



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:14 PM UTC

PDB ID : 8I0S / pdb_00008i0s
EMDB ID : EMD-35108
Title : The cryo-EM structure of human Bact-II complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2023-01-11
Resolution : 4.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

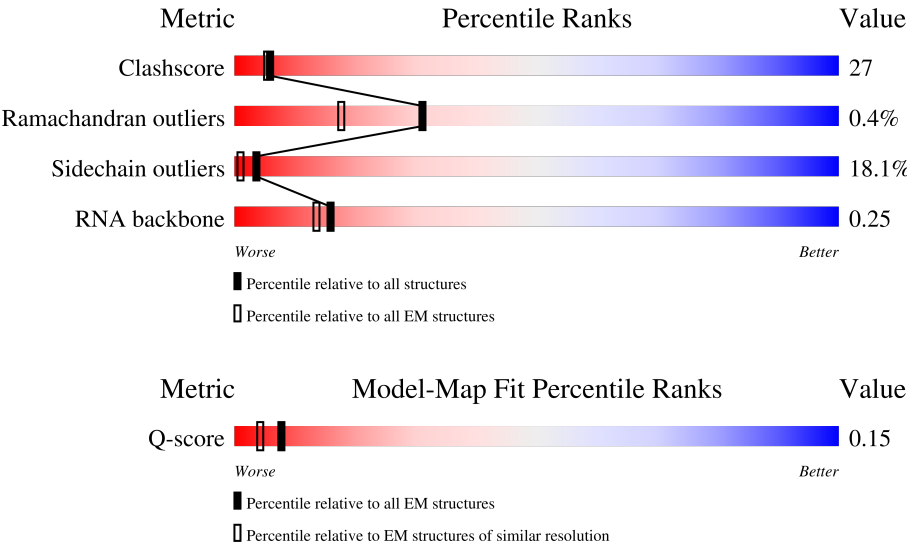
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	16% 53% 34% 8% ••
2	B	117	6% 24% 42% 18% 16%
3	C	972	35% 44% 10% 12%

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Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	F	107	
7	G	220	
8	H	188	
9	I	855	
10	J	848	
11	K	343	
12	L	802	
13	N	144	
14	O	420	
15	P	229	
16	Q	1485	
17	R	536	
18	S	166	
19	T	514	
20	U	2752	
21	V	908	
22	X	1041	
23	Y	492	
24	1	1304	
25	3	1217	
26	p	225	
27	w	501	
28	2	895	

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Mol	Chain	Length	Quality of chain
29	4	424	
30	7	110	
31	5	86	
32	y	301	
33	v	464	
34	u	793	
35	9	520	
36	a	240	
36	m	240	
37	b	119	
37	n	119	
38	c	118	
38	h	118	
39	d	86	
39	i	86	
40	e	92	
40	j	92	
41	f	76	
41	k	76	
42	g	126	
42	l	126	
43	o	255	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 112874 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2230	Total	C	N	O	S	0	0
			17607	11288	3122	3129	68		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	98	Total	C	N	O	P	0	0
			2066	925	347	696	98		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	860	Total	C	N	O	S	0	0
			6724	4298	1122	1272	32		

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

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

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

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

- Molecule 6 is a RNA chain called U6 snRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	72	Total	C	N	O	P	0	0
			1503	673	248	510	72		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	167	Total	C	N	O	P	0	0
			3539	1581	607	1184	167		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	571	Total	C	N	O	0	0
			2880	1738	571	571		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	249	Total	C	N	O	S	0	0
			2116	1355	380	375	6		

- Molecule 11 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	46	Total	C	N	O	S	0	0
			392	246	67	76	3		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	169	Total	C	N	O	S	0	0
			1403	890	262	247	4		

- Molecule 13 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	143	Total	C	N	O	S	0	0
			1174	740	213	209	12		

- Molecule 14 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	O	287	Total	C	N	O	0	0
			1432	853	289	290		

- Molecule 15 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	101	Total	C	N	O	S	0	0
			876	537	175	162	2		

- Molecule 16 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Q	1329	Total	C	N	O	0	0
			6730	4072	1329	1329		

- Molecule 17 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	361	Total	C	N	O	P	S	0	0
			2760	1694	524	529	1	12		

- Molecule 18 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	S	158	Total	C	N	O	0	0
			770	454	158	158		

- Molecule 19 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	320	Total	C	N	O	S	0	0
			2507	1582	456	462	7		

- Molecule 20 is a protein called Serine/arginine repetitive matrix protein 2.

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

- Molecule 21 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	462	Total	C	N	O	S	0	0
			2959	1842	537	567	13		

- Molecule 22 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	786	Total	C	N	O	S	0	0
			6357	4010	1133	1184	30		

- Molecule 23 is a protein called Peptidyl-prolyl cis-trans isomerase-like 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	320	Total	C	N	O	S	0	0
			2556	1616	420	508	12		

- Molecule 24 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	816	Total	C	N	O	S	0	0
			6468	4154	1110	1165	39		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	1177	Total	C	N	O	S	0	0
			9210	5849	1563	1753	45		

- Molecule 26 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	p	167	Total	C	N	O	0	0
			841	507	167	167		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	w	434	Total	C	N	O	S	0	0
			2275	1287	491	493	4		

- Molecule 28 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	250	Total	C	N	O	S	0	0
			1803	1132	340	324	7		

- Molecule 29 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	161	Total	C	N	O		0	0
			792	470	161	161			

- Molecule 30 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	7	81	Total	C	N	O	S	0	0
			613	376	109	115	13		

- Molecule 31 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	77	Total	C	N	O	S	0	0
			635	403	110	117	5		

- Molecule 32 is a protein called Peptidyl-prolyl cis-trans isomerase E.

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

- Molecule 33 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	v	158	Total	C	N	O	S	0	0
			964	558	203	200	3		

- Molecule 34 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	187	Total	C	N	O		0	0
			834	460	187	187			

- Molecule 35 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	338	Total	C	N	O	S	0	0
			2307	1429	420	450	8		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	a	86	Total	C	N	O		0	0
			344	172	86	86			
36	m	82	Total	C	N	O		0	0
			413	249	82	82			

- Molecule 37 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	82	Total	C	N	O		0	0
			328	164	82	82			
37	n	80	Total	C	N	O		0	0
			402	242	80	80			

- Molecule 38 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	97	Total	C	N	O		0	0
			388	194	97	97			
38	h	95	Total	C	N	O		0	0
			482	292	95	95			

- Molecule 39 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	74	Total	C	N	O		0	0
			296	148	74	74			
39	i	72	Total	C	N	O		0	0
			359	215	72	72			

- Molecule 40 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	79	Total	C	N	O		0	0
			316	158	79	79			
40	j	81	Total	C	N	O		0	0
			403	241	81	81			

- Molecule 41 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	f	74	Total	C	N	O	0	0
			296	148	74	74		
41	k	73	Total	C	N	O	0	0
			364	218	73	73		

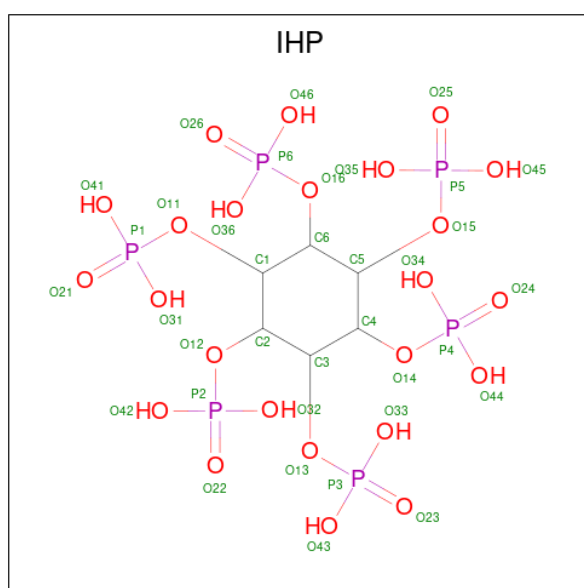
- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	g	81	Total	C	N	O	0	0
			324	162	81	81		
42	l	83	Total	C	N	O	0	0
			415	249	83	83		

- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein A'.

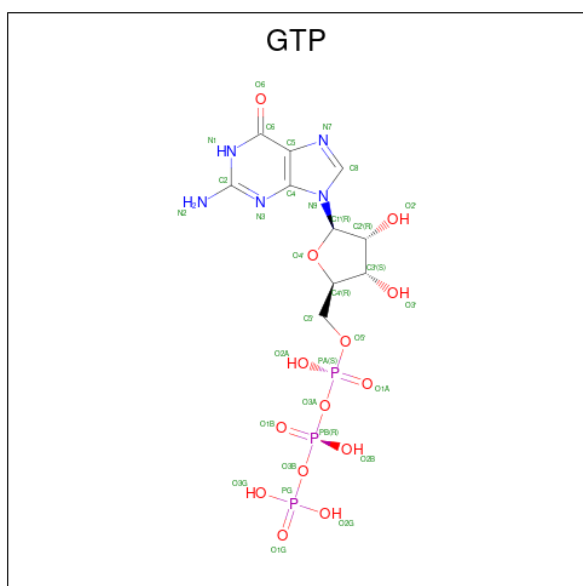
Mol	Chain	Residues	Atoms				AltConf	Trace
43	o	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 44 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



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

- Molecule 45 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 46 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	C	1	Total	Mg	0
			1	1	
46	F	6	Total	Mg	0
			6	6	

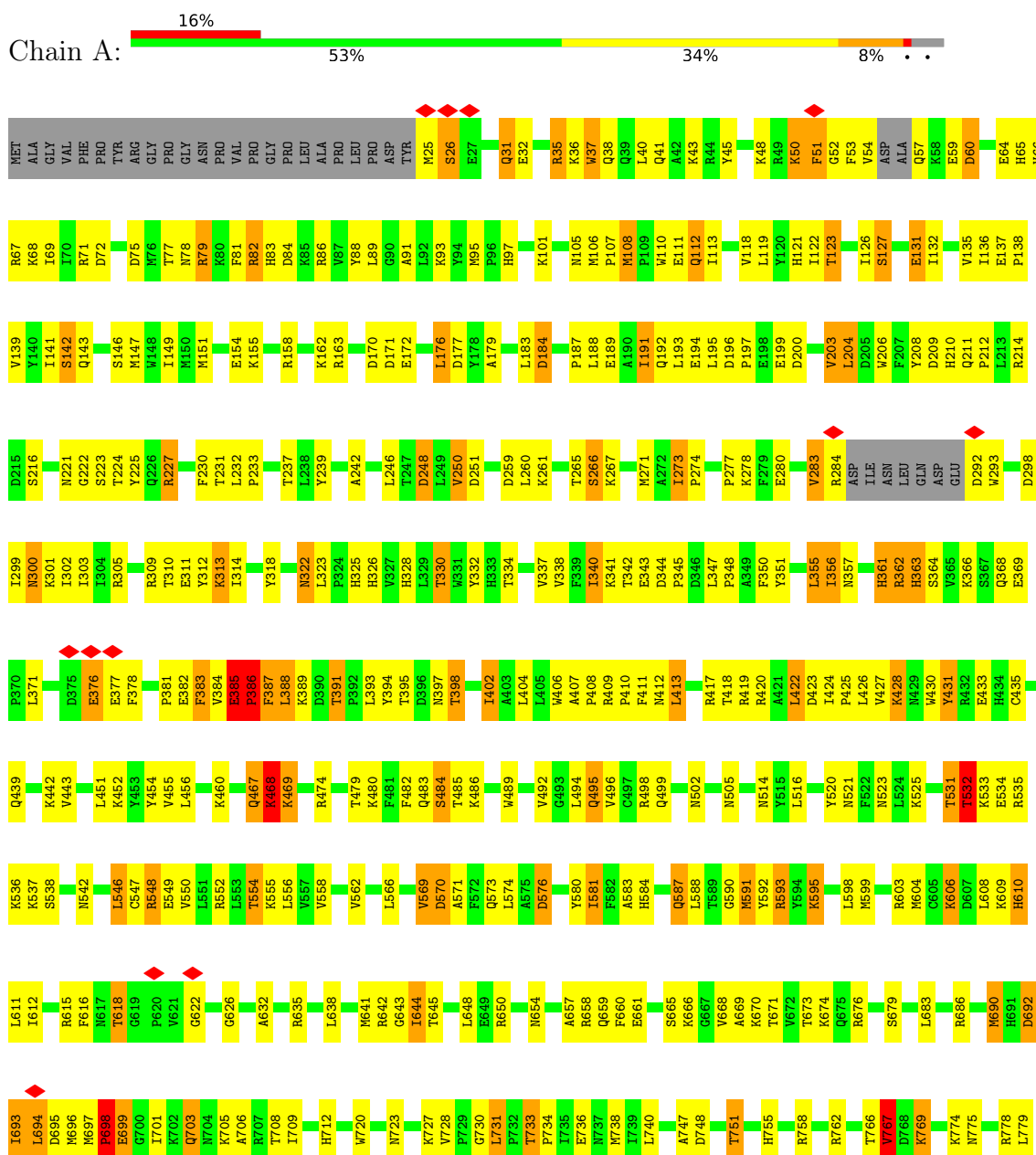
- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	K	1	Total	Zn	0
			1	1	
47	N	3	Total	Zn	0
			3	3	
47	7	3	Total	Zn	0
			3	3	

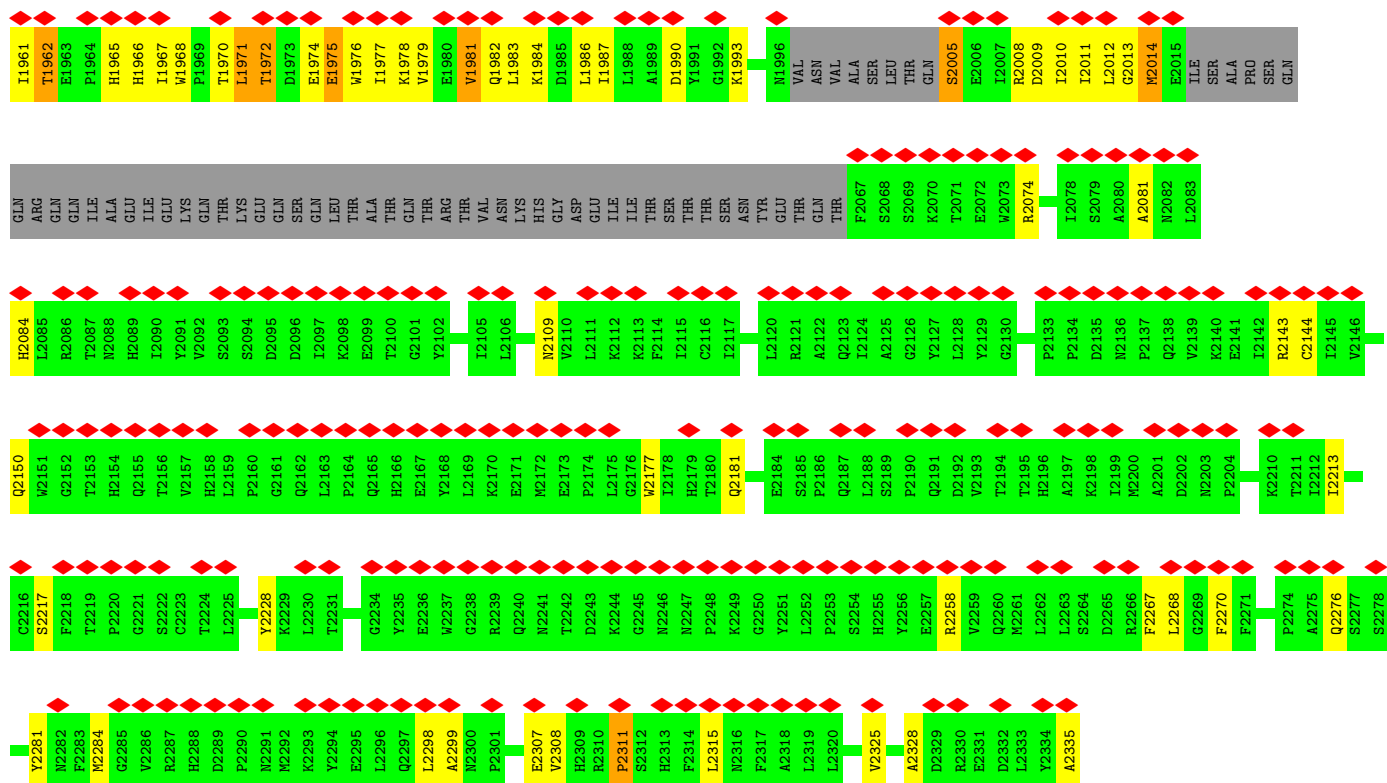
3 Residue-property plots

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

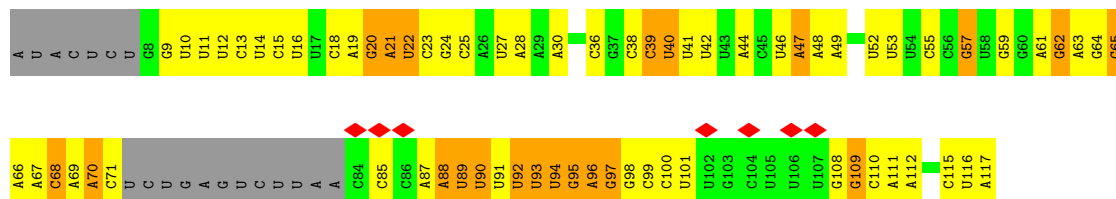
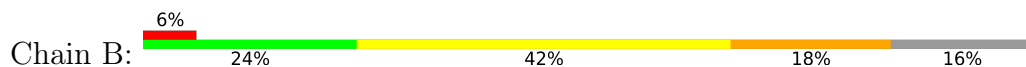
- Molecule 1: Pre-mRNA-processing-splicing factor 8



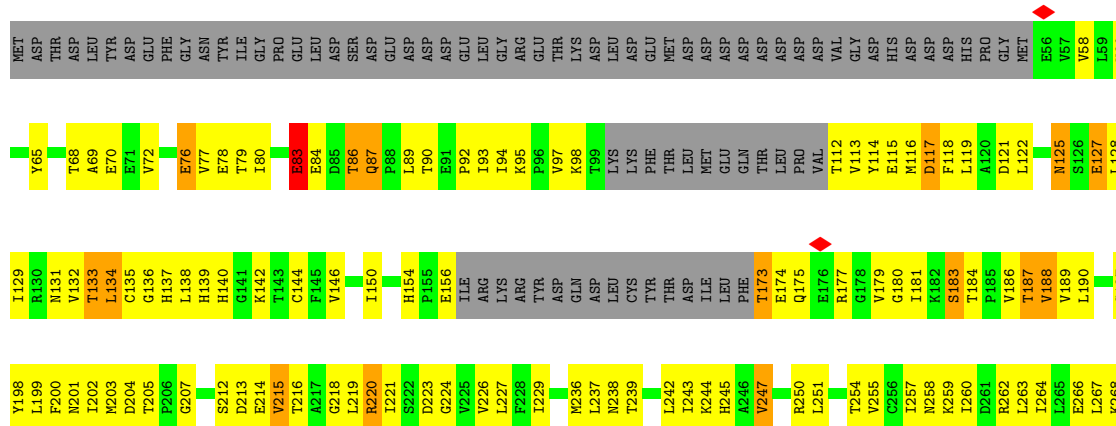




• Molecule 2: U5 snRNA

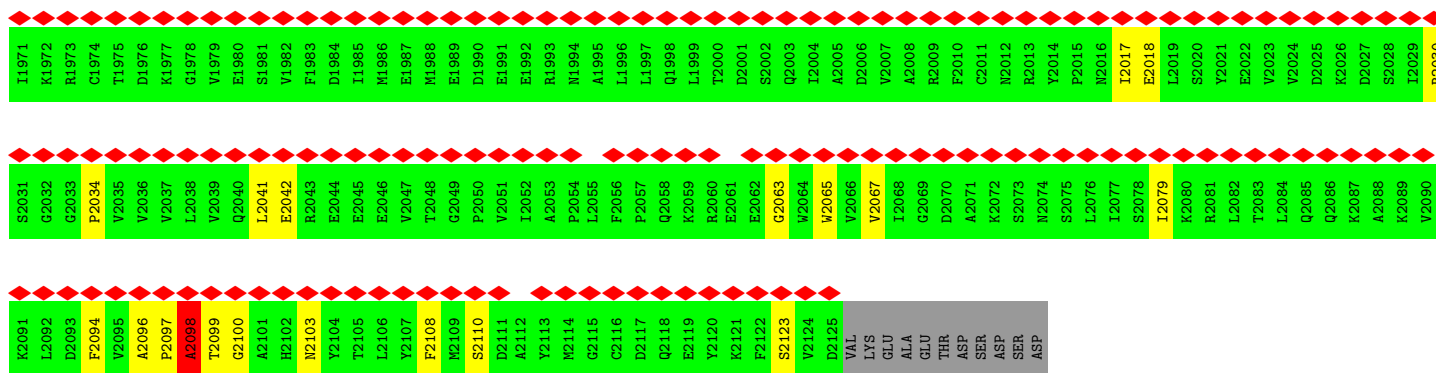


• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

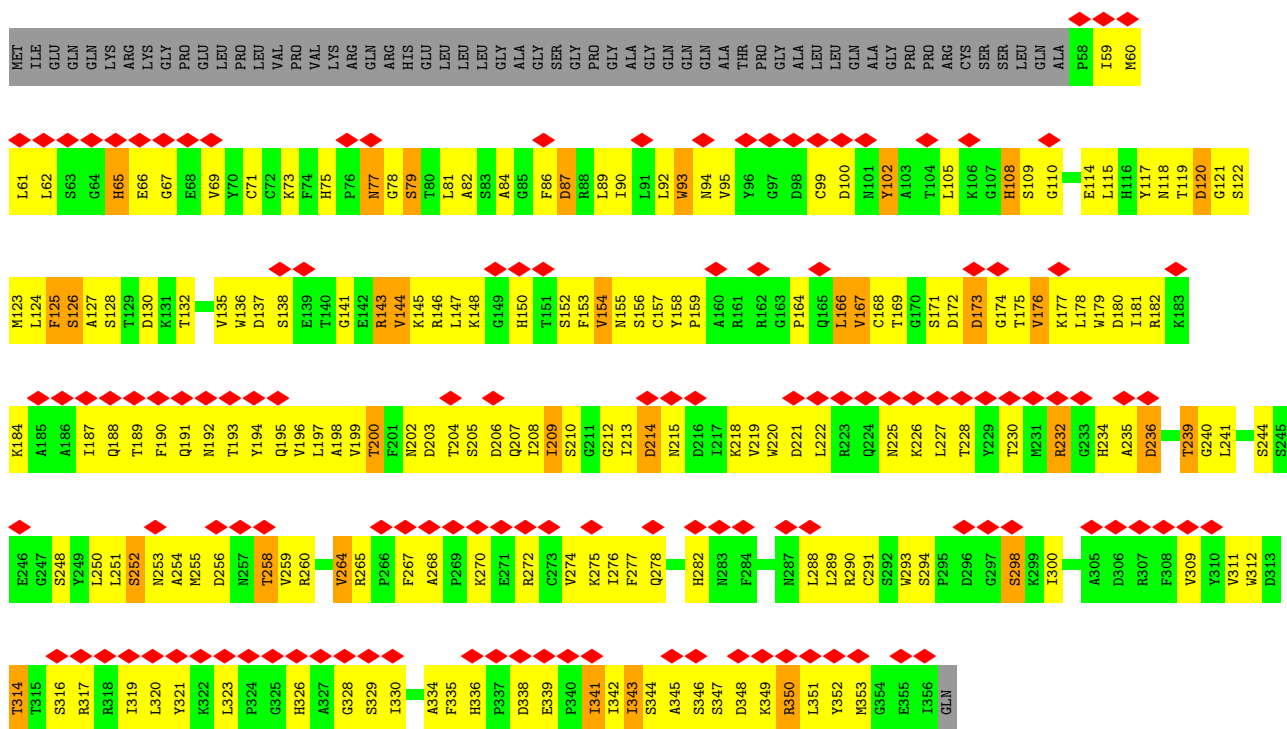




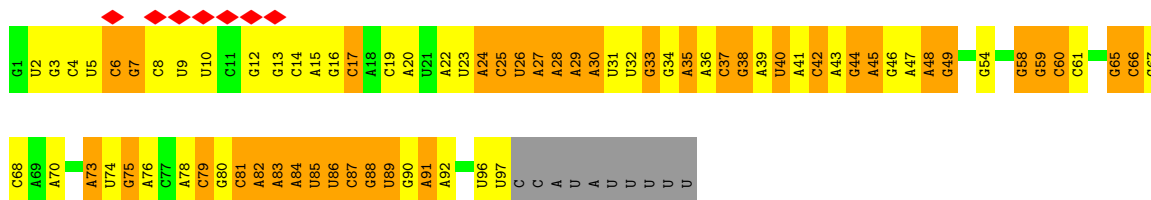
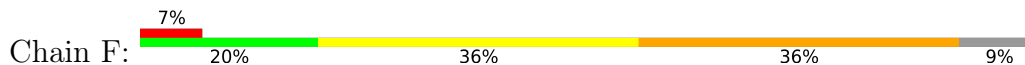
D1911	K1183	D1303	A1363	N1423	V1488	T1551	K1610	N1670	C1731	Q1791	N1851	D1911
T1912	L1184	L1304	I1364	I1424	A1489	K1552	E1611	G1671	M1732	T1792	A1852	T1912
E1913	E1185	L1305	L1365	I1425	A1490	H1553	T1612	K1672	H1733	L1793	A1853	E1913
E1914	L1186	P1306	A1246	I1426	S1491	S1554	L1613	I1673	D1734	S1794	E1854	E1914
I1915	S1187	L1307	Q1247	I1427	S1492	P1555	L1614	H1674	H1735	D1795	E1855	I1915
L1916	V1188	P1308	M1367	T1428	S1493	L1494	N1615	A1675	F1736	L1796	E1856	L1916
S1917	H1189	V1309	L1368	P1429	L1495	S1495	G1616	Y1676	M1737	E1797	N1857	S1917
K1918	L1190	S1310	L1369	P1428	N1496	N1496	V1617	V1677	E1738	Q1798	I1858	K1918
A1919	Q1191	A1311	Q1370	D1433	N1497	P1558	G1618	D1678	E1739	S1799	P1859	A1919
I1920	P1192	L1312	S1371	I1434	K1498	V1559	V1619	Y1679	I1740	K1800	I1860	I1920
R1921	I1193	R1313	E1373	R1437	D1499	I1560	L1620	P1680	V1741	C1801	R1861	R1921
L1922	T1194	M1314	G1374	R1438	K1499	V1561	H1621	I1681	T1742	T1802	H1862	L1922
Q1923	F1254	S1315	R1375	W1439	A1501	F1562	E1622	Y1682	K1743	S1803	H1863	Q1923
Q1924	R1195	A1316	Q1376	W1439	H1502	P1564	L1624	V1684	T1744	T1804	E1864	Q1924
A1925	S1196	F1317	V1377	Q1440	W1503	S1565	S1625	L1685	I1745	E1805	D1865	A1925
C1926	T1197	E1318	Y1378	Q1441	L1504	R1566	S1626	Q1686	E1746	D1806	N1866	C1926
V1927	L1198	S1319	I1379	Q1442	K1505	K1567	P1627	M1687	M1747	E1807	L1867	V1927
E1928	K1199	L1320	T1380	K1443	G1506	Q1568	E1628	M1687	K1748	M1808	L1868	E1928
P1929	V1200	Y1321	P1381	V1445	C1507	T1569	R1629	V1688	Q1749	D1809	R1869	P1929
L1930	E1201	Q1322	M1382	Q1446	S1507	R1670	L1630	A1691	D1750	V1810	Q1870	L1930
S1931	L1202	Q1322	E1383	Q1446	A1508	L1571	L1631	N1692	A1751	A1811	L1871	S1931
S1932	T1203	K1323	E1383	N1447	T1509	T1572	L1631	N1692	V1752	P1812	A1872	S1932
N1933	I1204	K1324	A1384	N1447	S1510	E1573	V1632	R1693	D1753	L1813	Q1873	N1933
G1934	T1205	F1325	L1385	N1448	T1511	I1574	E1633	P1694	Y1754	N1814	K1874	G1934
V1935	P1206	P1326	A1386	N1449	F1512	Q1575	Q1634	L1695	L1755	L1815	V1875	V1935
P1936	D1207	F1327	E1387	L1450	N1513	D1576	F1636	Q1696	T1756	K1816	P1876	P1936
L1937	F1208	F1328	Q1388	F1451	H1514	I1576	F1637	D1697	W1757	M1817	H1877	L1937
S1937	Q1209	F1328	W1389	F1452	F1514	T1578	S1637	E1698	F1758	L1818	K1878	S1937
P1938	W1210	M1329	V1390	V1453	H1515	C1579	S1638	E1699	F1759	A1819	L1879	P1938
A1939	D1211	P1330	M1391	D1454	H1516	T1578	G1639	G1700	L1760	A1820	M1880	A1939
L1940	E1212	Q1331	D1392	D1455	N1517	C1580	A1640	R1701	Y1761	Y1821	N1881	L1940
A1941	K1213	I1332	W1393	V1456	V1518	A1581	I1641	C1702	A1762	Y1822	M1882	A1941
E1942	W1214	Q1333	Y1394	H1457	R1519	A1582	Q1642	I1703	R1763	I1823	P1883	E1942
L1943	G1216	Q1334	E1395	L1458	V1520	E1583	V1643	I1704	M1764	M1824	K1884	L1943
Q1947	S1217	Q1336	K1396	I1459	P1522	I1584	V1644	M1705	T1765	N1825	F1884	E1947
M1948	C1278	M1337	F1397	G1460	L1523	R1586	V1645	Q1707	Q1766	Y1826	D1886	Q1947
V1949	S1218	T1338	Q1399	E1462	E1524	Q1587	A1646	G1708	M1767	T1827	P1887	V1949
Q1950	E1219	T1339	D1399	G1464	L1525	R1588	S1647	S1709	P1768	L1828	H1888	Q1950
Q1951	A1220	Y1340	R1400	G1464	H1526	F1589	R1648	K1710	M1769	I1829	V1889	Q1951
A1952	F1221	M1341	N1402	P1465	L1527	Q1528	S1649	K1711	Y1770	E1830	K1890	A1952
S1953	W1222	S1342	K1403	V1466	Q1528	L1590	S1649	K1711	Y1771	L1831	T1891	S1953
W1954	L1224	D1343	K1404	L1467	G1529	H1591	L1650	D1712	M1772	F1832	M1892	W1954
K1956	S1286	D1344	V1405	C1471	F1530	C1592	C1651	F1713	L1773	S1833	L1893	K1956
D1957	F1286	M1345	V1406	S1472	N1531	T1593	W1652	F1714	Q1774	M1834	L1894	D1957
S1958	D1227	V1346	L1407	R1473	I1532	E1594	G1653	K1715	G1775	S1835	L1895	S1958
Y1959	W1228	F1347	L1408	M1474	S1533	M1596	M1655	F1716	I1776	L1836	Q1896	Y1959
L1960	D1229	V1348	T1409	R1475	H1534	L1597	V1656	F1717	S1777	N1837	A1897	L1960
K1961	S1230	G1349	G1410	Y1476	T1535	I1598	A1657	L1718	H1778	A1838	H1898	K1961
Q1962	E1231	A1350	E1411	Y1477	Q1536	P1599	A1658	Y1719	R1779	L1839	L1899	Q1962
L1963	V1232	P1351	T1292	I1477	T1537	Y1600	E1659	E1720	H1780	T1840	S1900	L1963
I1964	I1233	T1352	E1293	S1478	R1538	Y1600	L1660	L1722	L1781	K1841	R1901	I1964
H1965	K1234	G1353	K1294	S1479	L1539	L1601	V1661	P1723	S1782	V1842	M1902	H1965
F1966	H1235	S1354	Y1296	Q1480	M1542	E1602	I1662	V1724	D1783	R1843	Q1903	F1966
P1967	H1236	G1355	P1296	I1481	A1543	K1603	T1663	E1725	H1784	G1844	L1904	P1967
S1968	H1237	K1356	P1297	I1482	E1544	L1604	M1664	S1726	L1785	L1845	S1905	S1968
E1969	Y1238	P1298	P1297	R1483	P1545	S1605	D1665	H1727	S1786	I1846	A1906	E1969
L1970	F1239	T1299	T1299	P1484	V1546	D1606	T1666	L1728	E1787	E1847	E1907	L1970
K1242	L1240	E1300	G1420	I1485	Y1547	S1607	Y1668	D1729	L1788	L1848	L1908	K1242
L1302	L1301	L1301	K1421	R1486	H1548	T1608	Y1669	H1730	E1790	I1849	Q1909	L1302
										S1850	S1910	



• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



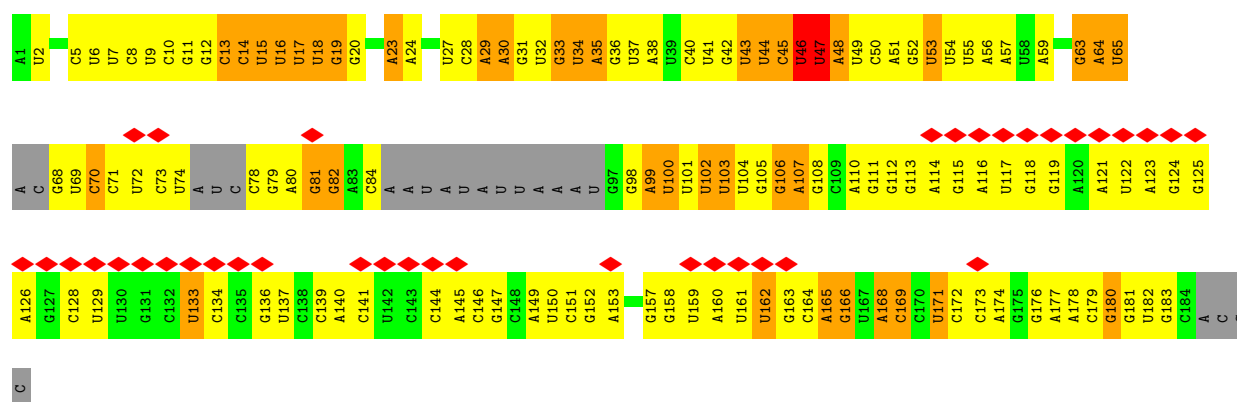
• Molecule 6: U6 snRNA



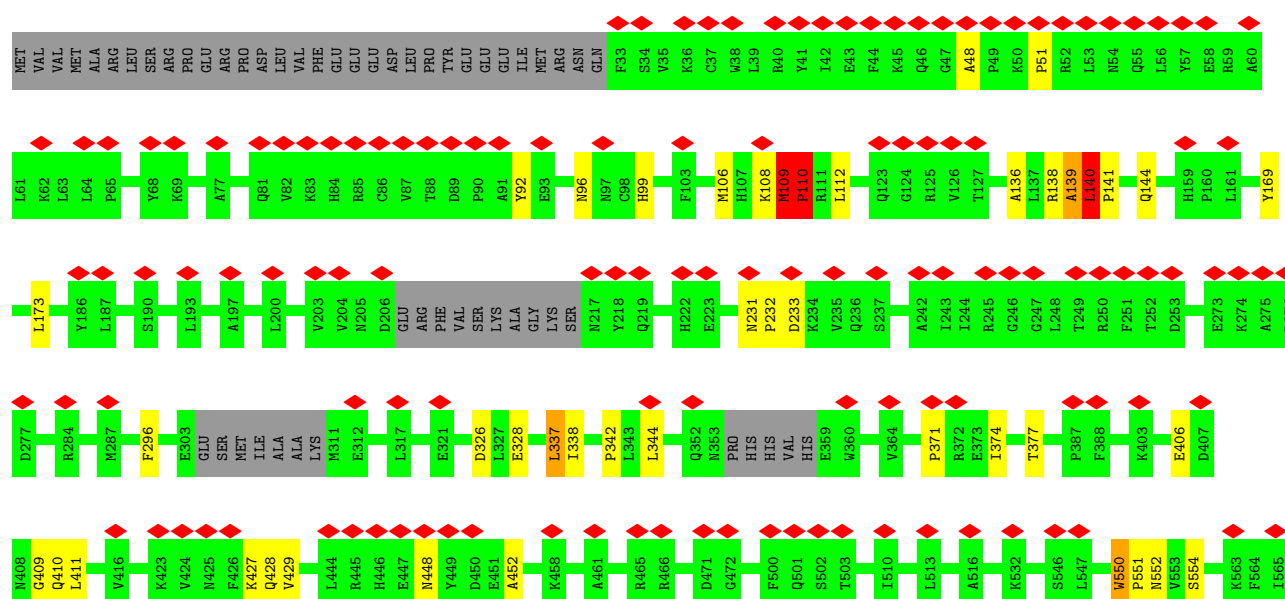
• Molecule 7: pre-mRNA

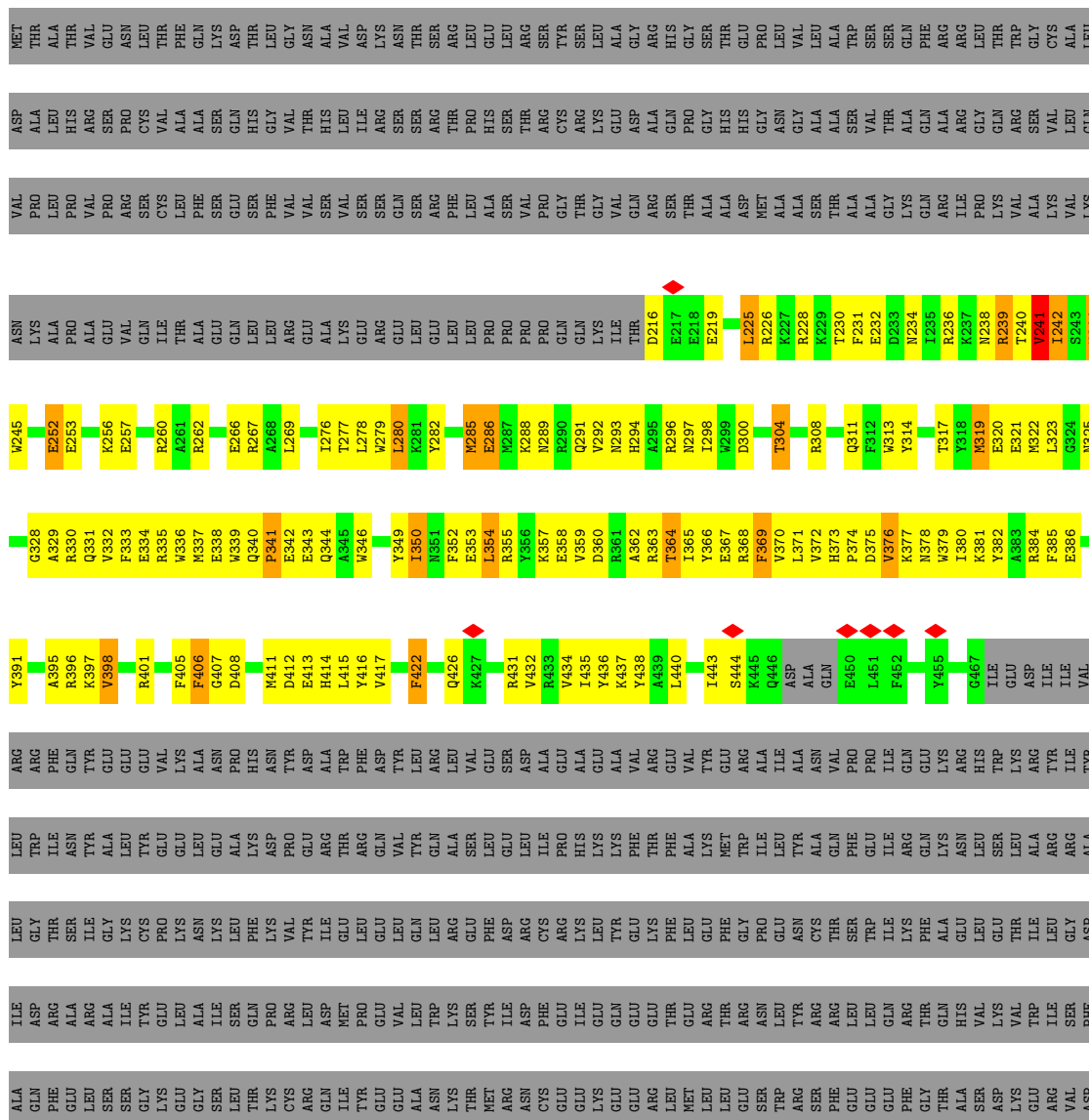
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	C	C	Grey
	U	C	Green
	C	C	Grey
	U	U	Grey
	C	U	Yellow
	U	U	Grey
	C	U	Grey
	U	G	Grey
	C	G	Grey
G	A83	U	Yellow
	U84	U	Grey
	G85	U	Grey
	C86	U	Grey
	U87	U	Green
	G88	U	Grey
	U89	U	Grey
	C90	U	Grey
	A91	U	Yellow
	U92	U	Yellow
C	A93	U	Yellow
	C	U	Grey
	A	U	Grey
	C	U	Grey
	U96	U	Grey
	G	U	Grey
	A97	U	Grey
	U98	U	Grey
	C99	U	Grey
	U100	U	Grey
G	C100	U	Grey
	G	U	Grey
	U101	U	Grey
	G102	U	Grey
	A	U	Grey
	U103	U	Grey
	C104	U	Grey
	C105	U	Grey
	G106	U	Grey
	U107	U	Grey
A	U108	U	Grey
	C	U	Green
	A	U	Grey
	U109	U	Green
	U	U	Grey
	C	U	Grey
	U110	U	Grey
	C	U	Grey
	U111	U	Grey
	C	U	Grey
G	U112	U	Grey
	C	U	Grey
	U113	U	Grey
	C	U	Grey
	U114	U	Grey
	C115	U	Grey
	C116	U	Yellow
	A117	U	Yellow
	C	U	Grey
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U	C	U	Grey
	G	U	Grey
	A	U	Grey
	C	U	Grey
	G	U	Grey
	U	U	Grey
	C	U	Grey
	U	U	Grey
	G	U	Grey
	A	U	Grey
U			

Chain H: 20% 17% 51% 20% 11%



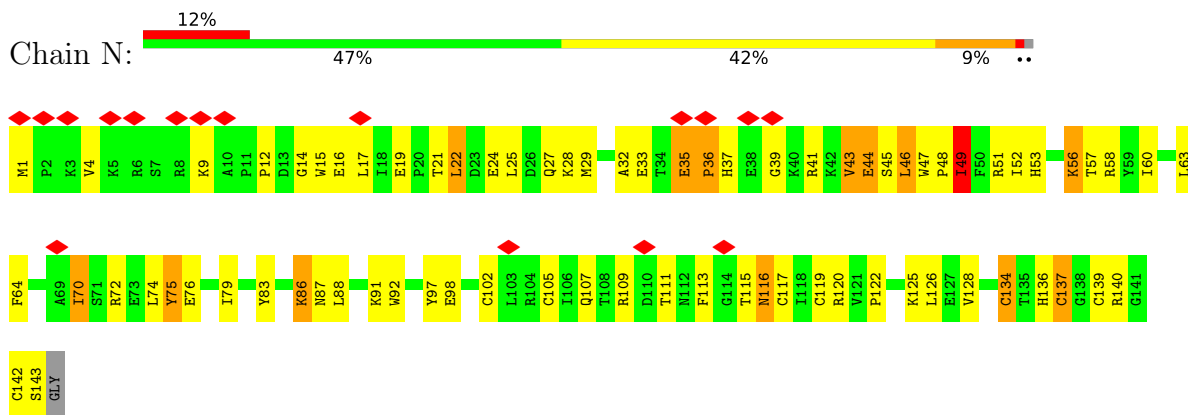
Chain I:



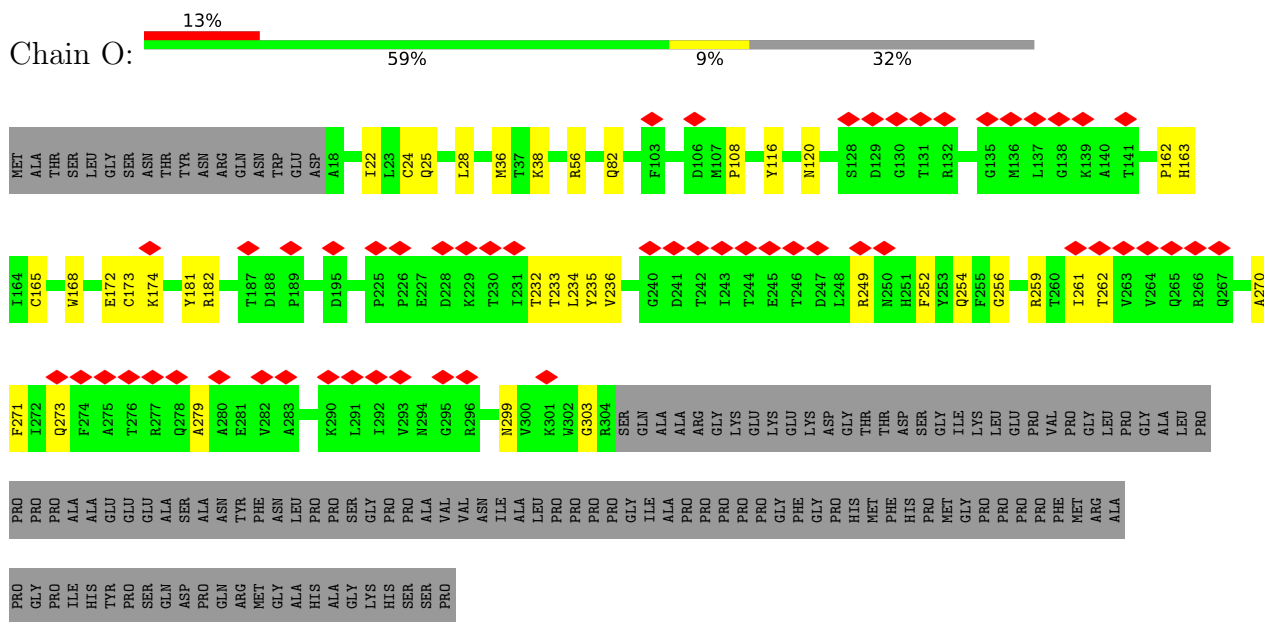


[illegible]

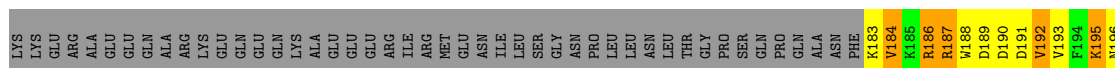
- Molecule 13: Protein BUD31 homolog



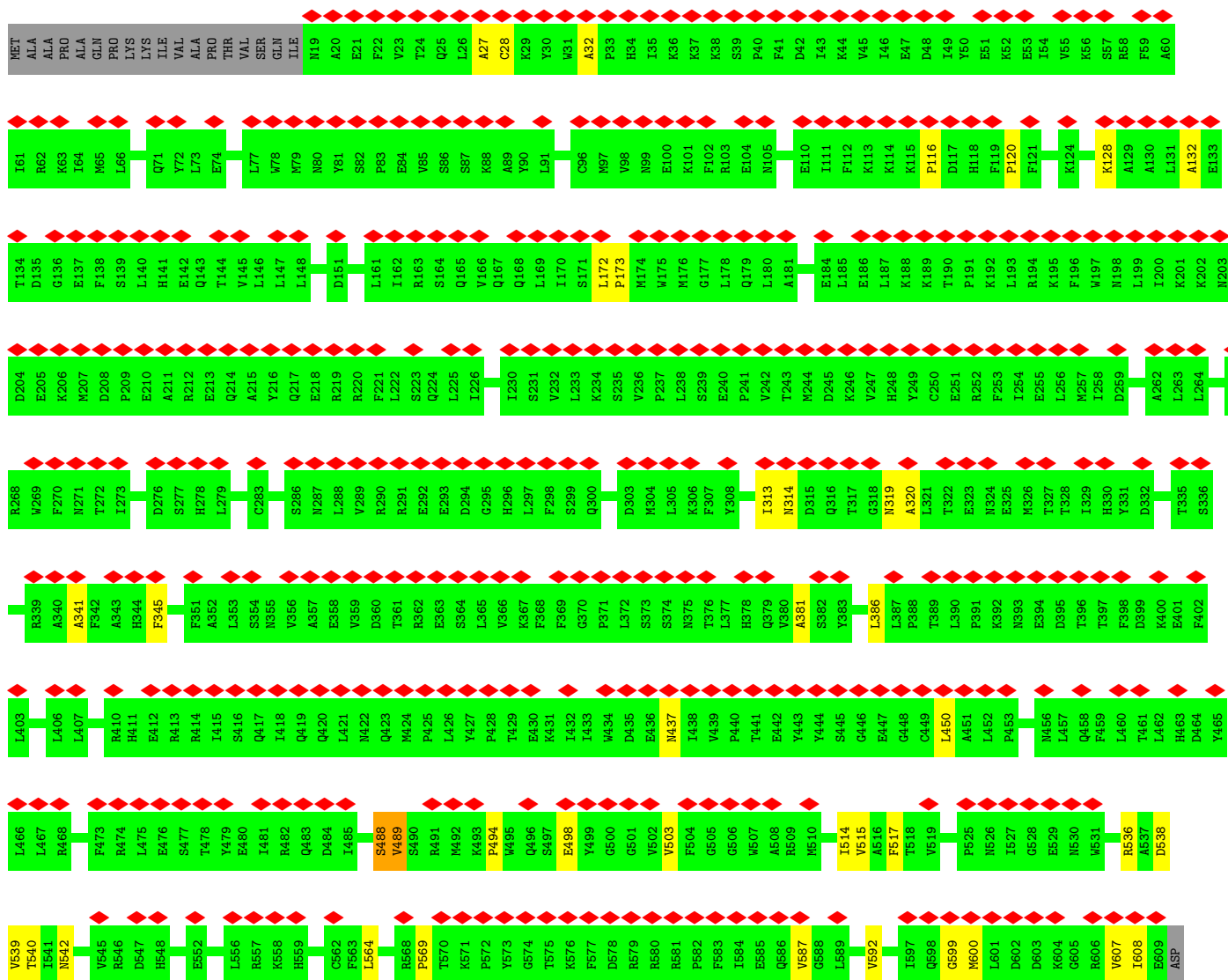
- Molecule 14: Pre-mRNA-splicing factor RBM22

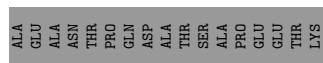


- Molecule 15: Spliceosome-associated protein CWC15 homolog

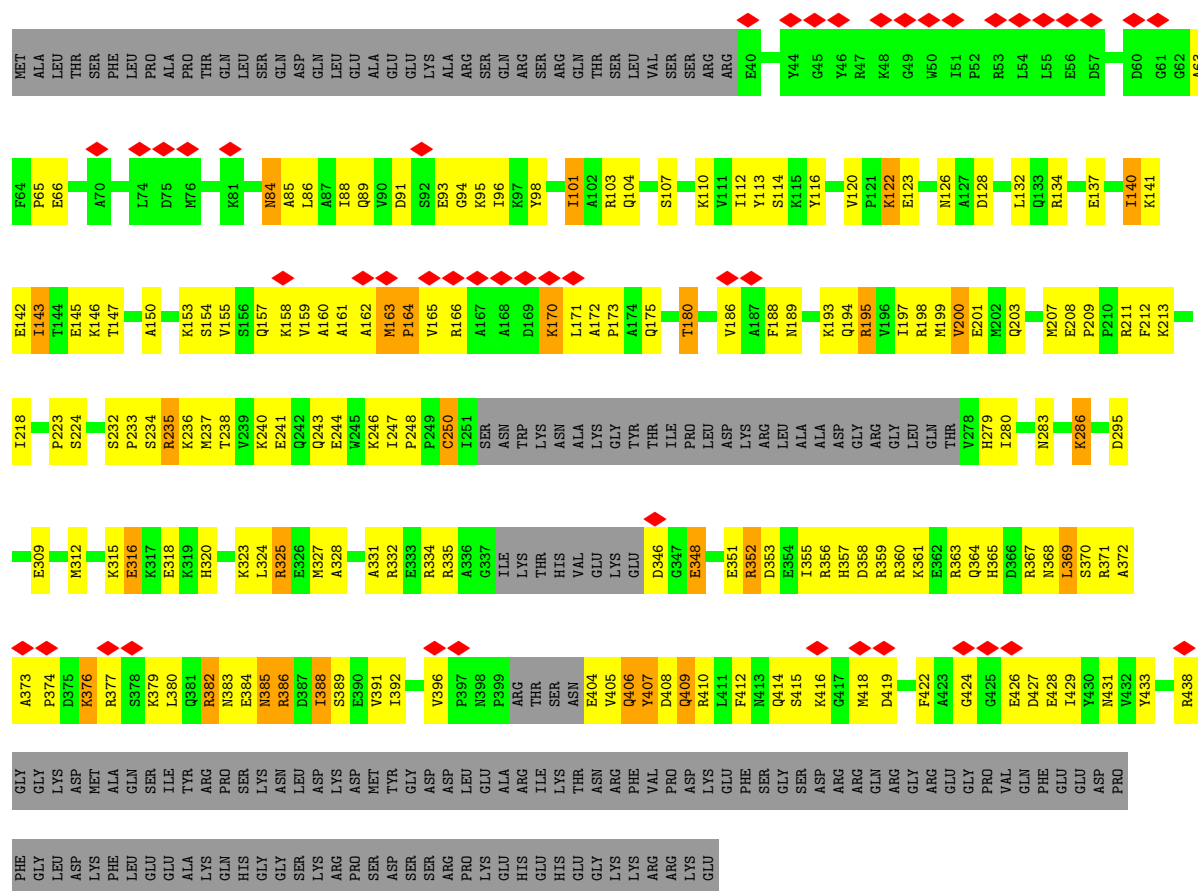


Chain Q: 59% 82% 7% 11%

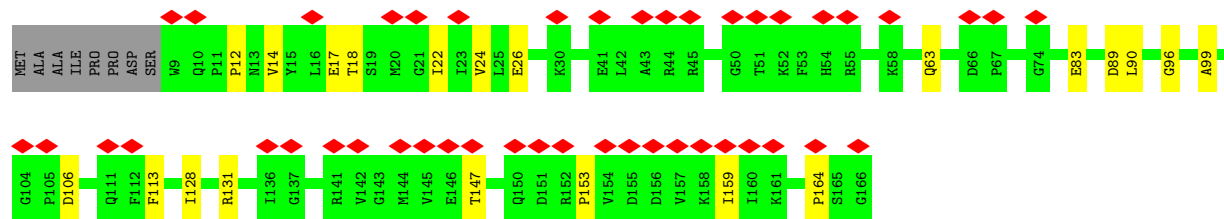
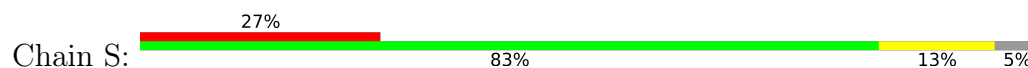




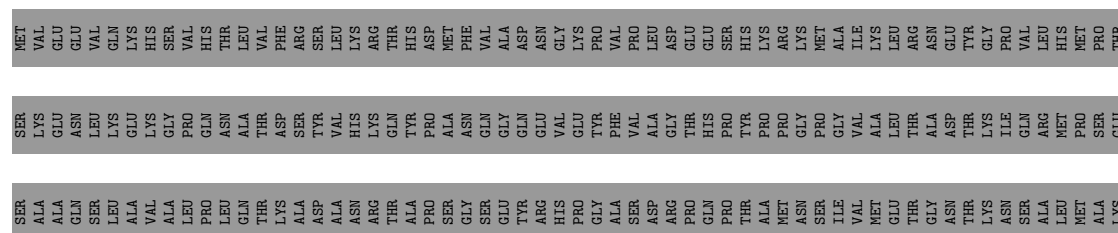
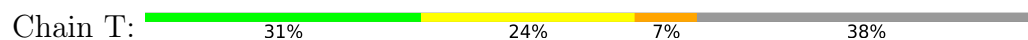
Chain R:

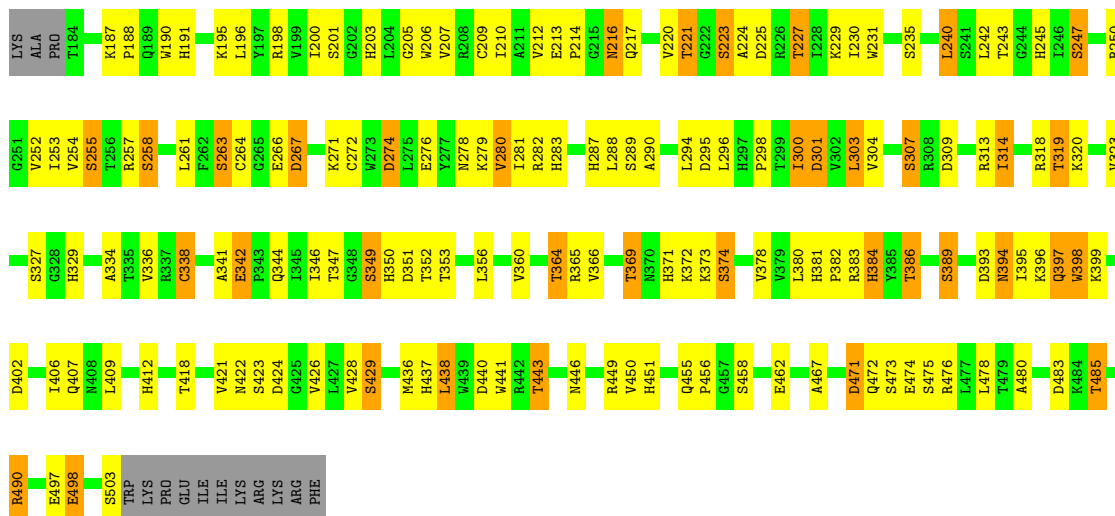


• Molecule 18: Peptidyl-prolyl cis-trans isomerase-like 1



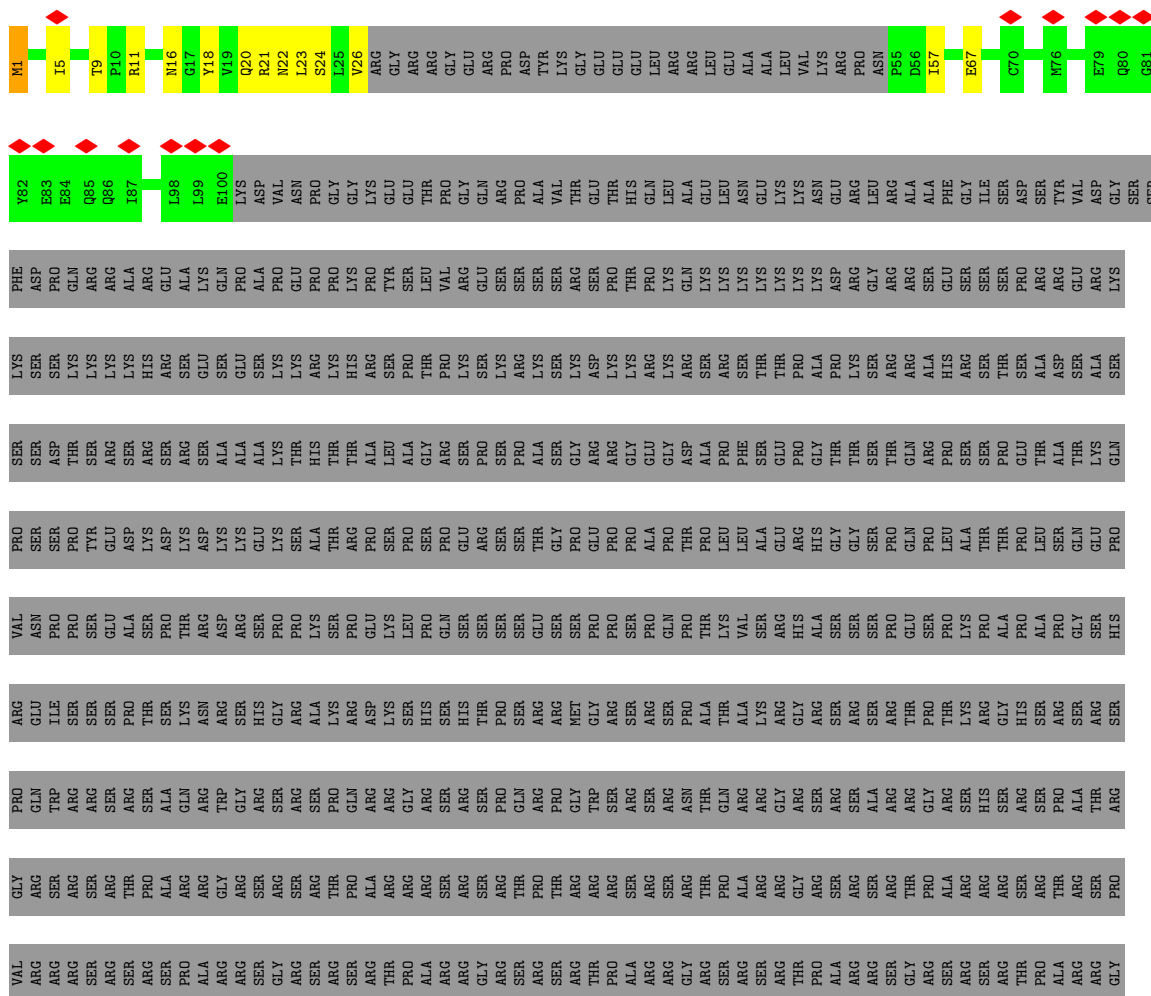
• Molecule 19: Pleiotropic regulator 1



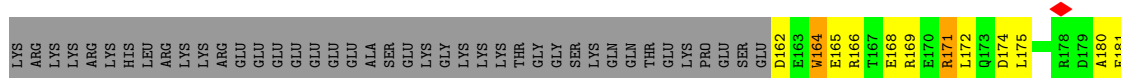


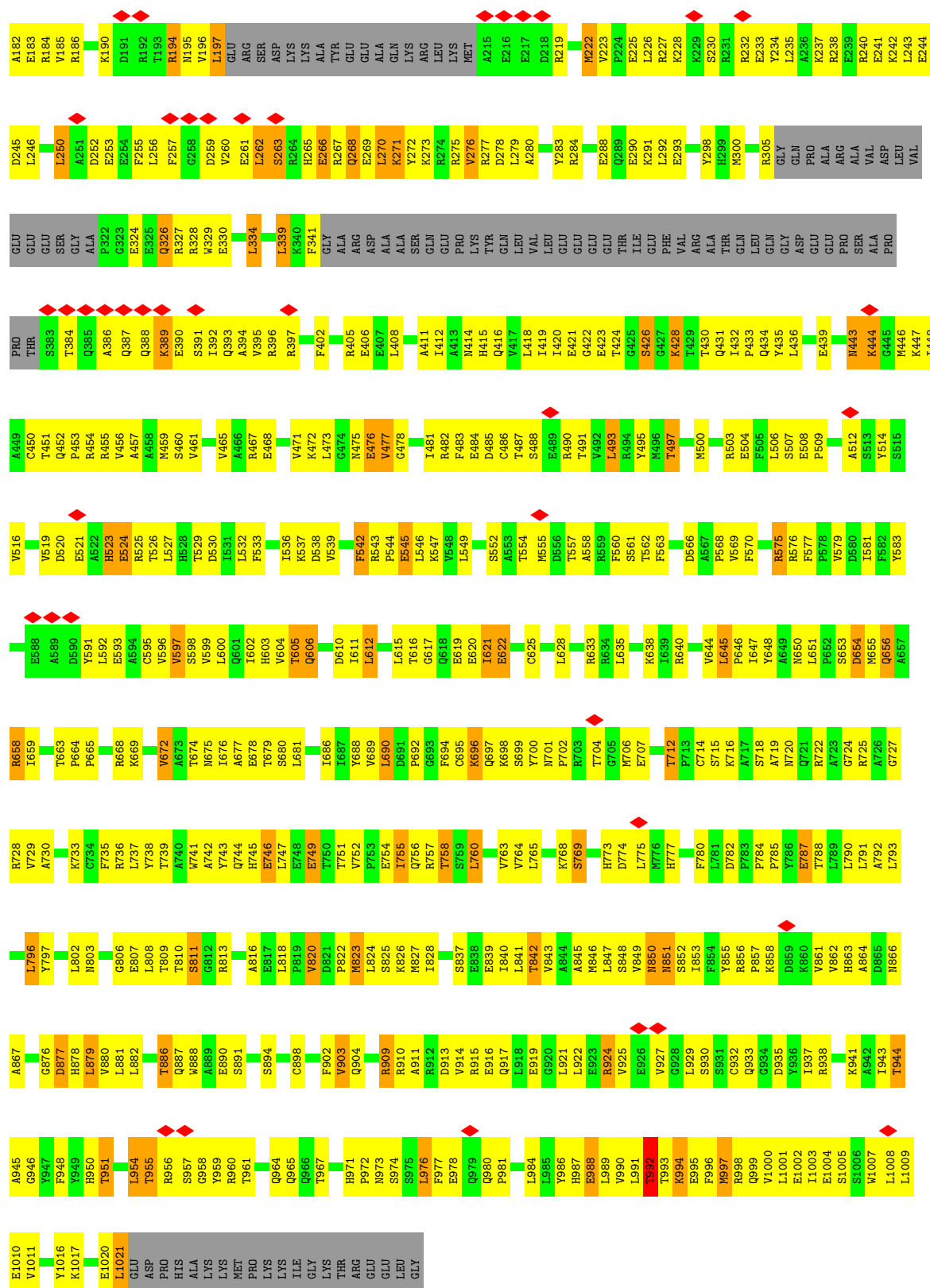
- Molecule 20: Serine/arginine repetitive matrix protein 2

Chain U: 97%



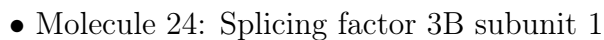






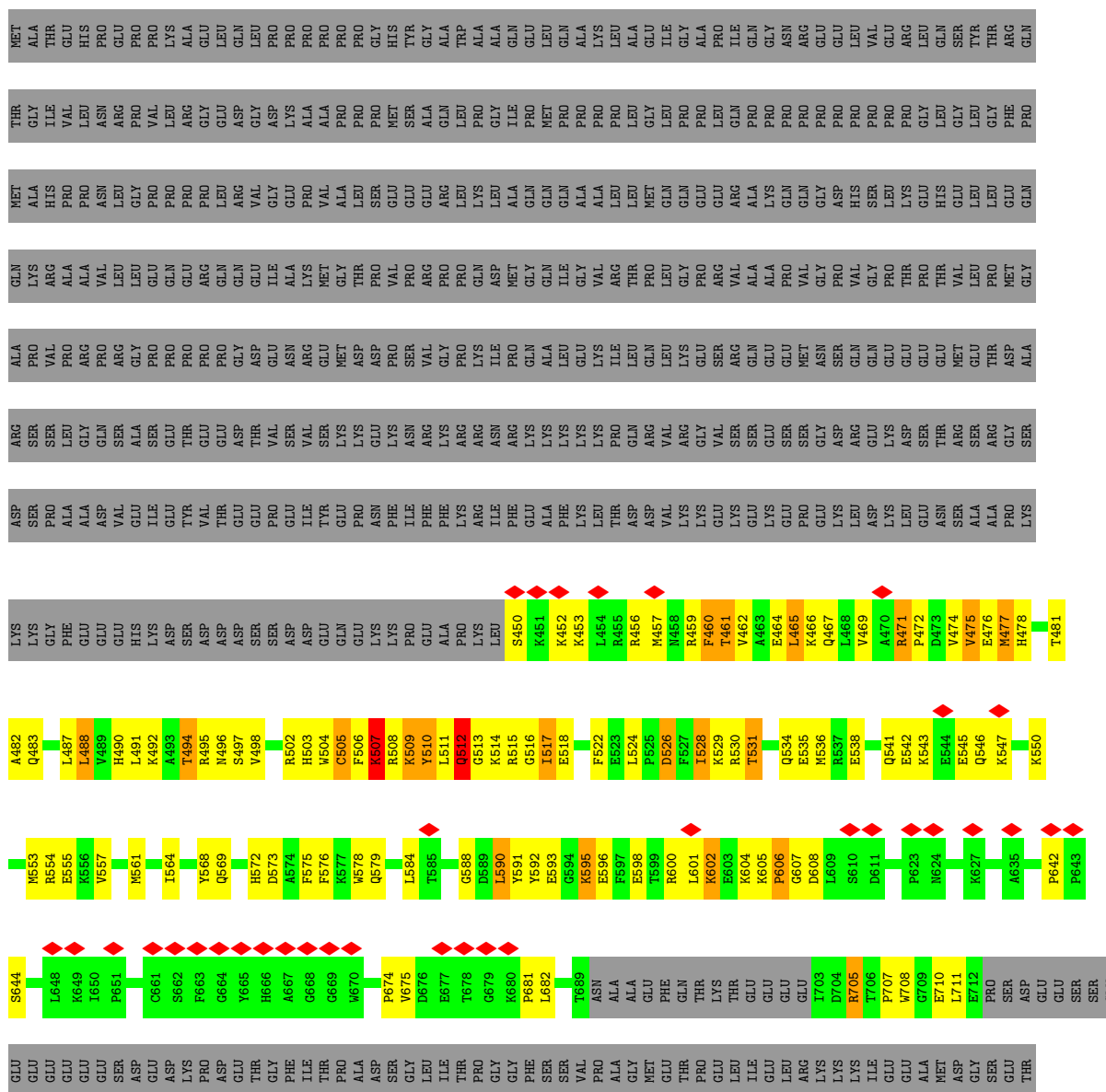
• Molecule 23: Peptidyl-prolyl cis-trans isomerase-like 4

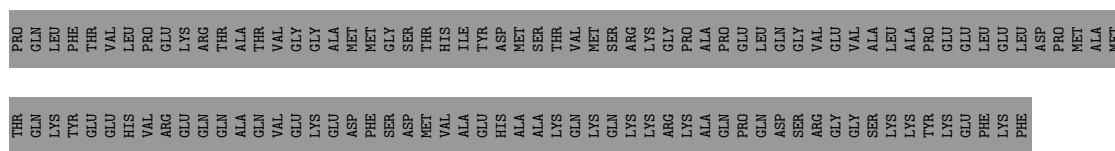
Chain Y: 22% 35% 8% 35%



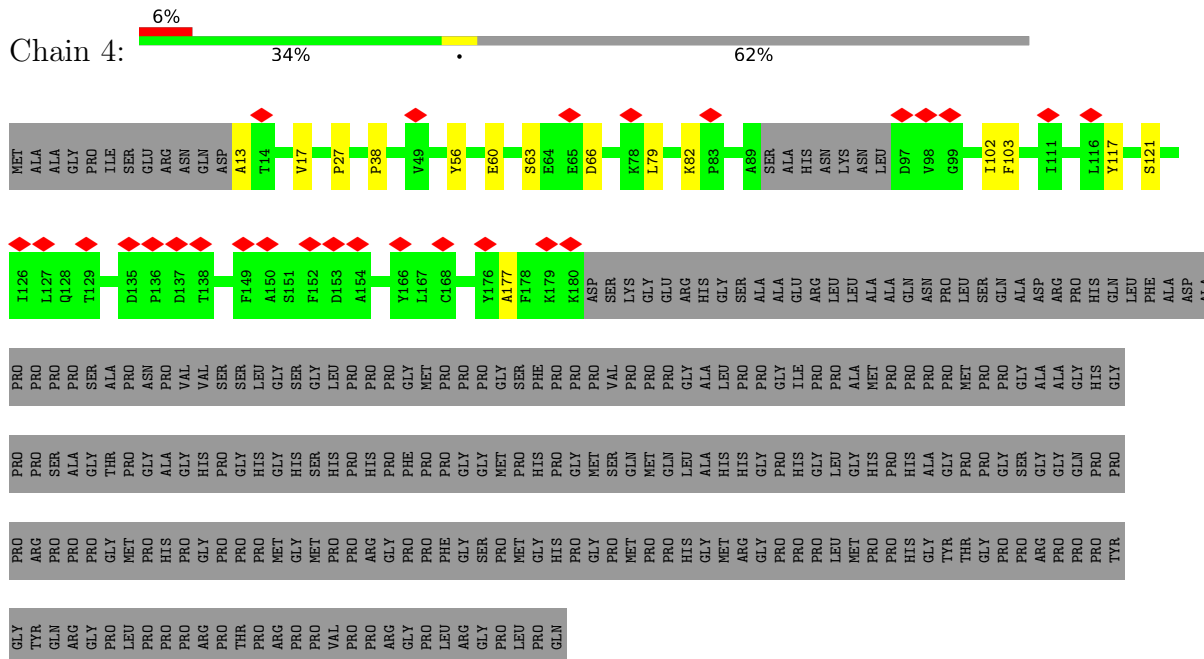


- Molecule 28: Splicing factor 3B subunit 2

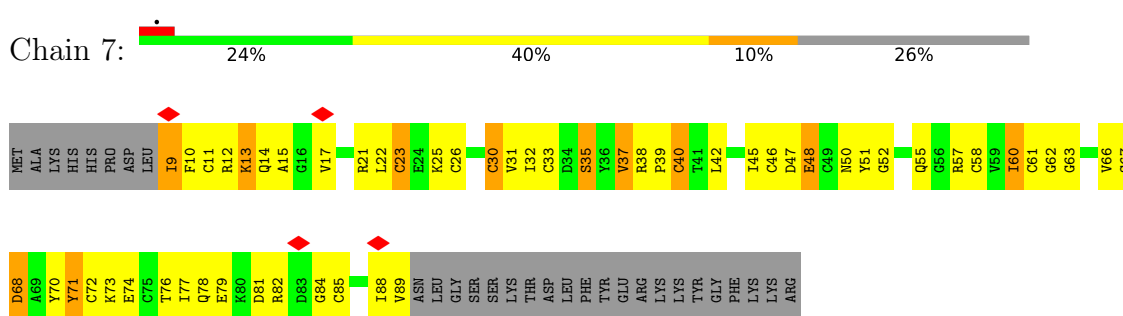




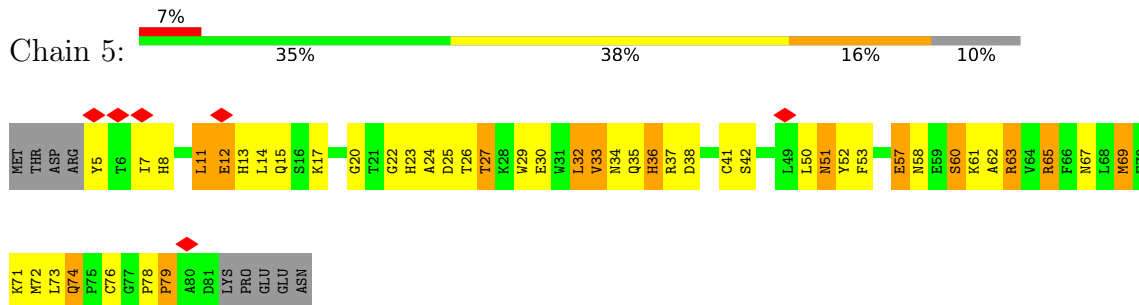
- Molecule 29: Splicing factor 3B subunit 4



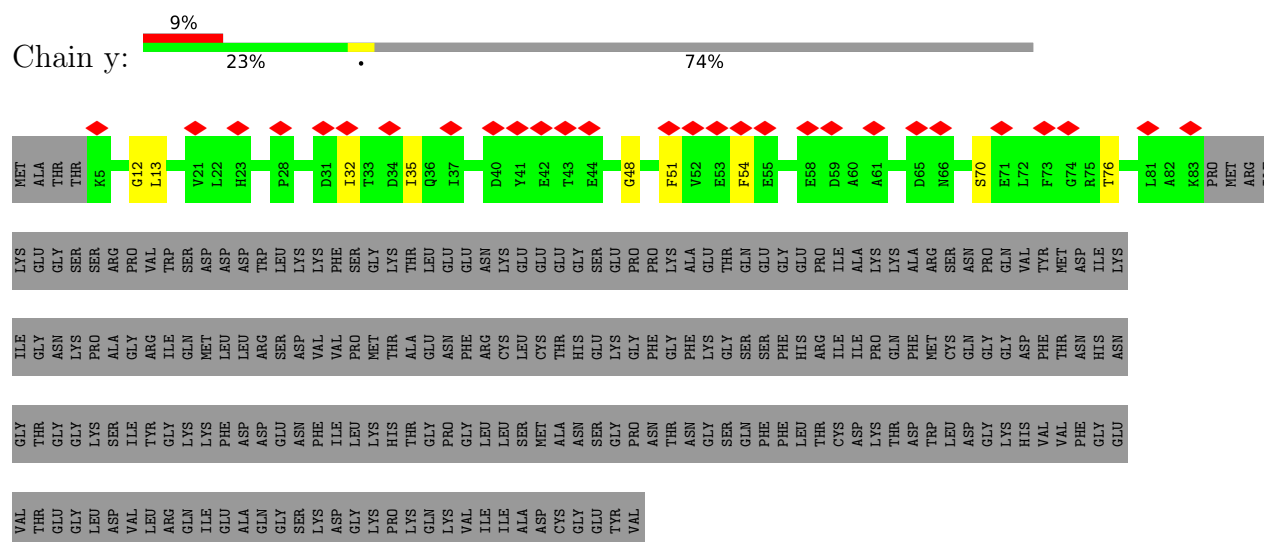
- Molecule 30: PHD finger-like domain-containing protein 5A



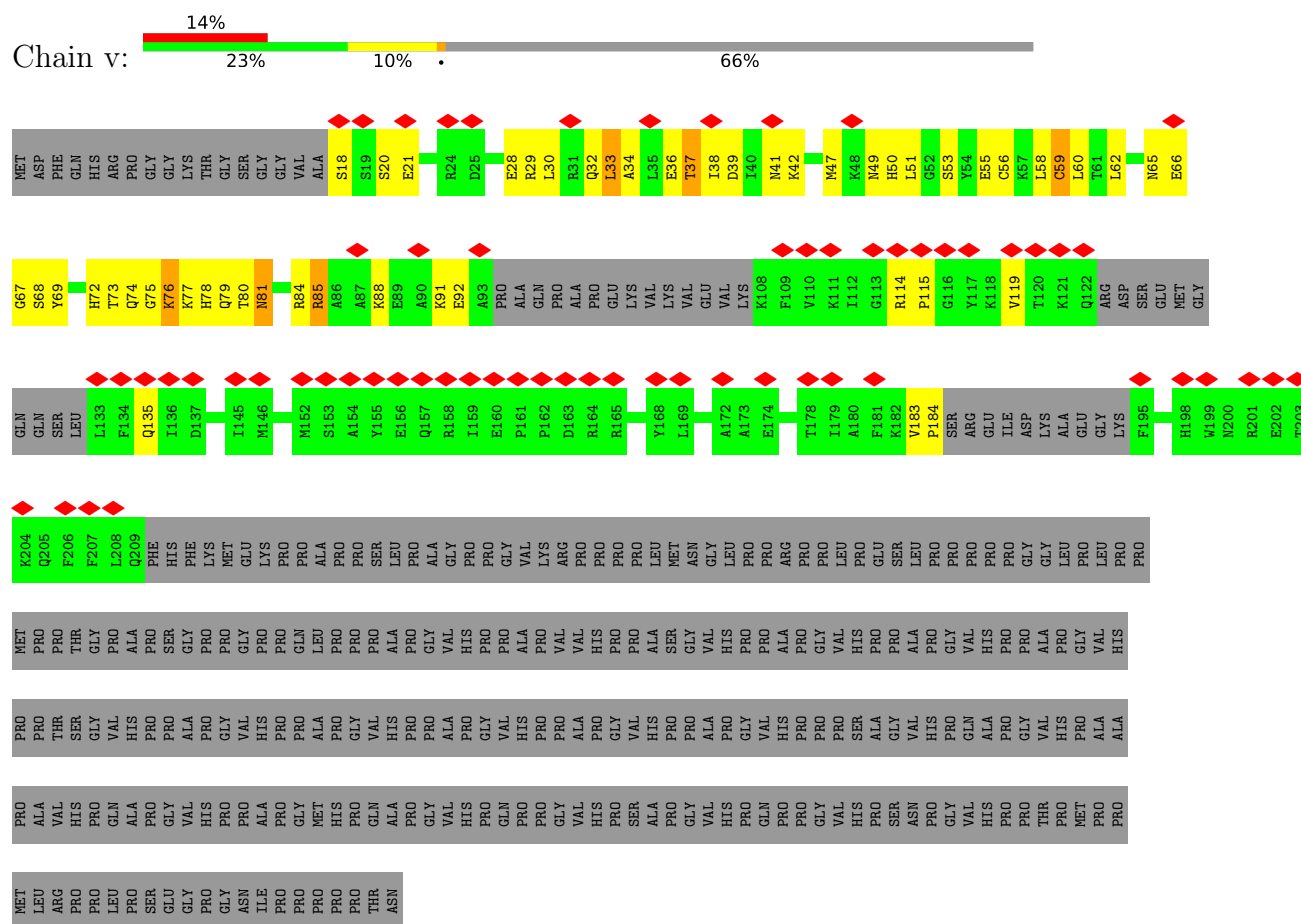
- Molecule 31: Splicing factor 3B subunit 5



