



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:13 AM UTC

PDB ID : 8I0P / pdb_00008i0p
EMDB ID : EMD-35105
Title : The cryo-EM structure of human pre-Bact complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2023-01-11
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

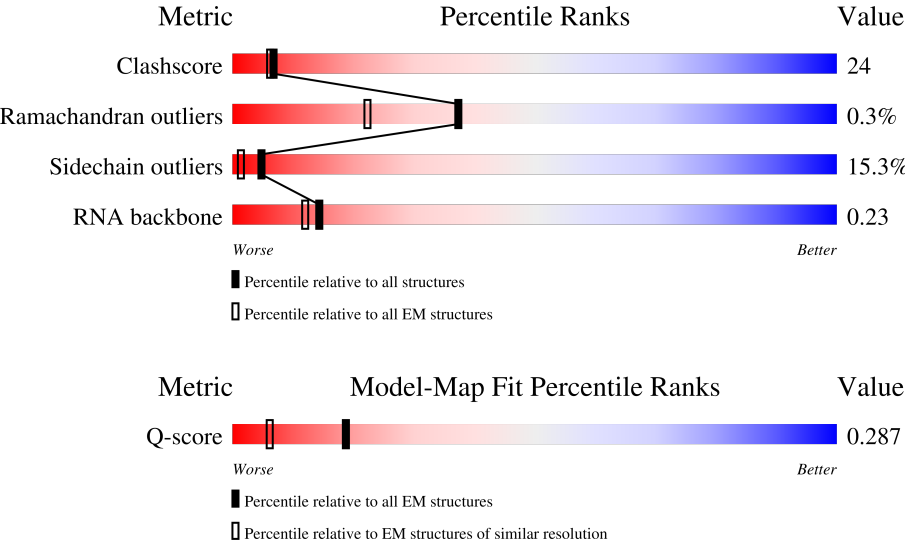
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	

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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	393	
12	L	802	
13	N	144	
14	O	420	
15	P	229	
16	Q	1485	
17	R	536	
18	T	514	
19	X	396	
20	Y	322	
21	Z	619	
22	1	1304	
23	3	1217	
24	o	255	
25	p	225	
26	c	118	
26	h	118	
27	d	86	

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Mol	Chain	Length	Quality of chain
27	i	86	
28	a	240	
28	m	240	
29	g	126	
29	l	126	
30	f	76	
30	k	76	
31	e	92	
31	j	92	
32	b	119	
32	n	119	
33	w	501	
34	u	793	
35	2	895	
36	4	424	
37	6	125	
38	7	110	
39	5	86	
40	9	520	
41	8	904	
42	y	301	
43	v	464	
44	z	25	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	SEP	1	129	-	-	X	-

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 103887 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	2149	Total	C	N	O	S	0	0
			16165	10296	2906	2900	63		

- 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	896	Total	C	N	O	S	0	0
			7077	4528	1176	1338	35		

- 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	95	Total	C	N	O	P	0	0
			2035	910	377	653	95		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	63	Total	C	N	O	P	0	0
			1321	592	217	449	63		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	165	Total	C	N	O	P	0	0
			3497	1562	600	1170	165		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	593	Total	C	N	O	0	0
			2991	1805	593	593		

- 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 DNA/RNA-binding protein KIN17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	312	Total	C	N	O	S	0	0
			2173	1338	413	412	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	99	Total	C	N	O	S	0	0
			829	532	149	144	4		

- Molecule 13 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	N	134	Total	C	N	O	0	0
			662	394	134	134		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	O	271	Total	C	N	O	0	0
			1340	798	271	271		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	42	Total	C	N	O	S	0	0
			362	231	63	66	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	192	Total	C	N	O	S	0	0
			1520	937	278	297	8		

- Molecule 18 is a protein called Pleiotropic regulator 1.

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

- Molecule 19 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	154	Total	C	N	O	S	0	0
			1279	819	231	227	2		

- Molecule 20 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	118	Total	C	N	O	S	0	0
			948	605	163	176	4		

- Molecule 21 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Z	55	Total	C	N	O	0	0
			439	282	85	72		

- Molecule 22 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	1	993	Total	C	N	O	P	S	0	0
			7845	5003	1360	1435	1	46		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1180	Total	C	N	O	S	0	0
			9240	5868	1569	1758	45		

- Molecule 24 is a protein called U2 small nuclear ribonucleoprotein A'.

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

- Molecule 25 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	p	169	Total	C	N	O	0	0
			851	513	169	169		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D2.

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

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

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

- Molecule 28 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	m	82	Total	C	N	O	0	0
			413	249	82	82		
28	a	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D3.

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

- Molecule 30 is a protein called Small nuclear ribonucleoprotein G.

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

- Molecule 31 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	j	81	Total	C	N	O	0	0
			403	241	81	81		
31	e	77	Total	C	N	O	0	0
			308	154	77	77		

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

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

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

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

- 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 Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	231	Total	C	N	O	S	0	0
			1651	1037	309	301	4		

- Molecule 36 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4	161	Total	C	N	O		0	0
			792	470	161	161			

- Molecule 37 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	6	109	Total	C	N	O	S	0	0
			906	582	157	163	4		

- Molecule 38 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	7	105	Total	C	N	O	S	0	0
			811	502	145	151	13		

- Molecule 39 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5	81	Total	C	N	O	S	0	0
			669	422	117	124	6		

- Molecule 40 is a protein called RING-type E3 ubiquitin-protein ligase PPIL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	9	384	Total	C	N	O	S	0	0
			2681	1665	484	524	8		

- Molecule 41 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	8	115	Total	C	N	O	S	0	0
			931	602	154	170	5		

- Molecule 42 is a protein called Peptidyl-prolyl cis-trans isomerase E.

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

- Molecule 43 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	166	Total	C	N	O	S	0	0
			997	576	211	207	3		

- Molecule 44 is a protein called Unknown polymer.

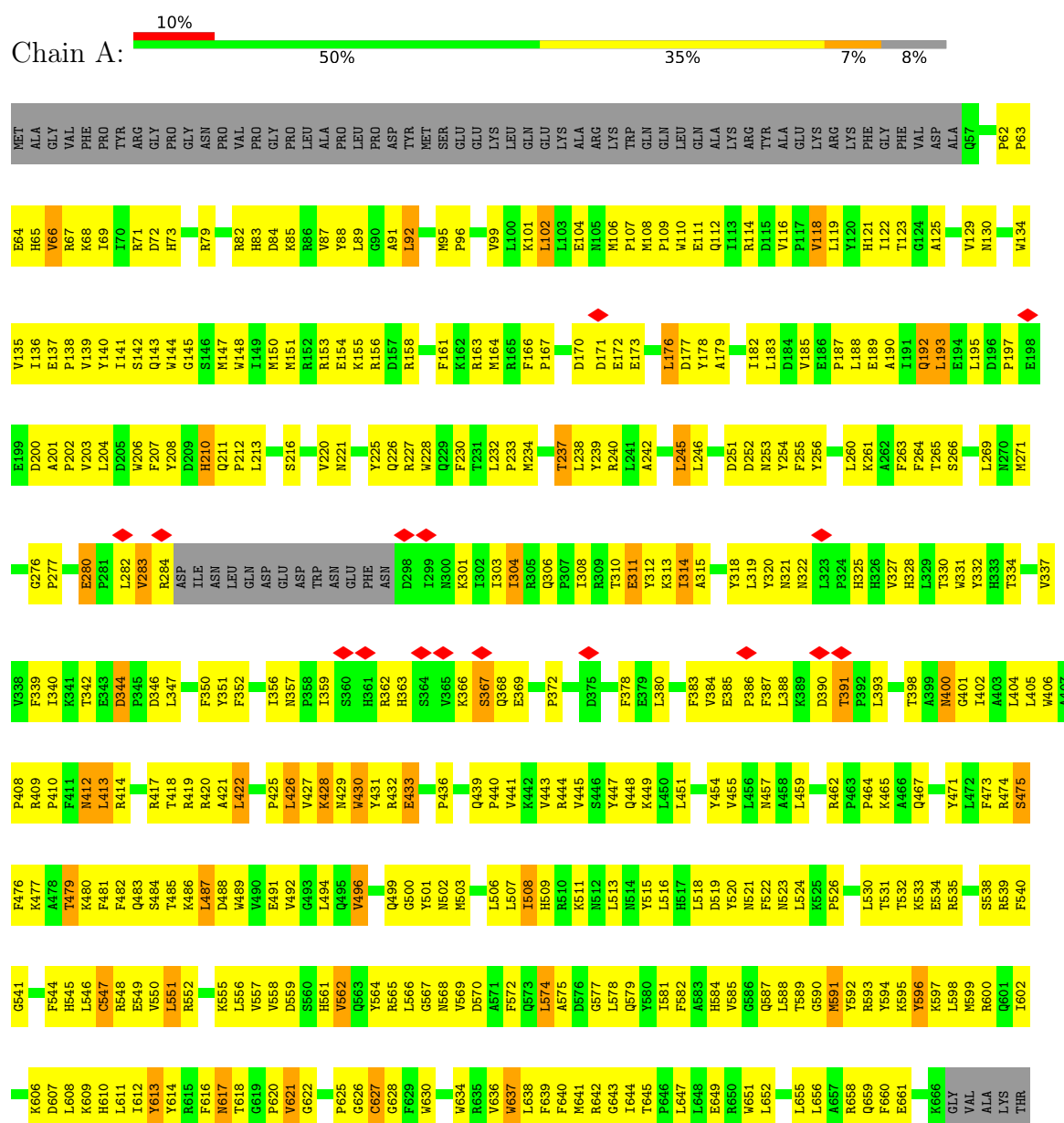
Mol	Chain	Residues	Atoms				AltConf	Trace
44	z	25	Total	C	N	O	0	0
			124	74	25	25		

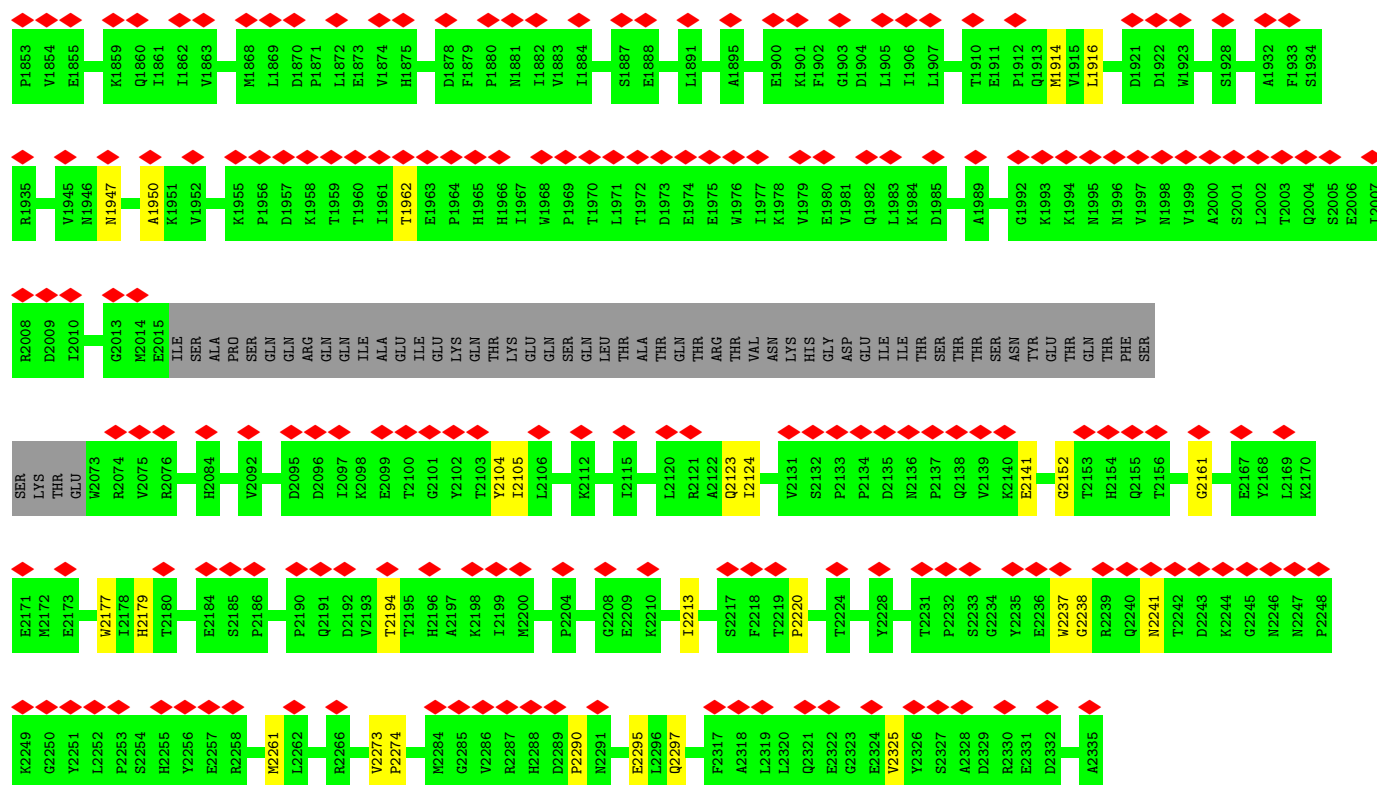
- Molecule 45 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

3 Residue-property plots

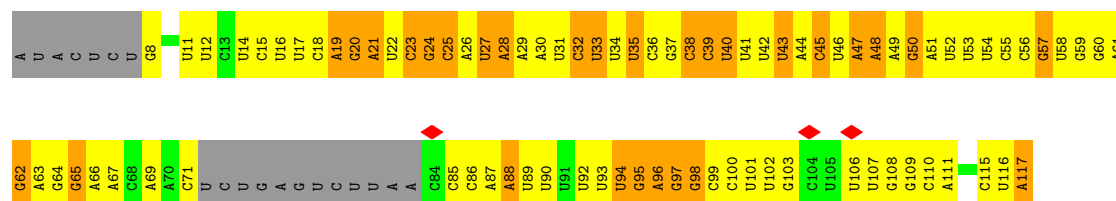
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

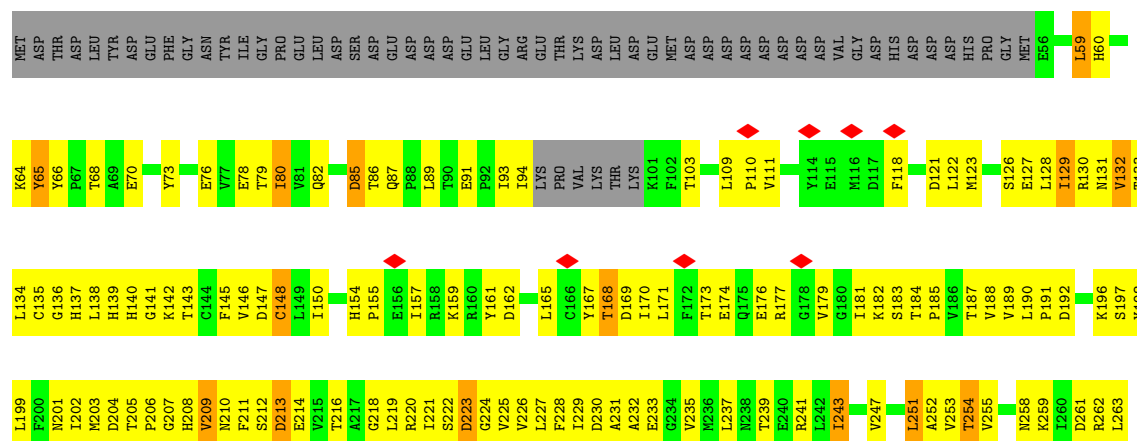




• Molecule 2: U5 snRNA

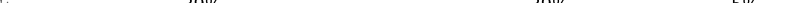


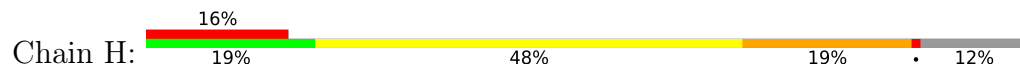
• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

