1252:GLY:HA2	1:A:1298:ARG:HH21	1.69	0.56
13:F:57:U:H2'	13:F:58:G:H8	1.69	0.56
14:G:7:G:H2'	14:G:8:C:C6	2.40	0.56
15:H:78:C:HO2'	15:H:79:G:H5'	1.70	0.56
15:H:141:C:C2	15:H:142:C:C5	2.94	0.56
23:3:327:LEU:O	23:3:373:PHE:HB2	2.05	0.56
23:3:478:PHE:O	23:3:504:PRO:HB3	2.05	0.56
28:J:273:TYR:CG	32:R:228:PRO:CG	2.88	0.56
32:R:409:VAL:O	32:R:410:GLN:HG2	2.05	0.56
37:Z:524:ARG:HB3	37:Z:524:ARG:CZ	2.35	0.56
1:A:296:PHE:CG	3:C:656:ALA:HB2	2.40	0.56
1:A:587:GLN:O	1:A:587:GLN:HG2	2.04	0.56
1:A:593:ARG:HH22	1:A:1551:PHE:HB3	1.71	0.56
1:A:1386:TRP:HZ2	1:A:1417:PRO:HB2	1.69	0.56
1:A:1548:TYR:CD2	1:A:1549:VAL:CG2	2.75	0.56
2:B:40:U:H3'	2:B:40:U:O2	2.05	0.56
3:C:426:GLU:O	3:C:427:PHE:HB2	2.05	0.56
3:C:449:ILE:CG2	3:C:457:VAL:HG11	2.30	0.56
5:E:250:LEU:CD2	5:E:262:TRP:HB2	2.35	0.56
15:H:152:G:N2	15:H:153:A:C8	2.73	0.56
21:1:847:ALA:O	21:1:851:SER:OG	2.24	0.56
22:2:643:PRO:CD	24:4:69:TYR:CG	2.88	0.56
23:3:438:LEU:HA	23:3:775:ASN:O	2.06	0.56
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:633:LEU:HD13	23:3:667:ILE:HG21	1.87	0.56
31:P:76:ARG:HG3	31:P:77:ASP:N	2.19	0.56
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.38	0.56
3:C:457:VAL:HA	3:C:462:GLY:HA3	1.88	0.56
3:C:673:LYS:HG3	3:C:686:THR:CG2	2.36	0.56
3:C:701:GLU:HA	3:C:740:THR:HG1	1.70	0.56
14:G:22:C:O2	14:G:22:C:H2'	2.06	0.56
21:1:944:SER:O	21:1:948:ARG:HG3	2.04	0.56
21:1:1279:ALA:HA	23:3:1167:TYR:CE1	2.41	0.56
24:4:75:ASN:ND2	24:4:86:VAL:O	2.38	0.56
30:M:201:ILE:HA	30:M:220:LEU:HB3	1.85	0.56
1:A:283:VAL:HG22	1:A:284:ARG:HG2	1.88	0.56
1:A:299:ILE:HD11	3:C:921:LEU:N	2.20	0.56
1:A:378:PHE:CZ	3:C:335:ASN:CB	2.89	0.56
1:A:569:VAL:O	1:A:570:ASP:HB2	2.04	0.56
1:A:692:ASP:OD1	33:T:376:ARG:NH2	2.38	0.56
1:A:1163:ARG:NH2	3:C:61:GLU:OE2	2.35	0.56
23:3:550:ASN:HD21	23:3:595:VAL:H	1.53	0.56
27:7:32:LEU:O	27:7:36:HIS:ND1	2.23	0.56
28:J:311:GLN:OE1	28:J:311:GLN:N	2.33	0.56
1:A:226:GLN:HA	1:A:418:THR:OG1	2.06	0.56
1:A:229:GLN:HG2	1:A:415:SER:CB	2.36	0.56
1:A:250:VAL:HG23	1:A:337:VAL:CG1	2.36	0.56
2:B:35:U:H6	2:B:35:U:OP2	1.89	0.56
3:C:301:SER:O	3:C:304:LEU:N	2.30	0.56
3:C:619:THR:C	3:C:620:LYS:HG3	2.25	0.56
13:F:50:A:O2'	13:F:51:U:OP1	2.23	0.56
1:A:402:ILE:HG13	3:C:385:VAL:CG2	2.28	0.56
1:A:579:GLN:NE2	1:A:613:TYR:CE1	2.74	0.56
1:A:812:THR:HG23	1:A:1055:LEU:HD11	1.88	0.56
1:A:2320:LEU:HD23	1:A:2322:GLU:H	1.71	0.56
3:C:140:HIS:CB	3:C:230:ASP:CB	2.66	0.56
24:4:79:LEU:HB2	24:4:84:ILE:HD11	1.88	0.56
1:A:44:ARG:NH2	5:E:285:GLU:O	2.38	0.56
1:A:849:ALA:O	1:A:1449:LYS:NZ	2.36	0.56
3:C:85:ASP:HB3	33:T:238:LEU:CG	2.27	0.56
3:C:677:GLU:HA	3:C:683:ASN:O	2.05	0.56
5:E:277:PHE:CE2	5:E:300:ILE:HD13	2.40	0.56
21:1:1026:ASN:ND2	21:1:1031:VAL:HG11	2.21	0.56
23:3:745:PHE:HE2	23:3:750:CYS:HB3	1.71	0.56
1:A:251:ASP:CA	1:A:337:VAL:HG21	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1306:LYS:NZ	2:B:38:C:C2'	2.68	0.56
3:C:385:VAL:HG23	3:C:386:GLY:N	2.20	0.56
5:E:153:PHE:HD1	5:E:153:PHE:H	1.54	0.56
15:H:150:U:C2	15:H:151:C:C5	2.94	0.56
21:1:689:ILE:O	21:1:692:HIS:ND1	2.39	0.56
21:1:718:PRO:HA	21:1:756:LEU:HG	1.88	0.56
23:3:669:LEU:HB2	23:3:673:VAL:HG22	1.88	0.56
25:5:93:ASN:OD1	25:5:94:ALA:N	2.34	0.56
28:J:433:ARG:HH12	28:J:461:LYS:CB	2.19	0.56
33:T:342:GLU:CB	33:T:343:PRO:CD	2.83	0.56
37:Z:612:TYR:O	37:Z:613:LYS:C	2.43	0.56
1:A:311:GLU:CB	3:C:885:THR:CG2	2.84	0.56
1:A:395:THR:HG21	3:C:383:GLN:NE2	2.15	0.56
1:A:1451:ASN:OD1	1:A:1453:PHE:N	2.39	0.56
3:C:631:GLY:HA3	3:C:637:LEU:HD21	1.88	0.56
15:H:83:A:N1	15:H:84:C:C4	2.74	0.56
21:1:1293:ASN:HA	27:7:76:CYS:O	2.05	0.56
21:1:1295:TYR:CE2	27:7:28:LYS:HE2	2.41	0.56
23:3:29:GLU:HB3	23:3:40:LEU:HD11	1.87	0.56
23:3:804:HIS:HD2	23:3:862:TRP:CZ2	2.24	0.56
23:3:1028:THR:HG22	23:3:1088:LYS:HD3	1.86	0.56
1:A:251:ASP:CA	1:A:337:VAL:CG2	2.84	0.55
1:A:319:LEU:HD13	3:C:637:LEU:HB3	1.86	0.55
1:A:434:HIS:HB3	3:C:892:GLN:OE1	2.07	0.55
1:A:783:TYR:CD1	31:P:228:ILE:HG12	2.41	0.55
14:G:16:G:H4'	14:G:17:U:O5'	2.04	0.55
15:H:154:C:O2'	15:H:155:C:H5'	2.04	0.55
21:1:570:TYR:HD1	21:1:573:LYS:HD2	1.71	0.55
1:A:89:LEU:O	1:A:89:LEU:HD23	2.06	0.55
1:A:91:ALA:O	1:A:92:LEU:C	2.45	0.55
1:A:387:PHE:HE1	3:C:327:TYR:CA	2.05	0.55
1:A:2113:LYS:CE	4:D:1229:ASP:CA	2.84	0.55
15:H:141:C:H2'	15:H:142:C:H6	1.71	0.55
15:H:149:A:C4	15:H:150:U:C5	2.95	0.55
15:H:180:G:C2	15:H:181:G:C5	2.94	0.55
1:A:530:LEU:CA	30:M:198:GLN:NE2	2.27	0.55
1:A:1321:GLU:O	1:A:1503:TRP:NE1	2.39	0.55
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.72	0.55
1:A:2325:VAL:CG1	4:D:788:GLY:O	2.33	0.55
3:C:674:CYS:HG	3:C:822:MET:CE	2.16	0.55
5:E:250:LEU:HD22	5:E:262:TRP:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1137:ARG:HH21	22:2:524:LEU:HD13	1.72	0.55
31:P:224:MET:HA	31:P:224:MET:HE3	1.88	0.55
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.71	0.55
1:A:280:GLU:HB2	2:B:48:A:C4'	2.36	0.55
3:C:77:VAL:HG13	33:T:196:LEU:C	1.90	0.55
3:C:706:GLN:NE2	3:C:708:THR:H	2.02	0.55
22:2:650:ILE:HG12	22:2:688:GLY:HA3	1.89	0.55
1:A:151:MET:SD	1:A:628:GLY:O	2.65	0.55
1:A:305:ARG:CG	3:C:878:ILE:CG2	2.85	0.55
1:A:1035:GLN:HA	1:A:1446:GLN:NE2	2.21	0.55
1:A:1690:ASP:OD1	1:A:1691:ASN:N	2.39	0.55
2:B:94:U:H2'	2:B:95:G:H5''	1.89	0.55
3:C:185:PRO:HG3	3:C:482:TYR:CZ	2.41	0.55
3:C:439:PRO:HB2	3:C:443:VAL:HB	1.88	0.55
21:1:1166:ILE:O	21:1:1170:THR:HG23	2.07	0.55
23:3:526:HIS:HB3	23:3:534:ASN:HB2	1.88	0.55
24:4:29:LEU:HD22	24:4:33:PHE:HE2	1.72	0.55
34:V:641:ASP:O	34:V:644:ARG:N	2.39	0.55
37:Z:566:TYR:CD2	37:Z:580:PRO:HG2	2.36	0.55
1:A:356:ILE:HG22	1:A:357:ASN:H	1.72	0.55
1:A:1607:GLU:N	1:A:1632:PHE:O	2.38	0.55
1:A:1930:TYR:O	1:A:1933:PHE:HB3	2.06	0.55
1:A:2073:TRP:HD1	1:A:2074:ARG:N	2.04	0.55
3:C:516:LEU:HD13	3:C:516:LEU:C	2.26	0.55
3:C:702:ASN:O	3:C:703:GLU:HB2	2.07	0.55
5:E:162:ARG:CZ	5:E:203:ASP:O	2.55	0.55
15:H:165:A:H2'	15:H:166:G:H5'	1.88	0.55
23:3:996:ILE:HG23	23:3:999:ARG:H	1.72	0.55
1:A:319:LEU:HB2	3:C:638:ASP:HA	1.89	0.55
1:A:1233:ASP:O	1:A:1236:SER:OG	2.23	0.55
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.71	0.55
3:C:78:GLU:OE1	33:T:198:ARG:NE	2.36	0.55
3:C:79:THR:CG2	33:T:199:VAL:CG1	2.84	0.55
3:C:567:GLU:OE1	3:C:572:GLU:HB3	2.06	0.55
5:E:260:ARG:NH1	5:E:276:ILE:HD11	2.22	0.55
14:G:23:U:O2	14:G:23:U:H2'	2.07	0.55
21:1:1255:PHE:CD2	22:2:487:LEU:HD22	2.42	0.55
31:P:33:ARG:HG3	31:P:33:ARG:HH11	1.72	0.55
36:Y:22:VAL:HG22	36:Y:26:VAL:HG13	1.88	0.55
37:Z:600:ARG:HB3	37:Z:600:ARG:NH1	2.08	0.55
1:A:283:VAL:HG13	1:A:284:ARG:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TYR:CD2	3:C:882:GLY:CA	2.86	0.55
1:A:715:GLU:CD	32:R:258:TRP:CZ3	2.79	0.55
1:A:1099:PHE:HE2	1:A:1153:VAL:HG13	1.72	0.55
1:A:1457:HIS:HE1	1:A:1459:ARG:HG3	1.68	0.55
1:A:1971:LEU:HB2	1:A:1976:TRP:CE2	2.42	0.55
2:B:63:A:O2'	5:E:106:LYS:NZ	2.39	0.55
21:1:1017:LEU:HD13	21:1:1050:VAL:HG21	1.89	0.55
21:1:1076:ALA:O	21:1:1080:THR:HG23	2.07	0.55
23:3:441:GLY:O	23:3:775:ASN:CB	2.55	0.55
32:R:74:LEU:HD23	32:R:75:ASP:OD1	2.06	0.55
32:R:436:VAL:CG2	32:R:437:TYR:CE1	2.89	0.55
36:Y:85:GLU:O	37:Z:502:ALA:CB	2.55	0.55
1:A:151:MET:CE	1:A:628:GLY:C	2.75	0.55
3:C:149:LEU:HA	3:C:427:PHE:CD2	2.41	0.55
5:E:114:GLU:CD	5:E:116:HIS:HE2	2.09	0.55
14:G:142:U:H2'	14:G:143:U:C6	2.42	0.55
15:H:150:U:H2'	15:H:151:C:H6	1.71	0.55
25:5:17:VAL:HG23	25:5:67:ILE:HD11	1.89	0.55
36:Y:37:TRP:HZ3	37:Z:498:GLY:HA3	1.66	0.55
1:A:1457:HIS:HE2	32:R:425:GLY:H	1.46	0.55
1:A:1505:LYS:HE3	37:Z:615:SER:HG	1.68	0.55
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.88	0.55
1:A:2306:HIS:HD2	1:A:2308:VAL:H	1.54	0.55
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.89	0.55
21:1:1174:GLU:OE2	21:1:1210:HIS:NE2	2.35	0.55
23:3:452:LEU:HB3	23:3:478:PHE:CE1	2.42	0.55
29:L:224:PHE:CD1	32:R:86:LEU:O	2.59	0.55
31:P:188:TRP:O	31:P:190:ASP:N	2.39	0.55
32:R:74:LEU:HD23	32:R:74:LEU:C	2.27	0.55
37:Z:574:ASN:O	37:Z:577:ASN:N	2.33	0.55
1:A:311:GLU:HB3	3:C:885:THR:HG21	1.89	0.54
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.54
23:3:309:ASP:HA	23:3:332:THR:HG22	1.88	0.54
23:3:848:PRO:HB2	23:3:851:ILE:HG22	1.89	0.54
24:4:14:THR:CA	24:4:59:VAL:O	2.28	0.54
26:6:39:PRO:HB3	26:6:70:TYR:HB2	1.88	0.54
28:J:294:HIS:HE1	29:L:227:THR:HB	1.70	0.54
31:P:228:ILE:O	31:P:229:LYS:C	2.45	0.54
32:R:86:LEU:HD12	32:R:86:LEU:O	2.06	0.54
1:A:350:PHE:CE2	1:A:398:THR:HG21	2.43	0.54
5:E:119:THR:HG21	5:E:161:ARG:HB2	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:153:A:C3'	15:H:154:C:C5'	2.86	0.54
21:1:1179:ASP:HB3	22:2:511:LEU:CD1	2.37	0.54
21:1:1279:ALA:HA	23:3:1167:TYR:HE1	1.70	0.54
35:X:312:GLU:O	35:X:327:TYR:HB2	2.07	0.54
1:A:148:TRP:CH2	1:A:616:PHE:HB2	2.42	0.54
1:A:420:ARG:CZ	2:B:56:C:O2'	2.55	0.54
1:A:436:PRO:O	1:A:437:ALA:HB3	2.07	0.54
3:C:140:HIS:CD2	3:C:233:GLU:HG3	2.41	0.54
3:C:510:LEU:HB3	3:C:576:ILE:HD11	1.89	0.54
13:F:36:A:H2'	13:F:37:C:H4'	1.89	0.54
13:F:38:G:H2'	13:F:39:A:C8	2.42	0.54
13:F:56:A:C2	15:H:20:G:C2	2.96	0.54
23:3:553:GLN:HA	23:3:566:PHE:O	2.07	0.54
23:3:1014:TYR:OH	23:3:1019:ASN:OD1	2.24	0.54
28:J:218:GLU:HG3	28:J:219:GLU:OE2	2.07	0.54
1:A:529:THR:HB	30:M:199:PRO:HD3	1.88	0.54
1:A:676:ARG:HG3	13:F:56:A:P	2.48	0.54
3:C:749:THR:HG1	3:C:752:SER:HB2	1.72	0.54
32:R:402:ASN:HB3	35:X:191:GLN:HB2	1.90	0.54
36:Y:10:ILE:HD13	36:Y:98:ASN:HD21	1.73	0.54
1:A:387:PHE:CD1	3:C:327:TYR:CD1	2.95	0.54
1:A:699:GLU:O	1:A:701:ILE:HD12	2.07	0.54
1:A:1306:LYS:HB2	14:G:-6:C:H4'	1.89	0.54
1:A:1459:ARG:HG3	32:R:424:SER:N	2.22	0.54
3:C:145:PHE:CZ	3:C:427:PHE:HE1	2.21	0.54
5:E:161:ARG:NH1	5:E:203:ASP:OD1	2.40	0.54
23:3:913:LEU:HD23	23:3:920:VAL:HG12	1.89	0.54
28:J:262:ARG:HD3	29:L:220:PRO:CG	2.38	0.54
29:L:224:PHE:HD1	32:R:86:LEU:O	1.91	0.54
31:P:63:LEU:HD23	31:P:63:LEU:C	2.28	0.54
33:T:455:GLN:NE2	33:T:456:PRO:HD2	2.22	0.54
1:A:705:LYS:HG2	32:R:251:ILE:CG1	2.38	0.54
1:A:1333:VAL:HG11	1:A:1367:ASN:HD22	1.73	0.54
1:A:2095:ASP:OD1	1:A:2095:ASP:N	2.41	0.54
5:E:108:HIS:ND1	5:E:128:SER:CB	2.70	0.54
5:E:310:TYR:CZ	5:E:322:LYS:HD2	2.42	0.54
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.43	0.54
23:3:336:ALA:HB2	23:3:349:VAL:HG13	1.90	0.54
32:R:131:ASP:OD2	32:R:132:LEU:HD23	2.07	0.54
1:A:592:TYR:HA	1:A:595:LYS:O	2.08	0.54
1:A:978:GLU:OE2	1:A:1187:PHE:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1328:LEU:HD22	1:A:1368:LEU:HD21	1.89	0.54
1:A:2325:VAL:O	4:D:788:GLY:CA	2.56	0.54
3:C:259:LYS:CE	3:C:262:ARG:HD2	2.36	0.54
3:C:482:TYR:CD2	3:C:493:PHE:HB2	2.42	0.54
3:C:700:ILE:CG2	3:C:735:PHE:CD2	2.83	0.54
21:1:470:ASP:OD1	21:1:471:ASP:N	2.41	0.54
21:1:624:VAL:O	21:1:628:THR:OG1	2.14	0.54
21:1:632:PHE:HA	21:1:635:VAL:HG22	1.90	0.54
23:3:144:LEU:HB3	23:3:152:LEU:HD11	1.89	0.54
23:3:253:GLU:OE2	23:3:254:ASN:ND2	2.41	0.54
23:3:440:HIS:C	23:3:733:PRO:HG2	2.28	0.54
28:J:408:ASP:OD1	28:J:443:ILE:HG22	2.07	0.54
1:A:119:LEU:HD11	1:A:477:LYS:HG3	1.88	0.54
1:A:173:GLU:O	1:A:520:TYR:CD2	2.61	0.54
3:C:230:ASP:CG	3:C:259:LYS:NZ	2.61	0.54
15:H:183:G:C4	15:H:184:C:C5	2.95	0.54
21:1:331:ALA:O	21:1:335:LYS:N	2.34	0.54
31:P:228:ILE:HD12	31:P:228:ILE:N	2.23	0.54
33:T:356:LEU:N	33:T:356:LEU:CD1	2.70	0.54
37:Z:612:TYR:O	37:Z:615:SER:N	2.29	0.54
1:A:120:TYR:N	1:A:483:GLN:O	2.33	0.54
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.90	0.54
1:A:254:TYR:O	1:A:434:HIS:HD2	1.91	0.54
1:A:278:LYS:O	1:A:452:LYS:HD2	2.08	0.54
1:A:384:VAL:CG2	3:C:334:ILE:HG23	2.35	0.54
1:A:384:VAL:HG21	3:C:334:ILE:CG1	2.38	0.54
1:A:465:LYS:HG3	1:A:465:LYS:O	2.08	0.54
1:A:1778:TRP:CE2	1:A:1858:PRO:HG3	2.42	0.54
1:A:2067:PHE:CE2	1:A:2069:SER:HA	2.43	0.54
3:C:135:CYS:SG	3:C:227:LEU:HB2	2.47	0.54
21:1:893:ILE:HG13	21:1:928:TYR:CD2	2.43	0.54
22:2:476:GLU:N	22:2:479:ASP:OD2	2.41	0.54
27:7:15:GLN:O	27:7:21:THR:OG1	2.22	0.54
28:J:255:LEU:HD22	29:L:235:LEU:CD1	2.35	0.54
32:R:232:MET:O	32:R:232:MET:HG2	2.07	0.54
1:A:256:TYR:CZ	3:C:888:ARG:CZ	2.91	0.54
1:A:264:PHE:CE1	1:A:455:VAL:CG1	2.75	0.54
1:A:1838:LYS:HG3	1:A:1868:MET:SD	2.49	0.54
1:A:2113:LYS:HE3	4:D:1229:ASP:CA	2.38	0.54
1:A:2325:VAL:HG13	4:D:789:MET:HA	1.88	0.54
3:C:79:THR:HA	33:T:199:VAL:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:137:C:H2'	14:G:138:A:O4'	2.07	0.54
15:H:3:C:H2'	15:H:4:G:H8	1.73	0.54
21:1:826:ASP:OD1	21:1:827:ARG:N	2.39	0.54
21:1:1010:THR:O	21:1:1012:PRO:HD3	2.08	0.54
27:7:60:SER:HG	27:7:63:ARG:H	1.55	0.54
32:R:135:PRO:HD2	33:T:341:ALA:HB1	1.90	0.54
32:R:442:ARG:CD	32:R:443:GLY:CA	2.70	0.54
1:A:335:PRO:HG3	3:C:139:HIS:CB	2.36	0.53
1:A:2117:ILE:O	1:A:2304:PHE:HB2	2.07	0.53
3:C:700:ILE:HA	3:C:705:VAL:HG12	1.89	0.53
3:C:742:PRO:HB2	3:C:786:ASN:H	1.72	0.53
5:E:178:LEU:CD1	5:E:222:LEU:HD22	2.37	0.53
32:R:442:ARG:NH1	32:R:444:GLY:N	2.41	0.53
33:T:287:HIS:CE1	33:T:313:ARG:HG3	2.43	0.53
37:Z:485:GLU:O	37:Z:489:GLU:CB	2.56	0.53
1:A:705:LYS:HG2	32:R:251:ILE:CG2	2.38	0.53
1:A:1403:LEU:O	32:R:412:ASP:HB2	2.08	0.53
1:A:1930:TYR:CD2	1:A:1931:THR:N	2.76	0.53
14:G:135:G:H1	15:H:41:U:H3	1.56	0.53
15:H:84:C:O2	15:H:84:C:H2'	2.09	0.53
23:3:166:LEU:O	23:3:186:GLU:HA	2.08	0.53
33:T:454:VAL:HG12	33:T:455:GLN:N	2.24	0.53
34:V:525:PHE:O	34:V:528:ILE:N	2.41	0.53
1:A:386:PRO:HB3	3:C:372:PHE:CD1	2.43	0.53
1:A:628:GLY:O	1:A:629:PHE:HB2	2.09	0.53
1:A:1118:PRO:CD	1:A:1119:ASP:H	2.19	0.53
1:A:1605:GLU:OE2	1:A:2286:VAL:HG21	2.07	0.53
1:A:1962:THR:CG2	37:Z:524:ARG:CG	2.86	0.53
5:E:87:ASP:O	5:E:88:ARG:HB2	2.07	0.53
13:F:53:A:H2'	13:F:54:G:O4'	2.09	0.53
21:1:626:ASN:ND2	21:1:630:ARG:HH12	2.06	0.53
21:1:1299:GLU:HA	21:1:1302:TYR:CE2	2.44	0.53
33:T:384:HIS:O	33:T:385:TYR:CB	2.55	0.53
35:X:181:PHE:HA	36:Y:50:GLY:H	1.73	0.53
1:A:664:HIS:CE1	1:A:666:LYS:CB	2.85	0.53
3:C:449:ILE:CD1	3:C:466:SER:N	2.71	0.53
21:1:822:ARG:HH11	36:Y:31:GLU:HG2	1.74	0.53
21:1:1077:THR:O	21:1:1080:THR:OG1	2.22	0.53
21:1:1127:THR:HA	22:2:571:LEU:HB3	1.88	0.53
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.48	0.53
28:J:218:GLU:HG3	28:J:219:GLU:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:103:ARG:HH11	32:R:103:ARG:CG	2.21	0.53
1:A:2073:TRP:CH2	1:A:2310:ARG:HG2	2.44	0.53
1:A:2298:LEU:HD13	4:D:1265:GLN:CB	2.39	0.53
3:C:481:MET:SD	3:C:559:ILE:HD11	2.48	0.53
23:3:712:VAL:HG23	23:3:722:SER:HB3	1.91	0.53
1:A:115:ASP:HB3	1:A:486:LYS:HE2	1.91	0.53
1:A:665:SER:HB3	32:R:215:ASN:HB2	1.90	0.53
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.88	0.53
1:A:1457:HIS:HE2	32:R:425:GLY:N	2.04	0.53
1:A:2310:ARG:HH12	1:A:2314:PHE:HE1	1.56	0.53
2:B:18:C:C2'	2:B:19:A:O5'	2.56	0.53
3:C:115:GLU:O	3:C:116:MET:C	2.43	0.53
3:C:220:ARG:O	3:C:448:LYS:HE2	2.08	0.53
3:C:360:ALA:N	3:C:361:PRO:CD	2.71	0.53
15:H:147:G:C2	15:H:148:C:C2	2.97	0.53
15:H:153:A:H3'	15:H:154:C:C5'	2.38	0.53
21:1:1157:TYR:O	26:6:38:ARG:NH2	2.40	0.53
23:3:195:ASP:OD1	23:3:197:THR:OG1	2.23	0.53
23:3:250:ILE:HD13	23:3:259:LYS:HB3	1.91	0.53
23:3:547:CYS:HB3	23:3:556:ILE:HG22	1.90	0.53
23:3:667:ILE:HB	23:3:675:LEU:HB2	1.91	0.53
31:P:41:ILE:HD11	33:T:318:ARG:HB2	1.90	0.53
1:A:393:LEU:HD13	3:C:375:GLU:O	2.08	0.53
1:A:586:GLY:O	1:A:1549:VAL:HG12	2.08	0.53
3:C:449:ILE:HG22	3:C:457:VAL:HG13	1.88	0.53
5:E:108:HIS:ND1	5:E:128:SER:HB2	2.24	0.53
5:E:178:LEU:CD2	5:E:208:ILE:CD1	2.87	0.53
15:H:68:G:C2'	15:H:69:U:H5'	2.37	0.53
23:3:141:VAL:HG11	23:3:213:LEU:HD12	1.89	0.53
23:3:440:HIS:CD2	23:3:733:PRO:CG	2.92	0.53
1:A:203:VAL:HG23	1:A:237:THR:CG2	2.35	0.53
1:A:308:ILE:HG22	1:A:308:ILE:O	2.09	0.53
1:A:384:VAL:HG21	3:C:334:ILE:HG23	1.80	0.53
3:C:82:GLN:CG	33:T:237:LYS:HA	2.38	0.53
15:H:79:G:C2	15:H:80:A:C5	2.97	0.53
21:1:944:SER:HA	21:1:948:ARG:NE	2.23	0.53
28:J:359:VAL:O	28:J:363:ARG:HG2	2.08	0.53
32:R:132:LEU:HB3	33:T:399:LYS:HZ2	1.70	0.53
33:T:318:ARG:HH11	33:T:318:ARG:CG	2.22	0.53
37:Z:571:PRO:HD3	37:Z:579:TRP:CH2	2.43	0.53
1:A:299:ILE:HD11	3:C:920:PRO:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:ARG:HH12	2:B:58:U:C5'	2.21	0.53
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.32	0.53
3:C:259:LYS:HG2	3:C:262:ARG:HG3	1.90	0.53
5:E:232:ARG:O	5:E:262:TRP:HH2	1.91	0.53
21:1:516:LEU:O	21:1:520:THR:HG23	2.08	0.53
24:4:47:ASP:HB3	24:4:52:GLN:O	2.08	0.53
1:A:148:TRP:CZ2	1:A:616:PHE:HA	2.44	0.53
1:A:264:PHE:CE1	1:A:459:LEU:CD1	2.81	0.53
1:A:405:LEU:CD1	3:C:265:LEU:HD22	2.39	0.53
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.41	0.53
1:A:748:ASP:HA	31:P:214:THR:CG2	2.34	0.53
1:A:1275:ARG:HD2	1:A:1375:TRP:CD1	2.44	0.53
1:A:1425:LYS:CG	32:R:417:ASN:OD1	2.56	0.53
1:A:1781:ASP:HB3	1:A:1808:PHE:HB3	1.90	0.53
3:C:250:ARG:NE	3:C:451:HIS:CD2	2.76	0.53
3:C:516:LEU:HB2	3:C:575:GLN:HE22	1.73	0.53
13:F:50:A:H2'	13:F:51:U:C6	2.44	0.53
13:F:56:A:C6	15:H:20:G:C6	2.96	0.53
22:2:614:ARG:HH11	22:2:614:ARG:CG	2.14	0.53
23:3:211:TYR:HE1	23:3:222:ARG:HG2	1.74	0.53
23:3:605:LEU:O	23:3:616:ILE:HA	2.08	0.53
23:3:719:SER:OG	23:3:739:LEU:HD11	2.09	0.53
34:V:530:LYS:O	34:V:532:GLN:N	2.42	0.53
1:A:121:HIS:CD2	1:A:481:PHE:HB3	2.36	0.52
1:A:891:PHE:O	29:L:83:ARG:NH1	2.42	0.52
3:C:671:SER:C	3:C:672:LEU:HD22	2.30	0.52
21:1:599:ASN:O	21:1:603:ALA:CB	2.57	0.52
23:3:519:VAL:HG22	23:3:524:ILE:HG12	1.90	0.52
23:3:639:SER:OG	23:3:701:LEU:N	2.42	0.52
23:3:1148:LEU:O	23:3:1152:HIS:N	2.39	0.52
32:R:95:LYS:HD3	32:R:95:LYS:N	2.25	0.52
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	1.90	0.52
3:C:943:LEU:HD23	3:C:943:LEU:N	2.24	0.52
13:F:48:A:N3	29:L:33:ARG:NH2	2.57	0.52
13:F:94:C:OP1	28:J:351:ASN:CB	2.57	0.52
14:G:153:C:H4'	14:G:154:U:OP1	2.10	0.52
15:H:81:G:C2	15:H:82:G:C5	2.97	0.52
23:3:550:ASN:HB3	23:3:553:GLN:HB2	1.90	0.52
3:C:97:VAL:HG12	31:P:47:THR:OG1	2.10	0.52
13:F:34:G:H2'	13:F:35:A:O5'	2.10	0.52
14:G:-4:A:H2'	14:G:-3:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:148:C:C2'	15:H:149:A:H5'	2.39	0.52
21:1:516:LEU:HD11	21:1:558:ARG:HD3	1.91	0.52
21:1:1090:PRO:HG3	21:1:1123:CYS:HB2	1.91	0.52
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.73	0.52
23:3:159:GLU:OE2	26:6:14:GLN:HB2	2.09	0.52
23:3:755:VAL:HG22	23:3:764:ILE:HD12	1.89	0.52
31:P:189:ASP:O	31:P:191:ASP:N	2.43	0.52
32:R:233:HIS:H	32:R:233:HIS:HD2	1.56	0.52
33:T:351:ASP:C	33:T:352:THR:HG1	2.11	0.52
1:A:830:LEU:HA	1:A:882:LYS:HZ2	1.74	0.52
1:A:1214:TRP:CE2	1:A:1230:LEU:HD11	2.45	0.52
1:A:1301:ILE:HD13	1:A:1306:LYS:CE	2.35	0.52
5:E:178:LEU:N	5:E:178:LEU:HD23	2.25	0.52
14:G:-12:G:H4'	14:G:-11:G:OP1	2.09	0.52
21:1:1108:ASN:OD1	21:1:1109:ARG:N	2.43	0.52
23:3:114:ARG:NE	23:3:136:GLU:OE1	2.32	0.52
32:R:52:PRO:O	32:R:53:ARG:HB2	2.09	0.52
32:R:81:LYS:HA	32:R:81:LYS:HE3	1.87	0.52
1:A:204:LEU:HD23	1:A:205:ASP:OD1	2.09	0.52
1:A:267:LYS:HZ1	2:B:49:A:P	2.24	0.52
1:A:338:VAL:O	3:C:266:GLU:HG2	2.10	0.52
1:A:384:VAL:HG22	3:C:334:ILE:CG2	2.33	0.52
1:A:387:PHE:CE1	3:C:326:ILE:HG22	2.45	0.52
1:A:664:HIS:NE2	1:A:666:LYS:CG	2.73	0.52
1:A:666:LYS:HB2	1:A:668:VAL:HG23	1.83	0.52
1:A:1275:ARG:NH1	1:A:1378:GLU:OE1	2.43	0.52
3:C:80:ILE:CD1	3:C:80:ILE:N	2.73	0.52
3:C:143:THR:HB	41:C:1500:GTP:O1A	2.09	0.52
3:C:700:ILE:CG2	3:C:741:GLY:O	2.57	0.52
13:F:36:A:C8	13:F:36:A:C4'	2.93	0.52
13:F:57:U:H2'	13:F:58:G:C8	2.45	0.52
21:1:717:THR:HG22	21:1:718:PRO:CD	2.39	0.52
21:1:762:ALA:O	21:1:766:THR:OG1	2.19	0.52
23:3:159:GLU:HB3	23:3:161:HIS:CD2	2.44	0.52
37:Z:524:ARG:HD2	37:Z:525:TYR:HB3	1.92	0.52
1:A:128:PHE:CD1	1:A:473:PHE:CZ	2.98	0.52
1:A:665:SER:OG	1:A:666:LYS:HD3	2.10	0.52
1:A:1113:TYR:C	1:A:1115:THR:H	2.13	0.52
1:A:1631:LEU:HD12	1:A:1660:TYR:HD2	1.74	0.52
1:A:2133:PRO:HD2	1:A:2139:VAL:HG13	1.92	0.52
3:C:78:GLU:O	33:T:198:ARG:C	2.47	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:78:GLU:CG	3:C:80:ILE:CD1	2.54	0.52
3:C:139:HIS:O	3:C:259:LYS:NZ	2.36	0.52
3:C:449:ILE:HD11	3:C:466:SER:HA	1.91	0.52
3:C:508:LYS:HB3	3:C:566:THR:CG2	2.39	0.52
3:C:710:ASN:O	3:C:712:LYS:N	2.42	0.52
21:1:1254:LEU:O	21:1:1262:ARG:HG2	2.09	0.52
23:3:1059:PRO:O	23:3:1062:THR:HG23	2.08	0.52
33:T:267:ASP:O	33:T:268:LYS:CG	2.56	0.52
33:T:351:ASP:C	33:T:352:THR:OG1	2.48	0.52
37:Z:597:ARG:NH1	37:Z:601:LEU:HD13	2.24	0.52
1:A:203:VAL:CG2	1:A:237:THR:CB	2.88	0.52
1:A:433:GLU:OE1	1:A:436:PRO:CB	2.54	0.52
1:A:661:GLU:CG	32:R:210:PRO:CB	2.88	0.52
1:A:1162:PRO:HG3	31:P:194:PHE:CG	2.44	0.52
1:A:1459:ARG:HD2	32:R:422:MET:O	2.09	0.52
2:B:27:U:O2'	2:B:28:A:O5'	2.23	0.52
14:G:11:A:N1	14:G:12:G:C8	2.77	0.52
23:3:285:MET:SD	23:3:305:THR:HB	2.49	0.52
23:3:304:GLN:HE22	23:3:335:VAL:HA	1.73	0.52
24:4:41:ASN:HB2	24:4:60:GLU:HB3	1.92	0.52
33:T:318:ARG:HH11	33:T:319:THR:HG23	1.74	0.52
1:A:47:GLU:OE1	1:A:47:GLU:N	2.35	0.52
3:C:711:ARG:CZ	3:C:730:ARG:O	2.57	0.52
3:C:902:HIS:ND1	3:C:903:HIS:HB2	2.25	0.52
21:1:1289:ASN:HB3	21:1:1295:TYR:H	1.75	0.52
23:3:108:GLY:O	26:6:82:ARG:HD3	2.09	0.52
23:3:232:GLY:HA2	23:3:252:SER:HA	1.90	0.52
24:4:34:LEU:HA	24:4:37:GLY:O	2.10	0.52
32:R:135:PRO:O	32:R:136:ASP:CB	2.58	0.52
1:A:191:ILE:HG23	1:A:572:PHE:CZ	2.44	0.52
1:A:339:PHE:C	1:A:340:ILE:HD13	2.31	0.52
3:C:259:LYS:HG2	3:C:262:ARG:CG	2.39	0.52
3:C:510:LEU:HD22	3:C:514:TYR:HE2	1.75	0.52
21:1:901:GLN:HA	21:1:939:ARG:HH22	1.72	0.52
31:P:193:VAL:HG23	31:P:194:PHE:N	2.25	0.52
33:T:347:THR:O	33:T:354:ILE:HG23	2.10	0.52
1:A:676:ARG:HG3	13:F:55:C:O3'	2.09	0.52
2:B:42:U:H3	14:G:-3:A:N1	1.47	0.52
3:C:449:ILE:CD1	3:C:466:SER:CA	2.88	0.52
3:C:600:LEU:N	3:C:601:PRO:HD2	2.25	0.52
21:1:661:ARG:NH1	21:1:696:ASP:OD2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1070:LYS:HB3	21:1:1073:ILE:HD12	1.91	0.52
21:1:1096:THR:HA	21:1:1099:ASN:ND2	2.25	0.52
23:3:259:LYS:HG3	23:3:266:ASP:OD1	2.09	0.52
23:3:1048:ASP:HB3	23:3:1052:ASN:H	1.75	0.52
31:P:189:ASP:OD2	31:P:192:VAL:CG2	2.59	0.52
32:R:70:ALA:O	32:R:71:GLN:C	2.48	0.52
32:R:442:ARG:CD	32:R:443:GLY:C	2.77	0.52
36:Y:69:ARG:NH2	36:Y:74:GLY:O	2.34	0.52
1:A:312:TYR:N	1:A:312:TYR:CD1	2.78	0.51
1:A:941:LYS:HG3	1:A:1071:PHE:CE1	2.46	0.51
1:A:1275:ARG:HD2	1:A:1375:TRP:NE1	2.25	0.51
1:A:1425:LYS:C	1:A:1425:LYS:HD3	2.31	0.51
3:C:64:LYS:NZ	31:P:206:LYS:HG3	2.22	0.51
3:C:89:LEU:O	3:C:91:GLU:N	2.43	0.51
21:1:1256:HIS:ND1	21:1:1261:VAL:HG11	2.24	0.51
23:3:460:TRP:CZ2	23:3:507:SER:HA	2.46	0.51
23:3:476:VAL:HG22	23:3:762:LEU:HD22	1.91	0.51
23:3:1134:SER:HB2	23:3:1136:GLU:OE1	2.09	0.51
31:P:32:SER:O	31:P:35:LEU:HD12	2.09	0.51
1:A:107:PRO:O	1:A:111:GLU:CD	2.48	0.51
1:A:245:LEU:HD22	1:A:430:TRP:CH2	2.44	0.51
1:A:664:HIS:NE2	1:A:666:LYS:CB	2.73	0.51
1:A:672:VAL:HG21	33:T:267:ASP:OD1	2.10	0.51
1:A:805:GLU:CB	31:P:194:PHE:CZ	2.89	0.51
3:C:77:VAL:HG13	33:T:196:LEU:HB3	1.91	0.51
13:F:36:A:H3'	13:F:37:C:C5'	2.26	0.51
21:1:1253:GLY:HA3	21:1:1265:TYR:CG	2.45	0.51
26:6:54:TYR:HA	26:6:57:ARG:HB2	1.92	0.51
29:L:224:PHE:CE1	32:R:86:LEU:HD13	2.44	0.51
33:T:392:PRO:HA	33:T:414:ALA:O	2.09	0.51
1:A:296:PHE:HB3	3:C:656:ALA:HB2	1.92	0.51
1:A:366:LYS:N	1:A:366:LYS:CD	2.73	0.51
1:A:589:THR:OG1	1:A:590:GLY:N	2.44	0.51
1:A:642:ARG:NH2	2:B:56:C:C2	2.78	0.51
1:A:750:TRP:CZ2	1:A:778:ARG:HG2	2.45	0.51
1:A:1179:SER:O	1:A:1182:ASN:N	2.44	0.51
1:A:1784:ASN:ND2	1:A:1897:LEU:HD12	2.22	0.51
3:C:674:CYS:SG	3:C:822:MET:CE	2.99	0.51
13:F:45:A:N1	22:2:554:ARG:NH2	2.53	0.51
21:1:1179:ASP:HB2	21:1:1185:ARG:HD3	1.93	0.51
23:3:331:ASP:OD2	23:3:394:ASN:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:125:MET:O	32:R:126:ASN:HB3	2.11	0.51
33:T:267:ASP:O	33:T:268:LYS:HB2	2.09	0.51
33:T:454:VAL:CG2	33:T:463:SER:OG	2.58	0.51
1:A:221:ASN:ND2	2:B:12:U:OP1	2.43	0.51
1:A:232:LEU:HB2	1:A:233:PRO:HD3	1.93	0.51
1:A:782:LEU:HB3	31:P:224:MET:SD	2.50	0.51
3:C:300:LEU:HD13	3:C:300:LEU:N	2.25	0.51
3:C:388:VAL:O	3:C:388:VAL:HG22	2.10	0.51
15:H:55:U:H1'	15:H:58:U:H5	1.74	0.51
15:H:107:A:C6	15:H:108:G:C5	2.99	0.51
37:Z:593:PHE:O	37:Z:597:ARG:CB	2.57	0.51
1:A:152:ARG:CG	1:A:152:ARG:NH1	2.73	0.51
1:A:227:ARG:H	1:A:417:ARG:HA	1.75	0.51
1:A:227:ARG:C	1:A:416:GLY:O	2.48	0.51
1:A:1667:ARG:HD2	1:A:1679:TYR:CE2	2.46	0.51
1:A:2147:MET:O	1:A:2274:PRO:HD3	2.10	0.51
3:C:678:THR:HG23	3:C:683:ASN:H	1.75	0.51
5:E:231:MET:SD	5:E:262:TRP:CE3	3.04	0.51
13:F:68:C:N4	31:P:33:ARG:CB	2.45	0.51
21:1:1054:GLU:OE1	21:1:1057:ARG:NH1	2.36	0.51
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.93	0.51
23:3:1002:VAL:HB	23:3:1010:ILE:HB	1.93	0.51
1:A:1447:VAL:HG12	1:A:1449:LYS:HG2	1.92	0.51
13:F:43:A:O2'	13:F:44:G:H5'	2.11	0.51
21:1:231:ARG:HA	21:1:607:ALA:HB2	1.92	0.51
23:3:264:GLN:HE22	23:3:322:VAL:H	1.58	0.51
23:3:745:PHE:CZ	23:3:747:SER:HB3	2.46	0.51
33:T:318:ARG:HG3	33:T:318:ARG:HH11	1.76	0.51
1:A:349:ALA:HB2	1:A:399:ALA:CB	2.19	0.51
1:A:978:GLU:CD	1:A:1188:ASN:H	2.14	0.51
1:A:1320:LYS:NZ	32:R:434:TYR:CD1	2.77	0.51
1:A:1962:THR:HG23	37:Z:524:ARG:CB	2.28	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:220:ARG:O	3:C:448:LYS:CE	2.58	0.51
13:F:34:G:N3	13:F:34:G:C3'	2.72	0.51
13:F:94:C:H5''	28:J:347:HIS:HB3	1.92	0.51
22:2:469:VAL:HG12	22:2:471:ARG:H	1.76	0.51
23:3:113:ARG:HB2	23:3:116:VAL:HB	1.91	0.51
23:3:971:ASP:OD1	23:3:972:LEU:N	2.43	0.51
33:T:459:LEU:HD12	33:T:460:ASP:N	2.25	0.51
36:Y:37:TRP:CH2	37:Z:498:GLY:N	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:MET:N	1:A:96:PRO:HD2	2.26	0.51
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.92	0.51
1:A:1923:TRP:HB3	1:A:1927:ILE:HD11	1.93	0.51
1:A:2081:ALA:HB1	4:D:1010:SER:CB	2.40	0.51
3:C:133:THR:O	3:C:226:VAL:O	2.29	0.51
13:F:34:G:N3	13:F:34:G:C5'	2.73	0.51
13:F:35:A:N3	13:F:35:A:C5'	2.73	0.51
23:3:354:GLY:HA3	23:3:432:ARG:HH12	1.76	0.51
24:4:16:TYR:HA	24:4:57:GLY:O	2.10	0.51
24:4:16:TYR:HD1	24:4:58:PHE:CE2	2.28	0.51
28:J:257:GLU:HA	29:L:232:TYR:CE2	2.46	0.51
28:J:273:TYR:CD2	32:R:228:PRO:CG	2.94	0.51
1:A:206:TRP:CD1	1:A:213:LEU:HD21	2.45	0.51
1:A:331:TRP:C	1:A:331:TRP:HE3	2.14	0.51
1:A:744:LYS:HZ1	31:P:212:ASN:C	2.14	0.51
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.93	0.51
1:A:1373:GLN:HB3	1:A:1378:GLU:OE2	2.11	0.51
1:A:1502:PHE:CZ	1:A:1505:LYS:HB3	2.45	0.51
3:C:131:ASN:ND2	3:C:223:ASP:OD2	2.44	0.51
14:G:11:A:N3	14:G:11:A:C5'	2.73	0.51
14:G:11:A:N1	14:G:12:G:N7	2.59	0.51
21:1:669:GLN:O	21:1:672:ALA:N	2.44	0.51
23:3:246:SER:O	23:3:260:ASN:ND2	2.44	0.51
23:3:404:LEU:HD23	23:3:407:ILE:HD11	1.92	0.51
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.46	0.51
23:3:896:PHE:HB2	23:3:899:THR:HG22	1.93	0.51
28:J:273:TYR:CD1	32:R:228:PRO:HG2	2.46	0.51
33:T:300:ILE:O	33:T:301:ASP:HB2	2.11	0.51
1:A:331:TRP:CE2	3:C:635:LEU:HD22	2.46	0.51
1:A:748:ASP:OD2	33:T:484:LYS:NZ	2.43	0.51
1:A:823:SER:OG	1:A:933:ARG:NH1	2.44	0.51
1:A:1276:GLU:O	1:A:1279:VAL:HG12	2.11	0.51
3:C:93:ILE:CD1	33:T:230:ILE:CD1	2.89	0.51
15:H:111:G:O3'	15:H:112:G:O4'	2.29	0.51
21:1:475:PHE:CE1	21:1:502:LEU:HB2	2.46	0.51
21:1:582:LEU:HD23	21:1:630:ARG:HB3	1.93	0.51
23:3:556:ILE:HD11	23:3:564:VAL:HB	1.93	0.51
23:3:1144:VAL:O	23:3:1148:LEU:HB2	2.11	0.51
33:T:385:TYR:CE2	33:T:400:PHE:HB3	2.46	0.51
34:V:576:THR:O	34:V:580:ARG:N	2.36	0.51
1:A:1435:GLY:O	1:A:1438:VAL:HG22	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:215:VAL:HG11	3:C:242:LEU:HD22	1.93	0.50
3:C:559:ILE:C	3:C:559:ILE:HD12	2.31	0.50
23:3:28:GLN:HE22	23:3:343:LYS:HG2	1.77	0.50
23:3:80:VAL:HB	23:3:88:VAL:HG23	1.93	0.50