- Molecule 32: Peptidyl-prolyl cis-trans isomerase E

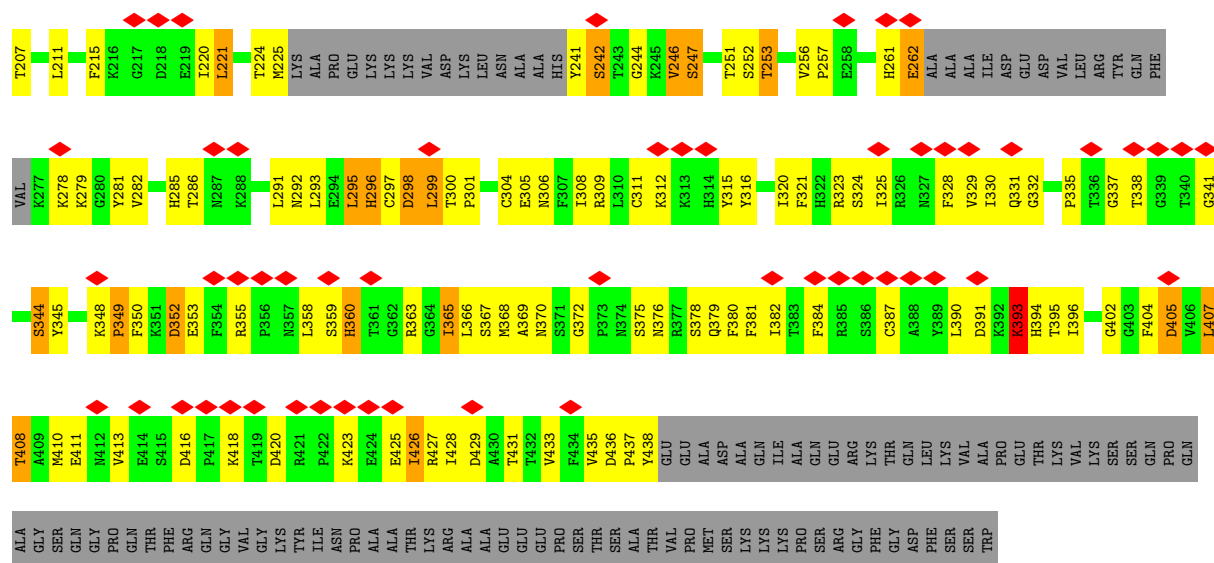


- Molecule 33: Splicing factor 3A subunit 2

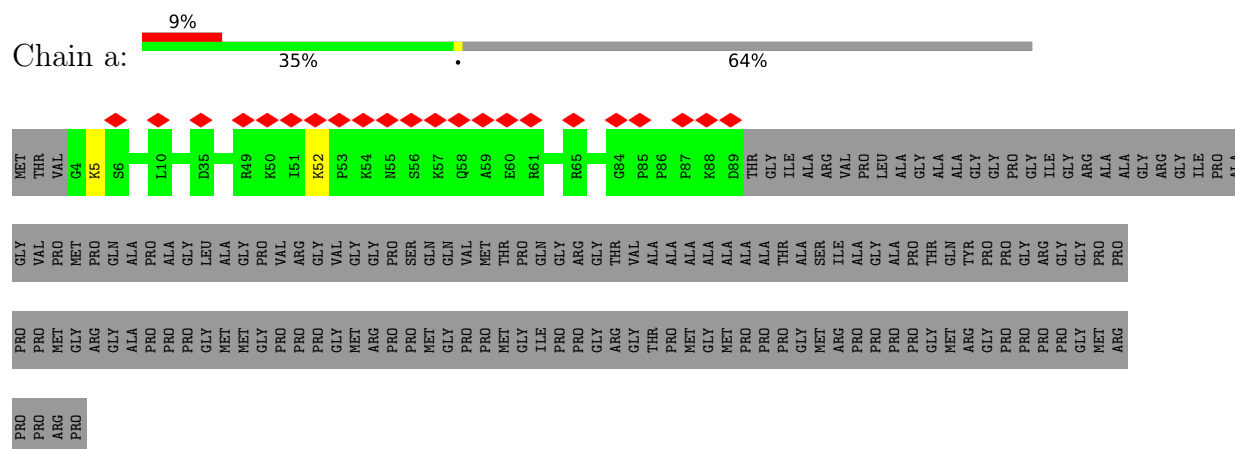


- Molecule 34: Splicing factor 3A subunit 1

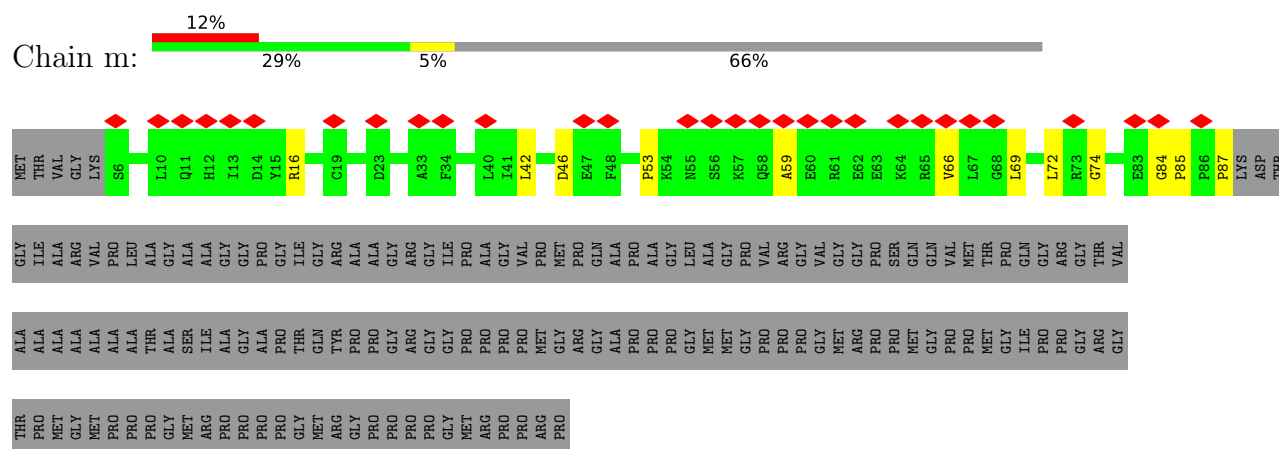




• Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 37: Small nuclear ribonucleoprotein Sm D1



-
- | Amino Acid | Count |
|------------|-------|
| MET | 1 |
| ALA | 1 |
| TYR | 1 |
| ARG | 1 |
| GLY | 1 |
| GLN | 1 |
| GLN | 1 |
| LYS | 1 |
| VAL | 1 |
| LYS | 1 |
| VAL | 1 |
| MET | 2 |
| L25 | 2 |
| F50 | 2 |
| K67 | 2 |
| T68 | 2 |
| K69 | 2 |
| S70 | 2 |
| Q73 | 2 |
| T85 | 2 |
| S89 | 2 |
| N92 | 2 |

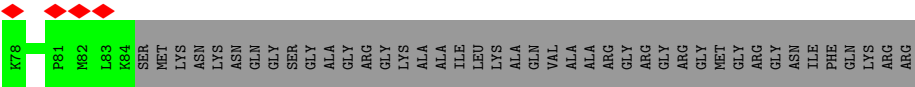
-

- | NET | SER |
|-----|-----|
| K3 | |
| A4 | |
| M13 | |
| S18 | |
| G23 | |
| G33 | |
| P36 | |
| C45 | |
| V46 | |
| E47 | |
| N48 | |
| A49 | |
| T50 | |
| S51 | |
| G52 | |
| Q53 | |
| Q54 | |
| N55 | |
| N56 | |
| I57 | |
| M69 | |
| E74 | |
| R75 | |
| V76 | |

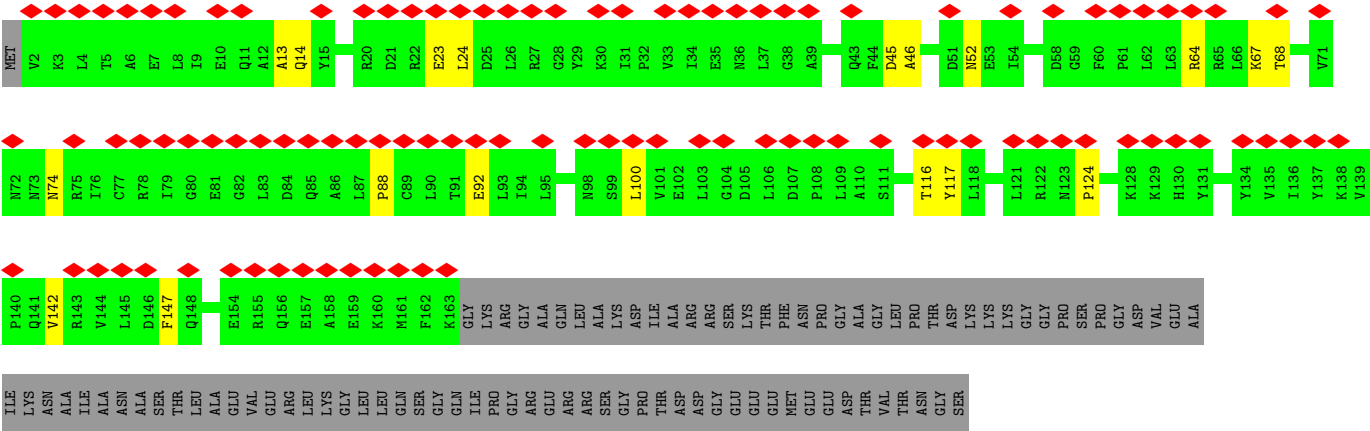
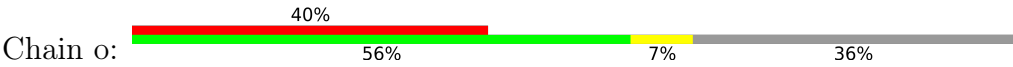
- | NET | SER | LYS |
|-----|-----|-----|
| A4 | | |
| H5 | | |
| P6 | | |
| P7 | | |
| E8 | | |
| K10 | | |
| K11 | | |
| F12 | | |
| M13 | | |
| D14 | | |
| K15 | | |
| S18 | | |
| L19 | | |
| E20 | | |
| L21 | | |
| H26 | | |
| V27 | | |
| Q28 | | |
| G29 | | |
| I30 | | |
| R31 | | |
| L32 | | |
| G33 | | |
| F34 | | |
| D35 | | |
| P36 | | |
| V41 | | |
| I42 | | |
| D43 | | |
| E44 | | |
| C45 | | |
| V46 | | |
| G52 | | |
| Q53 | | |
| Q54 | | |
| N55 | | |
| N56 | | |
| V60 | | |
| V61 | | |
| I67 | | |
| F68 | | |
| M69 | | |
| L70 | | |
| E71 | | |
| A72 | | |
| L73 | | |
| E74 | | |
| R75 | | |

- [illegible]

- [illegible]



• Molecule 43: U2 small nuclear ribonucleoprotein A'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13372	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.423	Depositor
Minimum map value	-0.641	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	516.96, 516.96, 516.96	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.077, 1.077, 1.077	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.87	3/18048 (0.0%)	0.84	26/24520 (0.1%)
2	B	0.56	0/2303	0.49	0/3579
3	C	0.33	0/6873	0.65	3/9346 (0.0%)
4	D	0.24	0/8527	0.56	0/11887
5	E	0.27	0/2392	0.63	0/3242
6	F	0.72	0/2323	0.58	0/3619
7	G	0.49	0/1673	0.64	0/2597
8	H	0.42	0/3947	0.60	9/6138 (0.1%)
9	I	0.49	3/2898 (0.1%)	0.83	7/4057 (0.2%)
10	J	0.36	0/2171	0.63	0/2929
11	K	0.52	0/404	0.68	0/541
12	L	0.57	1/1430 (0.1%)	0.66	0/1915
13	N	0.76	2/1200 (0.2%)	1.04	4/1611 (0.2%)
14	O	0.27	0/1432	0.59	0/1992
15	P	0.68	0/888	0.76	0/1177
16	Q	0.22	0/6796	0.50	2/9527 (0.0%)
17	R	0.46	0/2789	0.66	0/3747
18	S	0.22	0/769	0.57	0/1063
19	T	0.81	0/2574	0.74	0/3511
20	U	0.47	0/424	0.63	0/582
21	V	0.39	1/2993 (0.0%)	0.61	0/4088
22	X	0.38	1/6479 (0.0%)	0.66	0/8747
23	Y	0.33	0/2605	0.66	2/3522 (0.1%)
24	1	0.56	0/6591	0.74	2/8926 (0.0%)
25	3	0.51	4/9398 (0.0%)	0.80	15/12755 (0.1%)
26	p	0.22	0/847	0.49	0/1181
27	w	0.25	0/2311	0.54	0/3008
28	2	0.51	0/1833	0.78	1/2468 (0.0%)
29	4	0.22	0/790	0.54	0/1095
30	7	0.46	0/621	0.74	0/833
31	5	0.65	0/654	0.78	0/885
32	y	0.24	0/389	0.52	0/540

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	v	0.37	0/976	0.62	0/1282
34	u	0.22	0/842	0.43	0/1110
35	9	0.27	0/2342	0.61	2/3182 (0.1%)
36	a	0.87	0/343	1.20	3/427 (0.7%)
36	m	0.23	0/416	0.58	0/581
37	b	0.89	0/327	1.11	0/407
37	n	0.24	0/404	0.57	0/564
38	c	1.15	0/387	1.22	1/482 (0.2%)
38	h	0.21	0/485	0.46	0/677
39	d	1.23	0/295	1.26	0/367
39	i	0.23	0/362	0.52	0/502
40	e	1.03	0/315	1.27	1/392 (0.3%)
40	j	0.22	0/403	0.49	0/561
41	f	0.87	0/295	1.05	0/367
41	k	0.24	0/366	0.54	0/509
42	g	0.80	0/322	1.01	0/399
42	l	0.23	0/417	0.55	0/581
43	o	0.21	0/821	0.55	0/1149
All	All	0.54	15/115490 (0.0%)	0.70	78/159167 (0.0%)

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	15
3	C	0	6
4	D	0	2
9	I	0	4
10	J	0	3
11	K	0	1
12	L	0	2
13	N	0	1
15	P	0	2
16	Q	0	2
17	R	0	1
18	S	0	1
22	X	0	1
23	Y	0	3
24	1	0	3
25	3	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	2	0	1
30	7	0	1
31	5	0	1
35	9	0	2
38	c	0	1
All	All	0	58

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	N	36	PRO	N-CA	19.82	1.71	1.47
9	I	110	PRO	N-CA	17.78	1.70	1.47
25	3	570	PRO	N-CA	13.77	1.65	1.47
13	N	35	GLU	C-N	9.45	1.45	1.33
1	A	385	GLU	C-N	7.47	1.51	1.33
22	X	605	THR	C-N	-7.38	1.22	1.33
1	A	1281	THR	CA-CB	-7.33	1.43	1.53
9	I	140	LEU	C-N	7.32	1.50	1.33
12	L	81	GLN	CA-CB	-6.70	1.41	1.53
21	V	477	LEU	CA-C	-6.65	1.43	1.52
25	3	571	SER	N-CA	6.55	1.54	1.46
25	3	570	PRO	C-N	6.15	1.42	1.33
1	A	1182	ASN	C-N	-5.94	1.28	1.34
25	3	569	ASP	C-N	5.19	1.46	1.33
9	I	109	MET	C-N	5.15	1.45	1.33

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	N	35	GLU	CA-C-N	18.64	138.96	119.76
13	N	35	GLU	C-N-CA	18.64	138.96	119.76
9	I	109	MET	CA-C-N	17.98	142.32	119.84
9	I	109	MET	C-N-CA	17.98	142.32	119.84
25	3	569	ASP	CA-C-N	16.69	140.70	119.84
25	3	569	ASP	C-N-CA	16.69	140.70	119.84
25	3	570	PRO	N-CA-C	-16.05	79.40	112.47
8	H	46	U	C3'-C2'-O2'	15.14	137.31	114.60
8	H	47	U	C4'-C3'-O3'	12.92	128.78	109.40
1	A	385	GLU	CA-C-N	12.68	135.69	119.84
1	A	385	GLU	C-N-CA	12.68	135.69	119.84
9	I	140	LEU	CA-C-N	12.59	135.58	119.84
9	I	140	LEU	C-N-CA	12.59	135.58	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	386	PRO	CB-CA-C	11.97	131.32	111.56
1	A	692	ASP	CA-C-N	-11.06	111.93	122.66
1	A	692	ASP	C-N-CA	-11.06	111.93	122.66
25	3	569	ASP	O-C-N	11.05	132.69	121.30
25	3	570	PRO	CA-N-CD	-10.85	96.81	112.00
9	I	110	PRO	CA-N-CD	-10.78	96.91	112.00
25	3	570	PRO	CA-C-N	9.96	140.57	121.54
25	3	570	PRO	C-N-CA	9.96	140.57	121.54
25	3	568	MET	CA-C-N	9.85	134.08	120.39
25	3	568	MET	C-N-CA	9.85	134.08	120.39
13	N	36	PRO	CA-N-CD	-8.47	100.15	112.00
1	A	532	THR	CA-CB-OG1	-8.15	97.37	109.60
8	H	46	U	C4'-C3'-O3'	-7.61	97.98	109.40
1	A	1165	VAL	N-CA-C	-7.44	105.74	111.62
8	H	47	U	P-O3'-C3'	7.20	131.00	120.20
1	A	1343	SER	CA-C-N	-7.01	111.01	122.65
1	A	1343	SER	C-N-CA	-7.01	111.01	122.65
1	A	767	VAL	N-CA-C	-6.98	106.33	113.10
25	3	571	SER	CA-C-N	6.79	134.73	121.41
25	3	571	SER	C-N-CA	6.79	134.73	121.41
35	9	393	LYS	N-CA-C	-6.48	106.33	114.56
24	1	1105	GLU	CA-C-N	5.92	132.85	121.54
24	1	1105	GLU	C-N-CA	5.92	132.85	121.54
16	Q	750	THR	CA-C-N	-5.91	112.61	121.83
16	Q	750	THR	C-N-CA	-5.91	112.61	121.83
1	A	386	PRO	N-CA-CB	5.81	109.35	103.25
23	Y	48	ASP	CA-C-N	-5.74	114.67	121.90
23	Y	48	ASP	C-N-CA	-5.74	114.67	121.90
35	9	221	LEU	N-CA-C	-5.72	105.02	112.23
8	H	47	U	N1-C1'-C2'	5.71	122.57	114.00
25	3	570	PRO	CA-C-O	-5.69	110.24	120.60
1	A	1834	GLY	N-CA-C	5.68	119.08	112.50
9	I	138	ARG	CA-C-N	5.65	132.34	121.54
9	I	138	ARG	C-N-CA	5.65	132.34	121.54
3	C	94	ILE	CA-C-N	-5.62	104.51	121.98
3	C	94	ILE	C-N-CA	-5.62	104.51	121.98
1	A	1252	GLY	N-CA-C	-5.59	99.92	113.18
1	A	1418	ARG	N-CA-C	-5.59	98.90	110.80
1	A	383	PHE	CB-CA-C	5.55	118.40	109.07
36	a	52	LYS	CA-C-N	-5.53	114.23	119.76
36	a	52	LYS	C-N-CA	-5.53	114.23	119.76
1	A	1418	ARG	CA-C-N	-5.53	111.97	121.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1418	ARG	C-N-CA	-5.53	111.97	121.09
1	A	1771	LEU	CA-CB-CG	5.49	135.51	116.30
8	H	46	U	O4'-C1'-C2'	5.43	111.23	105.80
1	A	532	THR	O-C-N	5.42	127.88	122.03
1	A	532	THR	CA-C-O	-5.36	115.38	120.90
13	N	49	ILE	CA-C-O	-5.36	115.56	121.29
8	H	47	U	C2'-C3'-O3'	-5.33	101.50	109.50
36	a	5	LYS	N-CA-C	5.32	117.99	111.82
1	A	1303	LEU	CA-C-N	-5.31	111.40	121.54
1	A	1303	LEU	C-N-CA	-5.31	111.40	121.54
28	2	507	LYS	N-CA-C	-5.27	106.90	113.38
8	H	47	U	O4'-C1'-C2'	5.27	111.07	105.80
1	A	1607	GLU	CB-CA-C	5.25	119.20	110.90
3	C	98	LYS	N-CA-C	5.25	115.22	108.34
8	H	47	U	C3'-C2'-O2'	5.14	122.31	114.60
25	3	498	GLY	N-CA-C	-5.14	108.14	115.64
25	3	1008	SER	N-CA-C	5.13	114.60	107.73
38	c	99	MET	N-CA-C	5.12	116.86	108.76
40	e	85	THR	N-CA-C	-5.12	105.87	112.68
1	A	698	PRO	CA-C-N	5.12	131.32	121.54
1	A	698	PRO	C-N-CA	5.12	131.32	121.54
1	A	1539	SER	N-CA-C	5.12	121.12	109.81
25	3	917	PRO	N-CA-C	-5.04	102.08	112.47

There are no chirality outliers.

All (58) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	1	1105	GLU	Mainchain
24	1	1179	ASP	Peptide
24	1	717	THR	Peptide
28	2	502	ARG	Peptide
25	3	268	ARG	Peptide
25	3	342	LEU	Peptide
25	3	490	THR	Peptide
25	3	916	ASN	Peptide
25	3	971	ASP	Peptide
31	5	79	PRO	Peptide
30	7	13	LYS	Peptide
35	9	329	VAL	Peptide
35	9	349	PRO	Peptide
1	A	108	MET	Peptide

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Mol	Chain	Res	Type	Group
1	A	1338	SER	Peptide
1	A	1416	ILE	Peptide
1	A	187	PRO	Peptide
1	A	203	VAL	Peptide
1	A	2150	GLN	Peptide
1	A	376	GLU	Peptide
1	A	467	GLN	Peptide
1	A	468	LYS	Peptide
1	A	698	PRO	Peptide
1	A	703	GLN	Peptide
1	A	855	ARG	Peptide
1	A	940	ILE	Peptide
1	A	941	LYS	Peptide
1	A	982	GLU	Peptide
3	C	360	ALA	Peptide
3	C	427	PHE	Peptide
3	C	443	VAL	Peptide
3	C	533	SER	Peptide
3	C	534	VAL	Peptide
3	C	823	ALA	Peptide
4	D	1583	ASP	Peptide
4	D	2098	ALA	Peptide
9	I	109	MET	Mainchain
9	I	337	LEU	Peptide
9	I	338	ILE	Peptide
9	I	550	TRP	Peptide
10	J	241	VAL	Peptide
10	J	354	LEU	Peptide
10	J	413	GLU	Peptide
11	K	196	ASP	Peptide
12	L	200	LYS	Peptide
12	L	202	ARG	Peptide
13	N	12	PRO	Peptide
15	P	29	GLN	Peptide
15	P	56	ASN	Peptide
16	Q	488	SER	Peptide
16	Q	489	VAL	Peptide
17	R	163	MET	Peptide
18	S	164	PRO	Peptide
22	X	326	GLN	Peptide
23	Y	204	SER	Peptide
23	Y	274	ASP	Peptide