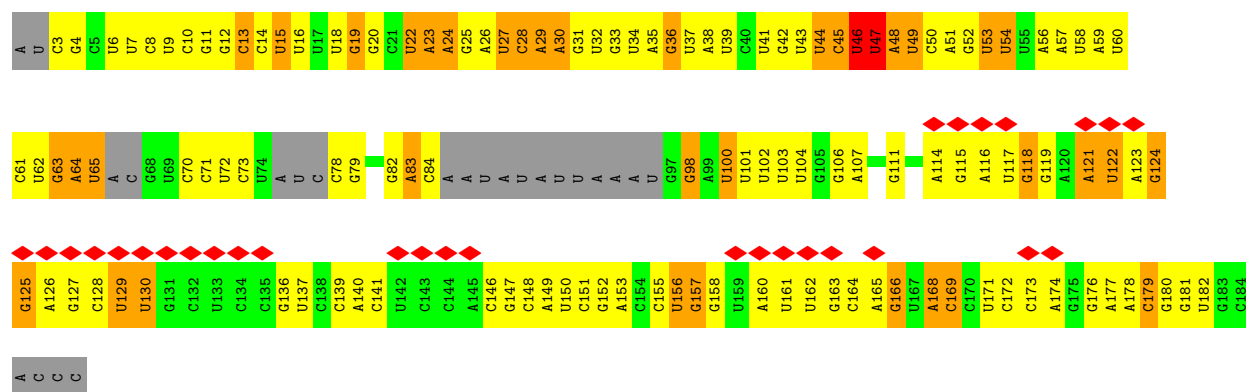




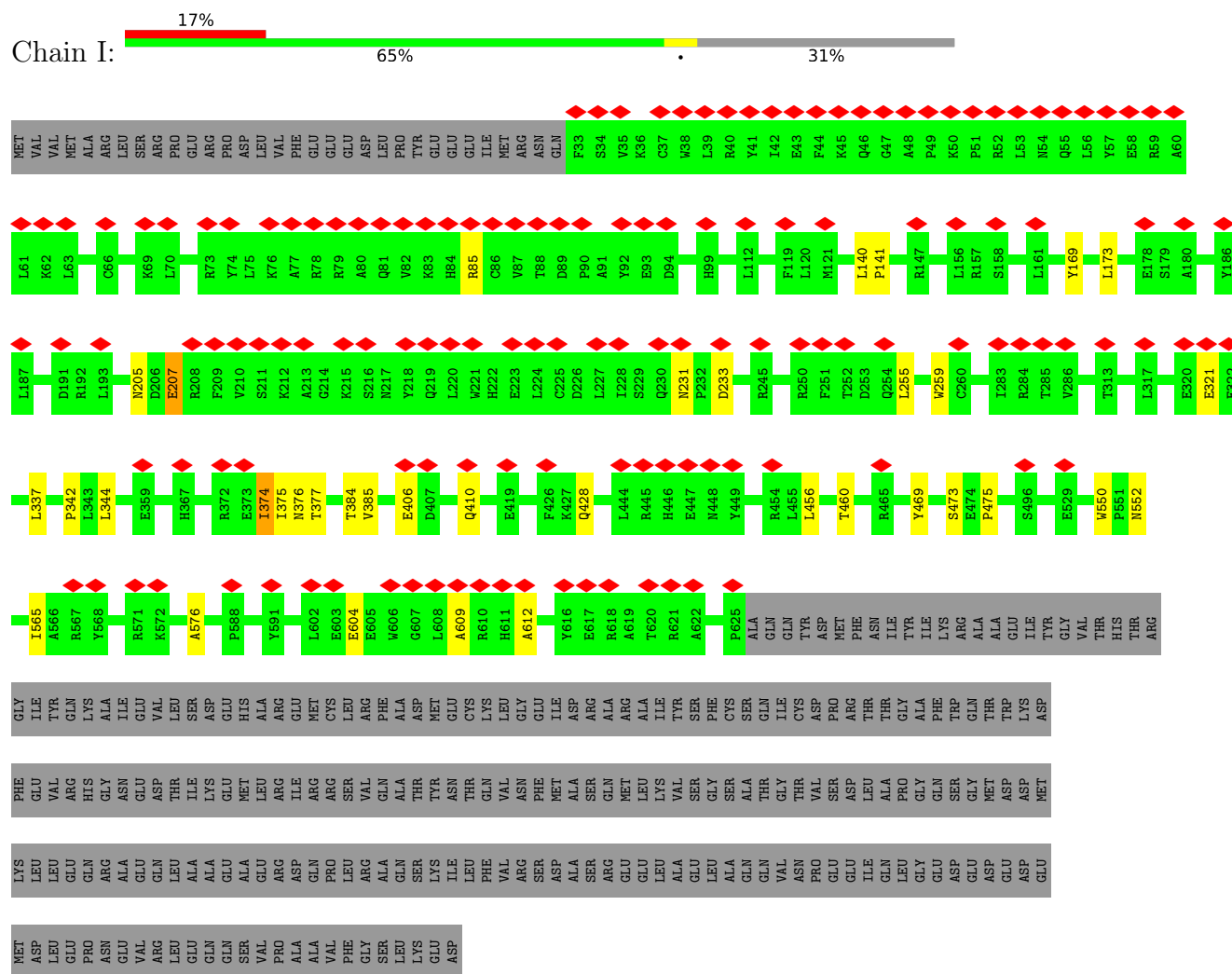
G2115	D1303	M1423	P1484	R1588	Q1667	D1750	A1811	A1872	W1935	A1995	L2055	G2115
C2116	L1304	I1424	I1485	F1589	Q1668	A1751	P1812	Q1873	L1936	L1996	P2056	C2116
D2117	Q1305	I1425	R1486	L1590	Y1668	W1752	L1813	K1874	S1937	L1997	P2057	D2117
Q2118	P1306	I1426	I1487	H1591	G1671	D1753	N1814	V1875	P1938	Q1998	Q2058	Q2118
E2119	L1307	S1427	V1488	C1592	Y1676	Y1754	L1815	H1876	L1939	L1999	K2059	E2119
V2120	P1308	T1428	A1489	E1594	Y1679	L1756	G1816	H1877	L1940	T2000	R2060	V2120
K2121	V1309	E1430	L1490	E1595	Y1679	W1757	M1817	K1878	A1941	D2001	E2061	K2121
F2122	A1311	K1431	S1491	D1596	Y1679	T1758	I1818	K1879	A1942	S2002	E2062	F2122
S2123	L1312	W1432	S1493	I1597	Y1682	F1759	A1820	N1880	M1943	Q2003	G2063	S2123
V2124	R1313	D1433	S1493	I1598	D1683	L1760	Y1821	N1881	E1944	L2004	W2064	V2124
D2125	R1314	I1434	S1495	I1599	L1684	Y1761	Y1822	P1882	L1945	A2005	W2065	D2125
VAL	S1315	L1435	M1496	Y1600	L1685	R1762	Y1823	F1884	A1946	D2006	V2066	VAL
LYS	S1316	S1436	A1497	L1601	Q1686	R1763	I1824	D1886	Q1947	V2007	P2067	LYS
GLU	A1317	R1437	K1498	E1602	Q1687	M1764	Y1825	D1887	M1948	A2008	I2068	GLU
ALA	C1376	R1438	V1500	K1603	V1688	T1765	T1827	V1888	V1949	R2009	G2069	ALA
GLU	Y1377	W1439	V1500	D1606	G1689	Q1766	T1828	H1888	T1950	F2010	D2070	GLU
THR	Y1378	K1440	A1501	D1607	H1690	N1769	T1829	V1889	Q1951	C2011	A2071	THR
ASP	T1379	Q1441	H1502	T1607	A1691	Y1770	I1829	K1890	A1952	N2012	K2072	ASP
ASP	P1381	R1442	W1503	T1608	N1692	Y1771	E1830	T1891	M1953	R2013	S2073	ASP
SER	E1383	K1443	L1504	L1609	P1693	M1772	L1831	N1892	W1954	Y2014	N2074	SER
SER	A1384	N1444	G1505	K1610	P1694	Q1773	F1832	L1893	S1955	P2015	S2075	SER
ASP	K1324	W1445	C1506	E1611	L1695	L1774	S1833	M1894	K1956	N2016	L2076	ASP
	F1325	Q1446	S1507	E1612	Q1696	Q1775	M1834	L1895	D1957	I2017	I2077	
	P1326	M1447	A1508	N1615	D1698	G1776	S1835	Q1896	S1958	E2018	S2078	
	F1327	I1448	Q1388	N1615	D1698	I1776	L1836	A1897	Y1959	L2019	I2079	
	F1328	V1389	V1390	Y1619	E1699	S1777	L1837	H1898	L1960	S2020	K2080	
	M1329	L1450	F1451	L1619	C1706	H1778	A1838	V1899	K1961	Y2021	R2081	
	P1330	F1452	V1452	L1624	Y1719	R1779	K1839	L1899	Q1962	E2022	L2082	
	I1331	V1453	D1454	S1625	E1720	H1781	L1781	S1900	L1963	V2023	T2083	
	Q1332	W1393	Y1394	P1626	Y1724	W1782	K1841	M1901	P1964	W2024	L2084	
	T1333	E1395	E1455	M1627	V1724	D1783	V1842	M1902	H1965	D2025	Q2085	
	Q1334	E1396	V1456	R1629	S1726	H1784	R1843	Q1903	F1966	K2026	Q2086	
	V1335	F1397	I1457	R1630	S1726	H1785	G1844	A1906	T1967	D2027	K2087	
	F1336	Q1398	M1337	L1631	H1727	L1786	L1845		S1968	S2028	A2088	
	M1337	D1399	T1338	V1632	L1728	E1787	I1846		E1969	I2029	K2089	
	V1339	R1400	V1340	E1633	D1729	L1788	E1847		H1970	R2030	V2090	
	N1341	L1401	N1402	Q1634	H1730	L1789	I1848		I1971	S2031	K2091	
	S1342	K1403	K1404	L1635	C1731	E1790	I1849		K1972	G2032	L2092	
	D1343	P1465	V1466	F1636	M1732	Q1791	S1850		A1973	G2033	D2093	
	D1344	V1467	L1467	S1637	H1733	L1793	N1851		C1974	P2034	F2094	
	M1345	E1468	A1549	A1640	D1734	L1793	A1852		T1975	V2035	V2095	
	V1346	V1469	I1550	I1641	W1735	S1794	E1853		D1976	V2036	A2096	
	L1407	I1470	T1551	Q1642	F1736	D1795	E1854		K1977	V2037	P2097	
	L1408	C1471	S1472	V1643	M1737	L1796	Y1855		G1978	L2038	A2098	
	V1348	C1471	S1472	V1644	A1738	E1797	I1858		V1979	V2039	T2099	
	G1349	R1473	M1474	V1644	A1739	Q1798	P1859		E1980	Q2040	G2100	
	A1350	R1473	M1474	R1648	I1740	S1799	I1860		S1981	L2041	A2101	
	P1351	T1412	R1475	P1558	V1741	K1800	R1861		V1982	E2042	H2102	
	G1352	T1414	Y1476	T1572	T1742	I1801	H1862		F1983	R2043	N2103	
	S1354	T1414	I1477	D1583	K1743	I1745	H1863		Q1924	E2044	T2105	
	G1355	D1415	I1478	I1584	N1655	L1746	E1864		C1926	E2045	L2106	
	K1356	L1416	S1478	Q1585	N1656	E1746	D1865		V1927	V2046	Y2107	
	T1357	K1417	S1479	Q1586	A1657	M1747	D1866		D1928	T2047	F2108	
	I1358	L1418	Q1480	Q1587	A1658	K1748	N1867		N1929	G2049	M2109	
	C1359	L1419	I1481	R1586	H1659	Q1749	L1868		L1930	P2050	S2110	
	A1360	G1420	E1482				R1869		S1931	D2051	D2111	
	E1361	K1421	R1483				Q1970		N1932	T2052	A2112	
	F1362	L1422					L1871		G1934	A2053	Y2113	
										P2054	M2114	

- Chain E: 

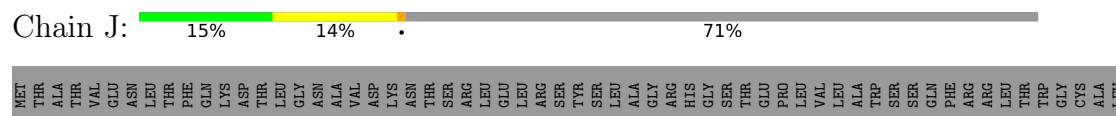


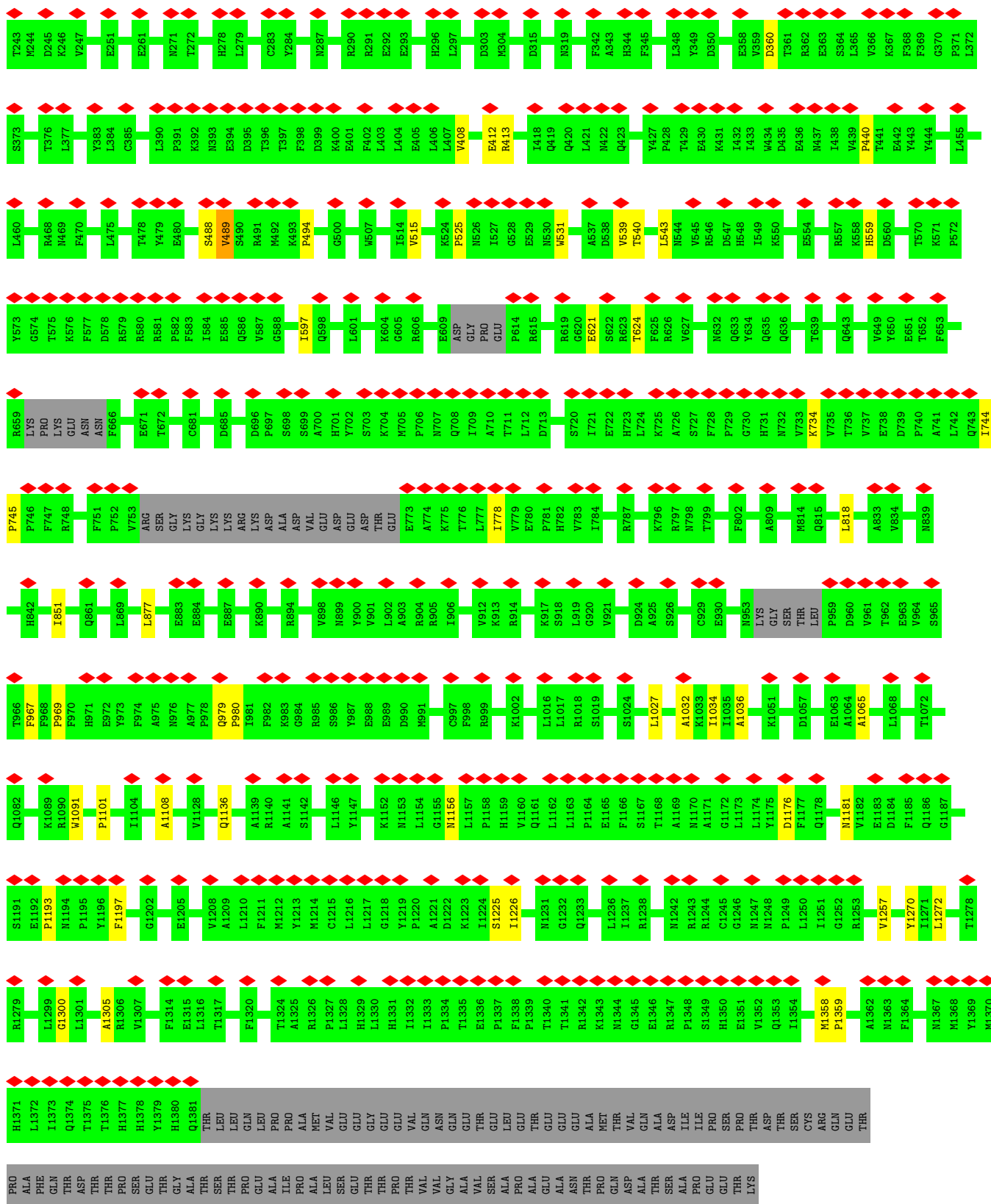


• Molecule 9: Pre-mRNA-splicing factor SYF1



• Molecule 10: Crooked neck-like protein 1





• Molecule 17: SNW domain-containing protein 1

Chain R:

20%

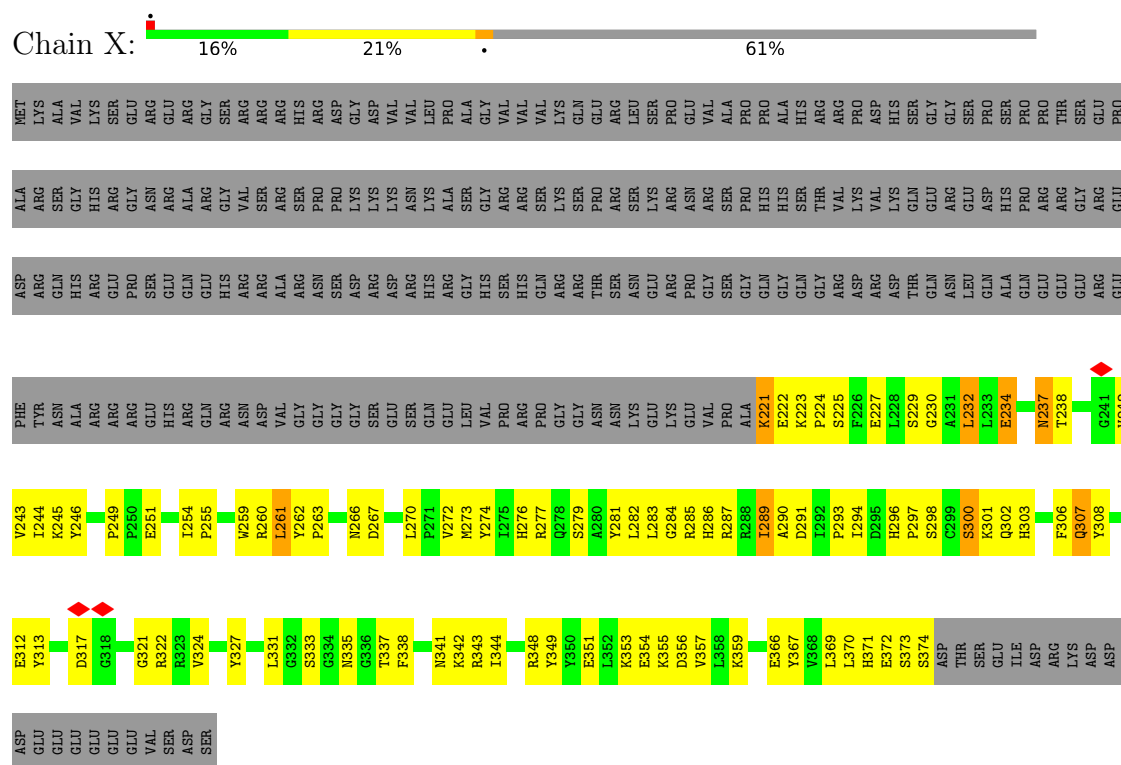
12%

.

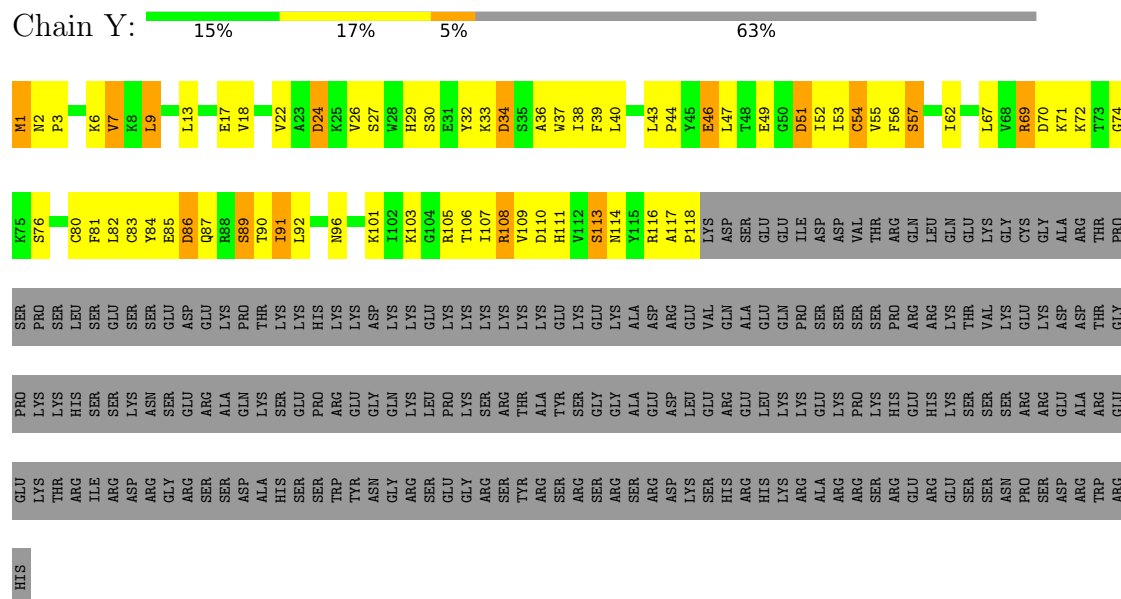
64%



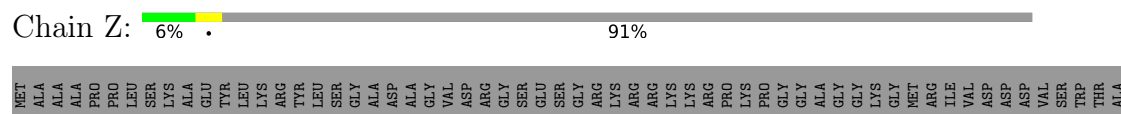
• Molecule 19: Smad nuclear-interacting protein 1