23:3:110:SER:HB3	26:6:82:ARG:HH12	1.75	0.50
28:J:252:GLU:OE1	28:J:260:ARG:HB3	2.12	0.50
28:J:360:ASP:HA	28:J:363:ARG:HD2	1.91	0.50
32:R:220:ARG:CB	32:R:220:ARG:HH11	2.24	0.50
33:T:233:LEU:HD23	33:T:233:LEU:C	2.32	0.50
1:A:251:ASP:N	1:A:337:VAL:HG21	2.26	0.50
1:A:863:GLU:OE2	1:A:916:LYS:NZ	2.36	0.50
1:A:1757:GLU:CD	32:R:451:ILE:HD11	2.30	0.50
1:A:1930:TYR:HD2	1:A:1931:THR:N	2.09	0.50
1:A:2298:LEU:CD1	4:D:1285:SER:CA	2.89	0.50
3:C:452:THR:O	3:C:578:ARG:N	2.43	0.50
3:C:457:VAL:HG12	3:C:462:GLY:CA	2.41	0.50
3:C:619:THR:O	3:C:620:LYS:HG3	2.11	0.50
5:E:229:TYR:CE2	5:E:272:ARG:NH1	2.77	0.50
15:H:51:A:N6	15:H:63:G:O6	2.44	0.50
23:3:506:LEU:HB3	23:3:547:CYS:SG	2.52	0.50
23:3:669:LEU:HD22	23:3:673:VAL:HG21	1.93	0.50
37:Z:574:ASN:O	37:Z:576:PHE:N	2.44	0.50
1:A:844:GLU:CB	32:R:422:MET:HE2	2.23	0.50
3:C:94:ILE:HG21	33:T:259:PRO:HB3	1.92	0.50
3:C:387:ASP:O	3:C:389:ASP:OD1	2.30	0.50
3:C:659:VAL:HG12	3:C:660:VAL:N	2.26	0.50
14:G:-12:G:O2'	14:G:-11:G:O5'	2.30	0.50
15:H:153:A:C2'	15:H:154:C:C5'	2.86	0.50
15:H:182:U:C2'	15:H:183:G:H5'	2.41	0.50
21:1:1156:GLU:O	26:6:38:ARG:NH1	2.45	0.50
27:7:32:LEU:HA	27:7:35:GLN:HG2	1.93	0.50
32:R:178:ARG:CD	32:R:194:GLN:HE22	2.07	0.50
32:R:422:MET:C	32:R:424:SER:H	2.12	0.50
32:R:434:TYR:CD1	37:Z:616:VAL:CB	2.95	0.50
33:T:329:HIS:CE1	33:T:355:ARG:HG3	2.46	0.50
1:A:89:LEU:CD2	1:A:656:LEU:HD22	2.42	0.50
1:A:232:LEU:CD1	3:C:412:ILE:HD11	2.37	0.50
1:A:329:LEU:HB3	3:C:177:ARG:HE	1.74	0.50
1:A:368:GLN:HA	1:A:369:GLU:OE2	2.10	0.50
1:A:480:LYS:CG	32:R:203:GLN:OE1	2.58	0.50
1:A:596:TYR:O	1:A:597:LYS:C	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:GLU:OE2	31:P:28:LYS:HB2	2.11	0.50
1:A:1379:PHE:O	1:A:1382:SER:OG	2.17	0.50
1:A:2073:TRP:HH2	1:A:2310:ARG:NH1	2.09	0.50
3:C:134:LEU:HD23	3:C:226:VAL:HB	1.94	0.50
3:C:140:HIS:HB3	3:C:230:ASP:N	2.26	0.50
3:C:456:GLY:O	3:C:457:VAL:HG13	2.11	0.50
5:E:277:PHE:CE2	5:E:300:ILE:HD12	2.46	0.50
13:F:35:A:C8	14:G:12:G:N1	2.80	0.50
13:F:37:C:N4	14:G:5:G:OP1	2.44	0.50
14:G:-4:A:H2'	14:G:-3:A:H8	1.76	0.50
21:1:897:LEU:HD11	21:1:932:ILE:HD13	1.93	0.50
23:3:757:ILE:HG23	23:3:762:LEU:HD13	1.94	0.50
23:3:996:ILE:HD13	23:3:1041:TYR:HD1	1.75	0.50
32:R:434:TYR:CE2	32:R:436:VAL:HG22	2.43	0.50
33:T:306:CYS:SG	33:T:336:VAL:CB	2.97	0.50
36:Y:86:ASP:HB2	37:Z:502:ALA:HB3	1.93	0.50
1:A:76:MET:SD	1:A:88:TYR:CE1	3.05	0.50
1:A:393:LEU:HD11	3:C:378:TYR:CB	2.41	0.50
1:A:393:LEU:CD1	3:C:379:LYS:HG3	2.36	0.50
1:A:693:ILE:O	1:A:697:MET:N	2.42	0.50
2:B:42:U:C2	14:G:-3:A:C2	2.82	0.50
3:C:93:ILE:HG21	33:T:218:TRP:CE2	2.46	0.50
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.94	0.50
14:G:132:G:H2'	14:G:133:A:C8	2.46	0.50
21:1:822:ARG:HD3	36:Y:32:TYR:OH	2.12	0.50
23:3:550:ASN:OD1	23:3:551:GLN:N	2.41	0.50
23:3:685:ASP:OD1	23:3:686:LEU:N	2.44	0.50
23:3:807:TYR:HE1	23:3:861:GLN:HG3	1.76	0.50
32:R:101:ILE:O	32:R:104:GLN:HG2	2.08	0.50
32:R:442:ARG:HH11	32:R:443:GLY:CA	2.15	0.50
33:T:297:HIS:HD2	33:T:338:CYS:SG	2.34	0.50
34:V:484:SER:C	34:V:486:THR:H	2.15	0.50
1:A:338:VAL:HG21	3:C:867:PRO:CG	2.42	0.50
1:A:361:HIS:HE2	3:C:279:ARG:NH2	2.10	0.50
1:A:848:GLU:CD	32:R:424:SER:OG	2.50	0.50
1:A:2073:TRP:CH2	1:A:2310:ARG:NH1	2.80	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
13:F:36:A:C3'	13:F:37:C:C5'	2.85	0.50
15:H:25:G:H2'	15:H:26:A:C8	2.45	0.50
15:H:46:U:O2'	15:H:47:U:OP2	2.25	0.50
15:H:70:C:O5'	15:H:70:C:H6	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:147:G:N2	15:H:148:C:C2	2.80	0.50
21:1:1003:VAL:HG23	21:1:1004:ILE:H	1.77	0.50
21:1:1132:LEU:O	21:1:1135:GLU:N	2.45	0.50
23:3:300:PHE:CG	23:3:312:LYS:HE2	2.46	0.50
31:P:41:ILE:HD11	33:T:318:ARG:HA	1.92	0.50
31:P:210:PHE:CG	33:T:201:SER:OG	2.64	0.50
1:A:117:PRO:HG2	1:A:131:GLU:HB2	1.94	0.50
1:A:121:HIS:HA	1:A:481:PHE:O	2.12	0.50
1:A:253:ASN:HB3	3:C:893:GLY:O	2.12	0.50
1:A:386:PRO:HB3	3:C:372:PHE:HD1	1.77	0.50
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.30	0.50
1:A:316:PHE:CE1	3:C:635:LEU:CA	2.94	0.50
1:A:948:PRO:O	1:A:951:LEU:HB2	2.12	0.50
1:A:1505:LYS:HE2	37:Z:615:SER:CA	2.40	0.50
1:A:1757:GLU:CD	32:R:451:ILE:CD1	2.80	0.50
3:C:66:TYR:CD2	33:T:457:GLY:CA	2.79	0.50
3:C:244:LYS:CA	3:C:292:TYR:CD2	2.92	0.50
15:H:148:C:HO2'	15:H:149:A:H5'	1.77	0.50
23:3:1050:PHE:HB3	23:3:1167:TYR:HE2	1.75	0.50
23:3:1147:HIS:O	23:3:1151:GLU:HB2	2.10	0.50
33:T:281:ILE:HD12	33:T:282:ARG:HG2	1.92	0.50
1:A:1119:ASP:N	1:A:1120:PRO:CA	2.74	0.50
1:A:1402:ARG:HH21	37:Z:573:PRO:HG3	1.77	0.50
3:C:259:LYS:HE2	3:C:262:ARG:HH11	1.77	0.50
5:E:228:THR:HG22	5:E:229:TYR:HD1	1.77	0.50
13:F:41:A:H2'	13:F:42:C:C6	2.47	0.50
15:H:74:U:O5'	15:H:74:U:H6	1.95	0.50
21:1:595:GLU:O	21:1:599:ASN:ND2	2.45	0.50
23:3:12:THR:HA	23:3:34:ARG:NH1	2.27	0.50
23:3:819:MET:O	23:3:823:MET:HG3	2.12	0.50
35:X:282:LEU:HD23	35:X:295:ASP:HA	1.94	0.50
1:A:122:ILE:HD12	1:A:483:GLN:HG3	1.94	0.49
1:A:686:ARG:HH11	1:A:710:LEU:HD13	1.77	0.49
1:A:1127:GLY:O	1:A:1128:TYR:C	2.48	0.49
3:C:144:CYS:C	3:C:312:SER:HB2	2.33	0.49
3:C:499:GLY:O	3:C:500:THR:CG2	2.60	0.49
21:1:1040:GLY:HA2	21:1:1080:THR:HG22	1.94	0.49
23:3:4:TYR:HB2	23:3:1132:PHE:CZ	2.47	0.49
23:3:458:ALA:HB3	23:3:477:SER:HB3	1.94	0.49
23:3:550:ASN:HD21	23:3:595:VAL:N	2.10	0.49
23:3:1188:ASN:O	23:3:1192:ASN:ND2	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:66:ARG:HH11	31:P:66:ARG:CG	2.24	0.49
37:Z:612:TYR:C	37:Z:614:TRP:N	2.63	0.49
37:Z:614:TRP:CD1	37:Z:614:TRP:C	2.85	0.49
1:A:348:PRO:O	1:A:350:PHE:N	2.45	0.49
1:A:965:VAL:HG13	1:A:966:TRP:CD1	2.47	0.49
1:A:1403:LEU:O	32:R:412:ASP:CB	2.60	0.49
1:A:1700:GLY:H	1:A:1717:ASN:HD22	1.60	0.49
3:C:116:MET:O	3:C:119:LEU:HB3	2.12	0.49
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.45	0.49
5:E:265:ARG:N	5:E:272:ARG:HH21	2.10	0.49
15:H:181:G:N2	15:H:182:U:C2	2.80	0.49
21:1:717:THR:HG22	21:1:718:PRO:HD3	1.93	0.49
23:3:274:ARG:HG2	23:3:387:PHE:CE1	2.47	0.49
23:3:755:VAL:HG13	23:3:762:LEU:HD11	1.93	0.49
32:R:132:LEU:HB3	33:T:399:LYS:HZ1	1.77	0.49
36:Y:48:THR:OG1	36:Y:49:GLU:OE1	2.30	0.49
1:A:387:PHE:CZ	3:C:330:THR:CB	2.96	0.49
1:A:1120:PRO:HG2	1:A:1121:ASN:H	1.78	0.49
1:A:2298:LEU:C	4:D:1283:PRO:CB	2.78	0.49
2:B:20:G:HI'	2:B:21:A:OP1	2.12	0.49
3:C:65:TYR:C	3:C:66:TYR:CG	2.86	0.49
3:C:78:GLU:OE1	33:T:198:ARG:NH2	2.45	0.49
3:C:297:ASN:HB3	3:C:298:LEU:HD13	1.95	0.49
3:C:493:PHE:HD2	3:C:551:LEU:HD21	1.76	0.49
3:C:715:GLY:HA2	3:C:729:ALA:HB1	1.93	0.49
5:E:164:PRO:O	5:E:166:LEU:HG	2.13	0.49
21:1:499:LYS:HD3	21:1:534:GLN:NE2	2.27	0.49
21:1:652:CYS:HB3	21:1:692:HIS:CE1	2.46	0.49
21:1:827:ARG:O	21:1:830:TYR:HB3	2.12	0.49
23:3:235:LEU:HG	23:3:250:ILE:HG13	1.93	0.49
23:3:1008:SER:OG	23:3:1009:PHE:N	2.45	0.49
1:A:235:MET:CE	1:A:411:PHE:CA	2.84	0.49
1:A:800:TYR:CB	3:C:59:LEU:HD13	2.43	0.49
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.44	0.49
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.45	0.49
1:A:1760:GLU:HB2	1:A:1761:PRO:HD2	1.93	0.49
1:A:1807:ILE:HB	1:A:1820:LYS:HB3	1.92	0.49
1:A:2325:VAL:HG11	4:D:789:MET:HA	1.94	0.49
3:C:62:ASP:HB3	31:P:206:LYS:NZ	2.27	0.49
3:C:66:TYR:CE2	31:P:211:VAL:HG11	2.45	0.49
3:C:349:PHE:CD1	3:C:356:PHE:HE1	2.22	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:37:U:H2'	15:H:38:A:H8	1.77	0.49
23:3:253:GLU:OE2	23:3:284:GLY:HA3	2.12	0.49
23:3:483:LEU:HD11	23:3:493:GLU:HG3	1.94	0.49
28:J:220:LEU:HD13	28:J:220:LEU:C	2.32	0.49
32:R:433:ILE:HG13	32:R:434:TYR:O	2.12	0.49
1:A:115:ASP:CB	1:A:486:LYS:HE2	2.42	0.49
1:A:366:LYS:N	1:A:366:LYS:CE	2.73	0.49
1:A:409:ARG:N	1:A:410:PRO:HD2	2.26	0.49
1:A:1405:LEU:N	32:R:415:LEU:HD21	2.27	0.49
1:A:1818:PHE:CD2	1:A:1848:LEU:HD21	2.47	0.49
1:A:1930:TYR:CD2	1:A:1930:TYR:C	2.85	0.49
3:C:133:THR:O	3:C:226:VAL:CB	2.60	0.49
3:C:335:ASN:OD1	3:C:336:TYR:N	2.45	0.49
3:C:709:TRP:N	3:C:709:TRP:CD1	2.79	0.49
23:3:994:GLN:HE22	23:3:1037:SER:HA	1.78	0.49
32:R:231:VAL:HG23	32:R:232:MET:N	2.26	0.49
32:R:241:MET:SD	32:R:245:GLU:CD	2.91	0.49
32:R:450:SER:OG	32:R:452:TYR:O	2.30	0.49
37:Z:563:ARG:CG	37:Z:563:ARG:NH2	2.73	0.49
1:A:690:MET:HG3	1:A:694:LEU:HD12	1.95	0.49
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.95	0.49
1:A:1809:ILE:HD11	1:A:1845:VAL:HG22	1.93	0.49
13:F:36:A:C8	13:F:36:A:H5'	2.48	0.49
21:1:805:TYR:CE1	21:1:809:GLU:HG3	2.46	0.49
23:3:23:SER:HA	23:3:94:PRO:HG3	1.95	0.49
23:3:794:SER:HB2	23:3:933:ASN:O	2.12	0.49
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.45	0.49
28:J:331:GLN:CG	32:R:98:TYR:OH	2.47	0.49
37:Z:526:ILE:N	37:Z:526:ILE:HD12	2.27	0.49
1:A:347:LEU:HD13	1:A:351:TYR:OH	2.12	0.49
1:A:800:TYR:HB3	3:C:59:LEU:HD13	1.95	0.49
1:A:2097:ILE:HD12	1:A:2099:GLU:HB2	1.93	0.49
3:C:140:HIS:O	3:C:258:ASN:HB3	2.13	0.49
3:C:363:SER:O	3:C:364:SER:CB	2.60	0.49
21:1:498:MET:HE1	21:1:531:LEU:HD12	1.93	0.49
21:1:1017:LEU:HD21	21:1:1058:ILE:HD11	1.93	0.49
21:1:1273:TYR:OH	21:1:1277:GLN:NE2	2.46	0.49
23:3:31:VAL:HG21	23:3:78:ILE:HD11	1.95	0.49
23:3:440:HIS:ND1	23:3:720:TRP:CH2	2.80	0.49
23:3:527:ILE:HA	23:3:532:ARG:O	2.12	0.49
31:P:30:TYR:OH	32:R:162:ALA:C	2.50	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Z:597:ARG:HH12	37:Z:601:LEU:CD1	2.22	0.49
1:A:251:ASP:HA	1:A:337:VAL:HG21	1.94	0.49
1:A:1618:LYS:HD2	1:A:1626:CYS:H	1.78	0.49
1:A:1718:TRP:HZ3	1:A:1726:ILE:HD12	1.77	0.49
1:A:2287:ARG:HH22	4:D:1147:ASN:CB	2.15	0.49
3:C:73:TYR:CZ	33:T:487:LYS:CE	2.95	0.49
3:C:137:HIS:NE2	3:C:236:MET:CE	2.75	0.49
3:C:705:VAL:HG21	3:C:718:PHE:CZ	2.47	0.49
5:E:74:PHE:HE1	5:E:95:VAL:CG2	2.25	0.49
13:F:53:A:C6	13:F:54:G:C5	3.00	0.49
14:G:5:G:H2'	14:G:5:G:N3	2.28	0.49
14:G:155:U:H4'	14:G:156:U:OP2	2.13	0.49
15:H:107:A:C2	15:H:108:G:C4	3.01	0.49
15:H:143:A:N3	15:H:143:A:C3'	2.73	0.49
21:1:175:LYS:O	21:1:179:GLY:HA3	2.11	0.49
21:1:1134:ASN:ND2	22:2:534:GLN:HA	2.28	0.49
23:3:47:THR:HG23	23:3:49:LYS:H	1.77	0.49
23:3:785:PRO:HA	23:3:801:GLU:HA	1.95	0.49
24:4:32:LEU:HD21	24:4:79:LEU:HD21	1.94	0.49
32:R:55:LEU:CA	32:R:73:PRO:O	2.61	0.49
1:A:87:VAL:HG13	32:R:205:ASP:OD2	2.13	0.49
1:A:1393:ARG:O	1:A:1397:ILE:HG13	2.12	0.49
3:C:301:SER:O	3:C:303:LEU:N	2.44	0.49
3:C:499:GLY:O	3:C:500:THR:HG23	2.13	0.49
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.95	0.49
26:6:43:VAL:HG21	26:6:69:ALA:HB3	1.94	0.49
32:R:131:ASP:OD2	32:R:132:LEU:CD2	2.60	0.49
32:R:171:LEU:HD11	32:R:201:GLU:CD	2.32	0.49
33:T:442:ARG:HB3	33:T:443:THR:HG23	1.95	0.49
36:Y:38:ILE:HG22	36:Y:90:THR:HG23	1.95	0.49
1:A:91:ALA:O	1:A:94:TYR:N	2.43	0.49
1:A:273:ILE:CG2	1:A:274:PRO:HD2	2.42	0.49
1:A:660:PHE:HB3	32:R:210:PRO:O	2.13	0.49
1:A:2113:LYS:HE2	4:D:1229:ASP:CA	2.41	0.49
3:C:381:LEU:CD2	3:C:416:LEU:HD22	2.42	0.49
5:E:74:PHE:HE1	5:E:95:VAL:HG22	1.77	0.49
15:H:71:C:H2'	15:H:72:U:H6	1.75	0.49
32:R:433:ILE:O	32:R:434:TYR:HB3	2.13	0.49
36:Y:24:ASP:CG	36:Y:25:LYS:H	2.14	0.49
1:A:44:ARG:CG	1:A:45:TYR:CE2	2.95	0.48
1:A:529:THR:HG22	30:M:197:TYR:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1870:ASP:HB2	1:A:1871:PRO:HD3	1.95	0.48
1:A:1998:ASN:O	1:A:2001:SER:OG	2.23	0.48
3:C:82:GLN:HG3	33:T:237:LYS:HA	1.94	0.48
3:C:334:ILE:HD12	3:C:334:ILE:O	2.13	0.48
5:E:153:PHE:N	5:E:153:PHE:CD1	2.78	0.48
13:F:26:U:H3'	13:F:27:A:C5'	2.37	0.48
15:H:182:U:HO2'	15:H:183:G:H5'	1.76	0.48
21:1:408:PHE:HB2	25:5:49:ARG:NH1	2.28	0.48
23:3:734:LEU:HD13	23:3:767:LEU:HD21	1.94	0.48
32:R:82:MET:HE2	32:R:82:MET:O	2.13	0.48
36:Y:32:TYR:C	36:Y:34:ASP:H	2.15	0.48
1:A:794:TYR:CD2	1:A:1028:TYR:HB2	2.47	0.48
1:A:1301:ILE:HD11	2:B:39:C:H5''	1.91	0.48
3:C:78:GLU:C	33:T:198:ARG:HA	2.25	0.48
3:C:508:LYS:HB3	3:C:566:THR:HG23	1.95	0.48
3:C:855:GLY:O	3:C:856:HIS:CB	2.44	0.48
5:E:162:ARG:HH22	5:E:204:THR:HA	1.74	0.48
13:F:54:G:N2	15:H:22:U:C2	2.81	0.48
14:G:11:A:N3	14:G:11:A:C3'	2.76	0.48
15:H:5:C:H2'	15:H:6:U:H6	1.78	0.48
21:1:483:ASP:OD1	21:1:484:GLU:N	2.46	0.48
28:J:360:ASP:HA	28:J:363:ARG:CG	2.44	0.48
1:A:267:LYS:NZ	2:B:49:A:P	2.85	0.48
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.95	0.48
1:A:828:PRO:HG3	1:A:925:TYR:CZ	2.48	0.48
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.48	0.48
1:A:2298:LEU:HD11	4:D:1285:SER:CA	2.43	0.48
3:C:73:TYR:CE1	33:T:453:ALA:O	2.67	0.48
3:C:297:ASN:HD22	3:C:298:LEU:CD1	2.26	0.48
3:C:333:ASP:OD1	3:C:333:ASP:N	2.42	0.48
3:C:401:ILE:HD11	3:C:423:PHE:HB2	1.96	0.48
13:F:49:G:H2'	13:F:50:A:H8	1.78	0.48
14:G:138:A:H5''	29:L:12:ARG:NE	2.28	0.48
15:H:10:C:H2'	15:H:11:G:C8	2.40	0.48
23:3:157:PRO:HD2	26:6:16:GLY:HA2	1.95	0.48
23:3:870:ASN:ND2	23:3:873:GLN:H	2.10	0.48
32:R:433:ILE:HG13	32:R:434:TYR:N	2.27	0.48
33:T:302:VAL:HG23	33:T:315:TRP:O	2.14	0.48
37:Z:604:LYS:HA	37:Z:607:VAL:HG23	1.94	0.48
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.13	0.48
1:A:2149:PRO:O	1:A:2160:PRO:HD3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:291:MET:CG	3:C:292:TYR:CE1	2.96	0.48
3:C:443:VAL:O	3:C:447:PRO:CD	2.62	0.48
3:C:452:THR:O	3:C:577:PHE:CA	2.60	0.48
13:F:8:C:H6	13:F:8:C:C5'	2.15	0.48
13:F:66:C:H2'	13:F:67:G:O4'	2.12	0.48
14:G:-8:U:H2'	14:G:-7:C:O4'	2.13	0.48
14:G:9:C:H2'	14:G:10:U:C6	2.48	0.48
15:H:25:G:N3	15:H:26:A:C8	2.82	0.48
23:3:886:GLU:OE1	23:3:926:TYR:OH	2.24	0.48
23:3:1149:ARG:HH12	23:3:1161:LEU:HD13	1.79	0.48
28:J:406:PHE:HB3	28:J:411:MET:HG2	1.96	0.48
35:X:212:ASN:H	35:X:307:GLN:HE22	1.60	0.48
1:A:258:PHE:HZ	1:A:275:GLY:O	1.96	0.48
1:A:387:PHE:HD1	3:C:327:TYR:CD1	2.31	0.48
1:A:774:LYS:HG2	15:H:23:A:C8	2.48	0.48
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.23	0.48
13:F:45:A:H4'	13:F:46:G:OP2	2.14	0.48
13:F:53:A:C6	15:H:25:G:C4	3.02	0.48
23:3:457:ASN:HD21	23:3:504:PRO:HB3	1.79	0.48
23:3:624:CYS:SG	23:3:625:LEU:HD13	2.54	0.48
23:3:930:LEU:HA	23:3:937:LEU:HD23	1.95	0.48
27:7:40:TYR:HA	27:7:43:TYR:CD2	2.49	0.48
32:R:103:ARG:CG	32:R:103:ARG:NH1	2.75	0.48
33:T:185:MET:CB	33:T:186:PRO:CD	2.90	0.48
33:T:213:GLU:HB2	33:T:218:TRP:O	2.14	0.48
34:V:549:LYS:O	34:V:552:ALA:CB	2.60	0.48
1:A:299:ILE:CD1	3:C:920:PRO:C	2.82	0.48
1:A:323:LEU:N	1:A:324:PRO:CD	2.77	0.48
1:A:366:LYS:N	1:A:366:LYS:HD3	2.27	0.48
1:A:595:LYS:CE	1:A:644:ILE:HD11	2.38	0.48
1:A:718:ARG:HH21	32:R:259:LYS:CE	2.25	0.48
1:A:1370:ARG:NH1	34:V:468:ASP:H	2.09	0.48
3:C:350:ASN:HB3	3:C:353:THR:HG23	1.94	0.48
3:C:445:ALA:O	3:C:449:ILE:HG13	2.12	0.48
3:C:678:THR:HG23	3:C:683:ASN:CA	2.43	0.48
3:C:736:GLY:N	3:C:770:PHE:HE2	2.10	0.48
21:1:1212:LEU:HD13	21:1:1237:LEU:HD13	1.96	0.48
23:3:142:TYR:CE1	23:3:157:PRO:HB3	2.48	0.48
23:3:565:TYR:CG	23:3:619:LEU:HD13	2.48	0.48
32:R:215:ASN:HD22	32:R:216:LYS:N	2.11	0.48
1:A:338:VAL:HG21	3:C:867:PRO:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1295:ILE:HG13	1:A:1296:GLN:N	2.29	0.48
3:C:135:CYS:SG	3:C:227:LEU:HA	2.54	0.48
3:C:149:LEU:CA	3:C:427:PHE:CE2	2.97	0.48
3:C:349:PHE:HB2	3:C:356:PHE:CE1	2.48	0.48
3:C:514:TYR:CD1	3:C:515:THR:N	2.82	0.48
15:H:83:A:C2	15:H:84:C:N3	2.82	0.48
23:3:842:PHE:HD2	23:3:843:LEU:HD12	1.78	0.48
23:3:926:TYR:HE1	23:3:942:LYS:HG3	1.77	0.48
28:J:273:TYR:CZ	32:R:228:PRO:CB	2.82	0.48
33:T:387:PHE:CD1	33:T:387:PHE:C	2.87	0.48
1:A:1332:HIS:HB3	1:A:1359:HIS:HE1	1.78	0.48
1:A:2298:LEU:HD11	4:D:1265:GLN:CB	2.44	0.48
3:C:82:GLN:O	33:T:202:GLY:HA3	2.13	0.48
3:C:457:VAL:HG12	3:C:462:GLY:HA3	1.96	0.48
3:C:477:HIS:HD1	3:C:478:THR:N	2.12	0.48
5:E:243:LEU:HD11	5:E:247:GLY:CA	2.41	0.48
14:G:17:U:H2'	14:G:18:A:C8	2.49	0.48
15:H:83:A:C2	15:H:84:C:C4	3.01	0.48
21:1:1297:ARG:NH1	27:7:39:SER:OG	2.46	0.48
22:2:504:TRP:C	22:2:506:PHE:H	2.17	0.48
33:T:384:HIS:O	33:T:385:TYR:HB3	2.13	0.48
1:A:405:LEU:HD11	3:C:265:LEU:HD22	1.96	0.48
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.79	0.48
3:C:128:LEU:O	3:C:199:LEU:N	2.37	0.48
3:C:690:GLU:HB2	3:C:691:PRO:HD2	1.95	0.48
13:F:44:G:H2'	22:2:554:ARG:HG2	1.96	0.48
15:H:37:U:H2'	15:H:38:A:C8	2.49	0.48
22:2:652:GLY:N	22:2:655:SER:O	2.45	0.48
23:3:21:ASN:HD21	23:3:28:GLN:HG2	1.77	0.48
23:3:58:VAL:HG12	23:3:1155:LEU:HB3	1.95	0.48
23:3:539:PRO:HD2	23:3:558:LEU:HD21	1.95	0.48
23:3:891:VAL:HA	23:3:906:LEU:O	2.13	0.48
23:3:1057:ARG:HG2	23:3:1058:LEU:O	2.13	0.48
32:R:184:GLN:O	32:R:188:PHE:HB2	2.13	0.48
34:V:576:THR:O	34:V:579:SER:N	2.47	0.48
36:Y:110:ASP:OD1	36:Y:111:HIS:N	2.43	0.48
1:A:356:ILE:CG2	3:C:865:GLY:C	2.82	0.48
1:A:417:ARG:NH1	2:B:58:U:C5'	2.77	0.48
1:A:529:THR:HB	30:M:199:PRO:CD	2.44	0.48
1:A:546:LEU:HD11	1:A:595:LYS:CG	2.43	0.48
1:A:731:LEU:HD23	1:A:736:GLU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2310:ARG:HH11	1:A:2310:ARG:CG	2.27	0.48
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.48
3:C:93:ILE:O	3:C:94:ILE:CB	2.62	0.48
3:C:145:PHE:HB2	3:C:312:SER:CB	2.32	0.48
21:1:208:PRO:N	21:1:656:LYS:HE3	2.29	0.48
23:3:476:VAL:O	23:3:482:THR:HA	2.14	0.48
23:3:981:CYS:SG	23:3:1021:LEU:HG	2.54	0.48
32:R:402:ASN:HB2	35:X:192:ARG:CG	2.43	0.48
34:V:527:GLY:O	34:V:530:LYS:N	2.47	0.48
1:A:171:ASP:CG	1:A:519:ASP:OD2	2.53	0.47
1:A:238:LEU:HB3	1:A:411:PHE:HE2	1.79	0.47
1:A:406:TRP:CH2	3:C:265:LEU:C	2.87	0.47
1:A:409:ARG:HD2	1:A:409:ARG:O	2.14	0.47
1:A:735:ILE:O	1:A:738:MET:HE2	2.14	0.47
1:A:758:ARG:HD2	1:A:775:ASN:ND2	2.28	0.47
1:A:1183:PRO:HA	1:A:1201:ARG:HE	1.78	0.47
1:A:1754:TYR:CD1	21:1:948:ARG:NH1	2.82	0.47
1:A:1768:TYR:HA	1:A:1771:LEU:CB	2.40	0.47
3:C:557:GLN:N	3:C:558:PRO:HD2	2.29	0.47
5:E:263:ASP:OD1	5:E:272:ARG:HB3	2.13	0.47
13:F:44:G:N2	14:G:3:A:C8	2.82	0.47
21:1:209:GLY:HA3	21:1:614:ARG:NH1	2.29	0.47
23:3:353:PHE:HB3	23:3:406:PRO:HD3	1.96	0.47
23:3:814:GLN:O	23:3:818:GLN:HB2	2.13	0.47
26:6:19:ILE:HD12	26:6:42:LEU:HD21	1.96	0.47
28:J:273:TYR:CD2	32:R:228:PRO:HG3	2.49	0.47
32:R:120:VAL:CG2	32:R:121:PRO:HD2	2.44	0.47
34:V:484:SER:C	34:V:486:THR:N	2.67	0.47
35:X:246:TYR:H	35:X:386:ASP:HA	1.79	0.47
1:A:134:TRP:HB3	1:A:418:THR:HG22	1.95	0.47
1:A:312:TYR:CZ	3:C:882:GLY:C	2.87	0.47
1:A:330:THR:O	1:A:331:TRP:CB	2.62	0.47
1:A:666:LYS:HE2	32:R:217:LYS:HG3	1.96	0.47
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.29	0.47
1:A:1270:LEU:HD12	1:A:1274:PHE:CD2	2.49	0.47
1:A:1551:PHE:O	1:A:1553:VAL:HG23	2.14	0.47
3:C:753:GLU:O	3:C:755:ASP:N	2.45	0.47
5:E:269:PRO:O	5:E:270:LYS:CB	2.54	0.47
13:F:12:G:H2'	13:F:13:G:O4'	2.14	0.47
15:H:151:C:C2	15:H:152:G:N7	2.82	0.47
23:3:675:LEU:HD23	23:3:686:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1095:TYR:CZ	23:3:1164:ARG:HD2	2.49	0.47
26:6:23:CYS:HB3	26:6:58:CYS:HB2	1.97	0.47
27:7:69:MET:HA	27:7:72:MET:HG2	1.96	0.47
28:J:436:TYR:OH	28:J:458:PHE:HA	2.14	0.47
33:T:416:ILE:O	33:T:416:ILE:HD13	2.14	0.47
1:A:350:PHE:HE2	1:A:398:THR:HG21	1.79	0.47
1:A:1258:LYS:HE2	32:R:432:GLU:CA	2.44	0.47
1:A:2148:VAL:O	1:A:2150:GLN:HG2	2.14	0.47
3:C:66:TYR:OH	31:P:216:ARG:HD2	2.13	0.47
3:C:73:TYR:HE1	33:T:453:ALA:O	1.97	0.47
3:C:441:PRO:O	3:C:444:GLY:CA	2.61	0.47
3:C:449:ILE:HD12	3:C:466:SER:OG	2.13	0.47
3:C:673:LYS:HB3	3:C:688:ILE:HG22	1.96	0.47
5:E:178:LEU:CD2	5:E:208:ILE:HD13	2.44	0.47
14:G:138:A:H2'	14:G:139:U:C6	2.49	0.47
21:1:1252:GLN:HG2	22:2:492:LYS:HA	1.96	0.47
23:3:240:GLY:HA3	23:3:246:SER:HB2	1.95	0.47
27:7:33:VAL:HG23	27:7:75:PRO:HG2	1.96	0.47
32:R:73:PRO:HG2	32:R:74:LEU:H	1.79	0.47
32:R:189:ASN:HD21	32:R:195:ARG:CZ	2.26	0.47
34:V:625:ARG:O	34:V:629:ASN:CB	2.62	0.47
36:Y:63:VAL:HG23	36:Y:64:ASN:H	1.78	0.47
1:A:121:HIS:O	1:A:123:THR:N	2.47	0.47
1:A:1192:PHE:HE1	1:A:1274:PHE:CD1	2.32	0.47
1:A:1439:ARG:O	1:A:1443:LYS:HG2	2.15	0.47
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.47
3:C:240:GLU:OE2	3:C:292:TYR:OH	2.18	0.47
3:C:438:ILE:CD1	3:C:438:ILE:N	2.76	0.47
14:G:17:U:H2'	14:G:18:A:H8	1.79	0.47
14:G:149:G:N2	14:G:150:U:H2'	2.29	0.47
21:1:464:LEU:HD23	21:1:478:LEU:HD21	1.95	0.47
21:1:781:ASP:HB3	21:1:784:MET:HB2	1.95	0.47
23:3:54:LEU:HD22	23:3:98:MET:HA	1.97	0.47
23:3:120:PHE:HB2	23:3:133:SER:OG	2.15	0.47
26:6:21:ARG:HG3	26:6:56:GLY:HA2	1.96	0.47
31:P:224:MET:HE2	31:P:228:ILE:CD1	2.39	0.47
31:P:228:ILE:CD1	31:P:228:ILE:N	2.78	0.47
1:A:203:VAL:HG12	1:A:207:PHE:CD1	2.49	0.47
1:A:2252:LEU:HD23	1:A:2253:PRO:HD2	1.96	0.47
2:B:44:A:H2	14:G:-5:G:O6	1.97	0.47
3:C:73:TYR:OH	33:T:487:LYS:CE	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:185:PRO:HD3	3:C:482:TYR:CE1	2.50	0.47
5:E:161:ARG:HH11	5:E:161:ARG:CG	2.26	0.47
21:1:1172:LEU:HA	22:2:522:PHE:HE1	1.79	0.47
23:3:354:GLY:HA3	23:3:432:ARG:NH1	2.30	0.47
31:P:192:VAL:HG12	31:P:193:VAL:N	2.29	0.47
32:R:103:ARG:NH2	32:R:110:LYS:O	2.40	0.47
32:R:178:ARG:CD	32:R:194:GLN:NE2	2.72	0.47
1:A:393:LEU:HD13	3:C:375:GLU:HG3	1.95	0.47
3:C:507:VAL:HG12	3:C:508:LYS:N	2.29	0.47
3:C:710:ASN:O	3:C:711:ARG:C	2.53	0.47
14:G:-5:G:O2'	14:G:-4:A:H8	1.98	0.47
15:H:57:A:H2'	15:H:58:U:O4'	2.14	0.47
21:1:1140:GLU:O	21:1:1144:GLN:HG3	2.15	0.47
23:3:459:VAL:HB	23:3:757:ILE:HG23	1.97	0.47
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.97	0.47
28:J:216:ASP:O	28:J:219:GLU:N	2.47	0.47
32:R:51:ILE:N	32:R:52:PRO:CD	2.77	0.47
33:T:318:ARG:HH11	33:T:319:THR:CG2	2.28	0.47
1:A:121:HIS:HE2	1:A:481:PHE:CB	2.14	0.47
1:A:340:ILE:HD13	1:A:340:ILE:N	2.29	0.47
1:A:363:HIS:HD2	3:C:283:ASP:O	1.98	0.47
1:A:639:PHE:O	2:B:28:A:O2'	2.31	0.47
1:A:664:HIS:HE1	1:A:666:LYS:HB2	1.71	0.47
1:A:735:ILE:O	1:A:738:MET:HB3	2.15	0.47
1:A:1241:HIS:ND1	1:A:1287:LEU:HD11	2.29	0.47
2:B:41:U:H2'	2:B:42:U:C6	2.49	0.47
3:C:78:GLU:CD	3:C:80:ILE:HD11	2.30	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.14	0.47
21:1:903:GLN:HE22	21:1:910:MET:HG3	1.80	0.47
23:3:18:ILE:HD13	23:3:65:LEU:HG	1.96	0.47
23:3:931:VAL:O	23:3:936:LYS:N	2.40	0.47
23:3:1032:TRP:O	23:3:1048:ASP:HA	2.15	0.47
28:J:273:TYR:CE2	32:R:228:PRO:HB3	2.46	0.47
31:P:227:TYR:N	31:P:227:TYR:CD1	2.81	0.47
33:T:257:ARG:HD3	33:T:301:ASP:OD1	2.14	0.47
36:Y:40:LEU:HB2	36:Y:43:LEU:HD11	1.96	0.47
1:A:195:LEU:H	1:A:195:LEU:HD12	1.80	0.47
1:A:592:TYR:O	1:A:595:LYS:O	2.32	0.47
1:A:1455:TRP:CE3	1:A:1456:THR:HB	2.50	0.47
2:B:43:U:H5'	13:F:67:G:H22	1.79	0.47
3:C:115:GLU:O	3:C:118:PHE:CA	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:457:VAL:CA	3:C:462:GLY:HA3	2.44	0.47
21:1:207:THR:HA	21:1:656:LYS:NZ	2.28	0.47
21:1:699:GLN:HA	21:1:702:ARG:CZ	2.45	0.47
23:3:164:ASN:ND2	23:3:189:TYR:OH	2.34	0.47
23:3:304:GLN:HA	23:3:309:ASP:O	2.15	0.47
23:3:931:VAL:HG12	23:3:932:ASN:N	2.26	0.47
25:5:14:PRO:HB2	25:5:16:GLU:OE1	2.15	0.47
33:T:246:ILE:HB	33:T:267:ASP:OD1	2.15	0.47
1:A:97:HIS:HD2	1:A:473:PHE:HZ	1.59	0.47
1:A:695:ASP:HB3	33:T:374:SER:CB	2.38	0.47
1:A:1608:THR:HG22	1:A:1632:PHE:HB2	1.97	0.47
21:1:535:ILE:O	21:1:538:LEU:N	2.47	0.47
21:1:760:GLU:N	21:1:760:GLU:OE1	2.47	0.47
21:1:1132:LEU:HD11	21:1:1150:SER:OG	2.14	0.47
23:3:5:ASN:OD1	23:3:6:LEU:N	2.47	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
23:3:498:GLY:HA3	23:3:531:LYS:NZ	2.30	0.47
32:R:67:ILE:HG22	32:R:69:VAL:HG21	1.97	0.47
32:R:82:MET:HE3	32:R:82:MET:C	2.36	0.47
34:V:467:LEU:O	34:V:468:ASP:CB	2.62	0.47
2:B:12:U:H3	2:B:65:G:H1	1.62	0.47
2:B:41:U:C4	14:G:-1:G:N1	2.83	0.47
3:C:470:PRO:CA	3:C:499:GLY:HA2	2.42	0.47
3:C:490:PHE:CE1	3:C:612:LYS:HD2	2.49	0.47
13:F:49:G:H2'	13:F:50:A:C8	2.50	0.47
14:G:156:U:P	14:G:156:U:H3'	2.54	0.47
15:H:6:U:H2'	15:H:7:U:H6	1.80	0.47
15:H:47:U:H4'	15:H:48:A:OP1	2.15	0.47
15:H:153:A:C8	15:H:154:C:H5'	2.50	0.47
21:1:1185:ARG:HD2	21:1:1218:ASN:CG	2.35	0.47
22:2:642:PRO:HG3	22:2:648:LEU:HD22	1.97	0.47
23:3:182:PHE:O	23:3:210:PHE:HA	2.15	0.47
23:3:458:ALA:HA	23:3:741:PHE:CB	2.45	0.47
28:J:255:LEU:CD2	29:L:235:LEU:HD13	2.38	0.47
1:A:67:ARG:HD3	1:A:179:ALA:CB	2.34	0.46
1:A:277:PRO:HA	1:A:448:GLN:HG3	1.96	0.46
1:A:316:PHE:HE1	3:C:635:LEU:CA	2.27	0.46
1:A:437:ALA:O	1:A:439:GLN:HG2	2.15	0.46
1:A:519:ASP:C	1:A:519:ASP:OD1	2.54	0.46
1:A:755:HIS:HE1	31:P:223:PHE:CB	2.14	0.46
1:A:1256:PHE:CZ	1:A:1302:GLY:HA3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1364:LEU:HD13	34:V:461:LEU:O	2.15	0.46
1:A:1718:TRP:CZ3	1:A:1723:LYS:HA	2.50	0.46
2:B:43:U:O4	14:G:-4:A:C6	2.68	0.46
3:C:82:GLN:HG3	33:T:238:LEU:N	2.30	0.46
3:C:244:LYS:HG3	3:C:292:TYR:CD2	2.50	0.46
3:C:449:ILE:HD11	3:C:465:MET:C	2.35	0.46
3:C:571:ASN:O	3:C:572:GLU:HB3	2.16	0.46
21:1:815:PHE:HA	21:1:819:TRP:HD1	1.81	0.46
21:1:1058:ILE:O	21:1:1062:LEU:HG	2.16	0.46
23:3:248:VAL:HG23	23:3:250:ILE:HD11	1.96	0.46
31:P:64:GLU:OE2	31:P:68:ARG:NE	2.48	0.46
1:A:280:GLU:HB2	2:B:48:A:O4'	2.15	0.46
1:A:414:ARG:NH1	3:C:408:LEU:O	2.43	0.46
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.83	0.46
1:A:1212:GLY:HA3	1:A:1280:ASN:ND2	2.31	0.46
1:A:1824:THR:HA	1:A:1827:TRP:HD1	1.80	0.46
1:A:1892:PRO:HG3	1:A:1941:ARG:HE	1.81	0.46
2:B:42:U:O5'	2:B:42:U:H6	1.97	0.46
2:B:44:A:C2	14:G:-5:G:O6	2.69	0.46
3:C:262:ARG:HG2	41:C:1500:GTP:N2	2.30	0.46
3:C:350:ASN:CB	3:C:353:THR:HG23	2.45	0.46
13:F:78:A:H8	13:F:78:A:OP2	1.98	0.46
15:H:150:U:H2'	15:H:151:C:C6	2.50	0.46
21:1:732:TRP:HB2	21:1:765:TYR:HE1	1.79	0.46
21:1:738:HIS:CE1	21:1:746:PHE:HE2	2.32	0.46
21:1:1169:VAL:HG12	21:1:1173:LEU:HG	1.97	0.46
23:3:28:GLN:NE2	23:3:343:LYS:HG2	2.31	0.46
23:3:1005:VAL:O	23:3:1032:TRP:HA	2.15	0.46
36:Y:48:THR:HG1	36:Y:49:GLU:H	1.63	0.46
1:A:388:LEU:HB3	1:A:391:THR:OG1	2.16	0.46
1:A:405:LEU:HD21	3:C:385:VAL:HG12	1.98	0.46
1:A:844:GLU:O	1:A:848:GLU:HG2	2.15	0.46
1:A:982:GLU:HG3	1:A:1169:GLN:HG3	1.97	0.46
1:A:1761:PRO:CB	1:A:1930:TYR:OH	2.55	0.46
1:A:1821:ILE:O	1:A:1912:PRO:HA	2.15	0.46
3:C:221:ILE:HG23	3:C:495:ARG:HB3	1.96	0.46
5:E:87:ASP:O	5:E:88:ARG:CG	2.63	0.46
21:1:728:LEU:O	21:1:731:LEU:N	2.48	0.46
23:3:274:ARG:NH2	23:3:307:GLN:OE1	2.48	0.46
32:R:195:ARG:HB3	32:R:195:ARG:HH11	1.80	0.46
36:Y:37:TRP:CZ3	37:Z:498:GLY:C	2.86	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ILE:CD1	1:A:483:GLN:CG	2.89	0.46
1:A:201:ALA:HA	1:A:204:LEU:HB3	1.98	0.46
1:A:468:LYS:HD3	1:A:468:LYS:C	2.35	0.46
1:A:1607:GLU:HB2	1:A:1634:SER:HA	1.96	0.46
1:A:1733:ILE:HG23	1:A:1737:ASN:HB2	1.98	0.46
1:A:2070:LYS:HA	1:A:2070:LYS:HD3	1.67	0.46
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.15	0.46
1:A:2314:PHE:HB3	4:D:1125:SER:N	2.29	0.46
2:B:29:A:O2'	2:B:30:A:H5'	2.15	0.46
3:C:66:TYR:CG	33:T:457:GLY:HA2	2.46	0.46
3:C:80:ILE:HD13	33:T:198:ARG:HG3	1.98	0.46
3:C:678:THR:HG21	3:C:683:ASN:CB	2.43	0.46
5:E:260:ARG:CZ	5:E:276:ILE:HD11	2.46	0.46
13:F:37:C:O2	13:F:37:C:H2'	2.15	0.46
14:G:149:G:H2'	14:G:150:U:C6	2.50	0.46
15:H:71:C:O5'	15:H:71:C:H6	1.98	0.46
15:H:79:G:N3	15:H:80:A:C8	2.83	0.46
15:H:142:C:H2'	15:H:143:A:H5'	1.98	0.46
21:1:572:HIS:HB2	21:1:612:THR:HG23	1.96	0.46
21:1:722:GLU:O	21:1:725:ASP:HB2	2.14	0.46
21:1:842:ASN:HA	21:1:879:LEU:HD11	1.96	0.46
21:1:1210:HIS:CD2	22:2:584:LEU:HD22	2.51	0.46
23:3:30:ILE:HG22	23:3:32:VAL:HG13	1.98	0.46
23:3:228:LEU:HD23	23:3:259:LYS:NZ	2.30	0.46
23:3:238:VAL:HB	23:3:247:GLY:O	2.16	0.46
23:3:718:ARG:HG2	23:3:719:SER:N	2.30	0.46
23:3:801:GLU:O	23:3:864:SER:HA	2.16	0.46
33:T:213:GLU:HG3	33:T:218:TRP:NE1	2.29	0.46
1:A:232:LEU:HD11	3:C:412:ILE:HD13	1.95	0.46
1:A:298:ASP:OD1	1:A:300:ASN:N	2.48	0.46
1:A:1370:ARG:HH12	34:V:468:ASP:H	1.58	0.46
1:A:1700:GLY:O	1:A:1717:ASN:N	2.41	0.46
1:A:1782:ASP:OD1	1:A:1865:ARG:HD3	2.15	0.46