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Mol	Chain	Res	Type	Group
23	Y	37	TYR	Peptide
38	c	112	ASN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	17607	0	16789	953	0
2	B	2066	0	1047	106	0
3	C	6724	0	6697	506	0
4	D	8528	0	3745	125	0
5	E	2338	0	2275	174	0
6	F	2075	0	1048	133	0
7	G	1503	0	766	165	0
8	H	3539	0	1791	180	0
9	I	2880	0	1411	41	0
10	J	2116	0	1977	123	0
11	K	392	0	343	49	0
12	L	1403	0	1431	98	0
13	N	1174	0	1168	103	0
14	O	1432	0	632	26	0
15	P	876	0	875	60	0
16	Q	6730	0	3268	69	0
17	R	2760	0	2639	298	0
18	S	770	0	356	20	0
19	T	2507	0	2451	118	0
20	U	422	0	291	31	0
21	V	2959	0	2237	131	0
22	X	6357	0	6349	581	0
23	Y	2556	0	2492	269	0
24	1	6468	0	6657	433	0
25	3	9210	0	9124	705	0
26	p	841	0	420	24	0
27	w	2275	0	1347	136	0
28	2	1803	0	1618	228	0
29	4	792	0	367	15	0
30	7	613	0	597	52	0
31	5	635	0	595	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	y	390	0	190	5	0
33	v	964	0	735	100	0
34	u	834	0	325	3	0
35	9	2307	0	1898	146	0
36	a	344	0	93	0	0
36	m	413	0	194	7	0
37	b	328	0	89	5	0
37	n	402	0	184	8	0
38	c	388	0	102	7	0
38	h	482	0	220	13	0
39	d	296	0	87	10	0
39	i	359	0	179	16	0
40	e	316	0	85	4	0
40	j	403	0	173	8	0
41	f	296	0	84	5	0
41	k	364	0	176	11	0
42	g	324	0	89	4	0
42	l	415	0	198	15	0
43	o	816	0	386	11	0
44	A	36	0	6	8	0
45	C	32	0	12	8	0
46	C	1	0	0	0	0
46	F	6	0	0	0	0
47	7	3	0	0	0	0
47	K	1	0	0	0	0
47	N	3	0	0	0	0
All	All	112874	0	88308	5357	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 (5357) 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)
27:w:387:TRP:CH2	33:v:84:ARG:HB2	1.26	1.61
1:A:2084:HIS:CB	4:D:1008:THR:CB	1.79	1.56
13:N:37:HIS:HB2	13:N:41:ARG:CB	1.10	1.52
1:A:2335:ALA:HA	4:D:592:LYS:CB	1.44	1.45
1:A:1889:LEU:HD12	1:A:2014:MET:N	1.21	1.44
26:p:191:PHE:CB	27:w:495:LEU:HD11	1.46	1.44
15:P:184:VAL:HG11	23:Y:50:ILE:CD1	1.43	1.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:p:152:ILE:CB	27:w:498:GLN:CG	1.96	1.42
13:N:37:HIS:CB	13:N:41:ARG:CB	1.97	1.42
25:3:1115:GLU:HG2	28:2:708:TRP:NE1	1.24	1.41
9:I:136:ALA:HB1	9:I:144:GLN:CB	1.51	1.40
25:3:1115:GLU:CG	28:2:708:TRP:HE1	1.34	1.40
9:I:110:PRO:N	9:I:110:PRO:CA	1.70	1.40
22:X:246:LEU:CD1	23:Y:227:VAL:HG11	1.49	1.40
27:w:387:TRP:HZ3	33:v:84:ARG:C	1.28	1.39
17:R:360:ARG:HH11	23:Y:275:TRP:CD1	1.41	1.38
17:R:360:ARG:HD2	23:Y:275:TRP:CD1	1.57	1.38
26:p:152:ILE:CB	27:w:498:GLN:CB	2.00	1.38
13:N:36:PRO:N	13:N:36:PRO:CA	1.71	1.37
17:R:348:GLU:HG3	22:X:262:LEU:CB	1.55	1.33
27:w:387:TRP:CH2	33:v:84:ARG:CB	2.08	1.33
25:3:1133:THR:C	28:2:711:LEU:HD22	1.51	1.32
1:A:2268:LEU:H	4:D:1263:PRO:CB	1.42	1.31
17:R:65:PRO:C	18:S:90:LEU:HA	1.55	1.31
15:P:184:VAL:HG21	23:Y:52:GLN:OE1	1.12	1.30
8:H:56:A:H4'	28:2:481:THR:OG1	1.19	1.29
1:A:442:LYS:HG3	1:A:610:HIS:NE2	1.42	1.29
6:F:79:C:O2'	12:L:170:LYS:HD2	1.23	1.28
26:p:152:ILE:CB	27:w:498:GLN:HB3	1.59	1.27
8:H:53:U:H5''	28:2:450:SER:CB	1.66	1.26
1:A:2074:ARG:CB	4:D:1047:PRO:CB	2.12	1.25
1:A:2268:LEU:N	4:D:1263:PRO:CB	1.99	1.25
3:C:673:LYS:HE2	20:U:57:ILE:CB	1.66	1.25
17:R:65:PRO:O	18:S:90:LEU:HA	1.17	1.25
27:w:387:TRP:CZ3	33:v:84:ARG:C	2.13	1.25
8:H:56:A:O2'	28:2:478:HIS:HB3	1.24	1.24
25:3:1133:THR:CA	28:2:711:LEU:CD2	2.16	1.24
17:R:348:GLU:CG	22:X:262:LEU:HB2	1.67	1.23
25:3:1116:SER:N	28:2:708:TRP:CZ2	2.05	1.22
15:P:184:VAL:CG1	23:Y:50:ILE:HD13	1.68	1.22
25:3:1133:THR:HA	28:2:711:LEU:CD2	1.70	1.22
1:A:2081:ALA:HA	4:D:1010:SER:CB	1.68	1.21
27:w:388:ASP:OD2	33:v:84:ARG:HD2	1.37	1.21
1:A:2298:LEU:O	4:D:1281:GLN:CB	1.88	1.20
17:R:360:ARG:CD	23:Y:275:TRP:CD1	2.23	1.20
22:X:164:TRP:CE3	22:X:542:PHE:CD1	2.30	1.20
15:P:184:VAL:CG2	23:Y:52:GLN:OE1	1.90	1.18
17:R:360:ARG:NH1	23:Y:276:LYS:H	1.39	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:226:LEU:HD22	23:Y:315:PHE:CE2	1.78	1.17
22:X:242:LYS:CG	23:Y:227:VAL:HG21	1.74	1.17
28:2:503:HIS:CD2	28:2:510:TYR:HB2	1.80	1.17
1:A:2143:ARG:CB	4:D:1264:PRO:CB	2.23	1.16
25:3:1116:SER:N	28:2:708:TRP:HZ2	1.43	1.15
26:p:191:PHE:CB	27:w:495:LEU:CD1	2.24	1.15
27:w:390:LYS:NZ	33:v:84:ARG:HD2	1.61	1.14
17:R:360:ARG:HD3	23:Y:275:TRP:NE1	1.60	1.14
25:3:1133:THR:C	28:2:711:LEU:CD2	2.21	1.14
9:I:109:MET:N	9:I:110:PRO:HD3	1.61	1.13
26:p:152:ILE:CB	27:w:498:GLN:HG2	1.66	1.13
8:H:53:U:H5'	28:2:450:SER:HB2	1.15	1.13
4:D:863:THR:H	25:3:599:GLU:HA	1.08	1.12
21:V:532:GLN:O	21:V:536:ILE:HB	1.47	1.13
22:X:242:LYS:HG3	23:Y:227:VAL:HG21	1.30	1.12
1:A:533:LYS:NZ	7:G:5:G:OP2	1.80	1.12
20:U:26:VAL:HB	21:V:517:LEU:HD21	1.29	1.12
25:3:1133:THR:HA	28:2:711:LEU:HD23	1.17	1.12
1:A:184:ASP:HB2	13:N:1:MET:H1	1.10	1.11
27:w:387:TRP:CZ3	33:v:84:ARG:CB	2.32	1.11
20:U:23:LEU:HD12	21:V:478:LYS:HB2	1.33	1.11
8:H:56:A:O2'	28:2:478:HIS:CB	1.99	1.11
25:3:1115:GLU:HB3	28:2:708:TRP:CZ2	1.85	1.11
17:R:355:ILE:HD11	22:X:266:GLU:OE2	1.51	1.10
1:A:48:LYS:HD3	1:A:53:PHE:CE1	1.87	1.09
28:2:518:GLU:HB2	33:v:47:MET:SD	1.92	1.09
22:X:164:TRP:CE3	22:X:542:PHE:CE1	2.40	1.09
1:A:442:LYS:CG	1:A:610:HIS:NE2	2.16	1.08
25:3:1041:TYR:CD2	28:2:705:ARG:HG3	1.88	1.08
22:X:238:ARG:HH22	23:Y:230:LEU:HG	0.98	1.08
22:X:226:LEU:HD22	23:Y:315:PHE:HE2	0.93	1.08
1:A:1889:LEU:CD1	1:A:2014:MET:N	2.16	1.08
22:X:246:LEU:HD12	23:Y:227:VAL:HG11	1.32	1.08
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.32	1.07
27:w:387:TRP:HZ3	33:v:85:ARG:N	1.51	1.07
22:X:238:ARG:NH2	23:Y:230:LEU:HG	1.67	1.07
22:X:242:LYS:O	22:X:246:LEU:HB2	1.53	1.07
25:3:616:ILE:HB	25:3:629:SER:O	1.54	1.07
25:3:1115:GLU:CG	28:2:708:TRP:NE1	2.01	1.07
6:F:79:C:O2'	12:L:170:LYS:CD	2.01	1.07
7:G:99:C:N4	8:H:32:U:H3	1.50	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2328:ALA:HB2	4:D:728:ARG:CB	1.84	1.06
25:3:114:ARG:NH1	31:5:38:ASP:OD1	1.87	1.06
25:3:1041:TYR:HD2	28:2:705:ARG:HG3	1.20	1.06
28:2:516:GLY:HA2	33:v:60:LEU:HD22	1.34	1.06
1:A:731:LEU:O	35:9:241:TYR:HB3	1.55	1.05
26:p:191:PHE:CB	27:w:495:LEU:HD21	1.83	1.05
17:R:360:ARG:CD	23:Y:275:TRP:NE1	2.19	1.05
17:R:360:ARG:NH1	23:Y:275:TRP:CD1	2.23	1.05
2:B:90:U:C5	42:g:38:ASN:O	2.09	1.05
27:w:388:ASP:CG	33:v:84:ARG:HB3	1.81	1.05
17:R:355:ILE:HG23	22:X:252:ASP:OD2	1.55	1.04
23:Y:246:LYS:HE3	23:Y:312:HIS:HB2	1.36	1.04
4:D:863:THR:N	25:3:599:GLU:HA	1.73	1.04
10:J:225:LEU:HB2	12:L:211:ASN:HD21	1.21	1.04
12:L:37:LEU:HD23	33:v:29:ARG:HH21	1.21	1.03
1:A:2328:ALA:CB	4:D:728:ARG:CB	2.36	1.03
17:R:65:PRO:O	18:S:90:LEU:CA	2.06	1.03
1:A:2335:ALA:CA	4:D:592:LYS:CB	2.37	1.03
15:P:184:VAL:HG11	23:Y:50:ILE:HD11	1.38	1.03
16:Q:1331:HIS:HA	16:Q:1353:GLN:O	1.59	1.02
1:A:1941:ARG:NH1	1:A:2010:ILE:O	1.90	1.02
15:P:186:ARG:HB2	15:P:186:ARG:HH11	1.20	1.02
17:R:351:GLU:HG3	22:X:260:VAL:HG21	1.41	1.02
27:w:387:TRP:HB2	33:v:88:LYS:HD2	1.41	1.02
9:I:136:ALA:CB	9:I:144:GLN:CB	2.38	1.02
1:A:1889:LEU:HD12	1:A:2013:GLY:C	1.84	1.01
8:H:48:A:C6	8:H:78:C:OP1	2.12	1.01
22:X:164:TRP:CD2	22:X:542:PHE:CD1	2.47	1.01
1:A:525:LYS:HB3	11:K:197:TYR:CE2	1.95	1.01
28:2:505:CYS:O	28:2:507:LYS:HE3	1.61	1.01
1:A:2267:PHE:CB	4:D:1262:LEU:O	2.08	1.01
1:A:2268:LEU:O	4:D:1263:PRO:CB	2.09	1.01
13:N:44:GLU:HA	13:N:47:TRP:CD1	1.96	1.01
4:D:754:GLU:HA	25:3:662:PHE:CD1	1.94	1.01
27:w:387:TRP:CZ3	33:v:84:ARG:HB2	1.93	1.00
8:H:56:A:C4'	28:2:481:THR:OG1	2.10	1.00
1:A:1889:LEU:CD1	1:A:2014:MET:O	2.08	1.00
43:o:46:ALA:HA	43:o:68:THR:O	1.60	1.00
2:B:95:G:H1'	39:d:24:LYS:CA	1.91	1.00
10:J:228:ARG:HG2	12:L:210:TYR:HB3	1.42	1.00
6:F:38:G:H2'	6:F:39:A:H8	1.25	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:358:ASP:OD2	22:X:255:PHE:HZ	1.45	0.99
1:A:48:LYS:CD	1:A:53:PHE:CE1	2.44	0.99
7:G:2:U:C4	11:K:219:PHE:CE2	2.51	0.99
15:P:184:VAL:CG1	23:Y:50:ILE:CD1	2.33	0.99
25:3:477:SER:HB2	25:3:505:THR:H	1.28	0.98
15:P:184:VAL:HG11	23:Y:50:ILE:HD13	1.00	0.98
31:5:36:HIS:HD1	31:5:76:CYS:HG	1.06	0.98
25:3:1115:GLU:HB3	28:2:708:TRP:CE2	1.99	0.98
1:A:523:ASN:HB3	11:K:194:ARG:HD3	1.44	0.98
22:X:242:LYS:HG3	23:Y:227:VAL:CG2	1.93	0.98
25:3:1115:GLU:CB	28:2:708:TRP:CZ2	2.47	0.98
1:A:184:ASP:HB2	13:N:1:MET:N	1.78	0.97
1:A:48:LYS:HD3	1:A:53:PHE:HE1	1.28	0.97
17:R:355:ILE:HD11	22:X:266:GLU:CD	1.89	0.97
1:A:1402:ARG:HB2	17:R:407:TYR:HA	1.45	0.97
22:X:165:GLU:HB2	22:X:542:PHE:CZ	1.98	0.97
28:2:642:PRO:CB	29:4:66:ASP:CB	2.42	0.97
1:A:789:GLU:HB2	35:9:253:THR:HB	1.47	0.97
7:G:84:U:OP2	27:w:396:LEU:CD1	2.12	0.97
6:F:59:G:N2	6:F:76:A:N1	2.12	0.97
7:G:117:A:C2'	23:Y:245:CYS:HG	1.78	0.97
3:C:255:VAL:O	3:C:307:VAL:HA	1.65	0.97
17:R:352:ARG:NH1	22:X:265:HIS:HB3	1.80	0.97
9:I:109:MET:N	9:I:110:PRO:CD	2.25	0.96
22:X:246:LEU:CD1	23:Y:227:VAL:CG1	2.43	0.96
6:F:36:A:H3'	6:F:37:C:H5''	1.44	0.96
17:R:358:ASP:OD2	22:X:255:PHE:CZ	2.18	0.96
28:2:644:SER:CB	29:4:63:SER:CB	2.44	0.96
1:A:35:ARG:HB3	1:A:35:ARG:HH11	1.29	0.96
1:A:1768:TYR:HA	1:A:1771:LEU:HB3	1.43	0.96
9:I:109:MET:H	9:I:110:PRO:HD3	1.25	0.96
20:U:22:ASN:HA	21:V:474:HIS:HD2	1.30	0.96
2:B:93:U:H1'	38:c:104:ASP:CA	1.96	0.95
10:J:411:MET:HE1	10:J:415:LEU:HB3	1.48	0.95
12:L:37:LEU:HD23	33:v:29:ARG:NH2	1.79	0.95
1:A:435:CYS:HG	7:G:-10:G:H1	1.14	0.95
13:N:46:LEU:H	13:N:46:LEU:HD22	1.30	0.95
1:A:2081:ALA:CA	4:D:1010:SER:CB	2.43	0.95
7:G:115:C:H1'	23:Y:309:ARG:HH21	1.31	0.95
7:G:1:G:C5	11:K:218:LYS:HD2	2.02	0.95
25:3:1116:SER:N	28:2:708:TRP:CH2	2.34	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:388:ASP:OD2	33:v:84:ARG:CD	2.15	0.94
22:X:164:TRP:CZ3	22:X:542:PHE:CD1	2.55	0.94
1:A:83:HIS:NE2	7:G:16:G:O6	2.01	0.94
6:F:59:G:H1	6:F:76:A:N6	1.64	0.94
25:3:1116:SER:H	28:2:708:TRP:HZ2	1.05	0.94
25:3:1132:PHE:O	28:2:711:LEU:CD2	2.14	0.94
25:3:108:GLY:O	30:7:82:ARG:NH1	2.00	0.94
43:o:13:ALA:O	43:o:24:LEU:HA	1.65	0.94
17:R:348:GLU:HB2	22:X:263:SER:H	1.33	0.94
17:R:360:ARG:HD3	23:Y:275:TRP:HE1	1.13	0.94
25:3:1116:SER:CA	28:2:708:TRP:HH2	1.80	0.94
1:A:2308:VAL:HA	4:D:1125:SER:N	1.84	0.93
25:3:1041:TYR:HD2	28:2:705:ARG:CG	1.80	0.93
1:A:525:LYS:HD2	11:K:197:TYR:CE2	2.04	0.93
1:A:1889:LEU:HA	1:A:2014:MET:H	1.32	0.93
20:U:23:LEU:CD1	21:V:478:LYS:HB2	1.98	0.93
24:1:1302:TYR:CE1	25:3:915:LEU:HB3	2.04	0.93
22:X:226:LEU:CD2	23:Y:315:PHE:HE2	1.82	0.93
25:3:1132:PHE:C	28:2:711:LEU:HD21	1.93	0.93
15:P:186:ARG:HB2	15:P:186:ARG:NH1	1.83	0.93
7:G:99:C:H42	8:H:32:U:H3	0.95	0.92
7:G:1:G:C4	11:K:218:LYS:HD2	2.05	0.92
25:3:516:LEU:O	25:3:527:ILE:HB	1.70	0.92
28:2:452:LYS:HE3	28:2:456:ARG:HB2	1.50	0.92
1:A:525:LYS:CD	11:K:197:TYR:HE2	1.82	0.92
4:D:1224:LEU:O	4:D:1268:ILE:HA	1.69	0.92
19:T:257:ARG:NH2	19:T:301:ASP:OD1	2.03	0.92
17:R:66:GLU:HA	18:S:89:ASP:C	1.95	0.91
8:H:48:A:C5	8:H:78:C:OP1	2.23	0.91
17:R:360:ARG:HH12	23:Y:276:LYS:H	1.09	0.91
1:A:48:LYS:HD2	1:A:53:PHE:CZ	2.05	0.91
8:H:56:A:O3'	28:2:481:THR:HG21	1.71	0.91
1:A:82:ARG:NH1	7:G:15:U:O4	2.02	0.91
25:3:1041:TYR:CD2	28:2:705:ARG:NE	2.38	0.91
23:Y:35:LYS:NZ	23:Y:159:THR:O	2.04	0.91
16:Q:851:ILE:HA	16:Q:1060:LEU:O	1.70	0.91
1:A:1889:LEU:HD12	1:A:2014:MET:H	1.26	0.91
1:A:388:LEU:HD11	3:C:395:THR:CG2	2.01	0.90
1:A:1768:TYR:CE2	1:A:2012:LEU:HD22	2.06	0.90
25:3:1116:SER:CA	28:2:708:TRP:CH2	2.53	0.90
1:A:385:GLU:OE1	1:A:386:PRO:HD2	1.72	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:84:U:OP2	27:w:396:LEU:HD11	1.72	0.90
25:3:1041:TYR:CE2	28:2:705:ARG:CZ	2.53	0.90
17:R:371:ARG:NH1	23:Y:282:CYS:HB2	1.86	0.90
22:X:182:ALA:HB2	22:X:924:ARG:HH11	1.36	0.90
12:L:225:TYR:O	17:R:85:ALA:HB2	1.71	0.90
1:A:523:ASN:HB3	11:K:194:ARG:CD	2.00	0.90
4:D:754:GLU:CB	25:3:662:PHE:HB2	2.02	0.90
6:F:85:U:H3	8:H:14:C:H42	1.20	0.90
8:H:57:A:P	28:2:481:THR:HG21	2.10	0.90
22:X:246:LEU:HD13	23:Y:227:VAL:HG11	1.53	0.90
22:X:768:LYS:HE3	22:X:773:HIS:HA	1.53	0.90
25:3:459:VAL:HG21	25:3:757:ILE:HG21	1.51	0.90
1:A:2308:VAL:HA	4:D:1124:GLN:C	1.97	0.89
17:R:360:ARG:HH11	23:Y:275:TRP:HD1	1.18	0.89
26:p:191:PHE:CB	27:w:495:LEU:CD2	2.50	0.89
1:A:1219:GLU:HG3	22:X:341:PHE:HD1	1.37	0.89
2:B:95:G:H21	2:B:96:A:H5''	1.36	0.89
17:R:280:ILE:H	35:9:225:MET:HG3	1.37	0.89
1:A:2308:VAL:O	4:D:1125:SER:CA	2.20	0.89
2:B:93:U:O4	39:d:66:CYS:N	2.06	0.89
8:H:57:A:OP1	28:2:481:THR:HG21	1.73	0.89
7:G:97:A:O4'	24:1:1110:VAL:HG11	1.73	0.89
24:1:564:ASP:O	24:1:568:ARG:NH2	2.06	0.89
25:3:463:ARG:H	25:3:510:LEU:HD22	1.36	0.89
8:H:56:A:C2'	28:2:478:HIS:HB3	2.03	0.88
10:J:225:LEU:HB2	12:L:211:ASN:ND2	1.87	0.88
25:3:1115:GLU:CG	28:2:708:TRP:CE2	2.56	0.88
30:7:33:CYS:HG	30:7:35:SER:HG	0.95	0.88
1:A:2328:ALA:N	4:D:728:ARG:CB	2.37	0.88
2:B:18:C:N3	2:B:59:G:N1	2.20	0.88
35:9:321:PHE:HA	35:9:332:GLY:HA3	1.54	0.88
17:R:348:GLU:O	17:R:352:ARG:HB2	1.74	0.88
8:H:53:U:C5'	28:2:450:SER:HB2	2.02	0.88
1:A:163:ARG:NH2	1:A:576:ASP:OD1	2.07	0.88
1:A:1889:LEU:CD1	1:A:2013:GLY:C	2.45	0.87
2:B:93:U:C1'	38:c:104:ASP:CA	2.52	0.87
22:X:171:ARG:HG2	22:X:509:PRO:HG3	1.55	0.87
27:w:387:TRP:CZ3	33:v:85:ARG:N	2.33	0.87
8:H:56:A:H1'	28:2:478:HIS:CB	2.05	0.87
22:X:650:ASN:O	22:X:904:GLN:NE2	2.07	0.87
25:3:668:GLY:HA3	25:3:699:VAL:HG11	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:53:U:H5''	28:2:450:SER:HB3	1.53	0.87
1:A:35:ARG:HB3	1:A:35:ARG:NH1	1.89	0.87
1:A:1889:LEU:HG	1:A:2013:GLY:HA3	1.54	0.87
13:N:44:GLU:HA	13:N:47:TRP:CG	2.08	0.87
40:j:63:GLU:O	40:j:71:ARG:HA	1.75	0.87
1:A:1637:TRP:O	1:A:1656:THR:HA	1.73	0.87
24:1:1262:ARG:HD2	31:5:24:ALA:O	1.73	0.87
26:p:152:ILE:CB	27:w:498:GLN:CD	2.47	0.87
7:G:2:U:C4	11:K:219:PHE:CZ	2.62	0.87
25:3:1116:SER:HA	28:2:708:TRP:HH2	1.36	0.87
17:R:147:THR:HG23	19:T:360:VAL:HG22	1.57	0.87
17:R:360:ARG:NH1	23:Y:276:LYS:N	2.22	0.87
25:3:139:LYS:HG3	25:3:160:ALA:HB3	1.57	0.87
28:2:595:LYS:HE2	28:2:595:LYS:O	1.74	0.87
2:B:40:U:O4	7:G:0:G:N2	2.07	0.86
8:H:19:G:N2	8:H:20:G:O6	2.08	0.86
13:N:58:ARG:NH2	13:N:98:GLU:O	2.08	0.86
24:1:1262:ARG:NH1	31:5:24:ALA:O	2.07	0.86
35:9:352:ASP:OD1	35:9:376:ASN:ND2	2.07	0.86
24:1:1110:VAL:O	24:1:1114:VAL:HG23	1.74	0.86
26:p:191:PHE:CB	27:w:495:LEU:CG	2.52	0.86
28:2:509:LYS:N	28:2:509:LYS:HE3	1.90	0.86
1:A:1011:ALA:HB2	12:L:80:THR:HB	1.58	0.86
22:X:165:GLU:HB2	22:X:542:PHE:HZ	1.38	0.86
25:3:1133:THR:O	28:2:711:LEU:HD22	1.74	0.86
3:C:480:LYS:HB2	3:C:493:PHE:HB3	1.58	0.86
17:R:331:ALA:HA	22:X:275:ARG:HH12	1.40	0.86
8:H:56:A:Cl'	28:2:478:HIS:HB3	2.06	0.86
18:S:18:THR:HA	18:S:159:ILE:HA	1.56	0.86
22:X:238:ARG:HH22	23:Y:230:LEU:CG	1.86	0.86
24:1:1157:TYR:CE2	30:7:37:VAL:HG11	2.09	0.86
27:w:387:TRP:HH2	33:v:84:ARG:HB2	1.05	0.86
28:2:452:LYS:CE	28:2:456:ARG:HB2	2.05	0.86
1:A:1431:ALA:HA	22:X:329:TRP:CD1	2.11	0.86
4:D:1558:PRO:HA	4:D:1642:GLN:O	1.75	0.86
25:3:806:ALA:HA	25:3:856:LYS:HB3	1.58	0.85
14:O:236:VAL:HA	14:O:299:ASN:O	1.76	0.85
22:X:725:ARG:HD3	22:X:728:ARG:HH12	1.42	0.85
43:o:23:GLU:HA	43:o:46:ALA:HB3	1.56	0.85
2:B:90:U:H5	42:g:38:ASN:O	1.53	0.85
17:R:360:ARG:HH12	23:Y:276:LYS:N	1.72	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:HIS:HD2	1:A:326:HIS:HD2	1.25	0.85
7:G:117:A:C2'	23:Y:245:CYS:SG	2.64	0.85
7:G:117:A:OP2	23:Y:246:LYS:HD3	1.75	0.85
17:R:360:ARG:HD2	23:Y:275:TRP:HD1	1.04	0.85
24:1:1292:LYS:NZ	31:5:79:PRO:O	2.09	0.85
1:A:957:GLN:O	1:A:961:ASN:ND2	2.08	0.85
19:T:483:ASP:OD2	19:T:485:THR:OG1	1.95	0.85
22:X:164:TRP:CZ3	22:X:542:PHE:CE1	2.65	0.85
3:C:673:LYS:CE	20:U:57:ILE:CB	2.53	0.85
27:w:388:ASP:OD2	27:w:390:LYS:NZ	2.10	0.84
1:A:1581:LEU:HD22	1:A:1746:ARG:HH11	1.41	0.84
3:C:605:ASP:HA	3:C:608:ARG:HD2	1.59	0.84
17:R:359:ARG:HB3	17:R:363:ARG:HH21	1.42	0.84
1:A:362:ARG:HD2	21:V:333:GLN:CB	2.06	0.84
13:N:49:ILE:O	13:N:49:ILE:HD12	1.77	0.84
17:R:103:ARG:NH1	17:R:110:LYS:O	2.11	0.84
22:X:878:HIS:HA	22:X:881:LEU:HD12	1.60	0.84
24:1:1203:GLY:HA2	25:3:1171:LYS:HG3	1.59	0.84
30:7:40:CYS:SG	30:7:73:LYS:NZ	2.50	0.84
22:X:246:LEU:HD12	23:Y:227:VAL:CG1	2.06	0.84
25:3:1106:LYS:HD2	28:2:708:TRP:CD1	2.13	0.84
1:A:888:GLN:O	1:A:889:ARG:NH1	2.10	0.84
4:D:863:THR:CB	25:3:599:GLU:C	2.50	0.84
12:L:227:THR:OG1	17:R:84:ASN:HB2	1.78	0.84
35:9:305:GLU:OE1	35:9:309:ARG:NH1	2.11	0.84
1:A:2328:ALA:H	4:D:728:ARG:CB	1.90	0.84
3:C:135:CYS:HA	3:C:205:THR:OG1	1.78	0.84
12:L:37:LEU:CD2	33:v:29:ARG:HH21	1.91	0.84
23:Y:245:CYS:SG	23:Y:246:LYS:N	2.51	0.84
27:w:390:LYS:NZ	33:v:84:ARG:CD	2.39	0.84
1:A:171:ASP:OD1	1:A:521:ASN:ND2	2.10	0.83
10:J:431:ARG:HA	10:J:434:VAL:HG12	1.60	0.83
22:X:238:ARG:CG	23:Y:224:LEU:HG	2.07	0.83
25:3:280:ASP:HB3	25:3:283:ARG:HG3	1.60	0.83
25:3:585:ALA:HB1	25:3:610:VAL:HG12	1.59	0.83
25:3:1115:GLU:C	28:2:708:TRP:CZ2	2.56	0.83
24:1:734:GLY:O	24:1:738:HIS:HB2	1.77	0.83
3:C:529:ARG:HH22	3:C:540:GLU:HB2	1.42	0.83
7:G:117:A:H2'	23:Y:245:CYS:SG	2.19	0.83
39:i:44:LEU:O	39:i:61:GLU:HA	1.79	0.83
13:N:43:VAL:O	13:N:47:TRP:NE1	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:386:ARG:HG2	22:X:909:ARG:HH22	1.44	0.83
23:Y:246:LYS:HB2	23:Y:311:ILE:HA	1.60	0.83
25:3:1132:PHE:O	28:2:711:LEU:HD21	1.78	0.83
3:C:301:SER:H	3:C:306:ASN:HD22	1.27	0.83
15:P:30:TYR:CE2	17:R:162:ALA:O	2.31	0.83
22:X:238:ARG:HE	23:Y:224:LEU:HD12	1.44	0.83
25:3:568:MET:HB3	25:3:574:LEU:HD12	1.60	0.83
2:B:18:C:N4	2:B:59:G:O6	2.10	0.82
17:R:175:GLN:HB2	17:R:199:MET:HB2	1.62	0.82
25:3:352:GLU:OE2	25:3:429:ARG:NH1	2.12	0.82
1:A:730:GLY:O	17:R:248:PRO:HG2	1.79	0.82
3:C:670:SER:HA	3:C:823:ALA:HB3	1.60	0.82
20:U:26:VAL:CB	21:V:517:LEU:HD21	2.08	0.82
24:1:725:ASP:HA	24:1:728:LEU:HG	1.61	0.82
41:k:21:LEU:HA	41:k:67:ILE:HA	1.62	0.82
1:A:214:ARG:NH2	1:A:223:SER:O	2.11	0.82
1:A:858:GLN:OE1	1:A:861:ARG:NH1	2.13	0.82
24:1:665:ILE:HD13	24:1:705:SER:HB2	1.61	0.82
5:E:61:LEU:HD21	5:E:350:ARG:HD3	1.62	0.82
6:F:91:A:H2'	6:F:92:A:H8	1.43	0.82
15:P:44:ARG:NH2	19:T:255:SER:O	2.12	0.82
1:A:946:GLU:HB3	1:A:950:LEU:HD23	1.62	0.82
27:w:387:TRP:CZ3	33:v:84:ARG:HB3	2.14	0.82
21:V:624:THR:HG21	21:V:647:LEU:HD13	1.61	0.81
1:A:135:VAL:O	1:A:418:THR:OG1	1.96	0.81
27:w:390:LYS:HZ1	33:v:84:ARG:HD2	1.42	0.81
1:A:361:HIS:HB2	3:C:280:HIS:ND1	1.96	0.81
1:A:1819:LEU:HB3	1:A:1915:VAL:HG23	1.62	0.81
13:N:113:PHE:HD1	17:R:198:ARG:HH11	1.25	0.81
20:U:26:VAL:HB	21:V:517:LEU:CD2	2.09	0.81
22:X:741:TRP:HE1	24:1:781:ASP:CG	1.89	0.81
17:R:360:ARG:CD	23:Y:275:TRP:HE1	1.84	0.81
14:O:234:LEU:O	14:O:271:PHE:HA	1.81	0.81
12:L:77:LEU:HD21	35:9:221:LEU:HD22	1.62	0.81
22:X:238:ARG:NH2	23:Y:230:LEU:CG	2.43	0.81
13:N:15:TRP:HZ3	13:N:22:LEU:HD12	1.46	0.81
24:1:652:CYS:HB2	24:1:692:HIS:HE1	1.46	0.81
25:3:412:ILE:HG12	25:3:423:LEU:HD22	1.63	0.81
25:3:1041:TYR:CE2	28:2:705:ARG:NH2	2.48	0.81
31:5:36:HIS:ND1	31:5:76:CYS:SG	2.49	0.81
1:A:1889:LEU:HD12	1:A:2014:MET:CA	2.11	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:105:C:O2'	22:X:619:GLU:OE2	1.98	0.81
13:N:29:MET:SD	13:N:49:ILE:HD13	2.21	0.81
1:A:1962:THR:HG23	1:A:1966:HIS:HB2	1.61	0.80
2:B:92:U:H3	37:b:36:MET:CA	1.93	0.80
25:3:1008:SER:OG	25:3:1009:PHE:N	2.07	0.80
1:A:1518:LEU:O	1:A:1523:ARG:NH1	2.12	0.80
5:E:239:THR:HG23	5:E:254:ALA:HA	1.63	0.80
5:E:240:GLY:O	5:E:252:SER:HA	1.80	0.80
6:F:85:U:H3	8:H:14:C:N4	1.78	0.80
17:R:233:PRO:O	17:R:235:ARG:NH2	2.13	0.80
22:X:234:TYR:OH	22:X:238:ARG:NH1	2.15	0.80
1:A:740:LEU:HD21	35:9:247:SER:HB3	1.64	0.80
20:U:22:ASN:HA	21:V:474:HIS:CD2	2.16	0.80
25:3:29:GLU:HG3	25:3:42:ARG:HG3	1.63	0.80
1:A:119:LEU:HD11	1:A:482:PHE:HB3	1.63	0.80
1:A:2308:VAL:HA	4:D:1125:SER:CA	2.11	0.80
3:C:561:LYS:NZ	3:C:614:TYR:O	2.15	0.80
15:P:67:GLU:OE2	19:T:476:ARG:NH2	2.15	0.80
17:R:357:HIS:HD2	23:Y:276:LYS:NZ	1.79	0.80
22:X:235:LEU:HA	23:Y:220:GLN:OE1	1.81	0.80
17:R:369:LEU:HA	17:R:376:LYS:HE3	1.64	0.80
1:A:361:HIS:HE1	21:V:324:HIS:CB	1.95	0.80
7:G:97:A:O4'	24:1:1110:VAL:CG1	2.29	0.80
12:L:223:GLY:HA2	17:R:86:LEU:HD21	1.64	0.80
21:V:521:TYR:HA	21:V:524:SER:HB2	1.63	0.80
25:3:162:LYS:HE3	25:3:165:THR:HG21	1.62	0.80
6:F:41:A:N1	7:G:6:A:N6	2.29	0.80
22:X:238:ARG:HG3	23:Y:224:LEU:HG	1.62	0.80
24:1:963:LYS:O	24:1:966:GLN:N	2.14	0.80
1:A:658:ARG:NH1	6:F:67:G:OP2	2.14	0.79
19:T:191:HIS:NE2	19:T:440:ASP:OD1	2.15	0.79
25:3:412:ILE:HD12	25:3:1107:THR:HG21	1.64	0.79
1:A:155:LYS:HG3	1:A:626:GLY:HA3	1.64	0.79
1:A:310:THR:HA	1:A:313:LYS:HG3	1.64	0.79
3:C:495:ARG:HD2	3:C:497:LEU:HG	1.62	0.79
1:A:388:LEU:HD11	3:C:395:THR:HG23	1.63	0.79
1:A:1768:TYR:CE2	1:A:2012:LEU:CD2	2.65	0.79
3:C:488:VAL:HG13	3:C:609:LYS:HD3	1.64	0.79
1:A:525:LYS:CD	11:K:197:TYR:CE2	2.64	0.79
3:C:464:ALA:HB1	3:C:473:PRO:HG3	1.65	0.79
25:3:170:VAL:HG23	25:3:184:CYS:HB3	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:255:VAL:HB	3:C:307:VAL:HG12	1.65	0.79
22:X:246:LEU:HD11	23:Y:227:VAL:HG11	1.61	0.79
23:Y:135:ILE:HA	23:Y:138:LYS:HD2	1.63	0.79
24:1:598:SER:O	24:1:602:LYS:HB2	1.83	0.79
1:A:712:HIS:ND1	17:R:250:CYS:SG	2.55	0.79
2:B:94:U:H1'	2:B:95:G:OP1	1.82	0.79
3:C:396:LEU:HD21	3:C:403:LEU:HB2	1.63	0.79
1:A:1412:TRP:O	1:A:1420:ASN:ND2	2.14	0.79
3:C:686:THR:HB	3:C:793:ASP:HB3	1.64	0.79
19:T:245:HIS:HE2	19:T:263:SER:HG	1.30	0.79
1:A:54:VAL:HB	13:N:109:ARG:HH22	1.45	0.79
13:N:120:ARG:NH1	13:N:142:CYS:SG	2.55	0.79
22:X:961:THR:O	22:X:965:GLN:NE2	2.15	0.79
25:3:136:GLU:OE2	25:3:189:TYR:OH	2.00	0.79
6:F:38:G:H2'	6:F:39:A:C8	2.16	0.79
10:J:266:GLU:OE2	10:J:282:TYR:OH	2.00	0.79
17:R:331:ALA:HA	22:X:275:ARG:NH1	1.98	0.79
22:X:324:GLU:OE1	22:X:327:ARG:NH2	2.16	0.79
24:1:805:TYR:O	24:1:809:GLU:HB2	1.82	0.79
6:F:59:G:H1	6:F:76:A:H61	0.84	0.78
19:T:307:SER:OG	19:T:309:ASP:OD1	2.00	0.78
22:X:263:SER:O	22:X:267:ARG:HB2	1.83	0.78
1:A:1320:LYS:NZ	1:A:1325:LEU:O	2.15	0.78
33:v:85:ARG:HH12	33:v:88:LYS:HB3	1.47	0.78
1:A:305:ARG:NH1	3:C:924:GLN:O	2.16	0.78
1:A:357:ASN:HD22	3:C:862:PRO:HB3	1.48	0.78
1:A:384:VAL:HG22	3:C:331:PHE:HB3	1.63	0.78
1:A:1889:LEU:HG	1:A:2013:GLY:CA	2.13	0.78
1:A:1889:LEU:HD11	1:A:2014:MET:O	1.80	0.78
12:L:73:HIS:CD2	35:9:220:ILE:HB	2.18	0.78
22:X:653:SER:HA	22:X:656:GLN:HG3	1.65	0.78
24:1:544:LEU:HD21	24:1:549:ARG:HG3	1.64	0.78
24:1:757:MET:HB3	24:1:762:ALA:HB2	1.64	0.78
3:C:300:LEU:HD23	3:C:306:ASN:HB3	1.64	0.78
16:Q:1272:LEU:HA	16:Q:1302:TYR:O	1.84	0.78
27:w:388:ASP:CG	33:v:84:ARG:CB	2.56	0.78
3:C:510:LEU:HB2	3:C:564:THR:O	1.82	0.78
3:C:677:GLU:HA	3:C:683:ASN:O	1.83	0.78
10:J:256:LYS:HE2	12:L:232:TYR:CE1	2.19	0.78
24:1:834:VAL:HG22	24:1:871:THR:HG23	1.65	0.78
1:A:54:VAL:HB	13:N:109:ARG:NH2	1.99	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2276:GLN:CB	4:D:1151:GLU:CB	2.62	0.78
22:X:882:LEU:O	22:X:886:THR:OG1	2.01	0.78
25:3:929:LYS:HE3	25:3:938:GLU:HB2	1.65	0.78
3:C:674:CYS:HB3	3:C:818:SER:HB2	1.66	0.78
22:X:698:LYS:HZ1	22:X:758:THR:HA	1.47	0.78
1:A:588:LEU:O	1:A:1551:PHE:HE2	1.68	0.77
11:K:206:LYS:O	11:K:223:ARG:NH1	2.16	0.77
19:T:267:ASP:N	19:T:267:ASP:OD1	2.17	0.77
19:T:349:SER:OG	19:T:351:ASP:OD1	1.99	0.77
20:U:26:VAL:CG1	21:V:517:LEU:HD23	2.14	0.77
22:X:610:ASP:HB3	22:X:686:ILE:HD13	1.67	0.77
25:3:1115:GLU:CB	28:2:708:TRP:CE2	2.65	0.77
1:A:891:PHE:O	12:L:83:ARG:NH2	2.17	0.77
1:A:1014:ASN:ND2	1:A:1014:ASN:O	2.17	0.77
10:J:293:ASN:HA	10:J:296:ARG:HD2	1.64	0.77
22:X:526:THR:HG23	22:X:529:THR:H	1.46	0.77
25:3:1115:GLU:CG	28:2:708:TRP:CZ2	2.68	0.77
3:C:117:ASP:N	3:C:117:ASP:OD1	2.14	0.77
17:R:65:PRO:C	18:S:90:LEU:CA	2.48	0.77
21:V:518:LYS:HD3	21:V:519:LYS:H	1.49	0.77
12:L:223:GLY:HA2	17:R:86:LEU:CD2	2.15	0.77
22:X:617:GLY:O	22:X:621:ILE:HB	1.84	0.77
7:G:1:G:C8	11:K:218:LYS:HD2	2.19	0.77
9:I:92:TYR:CB	16:Q:953:ASN:HA	2.14	0.77
12:L:77:LEU:HD21	35:9:221:LEU:CD2	2.15	0.77
22:X:263:SER:HA	22:X:267:ARG:HH21	1.49	0.77
1:A:1631:LEU:HB2	1:A:1660:TYR:HB3	1.67	0.77
3:C:852:ARG:HD2	7:G:-12:C:H5'	1.65	0.77
1:A:325:HIS:CD2	1:A:326:HIS:HD2	2.02	0.77
1:A:1497:THR:OG1	1:A:1499:GLU:OE1	2.02	0.77
5:E:255:MET:HB2	5:E:282:HIS:HB3	1.67	0.77
9:I:106:MET:O	9:I:110:PRO:HG2	1.84	0.77
19:T:406:ILE:HG22	19:T:407:GLN:HG2	1.67	0.77
8:H:56:A:H1'	28:2:478:HIS:HB3	1.62	0.77
17:R:386:ARG:CG	22:X:909:ARG:HH22	1.97	0.77
6:F:84:A:H1'	6:F:85:U:H5'	1.67	0.77
17:R:348:GLU:CB	22:X:263:SER:H	1.98	0.77
22:X:434:GLN:NE2	22:X:468:GLU:OE2	2.18	0.77
25:3:228:LEU:HD21	25:3:250:ILE:HG21	1.66	0.77
25:3:878:ASP:OD1	25:3:879:LEU:N	2.18	0.77
10:J:354:LEU:HD21	10:J:362:ALA:HB2	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:145:ASP:OD2	23:Y:190:ARG:NH2	2.18	0.76
25:3:592:LEU:HD22	25:3:605:LEU:HD13	1.65	0.76
6:F:31:U:O4	7:G:15:U:N3	2.17	0.76
6:F:36:A:N1	7:G:10:U:N3	2.32	0.76
7:G:84:U:OP2	27:w:396:LEU:HD12	1.86	0.76
37:n:32:VAL:HA	37:n:37:ASN:O	1.85	0.76
24:1:565:ASP:HA	24:1:568:ARG:HE	1.51	0.76
5:E:90:ILE:HD12	5:E:105:LEU:HD22	1.68	0.76
6:F:23:U:OP1	13:N:115:THR:OG1	2.02	0.76
24:1:524:ARG:NH1	24:1:562:LYS:O	2.18	0.76
24:1:972:GLY:HA2	24:1:1010:THR:HG21	1.64	0.76
27:w:388:ASP:HB3	33:v:84:ARG:O	1.85	0.76
1:A:361:HIS:CE1	21:V:324:HIS:CB	2.68	0.76
1:A:2325:VAL:O	4:D:728:ARG:CB	2.33	0.76
15:P:42:LYS:NZ	19:T:276:GLU:OE1	2.19	0.76
25:3:464:ARG:HG2	25:3:516:LEU:HD11	1.67	0.76
25:3:1013:ARG:NH2	25:3:1064:ASP:OD1	2.19	0.76
22:X:164:TRP:HE1	22:X:539:VAL:HA	1.49	0.76
22:X:605:THR:OG1	22:X:606:GLN:NE2	2.19	0.76
24:1:1273:TYR:OH	31:5:38:ASP:OD2	2.04	0.76
39:i:20:MET:HA	39:i:29:TYR:O	1.86	0.76
1:A:523:ASN:CB	11:K:194:ARG:HD3	2.16	0.76
24:1:554:LYS:HA	24:1:558:ARG:HH21	1.50	0.76
25:3:1133:THR:CA	28:2:711:LEU:HD21	2.12	0.76
27:w:390:LYS:HZ2	33:v:84:ARG:HD2	1.46	0.76
24:1:793:LYS:HE2	24:1:839:GLU:HG3	1.67	0.76
25:3:1026:ASP:OD1	25:3:1026:ASP:N	2.18	0.76
30:7:22:LEU:N	30:7:67:SER:O	2.18	0.76
1:A:435:CYS:SG	7:G:-10:G:N1	2.52	0.76
3:C:687:MET:HE2	3:C:791:ILE:HG12	1.66	0.76
8:H:181:G:N2	42:l:52:ASP:O	2.19	0.76
25:3:89:ILE:HD12	25:3:103:HIS:HB2	1.67	0.76
25:3:351:SER:H	25:3:356:HIS:HB3	1.51	0.76
25:3:1041:TYR:CD2	28:2:705:ARG:CG	2.61	0.76
28:2:595:LYS:HE2	28:2:595:LYS:C	2.11	0.76
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.18	0.76
1:A:1784:ASN:HD21	1:A:1894:GLN:HB2	1.51	0.76
22:X:164:TRP:HD1	22:X:538:ASP:C	1.94	0.76
25:3:902:ASP:OD1	25:3:902:ASP:N	2.19	0.76
6:F:28:A:O2'	13:N:39:GLY:HA2	1.86	0.75
17:R:160:ALA:HA	17:R:163:MET:HG2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:861:ALA:O	24:1:864:TYR:N	2.17	0.75
25:3:525:ARG:HG3	25:3:533:VAL:HG13	1.67	0.75
1:A:531:THR:OG1	1:A:534:GLU:OE1	2.04	0.75
1:A:2268:LEU:C	4:D:1263:PRO:CB	2.59	0.75
4:D:754:GLU:HA	25:3:662:PHE:HD1	1.49	0.75
22:X:620:GLU:OE1	22:X:696:LYS:NZ	2.19	0.75
17:R:371:ARG:HH12	23:Y:282:CYS:HB2	1.50	0.75
35:9:298:ASP:N	35:9:298:ASP:OD1	2.19	0.75
1:A:79:ARG:HH11	1:A:82:ARG:HH21	1.35	0.75
1:A:1403:LEU:O	17:R:407:TYR:HB2	1.85	0.75
2:B:93:U:O4	39:d:65:ARG:CA	2.35	0.75
13:N:32:ALA:HA	13:N:35:GLU:HG3	1.67	0.75
22:X:222:MET:HE3	23:Y:299:PHE:CZ	2.20	0.75
35:9:390:LEU:HD22	35:9:393:LYS:HE2	1.68	0.75
1:A:593:ARG:NH1	1:A:1565:LYS:NZ	2.33	0.75
1:A:1892:PRO:HG2	1:A:1940:LEU:HB2	1.67	0.75
3:C:154:HIS:HB3	3:C:156:GLU:HB3	1.66	0.75
1:A:972:GLU:N	1:A:972:GLU:OE1	2.19	0.75
8:H:56:A:N3	28:2:478:HIS:CE1	2.55	0.75
16:Q:1136:GLN:H	16:Q:1156:ASN:HA	1.50	0.75
21:V:589:GLU:O	21:V:593:TYR:HB2	1.86	0.75
22:X:164:TRP:CD1	22:X:542:PHE:HB2	2.20	0.75
22:X:741:TRP:NE1	24:1:781:ASP:OD2	2.20	0.75
25:3:459:VAL:HG22	25:3:476:VAL:HA	1.68	0.75
3:C:135:CYS:SG	3:C:242:LEU:HD13	2.26	0.75
21:V:490:CYS:HB2	21:V:525:PHE:HE2	1.51	0.75
20:U:26:VAL:HG12	21:V:517:LEU:HD23	1.68	0.74
24:1:630:ARG:HE	24:1:670:GLN:CD	1.95	0.74
24:1:1141:LEU:HD13	33:v:51:LEU:HD13	1.67	0.74
1:A:318:TYR:O	3:C:645:ARG:NH2	2.20	0.74
1:A:658:ARG:NH2	6:F:65:G:OP2	2.19	0.74
1:A:2109:ASN:CB	4:D:1228:VAL:CB	2.64	0.74
22:X:164:TRP:CD2	22:X:542:PHE:CG	2.74	0.74
3:C:392:LEU:O	3:C:396:LEU:HB2	1.87	0.74
25:3:463:ARG:HB2	25:3:510:LEU:HD13	1.66	0.74
27:w:421:ALA:HA	27:w:424:ARG:HE	1.53	0.74
5:E:87:ASP:N	5:E:87:ASP:OD1	2.19	0.74
24:1:838:VAL:HG13	24:1:875:ILE:HG12	1.67	0.74
25:3:969:VAL:HB	25:3:981:CYS:HB2	1.69	0.74
11:K:200:ASP:HB3	11:K:219:PHE:HD1	1.53	0.74
23:Y:12:VAL:HG22	23:Y:132:GLY:HA3	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:507:LYS:H	28:2:507:LYS:HD2	1.51	0.74
17:R:386:ARG:O	22:X:909:ARG:NH1	2.20	0.74
22:X:164:TRP:NE1	22:X:539:VAL:HA	2.02	0.74
25:3:412:ILE:H	25:3:1105:GLN:HE22	1.34	0.74
28:2:491:LEU:O	28:2:494:THR:OG1	2.06	0.74
1:A:105:ASN:O	1:A:489:TRP:NE1	2.21	0.74
1:A:1201:ARG:O	1:A:1203:SER:N	2.20	0.74
3:C:177:ARG:NH2	3:C:638:ASP:OD2	2.20	0.74
3:C:277:LYS:HD2	3:C:865:GLY:HA3	1.70	0.74
17:R:348:GLU:HG3	22:X:262:LEU:HB2	0.80	0.74
22:X:288:GLU:HA	22:X:291:LYS:HD3	1.70	0.74
25:3:487:ILE:HA	25:3:491:VAL:HG13	1.69	0.74
3:C:349:PHE:HE1	3:C:354:ARG:HA	1.53	0.74
6:F:91:A:H2'	6:F:92:A:C8	2.22	0.74
1:A:419:ARG:NH2	1:A:423:ASP:O	2.20	0.74
1:A:1864:THR:HG22	1:A:1890:GLN:CD	2.12	0.74
7:G:115:C:H3'	7:G:116:C:H4'	1.70	0.74
1:A:2328:ALA:H	4:D:728:ARG:N	1.85	0.74
1:A:265:THR:OG1	1:A:328:HIS:O	2.06	0.73
1:A:525:LYS:CB	11:K:197:TYR:CE2	2.70	0.73
1:A:1429:THR:HG21	17:R:418:MET:SD	2.28	0.73
6:F:42:C:H2'	6:F:43:A:O4'	1.88	0.73
8:H:59:A:OP1	27:w:404:ILE:HD11	1.88	0.73
9:I:140:LEU:N	9:I:141:PRO:HD3	2.03	0.73
10:J:232:GLU:HG3	12:L:210:TYR:CE1	2.22	0.73
25:3:932:ASN:HB2	25:3:936:LYS:HE3	1.69	0.73
6:F:90:G:H2'	6:F:91:A:C8	2.22	0.73
8:H:12:G:O2'	8:H:13:C:O4'	2.05	0.73
22:X:197:LEU:HD21	23:Y:299:PHE:O	1.87	0.73
24:1:1179:ASP:HB2	28:2:511:LEU:HD13	1.70	0.73
27:w:480:GLU:HA	27:w:486:VAL:HA	1.70	0.73
3:C:183:SER:HB3	3:C:205:THR:HA	1.70	0.73
25:3:325:ILE:N	25:3:375:SER:OG	2.20	0.73
1:A:498:ARG:O	1:A:502:ASN:ND2	2.21	0.73
3:C:476:CYS:HB2	3:C:565:ILE:HB	1.71	0.73
10:J:414:HIS:HA	10:J:417:VAL:HG22	1.71	0.73
13:N:46:LEU:HD22	13:N:46:LEU:N	2.02	0.73
21:V:616:LEU:HB2	21:V:643:LEU:HD12	1.71	0.73
22:X:850:ASN:O	22:X:852:SER:N	2.21	0.73
25:3:511:LEU:HD23	25:3:512:GLY:H	1.52	0.73
30:7:73:LYS:O	30:7:77:ILE:HG13	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:242:LYS:HB2	23:Y:224:LEU:HD23	1.70	0.73
25:3:228:LEU:HD12	25:3:229:GLU:H	1.52	0.73
28:2:526:ASP:OD1	28:2:526:ASP:N	2.17	0.73
2:B:117:A:N1	39:d:26:GLY:HA3	2.04	0.73
16:Q:515:VAL:N	16:Q:540:THR:O	2.21	0.73
17:R:161:ALA:HA	17:R:166:ARG:HH22	1.52	0.73
1:A:428:LYS:NZ	2:B:27:U:OP2	2.21	0.73
1:A:1219:GLU:HG3	22:X:341:PHE:CD1	2.23	0.73
1:A:1458:GLN:HG3	17:R:422:PHE:CZ	2.23	0.73
8:H:43:U:O2'	8:H:44:U:O5'	2.04	0.73
22:X:706:MET:HE2	22:X:991:LEU:HB3	1.71	0.73
1:A:1638:ASN:HA	1:A:1655:THR:O	1.89	0.73
12:L:225:TYR:C	17:R:85:ALA:HB2	2.14	0.73
28:2:642:PRO:CB	29:4:66:ASP:HA	2.17	0.73
1:A:1778:TRP:HH2	1:A:1852:LEU:HD21	1.52	0.73
3:C:262:ARG:NH2	3:C:266:GLU:OE2	2.21	0.73
21:V:622:ARG:HA	21:V:625:ARG:HH21	1.54	0.73
28:2:509:LYS:HB2	28:2:512:GLN:HB2	1.71	0.73
30:7:21:ARG:NH1	30:7:68:ASP:OD1	2.22	0.73
22:X:715:SER:OG	22:X:749:GLU:O	2.07	0.73
25:3:1132:PHE:O	28:2:711:LEU:HD23	1.89	0.73
38:h:73:MET:HA	38:h:92:LYS:O	1.89	0.73
1:A:588:LEU:O	1:A:1551:PHE:CE2	2.42	0.72
1:A:2328:ALA:HB3	4:D:728:ARG:HA	1.70	0.72
7:G:97:A:C4'	24:1:1110:VAL:HG11	2.19	0.72
15:P:30:TYR:CD1	17:R:164:PRO:HD2	2.24	0.72
22:X:422:GLY:O	22:X:428:LYS:NZ	2.22	0.72
25:3:208:LEU:HD13	25:3:250:ILE:HD11	1.71	0.72
26:p:152:ILE:CB	27:w:498:GLN:OE1	2.37	0.72
1:A:2109:ASN:O	4:D:1229:ASP:CB	2.36	0.72
19:T:349:SER:OG	19:T:350:HIS:N	2.17	0.72
5:E:172:ASP:HA	5:E:195:GLN:HB3	1.70	0.72
22:X:283:TYR:CG	23:Y:226:MET:HE3	2.24	0.72
28:2:515:ARG:HD3	33:v:60:LEU:O	1.89	0.72
1:A:57:GLN:O	13:N:107:GLN:NE2	2.22	0.72
22:X:182:ALA:CB	22:X:924:ARG:HH11	2.03	0.72
23:Y:40:CYS:O	23:Y:155:ARG:HA	1.90	0.72
25:3:565:TYR:HE1	25:3:619:LEU:HB2	1.54	0.72
25:3:1133:THR:N	28:2:711:LEU:HD21	2.04	0.72
27:w:387:TRP:CZ3	33:v:84:ARG:CA	2.72	0.72
3:C:131:ASN:ND2	3:C:495:ARG:HH12	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:208:LYS:O	15:P:208:LYS:NZ	2.20	0.72
17:R:414:GLN:HG2	22:X:633:ARG:HH12	1.55	0.72
24:1:1300:LEU:HB3	25:3:1032:TRP:CZ3	2.24	0.72
25:3:805:ASN:HB3	31:5:58:ASN:HB3	1.69	0.72
25:3:1040:ASP:OD2	25:3:1043:THR:N	2.20	0.72
1:A:2299:ALA:HB2	4:D:1281:GLN:CB	2.19	0.72
6:F:30:A:H61	7:G:16:G:H1'	1.54	0.72
7:G:115:C:H1'	23:Y:309:ARG:NH2	2.03	0.72
28:2:642:PRO:CB	29:4:66:ASP:CA	2.67	0.72
2:B:92:U:N3	37:b:36:MET:CA	2.53	0.72
22:X:197:LEU:C	22:X:197:LEU:HD12	2.14	0.72
24:1:600:LEU:O	24:1:604:ALA:HB2	1.90	0.72
25:3:1132:PHE:C	28:2:711:LEU:CD2	2.62	0.72
1:A:784:LEU:O	1:A:788:GLN:HG3	1.89	0.72
1:A:1104:ASP:OD1	1:A:1104:ASP:N	2.22	0.72
2:B:96:A:H61	41:f:23:GLY:H	1.38	0.72
25:3:206:GLN:HG3	25:3:231:HIS:HD2	1.52	0.72
25:3:581:LYS:HD2	25:3:625:LEU:HD22	1.71	0.72
7:G:110:U:H5''	22:X:455:ARG:HG3	1.71	0.72
17:R:163:MET:O	17:R:165:VAL:N	2.23	0.72
25:3:384:THR:OG1	25:3:385:PHE:O	2.08	0.72
2:B:96:A:H4'	2:B:97:G:H5''	1.72	0.71
3:C:137:HIS:CD2	3:C:238:ASN:HB2	2.25	0.71
8:H:43:U:H2'	8:H:44:U:C6	2.25	0.71
12:L:188:ARG:HA	12:L:191:LEU:HB2	1.71	0.71
17:R:373:ALA:HB3	17:R:376:LYS:HB2	1.71	0.71
19:T:201:SER:OG	19:T:455:GLN:NE2	2.23	0.71
22:X:171:ARG:HG2	22:X:509:PRO:CG	2.19	0.71
24:1:553:VAL:HA	24:1:556:ILE:HG22	1.72	0.71
24:1:1299:GLU:HA	24:1:1302:TYR:HE2	1.56	0.71
35:9:300:THR:HG1	35:9:304:CYS:HG	1.20	0.71
24:1:717:THR:HB	24:1:718:PRO:HD3	1.72	0.71
1:A:442:LYS:HG3	1:A:610:HIS:CE1	2.22	0.71
1:A:1835:GLN:HA	1:A:1838:LYS:HG3	1.72	0.71
3:C:642:HIS:O	3:C:646:LYS:HB2	1.91	0.71
17:R:331:ALA:HB2	22:X:275:ARG:CZ	2.20	0.71
22:X:232:ARG:HA	22:X:235:LEU:HG	1.73	0.71
22:X:242:LYS:HG2	23:Y:227:VAL:HG21	1.70	0.71
25:3:565:TYR:HB3	25:3:577:TYR:HB3	1.72	0.71
31:5:62:ALA:HA	31:5:65:ARG:HH12	1.55	0.71
3:C:313:GLN:O	3:C:417:ARG:NE	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:153:PHE:HB2	5:E:172:ASP:HB2	1.72	0.71
17:R:357:HIS:CD2	23:Y:276:LYS:NZ	2.59	0.71
23:Y:122:VAL:HB	23:Y:123:HIS:HD2	1.55	0.71
24:1:802:GLU:HB2	24:1:805:TYR:H	1.55	0.71
33:v:37:THR:O	33:v:41:ASN:ND2	2.19	0.71
7:G:2:U:N3	11:K:219:PHE:CD2	2.58	0.71
24:1:876:MET:HE3	24:1:920:ALA:HB3	1.72	0.71
1:A:835:ASP:N	1:A:835:ASP:OD1	2.19	0.71
1:A:979:SER:HB3	1:A:1173:SER:HB2	1.70	0.71
1:A:1660:TYR:OH	1:A:1717:ASN:O	2.06	0.71
1:A:1713:SER:OG	1:A:1714:ALA:N	2.21	0.71
3:C:496:VAL:HB	3:C:546:ALA:HA	1.71	0.71
10:J:350:ILE:HD11	10:J:365:ILE:HB	1.72	0.71
16:Q:971:HIS:O	16:Q:975:ALA:HB2	1.90	0.71
22:X:646:PRO:HA	22:X:672:VAL:HG12	1.71	0.71
22:X:991:LEU:HA	22:X:995:GLU:HA	1.72	0.71
28:2:675:VAL:HA	28:2:681:PRO:HA	1.73	0.71
1:A:64:GLU:N	1:A:64:GLU:OE1	2.22	0.71
1:A:1459:ARG:NE	17:R:419:ASP:O	2.16	0.71
24:1:503:LYS:HE2	24:1:511:MET:HG2	1.72	0.71
24:1:528:ALA:HA	24:1:531:LEU:HB2	1.72	0.71
1:A:391:THR:O	3:C:379:LYS:NZ	2.19	0.71
6:F:86:U:N3	8:H:12:G:O6	2.23	0.71
13:N:120:ARG:O	13:N:143:SER:OG	2.09	0.71
19:T:342:GLU:OE1	19:T:365:ARG:NH1	2.20	0.71
22:X:257:PHE:HA	22:X:262:LEU:HD21	1.72	0.71
22:X:774:ASP:CG	22:X:777:HIS:HD1	1.99	0.71
25:3:22:PHE:O	25:3:75:LYS:NZ	2.19	0.71
25:3:642:ILE:O	25:3:703:ARG:NE	2.24	0.71
1:A:2276:GLN:HA	4:D:1151:GLU:CB	2.21	0.71
22:X:862:VAL:O	22:X:866:ASN:ND2	2.24	0.71
23:Y:6:GLU:O	23:Y:157:ASN:N	2.24	0.71
23:Y:71:TYR:O	23:Y:74:GLN:NE2	2.23	0.71
39:i:33:LEU:HA	39:i:44:LEU:HA	1.73	0.71
3:C:711:ARG:NH2	3:C:732:ILE:O	2.23	0.71
16:Q:536:ARG:HA	16:Q:627:VAL:O	1.91	0.71
3:C:713:LYS:HA	3:C:716:GLU:CD	2.15	0.70
6:F:81:C:H1'	6:F:82:A:C5	2.25	0.70
17:R:348:GLU:CG	22:X:262:LEU:CB	2.46	0.70
17:R:367:ARG:HD3	17:R:371:ARG:HD2	1.71	0.70
19:T:471:ASP:OD2	19:T:472:GLN:N	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:487:ILE:HG13	25:3:491:VAL:HG22	1.73	0.70
1:A:1130:ASN:OD1	1:A:1130:ASN:N	2.22	0.70
1:A:1640:SER:OG	1:A:1641:ARG:N	2.21	0.70
24:1:1141:LEU:CD1	33:v:51:LEU:HD13	2.20	0.70
35:9:300:THR:HA	35:9:353:GLU:HG2	1.72	0.70
41:k:19:LEU:O	41:k:26:HIS:HA	1.90	0.70
1:A:1431:ALA:HB2	22:X:329:TRP:HB2	1.73	0.70
1:A:1838:LYS:HD3	1:A:1868:MET:HG3	1.73	0.70
2:B:87:A:N6	2:B:92:U:P	2.64	0.70
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.70	0.70
3:C:810:PRO:HB3	35:9:105:VAL:O	1.90	0.70
17:R:280:ILE:O	35:9:225:MET:HG3	1.90	0.70
22:X:846:MET:HG3	22:X:881:LEU:HB3	1.72	0.70
24:1:582:LEU:HG	24:1:634:VAL:HG21	1.72	0.70
1:A:1558:THR:OG1	1:A:1559:GLY:N	2.21	0.70
2:B:94:U:C1'	2:B:95:G:OP1	2.39	0.70
22:X:246:LEU:HG	22:X:277:ARG:HE	1.56	0.70
22:X:423:GLU:O	22:X:426:SER:OG	2.08	0.70
24:1:1103:VAL:HG11	24:1:1108:ASN:ND2	2.05	0.70
30:7:71:TYR:CE2	30:7:81:ASP:HB2	2.25	0.70
43:o:116:THR:HA	43:o:142:VAL:HA	1.74	0.70
1:A:442:LYS:CG	1:A:610:HIS:CE1	2.75	0.70
1:A:1070:ASP:OD1	1:A:1070:ASP:N	2.25	0.70
1:A:1132:LYS:HG3	1:A:1139:ARG:HH21	1.56	0.70
22:X:839:GLU:N	22:X:839:GLU:OE2	2.22	0.70
24:1:1181:ASP:OD1	24:1:1182:LEU:N	2.24	0.70
28:2:511:LEU:O	28:2:514:LYS:N	2.20	0.70
16:Q:875:HIS:HA	16:Q:1032:ALA:HA	1.72	0.70
22:X:283:TYR:CZ	23:Y:222:ILE:CG2	2.74	0.70
25:3:1048:ASP:OD1	25:3:1049:LYS:N	2.24	0.70
1:A:525:LYS:HB3	11:K:197:TYR:HE2	1.56	0.70
1:A:2307:GLU:O	4:D:1125:SER:N	2.24	0.70
8:H:28:C:O2'	8:H:29:A:N3	2.25	0.70
13:N:107:GLN:OE1	13:N:109:ARG:NH1	2.25	0.70
24:1:612:THR:HB	24:1:613:MET:HE2	1.73	0.70
24:1:699:GLN:HE22	24:1:738:HIS:HE1	1.40	0.70
33:v:88:LYS:HA	33:v:91:LYS:HE2	1.74	0.70
1:A:1807:ILE:HD11	1:A:1841:THR:HG22	1.74	0.70
3:C:394:ARG:NH1	3:C:395:THR:OG1	2.25	0.70
6:F:38:G:OP1	6:F:38:G:H8	1.74	0.70
6:F:48:A:O3'	12:L:33:ARG:NH1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:455:GLN:HG2	19:T:456:PRO:HD2	1.74	0.70
22:X:785:PRO:O	22:X:788:THR:OG1	2.09	0.70
23:Y:53:THR:OG1	23:Y:54:GLY:N	2.24	0.70
24:1:1139:PRO:O	33:v:50:HIS:O	2.09	0.70
1:A:1618:LYS:NZ	1:A:1663:ASP:OD1	2.24	0.70
3:C:509:VAL:O	3:C:522:SER:OG	2.07	0.70
3:C:818:SER:O	3:C:822:MET:HB2	1.92	0.70
19:T:371:HIS:NE2	19:T:389:SER:OG	2.23	0.70
22:X:701:ASN:ND2	22:X:704:THR:OG1	2.24	0.70
24:1:586:ASP:OD1	24:1:589:ALA:N	2.24	0.70
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.74	0.70
7:G:2:U:O2'	11:K:204:ASP:OD1	2.08	0.70
42:l:49:THR:HA	42:l:55:VAL:HA	1.74	0.70
24:1:1103:VAL:CG1	24:1:1108:ASN:ND2	2.55	0.69
1:A:857:ASN:ND2	1:A:860:GLN:OE1	2.25	0.69
6:F:41:A:H2'	6:F:42:C:C6	2.28	0.69
15:P:205:LYS:HB2	15:P:208:LYS:HB3	1.73	0.69
17:R:315:LYS:NZ	23:Y:191:ILE:HG12	2.07	0.69
22:X:695:CYS:HB3	22:X:722:ARG:HH22	1.58	0.69
38:h:108:VAL:HA	39:i:64:ILE:HA	1.72	0.69
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	2.25	0.69
1:A:1402:ARG:HD2	22:X:664:PRO:CB	2.23	0.69
1:A:1771:LEU:HD21	1:A:1779:PHE:HZ	1.54	0.69
3:C:667:VAL:HG22	3:C:824:THR:HG21	1.74	0.69
3:C:933:PHE:O	3:C:937:THR:OG1	2.07	0.69
8:H:48:A:C4	8:H:78:C:OP1	2.46	0.69
33:v:75:GLY:HA2	33:v:78:HIS:HB3	1.74	0.69
1:A:1181:ASP:OD1	1:A:1181:ASP:N	2.24	0.69
3:C:122:LEU:HD21	3:C:197:SER:OG	1.92	0.69
22:X:1009:LEU:HD23	22:X:1021:LEU:HD11	1.73	0.69
25:3:109:LYS:HA	30:7:82:ARG:NH1	2.07	0.69
25:3:1194:SER:OG	25:3:1199:ARG:O	2.10	0.69
2:B:12:U:O2	2:B:65:G:N2	2.19	0.69
3:C:852:ARG:HD2	7:G:-12:C:C5'	2.21	0.69
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.25	0.69
22:X:225:GLU:HA	22:X:228:LYS:HG2	1.73	0.69
22:X:654:ASP:OD1	22:X:654:ASP:N	2.25	0.69
24:1:948:ARG:NH2	24:1:984:GLU:OE2	2.25	0.69
2:B:66:A:H2'	2:B:67:A:C8	2.27	0.69
5:E:274:VAL:HG12	5:E:275:LYS:HG3	1.73	0.69
8:H:56:A:H1'	28:2:478:HIS:CG	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:188:PRO:HB3	19:T:443:THR:HG21	1.74	0.69
25:3:1182:PHE:O	25:3:1190:GLN:NE2	2.24	0.69
17:R:348:GLU:HG3	22:X:262:LEU:HB3	1.70	0.69
23:Y:251:THR:OG1	23:Y:307:ASP:OD2	2.08	0.69
1:A:35:ARG:HH11	1:A:35:ARG:CB	2.04	0.69
1:A:402:ILE:HG21	3:C:268:LYS:HE3	1.74	0.69
1:A:525:LYS:CG	11:K:197:TYR:HE2	2.05	0.69
1:A:606:LYS:NZ	44:A:3000:IHP:O26	2.26	0.69
1:A:712:HIS:CE1	17:R:250:CYS:HB2	2.28	0.69
1:A:1397:ILE:HG13	17:R:405:VAL:HG22	1.75	0.69
1:A:1431:ALA:CA	22:X:329:TRP:CD1	2.76	0.69
2:B:93:U:O4	39:d:65:ARG:C	2.36	0.69
5:E:158:TYR:CE1	5:E:200:THR:HG22	2.28	0.69
13:N:49:ILE:HD12	13:N:49:ILE:C	2.17	0.69
16:Q:1028:LEU:HA	16:Q:1032:ALA:HB3	1.74	0.69
17:R:348:GLU:HB2	22:X:263:SER:N	2.05	0.69
22:X:238:ARG:NH1	23:Y:319:VAL:HG23	2.08	0.69
24:1:621:ASP:HB3	24:1:624:VAL:HG22	1.75	0.69
27:w:422:PHE:O	27:w:425:HIS:ND1	2.20	0.69
30:7:46:CYS:H	30:7:85:CYS:HB2	1.58	0.69
42:l:62:TYR:N	41:k:70:LEU:O	2.22	0.69
3:C:737:PRO:HD2	3:C:741:GLY:HA3	1.74	0.69
6:F:36:A:C3'	6:F:37:C:H5''	2.21	0.69
6:F:81:C:H1'	6:F:82:A:C4	2.27	0.69
8:H:48:A:N1	8:H:78:C:OP1	2.26	0.69
14:O:165:CYS:O	14:O:168:TRP:N	2.26	0.69
22:X:516:VAL:HG22	22:X:547:LYS:HB2	1.75	0.69
22:X:554:THR:HG22	22:X:555:MET:H	1.58	0.69
25:3:812:LYS:HD2	25:3:856:LYS:HE3	1.74	0.69
28:2:452:LYS:HD3	28:2:452:LYS:C	2.17	0.69
31:5:62:ALA:HA	31:5:65:ARG:NH1	2.07	0.69
1:A:1676:ILE:HD12	1:A:1706:ASP:HB2	1.74	0.69
19:T:423:SER:OG	19:T:424:ASP:OD1	2.09	0.69
35:9:323:ARG:HB3	35:9:331:GLN:HB3	1.75	0.69
22:X:765:LEU:O	22:X:769:SER:OG	2.10	0.68
25:3:968:ARG:HB2	25:3:970:TYR:HE2	1.57	0.68
30:7:33:CYS:SG	30:7:35:SER:OG	2.31	0.68
30:7:37:VAL:HB	30:7:38:ARG:HG3	1.75	0.68
1:A:50:LYS:HB2	1:A:50:LYS:NZ	2.08	0.68
1:A:1427:ARG:HB3	22:X:329:TRP:CZ3	2.29	0.68
1:A:1516:LYS:H	1:A:1516:LYS:HD3	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:115:C:C1'	23:Y:309:ARG:HH21	2.04	0.68
17:R:382:ARG:HH21	17:R:385:ASN:HD22	1.40	0.68
20:U:26:VAL:CG1	21:V:517:LEU:CD2	2.71	0.68
25:3:775:ASN:HD22	25:3:775:ASN:H	1.40	0.68
5:E:202:ASN:ND2	5:E:204:THR:OG1	2.26	0.68
5:E:209:ILE:HG12	5:E:219:VAL:HG22	1.75	0.68
23:Y:30:LYS:HE3	23:Y:168:ASP:HA	1.74	0.68
24:1:680:LEU:HA	24:1:683:LEU:HB2	1.75	0.68
28:2:452:LYS:HD3	28:2:452:LYS:O	1.92	0.68
1:A:83:HIS:NE2	7:G:16:G:C6	2.56	0.68
4:D:913:ALA:N	4:D:977:GLY:O	2.23	0.68
6:F:26:U:H5'	6:F:27:A:H8	1.59	0.68
10:J:330:ARG:NE	10:J:353:GLU:OE2	2.25	0.68
22:X:387:GLN:NE2	22:X:390:GLU:OE2	2.26	0.68
22:X:595:CYS:O	22:X:598:SER:OG	2.12	0.68
28:2:596:GLU:OE2	28:2:596:GLU:N	2.21	0.68
1:A:731:LEU:C	35:9:241:TYR:HB3	2.19	0.68
4:D:971:LYS:O	4:D:980:GLN:N	2.26	0.68
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.75	0.68
6:F:30:A:H2'	6:F:31:U:O4'	1.94	0.68
24:1:734:GLY:O	24:1:738:HIS:CB	2.40	0.68
25:3:328:LYS:NZ	25:3:370:GLU:OE2	2.26	0.68
2:B:87:A:N6	2:B:92:U:OP2	2.26	0.68
3:C:188:VAL:HG23	3:C:190:LEU:HD11	1.75	0.68
3:C:495:ARG:HB2	3:C:495:ARG:HH11	1.58	0.68
8:H:173:C:H2'	8:H:174:A:C8	2.28	0.68
17:R:331:ALA:CB	22:X:275:ARG:CZ	2.71	0.68
22:X:845:ALA:HB2	22:X:915:ARG:HB2	1.76	0.68
24:1:498:MET:HE1	24:1:530:PRO:HB2	1.76	0.68
25:3:833:GLU:O	25:3:836:ALA:N	2.23	0.68
25:3:981:CYS:SG	25:3:1019:ASN:ND2	2.66	0.68
25:3:1115:GLU:C	28:2:708:TRP:HZ2	1.99	0.68
10:J:285:MET:O	10:J:289:ASN:ND2	2.26	0.68
17:R:360:ARG:HH11	23:Y:276:LYS:H	1.36	0.68
22:X:659:ILE:O	22:X:669:LYS:NZ	2.27	0.68
1:A:385:GLU:OE1	1:A:386:PRO:CD	2.42	0.68
3:C:480:LYS:NZ	3:C:482:TYR:OH	2.26	0.68
10:J:267:ARG:HD3	12:L:216:PHE:O	1.94	0.68
21:V:604:LYS:HZ2	21:V:639:LEU:HD23	1.59	0.68
7:G:117:A:HO2'	23:Y:245:CYS:HG	0.88	0.68
24:1:1276:SER:O	24:1:1276:SER:OG	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:449:VAL:HG13	25:3:763:ARG:HG2	1.76	0.68
25:3:1115:GLU:HG3	28:2:708:TRP:CZ2	2.28	0.68
35:9:143:ASP:N	35:9:148:GLU:O	2.23	0.68
4:D:1265:GLN:CB	4:D:1284:VAL:O	2.41	0.67
5:E:122:SER:HB3	5:E:123:MET:HE2	1.77	0.67
13:N:37:HIS:CG	13:N:41:ARG:CB	2.76	0.67
24:1:732:TRP:NE1	24:1:768:GLU:OE2	2.27	0.67
25:3:427:CYS:SG	25:3:428:GLY:N	2.66	0.67
28:2:516:GLY:CA	33:v:60:LEU:HD22	2.18	0.67
35:9:286:THR:HG22	35:9:428:ILE:HD13	1.76	0.67
3:C:604:LEU:HA	3:C:607:LEU:HG	1.74	0.67
25:3:485:LEU:HD23	25:3:491:VAL:HG12	1.76	0.67
25:3:697:ARG:NH2	25:3:717:SER:OG	2.28	0.67
25:3:745:PHE:HB2	25:3:755:VAL:HG23	1.75	0.67
27:w:461:LYS:NZ	28:2:466:LYS:O	2.25	0.67
1:A:720:TRP:HA	35:9:251:THR:HB	1.75	0.67
5:E:202:ASN:ND2	5:E:207:GLN:OE1	2.26	0.67
7:G:117:A:O2'	23:Y:245:CYS:SG	2.20	0.67
8:H:125:G:H2'	8:H:126:A:C8	2.30	0.67
25:3:215:LEU:H	25:3:215:LEU:HD12	1.59	0.67
25:3:840:ALA:O	25:3:844:ASN:ND2	2.27	0.67
27:w:461:LYS:HD3	28:2:467:GLN:HA	1.76	0.67
1:A:1719:PHE:HB2	1:A:1720:PRO:HD2	1.75	0.67
7:G:2:U:C5	11:K:219:PHE:CE2	2.82	0.67
9:I:108:LYS:O	9:I:112:LEU:CB	2.42	0.67
14:O:25:GLN:CB	17:R:188:PHE:HB3	2.23	0.67
21:V:609:GLN:HE22	21:V:616:LEU:HD21	1.58	0.67
25:3:603:ARG:HG3	25:3:604:PHE:CE1	2.29	0.67
1:A:2268:LEU:CA	4:D:1263:PRO:CB	2.72	0.67
2:B:93:U:O4'	38:c:104:ASP:CA	2.42	0.67
25:3:288:VAL:HG23	25:3:289:CYS:H	1.59	0.67
1:A:1792:LYS:HA	1:A:1798:LEU:HA	1.75	0.67
5:E:188:GLN:NE2	5:E:189:THR:H	1.91	0.67
8:H:48:A:C2	8:H:78:C:P	2.88	0.67
12:L:89:ILE:HD11	12:L:96:CYS:SG	2.34	0.67
21:V:636:LEU:HB3	21:V:639:LEU:HD12	1.77	0.67
25:3:700:LYS:HB3	25:3:702:PHE:CZ	2.30	0.67
25:3:983:ASN:ND2	25:3:1021:LEU:O	2.25	0.67
24:1:758:ASP:O	24:1:762:ALA:N	2.15	0.67
24:1:1052:ALA:HA	24:1:1088:ILE:HD11	1.75	0.67
1:A:142:SER:HA	1:A:242:ALA:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:97:G:H1	2:B:116:U:H3	1.41	0.67
3:C:673:LYS:HE2	20:U:57:ILE:CA	2.25	0.67
16:Q:517:PHE:HA	16:Q:538:ASP:O	1.94	0.67
25:3:705:ARG:HA	25:3:710:GLU:HA	1.76	0.67
27:w:473:PRO:O	27:w:477:GLU:HB3	1.95	0.67
1:A:727:LYS:HG3	35:9:244:GLY:HA3	1.75	0.67
1:A:2081:ALA:O	4:D:1010:SER:CB	2.43	0.67
2:B:95:G:H21	2:B:96:A:C5'	2.07	0.67
25:3:867:ARG:HD2	25:3:869:MET:HE3	1.76	0.67
25:3:1041:TYR:HB3	28:2:705:ARG:HG3	1.75	0.67
1:A:155:LYS:NZ	1:A:622:GLY:O	2.27	0.67
1:A:525:LYS:CG	11:K:197:TYR:CE2	2.78	0.67
3:C:810:PRO:CB	35:9:105:VAL:O	2.42	0.67
25:3:521:PRO:O	25:3:543:THR:OG1	2.12	0.67
25:3:1160:HIS:NE2	25:3:1175:ASP:OD2	2.20	0.67
41:k:42:ILE:N	41:k:60:VAL:O	2.27	0.67
1:A:1790:ILE:HG23	1:A:1800:THR:HB	1.77	0.66
3:C:129:ILE:HA	3:C:199:LEU:O	1.95	0.66
3:C:221:ILE:HD13	3:C:493:PHE:HE1	1.59	0.66
5:E:135:VAL:O	5:E:144:VAL:N	2.28	0.66
5:E:146:ARG:HD2	5:E:148:LYS:HE2	1.76	0.66
8:H:57:A:OP1	28:2:481:THR:CG2	2.43	0.66
14:O:36:MET:CB	17:R:199:MET:HE1	2.25	0.66
18:S:83:GLU:HA	18:S:106:ASP:HA	1.74	0.66
19:T:203:HIS:CE1	19:T:229:LYS:HG3	2.29	0.66
25:3:39:GLU:OE2	25:3:55:THR:OG1	2.12	0.66
35:9:142:ARG:HA	35:9:149:PRO:HA	1.77	0.66
1:A:184:ASP:CB	13:N:1:MET:N	2.55	0.66
1:A:593:ARG:HH12	1:A:1565:LYS:NZ	1.93	0.66
1:A:730:GLY:O	17:R:248:PRO:CG	2.43	0.66
1:A:1622:MET:O	1:A:1687:TYR:OH	2.12	0.66
3:C:774:THR:HG22	3:C:784:ILE:HD11	1.78	0.66
9:I:448:ASN:O	9:I:452:ALA:CB	2.42	0.66
12:L:79:PRO:O	12:L:80:THR:OG1	2.13	0.66
19:T:336:VAL:HG23	19:T:347:THR:HG22	1.77	0.66
22:X:957:SER:OG	22:X:960:ARG:NH2	2.28	0.66
25:3:620:ASP:N	25:3:620:ASP:OD1	2.27	0.66
35:9:341:GLY:O	35:9:379:GLN:NE2	2.28	0.66
3:C:807:GLN:NE2	35:9:145:LEU:C	2.52	0.66
3:C:887:LEU:O	3:C:891:THR:HG22	1.95	0.66
20:U:23:LEU:HD12	21:V:478:LYS:CB	2.20	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:238:ARG:HG2	23:Y:224:LEU:HG	1.77	0.66
1:A:712:HIS:CE1	17:R:250:CYS:CB	2.79	0.66
1:A:1866:LYS:HG3	1:A:1886:GLY:HA3	1.76	0.66
1:A:1984:LYS:HG2	1:A:2011:ILE:HD11	1.77	0.66
3:C:453:TYR:CE1	3:C:465:MET:HE1	2.30	0.66
4:D:2065:TRP:O	4:D:2108:PHE:HA	1.95	0.66
22:X:164:TRP:CH2	22:X:542:PHE:HD1	2.13	0.66
23:Y:42:ILE:HB	23:Y:154:ILE:HD12	1.76	0.66
25:3:434:SER:OG	25:3:436:ARG:NE	2.25	0.66
1:A:184:ASP:CB	13:N:1:MET:HA	2.25	0.66
22:X:592:LEU:HD12	22:X:593:GLU:H	1.61	0.66
25:3:147:ASP:OD1	25:3:151:ARG:N	2.28	0.66
25:3:665:LEU:HD11	25:3:667:ILE:HG13	1.77	0.66
1:A:762:ARG:HH12	15:P:226:LYS:HZ1	1.41	0.66
8:H:48:A:C2	8:H:78:C:OP1	2.48	0.66
25:3:777:VAL:HG22	25:3:779:PHE:HE1	1.61	0.66
7:G:99:C:N4	8:H:32:U:N3	2.25	0.66
22:X:164:TRP:CZ3	22:X:542:PHE:HD1	2.13	0.66
24:1:770:MET:HE1	24:1:795:CYS:SG	2.36	0.66
24:1:923:LYS:HG2	24:1:926:LYS:HE3	1.78	0.66
24:1:1299:GLU:HA	24:1:1302:TYR:CE2	2.30	0.66
25:3:169:HIS:ND1	25:3:234:PHE:HB2	2.10	0.66
25:3:191:GLU:HA	25:3:194:ASN:HD22	1.59	0.66
33:v:85:ARG:HA	33:v:85:ARG:NH1	2.11	0.66
1:A:660:PHE:CD2	17:R:209:PRO:HB2	2.31	0.66
1:A:2281:TYR:O	1:A:2284:MET:N	2.24	0.66
3:C:146:VAL:O	3:C:150:ILE:HG13	1.94	0.66
4:D:2098:ALA:O	4:D:2100:GLY:N	2.29	0.66
13:N:29:MET:HB2	13:N:52:ILE:HG21	1.78	0.66
25:3:926:TYR:HB3	25:3:928:TYR:HE2	1.60	0.66
35:9:118:ALA:O	35:9:155:ILE:HA	1.96	0.66
10:J:434:VAL:O	10:J:438:TYR:HB3	1.95	0.66
21:V:494:LEU:HD23	21:V:550:MET:HE1	1.76	0.66
22:X:238:ARG:HH12	23:Y:319:VAL:HG23	1.58	0.66
25:3:511:LEU:HD21	25:3:517:VAL:HG23	1.78	0.66
1:A:1403:LEU:HB2	17:R:407:TYR:HD1	1.61	0.66
2:B:63:A:H2'	2:B:64:G:C8	2.31	0.66
5:E:312:TRP:HD1	5:E:319:ILE:HA	1.60	0.66
25:3:169:HIS:HD2	25:3:170:VAL:H	1.44	0.66
25:3:499:PHE:HZ	25:3:516:LEU:HD22	1.57	0.66
25:3:1188:ASN:OD1	25:3:1189:LYS:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:476:GLU:HG2	28:2:477:MET:H	1.61	0.66
3:C:515:THR:HG22	3:C:518:ASP:HB2	1.77	0.65
24:1:1252:GLN:NE2	28:2:492:LYS:HA	2.11	0.65
25:3:1117:LEU:O	25:3:1128:ILE:HA	1.96	0.65
37:n:23:THR:HA	37:n:47:LEU:HA	1.77	0.65
3:C:778:PRO:HB2	3:C:821:LEU:HD21	1.78	0.65
5:E:120:ASP:OD1	5:E:120:ASP:N	2.28	0.65
23:Y:17:TYR:HB3	23:Y:20:GLU:HG3	1.79	0.65
24:1:796:CYS:HA	24:1:801:VAL:HG11	1.78	0.65
24:1:1203:GLY:HA2	25:3:1171:LYS:CG	2.25	0.65
25:3:586:ASP:HB3	25:3:610:VAL:HB	1.77	0.65
25:3:680:ASP:CG	25:3:681:PRO:HD2	2.21	0.65
1:A:2267:PHE:CB	4:D:1262:LEU:C	2.69	0.65
14:O:36:MET:HA	14:O:56:ARG:O	1.96	0.65
23:Y:183:ARG:HA	23:Y:183:ARG:HE	1.61	0.65
25:3:206:GLN:HG3	25:3:231:HIS:CD2	2.31	0.65
28:2:452:LYS:HE3	28:2:456:ARG:CB	2.27	0.65
30:7:26:CYS:SG	30:7:61:CYS:HB2	2.35	0.65
1:A:176:LEU:H	1:A:176:LEU:HD23	1.61	0.65
1:A:850:TYR:OH	1:A:863:GLU:OE1	2.13	0.65
5:E:75:HIS:HB3	5:E:78:GLY:H	1.60	0.65
5:E:135:VAL:HG21	5:E:181:ILE:HD13	1.77	0.65
15:P:30:TYR:CE1	17:R:164:PRO:HD2	2.31	0.65
17:R:386:ARG:HG2	22:X:909:ARG:NH2	2.10	0.65
23:Y:39:TYR:N	23:Y:156:ILE:O	2.29	0.65
24:1:862:GLU:OE1	24:1:904:THR:OG1	2.14	0.65
24:1:1302:TYR:HE1	25:3:915:LEU:HB3	1.57	0.65
26:p:185:GLY:HA2	27:w:485:ASN:HD22	1.62	0.65
27:w:390:LYS:HZ3	33:v:84:ARG:CZ	2.09	0.65
27:w:460:ALA:O	27:w:464:LEU:HG	1.97	0.65
28:2:505:CYS:O	28:2:507:LYS:CE	2.42	0.65
1:A:325:HIS:HD2	1:A:326:HIS:CD2	2.12	0.65
1:A:384:VAL:CG1	3:C:327:TYR:CE2	2.80	0.65
1:A:1780:VAL:HB	1:A:1863:VAL:HG23	1.77	0.65
7:G:98:U:O4	8:H:33:G:N1	2.25	0.65
23:Y:87:LYS:NZ	23:Y:120:ASP:OD2	2.30	0.65
24:1:694:LEU:HD12	24:1:694:LEU:H	1.59	0.65
24:1:712:LEU:O	24:1:716:ALA:HB3	1.97	0.65
24:1:1174:GLU:OE2	24:1:1210:HIS:NE2	2.26	0.65
38:h:107:ILE:O	39:i:65:ARG:N	2.29	0.65
3:C:709:TRP:HB3	3:C:713:LYS:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:348:GLU:OE1	22:X:263:SER:O	2.13	0.65
19:T:329:HIS:HE2	19:T:347:THR:HG1	1.45	0.65
24:1:696:ASP:O	24:1:702:ARG:NH1	2.29	0.65
1:A:1383:GLN:OE1	22:X:339:LEU:HB3	1.97	0.65
1:A:1889:LEU:HA	1:A:2014:MET:N	2.10	0.65
6:F:35:A:H8	7:G:12:G:C6	2.15	0.65
8:H:12:G:H2'	8:H:13:C:C6	2.31	0.65
10:J:300:ASP:O	10:J:304:THR:OG1	2.15	0.65
10:J:334:GLU:OE2	10:J:349:TYR:OH	2.11	0.65
25:3:185:LEU:HG	25:3:235:LEU:HD11	1.76	0.65
42:l:27:VAL:O	42:l:48:VAL:HA	1.96	0.65
1:A:525:LYS:CB	11:K:197:TYR:HE2	2.10	0.65
9:I:448:ASN:O	9:I:452:ALA:HB2	1.96	0.65
14:O:232:THR:O	14:O:273:GLN:HA	1.97	0.65
23:Y:244:VAL:HG12	23:Y:247:LEU:HD21	1.77	0.65
35:9:416:ASP:O	35:9:420:ASP:N	2.28	0.65
1:A:139:VAL:O	1:A:143:GLN:HG3	1.97	0.65
1:A:1431:ALA:HB2	22:X:329:TRP:CD1	2.32	0.65
1:A:1782:ASP:OD2	1:A:1782:ASP:N	2.28	0.65
5:E:105:LEU:HD11	5:E:136:TRP:CD2	2.32	0.65
6:F:60:C:C2	10:J:236:ARG:NH2	2.64	0.65
22:X:850:ASN:O	22:X:853:ILE:HG13	1.97	0.65
24:1:1157:TYR:CD2	30:7:37:VAL:HG11	2.32	0.65
1:A:1768:TYR:HA	1:A:1771:LEU:CB	2.23	0.65
22:X:164:TRP:CE2	22:X:542:PHE:CD1	2.84	0.65
25:3:911:LYS:HB3	25:3:922:GLY:O	1.96	0.65
25:3:1009:PHE:HE1	25:3:1036:ALA:HB2	1.61	0.65
35:9:360:HIS:HB2	35:9:387:CYS:O	1.97	0.65
3:C:759:LEU:HA	3:C:762:VAL:HG12	1.79	0.64
3:C:813:ARG:HH21	35:9:106:LEU:HA	1.62	0.64
8:H:119:G:H8	8:H:119:G:O5'	1.80	0.64
18:S:17:GLU:HA	18:S:22:ILE:HA	1.79	0.64
25:3:734:LEU:HD12	25:3:767:LEU:HD22	1.79	0.64
27:w:387:TRP:CH2	33:v:84:ARG:HB3	2.20	0.64
7:G:88:G:O2'	7:G:89:U:H5'	1.98	0.64
17:R:65:PRO:CB	18:S:90:LEU:CB	2.75	0.64
22:X:483:PHE:CE1	22:X:917:GLN:HG3	2.32	0.64
24:1:662:HIS:CE1	24:1:700:LYS:HB3	2.32	0.64
3:C:492:ALA:O	3:C:551:LEU:HA	1.97	0.64
17:R:280:ILE:N	35:9:225:MET:HG3	2.09	0.64
22:X:523:HIS:O	22:X:525:ARG:HG2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:662:HIS:CD2	24:1:704:ILE:HG21	2.33	0.64
24:1:843:LYS:HB3	24:1:844:VAL:HG22	1.80	0.64
25:3:121:LEU:HB2	25:3:132:ILE:HD12	1.78	0.64
25:3:805:ASN:HB3	31:5:58:ASN:CB	2.26	0.64
1:A:857:ASN:OD1	1:A:860:GLN:N	2.24	0.64
1:A:1937:ILE:CG2	1:A:2011:ILE:O	2.46	0.64
3:C:227:LEU:HD11	3:C:239:THR:HG22	1.80	0.64
7:G:107:U:OP1	22:X:696:LYS:NZ	2.22	0.64
9:I:406:GLU:HA	9:I:410:GLN:HA	1.79	0.64
17:R:357:HIS:CD2	23:Y:276:LYS:HZ2	2.16	0.64
24:1:717:THR:O	24:1:719:TYR:N	2.30	0.64
25:3:568:MET:HA	25:3:574:LEU:HA	1.79	0.64
25:3:1017:ASN:OD1	25:3:1018:GLU:N	2.31	0.64
26:p:178:LYS:H	26:p:194:PHE:HA	1.62	0.64
17:R:408:ASP:OD1	17:R:409:GLN:N	2.30	0.64
1:A:767:VAL:HG21	2:B:39:C:O2'	1.98	0.64
1:A:1431:ALA:CB	22:X:329:TRP:CD1	2.81	0.64
4:D:1264:PRO:O	4:D:1286:PHE:N	2.27	0.64
22:X:171:ARG:O	22:X:174:ASP:HB3	1.98	0.64
1:A:221:ASN:O	2:B:11:U:H5''	1.97	0.64
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.13	0.64
25:3:512:GLY:HA3	25:3:515:ALA:HB3	1.80	0.64
25:3:545:VAL:HG12	25:3:546:LYS:HG2	1.79	0.64
1:A:248:ASP:OD1	1:A:248:ASP:N	2.27	0.64
1:A:2143:ARG:O	4:D:1264:PRO:CB	2.46	0.64
2:B:89:U:H2'	2:B:90:U:H5''	1.79	0.64
3:C:137:HIS:HB3	3:C:140:HIS:CE1	2.33	0.64
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.31	0.64
5:E:174:GLY:HA2	5:E:194:TYR:C	2.23	0.64
24:1:1120:ALA:HB2	24:1:1128:VAL:HG21	1.80	0.64
25:3:1004:ASP:OD1	25:3:1006:GLN:N	2.28	0.64
25:3:1115:GLU:CB	28:2:708:TRP:NE1	2.61	0.64
1:A:60:ASP:OD1	1:A:60:ASP:N	2.30	0.64
1:A:1607:GLU:HB3	1:A:1633:ALA:O	1.98	0.64
2:B:85:C:OP1	38:c:20:GLU:CA	2.46	0.64
8:H:18:U:O2'	8:H:19:G:O5'	2.16	0.64
13:N:116:ASN:OD1	13:N:116:ASN:N	2.31	0.64
24:1:568:ARG:NH1	24:1:605:GLY:H	1.96	0.64
25:3:1031:ARG:HG2	25:3:1031:ARG:HH11	1.63	0.64
1:A:393:LEU:HD12	3:C:379:LYS:HE2	1.80	0.64
1:A:1544:ARG:NE	1:A:1672:ASP:OD2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:138:LEU:HA	3:C:207:GLY:HA3	1.80	0.64
3:C:877:ALA:O	3:C:880:SER:OG	2.16	0.64
16:Q:700:ALA:O	16:Q:818:LEU:N	2.31	0.64
27:w:390:LYS:HZ1	33:v:84:ARG:CD	2.06	0.64
2:B:12:U:H2'	2:B:13:C:C6	2.33	0.63
3:C:925:PRO:HG2	3:C:928:HIS:CE1	2.33	0.63
5:E:69:VAL:HG11	5:E:351:LEU:HD21	1.80	0.63
19:T:351:ASP:O	19:T:352:THR:OG1	2.15	0.63
21:V:509:LEU:HG	21:V:553:HIS:HE1	1.62	0.63
25:3:1010:ILE:HG12	25:3:1026:ASP:HB3	1.80	0.63
30:7:10:PHE:HB3	30:7:12:ARG:HG2	1.79	0.63
22:X:937:ILE:HG22	22:X:941:LYS:HD2	1.80	0.63
24:1:826:ASP:OD1	24:1:827:ARG:N	2.31	0.63
25:3:260:ASN:OD1	25:3:261:PHE:N	2.30	0.63
25:3:794:SER:O	25:3:796:ASN:ND2	2.31	0.63
25:3:958:ARG:NH2	25:3:1014:TYR:OH	2.31	0.63
25:3:1201:PRO:HA	25:3:1204:VAL:HG22	1.80	0.63
35:9:211:LEU:O	35:9:215:PHE:HB3	1.98	0.63
1:A:386:PRO:HG3	3:C:372:PHE:CE1	2.33	0.63
5:E:153:PHE:O	5:E:172:ASP:N	2.30	0.63
5:E:321:TYR:HB3	5:E:323:LEU:HG	1.79	0.63
22:X:625:CYS:HA	22:X:628:LEU:HD12	1.80	0.63
22:X:878:HIS:CE1	22:X:1001:LEU:HB2	2.33	0.63
28:2:592:TYR:H	28:2:595:LYS:HB2	1.61	0.63
1:A:223:SER:N	2:B:12:U:OP1	2.31	0.63
1:A:385:GLU:CD	1:A:386:PRO:HD2	2.22	0.63
3:C:173:THR:O	3:C:177:ARG:HB2	1.98	0.63
7:G:108:U:H5''	22:X:676:ILE:HB	1.80	0.63
21:V:525:PHE:HB3	21:V:560:LEU:HD21	1.81	0.63
24:1:1302:TYR:HD1	25:3:915:LEU:HD13	1.62	0.63
25:3:1136:GLU:OE1	25:3:1136:GLU:N	2.27	0.63
27:w:388:ASP:OD1	33:v:84:ARG:HB3	1.98	0.63
28:2:516:GLY:HA2	33:v:60:LEU:CD2	2.21	0.63
1:A:442:LYS:HG3	1:A:610:HIS:CD2	2.29	0.63
1:A:615:ARG:O	1:A:618:THR:OG1	2.16	0.63
1:A:1402:ARG:HA	17:R:406:GLN:O	1.98	0.63
21:V:621:PRO:O	21:V:625:ARG:NE	2.32	0.63
22:X:194:ARG:O	22:X:194:ARG:HD3	1.99	0.63
24:1:625:ARG:NH1	24:1:659:GLN:OE1	2.31	0.63
24:1:699:GLN:HE22	24:1:738:HIS:CE1	2.15	0.63
25:3:105:GLU:OE1	30:7:17:VAL:HG12	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:434:SER:HG	25:3:436:ARG:HE	1.45	0.63
25:3:635:ALA:HB3	25:3:669:LEU:HD13	1.78	0.63
27:w:429:TRP:O	27:w:432:ALA:N	2.31	0.63
1:A:988:ILE:HD12	1:A:1030:ILE:HD12	1.81	0.63
4:D:1583:ASP:O	4:D:1585:GLN:N	2.31	0.63
6:F:24:A:OP2	13:N:111:THR:OG1	2.15	0.63
7:G:2:U:C5	11:K:219:PHE:CZ	2.87	0.63
21:V:490:CYS:HB2	21:V:525:PHE:CE2	2.32	0.63
22:X:715:SER:O	22:X:718:SER:OG	2.10	0.63
24:1:967:GLU:HG3	24:1:970:LEU:HB3	1.81	0.63
25:3:452:LEU:HD12	25:3:453:PRO:HD2	1.80	0.63
25:3:884:GLN:NE2	25:3:884:GLN:O	2.32	0.63
12:L:61:THR:OG1	12:L:62:GLU:N	2.31	0.63
17:R:170:LYS:H	17:R:170:LYS:HD2	1.64	0.63
25:3:207:THR:O	25:3:209:THR:HG22	1.99	0.63
30:7:39:PRO:HB2	30:7:70:TYR:HD1	1.63	0.63
35:9:75:THR:HA	35:9:82:LYS:HA	1.79	0.63
1:A:68:LYS:O	1:A:72:ASP:HB2	1.98	0.63
3:C:286:ASN:HD21	3:C:300:LEU:H	1.45	0.63
5:E:260:ARG:HD3	5:E:276:ILE:HG12	1.79	0.63
7:G:-10:G:H8	20:U:1:MET:HE3	1.63	0.63
27:w:429:TRP:HB3	27:w:430:ARG:HH12	1.63	0.63
2:B:90:U:H5	42:g:38:ASN:C	2.06	0.63
3:C:604:LEU:HD23	3:C:607:LEU:HD21	1.80	0.63
3:C:685:ILE:HD11	3:C:808:ILE:HD11	1.81	0.63
21:V:620:ASN:ND2	21:V:623:ASN:OD1	2.31	0.63
22:X:164:TRP:CE2	22:X:542:PHE:CB	2.82	0.63
23:Y:62:GLY:O	23:Y:107:GLN:NE2	2.30	0.63
25:3:747:SER:N	25:3:750:CYS:O	2.31	0.63
25:3:966:LEU:HB2	25:3:968:ARG:HD2	1.81	0.63
30:7:30:CYS:SG	30:7:31:VAL:N	2.72	0.63
30:7:52:GLY:H	30:7:55:GLN:HE21	1.47	0.63
33:v:58:LEU:HD23	33:v:78:HIS:CE1	2.34	0.63
42:l:61:VAL:HA	41:k:71:GLU:HA	1.80	0.63
1:A:332:TYR:O	3:C:888:ARG:NH2	2.31	0.62
1:A:858:GLN:O	1:A:862:GLU:HG3	1.98	0.62
1:A:1892:PRO:HG3	1:A:1941:ARG:HE	1.64	0.62
2:B:88:A:H2'	2:B:88:A:N3	2.14	0.62
10:J:339:TRP:HA	17:R:116:TYR:CD2	2.33	0.62
17:R:315:LYS:O	17:R:318:GLU:HG3	1.99	0.62
19:T:195:LYS:NZ	19:T:490:ARG:HH21	1.96	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:741:TRP:CH2	24:1:782:GLU:HB3	2.34	0.62
22:X:784:PRO:HB2	22:X:788:THR:OG1	1.98	0.62
23:Y:244:VAL:HG13	23:Y:313:VAL:HG22	1.80	0.62
25:3:70:LEU:HD11	25:3:152:LEU:HD13	1.80	0.62
27:w:434:GLY:O	27:w:438:LEU:HG	1.99	0.62
4:D:1192:PRO:HA	4:D:1198:LEU:HA	1.81	0.62
15:P:212:ASN:ND2	19:T:458:SER:OG	2.32	0.62
22:X:615:LEU:HB2	22:X:621:ILE:HG13	1.81	0.62
23:Y:230:LEU:HD13	23:Y:231:PRO:HD2	1.81	0.62
24:1:1066:LEU:HD22	24:1:1111:CYS:HB3	1.80	0.62
27:w:387:TRP:CZ3	33:v:84:ARG:O	2.52	0.62
27:w:388:ASP:OD2	33:v:84:ARG:CG	2.46	0.62
30:7:33:CYS:HB3	30:7:72:CYS:SG	2.39	0.62
4:D:912:ASN:HA	4:D:978:ASN:HA	1.81	0.62
22:X:164:TRP:CE2	22:X:542:PHE:HB3	2.34	0.62
22:X:230:SER:O	22:X:234:TYR:HB2	1.99	0.62
22:X:648:TYR:CE2	22:X:651:LEU:HB3	2.34	0.62
24:1:742:GLY:O	24:1:746:PHE:HB2	2.00	0.62
24:1:859:ASP:O	24:1:865:ARG:NE	2.27	0.62
24:1:1013:ILE:HD11	24:1:1049:TYR:CD2	2.34	0.62
25:3:105:GLU:OE1	30:7:17:VAL:CG1	2.48	0.62
25:3:1041:TYR:CB	28:2:705:ARG:HG3	2.29	0.62
28:2:469:VAL:HG12	28:2:471:ARG:H	1.62	0.62
1:A:246:LEU:HD11	1:A:411:PHE:HE1	1.63	0.62
1:A:381:PRO:HG2	3:C:334:ILE:HG22	1.81	0.62
1:A:1681:ARG:NH1	1:A:1681:ARG:HB3	2.14	0.62
5:E:206:ASP:C	5:E:222:LEU:HG	2.24	0.62
10:J:375:ASP:OD2	10:J:378:ASN:ND2	2.31	0.62
17:R:348:GLU:OE1	22:X:263:SER:C	2.43	0.62
17:R:388:ILE:HG21	22:X:653:SER:HB3	1.81	0.62
22:X:419:ILE:HG22	22:X:569:VAL:HG13	1.81	0.62
25:3:1193:VAL:HA	25:3:1196:GLU:HG2	1.81	0.62
41:k:28:GLN:O	41:k:45:CYS:HA	1.98	0.62
1:A:171:ASP:O	1:A:520:TYR:HB2	1.99	0.62
3:C:112:THR:HB	3:C:115:GLU:HB2	1.81	0.62
3:C:201:ASN:HB3	3:C:549:TRP:CZ3	2.33	0.62
7:G:115:C:H5"	17:R:371:ARG:O	1.99	0.62
17:R:352:ARG:CZ	22:X:265:HIS:HB3	2.30	0.62
23:Y:244:VAL:HG22	23:Y:313:VAL:HG13	1.82	0.62
30:7:46:CYS:O	30:7:50:ASN:HB2	1.99	0.62
1:A:340:ILE:HG22	1:A:355:LEU:HD13	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:PRO:HG2	1:A:351:TYR:HB2	1.80	0.62
1:A:361:HIS:O	1:A:362:ARG:NH1	2.32	0.62
3:C:510:LEU:HD13	3:C:514:TYR:CE2	2.34	0.62
3:C:665:THR:OG1	3:C:666:VAL:N	2.33	0.62
22:X:645:LEU:HD11	22:X:669:LYS:HD2	1.81	0.62
24:1:1217:PRO:HD3	28:2:590:LEU:HD13	1.79	0.62
25:3:565:TYR:CE1	25:3:619:LEU:HB2	2.33	0.62
25:3:1180:GLU:CD	25:3:1212:ARG:HH21	2.08	0.62
27:w:387:TRP:O	33:v:88:LYS:HB2	1.99	0.62
1:A:1878:ASP:OD1	1:A:1878:ASP:N	2.21	0.62
3:C:384:VAL:HA	3:C:392:LEU:HD11	1.82	0.62
10:J:328:GLY:O	10:J:332:VAL:HG13	2.00	0.62
12:L:192:ARG:HA	12:L:196:ILE:O	1.99	0.62
19:T:450:VAL:C	19:T:451:HIS:HD1	2.06	0.62
22:X:765:LEU:HD22	22:X:822:PRO:HG3	1.82	0.62
24:1:617:ILE:HD12	24:1:660:ALA:HB1	1.81	0.62
27:w:464:LEU:O	27:w:468:SER:OG	2.18	0.62
28:2:674:PRO:O	28:2:682:LEU:N	2.24	0.62
1:A:246:LEU:HD11	1:A:411:PHE:CE1	2.34	0.62
1:A:889:ARG:HD2	12:L:80:THR:HG22	1.81	0.62
5:E:176:VAL:HG22	5:E:196:VAL:HG21	1.80	0.62
17:R:348:GLU:OE2	22:X:267:ARG:N	2.32	0.62
22:X:250:LEU:HA	22:X:253:GLU:HG2	1.82	0.62
39:i:72:ILE:O	40:j:78:MET:N	2.31	0.62
1:A:1494:TYR:HB2	1:A:1744:ARG:HD3	1.82	0.62
1:A:1889:LEU:CG	1:A:2013:GLY:HA3	2.27	0.62
3:C:281:ILE:O	3:C:285:VAL:HG12	1.99	0.62
21:V:544:LEU:HD21	21:V:582:PHE:HB2	1.82	0.62
22:X:846:MET:HB3	22:X:881:LEU:HD22	1.82	0.62
24:1:550:HIS:HD2	24:1:551:LEU:HD22	1.64	0.62
24:1:1212:LEU:HD13	24:1:1237:LEU:HD13	1.81	0.62
25:3:318:ASP:OD1	25:3:319:GLU:N	2.33	0.62
25:3:325:ILE:O	25:3:374:SER:HA	2.00	0.62
25:3:1009:PHE:HZ	25:3:1046:GLY:HA3	1.64	0.62
35:9:306:ASN:HD21	35:9:344:SER:HA	1.65	0.62
16:Q:28:CYS:HA	16:Q:32:ALA:HB3	1.80	0.62
22:X:164:TRP:CD1	22:X:539:VAL:HA	2.35	0.62
22:X:283:TYR:CZ	23:Y:222:ILE:HG22	2.35	0.62
25:3:639:SER:OG	25:3:699:VAL:O	2.14	0.62
25:3:1133:THR:N	28:2:711:LEU:CD2	2.62	0.62
35:9:221:LEU:HA	35:9:224:THR:HB	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1160:ARG:HD3	15:P:192:VAL:HG21	1.82	0.61
1:A:1428:HIS:HE1	22:X:326:GLN:HB2	1.64	0.61
17:R:147:THR:HG23	19:T:360:VAL:CG2	2.30	0.61
23:Y:21:ARG:NH1	23:Y:83:VAL:O	2.33	0.61
24:1:1295:TYR:OH	31:5:29:TRP:HD1	1.82	0.61
25:3:233:ASN:ND2	25:3:233:ASN:H	1.95	0.61
33:v:85:ARG:HA	33:v:85:ARG:HH11	1.65	0.61
35:9:349:PRO:HB2	35:9:375:SER:HA	1.82	0.61
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.82	0.61
1:A:2328:ALA:HB3	4:D:728:ARG:CA	2.29	0.61
3:C:614:TYR:OH	3:C:643:ASP:OD2	2.17	0.61
5:E:114:GLU:OE2	5:E:290:ARG:NH2	2.32	0.61
5:E:300:ILE:HD11	5:E:314:THR:HG23	1.82	0.61
25:3:928:TYR:HB3	25:3:937:LEU:HB3	1.81	0.61
1:A:712:HIS:ND1	17:R:250:CYS:HB2	2.15	0.61
1:A:1143:MET:O	1:A:1147:VAL:HG13	1.99	0.61
1:A:1346:THR:O	1:A:1346:THR:OG1	2.15	0.61
1:A:1352:HIS:CD2	20:U:5:ILE:HG13	2.35	0.61
1:A:1428:HIS:CE1	22:X:326:GLN:HB2	2.35	0.61
3:C:116:MET:HA	3:C:119:LEU:HG	1.82	0.61
3:C:216:THR:HG22	3:C:245:HIS:HE1	1.65	0.61
4:D:1223:ILE:HA	4:D:1269:ARG:O	2.00	0.61
22:X:525:ARG:NH1	22:X:530:ASP:OD1	2.33	0.61
1:A:343:GLU:HG3	1:A:344:ASP:H	1.62	0.61
3:C:609:LYS:HA	3:C:612:LYS:HD2	1.82	0.61
22:X:810:THR:HA	22:X:813:ARG:HE	1.65	0.61
24:1:490:GLU:O	24:1:494:GLU:HG2	1.98	0.61
24:1:743:LEU:O	24:1:747:LEU:HB2	2.01	0.61
25:3:1041:TYR:CE2	28:2:705:ARG:NE	2.63	0.61
25:3:1041:TYR:CG	28:2:705:ARG:HG3	2.35	0.61
1:A:595:LYS:NZ	2:B:30:A:OP1	2.33	0.61
1:A:1403:LEU:N	17:R:407:TYR:HB3	2.15	0.61
14:O:256:GLY:HA3	14:O:279:ALA:HB1	1.82	0.61
17:R:63:ALA:H	18:S:131:ARG:CB	2.14	0.61
22:X:557:THR:HA	22:X:560:PHE:HB2	1.82	0.61
24:1:669:GLN:HB2	24:1:708:ALA:HA	1.83	0.61
24:1:953:ASP:O	24:1:956:SER:OG	2.18	0.61
25:3:384:THR:OG1	25:3:385:PHE:N	2.31	0.61
33:v:18:SER:N	33:v:21:GLU:OE1	2.34	0.61
35:9:358:LEU:HD22	35:9:396:ILE:HB	1.83	0.61
1:A:1427:ARG:NE	22:X:326:GLN:OE1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:811:THR:O	3:C:815:VAL:HG23	1.99	0.61
6:F:90:G:H2'	6:F:91:A:H8	1.65	0.61
6:F:96:U:H2'	6:F:97:U:C6	2.36	0.61
17:R:367:ARG:NH2	23:Y:274:ASP:OD2	2.33	0.61
21:V:606:GLU:OE2	21:V:609:GLN:HG3	1.99	0.61
22:X:197:LEU:HD12	22:X:197:LEU:O	2.00	0.61
25:3:883:GLU:OE2	25:3:884:GLN:N	2.33	0.61
35:9:279:LYS:HA	35:9:295:LEU:O	2.00	0.61
1:A:48:LYS:CD	1:A:53:PHE:HE1	2.00	0.61
1:A:1554:GLN:NE2	1:A:1558:THR:O	2.34	0.61
44:A:3000:IHP:H2	44:A:3000:IHP:O21	1.94	0.61
3:C:855:GLY:HA2	3:C:875:ILE:HD12	1.83	0.61
4:D:530:THR:C	4:D:532:ASN:H	2.09	0.61
17:R:331:ALA:HB2	22:X:275:ARG:NH2	2.16	0.61
24:1:495:ARG:HH21	24:1:530:PRO:HB3	1.66	0.61
25:3:139:LYS:NZ	25:3:160:ALA:O	2.34	0.61
25:3:293:HIS:NE2	25:3:295:THR:HB	2.15	0.61
33:v:34:ALA:O	33:v:38:ILE:HD12	2.01	0.61
1:A:362:ARG:HD2	21:V:333:GLN:CA	2.31	0.61
1:A:641:MET:O	1:A:645:THR:HG23	2.01	0.61
1:A:1298:ARG:HH11	1:A:1298:ARG:HB2	1.65	0.61
2:B:95:G:H2'	2:B:95:G:N3	2.15	0.61
4:D:2063:GLY:O	4:D:2110:SER:HA	1.99	0.61
13:N:43:VAL:CG2	13:N:47:TRP:CZ2	2.83	0.61
1:A:1610:GLN:HB3	1:A:1630:LEU:HB3	1.83	0.61
1:A:1766:GLN:NE2	1:A:2009:ASP:OD1	2.34	0.61
3:C:137:HIS:CD2	3:C:138:LEU:H	2.18	0.61
4:D:1662:ILE:HA	4:D:1703:VAL:O	2.01	0.61
15:P:206:LYS:O	15:P:218:GLU:HG3	2.01	0.61
19:T:250:ARG:HD2	19:T:266:GLU:HG3	1.81	0.61
22:X:488:SER:O	22:X:491:THR:OG1	2.10	0.61
24:1:834:VAL:O	24:1:838:VAL:HG23	2.01	0.61
25:3:207:THR:O	25:3:207:THR:OG1	2.15	0.61
25:3:330:PHE:O	25:3:390:ARG:NH2	2.32	0.61
33:v:76:LYS:O	33:v:80:THR:HG23	2.01	0.61
1:A:1949:ARG:HA	1:A:1952:VAL:HG12	1.83	0.61
3:C:476:CYS:O	3:C:564:THR:HA	2.01	0.61
4:D:1201:GLU:HA	4:D:1253:THR:HA	1.83	0.61
16:Q:27:ALA:O	16:Q:32:ALA:N	2.28	0.61
16:Q:313:ILE:HA	16:Q:320:ALA:HA	1.82	0.61
17:R:137:GLU:HA	17:R:140:ILE:HB	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:371:ARG:NH1	23:Y:282:CYS:CB	2.63	0.61
21:V:620:ASN:HB3	21:V:623:ASN:HD21	1.64	0.61
22:X:619:GLU:HA	22:X:622:GLU:OE1	2.01	0.61
25:3:25:THR:OG1	25:3:27:GLN:N	2.31	0.61
25:3:138:GLN:HG2	25:3:161:HIS:CE1	2.36	0.61
25:3:387:PHE:HE1	25:3:389:PRO:HG3	1.64	0.61
3:C:463:GLU:H	3:C:463:GLU:CD	2.08	0.60
3:C:560:VAL:HG12	3:C:561:LYS:H	1.65	0.60
4:D:1404:LYS:O	4:D:1423:ASN:N	2.33	0.60
5:E:208:ILE:O	5:E:219:VAL:HA	2.01	0.60
8:H:56:A:H4'	28:2:481:THR:HG1	1.61	0.60
22:X:803:ASN:OD1	22:X:806:GLY:N	2.32	0.60
24:1:595:GLU:O	24:1:599:ASN:ND2	2.33	0.60
25:3:12:THR:O	25:3:34:ARG:NH1	2.34	0.60
25:3:947:GLU:HB3	25:3:963:VAL:HG13	1.82	0.60
25:3:1116:SER:C	28:2:708:TRP:CH2	2.79	0.60
7:G:2:U:N3	11:K:219:PHE:CE2	2.69	0.60
8:H:106:G:N2	39:i:24:LYS:O	2.34	0.60
10:J:262:ARG:O	10:J:266:GLU:HG2	2.01	0.60
19:T:295:ASP:OD1	19:T:296:LEU:N	2.31	0.60
22:X:418:LEU:HD13	22:X:568:PRO:HG2	1.82	0.60
22:X:621:ILE:HG12	22:X:672:VAL:HG13	1.82	0.60
25:3:1041:TYR:CZ	28:2:705:ARG:NH2	2.68	0.60
41:k:19:LEU:HA	41:k:70:LEU:HA	1.83	0.60
1:A:1089:CYS:SG	1:A:1096:HIS:HD2	2.24	0.60
1:A:1431:ALA:HB2	22:X:329:TRP:CG	2.36	0.60
1:A:1935:ARG:O	1:A:1939:ILE:HG13	2.01	0.60
3:C:712:LYS:O	3:C:716:GLU:HG3	2.01	0.60
24:1:1028:HIS:O	24:1:1032:GLN:HB2	2.01	0.60
25:3:71:THR:O	25:3:146:ARG:NH2	2.34	0.60
4:D:668:ASP:O	4:D:672:GLY:N	2.34	0.60
4:D:1219:GLU:O	4:D:1240:LEU:HA	2.02	0.60
5:E:277:PHE:CE2	5:E:300:ILE:HG13	2.36	0.60
6:F:36:A:N6	7:G:10:U:O4	2.33	0.60
8:H:56:A:O3'	28:2:481:THR:CG2	2.48	0.60
12:L:105:ASP:OD1	22:X:305:ARG:NH1	2.35	0.60
13:N:43:VAL:O	13:N:47:TRP:CD1	2.54	0.60
13:N:43:VAL:HG22	13:N:47:TRP:CZ2	2.36	0.60
17:R:328:ALA:HB2	22:X:279:LEU:HD13	1.83	0.60
19:T:356:LEU:HD13	19:T:366:VAL:HB	1.82	0.60
22:X:754:GLU:HA	22:X:757:ARG:NH2	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:807:TYR:H	25:3:856:LYS:HD2	1.65	0.60
1:A:1131:LYS:NZ	1:A:1193:GLU:OE2	2.29	0.60
6:F:36:A:H3'	6:F:37:C:C5'	2.28	0.60
8:H:99:A:O2'	8:H:100:U:OP2	2.18	0.60
13:N:16:GLU:H	13:N:16:GLU:CD	2.09	0.60
17:R:382:ARG:NH2	17:R:385:ASN:HD22	1.99	0.60
17:R:408:ASP:OD1	17:R:410:ARG:N	2.24	0.60
23:Y:207:GLU:HA	23:Y:210:GLU:HB3	1.82	0.60
24:1:508:THR:HB	24:1:510:PRO:HD2	1.84	0.60
25:3:1115:GLU:CB	28:2:708:TRP:HZ2	2.07	0.60
29:4:17:VAL:O	29:4:56:TYR:HA	2.01	0.60
35:9:315:TYR:CE1	35:9:335:PRO:HG2	2.36	0.60
39:i:30:LYS:O	39:i:47:THR:HA	2.02	0.60
1:A:51:PHE:O	1:A:53:PHE:N	2.33	0.60
3:C:444:GLY:O	3:C:447:PRO:HD2	2.01	0.60
8:H:16:U:H1'	8:H:17:U:H5'	1.83	0.60
24:1:1166:ILE:O	24:1:1170:THR:HG22	2.01	0.60
25:3:615:ARG:NH2	25:3:630:MET:HB3	2.17	0.60
1:A:1457:HIS:ND1	1:A:1460:HIS:HD2	2.00	0.60
5:E:264:VAL:HA	5:E:272:ARG:NH1	2.16	0.60
7:G:-8:C:O4'	20:U:18:TYR:HB2	2.00	0.60
17:R:66:GLU:O	18:S:89:ASP:CB	2.50	0.60
24:1:664:GLY:HA2	24:1:667:ILE:HD12	1.82	0.60
27:w:432:ALA:O	27:w:436:ARG:HD3	2.01	0.60
28:2:477:MET:SD	28:2:478:HIS:ND1	2.75	0.60
35:9:330:ILE:HD13	35:9:410:MET:HB3	1.84	0.60
1:A:361:HIS:HB2	3:C:280:HIS:CE1	2.36	0.60
1:A:1286:ASP:OD1	1:A:1286:ASP:N	2.26	0.60
8:H:29:A:N6	12:L:32:SER:OG	2.34	0.60
12:L:227:THR:HG1	17:R:84:ASN:HB2	1.66	0.60
14:O:233:THR:O	14:O:303:GLY:N	2.29	0.60
17:R:280:ILE:H	35:9:225:MET:CG	2.12	0.60
19:T:446:ASN:HD21	19:T:449:ARG:HE	1.49	0.60
23:Y:192:GLY:N	23:Y:195:GLU:OE2	2.35	0.60
24:1:1192:VAL:O	24:1:1196:SER:OG	2.20	0.60
35:9:316:TYR:HE1	35:9:378:SER:HB2	1.66	0.60
3:C:724:TRP:HE1	3:C:732:ILE:HD11	1.66	0.60
16:Q:489:VAL:O	16:Q:494:PRO:HD3	2.02	0.60
17:R:86:LEU:HD23	17:R:86:LEU:H	1.66	0.60
22:X:837:SER:O	22:X:841:LEU:HG	2.02	0.60
24:1:617:ILE:HD13	24:1:651:VAL:HB	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:1252:GLN:NE2	28:2:497:SER:OG	2.34	0.60
28:2:507:LYS:HD2	28:2:507:LYS:N	2.16	0.60
1:A:292:ASP:CG	1:A:293:TRP:H	2.10	0.60
1:A:570:ASP:OD1	1:A:571:ALA:N	2.34	0.60
1:A:1644:LEU:HD23	1:A:1715:TYR:HD1	1.67	0.60
18:S:147:THR:HA	18:S:153:PRO:HA	1.82	0.60
24:1:1295:TYR:HH	31:5:29:TRP:HD1	1.50	0.60
25:3:191:GLU:O	25:3:194:ASN:N	2.26	0.60
1:A:467:GLN:HE21	1:A:469:LYS:HG2	1.67	0.59
1:A:1303:LEU:HD12	1:A:1311:PHE:CE1	2.37	0.59
7:G:1:G:N9	11:K:218:LYS:HD2	2.16	0.59
24:1:590:ARG:O	24:1:594:ARG:HB2	2.02	0.59
25:3:910:ALA:HB1	25:3:913:LEU:HD11	1.83	0.59
25:3:994:GLN:HE22	25:3:1036:ALA:C	2.10	0.59
1:A:1124:ASN:ND2	1:A:1148:ASN:OD1	2.32	0.59
1:A:1189:MET:CG	1:A:1190:CYS:H	2.14	0.59
1:A:1581:LEU:O	1:A:1585:ILE:HG13	2.03	0.59
2:B:95:G:N2	2:B:96:A:H5"	2.13	0.59
3:C:630:LEU:HD21	3:C:661:THR:HG21	1.84	0.59
5:E:330:ILE:HA	5:E:346:SER:HA	1.83	0.59
17:R:66:GLU:HA	18:S:90:LEU:N	2.17	0.59
17:R:137:GLU:OE1	17:R:137:GLU:N	2.31	0.59
24:1:619:ASN:OD1	24:1:620:MET:N	2.32	0.59
25:3:212:GLU:HB2	25:3:223:LYS:HG3	1.84	0.59
1:A:875:HIS:HE1	22:X:866:ASN:HB3	1.66	0.59
4:D:754:GLU:CA	25:3:662:PHE:HD1	2.13	0.59
12:L:69:GLU:OE1	35:9:220:ILE:HD11	2.03	0.59
20:U:26:VAL:O	21:V:513:ARG:NH1	2.35	0.59
22:X:424:THR:HG21	22:X:728:ARG:HH21	1.67	0.59
24:1:605:GLY:O	24:1:608:THR:OG1	2.16	0.59
24:1:677:CYS:O	24:1:680:LEU:HD12	2.01	0.59
25:3:329:TYR:CE2	25:3:389:PRO:HA	2.37	0.59
31:5:65:ARG:HB3	31:5:65:ARG:CZ	2.32	0.59
1:A:184:ASP:HB2	13:N:1:MET:CA	2.31	0.59
1:A:848:GLU:OE1	17:R:424:GLY:HA2	2.02	0.59
2:B:87:A:N6	2:B:91:U:O3'	2.36	0.59
13:N:44:GLU:HA	13:N:47:TRP:CD2	2.37	0.59
14:O:116:TYR:O	14:O:120:ASN:ND2	2.35	0.59
17:R:150:ALA:O	17:R:153:LYS:HG3	2.02	0.59
22:X:405:ARG:HG3	22:X:435:TYR:CE2	2.37	0.59
1:A:388:LEU:HG	3:C:399:LEU:HD21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:531:TRP:CE3	3:C:540:GLU:HB3	2.37	0.59
5:E:180:ASP:HB2	5:E:187:ILE:HD11	1.84	0.59
10:J:238:ASN:C	10:J:240:THR:H	2.11	0.59
22:X:537:LYS:HD2	22:X:563:PHE:CE1	2.38	0.59
24:1:630:ARG:HG3	24:1:670:GLN:HG3	1.83	0.59
25:3:435:LEU:HD13	25:3:799:ILE:HD11	1.84	0.59
25:3:680:ASP:OD2	25:3:681:PRO:HD2	2.02	0.59
1:A:525:LYS:HB3	11:K:197:TYR:CD2	2.35	0.59
1:A:1211:ASP:O	1:A:1213:VAL:N	2.36	0.59
1:A:1870:ASP:OD1	1:A:1870:ASP:N	2.26	0.59
6:F:85:U:O2	8:H:14:C:N3	2.36	0.59
22:X:877:ASP:OD1	22:X:877:ASP:N	2.36	0.59
1:A:179:ALA:HA	1:A:183:LEU:HB2	1.84	0.59
1:A:693:ILE:O	1:A:695:ASP:N	2.34	0.59
3:C:133:THR:OG1	3:C:203:MET:HB3	2.02	0.59
16:Q:1306:ARG:O	16:Q:1310:PHE:CB	2.51	0.59
17:R:367:ARG:NH1	23:Y:281:LEU:HD23	2.18	0.59
21:V:613:GLU:OE1	21:V:618:ARG:NH2	2.36	0.59
22:X:182:ALA:N	22:X:924:ARG:NH1	2.50	0.59
23:Y:3:VAL:HG23	23:Y:16:LEU:HD21	1.85	0.59
24:1:1258:ALA:HB3	24:1:1261:VAL:HG13	1.83	0.59
35:9:42:CYS:N	35:9:47:GLN:O	2.33	0.59
35:9:366:LEU:HD11	35:9:380:PHE:HB2	1.84	0.59
1:A:1502:PHE:HZ	1:A:1505:LYS:HB2	1.68	0.59
1:A:1837:ALA:O	1:A:1841:THR:HG23	2.02	0.59
1:A:1888:GLU:O	1:A:2014:MET:HB2	2.02	0.59
1:A:2328:ALA:H	4:D:728:ARG:CA	2.15	0.59
9:I:106:MET:O	9:I:110:PRO:CG	2.50	0.59
21:V:505:LYS:NZ	21:V:593:TYR:OH	2.35	0.59
23:Y:33:LYS:HG3	23:Y:161:ILE:HG13	1.85	0.59
25:3:214:ASP:O	25:3:218:ASN:N	2.33	0.59
25:3:758:SER:N	25:3:761:THR:O	2.25	0.59
26:p:185:GLY:HA2	27:w:485:ASN:ND2	2.17	0.59
1:A:2276:GLN:CA	4:D:1151:GLU:CB	2.81	0.59
6:F:41:A:H2	7:G:6:A:N1	2.01	0.59
14:O:38:LYS:N	17:R:200:VAL:O	2.27	0.59
16:Q:1322:GLN:HA	16:Q:1325:ALA:HB2	1.85	0.59
19:T:255:SER:OG	19:T:258:SER:O	2.19	0.59
22:X:741:TRP:NE1	24:1:781:ASP:HA	2.17	0.59
24:1:1137:ARG:NH1	28:2:522:PHE:O	2.36	0.59
25:3:69:ARG:NH1	25:3:74:THR:HA	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:700:LYS:HE2	25:3:715:MET:HB3	1.84	0.59
25:3:706:MET:HG3	25:3:707:GLN:HG2	1.83	0.59
1:A:712:HIS:CE1	17:R:250:CYS:SG	2.96	0.59
3:C:500:THR:HG22	3:C:545:PRO:HA	1.83	0.59
5:E:345:ALA:HA	5:E:351:LEU:HD23	1.84	0.59
6:F:43:A:H2	7:G:4:A:H61	1.50	0.59
8:H:48:A:C2	8:H:65:U:H2'	2.37	0.59
17:R:91:ASP:OD1	17:R:94:GLY:N	2.36	0.59
17:R:240:LYS:O	17:R:244:GLU:HG3	2.03	0.59
19:T:383:ARG:O	19:T:384:HIS:ND1	2.31	0.59
42:I:36:GLU:O	42:I:39:MET:N	2.25	0.59
1:A:1937:ILE:HG21	1:A:2012:LEU:HA	1.84	0.58
3:C:493:PHE:HD2	3:C:551:LEU:HG	1.67	0.58
21:V:542:ASN:OD1	21:V:545:ARG:NH2	2.35	0.58
22:X:960:ARG:HG3	22:X:967:THR:HA	1.84	0.58
24:1:747:LEU:HA	24:1:750:ILE:HG12	1.85	0.58
24:1:854:VAL:HG23	24:1:855:ASP:H	1.68	0.58
25:3:876:THR:O	25:3:876:THR:OG1	2.12	0.58
1:A:41:GLN:HG3	1:A:45:TYR:HB3	1.85	0.58
1:A:442:LYS:HG2	1:A:610:HIS:NE2	2.14	0.58
1:A:840:ILE:CG2	17:R:418:MET:HE1	2.33	0.58
1:A:1427:ARG:HE	22:X:326:GLN:CD	2.11	0.58
6:F:89:U:H2'	6:F:90:G:O4'	2.03	0.58
20:U:26:VAL:CB	21:V:517:LEU:CD2	2.77	0.58
22:X:171:ARG:HD3	22:X:509:PRO:HB3	1.84	0.58
23:Y:51:ILE:O	23:Y:109:LEU:HA	2.02	0.58
24:1:898:TYR:OH	24:1:902:GLU:HG2	2.04	0.58
25:3:387:PHE:CE1	25:3:389:PRO:HG3	2.38	0.58
1:A:138:PRO:O	1:A:142:SER:OG	2.14	0.58
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.71	0.58
1:A:2267:PHE:CB	4:D:1263:PRO:HA	2.33	0.58
3:C:80:ILE:HD11	19:T:198:ARG:HD3	1.84	0.58
7:G:85:G:H2'	7:G:86:A:C8	2.38	0.58
8:H:13:C:H1'	8:H:14:C:H5'	1.84	0.58
11:K:218:LYS:HE2	11:K:218:LYS:O	2.03	0.58
13:N:44:GLU:H	13:N:44:GLU:CD	2.11	0.58
17:R:371:ARG:HH12	23:Y:282:CYS:CB	2.15	0.58
22:X:591:TYR:HD2	22:X:692:PRO:HB2	1.68	0.58
24:1:698:GLN:HB3	24:1:701:VAL:HG12	1.84	0.58
24:1:759:ALA:O	24:1:763:ASN:N	2.35	0.58
24:1:815:PHE:HZ	24:1:849:ILE:HG23	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:1074:ARG:NE	24:1:1107:GLN:HE22	2.00	0.58
25:3:246:SER:OG	25:3:247:GLY:N	2.35	0.58
25:3:583:MET:HE2	25:3:583:MET:HA	1.85	0.58
40:j:46:CYS:O	40:j:59:ASP:N	2.35	0.58
1:A:1817:LEU:HD11	1:A:1819:LEU:HD13	1.84	0.58
3:C:125:ASN:OD1	3:C:128:LEU:N	2.25	0.58
3:C:379:LYS:O	3:C:383:GLN:HG2	2.04	0.58
5:E:108:HIS:CD2	5:E:128:SER:HB3	2.38	0.58
7:G:7:G:C5	7:G:8:C:C4	2.92	0.58
22:X:219:ARG:HA	22:X:222:MET:SD	2.43	0.58
22:X:524:GLU:OE2	22:X:529:THR:OG1	2.20	0.58
23:Y:118:TYR:N	23:Y:118:TYR:CD1	2.72	0.58
24:1:1295:TYR:HH	31:5:29:TRP:CD1	2.21	0.58
25:3:642:ILE:H	25:3:703:ARG:HE	1.52	0.58
28:2:542:GLU:O	28:2:546:GLN:HG2	2.03	0.58
35:9:375:SER:O	35:9:375:SER:OG	2.22	0.58
1:A:361:HIS:HB2	3:C:280:HIS:CG	2.37	0.58
3:C:352:LYS:HE2	3:C:352:LYS:H	1.67	0.58
8:H:6:U:H2'	8:H:7:U:C6	2.38	0.58
13:N:63:LEU:HB3	13:N:70:ILE:HD12	1.85	0.58
24:1:850:ILE:O	24:1:854:VAL:HG13	2.04	0.58
25:3:195:ASP:OD2	25:3:198:GLY:N	2.36	0.58
27:w:411:CYS:SG	27:w:416:TYR:OH	2.61	0.58
33:v:56:CYS:SG	33:v:72:HIS:NE2	2.73	0.58
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.36	0.58
1:A:2308:VAL:CA	4:D:1125:SER:CA	2.80	0.58
6:F:22:A:C5'	13:N:115:THR:HB	2.33	0.58
8:H:125:G:H2'	8:H:126:A:H8	1.67	0.58
17:R:369:LEU:HD23	17:R:377:ARG:HA	1.85	0.58
22:X:797:TYR:HA	22:X:802:LEU:HB2	1.84	0.58
22:X:1004:GLU:HB2	22:X:1007:TRP:CD2	2.38	0.58
24:1:512:ARG:O	24:1:516:LEU:HB2	2.04	0.58
24:1:1104:GLN:O	24:1:1105:GLU:HB3	2.03	0.58
25:3:528:ARG:HG2	25:3:532:ARG:HH21	1.67	0.58
25:3:1147:HIS:O	25:3:1151:GLU:HG3	2.03	0.58
1:A:1889:LEU:HD13	1:A:2014:MET:O	1.97	0.58
2:B:20:G:O6	2:B:57:G:N2	2.37	0.58
3:C:115:GLU:OE1	3:C:115:GLU:N	2.37	0.58
3:C:441:PRO:HA	3:C:444:GLY:HA3	1.86	0.58
5:E:334:ALA:HB3	5:E:343:ILE:HG23	1.85	0.58
7:G:1:G:N7	11:K:218:LYS:HD2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:408:ASP:OD1	10:J:408:ASP:N	2.36	0.58
13:N:72:ARG:O	13:N:76:GLU:HG3	2.02	0.58
22:X:694:PHE:O	22:X:722:ARG:NH1	2.26	0.58
22:X:698:LYS:NZ	22:X:758:THR:HA	2.17	0.58
22:X:987:HIS:HB3	22:X:999:GLN:HB2	1.85	0.58
23:Y:42:ILE:HG21	23:Y:51:ILE:HG22	1.84	0.58
24:1:1066:LEU:HD22	24:1:1111:CYS:CB	2.34	0.58
25:3:982:GLU:HG2	25:3:984:LYS:HE3	1.84	0.58
28:2:509:LYS:HE3	28:2:509:LYS:CA	2.34	0.58
1:A:1251:SER:OG	1:A:1298:ARG:HD3	2.04	0.58
5:E:208:ILE:HG13	5:E:222:LEU:HD21	1.86	0.58
7:G:2:U:O4	11:K:219:PHE:CE1	2.57	0.58
8:H:50:C:H2'	8:H:51:A:C8	2.38	0.58
8:H:180:G:H2'	8:H:181:G:C8	2.38	0.58
11:K:205:TYR:O	11:K:209:GLY:N	2.37	0.58
17:R:315:LYS:HZ2	23:Y:191:ILE:HG12	1.66	0.58
21:V:456:ARG:NE	21:V:492:MET:SD	2.76	0.58
23:Y:5:LEU:HD22	23:Y:156:ILE:HG23	1.85	0.58
23:Y:90:LYS:HB2	23:Y:93:THR:HG23	1.84	0.58
23:Y:126:PHE:C	23:Y:126:PHE:CD2	2.82	0.58
24:1:675:MET:HB3	24:1:678:ALA:HB3	1.84	0.58
25:3:449:VAL:HG22	25:3:763:ARG:HB3	1.85	0.58
1:A:1819:LEU:HD22	1:A:1902:PHE:HD1	1.67	0.58
2:B:95:G:O2'	39:d:24:LYS:C	2.46	0.58
24:1:1074:ARG:O	24:1:1078:VAL:HG23	2.03	0.58
25:3:447:MET:HE2	25:3:766:ALA:HB2	1.86	0.58
25:3:538:THR:OG1	25:3:542:LYS:O	2.22	0.58
35:9:366:LEU:HD13	35:9:382:ILE:HG13	1.86	0.58
1:A:1502:PHE:CZ	1:A:1505:LYS:HB2	2.37	0.58
3:C:543:ARG:CZ	3:C:543:ARG:HB2	2.34	0.58
7:G:88:G:H4'	7:G:89:U:OP1	2.04	0.58
17:R:65:PRO:O	18:S:89:ASP:O	2.21	0.58
22:X:235:LEU:HD22	23:Y:220:GLN:CD	2.28	0.58
22:X:451:THR:HG22	22:X:519:VAL:HA	1.86	0.58
22:X:543:ARG:NE	22:X:545:GLU:OE1	2.34	0.58
22:X:741:TRP:NE1	24:1:781:ASP:CG	2.61	0.58
25:3:345:GLY:O	25:3:360:GLN:HG3	2.04	0.58
25:3:365:GLY:HA2	25:3:394:ASN:ND2	2.19	0.58
28:2:602:LYS:HE3	28:2:602:LYS:O	2.04	0.58
43:o:64:ARG:HA	43:o:88:PRO:HD2	1.85	0.58
3:C:925:PRO:O	3:C:928:HIS:ND1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:37:C:H4'	6:F:38:G:OP2	2.00	0.57
7:G:2:U:C4	11:K:219:PHE:CD2	2.92	0.57
22:X:583:TYR:HB3	22:X:739:THR:HA	1.86	0.57
22:X:948:PHE:O	22:X:1016:TYR:OH	2.21	0.57
25:3:310:ILE:O	25:3:311:PHE:HD2	1.87	0.57
30:7:33:CYS:HB2	30:7:74:GLU:OE1	2.04	0.57
35:9:312:LYS:NZ	35:9:436:ASP:OD2	2.37	0.57
35:9:360:HIS:HB3	35:9:365:ILE:HG21	1.85	0.57
3:C:803:ARG:O	3:C:807:GLN:HG2	2.04	0.57
8:H:68:G:H2'	8:H:69:U:C6	2.39	0.57
23:Y:30:LYS:HE3	23:Y:169:PRO:HD2	1.86	0.57
23:Y:263:PHE:CE1	23:Y:300:LYS:HD2	2.40	0.57
1:A:361:HIS:CB	3:C:280:HIS:CG	2.87	0.57
3:C:439:PRO:O	3:C:443:VAL:HB	2.04	0.57
6:F:82:A:H1'	6:F:83:A:H2'	1.85	0.57
23:Y:152:GLN:NE2	23:Y:193:ALA:HA	2.19	0.57
24:1:703:THR:HG22	24:1:745:ALA:HB3	1.87	0.57
25:3:329:TYR:HE2	25:3:389:PRO:HA	1.69	0.57
25:3:462:VAL:O	25:3:472:ALA:N	2.30	0.57
25:3:638:GLU:OE2	25:3:698:PRO:HB3	2.04	0.57
25:3:1148:LEU:HA	25:3:1151:GLU:OE2	2.05	0.57
35:9:363:ARG:HG3	35:9:384:PHE:HA	1.86	0.57
1:A:38:GLN:OE1	1:A:38:GLN:HA	2.02	0.57
1:A:1220:VAL:HG23	1:A:1221:THR:HG23	1.87	0.57
2:B:63:A:H2'	2:B:64:G:H8	1.67	0.57
12:L:213:GLU:OE1	14:O:108:PRO:HA	2.04	0.57
21:V:515:CYS:HA	21:V:521:TYR:HB2	1.84	0.57
22:X:182:ALA:CA	22:X:924:ARG:HH11	2.17	0.57
22:X:257:PHE:CZ	22:X:270:LEU:HB2	2.39	0.57
22:X:910:ARG:O	22:X:914:VAL:HG13	2.03	0.57
24:1:1266:TRP:CZ3	31:5:22:GLY:HA3	2.39	0.57
25:3:477:SER:CB	25:3:505:THR:H	2.11	0.57
25:3:479:VAL:HG23	25:3:480:ASN:ND2	2.20	0.57
28:2:457:MET:HE3	28:2:457:MET:HA	1.86	0.57
28:2:498:VAL:CG2	28:2:588:GLY:HA2	2.34	0.57
1:A:1403:LEU:H	17:R:407:TYR:HB3	1.69	0.57
1:A:1639:VAL:HG22	1:A:1719:PHE:HB3	1.86	0.57
1:A:1861:ILE:HG23	1:A:1884:ILE:HG23	1.86	0.57
1:A:2005:SER:HB2	1:A:2008:ARG:HH22	1.70	0.57
5:E:102:TYR:HD1	5:E:102:TYR:H	1.51	0.57
8:H:70:C:H2'	8:H:71:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:352:ARG:HH12	22:X:265:HIS:HB3	1.68	0.57
17:R:371:ARG:CZ	23:Y:282:CYS:HB2	2.34	0.57
22:X:521:GLU:HB3	22:X:523:HIS:CE1	2.38	0.57
23:Y:8:THR:HG23	23:Y:155:ARG:HB2	1.86	0.57
25:3:616:ILE:HG22	25:3:628:LEU:HB3	1.86	0.57
27:w:425:HIS:HA	27:w:428:GLU:HB2	1.85	0.57
31:5:7:ILE:HG13	31:5:8:HIS:N	2.18	0.57
1:A:1941:ARG:HH22	1:A:2012:LEU:C	2.13	0.57
2:B:96:A:N6	41:f:23:GLY:H	2.02	0.57
3:C:572:GLU:CD	3:C:573:GLU:H	2.11	0.57
4:D:668:ASP:O	4:D:672:GLY:CA	2.53	0.57
5:E:259:VAL:HG22	5:E:277:PHE:HB2	1.85	0.57
6:F:22:A:O5'	13:N:115:THR:HB	2.04	0.57
15:P:184:VAL:HG13	23:Y:50:ILE:HD13	1.77	0.57
15:P:216:ARG:NH1	35:9:257:PRO:HG3	2.20	0.57
21:V:609:GLN:HA	21:V:612:PHE:HB2	1.85	0.57
23:Y:74:GLN:CD	23:Y:74:GLN:H	2.13	0.57
24:1:1078:VAL:HG12	24:1:1118:ILE:HD12	1.85	0.57
30:7:68:ASP:OD1	30:7:68:ASP:N	2.38	0.57
35:9:308:ILE:HA	35:9:311:CYS:HB2	1.87	0.57
35:9:316:TYR:CE1	35:9:378:SER:HB2	2.39	0.57
1:A:1275:ARG:O	1:A:1369:TYR:HE1	1.88	0.57
3:C:670:SER:HB2	3:C:689:ALA:H	1.70	0.57
5:E:81:LEU:O	5:E:92:LEU:HA	2.04	0.57
10:J:406:PHE:HD1	10:J:411:MET:HA	1.69	0.57
22:X:238:ARG:HE	23:Y:224:LEU:CD1	2.17	0.57
25:3:552:ARG:HH21	25:3:567:GLU:HB3	1.69	0.57
1:A:2307:GLU:O	4:D:1125:SER:CA	2.53	0.57
3:C:78:GLU:HG3	3:C:79:THR:N	2.18	0.57
10:J:333:PHE:O	10:J:337:MET:HG2	2.05	0.57
22:X:238:ARG:HH12	23:Y:319:VAL:CG2	2.17	0.57
22:X:283:TYR:CE2	23:Y:222:ILE:HG21	2.39	0.57
24:1:631:ALA:O	24:1:635:VAL:HG13	2.05	0.57
25:3:607:VAL:HB	25:3:615:ARG:HB2	1.85	0.57
25:3:1140:PHE:HE1	25:3:1197:LEU:HD13	1.67	0.57
31:5:14:LEU:HA	31:5:17:LYS:HB2	1.86	0.57
1:A:123:THR:O	1:A:123:THR:OG1	2.23	0.57
1:A:357:ASN:ND2	3:C:862:PRO:HB3	2.16	0.57
1:A:1978:LYS:O	1:A:1981:VAL:HG12	2.05	0.57
1:A:2228:TYR:HA	1:A:2258:ARG:HA	1.86	0.57
3:C:216:THR:HG22	3:C:245:HIS:CE1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:704:VAL:HG12	3:C:717:PHE:HE1	1.68	0.57
5:E:75:HIS:ND1	5:E:77:ASN:HB2	2.19	0.57
5:E:197:LEU:HD21	5:E:213:ILE:HD11	1.87	0.57
10:J:300:ASP:OD2	17:R:101:ILE:CD1	2.53	0.57
10:J:360:ASP:O	10:J:364:THR:OG1	2.22	0.57
17:R:389:SER:HA	17:R:392:ILE:HD12	1.87	0.57
22:X:707:GLU:O	22:X:990:VAL:HA	2.05	0.57
25:3:1200:THR:O	25:3:1203:GLU:N	2.37	0.57
1:A:250:VAL:HG23	1:A:251:ASP:OD2	2.05	0.57
1:A:362:ARG:HD2	21:V:333:GLN:HA	1.87	0.57
1:A:827:PHE:HB2	1:A:1002:ASP:OD2	2.04	0.57
1:A:872:ASP:O	1:A:874:PRO:HD3	2.04	0.57
1:A:1771:LEU:HD13	1:A:1777:ILE:HD12	1.86	0.57
1:A:1836:LEU:HA	1:A:1839:TRP:HD1	1.70	0.57
1:A:1862:ILE:HG23	1:A:1885:LYS:HB3	1.86	0.57
3:C:560:VAL:HG12	3:C:561:LYS:HG2	1.87	0.57
7:G:111:U:P	22:X:482:ARG:HB2	2.45	0.57
13:N:97:TYR:HD1	13:N:120:ARG:HH21	1.53	0.57
17:R:367:ARG:CZ	23:Y:281:LEU:HD23	2.35	0.57
21:V:576:THR:O	21:V:579:SER:OG	2.16	0.57
22:X:265:HIS:O	22:X:268:GLN:HG2	2.04	0.57
23:Y:263:PHE:HE1	23:Y:300:LYS:HD2	1.69	0.57
24:1:716:ALA:O	24:1:756:LEU:HD21	2.05	0.57
24:1:1056:MET:HE2	24:1:1096:THR:HG21	1.86	0.57
24:1:1304:LEU:HD23	25:3:786:ARG:NH2	2.20	0.57
30:7:13:LYS:NZ	30:7:48:GLU:OE1	2.26	0.57
35:9:321:PHE:N	35:9:426:ILE:O	2.38	0.57
42:1:43:MET:O	42:1:60:GLN:HA	2.05	0.57
1:A:1116:GLU:OE1	15:P:196:ASN:ND2	2.37	0.56
1:A:1403:LEU:HB2	17:R:407:TYR:CD1	2.40	0.56
1:A:1923:TRP:HB3	1:A:1927:ILE:HD11	1.87	0.56
2:B:53:U:OP1	15:P:39:THR:OG1	2.23	0.56
6:F:35:A:OP1	12:L:203:LYS:NZ	2.38	0.56
7:G:116:C:C6	17:R:370:SER:O	2.58	0.56
8:H:41:U:H2'	8:H:42:G:C8	2.39	0.56
12:L:38:LEU:HB3	12:L:41:LYS:HB2	1.87	0.56
15:P:39:THR:O	19:T:318:ARG:HD3	2.05	0.56
23:Y:67:PHE:HB2	23:Y:75:ALA:O	2.05	0.56
24:1:784:MET:O	24:1:788:VAL:HG12	2.05	0.56
1:A:1889:LEU:HA	1:A:2014:MET:HB2	1.86	0.56
1:A:1937:ILE:HG22	1:A:2011:ILE:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1971:LEU:HD22	1:A:1972:THR:H	1.70	0.56
3:C:928:HIS:ND1	3:C:928:HIS:N	2.53	0.56
8:H:56:A:O2'	28:2:478:HIS:CA	2.53	0.56
23:Y:55:ASP:OD2	23:Y:60:GLY:N	2.37	0.56
24:1:557:ASP:HB2	24:1:558:ARG:NH2	2.20	0.56
24:1:954:LEU:O	24:1:958:THR:HG22	2.05	0.56
25:3:141:VAL:HB	25:3:158:LEU:HD12	1.86	0.56
25:3:169:HIS:CD2	25:3:170:VAL:H	2.23	0.56
25:3:326:ARG:NE	25:3:372:GLU:OE2	2.19	0.56
26:p:213:THR:O	26:p:215:SER:N	2.38	0.56
1:A:532:THR:HG23	1:A:536:LYS:HE3	1.86	0.56
1:A:731:LEU:O	35:9:241:TYR:CB	2.43	0.56
1:A:1402:ARG:HD2	22:X:664:PRO:HB2	1.87	0.56
2:B:87:A:C6	2:B:92:U:OP2	2.59	0.56
4:D:434:SER:HA	4:D:446:HIS:O	2.06	0.56
6:F:87:C:C2	6:F:88:G:C8	2.94	0.56
6:F:89:U:H3	8:H:9:U:H3	1.52	0.56
9:I:92:TYR:CB	16:Q:953:ASN:CB	2.83	0.56
13:N:97:TYR:HA	13:N:120:ARG:HH21	1.71	0.56
21:V:570:LEU:HD13	21:V:627:ALA:HB1	1.87	0.56
22:X:596:VAL:O	22:X:600:LEU:HG	2.05	0.56
22:X:598:SER:O	22:X:602:ILE:HG13	2.05	0.56
22:X:716:LYS:N	22:X:747:LEU:HD12	2.20	0.56
23:Y:268:SER:OG	23:Y:287:GLU:OE2	2.16	0.56
24:1:1139:PRO:O	33:v:51:LEU:HA	2.05	0.56
25:3:525:ARG:HD3	25:3:533:VAL:HG22	1.85	0.56
25:3:717:SER:HB2	25:3:718:ARG:NH1	2.21	0.56
29:4:13:ALA:O	29:4:60:GLU:HA	2.06	0.56
35:9:278:LYS:HG2	35:9:279:LYS:H	1.69	0.56
1:A:170:ASP:OD1	1:A:171:ASP:N	2.38	0.56
1:A:525:LYS:HB2	1:A:525:LYS:HZ3	1.70	0.56
1:A:587:GLN:HB3	1:A:1550:GLY:O	2.05	0.56
1:A:1359:HIS:HD2	1:A:1361:GLU:O	1.89	0.56
3:C:258:ASN:OD1	3:C:259:LYS:N	2.38	0.56
3:C:510:LEU:HB2	3:C:564:THR:HG23	1.87	0.56
8:H:165:A:O2'	8:H:166:G:O5'	2.24	0.56
10:J:342:GLU:OE2	10:J:344:GLN:N	2.37	0.56
12:L:187:LYS:O	12:L:191:LEU:N	2.35	0.56
17:R:348:GLU:CD	22:X:263:SER:N	2.64	0.56
17:R:372:ALA:HB3	17:R:376:LYS:HE2	1.87	0.56
19:T:381:HIS:HD2	19:T:441:TRP:CE2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:604:LYS:NZ	21:V:639:LEU:HD23	2.21	0.56
23:Y:257:GLU:O	23:Y:261:SER:HB3	2.06	0.56
23:Y:272:ILE:HG22	23:Y:281:LEU:HD12	1.86	0.56
24:1:720:GLY:HA2	24:1:756:LEU:HD23	1.85	0.56
25:3:791:HIS:HD2	25:3:794:SER:OG	1.87	0.56
1:A:875:HIS:CE1	22:X:866:ASN:HB3	2.40	0.56
1:A:1211:ASP:C	1:A:1213:VAL:H	2.14	0.56
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.88	0.56
2:B:110:C:H2'	2:B:111:A:H8	1.70	0.56
3:C:68:THR:OG1	3:C:69:ALA:N	2.37	0.56
3:C:129:ILE:HB	3:C:199:LEU:HD23	1.86	0.56
3:C:380:ILE:O	3:C:384:VAL:HG23	2.05	0.56
5:E:202:ASN:ND2	5:E:204:THR:HG1	2.03	0.56
5:E:214:ASP:N	5:E:214:ASP:OD1	2.39	0.56
8:H:72:U:H2'	8:H:73:C:C6	2.41	0.56
24:1:739:ARG:HA	24:1:743:LEU:HD22	1.88	0.56
25:3:206:GLN:NE2	25:3:231:HIS:HA	2.21	0.56
1:A:1813:ARG:HE	1:A:1814:THR:HG23	1.71	0.56
1:A:1926:THR:O	1:A:1926:THR:OG1	2.24	0.56
5:E:150:HIS:NE2	5:E:169:THR:OG1	2.32	0.56
17:R:180:THR:HG23	17:R:194:GLN:HE21	1.71	0.56
22:X:681:LEU:H	22:X:725:ARG:HH22	1.52	0.56
23:Y:267:ARG:N	23:Y:287:GLU:O	2.34	0.56
27:w:461:LYS:HA	27:w:464:LEU:HD12	1.86	0.56
1:A:693:ILE:HB	1:A:738:MET:SD	2.46	0.56
1:A:1482:GLU:O	1:A:1486:GLU:HG2	2.05	0.56
1:A:1655:THR:OG1	1:A:1656:THR:N	2.38	0.56
5:E:251:LEU:HD21	5:E:300:ILE:HG23	1.87	0.56
7:G:-10:G:C8	20:U:1:MET:HE3	2.40	0.56
7:G:116:C:C4	17:R:370:SER:HB3	2.40	0.56
10:J:296:ARG:HD3	12:L:225:TYR:CE1	2.40	0.56
10:J:416:TYR:HE2	10:J:443:ILE:HD13	1.70	0.56
13:N:44:GLU:HA	13:N:47:TRP:NE1	2.20	0.56
17:R:353:ASP:O	17:R:357:HIS:HB2	2.05	0.56
19:T:227:THR:HG22	19:T:243:THR:HG22	1.88	0.56
19:T:247:SER:OG	19:T:267:ASP:OD1	2.20	0.56
20:U:23:LEU:H	21:V:474:HIS:CD2	2.23	0.56
22:X:457:ALA:O	22:X:460:SER:OG	2.21	0.56
23:Y:87:LYS:O	23:Y:89:LYS:N	2.36	0.56
23:Y:253:ASP:OD1	23:Y:253:ASP:N	2.30	0.56
25:3:86:ARG:NH1	25:3:1157:GLY:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:804:HIS:O	31:5:58:ASN:ND2	2.38	0.56
42:l:31:LYS:O	42:l:44:SER:N	2.38	0.56
1:A:1773:SER:HB2	1:A:1775:GLN:HG3	1.87	0.56
3:C:350:ASN:ND2	3:C:353:THR:OG1	2.38	0.56
19:T:272:CYS:HB3	19:T:282:ARG:HB3	1.86	0.56
21:V:532:GLN:O	21:V:536:ILE:CB	2.39	0.56
22:X:741:TRP:CD1	24:1:781:ASP:HA	2.40	0.56
23:Y:217:ALA:O	23:Y:220:GLN:HG3	2.05	0.56
24:1:754:ILE:HG22	24:1:755:PRO:HD3	1.88	0.56
25:3:703:ARG:HH11	25:3:703:ARG:HB2	1.70	0.56
28:2:503:HIS:CD2	28:2:510:TYR:CB	2.71	0.56
28:2:601:LEU:CD1	29:4:27:PRO:HA	2.36	0.56
35:9:301:PRO:O	35:9:305:GLU:HB2	2.06	0.56
42:l:21:GLU:O	42:l:69:ARG:N	2.39	0.56
37:n:39:HIS:HA	37:n:59:SER:HA	1.87	0.56
1:A:184:ASP:CB	13:N:1:MET:CA	2.83	0.56
1:A:939:TRP:NE1	1:A:1049:ASP:OD2	2.33	0.56
1:A:2328:ALA:HB3	4:D:728:ARG:CB	2.31	0.56
2:B:13:C:H2'	2:B:14:U:O4'	2.05	0.56
3:C:587:VAL:HG11	3:C:830:PRO:HG3	1.87	0.56
3:C:694:LYS:HA	3:C:786:ASN:OD1	2.06	0.56
10:J:262:ARG:HH22	10:J:291:GLN:HG2	1.70	0.56
17:R:172:ALA:HB1	17:R:173:PRO:HD2	1.86	0.56
17:R:352:ARG:NH2	22:X:265:HIS:ND1	2.54	0.56
22:X:164:TRP:CH2	22:X:542:PHE:CD1	2.93	0.56
24:1:970:LEU:O	24:1:973:HIS:HB2	2.06	0.56
25:3:69:ARG:HH12	25:3:74:THR:HA	1.71	0.56
1:A:48:LYS:O	1:A:53:PHE:CD1	2.59	0.56
1:A:940:ILE:HD13	1:A:1090:ARG:HH12	1.71	0.56
1:A:1336:PRO:HB2	1:A:1350:ILE:HG12	1.88	0.56
1:A:1858:PRO:C	1:A:1859:LYS:HD2	2.31	0.56
3:C:286:ASN:HD21	3:C:300:LEU:N	2.02	0.56
3:C:461:LEU:HA	3:C:464:ALA:HB3	1.86	0.56
3:C:733:TRP:CG	3:C:763:LYS:HZ3	2.24	0.56
3:C:746:VAL:O	3:C:791:ILE:HG13	2.06	0.56
3:C:759:LEU:O	3:C:762:VAL:N	2.39	0.56
3:C:875:ILE:HG13	3:C:876:PRO:HD2	1.88	0.56
5:E:197:LEU:HD11	5:E:213:ILE:HD13	1.87	0.56
17:R:414:GLN:HG2	22:X:633:ARG:NH1	2.19	0.56
22:X:405:ARG:NH1	22:X:406:GLU:OE1	2.39	0.56
24:1:807:LYS:HG3	24:1:844:VAL:HG11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:68:PHE:CE2	25:3:77:TYR:HB2	2.41	0.56
25:3:510:LEU:HD23	25:3:510:LEU:H	1.70	0.56
25:3:1145:GLU:HA	25:3:1148:LEU:HB2	1.88	0.56
35:9:323:ARG:HB3	35:9:331:GLN:HE21	1.70	0.56
1:A:591:MET:HB3	1:A:598:LEU:HD21	1.87	0.55
1:A:1782:ASP:HB3	1:A:1807:ILE:HD13	1.88	0.55
1:A:2308:VAL:CA	4:D:1125:SER:N	2.65	0.55
3:C:478:THR:HA	3:C:494:GLY:HA3	1.87	0.55
13:N:21:THR:O	13:N:24:GLU:HG3	2.06	0.55
22:X:283:TYR:CZ	23:Y:222:ILE:HG21	2.41	0.55
22:X:706:MET:HE2	22:X:991:LEU:CB	2.36	0.55
23:Y:181:PRO:HB2	23:Y:186:LEU:HG	1.88	0.55
25:3:226:GLU:OE1	25:3:259:LYS:HD3	2.07	0.55
25:3:418:GLU:OE1	25:3:419:ASP:N	2.28	0.55
25:3:592:LEU:HD11	25:3:619:LEU:HD21	1.87	0.55
25:3:1083:ASN:OD1	25:3:1084:GLY:N	2.39	0.55
31:5:27:THR:HG23	31:5:30:GLU:HG3	1.88	0.55
1:A:82:ARG:CZ	7:G:15:U:O4	2.55	0.55
1:A:876:GLU:O	1:A:879:SER:OG	2.23	0.55
2:B:12:U:H2'	2:B:13:C:H6	1.70	0.55
3:C:827:LEU:HD12	3:C:911:PRO:HB3	1.88	0.55
3:C:913:ASP:O	3:C:931:ARG:NE	2.39	0.55
6:F:83:A:N6	8:H:16:U:C4	2.74	0.55
7:G:85:G:H1	8:H:45:C:H42	1.53	0.55
7:G:85:G:N2	8:H:45:C:N3	2.51	0.55
10:J:339:TRP:HE3	17:R:116:TYR:CD2	2.24	0.55
10:J:376:VAL:HA	10:J:379:TRP:HD1	1.71	0.55
13:N:48:PRO:O	13:N:51:ARG:HB2	2.06	0.55
17:R:143:ILE:O	17:R:147:THR:OG1	2.18	0.55
22:X:227:ARG:HH21	23:Y:239:GLU:HG2	1.72	0.55
22:X:388:GLN:O	22:X:392:ILE:HG13	2.06	0.55
25:3:819:MET:HA	25:3:822:GLU:CD	2.31	0.55
25:3:1191:LYS:O	25:3:1195:GLU:HG3	2.06	0.55
35:9:297:CYS:SG	35:9:437:PRO:HG3	2.46	0.55
1:A:848:GLU:OE1	17:R:424:GLY:CA	2.55	0.55
1:A:1787:ARG:NH1	1:A:1788:VAL:O	2.39	0.55
3:C:189:VAL:HA	3:C:198:TYR:O	2.06	0.55
8:H:28:C:O2'	8:H:29:A:O5'	2.25	0.55
8:H:107:A:H2'	8:H:108:G:C8	2.42	0.55
13:N:46:LEU:N	13:N:46:LEU:HD13	2.20	0.55
21:V:518:LYS:HD2	21:V:520:GLU:OE1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:233:ASN:HD21	25:3:286:ILE:CG2	2.19	0.55
25:3:926:TYR:HB3	25:3:928:TYR:CE2	2.41	0.55
37:n:40:LEU:N	37:n:58:LEU:O	2.39	0.55
1:A:84:ASP:O	1:A:88:TYR:HB2	2.07	0.55
1:A:172:GLU:OE1	1:A:172:GLU:N	2.39	0.55
1:A:398:THR:CG2	3:C:382:ALA:HB1	2.36	0.55
1:A:1131:LYS:HG2	1:A:1193:GLU:OE2	2.06	0.55
1:A:1339:ASP:OD1	1:A:1339:ASP:N	2.38	0.55
1:A:1787:ARG:HD3	1:A:1788:VAL:H	1.71	0.55
1:A:2081:ALA:C	4:D:1010:SER:CB	2.79	0.55
3:C:144:CYS:SG	3:C:312:SER:OG	2.65	0.55
5:E:255:MET:HB2	5:E:282:HIS:CB	2.35	0.55
13:N:46:LEU:H	13:N:46:LEU:CD2	2.13	0.55
23:Y:91:LYS:HG3	23:Y:114:GLU:HG3	1.88	0.55
24:1:549:ARG:NH2	24:1:592:GLU:OE1	2.30	0.55
24:1:818:PHE:HD1	24:1:823:MET:HE2	1.71	0.55
24:1:1098:LEU:HD12	24:1:1135:GLU:HG2	1.87	0.55
25:3:342:LEU:HB3	25:3:343:LYS:O	2.06	0.55
1:A:155:LYS:HE3	1:A:626:GLY:O	2.06	0.55
1:A:341:LYS:HA	1:A:341:LYS:HE2	1.87	0.55
1:A:1984:LYS:HA	1:A:1987:ILE:HD12	1.88	0.55
2:B:117:A:C2	39:d:26:GLY:HA3	2.41	0.55
3:C:375:GLU:O	3:C:379:LYS:HG3	2.06	0.55
5:E:62:LEU:HB2	5:E:351:LEU:HB2	1.89	0.55
5:E:110:GLY:H	5:E:130:ASP:CG	2.15	0.55
8:H:78:C:H2'	8:H:79:G:H8	1.72	0.55
9:I:169:TYR:O	9:I:173:LEU:CB	2.54	0.55
12:L:48:ALA:O	12:L:52:GLU:HG2	2.07	0.55
16:Q:514:ILE:H	16:Q:655:ILE:HA	1.71	0.55
17:R:110:LYS:NZ	19:T:364:THR:O	2.38	0.55
17:R:122:LYS:HE2	19:T:399:LYS:NZ	2.21	0.55
19:T:220:VAL:HG23	19:T:230:ILE:HG12	1.87	0.55
21:V:543:LYS:HA	21:V:546:ASN:ND2	2.22	0.55
21:V:553:HIS:CD2	21:V:556:TYR:HE1	2.25	0.55
28:2:452:LYS:CD	28:2:456:ARG:HB2	2.36	0.55
35:9:382:ILE:HG21	35:9:407:LEU:HD12	1.88	0.55
1:A:322:ASN:N	1:A:322:ASN:OD1	2.38	0.55
1:A:1889:LEU:CD2	1:A:2012:LEU:HG	2.36	0.55
1:A:1925:LYS:HD3	21:V:457:ARG:NH2	2.22	0.55
10:J:339:TRP:HA	17:R:116:TYR:HD2	1.70	0.55
21:V:618:ARG:HB3	21:V:646:HIS:CE1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:837:SER:HB3	22:X:930:SER:H	1.71	0.55
23:Y:247:LEU:HB2	23:Y:282:CYS:C	2.32	0.55
24:1:826:ASP:HB3	24:1:829:ASN:HB2	1.86	0.55
25:3:791:HIS:NE2	25:3:934:GLY:HA3	2.22	0.55
25:3:1015:LYS:O	25:3:1019:ASN:N	2.40	0.55
27:w:429:TRP:HB3	27:w:430:ARG:NH1	2.22	0.55
38:h:109:VAL:N	39:i:63:LEU:O	2.27	0.55
1:A:608:LEU:HD13	1:A:632:ALA:HB1	1.89	0.55
1:A:1579:ALA:HB2	11:K:226:TYR:CE2	2.41	0.55
1:A:1670:ASP:N	1:A:1670:ASP:OD1	2.37	0.55
3:C:465:MET:O	3:C:468:CYS:N	2.37	0.55
6:F:16:G:H2'	6:F:17:C:C6	2.41	0.55
10:J:226:ARG:O	10:J:230:THR:HG23	2.06	0.55
12:L:222:LEU:O	17:R:86:LEU:HD22	2.07	0.55
14:O:249:ARG:O	14:O:252:PHE:N	2.39	0.55
19:T:274:ASP:HB2	19:T:281:ILE:HD13	1.88	0.55
21:V:497:CYS:HB2	21:V:507:PHE:CB	2.36	0.55
21:V:622:ARG:CA	21:V:625:ARG:HH21	2.20	0.55
22:X:593:GLU:O	22:X:597:VAL:HG22	2.06	0.55
24:1:1203:GLY:CA	25:3:1171:LYS:HG3	2.34	0.55
25:3:373:PHE:HE1	25:3:385:PHE:HB3	1.70	0.55
1:A:298:ASP:CG	1:A:300:ASN:HD22	2.15	0.55
1:A:1889:LEU:CD1	1:A:2014:MET:C	2.79	0.55
1:A:2328:ALA:CA	4:D:728:ARG:CB	2.84	0.55
3:C:131:ASN:HD22	3:C:495:ARG:HH12	1.54	0.55
6:F:45:A:OP2	28:2:554:ARG:NH1	2.40	0.55
7:G:90:C:O5'	7:G:90:C:H6	1.89	0.55
8:H:50:C:H2'	8:H:51:A:H8	1.71	0.55
16:Q:1136:GLN:N	16:Q:1156:ASN:HA	2.21	0.55
21:V:529:PHE:CE1	21:V:564:VAL:HB	2.42	0.55
22:X:165:GLU:HB2	22:X:542:PHE:CE1	2.42	0.55
22:X:284:ARG:HD3	23:Y:223:LEU:HD21	1.88	0.55
23:Y:126:PHE:C	23:Y:126:PHE:HD2	2.14	0.55
25:3:1143:HIS:O	25:3:1147:HIS:ND1	2.39	0.55
1:A:176:LEU:H	1:A:176:LEU:CD2	2.20	0.55
1:A:762:ARG:HH22	15:P:226:LYS:HZ3	1.55	0.55
1:A:1091:TYR:O	1:A:1092:ILE:C	2.48	0.55
1:A:1275:ARG:C	1:A:1276:GLU:HG3	2.32	0.55
1:A:1771:LEU:HD21	1:A:1779:PHE:CZ	2.40	0.55
1:A:2308:VAL:C	4:D:1125:SER:CA	2.79	0.55
5:E:197:LEU:HG	5:E:212:GLY:HA2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:22:A:H5''	13:N:116:ASN:O	2.07	0.55
8:H:36:G:H2'	8:H:37:U:C6	2.42	0.55
10:J:230:THR:OG1	10:J:231:PHE:N	2.38	0.55
10:J:368:ARG:HA	10:J:368:ARG:NE	2.22	0.55
19:T:223:SER:OG	19:T:224:ALA:N	2.38	0.55
22:X:768:LYS:HZ2	22:X:775:LEU:HG	1.71	0.55
23:Y:147:ASP:OD2	23:Y:147:ASP:N	2.40	0.55
24:1:735:ILE:HD12	24:1:747:LEU:HD12	1.88	0.55
25:3:2:PHE:C	25:3:3:LEU:HD23	2.32	0.55
35:9:324:SER:O	35:9:420:ASP:HB3	2.06	0.55
38:h:45:ASN:O	38:h:107:ILE:N	2.39	0.55
1:A:81:PHE:O	1:A:83:HIS:N	2.39	0.55
1:A:378:PHE:HE2	3:C:338:GLU:HB3	1.72	0.55
1:A:1303:LEU:HD12	1:A:1311:PHE:HE1	1.72	0.55
1:A:1787:ARG:HD3	1:A:1788:VAL:N	2.22	0.55
3:C:276:TYR:OH	21:V:321:ASN:CB	2.55	0.55
10:J:407:GLY:O	10:J:411:MET:HB3	2.07	0.55
13:N:120:ARG:CZ	13:N:143:SER:HB3	2.37	0.55
17:R:312:MET:HE3	23:Y:191:ILE:HG13	1.90	0.55
21:V:244:GLY:O	21:V:249:ASP:N	2.30	0.55
22:X:280:ALA:HB2	23:Y:227:VAL:HG13	1.89	0.55
22:X:475:ASN:HB3	22:X:490:ARG:HD3	1.89	0.55
22:X:561:SER:O	22:X:566:ASP:N	2.32	0.55
22:X:600:LEU:O	22:X:604:VAL:HG23	2.06	0.55
24:1:819:TRP:HZ2	24:1:837:THR:HG21	1.71	0.55
25:3:747:SER:OG	25:3:748:GLU:N	2.40	0.55
25:3:883:GLU:HB3	25:3:886:GLU:HG3	1.89	0.55
35:9:306:ASN:OD1	35:9:345:TYR:N	2.27	0.55
35:9:368:MET:O	35:9:394:HIS:ND1	2.40	0.55
1:A:1777:ILE:HG23	1:A:1860:GLN:HG3	1.89	0.54
1:A:1947:ASN:O	1:A:1951:LYS:HG3	2.07	0.54
3:C:134:LEU:HB3	3:C:204:ASP:HA	1.89	0.54
3:C:719:GLN:HG3	3:C:724:TRP:O	2.06	0.54
5:E:221:ASP:HB2	5:E:228:THR:OG1	2.06	0.54
5:E:227:LEU:O	5:E:227:LEU:HD12	2.07	0.54
5:E:268:ALA:O	5:E:270:LYS:HD2	2.07	0.54
14:O:261:ILE:HA	14:O:271:PHE:O	2.07	0.54
23:Y:21:ARG:NH2	23:Y:81:GLU:O	2.41	0.54
25:3:234:PHE:CE1	25:3:236:ILE:HG12	2.42	0.54
25:3:527:ILE:HG12	25:3:532:ARG:O	2.06	0.54
25:3:718:ARG:HB2	25:3:720:TRP:NE1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:p:177:PHE:HA	26:p:194:PHE:HA	1.89	0.54
27:w:107:SER:O	27:w:119:ASN:N	2.38	0.54
30:7:57:ARG:NH1	30:7:62:GLY:O	2.39	0.54
38:h:58:ALA:O	38:h:65:MET:HA	2.07	0.54
1:A:705:LYS:O	1:A:708:THR:HG22	2.07	0.54
1:A:1979:VAL:HA	1:A:1982:GLN:HB2	1.89	0.54
3:C:215:VAL:HG11	3:C:242:LEU:HD21	1.89	0.54
3:C:260:ILE:HG13	3:C:310:SER:O	2.05	0.54
3:C:390:THR:O	3:C:393:PRO:HD2	2.07	0.54
3:C:404:THR:O	3:C:408:LEU:HD12	2.08	0.54
4:D:418:GLN:O	4:D:422:PHE:N	2.40	0.54
7:G:85:G:N1	8:H:44:U:N3	2.55	0.54
11:K:200:ASP:HB3	11:K:219:PHE:CD1	2.40	0.54
13:N:122:PRO:HG2	13:N:125:LYS:HE2	1.90	0.54
15:P:30:TYR:CZ	17:R:162:ALA:O	2.60	0.54
22:X:741:TRP:HE1	24:1:781:ASP:CB	2.20	0.54
24:1:769:VAL:HA	24:1:772:ILE:HD13	1.89	0.54
24:1:1206:ASP:OD1	24:1:1207:SER:N	2.41	0.54
25:3:18:ILE:HG21	25:3:67:ALA:H	1.72	0.54
33:v:183:VAL:N	33:v:184:PRO:HD3	2.22	0.54
1:A:233:PRO:O	1:A:237:THR:HG23	2.07	0.54
1:A:1224:ARG:HG3	1:A:1224:ARG:HH11	1.73	0.54
11:K:209:GLY:HA2	11:K:223:ARG:HD3	1.90	0.54
16:Q:564:LEU:O	16:Q:592:VAL:HA	2.07	0.54
16:Q:1049:LEU:O	16:Q:1054:PHE:N	2.39	0.54
22:X:597:VAL:HA	22:X:600:LEU:HD12	1.89	0.54
25:3:526:HIS:CG	25:3:573:GLN:HE21	2.25	0.54
28:2:511:LEU:C	28:2:513:GLY:N	2.65	0.54
3:C:118:PHE:O	3:C:122:LEU:HD12	2.07	0.54
3:C:224:GLY:HA2	3:C:251:LEU:HB3	1.89	0.54
3:C:441:PRO:O	3:C:444:GLY:HA3	2.07	0.54
3:C:857:VAL:HA	3:C:873:ALA:HB2	1.89	0.54
9:I:92:TYR:CB	16:Q:953:ASN:CA	2.85	0.54
17:R:357:HIS:HD2	23:Y:276:LYS:HZ2	1.52	0.54
19:T:243:THR:O	19:T:243:THR:OG1	2.24	0.54
22:X:164:TRP:NE1	22:X:542:PHE:HB2	2.23	0.54
22:X:769:SER:OG	22:X:816:ALA:HB1	2.08	0.54
24:1:1266:TRP:CE3	31:5:22:GLY:HA3	2.42	0.54
25:3:25:THR:OG1	25:3:26:LYS:N	2.35	0.54
25:3:542:LYS:HB2	25:3:558:LEU:HD11	1.88	0.54
35:9:300:THR:OG1	35:9:304:CYS:SG	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LEU:HD11	1:A:566:LEU:HD11	1.88	0.54
1:A:1793:THR:HB	1:A:1795:GLU:H	1.73	0.54
2:B:110:C:H2'	2:B:111:A:C8	2.41	0.54
3:C:891:THR:HG21	3:C:895:ALA:HB3	1.90	0.54
5:E:78:GLY:HA3	5:E:336:HIS:CE1	2.42	0.54
6:F:89:U:H2'	6:F:90:G:C8	2.42	0.54
8:H:56:A:OP1	24:1:1258:ALA:HA	2.08	0.54
22:X:454:ARG:NH1	22:X:680:SER:OG	2.40	0.54
22:X:809:THR:O	22:X:813:ARG:HG2	2.06	0.54
24:1:728:LEU:HB3	24:1:765:TYR:OH	2.08	0.54
1:A:657:ALA:O	1:A:661:GLU:HG3	2.08	0.54
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.42	0.54
3:C:715:GLY:HA2	3:C:719:GLN:HE22	1.73	0.54
5:E:253:ASN:ND2	5:E:291:CYS:HB3	2.23	0.54
5:E:330:ILE:H	5:E:330:ILE:HD12	1.72	0.54
8:H:151:C:H2'	8:H:152:G:C8	2.43	0.54
24:1:1062:LEU:HA	24:1:1065:LEU:HD12	1.88	0.54
28:2:510:TYR:C	28:2:510:TYR:CD2	2.85	0.54
31:5:14:LEU:HD23	31:5:17:LYS:HD2	1.88	0.54
1:A:224:THR:N	2:B:12:U:OP1	2.39	0.54
1:A:593:ARG:NH1	1:A:1565:LYS:HZ3	2.05	0.54
1:A:854:SER:OG	1:A:855:ARG:N	2.39	0.54
1:A:1536:LEU:HG	1:A:1572:SER:HB3	1.89	0.54
1:A:2268:LEU:CB	4:D:1228:VAL:CB	2.86	0.54
5:E:75:HIS:CE1	5:E:121:GLY:HA3	2.43	0.54
9:I:550:TRP:O	9:I:552:ASN:N	2.32	0.54
10:J:296:ARG:HD3	12:L:225:TYR:CZ	2.42	0.54
22:X:481:ILE:HD11	22:X:484:GLU:HB3	1.90	0.54
24:1:778:GLN:N	24:1:778:GLN:OE1	2.41	0.54
24:1:1122:THR:OG1	24:1:1123:CYS:N	2.41	0.54
24:1:1157:TYR:CE2	30:7:37:VAL:CG1	2.89	0.54
25:3:234:PHE:C	25:3:235:LEU:HD12	2.33	0.54
25:3:943:THR:HG23	25:3:976:LYS:HB3	1.89	0.54
27:w:390:LYS:HZ3	33:v:84:ARG:NH2	2.06	0.54
28:2:531:THR:O	28:2:531:THR:OG1	2.25	0.54
3:C:692:LEU:HB2	3:C:786:ASN:ND2	2.23	0.54
3:C:719:GLN:NE2	3:C:726:LEU:HA	2.23	0.54
3:C:884:GLU:O	3:C:888:ARG:HG3	2.07	0.54
7:G:7:G:H2'	7:G:8:C:C6	2.42	0.54
12:L:74:LEU:O	12:L:77:LEU:N	2.41	0.54
17:R:91:ASP:OD1	17:R:95:LYS:N	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:351:GLU:OE2	22:X:256:LEU:HA	2.08	0.54
19:T:213:GLU:OE1	19:T:217:GLN:N	2.30	0.54
23:Y:271:VAL:HG22	23:Y:284:ALA:HB2	1.88	0.54
24:1:652:CYS:SG	24:1:689:ILE:HG23	2.48	0.54
25:3:266:ASP:OD1	25:3:266:ASP:N	2.40	0.54
25:3:294:LYS:HZ2	25:3:294:LYS:C	2.16	0.54
25:3:530:ASP:O	25:3:532:ARG:N	2.40	0.54
25:3:642:ILE:N	25:3:703:ARG:HE	2.06	0.54
25:3:911:LYS:CB	25:3:922:GLY:O	2.55	0.54
28:2:518:GLU:CB	33:v:47:MET:SD	2.82	0.54
29:4:79:LEU:N	29:4:82:LYS:O	2.41	0.54
40:j:59:ASP:HA	40:j:76:ARG:HA	1.88	0.54
3:C:132:VAL:HG11	3:C:226:VAL:HG23	1.90	0.54
3:C:298:LEU:HD21	3:C:300:LEU:HG	1.89	0.54
6:F:38:G:H8	6:F:38:G:P	2.31	0.54
6:F:84:A:C1'	6:F:85:U:H5'	2.37	0.54
7:G:100:C:H4'	7:G:101:U:C6	2.42	0.54
23:Y:21:ARG:HH12	23:Y:83:VAL:N	2.06	0.54
24:1:565:ASP:OD1	24:1:566:LEU:N	2.40	0.54
24:1:785:LYS:O	24:1:789:LEU:HD12	2.07	0.54
24:1:933:CYS:O	24:1:936:VAL:N	2.41	0.54
24:1:1092:ASP:O	24:1:1096:THR:HG23	2.08	0.54
25:3:406:PRO:HG2	25:3:408:LEU:HD11	1.89	0.54
31:5:8:HIS:NE2	31:5:12:GLU:OE2	2.37	0.54
1:A:357:ASN:HD22	3:C:862:PRO:CB	2.17	0.54
1:A:703:GLN:O	1:A:705:LYS:N	2.41	0.54
15:P:186:ARG:HD2	15:P:190:ASP:HB3	1.90	0.54
22:X:932:CYS:HB2	22:X:938:ARG:HD2	1.90	0.54
24:1:1108:ASN:N	24:1:1108:ASN:OD1	2.39	0.54
28:2:601:LEU:HD11	29:4:27:PRO:CB	2.38	0.54
34:u:72:ARG:O	34:u:76:ILE:CB	2.55	0.54
1:A:852:VAL:HB	17:R:426:GLU:OE1	2.08	0.53
1:A:1431:ALA:HB2	22:X:329:TRP:CB	2.38	0.53
1:A:1889:LEU:HD11	1:A:2009:ASP:OD2	2.07	0.53
3:C:658:PRO:HB2	3:C:881:PHE:CZ	2.43	0.53
7:G:9:C:O2'	7:G:10:U:O4'	2.12	0.53
12:L:11:TRP:CD2	12:L:49:ARG:HD3	2.43	0.53
19:T:329:HIS:CE1	19:T:349:SER:HB3	2.43	0.53
25:3:623:ASP:OD2	25:3:626:GLN:NE2	2.41	0.53
1:A:299:ILE:HD12	3:C:920:PRO:HB2	1.90	0.53
1:A:1199:LYS:HE2	1:A:1206:GLU:CD	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1983:LEU:O	1:A:1987:ILE:HG13	2.08	0.53
3:C:320:LEU:HD22	3:C:343:LEU:HB2	1.90	0.53
6:F:49:G:N7	12:L:33:ARG:HB3	2.23	0.53
7:G:111:U:H4'	7:G:112:U:OP2	2.06	0.53
7:G:111:U:H2'	22:X:482:ARG:HD2	1.89	0.53
9:I:139:ALA:HA	16:Q:938:TYR:CB	2.38	0.53
17:R:348:GLU:CD	22:X:263:SER:H	2.16	0.53
23:Y:70:LEU:HD23	23:Y:171:ASP:HB2	1.89	0.53
24:1:523:ALA:C	24:1:563:LEU:HD11	2.33	0.53
25:3:642:ILE:HB	25:3:703:ARG:HH21	1.73	0.53
25:3:940:LEU:HB3	25:3:941:HIS:CE1	2.43	0.53
30:7:46:CYS:N	30:7:85:CYS:HB2	2.23	0.53
31:5:63:ARG:O	31:5:67:ASN:ND2	2.42	0.53
1:A:1768:TYR:CZ	1:A:2012:LEU:HD22	2.42	0.53
3:C:604:LEU:HD21	3:C:627:HIS:HE1	1.73	0.53
3:C:928:HIS:N	3:C:928:HIS:HD1	2.07	0.53
5:E:334:ALA:HB3	5:E:343:ILE:CG2	2.38	0.53
8:H:56:A:C4'	24:1:1257:PRO:HB3	2.38	0.53
9:I:136:ALA:C	9:I:144:GLN:CB	2.82	0.53
17:R:427:ASP:OD1	17:R:428:GLU:N	2.41	0.53
19:T:245:HIS:NE2	19:T:263:SER:OG	2.23	0.53
21:V:555:LEU:HG	21:V:586:PHE:HZ	1.73	0.53
23:Y:210:GLU:O	23:Y:214:GLU:HG3	2.08	0.53
24:1:806:ILE:HG23	24:1:810:ILE:HB	1.90	0.53
24:1:933:CYS:SG	24:1:970:LEU:HD21	2.48	0.53
25:3:34:ARG:HB2	25:3:37:ILE:HB	1.91	0.53
27:w:440:ILE:HG12	27:w:459:TRP:CG	2.44	0.53
28:2:509:LYS:CA	28:2:509:LYS:CE	2.87	0.53
1:A:75:ASP:O	1:A:77:THR:N	2.41	0.53
1:A:222:GLY:HA3	2:B:11:U:O3'	2.09	0.53
1:A:1661:TRP:HH2	1:A:1684:PHE:HE1	1.56	0.53
1:A:1780:VAL:HA	1:A:1808:PHE:O	2.09	0.53
7:G:88:G:O6	8:H:40:C:N4	2.41	0.53
8:H:36:G:H2'	8:H:37:U:H6	1.73	0.53
8:H:118:G:H2'	8:H:119:G:C8	2.43	0.53
23:Y:9:LEU:O	23:Y:135:ILE:HD13	2.08	0.53
25:3:289:CYS:SG	25:3:338:ALA:HA	2.48	0.53
27:w:429:TRP:CE3	27:w:430:ARG:HG3	2.43	0.53
27:w:430:ARG:HH11	27:w:430:ARG:H	1.56	0.53
28:2:601:LEU:HD11	29:4:27:PRO:HA	1.90	0.53
1:A:550:VAL:O	1:A:554:THR:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1019:TYR:O	1:A:1020:LYS:C	2.51	0.53
3:C:323:PHE:CE2	3:C:373:ILE:HG12	2.44	0.53
3:C:558:PRO:HG2	3:C:559:ILE:HG23	1.91	0.53
4:D:2018:GLU:O	4:D:2041:LEU:HA	2.09	0.53
5:E:312:TRP:CD1	5:E:319:ILE:HA	2.42	0.53
7:G:-10:G:H8	20:U:1:MET:CE	2.21	0.53
17:R:137:GLU:HB2	17:R:141:LYS:HE3	1.89	0.53
22:X:234:TYR:CD2	23:Y:317:GLN:HB3	2.43	0.53
22:X:803:ASN:OD1	22:X:807:GLU:N	2.37	0.53
23:Y:198:ASP:HA	23:Y:200:PHE:CE2	2.43	0.53
24:1:515:ALA:O	24:1:519:ILE:HG22	2.09	0.53
24:1:896:ILE:HD12	24:1:917:VAL:HG11	1.90	0.53
25:3:164:ASN:HA	25:3:189:TYR:CZ	2.43	0.53
33:v:28:GLU:O	33:v:32:GLN:NE2	2.41	0.53
1:A:378:PHE:CE2	3:C:338:GLU:HB3	2.43	0.53
1:A:384:VAL:CG1	3:C:327:TYR:HE2	2.21	0.53
1:A:699:GLU:OE1	1:A:699:GLU:HA	2.08	0.53
1:A:1362:ASP:CG	1:A:1363:GLN:H	2.17	0.53
3:C:711:ARG:HB3	3:C:730:ARG:HH22	1.74	0.53
4:D:1157:ASN:O	4:D:1161:ILE:N	2.31	0.53
5:E:294:SER:HB2	5:E:298:SER:H	1.73	0.53
7:G:116:C:H3'	7:G:117:A:H8	1.73	0.53
9:I:374:ILE:O	9:I:377:THR:N	2.42	0.53
10:J:377:LYS:NZ	10:J:381:LYS:HE3	2.23	0.53
13:N:139:CYS:SG	13:N:140:ARG:N	2.82	0.53
17:R:331:ALA:CA	22:X:275:ARG:NH1	2.71	0.53
22:X:180:ALA:O	22:X:184:ARG:HG3	2.09	0.53
23:Y:255:ASP:O	23:Y:258:ILE:HB	2.09	0.53
24:1:1136:TYR:HD2	28:2:522:PHE:CD1	2.26	0.53
25:3:769:LYS:HD3	25:3:769:LYS:N	2.24	0.53
28:2:530:ARG:HH12	28:2:578:TRP:CD1	2.26	0.53
28:2:604:LYS:HE2	29:4:38:PRO:HA	1.91	0.53
1:A:2311:PRO:O	1:A:2315:LEU:N	2.37	0.53
7:G:2:U:O4	11:K:219:PHE:CZ	2.62	0.53
12:L:68:GLU:OE2	12:L:99:HIS:NE2	2.38	0.53
17:R:162:ALA:C	17:R:164:PRO:HD3	2.33	0.53
22:X:238:ARG:NH2	23:Y:230:LEU:CD2	2.71	0.53
22:X:810:THR:HA	22:X:813:ARG:NE	2.24	0.53
24:1:1058:ILE:O	24:1:1062:LEU:HG	2.08	0.53
25:3:777:VAL:HG22	25:3:779:PHE:CE1	2.43	0.53
25:3:1083:ASN:HB3	28:2:496:ASN:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:1168:PHE:N	25:3:1168:PHE:CD2	2.77	0.53
28:2:460:PHE:HB3	28:2:464:GLU:HG2	1.91	0.53
40:j:60:ASP:N	40:j:75:GLY:O	2.42	0.53
1:A:48:LYS:CD	1:A:53:PHE:CZ	2.75	0.53
1:A:697:MET:N	1:A:698:PRO:HD3	2.24	0.53
1:A:1811:ASN:HB3	1:A:1814:THR:OG1	2.09	0.53
3:C:682:LYS:HB3	3:C:797:ALA:HB2	1.90	0.53
3:C:852:ARG:HD2	7:G:-12:C:O5'	2.08	0.53
5:E:239:THR:OG1	5:E:289:LEU:HB3	2.09	0.53
9:I:108:LYS:C	9:I:110:PRO:CD	2.81	0.53
16:Q:748:ARG:O	16:Q:779:VAL:HA	2.08	0.53
17:R:134:ARG:NH1	19:T:382:PRO:O	2.36	0.53
19:T:207:VAL:HG12	19:T:480:ALA:HB1	1.90	0.53
19:T:223:SER:OG	19:T:225:ASP:OD2	2.09	0.53
22:X:219:ARG:NH1	23:Y:292:GLU:OE2	2.41	0.53
22:X:689:VAL:C	22:X:690:LEU:HD23	2.34	0.53
24:1:731:LEU:O	24:1:735:ILE:HG12	2.08	0.53
24:1:796:CYS:C	24:1:801:VAL:HG21	2.34	0.53
38:h:69:ASN:N	38:h:97:SER:O	2.41	0.53
1:A:393:LEU:HA	3:C:379:LYS:HG2	1.91	0.53
1:A:712:HIS:ND1	17:R:250:CYS:CB	2.71	0.53
1:A:1108:ASP:O	1:A:1112:ARG:HG3	2.09	0.53
2:B:99:C:H2'	2:B:100:C:C6	2.43	0.53
3:C:622:GLU:O	3:C:625:GLY:N	2.41	0.53
5:E:65:HIS:CE1	5:E:84:ALA:HA	2.44	0.53
7:G:15:U:H3'	7:G:16:G:H8	1.73	0.53
12:L:73:HIS:HD2	35:9:220:ILE:CG2	2.22	0.53
16:Q:735:VAL:HA	16:Q:779:VAL:O	2.08	0.53
17:R:201:GLU:H	17:R:201:GLU:CD	2.16	0.53
17:R:335:ARG:CB	22:X:272:TYR:HB2	2.39	0.53
22:X:913:ASP:O	22:X:916:GLU:HG3	2.09	0.53
25:3:269:CYS:SG	25:3:327:LEU:HD11	2.48	0.53
25:3:939:PHE:CZ	25:3:942:LYS:HG2	2.44	0.53
1:A:267:LYS:NZ	2:B:49:A:OP1	2.37	0.53
1:A:283:VAL:HG13	1:A:284:ARG:H	1.74	0.53
1:A:1436:TRP:O	1:A:1440:THR:HG23	2.08	0.53
2:B:108:G:H3'	2:B:109:G:H8	1.73	0.53
13:N:57:THR:HG21	13:N:88:LEU:HD23	1.91	0.53
24:1:833:LEU:O	24:1:837:THR:OG1	2.23	0.53
25:3:695:GLY:O	25:3:697:ARG:NE	2.30	0.53
25:3:833:GLU:C	25:3:836:ALA:H	2.14	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:v:34:ALA:HB2	33:v:66:GLU:HG2	1.91	0.53
1:A:261:LYS:HB2	1:A:330:THR:HB	1.92	0.52
1:A:1767:ASN:O	1:A:1770:GLU:HB3	2.09	0.52
3:C:314:TYR:CD2	3:C:416:LEU:HD22	2.44	0.52
3:C:490:PHE:HB2	3:C:556:ASP:HB3	1.91	0.52
3:C:879:ASP:OD1	3:C:879:ASP:N	2.41	0.52
4:D:2103:ASN:HA	4:D:2123:SER:HA	1.91	0.52
5:E:191:GLN:HE21	5:E:193:THR:HA	1.74	0.52
8:H:172:C:N4	8:H:173:C:H41	2.07	0.52
10:J:292:VAL:HG12	10:J:296:ARG:HE	1.75	0.52
16:Q:599:GLY:HA3	16:Q:608:ILE:H	1.74	0.52
17:R:346:ASP:OD2	22:X:261:GLU:OE1	2.27	0.52
19:T:423:SER:HB3	19:T:474:GLU:OE1	2.09	0.52
23:Y:3:VAL:HG11	23:Y:32:CYS:SG	2.49	0.52
24:1:693:GLY:HA2	24:1:696:ASP:HB2	1.90	0.52
24:1:815:PHE:HA	24:1:819:TRP:CD1	2.43	0.52
25:3:312:LYS:HB2	25:3:330:PHE:HD1	1.72	0.52
25:3:442:LEU:HD13	25:3:770:LEU:HD23	1.91	0.52
28:2:495:ARG:O	28:2:497:SER:N	2.41	0.52
33:v:66:GLU:O	33:v:69:TYR:N	2.41	0.52
35:9:296:HIS:H	35:9:296:HIS:CD2	2.26	0.52
35:9:360:HIS:ND1	35:9:396:ILE:HD11	2.23	0.52
1:A:31:GLN:HA	1:A:31:GLN:OE1	2.09	0.52
1:A:857:ASN:OD1	1:A:859:SER:N	2.42	0.52
3:C:529:ARG:NH2	3:C:540:GLU:HB2	2.19	0.52
6:F:13:G:H2'	6:F:14:C:C6	2.44	0.52
7:G:8:C:H2'	7:G:9:C:C6	2.45	0.52
13:N:113:PHE:HD1	17:R:198:ARG:NH1	2.02	0.52
17:R:280:ILE:C	35:9:225:MET:HG3	2.33	0.52
17:R:383:ASN:HA	17:R:386:ARG:NH1	2.23	0.52
22:X:235:LEU:HD22	23:Y:220:GLN:CG	2.39	0.52
22:X:954:LEU:HG	22:X:956:ARG:NH1	2.24	0.52
24:1:846:ALA:HB1	24:1:850:ILE:HG12	1.91	0.52
25:3:803:ASP:OD1	25:3:804:HIS:N	2.41	0.52
28:2:596:GLU:H	28:2:596:GLU:CD	2.16	0.52
1:A:650:ARG:O	1:A:654:ASN:ND2	2.40	0.52
2:B:87:A:H61	2:B:92:U:P	2.32	0.52
4:D:2017:ILE:HA	4:D:2042:GLU:O	2.10	0.52
8:H:56:A:O4'	24:1:1257:PRO:CB	2.57	0.52
17:R:348:GLU:CD	22:X:263:SER:O	2.53	0.52
17:R:361:LYS:HA	17:R:364:GLN:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:369:LEU:HD12	17:R:376:LYS:NZ	2.24	0.52
21:V:642:GLU:O	21:V:645:GLU:HB3	2.10	0.52
22:X:234:TYR:CE1	23:Y:317:GLN:O	2.63	0.52
22:X:476:GLU:HA	22:X:491:THR:HA	1.90	0.52
22:X:558:ALA:O	22:X:562:THR:OG1	2.21	0.52
22:X:879:LEU:HD23	22:X:879:LEU:H	1.73	0.52
22:X:957:SER:OG	22:X:957:SER:O	2.19	0.52
23:Y:203:ARG:HH21	23:Y:203:ARG:HA	1.74	0.52
25:3:120:PHE:HB2	25:3:133:SER:OG	2.09	0.52
25:3:390:ARG:HD3	25:3:393:LYS:HE3	1.91	0.52
25:3:605:LEU:O	25:3:617:ILE:N	2.42	0.52
25:3:1025:ALA:HA	25:3:1087:GLN:O	2.09	0.52
29:4:102:ILE:C	29:4:177:ALA:HB2	2.33	0.52
39:i:21:VAL:O	39:i:28:GLU:HA	2.09	0.52
1:A:65:HIS:O	1:A:69:ILE:HG13	2.10	0.52
1:A:1437:ARG:NH1	1:A:1455:TRP:O	2.43	0.52
1:A:1889:LEU:CA	1:A:2014:MET:H	2.16	0.52
3:C:311:SER:OG	3:C:314:TYR:HB2	2.10	0.52
5:E:171:SER:OG	5:E:173:ASP:OD2	2.25	0.52
8:H:56:A:O2'	28:2:478:HIS:CG	2.62	0.52
17:R:280:ILE:O	35:9:225:MET:CG	2.57	0.52
17:R:348:GLU:HG2	22:X:266:GLU:OE1	2.08	0.52
19:T:418:THR:HG21	19:T:467:ALA:HA	1.90	0.52
25:3:229:GLU:HB2	25:3:230:GLU:OE1	2.09	0.52
25:3:700:LYS:HB3	25:3:702:PHE:HZ	1.74	0.52
25:3:872:ILE:HD12	25:3:872:ILE:H	1.75	0.52
35:9:94:SER:O	35:9:101:TYR:HA	2.09	0.52
35:9:413:VAL:HG11	35:9:426:ILE:HD11	1.91	0.52
3:C:441:PRO:C	3:C:444:GLY:HA3	2.35	0.52
3:C:480:LYS:HB3	3:C:482:TYR:CE1	2.44	0.52
3:C:693:GLU:HB3	3:C:696:LEU:HD21	1.92	0.52
6:F:31:U:H3'	6:F:32:U:H6	1.74	0.52
7:G:85:G:O6	8:H:44:U:O4	2.28	0.52
10:J:328:GLY:HA2	10:J:331:GLN:HE21	1.74	0.52
14:O:172:GLU:O	14:O:174:LYS:N	2.42	0.52
17:R:320:HIS:NE2	17:R:324:LEU:HD11	2.24	0.52
22:X:222:MET:HE3	23:Y:299:PHE:CE2	2.44	0.52
22:X:743:TYR:O	22:X:747:LEU:HB2	2.08	0.52
24:1:609:MET:HE1	24:1:635:VAL:HG11	1.91	0.52
24:1:842:ASN:OD1	24:1:879:LEU:HD11	2.10	0.52
24:1:1260:LYS:O	24:1:1264:VAL:HG22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:181:MET:HB3	25:3:212:GLU:HA	1.92	0.52
25:3:233:ASN:HD21	25:3:286:ILE:HG22	1.75	0.52
25:3:484:VAL:C	25:3:485:LEU:HD12	2.34	0.52
25:3:519:VAL:HB	25:3:524:ILE:HG23	1.92	0.52
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.10	0.52
1:A:1189:MET:HG3	1:A:1190:CYS:H	1.75	0.52
1:A:1838:LYS:HA	1:A:1868:MET:SD	2.49	0.52
1:A:2181:GLN:O	1:A:2217:SER:HA	2.09	0.52
3:C:223:ASP:HA	3:C:448:LYS:NZ	2.25	0.52
6:F:22:A:OP1	13:N:116:ASN:OD1	2.27	0.52
10:J:314:TYR:CE1	10:J:336:TRP:HH2	2.28	0.52
15:P:205:LYS:CB	15:P:208:LYS:HB3	2.39	0.52
22:X:171:ARG:HG2	22:X:509:PRO:CB	2.39	0.52
22:X:257:PHE:CE1	22:X:270:LEU:HB2	2.44	0.52
22:X:283:TYR:CB	23:Y:226:MET:HE3	2.38	0.52
22:X:991:LEU:HB2	22:X:995:GLU:OE1	2.10	0.52
24:1:886:HIS:HD2	24:1:887:LYS:HD3	1.74	0.52
28:2:507:LYS:N	28:2:507:LYS:CD	2.72	0.52
35:9:296:HIS:HE1	35:9:358:LEU:HD21	1.74	0.52
1:A:1818:PHE:HD1	1:A:1914:MET:HE3	1.74	0.52
1:A:1895:ALA:HB1	1:A:1943:LEU:HB2	1.92	0.52
3:C:227:LEU:HD21	3:C:229:ILE:HD11	1.91	0.52
3:C:724:TRP:HA	3:C:724:TRP:CE3	2.45	0.52
10:J:289:ASN:HB3	12:L:232:TYR:CE2	2.45	0.52
10:J:376:VAL:HG13	10:J:415:LEU:HB2	1.92	0.52
12:L:175:GLN:O	12:L:178:GLU:N	2.42	0.52
17:R:352:ARG:HG3	17:R:355:ILE:HD12	1.90	0.52
22:X:240:ARG:O	22:X:243:LEU:HB3	2.10	0.52
22:X:760:LEU:O	22:X:764:VAL:HG23	2.10	0.52
24:1:740:GLY:H	24:1:743:LEU:HD22	1.74	0.52
24:1:1007:HIS:HB3	24:1:1049:TYR:OH	2.10	0.52
25:3:550:ASN:HD22	25:3:553:GLN:HB2	1.75	0.52
25:3:991:SER:O	25:3:991:SER:OG	2.28	0.52
30:7:58:CYS:HB3	30:7:62:GLY:N	2.25	0.52
1:A:362:ARG:HA	1:A:362:ARG:HH11	1.74	0.52
3:C:135:CYS:HA	3:C:205:THR:HG1	1.74	0.52
5:E:117:TYR:HB3	5:E:118:ASN:O	2.09	0.52
6:F:87:C:H2'	6:F:88:G:O4'	2.08	0.52
16:Q:827:THR:HA	16:Q:1136:GLN:HA	1.92	0.52
17:R:355:ILE:HG12	22:X:256:LEU:CD1	2.39	0.52
19:T:371:HIS:CE1	19:T:396:LYS:HG3	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:164:TRP:NE1	22:X:542:PHE:CB	2.73	0.52
24:1:1210:HIS:ND1	28:2:584:LEU:HA	2.25	0.52
25:3:632:ALA:O	25:3:633:LEU:HD23	2.09	0.52
1:A:417:ARG:HB3	1:A:417:ARG:NH1	2.24	0.52
1:A:1957:ASP:OD1	1:A:1958:LYS:N	2.43	0.52
3:C:125:ASN:OD1	3:C:127:GLU:N	2.39	0.52
7:G:116:C:C5	17:R:370:SER:HB3	2.45	0.52
8:H:56:A:C2	28:2:478:HIS:CE1	2.98	0.52
10:J:357:LYS:O	10:J:359:VAL:N	2.43	0.52
12:L:178:GLU:O	12:L:181:ARG:HG3	2.09	0.52
13:N:44:GLU:HA	13:N:47:TRP:CE2	2.44	0.52
15:P:183:LYS:O	15:P:183:LYS:HG2	2.09	0.52
16:Q:1136:GLN:O	16:Q:1157:LEU:N	2.42	0.52
17:R:331:ALA:HA	22:X:275:ARG:CZ	2.40	0.52
17:R:369:LEU:HG	17:R:376:LYS:HG2	1.91	0.52
22:X:973:ASN:OD1	22:X:973:ASN:N	2.42	0.52
24:1:1257:PRO:HD3	28:2:482:ALA:HB2	1.91	0.52
25:3:91:GLU:HG2	25:3:92:TYR:N	2.25	0.52
25:3:92:TYR:OH	25:3:97:ASN:OD1	2.18	0.52
25:3:515:ALA:HB2	25:3:528:ARG:CZ	2.40	0.52
25:3:1125:GLY:C	25:3:1126:ILE:HG13	2.35	0.52
28:2:506:PHE:HB3	28:2:508:ARG:HG3	1.92	0.52
35:9:320:ILE:HD11	35:9:337:GLY:O	2.10	0.52
42:l:33:ILE:N	42:l:42:GLN:O	2.43	0.52
1:A:209:ASP:HB2	1:A:212:PRO:HA	1.92	0.52
2:B:95:G:N3	2:B:95:G:C2'	2.73	0.52
3:C:742:PRO:HG2	3:C:785:ARG:HA	1.92	0.52
5:E:191:GLN:NE2	5:E:193:THR:HA	2.24	0.52
10:J:337:MET:HE3	10:J:346:TRP:CE3	2.45	0.52
13:N:43:VAL:CG2	13:N:47:TRP:HZ2	2.23	0.52
17:R:160:ALA:O	17:R:166:ARG:NH1	2.43	0.52
22:X:263:SER:HA	22:X:267:ARG:NH2	2.22	0.52
22:X:504:GLU:O	22:X:507:SER:OG	2.21	0.52
22:X:603:HIS:HA	22:X:668:ARG:CZ	2.40	0.52
24:1:648:LEU:HA	24:1:651:VAL:HG22	1.92	0.52
24:1:1080:THR:HA	24:1:1083:TYR:HD2	1.74	0.52
24:1:1231:MET:HE1	24:1:1268:ILE:HG12	1.90	0.52
25:3:569:ASP:C	25:3:571:SER:N	2.65	0.52
25:3:695:GLY:HA3	25:3:717:SER:OG	2.10	0.52
27:w:496:LYS:HA	27:w:501:LEU:HB2	1.92	0.52
35:9:282:VAL:HG22	35:9:433:VAL:HG13	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:n:30:THR:N	37:n:39:HIS:O	2.31	0.52
1:A:273:ILE:HD11	1:A:314:ILE:HG21	1.92	0.51
1:A:1590:VAL:HG12	1:A:1664:ILE:HG13	1.92	0.51
3:C:673:LYS:HZ2	3:C:688:ILE:HG21	1.74	0.51
7:G:106:C:OP2	22:X:998:ARG:NH2	2.43	0.51
21:V:555:LEU:HD22	21:V:560:LEU:HB2	1.91	0.51
22:X:164:TRP:HB2	22:X:538:ASP:HB3	1.92	0.51
22:X:164:TRP:HE3	22:X:165:GLU:HA	1.75	0.51
22:X:242:LYS:HD2	22:X:246:LEU:HD22	1.92	0.51
22:X:242:LYS:CD	23:Y:227:VAL:HG21	2.36	0.51
22:X:257:PHE:CZ	22:X:267:ARG:HA	2.45	0.51
22:X:257:PHE:HZ	22:X:267:ARG:HA	1.74	0.51
22:X:527:LEU:N	22:X:754:GLU:OE2	2.38	0.51
22:X:714:CYS:SG	22:X:722:ARG:NH1	2.84	0.51
24:1:661:ARG:HG2	24:1:692:HIS:NE2	2.25	0.51
24:1:1289:ASN:HB3	24:1:1295:TYR:H	1.75	0.51
25:3:206:GLN:NE2	25:3:232:GLY:H	2.07	0.51
35:9:370:ASN:HB2	35:9:375:SER:O	2.10	0.51
40:j:32:GLN:HA	40:j:43:ILE:O	2.11	0.51
1:A:523:ASN:CG	11:K:194:ARG:HD3	2.35	0.51
1:A:758:ARG:HH21	1:A:775:ASN:HD22	1.58	0.51
1:A:1454:TRP:H	1:A:1454:TRP:CD1	2.26	0.51
1:A:1580:HIS:HD2	1:A:1583:GLN:NE2	2.08	0.51
1:A:1814:THR:OG1	1:A:1816:GLN:HB2	2.11	0.51
2:B:65:G:H2'	2:B:66:A:H8	1.75	0.51
2:B:90:U:C5	42:g:38:ASN:C	2.85	0.51
7:G:85:G:H2'	7:G:86:A:N9	2.25	0.51
10:J:431:ARG:HH11	10:J:434:VAL:HG11	1.76	0.51
21:V:539:LEU:HB3	21:V:543:LYS:HB2	1.91	0.51
22:X:171:ARG:HG2	22:X:509:PRO:HB3	1.91	0.51
22:X:182:ALA:CA	22:X:924:ARG:NH1	2.73	0.51
22:X:430:THR:O	22:X:433:PRO:HD2	2.10	0.51
23:Y:21:ARG:HH12	23:Y:83:VAL:H	1.58	0.51
25:3:317:THR:HB	25:3:322:VAL:HA	1.92	0.51
25:3:1015:LYS:HZ2	25:3:1016:ARG:N	2.09	0.51
35:9:95:LYS:HA	35:9:100:LYS:O	2.11	0.51
36:m:72:LEU:HA	42:l:70:PHE:HA	1.91	0.51
1:A:32:GLU:HG2	1:A:36:LYS:HE2	1.93	0.51
1:A:599:MET:O	1:A:603:ARG:HG3	2.10	0.51
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.28	0.51
2:B:85:C:OP1	38:c:20:GLU:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:750:LEU:O	3:C:754:VAL:HG23	2.10	0.51
5:E:166:LEU:HD12	5:E:178:LEU:HD11	1.91	0.51
5:E:190:PHE:HE1	5:E:225:ASN:HA	1.75	0.51
6:F:35:A:C8	7:G:12:G:C6	2.97	0.51
10:J:286:GLU:HG2	10:J:298:ILE:HD12	1.91	0.51
10:J:431:ARG:HD2	10:J:434:VAL:HG11	1.93	0.51
17:R:243:GLN:HA	17:R:243:GLN:OE1	2.11	0.51
17:R:357:HIS:HD2	23:Y:276:LYS:HZ1	1.59	0.51
21:V:571:SER:O	21:V:575:THR:OG1	2.27	0.51
21:V:628:ILE:O	21:V:632:THR:OG1	2.27	0.51
22:X:411:ALA:HA	22:X:414:ASN:HD22	1.75	0.51
22:X:790:LEU:HA	22:X:793:LEU:HD12	1.92	0.51
23:Y:23:ARG:O	23:Y:26:LEU:HG	2.09	0.51
24:1:823:MET:HE3	24:1:829:ASN:HB3	1.93	0.51
24:1:1056:MET:HE3	24:1:1059:CYS:HB2	1.92	0.51
25:3:147:ASP:OD1	25:3:150:ALA:N	2.43	0.51
25:3:606:ALA:HA	25:3:616:ILE:HA	1.92	0.51
25:3:674:LEU:C	25:3:675:LEU:HD12	2.34	0.51
25:3:1115:GLU:HG3	28:2:708:TRP:HZ2	1.72	0.51
26:p:185:GLY:CA	27:w:485:ASN:HD22	2.22	0.51
27:w:440:ILE:HG12	27:w:459:TRP:CD2	2.45	0.51
1:A:984:MET:O	1:A:988:ILE:HG13	2.11	0.51
1:A:1179:SER:O	1:A:1201:ARG:NH1	2.29	0.51
1:A:1401:ARG:HB2	1:A:1401:ARG:NH1	2.25	0.51
1:A:1406:GLU:N	1:A:1406:GLU:OE1	2.43	0.51
1:A:1778:TRP:CH2	1:A:1852:LEU:HD21	2.40	0.51
4:D:1523:LEU:HA	4:D:1700:GLY:O	2.10	0.51
6:F:2:U:H5'	13:N:98:GLU:HG2	1.92	0.51
6:F:36:A:H5''	6:F:37:C:OP2	2.10	0.51
7:G:6:A:C6	7:G:7:G:C5	2.98	0.51
8:H:41:U:H2'	8:H:42:G:H8	1.75	0.51
8:H:56:A:O4'	24:1:1257:PRO:HB2	2.10	0.51
11:K:228:HIS:HB2	11:K:231:GLN:NE2	2.25	0.51
13:N:37:HIS:HB3	13:N:41:ARG:CB	2.23	0.51
16:Q:1180:ILE:O	16:Q:1304:PHE:HA	2.10	0.51
17:R:113:TYR:OH	19:T:402:ASP:O	2.27	0.51
17:R:352:ARG:HD2	22:X:266:GLU:HB3	1.93	0.51
19:T:396:LYS:HB2	19:T:398:TRP:HE1	1.76	0.51
22:X:168:GLU:O	22:X:172:LEU:HG	2.11	0.51
22:X:194:ARG:CD	22:X:194:ARG:H	2.23	0.51
24:1:687:VAL:O	24:1:690:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:1274:ILE:O	25:3:113:ARG:NH1	2.44	0.51
27:w:472:GLN:O	27:w:476:GLU:HG3	2.10	0.51
1:A:79:ARG:HD2	1:A:82:ARG:HE	1.76	0.51
1:A:154:GLU:OE2	1:A:158:ARG:NE	2.32	0.51
1:A:1645:LEU:HD13	1:A:1718:TRP:CH2	2.46	0.51
9:I:139:ALA:HA	16:Q:938:TYR:HA	1.92	0.51
20:U:20:GLN:HG2	20:U:21:ARG:H	1.75	0.51
22:X:611:ILE:HG12	22:X:688:TYR:HB2	1.92	0.51
24:1:906:GLU:N	24:1:906:GLU:OE1	2.44	0.51
25:3:356:HIS:CD2	25:3:403:SER:HG	2.27	0.51
25:3:607:VAL:N	25:3:615:ARG:O	2.29	0.51
3:C:396:LEU:HG	3:C:401:ILE:O	2.11	0.51
3:C:737:PRO:HD3	3:C:743:ASN:ND2	2.26	0.51
7:G:84:U:H5'	27:w:395:TRP:CH2	2.46	0.51
10:J:336:TRP:CD1	10:J:341:PRO:HG3	2.45	0.51
17:R:367:ARG:O	17:R:371:ARG:HG3	2.10	0.51
22:X:272:TYR:O	22:X:276:VAL:HB	2.11	0.51
22:X:635:LEU:O	22:X:638:LYS:HB2	2.11	0.51
24:1:641:ILE:N	24:1:642:PRO:HD2	2.26	0.51
24:1:1302:TYR:CD1	25:3:915:LEU:HD13	2.44	0.51
25:3:1114:SER:HB2	25:3:1215:TYR:CE1	2.46	0.51
27:w:478:GLU:HA	27:w:488:ASN:HA	1.92	0.51
30:7:71:TYR:CD2	30:7:81:ASP:HB2	2.46	0.51
38:h:41:GLN:HA	38:h:55:ARG:HA	1.92	0.51
1:A:348:PRO:HB3	1:A:394:TYR:CZ	2.45	0.51
1:A:474:ARG:HH21	1:A:474:ARG:HB2	1.76	0.51
1:A:1268:ILE:O	1:A:1272:THR:OG1	2.25	0.51
1:A:1284:LEU:O	1:A:1287:LEU:N	2.43	0.51
8:H:151:C:H2'	8:H:152:G:H8	1.76	0.51
8:H:181:G:H2'	8:H:182:U:C6	2.46	0.51
9:I:326:ASP:C	9:I:328:GLU:H	2.17	0.51
12:L:30:GLN:HB3	12:L:33:ARG:HD2	1.92	0.51
22:X:911:ALA:O	22:X:914:VAL:HG22	2.10	0.51
24:1:1291:ASP:OD1	24:1:1292:LYS:N	2.43	0.51
25:3:413:ALA:HB1	25:3:415:LEU:HD13	1.92	0.51
25:3:644:GLU:HG2	25:3:645:MET:N	2.25	0.51
25:3:663:LEU:HD23	25:3:679:LEU:HB3	1.92	0.51
29:4:117:TYR:O	29:4:121:SER:CB	2.58	0.51
3:C:465:MET:HE2	3:C:475:MET:HB2	1.92	0.51
5:E:122:SER:O	5:E:138:SER:OG	2.29	0.51
10:J:377:LYS:HA	10:J:380:ILE:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:213:GLU:HG2	19:T:214:PRO:N	2.26	0.51
19:T:429:SER:O	19:T:429:SER:OG	2.29	0.51
22:X:242:LYS:HG3	23:Y:227:VAL:HG23	1.88	0.51
24:1:545:GLU:HG2	24:1:548:GLU:HG3	1.91	0.51
24:1:547:GLN:HA	24:1:550:HIS:HB3	1.92	0.51
25:3:43:PRO:HB3	25:3:50:VAL:HG22	1.93	0.51
25:3:613:THR:HB	25:3:630:MET:HE1	1.93	0.51
25:3:628:LEU:HD21	25:3:681:PRO:HA	1.92	0.51
25:3:819:MET:HA	25:3:822:GLU:OE1	2.10	0.51
25:3:929:LYS:HG3	25:3:931:VAL:HG22	1.93	0.51
1:A:83:HIS:CE1	7:G:16:G:C6	2.99	0.51
1:A:731:LEU:N	35:9:241:TYR:CD1	2.79	0.51
1:A:1661:TRP:CE3	1:A:1700:GLY:HA3	2.45	0.51
2:B:96:A:N6	41:f:23:GLY:N	2.58	0.51
3:C:510:LEU:HD12	3:C:576:ILE:HG22	1.92	0.51
8:H:102:U:O2	36:m:74:GLY:N	2.44	0.51
8:H:181:G:H21	42:l:52:ASP:C	2.19	0.51
16:Q:128:LYS:O	16:Q:132:ALA:HB2	2.10	0.51
16:Q:1061:MET:O	16:Q:1093:MET:HA	2.11	0.51
21:V:620:ASN:HB3	21:V:623:ASN:ND2	2.25	0.51
22:X:764:VAL:HG21	22:X:792:ALA:HB1	1.92	0.51
22:X:818:LEU:HB3	22:X:820:VAL:HG13	1.92	0.51
24:1:663:THR:HA	24:1:666:LYS:HE3	1.93	0.51
24:1:731:LEU:HD23	24:1:746:PHE:CD1	2.46	0.51
24:1:1103:VAL:HG13	24:1:1108:ASN:ND2	2.24	0.51
25:3:451:GLU:HA	25:3:761:THR:HG22	1.92	0.51
27:w:453:GLU:HA	27:w:456:VAL:HG22	1.93	0.51
27:w:479:TYR:N	27:w:487:VAL:O	2.40	0.51
35:9:292:ASN:HB2	35:9:402:GLY:H	1.75	0.51
40:j:64:ILE:HA	40:j:70:SER:O	2.11	0.51
1:A:411:PHE:C	1:A:413:LEU:H	2.19	0.51
1:A:976:MET:HE2	1:A:1098:PHE:HD1	1.76	0.51
1:A:1579:ALA:CB	11:K:226:TYR:CE2	2.94	0.51
1:A:2267:PHE:CB	4:D:1263:PRO:CA	2.88	0.51
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.39	0.51
3:C:134:LEU:N	3:C:203:MET:O	2.42	0.51
3:C:187:THR:HA	3:C:200:PHE:O	2.11	0.51
3:C:285:VAL:O	3:C:289:ILE:HG13	2.10	0.51
3:C:440:SER:O	3:C:442:LYS:N	2.44	0.51
3:C:694:LYS:O	3:C:698:GLU:HG2	2.11	0.51
5:E:328:GLY:N	5:E:348:ASP:HB3	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:73:A:OP1	6:F:75:G:O2'	2.28	0.51
7:G:12:G:H3'	7:G:13:C:C6	2.46	0.51
15:P:187:ARG:HG2	15:P:188:TRP:O	2.11	0.51
17:R:328:ALA:CB	22:X:279:LEU:HD13	2.41	0.51
19:T:386:THR:HG22	19:T:398:TRP:O	2.11	0.51
23:Y:306:ILE:HD12	23:Y:311:ILE:HD11	1.93	0.51
24:1:560:LEU:HD23	24:1:603:ALA:HB3	1.92	0.51
25:3:42:ARG:HB2	25:3:53:LEU:HD11	1.93	0.51
25:3:233:ASN:ND2	25:3:233:ASN:N	2.59	0.51
25:3:424:TYR:CD1	25:3:437:VAL:HG22	2.46	0.51
25:3:932:ASN:O	25:3:933:ASN:ND2	2.44	0.51