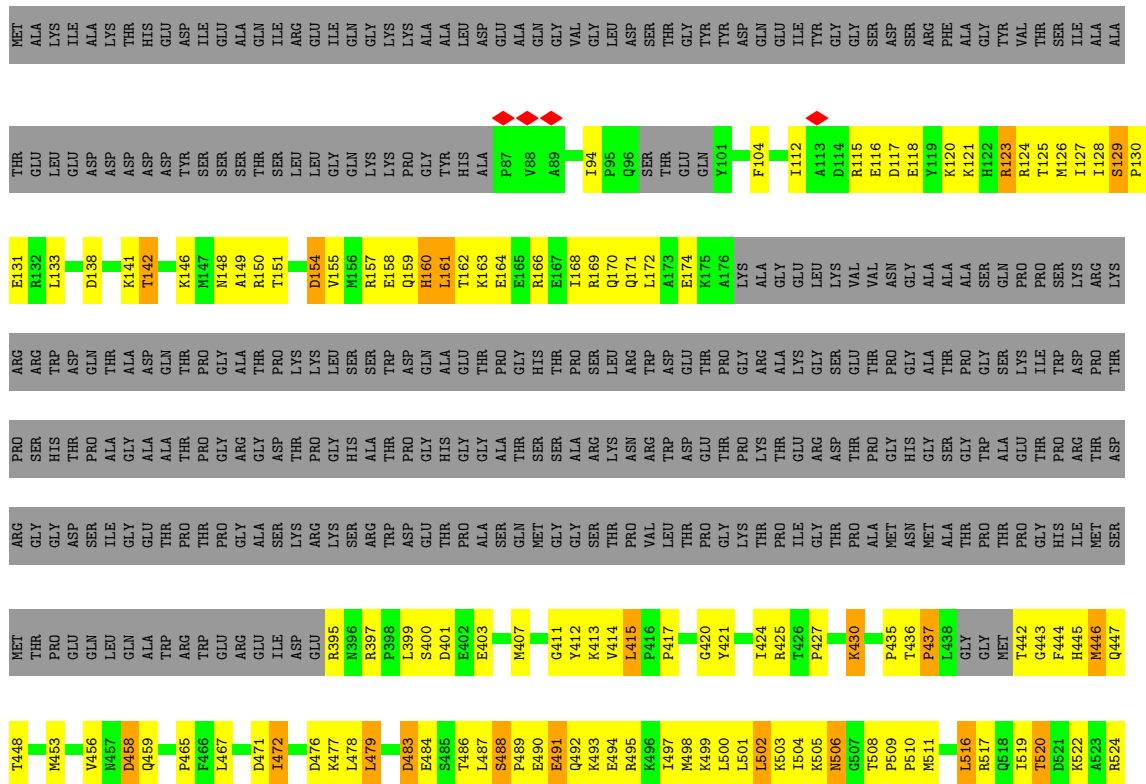


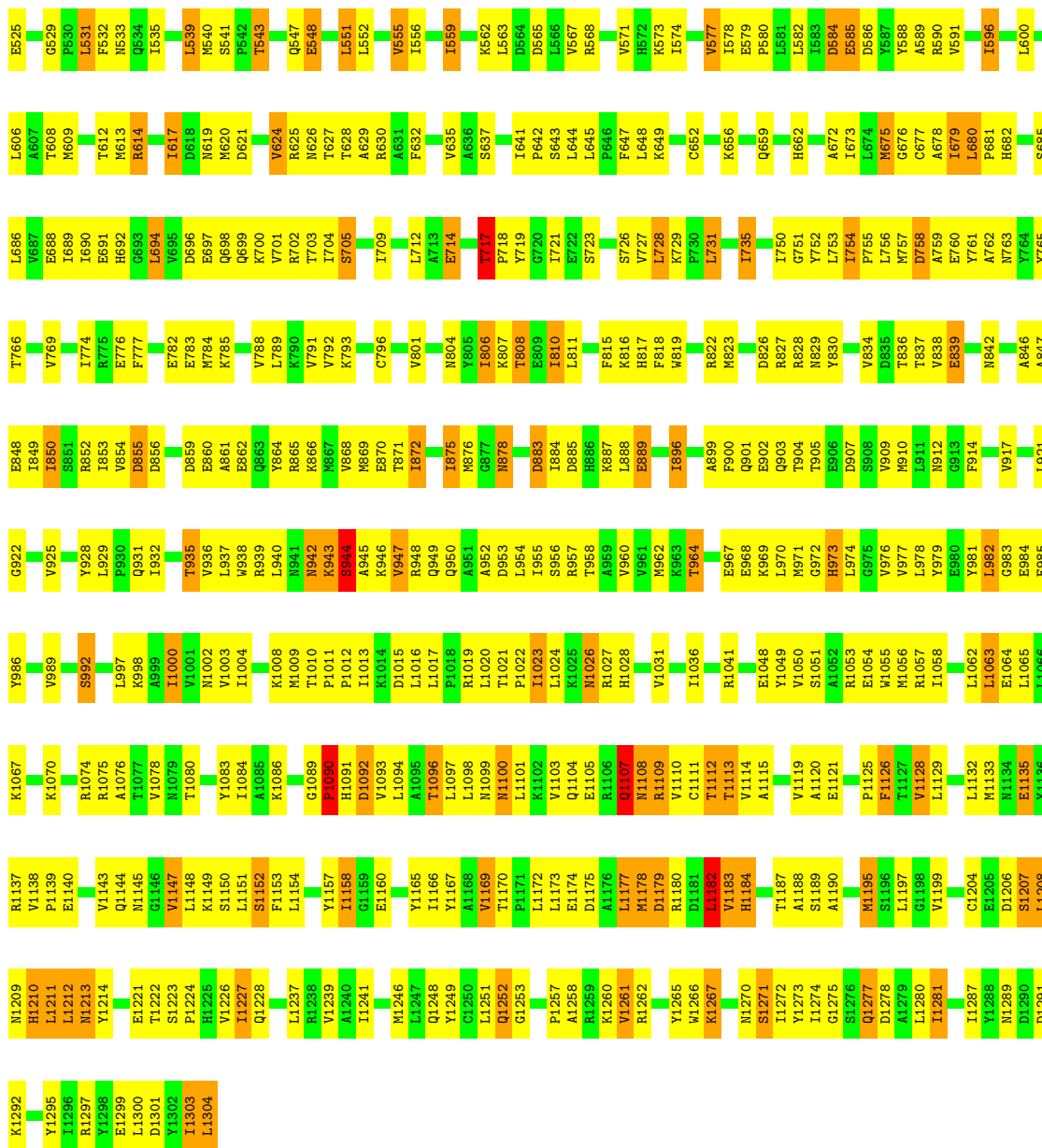
• Molecule 20: RNA-binding motif protein, X-linked 2



• Molecule 21: BUD13 homolog

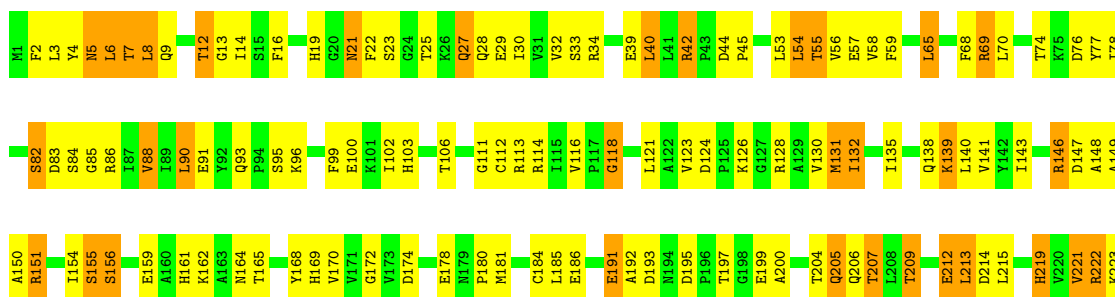


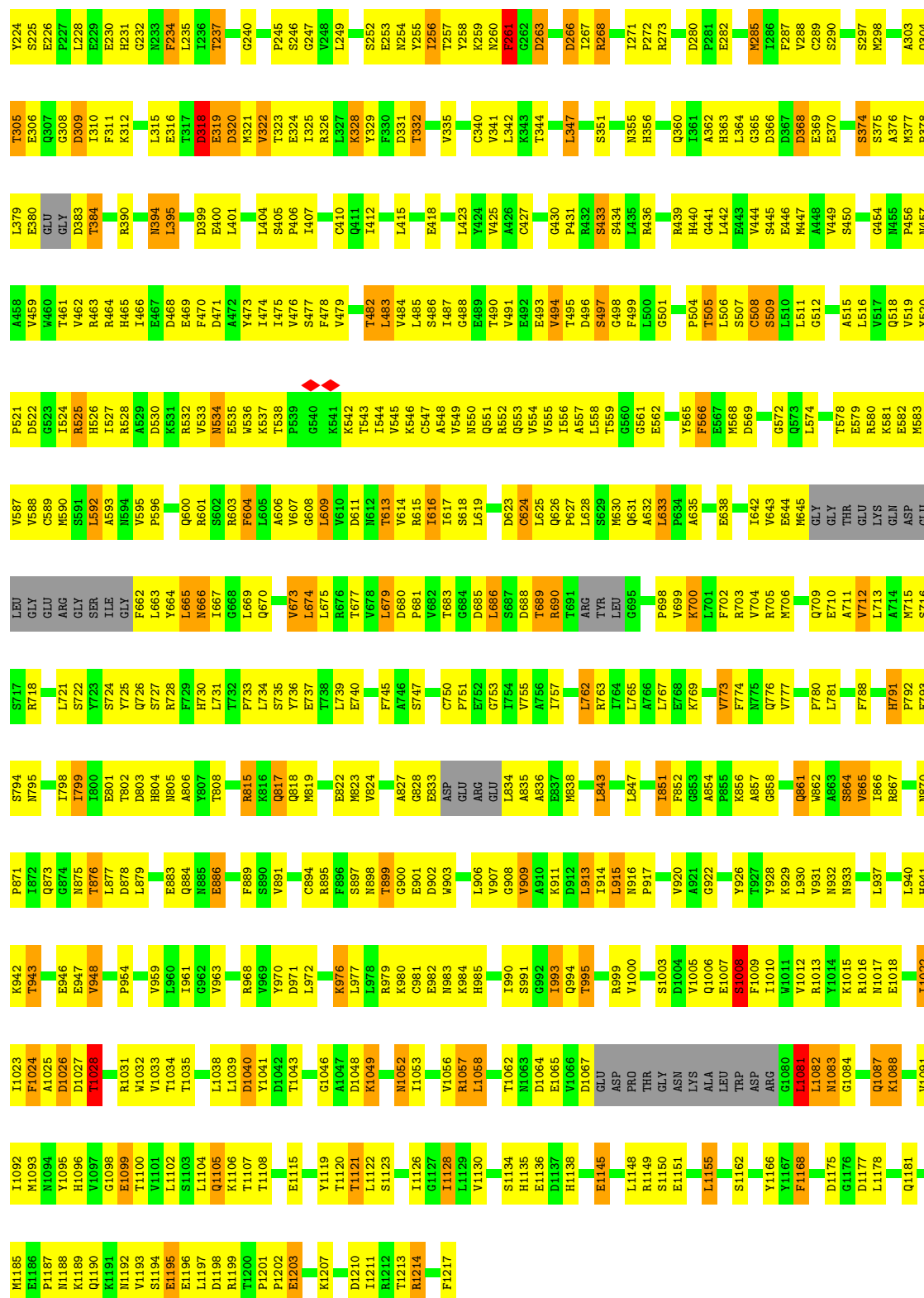




• Molecule 23: Splicing factor 3B subunit 3

Chain 3: 41% 46% 10%





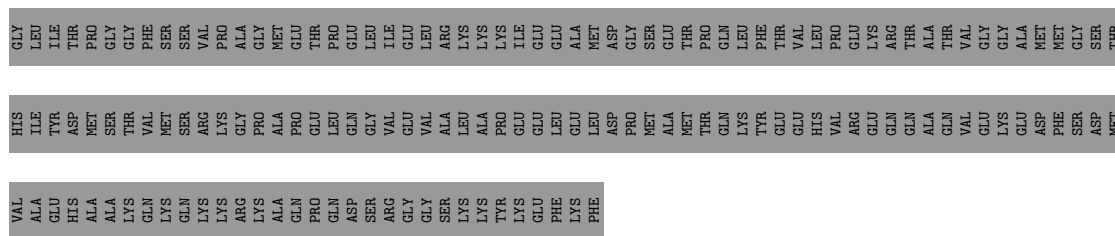
● Molecule 24: U2 small nuclear ribonucleoprotein A'



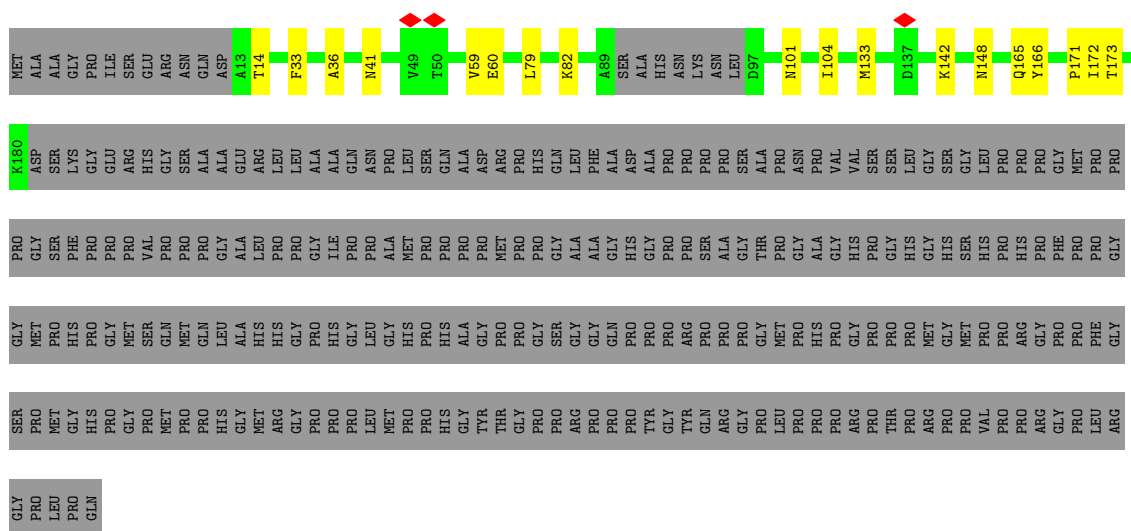
MET	SER	PRO	ALA
LEU	MET	PRO	PRO
ALA	MET	PRO	THR
GLY	PRO	PRO	ILE
GLN	GLU	SER	THR
LYS	GLU	ALA	SER
LEU	PHE	PRO	VAL
GLN	LEU	ILE	ARG
TYR	ARG	MET	PRO
GLU	ARG	ALA	PRO
GLY	ASN	PRO	THR
ILE	LYS	ARG	MET
PHE	GLY	PRO	PRO
ILE	PRO	PRO	PRO
LYS	VAL	PRO	PRO
ASP	SER	MET	VAL
SER	ILE	ILE	ARG
ASN	LYS	VAL	THR
LEU	VAL	PRO	THR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

- Molecule 35: Splicing factor 3B subunit 2

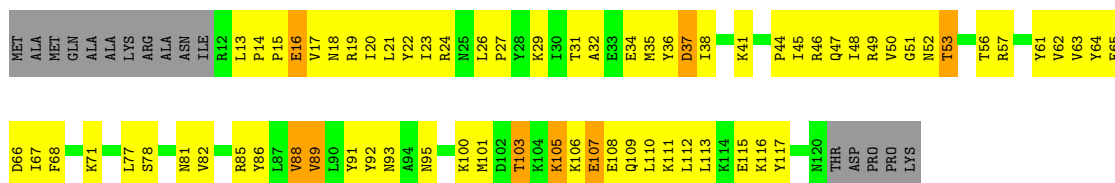
[illegible]



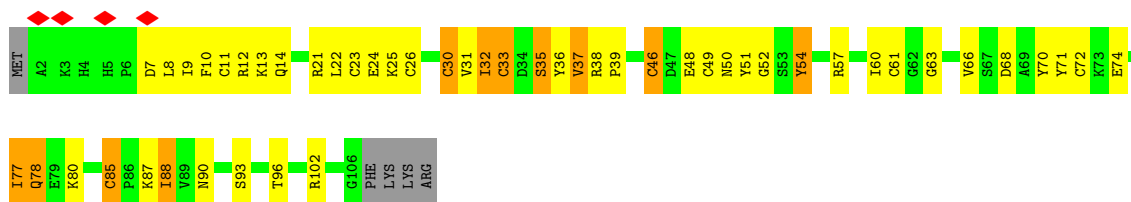
- Molecule 36: Splicing factor 3B subunit 4



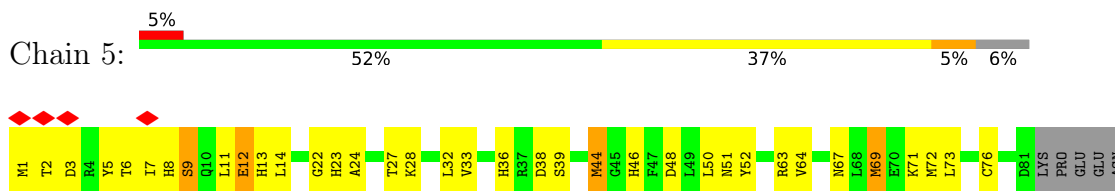
- Molecule 37: Splicing factor 3B subunit 6



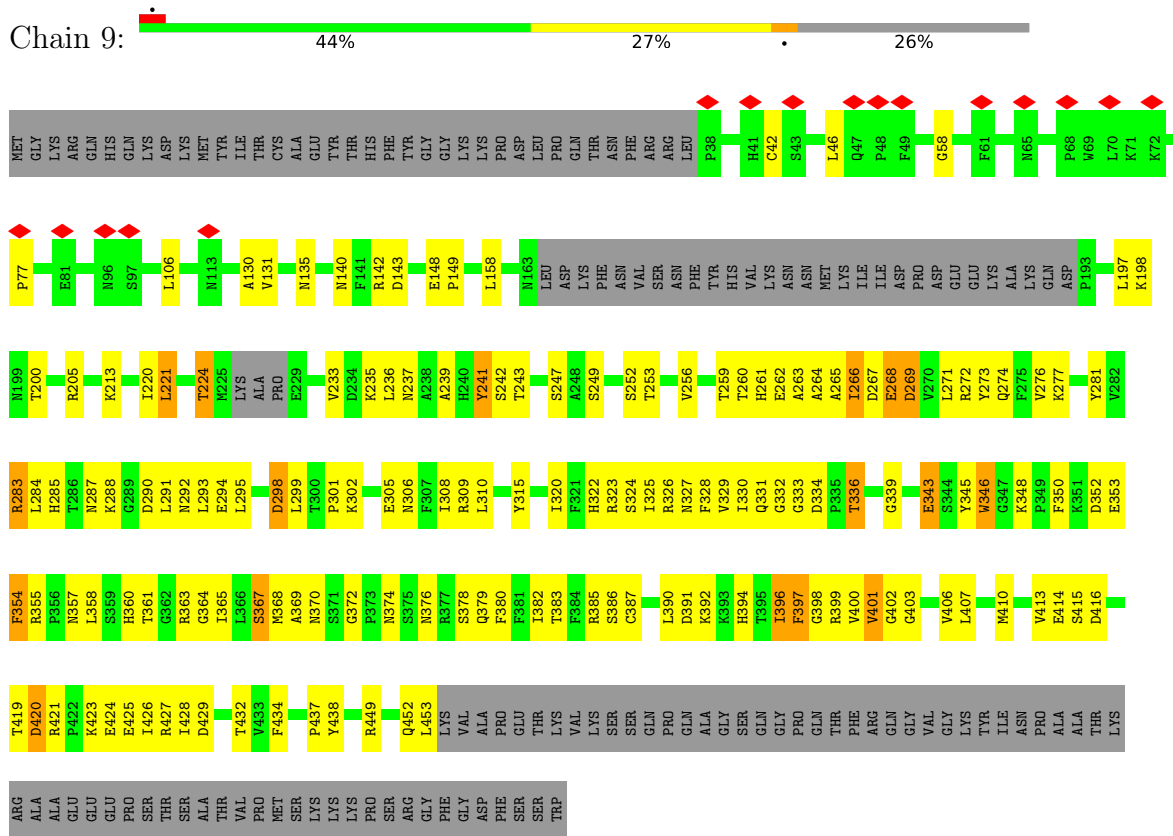
- Molecule 38: PHD finger-like domain-containing protein 5A



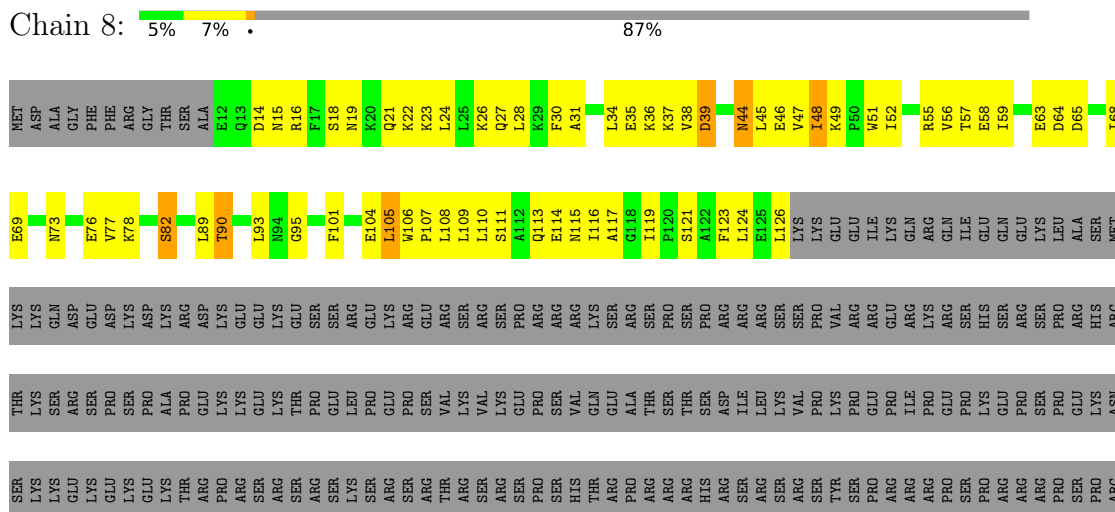
- Molecule 39: Splicing factor 3B subunit 5