3:C:385:VAL:CG2	3:C:386:GLY:N	2.78	0.46
15:H:80:A:N3	15:H:81:G:C8	2.84	0.46
21:1:478:LEU:HA	21:1:496:LYS:HE3	1.97	0.46
21:1:579:GLU:HB3	21:1:627:THR:OG1	2.16	0.46
21:1:903:GLN:HG3	21:1:950:GLN:HE22	1.81	0.46
21:1:1186:GLN:HE22	21:1:1225:HIS:HB3	1.79	0.46
21:1:1253:GLY:HA3	21:1:1265:TYR:CD1	2.51	0.46
23:3:195:ASP:OD2	23:3:200:ALA:N	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:787:LYS:HB3	23:3:800:ILE:HD11	1.96	0.46
23:3:828:GLY:O	23:3:834:LEU:N	2.49	0.46
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.50	0.46
25:5:78:SER:HA	25:5:89:VAL:HG21	1.97	0.46
32:R:134:ARG:O	32:R:135:PRO:C	2.54	0.46
1:A:91:ALA:CA	32:R:207:MET:HE2	2.38	0.46
1:A:229:GLN:CB	1:A:415:SER:HB2	2.45	0.46
1:A:748:ASP:CB	31:P:214:THR:HG21	2.46	0.46
1:A:1306:LYS:HZ2	2:B:38:C:C2'	2.27	0.46
1:A:1397:ILE:HG12	32:R:408:GLU:CG	2.45	0.46
3:C:145:PHE:CG	3:C:312:SER:HB3	2.49	0.46
3:C:149:LEU:N	3:C:427:PHE:HE2	2.14	0.46
21:1:862:GLU:O	21:1:865:ARG:N	2.48	0.46
21:1:972:GLY:O	21:1:976:VAL:HG22	2.15	0.46
23:3:253:GLU:HG3	23:3:254:ASN:HD22	1.81	0.46
23:3:488:GLY:C	23:3:490:THR:H	2.19	0.46
25:5:81:ASN:OD1	25:5:82:VAL:N	2.48	0.46
33:T:185:MET:HB2	33:T:186:PRO:HD3	1.98	0.46
1:A:132:ILE:CD1	2:B:57:G:OP1	2.64	0.46
1:A:374:ASP:O	1:A:375:ASP:HB3	2.16	0.46
1:A:384:VAL:HG22	3:C:334:ILE:HG21	1.82	0.46
1:A:1306:LYS:NZ	2:B:38:C:O2'	2.47	0.46
3:C:66:TYR:N	3:C:66:TYR:CD1	2.81	0.46
3:C:507:VAL:HG13	3:C:566:THR:O	2.16	0.46
3:C:559:ILE:HD12	3:C:559:ILE:O	2.15	0.46
3:C:569:ARG:O	3:C:569:ARG:HG2	2.16	0.46
3:C:671:SER:OG	3:C:672:LEU:HD22	2.15	0.46
3:C:853:ARG:O	3:C:854:ARG:CB	2.62	0.46
3:C:934:MET:HE2	3:C:934:MET:HB2	1.77	0.46
5:E:276:ILE:C	5:E:277:PHE:HD1	2.19	0.46
14:G:135:G:O6	14:G:137:C:N4	2.48	0.46
15:H:30:A:C8	29:L:7:LYS:HD3	2.51	0.46
15:H:107:A:C6	15:H:108:G:C6	3.04	0.46
21:1:859:ASP:OD1	21:1:860:GLU:N	2.47	0.46
23:3:448:ALA:HB3	23:3:764:ILE:HB	1.97	0.46
29:L:78:MET:HB3	29:L:81:GLN:OE1	2.16	0.46
37:Z:604:LYS:HA	37:Z:607:VAL:CG2	2.46	0.46
1:A:780:THR:HG22	1:A:898:PHE:CD2	2.50	0.46
1:A:802:THR:HG22	1:A:803:ALA:H	1.80	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD21	1.98	0.46
1:A:1312:PRO:O	1:A:1315:VAL:HG22	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1399:GLN:HB3	1:A:1401:ARG:HG2	1.98	0.46
1:A:2112:LYS:HE2	1:A:2112:LYS:HB3	1.67	0.46
13:F:56:A:N1	15:H:20:G:C6	2.84	0.46
15:H:78:C:O5'	15:H:78:C:H6	1.98	0.46
21:1:588:TYR:HA	21:1:591:VAL:HG12	1.98	0.46
21:1:608:THR:O	21:1:612:THR:OG1	2.15	0.46
21:1:759:ALA:O	21:1:763:ASN:HB2	2.16	0.46
23:3:69:ARG:HG2	23:3:70:LEU:O	2.16	0.46
23:3:509:SER:CB	23:3:549:VAL:HG21	2.45	0.46
32:R:88:ILE:HG22	32:R:96:ILE:HG23	1.98	0.46
32:R:220:ARG:NH1	32:R:220:ARG:CB	2.76	0.46
1:A:232:LEU:N	1:A:233:PRO:CD	2.78	0.46
1:A:434:HIS:C	1:A:434:HIS:HD1	2.19	0.46
1:A:841:LEU:HD13	1:A:1433:ASP:HB2	1.98	0.46
1:A:1388:GLU:O	1:A:1392:LYS:HG2	2.16	0.46
1:A:1718:TRP:CZ3	1:A:1726:ILE:HD12	2.50	0.46
3:C:725:ASP:OD1	3:C:727:LEU:CA	2.64	0.46
5:E:276:ILE:C	5:E:277:PHE:CD1	2.89	0.46
13:F:43:A:H2	14:G:4:A:H61	1.64	0.46
15:H:114:A:H2'	15:H:115:G:H8	1.81	0.46
21:1:647:PHE:O	21:1:651:VAL:HG23	2.16	0.46
21:1:1125:PRO:O	21:1:1128:VAL:N	2.49	0.46
21:1:1181:ASP:H	21:1:1184:HIS:HD2	1.64	0.46
23:3:71:THR:HG23	23:3:126:LYS:HD2	1.98	0.46
23:3:482:THR:HG23	23:3:503:THR:O	2.15	0.46
23:3:616:ILE:O	23:3:628:LEU:HB2	2.16	0.46
24:4:29:LEU:HD22	24:4:33:PHE:CE2	2.49	0.46
24:4:32:LEU:CD2	24:4:79:LEU:HD21	2.46	0.46
25:5:46:ARG:HB3	25:5:63:VAL:HG12	1.97	0.46
28:J:406:PHE:CG	28:J:411:MET:CE	2.97	0.46
31:P:54:VAL:HG13	31:P:59:PHE:HZ	1.80	0.46
32:R:185:GLY:C	32:R:186:VAL:HG13	2.35	0.46
1:A:34:ALA:HA	5:E:213:ILE:CD1	2.46	0.46
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.34	0.46
1:A:738:MET:HE3	1:A:739:ILE:HG13	1.97	0.46
1:A:1328:LEU:HD23	1:A:1470:TYR:CE2	2.51	0.46
1:A:1505:LYS:CD	37:Z:615:SER:CB	2.91	0.46
1:A:2272:MET:HB3	1:A:2272:MET:HE3	1.68	0.46
3:C:678:THR:HG23	3:C:683:ASN:N	2.31	0.46
5:E:248:SER:HB2	5:E:249:TYR:HD1	1.75	0.46
21:1:888:LEU:O	21:1:892:LEU:HG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.46
31:P:48:GLN:O	31:P:49:ASP:CB	2.64	0.46
32:R:148:ARG:HG3	32:R:148:ARG:NH1	2.31	0.46
1:A:378:PHE:HE2	3:C:335:ASN:HD22	1.62	0.45
1:A:892:LYS:HD2	1:A:912:GLU:OE1	2.16	0.45
1:A:903:SER:OG	1:A:904:HIS:N	2.48	0.45
1:A:1026:ASN:ND2	1:A:1029:GLY:O	2.45	0.45
2:B:22:U:O2	2:B:22:U:H2'	2.15	0.45
2:B:47:A:O2'	2:B:48:A:H8	1.98	0.45
5:E:232:ARG:O	5:E:262:TRP:CH2	2.69	0.45
21:1:744:ALA:O	21:1:787:ILE:HG21	2.16	0.45
21:1:1165:TYR:HE1	22:2:575:PHE:CG	2.33	0.45
23:3:58:VAL:HG12	23:3:1155:LEU:HD23	1.98	0.45
23:3:233:ASN:ND2	23:3:286:ILE:HD12	2.31	0.45
23:3:462:VAL:HG21	23:3:508:CYS:HB3	1.98	0.45
23:3:1012:VAL:HA	23:3:1022:ILE:O	2.17	0.45
1:A:666:LYS:HD3	1:A:666:LYS:N	2.31	0.45
1:A:671:THR:OG1	13:F:69:A:OP1	2.34	0.45
1:A:1084:PRO:HB3	1:A:1101:PHE:CE1	2.51	0.45
3:C:136:GLY:HA3	3:C:228:PHE:O	2.16	0.45
3:C:301:SER:C	3:C:303:LEU:N	2.68	0.45
3:C:499:GLY:C	3:C:500:THR:HG23	2.36	0.45
3:C:753:GLU:C	3:C:755:ASP:H	2.19	0.45
13:F:57:U:C2	13:F:58:G:N7	2.84	0.45
14:G:10:U:O2'	14:G:11:A:OP1	2.28	0.45
21:1:701:VAL:O	21:1:705:SER:HB3	2.16	0.45
23:3:536:TRP:CG	23:3:566:PHE:HZ	2.33	0.45
23:3:700:LYS:NZ	23:3:740:GLU:O	2.41	0.45
23:3:701:LEU:HA	23:3:713:LEU:O	2.16	0.45
1:A:61:MET:HB3	1:A:62:PRO:HD2	1.98	0.45
1:A:305:ARG:NH2	3:C:854:ARG:HD3	2.31	0.45
1:A:907:PRO:CD	31:P:229:LYS:HB2	2.39	0.45
1:A:1957:ASP:HB3	1:A:1960:THR:HG23	1.98	0.45
3:C:336:TYR:CD1	3:C:336:TYR:C	2.89	0.45
5:E:146:ARG:NH1	5:E:148:LYS:NZ	2.62	0.45
15:H:60:U:H2'	15:H:61:C:H6	1.81	0.45
21:1:1074:ARG:HD2	21:1:1111:CYS:SG	2.55	0.45
23:3:169:HIS:CD2	23:3:170:VAL:H	2.34	0.45
23:3:526:HIS:HB3	23:3:534:ASN:O	2.17	0.45
23:3:544:ILE:HD11	23:3:556:ILE:HG21	1.98	0.45
23:3:805:ASN:O	23:3:856:LYS:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:227:TYR:N	31:P:227:TYR:HD1	2.14	0.45
33:T:306:CYS:SG	33:T:336:VAL:HG12	2.56	0.45
1:A:305:ARG:HH21	3:C:854:ARG:CZ	2.29	0.45
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.45	0.45
2:B:57:G:H2'	2:B:58:U:H5'	1.99	0.45
3:C:193:THR:HG22	3:C:428:THR:HG21	1.97	0.45
3:C:482:TYR:CE2	3:C:493:PHE:CG	2.89	0.45
5:E:119:THR:CG2	5:E:161:ARG:CB	2.73	0.45
5:E:157:CYS:HA	5:E:168:CYS:O	2.16	0.45
15:H:181:G:C2	15:H:182:U:N3	2.84	0.45
21:1:427:PRO:O	21:1:431:LEU:N	2.45	0.45
21:1:834:VAL:O	21:1:838:VAL:HG23	2.16	0.45
21:1:1181:ASP:OD1	21:1:1182:LEU:N	2.46	0.45
23:3:257:THR:OG1	23:3:268:ARG:HG2	2.16	0.45
23:3:482:THR:HG21	23:3:505:THR:OG1	2.17	0.45
23:3:897:SER:HB2	23:3:957:GLY:HA3	1.97	0.45
23:3:905:VAL:HG23	23:3:930:LEU:HB2	1.98	0.45
27:7:73:LEU:HD12	27:7:74:GLN:N	2.32	0.45
31:P:193:VAL:CG2	31:P:194:PHE:N	2.79	0.45
32:R:88:ILE:HD12	32:R:88:ILE:N	2.29	0.45
32:R:181:PRO:O	32:R:182:SER:CB	2.58	0.45
1:A:966:TRP:HE3	1:A:1178:TYR:CZ	2.35	0.45
1:A:1426:ASP:OD2	32:R:421:GLY:CA	2.64	0.45
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.97	0.45
1:A:1900:GLU:OE2	37:Z:521:PRO:CA	2.64	0.45
3:C:183:SER:OG	3:C:480:LYS:NZ	2.50	0.45
3:C:230:ASP:CG	3:C:259:LYS:HZ1	2.19	0.45
5:E:243:LEU:CD1	5:E:247:GLY:CA	2.84	0.45
15:H:25:G:C2	15:H:26:A:C5	3.04	0.45
15:H:150:U:H3	15:H:181:G:H1	1.62	0.45
15:H:152:G:O2'	15:H:153:A:H1'	2.16	0.45
23:3:796:ASN:HA	23:3:871:PRO:HD3	1.98	0.45
28:J:360:ASP:HA	28:J:363:ARG:CD	2.46	0.45
33:T:409:LEU:HD12	33:T:409:LEU:N	2.31	0.45
1:A:75:ASP:HB2	1:A:77:THR:OG1	2.16	0.45
1:A:168:PRO:HG2	1:A:559:ASP:CB	2.36	0.45
1:A:466:ALA:HB3	2:B:54:U:OP2	2.17	0.45
1:A:730:GLY:O	1:A:731:LEU:HB2	2.16	0.45
1:A:1413:ASP:OD1	1:A:1414:ARG:HG3	2.17	0.45
1:A:1604:LEU:HD11	1:A:1725:LEU:HD22	1.98	0.45
1:A:2169:LEU:HD21	1:A:2272:MET:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2303:GLU:CD	1:A:2303:GLU:H	2.19	0.45
3:C:66:TYR:CB	33:T:456:PRO:O	2.51	0.45
3:C:495:ARG:HG3	3:C:495:ARG:O	2.16	0.45
3:C:497:LEU:CD1	3:C:577:PHE:CE1	2.94	0.45
3:C:852:ARG:NH2	14:G:-12:G:OP1	2.50	0.45
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.45
5:E:260:ARG:CD	5:E:276:ILE:HG12	2.47	0.45
13:F:94:C:H2'	13:F:95:G:H8	1.82	0.45
14:G:-12:G:HO2'	14:G:-11:G:C5'	2.29	0.45
23:3:115:ILE:HD11	27:7:18:TYR:CE1	2.51	0.45
32:R:179:TYR:CE2	32:R:181:PRO:HG3	2.52	0.45
33:T:297:HIS:CD2	33:T:338:CYS:SG	3.09	0.45
37:Z:525:TYR:CE1	37:Z:526:ILE:CG2	2.86	0.45
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.17	0.45
1:A:331:TRP:CE3	1:A:331:TRP:C	2.90	0.45
1:A:648:LEU:HD23	1:A:648:LEU:HA	1.79	0.45
1:A:1768:TYR:HE1	1:A:1930:TYR:CE1	2.34	0.45
3:C:926:ALA:N	3:C:927:PRO:HD2	2.32	0.45
5:E:178:LEU:HG	5:E:188:GLN:HB2	1.98	0.45
5:E:277:PHE:CD1	5:E:277:PHE:N	2.83	0.45
21:1:86:ALA:O	21:1:89:ALA:HB3	2.17	0.45
21:1:476:ASP:OD1	21:1:477:LYS:N	2.49	0.45
21:1:1110:VAL:O	21:1:1113:THR:HB	2.17	0.45
21:1:1251:LEU:HD12	22:2:497:SER:OG	2.16	0.45
23:3:223:LYS:HE2	23:3:224:TYR:CZ	2.52	0.45
23:3:429:ARG:HH12	27:7:59:GLU:H	1.65	0.45
23:3:1114:SER:HB2	23:3:1215:TYR:CE1	2.51	0.45
28:J:338:GLU:O	32:R:116:TYR:CE1	2.69	0.45
32:R:128:ASP:OD2	32:R:133:GLN:OE1	2.34	0.45
33:T:393:ASP:O	33:T:413:ASN:ND2	2.49	0.45
37:Z:564:PRO:O	37:Z:582:TYR:CG	2.69	0.45
37:Z:600:ARG:CG	37:Z:600:ARG:NH1	2.73	0.45
1:A:259:ASP:C	1:A:259:ASP:OD1	2.55	0.45
1:A:586:GLY:O	1:A:592:TYR:CE2	2.69	0.45
1:A:755:HIS:CG	31:P:219:PHE:HE2	2.35	0.45
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.52	0.45
1:A:975:VAL:HG11	1:A:1153:VAL:HG21	1.98	0.45
1:A:1963:GLU:HB2	1:A:1966:HIS:HD2	1.81	0.45
3:C:144:CYS:SG	3:C:148:CYS:SG	3.15	0.45
13:F:38:G:OP2	13:F:38:G:C8	2.70	0.45
14:G:6:A:H2'	14:G:7:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:501:LEU:O	21:1:504:ILE:N	2.48	0.45
21:1:592:GLU:O	21:1:596:ILE:HG23	2.16	0.45
21:1:629:ALA:HA	21:1:667:ILE:HG12	1.99	0.45
23:3:383:ASP:OD1	23:3:384:THR:N	2.50	0.45
23:3:1057:ARG:HB2	23:3:1092:ILE:HD13	1.98	0.45
32:R:82:MET:C	32:R:82:MET:CE	2.86	0.45
36:Y:41:GLY:HA2	36:Y:79:PHE:HB3	1.99	0.45
1:A:305:ARG:HG3	3:C:878:ILE:CB	2.46	0.45
1:A:318:TYR:O	3:C:641:MET:CB	2.65	0.45
1:A:660:PHE:CE2	32:R:209:PRO:CB	3.00	0.45
1:A:733:THR:OG1	1:A:734:PRO:HD3	2.16	0.45
1:A:1013:ASN:OD1	1:A:1030:ILE:HG13	2.16	0.45
1:A:1904:ASP:O	1:A:1908:LYS:HG2	2.16	0.45
1:A:1949:ARG:HA	1:A:1952:VAL:HG23	1.98	0.45
1:A:2074:ARG:O	1:A:2078:ILE:HD13	2.17	0.45
2:B:40:U:O4	14:G:-1:G:O6	2.35	0.45
3:C:137:HIS:HD2	3:C:236:MET:HB2	1.61	0.45
3:C:191:PRO:HG2	3:C:426:GLU:OE1	2.17	0.45
3:C:445:ALA:HB1	3:C:449:ILE:CG1	2.45	0.45
5:E:162:ARG:HH21	5:E:204:THR:HA	1.78	0.45
13:F:51:U:H2'	13:F:52:U:O4'	2.17	0.45
21:1:552:LEU:HA	21:1:555:VAL:HG12	1.98	0.45
21:1:822:ARG:NH1	36:Y:31:GLU:HG2	2.32	0.45
21:1:897:LEU:O	21:1:901:GLN:HG3	2.17	0.45
21:1:1186:GLN:NE2	21:1:1225:HIS:HB3	2.31	0.45
23:3:643:VAL:HG12	23:3:664:TYR:O	2.17	0.45
25:5:48:ILE:HG12	25:5:62:VAL:HG23	1.99	0.45
28:J:406:PHE:CB	28:J:411:MET:HG2	2.47	0.45
33:T:342:GLU:CB	33:T:343:PRO:HD2	2.47	0.45
33:T:454:VAL:HG22	33:T:463:SER:OG	2.16	0.45
33:T:455:GLN:CG	33:T:456:PRO:CD	2.94	0.45
1:A:44:ARG:CD	1:A:45:TYR:CE2	2.99	0.45
1:A:256:TYR:CG	3:C:888:ARG:NH2	2.85	0.45
1:A:382:GLU:O	1:A:383:PHE:CD2	2.70	0.45
1:A:507:LEU:HD12	1:A:507:LEU:HA	1.79	0.45
1:A:661:GLU:CG	32:R:210:PRO:HB3	2.47	0.45
1:A:845:ARG:NH2	1:A:1439:ARG:HE	2.15	0.45
1:A:1258:LYS:HE2	32:R:432:GLU:CB	2.47	0.45
1:A:1780:VAL:HG22	1:A:1809:ILE:HG12	1.99	0.45
3:C:65:TYR:O	3:C:66:TYR:CB	2.65	0.45
3:C:230:ASP:OD2	3:C:233:GLU:CG	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:502:HIS:ND1	3:C:543:ARG:HB3	2.32	0.45
3:C:926:ALA:HA	3:C:929:LEU:HG	1.98	0.45
13:F:50:A:H2'	13:F:51:U:H6	1.82	0.45
14:G:6:A:H2'	14:G:7:G:C8	2.52	0.45
14:G:12:G:N3	14:G:12:G:C2'	2.79	0.45
14:G:157:U:H5'	21:1:622:GLU:OE1	2.17	0.45
15:H:113:G:H2'	15:H:114:A:H8	1.82	0.45
21:1:1002:ASN:OD1	21:1:1041:ARG:NH2	2.50	0.45
22:2:611:ASP:O	22:2:614:ARG:CB	2.60	0.45
23:3:462:VAL:O	23:3:472:ALA:N	2.46	0.45
23:3:509:SER:OG	23:3:517:VAL:O	2.20	0.45
23:3:883:GLU:HG3	23:3:884:GLN:N	2.32	0.45
23:3:1051:GLY:HA2	23:3:1100:THR:HA	1.99	0.45
25:5:26:LEU:HD12	25:5:87:LEU:HD22	1.98	0.45
27:7:31:TRP:HE3	27:7:32:LEU:HD12	1.82	0.45
29:L:226:ASP:OD1	32:R:83:SER:HB2	2.16	0.45
32:R:88:ILE:HG21	32:R:96:ILE:CG2	2.46	0.45
32:R:408:GLU:CG	32:R:409:VAL:N	2.78	0.45
35:X:336:GLY:HA3	35:X:378:GLU:HB2	1.99	0.45
37:Z:524:ARG:HD2	37:Z:525:TYR:CB	2.46	0.45
1:A:76:MET:SD	1:A:88:TYR:CE2	3.10	0.44
1:A:193:LEU:HD12	1:A:194:GLU:N	2.29	0.44
1:A:1147:VAL:HG23	1:A:1148:ASN:N	2.33	0.44
3:C:93:ILE:CG2	33:T:218:TRP:NE1	2.80	0.44
5:E:276:ILE:O	5:E:277:PHE:HD1	2.00	0.44
13:F:68:C:C5	31:P:33:ARG:HG2	2.52	0.44
13:F:94:C:H2'	13:F:95:G:C8	2.52	0.44
15:H:7:U:H2'	15:H:8:C:C6	2.52	0.44
15:H:81:G:N3	15:H:82:G:C8	2.85	0.44
15:H:141:C:H2'	15:H:142:C:C6	2.50	0.44
21:1:810:ILE:O	21:1:813:PRO:HD2	2.17	0.44
23:3:460:TRP:CE2	23:3:507:SER:HA	2.52	0.44
23:3:723:TYR:CD1	23:3:725:TYR:HB2	2.53	0.44
23:3:1140:PHE:O	23:3:1144:VAL:HG23	2.17	0.44
32:R:147:THR:HG23	33:T:360:VAL:CG1	2.40	0.44
32:R:416:PHE:O	32:R:416:PHE:CG	2.70	0.44
1:A:89:LEU:CD2	1:A:656:LEU:CD2	2.95	0.44
1:A:1088:PHE:HD1	1:A:1097:ILE:HG12	1.82	0.44
1:A:1430:LEU:HD11	32:R:422:MET:HA	1.98	0.44
1:A:1591:MET:SD	1:A:1611:LYS:NZ	2.75	0.44
1:A:1788:VAL:HA	1:A:1802:PRO:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2196:HIS:HB3	1:A:2230:LEU:HD11	1.98	0.44
1:A:2222:SER:OG	1:A:2223:CYS:N	2.50	0.44
1:A:2334:TYR:CE1	4:D:591:GLU:CB	3.00	0.44
2:B:40:U:OP2	2:B:40:U:C6	2.70	0.44
3:C:93:ILE:CG2	33:T:218:TRP:CZ2	3.00	0.44
3:C:388:VAL:HA	3:C:392:LEU:HB2	1.99	0.44
5:E:132:THR:HG21	5:E:146:ARG:HG2	1.98	0.44
13:F:58:G:O2'	13:F:59:G:OP1	2.31	0.44
15:H:143:A:OP2	15:H:143:A:C2	2.71	0.44
15:H:157:G:H5''	15:H:157:G:C8	2.50	0.44
21:1:762:ALA:O	21:1:766:THR:CB	2.64	0.44
21:1:1252:GLN:NE2	22:2:492:LYS:O	2.51	0.44
22:2:613:LEU:HD21	24:4:32:LEU:HD13	1.99	0.44
23:3:404:LEU:HB3	23:3:407:ILE:HD11	1.99	0.44
23:3:536:TRP:CD1	23:3:566:PHE:HZ	2.35	0.44
23:3:607:VAL:HB	23:3:615:ARG:O	2.17	0.44
23:3:1159:ASP:OD1	23:3:1160:HIS:N	2.49	0.44
28:J:297:ASN:OD1	29:L:223:GLY:O	2.34	0.44
34:V:548:ALA:HB2	34:V:585:ILE:CB	2.42	0.44
1:A:317:PRO:HB2	1:A:327:VAL:HG11	1.98	0.44
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.75	0.44
1:A:1785:VAL:O	1:A:1805:GLY:HA3	2.17	0.44
1:A:2328:ALA:CB	4:D:788:GLY:N	2.79	0.44
3:C:140:HIS:HB3	3:C:230:ASP:CB	2.43	0.44
3:C:671:SER:CB	3:C:672:LEU:HD22	2.46	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.94	0.44
13:F:39:A:H2'	13:F:40:U:C6	2.52	0.44
21:1:529:GLY:HA2	21:1:570:TYR:CZ	2.51	0.44
23:3:205:GLN:HB2	23:3:228:LEU:O	2.17	0.44
23:3:747:SER:N	23:3:750:CYS:O	2.51	0.44
25:5:98:PHE:O	25:5:100:LYS:N	2.50	0.44
31:P:188:TRP:N	31:P:188:TRP:CD2	2.86	0.44
32:R:416:PHE:O	32:R:416:PHE:CD1	2.70	0.44
33:T:387:PHE:CZ	33:T:398:TRP:CD1	3.04	0.44
37:Z:500:GLY:O	37:Z:503:GLN:N	2.50	0.44
37:Z:573:PRO:O	37:Z:573:PRO:CD	2.65	0.44
37:Z:597:ARG:CZ	37:Z:601:LEU:HD13	2.47	0.44
1:A:777:GLY:O	1:A:780:THR:OG1	2.25	0.44
1:A:1074:PHE:HB3	1:A:1079:THR:OG1	2.17	0.44
1:A:1631:LEU:HD12	1:A:1660:TYR:CD2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:U:O2	14:G:-3:A:H2	2.00	0.44
13:F:5:U:H5'	13:F:6:C:OP2	2.17	0.44
15:H:159:U:H2'	15:H:160:A:C8	2.52	0.44
15:H:165:A:C6	15:H:166:G:O6	2.71	0.44
21:1:937:LEU:O	21:1:940:LEU:HB3	2.18	0.44
22:2:611:ASP:O	22:2:614:ARG:N	2.50	0.44
23:3:1063:ASN:H	23:3:1087:GLN:HE22	1.65	0.44
23:3:1096:HIS:NE2	23:3:1098:GLY:HA2	2.33	0.44
31:P:189:ASP:C	31:P:191:ASP:N	2.68	0.44
33:T:439:TRP:CE3	33:T:446:ASN:HB2	2.52	0.44
34:V:525:PHE:O	34:V:526:GLU:C	2.55	0.44
36:Y:36:ALA:CB	37:Z:499:LYS:O	2.54	0.44
1:A:359:ILE:O	1:A:360:SER:HB3	2.16	0.44
1:A:373:ASP:OD1	1:A:374:ASP:N	2.51	0.44
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.70	0.44
1:A:1110:ILE:HG22	1:A:1114:LEU:HD12	1.98	0.44
1:A:1402:ARG:HD2	32:R:412:ASP:HA	1.98	0.44
1:A:1533:ARG:HD2	1:A:1751:LEU:O	2.18	0.44
1:A:1553:VAL:O	1:A:1561:PHE:HA	2.18	0.44
1:A:1957:ASP:O	1:A:1960:THR:OG1	2.19	0.44
1:A:2073:TRP:CZ3	1:A:2313:HIS:CE1	3.05	0.44
3:C:135:CYS:SG	3:C:227:LEU:CB	3.06	0.44
3:C:259:LYS:HD2	41:C:1500:GTP:C5	2.52	0.44
3:C:673:LYS:HG3	3:C:686:THR:HG23	2.00	0.44
14:G:21:A:O3'	14:G:22:C:C6	2.71	0.44
15:H:60:U:H2'	15:H:61:C:C6	2.52	0.44
21:1:1211:LEU:O	21:1:1215:VAL:HG23	2.17	0.44
23:3:442:LEU:HD11	23:3:732:THR:OG1	2.17	0.44
23:3:636:GLN:O	23:3:670:GLN:HG2	2.17	0.44
26:6:58:CYS:N	26:6:63:GLY:O	2.46	0.44
36:Y:58:GLN:HB2	37:Z:584:TRP:NE1	2.33	0.44
1:A:121:HIS:CD2	1:A:481:PHE:O	2.70	0.44
1:A:381:PRO:HG2	3:C:333:ASP:HB2	2.00	0.44
1:A:707:ARG:O	1:A:711:GLN:HG3	2.17	0.44
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.44
1:A:1364:LEU:CD1	34:V:461:LEU:O	2.66	0.44
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.51	0.44
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.52	0.44
1:A:2125:ALA:O	1:A:2150:GLN:NE2	2.50	0.44
1:A:2237:TRP:HZ2	1:A:2248:PRO:HB2	1.81	0.44
3:C:457:VAL:CG1	3:C:462:GLY:HA3	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:34:U:C4	15:H:35:A:N7	2.85	0.44
15:H:73:C:O5'	15:H:73:C:H6	2.01	0.44
15:H:142:C:O2'	15:H:143:A:H5'	2.18	0.44
15:H:147:G:C6	15:H:148:C:N4	2.86	0.44
21:1:1108:ASN:OD1	21:1:1110:VAL:HG12	2.17	0.44
23:3:812:LYS:O	23:3:816:LYS:CB	2.57	0.44
31:P:193:VAL:HG23	31:P:194:PHE:CB	2.47	0.44
36:Y:63:VAL:HG23	36:Y:64:ASN:N	2.33	0.44
1:A:369:GLU:HB2	1:A:370:PRO:HD2	2.00	0.44
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.51	0.44
1:A:1674:HIS:HB3	1:A:1709:TYR:CE2	2.53	0.44
1:A:2121:ARG:HA	1:A:2121:ARG:HD2	1.55	0.44
3:C:145:PHE:HD1	3:C:312:SER:HB3	1.83	0.44
13:F:9:U:H2'	13:F:10:U:C6	2.52	0.44
13:F:68:C:C5	31:P:33:ARG:CG	2.95	0.44
15:H:26:A:C6	15:H:27:U:C4	3.05	0.44
21:1:1072:ALA:O	21:1:1075:ARG:HB3	2.18	0.44
23:3:929:LYS:HD3	23:3:938:GLU:OE2	2.17	0.44
29:L:224:PHE:CE1	32:R:86:LEU:HD12	2.43	0.44
33:T:342:GLU:O	33:T:343:PRO:C	2.56	0.44
37:Z:584:TRP:CZ3	37:Z:586:GLY:HA2	2.53	0.44
1:A:73:HIS:HA	1:A:81:PHE:CE2	2.53	0.44
1:A:121:HIS:CA	1:A:481:PHE:O	2.66	0.44
1:A:251:ASP:HA	1:A:337:VAL:CG2	2.48	0.44
1:A:363:HIS:CE1	3:C:287:GLY:CA	3.00	0.44
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.98	0.44
1:A:1457:HIS:CE1	32:R:424:SER:C	2.90	0.44
1:A:1555:LEU:HD12	1:A:1560:ILE:HB	2.00	0.44
1:A:1557:LEU:HD13	1:A:1580:HIS:CE1	2.53	0.44
1:A:2280:ASN:HB3	1:A:2309:HIS:CD2	2.53	0.44
21:1:601:ALA:HB2	21:1:635:VAL:HG12	2.00	0.44
21:1:969:LYS:O	21:1:973:HIS:ND1	2.36	0.44
23:3:353:PHE:CD1	23:3:406:PRO:HD3	2.53	0.44
23:3:607:VAL:HG21	23:3:617:ILE:HD12	1.99	0.44
23:3:930:LEU:HG	23:3:934:GLY:HA2	1.98	0.44
24:4:79:LEU:HG	24:4:84:ILE:HG13	2.00	0.44
31:P:66:ARG:HB2	31:P:66:ARG:NH1	2.30	0.44
32:R:124:VAL:HG22	32:R:125:MET:H	1.83	0.44
32:R:132:LEU:HD23	32:R:132:LEU:N	2.31	0.44
32:R:208:GLU:OE2	32:R:211:ARG:NH1	2.51	0.44
32:R:415:LEU:H	32:R:415:LEU:HG	1.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:358:ASP:HB2	33:T:365:ARG:HD2	2.00	0.44
37:Z:524:ARG:CD	37:Z:524:ARG:C	2.85	0.44
1:A:86:ARG:NH2	32:R:211:ARG:CG	2.63	0.44
1:A:94:TYR:CD2	32:R:207:MET:SD	3.11	0.44
1:A:941:LYS:HE3	1:A:951:LEU:HD21	2.00	0.44
1:A:1038:SER:HA	1:A:1442:PHE:HE2	1.83	0.44
1:A:1900:GLU:CG	37:Z:521:PRO:HG3	2.39	0.44
3:C:439:PRO:O	3:C:440:SER:CB	2.66	0.44
3:C:465:MET:HE1	3:C:475:MET:CE	2.47	0.44
3:C:779:LEU:HD11	3:C:825:PRO:HB2	1.99	0.44
14:G:11:A:C5	14:G:12:G:C8	3.06	0.44
14:G:21:A:O3'	14:G:22:C:H6	2.00	0.44
15:H:6:U:H2'	15:H:7:U:C6	2.53	0.44
21:1:503:LYS:HD2	21:1:515:ALA:HB2	2.00	0.44
21:1:779:SER:HB3	21:1:784:MET:HG2	2.00	0.44
21:1:1131:ALA:O	21:1:1135:GLU:HG2	2.17	0.44
23:3:411:GLN:HA	23:3:1105:GLN:OE1	2.18	0.44
23:3:798:ILE:HA	23:3:867:ARG:O	2.18	0.44
25:5:46:ARG:N	25:5:63:VAL:O	2.50	0.44
1:A:44:ARG:HG2	1:A:45:TYR:CD2	2.53	0.43
1:A:79:ARG:HD2	1:A:79:ARG:O	2.18	0.43
1:A:394:TYR:CD1	1:A:394:TYR:N	2.86	0.43
1:A:1118:PRO:O	1:A:1120:PRO:O	2.36	0.43
1:A:2073:TRP:CH2	1:A:2313:HIS:CG	3.06	0.43
3:C:229:ILE:CG2	3:C:234:GLY:O	2.66	0.43
5:E:248:SER:HB2	5:E:249:TYR:CE1	2.53	0.43
13:F:35:A:C8	14:G:12:G:O6	2.71	0.43
13:F:68:C:H42	33:T:283:HIS:CE1	2.35	0.43
21:1:903:GLN:HG3	21:1:950:GLN:NE2	2.33	0.43
23:3:176:GLY:O	23:3:178:GLU:HG2	2.17	0.43
23:3:446:GLU:CD	23:3:763:ARG:HD3	2.38	0.43
23:3:745:PHE:HB2	23:3:755:VAL:HG23	2.00	0.43
23:3:998:HIS:HE1	23:3:1064:ASP:OD2	2.00	0.43
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.18	0.43
25:5:53:THR:O	25:5:57:ARG:HG3	2.18	0.43
28:J:339:TRP:C	32:R:116:TYR:CE2	2.92	0.43
32:R:109:ASP:OD1	32:R:110:LYS:N	2.51	0.43
33:T:454:VAL:CG1	33:T:455:GLN:N	2.81	0.43
1:A:106:MET:HG2	1:A:489:TRP:CZ2	2.53	0.43
1:A:210:HIS:CD2	1:A:210:HIS:C	2.92	0.43
1:A:330:THR:O	1:A:331:TRP:HB2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:LEU:O	1:A:698:PRO:HG3	2.18	0.43
1:A:970:GLU:HB2	1:A:972:GLU:OE2	2.17	0.43
1:A:1301:ILE:HD11	2:B:39:C:OP1	2.18	0.43
1:A:1532:ARG:HG2	1:A:1572:SER:OG	2.18	0.43
1:A:2310:ARG:HH11	1:A:2310:ARG:HB3	1.83	0.43
3:C:135:CYS:N	3:C:226:VAL:O	2.50	0.43
3:C:392:LEU:HD12	3:C:392:LEU:O	2.18	0.43
3:C:508:LYS:O	3:C:566:THR:HG22	2.18	0.43
3:C:674:CYS:HB2	3:C:818:SER:HB3	2.00	0.43
3:C:703:GLU:OE2	3:C:740:THR:CG2	2.50	0.43
5:E:251:LEU:CG	5:E:291:CYS:SG	3.05	0.43
15:H:159:U:H2'	15:H:160:A:H8	1.83	0.43
15:H:182:U:H6	15:H:182:U:O5'	2.01	0.43
21:1:528:ALA:HB2	21:1:563:LEU:HD13	2.00	0.43
21:1:732:TRP:O	21:1:735:ILE:HB	2.19	0.43
22:2:556:LYS:O	22:2:559:PRO:HD3	2.18	0.43
23:3:409:PHE:HD2	23:3:788:PHE:CE2	2.36	0.43
23:3:484:VAL:HG21	23:3:499:PHE:HB2	1.99	0.43
23:3:791:HIS:ND1	23:3:794:SER:HB3	2.33	0.43
23:3:837:GLU:O	23:3:837:GLU:HG2	2.17	0.43
32:R:419:SER:C	32:R:420:LYS:O	2.55	0.43
1:A:345:PRO:O	1:A:346:ASP:O	2.35	0.43
1:A:525:LYS:HG2	30:M:194:ARG:CG	2.48	0.43
1:A:908:VAL:HA	1:A:1445:TYR:O	2.18	0.43
1:A:1071:PHE:CD2	1:A:1072:LEU:HG	2.53	0.43
1:A:1544:ARG:HB3	1:A:1672:ASP:OD2	2.19	0.43
1:A:2067:PHE:HB2	1:A:2072:GLU:HG2	2.00	0.43
2:B:12:U:O2'	2:B:13:C:P	2.77	0.43
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.52	0.43
3:C:524:ILE:O	3:C:525:CYS:SG	2.74	0.43
15:H:64:A:H2'	15:H:65:U:C6	2.53	0.43
15:H:153:A:H2'	15:H:154:C:H5''	1.99	0.43
21:1:840:LEU:O	21:1:844:VAL:HG12	2.19	0.43
22:2:482:ALA:O	22:2:485:PRO:HD3	2.18	0.43
23:3:88:VAL:HA	23:3:103:HIS:O	2.18	0.43
23:3:458:ALA:C	23:3:757:ILE:HG12	2.39	0.43
23:3:511:LEU:HB2	23:3:517:VAL:HG23	1.99	0.43
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	2.01	0.43
24:4:67:ALA:HA	24:4:70:ALA:HB3	2.00	0.43
32:R:88:ILE:HG22	32:R:96:ILE:CG2	2.49	0.43
33:T:406:ILE:HG22	33:T:407:GLN:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:LEU:HD21	3:C:388:VAL:CG1	2.32	0.43
1:A:305:ARG:CG	3:C:878:ILE:HG21	2.38	0.43
1:A:318:TYR:O	3:C:641:MET:HB2	2.19	0.43
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.75	0.43
1:A:741:ARG:NH2	33:T:432:ASP:O	2.41	0.43
1:A:1113:TYR:O	1:A:1117:HIS:CB	2.66	0.43
1:A:1263:TRP:CE3	1:A:1295:ILE:HD13	2.53	0.43
2:B:64:G:C5'	5:E:106:LYS:HZ3	2.13	0.43
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.43
3:C:133:THR:CB	3:C:225:VAL:HG23	2.43	0.43
3:C:297:ASN:HD22	3:C:298:LEU:HD12	1.83	0.43
3:C:350:ASN:HB3	3:C:353:THR:CG2	2.49	0.43
3:C:505:GLN:HG2	3:C:506:PRO:HD2	2.00	0.43
3:C:776:GLU:O	3:C:781:ASP:HA	2.18	0.43
13:F:42:C:H2'	13:F:43:A:C8	2.53	0.43
21:1:885:ASP:OD1	21:1:888:LEU:HB3	2.18	0.43
21:1:1119:VAL:O	21:1:1122:THR:HG22	2.17	0.43
21:1:1120:ALA:HB1	21:1:1125:PRO:HB3	2.01	0.43
21:1:1179:ASP:HB3	22:2:511:LEU:HD12	2.00	0.43
22:2:630:PRO:HA	22:2:631:PRO:HD3	1.77	0.43
23:3:136:GLU:OE2	23:3:189:TYR:OH	2.10	0.43
29:L:63:TRP:CH2	29:L:99:HIS:HB2	2.54	0.43
29:L:101:GLU:O	29:L:105:ASP:HB2	2.18	0.43
32:R:54:LEU:HD12	32:R:54:LEU:HA	1.86	0.43
32:R:55:LEU:C	32:R:73:PRO:O	2.56	0.43
33:T:399:LYS:HG3	33:T:406:ILE:CD1	2.37	0.43
36:Y:36:ALA:HB3	37:Z:498:GLY:O	2.18	0.43
1:A:141:ILE:HG12	1:A:426:LEU:HD23	1.99	0.43
1:A:643:GLY:O	1:A:646:PRO:HD2	2.19	0.43
3:C:145:PHE:N	3:C:312:SER:OG	2.50	0.43
3:C:736:GLY:HA3	3:C:770:PHE:CE2	2.53	0.43
5:E:67:GLY:N	5:E:87:ASP:OD1	2.42	0.43
14:G:-5:G:O2'	14:G:-4:A:H5''	2.18	0.43
15:H:83:A:C4	15:H:84:C:C6	3.07	0.43
15:H:98:G:H5'	15:H:104:U:OP2	2.18	0.43
15:H:154:C:O2'	15:H:155:C:C5'	2.66	0.43
15:H:181:G:C2	15:H:182:U:C4	3.07	0.43
21:1:897:LEU:HD21	21:1:932:ILE:HD13	2.00	0.43
21:1:1235:GLU:O	21:1:1238:ARG:HB3	2.18	0.43
23:3:139:LYS:HB2	23:3:160:ALA:HB3	2.00	0.43
23:3:868:VAL:HG12	23:3:877:LEU:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:126:ASN:HD22	32:R:128:ASP:H	1.66	0.43
36:Y:29:HIS:CG	36:Y:91:ILE:HG23	2.53	0.43
1:A:148:TRP:HE3	1:A:629:PHE:CD1	2.35	0.43
1:A:253:ASN:CG	1:A:334:THR:O	2.57	0.43
1:A:417:ARG:NH1	2:B:58:U:H4'	2.33	0.43
1:A:549:GLU:CD	1:A:552:ARG:NH1	2.72	0.43
1:A:1382:SER:HB3	1:A:1416:ILE:HG12	2.00	0.43
1:A:1771:LEU:HD12	1:A:1777:ILE:HD13	2.00	0.43
1:A:2284:MET:HE1	1:A:2311:PRO:HG3	2.01	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
13:F:36:A:C3'	13:F:36:A:C8	3.01	0.43
15:H:157:G:H2'	15:H:158:G:O4'	2.19	0.43
21:1:889:GLU:HA	21:1:892:LEU:HD12	2.00	0.43
22:2:613:LEU:HD11	24:4:32:LEU:HD13	1.99	0.43
23:3:32:VAL:HG23	23:3:39:GLU:HB3	1.99	0.43
25:5:114:LYS:HA	25:5:119:ILE:O	2.19	0.43
29:L:73:HIS:CD2	29:L:77:LEU:HD11	2.53	0.43
32:R:52:PRO:HB3	32:R:57:ASP:OD2	2.17	0.43
32:R:119:LEU:HA	32:R:232:MET:CE	2.49	0.43
32:R:120:VAL:HG23	32:R:121:PRO:HD2	2.01	0.43
33:T:459:LEU:HG	33:T:461:SER:OG	2.18	0.43
1:A:661:GLU:HG3	32:R:210:PRO:HB2	2.00	0.43
1:A:790:ARG:HG3	3:C:60:HIS:HD2	1.82	0.43
1:A:1921:ASP:OD2	1:A:1966:HIS:HB3	2.19	0.43
1:A:2073:TRP:CD1	1:A:2073:TRP:C	2.91	0.43
1:A:2328:ALA:HB3	4:D:787:ALA:C	2.38	0.43
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.43
3:C:61:GLU:OE1	3:C:62:ASP:N	2.51	0.43
3:C:295:ASP:OD1	3:C:297:ASN:HB2	2.19	0.43
3:C:461:LEU:HD23	3:C:461:LEU:HA	1.78	0.43
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.43
21:1:471:ASP:OD2	21:1:505:LYS:NZ	2.34	0.43
32:R:242:THR:HG22	32:R:244:LYS:H	1.84	0.43
32:R:443:GLY:O	32:R:447:MET:CB	2.67	0.43
1:A:356:ILE:HG23	3:C:865:GLY:C	2.39	0.43
1:A:781:ARG:NH2	15:H:24:A:H5'	2.34	0.43
1:A:1433:ASP:O	1:A:1434:LYS:HD3	2.19	0.43
1:A:1437:ARG:O	1:A:1440:THR:OG1	2.36	0.43
3:C:73:TYR:CE1	33:T:487:LYS:HE2	2.52	0.43
3:C:137:HIS:HD2	3:C:236:MET:CB	2.22	0.43
3:C:275:TYR:OH	3:C:345:GLY:HA2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:349:PHE:CG	3:C:356:PHE:HE1	2.36	0.43
3:C:941:LYS:HG2	3:C:942:GLY:N	2.34	0.43
13:F:46:G:H2'	13:F:47:A:C8	2.54	0.43
15:H:166:G:N3	15:H:166:G:H2'	2.33	0.43
15:H:180:G:N3	15:H:181:G:C8	2.87	0.43
21:1:892:LEU:HD23	21:1:892:LEU:HA	1.91	0.43
27:7:51:ASN:OD1	27:7:61:LYS:HE2	2.18	0.43
31:P:191:ASP:O	31:P:192:VAL:HG23	2.18	0.43
33:T:225:ASP:O	33:T:226:ARG:HB2	2.18	0.43
1:A:151:MET:SD	1:A:628:GLY:HA3	2.59	0.43
1:A:175:PRO:CG	1:A:498:ARG:NH2	2.73	0.43
1:A:331:TRP:HZ3	3:C:179:VAL:HG22	1.82	0.43
1:A:843:LEU:HD22	1:A:867:ILE:HG23	2.01	0.43
3:C:289:ILE:CD1	3:C:300:LEU:HD21	2.49	0.43
3:C:381:LEU:HD23	3:C:416:LEU:HD22	1.99	0.43
5:E:255:MET:C	5:E:257:ASN:H	2.22	0.43
13:F:39:A:H61	14:G:8:C:N4	2.11	0.43
14:G:12:G:C2	14:G:13:C:O4'	2.71	0.43
21:1:184:VAL:O	21:1:188:ALA:CB	2.66	0.43
23:3:633:LEU:HD12	23:3:637:PRO:HG2	2.00	0.43
28:J:339:TRP:CG	32:R:116:TYR:CD2	3.06	0.43