25:3:940:LEU:HB3	25:3:941:HIS:ND1	2.26	0.51
27:w:387:TRP:O	33:v:88:LYS:HG3	2.11	0.51
35:9:405:ASP:OD1	35:9:405:ASP:N	2.38	0.51
1:A:25:MET:SD	1:A:26:SER:N	2.85	0.50
1:A:50:LYS:HB2	1:A:50:LYS:HZ3	1.76	0.50
1:A:136:ILE:HG22	1:A:138:PRO:HD2	1.93	0.50
1:A:762:ARG:NH1	15:P:226:LYS:HZ1	2.08	0.50
2:B:66:A:H2'	2:B:67:A:H8	1.73	0.50
3:C:369:PHE:CE1	3:C:373:ILE:HD12	2.46	0.50
3:C:854:ARG:NH1	3:C:876:PRO:HG2	2.26	0.50
4:D:863:THR:H	25:3:599:GLU:CA	2.01	0.50
6:F:31:U:H3'	6:F:32:U:C6	2.46	0.50
13:N:119:CYS:HB2	13:N:134:CYS:HB3	1.93	0.50
15:P:73:GLU:HG2	15:P:76:ARG:HH21	1.76	0.50
17:R:137:GLU:H	17:R:137:GLU:CD	2.15	0.50
22:X:386:ALA:O	22:X:390:GLU:HG3	2.11	0.50
23:Y:44:ASN:HD22	23:Y:52:GLN:CB	2.24	0.50
24:1:573:LYS:H	24:1:573:LYS:HD2	1.76	0.50
24:1:618:ASP:HA	24:1:660:ALA:HB2	1.92	0.50
24:1:831:ARG:O	24:1:834:VAL:HB	2.10	0.50
24:1:908:SER:OG	24:1:912:ASN:OD1	2.28	0.50
25:3:720:TRP:CE3	25:3:731:LEU:HG	2.45	0.50
30:7:39:PRO:HB2	30:7:70:TYR:CD1	2.45	0.50
1:A:451:LEU:O	1:A:455:VAL:HG23	2.11	0.50
1:A:1942:ALA:HB2	1:A:1983:LEU:HD23	1.93	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.46	0.50
3:C:461:LEU:HB3	3:C:465:MET:HE3	1.93	0.50
3:C:559:ILE:HD12	3:C:560:VAL:O	2.10	0.50
4:D:863:THR:CB	25:3:600:GLN:N	2.74	0.50
5:E:218:LYS:HG3	5:E:230:THR:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:248:SER:OG	5:E:265:ARG:NH2	2.44	0.50
7:G:84:U:H5'	27:w:395:TRP:HH2	1.75	0.50
10:J:339:TRP:CE3	17:R:116:TYR:CD2	2.99	0.50
10:J:386:GLU:O	10:J:391:TYR:N	2.40	0.50
16:Q:893:SER:O	16:Q:897:ARG:CB	2.59	0.50
19:T:203:HIS:HE1	19:T:229:LYS:HG3	1.73	0.50
22:X:397:ARG:HA	22:X:402:PHE:CG	2.47	0.50
22:X:454:ARG:HH12	22:X:679:THR:CB	2.25	0.50
23:Y:18:THR:HB	23:Y:166:PHE:CE2	2.46	0.50
23:Y:117:ASP:N	23:Y:117:ASP:OD1	2.44	0.50
25:3:614:VAL:HG23	25:3:633:LEU:HD11	1.93	0.50
25:3:677:THR:HA	25:3:685:ASP:O	2.12	0.50
28:2:498:VAL:HG11	28:2:590:LEU:HD21	1.92	0.50
1:A:948:PRO:O	1:A:952:VAL:HG23	2.12	0.50
3:C:692:LEU:HB2	3:C:786:ASN:HD22	1.77	0.50
3:C:918:ILE:HG22	3:C:920:PRO:HA	1.93	0.50
5:E:118:ASN:ND2	5:E:121:GLY:H	2.09	0.50
6:F:81:C:H4'	6:F:82:A:H5'	1.92	0.50
7:G:104:C:O2'	7:G:105:C:OP2	2.26	0.50
10:J:313:TRP:HB3	10:J:336:TRP:CZ3	2.46	0.50
22:X:472:LYS:HB3	22:X:475:ASN:ND2	2.26	0.50
23:Y:27:ASN:OD1	23:Y:66:ILE:N	2.28	0.50
24:1:699:GLN:NE2	24:1:738:HIS:HE1	2.08	0.50
24:1:712:LEU:O	24:1:716:ALA:CB	2.58	0.50
1:A:146:SER:HA	1:A:149:ILE:HD12	1.94	0.50
1:A:266:SER:OG	1:A:267:LYS:N	2.42	0.50
1:A:516:LEU:HD11	1:A:538:SER:HB2	1.92	0.50
1:A:570:ASP:HB3	1:A:573:GLN:HB2	1.93	0.50
1:A:1864:THR:HG22	1:A:1890:GLN:OE1	2.10	0.50
3:C:243:ILE:HD11	3:C:288:LEU:HB3	1.93	0.50
3:C:283:ASP:OD2	3:C:284:GLU:N	2.45	0.50
3:C:442:LYS:HZ1	3:C:469:ASP:HA	1.75	0.50
3:C:508:LYS:HB2	3:C:524:ILE:HD13	1.93	0.50
3:C:810:PRO:HA	3:C:813:ARG:HG2	1.93	0.50
5:E:66:GLU:N	5:E:87:ASP:OD2	2.44	0.50
5:E:203:ASP:N	5:E:203:ASP:OD1	2.43	0.50
5:E:346:SER:HB3	5:E:348:ASP:OD1	2.12	0.50
8:H:133:U:H2'	8:H:134:C:C6	2.46	0.50
9:I:342:PRO:C	9:I:344:LEU:H	2.20	0.50
10:J:314:TYR:CD1	10:J:336:TRP:HH2	2.30	0.50
15:P:216:ARG:HH12	35:9:257:PRO:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:1060:LEU:HA	16:Q:1092:ILE:O	2.12	0.50
17:R:331:ALA:CA	22:X:275:ARG:NH2	2.74	0.50
21:V:646:HIS:C	21:V:646:HIS:ND1	2.69	0.50
24:1:495:ARG:HA	24:1:498:MET:HE3	1.94	0.50
24:1:824:ALA:HB3	24:1:864:TYR:HD1	1.76	0.50
25:3:185:LEU:HD13	25:3:206:GLN:OE1	2.11	0.50
25:3:259:LYS:HE2	25:3:266:ASP:HB3	1.93	0.50
25:3:642:ILE:H	25:3:703:ARG:NE	2.09	0.50
25:3:757:ILE:HA	25:3:762:LEU:HA	1.94	0.50
25:3:1011:TRP:HB2	25:3:1025:ALA:O	2.11	0.50
33:v:80:THR:OG1	33:v:81:ASN:N	2.45	0.50
1:A:196:ASP:OD2	1:A:199:GLU:N	2.29	0.50
1:A:378:PHE:CG	3:C:342:ARG:HD2	2.47	0.50
2:B:98:G:H2'	2:B:99:C:C6	2.46	0.50
3:C:377:LEU:HA	3:C:380:ILE:HB	1.94	0.50
5:E:167:VAL:O	5:E:178:LEU:HD12	2.12	0.50
6:F:58:G:O2'	6:F:59:G:H5'	2.11	0.50
7:G:85:G:H2'	7:G:86:A:C4	2.47	0.50
8:H:152:G:H2'	8:H:153:A:C8	2.47	0.50
10:J:374:PRO:HB3	10:J:405:PHE:HZ	1.76	0.50
19:T:190:TRP:CG	19:T:497:GLU:HG3	2.46	0.50
19:T:428:VAL:HG22	19:T:438:LEU:HD22	1.92	0.50
22:X:745:HIS:HB2	22:X:746:GLU:OE2	2.11	0.50
23:Y:64:GLU:HB3	23:Y:76:SER:HB2	1.93	0.50
24:1:652:CYS:HB2	24:1:692:HIS:CE1	2.35	0.50
24:1:898:TYR:CZ	24:1:902:GLU:HG2	2.47	0.50
24:1:972:GLY:O	24:1:976:VAL:HG12	2.10	0.50
24:1:1003:VAL:HG22	24:1:1004:ILE:N	2.27	0.50
25:3:805:ASN:CB	31:5:58:ASN:CB	2.90	0.50
33:v:73:THR:HA	33:v:78:HIS:CD2	2.46	0.50
1:A:1493:THR:O	1:A:1748:ARG:NE	2.45	0.50
1:A:1628:ASP:OD2	1:A:1663:ASP:HA	2.12	0.50
3:C:531:TRP:CZ3	3:C:540:GLU:HB3	2.47	0.50
5:E:219:VAL:O	5:E:228:THR:N	2.42	0.50
12:L:222:LEU:H	12:L:222:LEU:HD22	1.77	0.50
25:3:458:ALA:HB1	25:3:460:TRP:HZ3	1.75	0.50
25:3:700:LYS:O	25:3:714:ALA:HA	2.11	0.50
25:3:1188:ASN:HA	25:3:1191:LYS:HZ2	1.76	0.50
35:9:350:PHE:CE1	35:9:376:ASN:HB3	2.46	0.50
1:A:386:PRO:HG3	3:C:372:PHE:HE1	1.75	0.50
1:A:1719:PHE:CD1	1:A:1719:PHE:C	2.90	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:203:MET:HG3	3:C:221:ILE:HD11	1.92	0.50
5:E:268:ALA:O	5:E:270:LYS:N	2.44	0.50
17:R:348:GLU:CD	22:X:262:LEU:HB2	2.35	0.50
21:V:617:PRO:HB3	21:V:623:ASN:HD22	1.77	0.50
23:Y:305:LEU:HD21	23:Y:308:ASP:HA	1.93	0.50
24:1:830:TYR:O	24:1:834:VAL:HG23	2.11	0.50
25:3:713:LEU:HD13	25:3:714:ALA:N	2.27	0.50
25:3:1040:ASP:OD2	25:3:1042:ASP:N	2.45	0.50
27:w:421:ALA:HA	27:w:424:ARG:NE	2.24	0.50
1:A:1778:TRP:C	1:A:1779:PHE:HD2	2.19	0.50
1:A:1946:ASN:HD22	1:A:1949:ARG:HB2	1.76	0.50
2:B:96:A:H61	41:f:23:GLY:N	2.07	0.50
3:C:300:LEU:HA	3:C:306:ASN:ND2	2.27	0.50
5:E:236:ASP:HB2	5:E:256:ASP:HB3	1.94	0.50
6:F:7:G:C6	6:F:15:A:C6	3.00	0.50
6:F:41:A:C2	7:G:7:G:N1	2.80	0.50
16:Q:1269:ASP:O	16:Q:1300:GLY:N	2.45	0.50
17:R:408:ASP:OD2	17:R:410:ARG:NH1	2.44	0.50
22:X:612:LEU:HD23	22:X:686:ILE:HG13	1.94	0.50
22:X:752:VAL:O	22:X:757:ARG:NH2	2.44	0.50
22:X:1005:SER:HA	22:X:1008:LEU:HG	1.94	0.50
25:3:275:ARG:HB3	25:3:275:ARG:HH21	1.75	0.50
25:3:488:GLY:C	25:3:490:THR:H	2.20	0.50
25:3:665:LEU:HD21	25:3:667:ILE:HD11	1.94	0.50
25:3:776:GLN:HG2	25:3:777:VAL:N	2.27	0.50
35:9:323:ARG:HE	35:9:325:ILE:HD11	1.76	0.50
1:A:246:LEU:HD22	1:A:408:PRO:HG2	1.93	0.50
3:C:474:LEU:O	3:C:566:THR:HA	2.12	0.50
3:C:823:ALA:O	3:C:824:THR:OG1	2.26	0.50
6:F:88:G:C2	8:H:11:G:C2	3.00	0.50
10:J:382:TYR:O	10:J:386:GLU:HG2	2.11	0.50
16:Q:817:GLY:O	16:Q:1090:ARG:HA	2.12	0.50
17:R:351:GLU:O	17:R:355:ILE:HG13	2.11	0.50
19:T:399:LYS:HB2	19:T:406:ILE:HD11	1.94	0.50
20:U:26:VAL:HG12	21:V:517:LEU:CD2	2.38	0.50
25:3:22:PHE:N	25:3:29:GLU:OE1	2.45	0.50
25:3:379:LEU:HD12	25:3:380:GLU:H	1.76	0.50
35:9:281:TYR:H	35:9:435:VAL:HG22	1.77	0.50
40:e:15:VAL:O	41:f:33:GLY:HA3	2.12	0.50
1:A:216:SER:O	1:A:216:SER:OG	2.24	0.49
1:A:303:ILE:HG12	3:C:932:GLU:OE2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:514:ASN:ND2	6:F:36:A:O2'	2.39	0.49
1:A:1868:MET:O	1:A:1871:PRO:HD2	2.11	0.49
1:A:1874:VAL:O	1:A:1877:LEU:HG	2.12	0.49
3:C:137:HIS:HA	3:C:238:ASN:HB3	1.94	0.49
3:C:301:SER:H	3:C:306:ASN:ND2	2.04	0.49
3:C:568:PRO:C	3:C:570:GLY:H	2.20	0.49
8:H:46:U:O2	8:H:46:U:O2'	2.27	0.49
8:H:103:U:H4'	8:H:104:U:H5'	1.92	0.49
12:L:77:LEU:CD2	35:9:221:LEU:HD22	2.39	0.49
22:X:592:LEU:HD12	22:X:593:GLU:N	2.27	0.49
23:Y:30:LYS:NZ	23:Y:168:ASP:OD1	2.29	0.49
25:3:704:VAL:C	25:3:710:GLU:HG3	2.37	0.49
25:3:706:MET:HG2	25:3:770:LEU:HD12	1.94	0.49
25:3:823:MET:SD	25:3:838:MET:HG3	2.52	0.49
25:3:1187:PRO:O	25:3:1191:LYS:HG3	2.12	0.49
28:2:534:GLN:O	28:2:538:GLU:HG3	2.11	0.49
35:9:242:SER:HB2	35:9:262:GLU:C	2.37	0.49
1:A:137:GLU:O	1:A:141:ILE:HG13	2.12	0.49
1:A:542:ASN:O	1:A:546:LEU:HB2	2.11	0.49
1:A:1218:ASN:OD1	1:A:1220:VAL:HG22	2.12	0.49
1:A:1817:LEU:HD22	1:A:1917:PHE:HB2	1.93	0.49
2:B:115:C:OP1	40:e:67:LYS:O	2.30	0.49
3:C:709:TRP:HZ3	3:C:717:PHE:HB2	1.76	0.49
4:D:538:ILE:O	4:D:585:ILE:HA	2.12	0.49
8:H:43:U:HO2'	8:H:44:U:P	2.34	0.49
8:H:165:A:O2'	8:H:166:G:O4'	2.29	0.49
12:L:222:LEU:O	17:R:86:LEU:CD2	2.60	0.49
14:O:259:ARG:O	16:Q:498:GLU:CB	2.60	0.49
22:X:162:ASP:O	22:X:165:GLU:N	2.45	0.49
22:X:284:ARG:HD3	23:Y:223:LEU:CD2	2.43	0.49
22:X:651:LEU:HD13	22:X:655:MET:HB2	1.94	0.49
24:1:522:LYS:HD3	24:1:526:PHE:CE2	2.48	0.49
27:w:388:ASP:HA	33:v:88:LYS:HB2	1.93	0.49
35:9:102:HIS:HA	35:9:110:PHE:H	1.77	0.49
35:9:323:ARG:HD2	35:9:324:SER:H	1.77	0.49
36:m:46:ASP:HA	36:m:66:VAL:HA	1.93	0.49
1:A:122:ILE:HD13	1:A:483:GLN:HG2	1.94	0.49
1:A:389:LYS:HA	3:C:379:LYS:NZ	2.27	0.49
1:A:727:LYS:CG	35:9:244:GLY:HA3	2.42	0.49
1:A:845:ARG:HH12	1:A:1440:THR:HG22	1.77	0.49
2:B:21:A:H2'	2:B:21:A:N3	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:GLY:HA3	45:C:1500:GTP:O3G	2.12	0.49
5:E:118:ASN:HD21	5:E:122:SER:H	1.61	0.49
7:G:97:A:H4'	24:1:1110:VAL:HG11	1.95	0.49
10:J:313:TRP:HB3	10:J:336:TRP:CE3	2.47	0.49
17:R:348:GLU:CG	22:X:263:SER:H	2.26	0.49
19:T:221:THR:OG1	19:T:231:TRP:NE1	2.36	0.49
19:T:422:ASN:OD1	19:T:474:GLU:HB3	2.11	0.49
22:X:443:ASN:O	22:X:444:LYS:HB2	2.12	0.49
22:X:736:ARG:HB3	22:X:738:TYR:CE1	2.48	0.49
25:3:159:GLU:CD	25:3:161:HIS:H	2.19	0.49
25:3:331:ASP:CG	25:3:390:ARG:HH21	2.20	0.49
1:A:1089:CYS:SG	1:A:1096:HIS:CD2	3.05	0.49
1:A:1850:ARG:HG2	1:A:1879:PHE:HE2	1.77	0.49
1:A:1902:PHE:CE2	1:A:1967:ILE:HD12	2.47	0.49
1:A:1902:PHE:HE2	1:A:1967:ILE:HD12	1.77	0.49
3:C:302:PRO:HG2	3:C:320:LEU:HD11	1.94	0.49
3:C:670:SER:OG	3:C:819:ALA:O	2.31	0.49
3:C:813:ARG:NH2	35:9:106:LEU:HA	2.24	0.49
6:F:22:A:H5''	13:N:115:THR:HB	1.93	0.49
7:G:7:G:O2'	7:G:8:C:H5'	2.13	0.49
17:R:243:GLN:OE1	17:R:246:LYS:HD2	2.11	0.49
17:R:376:LYS:HA	17:R:379:LYS:HB2	1.94	0.49
21:V:490:CYS:SG	21:V:524:SER:HB3	2.51	0.49
25:3:238:VAL:HB	25:3:247:GLY:O	2.12	0.49
25:3:316:GLU:O	25:3:323:THR:OG1	2.29	0.49
25:3:616:ILE:O	25:3:628:LEU:N	2.45	0.49
1:A:1382:SER:HB2	1:A:1415:GLY:HA2	1.93	0.49
1:A:1817:LEU:HD23	1:A:1917:PHE:H	1.77	0.49
1:A:2307:GLU:C	4:D:1125:SER:N	2.70	0.49
3:C:850:LEU:O	3:C:855:GLY:N	2.45	0.49
5:E:126:SER:OG	5:E:136:TRP:NE1	2.46	0.49
7:G:117:A:H2'	23:Y:245:CYS:HG	1.56	0.49
17:R:355:ILE:HG13	22:X:256:LEU:HD13	1.94	0.49
22:X:478:GLY:HA3	22:X:487:THR:HG22	1.94	0.49
23:Y:13:VAL:HB	23:Y:131:GLU:HG3	1.95	0.49
24:1:563:LEU:HB2	24:1:567:VAL:HG13	1.95	0.49
25:3:18:ILE:HD12	25:3:67:ALA:HB2	1.95	0.49
25:3:146:ARG:HB3	25:3:150:ALA:HA	1.93	0.49
25:3:1207:LYS:O	25:3:1211:ILE:HG12	2.12	0.49
28:2:498:VAL:HG22	28:2:588:GLY:HA2	1.95	0.49
33:v:50:HIS:CE1	33:v:51:LEU:HG	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:9:323:ARG:O	35:9:331:GLN:N	2.36	0.49
1:A:347:LEU:HD22	1:A:351:TYR:CZ	2.48	0.49
1:A:362:ARG:NH2	21:V:323:LEU:C	2.71	0.49
1:A:384:VAL:HA	3:C:331:PHE:HD2	1.78	0.49
1:A:671:THR:O	1:A:676:ARG:NH1	2.46	0.49
1:A:723:ASN:OD1	35:9:252:SER:HA	2.13	0.49
2:B:14:U:H2'	2:B:15:C:H6	1.78	0.49
2:B:92:U:H3'	2:B:92:U:H6	1.77	0.49
3:C:296:GLU:H	3:C:296:GLU:CD	2.21	0.49
3:C:807:GLN:NE2	35:9:145:LEU:O	2.46	0.49
7:G:116:C:C2	17:R:374:PRO:HA	2.48	0.49
8:H:7:U:H2'	8:H:8:C:C6	2.47	0.49
8:H:33:G:C6	8:H:34:U:C4	3.01	0.49
10:J:366:TYR:O	10:J:370:VAL:HG23	2.13	0.49
12:L:227:THR:OG1	17:R:84:ASN:CB	2.56	0.49
17:R:351:GLU:OE2	22:X:256:LEU:O	2.30	0.49
22:X:234:TYR:CG	23:Y:317:GLN:HB3	2.47	0.49
22:X:416:GLN:NE2	22:X:546:LEU:O	2.28	0.49
22:X:842:THR:HB	22:X:882:LEU:HD12	1.94	0.49
23:Y:74:GLN:OE1	23:Y:74:GLN:N	2.45	0.49
24:1:569:PRO:HD2	24:1:570:TYR:CE2	2.48	0.49
24:1:663:THR:HA	24:1:666:LYS:CE	2.43	0.49
25:3:209:THR:OG1	25:3:210:PHE:N	2.45	0.49
25:3:463:ARG:HD3	25:3:468:ASP:HB3	1.94	0.49
25:3:642:ILE:H	25:3:703:ARG:HH21	1.61	0.49
25:3:740:GLU:HB2	25:3:758:SER:HA	1.95	0.49
28:2:462:VAL:O	28:2:466:LYS:HG3	2.12	0.49
1:A:1623:ASN:HD22	1:A:1623:ASN:C	2.19	0.49
1:A:1635:TYR:O	1:A:1636:LYS:HG3	2.12	0.49
2:B:98:G:H2'	2:B:99:C:H6	1.77	0.49
3:C:528:GLY:HA3	3:C:553:GLU:HG2	1.95	0.49
3:C:530:LEU:O	3:C:540:GLU:HA	2.12	0.49
5:E:137:ASP:O	5:E:141:GLY:N	2.26	0.49
5:E:188:GLN:CD	5:E:189:THR:H	2.21	0.49
7:G:100:C:C5	24:1:1069:HIS:CD2	2.99	0.49
8:H:182:U:H2'	8:H:183:G:C8	2.48	0.49
16:Q:341:ALA:O	16:Q:345:PHE:N	2.36	0.49
21:V:620:ASN:HD22	21:V:623:ASN:H	1.60	0.49
22:X:620:GLU:CD	22:X:620:GLU:H	2.17	0.49
22:X:655:MET:O	22:X:658:ARG:HG2	2.12	0.49
22:X:986:TYR:HB3	22:X:997:MET:HE2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:469:GLU:HG2	25:3:470:PHE:CD1	2.47	0.49
25:3:1041:TYR:CB	28:2:705:ARG:HA	2.42	0.49
25:3:1098:GLY:C	25:3:1099:GLU:HG3	2.38	0.49
25:3:1165:SER:HB2	25:3:1169:PRO:HA	1.94	0.49
1:A:197:PRO:HA	1:A:204:LEU:HD13	1.94	0.49
1:A:590:GLY:HA2	1:A:592:TYR:CE2	2.47	0.49
1:A:1076:ASP:N	1:A:1076:ASP:OD2	2.43	0.49
1:A:1914:MET:HE1	1:A:1916:LEU:HB2	1.94	0.49
3:C:496:VAL:HG13	3:C:501:ILE:HD11	1.94	0.49
3:C:500:THR:HB	3:C:502:HIS:CE1	2.48	0.49
6:F:86:U:C4	8:H:12:G:O6	2.66	0.49
8:H:54:U:H2'	8:H:55:U:C6	2.48	0.49
12:L:52:GLU:O	12:L:58:ILE:HD13	2.12	0.49
17:R:237:MET:HE3	17:R:241:GLU:HB3	1.94	0.49
22:X:485:ASP:OD1	22:X:487:THR:OG1	2.24	0.49
24:1:581:LEU:O	24:1:584:ASP:HB3	2.12	0.49
25:3:388:GLN:NE2	25:3:845:GLU:OE1	2.46	0.49
28:2:705:ARG:N	28:2:705:ARG:HD2	2.28	0.49
30:7:73:LYS:HA	30:7:76:THR:HG22	1.95	0.49
1:A:498:ARG:HG2	1:A:502:ASN:HD21	1.77	0.49
1:A:693:ILE:C	1:A:695:ASP:N	2.70	0.49
1:A:1642:PRO:HA	1:A:1716:GLY:O	2.13	0.49
1:A:1860:GLN:HA	1:A:1883:VAL:O	2.13	0.49
1:A:1984:LYS:HG2	1:A:2011:ILE:CD1	2.43	0.49
3:C:259:LYS:HE3	45:C:1500:GTP:H1'	1.95	0.49
3:C:693:GLU:OE1	3:C:695:GLY:N	2.45	0.49
4:D:537:LYS:O	4:D:609:VAL:HA	2.13	0.49
6:F:19:C:H2'	6:F:20:A:C8	2.47	0.49
7:G:84:U:P	27:w:395:TRP:HH2	2.35	0.49
8:H:64:A:H2'	8:H:65:U:C6	2.48	0.49
8:H:139:C:H2'	8:H:140:A:H8	1.78	0.49
10:J:320:GLU:OE1	10:J:325:ASN:HB3	2.12	0.49
17:R:154:SER:O	17:R:157:GLN:HG2	2.12	0.49
22:X:716:LYS:O	22:X:720:ASN:ND2	2.46	0.49
22:X:827:MET:HE3	22:X:840:ILE:HG23	1.94	0.49
22:X:932:CYS:HA	22:X:938:ARG:HH11	1.77	0.49
24:1:869:MET:HE2	24:1:896:ILE:HD13	1.95	0.49
27:w:405:ASN:HA	27:w:416:TYR:O	2.13	0.49
30:7:42:LEU:HG	30:7:70:TYR:CE2	2.47	0.49
1:A:872:ASP:C	1:A:874:PRO:HD3	2.38	0.49
1:A:1845:VAL:O	1:A:1849:ILE:HG13	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1894:GLN:HE21	1:A:1944:HIS:CE1	2.31	0.49
3:C:89:LEU:HD12	19:T:240:LEU:HD11	1.94	0.49
10:J:269:LEU:HD21	10:J:279:TRP:CZ3	2.47	0.49
12:L:224:PHE:CD1	17:R:88:ILE:HG12	2.48	0.49
13:N:70:ILE:HG23	13:N:74:LEU:HD23	1.94	0.49
15:P:68:ARG:HB3	15:P:68:ARG:HH11	1.77	0.49
19:T:395:ILE:HD12	19:T:395:ILE:H	1.78	0.49
21:V:320:ARG:O	21:V:324:HIS:CB	2.61	0.49
22:X:888:TRP:O	22:X:891:SER:OG	2.25	0.49
24:1:862:GLU:HA	24:1:865:ARG:NH1	2.27	0.49
24:1:1076:ALA:O	24:1:1080:THR:HG23	2.12	0.49
25:3:249:LEU:HA	25:3:257:THR:O	2.12	0.49
25:3:952:ILE:HG12	25:3:961:ILE:HG12	1.95	0.49
1:A:214:ARG:NH2	1:A:223:SER:OG	2.46	0.48
1:A:1131:LYS:HE2	1:A:1174:PHE:CE2	2.48	0.48
1:A:1455:TRP:H	1:A:1455:TRP:CD1	2.30	0.48
3:C:711:ARG:HH22	3:C:733:TRP:HA	1.78	0.48
4:D:1188:VAL:HA	4:D:1201:GLU:O	2.13	0.48
6:F:48:A:O2'	12:L:33:ARG:NH1	2.39	0.48
10:J:346:TRP:CD1	10:J:369:PHE:HD1	2.30	0.48
13:N:53:HIS:O	13:N:57:THR:HG22	2.13	0.48
22:X:194:ARG:H	22:X:194:ARG:HD2	1.78	0.48
22:X:283:TYR:OH	23:Y:222:ILE:HB	2.12	0.48
22:X:715:SER:OG	22:X:716:LYS:N	2.45	0.48
22:X:855:TYR:CE2	22:X:857:PRO:HG3	2.48	0.48
22:X:932:CYS:SG	22:X:935:ASP:N	2.86	0.48
22:X:955:THR:OG1	22:X:958:GLY:O	2.15	0.48
24:1:796:CYS:HA	24:1:801:VAL:HG21	1.94	0.48
25:3:484:VAL:O	25:3:485:LEU:HD12	2.13	0.48
25:3:945:VAL:HG21	25:3:963:VAL:HG21	1.93	0.48
27:w:408:CYS:HG	27:w:425:HIS:CE1	2.27	0.48
27:w:410:ILE:HD12	27:w:438:LEU:HD11	1.95	0.48
1:A:369:GLU:HB2	1:A:371:LEU:HD13	1.95	0.48
1:A:1637:TRP:O	1:A:1656:THR:CA	2.56	0.48
1:A:1925:LYS:HD3	21:V:457:ARG:HH22	1.77	0.48
3:C:201:ASN:HB3	3:C:549:TRP:CE3	2.48	0.48
3:C:475:MET:HA	3:C:565:ILE:O	2.12	0.48
3:C:938:ARG:HG2	3:C:942:GLY:HA3	1.95	0.48
6:F:5:U:H5'	6:F:6:C:H4'	1.94	0.48
8:H:56:A:C5	28:2:504:TRP:HZ3	2.31	0.48
8:H:163:G:O2'	26:p:48:MET:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:352:PHE:HA	10:J:355:ARG:NE	2.27	0.48
10:J:364:THR:O	10:J:367:GLU:HB3	2.13	0.48
19:T:342:GLU:CD	19:T:365:ARG:HH12	2.16	0.48
24:1:796:CYS:HB3	24:1:806:ILE:HG12	1.95	0.48
25:3:477:SER:HA	25:3:482:THR:HG23	1.95	0.48
25:3:603:ARG:HD2	25:3:603:ARG:O	2.13	0.48
25:3:914:ILE:HD12	25:3:919:SER:HB3	1.95	0.48
28:2:591:TYR:HA	28:2:595:LYS:HG3	1.95	0.48
30:7:15:ALA:HB2	30:7:84:GLY:HA2	1.94	0.48
35:9:306:ASN:CG	35:9:345:TYR:H	2.17	0.48
1:A:1413:ASP:O	1:A:1414:ARG:HG3	2.13	0.48
6:F:23:U:H5'	13:N:116:ASN:O	2.14	0.48
10:J:406:PHE:HB3	10:J:411:MET:SD	2.54	0.48
17:R:331:ALA:HA	22:X:275:ARG:NH2	2.29	0.48
19:T:257:ARG:HD3	19:T:298:PRO:O	2.13	0.48
21:V:551:PHE:O	21:V:555:LEU:HD23	2.14	0.48
21:V:616:LEU:HD12	21:V:616:LEU:O	2.13	0.48
21:V:647:LEU:O	21:V:651:PRO:HD3	2.14	0.48
24:1:795:CYS:O	24:1:798:THR:HG23	2.13	0.48
24:1:1074:ARG:NE	24:1:1107:GLN:NE2	2.61	0.48
25:3:181:MET:HB2	25:3:211:TYR:O	2.13	0.48
30:7:30:CYS:SG	30:7:33:CYS:HB3	2.54	0.48
31:5:60:SER:O	31:5:63:ARG:N	2.46	0.48
43:o:100:LEU:O	43:o:124:PRO:HD2	2.13	0.48
1:A:385:GLU:OE1	1:A:389:LYS:HG3	2.13	0.48
1:A:693:ILE:HG22	1:A:694:LEU:HD23	1.94	0.48
1:A:1258:LYS:O	1:A:1262:LYS:HG3	2.13	0.48
1:A:1384:ARG:HH22	1:A:1414:ARG:NH1	2.11	0.48
1:A:1431:ALA:HA	22:X:329:TRP:HD1	1.68	0.48
1:A:1788:VAL:HB	1:A:1800:THR:OG1	2.14	0.48
1:A:2328:ALA:CB	4:D:728:ARG:CA	2.89	0.48
3:C:250:ARG:NH1	3:C:447:PRO:O	2.46	0.48
3:C:366:GLN:HG3	3:C:371:GLU:HG3	1.96	0.48
3:C:495:ARG:HB2	3:C:495:ARG:NH1	2.27	0.48
3:C:938:ARG:HA	3:C:942:GLY:H	1.76	0.48
4:D:754:GLU:CA	25:3:662:PHE:CD1	2.79	0.48
5:E:136:TRP:CZ3	5:E:143:ARG:HB3	2.48	0.48
7:G:111:U:C2'	22:X:482:ARG:HD2	2.43	0.48
8:H:106:G:N3	8:H:107:A:C6	2.81	0.48
19:T:497:GLU:OE1	19:T:497:GLU:N	2.29	0.48
22:X:164:TRP:CZ2	22:X:542:PHE:HD1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:37:TYR:OH	23:Y:106:SER:HB3	2.13	0.48
23:Y:224:LEU:HD11	23:Y:229:ASP:HB2	1.94	0.48
24:1:717:THR:HB	24:1:718:PRO:CD	2.41	0.48
24:1:815:PHE:O	24:1:819:TRP:HB2	2.13	0.48
24:1:889:GLU:OE2	24:1:928:TYR:OH	2.31	0.48
24:1:933:CYS:SG	24:1:970:LEU:HD11	2.52	0.48
25:3:968:ARG:HG2	25:3:982:GLU:OE1	2.12	0.48
28:2:452:LYS:C	28:2:452:LYS:CD	2.86	0.48
33:v:85:ARG:NH1	33:v:88:LYS:HB3	2.22	0.48
39:i:19:VAL:HA	39:i:73:ARG:O	2.13	0.48
1:A:91:ALA:HA	17:R:207:MET:HB3	1.96	0.48
1:A:420:ARG:NH2	1:A:423:ASP:OD1	2.47	0.48
1:A:427:VAL:HG12	1:A:430:TRP:CE3	2.49	0.48
1:A:485:THR:HG22	1:A:486:LYS:N	2.27	0.48
3:C:509:VAL:HG22	3:C:523:GLN:O	2.14	0.48
3:C:561:LYS:NZ	3:C:615:PRO:O	2.41	0.48
3:C:807:GLN:NE2	35:9:145:LEU:CA	2.76	0.48
5:E:176:VAL:O	5:E:189:THR:HA	2.14	0.48
5:E:202:ASN:OD1	5:E:207:GLN:N	2.38	0.48
6:F:15:A:H2'	6:F:16:G:C8	2.48	0.48
6:F:39:A:C5	6:F:40:U:C5	3.02	0.48
7:G:116:C:C2	17:R:370:SER:O	2.67	0.48
21:V:451:ASN:O	21:V:455:PHE:HB2	2.13	0.48
22:X:235:LEU:HB3	23:Y:220:GLN:HG2	1.95	0.48
24:1:517:ARG:HB3	24:1:517:ARG:CZ	2.43	0.48
24:1:970:LEU:O	24:1:974:LEU:HG	2.13	0.48
25:3:143:ILE:H	25:3:143:ILE:HD12	1.79	0.48
25:3:357:TYR:HE1	25:3:400:GLU:HG3	1.77	0.48
25:3:503:THR:HG22	25:3:504:PRO:HD2	1.95	0.48
25:3:543:THR:C	25:3:558:LEU:HD12	2.38	0.48
25:3:804:HIS:NE2	25:3:859:ASN:O	2.46	0.48
1:A:929:GLU:OE1	1:A:933:ARG:NH2	2.40	0.48
1:A:1809:ILE:O	1:A:1817:LEU:HA	2.13	0.48
1:A:1819:LEU:HB3	1:A:1915:VAL:CG2	2.37	0.48
3:C:183:SER:OG	3:C:214:GLU:OE1	2.31	0.48
3:C:286:ASN:ND2	3:C:300:LEU:O	2.46	0.48
10:J:375:ASP:HB2	10:J:378:ASN:CG	2.38	0.48
13:N:120:ARG:HA	13:N:120:ARG:HD2	1.51	0.48
15:P:45:GLN:HA	15:P:45:GLN:HE21	1.79	0.48
16:Q:600:MET:O	16:Q:607:VAL:HA	2.13	0.48
17:R:66:GLU:HA	18:S:89:ASP:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:96:GLY:O	18:S:131:ARG:HA	2.14	0.48
19:T:369:THR:O	19:T:369:THR:OG1	2.27	0.48
21:V:505:LYS:HE3	21:V:553:HIS:NE2	2.28	0.48
22:X:450:CYS:HB2	22:X:495:TYR:CD1	2.48	0.48
22:X:592:LEU:O	22:X:595:CYS:HB2	2.14	0.48
23:Y:1:MET:HG2	23:Y:163:ASP:OD2	2.13	0.48
23:Y:246:LYS:HD2	23:Y:310:ARG:O	2.14	0.48
25:3:1095:TYR:CE1	25:3:1164:ARG:HD2	2.48	0.48
27:w:383:LEU:CD1	27:w:391:PRO:HB3	2.43	0.48
33:v:39:ASP:O	33:v:42:LYS:NZ	2.28	0.48
1:A:523:ASN:OD1	1:A:552:ARG:NH1	2.43	0.48
1:A:643:GLY:HA3	2:B:28:A:O2'	2.13	0.48
1:A:1289:VAL:HG21	1:A:1335:ILE:HD11	1.95	0.48
1:A:1375:TRP:O	1:A:1378:GLU:N	2.46	0.48
1:A:1726:ILE:O	1:A:1727:GLN:C	2.54	0.48
1:A:1768:TYR:CA	1:A:1771:LEU:HB3	2.31	0.48
3:C:313:GLN:HG3	3:C:417:ARG:HH21	1.78	0.48
3:C:666:VAL:HG12	3:C:667:VAL:N	2.29	0.48
4:D:463:PRO:HA	4:D:480:THR:HA	1.95	0.48
7:G:84:U:C5'	27:w:395:TRP:HH2	2.25	0.48
8:H:107:A:C6	8:H:108:G:C6	3.02	0.48
12:L:178:GLU:HB3	12:L:181:ARG:HH11	1.79	0.48
17:R:283:ASN:N	17:R:283:ASN:OD1	2.44	0.48
17:R:346:ASP:N	22:X:261:GLU:O	2.46	0.48
21:V:584:LYS:HG3	21:V:634:ILE:HG22	1.96	0.48
22:X:411:ALA:HA	22:X:414:ASN:ND2	2.28	0.48
22:X:487:THR:HG22	22:X:491:THR:HG21	1.95	0.48
22:X:606:GLN:HB2	22:X:668:ARG:HH22	1.79	0.48
22:X:813:ARG:O	22:X:816:ALA:N	2.46	0.48
23:Y:291:GLU:O	23:Y:295:GLU:HG3	2.14	0.48
24:1:770:MET:HA	24:1:773:LEU:HG	1.95	0.48
24:1:914:PHE:O	24:1:918:VAL:HG23	2.14	0.48
25:3:605:LEU:HD23	25:3:617:ILE:HG22	1.95	0.48
28:2:595:LYS:C	28:2:595:LYS:CE	2.86	0.48
35:9:365:ILE:HG23	35:9:396:ILE:HD13	1.95	0.48
1:A:723:ASN:HD22	1:A:788:GLN:NE2	2.12	0.48
1:A:1209:HIS:ND1	1:A:1210:LYS:HE2	2.29	0.48
1:A:2307:GLU:CB	4:D:1124:GLN:H	2.27	0.48
3:C:69:ALA:HA	3:C:72:VAL:HG12	1.95	0.48
3:C:618:THR:HG23	3:C:630:LEU:HB3	1.94	0.48
3:C:624:SER:HB2	3:C:626:GLU:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:799:GLU:O	3:C:801:LEU:N	2.46	0.48
4:D:1199:LYS:HA	4:D:1255:PHE:HA	1.95	0.48
6:F:23:U:H2'	6:F:24:A:O4'	2.14	0.48
6:F:82:A:H2'	6:F:82:A:OP2	2.14	0.48
7:G:84:U:OP1	27:w:395:TRP:HH2	1.97	0.48
8:H:106:G:H1'	8:H:107:A:N7	2.29	0.48
10:J:257:GLU:OE1	10:J:257:GLU:N	2.47	0.48
14:O:162:PRO:CB	14:O:181:TYR:HA	2.43	0.48
17:R:348:GLU:OE2	22:X:266:GLU:HG2	2.13	0.48
19:T:195:LYS:HZ1	19:T:490:ARG:HH21	1.61	0.48
19:T:271:LYS:HG2	19:T:280:VAL:HG11	1.96	0.48
21:V:496:CYS:HG	21:V:507:PHE:HE1	1.61	0.48
22:X:391:SER:O	22:X:395:VAL:HG23	2.13	0.48
23:Y:195:GLU:H	23:Y:195:GLU:HG3	1.43	0.48
24:1:495:ARG:HA	24:1:498:MET:HB3	1.95	0.48
24:1:524:ARG:HD3	24:1:563:LEU:HD12	1.96	0.48
24:1:823:MET:O	24:1:829:ASN:HB2	2.14	0.48
24:1:967:GLU:CG	24:1:970:LEU:HB3	2.43	0.48
24:1:972:GLY:CA	24:1:1010:THR:HG21	2.40	0.48
24:1:1159:GLY:O	24:1:1161:MET:N	2.46	0.48
25:3:329:TYR:HB3	25:3:370:GLU:CD	2.39	0.48
25:3:415:LEU:HB2	25:3:424:TYR:CE2	2.49	0.48
25:3:449:VAL:HG11	25:3:763:ARG:NH1	2.29	0.48
25:3:745:PHE:CB	25:3:755:VAL:HG23	2.43	0.48
27:w:453:GLU:OE1	27:w:454:ASP:N	2.44	0.48
28:2:461:THR:HG1	28:2:464:GLU:H	1.56	0.48
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.31	0.48
1:A:612:ILE:O	1:A:616:PHE:HB2	2.13	0.48
3:C:212:SER:O	3:C:216:THR:HG23	2.13	0.48
3:C:213:ASP:OD2	3:C:616:SER:OG	2.17	0.48
3:C:483:SER:HA	3:C:490:PHE:HA	1.96	0.48
3:C:850:LEU:HB3	3:C:855:GLY:HA3	1.95	0.48
4:D:898:PRO:HA	4:D:960:ALA:HB1	1.96	0.48
5:E:67:GLY:C	5:E:349:LYS:HG2	2.39	0.48
5:E:75:HIS:O	5:E:78:GLY:N	2.46	0.48
5:E:164:PRO:O	5:E:166:LEU:HD23	2.14	0.48
6:F:22:A:H5''	13:N:116:ASN:H	1.79	0.48
7:G:5:G:N1	7:G:6:A:N6	2.62	0.48
7:G:90:C:H42	8:H:40:C:H42	1.60	0.48
8:H:176:G:H8	8:H:176:G:O5'	1.97	0.48
10:J:396:ARG:HH22	10:J:426:GLN:HG3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:529:PHE:CD1	21:V:564:VAL:HB	2.49	0.48
21:V:537:HIS:CE1	21:V:538:ARG:HG2	2.49	0.48
25:3:563:LEU:O	25:3:580:ARG:HB3	2.14	0.48
25:3:604:PHE:HA	25:3:618:SER:HA	1.96	0.48
25:3:926:TYR:CZ	25:3:942:LYS:HD2	2.48	0.48
43:o:45:ASP:O	43:o:67:LYS:N	2.35	0.48
38:h:100:PHE:N	37:n:68:PHE:O	2.43	0.48
1:A:888:GLN:C	1:A:889:ARG:HG2	2.39	0.48
1:A:1846:ALA:O	1:A:1850:ARG:HG3	2.13	0.48
1:A:1939:ILE:HG21	1:A:1968:TRP:CE2	2.49	0.48
2:B:111:A:H2'	2:B:112:A:C8	2.49	0.48
3:C:607:LEU:HA	3:C:610:VAL:HG22	1.96	0.48
5:E:168:CYS:SG	5:E:199:VAL:HG21	2.54	0.48
7:G:7:G:C2	7:G:8:C:C2	3.02	0.48
7:G:111:U:OP1	22:X:482:ARG:HB2	2.14	0.48
17:R:122:LYS:HE2	19:T:399:LYS:HZ3	1.78	0.48
17:R:213:LYS:HB3	17:R:213:LYS:HE3	1.63	0.48
22:X:446:MET:HE1	22:X:512:ALA:O	2.14	0.48
23:Y:214:GLU:O	23:Y:218:LYS:HG3	2.13	0.48
24:1:770:MET:O	24:1:774:ILE:HG12	2.14	0.48
25:3:16:PHE:HE2	25:3:63:ARG:C	2.22	0.48
25:3:581:LYS:HB2	25:3:625:LEU:HD22	1.94	0.48
25:3:612:ASN:HA	25:3:636:GLN:HA	1.95	0.48
25:3:805:ASN:CB	31:5:58:ASN:HB3	2.40	0.48
25:3:839:ALA:O	25:3:843:LEU:HD12	2.14	0.48
25:3:1034:THR:HG22	25:3:1049:LYS:HG3	1.96	0.48
26:p:193:GLU:CB	27:w:498:GLN:OE1	2.62	0.48
34:u:90:TYR:O	34:u:94:TYR:CB	2.62	0.48
1:A:332:TYR:O	3:C:888:ARG:NH1	2.45	0.47
1:A:1014:ASN:OD1	12:L:84:THR:OG1	2.26	0.47
1:A:1019:TYR:O	1:A:1021:ASP:N	2.47	0.47
1:A:1382:SER:HA	1:A:1415:GLY:HA2	1.96	0.47
1:A:1490:PHE:O	1:A:1493:THR:OG1	2.30	0.47
1:A:2311:PRO:CB	4:D:1125:SER:O	2.62	0.47
3:C:389:ASP:OD2	3:C:389:ASP:N	2.29	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.13	0.47
6:F:49:G:H8	6:F:49:G:OP1	1.97	0.47
7:G:85:G:N2	8:H:45:C:C2	2.80	0.47
9:I:99:HIS:CB	16:Q:946:GLU:HA	2.43	0.47
10:J:285:MET:HE3	10:J:285:MET:HB3	1.73	0.47
10:J:411:MET:HE3	10:J:412:ASP:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:24:SER:O	20:U:24:SER:OG	2.28	0.47
22:X:961:THR:HG21	22:X:964:GLN:NE2	2.29	0.47
23:Y:9:LEU:HD23	23:Y:138:LYS:HD3	1.95	0.47
24:1:570:TYR:HA	24:1:573:LYS:HD3	1.96	0.47
24:1:625:ARG:HH21	24:1:662:HIS:HB3	1.78	0.47
24:1:789:LEU:HB3	24:1:836:THR:HG21	1.96	0.47
25:3:19:HIS:ND1	25:3:19:HIS:O	2.46	0.47
25:3:594:ASN:OD1	25:3:594:ASN:N	2.46	0.47
25:3:1191:LYS:O	25:3:1192:ASN:C	2.57	0.47
30:7:52:GLY:N	30:7:55:GLN:HE21	2.10	0.47
30:7:58:CYS:HB3	30:7:62:GLY:H	1.79	0.47
35:9:73:TYR:O	35:9:75:THR:N	2.47	0.47
1:A:408:PRO:C	1:A:410:PRO:HD2	2.38	0.47
1:A:1719:PHE:C	1:A:1719:PHE:HD1	2.22	0.47
3:C:725:ASP:HB3	3:C:728:ALA:H	1.79	0.47
3:C:891:THR:O	3:C:894:GLN:HG2	2.14	0.47
4:D:735:ALA:C	4:D:737:ALA:H	2.22	0.47
4:D:1459:ILE:HA	4:D:1464:GLY:HA3	1.96	0.47
8:H:34:U:H2'	8:H:35:A:C8	2.49	0.47
13:N:24:GLU:HB2	13:N:28:LYS:HE2	1.95	0.47
13:N:102:CYS:SG	13:N:137:CYS:HB2	2.54	0.47
17:R:331:ALA:CB	22:X:275:ARG:NH1	2.77	0.47
17:R:335:ARG:HA	22:X:271:LYS:HZ1	1.79	0.47
19:T:412:HIS:ND1	19:T:429:SER:OG	2.44	0.47
23:Y:211:ILE:O	23:Y:215:LYS:HG2	2.15	0.47
24:1:529:GLY:HA2	24:1:570:TYR:CZ	2.49	0.47
24:1:632:PHE:O	24:1:635:VAL:HG22	2.13	0.47
24:1:1091:HIS:HE2	28:2:568:TYR:HE1	1.62	0.47
25:3:407:ILE:HD11	25:3:1124:GLY:CA	2.44	0.47
25:3:477:SER:HB2	25:3:505:THR:N	2.11	0.47
25:3:757:ILE:HG22	25:3:762:LEU:HG	1.94	0.47
28:2:461:THR:OG1	28:2:464:GLU:N	2.26	0.47
31:5:51:ASN:OD1	31:5:51:ASN:N	2.46	0.47
1:A:1784:ASN:CG	1:A:1897:LEU:HD11	2.39	0.47
1:A:1841:THR:OG1	1:A:1868:MET:SD	2.64	0.47
1:A:1865:ARG:NH2	1:A:1865:ARG:HA	2.29	0.47
3:C:384:VAL:HG11	3:C:416:LEU:HG	1.97	0.47
3:C:589:LYS:HB3	3:C:659:VAL:HG23	1.96	0.47
12:L:86:ALA:HB1	12:L:91:ARG:O	2.14	0.47
15:P:217:SER:OG	15:P:218:GLU:N	2.47	0.47
17:R:391:VAL:HG13	17:R:396:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:431:GLN:HA	22:X:434:GLN:NE2	2.30	0.47
22:X:864:ALA:HA	22:X:902:PHE:CD2	2.48	0.47
24:1:720:GLY:HA2	24:1:756:LEU:HB3	1.97	0.47
24:1:854:VAL:HG11	24:1:891:GLN:HE21	1.79	0.47
24:1:1140:GLU:HB2	24:1:1143:VAL:CG1	2.44	0.47
25:3:169:HIS:HD2	25:3:170:VAL:N	2.09	0.47
25:3:412:ILE:H	25:3:1105:GLN:NE2	2.09	0.47
30:7:13:LYS:HD2	30:7:48:GLU:OE2	2.14	0.47
30:7:23:CYS:N	30:7:58:CYS:SG	2.73	0.47
33:v:49:ASN:ND2	33:v:53:SER:OG	2.39	0.47
33:v:66:GLU:H	33:v:66:GLU:CD	2.20	0.47
35:9:246:VAL:HG21	35:9:261:HIS:CG	2.50	0.47
1:A:121:HIS:ND1	1:A:123:THR:HG23	2.30	0.47
1:A:363:HIS:NE2	3:C:283:ASP:O	2.45	0.47
1:A:425:PRO:HB3	1:A:635:ARG:NH1	2.30	0.47
1:A:1361:GLU:OE1	1:A:1361:GLU:HA	2.14	0.47
1:A:1645:LEU:HD13	1:A:1718:TRP:HH2	1.80	0.47
1:A:1869:LEU:O	1:A:1873:GLU:HB2	2.14	0.47
2:B:117:A:C2	39:d:26:GLY:O	2.68	0.47
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.42	0.47
3:C:719:GLN:OE1	3:C:724:TRP:HB3	2.13	0.47
5:E:178:LEU:HB3	5:E:187:ILE:HB	1.96	0.47
5:E:244:SER:HB2	5:E:293:TRP:CE2	2.49	0.47
5:E:312:TRP:HE1	5:E:319:ILE:HG12	1.80	0.47
6:F:29:A:H2'	6:F:30:A:C8	2.49	0.47
16:Q:314:ASN:N	16:Q:319:ASN:O	2.43	0.47
17:R:357:HIS:CD2	23:Y:276:LYS:HZ1	2.29	0.47
17:R:367:ARG:CD	17:R:371:ARG:HD2	2.42	0.47
21:V:617:PRO:HG2	21:V:623:ASN:O	2.14	0.47
22:X:516:VAL:HG13	22:X:549:LEU:HD13	1.95	0.47
22:X:919:GLU:O	22:X:922:LEU:HB2	2.14	0.47
22:X:929:LEU:H	22:X:929:LEU:HD12	1.78	0.47
23:Y:21:ARG:HH22	23:Y:82:LYS:C	2.21	0.47
23:Y:45:VAL:HG22	23:Y:51:ILE:HG23	1.95	0.47
23:Y:224:LEU:CD1	23:Y:229:ASP:HB2	2.45	0.47
25:3:22:PHE:HA	25:3:76:ASP:HB2	1.94	0.47
25:3:664:TYR:CG	25:3:729:PHE:HZ	2.32	0.47
1:A:67:ARG:HD2	13:N:33:GLU:OE2	2.15	0.47
1:A:110:TRP:O	1:A:192:GLN:NE2	2.47	0.47
1:A:119:LEU:HD12	1:A:483:GLN:O	2.14	0.47
1:A:386:PRO:CG	1:A:389:LYS:HD2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1332:HIS:CE1	1:A:1359:HIS:HB3	2.49	0.47
6:F:41:A:C2	7:G:7:G:C2	3.03	0.47
6:F:84:A:H4'	6:F:85:U:OP1	2.13	0.47
8:H:166:G:N3	8:H:166:G:H2'	2.29	0.47
8:H:171:U:N3	8:H:172:C:C4	2.83	0.47
10:J:406:PHE:HB3	10:J:411:MET:HB2	1.97	0.47
11:K:218:LYS:HD3	11:K:219:PHE:CE2	2.49	0.47
12:L:233:GLN:HG3	12:L:234:ALA:H	1.79	0.47
21:V:452:LEU:O	21:V:456:ARG:HG3	2.14	0.47
22:X:702:PRO:HB2	22:X:791:LEU:HD13	1.96	0.47
24:1:647:PHE:O	24:1:651:VAL:HG13	2.15	0.47
25:3:70:LEU:HD13	25:3:146:ARG:HG2	1.96	0.47
25:3:302:LEU:HA	25:3:311:PHE:O	2.14	0.47
25:3:346:PHE:HA	25:3:360:GLN:HA	1.95	0.47
25:3:457:ASN:ND2	25:3:479:VAL:HG12	2.29	0.47
33:v:47:MET:HB3	33:v:55:GLU:HB2	1.96	0.47
33:v:85:ARG:HH12	33:v:88:LYS:HD3	1.79	0.47
35:9:300:THR:HA	35:9:353:GLU:CG	2.43	0.47
1:A:902:TYR:HE2	1:A:1246:GLN:HB3	1.79	0.47
1:A:1427:ARG:HB3	22:X:329:TRP:CE3	2.50	0.47
1:A:1862:ILE:HG21	1:A:1885:LYS:HE2	1.95	0.47
3:C:125:ASN:CG	3:C:127:GLU:H	2.23	0.47
3:C:238:ASN:O	3:C:242:LEU:HB2	2.15	0.47
6:F:36:A:N6	6:F:38:G:O6	2.48	0.47
7:G:84:U:OP1	27:w:395:TRP:CH2	2.67	0.47
12:L:202:ARG:O	12:L:203:LYS:HE3	2.14	0.47
21:V:473:ALA:O	21:V:477:LEU:HG	2.15	0.47
21:V:563:SER:HA	21:V:611:PHE:CD2	2.50	0.47
22:X:238:ARG:NH1	23:Y:319:VAL:CG2	2.76	0.47
22:X:754:GLU:HA	22:X:757:ARG:HH22	1.78	0.47
22:X:842:THR:HA	22:X:915:ARG:HD2	1.97	0.47
22:X:981:PRO:HB3	22:X:1002:GLU:OE1	2.14	0.47
23:Y:43:HIS:O	23:Y:149:VAL:HG22	2.13	0.47
23:Y:214:GLU:HB3	23:Y:218:LYS:NZ	2.29	0.47
24:1:933:CYS:O	24:1:934:GLY:C	2.58	0.47
24:1:1233:ALA:O	24:1:1237:LEU:HB2	2.15	0.47
25:3:333:VAL:HG21	25:3:349:VAL:HG21	1.97	0.47
25:3:436:ARG:HD3	25:3:776:GLN:OE1	2.14	0.47
25:3:595:VAL:HG21	25:3:600:GLN:C	2.39	0.47
25:3:636:GLN:HG2	25:3:637:PRO:HD2	1.96	0.47
25:3:665:LEU:CB	25:3:679:LEU:HD23	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:426:PHE:CZ	27:w:448:ASN:HA	2.49	0.47
28:2:529:LYS:HB2	28:2:529:LYS:HE2	1.61	0.47
31:5:13:HIS:ND1	31:5:17:LYS:HE3	2.30	0.47
1:A:79:ARG:HH11	1:A:82:ARG:NH2	2.09	0.47
1:A:309:ARG:HD3	1:A:311:GLU:OE1	2.15	0.47
1:A:361:HIS:CD2	3:C:280:HIS:HB2	2.48	0.47
1:A:381:PRO:HD2	3:C:334:ILE:CG2	2.44	0.47
1:A:1283:GLU:OE1	1:A:1283:GLU:N	2.48	0.47
1:A:1352:HIS:HD2	20:U:5:ILE:HG13	1.78	0.47
1:A:1401:ARG:HB2	1:A:1401:ARG:CZ	2.44	0.47
1:A:1425:LYS:HD2	17:R:416:LYS:HB2	1.96	0.47
1:A:1429:THR:CG2	17:R:418:MET:SD	3.02	0.47
1:A:1768:TYR:CE2	1:A:2012:LEU:HD21	2.48	0.47
1:A:1860:GLN:HB3	1:A:1883:VAL:HB	1.97	0.47
1:A:1928:SER:HB2	1:A:1931:THR:H	1.80	0.47
2:B:64:G:C4	2:B:65:G:C8	3.02	0.47
3:C:133:THR:OG1	3:C:218:GLY:HA3	2.15	0.47
3:C:139:HIS:O	45:C:1500:GTP:O1A	2.33	0.47
3:C:514:TYR:CE2	3:C:522:SER:HB2	2.49	0.47
3:C:595:VAL:HG13	3:C:652:ASP:O	2.15	0.47
3:C:636:TYR:O	3:C:640:VAL:HG23	2.15	0.47
8:H:14:C:H1'	8:H:15:U:H5'	1.97	0.47
8:H:48:A:N3	8:H:78:C:P	2.88	0.47
10:J:376:VAL:O	10:J:379:TRP:HB2	2.15	0.47
19:T:253:ILE:O	19:T:261:LEU:HD12	2.15	0.47
23:Y:38:ASN:OD1	23:Y:158:HIS:HA	2.14	0.47
24:1:582:LEU:HA	24:1:590:ARG:HA	1.97	0.47
24:1:1299:GLU:O	24:1:1302:TYR:HD2	1.97	0.47
25:3:75:LYS:HE3	25:3:76:ASP:H	1.79	0.47
25:3:373:PHE:CE1	25:3:385:PHE:HB3	2.48	0.47
25:3:442:LEU:HD23	25:3:442:LEU:HA	1.71	0.47
25:3:617:ILE:HG12	25:3:627:PRO:HA	1.95	0.47
25:3:867:ARG:NH1	25:3:879:LEU:HD13	2.30	0.47
25:3:979:ARG:NH2	27:w:478:GLU:OE1	2.47	0.47
27:w:397:TYR:CE2	27:w:402:LEU:HB2	2.50	0.47
27:w:461:LYS:HZ2	28:2:467:GLN:C	2.23	0.47
28:2:466:LYS:HG2	28:2:475:VAL:HG21	1.97	0.47
28:2:530:ARG:HH12	28:2:578:TRP:CG	2.32	0.47
33:v:32:GLN:O	33:v:36:GLU:HG2	2.15	0.47
33:v:80:THR:O	33:v:84:ARG:HG2	2.15	0.47
1:A:184:ASP:HB2	13:N:1:MET:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:GLN:HB3	1:A:225:TYR:CE1	2.49	0.47
1:A:397:ASN:HB3	3:C:386:GLY:O	2.15	0.47
1:A:1014:ASN:ND2	1:A:1014:ASN:C	2.73	0.47
1:A:1373:GLN:NE2	1:A:1377:SER:OG	2.48	0.47
2:B:21:A:O3'	2:B:22:U:H4'	2.15	0.47
3:C:142:LYS:NZ	45:C:1500:GTP:O1G	2.48	0.47
5:E:100:ASP:N	5:E:100:ASP:OD1	2.48	0.47
5:E:177:LYS:HB3	5:E:179:TRP:NE1	2.30	0.47
5:E:180:ASP:OD1	5:E:182:ARG:N	2.24	0.47
7:G:15:U:H3'	7:G:16:G:C8	2.49	0.47
8:H:173:C:H2'	8:H:174:A:H8	1.76	0.47
9:I:136:ALA:CA	9:I:144:GLN:CB	2.92	0.47
9:I:231:ASN:O	9:I:233:ASP:N	2.47	0.47
10:J:328:GLY:HA2	10:J:331:GLN:NE2	2.30	0.47
15:P:26:LEU:HD12	15:P:26:LEU:HA	1.62	0.47
16:Q:1082:GLN:N	16:Q:1085:PHE:O	2.29	0.47
22:X:787:GLU:O	22:X:791:LEU:HD12	2.15	0.47
23:Y:9:LEU:CD2	23:Y:138:LYS:HD3	2.45	0.47
23:Y:30:LYS:CE	23:Y:169:PRO:HD2	2.45	0.47
23:Y:215:LYS:O	23:Y:218:LYS:N	2.48	0.47
24:1:573:LYS:O	24:1:577:VAL:HG23	2.15	0.47
24:1:860:GLU:O	24:1:865:ARG:NH2	2.48	0.47
24:1:1135:GLU:HG3	24:1:1135:GLU:O	2.15	0.47
24:1:1279:ALA:O	24:1:1281:ILE:N	2.48	0.47
25:3:164:ASN:HA	25:3:189:TYR:OH	2.15	0.47
25:3:565:TYR:HE1	25:3:619:LEU:HD12	1.80	0.47
33:v:85:ARG:NH1	33:v:88:LYS:HD3	2.30	0.47
1:A:112:GLN:O	1:A:113:ILE:HG13	2.15	0.47
1:A:569:VAL:O	1:A:570:ASP:HB2	2.14	0.47
1:A:1661:TRP:HH2	1:A:1684:PHE:CE1	2.33	0.47
1:A:1685:LEU:O	1:A:1689:THR:HG23	2.14	0.47
1:A:1768:TYR:HE2	1:A:2012:LEU:CD2	2.23	0.47
1:A:1771:LEU:HD11	1:A:1779:PHE:CE2	2.49	0.47
3:C:135:CYS:HG	3:C:242:LEU:HD13	1.77	0.47
3:C:302:PRO:HD2	3:C:344:TRP:CD1	2.50	0.47
4:D:1598:ILE:O	4:D:1601:LEU:N	2.46	0.47
5:E:193:THR:HG23	5:E:194:TYR:CG	2.50	0.47
5:E:198:ALA:O	5:E:210:SER:HA	2.14	0.47
5:E:288:LEU:HD21	5:E:290:ARG:HE	1.80	0.47
13:N:41:ARG:HA	13:N:45:SER:HB2	1.95	0.47
13:N:47:TRP:HB2	13:N:48:PRO:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:542:ASN:HA	16:Q:622:SER:HA	1.96	0.47
16:Q:1224:ILE:O	16:Q:1255:ASN:N	2.46	0.47
23:Y:298:PHE:CE2	23:Y:314:ASP:HA	2.50	0.47
24:1:666:LYS:HB3	24:1:704:ILE:HD13	1.96	0.47
25:3:272:PRO:HD3	25:3:327:LEU:HD13	1.97	0.47
25:3:864:SER:O	25:3:865:VAL:HG23	2.15	0.47
27:w:397:TYR:HE2	27:w:402:LEU:HB2	1.80	0.47
29:4:103:PHE:N	29:4:177:ALA:HB2	2.29	0.47
39:i:50:TYR:HA	39:i:54:ALA:O	2.14	0.47
39:i:71:TYR:HA	40:j:79:LEU:HA	1.96	0.47
1:A:747:ALA:O	1:A:751:THR:OG1	2.29	0.47
1:A:1206:GLU:HG2	1:A:1207:PHE:N	2.28	0.47
3:C:86:THR:OG1	3:C:87:GLN:N	2.47	0.47
3:C:350:ASN:ND2	3:C:353:THR:H	2.13	0.47
6:F:88:G:H2'	6:F:89:U:H5'	1.96	0.47
10:J:289:ASN:O	10:J:291:GLN:NE2	2.48	0.47
13:N:15:TRP:NE1	13:N:19:GLU:OE1	2.47	0.47
13:N:44:GLU:CD	13:N:44:GLU:N	2.72	0.47
13:N:57:THR:HG23	13:N:92:TRP:CH2	2.50	0.47
21:V:550:MET:O	21:V:554:LEU:HG	2.15	0.47
22:X:172:LEU:O	22:X:175:LEU:HG	2.15	0.47
22:X:976:LEU:HD12	22:X:1000:VAL:HG23	1.96	0.47
24:1:929:LEU:N	24:1:930:PRO:HD2	2.30	0.47
25:3:24:GLY:HA2	25:3:74:THR:O	2.14	0.47
25:3:69:ARG:HG3	25:3:75:LYS:O	2.15	0.47
25:3:347:LEU:CD2	25:3:359:TYR:HB2	2.44	0.47
25:3:1181:GLN:O	25:3:1185:MET:HG3	2.14	0.47
30:7:21:ARG:NH1	30:7:66:VAL:O	2.27	0.47
32:y:13:LEU:H	32:y:48:GLY:HA2	1.80	0.47
1:A:196:ASP:HB3	1:A:199:GLU:HB2	1.97	0.46
1:A:344:ASP:OD2	1:A:347:LEU:HD12	2.15	0.46
1:A:644:ILE:HD12	1:A:644:ILE:HA	1.73	0.46
1:A:1675:ASP:OD1	1:A:1678:ARG:N	2.41	0.46
3:C:510:LEU:HD13	3:C:514:TYR:CD2	2.50	0.46
3:C:601:PRO:HA	3:C:604:LEU:HD12	1.97	0.46
4:D:777:LEU:O	4:D:780:TYR:N	2.40	0.46
13:N:91:LYS:HA	13:N:91:LYS:HD3	1.72	0.46
22:X:162:ASP:N	22:X:542:PHE:CE2	2.82	0.46
22:X:273:LYS:HA	22:X:276:VAL:HG12	1.96	0.46
22:X:394:ALA:HA	22:X:397:ARG:HD2	1.96	0.46
22:X:452:GLN:O	22:X:497:THR:HA	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:576:ARG:HA	22:X:576:ARG:NH2	2.30	0.46
24:1:864:TYR:O	24:1:868:VAL:HG13	2.15	0.46
25:3:169:HIS:CD2	25:3:170:VAL:N	2.82	0.46
25:3:511:LEU:HD21	25:3:517:VAL:CG2	2.44	0.46
30:7:12:ARG:NH1	30:7:84:GLY:O	2.48	0.46
35:9:325:ILE:HD13	35:9:328:PHE:HD1	1.79	0.46
36:m:16:ARG:O	36:m:84:GLY:N	2.44	0.46
1:A:191:ILE:HG12	1:A:571:ALA:HB1	1.97	0.46
1:A:976:MET:HE2	1:A:976:MET:HB2	1.68	0.46
1:A:1411:SER:O	1:A:1419:ILE:HG12	2.15	0.46
1:A:1852:LEU:HD23	1:A:1858:PRO:HD3	1.96	0.46
1:A:1974:GLU:O	1:A:1978:LYS:HG3	2.15	0.46
3:C:122:LEU:O	3:C:125:ASN:HB3	2.15	0.46
3:C:226:VAL:HG22	3:C:254:THR:HB	1.98	0.46
3:C:377:LEU:HD12	3:C:380:ILE:HD12	1.97	0.46
3:C:826:ARG:HA	3:C:911:PRO:HG3	1.97	0.46
8:H:13:C:H1'	8:H:14:C:OP2	2.15	0.46
8:H:53:U:C5'	28:2:450:SER:HB3	2.37	0.46
10:J:411:MET:SD	10:J:415:LEU:HD23	2.56	0.46
12:L:92:THR:OG1	12:L:95:GLN:HG3	2.15	0.46
13:N:47:TRP:N	13:N:48:PRO:CD	2.78	0.46
15:P:184:VAL:HG23	23:Y:52:GLN:OE1	2.02	0.46
22:X:575:ARG:HH22	22:X:724:GLY:HA2	1.79	0.46
22:X:876:GLY:O	22:X:880:VAL:HG23	2.16	0.46
24:1:503:LYS:HE2	24:1:511:MET:CG	2.44	0.46
24:1:568:ARG:HG3	24:1:568:ARG:HH11	1.79	0.46
24:1:854:VAL:HG12	24:1:892:LEU:CD2	2.45	0.46
25:3:312:LYS:HB2	25:3:330:PHE:CD1	2.50	0.46
25:3:558:LEU:HG	25:3:559:THR:N	2.29	0.46
25:3:817:GLN:HG3	25:3:818:GLN:OE1	2.15	0.46
25:3:1199:ARG:HH21	25:3:1207:LYS:HD3	1.80	0.46
31:5:50:LEU:HD12	31:5:50:LEU:HA	1.54	0.46
43:o:14:GLN:HA	43:o:23:GLU:O	2.15	0.46
1:A:409:ARG:N	1:A:410:PRO:HD2	2.30	0.46
1:A:1885:LYS:HG2	1:A:1886:GLY:N	2.30	0.46
2:B:38:C:C5	2:B:39:C:C4	3.03	0.46
5:E:202:ASN:HD21	5:E:204:THR:HG1	1.57	0.46
10:J:300:ASP:OD2	17:R:101:ILE:HD11	2.14	0.46
12:L:166:LYS:HB3	12:L:167:ALA:H	1.59	0.46
17:R:352:ARG:NH1	22:X:265:HIS:CB	2.67	0.46
19:T:266:GLU:HG2	19:T:290:ALA:HB1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:543:LYS:HA	21:V:546:ASN:HD21	1.81	0.46
22:X:503:ARG:O	22:X:506:LEU:HB2	2.16	0.46
23:Y:17:TYR:HD1	23:Y:17:TYR:HA	1.67	0.46
23:Y:31:LEU:HG	23:Y:66:ILE:HB	1.98	0.46
23:Y:33:LYS:NZ	23:Y:168:ASP:OD1	2.29	0.46
24:1:746:PHE:O	24:1:750:ILE:HG23	2.15	0.46
24:1:848:GLU:O	24:1:852:ARG:HG3	2.15	0.46
24:1:967:GLU:HB3	24:1:970:LEU:HB3	1.98	0.46
24:1:1277:GLN:NE2	24:1:1277:GLN:O	2.48	0.46
25:3:515:ALA:HA	25:3:528:ARG:HA	1.97	0.46
25:3:592:LEU:HD11	25:3:619:LEU:HD11	1.97	0.46
27:w:458:LEU:HD11	28:2:466:LYS:HB2	1.96	0.46
1:A:1417:PRO:O	1:A:1461:ASP:O	2.33	0.46
3:C:175:GLN:OE1	3:C:175:GLN:N	2.47	0.46
3:C:721:LYS:HD3	3:C:722:TYR:CZ	2.50	0.46
5:E:125:PHE:N	5:E:125:PHE:CD2	2.83	0.46
5:E:135:VAL:HG21	5:E:181:ILE:CD1	2.45	0.46
5:E:251:LEU:HB2	5:E:293:TRP:NE1	2.31	0.46
17:R:331:ALA:HA	22:X:275:ARG:HH22	1.81	0.46
19:T:210:ILE:HG22	19:T:467:ALA:HB1	1.98	0.46
19:T:301:ASP:OD1	19:T:301:ASP:N	2.48	0.46
22:X:415:HIS:CD2	22:X:568:PRO:HG3	2.50	0.46
22:X:508:GLU:OE1	22:X:512:ALA:N	2.48	0.46
22:X:675:ASN:O	22:X:678:GLU:HB2	2.16	0.46
23:Y:242:LEU:HD23	23:Y:315:PHE:HA	1.96	0.46
24:1:554:LYS:HD2	24:1:558:ARG:HE	1.80	0.46
24:1:867:MET:HE2	24:1:867:MET:HB3	1.82	0.46
24:1:881:ALA:HB1	24:1:884:ILE:HG12	1.97	0.46
24:1:903:GLN:HG2	24:1:910:MET:HG3	1.98	0.46
24:1:1067:LYS:HB3	24:1:1067:LYS:HE2	1.67	0.46
25:3:524:ILE:O	25:3:535:GLU:HA	2.15	0.46
25:3:809:GLU:O	25:3:812:LYS:HB2	2.15	0.46
28:2:515:ARG:HG3	33:v:62:LEU:HD11	1.97	0.46
1:A:549:GLU:HB2	1:A:591:MET:HG3	1.97	0.46
1:A:955:TRP:HE1	1:A:976:MET:HE1	1.80	0.46
1:A:1908:LYS:HA	1:A:1908:LYS:HD3	1.69	0.46
1:A:1920:TYR:HD2	1:A:1924:LEU:HD11	1.80	0.46
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.50	0.46
4:D:2034:PRO:HA	4:D:2094:PHE:O	2.14	0.46
8:H:51:A:H2'	8:H:52:G:O4'	2.15	0.46
12:L:168:LYS:HD3	12:L:171:ALA:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:315:LYS:HG2	17:R:316:GLU:N	2.31	0.46
19:T:287:HIS:CE1	19:T:313:ARG:HG3	2.50	0.46
22:X:164:TRP:CE2	22:X:542:PHE:CG	3.04	0.46
22:X:454:ARG:HH12	22:X:679:THR:HB	1.81	0.46
22:X:612:LEU:HB2	22:X:686:ILE:HG21	1.97	0.46
22:X:700:TYR:HB3	22:X:757:ARG:O	2.15	0.46
22:X:727:GLY:HA2	22:X:730:ALA:O	2.15	0.46
23:Y:275:TRP:CD1	23:Y:276:LYS:H	2.34	0.46
23:Y:290:LYS:HB2	23:Y:293:ASP:CG	2.40	0.46
24:1:869:MET:O	24:1:873:GLU:HB3	2.15	0.46
24:1:898:TYR:HA	24:1:901:GLN:OE1	2.15	0.46
25:3:528:ARG:NH1	25:3:572:GLY:O	2.49	0.46
25:3:745:PHE:CG	25:3:755:VAL:HG23	2.51	0.46
25:3:1158:ARG:HG3	25:3:1159:ASP:H	1.79	0.46
25:3:1210:ASP:HA	25:3:1213:THR:OG1	2.15	0.46
26:p:75:TYR:N	43:o:147:PHE:O	2.49	0.46
28:2:606:PRO:C	28:2:608:ASP:H	2.23	0.46
35:9:323:ARG:HD2	35:9:420:ASP:HB2	1.97	0.46
1:A:83:HIS:CE1	7:G:16:G:O6	2.67	0.46
1:A:105:ASN:O	1:A:489:TRP:CD1	2.69	0.46
1:A:1275:ARG:NH1	1:A:1373:GLN:O	2.43	0.46
1:A:1889:LEU:HD23	1:A:2012:LEU:HG	1.98	0.46
4:D:492:ALA:O	4:D:516:CYS:HA	2.16	0.46
4:D:621:HIS:HA	4:D:890:GLU:O	2.16	0.46
6:F:29:A:H61	7:G:17:U:P	2.39	0.46
7:G:116:C:O4'	17:R:371:ARG:HA	2.14	0.46
10:J:256:LYS:HE2	12:L:232:TYR:HE1	1.74	0.46
10:J:395:ALA:O	10:J:398:VAL:HG12	2.16	0.46
17:R:170:LYS:H	17:R:170:LYS:CD	2.21	0.46
22:X:164:TRP:CZ3	22:X:542:PHE:HE1	2.31	0.46
22:X:389:LYS:HE2	22:X:389:LYS:O	2.16	0.46
22:X:676:ILE:HG12	22:X:681:LEU:HD11	1.97	0.46
24:1:830:TYR:CG	24:1:867:MET:HG3	2.51	0.46
24:1:871:THR:O	24:1:875:ILE:HG13	2.15	0.46
24:1:1135:GLU:O	24:1:1138:VAL:HG12	2.16	0.46
25:3:451:GLU:HG3	25:3:760:ASN:O	2.16	0.46
25:3:604:PHE:CE1	25:3:681:PRO:HD3	2.51	0.46
25:3:676:ARG:HD2	25:3:729:PHE:CD2	2.51	0.46
27:w:118:GLU:O	27:w:121:SER:N	2.48	0.46
27:w:410:ILE:HG23	27:w:438:LEU:HD11	1.98	0.46
30:7:12:ARG:HD2	30:7:12:ARG:HA	1.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:9:369:ALA:HA	35:9:394:HIS:CE1	2.51	0.46
1:A:108:MET:O	1:A:110:TRP:N	2.48	0.46
1:A:310:THR:O	1:A:314:ILE:HG22	2.16	0.46
2:B:69:A:H3'	2:B:70:A:C8	2.51	0.46
3:C:118:PHE:CE2	3:C:122:LEU:HD11	2.51	0.46
3:C:220:ARG:HA	3:C:220:ARG:HE	1.81	0.46
3:C:366:GLN:H	3:C:366:GLN:HG2	1.37	0.46
9:I:551:PRO:HB3	9:I:554:SER:CB	2.46	0.46
10:J:432:VAL:O	10:J:435:ILE:HG13	2.16	0.46
12:L:40:ARG:O	12:L:40:ARG:HG2	2.16	0.46
17:R:286:LYS:NZ	35:9:211:LEU:HD21	2.31	0.46
22:X:223:VAL:O	22:X:227:ARG:HG3	2.16	0.46
24:1:1231:MET:HE1	24:1:1268:ILE:CG1	2.46	0.46
25:3:1115:GLU:C	28:2:708:TRP:CH2	2.88	0.46
25:3:1204:VAL:HG23	25:3:1205:SER:N	2.30	0.46
28:2:504:TRP:CD1	28:2:504:TRP:H	2.34	0.46
30:7:47:ASP:HA	30:7:50:ASN:HB3	1.97	0.46
31:5:8:HIS:HA	31:5:11:LEU:HB2	1.97	0.46
1:A:660:PHE:CE2	17:R:209:PRO:CB	2.99	0.46
1:A:1580:HIS:CD2	1:A:1583:GLN:NE2	2.84	0.46
1:A:1614:ILE:H	1:A:1614:ILE:HG13	1.60	0.46
1:A:1889:LEU:HG	1:A:2013:GLY:N	2.31	0.46
1:A:1914:MET:HE2	1:A:1915:VAL:O	2.16	0.46
2:B:99:C:H2'	2:B:100:C:H6	1.80	0.46
3:C:857:VAL:HA	3:C:873:ALA:CB	2.46	0.46
5:E:342:ILE:O	5:E:353:MET:HA	2.16	0.46
8:H:14:C:OP2	8:H:14:C:H2'	2.16	0.46
12:L:11:TRP:CZ2	12:L:41:LYS:HD2	2.51	0.46
12:L:73:HIS:CD2	35:9:220:ILE:CB	2.96	0.46
12:L:188:ARG:HD2	12:L:191:LEU:HD12	1.98	0.46
13:N:64:PHE:CZ	13:N:72:ARG:HD2	2.51	0.46
22:X:453:PRO:HB3	22:X:524:GLU:CD	2.40	0.46
22:X:456:VAL:HA	22:X:459:MET:HG3	1.97	0.46
24:1:536:LEU:O	24:1:540:MET:HG2	2.16	0.46
24:1:1216:TRP:O	24:1:1219:VAL:HB	2.16	0.46
25:3:185:LEU:O	25:3:186:GLU:HG3	2.16	0.46
25:3:304:GLN:HE21	25:3:308:GLY:HA2	1.80	0.46
25:3:642:ILE:H	25:3:703:ARG:NH2	2.13	0.46
25:3:945:VAL:HG23	25:3:968:ARG:HH12	1.80	0.46
25:3:1085:ALA:HB3	25:3:1088:LYS:HE2	1.97	0.46
27:w:433:HIS:O	27:w:434:GLY:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:496:LYS:HG3	27:w:501:LEU:C	2.41	0.46
33:v:88:LYS:O	33:v:92:GLU:HG3	2.16	0.46
35:9:363:ARG:HB3	35:9:363:ARG:CZ	2.45	0.46
1:A:41:GLN:C	1:A:43:LYS:H	2.23	0.46
1:A:79:ARG:HD2	1:A:82:ARG:NE	2.31	0.46
1:A:1489:LEU:HD12	1:A:1536:LEU:HD22	1.98	0.46
1:A:1784:ASN:ND2	1:A:1894:GLN:HB2	2.27	0.46
3:C:442:LYS:CD	3:C:468:CYS:HB3	2.46	0.46
5:E:105:LEU:HD11	5:E:136:TRP:CE3	2.50	0.46
8:H:15:U:O2'	8:H:16:U:OP2	2.26	0.46
10:J:342:GLU:CD	10:J:343:GLU:N	2.74	0.46
10:J:367:GLU:O	10:J:371:LEU:HG	2.16	0.46
12:L:227:THR:OG1	17:R:84:ASN:ND2	2.49	0.46
17:R:383:ASN:N	17:R:383:ASN:OD1	2.48	0.46
21:V:540:GLU:H	21:V:540:GLU:HG3	1.51	0.46
22:X:725:ARG:HD3	22:X:728:ARG:NH1	2.21	0.46
22:X:858:LYS:O	22:X:861:VAL:HG23	2.16	0.46
25:3:615:ARG:C	25:3:616:ILE:HD12	2.41	0.46
27:w:383:LEU:HA	27:w:383:LEU:HD23	1.67	0.46
28:2:601:LEU:HD11	29:4:27:PRO:CA	2.46	0.46
41:k:30:ILE:O	41:k:42:ILE:HA	2.15	0.46
1:A:93:LYS:NZ	17:R:165:VAL:HG22	2.30	0.46
1:A:340:ILE:H	1:A:340:ILE:HG12	1.37	0.46
1:A:361:HIS:HB3	3:C:280:HIS:CG	2.52	0.46
1:A:796:LYS:HB3	1:A:796:LYS:HE3	1.76	0.46
1:A:977:LEU:HG	1:A:978:GLU:N	2.30	0.46
1:A:1189:MET:HG3	1:A:1190:CYS:N	2.31	0.46
1:A:1310:ARG:HD3	1:A:1542:ILE:O	2.16	0.46
2:B:65:G:H2'	2:B:66:A:C8	2.51	0.46
3:C:174:GLU:CD	3:C:180:GLY:HA2	2.41	0.46
3:C:360:ALA:H	3:C:361:PRO:HD3	1.81	0.46
3:C:388:VAL:HA	3:C:392:LEU:CD1	2.46	0.46
3:C:700:ILE:HG13	3:C:705:VAL:HG11	1.98	0.46
3:C:921:LEU:HD23	3:C:921:LEU:HA	1.68	0.46
3:C:938:ARG:O	3:C:942:GLY:N	2.49	0.46
15:P:27:SER:HB2	15:P:29:GLN:OE1	2.15	0.46
15:P:195:LYS:O	15:P:196:ASN:C	2.59	0.46
16:Q:116:PRO:O	16:Q:120:PRO:HD2	2.16	0.46
17:R:189:ASN:ND2	17:R:195:ARG:HG2	2.30	0.46
19:T:334:ALA:HB2	19:T:350:HIS:CE1	2.51	0.46
19:T:394:ASN:N	19:T:394:ASN:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:182:ALA:N	22:X:924:ARG:HH12	2.12	0.46
22:X:867:ALA:HB3	22:X:902:PHE:HD2	1.80	0.46
23:Y:188:SER:HB2	23:Y:190:ARG:HB2	1.98	0.46
23:Y:204:SER:OG	23:Y:206:GLU:N	2.49	0.46
23:Y:241:VAL:HA	23:Y:286:ILE:O	2.16	0.46
24:1:662:HIS:HB2	24:1:701:VAL:HB	1.99	0.46
24:1:1000:ILE:O	24:1:1003:VAL:HG13	2.16	0.46
24:1:1015:ASP:OD1	24:1:1015:ASP:N	2.49	0.46
25:3:5:ASN:O	25:3:1176:GLY:HA3	2.16	0.46
25:3:565:TYR:CE1	25:3:619:LEU:HD12	2.51	0.46
25:3:633:LEU:HD12	25:3:637:PRO:HG3	1.97	0.46
25:3:725:TYR:O	25:3:728:ARG:HB2	2.16	0.46
25:3:1041:TYR:CD2	28:2:705:ARG:CD	2.99	0.46
27:w:466:LYS:HE3	27:w:466:LYS:HB2	1.73	0.46
28:2:542:GLU:HA	28:2:545:GLU:HG2	1.98	0.46
28:2:604:LYS:O	28:2:604:LYS:HD3	2.15	0.46
35:9:203:GLU:O	35:9:207:THR:OG1	2.12	0.46
35:9:282:VAL:HG13	35:9:433:VAL:HG22	1.98	0.46
35:9:370:ASN:ND2	35:9:372:GLY:O	2.45	0.46
1:A:593:ARG:HH12	1:A:1565:LYS:HZ2	1.64	0.45
1:A:1030:ILE:HD11	1:A:1040:ILE:HG21	1.98	0.45
3:C:139:HIS:C	45:C:1500:GTP:O1A	2.58	0.45
6:F:36:A:C6	6:F:38:G:C6	3.04	0.45
6:F:88:G:C2	6:F:89:U:C6	3.04	0.45
7:G:9:C:H2'	7:G:10:U:C2	2.51	0.45
16:Q:172:LEU:N	16:Q:173:PRO:HD2	2.31	0.45
17:R:355:ILE:CG1	22:X:256:LEU:HD13	2.46	0.45
22:X:290:GLU:O	22:X:293:GLU:HG3	2.16	0.45
22:X:436:LEU:CD2	22:X:516:VAL:HG11	2.46	0.45
23:Y:65:SER:N	23:Y:76:SER:O	2.33	0.45
23:Y:144:VAL:HA	23:Y:150:PRO:HA	1.98	0.45
24:1:586:ASP:O	24:1:590:ARG:HG3	2.16	0.45
25:3:49:LYS:HD3	25:3:49:LYS:HA	1.59	0.45
25:3:226:GLU:HB3	25:3:261:PHE:CE2	2.51	0.45
25:3:569:ASP:O	25:3:572:GLY:N	2.45	0.45
28:2:511:LEU:C	28:2:513:GLY:H	2.24	0.45
43:o:52:ASN:O	43:o:74:ASN:HA	2.17	0.45
1:A:184:ASP:HB3	13:N:1:MET:HA	1.96	0.45
1:A:758:ARG:HD3	1:A:779:LEU:HD11	1.97	0.45
1:A:1634:SER:OG	1:A:1635:TYR:N	2.50	0.45
1:A:1836:LEU:HA	1:A:1839:TRP:CD1	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:114:TYR:N	3:C:115:GLU:OE1	2.49	0.45
3:C:237:LEU:HD21	3:C:900:VAL:HG13	1.98	0.45
3:C:724:TRP:HA	3:C:724:TRP:HE3	1.80	0.45
5:E:171:SER:O	5:E:196:VAL:N	2.44	0.45
5:E:270:LYS:HA	5:E:270:LYS:HE3	1.98	0.45
5:E:311:VAL:HB	5:E:321:TYR:HB2	1.97	0.45
6:F:38:G:C4	6:F:39:A:N7	2.84	0.45
7:G:5:G:H2'	7:G:5:G:N3	2.31	0.45
7:G:99:C:N4	8:H:32:U:C4	2.84	0.45
8:H:53:U:C5'	28:2:450:SER:CB	2.62	0.45
12:L:63:TRP:HB3	12:L:68:GLU:HG3	1.99	0.45
13:N:64:PHE:HZ	13:N:72:ARG:HD2	1.81	0.45
17:R:334:ARG:O	22:X:271:LYS:NZ	2.49	0.45
23:Y:88:HIS:CE1	23:Y:125:VAL:HG22	2.51	0.45
24:1:516:LEU:HD12	24:1:516:LEU:HA	1.69	0.45
24:1:609:MET:HB3	24:1:609:MET:HE2	1.51	0.45
24:1:893:ILE:HD13	24:1:893:ILE:HA	1.68	0.45
24:1:1302:TYR:CD1	25:3:915:LEU:HB3	2.49	0.45
25:3:232:GLY:HA3	25:3:252:SER:HA	1.97	0.45
25:3:696:SER:O	25:3:696:SER:OG	2.32	0.45
25:3:788:PHE:HB2	25:3:799:ILE:HA	1.98	0.45
25:3:1117:LEU:HD12	25:3:1117:LEU:HA	1.60	0.45
25:3:1159:ASP:OD1	25:3:1160:HIS:N	2.50	0.45
27:w:408:CYS:HB2	27:w:416:TYR:CE2	2.50	0.45
27:w:461:LYS:NZ	28:2:467:GLN:HA	2.31	0.45
28:2:452:LYS:HD3	28:2:456:ARG:HB2	1.98	0.45
35:9:295:LEU:HD13	35:9:308:ILE:HD11	1.99	0.45
41:k:41:VAL:HA	41:k:61:VAL:HA	1.98	0.45
1:A:531:THR:O	1:A:535:ARG:HB2	2.16	0.45
1:A:547:CYS:O	1:A:548:ARG:C	2.58	0.45
1:A:1934:SER:O	1:A:1938:LEU:HG	2.17	0.45
3:C:118:PHE:CZ	3:C:122:LEU:HD11	2.51	0.45
3:C:711:ARG:HB3	3:C:730:ARG:NH2	2.31	0.45
3:C:718:PHE:HB3	3:C:724:TRP:CD1	2.51	0.45
3:C:902:HIS:ND1	3:C:903:HIS:HD2	2.14	0.45
3:C:914:LYS:HA	3:C:914:LYS:HD2	1.89	0.45
5:E:156:SER:OG	5:E:197:LEU:O	2.33	0.45
6:F:22:A:H3'	13:N:115:THR:HG21	1.98	0.45
6:F:85:U:H1'	6:F:86:U:C6	2.51	0.45
7:G:92:U:O2'	33:v:65:ASN:ND2	2.49	0.45
7:G:111:U:OP2	22:X:482:ARG:HD3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:43:U:H2'	8:H:44:U:C5	2.51	0.45
10:J:334:GLU:O	10:J:338:GLU:HG3	2.16	0.45
17:R:315:LYS:HZ3	23:Y:191:ILE:HG12	1.81	0.45
23:Y:186:LEU:HD23	23:Y:186:LEU:HA	1.79	0.45
23:Y:276:LYS:HB3	23:Y:276:LYS:HE2	1.75	0.45
24:1:769:VAL:HG13	24:1:773:LEU:HD21	1.99	0.45
24:1:1142:ASN:H	24:1:1142:ASN:HD22	1.64	0.45
24:1:1226:VAL:O	24:1:1230:VAL:HG23	2.17	0.45
25:3:14:ILE:HD11	25:3:356:HIS:CD2	2.51	0.45
25:3:93:GLN:O	25:3:97:ASN:N	2.50	0.45
25:3:278:LEU:HD21	25:3:816:LYS:NZ	2.32	0.45
25:3:528:ARG:HG3	25:3:529:ALA:N	2.32	0.45
32:y:35:ILE:HA	32:y:51:PHE:O	2.15	0.45
1:A:259:ASP:OD1	1:A:259:ASP:N	2.39	0.45
1:A:260:LEU:HD21	1:A:454:TYR:CZ	2.52	0.45
1:A:774:LYS:HE3	8:H:23:A:OP1	2.15	0.45
1:A:1644:LEU:HD23	1:A:1644:LEU:HA	1.71	0.45
3:C:453:TYR:CE2	3:C:575:GLN:HB2	2.52	0.45
3:C:574:ALA:O	3:C:575:GLN:NE2	2.46	0.45
3:C:651:ILE:HG22	3:C:652:ASP:N	2.31	0.45
3:C:776:GLU:O	3:C:781:ASP:HA	2.16	0.45
3:C:827:LEU:O	3:C:907:VAL:HG23	2.17	0.45
4:D:668:ASP:O	4:D:672:GLY:HA3	2.16	0.45
5:E:124:LEU:C	5:E:125:PHE:HD2	2.24	0.45
5:E:145:LYS:HD2	5:E:184:LYS:HE2	1.98	0.45
12:L:178:GLU:HB3	12:L:181:ARG:NH1	2.32	0.45
17:R:364:GLN:O	17:R:368:ASN:ND2	2.50	0.45
17:R:376:LYS:HE3	17:R:376:LYS:HB3	1.75	0.45
19:T:498:GLU:H	19:T:498:GLU:HG3	1.42	0.45
21:V:562:TRP:CD2	21:V:602:ARG:HD3	2.51	0.45
22:X:997:MET:C	22:X:998:ARG:HD2	2.42	0.45
23:Y:104:HIS:NE2	23:Y:124:THR:OG1	2.29	0.45
24:1:644:LEU:HB3	24:1:648:LEU:CD1	2.46	0.45
24:1:854:VAL:HG11	24:1:891:GLN:HG3	1.97	0.45
24:1:856:ASP:HB3	24:1:864:TYR:CE2	2.51	0.45
25:3:698:PRO:O	25:3:700:LYS:NZ	2.34	0.45
27:w:445:HIS:CD2	27:w:445:HIS:N	2.83	0.45
35:9:325:ILE:HB	35:9:328:PHE:HB3	1.98	0.45
1:A:1418:ARG:HB2	1:A:1462:GLY:HA3	1.98	0.45
1:A:1625:SER:OG	1:A:1687:TYR:HD2	1.99	0.45
3:C:113:VAL:HG23	3:C:114:TYR:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:684:LYS:HB3	3:C:795:VAL:HB	1.98	0.45
4:D:783:ALA:O	4:D:809:LEU:HA	2.17	0.45
5:E:329:SER:N	5:E:347:SER:OG	2.49	0.45
8:H:99:A:HO2'	8:H:100:U:P	2.38	0.45
11:K:218:LYS:HB2	11:K:218:LYS:HE3	1.36	0.45
16:Q:1144:CYS:O	16:Q:1148:ASN:N	2.47	0.45
17:R:158:LYS:O	17:R:161:ALA:HB3	2.17	0.45
17:R:171:LEU:HD11	17:R:203:GLN:OE1	2.16	0.45
21:V:533:TYR:CE2	21:V:568:ILE:HG23	2.52	0.45
22:X:447:LYS:HB2	22:X:514:TYR:CD1	2.51	0.45
22:X:1017:LYS:HB2	22:X:1020:GLU:OE2	2.17	0.45
23:Y:70:LEU:HD22	23:Y:169:PRO:HB2	1.98	0.45
24:1:974:LEU:HG	24:1:974:LEU:H	1.46	0.45
24:1:1298:TYR:CD1	25:3:918:ARG:HB2	2.51	0.45
27:w:388:ASP:OD2	33:v:84:ARG:CB	2.64	0.45
27:w:388:ASP:HB3	33:v:84:ARG:C	2.40	0.45
28:2:541:GLN:O	28:2:545:GLU:HG2	2.17	0.45
30:7:48:GLU:H	30:7:48:GLU:HG3	1.32	0.45
35:9:370:ASN:ND2	35:9:375:SER:H	2.15	0.45
1:A:642:ARG:NH2	2:B:55:C:N3	2.60	0.45
1:A:929:GLU:O	1:A:933:ARG:HG3	2.17	0.45
1:A:1473:ASP:OD1	1:A:1473:ASP:N	2.46	0.45
1:A:1781:ASP:HB2	1:A:1808:PHE:HB3	1.99	0.45
1:A:1903:GLY:O	1:A:1907:LEU:HG	2.16	0.45
2:B:14:U:H2'	2:B:15:C:C6	2.51	0.45
3:C:339:PHE:HE1	3:C:356:PHE:HZ	1.62	0.45
5:E:71:CYS:HB2	5:E:115:LEU:HG	1.99	0.45
5:E:94:ASN:N	5:E:100:ASP:O	2.40	0.45
5:E:343:ILE:HA	5:E:352:TYR:O	2.17	0.45
7:G:-7:U:H5'	7:G:-6:C:OP2	2.17	0.45
7:G:90:C:H42	8:H:40:C:N4	2.14	0.45
8:H:105:G:N2	8:H:107:A:H5'	2.31	0.45
9:I:427:LYS:O	9:I:429:VAL:N	2.48	0.45
10:J:262:ARG:NH2	10:J:291:GLN:HG2	2.32	0.45
12:L:201:LYS:HD2	12:L:201:LYS:HA	1.61	0.45
15:P:30:TYR:CG	17:R:164:PRO:HD2	2.51	0.45
21:V:450:ILE:HD12	21:V:450:ILE:HA	1.83	0.45
22:X:396:ARG:NE	22:X:431:GLN:HE22	2.15	0.45
22:X:845:ALA:CB	22:X:915:ARG:HB2	2.46	0.45
23:Y:80:ALA:HB2	23:Y:102:ASP:O	2.16	0.45
24:1:560:LEU:HD11	24:1:600:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:334:PRO:HB3	25:3:432:ARG:NH1	2.30	0.45
25:3:343:LYS:C	25:3:345:GLY:H	2.24	0.45
25:3:404:LEU:HB3	25:3:407:ILE:HG12	1.99	0.45
25:3:996:ILE:HG21	25:3:1041:TYR:CD1	2.52	0.45
27:w:108:VAL:O	27:w:120:PRO:HD2	2.17	0.45
27:w:383:LEU:HD13	27:w:391:PRO:HB3	1.98	0.45
28:2:553:MET:HE3	28:2:553:MET:HB2	1.75	0.45
32:y:70:SER:O	32:y:76:THR:HA	2.17	0.45
35:9:285:HIS:O	35:9:429:ASP:HB2	2.16	0.45
35:9:315:TYR:CZ	35:9:335:PRO:HG2	2.52	0.45
35:9:437:PRO:HG2	35:9:438:TYR:CE2	2.52	0.45
1:A:126:ILE:HA	1:A:499:GLN:OE1	2.17	0.45
1:A:273:ILE:HG23	1:A:274:PRO:HD2	1.99	0.45
1:A:389:LYS:HA	3:C:379:LYS:HZ2	1.82	0.45
1:A:1536:LEU:HD11	1:A:1576:ILE:HD11	1.97	0.45
3:C:121:ASP:OD1	3:C:122:LEU:N	2.50	0.45
3:C:510:LEU:CB	3:C:564:THR:HG23	2.47	0.45
5:E:146:ARG:HD2	5:E:148:LYS:CE	2.47	0.45
6:F:40:U:H2'	6:F:41:A:C8	2.51	0.45
6:F:83:A:H1'	6:F:84:A:C8	2.52	0.45
7:G:105:C:H5'	7:G:105:C:O2	2.17	0.45
8:H:150:U:H3	8:H:181:G:H22	1.64	0.45
14:O:256:GLY:HA3	14:O:279:ALA:CB	2.47	0.45
17:R:351:GLU:OE2	22:X:256:LEU:CA	2.64	0.45
21:V:596:LEU:N	21:V:597:PRO:HD2	2.32	0.45
22:X:263:SER:O	22:X:267:ARG:CB	2.60	0.45
22:X:444:LYS:N	22:X:444:LYS:HD2	2.32	0.45
22:X:698:LYS:HD3	22:X:707:GLU:HB2	1.99	0.45
24:1:1195:MET:O	24:1:1199:VAL:HG23	2.16	0.45
25:3:185:LEU:HD23	25:3:185:LEU:HA	1.69	0.45
25:3:193:ASP:OD2	31:5:37:ARG:NH2	2.46	0.45
25:3:458:ALA:O	25:3:459:VAL:HG23	2.16	0.45
25:3:592:LEU:HA	25:3:592:LEU:HD13	1.64	0.45
25:3:739:LEU:HD23	25:3:739:LEU:HA	1.70	0.45
28:2:595:LYS:NZ	28:2:596:GLU:HA	2.32	0.45
30:7:9:ILE:O	30:7:88:ILE:HG22	2.17	0.45
31:5:69:MET:HE2	31:5:69:MET:HB2	1.52	0.45
1:A:1007:ASP:HB3	12:L:80:THR:HG21	1.98	0.45
1:A:1712:HIS:ND1	1:A:1734:MET:HG3	2.32	0.45
1:A:1971:LEU:HD23	1:A:1971:LEU:HA	1.82	0.45
2:B:92:U:C4	37:b:36:MET:N	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:247:VAL:HG11	3:C:292:TYR:HB3	1.98	0.45
3:C:686:THR:CB	3:C:793:ASP:HB3	2.42	0.45
3:C:853:ARG:HD3	3:C:879:ASP:O	2.17	0.45
6:F:25:C:H4'	6:F:26:U:OP2	2.17	0.45
6:F:39:A:C2'	6:F:40:U:H5'	2.47	0.45
8:H:47:U:C6	8:H:47:U:OP1	2.70	0.45
8:H:158:G:H2'	8:H:159:U:O4'	2.16	0.45
9:I:296:PHE:CB	9:I:337:LEU:HA	2.46	0.45
13:N:15:TRP:CZ3	13:N:22:LEU:HD12	2.38	0.45
14:O:235:TYR:HA	14:O:270:ALA:O	2.17	0.45
16:Q:437:ASN:O	16:Q:450:LEU:HA	2.16	0.45
17:R:331:ALA:CA	22:X:275:ARG:HH22	2.30	0.45
17:R:355:ILE:CG1	22:X:256:LEU:CD1	2.95	0.45
19:T:422:ASN:HB2	19:T:426:VAL:HB	1.97	0.45
21:V:553:HIS:CD2	21:V:556:TYR:CE1	3.05	0.45
22:X:257:PHE:O	22:X:259:ASP:N	2.49	0.45
22:X:525:ARG:O	22:X:754:GLU:HB2	2.16	0.45
22:X:826:LYS:HA	22:X:826:LYS:HD2	1.68	0.45
24:1:907:ASP:OD2	24:1:909:VAL:HB	2.16	0.45
24:1:1130:PRO:HD3	28:2:575:PHE:CE2	2.52	0.45
25:3:124:ASP:OD2	25:3:128:ARG:HG3	2.17	0.45
25:3:325:ILE:HB	25:3:375:SER:HB3	1.99	0.45
25:3:590:MET:HE3	25:3:607:VAL:HG22	1.99	0.45
27:w:390:LYS:NZ	33:v:84:ARG:NH2	2.64	0.45
28:2:506:PHE:HB3	28:2:508:ARG:CG	2.46	0.45
1:A:693:ILE:C	1:A:695:ASP:H	2.25	0.45
1:A:701:ILE:HD11	17:R:237:MET:HE2	1.99	0.45
1:A:839:LEU:O	1:A:843:LEU:HG	2.17	0.45
1:A:1301:ILE:HA	1:A:1301:ILE:HD13	1.67	0.45
3:C:137:HIS:HB3	3:C:140:HIS:ND1	2.32	0.45
3:C:267:LEU:HD23	3:C:267:LEU:HA	1.74	0.45
3:C:349:PHE:CZ	3:C:351:PRO:HA	2.52	0.45
4:D:1581:ALA:O	4:D:1584:ILE:HA	2.17	0.45
6:F:65:G:H5''	6:F:66:C:OP2	2.17	0.45
6:F:84:A:O2'	6:F:85:U:H2'	2.17	0.45
8:H:160:A:C2	8:H:171:U:C2	3.05	0.45
10:J:231:PHE:HA	10:J:234:ASN:HD22	1.82	0.45
16:Q:599:GLY:HA3	16:Q:608:ILE:N	2.31	0.45
17:R:328:ALA:HA	22:X:279:LEU:CD1	2.47	0.45
21:V:374:ASP:O	21:V:376:TYR:N	2.45	0.45
21:V:570:LEU:HD23	21:V:575:THR:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:770:MET:HE2	24:1:770:MET:HB2	1.79	0.45
24:1:857:LEU:HA	24:1:865:ARG:HB3	1.99	0.45
24:1:1017:LEU:HD22	24:1:1050:VAL:HG11	1.98	0.45
35:9:41:HIS:HA	35:9:48:PRO:HA	1.99	0.45
1:A:37:TRP:CE3	1:A:37:TRP:O	2.70	0.45
1:A:364:SER:O	1:A:366:LYS:HD3	2.17	0.45
2:B:18:C:O2	2:B:59:G:N2	2.33	0.45
2:B:92:U:N3	37:b:36:MET:N	2.64	0.45
3:C:259:LYS:HE3	45:C:1500:GTP:C1'	2.47	0.45
5:E:192:ASN:CG	5:E:193:THR:H	2.24	0.45
7:G:99:C:N3	8:H:33:G:C4	2.84	0.45
8:H:48:A:C4	8:H:78:C:P	3.10	0.45
8:H:106:G:N3	8:H:107:A:N6	2.65	0.45
10:J:381:LYS:O	10:J:384:ARG:HB3	2.17	0.45
16:Q:494:PRO:HB2	16:Q:503:VAL:O	2.17	0.45
17:R:429:ILE:CD1	17:R:431:ASN:HD22	2.30	0.45
21:V:219:VAL:O	21:V:223:ASN:CB	2.65	0.45
22:X:181:PHE:O	22:X:185:VAL:HG23	2.16	0.45
25:3:147:ASP:OD2	25:3:151:ARG:HG2	2.16	0.45
25:3:184:CYS:SG	25:3:211:TYR:HE1	2.40	0.45
25:3:407:ILE:HD11	25:3:1124:GLY:HA2	1.99	0.45
25:3:485:LEU:CD2	25:3:491:VAL:HG12	2.46	0.45
25:3:543:THR:O	25:3:558:LEU:HD12	2.17	0.45
25:3:911:LYS:HG3	25:3:912:ASP:CG	2.42	0.45
26:p:10:TYR:O	26:p:81:ILE:HA	2.16	0.45
39:i:24:LYS:N	39:i:68:ASN:O	2.50	0.45
1:A:232:LEU:N	1:A:233:PRO:HD2	2.32	0.44
1:A:406:TRP:CZ2	3:C:266:GLU:HG3	2.52	0.44
1:A:974:ASN:OD1	1:A:1100:ARG:NH1	2.50	0.44
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.99	0.44
1:A:1361:GLU:HG3	1:A:1362:ASP:OD2	2.17	0.44
1:A:1645:LEU:HD11	1:A:1727:GLN:HG3	1.99	0.44
1:A:1681:ARG:HB3	1:A:1681:ARG:HH11	1.82	0.44
1:A:1687:TYR:HA	1:A:1690:ASP:OD2	2.17	0.44
3:C:733:TRP:CD1	3:C:763:LYS:HZ3	2.34	0.44
5:E:75:HIS:HB3	5:E:79:SER:H	1.82	0.44
6:F:81:C:N4	8:H:17:U:H3	2.15	0.44
7:G:6:A:H2'	7:G:7:G:C8	2.53	0.44
7:G:12:G:H3'	7:G:13:C:C5	2.51	0.44
7:G:110:U:H5''	22:X:455:ARG:H	1.83	0.44
15:P:50:ALA:O	15:P:54:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:52:GLU:HB2	15:P:53:GLU:OE1	2.17	0.44
17:R:153:LYS:HD2	17:R:154:SER:N	2.32	0.44
17:R:325:ARG:HH11	23:Y:222:ILE:HG23	1.82	0.44
22:X:246:LEU:HG	22:X:277:ARG:NE	2.27	0.44
22:X:421:GLU:HB2	22:X:557:THR:HG21	1.99	0.44
22:X:644:VAL:O	22:X:645:LEU:HD23	2.18	0.44
22:X:988:GLU:CB	22:X:998:ARG:HB2	2.48	0.44
23:Y:298:PHE:HE2	23:Y:314:ASP:HA	1.82	0.44
24:1:581:LEU:HD13	24:1:589:ALA:HB1	1.98	0.44
25:3:27:GLN:OE1	25:3:42:ARG:NH1	2.50	0.44
25:3:114:ARG:HD2	31:5:41:CYS:SG	2.57	0.44
25:3:243:ASP:OD1	25:3:244:GLY:N	2.50	0.44
25:3:595:VAL:HG22	25:3:596:PRO:O	2.17	0.44
25:3:910:ALA:HB2	25:3:948:VAL:HG23	1.98	0.44
25:3:988:ASN:ND2	25:3:1004:ASP:OD1	2.50	0.44
25:3:1102:LEU:HD12	25:3:1102:LEU:HA	1.66	0.44
25:3:1133:THR:C	28:2:711:LEU:HD21	2.28	0.44
28:2:477:MET:SD	28:2:478:HIS:CE1	3.10	0.44
28:2:516:GLY:CA	33:v:60:LEU:CD2	2.91	0.44
28:2:517:ILE:H	28:2:517:ILE:HG13	1.27	0.44
28:2:569:GLN:O	28:2:573:ASP:HB2	2.17	0.44
28:2:600:ARG:H	28:2:600:ARG:HG2	1.61	0.44
1:A:246:LEU:HA	1:A:246:LEU:HD23	1.68	0.44
1:A:350:PHE:HE1	3:C:264:ILE:HG23	1.82	0.44
1:A:363:HIS:HB2	1:A:366:LYS:NZ	2.31	0.44
1:A:599:MET:H	1:A:599:MET:HG2	1.54	0.44
1:A:1207:PHE:CD1	1:A:1207:PHE:C	2.96	0.44
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.98	0.44
1:A:1866:LYS:HE2	1:A:1866:LYS:HB2	1.84	0.44
1:A:2307:GLU:C	4:D:1125:SER:H	2.24	0.44
4:D:864:LYS:N	25:3:598:GLY:O	2.46	0.44
6:F:28:A:H61	14:O:173:CYS:HA	1.82	0.44
6:F:40:U:H3	7:G:7:G:H1	1.65	0.44
8:H:161:U:H2'	8:H:163:G:N2	2.32	0.44
13:N:75:TYR:O	13:N:79:ILE:HD12	2.18	0.44
15:P:74:LYS:HA	15:P:77:ASP:HB3	1.99	0.44
15:P:186:ARG:CD	15:P:190:ASP:HB3	2.47	0.44
16:Q:698:SER:HA	16:Q:1129:PRO:HD3	1.98	0.44
17:R:211:ARG:HB2	17:R:212:PHE:CE2	2.52	0.44
19:T:195:LYS:HZ3	19:T:490:ARG:HH21	1.62	0.44
22:X:242:LYS:HE3	22:X:242:LYS:HB3	1.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:419:ILE:O	22:X:569:VAL:HA	2.17	0.44
24:1:781:ASP:O	24:1:785:LYS:HG3	2.17	0.44
24:1:1017:LEU:HD21	24:1:1058:ILE:HD11	1.99	0.44
25:3:101:LYS:HE3	25:3:101:LYS:HB2	1.65	0.44
25:3:275:ARG:HH21	25:3:275:ARG:CB	2.31	0.44
25:3:499:PHE:CZ	25:3:516:LEU:HD22	2.46	0.44
27:w:408:CYS:SG	27:w:431:HIS:CE1	3.11	0.44
28:2:452:LYS:HE3	28:2:456:ARG:CG	2.46	0.44
28:2:526:ASP:O	28:2:528:ILE:N	2.50	0.44
31:5:33:VAL:CG2	31:5:76:CYS:HB2	2.47	0.44
38:h:34:GLN:O	38:h:38:ASN:CB	2.65	0.44
1:A:51:PHE:C	1:A:53:PHE:H	2.23	0.44
1:A:67:ARG:HE	1:A:67:ARG:HB2	1.46	0.44
1:A:485:THR:HG22	1:A:486:LYS:H	1.83	0.44
1:A:864:LEU:HD12	1:A:864:LEU:HA	1.52	0.44
1:A:1309:SER:O	1:A:1544:ARG:HD3	2.17	0.44
1:A:1893:PHE:O	1:A:1896:CYS:HB2	2.17	0.44
3:C:95:LYS:HE2	3:C:95:LYS:HB2	1.58	0.44
3:C:403:LEU:HD23	3:C:403:LEU:HA	1.87	0.44
3:C:788:LYS:HE2	3:C:790:LYS:HE3	1.98	0.44
6:F:5:U:N3	6:F:7:G:N7	2.65	0.44
6:F:7:G:H2'	6:F:8:C:C6	2.52	0.44
7:G:99:C:C4	8:H:33:G:C5	3.05	0.44
12:L:225:TYR:N	17:R:85:ALA:CB	2.80	0.44
22:X:448:ILE:HB	22:X:493:LEU:HD22	1.98	0.44
22:X:898:CYS:SG	22:X:903:VAL:HB	2.57	0.44
23:Y:44:ASN:HD22	23:Y:52:GLN:HB3	1.82	0.44
23:Y:64:GLU:HG2	23:Y:77:PHE:CE1	2.52	0.44
24:1:658:TRP:CZ3	24:1:698:GLN:HG2	2.52	0.44
24:1:1149:LYS:O	24:1:1152:SER:HB3	2.17	0.44
25:3:288:VAL:HG23	25:3:289:CYS:N	2.30	0.44
1:A:298:ASP:HB3	1:A:301:LYS:HD3	1.99	0.44
1:A:325:HIS:CD2	1:A:326:HIS:CD2	2.93	0.44
1:A:407:ALA:O	1:A:412:ASN:HB3	2.17	0.44
1:A:591:MET:HB3	1:A:598:LEU:CD2	2.48	0.44
1:A:779:LEU:HD12	1:A:905:LEU:HD11	2.00	0.44
1:A:1000:ILE:HA	1:A:1000:ILE:HD12	1.58	0.44
1:A:1210:LYS:HE2	1:A:1210:LYS:HB2	1.75	0.44
1:A:1725:LEU:HD12	1:A:1725:LEU:HA	1.75	0.44
44:A:3000:IHP:O45	44:A:3000:IHP:H6	2.16	0.44
3:C:474:LEU:HD11	3:C:501:ILE:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:742:PRO:CG	3:C:785:ARG:HG2	2.48	0.44
3:C:802:HIS:CE1	3:C:803:ARG:HH11	2.36	0.44
3:C:909:GLY:HA3	3:C:930:ALA:HB3	1.99	0.44
4:D:1526:HIS:O	4:D:1703:VAL:HA	2.18	0.44
5:E:326:HIS:CE1	5:E:346:SER:HB2	2.53	0.44
7:G:99:C:N3	8:H:33:G:C5	2.85	0.44
8:H:56:A:C4	28:2:504:TRP:CZ3	3.06	0.44
10:J:225:LEU:CB	12:L:211:ASN:ND2	2.70	0.44
11:K:232:ILE:O	11:K:236:LEU:HG	2.18	0.44
15:P:28:LYS:HD2	17:R:164:PRO:HB3	2.00	0.44
15:P:45:GLN:HA	15:P:45:GLN:NE2	2.33	0.44
19:T:203:HIS:CD2	19:T:207:VAL:HG22	2.52	0.44
19:T:295:ASP:O	19:T:303:LEU:HD23	2.18	0.44
21:V:593:TYR:HD1	21:V:593:TYR:HA	1.73	0.44
22:X:497:THR:H	22:X:500:MET:HB2	1.81	0.44
22:X:610:ASP:CG	22:X:669:LYS:HB3	2.42	0.44
24:1:781:ASP:HB3	24:1:784:MET:HB2	2.00	0.44
24:1:946:LYS:O	24:1:950:GLN:HG3	2.17	0.44
24:1:963:LYS:O	24:1:965:CYS:N	2.50	0.44
25:3:109:LYS:NZ	30:7:79:GLU:O	2.50	0.44
25:3:249:LEU:HD23	25:3:256:ILE:HD11	1.98	0.44
25:3:424:TYR:HD1	25:3:437:VAL:HG22	1.82	0.44
25:3:485:LEU:HA	25:3:494:VAL:HB	1.98	0.44
25:3:741:PHE:HB3	25:3:757:ILE:HG13	1.99	0.44
25:3:753:GLY:O	25:3:754:ILE:HD13	2.17	0.44
28:2:596:GLU:N	28:2:596:GLU:CD	2.73	0.44
33:v:60:LEU:HD23	33:v:60:LEU:HA	1.58	0.44
35:9:366:LEU:HD11	35:9:380:PHE:CD2	2.52	0.44
1:A:533:LYS:HE2	7:G:4:A:H5''	1.99	0.44
1:A:863:GLU:HG3	1:A:913:PRO:HB3	2.00	0.44
1:A:1660:TYR:CE1	1:A:1699:THR:HG22	2.53	0.44
2:B:117:A:C6	39:d:26:GLY:HA3	2.52	0.44
3:C:69:ALA:O	3:C:72:VAL:N	2.45	0.44
3:C:485:ASP:OD1	3:C:486:ASP:N	2.51	0.44
3:C:766:ILE:HD12	3:C:766:ILE:HA	1.87	0.44
4:D:824:HIS:HA	4:D:862:ASP:CB	2.47	0.44
5:E:125:PHE:CE2	5:E:135:VAL:HG13	2.52	0.44
6:F:82:A:O2'	6:F:83:A:H2'	2.17	0.44
6:F:83:A:H1'	6:F:84:A:C4	2.53	0.44
7:G:88:G:H1'	8:H:42:G:N2	2.33	0.44
8:H:30:A:H2'	8:H:30:A:N3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:114:A:H2'	8:H:115:G:C8	2.53	0.44
9:I:96:ASN:N	16:Q:949:SER:CB	2.81	0.44
10:J:339:TRP:CE3	17:R:116:TYR:HD2	2.36	0.44
10:J:346:TRP:CG	10:J:369:PHE:HD1	2.35	0.44
14:O:163:HIS:O	14:O:182:ARG:N	2.51	0.44
19:T:341:ALA:O	19:T:344:GLN:HG3	2.17	0.44
22:X:849:VAL:O	22:X:850:ASN:C	2.60	0.44
23:Y:30:LYS:C	23:Y:66:ILE:HD13	2.42	0.44
24:1:761:TYR:O	24:1:765:TYR:HB2	2.17	0.44
24:1:834:VAL:O	24:1:835:ASP:C	2.60	0.44
25:3:187:MET:HE3	25:3:231:HIS:NE2	2.32	0.44
25:3:341:VAL:HG12	25:3:347:LEU:HB2	2.00	0.44
25:3:1151:GLU:OE2	25:3:1193:VAL:HG21	2.18	0.44
28:2:510:TYR:CD2	28:2:510:TYR:O	2.71	0.44
28:2:512:GLN:N	28:2:512:GLN:OE1	2.51	0.44
28:2:528:ILE:O	28:2:531:THR:HG23	2.18	0.44
28:2:535:GLU:H	28:2:535:GLU:CD	2.26	0.44
28:2:707:PRO:HG2	28:2:710:GLU:HG2	2.00	0.44
30:7:21:ARG:HH11	30:7:66:VAL:C	2.19	0.44
31:5:63:ARG:HD3	31:5:63:ARG:HA	1.77	0.44
33:v:33:LEU:O	33:v:37:THR:HG22	2.17	0.44
42:l:32:LEU:HA	42:l:43:MET:HA	1.99	0.44
1:A:384:VAL:HG12	3:C:327:TYR:CE2	2.53	0.44
1:A:384:VAL:HG13	3:C:331:PHE:CD2	2.53	0.44
1:A:758:ARG:HA	1:A:758:ARG:HD2	1.78	0.44
1:A:1368:LEU:HA	1:A:1368:LEU:HD23	1.56	0.44
1:A:1457:HIS:CE1	1:A:1460:HIS:HD2	2.35	0.44
1:A:1838:LYS:HB3	1:A:1868:MET:HG3	1.99	0.44
1:A:1891:LEU:O	1:A:1893:PHE:N	2.47	0.44
1:A:1933:PHE:O	1:A:1937:ILE:HG13	2.17	0.44
2:B:64:G:C6	2:B:65:G:C5	3.05	0.44
3:C:530:LEU:HD23	3:C:530:LEU:HA	1.67	0.44
3:C:743:ASN:HB3	3:C:787:VAL:HG13	2.00	0.44
5:E:81:LEU:HB2	5:E:95:VAL:HG22	1.99	0.44
5:E:259:VAL:CG2	5:E:277:PHE:HB2	2.48	0.44
6:F:28:A:N6	14:O:173:CYS:HA	2.33	0.44
6:F:43:A:N6	6:F:44:G:O6	2.50	0.44
13:N:37:HIS:CG	13:N:37:HIS:O	2.69	0.44
21:V:525:PHE:HA	21:V:528:ILE:HB	1.99	0.44
21:V:648:LYS:HD3	21:V:648:LYS:C	2.43	0.44
22:X:408:LEU:HB2	22:X:570:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:591:TYR:CD2	22:X:692:PRO:HB2	2.50	0.44
22:X:620:GLU:OE2	22:X:620:GLU:N	2.44	0.44
22:X:961:THR:H	22:X:961:THR:HG1	1.53	0.44
23:Y:47:ARG:NH2	23:Y:141:GLU:O	2.51	0.44
24:1:1244:CYS:O	24:1:1245:ARG:C	2.60	0.44
25:3:249:LEU:HD12	25:3:249:LEU:N	2.33	0.44
33:v:74:GLN:HA	33:v:74:GLN:OE1	2.17	0.44
35:9:423:LYS:HE3	35:9:423:LYS:HB3	1.67	0.44
1:A:431:TYR:C	1:A:431:TYR:CD1	2.96	0.44
1:A:1391:LEU:HD23	1:A:1391:LEU:HA	1.73	0.44
3:C:83:GLU:H	3:C:83:GLU:HG2	1.34	0.44
3:C:291:MET:HA	3:C:291:MET:HE3	1.99	0.44
3:C:471:ASP:O	3:C:499:GLY:HA2	2.18	0.44
3:C:745:LEU:HB2	3:C:770:PHE:CD2	2.53	0.44
4:D:530:THR:C	4:D:532:ASN:N	2.75	0.44
5:E:235:ALA:HB3	5:E:256:ASP:HB2	1.99	0.44
5:E:316:SER:O	5:E:317:ARG:HG3	2.18	0.44
6:F:60:C:O2	12:L:206:ARG:HG2	2.17	0.44
7:G:99:C:C4	8:H:33:G:C6	3.05	0.44
13:N:16:GLU:CD	13:N:16:GLU:N	2.75	0.44
16:Q:569:PRO:HA	16:Q:587:VAL:O	2.18	0.44
18:S:12:PRO:O	18:S:26:GLU:HA	2.18	0.44
18:S:99:ALA:HB2	18:S:128:ILE:HA	1.99	0.44
22:X:581:ILE:HG21	22:X:736:ARG:NH1	2.33	0.44
22:X:992:THR:O	22:X:994:LYS:N	2.51	0.44
22:X:1003:ILE:HD12	22:X:1008:LEU:HD21	1.99	0.44
23:Y:37:TYR:CE1	23:Y:106:SER:HB3	2.52	0.44
23:Y:303:ASN:HA	23:Y:311:ILE:O	2.18	0.44
24:1:750:ILE:HG13	24:1:751:GLY:N	2.32	0.44
25:3:554:VAL:HG12	25:3:556:ILE:HG23	2.00	0.44
25:3:910:ALA:CB	25:3:913:LEU:HD11	2.45	0.44
27:w:413:ASN:HD22	27:w:413:ASN:HA	1.61	0.44
27:w:477:GLU:HG2	27:w:479:TYR:HE2	1.83	0.44
28:2:498:VAL:HG21	28:2:588:GLY:HA2	1.99	0.44
33:v:66:GLU:O	33:v:67:GLY:C	2.61	0.44
35:9:300:THR:O	35:9:304:CYS:HB2	2.17	0.44
1:A:388:LEU:HD23	1:A:388:LEU:HA	1.66	0.44
1:A:1661:TRP:CH2	1:A:1684:PHE:HE1	2.36	0.44
1:A:1935:ARG:HA	1:A:1938:LEU:HD12	2.00	0.44
3:C:502:HIS:CE1	3:C:543:ARG:HH12	2.35	0.44
3:C:608:ARG:HB3	3:C:612:LYS:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:114:GLU:O	5:E:126:SER:HA	2.18	0.44
5:E:150:HIS:CE1	5:E:177:LYS:HD2	2.53	0.44
8:H:5:C:H2'	8:H:6:U:C6	2.53	0.44
10:J:436:TYR:O	10:J:440:LEU:HD23	2.18	0.44
12:L:76:LYS:NZ	12:L:76:LYS:HB3	2.31	0.44
21:V:572:GLU:OE1	21:V:580:ARG:NH2	2.51	0.44
21:V:628:ILE:HG21	21:V:644:ARG:HD2	1.98	0.44
22:X:279:LEU:HB3	23:Y:226:MET:SD	2.58	0.44
22:X:327:ARG:NH1	22:X:327:ARG:HB3	2.32	0.44
22:X:972:PRO:HA	22:X:977:PHE:CD2	2.52	0.44
23:Y:8:THR:CG2	23:Y:155:ARG:HB2	2.47	0.44
24:1:532:PHE:HD2	24:1:570:TYR:CD2	2.35	0.44
24:1:967:GLU:HB3	24:1:971:MET:H	1.83	0.44
25:3:164:ASN:HD22	25:3:190:GLU:HG2	1.82	0.44
25:3:569:ASP:HA	25:3:570:PRO:HD2	1.49	0.44
25:3:769:LYS:HD3	25:3:769:LYS:H	1.81	0.44
27:w:381:LYS:HE2	27:w:381:LYS:HB2	1.70	0.44
27:w:458:LEU:HD11	28:2:466:LYS:HD2	2.00	0.44
32:y:32:ILE:HA	32:y:54:PHE:HA	1.98	0.44
1:A:694:LEU:HD22	1:A:709:ILE:HD12	2.00	0.44
1:A:785:LYS:HE3	1:A:785:LYS:HB3	1.56	0.44
1:A:984:MET:HG3	1:A:985:TYR:CD1	2.53	0.44
1:A:1108:ASP:OD1	1:A:1108:ASP:N	2.49	0.44
1:A:1853:PRO:HD2	1:A:1856:GLU:OE2	2.17	0.44
1:A:1917:PHE:HD1	1:A:1967:ILE:HD11	1.83	0.44
2:B:36:C:O2	20:U:11:ARG:NH2	2.51	0.44
3:C:203:MET:CG	3:C:221:ILE:HD11	2.48	0.44
3:C:219:LEU:HD22	3:C:251:LEU:HG	2.00	0.44
3:C:243:ILE:HG13	3:C:244:LYS:N	2.32	0.44
3:C:259:LYS:CE	45:C:1500:GTP:O2'	2.66	0.44
4:D:1915:ILE:O	4:D:1919:ALA:HB2	2.17	0.44
7:G:84:U:C5'	27:w:395:TRP:CH2	3.00	0.44
8:H:105:G:O2'	8:H:107:A:OP1	2.23	0.44
10:J:342:GLU:O	10:J:346:TRP:CD1	2.71	0.44
12:L:62:GLU:N	12:L:62:GLU:OE1	2.51	0.44
12:L:197:GLU:H	12:L:197:GLU:CD	2.26	0.44
19:T:352:THR:HG22	19:T:373:LYS:C	2.43	0.44
21:V:571:SER:HB3	21:V:574:THR:OG1	2.17	0.44
21:V:609:GLN:N	21:V:610:PRO:HD2	2.33	0.44
21:V:636:LEU:HD23	21:V:636:LEU:HA	1.57	0.44
22:X:416:GLN:NE2	22:X:544:PRO:HA	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:482:ARG:NH2	22:X:914:VAL:HG12	2.33	0.44
22:X:576:ARG:HB3	22:X:577:PHE:CD2	2.53	0.44
22:X:808:LEU:HD21	22:X:813:ARG:HB3	2.00	0.44
23:Y:27:ASN:HD21	23:Y:65:SER:HA	1.83	0.44
23:Y:246:LYS:O	23:Y:311:ILE:HG22	2.17	0.44
24:1:694:LEU:HD13	24:1:727:VAL:HG21	2.00	0.44
24:1:1158:ILE:HG13	24:1:1159:GLY:N	2.32	0.44
25:3:190:GLU:CD	25:3:194:ASN:HD21	2.26	0.44
25:3:1211:ILE:HD12	25:3:1214:ARG:HE	1.82	0.44
35:9:241:TYR:HB2	35:9:242:SER:H	1.61	0.44
1:A:858:GLN:OE1	1:A:858:GLN:HA	2.17	0.43
1:A:983:LYS:HE2	1:A:983:LYS:HB2	1.53	0.43
1:A:1109:LEU:HG	1:A:1152:ALA:HB1	2.00	0.43
1:A:1224:ARG:HG3	1:A:1224:ARG:NH1	2.33	0.43
1:A:1276:GLU:OE1	1:A:1375:TRP:N	2.37	0.43
1:A:1375:TRP:O	1:A:1377:SER:N	2.51	0.43
1:A:1978:LYS:HE2	1:A:1978:LYS:HB3	1.76	0.43
2:B:61:A:H2'	2:B:62:G:O4'	2.18	0.43
3:C:280:HIS:HA	3:C:283:ASP:OD1	2.17	0.43
3:C:436:GLN:C	3:C:437:HIS:HD2	2.26	0.43
3:C:839:PRO:HG2	3:C:894:GLN:HB3	1.99	0.43
5:E:84:ALA:HB2	5:E:90:ILE:HG12	1.99	0.43
7:G:1:G:H8	7:G:1:G:H2'	1.59	0.43
7:G:6:A:C4	7:G:7:G:C8	3.06	0.43
7:G:88:G:H2'	7:G:88:G:N3	2.33	0.43
7:G:116:C:N1	17:R:370:SER:O	2.51	0.43
8:H:162:U:H4'	8:H:163:G:O4'	2.18	0.43
9:I:140:LEU:N	9:I:141:PRO:CD	2.80	0.43
10:J:241:VAL:O	10:J:244:ASN:ND2	2.51	0.43
10:J:291:GLN:HB3	10:J:294:HIS:ND1	2.33	0.43
13:N:14:GLY:C	13:N:74:LEU:HD22	2.43	0.43
15:P:212:ASN:O	15:P:212:ASN:CG	2.61	0.43
16:Q:1317:THR:N	16:Q:1318:PRO:HD2	2.33	0.43
19:T:467:ALA:HB3	19:T:480:ALA:HB3	2.00	0.43
22:X:697:GLN:HB2	22:X:712:THR:HG21	1.99	0.43
23:Y:21:ARG:O	23:Y:25:CYS:HB2	2.18	0.43
23:Y:215:LYS:O	23:Y:216:GLU:C	2.61	0.43
24:1:806:ILE:HA	24:1:810:ILE:HD12	2.00	0.43
24:1:969:LYS:HD2	24:1:969:LYS:H	1.83	0.43
24:1:1080:THR:HA	24:1:1083:TYR:CD2	2.52	0.43
24:1:1136:TYR:HD2	28:2:522:PHE:HD1	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:373:PHE:HD1	25:3:385:PHE:CD2	2.36	0.43
25:3:404:LEU:HD12	25:3:404:LEU:HA	1.77	0.43
25:3:462:VAL:HG11	25:3:516:LEU:HD23	2.00	0.43
25:3:613:THR:CB	25:3:630:MET:HE1	2.48	0.43
25:3:1031:ARG:HG2	25:3:1031:ARG:NH1	2.26	0.43
25:3:1115:GLU:CG	28:2:708:TRP:HZ2	2.22	0.43
25:3:1156:CYS:O	25:3:1158:ARG:N	2.50	0.43
1:A:75:ASP:O	1:A:77:THR:HG22	2.18	0.43
1:A:214:ARG:HH22	1:A:223:SER:C	2.14	0.43
1:A:736:GLU:OE2	35:9:247:SER:OG	2.29	0.43
1:A:923:ASP:OD2	1:A:1439:ARG:NH1	2.49	0.43
1:A:1769:GLY:HA2	1:A:1772:PHE:CE1	2.53	0.43
1:A:1777:ILE:HA	1:A:1860:GLN:O	2.18	0.43
3:C:502:HIS:CE1	3:C:543:ARG:NH1	2.86	0.43
3:C:560:VAL:O	3:C:561:LYS:C	2.61	0.43
3:C:750:LEU:HD11	20:U:67:GLU:CB	2.48	0.43
3:C:848:THR:O	3:C:852:ARG:HG3	2.18	0.43
5:E:110:GLY:N	5:E:130:ASP:OD1	2.35	0.43
6:F:36:A:N6	6:F:38:G:C6	2.86	0.43
8:H:10:C:H2'	8:H:11:G:C8	2.52	0.43
8:H:48:A:N3	8:H:78:C:OP2	2.51	0.43
12:L:200:LYS:O	12:L:201:LYS:HB2	2.18	0.43
16:Q:381:ALA:O	16:Q:386:LEU:N	2.30	0.43
17:R:369:LEU:HD12	17:R:376:LYS:HZ2	1.83	0.43
21:V:537:HIS:CE1	21:V:538:ARG:HE	2.36	0.43
22:X:269:GLU:HA	22:X:272:TYR:HB3	2.00	0.43
22:X:849:VAL:O	22:X:851:ASN:N	2.51	0.43
22:X:950:HIS:CG	22:X:986:TYR:CE2	3.06	0.43
23:Y:240:ASN:ND2	23:Y:289:GLU:O	2.51	0.43
23:Y:275:TRP:CG	23:Y:276:LYS:N	2.86	0.43
24:1:645:LEU:HD13	24:1:682:HIS:CD2	2.52	0.43
25:3:1:MET:HE3	25:3:3:LEU:HD21	1.99	0.43
25:3:549:VAL:HG12	25:3:550:ASN:O	2.18	0.43
25:3:803:ASP:OD2	31:5:58:ASN:ND2	2.51	0.43
25:3:1183:ASN:OD1	25:3:1183:ASN:N	2.51	0.43
27:w:419:PRO:O	27:w:422:PHE:HB3	2.18	0.43
1:A:71:ARG:HG3	1:A:71:ARG:HH11	1.83	0.43
1:A:75:ASP:OD1	1:A:75:ASP:N	2.52	0.43
1:A:118:VAL:O	1:A:484:SER:HA	2.18	0.43
1:A:593:ARG:CZ	1:A:1565:LYS:HZ3	2.31	0.43
1:A:1189:MET:O	1:A:1190:CYS:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1337:GLN:HA	1:A:1337:GLN:HE21	1.82	0.43
1:A:1793:THR:C	1:A:1795:GLU:H	2.25	0.43
1:A:1889:LEU:CG	1:A:2013:GLY:CA	2.88	0.43
4:D:606:THR:C	4:D:608:LEU:H	2.26	0.43
5:E:328:GLY:O	5:E:346:SER:OG	2.37	0.43
8:H:70:C:H2'	8:H:71:C:H6	1.80	0.43
19:T:288:LEU:O	19:T:289:SER:OG	2.31	0.43
19:T:320:LYS:HE2	19:T:320:LYS:HB2	1.72	0.43
21:V:451:ASN:OD1	21:V:452:LEU:N	2.51	0.43
22:X:164:TRP:CE3	22:X:165:GLU:HA	2.53	0.43
23:Y:177:ARG:HG2	23:Y:178:SER:H	1.83	0.43
24:1:685:SER:O	24:1:689:ILE:HG12	2.17	0.43
25:3:278:LEU:HD21	25:3:816:LYS:HZ3	1.83	0.43
25:3:568:MET:H	25:3:568:MET:HG2	1.58	0.43
25:3:705:ARG:NH2	25:3:746:ALA:HB2	2.34	0.43
25:3:779:PHE:N	25:3:779:PHE:CD1	2.86	0.43
25:3:798:ILE:H	25:3:798:ILE:HG12	1.47	0.43
25:3:986:ILE:HG21	25:3:990:ILE:HG12	1.99	0.43
28:2:465:LEU:HB3	28:2:475:VAL:HG11	2.00	0.43
28:2:511:LEU:O	28:2:513:GLY:N	2.51	0.43
33:v:30:LEU:HD23	33:v:30:LEU:HA	1.72	0.43
33:v:119:VAL:CA	33:v:135:GLN:O	2.66	0.43
1:A:606:LYS:HD2	44:A:3000:IHP:O26	2.18	0.43
1:A:1012:LYS:O	1:A:1012:LYS:HG3	2.19	0.43
1:A:1050:LEU:HA	1:A:1050:LEU:HD23	1.80	0.43
2:B:63:A:C2	2:B:64:G:C5	3.06	0.43
2:B:92:U:O4	37:b:34:VAL:O	2.37	0.43
3:C:219:LEU:HD23	3:C:219:LEU:HA	1.67	0.43
3:C:366:GLN:HB2	3:C:370:VAL:HB	1.99	0.43
5:E:125:PHE:N	5:E:125:PHE:HD2	2.16	0.43
5:E:258:THR:HG23	5:E:278:GLN:HE22	1.84	0.43
7:G:90:C:H2'	7:G:91:A:C8	2.53	0.43
8:H:7:U:H2'	8:H:8:C:O4'	2.18	0.43
10:J:252:GLU:CD	10:J:260:ARG:HD2	2.43	0.43
17:R:279:HIS:C	17:R:280:ILE:HG12	2.43	0.43
22:X:482:ARG:HH21	22:X:914:VAL:HG12	1.83	0.43
22:X:809:THR:HG22	22:X:810:THR:N	2.34	0.43
22:X:877:ASP:O	22:X:880:VAL:HB	2.19	0.43
22:X:921:LEU:O	22:X:925:VAL:HG22	2.17	0.43
23:Y:26:LEU:HB3	23:Y:166:PHE:CE1	2.53	0.43
24:1:1286:ARG:O	28:2:490:HIS:NE2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:192:ALA:CB	31:5:73:LEU:HD11	2.49	0.43
25:3:925:VAL:O	25:3:942:LYS:HA	2.18	0.43
28:2:510:TYR:CE1	28:2:511:LEU:HG	2.53	0.43
28:2:536:MET:HE2	28:2:536:MET:HB3	1.76	0.43
31:5:20:GLY:HA2	31:5:34:ASN:ND2	2.33	0.43
33:v:58:LEU:HG	33:v:59:CYS:SG	2.59	0.43
35:9:292:ASN:HB2	35:9:402:GLY:N	2.33	0.43
3:C:453:TYR:HB3	3:C:456:GLY:H	1.83	0.43
3:C:632:THR:H	3:C:636:TYR:HD2	1.66	0.43
4:D:1189:HIS:O	4:D:1200:VAL:HA	2.18	0.43
5:E:75:HIS:HB3	5:E:78:GLY:N	2.29	0.43
7:G:6:A:C6	7:G:7:G:C6	3.06	0.43
11:K:198:GLN:NE2	11:K:198:GLN:HA	2.34	0.43
17:R:335:ARG:HA	22:X:271:LYS:NZ	2.34	0.43
17:R:360:ARG:CZ	23:Y:275:TRP:CD1	2.97	0.43
22:X:269:GLU:HA	22:X:269:GLU:OE2	2.18	0.43
23:Y:26:LEU:HB3	23:Y:166:PHE:CD1	2.53	0.43
23:Y:223:LEU:O	23:Y:226:MET:HB3	2.18	0.43
24:1:551:LEU:O	24:1:555:VAL:HG23	2.18	0.43
24:1:630:ARG:O	24:1:634:VAL:HG23	2.18	0.43
24:1:666:LYS:HB3	24:1:704:ILE:CD1	2.48	0.43
24:1:857:LEU:HD13	24:1:895:GLY:C	2.44	0.43
25:3:123:VAL:HG22	25:3:124:ASP:H	1.84	0.43
25:3:125:PRO:HG2	25:3:174:ASP:HA	1.98	0.43
25:3:558:LEU:HD23	25:3:562:GLU:HB3	1.99	0.43
25:3:590:MET:HB2	25:3:606:ALA:O	2.18	0.43
25:3:679:LEU:HD22	25:3:679:LEU:HA	1.78	0.43
1:A:312:TYR:N	1:A:312:TYR:CD1	2.83	0.43
1:A:1607:GLU:C	1:A:1607:GLU:CD	2.84	0.43
1:A:1636:LYS:HG3	1:A:1658:GLN:HE21	1.84	0.43
1:A:1975:GLU:O	1:A:1979:VAL:HG22	2.19	0.43
3:C:223:ASP:HA	3:C:448:LYS:HZ1	1.83	0.43
3:C:643:ASP:OD1	3:C:643:ASP:N	2.52	0.43
3:C:664:GLU:HG3	3:C:784:ILE:HG22	1.99	0.43
3:C:721:LYS:HB2	3:C:722:TYR:CE2	2.54	0.43
3:C:801:LEU:HD23	3:C:801:LEU:HA	1.76	0.43
3:C:807:GLN:HE21	35:9:145:LEU:HA	1.83	0.43
3:C:914:LYS:HD2	3:C:931:ARG:NH2	2.33	0.43
5:E:177:LYS:HB3	5:E:179:TRP:HE1	1.83	0.43
5:E:343:ILE:HD11	5:E:351:LEU:HD13	2.01	0.43
6:F:58:G:HO2'	6:F:59:G:P	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:104:C:O2	7:G:104:C:H2'	2.18	0.43
10:J:242:ILE:HA	10:J:245:TRP:HD1	1.83	0.43
10:J:339:TRP:HA	17:R:116:TYR:CE2	2.53	0.43
17:R:91:ASP:CG	17:R:93:GLU:H	2.26	0.43
17:R:386:ARG:HG3	22:X:909:ARG:HH22	1.77	0.43
21:V:497:CYS:HB2	21:V:507:PHE:HB2	1.99	0.43
22:X:164:TRP:CD1	22:X:538:ASP:C	2.84	0.43
22:X:226:LEU:CD2	23:Y:315:PHE:CE2	2.70	0.43
22:X:412:ILE:HB	22:X:418:LEU:HD23	2.01	0.43
22:X:516:VAL:HG22	22:X:547:LYS:CB	2.47	0.43
22:X:529:THR:O	22:X:532:LEU:HG	2.19	0.43
22:X:792:ALA:O	22:X:796:LEU:HG	2.19	0.43
24:1:830:TYR:HA	24:1:867:MET:SD	2.57	0.43
24:1:963:LYS:HG3	24:1:964:THR:N	2.33	0.43
24:1:1156:GLU:O	30:7:38:ARG:NH1	2.51	0.43
24:1:1292:LYS:O	31:5:78:PRO:HD2	2.18	0.43
25:3:234:PHE:CD1	25:3:235:LEU:N	2.86	0.43
25:3:604:PHE:CZ	25:3:681:PRO:HD3	2.53	0.43
25:3:611:ASP:O	25:3:612:ASN:HB2	2.17	0.43
25:3:955:PHE:HZ	25:3:1014:TYR:CD2	2.36	0.43
25:3:993:ILE:HG23	25:3:1002:VAL:HG23	1.99	0.43
25:3:1041:TYR:HB3	28:2:705:ARG:HA	1.99	0.43
25:3:1158:ARG:HG3	25:3:1159:ASP:N	2.34	0.43
28:2:509:LYS:N	28:2:509:LYS:CE	2.73	0.43
30:7:74:GLU:O	30:7:78:GLN:HG3	2.18	0.43
34:u:60:VAL:HA	34:u:64:GLY:H	1.83	0.43
35:9:285:HIS:N	35:9:285:HIS:CD2	2.87	0.43
35:9:300:THR:OG1	35:9:300:THR:O	2.37	0.43
35:9:370:ASN:HD22	35:9:375:SER:H	1.66	0.43
1:A:1500:GLY:O	1:A:1501:LEU:C	2.62	0.43
1:A:1593:LEU:HD23	1:A:1593:LEU:HA	1.55	0.43
1:A:1889:LEU:CD1	1:A:2013:GLY:CA	2.96	0.43
3:C:259:LYS:H	3:C:311:SER:HA	1.83	0.43
3:C:710:ASN:OD1	3:C:713:LYS:HG3	2.19	0.43
3:C:833:PHE:CZ	3:C:872:LYS:HB3	2.54	0.43
3:C:909:GLY:HA3	3:C:930:ALA:H	1.83	0.43
5:E:125:PHE:CD1	5:E:159:PRO:HG3	2.54	0.43
5:E:267:PHE:HD2	5:E:268:ALA:N	2.16	0.43
7:G:90:C:N4	8:H:40:C:H42	2.16	0.43
8:H:56:A:C5	28:2:504:TRP:CZ3	3.07	0.43
8:H:118:G:C6	8:H:140:A:N6	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:363:ARG:HB2	10:J:382:TYR:OH	2.18	0.43
10:J:372:VAL:HG12	10:J:373:HIS:CE1	2.53	0.43
15:P:74:LYS:O	15:P:77:ASP:HB3	2.18	0.43
17:R:369:LEU:HA	17:R:376:LYS:CE	2.41	0.43
19:T:473:SER:OG	19:T:475:SER:HB3	2.18	0.43
21:V:506:PHE:CD1	21:V:506:PHE:C	2.96	0.43
21:V:563:SER:O	21:V:565:LEU:N	2.52	0.43
21:V:643:LEU:HD23	21:V:643:LEU:HA	1.48	0.43
22:X:164:TRP:CE3	22:X:164:TRP:C	2.96	0.43
22:X:647:ILE:HA	22:X:651:LEU:HD21	2.01	0.43
23:Y:208:VAL:O	23:Y:212:LYS:HG3	2.18	0.43
25:3:788:PHE:CD1	25:3:788:PHE:C	2.97	0.43
35:9:321:PHE:HB2	35:9:426:ILE:HB	2.00	0.43
1:A:191:ILE:CG1	1:A:571:ALA:HB1	2.49	0.43
1:A:456:LEU:O	1:A:460:LYS:HG2	2.18	0.43
1:A:755:HIS:HE1	15:P:220:HIS:CE1	2.35	0.43
1:A:1255:THR:O	1:A:1256:PHE:C	2.62	0.43
1:A:1402:ARG:NH1	17:R:406:GLN:HE21	2.17	0.43
1:A:1840:LYS:O	1:A:1844:GLU:HG2	2.19	0.43
1:A:1990:ASP:HA	1:A:1993:LYS:HD3	2.01	0.43
4:D:1590:LEU:HA	4:D:1640:ALA:O	2.19	0.43
7:G:-8:C:C4'	20:U:18:TYR:HB2	2.49	0.43
7:G:21:A:H4'	7:G:22:C:OP1	2.18	0.43
7:G:86:A:H2	8:H:44:U:O2	2.02	0.43
7:G:100:C:H3'	7:G:100:C:OP2	2.19	0.43
17:R:155:VAL:HG22	19:T:323:VAL:HG12	2.00	0.43
21:V:555:LEU:HG	21:V:586:PHE:CZ	2.53	0.43
21:V:571:SER:HA	21:V:623:ASN:HB3	2.01	0.43
22:X:390:GLU:O	22:X:393:GLN:HG3	2.18	0.43
22:X:974:SER:HB3	22:X:977:PHE:HB2	1.99	0.43
23:Y:91:LYS:C	23:Y:93:THR:H	2.27	0.43
24:1:666:LYS:O	24:1:670:GLN:HG2	2.19	0.43
24:1:668:VAL:HG22	24:1:686:LEU:HD23	1.99	0.43
25:3:182:PHE:O	25:3:210:PHE:HA	2.19	0.43
25:3:526:HIS:HB2	25:3:574:LEU:CD2	2.48	0.43
25:3:822:GLU:H	25:3:822:GLU:HG3	1.64	0.43
25:3:838:MET:H	25:3:838:MET:HG2	1.73	0.43
25:3:924:PHE:HA	25:3:943:THR:O	2.18	0.43
28:2:487:LEU:O	28:2:488:LEU:C	2.61	0.43
28:2:534:GLN:HG2	28:2:538:GLU:OE1	2.18	0.43
43:o:92:GLU:HA	43:o:117:TYR:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ASP:CG	1:A:171:ASP:N	2.76	0.43
1:A:206:TRP:HA	1:A:209:ASP:OD2	2.19	0.43
1:A:1489:LEU:HD23	1:A:1489:LEU:HA	1.85	0.43
1:A:1781:ASP:OD2	1:A:1893:PHE:HB2	2.18	0.43
2:B:40:U:H5'	2:B:41:U:OP2	2.19	0.43
3:C:226:VAL:HG13	3:C:254:THR:HG22	2.00	0.43
3:C:745:LEU:HD22	3:C:770:PHE:HB2	1.99	0.43
3:C:834:VAL:HG22	3:C:899:SER:HB2	2.01	0.43
3:C:846:VAL:HG11	3:C:871:ILE:HD12	1.99	0.43
5:E:154:VAL:HG13	5:E:171:SER:HB3	2.00	0.43
5:E:207:GLN:HB3	5:E:219:VAL:HG12	2.01	0.43
5:E:215:ASN:HB2	5:E:232:ARG:NH1	2.34	0.43
8:H:63:G:N1	8:H:64:A:N6	2.67	0.43
13:N:56:LYS:HD2	13:N:83:TYR:HB3	2.01	0.43
15:P:68:ARG:HB3	15:P:68:ARG:NH1	2.33	0.43
17:R:335:ARG:O	22:X:268:GLN:HB2	2.19	0.43
19:T:300:ILE:H	19:T:300:ILE:HG13	1.65	0.43
19:T:346:ILE:HD13	19:T:380:LEU:HD21	1.99	0.43
19:T:462:GLU:O	19:T:483:ASP:HB3	2.18	0.43
22:X:283:TYR:CE2	23:Y:222:ILE:CG2	2.99	0.43
24:1:823:MET:SD	24:1:829:ASN:ND2	2.92	0.43
24:1:998:LYS:HZ1	24:1:1041:ARG:NH1	2.17	0.43
24:1:1287:ILE:HB	31:5:32:LEU:HD11	2.00	0.43
25:3:436:ARG:HG2	25:3:778:ALA:CB	2.49	0.43
25:3:483:LEU:HD11	25:3:493:GLU:OE2	2.19	0.43
25:3:565:TYR:HB3	25:3:577:TYR:CB	2.46	0.43
25:3:791:HIS:NE2	25:3:793:GLU:HB2	2.34	0.43
25:3:1022:ILE:HD13	25:3:1022:ILE:HA	1.77	0.43
35:9:312:LYS:HE2	35:9:312:LYS:HB2	1.76	0.43
1:A:101:LYS:HD3	1:A:101:LYS:HA	1.65	0.43
1:A:131:GLU:HG3	1:A:132:ILE:N	2.33	0.43
1:A:277:PRO:HD3	1:A:451:LEU:HB3	2.01	0.43
1:A:356:ILE:H	1:A:356:ILE:HG13	1.19	0.43
1:A:1585:ILE:O	1:A:1589:ILE:HD12	2.18	0.43
4:D:1271:VAL:HA	4:D:1279:GLU:HA	2.00	0.43
4:D:1771:TYR:C	4:D:1773:LEU:H	2.27	0.43
7:G:13:C:H2'	7:G:14:A:O4'	2.19	0.43
7:G:105:C:H5''	22:X:972:PRO:HG2	2.01	0.43
10:J:397:LYS:O	10:J:401:ARG:HD3	2.19	0.43
17:R:371:ARG:NH1	23:Y:282:CYS:SG	2.92	0.43
17:R:382:ARG:HH12	17:R:386:ARG:NE	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:164:TRP:CD1	22:X:542:PHE:CB	2.98	0.43
22:X:733:LYS:HB3	22:X:735:PHE:HE2	1.84	0.43
22:X:737:LEU:O	22:X:737:LEU:HD23	2.18	0.43
24:1:508:THR:HB	24:1:510:PRO:CD	2.46	0.43
24:1:609:MET:HE1	24:1:635:VAL:CG1	2.49	0.43
24:1:936:VAL:HG12	24:1:937:LEU:HD12	2.01	0.43
24:1:1227:ILE:O	24:1:1231:MET:HG2	2.19	0.43
24:1:1273:TYR:O	24:1:1277:GLN:HB3	2.19	0.43
25:3:514:ASP:OD1	25:3:514:ASP:N	2.52	0.43
25:3:665:LEU:HB2	25:3:679:LEU:HD23	2.00	0.43
25:3:690:ARG:HH12	25:3:696:SER:H	1.67	0.43
28:2:483:GLN:OE1	28:2:483:GLN:N	2.51	0.43
30:7:58:CYS:N	30:7:63:GLY:O	2.52	0.43
35:9:320:ILE:HG13	35:9:337:GLY:HA2	2.01	0.43
35:9:331:GLN:HG3	35:9:381:PHE:HB3	2.00	0.43
38:h:71:LYS:HA	38:h:95:TYR:HA	2.01	0.43
1:A:407:ALA:HB1	1:A:411:PHE:HB2	2.01	0.42
1:A:733:THR:O	1:A:734:PRO:C	2.60	0.42
1:A:793:ASN:HD22	3:C:60:HIS:CE1	2.36	0.42
1:A:1406:GLU:N	1:A:1406:GLU:CD	2.76	0.42
1:A:1457:HIS:ND1	1:A:1460:HIS:CD2	2.84	0.42
1:A:2144:CYS:HA	1:A:2270:PHE:O	2.19	0.42
2:B:67:A:H2'	2:B:68:C:O4'	2.19	0.42
3:C:263:LEU:HA	3:C:267:LEU:HB2	1.99	0.42
3:C:298:LEU:O	3:C:299:ILE:HD13	2.19	0.42
3:C:312:SER:OG	45:C:1500:GTP:N7	2.52	0.42
3:C:349:PHE:CE1	3:C:354:ARG:HA	2.43	0.42
3:C:351:PRO:O	3:C:354:ARG:HD3	2.19	0.42
3:C:474:LEU:HA	3:C:498:SER:O	2.19	0.42
3:C:493:PHE:HB2	3:C:551:LEU:HD23	2.01	0.42
4:D:784:ILE:HA	4:D:810:VAL:O	2.19	0.42
5:E:145:LYS:CD	5:E:184:LYS:HE2	2.49	0.42
5:E:178:LEU:HD12	5:E:178:LEU:HA	1.89	0.42
5:E:244:SER:HB2	5:E:293:TRP:CD2	2.54	0.42
6:F:36:A:C8	6:F:36:A:O5'	2.72	0.42
7:G:11:A:H2'	7:G:12:G:O4'	2.19	0.42
7:G:90:C:H2'	7:G:91:A:C4	2.54	0.42
8:H:8:C:H2'	8:H:9:U:C6	2.54	0.42
13:N:46:LEU:HA	13:N:49:ILE:HG22	2.01	0.42
17:R:367:ARG:NH2	23:Y:281:LEU:HD23	2.34	0.42
19:T:423:SER:N	19:T:474:GLU:OE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:164:TRP:CD1	22:X:538:ASP:O	2.71	0.42
22:X:234:TYR:CZ	23:Y:317:GLN:O	2.72	0.42
22:X:482:ARG:HE	22:X:483:PHE:HE2	1.65	0.42
24:1:493:LYS:O	24:1:496:LYS:N	2.52	0.42
24:1:679:ILE:O	24:1:682:HIS:N	2.46	0.42
25:3:58:VAL:HG21	25:3:62:ILE:CD1	2.49	0.42
25:3:1021:LEU:HD23	25:3:1021:LEU:HA	1.77	0.42
27:w:387:TRP:HH2	33:v:81:ASN:O	2.02	0.42
28:2:472:PRO:O	28:2:475:VAL:HG23	2.19	0.42
28:2:514:LYS:N	28:2:593:GLU:OE2	2.52	0.42
28:2:711:LEU:HD23	28:2:711:LEU:HA	1.80	0.42
31:5:11:LEU:O	31:5:14:LEU:HB2	2.19	0.42
33:v:47:MET:HB2	33:v:47:MET:HE3	1.71	0.42
39:i:23:LEU:N	39:i:27:MET:O	2.42	0.42
39:i:43:GLN:HA	39:i:63:LEU:HA	2.01	0.42
1:A:106:MET:HA	1:A:107:PRO:HD3	1.77	0.42
1:A:298:ASP:O	1:A:302:ILE:HG12	2.19	0.42
1:A:355:LEU:O	3:C:867:PRO:HB3	2.19	0.42
1:A:606:LYS:HZ2	44:A:3000:IHP:P6	2.42	0.42
1:A:1284:LEU:O	1:A:1285:LEU:C	2.60	0.42
3:C:463:GLU:HA	3:C:466:SER:HB3	2.01	0.42
3:C:692:LEU:CD2	3:C:788:LYS:HB2	2.50	0.42
3:C:757:ALA:O	3:C:761:SER:HB2	2.19	0.42
3:C:807:GLN:HE21	35:9:145:LEU:C	2.25	0.42
4:D:444:GLU:HA	4:D:690:VAL:HA	2.02	0.42
5:E:90:ILE:HB	5:E:105:LEU:HB3	2.01	0.42
5:E:94:ASN:O	5:E:99:CYS:HA	2.19	0.42
5:E:175:THR:HB	5:E:189:THR:CG2	2.49	0.42
15:P:53:GLU:H	15:P:53:GLU:CD	2.27	0.42
15:P:69:ALA:HA	15:P:72:ARG:NH1	2.34	0.42
16:Q:488:SER:O	16:Q:489:VAL:C	2.62	0.42
16:Q:1224:ILE:HA	16:Q:1270:TYR:O	2.19	0.42
21:V:468:ASP:OD1	21:V:468:ASP:N	2.52	0.42
22:X:527:LEU:HD21	22:X:755:ILE:HA	2.01	0.42
22:X:948:PHE:O	22:X:951:THR:OG1	2.35	0.42
22:X:1004:GLU:HG3	22:X:1007:TRP:CZ2	2.54	0.42
23:Y:4:LEU:HD11	23:Y:11:ASP:HB3	2.01	0.42
24:1:548:GLU:O	24:1:552:LEU:HG	2.18	0.42
24:1:1200:TYR:C	24:1:1200:TYR:CD1	2.95	0.42
24:1:1262:ARG:HB3	31:5:24:ALA:HB1	2.01	0.42
25:3:83:ASP:OD1	25:3:83:ASP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:131:MET:HB2	25:3:141:VAL:HG22	2.01	0.42
25:3:234:PHE:HE1	25:3:236:ILE:HG12	1.81	0.42
25:3:641:CYS:H	25:3:701:LEU:HD23	1.83	0.42
25:3:768:GLU:HB3	25:3:769:LYS:H	1.63	0.42
31:5:71:LYS:C	31:5:73:LEU:H	2.26	0.42
33:v:42:LYS:N	33:v:42:LYS:HD2	2.34	0.42
35:9:299:LEU:H	35:9:299:LEU:HD23	1.85	0.42
35:9:355:ARG:HB3	35:9:358:LEU:HD12	1.99	0.42
41:k:7:PRO:HD3	41:k:36:PRO:HA	2.00	0.42
1:A:79:ARG:NH1	1:A:82:ARG:HH21	2.11	0.42
1:A:371:LEU:HD12	1:A:371:LEU:HA	1.81	0.42
1:A:386:PRO:HD2	1:A:389:LYS:HD2	2.01	0.42
1:A:599:MET:HE3	1:A:599:MET:HB3	1.81	0.42
1:A:1779:PHE:HB3	1:A:1893:PHE:HE2	1.84	0.42
2:B:115:C:OP1	40:e:67:LYS:CA	2.67	0.42
3:C:131:ASN:HD22	3:C:495:ARG:HH22	1.67	0.42
3:C:481:MET:HB3	3:C:490:PHE:CD2	2.55	0.42
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.84	0.42
6:F:39:A:C4	6:F:40:U:C6	3.07	0.42
6:F:43:A:C2	7:G:5:G:C6	3.06	0.42
8:H:152:G:C6	8:H:153:A:N6	2.87	0.42
13:N:25:LEU:HD23	13:N:25:LEU:HA	1.84	0.42
13:N:98:GLU:CD	13:N:98:GLU:N	2.77	0.42
17:R:365:HIS:O	17:R:369:LEU:HD13	2.20	0.42
21:V:476:LEU:HD23	21:V:476:LEU:HA	1.77	0.42
21:V:585:ILE:H	21:V:585:ILE:HG13	1.71	0.42
22:X:162:ASP:N	22:X:542:PHE:HE2	2.16	0.42
22:X:234:TYR:HB2	23:Y:317:GLN:HG2	2.00	0.42
22:X:546:LEU:HD12	22:X:546:LEU:HA	1.87	0.42
22:X:577:PHE:HB2	22:X:727:GLY:O	2.19	0.42
22:X:959:TYR:OH	22:X:980:GLN:O	2.37	0.42
23:Y:12:VAL:HG13	23:Y:131:GLU:O	2.20	0.42
23:Y:290:LYS:HB2	23:Y:293:ASP:OD2	2.19	0.42
24:1:902:GLU:O	24:1:903:GLN:C	2.62	0.42
24:1:1254:LEU:O	24:1:1262:ARG:HG2	2.19	0.42
25:3:192:ALA:HA	25:3:200:ALA:HB3	2.01	0.42
25:3:671:ASN:HB3	25:3:696:SER:HA	2.01	0.42
25:3:966:LEU:H	25:3:966:LEU:HG	1.72	0.42
38:h:52:LEU:HA	38:h:71:LYS:O	2.19	0.42
1:A:127:SER:HG	1:A:499:GLN:HE22	1.61	0.42
1:A:435:CYS:HA	7:G:-10:G:H22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:GLU:CB	1:A:591:MET:HG3	2.50	0.42
1:A:690:MET:SD	1:A:706:ALA:HB1	2.59	0.42
1:A:858:GLN:HA	1:A:861:ARG:NH1	2.34	0.42
1:A:940:ILE:HD13	1:A:1090:ARG:NH1	2.34	0.42
1:A:1384:ARG:NH1	1:A:1384:ARG:HB2	2.35	0.42
1:A:1600:GLU:OE1	1:A:1604:LEU:HG	2.19	0.42
1:A:1695:TYR:HD1	1:A:1695:TYR:HA	1.71	0.42
1:A:1891:LEU:CD2	1:A:2012:LEU:O	2.67	0.42
1:A:1939:ILE:HG21	1:A:1968:TRP:NE1	2.35	0.42
3:C:508:LYS:O	3:C:566:THR:HG22	2.19	0.42
5:E:226:LYS:HD3	5:E:226:LYS:HA	1.87	0.42
5:E:251:LEU:HB2	5:E:293:TRP:CE2	2.54	0.42
6:F:6:C:O2'	6:F:7:G:OP1	2.34	0.42
10:J:292:VAL:HG12	10:J:296:ARG:NE	2.35	0.42
10:J:317:THR:O	10:J:320:GLU:N	2.52	0.42
10:J:416:TYR:CE2	10:J:443:ILE:HD13	2.52	0.42
12:L:169:ARG:HE	12:L:169:ARG:HB2	1.58	0.42
12:L:169:ARG:O	12:L:172:ARG:N	2.48	0.42
20:U:24:SER:HA	21:V:477:LEU:HD12	2.01	0.42
21:V:556:TYR:CE1	21:V:557:THR:HG23	2.54	0.42
22:X:327:ARG:HH12	22:X:328:ARG:NH2	2.17	0.42
22:X:408:LEU:HD13	22:X:570:PHE:CD2	2.55	0.42
22:X:428:LYS:H	22:X:428:LYS:HG3	1.58	0.42
22:X:664:PRO:HA	22:X:665:PRO:HD2	1.91	0.42
24:1:551:LEU:O	24:1:554:LYS:HB3	2.19	0.42
24:1:876:MET:HE1	24:1:917:VAL:HG23	2.01	0.42
24:1:962:MET:O	24:1:967:GLU:HB2	2.18	0.42
24:1:1046:GLY:O	24:1:1048:GLU:N	2.50	0.42
24:1:1199:VAL:HG12	24:1:1199:VAL:O	2.19	0.42
25:3:169:HIS:HD2	25:3:170:VAL:O	2.02	0.42
25:3:671:ASN:HA	25:3:696:SER:C	2.44	0.42
25:3:675:LEU:HB3	25:3:686:LEU:HD12	2.02	0.42
25:3:896:PHE:H	25:3:896:PHE:HD2	1.68	0.42
27:w:387:TRP:O	33:v:88:LYS:CG	2.68	0.42
28:2:526:ASP:HA	28:2:529:LYS:NZ	2.35	0.42
33:v:114:ARG:N	33:v:115:PRO:HD3	2.35	0.42
1:A:41:GLN:C	1:A:43:LYS:N	2.77	0.42
1:A:525:LYS:CB	11:K:197:TYR:CD2	2.99	0.42
1:A:1198:PRO:HG2	1:A:1201:ARG:HB2	2.00	0.42
1:A:1215:ASN:HB3	1:A:1224:ARG:NH1	2.34	0.42
1:A:1298:ARG:O	1:A:1298:ARG:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1839:TRP:CE3	1:A:1871:PRO:HB3	2.53	0.42
1:A:1840:LYS:O	1:A:1841:THR:C	2.62	0.42
44:A:3000:IHP:P3	44:A:3000:IHP:O42	2.77	0.42
3:C:366:GLN:HG3	3:C:371:GLU:CD	2.44	0.42
3:C:503:ALA:C	3:C:505:GLN:H	2.27	0.42
3:C:529:ARG:O	3:C:530:LEU:HD23	2.19	0.42
3:C:561:LYS:H	3:C:561:LYS:HG2	1.48	0.42
3:C:680:ASN:O	3:C:682:LYS:N	2.53	0.42
3:C:830:PRO:HA	3:C:904:TRP:HA	2.00	0.42
5:E:176:VAL:HG21	5:E:220:TRP:HE1	1.83	0.42
6:F:22:A:H3'	13:N:115:THR:CB	2.49	0.42
8:H:35:A:H3'	8:H:36:G:H8	1.83	0.42
10:J:319:MET:HG3	10:J:320:GLU:N	2.33	0.42
10:J:396:ARG:NH2	10:J:426:GLN:HG3	2.35	0.42
17:R:384:GLU:HG3	22:X:484:GLU:OE1	2.19	0.42
19:T:393:ASP:OD2	19:T:393:ASP:N	2.53	0.42
22:X:164:TRP:CG	22:X:542:PHE:CG	3.06	0.42
22:X:610:ASP:OD2	22:X:669:LYS:HB3	2.19	0.42
22:X:718:SER:OG	22:X:719:ALA:N	2.52	0.42
22:X:976:LEU:HD11	22:X:1001:LEU:HA	2.01	0.42
24:1:592:GLU:O	24:1:596:ILE:HG23	2.19	0.42
24:1:826:ASP:OD1	24:1:828:ARG:N	2.42	0.42
24:1:1178:MET:O	24:1:1179:ASP:C	2.62	0.42
24:1:1251:LEU:HD23	24:1:1251:LEU:HA	1.68	0.42
25:3:1115:GLU:HG2	28:2:708:TRP:HE1	0.42	0.42
27:w:429:TRP:O	27:w:430:ARG:C	2.62	0.42
28:2:508:ARG:C	28:2:509:LYS:HE3	2.43	0.42
1:A:71:ARG:HG3	1:A:71:ARG:NH1	2.35	0.42
1:A:147:MET:O	1:A:151:MET:HG2	2.19	0.42
1:A:193:LEU:HG	1:A:194:GLU:N	2.35	0.42
2:B:15:C:H2'	2:B:16:U:H6	1.83	0.42
3:C:137:HIS:CD2	3:C:238:ASN:CB	3.01	0.42
3:C:336:TYR:CE1	3:C:337:GLN:HG2	2.54	0.42
3:C:604:LEU:HD21	3:C:627:HIS:CE1	2.53	0.42
3:C:660:VAL:HG22	3:C:661:THR:O	2.20	0.42
3:C:928:HIS:HD1	3:C:928:HIS:H	1.67	0.42
5:E:241:LEU:HA	5:E:251:LEU:O	2.19	0.42
6:F:32:U:H2'	6:F:33:G:C8	2.54	0.42
6:F:83:A:C5	6:F:84:A:C6	3.08	0.42
6:F:88:G:H2'	6:F:89:U:C5'	2.50	0.42
8:H:12:G:H2'	8:H:13:C:N1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:99:HIS:CB	16:Q:946:GLU:CA	2.98	0.42
17:R:331:ALA:CB	22:X:275:ARG:NH2	2.80	0.42
17:R:407:TYR:HE2	17:R:412:PHE:HZ	1.66	0.42
22:X:477:VAL:HG22	22:X:493:LEU:HB2	2.01	0.42
22:X:677:ALA:O	22:X:725:ARG:NE	2.53	0.42
22:X:809:THR:HG22	22:X:811:SER:H	1.85	0.42
23:Y:249:PRO:HA	23:Y:280:SER:HB2	2.01	0.42
24:1:636:ALA:HB3	24:1:675:MET:HE1	2.02	0.42
24:1:903:GLN:OE1	24:1:910:MET:HB2	2.19	0.42
25:3:212:GLU:CB	25:3:223:LYS:HG3	2.49	0.42
25:3:717:SER:HB2	25:3:718:ARG:HH12	1.82	0.42
31:5:61:LYS:HB3	31:5:65:ARG:HH22	1.83	0.42
32:y:12:GLY:H	32:y:48:GLY:HA2	1.84	0.42
35:9:350:PHE:O	35:9:376:ASN:HB2	2.20	0.42
1:A:227:ARG:HE	1:A:227:ARG:HB2	1.70	0.42
1:A:239:TYR:C	1:A:239:TYR:CD1	2.97	0.42
1:A:344:ASP:HB2	1:A:345:PRO:HD2	2.01	0.42
1:A:727:LYS:HE2	1:A:727:LYS:HB3	1.74	0.42
1:A:1200:CYS:SG	1:A:1201:ARG:N	2.92	0.42
1:A:1287:LEU:HD12	1:A:1287:LEU:HA	1.83	0.42
1:A:1337:GLN:HA	1:A:1337:GLN:NE2	2.35	0.42
1:A:1424:GLN:O	1:A:1427:ARG:NH2	2.45	0.42
1:A:1832:ARG:O	1:A:1836:LEU:HD13	2.20	0.42
1:A:1891:LEU:HD21	1:A:2012:LEU:O	2.18	0.42
2:B:46:U:C2'	2:B:47:A:H5'	2.49	0.42
3:C:481:MET:CE	3:C:612:LYS:HB3	2.50	0.42
3:C:567:GLU:HG3	3:C:570:GLY:O	2.19	0.42
3:C:860:ASP:OD1	3:C:860:ASP:N	2.53	0.42
6:F:38:G:C4	6:F:39:A:C8	3.08	0.42
8:H:27:U:O2'	8:H:28:C:H5'	2.20	0.42
11:K:228:HIS:HD2	11:K:230:TRP:CE2	2.37	0.42
12:L:225:TYR:N	17:R:85:ALA:HB2	2.35	0.42
21:V:543:LYS:O	21:V:547:VAL:HG23	2.20	0.42
22:X:430:THR:O	22:X:434:GLN:HG3	2.19	0.42
22:X:500:MET:HE3	22:X:500:MET:HB3	1.73	0.42
22:X:543:ARG:NH2	22:X:546:LEU:HD13	2.35	0.42
24:1:606:LEU:HA	24:1:606:LEU:HD12	1.76	0.42
24:1:621:ASP:CG	24:1:623:TYR:HB3	2.45	0.42
24:1:1245:ARG:HH22	25:3:1028:THR:HB	1.84	0.42
25:3:164:ASN:ND2	25:3:190:GLU:HG2	2.35	0.42
25:3:199:GLU:OE2	25:3:199:GLU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:459:VAL:CG2	25:3:476:VAL:HA	2.45	0.42
25:3:484:VAL:O	25:3:494:VAL:HB	2.19	0.42
25:3:582:GLU:H	25:3:582:GLU:CD	2.27	0.42
25:3:595:VAL:HG21	25:3:601:ARG:N	2.34	0.42
25:3:610:VAL:HA	25:3:636:GLN:HE21	1.85	0.42
25:3:789:VAL:HG13	25:3:891:VAL:HG13	2.01	0.42
25:3:791:HIS:CB	25:3:796:ASN:O	2.68	0.42
35:9:323:ARG:CB	35:9:331:GLN:HE21	2.32	0.42
35:9:360:HIS:CE1	35:9:391:ASP:HB2	2.55	0.42
1:A:210:HIS:CE1	1:A:211:GLN:HG3	2.55	0.42
1:A:615:ARG:HE	1:A:615:ARG:HB2	1.62	0.42
1:A:659:GLN:O	1:A:659:GLN:NE2	2.53	0.42
1:A:1402:ARG:NH1	17:R:406:GLN:NE2	2.68	0.42
1:A:1810:PHE:CE1	1:A:1919:LEU:HG	2.55	0.42
2:B:116:U:OP2	40:e:68:THR:CA	2.67	0.42
3:C:131:ASN:HA	3:C:201:ASN:HB2	2.00	0.42
3:C:308:CYS:SG	3:C:433:MET:HE1	2.59	0.42
3:C:311:SER:OG	3:C:311:SER:O	2.32	0.42
3:C:366:GLN:HG3	3:C:371:GLU:CG	2.50	0.42
3:C:767:VAL:O	3:C:771:GLN:HG3	2.19	0.42
5:E:118:ASN:ND2	5:E:122:SER:H	2.17	0.42
6:F:3:G:H2'	6:F:4:C:C6	2.55	0.42
6:F:82:A:C4	6:F:83:A:C8	3.07	0.42
9:I:139:ALA:HA	16:Q:938:TYR:CA	2.50	0.42
10:J:329:ALA:O	10:J:332:VAL:HG22	2.19	0.42
10:J:335:ARG:NE	17:R:98:TYR:CE2	2.87	0.42
16:Q:1227:LEU:HA	16:Q:1258:THR:O	2.20	0.42
17:R:352:ARG:HG2	17:R:356:ARG:HH21	1.85	0.42
22:X:393:GLN:O	22:X:397:ARG:HG3	2.19	0.42
22:X:485:ASP:OD1	22:X:486:CYS:N	2.53	0.42
22:X:648:TYR:O	22:X:656:GLN:NE2	2.51	0.42
22:X:743:TYR:CD1	22:X:744:GLN:HG3	2.55	0.42
24:1:500:LEU:C	24:1:502:LEU:N	2.76	0.42
24:1:632:PHE:HA	24:1:635:VAL:HG22	2.02	0.42
25:3:206:GLN:HE22	25:3:232:GLY:H	1.66	0.42
25:3:469:GLU:OE1	25:3:469:GLU:N	2.53	0.42
25:3:996:ILE:O	25:3:998:HIS:N	2.53	0.42
25:3:1035:THR:HG21	25:3:1103:SER:HA	2.01	0.42
25:3:1040:ASP:OD2	25:3:1040:ASP:C	2.63	0.42
25:3:1049:LYS:HE3	31:5:52:TYR:CZ	2.55	0.42
28:2:547:LYS:NZ	28:2:555:GLU:HG2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:592:TYR:CD1	28:2:595:LYS:HB2	2.55	0.42
31:5:12:GLU:HA	31:5:15:GLN:HB3	2.01	0.42
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.20	0.42
1:A:203:VAL:HG12	1:A:206:TRP:CZ2	2.55	0.42
1:A:694:LEU:HD23	1:A:694:LEU:N	2.34	0.42
1:A:720:TRP:CA	35:9:251:THR:HB	2.48	0.42
1:A:1649:LYS:HA	1:A:1649:LYS:HD2	1.58	0.42
2:B:93:U:C4'	38:c:104:ASP:CA	2.97	0.42
3:C:369:PHE:HE1	3:C:373:ILE:HD12	1.84	0.42
3:C:433:MET:HE2	3:C:433:MET:HB3	1.75	0.42
3:C:598:SER:OG	3:C:599:GLU:HG2	2.20	0.42
3:C:911:PRO:O	3:C:934:MET:HE2	2.20	0.42
4:D:1200:VAL:N	4:D:1254:PHE:O	2.45	0.42
5:E:268:ALA:C	5:E:270:LYS:H	2.28	0.42
12:L:225:TYR:O	17:R:85:ALA:CB	2.54	0.42
13:N:86:LYS:HG3	13:N:87:ASN:N	2.33	0.42
17:R:141:LYS:O	17:R:145:GLU:HG2	2.20	0.42
21:V:542:ASN:HA	21:V:545:ARG:NH2	2.34	0.42
21:V:561:PRO:C	21:V:563:SER:N	2.78	0.42
21:V:617:PRO:HB2	21:V:624:THR:HA	2.02	0.42
22:X:165:GLU:HG2	22:X:169:ARG:NH2	2.35	0.42
22:X:228:LYS:HE3	22:X:232:ARG:NH2	2.35	0.42
22:X:742:ALA:O	22:X:747:LEU:HD23	2.20	0.42
23:Y:274:ASP:O	23:Y:278:GLY:N	2.41	0.42
24:1:722:GLU:OE1	24:1:722:GLU:N	2.37	0.42
24:1:981:TYR:C	24:1:983:GLY:H	2.27	0.42
24:1:1041:ARG:HA	24:1:1041:ARG:HD2	1.48	0.42
25:3:275:ARG:HB3	25:3:386:PHE:HB3	2.02	0.42
25:3:898:ASN:OD1	25:3:899:THR:N	2.52	0.42
25:3:1015:LYS:NZ	25:3:1016:ARG:H	2.18	0.42
27:w:388:ASP:CB	33:v:84:ARG:HB3	2.46	0.42
1:A:54:VAL:HB	1:A:57:GLN:OE1	2.19	0.42
1:A:532:THR:CG2	1:A:536:LYS:HE3	2.49	0.42
1:A:1249:MET:HE3	1:A:1249:MET:HB2	1.66	0.42
1:A:1352:HIS:HD2	20:U:5:ILE:CD1	2.33	0.42
1:A:2177:TRP:O	1:A:2213:ILE:HA	2.20	0.42
3:C:136:GLY:O	3:C:238:ASN:ND2	2.53	0.42
3:C:142:LYS:HZ1	3:C:207:GLY:CA	2.33	0.42
3:C:383:GLN:C	3:C:392:LEU:HD21	2.45	0.42
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.55	0.42
3:C:833:PHE:HD1	3:C:874:PHE:CE1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:60:MET:H	5:E:60:MET:HE2	1.84	0.42
5:E:124:LEU:HD21	5:E:138:SER:HB3	2.01	0.42
6:F:13:G:H8	6:F:13:G:O5'	2.03	0.42
9:I:48:ALA:O	9:I:51:PRO:HD2	2.20	0.42
10:J:256:LYS:HE2	12:L:232:TYR:CZ	2.53	0.42
12:L:168:LYS:HA	12:L:168:LYS:HE3	2.01	0.42
12:L:188:ARG:O	12:L:192:ARG:HG2	2.20	0.42
16:Q:539:VAL:O	16:Q:624:THR:HA	2.20	0.42
22:X:164:TRP:HE3	22:X:165:GLU:CA	2.33	0.42
22:X:330:GLU:O	22:X:334:LEU:HD12	2.19	0.42
22:X:768:LYS:HD3	22:X:768:LYS:HA	1.80	0.42
22:X:774:ASP:OD2	22:X:777:HIS:ND1	2.45	0.42
24:1:534:GLN:O	24:1:538:LEU:HD12	2.20	0.42
25:3:701:LEU:C	25:3:702:PHE:CG	2.98	0.42
25:3:855:PRO:O	25:3:856:LYS:HD3	2.20	0.42
25:3:914:ILE:HG22	25:3:917:PRO:HD2	2.02	0.42
27:w:390:LYS:HZ3	33:v:84:ARG:NE	2.17	0.42
28:2:456:ARG:HA	28:2:459:ARG:HB2	2.02	0.42
35:9:408:THR:O	35:9:411:GLU:HB3	2.20	0.42
1:A:692:ASP:OD1	1:A:692:ASP:C	2.63	0.41
1:A:748:ASP:OD1	15:P:214:THR:HB	2.20	0.41
1:A:883:ARG:O	1:A:887:THR:HG23	2.20	0.41
1:A:984:MET:C	1:A:986:GLU:H	2.28	0.41
1:A:1607:GLU:HB3	1:A:1633:ALA:C	2.45	0.41
1:A:1889:LEU:HD11	1:A:2013:GLY:C	2.37	0.41
3:C:904:TRP:CD1	3:C:904:TRP:H	2.38	0.41
6:F:79:C:C2'	12:L:170:LYS:HD2	2.35	0.41
7:G:116:C:N4	17:R:370:SER:HB3	2.34	0.41
8:H:47:U:O2	8:H:47:U:C2'	2.68	0.41
12:L:31:TRP:HB3	12:L:43:ALA:HB1	2.02	0.41
12:L:66:GLU:HA	12:L:69:GLU:HG3	2.02	0.41
17:R:388:ILE:HD12	17:R:388:ILE:HA	1.76	0.41
19:T:209:CYS:SG	19:T:252:VAL:HG13	2.60	0.41
19:T:319:THR:O	19:T:319:THR:OG1	2.30	0.41
22:X:233:GLU:O	22:X:237:LYS:HB3	2.19	0.41
22:X:621:ILE:HG12	22:X:672:VAL:CG1	2.50	0.41
24:1:555:VAL:HG12	24:1:559:ILE:HD13	2.02	0.41
24:1:802:GLU:HG2	24:1:805:TYR:HB2	2.02	0.41
25:3:311:PHE:HZ	25:3:387:PHE:CE2	2.38	0.41
25:3:576:GLU:OE1	25:3:580:ARG:NH2	2.52	0.41
25:3:605:LEU:HB3	25:3:619:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:947:GLU:HG3	25:3:948:VAL:H	1.84	0.41
27:w:471:TRP:CZ3	27:w:476:GLU:HB2	2.55	0.41
35:9:418:LYS:HA	35:9:418:LYS:HD2	1.89	0.41
1:A:196:ASP:N	1:A:200:ASP:OD2	2.50	0.41
1:A:388:LEU:CD1	3:C:395:THR:CG2	2.87	0.41
1:A:696:MET:C	1:A:698:PRO:HD3	2.45	0.41
1:A:1403:LEU:O	17:R:407:TYR:CB	2.63	0.41
3:C:198:TYR:CZ	3:C:435:VAL:HG11	2.55	0.41
3:C:258:ASN:HD21	3:C:312:SER:HB3	1.85	0.41
3:C:919:ARG:HB2	3:C:922:GLU:HG2	2.03	0.41
5:E:199:VAL:HA	5:E:209:ILE:O	2.20	0.41
5:E:339:GLU:HB3	5:E:341:ILE:HG13	2.02	0.41
7:G:113:U:H1'	7:G:114:U:OP2	2.19	0.41
9:I:231:ASN:HA	9:I:232:PRO:HD3	1.94	0.41
10:J:321:GLU:OE1	10:J:329:ALA:HB2	2.21	0.41
10:J:331:GLN:HA	10:J:334:GLU:HG2	2.02	0.41
10:J:362:ALA:O	10:J:366:TYR:HD2	2.03	0.41
14:O:254:GLN:C	14:O:256:GLY:H	2.27	0.41
14:O:262:THR:O	14:O:270:ALA:HA	2.21	0.41
16:Q:1064:ALA:HB3	16:Q:1095:GLY:HA3	2.02	0.41
17:R:241:GLU:HA	17:R:244:GLU:OE2	2.21	0.41
17:R:404:GLU:HG3	17:R:405:VAL:N	2.34	0.41
19:T:205:GLY:O	19:T:206:TRP:C	2.63	0.41
22:X:242:LYS:HG2	22:X:246:LEU:HD13	2.01	0.41
22:X:543:ARG:HH21	22:X:545:GLU:CD	2.28	0.41
22:X:756:GLN:NE2	22:X:782:ASP:OD2	2.53	0.41
22:X:1007:TRP:HA	22:X:1010:GLU:HB2	2.02	0.41
24:1:816:LYS:HB3	24:1:816:LYS:HE3	1.82	0.41
25:3:228:LEU:HD12	25:3:229:GLU:N	2.28	0.41
25:3:638:GLU:O	25:3:638:GLU:HG3	2.19	0.41
25:3:1001:ILE:HD12	25:3:1011:TRP:NE1	2.36	0.41
25:3:1115:GLU:CA	28:2:708:TRP:CZ2	3.03	0.41
28:2:550:LYS:HG2	28:2:554:ARG:HH21	1.84	0.41
35:9:437:PRO:HG2	35:9:438:TYR:CD2	2.55	0.41
1:A:283:VAL:O	1:A:284:ARG:HG2	2.20	0.41
1:A:368:GLN:OE1	1:A:368:GLN:HA	2.21	0.41
1:A:468:LYS:HD3	1:A:468:LYS:HA	1.53	0.41
1:A:668:VAL:HG23	1:A:669:ALA:H	1.84	0.41
1:A:1166:THR:HG23	1:A:1167:THR:N	2.35	0.41
1:A:1362:ASP:OD1	1:A:1363:GLN:N	2.34	0.41
1:A:1436:TRP:CD1	1:A:1436:TRP:H	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1675:ASP:OD1	1:A:1675:ASP:C	2.63	0.41
1:A:1677:GLU:HA	1:A:1677:GLU:OE2	2.19	0.41
1:A:1850:ARG:NH1	1:A:1878:ASP:OD2	2.54	0.41
1:A:1938:LEU:HD22	1:A:1984:LYS:HG3	2.02	0.41
3:C:78:GLU:HG3	3:C:79:THR:H	1.83	0.41
3:C:92:PRO:HA	19:T:278:ASN:HD21	1.85	0.41
3:C:334:ILE:HD11	3:C:339:PHE:CD2	2.55	0.41
3:C:932:GLU:O	3:C:933:PHE:C	2.64	0.41
4:D:696:LYS:O	4:D:700:ARG:CB	2.69	0.41
5:E:147:LEU:HD21	5:E:179:TRP:HB3	2.01	0.41
5:E:193:THR:HG23	5:E:194:TYR:CD2	2.55	0.41
9:I:139:ALA:CA	16:Q:938:TYR:HA	2.49	0.41
10:J:238:ASN:C	10:J:240:THR:N	2.77	0.41
12:L:184:ALA:O	12:L:188:ARG:HB2	2.20	0.41
18:S:14:VAL:O	18:S:24:VAL:HA	2.20	0.41
19:T:352:THR:HG22	19:T:374:SER:N	2.35	0.41
22:X:416:GLN:HE22	22:X:544:PRO:HA	1.86	0.41
22:X:754:GLU:HG3	22:X:757:ARG:HH12	1.84	0.41
22:X:823:MET:HE3	22:X:823:MET:HB2	1.82	0.41
22:X:994:LYS:HD2	22:X:996:PHE:CZ	2.56	0.41
23:Y:63:GLY:O	23:Y:105:GLY:HA3	2.19	0.41
23:Y:242:LEU:HD13	23:Y:313:VAL:HG11	2.01	0.41
24:1:1142:ASN:HD22	24:1:1142:ASN:N	2.19	0.41
24:1:1212:LEU:HD12	24:1:1212:LEU:HA	1.75	0.41
25:3:70:LEU:HA	25:3:70:LEU:HD23	1.78	0.41
25:3:299:PHE:CD1	25:3:299:PHE:C	2.99	0.41
25:3:408:LEU:HD12	25:3:427:CYS:HA	2.02	0.41
25:3:528:ARG:HG3	25:3:529:ALA:H	1.83	0.41
26:p:194:PHE:CB	26:p:200:ALA:HB2	2.50	0.41
31:5:74:GLN:NE2	31:5:78:PRO:HA	2.36	0.41
33:v:85:ARG:HA	33:v:85:ARG:HD2	1.78	0.41
1:A:520:TYR:O	1:A:555:LYS:NZ	2.26	0.41
1:A:694:LEU:HD22	1:A:709:ILE:CD1	2.50	0.41
1:A:769:LYS:HA	1:A:769:LYS:HD2	1.44	0.41
1:A:789:GLU:CB	35:9:253:THR:HB	2.34	0.41
1:A:1235:GLU:O	1:A:1235:GLU:HG2	2.19	0.41
1:A:1661:TRP:CD2	1:A:1700:GLY:HA3	2.55	0.41
1:A:1806:ALA:HA	1:A:1821:ILE:HA	2.01	0.41
3:C:154:HIS:C	3:C:156:GLU:H	2.29	0.41
3:C:517:GLU:H	3:C:517:GLU:CD	2.28	0.41
3:C:716:GLU:HG3	3:C:716:GLU:H	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:2030:ARG:O	4:D:2096:ALA:HB3	2.20	0.41
5:E:168:CYS:SG	5:E:208:ILE:HD13	2.60	0.41
7:G:12:G:H8	7:G:12:G:O5'	2.03	0.41
8:H:42:G:C6	8:H:43:U:C4	3.09	0.41
8:H:44:U:OP2	8:H:44:U:H6	2.02	0.41
8:H:168:A:H5''	8:H:169:C:C6	2.56	0.41
10:J:289:ASN:HB2	10:J:291:GLN:OE1	2.20	0.41
12:L:63:TRP:HD1	12:L:67:GLU:HB3	1.85	0.41
13:N:27:GLN:OE1	13:N:27:GLN:HA	2.21	0.41
16:Q:877:LEU:O	16:Q:1035:ILE:HA	2.21	0.41
22:X:408:LEU:HD13	22:X:570:PHE:CG	2.55	0.41
22:X:497:THR:HG23	22:X:500:MET:HG3	2.01	0.41
22:X:563:PHE:HE2	22:X:780:PHE:O	2.04	0.41
23:Y:134:ASP:O	23:Y:138:LYS:HG3	2.20	0.41
25:3:52:THR:O	25:3:52:THR:OG1	2.34	0.41
25:3:289:CYS:SG	25:3:290:SER:N	2.94	0.41
25:3:577:TYR:HE2	25:3:579:GLU:HB3	1.85	0.41
25:3:820:ALA:HA	25:3:823:MET:HE2	2.03	0.41
33:v:49:ASN:OD1	33:v:49:ASN:N	2.50	0.41
33:v:75:GLY:C	33:v:79:GLN:HB2	2.45	0.41
35:9:296:HIS:CD2	35:9:296:HIS:N	2.89	0.41
35:9:404:PHE:O	35:9:407:LEU:HD23	2.19	0.41
1:A:280:GLU:OE2	2:B:47:A:H1'	2.20	0.41
1:A:387:PHE:CE1	3:C:327:TYR:HA	2.56	0.41
1:A:495:GLN:HE21	1:A:495:GLN:HB2	1.62	0.41
1:A:856:LEU:H	1:A:856:LEU:HG	1.38	0.41
1:A:1579:ALA:HB1	11:K:226:TYR:CZ	2.55	0.41
1:A:1610:GLN:HB3	1:A:1630:LEU:CB	2.51	0.41
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	2.02	0.41
1:A:1872:LEU:HD12	1:A:1884:ILE:HD13	2.02	0.41
3:C:221:ILE:O	3:C:549:TRP:NE1	2.53	0.41
3:C:372:PHE:O	3:C:376:PRO:HG3	2.20	0.41
3:C:695:GLY:O	3:C:698:GLU:HB2	2.20	0.41
3:C:700:ILE:HG21	3:C:742:PRO:HA	2.02	0.41
3:C:758:LEU:HD22	3:C:800:PRO:HD3	2.02	0.41
5:E:326:HIS:CE1	5:E:344:SER:HG	2.24	0.41
6:F:88:G:N3	8:H:11:G:C2	2.88	0.41
7:G:93:A:C2	8:H:38:A:C2	3.08	0.41
9:I:326:ASP:C	9:I:328:GLU:N	2.78	0.41
9:I:448:ASN:O	9:I:452:ALA:HB3	2.18	0.41
13:N:37:HIS:CD2	13:N:41:ARG:CB	3.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:O:24:CYS:O	14:O:28:LEU:CB	2.68	0.41
17:R:160:ALA:O	17:R:163:MET:HB2	2.21	0.41
17:R:331:ALA:CA	22:X:275:ARG:CZ	2.97	0.41
22:X:268:GLN:HE21	22:X:268:GLN:HB3	1.67	0.41
23:Y:96:MET:HE3	23:Y:96:MET:HB3	1.83	0.41
24:1:769:VAL:O	24:1:772:ILE:HB	2.21	0.41
24:1:892:LEU:HD22	24:1:892:LEU:HA	1.70	0.41
24:1:914:PHE:O	24:1:917:VAL:HG12	2.21	0.41
24:1:1029:GLU:H	24:1:1029:GLU:HG3	1.73	0.41
24:1:1063:LEU:HD23	24:1:1063:LEU:HA	1.64	0.41
24:1:1276:SER:H	25:3:113:ARG:NH2	2.18	0.41
25:3:637:PRO:HB3	25:3:640:LEU:HD21	2.03	0.41
25:3:1004:ASP:OD2	25:3:1007:GLU:HB2	2.21	0.41
27:w:387:TRP:O	33:v:88:LYS:CB	2.68	0.41
27:w:387:TRP:CB	33:v:88:LYS:HD2	2.29	0.41
27:w:411:CYS:O	27:w:414:TYR:HB2	2.21	0.41
27:w:445:HIS:CD2	27:w:445:HIS:H	2.38	0.41
1:A:384:VAL:HA	3:C:331:PHE:CD2	2.55	0.41
1:A:1173:SER:OG	1:A:1174:PHE:N	2.52	0.41
1:A:1543:ASN:HB2	1:A:1569:LEU:HD21	2.02	0.41
1:A:1949:ARG:NH2	1:A:1986:LEU:HD21	2.36	0.41
2:B:95:G:C1'	39:d:24:LYS:CA	2.80	0.41
3:C:666:VAL:HG12	3:C:667:VAL:H	1.84	0.41
3:C:736:GLY:O	3:C:771:GLN:HG2	2.21	0.41
3:C:940:ARG:HG2	3:C:941:LYS:HG3	2.01	0.41
7:G:7:G:C6	7:G:8:C:N3	2.88	0.41
8:H:41:U:C2	8:H:42:G:C8	3.08	0.41
8:H:56:A:O2'	28:2:478:HIS:HA	2.21	0.41
11:K:232:ILE:H	11:K:232:ILE:HG13	1.74	0.41
12:L:19:LEU:O	12:L:20:LYS:C	2.63	0.41
13:N:63:LEU:O	13:N:70:ILE:HB	2.21	0.41
19:T:437:HIS:C	19:T:438:LEU:HD23	2.45	0.41
22:X:171:ARG:NH2	22:X:506:LEU:C	2.78	0.41
22:X:275:ARG:O	22:X:279:LEU:HG	2.21	0.41
22:X:736:ARG:C	22:X:738:TYR:H	2.27	0.41
23:Y:27:ASN:ND2	23:Y:65:SER:HB2	2.36	0.41
24:1:504:ILE:HG13	24:1:515:ALA:HB3	2.02	0.41
24:1:550:HIS:CD2	24:1:551:LEU:HD22	2.49	0.41
24:1:703:THR:HG23	24:1:742:GLY:HA2	2.03	0.41
24:1:1244:CYS:SG	25:3:1030:PRO:HD2	2.60	0.41
25:3:1199:ARG:HH21	25:3:1207:LYS:NZ	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:w:400:HIS:HB3	27:w:402:LEU:HD22	2.02	0.41
27:w:407:ASN:O	27:w:407:ASN:ND2	2.54	0.41
28:2:529:LYS:O	28:2:530:ARG:C	2.64	0.41
30:7:26:CYS:SG	30:7:60:ILE:HG13	2.61	0.41
35:9:323:ARG:CD	35:9:420:ASP:HB2	2.51	0.41
37:n:62:GLY:O	37:n:65:ILE:N	2.54	0.41
1:A:824:PRO:HG3	22:X:298:TYR:HE2	1.86	0.41
1:A:845:ARG:HH12	1:A:1440:THR:CG2	2.32	0.41
1:A:1220:VAL:HG23	1:A:1221:THR:N	2.36	0.41
1:A:1936:LEU:HG	1:A:1940:LEU:HD21	2.02	0.41
2:B:42:U:H1'	6:F:70:A:H4'	2.02	0.41
3:C:69:ALA:O	3:C:72:VAL:HG12	2.20	0.41
3:C:93:ILE:HD11	19:T:230:ILE:HG21	2.02	0.41
3:C:901:PHE:CD2	3:C:901:PHE:C	2.97	0.41
5:E:86:PHE:HD2	5:E:86:PHE:O	2.04	0.41
6:F:44:G:O2'	28:2:554:ARG:NH1	2.53	0.41
8:H:81:G:H2'	8:H:82:G:O4'	2.21	0.41
10:J:280:LEU:HD23	10:J:280:LEU:HA	1.75	0.41
10:J:411:MET:HE2	10:J:416:TYR:CE2	2.56	0.41
11:K:230:TRP:CZ3	11:K:231:GLN:HG3	2.55	0.41
13:N:22:LEU:HD23	13:N:22:LEU:HA	1.78	0.41
19:T:289:SER:O	19:T:290:ALA:C	2.62	0.41
19:T:350:HIS:HA	19:T:374:SER:HB3	2.03	0.41
19:T:424:ASP:OD1	19:T:424:ASP:N	2.53	0.41
24:1:556:ILE:O	24:1:560:LEU:HB2	2.21	0.41
24:1:1262:ARG:HH11	31:5:24:ALA:C	2.14	0.41
25:3:91:GLU:OE1	25:3:102:ILE:HD11	2.20	0.41
25:3:128:ARG:HH21	25:3:180:PRO:HG3	1.85	0.41
25:3:459:VAL:HA	25:3:475:ILE:O	2.21	0.41
25:3:1001:ILE:HG21	25:3:1044:VAL:HG21	2.02	0.41
25:3:1140:PHE:CE1	25:3:1197:LEU:HD13	2.53	0.41
28:2:471:ARG:HE	28:2:471:ARG:HB3	1.49	0.41
41:k:42:ILE:O	41:k:60:VAL:N	2.48	0.41
1:A:1284:LEU:HD23	1:A:1284:LEU:HA	1.77	0.41
2:B:89:U:C2'	2:B:90:U:H5''	2.47	0.41
3:C:465:MET:HE2	3:C:475:MET:CB	2.50	0.41
3:C:496:VAL:HG23	3:C:548:ASN:H	1.86	0.41
3:C:727:LEU:HA	3:C:730:ARG:HG2	2.03	0.41
3:C:764:ASP:OD2	3:C:764:ASP:N	2.48	0.41
3:C:810:PRO:HG3	3:C:813:ARG:HH22	1.85	0.41
3:C:932:GLU:HA	3:C:935:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:541:ILE:HA	4:D:588:CYS:O	2.21	0.41
4:D:2067:VAL:HA	4:D:2079:ILE:HA	2.02	0.41
7:G:96:U:H5''	7:G:97:A:OP2	2.21	0.41
8:H:55:U:H2'	8:H:57:A:OP2	2.21	0.41
15:P:41:ILE:HG13	19:T:318:ARG:HG3	2.02	0.41
16:Q:745:PRO:HG2	16:Q:781:PRO:HA	2.03	0.41
17:R:355:ILE:CD1	22:X:266:GLU:CD	2.78	0.41
17:R:360:ARG:HH22	23:Y:277:THR:HG23	1.85	0.41
17:R:367:ARG:HH12	23:Y:281:LEU:HA	1.85	0.41
22:X:716:LYS:HG3	22:X:747:LEU:HB3	2.03	0.41
22:X:887:GLN:O	22:X:890:GLU:HB3	2.20	0.41
22:X:989:LEU:HD12	22:X:989:LEU:HA	1.84	0.41
23:Y:64:GLU:HG2	23:Y:77:PHE:CZ	2.56	0.41
24:1:641:ILE:H	24:1:641:ILE:HG13	1.56	0.41
24:1:673:ILE:HD13	24:1:673:ILE:HA	1.76	0.41
24:1:862:GLU:O	24:1:866:LYS:HB2	2.21	0.41
25:3:43:PRO:HA	25:3:50:VAL:HA	2.01	0.41
25:3:280:ASP:H	25:3:857:ALA:CB	2.33	0.41
25:3:823:MET:HE2	25:3:823:MET:HB3	1.70	0.41
25:3:969:VAL:HB	25:3:981:CYS:CB	2.45	0.41
25:3:1096:HIS:ND1	25:3:1166:TYR:HB2	2.36	0.41
27:w:387:TRP:C	33:v:88:LYS:HB2	2.45	0.41
28:2:606:PRO:C	28:2:608:ASP:N	2.79	0.41
31:5:53:PHE:O	31:5:57:GLU:HG2	2.21	0.41
1:A:136:ILE:HG13	1:A:225:TYR:HE2	1.85	0.41
1:A:583:ALA:HB3	1:A:584:HIS:HD2	1.85	0.41
1:A:778:ARG:HH11	1:A:778:ARG:HD2	1.65	0.41
1:A:1161:LEU:HD22	1:A:1166:THR:HG22	2.03	0.41
1:A:1178:TYR:CD2	1:A:1178:TYR:C	2.99	0.41
1:A:1268:ILE:HD13	1:A:1268:ILE:HG21	1.77	0.41
1:A:1638:ASN:O	1:A:1652:MET:HB3	2.21	0.41
44:A:3000:IHP:O41	44:A:3000:IHP:P2	2.79	0.41
3:C:700:ILE:O	3:C:740:THR:OG1	2.33	0.41
3:C:930:ALA:HA	3:C:933:PHE:HB2	2.02	0.41
5:E:81:LEU:HD12	5:E:95:VAL:HG22	2.03	0.41
5:E:348:ASP:OD1	5:E:350:ARG:HG3	2.20	0.41
7:G:85:G:H1	8:H:45:C:N4	2.18	0.41
7:G:90:C:N3	8:H:40:C:N3	2.68	0.41
8:H:5:C:O2'	8:H:6:U:H5'	2.20	0.41
8:H:160:A:H2'	8:H:161:U:O4'	2.20	0.41
10:J:239:ARG:O	10:J:239:ARG:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:328:GLY:O	10:J:331:GLN:HG2	2.21	0.41
11:K:237:ASP:OD1	11:K:238:GLU:N	2.54	0.41
13:N:9:LYS:HA	13:N:9:LYS:HD3	1.91	0.41
13:N:49:ILE:C	13:N:49:ILE:CD1	2.85	0.41
13:N:58:ARG:HA	13:N:58:ARG:HD3	1.78	0.41
15:P:208:LYS:HA	15:P:208:LYS:HD2	1.52	0.41
17:R:348:GLU:OE1	22:X:263:SER:N	2.54	0.41
19:T:213:GLU:OE1	19:T:216:ASN:N	2.54	0.41
21:V:520:GLU:O	21:V:524:SER:OG	2.27	0.41
21:V:562:TRP:CE2	21:V:602:ARG:HD3	2.55	0.41
22:X:227:ARG:HH12	23:Y:237:PRO:HD2	1.85	0.41
22:X:431:GLN:HA	22:X:434:GLN:HE21	1.86	0.41
22:X:606:GLN:HG3	22:X:688:TYR:CE1	2.56	0.41
22:X:826:LYS:HB3	22:X:946:GLY:HA2	2.02	0.41
22:X:843:VAL:HG23	22:X:882:LEU:HD13	2.02	0.41
22:X:1007:TRP:HA	22:X:1010:GLU:OE2	2.20	0.41
23:Y:41:LEU:HB3	23:Y:155:ARG:NH1	2.36	0.41
23:Y:49:PHE:N	23:Y:112:THR:OG1	2.54	0.41
23:Y:194:ASP:OD2	23:Y:194:ASP:N	2.53	0.41
23:Y:242:LEU:HD12	23:Y:288:PHE:CZ	2.56	0.41
24:1:686:LEU:HA	24:1:689:ILE:HG12	2.03	0.41
25:3:66:MET:HE3	25:3:123:VAL:HG12	2.03	0.41
25:3:77:TYR:HE2	25:3:152:LEU:HD22	1.85	0.41
25:3:180:PRO:HD2	25:3:215:LEU:HD11	2.03	0.41
25:3:212:GLU:HG2	25:3:213:LEU:N	2.35	0.41
25:3:224:TYR:HB3	25:3:261:PHE:CD1	2.56	0.41
25:3:259:LYS:HE3	25:3:259:LYS:HB2	1.68	0.41
25:3:334:PRO:HG2	25:3:357:TYR:CD2	2.56	0.41
25:3:497:SER:OG	25:3:499:PHE:HB2	2.21	0.41
25:3:615:ARG:O	25:3:616:ILE:HD12	2.21	0.41
25:3:715:MET:HE3	25:3:739:LEU:H	1.86	0.41
25:3:724:SER:HB2	25:3:727:SER:HA	2.01	0.41
25:3:998:HIS:HE1	25:3:1041:TYR:OH	2.04	0.41
25:3:1175:ASP:OD1	25:3:1178:LEU:N	2.52	0.41
27:w:387:TRP:CZ3	33:v:85:ARG:CA	3.03	0.41
28:2:506:PHE:N	28:2:506:PHE:CD1	2.88	0.41
28:2:572:HIS:O	28:2:576:PHE:HB2	2.20	0.41
38:h:42:VAL:N	38:h:54:GLY:O	2.50	0.41
36:m:42:LEU:O	36:m:69:LEU:HA	2.21	0.41
36:m:53:PRO:HG3	36:m:59:ALA:C	2.46	0.41
42:l:13:ALA:HA	42:l:74:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:TYR:HB3	1:A:611:LEU:HD21	2.02	0.41
1:A:580:TYR:O	1:A:581:ILE:C	2.63	0.41
1:A:648:LEU:HD23	1:A:648:LEU:HA	1.86	0.41
1:A:1495:PHE:HD1	1:A:1495:PHE:HA	1.74	0.41
3:C:271:PRO:HG3	3:C:378:TYR:CD2	2.56	0.41
3:C:336:TYR:CZ	3:C:337:GLN:HG2	2.56	0.41
3:C:678:THR:HG23	3:C:683:ASN:HB2	2.03	0.41
3:C:718:PHE:HB3	3:C:724:TRP:HD1	1.86	0.41
5:E:123:MET:HE3	5:E:123:MET:HB2	1.87	0.41
7:G:115:C:H1'	23:Y:309:ARG:HE	1.85	0.41
8:H:34:U:H2'	8:H:35:A:C1'	2.51	0.41
8:H:139:C:H2'	8:H:140:A:C8	2.56	0.41
11:K:232:ILE:HA	11:K:235:GLU:HG2	2.03	0.41
17:R:116:TYR:HD1	17:R:120:VAL:HG13	1.86	0.41
19:T:314:ILE:O	19:T:323:VAL:HG22	2.21	0.41
19:T:397:GLN:C	19:T:398:TRP:CD1	2.99	0.41
21:V:469:PHE:CE1	21:V:509:LEU:HD13	2.56	0.41
22:X:616:THR:HB	22:X:696:LYS:HE2	2.03	0.41
22:X:856:ARG:CZ	22:X:856:ARG:HB3	2.51	0.41
23:Y:183:ARG:HH21	23:Y:186:LEU:HB3	1.85	0.41
23:Y:267:ARG:HB3	23:Y:287:GLU:HG2	2.02	0.41
24:1:572:HIS:CE1	24:1:613:MET:HE1	2.55	0.41
24:1:1208:LEU:HB3	24:1:1237:LEU:HD21	2.03	0.41
25:3:164:ASN:OD1	25:3:164:ASN:N	2.53	0.41
25:3:672:GLY:H	25:3:696:SER:CA	2.34	0.41
25:3:805:ASN:CB	31:5:58:ASN:HB2	2.50	0.41
27:w:388:ASP:CB	33:v:84:ARG:HA	2.51	0.41
28:2:592:TYR:CZ	28:2:595:LYS:HA	2.56	0.41
30:7:51:TYR:CG	30:7:52:GLY:N	2.89	0.41
35:9:324:SER:HA	35:9:330:ILE:HA	2.03	0.41
1:A:147:MET:HE1	1:A:191:ILE:O	2.21	0.40
1:A:184:ASP:HB3	13:N:1:MET:CA	2.51	0.40
1:A:674:LYS:HB3	1:A:674:LYS:HE3	1.75	0.40
1:A:1136:ARG:HG2	1:A:1139:ARG:NH1	2.36	0.40
1:A:1376:GLU:O	1:A:1376:GLU:HG3	2.14	0.40
1:A:1839:TRP:CZ3	1:A:1871:PRO:HB3	2.56	0.40
3:C:258:ASN:HA	3:C:310:SER:O	2.21	0.40
3:C:286:ASN:OD1	3:C:300:LEU:HD12	2.22	0.40
3:C:366:GLN:NE2	3:C:375:GLU:OE1	2.53	0.40
3:C:519:GLU:H	3:C:519:GLU:CD	2.28	0.40
3:C:556:ASP:OD1	3:C:556:ASP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1350:ALA:O	4:D:1492:SER:HA	2.21	0.40
6:F:40:U:H3'	6:F:41:A:C8	2.56	0.40
6:F:84:A:C4	6:F:85:U:C6	3.09	0.40
8:H:28:C:N4	12:L:32:SER:OG	2.54	0.40
10:J:319:MET:O	10:J:323:LEU:HD13	2.20	0.40
19:T:338:CYS:HA	19:T:344:GLN:O	2.20	0.40
19:T:471:ASP:CG	19:T:472:GLN:N	2.79	0.40
21:V:501:ARG:HH11	21:V:501:ARG:HB2	1.86	0.40
22:X:482:ARG:O	22:X:483:PHE:HB2	2.21	0.40
22:X:747:LEU:HA	22:X:747:LEU:HD13	1.86	0.40
22:X:941:LYS:HE2	22:X:1007:TRP:NE1	2.37	0.40
22:X:941:LYS:HA	22:X:944:THR:OG1	2.21	0.40
22:X:978:GLU:OE1	22:X:978:GLU:HA	2.21	0.40
24:1:646:PRO:O	24:1:649:LYS:HB2	2.20	0.40
24:1:664:GLY:O	24:1:668:VAL:HG23	2.20	0.40
24:1:953:ASP:O	24:1:956:SER:N	2.55	0.40
24:1:1028:HIS:HB3	24:1:1031:VAL:HG13	2.02	0.40
24:1:1080:THR:O	24:1:1084:ILE:HG13	2.21	0.40
25:3:1:MET:HG3	25:3:1092:ILE:HD12	2.02	0.40
25:3:258:TYR:CG	25:3:259:LYS:N	2.90	0.40
25:3:423:LEU:HB2	25:3:438:LEU:HB2	2.02	0.40
25:3:706:MET:HG2	25:3:770:LEU:CD1	2.51	0.40
25:3:1114:SER:HB2	25:3:1215:TYR:HE1	1.83	0.40
35:9:350:PHE:CZ	35:9:376:ASN:HB3	2.55	0.40
38:c:62:HIS:O	38:c:103:GLY:HA3	2.21	0.40
42:l:19:THR:HA	42:l:29:ARG:HA	2.02	0.40
1:A:59:GLU:HA	1:A:59:GLU:OE2	2.20	0.40
1:A:303:ILE:HG22	1:A:305:ARG:HG2	2.03	0.40
1:A:1070:ASP:O	1:A:1071:PHE:C	2.64	0.40
1:A:1936:LEU:O	1:A:1940:LEU:HG	2.21	0.40
2:B:14:U:C2	2:B:15:C:C5	3.10	0.40
3:C:690:GLU:CD	3:C:788:LYS:HD3	2.46	0.40
7:G:7:G:C5	7:G:8:C:N4	2.90	0.40
14:O:22:ILE:O	14:O:82:GLN:N	2.43	0.40
15:P:74:LYS:HA	15:P:77:ASP:CB	2.51	0.40
21:V:636:LEU:HD13	21:V:639:LEU:HD11	2.03	0.40
22:X:532:LEU:O	22:X:536:ILE:HG13	2.21	0.40
22:X:760:LEU:O	22:X:763:VAL:HG22	2.20	0.40
22:X:887:GLN:HA	22:X:890:GLU:HB3	2.03	0.40
24:1:501:LEU:HD23	24:1:501:LEU:HA	1.72	0.40
24:1:850:ILE:HG22	24:1:888:LEU:HD11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:926:LYS:HE2	24:1:965:CYS:HA	2.03	0.40
24:1:1216:TRP:CH2	24:1:1268:ILE:HD13	2.56	0.40
25:3:610:VAL:HG23	25:3:636:GLN:NE2	2.36	0.40
25:3:927:THR:HG23	25:3:940:LEU:HB2	2.04	0.40
26:p:159:PRO:HB2	26:p:162:THR:H	1.85	0.40
27:w:429:TRP:HE3	27:w:430:ARG:NH1	2.19	0.40
35:9:367:SER:HA	35:9:395:THR:O	2.21	0.40
1:A:40:LEU:HD12	1:A:40:LEU:HA	1.86	0.40
1:A:162:LYS:HA	1:A:162:LYS:HD2	1.73	0.40
1:A:162:LYS:HE2	1:A:163:ARG:O	2.21	0.40
1:A:660:PHE:CD2	17:R:209:PRO:CB	3.03	0.40
1:A:829:PRO:HD2	1:A:832:TYR:CG	2.56	0.40
1:A:1518:LEU:HD23	1:A:1518:LEU:N	2.36	0.40
1:A:1618:LYS:HG3	1:A:1626:CYS:HB2	2.02	0.40
1:A:1889:LEU:HD12	1:A:1889:LEU:HA	1.80	0.40
44:A:3000:IHP:O45	44:A:3000:IHP:C6	2.69	0.40
3:C:69:ALA:O	3:C:70:GLU:C	2.64	0.40
3:C:76:GLU:H	3:C:76:GLU:CD	2.29	0.40
3:C:83:GLU:HB2	3:C:84:GLU:H	1.75	0.40
3:C:140:HIS:NE2	3:C:236:MET:HE1	2.37	0.40
3:C:804:GLY:O	3:C:808:ILE:HB	2.22	0.40
5:E:309:VAL:HG22	5:E:330:ILE:HG12	2.04	0.40
9:I:409:GLY:C	9:I:411:LEU:H	2.30	0.40
10:J:278:LEU:HD12	10:J:278:LEU:HA	1.83	0.40
10:J:291:GLN:O	10:J:294:HIS:N	2.54	0.40
10:J:308:ARG:NH2	17:R:233:PRO:HD3	2.37	0.40
16:Q:1110:GLN:HA	16:Q:1115:MET:H	1.85	0.40
17:R:334:ARG:C	22:X:271:LYS:NZ	2.79	0.40
19:T:280:VAL:H	19:T:280:VAL:HG23	1.68	0.40
19:T:395:ILE:HB	19:T:409:LEU:HB2	2.03	0.40
22:X:461:VAL:O	22:X:465:VAL:HG23	2.22	0.40
22:X:850:ASN:C	22:X:852:SER:N	2.80	0.40
23:Y:95:SER:OG	23:Y:109:LEU:HD21	2.20	0.40
23:Y:161:ILE:HG21	23:Y:164:ASP:HB2	2.03	0.40
24:1:669:GLN:NE2	24:1:707:LEU:HD22	2.37	0.40
24:1:893:ILE:HG22	24:1:894:ASP:OD2	2.22	0.40
24:1:1027:ARG:HD3	24:1:1027:ARG:HA	1.83	0.40
24:1:1167:TYR:HB2	28:2:579:GLN:HE21	1.86	0.40
24:1:1173:LEU:HD21	24:1:1191:VAL:HG11	2.03	0.40
25:3:1:MET:HE3	25:3:1:MET:HB3	1.87	0.40
25:3:174:ASP:HB3	25:3:240:GLY:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:664:TYR:HA	25:3:677:THR:O	2.21	0.40
25:3:775:ASN:HD22	25:3:775:ASN:N	2.11	0.40
25:3:804:HIS:ND1	31:5:57:GLU:HA	2.37	0.40
25:3:889:PHE:HD1	25:3:889:PHE:HA	1.74	0.40
25:3:1014:TYR:OH	25:3:1019:ASN:OD1	2.25	0.40
27:w:410:ILE:H	27:w:410:ILE:HG12	1.73	0.40
27:w:414:TYR:HD1	27:w:416:TYR:CE1	2.38	0.40
28:2:459:ARG:HD2	28:2:481:THR:HA	2.03	0.40
36:m:85:PRO:O	36:m:87:PRO:HD3	2.22	0.40
1:A:467:GLN:HG2	2:B:19:A:H62	1.87	0.40
1:A:1838:LYS:HD3	1:A:1868:MET:CG	2.48	0.40
1:A:2308:VAL:HA	4:D:1124:GLN:O	2.19	0.40
2:B:20:G:O6	2:B:57:G:C2	2.74	0.40
2:B:38:C:H2'	2:B:39:C:H5'	2.02	0.40
5:E:62:LEU:HD22	5:E:93:TRP:CZ3	2.57	0.40
5:E:123:MET:C	5:E:124:LEU:HD23	2.47	0.40
10:J:396:ARG:HG3	10:J:422:PHE:HZ	1.87	0.40
12:L:98:GLU:O	12:L:101:GLU:HG3	2.21	0.40
13:N:75:TYR:CZ	13:N:79:ILE:HD11	2.57	0.40
22:X:432:ILE:HB	22:X:433:PRO:HD3	2.02	0.40
22:X:796:LEU:HB2	22:X:802:LEU:CD1	2.51	0.40
22:X:945:ALA:HA	22:X:1011:VAL:HG11	2.04	0.40
24:1:517:ARG:HB3	24:1:517:ARG:NH1	2.37	0.40
24:1:549:ARG:O	24:1:553:VAL:HG22	2.22	0.40
24:1:614:ARG:C	24:1:614:ARG:HD3	2.47	0.40
24:1:620:MET:HE3	24:1:620:MET:HB3	1.90	0.40
24:1:811:LEU:HB2	24:1:812:PRO:HD3	2.03	0.40
24:1:834:VAL:HG22	24:1:871:THR:CG2	2.44	0.40
25:3:183:ALA:HA	25:3:209:THR:O	2.22	0.40
25:3:226:GLU:HG3	25:3:226:GLU:O	2.22	0.40
25:3:1057:ARG:O	25:3:1090:GLU:HG3	2.22	0.40
26:p:223:ALA:CB	27:w:498:GLN:O	2.69	0.40
1:A:278:LYS:O	1:A:452:LYS:HE2	2.21	0.40
1:A:422:LEU:HD22	1:A:638:LEU:HD13	2.02	0.40
1:A:1937:ILE:HG21	1:A:2011:ILE:O	2.21	0.40
5:E:82:ALA:HA	5:E:92:LEU:HD23	2.02	0.40
5:E:127:ALA:HB2	5:E:157:CYS:HB2	2.03	0.40
6:F:85:U:C2	8:H:14:C:N3	2.89	0.40
7:G:8:C:OP1	12:L:201:LYS:HB2	2.21	0.40
12:L:85:ILE:O	12:L:88:ILE:HG13	2.22	0.40
15:P:77:ASP:O	15:P:78:ARG:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:744:ILE:N	16:Q:745:PRO:HD3	2.36	0.40
17:R:126:ASN:C	17:R:128:ASP:H	2.29	0.40
17:R:374:PRO:HD2	17:R:379:LYS:NZ	2.37	0.40
18:S:63:GLN:HA	18:S:113:PHE:HA	2.03	0.40
21:V:503:TYR:OH	21:V:550:MET:HA	2.21	0.40
21:V:616:LEU:HB2	21:V:643:LEU:CD1	2.48	0.40
21:V:618:ARG:HE	21:V:618:ARG:HB2	1.78	0.40
22:X:164:TRP:HE3	22:X:164:TRP:C	2.30	0.40
22:X:197:LEU:C	22:X:197:LEU:CD1	2.85	0.40
22:X:326:GLN:O	22:X:326:GLN:HG2	2.21	0.40
22:X:328:ARG:HA	22:X:328:ARG:HD3	1.88	0.40
22:X:971:HIS:HA	22:X:996:PHE:CE1	2.56	0.40
22:X:984:LEU:HD23	22:X:984:LEU:HA	1.96	0.40
22:X:988:GLU:HB2	22:X:998:ARG:HB2	2.02	0.40
25:3:526:HIS:HB2	25:3:574:LEU:HD21	2.03	0.40
25:3:1115:GLU:CA	28:2:708:TRP:HZ2	2.35	0.40
25:3:1135:HIS:HA	25:3:1138:HIS:HB3	2.03	0.40
27:w:441:PRO:HB2	27:w:443:THR:HG23	2.04	0.40
35:9:425:GLU:HB3	35:9:427:ARG:NH1	2.37	0.40
37:n:25:VAL:HA	37:n:44:LYS:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2216/2335 (95%)	1957 (88%)	246 (11%)	13 (1%)	21	58
3	C	854/972 (88%)	737 (86%)	110 (13%)	7 (1%)	16	52
4	D	1720/2136 (80%)	1585 (92%)	124 (7%)	11 (1%)	21	58
5	E	297/357 (83%)	271 (91%)	26 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	563/855 (66%)	479 (85%)	79 (14%)	5 (1%)	14	49
10	J	245/848 (29%)	214 (87%)	28 (11%)	3 (1%)	10	42
11	K	44/343 (13%)	39 (89%)	5 (11%)	0	100	100
12	L	165/802 (21%)	142 (86%)	23 (14%)	0	100	100
13	N	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
14	O	285/420 (68%)	239 (84%)	46 (16%)	0	100	100
15	P	97/229 (42%)	86 (89%)	9 (9%)	2 (2%)	5	30
16	Q	1319/1485 (89%)	1208 (92%)	111 (8%)	0	100	100
17	R	352/536 (66%)	314 (89%)	36 (10%)	2 (1%)	21	58
18	S	156/166 (94%)	147 (94%)	9 (6%)	0	100	100
19	T	318/514 (62%)	289 (91%)	29 (9%)	0	100	100
20	U	68/2752 (2%)	62 (91%)	6 (9%)	0	100	100
21	V	458/908 (50%)	430 (94%)	28 (6%)	0	100	100
22	X	778/1041 (75%)	692 (89%)	82 (10%)	4 (0%)	24	62
23	Y	318/492 (65%)	277 (87%)	41 (13%)	0	100	100
24	1	814/1304 (62%)	706 (87%)	104 (13%)	4 (0%)	24	62
25	3	1165/1217 (96%)	991 (85%)	172 (15%)	2 (0%)	43	77
26	p	163/225 (72%)	147 (90%)	15 (9%)	1 (1%)	21	58
27	w	428/501 (85%)	381 (89%)	47 (11%)	0	100	100
28	2	246/895 (28%)	210 (85%)	31 (13%)	5 (2%)	6	32
29	4	157/424 (37%)	138 (88%)	19 (12%)	0	100	100
30	7	79/110 (72%)	65 (82%)	14 (18%)	0	100	100
31	5	75/86 (87%)	64 (85%)	11 (15%)	0	100	100
32	y	77/301 (26%)	64 (83%)	13 (17%)	0	100	100
33	v	150/464 (32%)	134 (89%)	16 (11%)	0	100	100
34	u	183/793 (23%)	170 (93%)	13 (7%)	0	100	100
35	9	330/520 (64%)	292 (88%)	38 (12%)	0	100	100
36	a	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
36	m	80/240 (33%)	72 (90%)	8 (10%)	0	100	100
37	b	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
37	n	78/119 (66%)	67 (86%)	11 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	c	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
38	h	91/118 (77%)	82 (90%)	9 (10%)	0	100	100
39	d	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
39	i	70/86 (81%)	64 (91%)	6 (9%)	0	100	100
40	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
40	j	79/92 (86%)	73 (92%)	6 (8%)	0	100	100
41	f	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
41	k	71/76 (93%)	63 (89%)	8 (11%)	0	100	100
42	g	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
42	l	81/126 (64%)	70 (86%)	11 (14%)	0	100	100
43	o	160/255 (63%)	136 (85%)	24 (15%)	0	100	100
All	All	15528/26144 (59%)	13822 (89%)	1647 (11%)	59 (0%)	31	66