- Molecule 40: RING-type E3 ubiquitin-protein ligase PPIL2

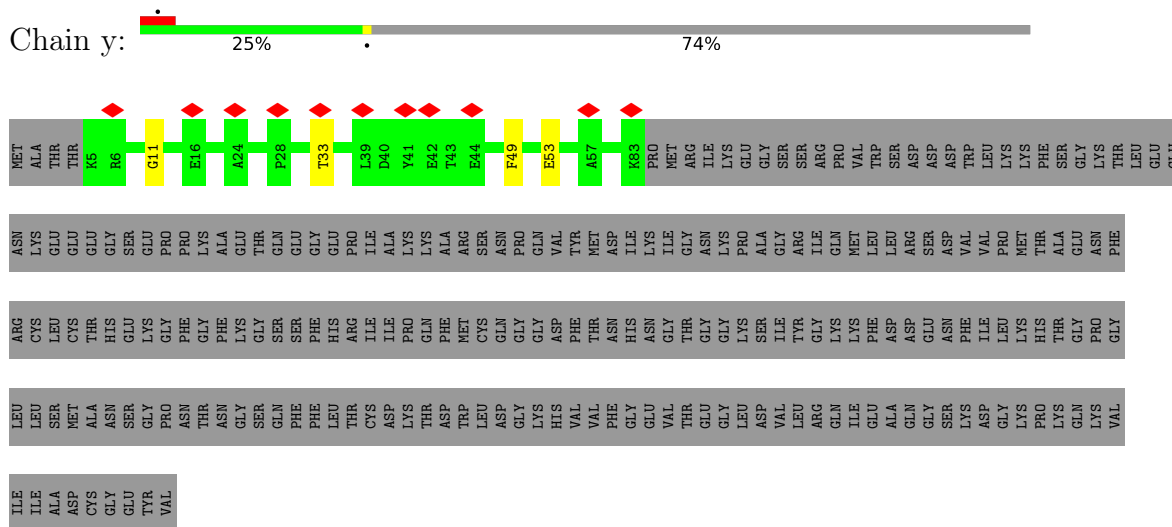


- Molecule 41: Serine/arginine repetitive matrix protein 1

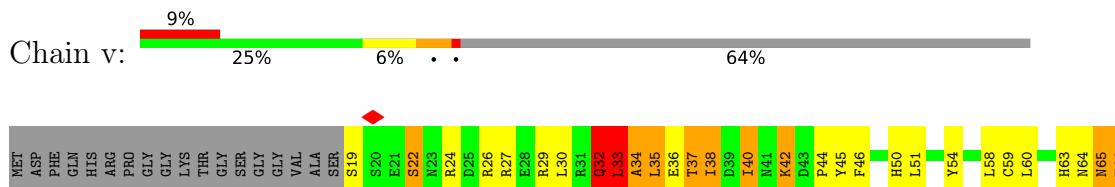


ALA	GLU	ARG	SER	ALA	PRO	ALA	PRO	GLY	THR	GLU	THR	THR	ARG
PRO	GLY	ARG	PRO	SER	PRO	SER	PRO	ARG	GLY	ARG	GLY	ARG	ARG
GLU	GLY	VAL	ARG	PRO	PRO	PRO	PRO	ARG	PRO	THR	THR	THR	ARG
PRO	GLY	SER	PRO	SER	ARG	PRO	ARG	ARG	GLY	SER	GLY	LEU	PRO
LYS	LYS	SER	ALA	PRO	ALA	PRO	ARG	ARG	PRO	SER	PRO	PRO	ARG
GLY	LYS	ARG	PRO	PRO	PRO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

- Molecule 42: Peptidyl-prolyl cis-trans isomerase E



- Molecule 43: Splicing factor 3A subunit 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46696	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	2.456	Depositor
Minimum map value	-1.255	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.19	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: SEP, ZN, MG, GTP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.68	6/16545 (0.0%)	0.76	27/22533 (0.1%)
2	B	0.26	0/2303	0.46	0/3579
3	C	0.26	0/7237	0.55	0/9834
4	D	0.18	0/8527	0.47	0/11887
5	E	0.24	0/2392	0.54	0/3242
6	F	0.30	0/2279	0.56	0/3551
7	G	0.43	0/1470	0.65	0/2281
8	H	0.34	0/3900	0.52	6/6065 (0.1%)
9	I	0.22	0/3013	0.62	0/4223
10	J	0.26	0/2171	0.56	0/2929
11	K	0.47	0/2203	0.81	0/2983
12	L	0.69	0/850	0.73	0/1146
13	N	0.19	0/661	0.42	0/919
14	O	0.20	0/1338	0.45	0/1861
15	P	0.65	0/369	0.83	0/489
16	Q	0.18	0/6796	0.43	0/9527
17	R	0.56	0/1544	0.84	3/2074 (0.1%)
18	T	0.64	0/2574	0.74	1/3511 (0.0%)
19	X	0.31	0/1312	0.57	0/1769
20	Y	0.54	0/966	0.58	0/1303
21	Z	0.40	0/455	0.59	0/617
22	1	0.83	11/7983 (0.1%)	0.88	19/10805 (0.2%)
23	3	0.94	1/9428 (0.0%)	0.87	13/12794 (0.1%)
24	o	0.19	0/821	0.47	0/1149
25	p	0.26	0/857	0.48	0/1196
26	c	0.19	0/387	0.53	0/482
26	h	0.21	0/485	0.48	0/677
27	d	0.18	0/295	0.49	0/367
27	i	0.19	0/362	0.48	0/502
28	a	0.19	0/335	0.54	0/417
28	m	0.22	0/416	0.53	0/581
29	g	0.18	0/322	0.48	0/399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	l	0.21	0/417	0.44	0/581
30	f	0.17	0/295	0.45	0/367
30	k	0.20	0/366	0.49	0/509
31	e	0.17	0/307	0.50	0/382
31	j	0.20	0/403	0.45	0/561
32	b	0.18	0/327	0.47	0/407
32	n	0.20	0/404	0.56	0/564
33	w	0.71	2/2311 (0.1%)	1.17	19/3008 (0.6%)
34	u	0.18	0/842	0.38	0/1110
35	2	1.28	21/1679 (1.3%)	1.71	31/2267 (1.4%)
36	4	0.22	0/790	0.51	0/1095
37	6	0.40	0/925	0.57	0/1247
38	7	0.70	1/825 (0.1%)	0.73	0/1106
39	5	1.07	0/688	0.86	0/930
40	9	0.29	0/2723	0.57	0/3697
41	8	0.46	0/946	0.59	0/1270
42	y	0.18	0/389	0.45	0/540
43	v	1.10	9/1010 (0.9%)	1.59	23/1326 (1.7%)
All	All	0.57	51/106243 (0.0%)	0.71	142/146659 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	11
4	D	0	1
5	E	0	1
9	I	0	4
11	K	0	2
16	Q	0	1
22	1	0	8
23	3	0	3
33	w	0	1
35	2	0	1
40	9	0	1
43	v	0	1
All	All	0	35

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1	1090	PRO	N-CA	15.73	1.67	1.47
1	A	827	PHE	C-N	14.23	1.50	1.33
35	2	485	PRO	N-CA	13.35	1.65	1.47
33	w	496	LYS	C-O	12.57	1.38	1.24
35	2	510	TYR	C-O	12.53	1.39	1.24
43	v	93	ALA	C-N	10.84	1.51	1.34
35	2	499	PRO	C-O	-10.50	1.11	1.23
22	1	1211	LEU	C-O	-8.46	1.14	1.24
35	2	501	PRO	C-O	-8.19	1.14	1.23
35	2	487	LEU	C-O	-8.05	1.14	1.24
1	A	1312	PRO	C-O	-7.21	1.16	1.24
22	1	1212	LEU	C-O	-7.13	1.15	1.24
35	2	484	ASP	C-N	6.83	1.43	1.33
22	1	1208	LEU	C-O	-6.78	1.16	1.24
35	2	485	PRO	C-O	-6.76	1.15	1.24
1	A	824	PRO	C-O	-6.61	1.15	1.23
35	2	520	PRO	C-O	-6.55	1.19	1.24
35	2	488	LEU	C-O	-6.37	1.16	1.24
43	v	72	HIS	C-O	-6.36	1.16	1.24
38	7	85	CYS	C-N	-6.31	1.28	1.33
35	2	496	ASN	C-O	-6.16	1.14	1.24
35	2	497	SER	CA-CB	-6.09	1.43	1.53
33	w	498	GLN	N-CA	6.05	1.53	1.46
35	2	494	THR	C-O	-5.96	1.16	1.23
35	2	491	LEU	C-O	-5.95	1.16	1.24
43	v	80	THR	C-O	-5.92	1.17	1.24
35	2	500	VAL	C-O	-5.89	1.17	1.25
35	2	472	PRO	C-O	-5.86	1.16	1.24
22	1	1189	SER	CA-CB	-5.82	1.44	1.53
22	1	1190	ALA	C-O	-5.82	1.17	1.24
35	2	502	ARG	C-O	-5.80	1.16	1.24
22	1	1189	SER	C-O	-5.79	1.17	1.24
22	1	1214	TYR	C-O	-5.74	1.17	1.24
35	2	490	HIS	C-O	-5.62	1.17	1.24
1	A	826	PRO	C-O	-5.61	1.16	1.24
1	A	1313	PRO	C-O	-5.57	1.16	1.24
35	2	498	VAL	C-O	-5.52	1.17	1.23
35	2	506	PHE	C-O	-5.51	1.17	1.23
22	1	1090	PRO	C-O	-5.50	1.16	1.24
35	2	503	HIS	C-O	-5.45	1.16	1.24
43	v	68	SER	CA-CB	-5.41	1.44	1.53
43	v	34	ALA	C-O	-5.40	1.16	1.24
1	A	825	ILE	C-O	-5.39	1.18	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1	1182	LEU	C-O	-5.33	1.17	1.24
43	v	66	GLU	C-O	-5.30	1.17	1.24
43	v	68	SER	C-O	-5.29	1.18	1.24
35	2	492	LYS	C-O	-5.28	1.17	1.24
43	v	71	ALA	C-O	-5.28	1.18	1.24
22	1	1188	ALA	C-O	-5.22	1.17	1.24
43	v	78	HIS	C-O	-5.09	1.18	1.24
23	3	1025	ALA	C-O	-5.03	1.17	1.23

All (142) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	2	484	ASP	CA-C-N	18.14	138.10	119.24
35	2	484	ASP	C-N-CA	18.14	138.10	119.24
22	1	1089	GLY	CA-C-N	16.27	140.18	119.84
22	1	1089	GLY	C-N-CA	16.27	140.18	119.84
1	A	827	PHE	CA-C-N	14.15	134.95	120.38
1	A	827	PHE	C-N-CA	14.15	134.95	120.38
33	w	500	LEU	CA-C-N	-13.61	97.21	121.70
33	w	500	LEU	C-N-CA	-13.61	97.21	121.70
35	2	515	ARG	CA-C-N	11.75	133.19	120.03
35	2	515	ARG	C-N-CA	11.75	133.19	120.03
23	3	1026	ASP	CA-CB-CG	-11.06	101.53	112.60
35	2	516	GLY	N-CA-C	10.90	126.13	112.83
8	H	47	U	C4'-C3'-O3'	10.50	125.14	109.40
35	2	485	PRO	N-CA-C	-10.02	97.55	113.78
33	w	494	ASP	CB-CA-C	-9.80	95.50	110.88
35	2	587	HIS	CA-C-N	9.53	137.47	122.51
35	2	587	HIS	C-N-CA	9.53	137.47	122.51
8	H	46	U	C2'-C3'-O3'	9.22	123.34	109.50
23	3	1028	THR	CB-CA-C	-9.17	95.06	110.56
8	H	46	U	C3'-C2'-O2'	9.11	128.26	114.60
43	v	65	ASN	CB-CA-C	-8.73	95.34	110.45
35	2	494	THR	CB-CA-C	-8.67	94.85	109.50
33	w	497	ARG	N-CA-C	-8.67	101.78	111.14
43	v	35	LEU	N-CA-C	-8.66	101.79	111.14
33	w	498	GLN	CA-C-N	8.52	136.33	121.07
33	w	498	GLN	C-N-CA	8.52	136.33	121.07
35	2	502	ARG	CG-CD-NE	-8.52	93.25	112.00
35	2	514	LYS	CA-C-O	-8.44	111.87	120.90
33	w	499	GLY	CA-C-N	-8.35	105.60	121.54
33	w	499	GLY	C-N-CA	-8.35	105.60	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	1	1187	THR	CA-CB-OG1	-8.18	97.33	109.60
43	v	72	HIS	CB-CA-C	-7.83	97.79	110.79
35	2	502	ARG	CB-CA-C	-7.81	93.85	110.32
8	H	46	U	C4'-C3'-O3'	-7.74	97.79	109.40
33	w	496	LYS	O-C-N	7.60	129.94	122.03
43	v	36	GLU	CB-CA-C	-7.52	99.07	110.88
35	2	520	PRO	CB-CA-C	-7.51	104.11	111.17
1	A	1962	THR	CA-C-N	-7.45	110.69	120.67
1	A	1962	THR	C-N-CA	-7.45	110.69	120.67
43	v	75	GLY	O-C-N	7.42	129.90	123.37
1	A	824	PRO	CB-CA-C	-7.35	102.38	111.64
35	2	485	PRO	CA-N-CD	-7.34	101.72	112.00
33	w	500	LEU	O-C-N	7.33	132.33	122.59
1	A	1544	ARG	N-CA-C	-7.27	99.13	109.96
43	v	33	LEU	CA-C-O	-7.26	113.20	120.82
43	v	85	ARG	CB-CA-C	-7.23	97.25	110.63
22	1	1090	PRO	CA-N-CD	-7.07	102.10	112.00
22	1	1107	GLN	N-CA-C	-7.07	102.64	110.91
35	2	510	TYR	CA-C-O	7.06	130.60	120.51
23	3	431	PRO	CA-C-N	-7.00	111.46	122.73
23	3	431	PRO	C-N-CA	-7.00	111.46	122.73
35	2	597	PHE	CB-CA-C	-6.94	98.70	110.64
22	1	1187	THR	CB-CA-C	6.84	123.81	110.67
1	A	826	PRO	N-CA-CB	-6.76	96.15	103.25
22	1	1213	ASN	CB-CA-C	-6.70	99.67	110.79
22	1	1180	ARG	CA-C-N	-6.65	112.16	122.87
22	1	1180	ARG	C-N-CA	-6.65	112.16	122.87
1	A	1304	ASN	CA-CB-CG	6.58	119.18	112.60
35	2	492	LYS	CB-CA-C	-6.55	96.91	109.95
35	2	506	PHE	CB-CA-C	-6.54	100.02	109.84
17	R	144	THR	CB-CA-C	-6.40	100.84	110.88
35	2	493	ALA	CA-C-O	-6.33	112.25	119.78
43	v	73	THR	CA-CB-OG1	-6.32	100.12	109.60
33	w	477	GLU	CB-CA-C	-6.32	98.32	109.62
22	1	1180	ARG	N-CA-C	6.30	118.96	111.71
1	A	1551	PHE	CB-CA-C	-6.20	96.68	110.19
1	A	1546	ASN	N-CA-C	-6.17	104.24	110.97
22	1	1180	ARG	CA-C-O	-6.16	113.14	120.10
35	2	510	TYR	CB-CA-C	6.15	122.67	110.42
35	2	544	GLU	CA-C-N	6.12	128.47	120.28
35	2	544	GLU	C-N-CA	6.12	128.47	120.28
1	A	692	ASP	CA-C-N	-6.07	112.79	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	692	ASP	C-N-CA	-6.07	112.79	120.56
33	w	473	PRO	CB-CA-C	-6.05	103.44	113.06
1	A	428	LYS	CA-C-N	-6.04	112.58	122.54
1	A	428	LYS	C-N-CA	-6.04	112.58	122.54
43	v	66	GLU	N-CA-C	-5.99	104.83	111.36
43	v	73	THR	CA-C-N	-5.96	113.39	122.21
43	v	73	THR	C-N-CA	-5.96	113.39	122.21
23	3	1081	LEU	O-C-N	5.91	125.20	120.83
22	1	1189	SER	CA-C-O	-5.89	114.31	120.55
35	2	499	PRO	CB-CA-C	-5.88	103.71	111.23
22	1	1182	LEU	CA-C-O	-5.87	114.33	120.55
22	1	1183	VAL	CA-C-O	-5.83	114.89	120.95
1	A	1296	GLN	CB-CG-CD	-5.82	102.70	112.60
35	2	525	PRO	CB-CA-C	-5.81	104.18	111.56
22	1	1210	HIS	CB-CA-C	-5.75	101.07	110.85
33	w	497	ARG	CA-C-N	5.71	132.45	121.54
33	w	497	ARG	C-N-CA	5.71	132.45	121.54
1	A	1547	VAL	CA-C-O	-5.70	115.72	121.59
33	w	500	LEU	CA-C-O	-5.69	112.37	120.51
1	A	1133	CYS	CA-C-N	5.67	130.68	122.29
1	A	1133	CYS	C-N-CA	5.67	130.68	122.29
35	2	582	PRO	CB-CA-C	-5.64	102.25	111.56
33	w	470	ARG	CA-C-N	-5.63	115.17	123.05
33	w	470	ARG	C-N-CA	-5.63	115.17	123.05
43	v	34	ALA	N-CA-CB	5.62	118.77	110.56
33	w	501	LEU	N-CA-CB	5.59	120.01	110.50
35	2	474	VAL	N-CA-CB	-5.59	102.01	111.23
1	A	1299	ILE	N-CA-CB	5.54	118.90	110.58
43	v	80	THR	CB-CA-C	5.54	120.27	110.85
43	v	72	HIS	CA-C-O	-5.50	114.72	120.55
43	v	78	HIS	CA-C-N	5.47	128.06	120.29
43	v	78	HIS	C-N-CA	5.47	128.06	120.29
22	1	1209	ASN	CA-CB-CG	-5.46	107.14	112.60
43	v	34	ALA	CA-C-N	-5.46	113.02	120.44
43	v	34	ALA	C-N-CA	-5.46	113.02	120.44
22	1	944	SER	N-CA-C	5.45	119.48	111.04
8	H	47	U	N1-C1'-C2'	5.44	122.16	114.00
35	2	510	TYR	N-CA-CB	-5.40	101.37	110.49
1	A	821	ARG	CG-CD-NE	-5.37	100.18	112.00
1	A	1298	ARG	CG-CD-NE	-5.33	100.27	112.00
43	v	32	GLN	CB-CA-C	-5.32	100.78	110.63
23	3	1024	PHE	CA-C-O	-5.30	112.44	119.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	T	309	ASP	CB-CA-C	5.29	119.50	110.56
1	A	1547	VAL	CA-C-N	5.28	131.63	121.54
1	A	1547	VAL	C-N-CA	5.28	131.63	121.54
23	3	917	PRO	N-CA-C	-5.28	101.59	112.47
43	v	79	GLN	CB-CA-C	-5.27	101.89	110.85
35	2	516	GLY	CA-C-O	-5.26	115.64	120.80
17	R	136	ASP	CA-C-N	5.25	128.05	120.38
17	R	136	ASP	C-N-CA	5.25	128.05	120.38
35	2	511	LEU	CB-CA-C	5.23	119.76	109.72
23	3	118	GLY	CA-C-N	-5.21	113.54	120.63
23	3	118	GLY	C-N-CA	-5.21	113.54	120.63
8	H	47	U	O4'-C1'-C2'	5.20	111.00	105.80
23	3	1026	ASP	CA-C-N	5.19	128.58	120.75
23	3	1026	ASP	C-N-CA	5.19	128.58	120.75
1	A	1293	ASN	CA-CB-CG	-5.17	107.43	112.60
1	A	1308	PRO	N-CA-CB	-5.16	97.83	103.25
35	2	528	ILE	N-CA-C	-5.15	105.52	110.72
22	1	1207	SER	N-CA-C	-5.14	106.16	112.90
22	1	1126	PHE	CB-CA-C	-5.13	102.22	110.74
35	2	520	PRO	CA-C-O	-5.10	116.70	120.73
43	v	33	LEU	CA-C-N	-5.10	114.49	122.65
43	v	33	LEU	C-N-CA	-5.10	114.49	122.65
33	w	465	GLN	CB-CA-C	-5.09	102.89	110.88
1	A	827	PHE	CA-C-O	-5.07	115.45	119.71
1	A	1298	ARG	CA-C-O	-5.05	115.52	120.82
23	3	1083	ASN	CB-CA-C	5.04	114.82	109.83
23	3	1092	ILE	CB-CA-C	-5.04	105.50	111.65
43	v	36	GLU	CA-C-O	-5.01	115.56	120.82

There are no chirality outliers.