32:R:250:LYS:HD3	32:R:250:LYS:C	2.39	0.43
33:T:347:THR:HG21	33:T:357:TRP:HE1	1.82	0.43
35:X:307:GLN:HB3	35:X:331:LEU:HD13	2.01	0.43
1:A:30:LEU:HB3	5:E:194:TYR:CZ	2.53	0.43
1:A:1735:LYS:NZ	1:A:1765:SER:O	2.50	0.43
3:C:669:THR:HG22	3:C:690:GLU:CB	2.48	0.43
5:E:178:LEU:CD1	5:E:222:LEU:HD21	2.46	0.43
5:E:321:TYR:OH	5:E:356:ILE:HG23	2.19	0.43
15:H:68:G:C6	15:H:84:C:N4	2.85	0.43
21:1:900:PHE:HA	21:1:903:GLN:HE21	1.83	0.43
21:1:968:GLU:OE1	21:1:968:GLU:N	2.51	0.43
23:3:253:GLU:HA	23:3:286:ILE:HG22	2.01	0.43
23:3:820:ALA:HB2	23:3:843:LEU:HD11	2.00	0.43
23:3:1055:VAL:HB	23:3:1093:MET:HB3	2.00	0.43
26:6:14:GLN:O	26:6:46:CYS:HB3	2.18	0.43
32:R:113:TYR:CG	32:R:118:ASP:OD2	2.72	0.43
33:T:399:LYS:CG	33:T:406:ILE:CD1	2.78	0.43
34:V:585:ILE:O	34:V:586:PHE:C	2.58	0.43
36:Y:37:TRP:CE2	36:Y:83:CYS:SG	3.11	0.43
36:Y:85:GLU:O	37:Z:502:ALA:CA	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:TYR:CE1	1:A:485:THR:HG22	2.54	0.42
1:A:405:LEU:HD11	3:C:265:LEU:HD13	2.00	0.42
1:A:532:THR:HG21	14:G:2:U:O5'	2.19	0.42
1:A:1373:GLN:NE2	1:A:1381:ASP:OD2	2.52	0.42
1:A:1539:SER:OG	1:A:1540:PRO:HD3	2.19	0.42
1:A:1630:LEU:HA	1:A:1630:LEU:HD23	1.80	0.42
1:A:1900:GLU:CD	37:Z:521:PRO:HB2	2.34	0.42
1:A:2302:LYS:HD2	1:A:2306:HIS:CE1	2.54	0.42
1:A:2328:ALA:CB	4:D:787:ALA:C	2.87	0.42
3:C:77:VAL:CB	33:T:196:LEU:HG	2.41	0.42
3:C:457:VAL:O	3:C:458:ASP:CB	2.67	0.42
13:F:55:C:OP2	13:F:74:U:O2'	2.36	0.42
23:3:169:HIS:H	23:3:185:LEU:HB2	1.83	0.42
23:3:226:GLU:HG3	23:3:261:PHE:CZ	2.51	0.42
23:3:498:GLY:HA3	23:3:531:LYS:HZ3	1.83	0.42
23:3:520:TYR:HE1	23:3:522:ASP:HB2	1.83	0.42
23:3:640:LEU:HD22	23:3:667:ILE:HG12	2.01	0.42
23:3:1188:ASN:OD1	23:3:1189:LYS:N	2.51	0.42
26:6:57:ARG:HD2	26:6:62:GLY:C	2.40	0.42
32:R:124:VAL:HG22	32:R:126:ASN:N	2.34	0.42
33:T:284:TYR:N	33:T:284:TYR:CD1	2.87	0.42
36:Y:92:LEU:O	36:Y:96:ASN:CB	2.67	0.42
1:A:250:VAL:HG21	1:A:337:VAL:HG12	2.01	0.42
1:A:284:ARG:HE	1:A:284:ARG:HB3	1.70	0.42
1:A:311:GLU:CB	3:C:885:THR:HG21	2.47	0.42
1:A:349:ALA:CB	1:A:399:ALA:CB	2.74	0.42
1:A:1425:LYS:HG2	32:R:417:ASN:OD1	2.18	0.42
1:A:2072:GLU:O	1:A:2076:ARG:HG3	2.18	0.42
1:A:2310:ARG:HG2	1:A:2310:ARG:HH11	1.84	0.42
3:C:93:ILE:HG21	33:T:218:TRP:CZ2	2.54	0.42
3:C:481:MET:SD	3:C:492:ALA:CB	3.06	0.42
15:H:168:A:N3	15:H:168:A:C2'	2.77	0.42
21:1:404:LEU:HD23	25:5:47:GLN:CD	2.39	0.42
21:1:744:ALA:HB2	21:1:784:MET:SD	2.59	0.42
21:1:1289:ASN:HB2	21:1:1294:THR:HA	2.00	0.42
23:3:274:ARG:NH2	23:3:309:ASP:OD2	2.50	0.42
32:R:118:ASP:OD1	32:R:232:MET:HE1	2.19	0.42
32:R:220:ARG:HB2	32:R:220:ARG:CZ	2.49	0.42
36:Y:37:TRP:NE1	36:Y:83:CYS:CB	2.70	0.42
1:A:32:GLU:OE2	1:A:36:LYS:CE	2.68	0.42
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:VAL:HG22	1:A:1161:LEU:HD21	2.01	0.42
1:A:1099:PHE:HZ	1:A:1157:ILE:HD11	1.85	0.42
1:A:1457:HIS:HE2	32:R:424:SER:CB	2.32	0.42
1:A:1772:PHE:CD1	1:A:1773:SER:N	2.87	0.42
1:A:1810:PHE:CE1	1:A:1919:LEU:HD12	2.55	0.42
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.84	0.42
3:C:413:ARG:HB2	3:C:414:PRO:HD3	1.99	0.42
15:H:3:C:H2'	15:H:4:G:C8	2.53	0.42
15:H:178:A:N3	15:H:178:A:H2'	2.34	0.42
21:1:707:LEU:O	21:1:710:ALA:HB3	2.20	0.42
21:1:811:LEU:HB2	21:1:812:PRO:HD3	2.00	0.42
21:1:1040:GLY:CA	21:1:1080:THR:HG22	2.48	0.42
22:2:613:LEU:HA	22:2:616:SER:OG	2.20	0.42
23:3:310:ILE:O	23:3:330:PHE:HB3	2.19	0.42
23:3:961:ILE:HB	23:3:970:TYR:CD2	2.54	0.42
28:J:375:ASP:O	28:J:376:VAL:C	2.58	0.42
1:A:32:GLU:CD	1:A:36:LYS:HE3	2.39	0.42
1:A:94:TYR:HD2	32:R:207:MET:SD	2.43	0.42
1:A:319:LEU:CD1	3:C:637:LEU:HB3	2.48	0.42
1:A:361:HIS:CD2	3:C:279:ARG:CZ	3.03	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:323:PHE:CE1	3:C:424:PHE:HE1	2.37	0.42
3:C:706:GLN:HE21	3:C:708:THR:N	2.12	0.42
3:C:863:ILE:HA	3:C:864:PRO:HD3	1.88	0.42
5:E:67:GLY:H	5:E:87:ASP:CG	2.20	0.42
15:H:5:C:H2'	15:H:6:U:C6	2.54	0.42
21:1:413:LYS:HG3	21:1:415:LEU:HD11	2.01	0.42
21:1:619:ASN:ND2	21:1:624:VAL:HG21	2.34	0.42
21:1:619:ASN:OD1	21:1:620:MET:N	2.52	0.42
21:1:722:GLU:O	21:1:725:ASP:CB	2.67	0.42
23:3:185:LEU:HD11	23:3:235:LEU:HD13	2.01	0.42
23:3:287:PHE:HA	23:3:304:GLN:O	2.19	0.42
23:3:1014:TYR:CE2	23:3:1016:ARG:HA	2.55	0.42
23:3:1052:ASN:OD1	23:3:1096:HIS:ND1	2.39	0.42
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	2.02	0.42
26:6:47:ASP:HA	26:6:50:ASN:O	2.20	0.42
28:J:331:GLN:HG2	32:R:98:TYR:HH	1.76	0.42
28:J:339:TRP:CD2	32:R:116:TYR:CD2	2.85	0.42
29:L:63:TRP:CZ2	29:L:99:HIS:HB2	2.54	0.42
31:P:188:TRP:C	31:P:190:ASP:H	2.21	0.42
32:R:183:GLN:HB3	32:R:188:PHE:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:69:ARG:HA	36:Y:76:SER:HA	2.02	0.42
1:A:211:GLN:HA	1:A:212:PRO:HD3	1.82	0.42
1:A:258:PHE:CD2	1:A:434:HIS:HA	2.55	0.42
1:A:303:ILE:HG23	3:C:933:PHE:CD1	2.53	0.42
1:A:378:PHE:CD1	1:A:378:PHE:C	2.93	0.42
1:A:380:LEU:H	1:A:380:LEU:HD22	1.84	0.42
1:A:718:ARG:NH2	32:R:259:LYS:CE	2.78	0.42
1:A:1263:TRP:CD2	1:A:1295:ILE:HD13	2.54	0.42
1:A:1363:GLN:O	1:A:1364:LEU:HG	2.18	0.42
3:C:669:THR:HG22	3:C:690:GLU:OE1	2.19	0.42
3:C:712:LYS:O	3:C:716:GLU:HG3	2.18	0.42
5:E:277:PHE:CE1	5:E:317:ARG:HG2	2.53	0.42
14:G:5:G:C2	14:G:6:A:C5	3.08	0.42
14:G:136:U:O4	21:1:515:ALA:HA	2.19	0.42
21:1:494:GLU:HA	21:1:497:ILE:HG22	2.01	0.42
21:1:940:LEU:O	21:1:948:ARG:NH2	2.51	0.42
21:1:1255:PHE:HD2	22:2:487:LEU:HD22	1.81	0.42
23:3:456:PRO:HB2	23:3:757:ILE:HD13	2.02	0.42
23:3:508:CYS:SG	23:3:518:GLN:NE2	2.92	0.42
23:3:784:THR:HB	23:3:786:ARG:NH1	2.32	0.42
32:R:129:ASP:HB3	32:R:131:ASP:CG	2.40	0.42
33:T:318:ARG:CG	33:T:318:ARG:NH1	2.82	0.42
34:V:484:SER:O	34:V:486:THR:N	2.53	0.42
1:A:715:GLU:OE1	32:R:258:TRP:CE3	2.73	0.42
1:A:791:GLN:NE2	1:A:1026:ASN:OD1	2.52	0.42
1:A:1759:THR:N	21:1:938:TRP:CD1	2.88	0.42
1:A:1948:ASP:O	1:A:1951:LYS:HB2	2.20	0.42
1:A:1953:ILE:HD11	1:A:1986:LEU:HD13	2.01	0.42
1:A:2216:CYS:HA	1:A:2225:LEU:HB3	2.01	0.42
3:C:85:ASP:OD2	33:T:240:LEU:HA	2.20	0.42
3:C:90:THR:O	3:C:92:PRO:HD3	2.19	0.42
15:H:107:A:N1	15:H:108:G:C5	2.88	0.42
21:1:1075:ARG:HE	21:1:1075:ARG:HB2	1.64	0.42
23:3:146:ARG:HB2	23:3:150:ALA:HA	2.02	0.42
23:3:353:PHE:O	23:3:432:ARG:NH1	2.44	0.42
23:3:774:PHE:N	23:3:774:PHE:CD2	2.86	0.42
27:7:30:GLU:HA	27:7:33:VAL:HG12	2.02	0.42
30:M:202:CYS:HB2	30:M:219:PHE:HB2	2.02	0.42
32:R:71:GLN:HE21	32:R:71:GLN:HB2	1.61	0.42
33:T:188:PRO:HG3	33:T:443:THR:HG21	2.01	0.42
36:Y:38:ILE:HG12	36:Y:82:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:LYS:HG2	1:A:49:ARG:N	2.35	0.42
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.49	0.42
1:A:1889:LEU:HD11	1:A:2012:LEU:HG	2.02	0.42
3:C:77:VAL:HG13	33:T:196:LEU:CB	2.41	0.42
3:C:140:HIS:CB	3:C:230:ASP:H	2.33	0.42
3:C:259:LYS:HD2	41:C:1500:GTP:C4	2.55	0.42
3:C:452:THR:HB	3:C:577:PHE:CE2	2.55	0.42
5:E:152:SER:OG	5:E:153:PHE:HD1	2.03	0.42
13:F:58:G:O2'	13:F:59:G:P	2.78	0.42
14:G:141:C:H2'	14:G:142:U:C6	2.52	0.42
15:H:179:C:C2	15:H:180:G:C8	3.07	0.42
21:1:401:ASP:HA	21:1:404:LEU:HB2	2.00	0.42
21:1:848:GLU:O	21:1:851:SER:OG	2.32	0.42
21:1:1179:ASP:OD1	21:1:1181:ASP:N	2.52	0.42
23:3:3:LEU:HA	23:3:1130:VAL:O	2.20	0.42
23:3:228:LEU:HD23	23:3:259:LYS:HZ2	1.84	0.42
23:3:482:THR:OG1	23:3:501:GLY:HA3	2.19	0.42
23:3:691:THR:HG22	23:3:716:SER:HB3	2.02	0.42
23:3:718:ARG:HG2	23:3:719:SER:H	1.84	0.42
25:5:25:ASN:HB3	25:5:87:LEU:HA	2.02	0.42
28:J:294:HIS:HE1	29:L:227:THR:CB	2.26	0.42
31:P:226:LYS:HD3	31:P:227:TYR:HE1	1.83	0.42
32:R:67:ILE:CG1	32:R:71:GLN:OE1	2.68	0.42
34:V:547:VAL:O	34:V:548:ALA:C	2.58	0.42
1:A:371:LEU:HD12	1:A:372:PRO:HD2	2.00	0.42
1:A:380:LEU:HD12	3:C:334:ILE:HA	2.02	0.42
1:A:382:GLU:O	1:A:383:PHE:CG	2.73	0.42
1:A:611:LEU:HA	1:A:611:LEU:HD12	1.85	0.42
1:A:816:TRP:CE2	1:A:820:ARG:HG3	2.55	0.42
1:A:1436:TRP:HA	1:A:1439:ARG:CZ	2.50	0.42
3:C:149:LEU:HA	3:C:427:PHE:HD2	1.82	0.42
14:G:-3:A:H2'	14:G:-2:C:C6	2.55	0.42
15:H:82:G:C2	15:H:83:A:C5	3.08	0.42
21:1:527:GLY:O	21:1:531:LEU:HD13	2.20	0.42
22:2:525:PRO:HD2	22:2:528:ILE:HD12	2.00	0.42
23:3:412:ILE:HD12	23:3:1118:VAL:HG11	2.01	0.42
33:T:187:LYS:N	33:T:188:PRO:CD	2.83	0.42
33:T:233:LEU:HD23	33:T:233:LEU:O	2.20	0.42
36:Y:37:TRP:HH2	37:Z:498:GLY:N	2.15	0.42
36:Y:59:TYR:HB3	36:Y:92:LEU:HD23	2.01	0.42
1:A:109:PRO:HD3	1:A:630:TRP:HZ2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TYR:HH	3:C:853:ARG:NH2	2.07	0.42
1:A:697:MET:N	1:A:698:PRO:HD3	2.34	0.42
1:A:833:LYS:HE3	1:A:834:HIS:NE2	2.35	0.42
1:A:1301:ILE:CD1	2:B:39:C:OP1	2.67	0.42
1:A:1416:ILE:HB	1:A:1417:PRO:HD3	2.01	0.42
1:A:1457:HIS:HE1	32:R:424:SER:HA	1.74	0.42
1:A:1529:ILE:O	1:A:1530:PRO:C	2.59	0.42
2:B:41:U:C4	2:B:42:U:O4	2.73	0.42
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.42
3:C:140:HIS:HB3	3:C:230:ASP:H	1.85	0.42
3:C:149:LEU:HA	3:C:427:PHE:CE2	2.54	0.42
14:G:139:U:H2'	14:G:140:A:C8	2.55	0.42
15:H:26:A:C5	15:H:27:U:C5	3.08	0.42
21:1:687:VAL:HA	21:1:690:ILE:HG22	2.01	0.42
21:1:727:VAL:HG12	21:1:731:LEU:HD11	2.02	0.42
21:1:790:LYS:O	21:1:793:LYS:HB3	2.19	0.42
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.20	0.42
28:J:240:THR:O	28:J:241:VAL:HB	2.19	0.42
28:J:259:GLN:HE21	29:L:220:PRO:HD3	1.82	0.42
31:P:58:ASP:OD2	31:P:61:ARG:HB2	2.19	0.42
31:P:192:VAL:CG1	31:P:193:VAL:N	2.83	0.42
1:A:428:LYS:HE3	1:A:454:TYR:CE1	2.55	0.42
1:A:479:THR:HG23	32:R:203:GLN:NE2	2.35	0.42
1:A:1188:ASN:ND2	1:A:1233:ASP:OD2	2.47	0.42
1:A:1399:GLN:C	1:A:1401:ARG:H	2.24	0.42
1:A:1489:LEU:O	1:A:1492:GLY:N	2.45	0.42
1:A:1503:TRP:CZ2	1:A:1753:LEU:HD21	2.55	0.42
1:A:1555:LEU:HB2	1:A:1558:THR:OG1	2.19	0.42
1:A:1763:LEU:HD23	1:A:1764:SER:O	2.20	0.42
1:A:2117:ILE:H	1:A:2117:ILE:HG12	1.64	0.42
3:C:220:ARG:HD3	3:C:477:HIS:NE2	2.34	0.42
3:C:474:LEU:HD12	3:C:500:THR:O	2.20	0.42
5:E:274:VAL:C	5:E:275:LYS:HG3	2.40	0.42
15:H:147:G:C2	15:H:148:C:N3	2.87	0.42
15:H:155:C:H2'	15:H:156:U:H5''	2.02	0.42
15:H:179:C:O2	15:H:180:G:C8	2.72	0.42
21:1:555:VAL:O	21:1:559:ILE:HG12	2.19	0.42
22:2:643:PRO:HG2	24:4:66:ASP:HA	2.01	0.42
23:3:259:LYS:HE3	23:3:266:ASP:OD2	2.20	0.42
23:3:261:PHE:HD1	23:3:261:PHE:HA	1.72	0.42
23:3:288:VAL:HG23	23:3:289:CYS:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:519:VAL:HG22	23:3:524:ILE:HG23	2.02	0.42
23:3:673:VAL:HA	23:3:690:ARG:HA	2.02	0.42
23:3:968:ARG:CZ	23:3:979:ARG:HH11	2.33	0.42
23:3:1011:TRP:HB3	23:3:1024:PHE:CZ	2.55	0.42
28:J:216:ASP:O	28:J:218:GLU:N	2.53	0.42
33:T:281:ILE:CD1	33:T:282:ARG:HG2	2.50	0.42
1:A:121:HIS:C	1:A:123:THR:H	2.23	0.41
1:A:1320:LYS:NZ	32:R:434:TYR:CE1	2.88	0.41
1:A:1402:ARG:CD	32:R:412:ASP:HA	2.50	0.41
1:A:1942:ALA:CB	1:A:1983:LEU:HD22	2.50	0.41
3:C:291:MET:HG2	3:C:292:TYR:CE1	2.54	0.41
3:C:445:ALA:HB1	3:C:449:ILE:HG13	2.02	0.41
3:C:829:GLU:HG3	3:C:830:PRO:HD2	2.01	0.41
13:F:8:C:C6	13:F:8:C:C5'	2.98	0.41
13:F:31:U:H2'	13:F:32:U:C6	2.55	0.41
15:H:68:G:H2'	15:H:69:U:H6	1.82	0.41
21:1:783:GLU:O	21:1:787:ILE:HG12	2.20	0.41
21:1:1025:LYS:HE2	30:M:210:PHE:CE1	2.55	0.41
23:3:443:GLU:HA	23:3:735:SER:OG	2.20	0.41
23:3:812:LYS:NZ	23:3:855:PRO:HG2	2.35	0.41
27:7:23:HIS:H	27:7:26:THR:HG1	1.68	0.41
28:J:239:ARG:C	28:J:239:ARG:HD3	2.40	0.41
28:J:262:ARG:HB3	29:L:220:PRO:HG3	2.02	0.41
28:J:368:ARG:O	28:J:372:VAL:HG23	2.20	0.41
32:R:131:ASP:OD2	32:R:132:LEU:N	2.53	0.41
1:A:120:TYR:HE1	1:A:485:THR:HB	1.84	0.41
1:A:137:GLU:N	1:A:138:PRO:HD2	2.35	0.41
1:A:143:GLN:O	1:A:146:SER:HB3	2.20	0.41
1:A:148:TRP:CZ2	1:A:616:PHE:CA	3.02	0.41
1:A:252:ASP:HB2	1:A:334:THR:CB	2.48	0.41
1:A:344:ASP:OD1	1:A:347:LEU:HD11	2.19	0.41
1:A:470:ARG:CZ	1:A:470:ARG:HB2	2.49	0.41
1:A:615:ARG:HE	1:A:615:ARG:HB2	1.59	0.41
1:A:1051:LEU:HD22	31:P:193:VAL:HG11	2.00	0.41
1:A:1428:HIS:O	1:A:1429:THR:C	2.59	0.41
1:A:1823:HIS:O	1:A:1826:VAL:HG22	2.20	0.41
3:C:73:TYR:HB3	3:C:77:VAL:HG21	2.02	0.41
3:C:89:LEU:C	3:C:89:LEU:CD2	2.82	0.41
3:C:259:LYS:HG2	3:C:262:ARG:HD3	1.99	0.41
3:C:449:ILE:CD1	3:C:466:SER:HA	2.50	0.41
15:H:80:A:C2	15:H:81:G:N7	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:153:A:H62	15:H:177:A:H2	1.67	0.41
21:1:1185:ARG:HD2	21:1:1218:ASN:OD1	2.20	0.41
23:3:425:VAL:O	23:3:435:LEU:HD12	2.20	0.41
23:3:436:ARG:HG2	23:3:778:ALA:HA	2.01	0.41
29:L:31:TRP:CH2	29:L:47:LYS:HA	2.55	0.41
32:R:88:ILE:CG2	32:R:96:ILE:HG23	2.48	0.41
32:R:418:GLN:HE21	32:R:418:GLN:HB2	1.64	0.41
32:R:442:ARG:NH1	32:R:443:GLY:CA	2.78	0.41
36:Y:64:ASN:O	36:Y:83:CYS:HB3	2.19	0.41
37:Z:572:PRO:CG	37:Z:588:ASP:OD2	2.67	0.41
1:A:305:ARG:HE	3:C:854:ARG:NH1	2.18	0.41
1:A:629:PHE:CD2	1:A:629:PHE:O	2.73	0.41
1:A:1118:PRO:CD	1:A:1119:ASP:N	2.82	0.41
1:A:1883:VAL:HG12	1:A:1885:LYS:HG3	2.01	0.41
1:A:2111:LEU:HD21	1:A:2225:LEU:HD21	2.03	0.41
2:B:35:U:OP2	2:B:35:U:C6	2.70	0.41
3:C:148:CYS:SG	3:C:312:SER:O	2.78	0.41
3:C:512:GLU:HG3	3:C:562:THR:O	2.19	0.41
5:E:263:ASP:O	5:E:272:ARG:NE	2.32	0.41
21:1:520:THR:HG21	21:1:558:ARG:HE	1.85	0.41
21:1:1124:SER:O	21:1:1127:THR:OG1	2.28	0.41
23:3:8:LEU:HD23	23:3:774:PHE:CZ	2.52	0.41
33:T:225:ASP:O	33:T:226:ARG:CB	2.67	0.41
1:A:206:TRP:CE3	1:A:212:PRO:HB3	2.55	0.41
1:A:592:TYR:O	1:A:593:ARG:C	2.59	0.41
1:A:800:TYR:HB3	3:C:59:LEU:HD11	2.02	0.41
1:A:1554:GLN:NE2	1:A:1620:TYR:O	2.49	0.41
1:A:1730:MET:O	1:A:1734:MET:HG2	2.19	0.41
1:A:2172:MET:HB2	1:A:2172:MET:HE3	1.79	0.41
3:C:261:ASP:CG	41:C:1500:GTP:N1	2.61	0.41
3:C:445:ALA:CB	3:C:449:ILE:HD11	2.43	0.41
3:C:853:ARG:O	3:C:854:ARG:HB3	2.20	0.41
15:H:152:G:H2'	15:H:152:G:N3	2.36	0.41
15:H:154:C:N3	15:H:176:G:N1	2.61	0.41
21:1:642:PRO:HB3	21:1:682:HIS:NE2	2.36	0.41
21:1:1136:TYR:CE1	21:1:1144:GLN:HB3	2.55	0.41
23:3:199:GLU:HB3	23:3:203:ASN:HD21	1.85	0.41
28:J:220:LEU:O	28:J:223:TYR:HB3	2.21	0.41
32:R:155:VAL:O	32:R:159:VAL:HG23	2.20	0.41
1:A:368:GLN:C	1:A:369:GLU:OE2	2.57	0.41
1:A:387:PHE:HD1	3:C:327:TYR:CE1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:589:LYS:HB3	3:C:659:VAL:O	2.20	0.41
3:C:704:VAL:O	3:C:709:TRP:CZ2	2.74	0.41
3:C:707:ILE:HD11	3:C:735:PHE:HB2	2.01	0.41
13:F:40:U:O4	13:F:41:A:N6	2.54	0.41
15:H:103:U:C3'	15:H:104:U:H5'	2.51	0.41
21:1:621:ASP:OD2	21:1:623:TYR:HB3	2.19	0.41
21:1:719:TYR:CD1	23:3:218:ASN:HB2	2.56	0.41
23:3:116:VAL:HA	23:3:117:PRO:HD3	1.95	0.41
23:3:896:PHE:CZ	23:3:972:LEU:HB2	2.55	0.41
24:4:69:TYR:OH	24:4:73:ILE:HG13	2.20	0.41
28:J:340:GLN:N	28:J:341:PRO:HD3	2.35	0.41
31:P:189:ASP:O	31:P:190:ASP:C	2.58	0.41
33:T:223:SER:OG	33:T:224:ALA:N	2.53	0.41
35:X:173:GLN:NE2	35:X:176:GLU:HA	2.36	0.41
1:A:151:MET:SD	1:A:628:GLY:CA	3.09	0.41
1:A:280:GLU:HB2	2:B:48:A:H4'	2.01	0.41
1:A:335:PRO:HG3	3:C:139:HIS:CG	2.56	0.41
1:A:362:ARG:CD	1:A:362:ARG:C	2.88	0.41
1:A:398:THR:CG2	3:C:382:ALA:CB	2.96	0.41
1:A:434:HIS:ND1	1:A:434:HIS:C	2.73	0.41
1:A:1325:LEU:HD23	1:A:1325:LEU:HA	1.86	0.41
1:A:1948:ASP:HA	1:A:1951:LYS:HD2	2.01	0.41
1:A:2073:TRP:CZ3	1:A:2313:HIS:CG	3.09	0.41
1:A:2117:ILE:HG21	1:A:2301:PRO:HB2	2.02	0.41
1:A:2120:LEU:HD12	1:A:2120:LEU:N	2.35	0.41
3:C:97:VAL:HG21	31:P:45:GLN:CG	2.46	0.41
3:C:137:HIS:NE2	3:C:236:MET:SD	2.93	0.41
13:F:39:A:H2'	13:F:40:U:O4'	2.21	0.41
14:G:-2:C:H2'	14:G:-1:G:H8	1.82	0.41
15:H:72:U:H6	15:H:72:U:O5'	2.03	0.41
15:H:171:U:H2'	15:H:172:C:O4'	2.21	0.41
21:1:815:PHE:HA	21:1:819:TRP:CD1	2.56	0.41
23:3:168:TYR:CE1	27:7:69:MET:HB3	2.55	0.41
23:3:442:LEU:HD13	23:3:734:LEU:HD23	1.99	0.41
23:3:587:VAL:CG1	23:3:590:MET:HG3	2.49	0.41
33:T:297:HIS:CE1	33:T:300:ILE:HD12	2.56	0.41
33:T:455:GLN:CG	33:T:456:PRO:HD2	2.51	0.41
36:Y:24:ASP:O	36:Y:26:VAL:N	2.54	0.41
1:A:296:PHE:CZ	3:C:593:GLU:HB2	2.56	0.41
1:A:530:LEU:CB	30:M:198:GLN:HE21	2.17	0.41
1:A:866:LEU:O	1:A:869:GLN:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:GLN:HA	1:A:1446:GLN:HE22	1.84	0.41
1:A:1099:PHE:CE2	1:A:1153:VAL:HG13	2.53	0.41
1:A:1221:THR:O	1:A:1223:GLU:HG3	2.20	0.41
1:A:1430:LEU:HD21	32:R:422:MET:HA	2.03	0.41
1:A:1458:GLN:HE21	1:A:1463:LYS:HG3	1.86	0.41
3:C:230:ASP:OD1	3:C:259:LYS:HB2	2.17	0.41
3:C:270:PRO:HA	3:C:271:PRO:HD3	1.87	0.41
4:D:577:LYS:O	4:D:581:SER:N	2.54	0.41
14:G:155:U:C4'	14:G:156:U:H5'	2.49	0.41
15:H:4:G:H2'	15:H:5:C:C6	2.55	0.41
15:H:83:A:H2'	15:H:84:C:H1'	2.00	0.41
21:1:1127:THR:O	22:2:571:LEU:HD13	2.21	0.41
23:3:314:THR:HG22	23:3:315:LEU:N	2.36	0.41
23:3:521:PRO:HA	23:3:544:ILE:CG2	2.49	0.41
23:3:524:ILE:CD1	23:3:556:ILE:HD13	2.49	0.41
24:4:67:ALA:O	24:4:70:ALA:HB3	2.21	0.41
28:J:273:TYR:CD1	32:R:228:PRO:CB	3.04	0.41
1:A:61:MET:HB3	1:A:62:PRO:CD	2.50	0.41
1:A:1891:LEU:HB2	1:A:1893:PHE:CE2	2.55	0.41
1:A:2090:ILE:H	1:A:2090:ILE:HD13	1.86	0.41
1:A:2259:VAL:HG22	1:A:2260:GLN:H	1.86	0.41
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.41
3:C:300:LEU:N	3:C:300:LEU:CD1	2.84	0.41
13:F:60:C:H5''	32:R:219:PRO:HB3	2.01	0.41
15:H:160:A:H2'	15:H:161:U:C6	2.55	0.41
21:1:719:TYR:HB3	23:3:216:GLY:O	2.20	0.41
21:1:1016:LEU:O	21:1:1019:ARG:HB3	2.20	0.41
21:1:1055:TRP:O	21:1:1058:ILE:HB	2.20	0.41
21:1:1092:ASP:OD1	21:1:1092:ASP:N	2.53	0.41
23:3:86:ARG:CD	23:3:104:GLN:HE21	2.33	0.41
23:3:205:GLN:HE21	23:3:227:PRO:HB3	1.85	0.41
23:3:554:VAL:HG12	23:3:556:ILE:HG23	2.01	0.41
26:6:90:ASN:OD1	26:6:91:LEU:N	2.54	0.41
30:M:208:THR:HG22	30:M:210:PHE:HD2	1.85	0.41
32:R:129:ASP:C	32:R:131:ASP:N	2.73	0.41
33:T:309:ASP:C	33:T:309:ASP:OD1	2.59	0.41
37:Z:522:LEU:HD13	37:Z:522:LEU:C	2.41	0.41
37:Z:525:TYR:HD1	37:Z:526:ILE:CG2	2.29	0.41
1:A:121:HIS:C	1:A:123:THR:N	2.74	0.41
1:A:128:PHE:CD1	1:A:473:PHE:CE1	3.09	0.41
1:A:155:LYS:CE	1:A:624:GLY:O	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:GLU:O	1:A:520:TYR:HD2	2.02	0.41
1:A:292:ASP:O	1:A:294:ASN:ND2	2.54	0.41
1:A:331:TRP:CD1	3:C:635:LEU:HD13	2.55	0.41
1:A:596:TYR:O	1:A:598:LEU:N	2.54	0.41
1:A:965:VAL:O	1:A:1100:ARG:NH1	2.54	0.41
1:A:1052:VAL:CG2	1:A:1161:LEU:HD21	2.51	0.41
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.53	0.41
1:A:1757:GLU:CG	32:R:451:ILE:HG13	2.51	0.41
1:A:1776:ILE:O	1:A:1859:LYS:N	2.48	0.41
1:A:1788:VAL:HG21	1:A:1800:THR:HB	2.03	0.41
1:A:2117:ILE:HG22	1:A:2303:GLU:HA	2.03	0.41
1:A:2320:LEU:HD21	1:A:2322:GLU:CD	2.41	0.41
2:B:27:U:HO2'	2:B:28:A:P	2.42	0.41
2:B:64:G:H5'	5:E:106:LYS:HZ2	1.78	0.41
3:C:64:LYS:HE2	3:C:64:LYS:HA	2.02	0.41
3:C:65:TYR:O	3:C:66:TYR:CG	2.73	0.41
3:C:79:THR:HA	33:T:199:VAL:O	2.20	0.41
3:C:132:VAL:HG11	3:C:226:VAL:CG2	2.49	0.41
3:C:133:THR:HB	3:C:225:VAL:HA	2.02	0.41
3:C:513:ASN:O	3:C:513:ASN:ND2	2.54	0.41
3:C:518:ASP:N	3:C:519:GLU:OE2	2.54	0.41
5:E:115:LEU:O	5:E:116:HIS:CD2	2.74	0.41
5:E:177:LYS:C	5:E:178:LEU:HD23	2.41	0.41
5:E:243:LEU:HD22	5:E:243:LEU:HA	1.80	0.41
15:H:152:G:H2'	15:H:153:A:C1'	2.51	0.41
21:1:184:VAL:O	21:1:188:ALA:HB2	2.21	0.41
21:1:517:ARG:O	21:1:520:THR:OG1	2.20	0.41
21:1:664:GLY:O	21:1:667:ILE:HB	2.21	0.41
21:1:770:MET:O	21:1:774:ILE:HG12	2.21	0.41
21:1:963:LYS:HG2	21:1:1003:VAL:HB	2.02	0.41
21:1:1080:THR:HA	21:1:1083:TYR:CD2	2.56	0.41
21:1:1092:ASP:OD1	21:1:1093:VAL:N	2.54	0.41
21:1:1227:ILE:O	21:1:1231:MET:HG2	2.20	0.41
21:1:1252:GLN:OE1	22:2:499:PRO:HA	2.20	0.41
23:3:65:LEU:HD12	23:3:79:VAL:O	2.21	0.41
23:3:631:GLN:HG2	23:3:632:ALA:O	2.21	0.41
23:3:910:ALA:HB2	23:3:948:VAL:HG23	2.02	0.41
32:R:69:VAL:HG12	32:R:70:ALA:N	2.36	0.41
32:R:132:LEU:HD13	33:T:399:LYS:HE3	2.02	0.41
32:R:414:ARG:NH2	32:R:414:ARG:CB	2.73	0.41
33:T:209:CYS:O	33:T:221:THR:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:210:ILE:HG12	33:T:221:THR:HG22	2.03	0.41
33:T:294:LEU:N	33:T:294:LEU:HD23	2.36	0.41
33:T:400:PHE:HD1	33:T:401:PRO:HA	1.86	0.41
36:Y:10:ILE:O	36:Y:13:LEU:N	2.53	0.41
36:Y:67:LEU:HA	36:Y:80:CYS:HA	2.02	0.41
37:Z:566:TYR:CE2	37:Z:584:TRP:HE3	2.29	0.41
1:A:107:PRO:O	1:A:108:MET:HB2	2.21	0.41
1:A:118:VAL:HG12	1:A:119:LEU:N	2.36	0.41
1:A:164:MET:CE	1:A:560:SER:HA	2.51	0.41
1:A:247:THR:OG1	1:A:429:ASN:CB	2.60	0.41
1:A:384:VAL:O	1:A:385:GLU:HG2	2.21	0.41
1:A:395:THR:HG23	3:C:383:GLN:NE2	2.24	0.41
1:A:842:ALA:HB1	1:A:920:ALA:HB1	2.03	0.41
1:A:1425:LYS:CB	32:R:417:ASN:OD1	2.69	0.41
1:A:1771:LEU:O	1:A:1777:ILE:HD12	2.20	0.41
1:A:1776:ILE:HD13	1:A:1813:ARG:HD3	2.03	0.41
2:B:19:A:HO2'	2:B:20:G:P	2.38	0.41
3:C:149:LEU:HD11	3:C:427:PHE:CB	2.51	0.41
3:C:354:ARG:CG	3:C:354:ARG:HH11	2.34	0.41
13:F:42:C:C2	13:F:43:A:C8	3.09	0.41
21:1:1286:ARG:N	23:3:1006:GLN:HE22	2.19	0.41
23:3:274:ARG:HD2	23:3:389:PRO:HD3	2.02	0.41
25:5:14:PRO:O	25:5:17:VAL:HG22	2.21	0.41
28:J:423:GLU:OE1	28:J:423:GLU:HA	2.21	0.41
29:L:49:ARG:NH1	29:L:53:TRP:HB3	2.36	0.41
33:T:399:LYS:HB2	33:T:404:SER:HB3	2.03	0.41
33:T:434:GLY:HA2	33:T:464:GLY:N	2.36	0.41
34:V:512:GLY:O	34:V:513:ARG:C	2.60	0.41
1:A:265:THR:HG22	1:A:314:ILE:HG12	2.03	0.40
1:A:393:LEU:N	3:C:379:LYS:HE3	2.13	0.40
1:A:1528:GLN:HG3	1:A:1530:PRO:CD	2.51	0.40
1:A:1957:ASP:OD2	1:A:1959:THR:OG1	2.37	0.40
2:B:19:A:H2'	2:B:20:G:C5'	2.49	0.40
3:C:221:ILE:HG13	3:C:479:THR:OG1	2.21	0.40
3:C:235:VAL:HG13	3:C:239:THR:OG1	2.22	0.40
3:C:392:LEU:N	3:C:393:PRO:CD	2.84	0.40
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.40
5:E:178:LEU:CD2	5:E:208:ILE:HD11	2.51	0.40
14:G:146:C:C4	14:G:147:C:N4	2.89	0.40
15:H:112:G:O5'	15:H:112:G:H8	2.04	0.40
21:1:498:MET:HE1	21:1:530:PRO:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:765:TYR:O	21:1:769:VAL:HG23	2.20	0.40
21:1:806:ILE:HG12	21:1:810:ILE:HD12	2.03	0.40
21:1:997:LEU:O	21:1:1001:VAL:HG23	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CZ	2.56	0.40
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	2.03	0.40
23:3:194:ASN:O	23:3:196:PRO:HD3	2.21	0.40
23:3:259:LYS:HG3	23:3:266:ASP:CG	2.42	0.40
25:5:27:PRO:HG3	25:5:85:ARG:NH1	2.36	0.40
34:V:585:ILE:O	34:V:588:GLN:N	2.54	0.40
35:X:263:PRO:CG	35:X:265:LYS:H	2.34	0.40
37:Z:563:ARG:HH21	37:Z:563:ARG:HG3	1.83	0.40
1:A:76:MET:SD	1:A:88:TYR:CZ	3.15	0.40
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.21	0.40
1:A:225:TYR:O	1:A:418:THR:CB	2.68	0.40
1:A:254:TYR:HH	1:A:434:HIS:HB3	1.85	0.40
1:A:363:HIS:NE2	3:C:287:GLY:CA	2.74	0.40
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.55	0.40
1:A:1263:TRP:CZ2	1:A:1292:GLU:HG2	2.56	0.40
1:A:1451:ASN:HB2	32:R:428:GLY:O	2.21	0.40
1:A:1529:ILE:HG13	1:A:1530:PRO:HD3	2.03	0.40
3:C:64:LYS:NZ	31:P:209:ARG:NH1	2.70	0.40
3:C:85:ASP:HA	33:T:238:LEU:HB3	2.03	0.40
3:C:534:VAL:HG12	3:C:535:ALA:N	2.31	0.40
13:F:42:C:H2'	13:F:43:A:O4'	2.21	0.40
15:H:2:U:H2'	15:H:3:C:C6	2.55	0.40
15:H:149:A:N3	15:H:150:U:C6	2.89	0.40
21:1:658:TRP:CZ3	21:1:700:LYS:HD2	2.55	0.40
21:1:935:THR:O	21:1:939:ARG:HG2	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CE2	2.56	0.40
22:2:614:ARG:O	22:2:618:GLY:N	2.51	0.40
22:2:648:LEU:O	22:2:649:LYS:HD3	2.21	0.40
23:3:983:ASN:HB2	23:3:1021:LEU:HB2	2.03	0.40
24:4:17:VAL:HG13	24:4:84:ILE:CG2	2.48	0.40
28:J:338:GLU:O	32:R:116:TYR:CD2	2.75	0.40
28:J:376:VAL:HG13	28:J:377:LYS:N	2.36	0.40
31:P:44:ARG:HG3	33:T:258:SER:CA	2.51	0.40
34:V:530:LYS:C	34:V:532:GLN:N	2.74	0.40
35:X:238:THR:O	35:X:393:VAL:HG23	2.21	0.40
1:A:82:ARG:HB3	1:A:83:HIS:HD1	1.86	0.40
1:A:247:THR:HG23	1:A:249:LEU:HD12	2.03	0.40
1:A:378:PHE:CE2	3:C:335:ASN:HB2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:LEU:HD23	1:A:652:LEU:HA	1.84	0.40
1:A:1057:ARG:O	1:A:1060:GLU:HB2	2.22	0.40
1:A:1273:TYR:HD2	1:A:1274:PHE:CD2	2.39	0.40
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.36	0.40
1:A:2144:CYS:HB2	1:A:2270:PHE:CE1	2.57	0.40
3:C:375:GLU:N	3:C:376:PRO:HD2	2.37	0.40
5:E:255:MET:O	5:E:257:ASN:N	2.54	0.40
21:1:922:GLY:O	21:1:925:VAL:HG12	2.22	0.40
21:1:933:CYS:HA	21:1:936:VAL:HB	2.02	0.40
21:1:1130:PRO:HB3	22:2:528:ILE:HG23	2.04	0.40
23:3:63:ARG:HD2	23:3:83:ASP:HA	2.03	0.40
23:3:379:LEU:HB2	23:3:383:ASP:HB3	2.04	0.40
23:3:388:GLN:NE2	23:3:389:PRO:HD2	2.36	0.40
23:3:606:ALA:HA	23:3:616:ILE:HD13	2.04	0.40
33:T:339:GLN:CG	33:T:340:ALA:N	2.84	0.40
36:Y:37:TRP:HH2	37:Z:498:GLY:HA3	1.59	0.40
37:Z:491:ASP:O	37:Z:495:ALA:HB3	2.21	0.40
1:A:293:TRP:CE3	1:A:293:TRP:C	2.94	0.40
1:A:457:ASN:ND2	2:B:27:U:H3'	2.36	0.40
1:A:938:PRO:O	1:A:941:LYS:HD3	2.22	0.40
1:A:2120:LEU:HD12	1:A:2120:LEU:H	1.86	0.40
3:C:229:ILE:HG12	3:C:239:THR:HG21	2.04	0.40
3:C:567:GLU:O	3:C:567:GLU:HG3	2.20	0.40
13:F:96:U:H2'	13:F:97:U:C6	2.56	0.40
21:1:1052:ALA:HA	21:1:1055:TRP:CD1	2.51	0.40
21:1:1248:GLN:NE2	23:3:1030:PRO:HD3	2.36	0.40
23:3:179:ASN:HB3	23:3:213:LEU:O	2.22	0.40
23:3:192:ALA:HA	23:3:200:ALA:HB3	2.02	0.40
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.53	0.40
23:3:535:GLU:HG2	23:3:536:TRP:N	2.36	0.40
25:5:42:TYR:CZ	25:5:73:ALA:HA	2.56	0.40
33:T:220:VAL:HG12	33:T:221:THR:N	2.37	0.40
1:A:148:TRP:CZ3	1:A:612:ILE:HG23	2.56	0.40
1:A:283:VAL:O	1:A:284:ARG:CZ	2.67	0.40
1:A:361:HIS:HE2	3:C:279:ARG:HH22	1.68	0.40
1:A:692:ASP:HA	33:T:376:ARG:HH21	1.72	0.40
1:A:718:ARG:NH2	32:R:259:LYS:HG3	2.36	0.40
1:A:787:GLU:OE1	1:A:790:ARG:NH2	2.53	0.40
1:A:923:ASP:OD2	1:A:1439:ARG:HD3	2.22	0.40
1:A:1161:LEU:HD23	1:A:1161:LEU:HA	1.85	0.40
1:A:2195:THR:O	1:A:2199:ILE:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2332:ASP:O	1:A:2334:TYR:N	2.54	0.40
3:C:259:LYS:HG3	41:C:1500:GTP:C5	2.57	0.40
3:C:592:VAL:HG12	3:C:603:MET:SD	2.62	0.40
3:C:673:LYS:HD3	3:C:673:LYS:H	1.86	0.40
3:C:738:ASP:N	3:C:738:ASP:OD1	2.54	0.40
3:C:926:ALA:N	3:C:927:PRO:CD	2.84	0.40
13:F:58:G:HO2'	13:F:59:G:P	2.44	0.40
21:1:570:TYR:O	21:1:574:ILE:HG12	2.22	0.40
21:1:839:GLU:O	21:1:842:ASN:HB2	2.22	0.40
21:1:1023:ILE:O	21:1:1026:ASN:HB2	2.21	0.40
23:3:561:GLY:O	23:3:582:GLU:HA	2.22	0.40
23:3:999:ARG:NE	23:3:1041:TYR:OH	2.54	0.40
32:R:123:GLU:C	32:R:124:VAL:HG12	2.41	0.40
33:T:218:TRP:HZ3	33:T:220:VAL:CG2	2.35	0.40
35:X:231:ALA:O	35:X:236:THR:OG1	2.39	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2199/2335 (94%)	2049 (93%)	117 (5%)	33 (2%)	10	46
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	6	36
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	47	81
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	4	31
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100	100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	12	48
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	15
18	w	419/501 (84%)	379 (90%)	37 (9%)	3 (1%)	22	62
19	u	93/793 (12%)	87 (94%)	4 (4%)	2 (2%)	6	37
20	v	90/464 (19%)	67 (74%)	16 (18%)	7 (8%)	1	14
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	25	65
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1086 (93%)	78 (7%)	1 (0%)	51	85
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	12	48
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	11	46
29	L	128/802 (16%)	119 (93%)	8 (6%)	1 (1%)	19	60
30	M	34/343 (10%)	30 (88%)	3 (9%)	1 (3%)	4	31
31	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	6	37
32	R	295/540 (55%)	249 (84%)	31 (10%)	15 (5%)	2	21
33	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	3	26
34	V	443/908 (49%)	412 (93%)	26 (6%)	5 (1%)	14	52
35	X	142/396 (36%)	131 (92%)	11 (8%)	0	100	100
36	Y	102/322 (32%)	91 (89%)	11 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	2	21
38	z	176/472 (37%)	170 (97%)	6 (3%)	0	100	100
39	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	17	56
All	All	12645/20929 (60%)	11680 (92%)	812 (6%)	153 (1%)	17	50