All (59) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1258	VAL
9	I	139	ALA
17	R	164	PRO
17	R	223	PRO
24	1	1106	ARG
25	3	570	PRO
28	2	605	LYS
28	2	606	PRO
1	A	51	PHE
1	A	699	GLU
1	A	1417	PRO
3	C	83	GLU
3	C	824	THR
4	D	2098	ALA
4	D	2099	THR
10	J	241	VAL
22	X	851	ASN
28	2	512	GLN
28	2	607	GLY
1	A	698	PRO
1	A	856	LEU
1	A	1548	TYR

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Mol	Chain	Res	Type
3	C	359	LYS
4	D	1261	PRO
4	D	1263	PRO
4	D	1584	ILE
9	I	110	PRO
9	I	371	PRO
22	X	993	THR
24	1	717	THR
24	1	718	PRO
1	A	1418	ARG
4	D	1007	PRO
10	J	358	GLU
22	X	523	HIS
22	X	992	THR
24	1	1105	GLU
28	2	453	LYS
1	A	570	ASP
1	A	942	PRO
3	C	440	SER
4	D	1227	ASP
4	D	1666	THR
9	I	428	GLN
15	P	184	VAL
1	A	189	GLU
3	C	441	PRO
15	P	48	GLN
26	p	214	PRO
3	C	444	GLY
9	I	140	LEU
1	A	386	PRO
4	D	2097	PRO
10	J	341	PRO
25	3	672	GLY
1	A	52	GLY
4	D	531	ILE
1	A	2311	PRO
3	C	615	PRO