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	1	1101	LEU	Peptide
22	1	1107	GLN	Peptide
22	1	1108	ASN	Peptide
22	1	1177	LEU	Mainchain
22	1	415	LEU	Peptide
22	1	717	THR	Peptide
22	1	943	LYS	Peptide
22	1	944	SER	Peptide
35	2	493	ALA	Mainchain

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Mol	Chain	Res	Type	Group
23	3	261	PHE	Peptide
23	3	318	ASP	Peptide
23	3	916	ASN	Peptide
40	9	343	GLU	Peptide
1	A	1019	TYR	Peptide
1	A	109	PRO	Peptide
1	A	1543	ASN	Mainchain
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	698	PRO	Peptide
1	A	699	GLU	Peptide
1	A	700	GLY	Peptide
1	A	801	ILE	Peptide
1	A	940	ILE	Peptide
1	A	941	LYS	Peptide
4	D	2098	ALA	Peptide
5	E	192	ASN	Peptide
9	I	321	GLU	Peptide
9	I	337	LEU	Peptide
9	I	374	ILE	Peptide
9	I	384	THR	Peptide
11	K	275	ALA	Peptide
11	K	36	ARG	Peptide
16	Q	488	SER	Peptide
43	v	64	ASN	Mainchain
33	w	498	GLN	Mainchain

5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16165	0	14621	996	0
2	B	2066	0	1047	128	0
3	C	7077	0	7067	520	0
4	D	8528	0	3745	31	0
5	E	2338	0	2275	129	0
6	F	2035	0	1028	165	0
7	G	1321	0	673	146	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	3497	0	1770	143	0
9	I	2991	0	1473	17	0
10	J	2116	0	1977	96	0
11	K	2173	0	1770	128	0
12	L	829	0	837	61	0
13	N	662	0	284	5	0
14	O	1340	0	581	11	0
15	P	362	0	356	18	0
16	Q	6730	0	3268	30	0
17	R	1520	0	1482	101	0
18	T	2507	0	2451	196	0
19	X	1279	0	1284	81	0
20	Y	948	0	954	64	0
21	Z	439	0	410	16	0
22	1	7845	0	7915	525	0
23	3	9240	0	9164	554	0
24	o	816	0	386	16	0
25	p	851	0	423	23	0
26	c	388	0	102	1	0
26	h	482	0	220	5	0
27	d	296	0	87	5	0
27	i	359	0	179	7	0
28	a	336	0	89	2	0
28	m	413	0	194	11	0
29	g	324	0	89	3	0
29	l	415	0	198	14	0
30	f	296	0	84	2	0
30	k	364	0	176	10	0
31	e	308	0	83	3	0
31	j	403	0	173	12	0
32	b	328	0	89	4	0
32	n	402	0	184	7	0
33	w	2275	0	1347	106	0
34	u	834	0	325	0	0
35	2	1651	0	1438	163	0
36	4	792	0	367	9	0
37	6	906	0	913	69	0
38	7	811	0	789	42	0
39	5	669	0	631	31	0
40	9	2681	0	2270	141	0
41	8	931	0	960	66	0
42	y	390	0	190	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	v	997	0	745	60	0
44	z	124	0	26	0	0
45	C	32	0	12	8	0
46	C	1	0	0	0	0
47	7	3	0	0	0	0
47	K	1	0	0	0	0
All	All	103887	0	79201	4466	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 24.