All (153) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP
1	A	346	ASP
1	A	383	PHE
1	A	570	ASP
1	A	629	PHE
1	A	701	ILE
1	A	1119	ASP
3	C	388	VAL
3	C	427	PHE
3	C	444	GLY
3	C	457	VAL
3	C	458	ASP
3	C	516	LEU
3	C	824	THR
4	D	957	VAL
4	D	1584	ILE
5	E	193	THR
17	p	157	ASN
17	p	183	VAL
17	p	195	GLU
18	w	284	ARG
20	v	139	PRO
20	v	165	ARG
20	v	218	PRO
28	J	413	GLU
31	P	49	ASP
32	R	71	GLN
32	R	135	PRO
32	R	136	ASP

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Mol	Chain	Res	Type
32	R	186	VAL
32	R	412	ASP
32	R	416	PHE
32	R	420	LYS
32	R	425	GLY
33	T	186	PRO
33	T	268	LYS
33	T	341	ALA
33	T	343	PRO
33	T	495	ALA
34	V	596	LEU
34	V	597	PRO
37	Z	499	LYS
37	Z	531	LEU
37	Z	536	ARG
37	Z	569	PRO
39	x	937	ILE
1	A	122	ILE
1	A	308	ILE
1	A	349	ALA
1	A	367	SER
1	A	370	PRO
1	A	374	ASP
1	A	631	ALA
1	A	1141	ARG
3	C	90	THR
3	C	364	SER
3	C	572	GLU
3	C	711	ARG
16	o	160	LYS
17	p	159	PRO
17	p	160	GLU
17	p	177	PHE
17	p	186	ARG
19	u	280	VAL
20	v	115	PRO
21	1	112	ILE
28	J	217	GLU
28	J	341	PRO
28	J	376	VAL
28	J	709	VAL
31	P	190	ASP