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	1762/2108 (84%)	1441 (82%)	321 (18%)	2	11
3	C	747/866 (86%)	614 (82%)	133 (18%)	2	11
5	E	256/300 (85%)	212 (83%)	44 (17%)	2	12
9	I	22/749 (3%)	22 (100%)	0	100	100
10	J	205/751 (27%)	175 (85%)	30 (15%)	3	15
11	K	41/294 (14%)	36 (88%)	5 (12%)	5	19
12	L	141/709 (20%)	118 (84%)	23 (16%)	2	13
13	N	128/130 (98%)	108 (84%)	20 (16%)	2	14
14	O	3/361 (1%)	3 (100%)	0	100	100
15	P	95/203 (47%)	77 (81%)	18 (19%)	1	10
16	Q	71/1336 (5%)	71 (100%)	0	100	100
17	R	268/458 (58%)	213 (80%)	55 (20%)	1	8
19	T	273/441 (62%)	216 (79%)	57 (21%)	1	7
20	U	21/2432 (1%)	18 (86%)	3 (14%)	3	16
21	V	188/838 (22%)	150 (80%)	38 (20%)	1	9
22	X	682/897 (76%)	573 (84%)	109 (16%)	2	13
23	Y	286/451 (63%)	235 (82%)	51 (18%)	2	11
24	1	697/1104 (63%)	572 (82%)	125 (18%)	2	11
25	3	1016/1051 (97%)	789 (78%)	227 (22%)	1	6
26	p	8/195 (4%)	8 (100%)	0	100	100
27	w	112/446 (25%)	95 (85%)	17 (15%)	3	14
28	2	151/776 (20%)	123 (82%)	28 (18%)	1	10
30	7	69/95 (73%)	53 (77%)	16 (23%)	1	5
31	5	68/77 (88%)	48 (71%)	20 (29%)	0	2
33	v	73/382 (19%)	64 (88%)	9 (12%)	4	19
34	u	10/709 (1%)	10 (100%)	0	100	100
35	9	185/456 (41%)	159 (86%)	26 (14%)	3	16
36	m	4/177 (2%)	4 (100%)	0	100	100
37	n	3/101 (3%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	h	5/110 (4%)	5 (100%)	0	100	100
39	i	4/74 (5%)	4 (100%)	0	100	100
40	j	1/84 (1%)	1 (100%)	0	100	100
41	k	3/66 (4%)	3 (100%)	0	100	100
42	l	3/101 (3%)	3 (100%)	0	100	100
43	o	6/218 (3%)	6 (100%)	0	100	100
All	All	7607/19546 (39%)	6232 (82%)	1375 (18%)	3	11