All (4466) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1308:PRO:HB3	1:A:1548:TYR:CE2	1.15	1.65
35:2:530:ARG:HG2	35:2:578:TRP:CH2	1.15	1.64
35:2:530:ARG:CG	35:2:578:TRP:HH2	1.19	1.53
35:2:530:ARG:CG	35:2:578:TRP:CH2	1.89	1.53
35:2:530:ARG:HG2	35:2:578:TRP:CZ3	1.46	1.50
1:A:1307:MET:SD	1:A:1308:PRO:HD2	1.48	1.49
1:A:1308:PRO:CB	1:A:1548:TYR:CE2	1.93	1.48
33:w:488:ASN:HD21	33:w:491:THR:N	0.99	1.46
23:3:146:ARG:HD3	23:3:150:ALA:CB	1.47	1.43
22:1:1090:PRO:N	22:1:1090:PRO:CA	1.67	1.42
33:w:488:ASN:ND2	33:w:491:THR:H	1.03	1.42
35:2:533:ILE:HD11	35:2:566:ILE:CD1	1.50	1.41
1:A:1307:MET:SD	1:A:1308:PRO:CD	2.13	1.34
25:p:184:PRO:HG3	33:w:487:VAL:CG1	1.57	1.33
1:A:1308:PRO:HB3	1:A:1548:TYR:CD2	1.61	1.32
22:1:1210:HIS:CE1	35:2:585:THR:HG23	1.65	1.31
1:A:1545:ALA:HB2	1:A:1563:HIS:CG	1.66	1.29
7:G:99:C:N4	8:H:32:U:H3	1.29	1.28
7:G:85:G:C8	33:w:395:TRP:CH2	2.25	1.24
1:A:1308:PRO:CB	1:A:1548:TYR:CD2	2.16	1.23
12:L:38:LEU:CD1	12:L:41:LYS:HG2	1.69	1.23
2:B:8:G:H1	2:B:69:A:N6	1.38	1.22
33:w:383:LEU:HD21	33:w:397:TYR:CG	1.75	1.21
23:3:146:ARG:CD	23:3:150:ALA:HB1	1.71	1.21
1:A:1545:ALA:HB2	1:A:1563:HIS:CD2	1.75	1.20
33:w:383:LEU:CD2	33:w:384:PRO:HD2	1.72	1.19
6:F:85:U:H3	8:H:14:C:N4	1.42	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1545:ALA:HB2	1:A:1563:HIS:CE1	1.79	1.16
12:L:38:LEU:HD12	12:L:41:LYS:HG2	1.17	1.15
1:A:1308:PRO:CB	1:A:1548:TYR:HE2	1.41	1.14
23:3:146:ARG:CD	23:3:150:ALA:CB	2.25	1.13
23:3:146:ARG:HG2	23:3:150:ALA:HA	1.30	1.13
33:w:383:LEU:HD21	33:w:397:TYR:CD2	1.86	1.10
23:3:146:ARG:NE	23:3:150:ALA:HB1	1.67	1.09
22:1:129:SEP:O2P	22:1:573:LYS:NZ	1.85	1.09
33:w:383:LEU:HD23	33:w:384:PRO:HD2	1.29	1.08
1:A:1545:ALA:HB2	1:A:1563:HIS:ND1	1.68	1.07
35:2:533:ILE:HD11	35:2:566:ILE:HD11	1.36	1.07
23:3:146:ARG:HD3	23:3:150:ALA:HB2	1.34	1.07
22:1:1210:HIS:CE1	35:2:585:THR:H	1.71	1.07
33:w:383:LEU:HD23	33:w:384:PRO:CD	1.85	1.06
23:3:146:ARG:CG	23:3:150:ALA:HA	1.84	1.06
33:w:488:ASN:HD22	33:w:491:THR:HB	1.17	1.06
22:1:1182:LEU:H	22:1:1182:LEU:HD12	1.20	1.06
35:2:533:ILE:CD1	35:2:566:ILE:CD1	2.34	1.05
8:H:46:U:C5	33:w:394:TYR:HB2	1.92	1.05
35:2:533:ILE:HD11	35:2:566:ILE:HD12	1.15	1.05
3:C:118:PHE:CE1	29:g:15:GLY:O	2.10	1.04
11:K:360:ILE:O	20:Y:72:LYS:HE2	1.55	1.04
35:2:530:ARG:HG3	35:2:578:TRP:HH2	1.19	1.04
1:A:1545:ALA:CB	1:A:1563:HIS:CG	2.40	1.03
35:2:465:LEU:O	35:2:469:VAL:CG2	2.07	1.02
1:A:1304:ASN:OD1	1:A:1548:TYR:CE1	2.12	1.02
12:L:38:LEU:HD12	12:L:41:LYS:CG	1.89	1.02
22:1:1210:HIS:HE1	35:2:585:THR:CG2	1.72	1.02
1:A:1304:ASN:OD1	1:A:1548:TYR:CZ	2.12	1.01
25:p:184:PRO:CG	33:w:487:VAL:CG1	2.37	1.01
35:2:469:VAL:HG11	35:2:489:VAL:HG11	1.38	1.00
35:2:465:LEU:O	35:2:469:VAL:HG23	1.62	1.00
25:p:184:PRO:HG3	33:w:487:VAL:HG13	1.40	0.99
33:w:448:ASN:OD1	35:2:477:MET:HE2	1.62	0.99
33:w:488:ASN:ND2	33:w:491:THR:HB	1.76	0.99
14:O:55:PHE:O	14:O:67:LYS:HA	1.63	0.99
22:1:1139:PRO:CB	43:v:50:HIS:O	2.09	0.99
23:3:146:ARG:HH21	23:3:146:ARG:HB2	1.26	0.99
35:2:533:ILE:CD1	35:2:566:ILE:HD12	1.90	0.99
22:1:1137:ARG:HH22	35:2:534:GLN:HG2	1.27	0.98
1:A:827:PHE:HB2	1:A:1002:ASP:OD2	1.65	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1139:PRO:HB2	43:v:50:HIS:O	1.63	0.97
25:p:191:PHE:CB	33:w:498:GLN:OE1	2.12	0.97
18:T:245:HIS:HE2	18:T:263:SER:HG	1.12	0.96
11:K:362:GLU:CB	20:Y:71:LYS:HG2	1.95	0.96
23:3:146:ARG:HD3	23:3:150:ALA:HB1	1.30	0.96
22:1:1210:HIS:HE1	35:2:585:THR:HG23	0.80	0.96
1:A:1308:PRO:HB2	1:A:1548:TYR:CD2	1.99	0.96
1:A:508:ILE:HG23	1:A:513:LEU:HB2	1.47	0.96
6:F:33:G:N1	7:G:14:A:C6	2.34	0.95
33:w:383:LEU:HD21	33:w:397:TYR:CB	1.94	0.95
25:p:184:PRO:HG3	33:w:487:VAL:HG11	1.48	0.95
1:A:1545:ALA:HB2	1:A:1563:HIS:NE2	1.80	0.95
25:p:152:ILE:CB	33:w:498:GLN:NE2	2.30	0.95
2:B:17:U:H3	2:B:60:G:H1	1.16	0.94
33:w:383:LEU:CD2	33:w:397:TYR:CD2	2.51	0.94
25:p:184:PRO:CG	33:w:487:VAL:HG11	1.94	0.94
6:F:33:G:C6	7:G:14:A:N6	2.36	0.93
33:w:488:ASN:OD1	33:w:490:LYS:HB3	1.68	0.93
3:C:686:THR:HB	3:C:793:ASP:HB3	1.49	0.93
40:9:449:ARG:HA	40:9:452:GLN:HE21	1.35	0.92
33:w:383:LEU:HD21	33:w:397:TYR:HB2	1.51	0.92
33:w:464:LEU:O	33:w:467:ALA:HB3	1.70	0.91
35:2:533:ILE:CD1	35:2:566:ILE:HD11	2.00	0.91
35:2:530:ARG:HG3	35:2:578:TRP:CH2	1.93	0.91
8:H:46:U:H5	33:w:394:TYR:HB2	1.30	0.91
6:F:85:U:H3	8:H:14:C:H42	0.91	0.90
11:K:362:GLU:CB	20:Y:71:LYS:CG	2.48	0.90
22:1:1036:ILE:HD11	22:1:1065:LEU:HD13	1.53	0.90
6:F:85:U:O2	8:H:14:C:N3	2.05	0.90
8:H:56:A:O2'	35:2:481:THR:HG21	1.70	0.89
18:T:292:TYR:OH	18:T:308:ARG:HD3	1.71	0.89
19:X:312:GLU:HG2	19:X:322:ARG:HG2	1.54	0.89
1:A:1330:MET:HE1	1:A:1369:TYR:HB2	1.55	0.89
17:R:241:GLU:HA	17:R:244:GLU:HB2	1.53	0.89
1:A:1410:ASP:OD1	1:A:1410:ASP:N	2.06	0.88
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.55	0.88
3:C:182:LYS:HG3	3:C:214:GLU:HG2	1.55	0.88
23:3:456:PRO:HA	23:3:478:PHE:HA	1.55	0.88
22:1:1108:ASN:ND2	22:1:1111:CYS:SG	2.46	0.88
8:H:46:U:C6	33:w:394:TYR:CG	2.62	0.88
33:w:383:LEU:HD22	33:w:384:PRO:HD2	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.07	0.87
1:A:188:LEU:HD22	1:A:567:GLY:HA2	1.57	0.87
23:3:902:ASP:OD2	23:3:929:LYS:NZ	2.08	0.87
35:2:451:LYS:H	35:2:451:LYS:HD2	1.40	0.87
1:A:1304:ASN:OD1	1:A:1548:TYR:OH	1.93	0.86
23:3:552:ARG:NE	23:3:568:MET:O	2.07	0.86
1:A:158:ARG:HH21	1:A:572:PHE:HB2	1.40	0.86
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.54	0.86
22:1:967:GLU:HB3	22:1:970:LEU:HB3	1.56	0.86
35:2:530:ARG:CG	35:2:578:TRP:CZ3	2.33	0.86
35:2:585:THR:HB	35:2:589:ASP:OD2	1.74	0.86
17:R:148:ARG:CZ	17:R:148:ARG:HB3	2.05	0.86
3:C:258:ASN:HD21	3:C:312:SER:HB3	1.38	0.86
18:T:292:TYR:CE1	18:T:308:ARG:HB2	2.11	0.86
1:A:1307:MET:SD	1:A:1308:PRO:HD3	2.14	0.86
3:C:590:ILE:HB	3:C:637:LEU:HD21	1.57	0.86
6:F:30:A:OP2	7:G:16:G:N2	2.07	0.86
1:A:1308:PRO:CG	1:A:1548:TYR:HE2	1.88	0.85
22:1:1210:HIS:HE1	35:2:585:THR:H	1.19	0.85
11:K:21:LEU:HD11	11:K:102:ARG:HG2	1.56	0.85
23:3:114:ARG:NH1	39:5:38:ASP:OD1	2.09	0.85
23:3:146:ARG:HH21	23:3:146:ARG:CB	1.88	0.85
35:2:469:VAL:HG11	35:2:489:VAL:CG1	2.06	0.85
7:G:85:G:C8	33:w:395:TRP:HH2	1.93	0.85
17:R:329:GLN:HE22	17:R:332:ARG:HD2	1.42	0.85
23:3:461:THR:HA	23:3:473:TYR:O	1.75	0.85
1:A:1220:VAL:HG23	1:A:1221:THR:HG23	1.58	0.85
35:2:581:LYS:HB3	35:2:581:LYS:HZ2	1.42	0.84
1:A:110:TRP:O	1:A:192:GLN:NE2	2.10	0.84
22:1:154:ASP:O	22:1:158:GLU:HG3	1.77	0.84
23:3:805:ASN:ND2	23:3:858:GLY:O	2.10	0.84
33:w:495:LEU:HA	33:w:498:GLN:HB2	1.58	0.84
1:A:1256:PHE:CD1	1:A:1299:ILE:CG2	2.60	0.84
11:K:146:PRO:HB2	11:K:150:ARG:HH21	1.42	0.84
11:K:360:ILE:O	20:Y:72:LYS:CE	2.25	0.84
23:3:700:LYS:NZ	23:3:740:GLU:O	2.11	0.84
7:G:-3:A:H2'	7:G:-2:A:H8	1.41	0.84
43:v:54:TYR:CZ	43:v:66:GLU:HG3	2.11	0.84
23:3:93:GLN:NE2	23:3:100:GLU:OE1	2.10	0.84
23:3:617:ILE:HG12	23:3:627:PRO:HA	1.59	0.84
18:T:422:ASN:HB3	18:T:426:VAL:HG23	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2:530:ARG:O	35:2:530:ARG:HD3	1.78	0.84
1:A:82:ARG:H	1:A:85:LYS:HZ2	1.23	0.84
19:X:232:LEU:HD21	20:Y:51:ASP:HB3	1.60	0.84
23:3:675:LEU:HG	23:3:688:ASP:HB3	1.59	0.84
1:A:982:GLU:OE2	1:A:1172:ASN:ND2	2.10	0.84
1:A:1299:ILE:HD13	1:A:1316:PHE:CE1	2.13	0.84
22:1:1252:GLN:NE2	35:2:492:LYS:HA	1.91	0.83
33:w:447:ALA:O	35:2:466:LYS:HE3	1.77	0.83
43:v:32:GLN:HA	43:v:32:GLN:HE21	1.43	0.83
1:A:1545:ALA:CB	1:A:1563:HIS:CD2	2.59	0.83
3:C:396:LEU:HD13	3:C:403:LEU:HD13	1.60	0.83
17:R:389:SER:O	19:X:348:ARG:NE	2.10	0.83
8:H:78:C:H2'	8:H:79:G:H8	1.42	0.83
18:T:394:ASN:ND2	18:T:410:SER:OG	2.11	0.83
7:G:90:C:H2'	7:G:91:A:C8	2.14	0.83
35:2:473:ASP:OD1	35:2:473:ASP:N	2.07	0.83
1:A:617:ASN:ND2	1:A:622:GLY:O	2.12	0.83
1:A:1545:ALA:CB	1:A:1563:HIS:CE1	2.61	0.83
6:F:38:G:N2	7:G:9:C:O2	2.12	0.83
35:2:581:LYS:HD2	35:2:581:LYS:O	1.78	0.82
22:1:806:ILE:HA	22:1:810:ILE:HG13	1.61	0.82
22:1:1126:PHE:CE2	35:2:572:HIS:HD2	1.96	0.82
1:A:393:LEU:HA	3:C:379:LYS:HG2	1.62	0.82
35:2:537:ARG:HH11	35:2:537:ARG:HG3	1.44	0.82
1:A:1298:ARG:HB3	1:A:1298:ARG:NH2	1.94	0.82
20:Y:24:ASP:OD1	20:Y:24:ASP:N	2.10	0.82
23:3:828:GLY:O	23:3:834:LEU:N	2.12	0.82
18:T:316:ASP:OD1	18:T:319:THR:N	2.13	0.81
22:1:699:GLN:OE1	22:1:702:ARG:NH2	2.11	0.81
23:3:726:GLN:O	23:3:728:ARG:NH2	2.13	0.81
35:2:575:PHE:O	35:2:579:GLN:NE2	2.12	0.81
3:C:399:LEU:HB3	3:C:401:ILE:HG12	1.62	0.81
1:A:539:ARG:HH12	7:G:-1:C:H5''	1.44	0.81
18:T:245:HIS:NE2	18:T:263:SER:OG	2.12	0.81
11:K:73:ARG:HH12	11:K:77:LEU:HD11	1.44	0.81
3:C:237:LEU:HD22	3:C:898:LEU:HD22	1.62	0.81
21:Z:585:ASP:OD2	21:Z:589:ARG:NH2	2.12	0.81
23:3:499:PHE:O	23:3:525:ARG:NH1	2.13	0.81
1:A:232:LEU:HD22	1:A:404:LEU:HD13	1.62	0.81
17:R:386:ARG:NH2	19:X:356:ASP:OD2	2.13	0.81
41:8:121:SER:HA	41:8:124:LEU:HD12	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:129:SEP:HB3	22:1:130:PRO:HD2	1.64	0.81
22:1:571:VAL:HG22	22:1:600:LEU:HD11	1.63	0.81
23:3:70:LEU:HD12	23:3:146:ARG:HH22	1.46	0.81
33:w:488:ASN:HD21	33:w:491:THR:CA	1.94	0.81
8:H:155:C:N3	8:H:176:G:N2	2.29	0.80
12:L:24:MET:HE1	43:v:40:ILE:CD1	2.10	0.80
12:L:38:LEU:HD11	12:L:41:LYS:HG2	1.63	0.80
3:C:85:ASP:OD1	3:C:85:ASP:N	2.13	0.80
22:1:157:ARG:NH1	37:6:103:THR:OG1	2.14	0.80
35:2:581:LYS:H	35:2:581:LYS:HZ3	1.25	0.80
37:6:113:LEU:HA	37:6:116:LYS:HE3	1.63	0.80
22:1:141:LYS:NZ	22:1:142:THR:O	2.15	0.80
22:1:1137:ARG:NH2	35:2:534:GLN:HG2	1.96	0.80
33:w:448:ASN:HB2	35:2:462:VAL:HG11	1.63	0.80
5:E:341:ILE:HG12	5:E:355:GLU:HG3	1.64	0.80
18:T:386:THR:HG22	18:T:399:LYS:HA	1.63	0.80
6:F:38:G:C2	7:G:9:C:C2	2.70	0.80
22:1:1248:GLN:OE1	35:2:587:HIS:HE1	1.65	0.80
10:J:238:ASN:HB3	10:J:240:THR:HG22	1.64	0.80
33:w:488:ASN:ND2	33:w:491:THR:CB	2.43	0.80
23:3:146:ARG:CG	23:3:150:ALA:CA	2.59	0.79
1:A:319:LEU:HD22	3:C:637:LEU:HG	1.64	0.79
1:A:1308:PRO:CB	1:A:1548:TYR:HD2	1.86	0.79
1:A:1545:ALA:CB	1:A:1563:HIS:ND1	2.43	0.79
3:C:509:VAL:HG12	3:C:565:ILE:HG12	1.64	0.79
40:9:236:LEU:HD22	40:9:452:GLN:HE22	1.46	0.79
4:D:1376:CYS:HA	4:D:1450:LEU:O	1.82	0.79
6:F:38:G:N1	7:G:9:C:N3	2.31	0.79
22:1:1178:MET:CE	35:2:591:TYR:CE2	2.66	0.79
11:K:39:ASN:OD1	11:K:43:CYS:N	2.16	0.79
3:C:589:LYS:HE2	3:C:628:VAL:HG11	1.62	0.79
3:C:118:PHE:HE1	29:g:15:GLY:O	1.59	0.79
3:C:347:ILE:HD11	3:C:356:PHE:HB3	1.65	0.79
22:1:1260:LYS:NZ	35:2:504:TRP:O	2.16	0.79
8:H:54:U:O2	8:H:59:A:N6	2.16	0.79
35:2:514:LYS:N	35:2:593:GLU:OE1	2.16	0.79
22:1:138:ASP:HB3	22:1:141:LYS:HB3	1.63	0.79
23:3:609:LEU:HB2	23:3:611:ASP:HB3	1.64	0.79
22:1:1137:ARG:HH22	35:2:534:GLN:CG	1.96	0.78
23:3:553:GLN:NE2	23:3:600:GLN:O	2.16	0.78
22:1:626:ASN:OD1	22:1:630:ARG:NH1	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.16	0.78
5:E:90:ILE:HB	5:E:105:LEU:HB2	1.65	0.78
1:A:401:GLY:HA3	3:C:386:GLY:HA2	1.65	0.78
23:3:581:LYS:NZ	23:3:583:MET:SD	2.56	0.78
1:A:979:SER:OG	1:A:980:ARG:N	2.13	0.78
23:3:483:LEU:HD23	23:3:485:LEU:HD11	1.65	0.78
23:3:932:ASN:O	23:3:933:ASN:ND2	2.17	0.78
43:v:85:ARG:HA	43:v:85:ARG:HE	1.47	0.78
23:3:206:GLN:NE2	23:3:232:GLY:H	1.80	0.78
22:1:1210:HIS:CE1	35:2:585:THR:CG2	2.54	0.78
1:A:535:ARG:NH2	1:A:1551:PHE:HE1	1.82	0.78
3:C:441:PRO:HB3	3:C:495:ARG:HH22	1.48	0.78
17:R:137:GLU:CD	17:R:137:GLU:H	1.92	0.78
18:T:350:HIS:HA	18:T:374:SER:HB2	1.65	0.77
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.66	0.77
23:3:943:THR:HG21	23:3:977:LEU:HB2	1.66	0.77
41:8:115:ASN:OD1	41:8:116:ILE:N	2.17	0.77
1:A:1021:ASP:N	1:A:1021:ASP:OD1	2.14	0.77
22:1:859:ASP:OD1	22:1:860:GLU:N	2.17	0.77
23:3:946:GLU:OE1	23:3:946:GLU:N	2.16	0.77
33:w:488:ASN:ND2	33:w:488:ASN:O	2.17	0.77
1:A:1303:LEU:HD13	1:A:1303:LEU:N	2.00	0.77
12:L:41:LYS:HA	12:L:41:LYS:CE	2.15	0.77
23:3:941:HIS:CD2	23:3:976:LYS:HA	2.19	0.77
20:Y:53:ILE:HG23	20:Y:62:ILE:HD12	1.65	0.77
7:G:111:U:O2	20:Y:105:ARG:NH2	2.16	0.77
23:3:146:ARG:HD3	23:3:150:ALA:CA	2.15	0.77
43:v:38:ILE:HG21	43:v:46:PHE:CD1	2.18	0.77
23:3:473:TYR:HB3	23:3:475:ILE:HD11	1.66	0.77
27:i:23:LEU:HA	27:i:69:VAL:HA	1.67	0.77
7:G:85:G:N7	33:w:395:TRP:CH2	2.53	0.77
22:1:758:ASP:N	22:1:758:ASP:OD1	2.16	0.77
23:3:745:PHE:HB2	23:3:755:VAL:HG23	1.65	0.77
3:C:304:LEU:O	3:C:436:GLN:NE2	2.18	0.77
16:Q:1270:TYR:HA	16:Q:1300:GLY:O	1.84	0.77
1:A:82:ARG:NH1	7:G:16:G:O6	2.18	0.77
6:F:32:U:H3	7:G:15:U:H3	1.29	0.77
23:3:34:ARG:NH1	23:3:39:GLU:OE1	2.18	0.77
23:3:528:ARG:NH1	23:3:572:GLY:O	2.17	0.77
22:1:1074:ARG:NH1	22:1:1107:GLN:OE1	2.17	0.76
22:1:1126:PHE:HA	35:2:575:PHE:CD2	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:550:ASN:HD21	23:3:595:VAL:H	1.30	0.76
6:F:69:A:H3'	6:F:70:A:H8	1.50	0.76
1:A:420:ARG:NH1	2:B:56:C:O2'	2.18	0.76
6:F:30:A:N6	7:G:17:U:O5'	2.18	0.76
23:3:473:TYR:OH	23:3:497:SER:O	2.02	0.76
6:F:26:U:H3'	6:F:27:A:H5''	1.66	0.76
22:1:1277:GLN:NE2	22:1:1277:GLN:O	2.18	0.76
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.18	0.76
23:3:926:TYR:HB3	23:3:928:TYR:HE2	1.51	0.76
8:H:29:A:H1'	8:H:30:A:H5'	1.68	0.76
8:H:163:G:O2'	25:p:47:LYS:O	2.03	0.76
12:L:24:MET:HE1	43:v:40:ILE:HD11	1.66	0.76
1:A:457:ASN:ND2	2:B:28:A:OP2	2.18	0.76
3:C:813:ARG:NH2	40:9:106:LEU:O	2.18	0.76
29:l:49:THR:HA	29:l:55:VAL:HA	1.68	0.76
1:A:79:ARG:HH22	6:F:29:A:H5'	1.51	0.75
1:A:1312:PRO:HG3	1:A:1541:THR:HG22	1.68	0.75
3:C:448:LYS:O	3:C:452:THR:HB	1.86	0.75
18:T:287:HIS:HE2	18:T:305:THR:HG1	1.32	0.75
6:F:38:G:C2	7:G:9:C:O2	2.39	0.75
23:3:444:VAL:HG11	23:3:736:TYR:HB2	1.68	0.75
22:1:1139:PRO:O	43:v:51:LEU:HA	1.86	0.75
2:B:42:U:O4	7:G:-2:A:N6	2.17	0.75
3:C:313:GLN:HB2	45:C:1500:GTP:C5	2.21	0.75
19:X:234:GLU:O	19:X:238:THR:OG1	2.05	0.75
22:1:1248:GLN:OE1	35:2:587:HIS:CE1	2.39	0.75
23:3:547:CYS:HA	23:3:555:VAL:O	1.85	0.75
23:3:590:MET:HG2	23:3:607:VAL:HA	1.68	0.75
35:2:586:ILE:O	35:2:586:ILE:HD13	1.85	0.75
23:3:631:GLN:NE2	23:3:632:ALA:O	2.19	0.75
1:A:684:GLU:OE2	18:T:308:ARG:NH2	2.19	0.75
33:w:462:LEU:O	33:w:462:LEU:HD23	1.86	0.75
35:2:465:LEU:O	35:2:469:VAL:HG21	1.86	0.75
1:A:837:LYS:HD3	1:A:1432:TYR:HE2	1.51	0.75
1:A:1261:ASN:ND2	17:R:428:GLU:O	2.17	0.75
35:2:581:LYS:H	35:2:581:LYS:NZ	1.85	0.75
1:A:315:ALA:O	1:A:330:THR:OG1	2.05	0.75
22:1:1210:HIS:CE1	35:2:585:THR:N	2.53	0.75
1:A:873:ASN:N	1:A:873:ASN:OD1	2.20	0.74
3:C:225:VAL:HB	3:C:251:LEU:HD12	1.67	0.74
3:C:255:VAL:HG23	3:C:300:LEU:HD22	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:v:91:LYS:HZ2	43:v:91:LYS:HB2	1.51	0.74
1:A:425:PRO:HB2	1:A:428:LYS:HB2	1.69	0.74
23:3:155:SER:OG	23:3:156:SER:N	2.13	0.74
23:3:555:VAL:HG13	23:3:590:MET:HE3	1.68	0.74
7:G:98:U:O4	8:H:33:G:N1	2.19	0.74
43:v:91:LYS:HB2	43:v:91:LYS:NZ	2.01	0.74