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Mol	Chain	Res	Type
32	R	191	GLY
32	R	422	MET
33	T	301	ASP
34	V	485	GLN
37	Z	613	LYS
1	A	51	PHE
1	A	212	PRO
1	A	378	PHE
1	A	699	GLU
1	A	1118	PRO
1	A	1140	MET
5	E	60	MET
5	E	88	ARG
5	E	256	ASP
17	p	222	TYR
18	w	177	ARG
30	M	197	TYR
32	R	104	GLN
32	R	173	PRO
33	T	406	ILE
34	V	578	SER
39	x	1005	SER
1	A	363	HIS
1	A	480	LYS
1	A	698	PRO
1	A	1092	ILE
1	A	1114	LEU
1	A	1828	ALA
3	C	63	LYS
3	C	754	VAL
3	C	856	HIS
5	E	162	ARG
16	o	32	PRO
17	p	208	GLN
17	p	209	GLY
21	1	417	PRO
21	1	456	VAL
28	J	604	PRO
32	R	124	VAL
33	T	401	PRO
39	x	935	ASP
1	A	359	ILE

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Mol	Chain	Res	Type
3	C	361	PRO
3	C	615	PRO
5	E	159	PRO
20	v	217	PRO
32	R	126	ASN
32	R	423	ASP
33	T	185	MET
33	T	189	GLN
33	T	226	ARG
39	x	980	GLN
39	x	981	PRO
3	C	94	ILE
3	C	360	ALA
3	C	623	GLU
5	E	270	LYS
17	p	173	GLN
20	v	141	ILE
20	v	220	PRO
21	1	944	SER
29	L	215	PRO
34	V	609	GLN
3	C	66	TYR
5	E	149	GLY
37	Z	571	PRO
1	A	186	GLU
19	u	221	PRO
18	w	229	TRP
21	1	418	PRO
24	4	27	PRO
28	J	241	VAL
33	T	411	GLY
4	D	585	ILE
5	E	324	PRO
17	p	184	PRO
21	1	932	ILE
23	3	491	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1954/2108 (93%)	1850 (95%)	104 (5%)	22	49
3	C	745/866 (86%)	677 (91%)	68 (9%)	9	31
5	E	256/300 (85%)	244 (95%)	12 (5%)	26	52
18	w	49/446 (11%)	47 (96%)	2 (4%)	30	55
21	1	735/1104 (67%)	735 (100%)	0	100	100
22	2	94/776 (12%)	90 (96%)	4 (4%)	29	54
23	3	1018/1051 (97%)	1017 (100%)	1 (0%)	93	96
24	4	39/336 (12%)	37 (95%)	2 (5%)	24	50
25	5	74/109 (68%)	74 (100%)	0	100	100
26	6	76/95 (80%)	76 (100%)	0	100	100
27	7	57/77 (74%)	57 (100%)	0	100	100
28	J	205/751 (27%)	194 (95%)	11 (5%)	22	49
29	L	110/709 (16%)	105 (96%)	5 (4%)	27	53
30	M	25/294 (8%)	25 (100%)	0	100	100
31	P	90/203 (44%)	77 (86%)	13 (14%)	3	17
32	R	220/463 (48%)	170 (77%)	50 (23%)	1	6
33	T	268/441 (61%)	251 (94%)	17 (6%)	18	44
35	X	50/349 (14%)	44 (88%)	6 (12%)	5	22
36	Y	57/291 (20%)	56 (98%)	1 (2%)	59	77
37	Z	47/545 (9%)	39 (83%)	8 (17%)	2	13
38	z	146/416 (35%)	146 (100%)	0	100	100
39	x	1/897 (0%)	1 (100%)	0	100	100
All	All	6316/12627 (50%)	6012 (95%)	304 (5%)	29	51