All (1375) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	SER
1	A	31	GLN
1	A	35	ARG
1	A	37	TRP
1	A	50	LYS
1	A	60	ASP
1	A	66	VAL
1	A	78	ASN
1	A	79	ARG
1	A	82	ARG
1	A	86	ARG
1	A	89	LEU
1	A	95	MET
1	A	97	HIS
1	A	111	GLU
1	A	112	GLN
1	A	123	THR
1	A	127	SER
1	A	131	GLU
1	A	142	SER
1	A	176	LEU
1	A	177	ASP
1	A	184	ASP
1	A	188	LEU
1	A	191	ILE
1	A	195	LEU
1	A	204	LEU
1	A	227	ARG
1	A	230	PHE

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Mol	Chain	Res	Type
1	A	231	THR
1	A	248	ASP
1	A	250	VAL
1	A	266	SER
1	A	271	MET
1	A	273	ILE
1	A	283	VAL
1	A	300	ASN
1	A	313	LYS
1	A	322	ASN
1	A	323	LEU
1	A	330	THR
1	A	334	THR
1	A	337	VAL
1	A	338	VAL
1	A	340	ILE
1	A	342	THR
1	A	355	LEU
1	A	356	ILE
1	A	361	HIS
1	A	362	ARG
1	A	363	HIS
1	A	376	GLU
1	A	377	GLU
1	A	382	GLU
1	A	383	PHE
1	A	385	GLU
1	A	387	PHE
1	A	388	LEU
1	A	391	THR
1	A	395	THR
1	A	398	THR
1	A	402	ILE
1	A	404	LEU
1	A	413	LEU
1	A	422	LEU
1	A	424	ILE
1	A	426	LEU
1	A	428	LYS
1	A	431	TYR
1	A	433	GLU
1	A	439	GLN

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Mol	Chain	Res	Type
1	A	443	VAL
1	A	468	LYS
1	A	469	LYS
1	A	479	THR
1	A	480	LYS
1	A	484	SER
1	A	492	VAL
1	A	495	GLN
1	A	496	VAL
1	A	505	ASN
1	A	531	THR
1	A	532	THR
1	A	537	LYS
1	A	546	LEU
1	A	548	ARG
1	A	554	THR
1	A	556	LEU
1	A	558	VAL
1	A	569	VAL
1	A	574	LEU
1	A	576	ASP
1	A	581	ILE
1	A	587	GLN
1	A	591	MET
1	A	593	ARG
1	A	595	LYS
1	A	604	MET
1	A	606	LYS
1	A	609	LYS
1	A	610	HIS
1	A	618	THR
1	A	644	ILE
1	A	665	SER
1	A	666	LYS
1	A	670	LYS
1	A	673	THR
1	A	679	SER
1	A	683	LEU
1	A	686	ARG
1	A	690	MET
1	A	693	ILE
1	A	694	LEU

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Mol	Chain	Res	Type
1	A	728	VAL
1	A	731	LEU
1	A	733	THR
1	A	751	THR
1	A	766	THR
1	A	767	VAL
1	A	769	LYS
1	A	802	THR
1	A	807	VAL
1	A	830	LEU
1	A	831	SER
1	A	833	LYS
1	A	835	ASP
1	A	836	THR
1	A	839	LEU
1	A	840	ILE
1	A	845	ARG
1	A	854	SER
1	A	855	ARG
1	A	856	LEU
1	A	859	SER
1	A	861	ARG
1	A	864	LEU
1	A	866	LEU
1	A	885	LEU
1	A	887	THR
1	A	893	GLU
1	A	894	VAL
1	A	914	LEU
1	A	916	LYS
1	A	931	ASP
1	A	940	ILE
1	A	946	GLU
1	A	976	MET
1	A	977	LEU
1	A	978	GLU
1	A	983	LYS
1	A	993	LEU
1	A	1000	ILE
1	A	1010	THR
1	A	1014	ASN
1	A	1017	ILE

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Mol	Chain	Res	Type
1	A	1018	ASN
1	A	1022	MET
1	A	1027	SER
1	A	1030	ILE
1	A	1031	ILE
1	A	1032	ARG
1	A	1038	SER
1	A	1070	ASP
1	A	1076	ASP
1	A	1079	THR
1	A	1089	CYS
1	A	1095	ILE
1	A	1104	ASP
1	A	1108	ASP
1	A	1123	GLU
1	A	1126	VAL
1	A	1130	ASN
1	A	1131	LYS
1	A	1143	MET
1	A	1144	LYS
1	A	1147	VAL
1	A	1163	ARG
1	A	1166	THR
1	A	1168	VAL
1	A	1173	SER
1	A	1181	ASP
1	A	1186	LEU
1	A	1189	MET
1	A	1207	PHE
1	A	1209	HIS
1	A	1223	GLU
1	A	1270	LEU
1	A	1276	GLU
1	A	1286	ASP
1	A	1293	ASN
1	A	1295	ILE
1	A	1298	ARG
1	A	1306	LYS
1	A	1315	VAL
1	A	1321	GLU
1	A	1340	LEU
1	A	1348	VAL

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Mol	Chain	Res	Type
1	A	1351	THR
1	A	1367	ASN
1	A	1370	ARG
1	A	1372	ILE
1	A	1376	GLU
1	A	1377	SER
1	A	1382	SER
1	A	1383	GLN
1	A	1394	GLN
1	A	1399	GLN
1	A	1400	ASN
1	A	1401	ARG
1	A	1402	ARG
1	A	1405	LEU
1	A	1406	GLU
1	A	1407	ASP
1	A	1409	GLU
1	A	1410	ASP
1	A	1413	ASP
1	A	1419	ILE
1	A	1427	ARG
1	A	1438	VAL
1	A	1450	GLN
1	A	1458	GLN
1	A	1467	LEU
1	A	1486	GLU
1	A	1489	LEU
1	A	1491	LYS
1	A	1518	LEU
1	A	1526	LEU
1	A	1533	ARG
1	A	1536	LEU
1	A	1539	SER
1	A	1549	VAL
1	A	1553	VAL
1	A	1554	GLN
1	A	1555	LEU
1	A	1558	THR
1	A	1568	THR
1	A	1574	ILE
1	A	1575	GLN
1	A	1593	LEU

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Mol	Chain	Res	Type
1	A	1600	GLU
1	A	1601	LEU
1	A	1606	ILE
1	A	1607	GLU
1	A	1608	THR
1	A	1609	VAL
1	A	1614	ILE
1	A	1622	MET
1	A	1623	ASN
1	A	1624	SER
1	A	1630	LEU
1	A	1631	LEU
1	A	1635	TYR
1	A	1640	SER
1	A	1653	ASP
1	A	1655	THR
1	A	1662	ILE
1	A	1664	ILE
1	A	1667	ARG
1	A	1675	ASP
1	A	1691	ASN
1	A	1697	SER
1	A	1701	VAL
1	A	1705	ILE
1	A	1719	PHE
1	A	1722	SER
1	A	1723	LYS
1	A	1726	ILE
1	A	1730	MET
1	A	1756	SER
1	A	1757	GLU
1	A	1759	THR
1	A	1766	GLN
1	A	1768	TYR
1	A	1771	LEU
1	A	1772	PHE
1	A	1773	SER
1	A	1774	ASN
1	A	1775	GLN
1	A	1776	ILE
1	A	1780	VAL
1	A	1782	ASP

Continued on next page...

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Mol	Chain	Res	Type
1	A	1788	VAL
1	A	1789	THR
1	A	1790	ILE
1	A	1792	LYS
1	A	1793	THR
1	A	1798	LEU
1	A	1804	ASN
1	A	1813	ARG
1	A	1817	LEU
1	A	1820	LYS
1	A	1825	SER
1	A	1830	GLN
1	A	1852	LEU
1	A	1862	ILE
1	A	1870	ASP
1	A	1872	LEU
1	A	1876	LEU
1	A	1878	ASP
1	A	1882	ILE
1	A	1888	GLU
1	A	1889	LEU
1	A	1898	LYS
1	A	1900	GLU
1	A	1919	LEU
1	A	1926	THR
1	A	1934	SER
1	A	1935	ARG
1	A	1960	THR
1	A	1961	ILE
1	A	1962	THR
1	A	1965	HIS
1	A	1970	THR
1	A	1971	LEU
1	A	1972	THR
1	A	1975	GLU
1	A	1976	TRP
1	A	1977	ILE
1	A	1981	VAL
1	A	2005	SER
1	A	2014	MET
3	C	58	VAL
3	C	65	TYR

Continued on next page...