1:A:1601:LEU:HD12	1:A:1606:ILE:HB	1.69	0.74
6:F:65:G:H21	6:F:69:A:H2	1.35	0.74
1:A:1171:GLU:OE1	1:A:1171:GLU:N	2.20	0.74
3:C:664:GLU:O	3:C:785:ARG:N	2.19	0.74
18:T:197:TYR:OH	18:T:476:ARG:NH1	2.20	0.74
33:w:383:LEU:HD23	33:w:384:PRO:HD3	1.70	0.74
33:w:488:ASN:ND2	33:w:491:THR:N	1.82	0.74
1:A:62:PRO:HB2	1:A:64:GLU:HG2	1.67	0.74
1:A:1301:ILE:O	1:A:1301:ILE:HD13	1.88	0.74
3:C:496:VAL:HB	3:C:546:ALA:HA	1.68	0.74
35:2:509:LYS:HB2	35:2:512:GLN:HB3	1.68	0.74
1:A:1298:ARG:C	1:A:1298:ARG:HH21	1.95	0.74
3:C:170:ILE:HD11	3:C:535:ALA:HB1	1.68	0.74
9:I:169:TYR:O	9:I:173:LEU:CB	2.35	0.74
11:K:360:ILE:C	20:Y:72:LYS:HE2	2.13	0.74
43:v:65:ASN:HB2	43:v:68:SER:H	1.52	0.74
6:F:33:G:C2	7:G:14:A:C6	2.75	0.74
7:G:84:U:O2	33:w:396:LEU:HD11	1.88	0.74
23:3:1100:THR:OG1	39:5:48:ASP:OD2	2.05	0.74
7:G:99:C:N4	8:H:32:U:N3	2.05	0.74
17:R:407:TYR:HB3	17:R:411:LEU:HD12	1.69	0.74
22:1:984:GLU:OE2	22:1:986:TYR:N	2.20	0.74
23:3:5:ASN:ND2	23:3:1095:TYR:OH	2.21	0.74
31:j:32:GLN:O	31:j:88:GLN:N	2.16	0.74
35:2:517:ILE:N	35:2:517:ILE:HD12	2.03	0.74
1:A:821:ARG:HG2	1:A:821:ARG:NH1	2.00	0.74
22:1:458:ASP:O	22:1:459:GLN:NE2	2.21	0.74
28:m:71:LEU:N	29:l:71:LEU:O	2.16	0.74
3:C:76:GLU:OE1	3:C:76:GLU:N	2.18	0.73
5:E:251:LEU:HD13	5:E:300:ILE:HD13	1.70	0.73
12:L:74:LEU:O	12:L:77:LEU:N	2.20	0.73
1:A:1201:ARG:O	1:A:1203:SER:N	2.20	0.73
12:L:38:LEU:HD23	12:L:38:LEU:H	1.53	0.73
23:3:399:ASP:OD1	23:3:400:GLU:N	2.21	0.73
39:5:11:LEU:HD22	39:5:23:HIS:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:TRP:NE1	1:A:1049:ASP:OD2	2.21	0.73
17:R:148:ARG:HA	17:R:151:LEU:HD23	1.70	0.73
5:E:208:ILE:O	5:E:219:VAL:HA	1.89	0.73
10:J:224:LYS:NZ	10:J:257:GLU:OE2	2.21	0.73
22:1:129:SEP:HB3	22:1:130:PRO:CD	2.19	0.73
35:2:537:ARG:HG3	35:2:537:ARG:NH1	2.01	0.73
22:1:838:VAL:O	22:1:842:ASN:ND2	2.21	0.73
17:R:434:ASP:N	17:R:434:ASP:OD1	2.20	0.73
22:1:931:GLN:O	22:1:935:THR:OG1	2.07	0.73
22:1:1212:LEU:HD12	22:1:1212:LEU:O	1.88	0.73
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.70	0.73
1:A:1022:MET:C	1:A:1023:ASN:HD22	1.97	0.73
1:A:1308:PRO:HB2	1:A:1548:TYR:CE2	2.11	0.73
2:B:20:G:N1	2:B:58:U:O2	2.20	0.73
20:Y:92:LEU:O	20:Y:96:ASN:ND2	2.20	0.73
1:A:578:LEU:HA	1:A:581:ILE:HD12	1.70	0.73
23:3:430:GLY:O	23:3:433:SER:OG	2.06	0.73
1:A:902:TYR:OH	1:A:1249:MET:SD	2.46	0.72
6:F:38:G:N2	7:G:9:C:C2	2.57	0.72
6:F:38:G:N1	7:G:9:C:C2	2.57	0.72
20:Y:113:SER:OG	20:Y:114:ASN:ND2	2.22	0.72
22:1:491:GLU:OE2	22:1:492:GLN:N	2.22	0.72
33:w:383:LEU:CD2	33:w:397:TYR:HB2	2.20	0.72
22:1:694:LEU:HD11	22:1:731:LEU:HD23	1.71	0.72
23:3:266:ASP:OD1	23:3:266:ASP:N	2.20	0.72
23:3:1013:ARG:NH1	23:3:1065:GLU:OE2	2.22	0.72
1:A:798:GLY:HA3	17:R:281:ASN:HD22	1.54	0.72
3:C:318:PHE:HE1	3:C:373:ILE:HD13	1.52	0.72
23:3:685:ASP:OD1	23:3:686:LEU:N	2.22	0.72
1:A:471:TYR:HB3	1:A:474:ARG:HG3	1.71	0.72
3:C:685:ILE:HD11	3:C:811:THR:HG23	1.69	0.72
22:1:476:ASP:OD1	22:1:477:LYS:N	2.22	0.72
22:1:848:GLU:OE2	22:1:852:ARG:NE	2.23	0.72
22:1:1289:ASN:HB3	22:1:1295:TYR:H	1.53	0.72
1:A:639:PHE:O	2:B:28:A:O2'	2.05	0.72
1:A:941:LYS:NZ	1:A:946:GLU:OE2	2.23	0.72
3:C:913:ASP:HB3	3:C:916:ILE:HG13	1.70	0.72
18:T:213:GLU:CD	18:T:215:GLY:H	1.96	0.72
1:A:762:ARG:HH12	15:P:226:LYS:HZ1	1.37	0.72
1:A:798:GLY:HA2	17:R:284:PHE:HE2	1.55	0.72
2:B:58:U:H2'	2:B:59:G:H8	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:94:ILE:HG21	18:T:259:PRO:HB3	1.71	0.72
3:C:454:THR:OG1	3:C:576:ILE:O	2.06	0.72
3:C:495:ARG:HB3	3:C:549:TRP:HD1	1.53	0.72
18:T:287:HIS:NE2	18:T:305:THR:OG1	2.19	0.72
20:Y:86:ASP:OD1	20:Y:89:SER:OG	2.08	0.72
22:1:1262:ARG:NH1	39:5:24:ALA:O	2.23	0.72
23:3:946:GLU:OE2	23:3:968:ARG:NH2	2.20	0.72
18:T:329:HIS:ND1	18:T:351:ASP:OD2	2.20	0.72
43:v:63:HIS:CE1	43:v:72:HIS:HB2	2.25	0.72
1:A:2104:TYR:O	1:A:2261:MET:HA	1.90	0.72
3:C:448:LYS:HZ2	3:C:497:LEU:HD22	1.54	0.72
19:X:298:SER:O	19:X:335:ASN:ND2	2.22	0.72
23:3:21:ASN:N	23:3:76:ASP:OD2	2.21	0.72
41:8:14:ASP:OD1	41:8:16:ARG:N	2.23	0.72
1:A:66:VAL:HG11	1:A:485:THR:HG21	1.72	0.72
23:3:263:ASP:OD1	23:3:263:ASP:N	2.21	0.72
23:3:1008:SER:OG	23:3:1027:ASP:OD2	2.08	0.72
1:A:1551:PHE:HB3	1:A:1553:VAL:HG23	1.72	0.71
23:3:280:ASP:H	23:3:857:ALA:HB3	1.54	0.71
6:F:75:G:OP2	6:F:75:G:N2	2.22	0.71
8:H:139:C:H2'	8:H:140:A:H8	1.55	0.71
18:T:349:SER:OG	18:T:350:HIS:N	2.21	0.71
3:C:698:GLU:O	3:C:702:ASN:ND2	2.22	0.71
22:1:1064:GLU:OE1	22:1:1064:GLU:N	2.22	0.71
23:3:587:VAL:HG11	23:3:590:MET:HE2	1.70	0.71
1:A:63:PRO:HB2	1:A:67:ARG:HH22	1.55	0.71
6:F:79:C:H4'	6:F:80:G:OP1	1.90	0.71
40:9:352:ASP:OD1	40:9:376:ASN:ND2	2.23	0.71
1:A:1373:GLN:NE2	1:A:1377:SER:OG	2.22	0.71
3:C:313:GLN:O	3:C:417:ARG:NH1	2.24	0.71
22:1:804:ASN:O	22:1:808:THR:OG1	2.08	0.71
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.23	0.71
28:m:70:VAL:HA	29:l:72:ILE:HA	1.71	0.71
30:k:7:PRO:HD3	30:k:36:PRO:HA	1.71	0.71
22:1:1092:ASP:N	22:1:1092:ASP:OD1	2.22	0.71
14:O:81:CYS:O	14:O:85:LEU:N	2.23	0.71
20:Y:32:TYR:O	20:Y:87:GLN:NE2	2.23	0.71
22:1:1054:GLU:OE1	22:1:1057:ARG:NH1	2.24	0.71
33:w:462:LEU:HD23	33:w:462:LEU:C	2.16	0.71
33:w:488:ASN:CG	33:w:491:THR:H	1.95	0.71
35:2:530:ARG:HG2	35:2:578:TRP:HZ3	1.47	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:6:47:GLN:OE1	37:6:49:ARG:NE	2.24	0.71
19:X:263:PRO:HB2	19:X:270:LEU:HB2	1.73	0.71
22:1:884:ILE:HG23	22:1:888:LEU:HB3	1.73	0.71
22:1:1252:GLN:OE1	35:2:499:PRO:HA	1.91	0.71
1:A:276:GLY:O	1:A:448:GLN:NE2	2.23	0.71
1:A:578:LEU:HB2	1:A:630:TRP:CD1	2.26	0.71
23:3:206:GLN:HE21	23:3:232:GLY:H	1.36	0.71
1:A:96:PRO:HB2	1:A:645:THR:HG23	1.73	0.71
43:v:34:ALA:HA	43:v:37:THR:HG23	1.73	0.71
1:A:200:ASP:OD1	1:A:240:ARG:NH1	2.24	0.70
3:C:599:GLU:HG2	3:C:651:ILE:HD12	1.72	0.70
35:2:532:GLY:O	35:2:535:GLU:N	2.24	0.70
1:A:363:HIS:HD2	3:C:284:GLU:HA	1.56	0.70
10:J:275:ASN:OD1	10:J:278:LEU:N	2.23	0.70
22:1:946:LYS:HD2	22:1:946:LYS:H	1.57	0.70
23:3:705:ARG:HA	23:3:710:GLU:HA	1.73	0.70
6:F:46:G:H5''	11:K:19:LYS:HD3	1.71	0.70
40:9:287:ASN:ND2	40:9:425:GLU:O	2.24	0.70
1:A:1622:MET:O	1:A:1687:TYR:OH	2.10	0.70
2:B:50:G:H2'	2:B:51:A:O4'	1.91	0.70
19:X:224:PRO:HG3	20:Y:69:ARG:HD2	1.72	0.70
23:3:487:ILE:HA	23:3:491:VAL:HG13	1.74	0.70
37:6:17:VAL:HG13	37:6:67:ILE:HD11	1.73	0.70
36:4:79:LEU:N	36:4:82:LYS:O	2.24	0.70
3:C:210:ASN:HB3	3:C:636:TYR:HB2	1.74	0.70
3:C:366:GLN:HG3	3:C:371:GLU:HB2	1.71	0.70
19:X:286:HIS:HB2	19:X:301:LYS:HG2	1.72	0.70
1:A:1404:THR:OG1	1:A:1405:LEU:N	2.25	0.70
1:A:1655:THR:OG1	1:A:1656:THR:N	2.23	0.70
11:K:98:TYR:OH	11:K:105:ILE:N	2.20	0.70
17:R:299:ARG:NH1	22:1:447:GLN:O	2.24	0.70
1:A:1166:THR:OG1	1:A:1167:THR:N	2.18	0.70
1:A:1415:GLY:O	1:A:1418:ARG:NH1	2.25	0.70
2:B:97:G:H1	2:B:116:U:H3	1.37	0.70
11:K:40:GLY:O	11:K:44:HIS:CD2	2.45	0.70
17:R:407:TYR:HB2	17:R:412:PHE:HE1	1.57	0.70
31:j:32:GLN:N	31:j:88:GLN:O	2.22	0.70
1:A:1554:GLN:OE1	1:A:1622:MET:CE	2.40	0.70
4:D:1204:ILE:O	4:D:1250:HIS:N	2.22	0.70
5:E:202:ASN:ND2	5:E:204:THR:OG1	2.24	0.70
8:H:181:G:O2'	29:l:51:ARG:O	2.10	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:26:TRP:CD1	11:K:37:ASP:H	2.10	0.70
18:T:424:ASP:OD1	18:T:424:ASP:N	2.24	0.70
19:X:354:GLU:HG2	19:X:355:LYS:HG3	1.73	0.70
22:1:471:ASP:OD2	22:1:505:LYS:NZ	2.24	0.70
35:2:451:LYS:H	35:2:451:LYS:CD	2.02	0.70
35:2:581:LYS:HZ3	35:2:581:LYS:N	1.90	0.70
1:A:837:LYS:HD3	1:A:1432:TYR:CE2	2.27	0.69
1:A:1110:ILE:HG22	1:A:1114:LEU:HD12	1.74	0.69
2:B:29:A:H2'	2:B:30:A:H8	1.57	0.69
22:1:1133:MET:SD	35:2:528:ILE:HD11	2.32	0.69
23:3:368:ASP:OD1	23:3:368:ASP:N	2.17	0.69
40:9:360:HIS:NE2	40:9:394:HIS:O	2.25	0.69
1:A:835:ASP:N	1:A:835:ASP:OD1	2.23	0.69
10:J:236:ARG:HA	10:J:239:ARG:CZ	2.22	0.69
17:R:134:ARG:HH22	18:T:383:ARG:HA	1.56	0.69
23:3:561:GLY:O	23:3:582:GLU:HA	1.93	0.69
1:A:499:GLN:O	1:A:503:MET:HG2	1.93	0.69
6:F:36:A:N6	7:G:10:U:C2	2.60	0.69
11:K:121:TRP:HA	11:K:124:ARG:HH21	1.56	0.69
19:X:255:PRO:HA	19:X:324:VAL:HG11	1.73	0.69
23:3:285:MET:SD	23:3:305:THR:OG1	2.49	0.69
23:3:1150:SER:OG	23:3:1151:GLU:OE1	2.09	0.69
2:B:98:G:H2'	2:B:99:C:C6	2.28	0.69
17:R:281:ASN:OD1	17:R:282:GLU:N	2.25	0.69
23:3:146:ARG:CD	23:3:150:ALA:CA	2.70	0.69
23:3:351:SER:OG	23:3:355:ASN:O	2.10	0.69
23:3:736:TYR:HE2	23:3:739:LEU:HD21	1.56	0.69
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.75	0.69
22:1:1108:ASN:HB2	22:1:1111:CYS:H	1.57	0.69
23:3:550:ASN:OD1	23:3:551:GLN:N	2.24	0.69
23:3:895:ARG:NH1	23:3:901:GLU:OE2	2.25	0.69
1:A:1670:ASP:OD1	1:A:1673:SER:N	2.25	0.69
7:G:85:G:C8	33:w:395:TRP:CZ3	2.80	0.69
8:H:50:C:H2'	8:H:51:A:C8	2.28	0.69
23:3:527:ILE:HA	23:3:532:ARG:O	1.93	0.69
1:A:1375:TRP:O	1:A:1378:GLU:N	2.25	0.69
5:E:304:SER:H	5:E:330:ILE:HB	1.56	0.69
7:G:91:A:H2'	7:G:92:U:C6	2.27	0.69
11:K:67:TYR:O	11:K:71:GLU:HG2	1.91	0.69
19:X:281:TYR:HB2	19:X:306:PHE:HB3	1.74	0.69
23:3:380:GLU:O	23:3:383:ASP:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1684:PHE:HB3	1:A:1715:TYR:HD2	1.57	0.69
22:1:1017:LEU:HD21	22:1:1058:ILE:HD11	1.75	0.69
38:7:11:CYS:HB3	38:7:85:CYS:HB3	1.74	0.69
1:A:145:GLY:HA2	1:A:245:LEU:HD21	1.75	0.69
2:B:30:A:H2'	2:B:31:U:H6	1.56	0.69
3:C:300:LEU:HD23	3:C:306:ASN:HB2	1.73	0.69
7:G:-3:A:H2'	7:G:-2:A:C8	2.26	0.69
12:L:38:LEU:CD1	12:L:41:LYS:CG	2.57	0.69
1:A:1256:PHE:CG	1:A:1299:ILE:CG2	2.76	0.69
1:A:1437:ARG:NH2	1:A:1461:ASP:OD2	2.26	0.69
3:C:556:ASP:HA	3:C:559:ILE:HD12	1.75	0.69
5:E:224:GLN:HG3	5:E:226:LYS:H	1.59	0.69
19:X:237:ASN:ND2	19:X:244:ILE:O	2.25	0.69
20:Y:49:GLU:N	20:Y:49:GLU:OE2	2.25	0.69
37:6:18:ASN:OD1	37:6:19:ARG:N	2.25	0.69
2:B:18:C:O2	2:B:59:G:N2	2.20	0.68
3:C:879:ASP:OD1	3:C:879:ASP:N	2.25	0.68
22:1:400:SER:N	22:1:403:GLU:OE1	2.26	0.68
23:3:146:ARG:HB2	23:3:146:ARG:NH2	2.04	0.68
23:3:282:GLU:OE1	23:3:282:GLU:N	2.26	0.68
1:A:266:SER:OG	1:A:271:MET:O	2.08	0.68
1:A:318:TYR:HD1	3:C:645:ARG:HH11	1.40	0.68
2:B:100:C:H2'	2:B:101:U:C6	2.27	0.68
17:R:238:THR:O	17:R:242:GLN:HB2	1.94	0.68
22:1:158:GLU:O	22:1:162:THR:HG23	1.93	0.68
1:A:398:THR:HA	3:C:386:GLY:HA3	1.74	0.68
22:1:901:GLN:HA	22:1:939:ARG:HH22	1.58	0.68
3:C:64:LYS:HE3	15:P:206:LYS:HB3	1.75	0.68
20:Y:80:CYS:SG	20:Y:81:PHE:N	2.65	0.68
3:C:128:LEU:HD21	3:C:196:LYS:HE3	1.76	0.68
23:3:644:GLU:HG3	23:3:662:PHE:HB3	1.75	0.68
1:A:443:VAL:HG12	1:A:610:HIS:HB3	1.76	0.68
1:A:1310:ARG:HB3	1:A:1310:ARG:CZ	2.23	0.68
3:C:392:LEU:O	3:C:396:LEU:HG	1.93	0.68
3:C:531:TRP:HB3	3:C:538:HIS:HB3	1.76	0.68
6:F:42:C:H42	7:G:6:A:N6	1.91	0.68
23:3:146:ARG:CG	23:3:146:ARG:HH21	2.06	0.68
1:A:462:ARG:HH21	1:A:465:LYS:HG2	1.58	0.68
1:A:643:GLY:N	2:B:28:A:O2'	2.27	0.68
2:B:8:G:N1	2:B:69:A:N6	2.13	0.68
3:C:286:ASN:HB3	3:C:299:ILE:HG23	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:2098:ALA:O	4:D:2100:GLY:N	2.27	0.68
6:F:85:U:C2	8:H:14:C:N3	2.60	0.68
6:F:86:U:C2	8:H:12:G:O6	2.47	0.68
7:G:98:U:H3	8:H:33:G:H22	1.40	0.68
23:3:82:SER:HG	23:3:84:SER:H	1.39	0.68
23:3:971:ASP:OD1	23:3:972:LEU:N	2.25	0.68
23:3:1136:GLU:OE1	23:3:1136:GLU:N	2.21	0.68
8:H:165:A:O2'	8:H:166:G:O4'	2.12	0.68
17:R:148:ARG:HG2	17:R:148:ARG:HH21	1.59	0.68
18:T:325:THR:O	18:T:325:THR:OG1	2.11	0.68
23:3:878:ASP:OD1	23:3:879:LEU:N	2.25	0.68
38:7:11:CYS:SG	38:7:13:LYS:HG3	2.34	0.68
38:7:35:SER:OG	38:7:36:TYR:N	2.24	0.68
1:A:150:MET:HG3	1:A:572:PHE:HE1	1.59	0.68
1:A:1580:HIS:HB2	1:A:1584:LYS:HE3	1.76	0.68
5:E:239:THR:HB	5:E:289:LEU:H	1.57	0.68
22:1:1078:VAL:HG11	22:1:1114:VAL:HG12	1.75	0.68
40:9:276:VAL:HG21	40:9:438:TYR:CD1	2.29	0.68
1:A:1488:THR:OG1	1:A:1489:LEU:N	2.25	0.68
23:3:498:GLY:O	23:3:525:ARG:NH2	2.27	0.68
33:w:383:LEU:CD2	33:w:397:TYR:CG	2.68	0.68
1:A:467:GLN:NE2	2:B:57:G:O6	2.27	0.67
5:E:304:SER:OG	5:E:305:ALA:N	2.26	0.67
18:T:213:GLU:HG2	18:T:214:PRO:HD2	1.76	0.67
19:X:279:SER:O	19:X:307:GLN:NE2	2.27	0.67
22:1:944:SER:HB2	22:1:948:ARG:CZ	2.24	0.67
22:1:1178:MET:HE3	35:2:591:TYR:CE2	2.28	0.67
40:9:425:GLU:OE1	40:9:427:ARG:NH1	2.27	0.67
3:C:589:LYS:HG3	3:C:630:LEU:HD23	1.75	0.67
6:F:33:G:N1	7:G:14:A:C5	2.62	0.67
23:3:1013:ARG:NH2	23:3:1064:ASP:OD1	2.26	0.67
14:O:63:MET:HA	14:O:161:ARG:HA	1.75	0.67
23:3:947:GLU:HG3	23:3:948:VAL:H	1.60	0.67
38:7:8:LEU:HA	38:7:90:ASN:HD21	1.58	0.67
1:A:104:GLU:HG3	1:A:638:LEU:HD13	1.74	0.67
1:A:253:ASN:OD1	3:C:888:ARG:NH2	2.28	0.67
3:C:230:ASP:OD2	3:C:262:ARG:NH2	2.27	0.67
6:F:62:C:O2'	11:K:38:GLU:OE2	2.11	0.67
10:J:319:MET:O	10:J:323:LEU:HG	1.95	0.67
11:K:79:LEU:HD11	11:K:97:GLU:HG3	1.74	0.67
22:1:1108:ASN:HB3	22:1:1110:VAL:HB	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1278:ASP:OD2	23:3:112:CYS:N	2.28	0.67
37:6:46:ARG:HB3	37:6:63:VAL:HG12	1.76	0.67
3:C:320:LEU:HD21	3:C:344:TRP:HB2	1.76	0.67
22:1:614:ARG:HG3	22:1:647:PHE:HZ	1.58	0.67
1:A:429:ASN:ND2	1:A:432:ARG:HH11	1.91	0.67
1:A:1531:ASN:OD1	1:A:1531:ASN:N	2.24	0.67
3:C:241:ARG:NH2	3:C:583:ASN:O	2.27	0.67
3:C:475:MET:HB2	3:C:498:SER:HB2	1.75	0.67
6:F:85:U:N3	8:H:14:C:N4	2.25	0.67
11:K:360:ILE:O	20:Y:72:LYS:HG3	1.95	0.67
19:X:277:ARG:NH2	22:1:437:PRO:HA	2.09	0.67
27:i:34:VAL:N	27:i:43:GLN:O	2.27	0.67
2:B:33:U:H1'	18:T:279:LYS:HD3	1.77	0.67
3:C:259:LYS:HB3	3:C:262:ARG:HG3	1.76	0.67
3:C:645:ARG:NH2	3:C:653:ILE:O	2.27	0.67
5:E:95:VAL:HG13	5:E:353:MET:HE1	1.77	0.67
10:J:241:VAL:HG22	10:J:243:SER:H	1.58	0.67
38:7:46:CYS:HB3	38:7:85:CYS:HB2	1.77	0.67
1:A:101:LYS:HG3	1:A:473:PHE:HE2	1.59	0.67
2:B:29:A:H2'	2:B:30:A:C8	2.30	0.67
5:E:114:GLU:OE2	5:E:157:CYS:N	2.25	0.67
1:A:617:ASN:HA	1:A:621:VAL:HG22	1.76	0.67
1:A:1295:ILE:HD13	1:A:1295:ILE:C	2.20	0.67
12:L:38:LEU:HD12	12:L:41:LYS:CB	2.25	0.67
12:L:41:LYS:HA	12:L:41:LYS:HE3	1.75	0.67
17:R:385:ASN:O	17:R:386:ARG:NH1	2.28	0.67
18:T:245:HIS:ND1	18:T:267:ASP:OD2	2.28	0.67
22:1:659:GLN:OE1	22:1:659:GLN:N	2.28	0.67
23:3:578:THR:O	23:3:580:ARG:NH1	2.28	0.67
35:2:581:LYS:HD2	35:2:581:LYS:C	2.19	0.67
1:A:582:PHE:CE2	1:A:634:TRP:HB2	2.30	0.67
22:1:1004:ILE:HD11	22:1:1008:LYS:HB2	1.76	0.67
12:L:66:GLU:OE1	12:L:66:GLU:N	2.24	0.66
20:Y:54:CYS:HB3	21:Z:585:ASP:HB2	1.75	0.66
22:1:793:LYS:HB2	22:1:836:THR:HG22	1.77	0.66
23:3:507:SER:OG	23:3:509:SER:OG	2.12	0.66
1:A:508:ILE:HG22	1:A:509:HIS:HD2	1.60	0.66
1:A:535:ARG:NH2	1:A:1551:PHE:CE1	2.62	0.66
1:A:802:THR:OG1	1:A:803:ALA:N	2.23	0.66
1:A:1119:ASP:OD2	1:A:1124:ASN:ND2	2.28	0.66
6:F:78:A:H5''	6:F:79:C:H5	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:332:ARG:NH2	19:X:267:ASP:H	1.93	0.66
22:1:942:ASN:ND2	22:1:943:LYS:O	2.27	0.66
1:A:1295:ILE:CD1	1:A:1327:MET:HE1	2.25	0.66
8:H:100:U:O2	30:k:64:GLY:N	2.25	0.66
23:3:858:GLY:HA3	23:3:861:GLN:HG3	1.77	0.66