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	48	LYS
1	A	49	ARG
1	A	50	LYS
1	A	59	GLU
1	A	60	ASP

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Mol	Chain	Res	Type
1	A	75	ASP
1	A	77	THR
1	A	78	ASN
1	A	82	ARG
1	A	86	ARG
1	A	88	TYR
1	A	89	LEU
1	A	152	ARG
1	A	163	ARG
1	A	177	ASP
1	A	181	ASN
1	A	185	VAL
1	A	204	LEU
1	A	233	PRO
1	A	250	VAL
1	A	258	PHE
1	A	284	ARG
1	A	294	ASN
1	A	295	GLU
1	A	325	HIS
1	A	330	THR
1	A	331	TRP
1	A	334	THR
1	A	336	ASN
1	A	344	ASP
1	A	352	PHE
1	A	359	ILE
1	A	362	ARG
1	A	363	HIS
1	A	364	SER
1	A	366	LYS
1	A	367	SER
1	A	368	GLN
1	A	371	LEU
1	A	377	GLU
1	A	382	GLU
1	A	383	PHE
1	A	389	LYS
1	A	391	THR
1	A	394	TYR
1	A	409	ARG
1	A	413	LEU

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Mol	Chain	Res	Type
1	A	433	GLU
1	A	452	LYS
1	A	459	LEU
1	A	462	ARG
1	A	467	GLN
1	A	468	LYS
1	A	535	ARG
1	A	546	LEU
1	A	579	GLN
1	A	606	LYS
1	A	627	CYS
1	A	630	TRP
1	A	642	ARG
1	A	671	THR
1	A	673	THR
1	A	674	LYS
1	A	675	GLN
1	A	679	SER
1	A	1146	ASP
1	A	1163	ARG
1	A	1425	LYS
1	A	1549	VAL
1	A	1930	TYR
1	A	2067	PHE
1	A	2073	TRP
1	A	2074	ARG
1	A	2078	ILE
1	A	2085	LEU
1	A	2087	THR
1	A	2090	ILE
1	A	2103	THR
1	A	2108	LYS
1	A	2117	ILE
1	A	2143	ARG
1	A	2156	THR
1	A	2157	VAL
1	A	2159	LEU
1	A	2171	GLU
1	A	2193	VAL
1	A	2194	THR
1	A	2219	THR
1	A	2223	CYS

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Mol	Chain	Res	Type
1	A	2233	SER
1	A	2239	ARG
1	A	2242	THR
1	A	2254	SER
1	A	2259	VAL
1	A	2261	MET
1	A	2273	VAL
1	A	2284	MET
1	A	2293	LYS
1	A	2298	LEU
1	A	2310	ARG
1	A	2312	SER
1	A	2319	LEU
1	A	2329	ASP
3	C	61	GLU
3	C	62	ASP
3	C	63	LYS
3	C	64	LYS
3	C	66	TYR
3	C	68	THR
3	C	71	GLU
3	C	79	THR
3	C	97	VAL
3	C	131	ASN
3	C	227	LEU
3	C	256	CYS
3	C	259	LYS
3	C	295	ASP
3	C	296	GLU
3	C	297	ASN
3	C	298	LEU
3	C	300	LEU
3	C	333	ASP
3	C	336	TYR
3	C	354	ARG
3	C	359	LYS
3	C	362	THR
3	C	366	GLN
3	C	387	ASP
3	C	389	ASP
3	C	427	PHE
3	C	428	THR

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Mol	Chain	Res	Type
3	C	438	ILE
3	C	446	LYS
3	C	452	THR
3	C	454	THR
3	C	457	VAL
3	C	458	ASP
3	C	459	SER
3	C	463	GLU
3	C	468	CYS
3	C	474	LEU
3	C	475	MET
3	C	477	HIS
3	C	489	GLN
3	C	490	PHE
3	C	495	ARG
3	C	512	GLU
3	C	517	GLU
3	C	519	GLU
3	C	571	ASN
3	C	572	GLU
3	C	573	GLU
3	C	596	ASN
3	C	673	LYS
3	C	675	PHE
3	C	677	GLU
3	C	704	VAL
3	C	706	GLN
3	C	709	TRP
3	C	712	LYS
3	C	724	TRP
3	C	725	ASP
3	C	730	ARG
3	C	738	ASP
3	C	749	THR
3	C	750	LEU
3	C	763	LYS
3	C	826	ARG
3	C	856	HIS
3	C	941	LYS
3	C	943	LEU
5	E	74	PHE
5	E	153	PHE

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Mol	Chain	Res	Type
5	E	161	ARG
5	E	229	TYR
5	E	243	LEU
5	E	248	SER
5	E	250	LEU
5	E	265	ARG
5	E	270	LYS
5	E	271	GLU
5	E	289	LEU
5	E	290	ARG
18	w	419	PRO
18	w	441	PRO
22	2	498	VAL
22	2	520	PRO
22	2	614	ARG
22	2	616	SER
23	3	442	LEU
24	4	27	PRO
24	4	83	PRO
28	J	217	GLU
28	J	218	GLU
28	J	219	GLU
28	J	221	ASN
28	J	229	LYS
28	J	239	ARG
28	J	281	LYS
28	J	308	ARG
28	J	363	ARG
28	J	410	HIS
28	J	411	MET
29	L	219	LYS
29	L	222	LEU
29	L	227	THR
29	L	228	SER
29	L	235	LEU
31	P	28	LYS
31	P	29	GLN
31	P	30	TYR
31	P	33	ARG
31	P	66	ARG
31	P	67	GLU
31	P	76	ARG

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Mol	Chain	Res	Type
31	P	78	ARG
31	P	188	TRP
31	P	190	ASP
31	P	191	ASP
31	P	212	ASN
31	P	224	MET
32	R	56	GLU
32	R	66	GLU
32	R	71	GLN
32	R	72	TYR
32	R	75	ASP
32	R	80	LYS
32	R	81	LYS
32	R	82	MET
32	R	86	LEU
32	R	89	GLN
32	R	92	SER
32	R	95	LYS
32	R	103	ARG
32	R	104	GLN
32	R	106	GLN
32	R	118	ASP
32	R	122	LYS
32	R	125	MET
32	R	128	ASP
32	R	129	ASP
32	R	137	GLU
32	R	158	LYS
32	R	170	LYS
32	R	171	LEU
32	R	175	GLN
32	R	181	PRO
32	R	183	GLN
32	R	186	VAL
32	R	188	PHE
32	R	189	ASN
32	R	195	ARG
32	R	211	ARG
32	R	212	PHE
32	R	213	LYS
32	R	214	ILE
32	R	215	ASN

Continued on next page...

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Mol	Chain	Res	Type
32	R	220	ARG
32	R	233	HIS
32	R	245	GLU
32	R	250	LYS
32	R	403	PRO
32	R	409	VAL
32	R	411	TYR
32	R	415	LEU
32	R	418	GLN
32	R	420	LYS
32	R	422	MET
32	R	426	PHE
32	R	434	TYR
32	R	435	ASN
33	T	257	ARG
33	T	282	ARG
33	T	308	ARG
33	T	318	ARG
33	T	387	PHE
33	T	399	LYS
33	T	400	PHE
33	T	401	PRO
33	T	402	ASP
33	T	412	HIS
33	T	416	ILE
33	T	418	THR
33	T	455	GLN
33	T	460	ASP
33	T	461	SER
33	T	463	SER
33	T	478	LEU
35	X	209	PRO
35	X	224	PRO
35	X	249	PRO
35	X	263	PRO
35	X	293	PRO
35	X	297	PRO
36	Y	44	PRO
37	Z	524	ARG
37	Z	526	ILE
37	Z	563	ARG
37	Z	569	PRO

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Mol	Chain	Res	Type
37	Z	597	ARG
37	Z	598	PHE
37	Z	600	ARG
37	Z	613	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	73	HIS
1	A	78	ASN
1	A	97	HIS
1	A	210	HIS
1	A	297	ASN
1	A	325	HIS
1	A	363	HIS
1	A	573	GLN
1	A	584	HIS
1	A	601	GLN
1	A	675	GLN
1	A	775	ASN
1	A	924	GLN
1	A	1024	HIS
1	A	1069	ASN
1	A	1075	GLN
1	A	1096	HIS
1	A	1296	GLN
1	A	1359	HIS
1	A	1458	GLN
1	A	1460	HIS
1	A	1527	ASN
1	A	1580	HIS
1	A	1717	ASN
1	A	1784	ASN
1	A	1966	HIS
1	A	2123	GLN
1	A	2300	ASN
1	A	2306	HIS
3	C	87	GLN
3	C	245	HIS
3	C	297	ASN
3	C	383	GLN

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Mol	Chain	Res	Type
3	C	437	HIS
3	C	513	ASN
3	C	575	GLN
3	C	583	ASN
3	C	596	ASN
3	C	706	GLN
3	C	924	GLN
5	E	165	GLN
18	w	425	HIS
18	w	485	ASN
21	1	473	GLN
21	1	599	ASN
21	1	903	GLN
21	1	942	ASN
21	1	1026	ASN
21	1	1186	GLN
21	1	1209	ASN
21	1	1248	GLN
21	1	1277	GLN
22	2	490	HIS
23	3	21	ASN
23	3	104	GLN
23	3	254	ASN
23	3	264	GLN
23	3	293	HIS
23	3	304	GLN
23	3	388	GLN
23	3	440	HIS
23	3	518	GLN
23	3	775	ASN
23	3	870	ASN
23	3	1087	GLN
28	J	221	ASN
28	J	259	GLN
28	J	294	HIS
28	J	351	ASN
29	L	73	HIS
30	M	198	GLN
31	P	212	ASN
31	P	220	HIS
32	R	89	GLN
32	R	104	GLN

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Mol	Chain	Res	Type
32	R	106	GLN
32	R	126	ASN
32	R	189	ASN
32	R	194	GLN
32	R	215	ASN
32	R	233	HIS
32	R	283	HIS
32	R	418	GLN
33	T	217	GLN
33	T	278	ASN
33	T	297	HIS
33	T	413	ASN
33	T	417	ASN
33	T	446	ASN
33	T	451	HIS
33	T	455	GLN
35	X	307	GLN
36	Y	87	GLN
38	z	112	GLN
38	z	127	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	37 (40%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	21 (25%)	10 (12%)
All	All	379/686 (55%)	139 (36%)	35 (9%)

All (139) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G

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Mol	Chain	Res	Type
2	B	25	C
2	B	26	A
2	B	28	A
2	B	35	U
2	B	36	C
2	B	38	C
2	B	40	U
2	B	41	U
2	B	45	C
2	B	47	A
2	B	57	G
2	B	70	A
2	B	71	C
13	F	6	C
13	F	7	G
13	F	8	C
13	F	10	U
13	F	12	G
13	F	25	C
13	F	26	U
13	F	27	A
13	F	28	A
13	F	29	A
13	F	33	G
13	F	34	G
13	F	36	A
13	F	37	C
13	F	38	G
13	F	44	G
13	F	45	A
13	F	46	G
13	F	47	A
13	F	48	A
13	F	49	G
13	F	51	U
13	F	54	G
13	F	55	C
13	F	56	A
13	F	58	G
13	F	59	G
13	F	60	C
13	F	61	C

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Mol	Chain	Res	Type
13	F	62	C
13	F	68	C
13	F	74	U
13	F	78	A
13	F	79	C
13	F	85	U
13	F	86	U
13	F	87	C
14	G	-11	G
14	G	-6	C
14	G	-4	A
14	G	-3	A
14	G	1	G
14	G	2	U
14	G	3	A
14	G	4	A
14	G	5	G
14	G	7	G
14	G	8	C
14	G	10	U
14	G	11	A
14	G	12	G
14	G	13	C
14	G	17	U
14	G	21	A
14	G	22	C
14	G	23	U
14	G	24	G
14	G	25	G
14	G	26	U
14	G	27	U
14	G	28	A
14	G	29	C
14	G	30	C
14	G	31	U
14	G	131	U
14	G	132	G
14	G	135	G
14	G	136	U
14	G	137	C
14	G	143	U
14	G	144	A

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Mol	Chain	Res	Type
14	G	145	U
14	G	146	C
14	G	147	C
14	G	148	U
14	G	149	G
14	G	150	U
14	G	151	C
14	G	152	C
14	G	154	U
14	G	156	U
14	G	159	U
14	G	161	U
14	G	162	C
14	G	163	C
15	H	14	C
15	H	20	G
15	H	23	A
15	H	24	A
15	H	25	G
15	H	29	A
15	H	30	A
15	H	31	G
15	H	44	U
15	H	45	C
15	H	46	U
15	H	47	U
15	H	48	A
15	H	65	U
15	H	112	G
15	H	143	A
15	H	147	G
15	H	149	A
15	H	152	G
15	H	153	A
15	H	154	C
15	H	156	U
15	H	157	G
15	H	160	A
15	H	163	G
15	H	164	C
15	H	166	G
15	H	167	U

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Mol	Chain	Res	Type
15	H	169	C
15	H	177	A
15	H	178	A
15	H	179	C
15	H	183	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	18	C
2	B	19	A
2	B	20	G
2	B	23	C
2	B	24	G
2	B	25	C
2	B	27	U
2	B	39	C
2	B	40	U
13	F	5	U
13	F	7	G
13	F	25	C
13	F	33	G
13	F	35	A
13	F	36	A
13	F	37	C
13	F	47	A
13	F	48	A
13	F	50	A
13	F	58	G
13	F	59	G
14	G	-12	G
14	G	16	G
14	G	21	A
14	G	22	C
14	G	136	U
14	G	148	U
14	G	151	C
14	G	153	C
14	G	155	U
15	H	29	A
15	H	46	U

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Mol	Chain	Res	Type
15	H	47	U
15	H	156	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 10 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
40	IHP	A	3000	-	36,36,36	1.01	2 (5%)	54,60,60	1.62	12 (22%)
41	GTP	C	1500	42	26,34,34	1.18	1 (3%)	32,54,54	1.81	8 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
40	IHP	A	3000	-	-	6/30/54/54	0/1/1/1
41	GTP	C	1500	42	-	7/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	C	1500	GTP	C6-N1	-3.52	1.32	1.37
40	A	3000	IHP	P5-O45	-2.86	1.43	1.54
40	A	3000	IHP	P2-O12	2.65	1.64	1.59

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	A	3000	IHP	O45-P5-O35	4.10	123.30	107.64
40	A	3000	IHP	O35-P5-O15	-3.97	88.19	105.99
41	C	1500	GTP	C5-C6-N1	3.79	120.64	113.95
41	C	1500	GTP	PA-O3A-PB	-3.79	119.84	132.83
41	C	1500	GTP	O6-C6-C5	-3.73	117.08	124.37
40	A	3000	IHP	O16-C6-C1	3.32	116.50	108.69
40	A	3000	IHP	C6-C1-C2	-3.22	103.37	110.41
41	C	1500	GTP	PB-O3B-PG	-3.16	121.97	132.83
41	C	1500	GTP	C2-N1-C6	-3.02	119.53	125.10
41	C	1500	GTP	O2G-PG-O3B	2.89	114.34	104.64
40	A	3000	IHP	O44-P4-O34	2.73	118.06	107.64
40	A	3000	IHP	C5-C6-C1	-2.65	104.62	110.41
41	C	1500	GTP	C3'-C2'-C1'	2.32	104.47	100.98
41	C	1500	GTP	O4'-C4'-C3'	2.30	109.66	105.11
40	A	3000	IHP	O35-P5-O25	2.25	119.48	110.68
40	A	3000	IHP	O12-C2-C3	2.14	113.74	108.69
40	A	3000	IHP	O15-C5-C4	-2.13	103.66	108.69
40	A	3000	IHP	O42-P2-O22	2.10	118.91	110.68
40	A	3000	IHP	O31-P1-O11	-2.09	96.62	105.99
40	A	3000	IHP	C4-C3-C2	2.08	114.96	110.41

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C4-C5-O15-P5
40	A	3000	IHP	C6-C5-O15-P5
41	C	1500	GTP	PB-O3B-PG-O3G
41	C	1500	GTP	C5'-O5'-PA-O3A
41	C	1500	GTP	C5'-O5'-PA-O1A
41	C	1500	GTP	C5'-O5'-PA-O2A
41	C	1500	GTP	O4'-C4'-C5'-O5'
41	C	1500	GTP	C3'-C4'-C5'-O5'
40	A	3000	IHP	C2-O12-P2-O22
40	A	3000	IHP	C1-O11-P1-O21

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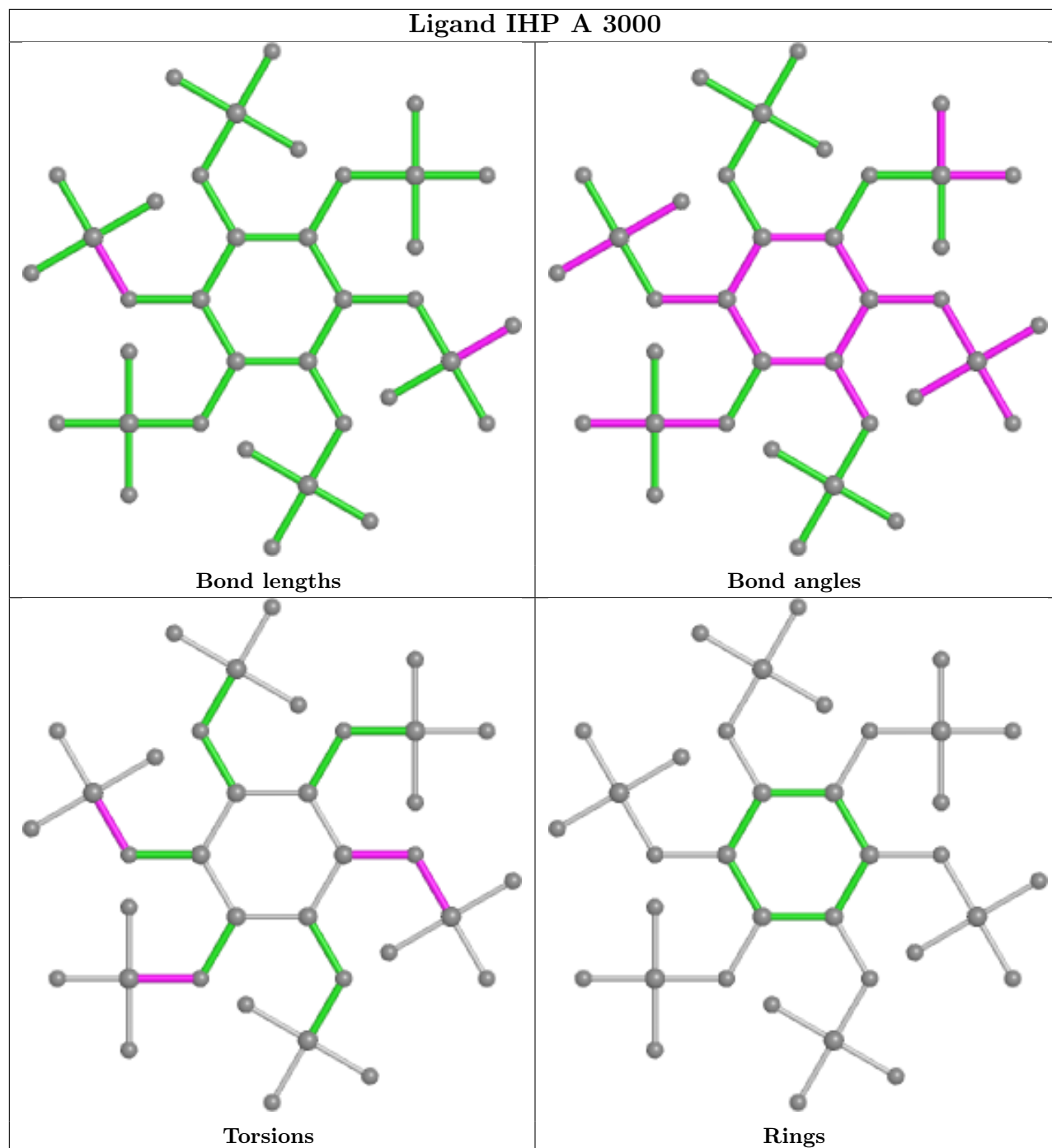
Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C1-O11-P1-O31
40	A	3000	IHP	C5-O15-P5-O35
41	C	1500	GTP	PG-O3B-PB-O2B

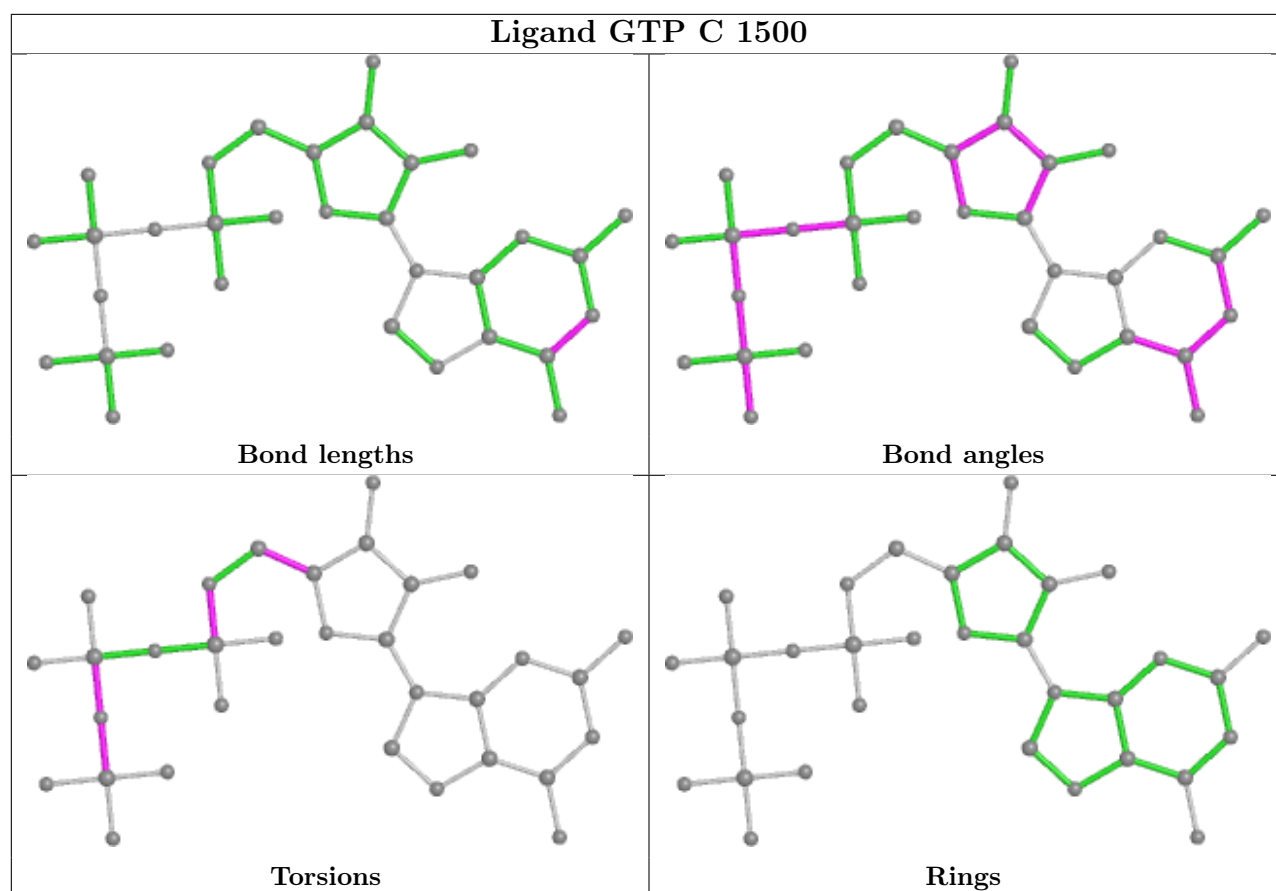
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	C	1500	GTP	11	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.