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Mol	Chain	Res	Type
3	C	76	GLU
3	C	77	VAL
3	C	83	GLU
3	C	86	THR
3	C	87	GLN
3	C	90	THR
3	C	97	VAL
3	C	117	ASP
3	C	125	ASN
3	C	127	GLU
3	C	133	THR
3	C	134	LEU
3	C	173	THR
3	C	179	VAL
3	C	181	ILE
3	C	183	SER
3	C	184	THR
3	C	186	VAL
3	C	187	THR
3	C	188	VAL
3	C	202	ILE
3	C	215	VAL
3	C	220	ARG
3	C	247	VAL
3	C	257	ILE
3	C	278	LEU
3	C	279	ARG
3	C	288	LEU
3	C	298	LEU
3	C	301	SER
3	C	316	ILE
3	C	319	THR
3	C	320	LEU
3	C	326	ILE
3	C	334	ILE
3	C	353	THR
3	C	359	LYS
3	C	362	THR
3	C	365	SER
3	C	366	GLN
3	C	371	GLU
3	C	385	VAL

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Mol	Chain	Res	Type
3	C	388	VAL
3	C	389	ASP
3	C	394	ARG
3	C	402	HIS
3	C	404	THR
3	C	406	GLU
3	C	412	ILE
3	C	417	ARG
3	C	431	VAL
3	C	449	ILE
3	C	452	THR
3	C	454	THR
3	C	457	VAL
3	C	465	MET
3	C	471	ASP
3	C	483	SER
3	C	484	THR
3	C	495	ARG
3	C	496	VAL
3	C	498	SER
3	C	501	ILE
3	C	510	LEU
3	C	513	ASN
3	C	522	SER
3	C	524	ILE
3	C	538	HIS
3	C	543	ARG
3	C	548	ASN
3	C	553	GLU
3	C	559	ILE
3	C	560	VAL
3	C	561	LYS
3	C	562	THR
3	C	564	THR
3	C	565	ILE
3	C	567	GLU
3	C	572	GLU
3	C	573	GLU
3	C	580	LEU
3	C	587	VAL
3	C	593	GLU
3	C	596	ASN

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Mol	Chain	Res	Type
3	C	598	SER
3	C	603	MET
3	C	612	LYS
3	C	617	LEU
3	C	618	THR
3	C	619	THR
3	C	630	LEU
3	C	635	LEU
3	C	643	ASP
3	C	661	THR
3	C	664	GLU
3	C	672	LEU
3	C	673	LYS
3	C	675	PHE
3	C	685	ILE
3	C	696	LEU
3	C	700	ILE
3	C	704	VAL
3	C	716	GLU
3	C	722	TYR
3	C	724	TRP
3	C	726	LEU
3	C	743	ASN
3	C	746	VAL
3	C	749	THR
3	C	750	LEU
3	C	759	LEU
3	C	766	ILE
3	C	767	VAL
3	C	785	ARG
3	C	799	GLU
3	C	807	GLN
3	C	809	ILE
3	C	826	ARG
3	C	827	LEU
3	C	836	VAL
3	C	866	SER
3	C	875	ILE
3	C	879	ASP
3	C	885	THR
3	C	897	SER
3	C	900	VAL

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Mol	Chain	Res	Type
3	C	907	VAL
3	C	916	ILE
3	C	922	GLU
3	C	928	HIS
3	C	940	ARG
5	E	59	ILE
5	E	65	HIS
5	E	73	LYS
5	E	77	ASN
5	E	79	SER
5	E	87	ASP
5	E	89	LEU
5	E	93	TRP
5	E	102	TYR
5	E	108	HIS
5	E	109	SER
5	E	119	THR
5	E	120	ASP
5	E	125	PHE
5	E	126	SER
5	E	132	THR
5	E	143	ARG
5	E	144	VAL
5	E	152	SER
5	E	154	VAL
5	E	155	ASN
5	E	166	LEU
5	E	167	VAL
5	E	173	ASP
5	E	176	VAL
5	E	200	THR
5	E	205	SER
5	E	209	ILE
5	E	214	ASP
5	E	232	ARG
5	E	234	HIS
5	E	236	ASP
5	E	239	THR
5	E	252	SER
5	E	258	THR
5	E	264	VAL
5	E	298	SER

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Mol	Chain	Res	Type
5	E	314	THR
5	E	320	LEU
5	E	335	PHE
5	E	338	ASP
5	E	341	ILE
5	E	343	ILE
5	E	350	ARG
10	J	216	ASP
10	J	219	GLU
10	J	225	LEU
10	J	239	ARG
10	J	242	ILE
10	J	244	ASN
10	J	252	GLU
10	J	253	GLU
10	J	276	ILE
10	J	277	THR
10	J	280	LEU
10	J	285	MET
10	J	286	GLU
10	J	288	LYS
10	J	297	ASN
10	J	304	THR
10	J	311	GLN
10	J	319	MET
10	J	322	MET
10	J	340	GLN
10	J	350	ILE
10	J	364	THR
10	J	369	PHE
10	J	376	VAL
10	J	385	PHE
10	J	398	VAL
10	J	406	PHE
10	J	422	PHE
10	J	437	LYS
10	J	444	SER
11	K	208	THR
11	K	215	ASP
11	K	218	LYS
11	K	222	ASP
11	K	228	HIS

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Mol	Chain	Res	Type
12	L	24	MET
12	L	33	ARG
12	L	40	ARG
12	L	45	GLN
12	L	53	TRP
12	L	59	LYS
12	L	60	LYS
12	L	61	THR
12	L	64	SER
12	L	77	LEU
12	L	88	ILE
12	L	91	ARG
12	L	104	LEU
12	L	106	LYS
12	L	169	ARG
12	L	170	LYS
12	L	174	LYS
12	L	182	LEU
12	L	190	GLU
12	L	196	ILE
12	L	209	ASP
12	L	222	LEU
12	L	231	ASN
13	N	4	VAL
13	N	17	LEU
13	N	22	LEU
13	N	43	VAL
13	N	44	GLU
13	N	46	LEU
13	N	49	ILE
13	N	56	LYS
13	N	60	ILE
13	N	70	ILE
13	N	75	TYR
13	N	86	LYS
13	N	105	CYS
13	N	116	ASN
13	N	117	CYS
13	N	126	LEU
13	N	128	VAL
13	N	134	CYS
13	N	136	HIS

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Mol	Chain	Res	Type
13	N	137	CYS
15	P	31	SER
15	P	32	SER
15	P	39	THR
15	P	55	ARG
15	P	186	ARG
15	P	187	ARG
15	P	189	ASP
15	P	191	ASP
15	P	192	VAL
15	P	193	VAL
15	P	195	LYS
15	P	204	GLN
15	P	208	LYS
15	P	215	LEU
15	P	224	MET
15	P	225	GLU
15	P	228	ILE
15	P	229	LYS
17	R	84	ASN
17	R	89	GLN
17	R	96	ILE
17	R	101	ILE
17	R	104	GLN
17	R	107	SER
17	R	112	ILE
17	R	114	SER
17	R	122	LYS
17	R	123	GLU
17	R	132	LEU
17	R	140	ILE
17	R	142	GLU
17	R	143	ILE
17	R	146	LYS
17	R	159	VAL
17	R	170	LYS
17	R	180	THR
17	R	186	VAL
17	R	193	LYS
17	R	195	ARG
17	R	197	ILE
17	R	200	VAL

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Mol	Chain	Res	Type
17	R	208	GLU
17	R	218	ILE
17	R	232	SER
17	R	234	SER
17	R	235	ARG
17	R	236	LYS
17	R	238	THR
17	R	247	ILE
17	R	250	CYS
17	R	286	LYS
17	R	295	ASP
17	R	309	GLU
17	R	316	GLU
17	R	323	LYS
17	R	325	ARG
17	R	327	MET
17	R	332	ARG
17	R	348	GLU
17	R	352	ARG
17	R	369	LEU
17	R	376	LYS
17	R	380	LEU
17	R	382	ARG
17	R	385	ASN
17	R	386	ARG
17	R	388	ILE
17	R	406	GLN
17	R	407	TYR
17	R	409	GLN
17	R	415	SER
17	R	433	TYR
17	R	438	ARG
19	T	187	LYS
19	T	196	LEU
19	T	200	ILE
19	T	212	VAL
19	T	216	ASN
19	T	221	THR
19	T	223	SER
19	T	227	THR
19	T	235	SER
19	T	240	LEU

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Mol	Chain	Res	Type
19	T	242	LEU
19	T	247	SER
19	T	254	VAL
19	T	255	SER
19	T	258	SER
19	T	263	SER
19	T	264	CYS
19	T	267	ASP
19	T	274	ASP
19	T	279	LYS
19	T	280	VAL
19	T	283	HIS
19	T	294	LEU
19	T	300	ILE
19	T	301	ASP
19	T	303	LEU
19	T	304	VAL
19	T	307	SER
19	T	314	ILE
19	T	319	THR
19	T	327	SER
19	T	338	CYS
19	T	342	GLU
19	T	349	SER
19	T	353	THR
19	T	364	THR
19	T	369	THR
19	T	372	LYS
19	T	374	SER
19	T	378	VAL
19	T	384	HIS
19	T	386	THR
19	T	389	SER
19	T	394	ASN
19	T	397	GLN
19	T	398	TRP
19	T	421	VAL
19	T	429	SER
19	T	436	MET
19	T	438	LEU
19	T	443	THR
19	T	471	ASP

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Mol	Chain	Res	Type
19	T	478	LEU
19	T	485	THR
19	T	490	ARG
19	T	498	GLU
19	T	503	SER
20	U	1	MET
20	U	9	THR
20	U	16	ASN
21	V	450	ILE
21	V	458	THR
21	V	461	LEU
21	V	465	SER
21	V	470	GLU
21	V	479	MET
21	V	480	GLU
21	V	481	PHE
21	V	483	GLU
21	V	485	GLN
21	V	487	LYS
21	V	494	LEU
21	V	501	ARG
21	V	505	LYS
21	V	516	MET
21	V	518	LYS
21	V	526	GLU
21	V	528	ILE
21	V	536	ILE
21	V	540	GLU
21	V	541	THR
21	V	545	ARG
21	V	565	LEU
21	V	581	ILE
21	V	593	TYR
21	V	607	THR
21	V	616	LEU
21	V	623	ASN
21	V	628	ILE
21	V	632	THR
21	V	633	SER
21	V	634	ILE
21	V	639	LEU
21	V	643	LEU

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Mol	Chain	Res	Type
21	V	644	ARG
21	V	646	HIS
21	V	647	LEU
21	V	650	THR
22	X	164	TRP
22	X	166	ARG
22	X	171	ARG
22	X	183	GLU
22	X	186	ARG
22	X	190	LYS
22	X	194	ARG
22	X	195	ASN
22	X	196	VAL
22	X	197	LEU
22	X	222	MET
22	X	241	GLU
22	X	244	GLU
22	X	245	ASP
22	X	250	LEU
22	X	262	LEU
22	X	263	SER
22	X	266	GLU
22	X	268	GLN
22	X	270	LEU
22	X	271	LYS
22	X	276	VAL
22	X	278	ASP
22	X	292	LEU
22	X	300	MET
22	X	334	LEU
22	X	339	LEU
22	X	384	THR
22	X	389	LYS
22	X	420	ILE
22	X	426	SER
22	X	428	LYS
22	X	439	GLU
22	X	443	ASN
22	X	444	LYS
22	X	467	ARG
22	X	471	VAL
22	X	473	LEU

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Mol	Chain	Res	Type
22	X	476	GLU
22	X	477	VAL
22	X	493	LEU
22	X	497	THR
22	X	520	ASP
22	X	524	GLU
22	X	533	PHE
22	X	542	PHE
22	X	545	GLU
22	X	552	SER
22	X	575	ARG
22	X	579	VAL
22	X	597	VAL
22	X	599	VAL
22	X	606	GLN
22	X	612	LEU
22	X	621	ILE
22	X	622	GLU
22	X	640	ARG
22	X	645	LEU
22	X	654	ASP
22	X	656	GLN
22	X	658	ARG
22	X	663	THR
22	X	672	VAL
22	X	674	THR
22	X	690	LEU
22	X	696	LYS
22	X	699	SER
22	X	712	THR
22	X	729	VAL
22	X	746	GLU
22	X	749	GLU
22	X	751	THR
22	X	755	ILE
22	X	758	THR
22	X	760	LEU
22	X	769	SER
22	X	787	GLU
22	X	796	LEU
22	X	811	SER
22	X	820	VAL

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Mol	Chain	Res	Type
22	X	823	MET
22	X	824	LEU
22	X	825	SER
22	X	828	ILE
22	X	842	THR
22	X	847	LEU
22	X	848	SER
22	X	850	ASN
22	X	863	HIS
22	X	877	ASP
22	X	879	LEU
22	X	886	THR
22	X	894	SER
22	X	903	VAL
22	X	909	ARG
22	X	924	ARG
22	X	927	VAL
22	X	933	GLN
22	X	943	ILE
22	X	944	THR
22	X	951	THR
22	X	954	LEU
22	X	955	THR
22	X	976	LEU
22	X	988	GLU
22	X	992	THR
22	X	994	LYS
22	X	997	MET
22	X	1021	LEU
23	Y	3	VAL
23	Y	16	LEU
23	Y	17	TYR
23	Y	18	THR
23	Y	23	ARG
23	Y	33	LYS
23	Y	40	CYS
23	Y	41	LEU
23	Y	51	ILE
23	Y	53	THR
23	Y	66	ILE
23	Y	79	GLU
23	Y	86	ILE

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Mol	Chain	Res	Type
23	Y	93	THR
23	Y	109	LEU
23	Y	118	TYR
23	Y	122	VAL
23	Y	125	VAL
23	Y	126	PHE
23	Y	129	VAL
23	Y	130	THR
23	Y	135	ILE
23	Y	147	ASP
23	Y	154	ILE
23	Y	159	THR
23	Y	162	LEU
23	Y	176	ASP
23	Y	182	THR
23	Y	188	SER
23	Y	191	ILE
23	Y	195	GLU
23	Y	197	ILE
23	Y	198	ASP
23	Y	200	PHE
23	Y	203	ARG
23	Y	210	GLU
23	Y	211	ILE
23	Y	216	GLU
23	Y	219	THR
23	Y	227	VAL
23	Y	235	ILE
23	Y	245	CYS
23	Y	250	VAL
23	Y	252	THR
23	Y	253	ASP
23	Y	257	GLU
23	Y	258	ILE
23	Y	273	ARG
23	Y	307	ASP
23	Y	309	ARG
23	Y	319	VAL
24	1	493	LYS
24	1	498	MET
24	1	544	LEU
24	1	545	GLU

Continued on next page...

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Mol	Chain	Res	Type
24	1	560	LEU
24	1	562	LYS
24	1	563	LEU
24	1	564	ASP
24	1	566	LEU
24	1	568	ARG
24	1	571	VAL
24	1	581	LEU
24	1	582	LEU
24	1	585	GLU
24	1	591	VAL
24	1	596	ILE
24	1	598	SER
24	1	609	MET
24	1	610	ILE
24	1	630	ARG
24	1	635	VAL
24	1	641	ILE
24	1	645	LEU
24	1	673	ILE
24	1	685	SER
24	1	687	VAL
24	1	691	GLU
24	1	698	GLN
24	1	701	VAL
24	1	707	LEU
24	1	719	TYR
24	1	721	ILE
24	1	736	ARG
24	1	754	ILE
24	1	760	GLU
24	1	768	GLU
24	1	769	VAL
24	1	771	LEU
24	1	779	SER
24	1	790	LYS
24	1	793	LYS
24	1	795	CYS
24	1	801	VAL
24	1	836	THR
24	1	837	THR
24	1	840	LEU

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Mol	Chain	Res	Type
24	1	844	VAL
24	1	850	ILE
24	1	858	LYS
24	1	868	VAL
24	1	873	GLU
24	1	876	MET
24	1	890	GLU
24	1	891	GLN
24	1	892	LEU
24	1	893	ILE
24	1	901	GLN
24	1	903	GLN
24	1	904	THR
24	1	905	THR
24	1	918	VAL
24	1	921	LEU
24	1	923	LYS
24	1	925	VAL
24	1	926	LYS
24	1	928	TYR
24	1	936	VAL
24	1	947	VAL
24	1	958	THR
24	1	963	LYS
24	1	964	THR
24	1	967	GLU
24	1	968	GLU
24	1	971	MET
24	1	973	HIS
24	1	980	GLU
24	1	982	LEU
24	1	989	VAL
24	1	1001	VAL
24	1	1003	VAL
24	1	1004	ILE
24	1	1009	MET
24	1	1010	THR
24	1	1014	LYS
24	1	1015	ASP
24	1	1021	THR
24	1	1030	LYS
24	1	1031	VAL

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Mol	Chain	Res	Type
24	1	1038	LEU
24	1	1041	ARG
24	1	1048	GLU
24	1	1050	VAL
24	1	1065	LEU
24	1	1067	LYS
24	1	1080	THR
24	1	1093	VAL
24	1	1108	ASN
24	1	1113	THR
24	1	1118	ILE
24	1	1121	GLU
24	1	1122	THR
24	1	1128	VAL
24	1	1138	VAL
24	1	1143	VAL
24	1	1161	MET
24	1	1164	ASP
24	1	1170	THR
24	1	1174	GLU
24	1	1182	LEU
24	1	1187	THR
24	1	1196	SER
24	1	1219	VAL
24	1	1237	LEU
24	1	1241	ILE
24	1	1245	ARG
24	1	1250	CYS
24	1	1251	LEU
24	1	1260	LYS
24	1	1261	VAL
24	1	1277	GLN
24	1	1281	ILE
24	1	1294	THR
24	1	1296	ILE
24	1	1303	ILE
24	1	1304	LEU
25	3	18	ILE
25	3	25	THR
25	3	30	ILE
25	3	33	SER
25	3	36	LYS

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Mol	Chain	Res	Type
25	3	41	LEU
25	3	44	ASP
25	3	49	LYS
25	3	52	THR
25	3	56	VAL
25	3	57	GLU
25	3	66	MET
25	3	68	PHE
25	3	74	THR
25	3	78	ILE
25	3	79	VAL
25	3	80	VAL
25	3	90	LEU
25	3	98	MET
25	3	106	THR
25	3	110	SER
25	3	116	VAL
25	3	121	LEU
25	3	124	ASP
25	3	126	LYS
25	3	130	VAL
25	3	131	MET
25	3	135	ILE
25	3	139	LYS
25	3	143	ILE
25	3	153	THR
25	3	156	SER
25	3	162	LYS
25	3	170	VAL
25	3	173	VAL
25	3	188	ASP
25	3	195	ASP
25	3	204	THR
25	3	207	THR
25	3	209	THR
25	3	221	VAL
25	3	225	SER
25	3	226	GLU
25	3	230	GLU
25	3	233	ASN
25	3	235	LEU
25	3	236	ILE

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Mol	Chain	Res	Type
25	3	237	THR
25	3	256	ILE
25	3	257	THR
25	3	261	PHE
25	3	264	GLN
25	3	266	ASP
25	3	271	ILE
25	3	273	ARG
25	3	275	ARG
25	3	286	ILE
25	3	294	LYS
25	3	297	SER
25	3	310	ILE
25	3	315	LEU
25	3	317	THR
25	3	320	ASP
25	3	321	MET
25	3	327	LEU
25	3	332	THR
25	3	333	VAL
25	3	335	VAL
25	3	340	CYS
25	3	343	LYS
25	3	344	THR
25	3	347	LEU
25	3	355	ASN
25	3	356	HIS
25	3	364	LEU
25	3	370	GLU
25	3	384	THR
25	3	390	ARG
25	3	392	LEU
25	3	403	SER
25	3	404	LEU
25	3	412	ILE
25	3	427	CYS
25	3	433	SER
25	3	435	LEU
25	3	439	ARG
25	3	443	GLU
25	3	459	VAL
25	3	461	THR

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Mol	Chain	Res	Type
25	3	462	VAL
25	3	464	ARG
25	3	465	HIS
25	3	466	ILE
25	3	469	GLU
25	3	471	ASP
25	3	474	ILE
25	3	475	ILE
25	3	482	THR
25	3	492	GLU
25	3	511	LEU
25	3	514	ASP
25	3	527	ILE
25	3	537	LYS
25	3	541	LYS
25	3	543	THR
25	3	544	ILE
25	3	555	VAL
25	3	556	ILE
25	3	563	LEU
25	3	564	VAL
25	3	568	MET
25	3	570	PRO
25	3	574	LEU
25	3	578	THR
25	3	584	SER
25	3	592	LEU
25	3	594	ASN
25	3	595	VAL
25	3	603	ARG
25	3	604	PHE
25	3	605	LEU
25	3	614	VAL
25	3	617	ILE
25	3	620	ASP
25	3	626	GLN
25	3	630	MET
25	3	642	ILE
25	3	643	VAL
25	3	665	LEU
25	3	669	LEU
25	3	675	LEU

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Mol	Chain	Res	Type
25	3	676	ARG
25	3	677	THR
25	3	678	VAL
25	3	679	LEU
25	3	685	ASP
25	3	689	THR
25	3	697	ARG
25	3	703	ARG
25	3	704	VAL
25	3	715	MET
25	3	721	LEU
25	3	726	GLN
25	3	727	SER
25	3	732	THR
25	3	738	THR
25	3	758	SER
25	3	761	THR
25	3	775	ASN
25	3	776	GLN
25	3	797	LEU
25	3	798	ILE
25	3	802	THR
25	3	818	GLN
25	3	821	GLU
25	3	822	GLU
25	3	834	LEU
25	3	837	GLU
25	3	850	SER
25	3	851	ILE
25	3	865	VAL
25	3	867	ARG
25	3	868	VAL
25	3	876	THR
25	3	882	LEU
25	3	883	GLU
25	3	897	SER
25	3	901	GLU
25	3	902	ASP
25	3	920	VAL
25	3	925	VAL
25	3	927	THR
25	3	931	VAL

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Mol	Chain	Res	Type
25	3	937	LEU
25	3	941	HIS
25	3	942	LYS
25	3	943	THR
25	3	945	VAL
25	3	948	VAL
25	3	958	ARG
25	3	959	VAL
25	3	960	LEU
25	3	961	ILE
25	3	966	LEU
25	3	968	ARG
25	3	969	VAL
25	3	978	LEU
25	3	981	CYS
25	3	988	ASN
25	3	991	SER
25	3	993	ILE
25	3	995	THR
25	3	996	ILE
25	3	998	HIS
25	3	1000	VAL
25	3	1002	VAL
25	3	1012	VAL
25	3	1022	ILE
25	3	1026	ASP
25	3	1028	THR
25	3	1033	VAL
25	3	1035	THR
25	3	1042	ASP
25	3	1056	VAL
25	3	1062	THR
25	3	1066	VAL
25	3	1090	GLU
25	3	1093	MET
25	3	1094	ASN
25	3	1099	GLU
25	3	1101	VAL
25	3	1103	SER
25	3	1107	THR
25	3	1114	SER
25	3	1116	SER

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Mol	Chain	Res	Type
25	3	1118	VAL
25	3	1120	THR
25	3	1121	THR
25	3	1135	HIS
25	3	1148	LEU
25	3	1150	SER
25	3	1151	GLU
25	3	1168	PHE
25	3	1170	VAL
25	3	1183	ASN
25	3	1184	SER
25	3	1193	VAL
27	w	390	LYS
27	w	400	HIS
27	w	403	ASN
27	w	414	TYR
27	w	415	THR
27	w	425	HIS
27	w	430	ARG
27	w	437	CYS
27	w	446	PHE
27	w	453	GLU
27	w	458	LEU
27	w	463	LYS
27	w	468	SER
27	w	471	TRP
27	w	475	THR
27	w	487	VAL
27	w	500	LEU
28	2	460	PHE
28	2	461	THR
28	2	465	LEU
28	2	471	ARG
28	2	474	VAL
28	2	475	VAL
28	2	477	MET
28	2	488	LEU
28	2	494	THR
28	2	505	CYS
28	2	507	LYS
28	2	509	LYS
28	2	510	TYR

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Mol	Chain	Res	Type
28	2	512	GLN
28	2	517	ILE
28	2	524	LEU
28	2	526	ASP
28	2	528	ILE
28	2	531	THR
28	2	543	LYS
28	2	557	VAL
28	2	561	MET
28	2	564	ILE
28	2	590	LEU
28	2	595	LYS
28	2	598	GLU
28	2	602	LYS
28	2	705	ARG
30	7	9	ILE
30	7	11	CYS
30	7	14	GLN
30	7	23	CYS
30	7	25	LYS
30	7	30	CYS
30	7	32	ILE
30	7	35	SER
30	7	37	VAL
30	7	40	CYS
30	7	45	ILE
30	7	48	GLU
30	7	60	ILE
30	7	68	ASP
30	7	71	TYR
30	7	89	VAL
31	5	5	TYR
31	5	11	LEU
31	5	12	GLU
31	5	23	HIS
31	5	25	ASP
31	5	26	THR
31	5	27	THR
31	5	32	LEU
31	5	33	VAL
31	5	35	GLN
31	5	36	HIS

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Mol	Chain	Res	Type
31	5	42	SER
31	5	51	ASN
31	5	57	GLU
31	5	60	SER
31	5	63	ARG
31	5	65	ARG
31	5	69	MET
31	5	72	MET
31	5	74	GLN
33	v	20	SER
33	v	33	LEU
33	v	37	THR
33	v	59	CYS
33	v	68	SER
33	v	76	LYS
33	v	77	LYS
33	v	81	ASN
33	v	85	ARG
35	9	201	ASN
35	9	242	SER
35	9	246	VAL
35	9	247	SER
35	9	253	THR
35	9	256	VAL
35	9	262	GLU
35	9	291	LEU
35	9	293	LEU
35	9	295	LEU
35	9	296	HIS
35	9	298	ASP
35	9	299	LEU
35	9	338	THR
35	9	344	SER
35	9	348	LYS
35	9	352	ASP
35	9	359	SER
35	9	360	HIS
35	9	365	ILE
35	9	393	LYS
35	9	405	ASP
35	9	407	LEU
35	9	408	THR

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Mol	Chain	Res	Type
35	9	426	ILE
35	9	431	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (192) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	78	ASN
1	A	121	HIS
1	A	181	ASN
1	A	244	GLN
1	A	270	ASN
1	A	300	ASN
1	A	325	HIS
1	A	326	HIS
1	A	328	HIS
1	A	357	ASN
1	A	361	HIS
1	A	368	GLN
1	A	439	GLN
1	A	467	GLN
1	A	495	GLN
1	A	499	GLN
1	A	502	ASN
1	A	584	HIS
1	A	659	GLN
1	A	675	GLN
1	A	752	ASN
1	A	755	HIS
1	A	775	ASN
1	A	788	GLN
1	A	792	HIS
1	A	815	HIS
1	A	1096	HIS
1	A	1293	ASN
1	A	1304	ASN
1	A	1337	GLN
1	A	1345	GLN
1	A	1352	HIS
1	A	1400	ASN
1	A	1424	GLN
1	A	1428	HIS

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Mol	Chain	Res	Type
1	A	1460	HIS
1	A	1487	HIS
1	A	1527	ASN
1	A	1552	GLN
1	A	1580	HIS
1	A	1583	GLN
1	A	1623	ASN
1	A	1710	ASN
1	A	1766	GLN
1	A	1784	ASN
1	A	1811	ASN
1	A	1830	GLN
1	A	1875	HIS
1	A	1894	GLN
1	A	1947	ASN
1	A	1965	HIS
3	C	82	GLN
3	C	131	ASN
3	C	137	HIS
3	C	139	HIS
3	C	210	ASN
3	C	245	HIS
3	C	280	HIS
3	C	286	ASN
3	C	306	ASN
3	C	313	GLN
3	C	350	ASN
3	C	627	HIS
3	C	743	ASN
3	C	802	HIS
3	C	807	GLN
5	E	94	ASN
5	E	101	ASN
5	E	116	HIS
5	E	188	GLN
5	E	287	ASN
5	E	331	ASN
10	J	234	ASN
10	J	238	ASN
10	J	244	ASN
10	J	331	GLN
10	J	347	HIS

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Mol	Chain	Res	Type
11	K	198	GLN
11	K	228	HIS
12	L	29	ASN
12	L	73	HIS
12	L	81	GLN
12	L	175	GLN
14	O	120	ASN
15	P	45	GLN
15	P	204	GLN
15	P	212	ASN
17	R	175	GLN
17	R	184	GLN
17	R	279	HIS
17	R	357	HIS
17	R	385	ASN
17	R	398	ASN
17	R	406	GLN
17	R	431	ASN
19	T	203	HIS
19	T	269	GLN
19	T	278	ASN
19	T	407	GLN
19	T	437	HIS
19	T	446	ASN
19	T	455	GLN
20	U	20	GLN
21	V	474	HIS
21	V	499	GLN
21	V	553	HIS
21	V	609	GLN
21	V	620	ASN
22	X	195	ASN
22	X	265	HIS
22	X	414	ASN
22	X	475	ASN
22	X	606	GLN
22	X	656	GLN
22	X	720	ASN
22	X	745	HIS
22	X	866	ASN
22	X	870	ASN
22	X	904	GLN

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Mol	Chain	Res	Type
22	X	950	HIS
22	X	964	GLN
22	X	971	HIS
22	X	979	GLN
22	X	987	HIS
23	Y	44	ASN
23	Y	158	HIS
24	1	550	HIS
24	1	599	ASN
24	1	669	GLN
24	1	682	HIS
24	1	817	HIS
24	1	829	ASN
24	1	886	HIS
24	1	1026	ASN
24	1	1028	HIS
24	1	1032	GLN
24	1	1069	HIS
24	1	1100	ASN
24	1	1142	ASN
24	1	1225	HIS
24	1	1252	GLN
24	1	1277	GLN
25	3	5	ASN
25	3	19	HIS
25	3	46	ASN
25	3	145	ASN
25	3	169	HIS
25	3	179	ASN
25	3	194	ASN
25	3	205	GLN
25	3	206	GLN
25	3	219	HIS
25	3	231	HIS
25	3	233	ASN
25	3	264	GLN
25	3	304	GLN
25	3	411	GLN
25	3	440	HIS
25	3	480	ASN
25	3	518	GLN
25	3	550	ASN

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Mol	Chain	Res	Type
25	3	573	GLN
25	3	612	ASN
25	3	636	GLN
25	3	671	ASN
25	3	709	GLN
25	3	730	HIS
25	3	775	ASN
25	3	796	ASN
25	3	844	ASN
25	3	861	GLN
25	3	881	GLN
25	3	933	ASN
25	3	956	GLN
25	3	994	GLN
25	3	1019	ASN
25	3	1052	ASN
25	3	1105	GLN
27	w	407	ASN
27	w	413	ASN
27	w	445	HIS
27	w	485	ASN
28	2	546	GLN
28	2	579	GLN
30	7	55	GLN
33	v	79	GLN
35	9	209	GLN
35	9	287	ASN
35	9	327	ASN
35	9	331	GLN
35	9	412	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	96/117 (82%)	29 (30%)	3 (3%)
6	F	96/107 (89%)	48 (50%)	4 (4%)
7	G	71/220 (32%)	44 (61%)	9 (12%)
8	H	163/188 (86%)	73 (44%)	6 (3%)
All	All	426/632 (67%)	194 (45%)	22 (5%)

All (194) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	9	G
2	B	10	U
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	40	U
2	B	44	A
2	B	47	A
2	B	48	A
2	B	52	U
2	B	57	G
2	B	62	G
2	B	65	G
2	B	68	C
2	B	70	A
2	B	71	C
2	B	88	A
2	B	89	U
2	B	90	U
2	B	92	U
2	B	93	U
2	B	94	U
2	B	95	G
2	B	96	A
2	B	97	G
2	B	109	G
6	F	6	C
6	F	7	G
6	F	9	U
6	F	10	U
6	F	12	G
6	F	17	C
6	F	24	A
6	F	25	C
6	F	26	U
6	F	27	A
6	F	28	A
6	F	29	A
6	F	30	A
6	F	33	G

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Mol	Chain	Res	Type
6	F	34	G
6	F	35	A
6	F	37	C
6	F	38	G
6	F	40	U
6	F	42	C
6	F	44	G
6	F	45	A
6	F	46	G
6	F	48	A
6	F	49	G
6	F	54	G
6	F	59	G
6	F	60	C
6	F	61	C
6	F	65	G
6	F	66	C
6	F	68	C
6	F	73	A
6	F	74	U
6	F	75	G
6	F	78	A
6	F	79	C
6	F	80	G
6	F	81	C
6	F	82	A
6	F	83	A
6	F	84	A
6	F	85	U
6	F	86	U
6	F	87	C
6	F	88	G
6	F	89	U
6	F	91	A
7	G	-10	G
7	G	-9	C
7	G	-8	C
7	G	-7	U
7	G	-6	C
7	G	-5	C
7	G	-4	G
7	G	1	G

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Mol	Chain	Res	Type
7	G	3	A
7	G	4	A
7	G	8	C
7	G	9	C
7	G	10	U
7	G	11	A
7	G	13	C
7	G	17	U
7	G	19	G
7	G	20	A
7	G	21	A
7	G	22	C
7	G	23	U
7	G	24	G
7	G	84	U
7	G	85	G
7	G	88	G
7	G	89	U
7	G	90	C
7	G	92	U
7	G	97	A
7	G	98	U
7	G	100	C
7	G	101	U
7	G	102	G
7	G	103	U
7	G	104	C
7	G	105	C
7	G	106	C
7	G	111	U
7	G	112	U
7	G	113	U
7	G	114	U
7	G	115	C
7	G	116	C
7	G	117	A
8	H	2	U
8	H	13	C
8	H	14	C
8	H	15	U
8	H	16	U
8	H	17	U

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Mol	Chain	Res	Type
8	H	18	U
8	H	19	G
8	H	23	A
8	H	24	A
8	H	29	A
8	H	30	A
8	H	31	G
8	H	33	G
8	H	34	U
8	H	35	A
8	H	44	U
8	H	45	C
8	H	46	U
8	H	47	U
8	H	48	A
8	H	49	U
8	H	53	U
8	H	63	G
8	H	64	A
8	H	65	U
8	H	70	C
8	H	74	U
8	H	80	A
8	H	81	G
8	H	82	G
8	H	84	C
8	H	98	G
8	H	99	A
8	H	100	U
8	H	101	U
8	H	102	U
8	H	103	U
8	H	106	G
8	H	107	A
8	H	110	A
8	H	111	G
8	H	112	G
8	H	113	G
8	H	116	A
8	H	117	U
8	H	121	A
8	H	122	U

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Mol	Chain	Res	Type
8	H	123	A
8	H	124	G
8	H	128	C
8	H	129	U
8	H	133	U
8	H	136	G
8	H	137	U
8	H	141	C
8	H	144	C
8	H	145	A
8	H	146	C
8	H	147	G
8	H	149	A
8	H	157	G
8	H	162	U
8	H	164	C
8	H	165	A
8	H	166	G
8	H	168	A
8	H	169	C
8	H	171	U
8	H	177	A
8	H	178	A
8	H	179	C
8	H	180	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	39	C
2	B	94	U
2	B	96	A
6	F	37	C
6	F	47	A
6	F	48	A
6	F	58	G
7	G	21	A
7	G	83	A
7	G	84	U
7	G	88	G
7	G	89	U
7	G	101	U

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Mol	Chain	Res	Type
7	G	105	C
7	G	111	U
7	G	113	U
8	H	13	C
8	H	18	U
8	H	43	U
8	H	46	U
8	H	47	U
8	H	165	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	SEP	R	224	17	8,9,10	1.47	1 (12%)	7,12,14	1.48	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	SEP	R	224	17	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	R	224	SEP	P-O1P	3.24	1.60	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	R	224	SEP	OG-CB-CA	3.45	111.50	108.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 14 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	$\# Z > 2$
45	GTP	C	1500	46	33,34,34	0.83	0	50,54,54	1.65	9 (18%)
44	IHP	A	3000	-	36,36,36	0.95	0	60,60,60	1.71	15 (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
45	GTP	C	1500	46	-	4/22/38/38	0/3/3/3
44	IHP	A	3000	-	-	7/30/54/54	0/1/1/1

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C	1500	GTP	C5-C4-N3	-5.47	119.69	128.39
45	C	1500	GTP	C2-N3-C4	4.97	120.86	112.30
44	A	3000	IHP	P4-O14-C4	-4.00	112.74	123.43
44	A	3000	IHP	C6-C5-C4	3.75	118.65	110.43
44	A	3000	IHP	C5-C4-C3	3.69	118.52	110.43
44	A	3000	IHP	O11-C1-C2	-3.59	101.13	108.76
45	C	1500	GTP	N9-C4-N3	3.49	132.94	125.95
44	A	3000	IHP	O13-C3-C4	3.43	116.05	108.76
45	C	1500	GTP	C2-N1-C6	-3.17	119.36	125.11
44	A	3000	IHP	O12-C2-C1	2.88	114.88	108.76
45	C	1500	GTP	C5-C6-N1	2.65	119.99	113.25
44	A	3000	IHP	O45-P5-O35	2.61	117.58	107.80
45	C	1500	GTP	O6-C6-C5	-2.50	119.93	126.53
45	C	1500	GTP	C8-N7-C5	2.49	108.69	104.26
44	A	3000	IHP	P1-O11-C1	-2.40	117.01	123.43
45	C	1500	GTP	N9-C8-N7	-2.39	108.98	113.40
45	C	1500	GTP	C3'-C2'-C1'	2.36	105.93	101.46
44	A	3000	IHP	O16-C6-C5	2.35	113.75	108.76
44	A	3000	IHP	P5-O15-C5	-2.26	117.38	123.43
44	A	3000	IHP	O42-P2-O32	2.26	116.27	107.80
44	A	3000	IHP	O13-C3-C2	-2.24	104.00	108.76
44	A	3000	IHP	O14-C4-C5	2.24	113.52	108.76
44	A	3000	IHP	P3-O13-C3	-2.20	117.56	123.43
44	A	3000	IHP	O44-P4-O34	2.18	115.98	107.80

There are no chirality outliers.

All (11) torsion outliers are listed below:

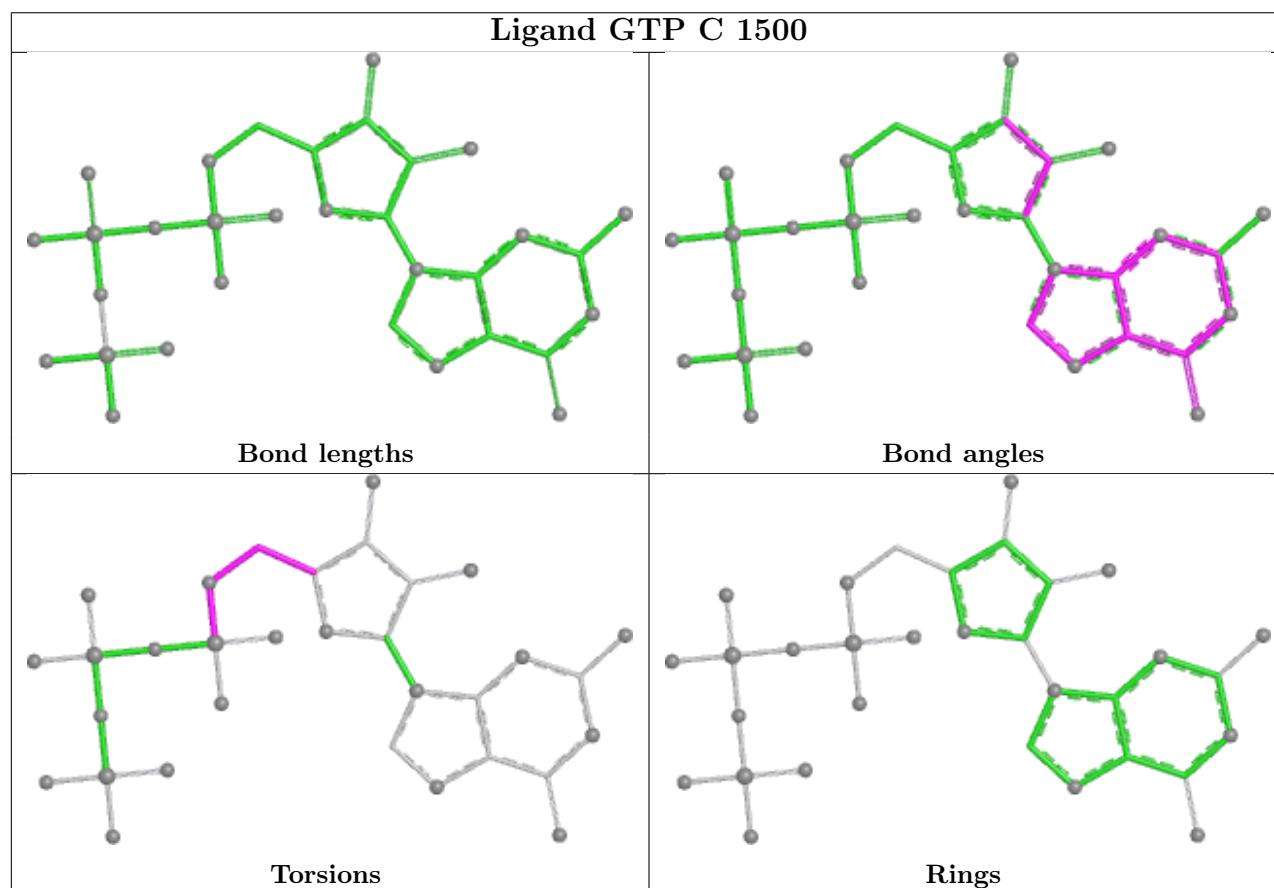
Mol	Chain	Res	Type	Atoms
44	A	3000	IHP	C2-C1-O11-P1
44	A	3000	IHP	C4-C5-O15-P5
44	A	3000	IHP	C6-C5-O15-P5
45	C	1500	GTP	C4'-C5'-O5'-PA
45	C	1500	GTP	C3'-C4'-C5'-O5'
45	C	1500	GTP	O4'-C4'-C5'-O5'
44	A	3000	IHP	C6-C1-O11-P1
45	C	1500	GTP	C5'-O5'-PA-O1A
44	A	3000	IHP	C4-O14-P4-O34
44	A	3000	IHP	C6-O16-P6-O26
44	A	3000	IHP	C1-C6-O16-P6

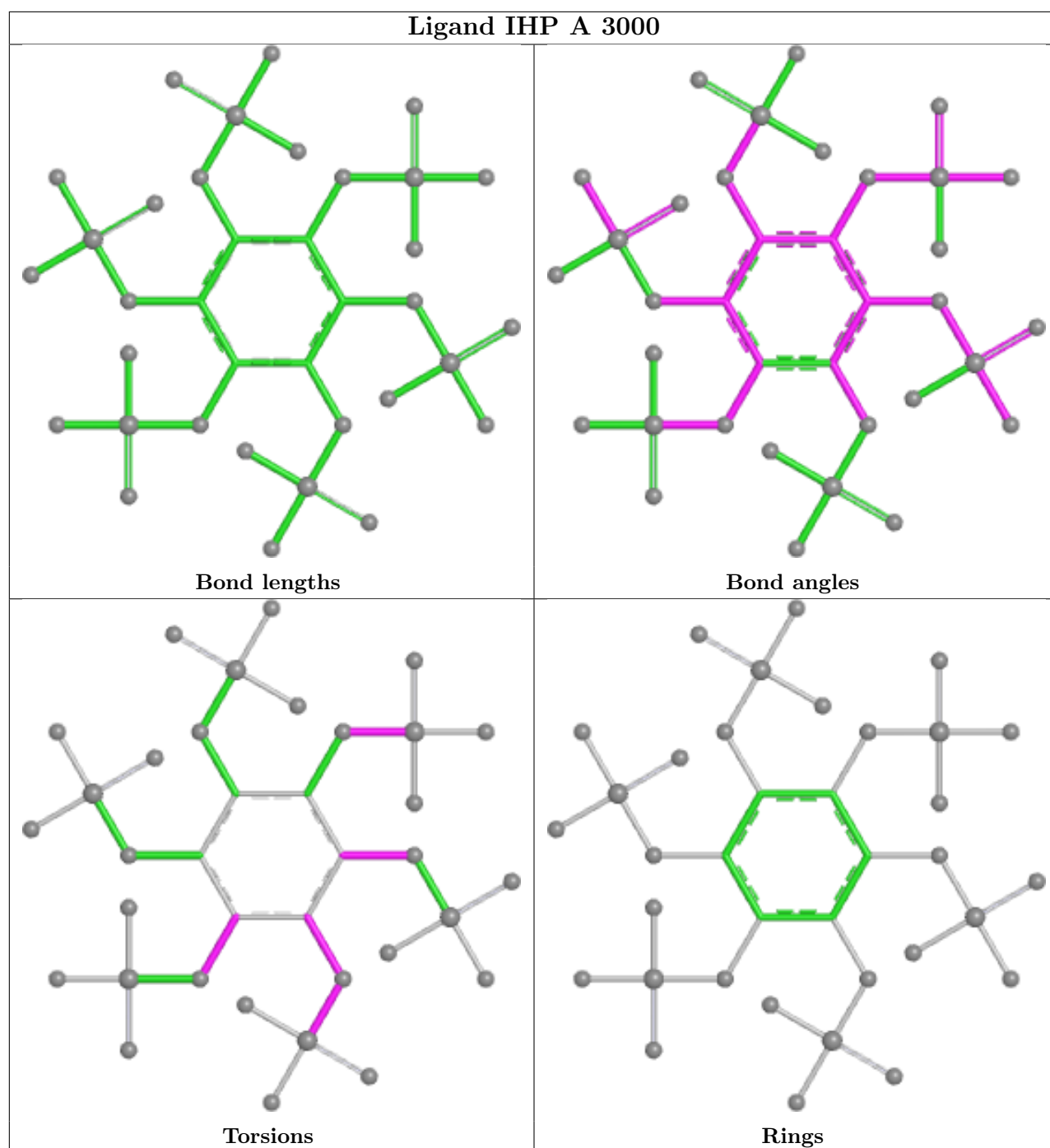
There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	C	1500	GTP	8	0
44	A	3000	IHP	8	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.

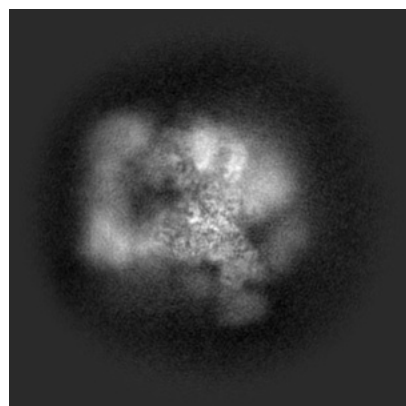
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35108. These allow visual inspection of the internal detail of the map and identification of artifacts.

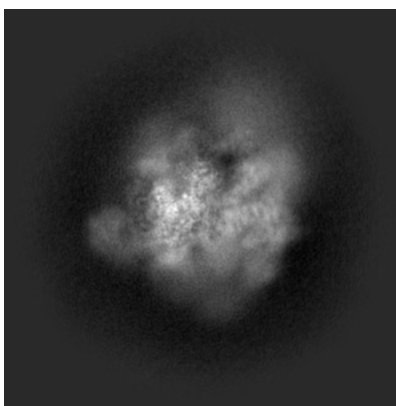
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

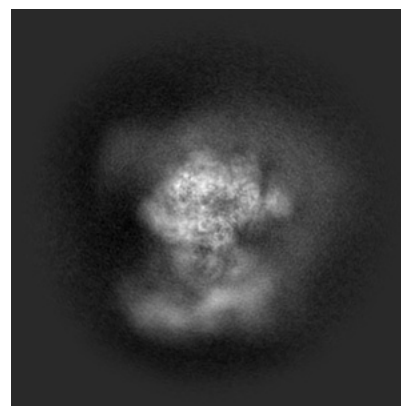
6.1.1 Primary map



X

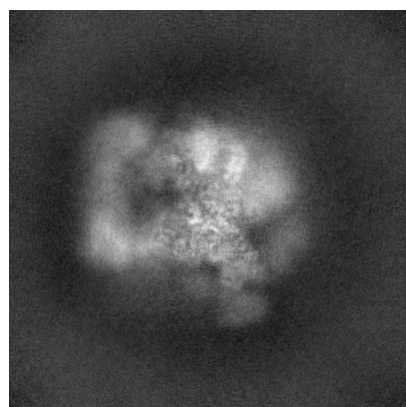


Y

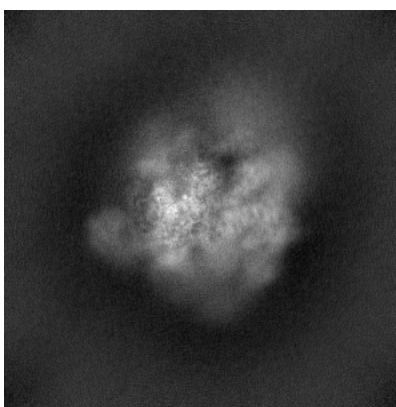


Z

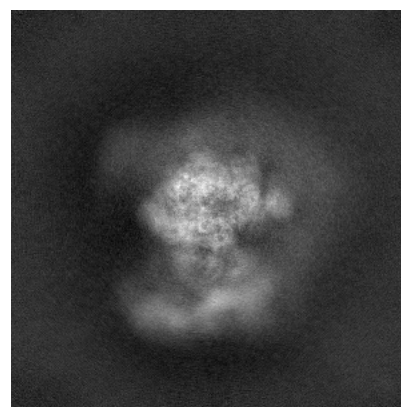
6.1.2 Raw map



X



Y

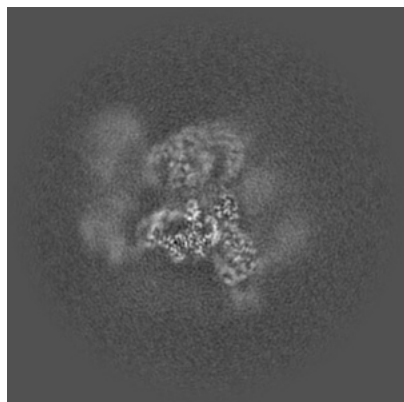


Z

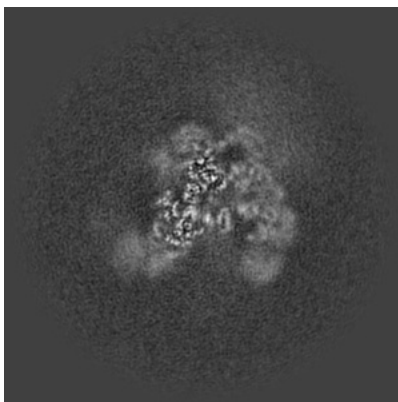
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

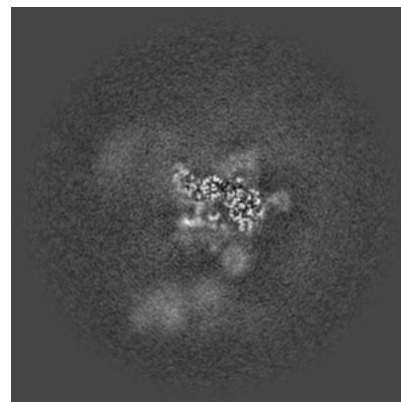
6.2.1 Primary map



X Index: 240

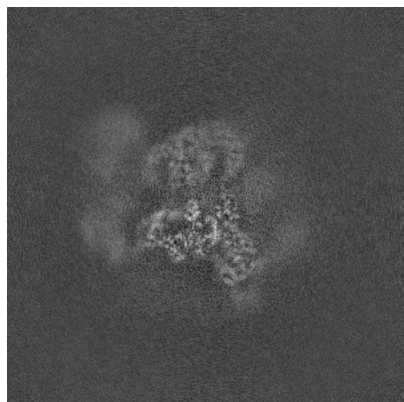


Y Index: 240

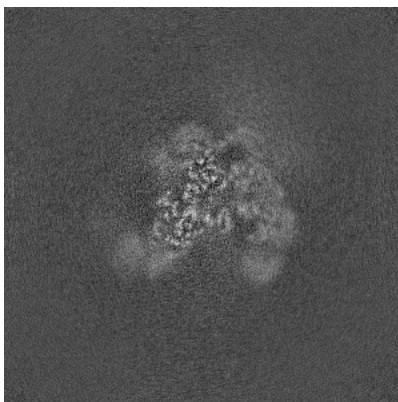


Z Index: 240

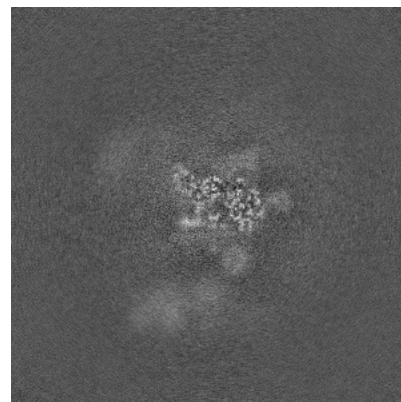
6.2.2 Raw map



X Index: 240



Y Index: 240

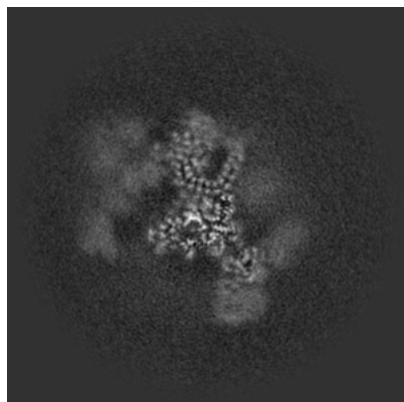


Z Index: 240

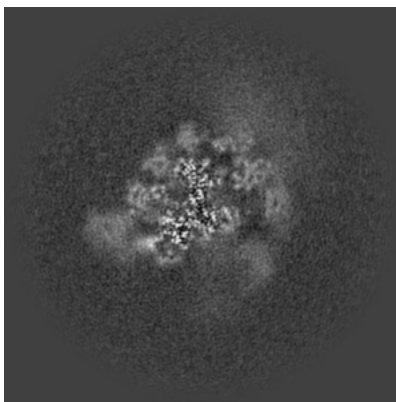
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

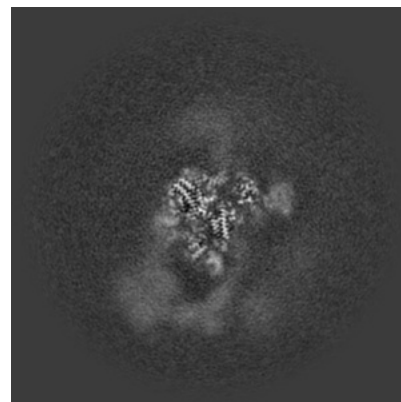
6.3.1 Primary map



X Index: 226

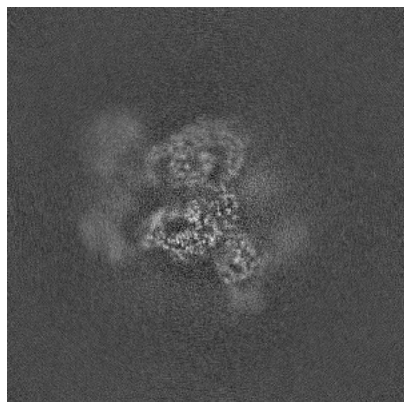


Y Index: 258

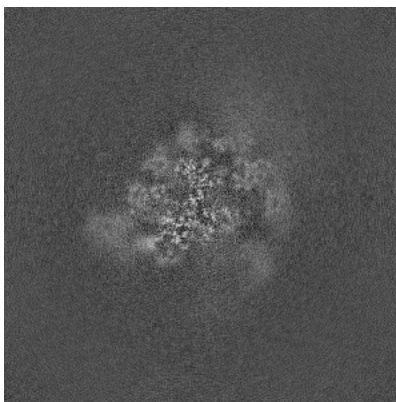


Z Index: 216

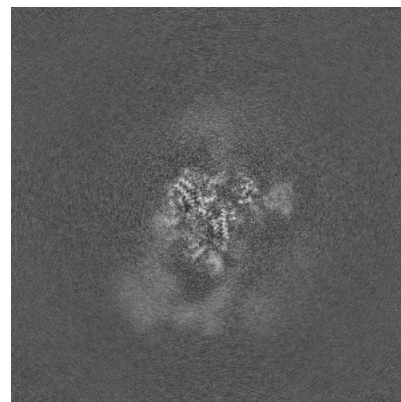
6.3.2 Raw map



X Index: 238



Y Index: 258

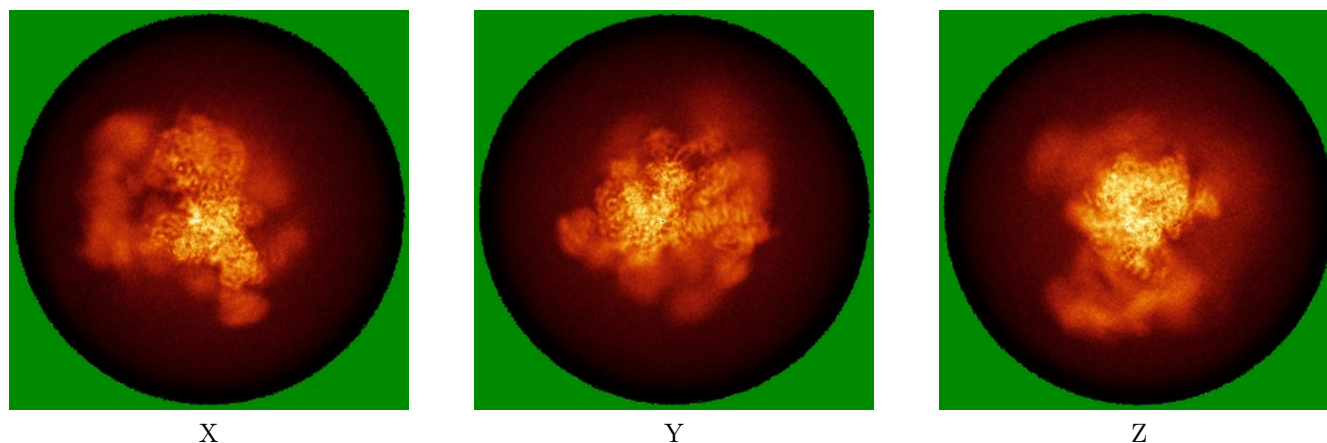


Z Index: 216

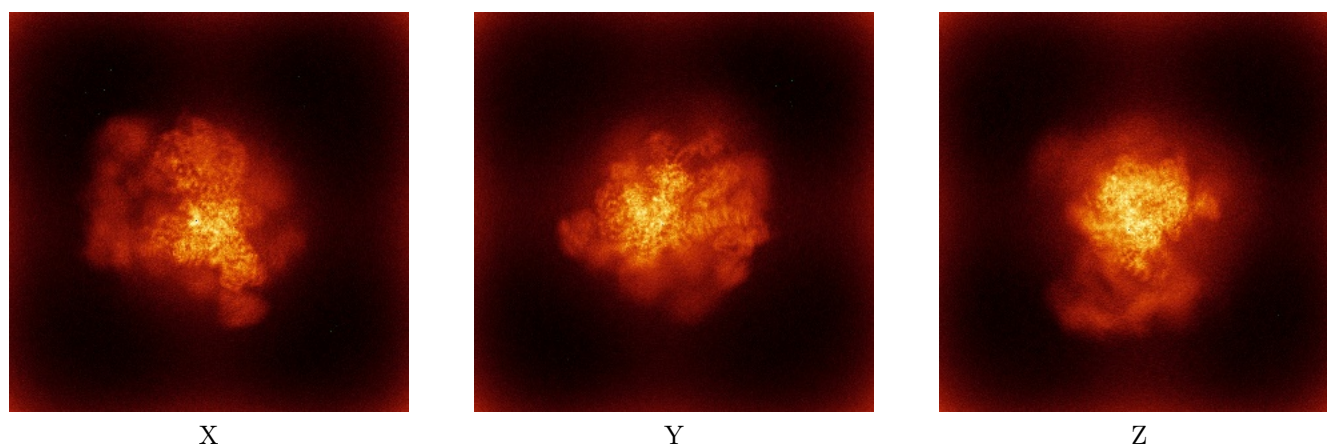
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

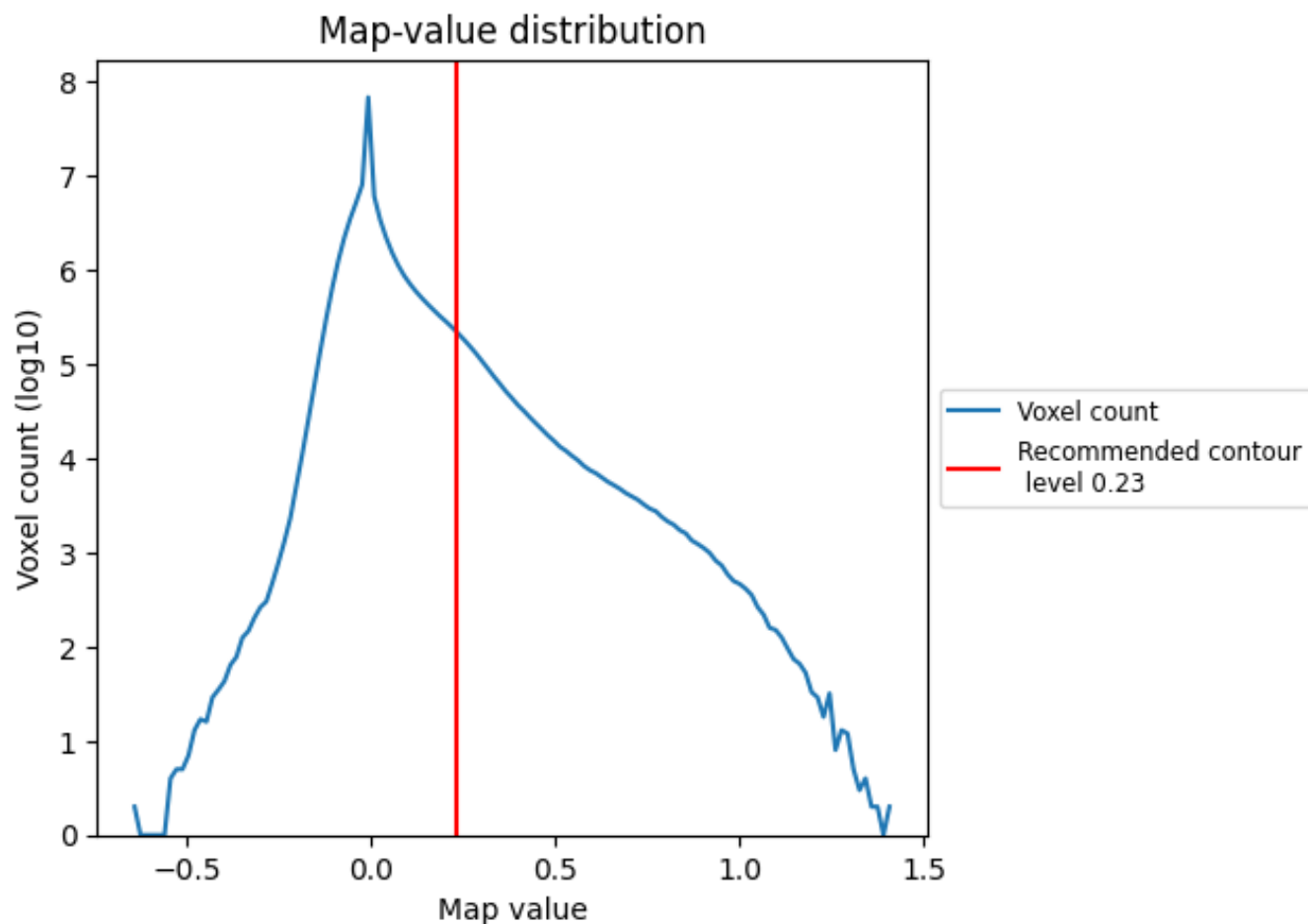
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

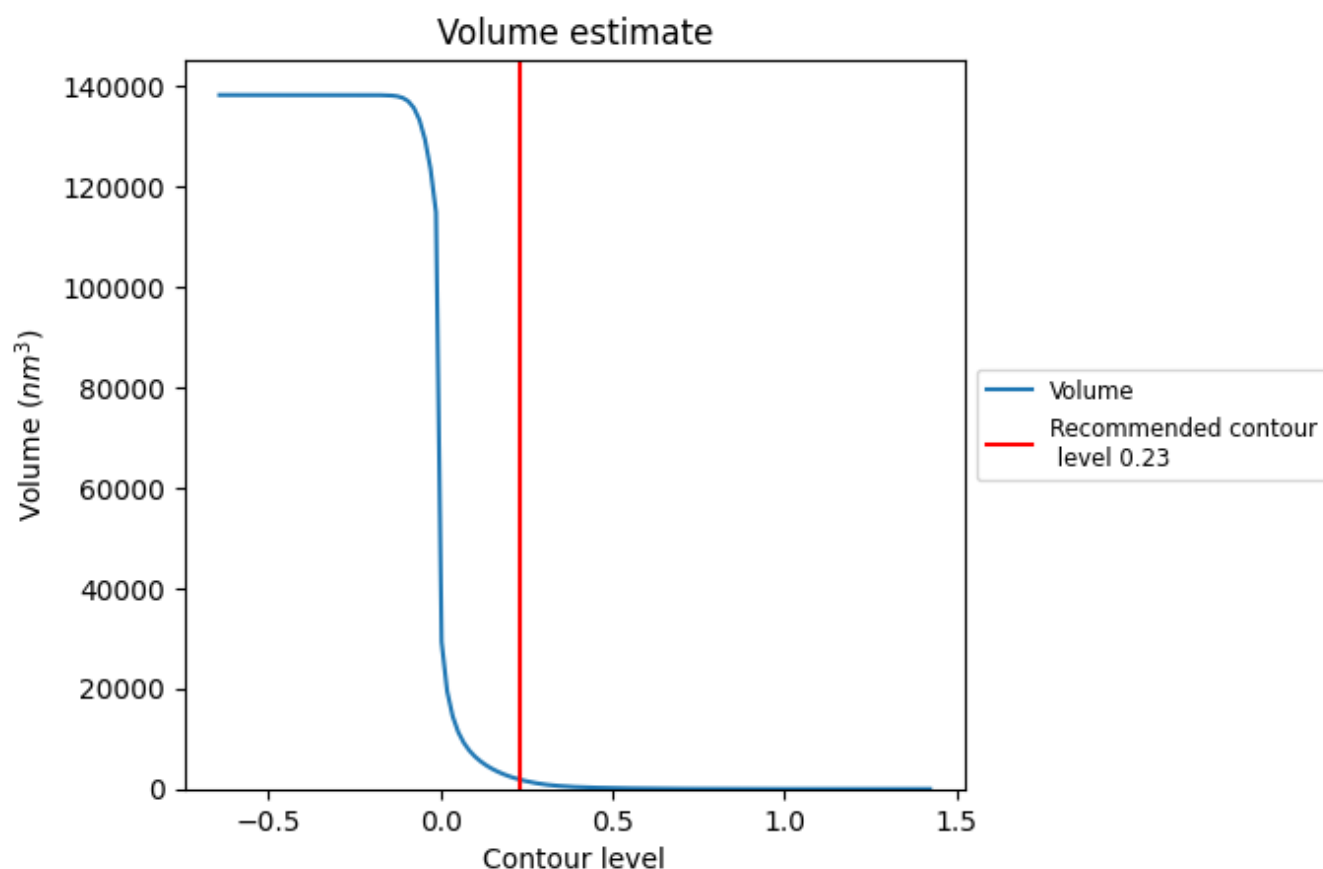
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

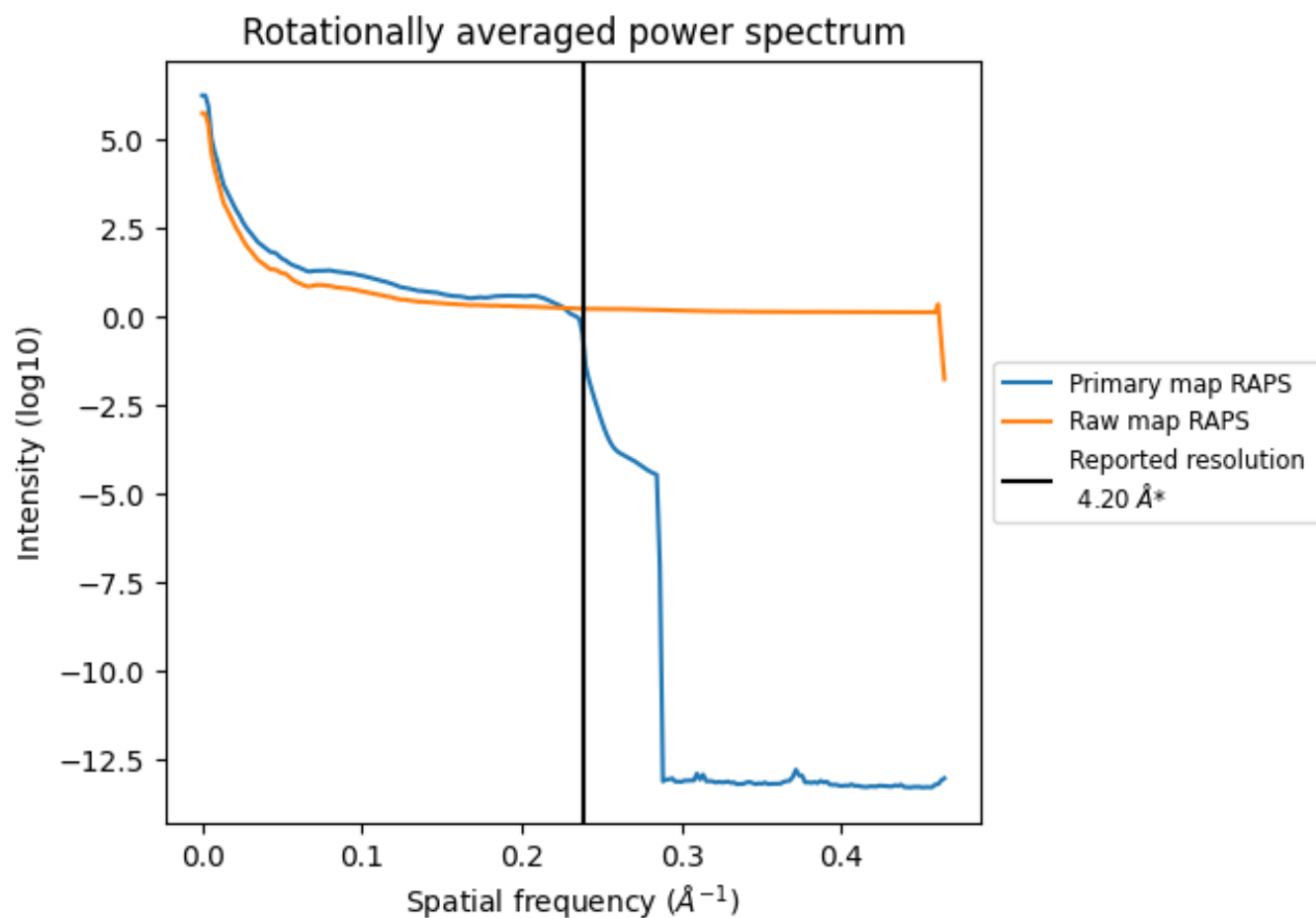
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1882 nm^3 ; this corresponds to an approximate mass of 1700 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

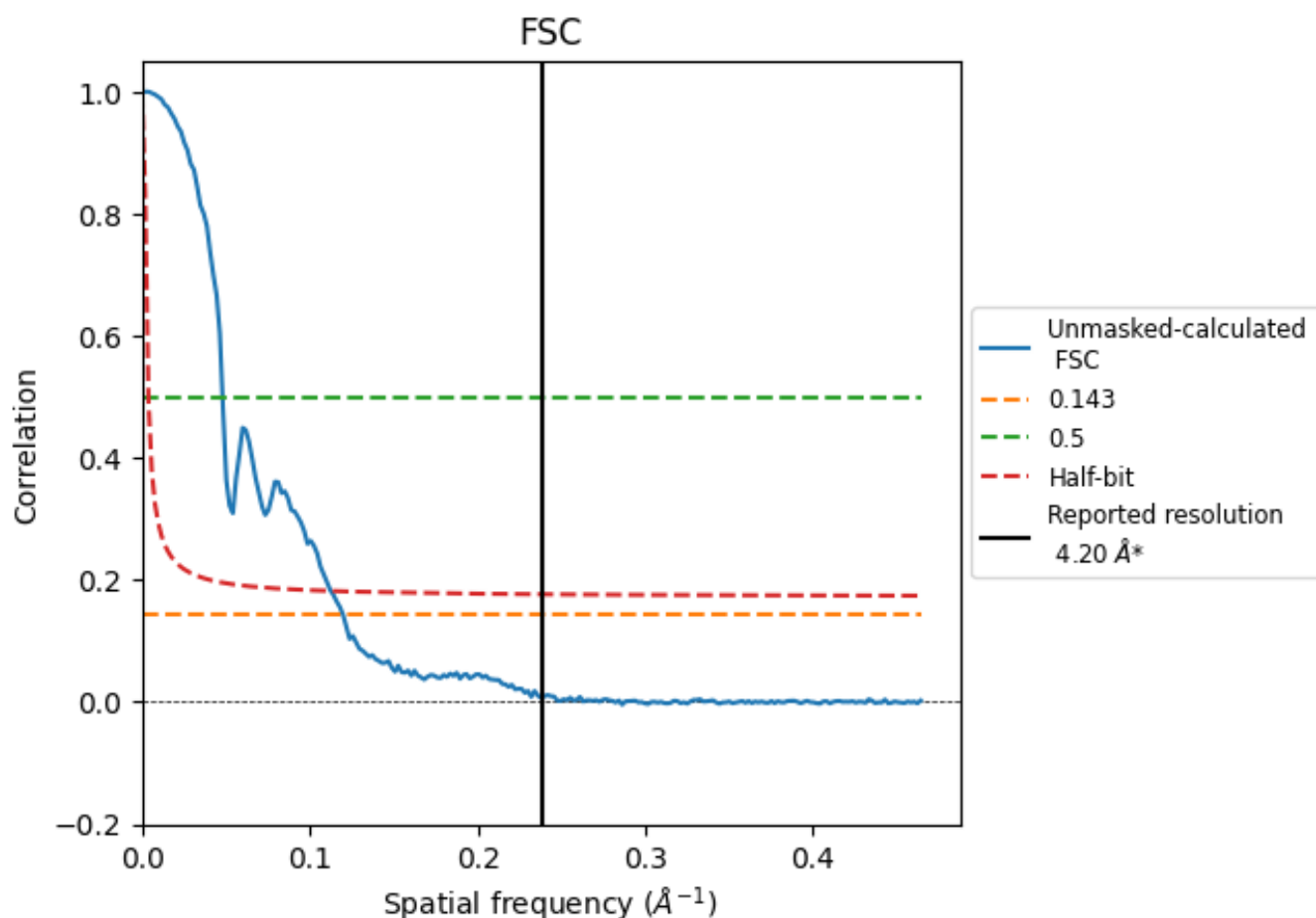


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.35	20.83	8.88

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.35 differs from the reported value 4.2 by more than 10 %

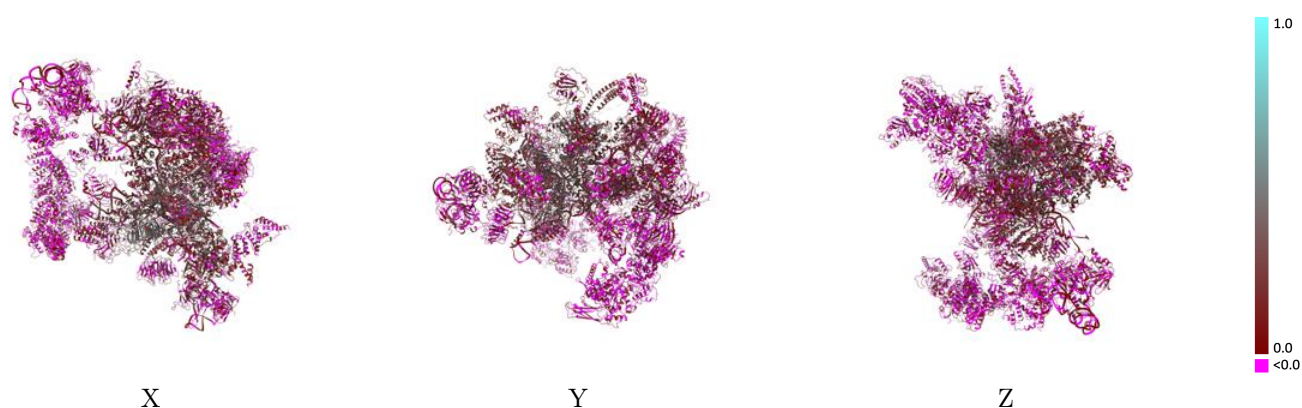
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35108 and PDB model 8I0S. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

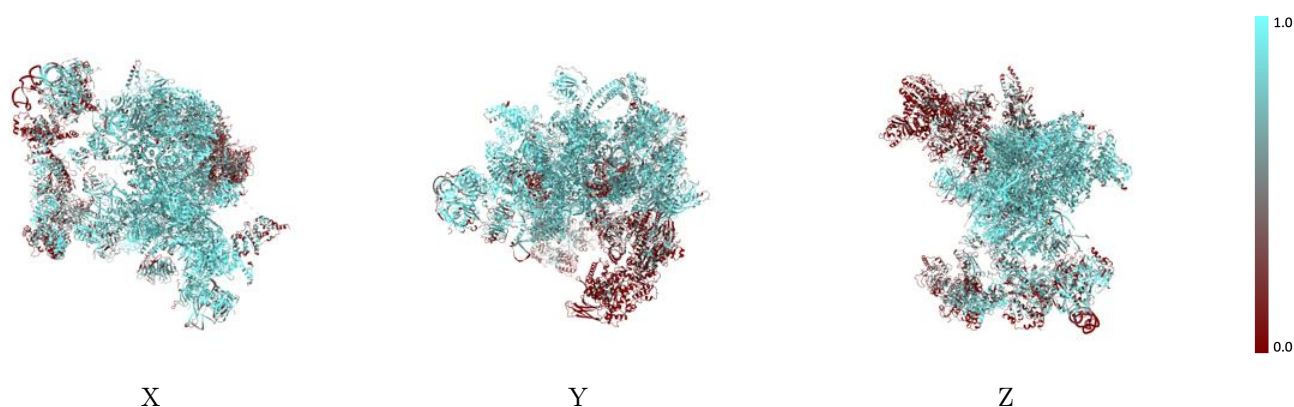
This section was not generated.

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



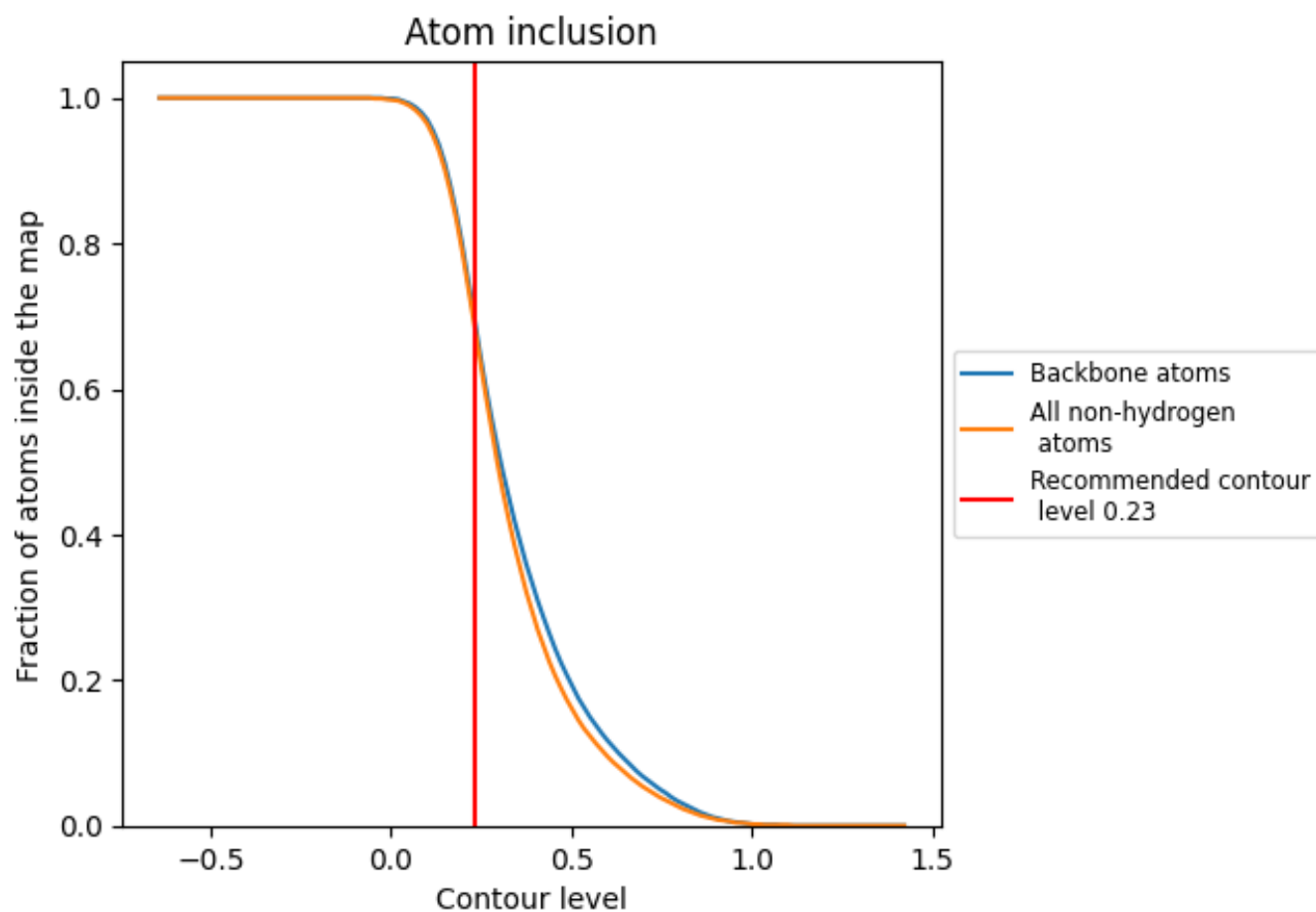
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 69% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6910	 0.1500
1	 0.8260	 0.1670
2	 0.7660	 0.1690
3	 0.8130	 0.1010
4	 0.7950	 0.1090
5	 0.7970	 0.1510
7	 0.8350	 0.1360
9	 0.7080	 0.1070
A	 0.7710	 0.2800
B	 0.8870	 0.2130
C	 0.8870	 0.2460
D	 0.1440	 0.0090
E	 0.5050	 0.0060
F	 0.8820	 0.2120
G	 0.8800	 0.1740
H	 0.6840	 0.0940
I	 0.6980	 0.0410
J	 0.8680	 0.2330
K	 0.7200	 0.1860
L	 0.7620	 0.2020
N	 0.7390	 0.1910
O	 0.7870	 0.1710
P	 0.8120	 0.2930
Q	 0.3560	 0.0320
R	 0.7710	 0.2270
S	 0.6420	 0.0810
T	 0.9300	 0.4050
U	 0.7620	 0.2050
V	 0.6430	 0.1150
X	 0.8030	 0.1600
Y	 0.8260	 0.1320
a	 0.7090	 0.0930
b	 0.8480	 0.0790
c	 0.7290	 0.0670
d	 0.7740	 0.0580



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Chain	Atom inclusion	Q-score
e	 0.8290	 0.0740
f	 0.6990	 0.0610
g	 0.8270	 0.0670
h	 0.6390	 0.0150
i	 0.6320	 0.0050
j	 0.6280	 0.0460
k	 0.5190	 0.0200
l	 0.5660	 0.0070
m	 0.5810	 0.0300
n	 0.6140	 -0.0020
o	 0.3680	 0.0010
p	 0.5760	 0.0540
u	 0.4830	 0.0420
v	 0.5610	 0.1100
w	 0.4710	 0.0410
y	 0.6460	 0.0790