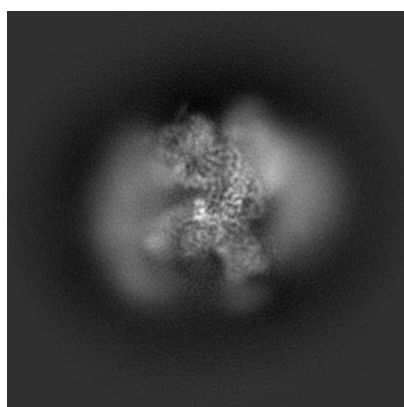
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6891. These allow visual inspection of the internal detail of the map and identification of artifacts.

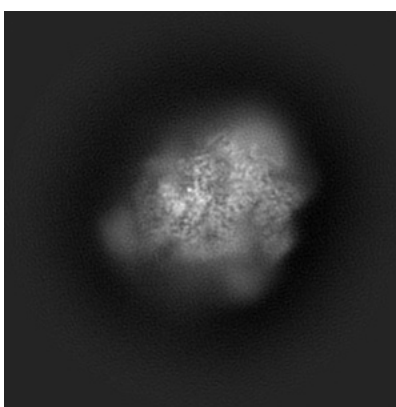
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

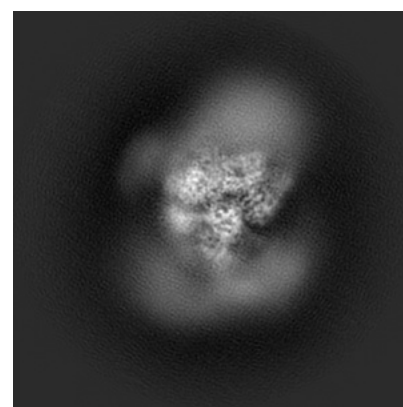
6.1.1 Primary map



X



Y

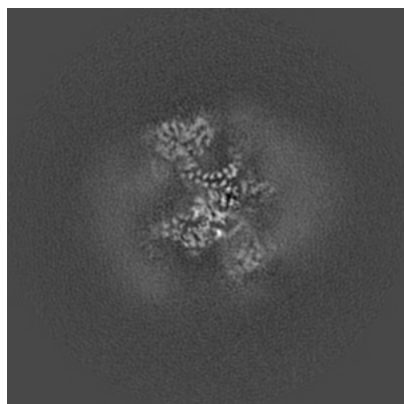


Z

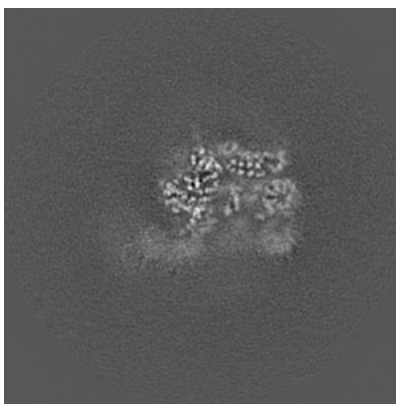
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

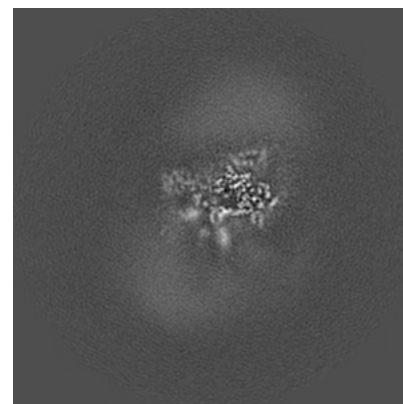
6.2.1 Primary map



X Index: 200



Y Index: 200

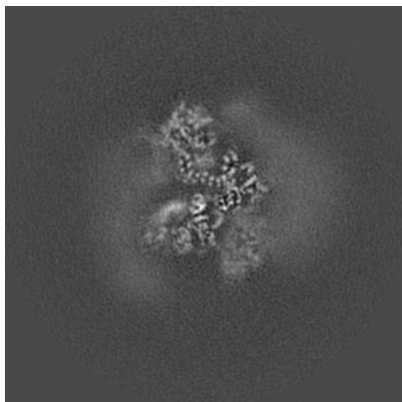


Z Index: 200

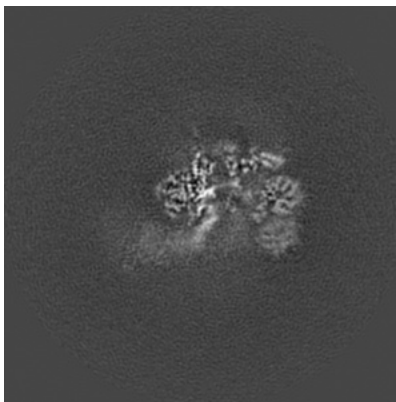
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

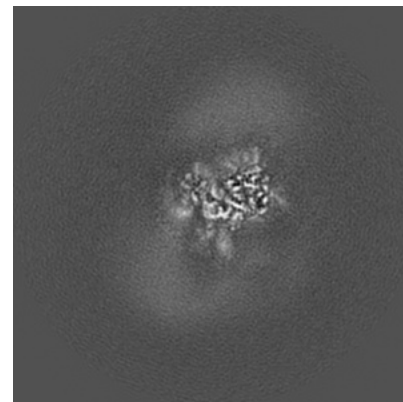
6.3.1 Primary map



X Index: 210



Y Index: 195



Z Index: 193

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0346. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

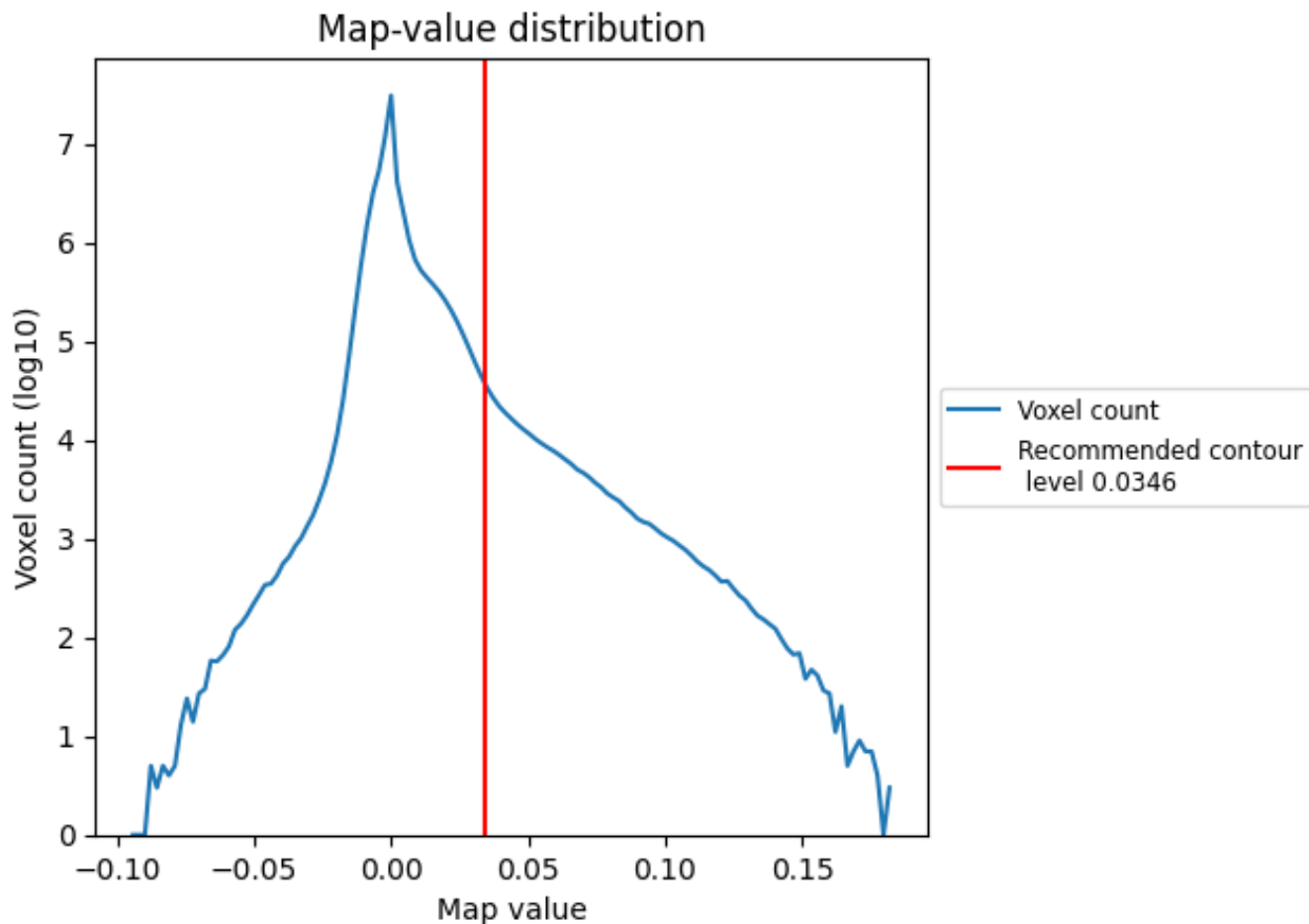
6.5 Mask visualisation

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

7 Map analysis [i](#)

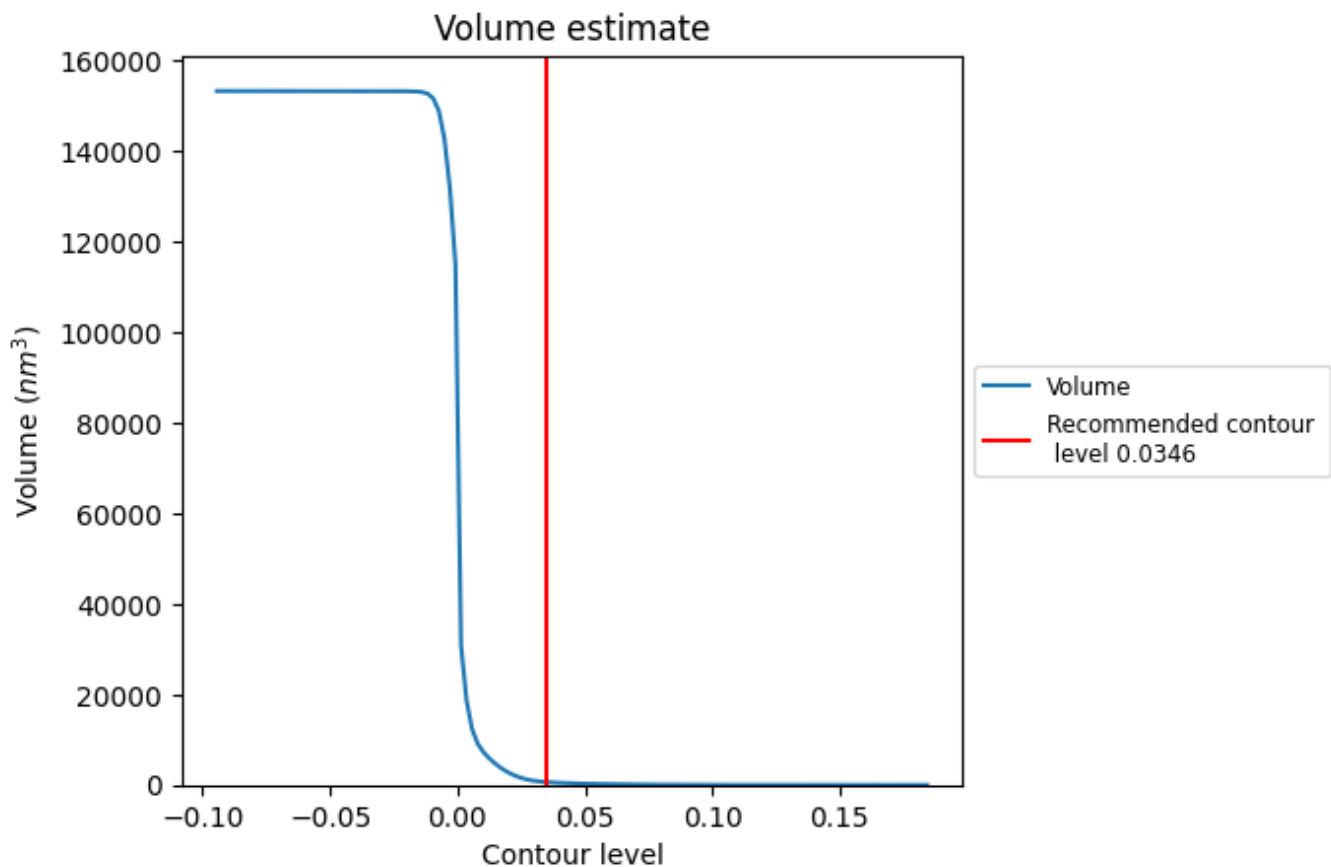
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

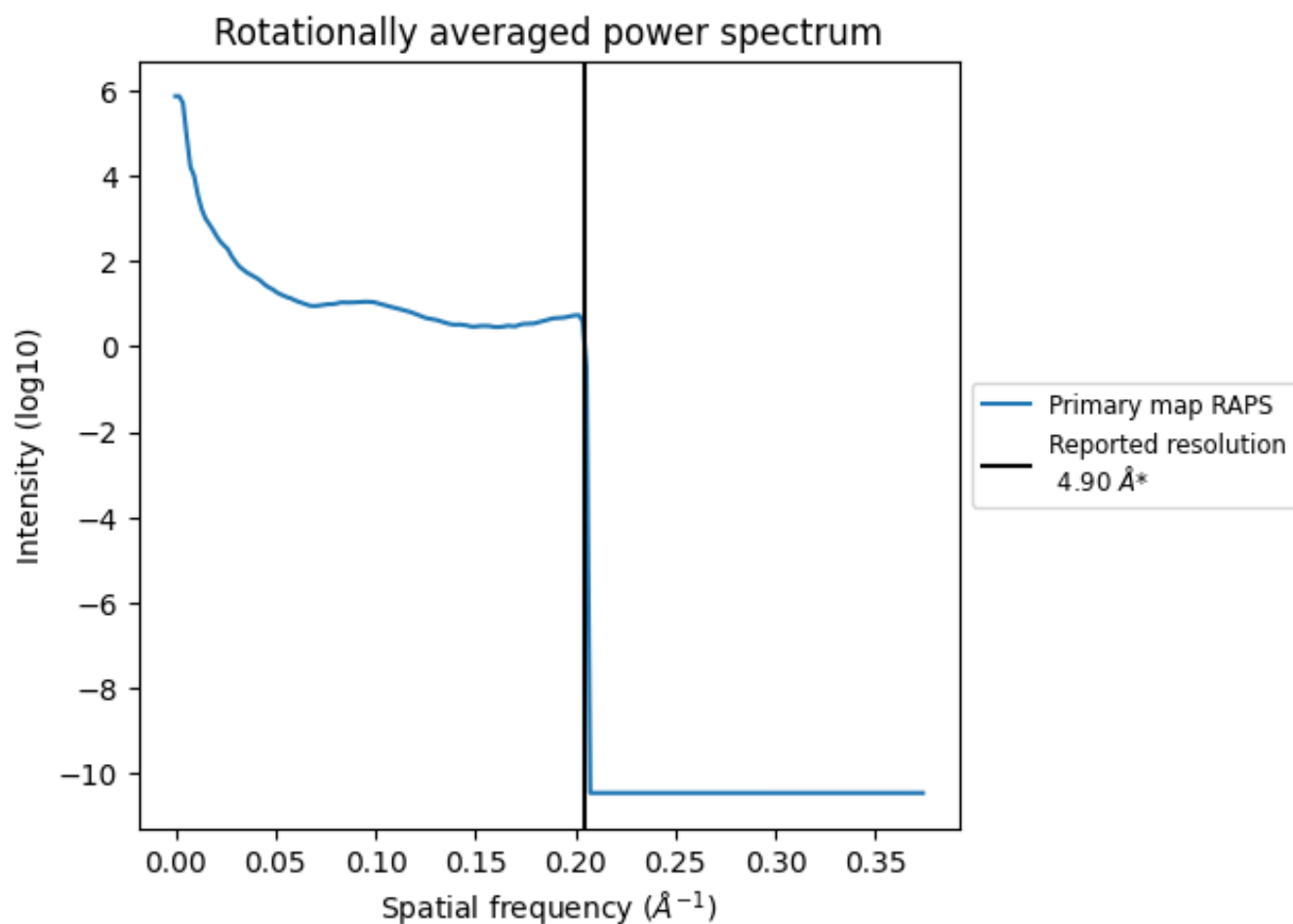
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 642 nm³; this corresponds to an approximate mass of 580 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

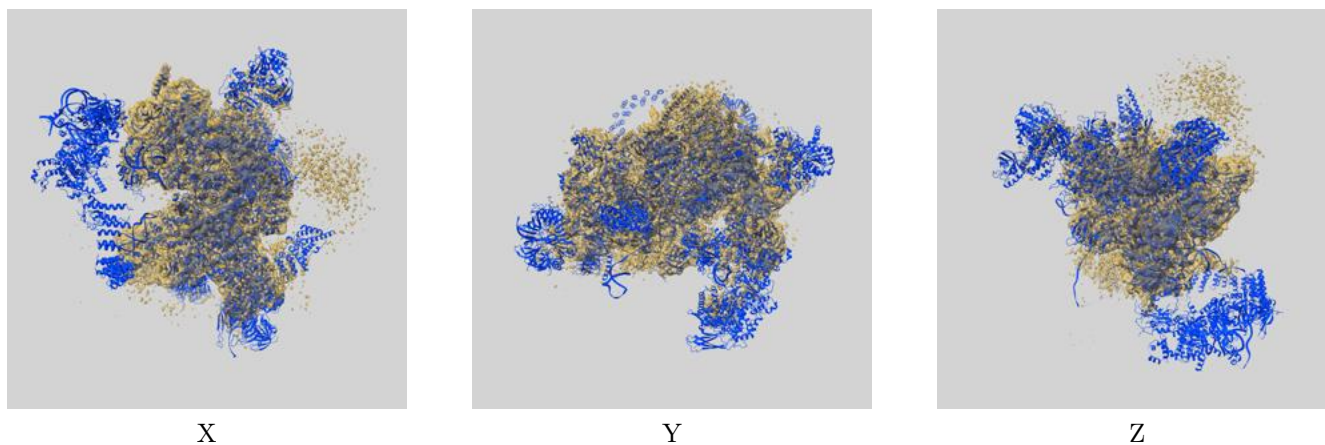
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

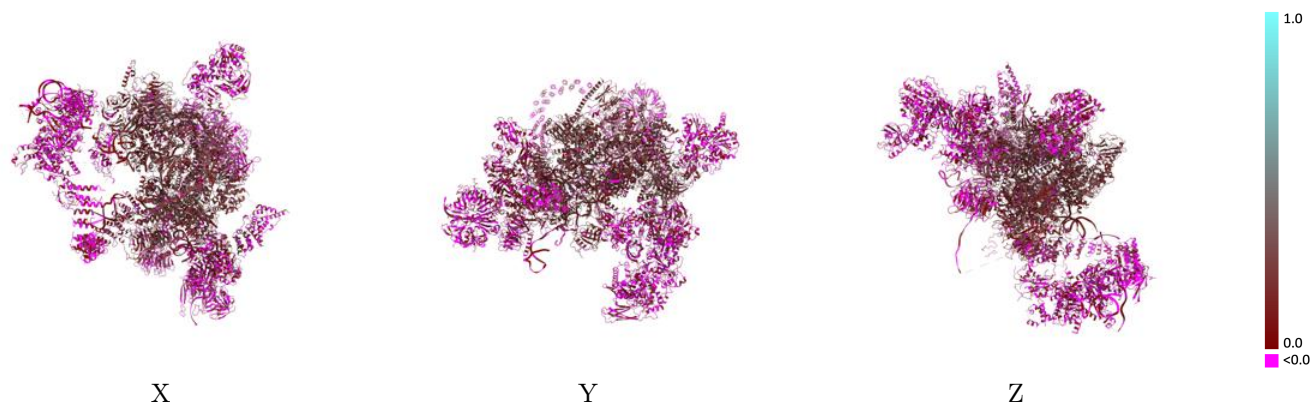
This section contains information regarding the fit between EMDB map EMD-6891 and PDB model 5Z58. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



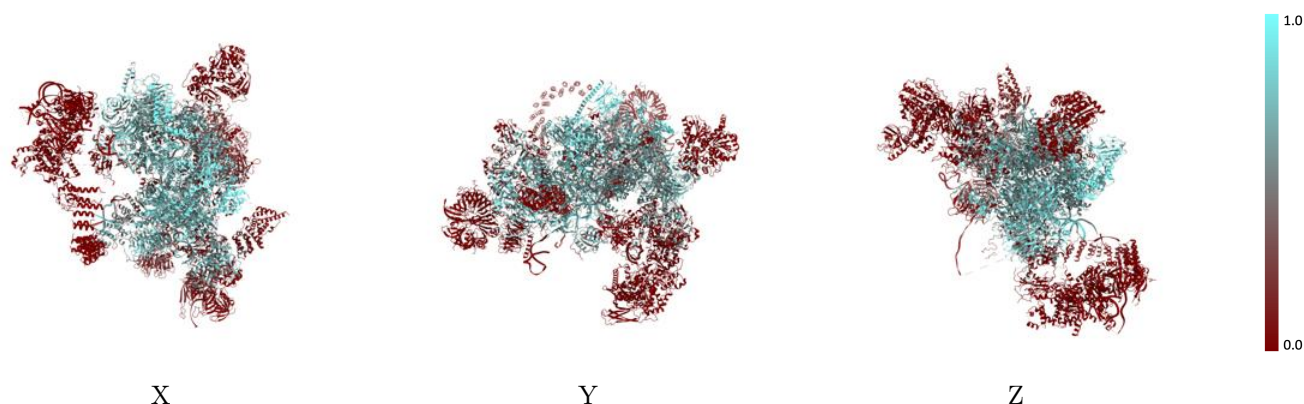
The images above show the 3D surface view of the map at the recommended contour level 0.0346 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



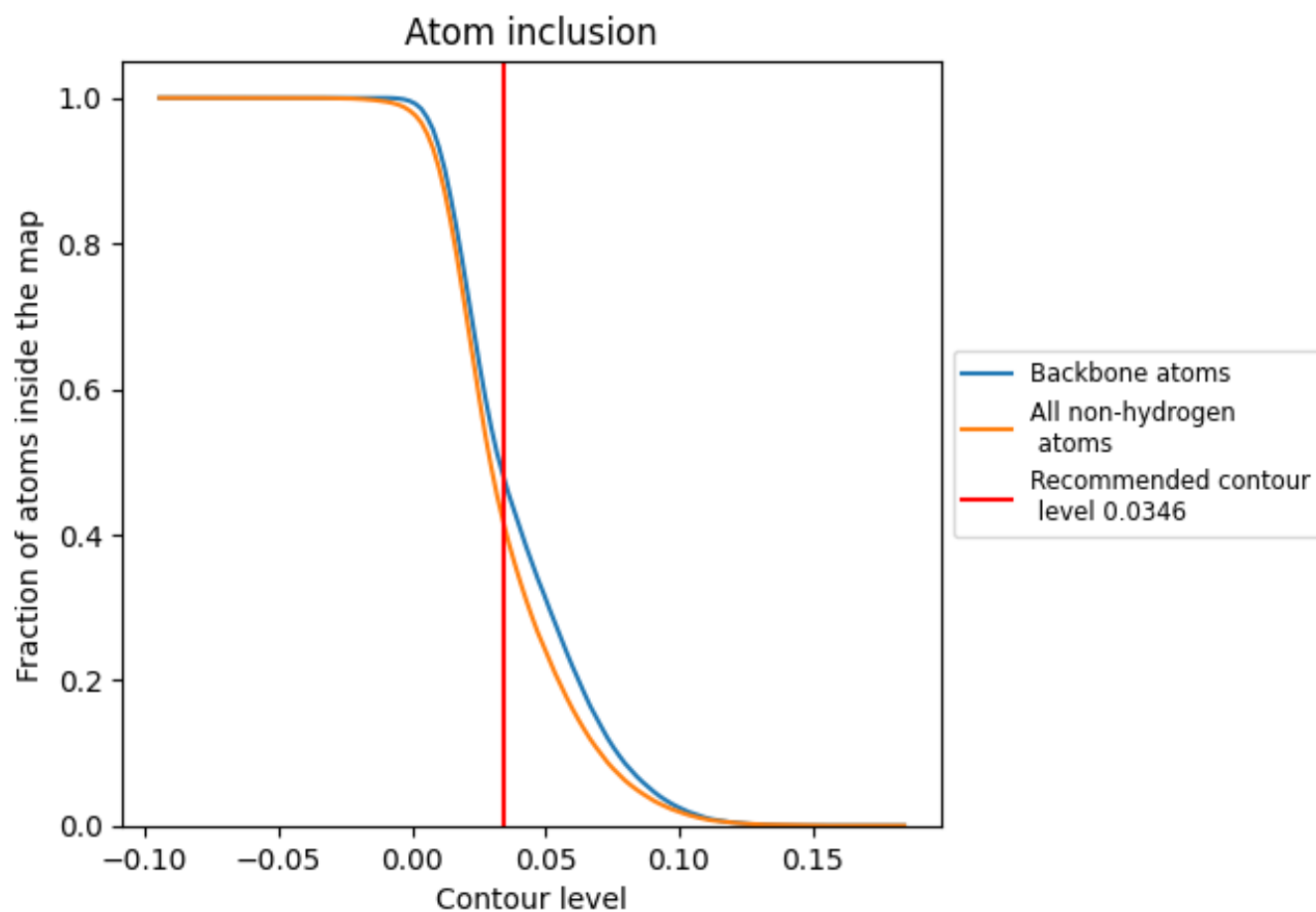
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0346).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 41% 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 (0.0346) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4117	 0.1310
1	 0.6673	 0.2300
2	 0.2970	 0.1480
3	 0.6080	 0.1670
4	 0.0727	 0.0080
5	 0.7299	 0.2390
6	 0.5061	 0.1590
7	 0.6799	 0.2240
A	 0.5571	 0.1970
B	 0.5984	 0.1040
C	 0.4527	 0.0960
D	 0.1161	 0.0400
E	 0.0258	 0.0260
F	 0.5991	 0.1470
G	 0.6227	 0.1490
H	 0.3416	 0.0880
J	 0.2791	 0.0660
L	 0.4753	 0.2070
M	 0.7170	 0.2530
P	 0.3091	 0.1160
R	 0.4076	 0.1660
T	 0.7535	 0.2280
V	 0.3423	 0.1200
X	 0.7089	 0.2160
Y	 0.6253	 0.2470
Z	 0.5948	 0.2670
a	 0.0000	 0.0170
b	 0.0049	 0.0410
c	 0.0222	 0.0060
d	 0.0938	 -0.0040
e	 0.0051	 0.0020
f	 0.0166	 -0.0230
g	 0.0000	 0.0030
h	 0.0000	 0.0340
i	 0.0000	 0.0210



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Chain	Atom inclusion	Q-score
j	0.0000	-0.0440
k	0.0000	0.0110
l	0.0000	0.0140
m	0.0000	-0.0500
n	0.0000	0.0110
o	0.0000	0.0280
p	0.0000	0.0170
u	0.0000	0.0040
v	0.0000	0.0460
w	0.1146	0.0420
x	0.0288	0.0110
z	0.4985	0.1870