37:6:34:GLU:O	37:6:38:ILE:HG13	1.95	0.66
1:A:1580:HIS:O	1:A:1584:LYS:HG2	1.96	0.66
2:B:99:C:H2'	2:B:100:C:C6	2.31	0.66
22:1:1076:ALA:O	22:1:1080:THR:HG23	1.96	0.66
23:3:21:ASN:HD22	23:3:28:GLN:HG3	1.60	0.66
35:2:536:MET:SD	35:2:536:MET:N	2.67	0.66
1:A:344:ASP:N	1:A:344:ASP:OD1	2.26	0.66
1:A:401:GLY:HA2	1:A:404:LEU:HD12	1.76	0.66
1:A:1102:THR:OG1	1:A:1104:ASP:OD1	2.10	0.66
3:C:387:ASP:OD1	3:C:390:THR:OG1	2.11	0.66
3:C:470:PRO:HB3	3:C:545:PRO:HB3	1.77	0.66
3:C:731:SER:HB2	3:C:747:ASP:HB3	1.76	0.66
20:Y:110:ASP:OD1	20:Y:111:HIS:N	2.29	0.66
43:v:66:GLU:H	43:v:66:GLU:CD	2.02	0.66
1:A:1256:PHE:CD1	1:A:1299:ILE:HG22	2.31	0.66
3:C:602:LYS:HD2	3:C:651:ILE:HD11	1.76	0.66
8:H:50:C:H2'	8:H:51:A:H8	1.59	0.66
22:1:698:GLN:O	22:1:702:ARG:NH1	2.29	0.66
23:3:854:ALA:O	23:3:856:LYS:N	2.29	0.66
1:A:843:LEU:HD22	1:A:867:ILE:HG23	1.78	0.66
2:B:23:C:H1'	2:B:24:G:H2'	1.78	0.66
18:T:399:LYS:HB2	18:T:406:ILE:HD11	1.76	0.66
22:1:855:ASP:OD1	22:1:855:ASP:N	2.15	0.66
23:3:1194:SER:OG	23:3:1199:ARG:O	2.13	0.66
43:v:85:ARG:HG3	43:v:85:ARG:O	1.96	0.66
1:A:253:ASN:ND2	1:A:334:THR:O	2.25	0.66
2:B:18:C:N3	2:B:59:G:N1	2.41	0.66
11:K:14:ASN:O	11:K:18:SER:OG	2.13	0.66
12:L:77:LEU:HD21	17:R:285:ALA:HA	1.77	0.66
17:R:332:ARG:HH22	19:X:267:ASP:H	1.42	0.66
18:T:247:SER:OG	18:T:248:THR:N	2.22	0.66
40:9:360:HIS:HA	40:9:365:ILE:HG13	1.78	0.66
3:C:279:ARG:HA	3:C:282:VAL:HG12	1.78	0.66
22:1:899:ALA:O	22:1:903:GLN:NE2	2.28	0.66
43:v:32:GLN:HA	43:v:32:GLN:NE2	2.10	0.66
1:A:733:THR:HG22	40:9:241:TYR:HA	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1018:ASN:OD1	1:A:1019:TYR:N	2.28	0.66
1:A:2105:ILE:O	1:A:2141:GLU:HA	1.96	0.66
3:C:322:SER:O	3:C:326:ILE:HG13	1.96	0.66
35:2:534:GLN:CA	35:2:534:GLN:HE21	2.07	0.66
43:v:93:ALA:HB1	43:v:94:PRO:HD2	1.76	0.66
18:T:356:LEU:HD13	18:T:366:VAL:HB	1.77	0.65
1:A:363:HIS:HE1	3:C:291:MET:HE3	1.61	0.65
1:A:1256:PHE:CD1	1:A:1299:ILE:HG23	2.29	0.65
18:T:264:CYS:HB2	18:T:291:VAL:HG11	1.78	0.65
20:Y:7:VAL:HG23	20:Y:108:ARG:HB3	1.78	0.65
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.61	0.65
33:w:488:ASN:ND2	33:w:491:THR:CA	2.55	0.65
37:6:37:ASP:O	37:6:41:LYS:NZ	2.29	0.65
43:v:54:TYR:OH	43:v:66:GLU:HG3	1.96	0.65
1:A:522:PHE:O	1:A:552:ARG:NH2	2.21	0.65
3:C:749:THR:O	3:C:749:THR:OG1	2.14	0.65
7:G:99:C:H42	8:H:32:U:H3	0.66	0.65
23:3:457:ASN:OD1	23:3:477:SER:OG	2.13	0.65
19:X:353:LYS:HG3	19:X:354:GLU:H	1.61	0.65
22:1:649:LYS:HG2	22:1:689:ILE:HG12	1.79	0.65
22:1:1107:GLN:N	22:1:1108:ASN:OD1	2.29	0.65
23:3:1043:THR:HG22	23:3:1057:ARG:HB2	1.79	0.65
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	1.78	0.65
1:A:1209:HIS:CD2	1:A:1210:LYS:HE2	2.31	0.65
10:J:396:ARG:NH2	10:J:423:GLU:OE2	2.30	0.65
11:K:27:TYR:HA	11:K:34:GLN:HA	1.78	0.65
23:3:394:ASN:OD1	23:3:394:ASN:N	2.29	0.65
33:w:381:LYS:HD2	33:w:381:LYS:O	1.96	0.65
1:A:136:ILE:HG12	1:A:228:TRP:HB3	1.79	0.65
1:A:163:ARG:HD3	1:A:625:PRO:HB3	1.77	0.65
1:A:369:GLU:HG3	3:C:303:LEU:HD22	1.79	0.65
1:A:857:ASN:HB3	1:A:860:GLN:HG3	1.77	0.65
1:A:1167:THR:OG1	1:A:1168:VAL:N	2.26	0.65
22:1:492:GLN:HA	22:1:495:ARG:HD3	1.78	0.65
22:1:902:GLU:O	22:1:903:GLN:NE2	2.29	0.65
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.31	0.65
1:A:1295:ILE:HD11	1:A:1327:MET:HE1	1.79	0.65
22:1:565:ASP:O	22:1:568:ARG:HG3	1.96	0.65
32:b:28:THR:O	32:b:41:LYS:N	2.24	0.65
1:A:357:ASN:ND2	3:C:866:SER:O	2.30	0.65
1:A:1638:ASN:HA	1:A:1656:THR:HA	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:110:PRO:HD2	3:C:537:TYR:CZ	2.32	0.65
3:C:253:VAL:HG11	3:C:289:ILE:HD11	1.79	0.65
3:C:490:PHE:HE2	3:C:612:LYS:HB3	1.62	0.65
5:E:127:ALA:HB1	5:E:154:VAL:HG12	1.79	0.65
7:G:-2:A:H2'	7:G:-1:C:H6	1.61	0.65
7:G:8:C:H2'	7:G:9:C:H6	1.61	0.65
15:P:195:LYS:HB3	40:9:198:LYS:HB2	1.78	0.65
22:1:977:VAL:HG12	22:1:981:TYR:HE2	1.62	0.65
24:o:143:ARG:O	24:o:150:VAL:N	2.28	0.65
1:A:550:VAL:HG22	1:A:591:MET:HE2	1.79	0.65
18:T:370:ASN:OD1	18:T:370:ASN:N	2.30	0.65
18:T:455:GLN:HG3	18:T:485:THR:HG21	1.79	0.65
8:H:126:A:H2'	8:H:127:G:C8	2.31	0.65
23:3:614:VAL:HG12	23:3:633:LEU:HD21	1.79	0.65
23:3:1107:THR:OG1	23:3:1108:THR:N	2.30	0.65
35:2:534:GLN:HE21	35:2:534:GLN:C	2.05	0.65
37:6:47:GLN:HE22	37:6:49:ARG:HH21	1.44	0.65
1:A:95:MET:HE1	1:A:496:VAL:HG13	1.78	0.64
1:A:693:ILE:O	1:A:696:MET:N	2.29	0.64
1:A:1181:ASP:OD1	1:A:1181:ASP:N	2.28	0.64
3:C:663:CYS:HB3	3:C:785:ARG:HB2	1.79	0.64
8:H:46:U:C5	33:w:394:TYR:CB	2.76	0.64
40:9:333:GLY:O	40:9:378:SER:OG	2.13	0.64
1:A:447:TYR:CE2	1:A:611:LEU:HD13	2.32	0.64
1:A:582:PHE:CD2	1:A:630:TRP:HB2	2.33	0.64
22:1:1178:MET:HE2	35:2:591:TYR:CZ	2.32	0.64
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.25	0.64
2:B:30:A:H2'	2:B:31:U:C6	2.32	0.64
7:G:91:A:H2'	7:G:92:U:H6	1.63	0.64
19:X:222:GLU:HG2	20:Y:69:ARG:HH12	1.61	0.64
22:1:619:ASN:OD1	22:1:620:MET:N	2.31	0.64
22:1:839:GLU:HA	22:1:842:ASN:HD22	1.62	0.64
23:3:550:ASN:ND2	23:3:593:ALA:O	2.31	0.64
1:A:254:TYR:HE2	1:A:433:GLU:HA	1.62	0.64
3:C:111:VAL:HG13	3:C:155:PRO:HD2	1.79	0.64
6:F:44:G:H21	7:G:5:G:H22	1.43	0.64
10:J:252:GLU:OE2	10:J:260:ARG:HD3	1.97	0.64
11:K:35:CYS:HB3	11:K:40:GLY:HA2	1.77	0.64
35:2:514:LYS:CA	35:2:593:GLU:OE1	2.46	0.64
1:A:387:PHE:HE1	3:C:326:ILE:HG22	1.62	0.64
1:A:1310:ARG:HG2	1:A:1310:ARG:HH21	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:223:ASP:OD1	3:C:223:ASP:N	2.28	0.64
3:C:224:GLY:HA3	3:C:438:ILE:HD12	1.78	0.64
3:C:853:ARG:O	3:C:876:PRO:HD2	1.97	0.64
5:E:126:SER:HG	5:E:136:TRP:CD1	2.15	0.64
22:1:754:ILE:HA	22:1:757:MET:HE3	1.80	0.64
25:p:223:ALA:HB1	33:w:498:GLN:HG2	1.80	0.64
29:l:33:ILE:H	29:l:43:MET:HA	1.63	0.64
41:8:105:LEU:O	41:8:108:LEU:N	2.31	0.64
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.31	0.64
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.80	0.64
9:I:609:ALA:HA	9:I:612:ALA:HB3	1.79	0.64
10:J:297:ASN:O	10:J:301:ARG:HG3	1.98	0.64
19:X:282:LEU:N	19:X:291:ASP:OD2	2.23	0.64
17:R:150:ALA:CB	18:T:360:VAL:HG21	2.28	0.64
18:T:257:ARG:NH2	18:T:297:HIS:O	2.31	0.64
20:Y:56:PHE:O	20:Y:84:TYR:OH	2.11	0.64
22:1:1126:PHE:HA	35:2:575:PHE:HD2	1.59	0.64
35:2:581:LYS:HB3	35:2:581:LYS:NZ	2.13	0.64
40:9:365:ILE:HB	40:9:383:THR:OG1	1.98	0.64
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.79	0.64
7:G:-2:A:H2'	7:G:-1:C:C6	2.33	0.64
22:1:489:PRO:O	22:1:492:GLN:N	2.30	0.64
23:3:581:LYS:HD2	23:3:625:LEU:HD22	1.79	0.64
25:p:152:ILE:CB	33:w:498:GLN:HE21	2.06	0.64
27:d:35:SER:O	27:d:43:GLN:N	2.25	0.64
1:A:634:TRP:NE1	1:A:638:LEU:HD11	2.12	0.64
6:F:40:U:C2	6:F:41:A:C8	2.86	0.64
7:G:6:A:H8	7:G:7:G:N7	1.96	0.64
9:I:374:ILE:O	9:I:376:ASN:N	2.31	0.64
17:R:306:ALA:HB1	17:R:310:ARG:HH12	1.63	0.64
22:1:1257:PRO:HB3	35:2:481:THR:OG1	1.98	0.64
23:3:320:ASP:OD1	23:3:320:ASP:N	2.29	0.64
23:3:447:MET:HE3	23:3:750:CYS:HA	1.80	0.64
23:3:999:ARG:HH11	23:3:1024:PHE:HZ	1.46	0.64
23:3:1188:ASN:OD1	23:3:1188:ASN:N	2.28	0.64
1:A:135:VAL:HA	1:A:225:TYR:CE2	2.32	0.63
8:H:43:U:H2'	8:H:44:U:C5	2.33	0.63
18:T:203:HIS:CE1	18:T:229:LYS:HD2	2.33	0.63
18:T:213:GLU:HG3	18:T:218:TRP:CE2	2.33	0.63
25:p:184:PRO:CG	33:w:487:VAL:HG13	2.15	0.63
1:A:108:MET:HG2	1:A:114:ARG:HH22	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:ASP:HA	1:A:562:VAL:HB	1.80	0.63
1:A:589:THR:OG1	1:A:591:MET:SD	2.49	0.63
3:C:460:ASP:OD1	3:C:460:ASP:N	2.29	0.63
10:J:434:VAL:O	10:J:438:TYR:HB3	1.99	0.63
18:T:394:ASN:ND2	18:T:408:ASN:OD1	2.31	0.63
40:9:242:SER:HA	40:9:263:ALA:HA	1.81	0.63
29:g:21:GLU:O	29:g:69:ARG:N	2.31	0.63
3:C:212:SER:O	3:C:216:THR:HG23	1.98	0.63
17:R:148:ARG:HH21	17:R:148:ARG:CG	2.12	0.63
23:3:316:GLU:OE2	23:3:326:ARG:NH2	2.32	0.63
1:A:200:ASP:HA	1:A:237:THR:HG21	1.79	0.63
1:A:508:ILE:HG22	1:A:509:HIS:CD2	2.33	0.63
2:B:62:G:H2'	2:B:63:A:C8	2.32	0.63
3:C:210:ASN:OD1	3:C:633:GLY:HA3	1.99	0.63
5:E:221:ASP:HB3	5:E:224:GLN:HG2	1.81	0.63
22:1:1145:ASN:ND2	22:1:1183:VAL:HG11	2.14	0.63
1:A:67:ARG:NH2	1:A:487:LEU:HD23	2.13	0.63
1:A:145:GLY:HA3	1:A:242:ALA:HA	1.80	0.63
1:A:1947:ASN:HA	1:A:1950:ALA:HB3	1.81	0.63
6:F:15:A:H2'	6:F:16:G:C8	2.34	0.63
8:H:46:U:C6	33:w:394:TYR:CD2	2.86	0.63
8:H:50:C:N3	8:H:64:A:N6	2.46	0.63
1:A:1660:TYR:OH	1:A:1717:ASN:O	2.17	0.63
5:E:336:HIS:HB2	5:E:341:ILE:HB	1.81	0.63
8:H:70:C:H2'	8:H:71:C:C6	2.34	0.63
8:H:78:C:H2'	8:H:79:G:C8	2.29	0.63
11:K:179:ARG:HA	11:K:182:GLU:OE2	1.99	0.63
22:1:762:ALA:O	22:1:766:THR:OG1	2.17	0.63
22:1:1133:MET:SD	35:2:528:ILE:CD1	2.87	0.63
1:A:1491:LYS:O	1:A:1710:ASN:ND2	2.32	0.63
1:A:1579:ALA:O	1:A:1584:LYS:NZ	2.24	0.63
3:C:911:PRO:HG2	3:C:912:LEU:HD12	1.80	0.63
23:3:260:ASN:OD1	23:3:261:PHE:N	2.32	0.63
23:3:552:ARG:HH21	23:3:569:ASP:HA	1.64	0.63
1:A:277:PRO:HD3	1:A:451:LEU:HB3	1.80	0.63
1:A:301:LYS:HG2	3:C:939:ARG:HB3	1.81	0.63
2:B:31:U:H2'	2:B:32:C:C6	2.34	0.63
8:H:180:G:H21	29:l:53:GLY:HA3	1.64	0.63
18:T:307:SER:C	18:T:309:ASP:H	2.06	0.63
33:w:456:VAL:O	33:w:459:TRP:HB3	1.98	0.63
1:A:799:PRO:HD3	17:R:284:PHE:CD2	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.31	0.63
8:H:139:C:H2'	8:H:140:A:C8	2.34	0.63
10:J:343:GLU:OE1	10:J:378:ASN:ND2	2.19	0.63
22:1:543:THR:O	22:1:543:THR:OG1	2.14	0.63
33:w:448:ASN:CB	35:2:462:VAL:HG11	2.29	0.63
35:2:537:ARG:HH11	35:2:537:ARG:CG	2.10	0.63
40:9:367:SER:HB2	40:9:394:HIS:HB3	1.81	0.63
1:A:1209:HIS:HD2	1:A:1210:LYS:H	1.47	0.62
1:A:1307:MET:HA	1:A:1307:MET:CE	2.29	0.62
3:C:122:LEU:HB3	3:C:199:LEU:HD22	1.79	0.62
3:C:381:LEU:HD22	3:C:416:LEU:HD11	1.80	0.62
3:C:780:CYS:HB3	3:C:934:MET:HG2	1.81	0.62
18:T:295:ASP:OD1	18:T:296:LEU:N	2.31	0.62
20:Y:101:LYS:HG2	20:Y:106:THR:HG22	1.81	0.62
23:3:550:ASN:HD21	23:3:595:VAL:N	1.97	0.62
40:9:370:ASN:ND2	40:9:372:GLY:O	2.32	0.62
5:E:65:HIS:HD2	5:E:351:LEU:HD11	1.64	0.62
22:1:826:ASP:OD1	22:1:827:ARG:N	2.32	0.62
1:A:501:TYR:HE1	1:A:518:LEU:HB3	1.64	0.62
1:A:1596:VAL:O	1:A:1600:GLU:HG2	2.00	0.62
18:T:415:ILE:O	18:T:432:ASP:N	2.31	0.62
19:X:327:TYR:HD1	19:X:349:TYR:HB3	1.65	0.62
23:3:405:SER:HB2	23:3:1123:SER:O	1.99	0.62
23:3:477:SER:HB2	23:3:504:PRO:HA	1.81	0.62
23:3:700:LYS:HE2	23:3:702:PHE:HZ	1.63	0.62
3:C:139:HIS:O	3:C:259:LYS:NZ	2.32	0.62
3:C:448:LYS:O	3:C:452:THR:CB	2.47	0.62
11:K:47:SER:HG	11:K:49:SER:HG	1.34	0.62
1:A:112:GLN:HG3	1:A:190:ALA:HB2	1.80	0.62
1:A:118:VAL:HG22	1:A:129:VAL:HA	1.82	0.62
1:A:1134:TRP:NE1	1:A:1193:GLU:OE2	2.31	0.62
1:A:1554:GLN:OE1	1:A:1622:MET:HE3	1.98	0.62
3:C:139:HIS:HB3	45:C:1500:GTP:H5''	1.81	0.62
17:R:123:GLU:OE1	17:R:125:MET:N	2.32	0.62
33:w:477:GLU:HB3	33:w:489:LYS:HB2	1.81	0.62
38:7:23:CYS:SG	38:7:26:CYS:N	2.64	0.62
32:b:13:GLU:O	32:b:29:ILE:N	2.32	0.62
1:A:690:MET:HA	1:A:694:LEU:HD12	1.82	0.62
3:C:129:ILE:HD12	3:C:441:PRO:HG2	1.80	0.62
3:C:607:LEU:HD21	3:C:644:LEU:HD22	1.82	0.62
17:R:332:ARG:NH2	19:X:366:GLU:OE1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:213:GLU:HG3	18:T:218:TRP:CZ2	2.35	0.62
27:d:42:MET:O	27:d:64:ILE:N	2.21	0.62
1:A:170:ASP:HB3	1:A:173:GLU:HB2	1.80	0.62
1:A:518:LEU:HD11	1:A:522:PHE:HA	1.82	0.62
1:A:569:VAL:HG23	1:A:570:ASP:H	1.64	0.62
1:A:684:GLU:CD	18:T:308:ARG:HH21	2.06	0.62
1:A:1272:THR:HG22	1:A:1372:ILE:HD11	1.81	0.62
1:A:1551:PHE:CB	1:A:1553:VAL:HG23	2.29	0.62
1:A:1629:ILE:O	1:A:1661:TRP:HA	1.98	0.62
3:C:854:ARG:HB3	3:C:876:PRO:HG2	1.80	0.62
8:H:70:C:H2'	8:H:71:C:H6	1.65	0.62
18:T:190:TRP:NE1	18:T:500:HIS:O	2.33	0.62
21:Z:600:ARG:HH22	21:Z:601:LEU:HD13	1.64	0.62
23:3:209:THR:O	23:3:209:THR:OG1	2.15	0.62
1:A:1734:MET:SD	1:A:1734:MET:N	2.73	0.62
3:C:664:GLU:HB3	3:C:820:PHE:CZ	2.35	0.62
22:1:1054:GLU:O	22:1:1058:ILE:HG13	2.00	0.62
22:1:1126:PHE:O	35:2:575:PHE:HE2	1.82	0.62
43:v:85:ARG:HE	43:v:85:ARG:CA	2.05	0.62
1:A:197:PRO:HA	1:A:204:LEU:HD13	1.81	0.62
1:A:261:LYS:HA	1:A:328:HIS:CD2	2.35	0.62
1:A:1607:GLU:N	1:A:1632:PHE:O	2.25	0.62
6:F:41:A:H2'	6:F:42:C:C6	2.35	0.62
8:H:82:G:H2'	8:H:83:A:H8	1.65	0.62
22:1:1133:MET:CE	35:2:528:ILE:HD12	2.29	0.62
23:3:146:ARG:HE	23:3:150:ALA:HB1	1.61	0.62
23:3:186:GLU:O	23:3:206:GLN:HB2	1.99	0.62
43:v:45:TYR:CD1	43:v:58:LEU:HB2	2.35	0.62
2:B:52:U:H2'	2:B:53:U:H6	1.65	0.62
2:B:62:G:H2'	2:B:63:A:H8	1.65	0.62
11:K:73:ARG:NH1	11:K:77:LEU:HD11	2.14	0.62
12:L:37:LEU:CD2	43:v:30:LEU:HG	2.30	0.62
41:8:64:ASP:O	41:8:68:ILE:HG12	2.00	0.62
27:d:34:VAL:N	27:d:43:GLN:O	2.32	0.62
1:A:350:PHE:HA	3:C:268:LYS:HB3	1.81	0.61
3:C:749:THR:O	3:C:753:GLU:N	2.33	0.61
6:F:47:A:H3'	6:F:48:A:H4'	1.81	0.61
12:L:62:GLU:OE1	12:L:62:GLU:N	2.33	0.61
22:1:584:ASP:O	22:1:590:ARG:NH2	2.31	0.61
24:o:45:ASP:HA	24:o:66:LEU:HA	1.81	0.61
41:8:47:VAL:HG13	41:8:48:ILE:HG12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:LYS:NZ	1:A:622:GLY:O	2.33	0.61
11:K:159:LYS:HA	11:K:162:ASP:OD2	2.00	0.61
22:1:1262:ARG:HH12	35:2:483:GLN:NE2	1.98	0.61
23:3:370:GLU:OE2	23:3:390:ARG:NH1	2.32	0.61
23:3:462:VAL:HG21	23:3:508:CYS:HB2	1.81	0.61
23:3:553:GLN:OE1	23:3:553:GLN:N	2.33	0.61
23:3:727:SER:O	23:3:728:ARG:NH1	2.34	0.61
23:3:730:HIS:HE1	23:3:773:VAL:HG13	1.63	0.61
1:A:467:GLN:HB3	2:B:19:A:N6	2.15	0.61
8:H:124:G:H2'	8:H:125:G:C8	2.36	0.61
17:R:152:GLU:HA	17:R:152:GLU:OE2	1.98	0.61
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.82	0.61
3:C:203:MET:HG2	3:C:218:GLY:HA3	1.83	0.61
18:T:292:TYR:HE1	18:T:308:ARG:HB2	1.65	0.61
18:T:412:HIS:ND1	18:T:437:HIS:HB2	2.15	0.61
22:1:1074:ARG:O	22:1:1078:VAL:HG23	1.99	0.61
23:3:200:ALA:O	23:3:204:THR:OG1	2.18	0.61
23:3:1175:ASP:OD1	23:3:1177:ASP:N	2.34	0.61
1:A:134:TRP:CZ3	1:A:420:ARG:HG3	2.35	0.61
1:A:582:PHE:HD2	1:A:630:TRP:HB2	1.65	0.61
1:A:1057:ARG:NH1	1:A:1060:GLU:OE1	2.31	0.61
1:A:1719:PHE:O	1:A:1722:SER:OG	2.10	0.61
3:C:774:THR:HA	3:C:784:ILE:HD12	1.81	0.61
7:G:101:U:O5'	22:1:1070:LYS:NZ	2.34	0.61
17:R:238:THR:O	17:R:242:GLN:CB	2.48	0.61
19:X:371:HIS:N	19:X:374:SER:OG	2.20	0.61
23:3:95:SER:OG	23:3:96:LYS:N	2.31	0.61
37:6:82:VAL:O	37:6:85:ARG:HG2	2.01	0.61
1:A:206:TRP:CZ2	1:A:234:MET:HE2	2.36	0.61
1:A:269:LEU:HD22	1:A:321:ASN:HD21	1.65	0.61
5:E:75:HIS:ND1	5:E:77:ASN:OD1	2.33	0.61
5:E:209:ILE:HG21	5:E:250:LEU:HD22	1.83	0.61
5:E:343:ILE:HD11	5:E:353:MET:HE3	1.83	0.61
7:G:85:G:N9	33:w:395:TRP:CZ3	2.69	0.61
18:T:308:ARG:HG2	18:T:308:ARG:NH1	2.16	0.61
23:3:55:THR:O	23:3:55:THR:OG1	2.18	0.61
40:9:397:PHE:N	40:9:397:PHE:CD1	2.68	0.61
1:A:1609:VAL:HG13	1:A:1631:LEU:HD23	1.81	0.61
6:F:86:U:O2	8:H:12:G:O6	2.18	0.61
23:3:174:ASP:CG	23:3:240:GLY:H	2.08	0.61
23:3:898:ASN:OD1	23:3:899:THR:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2:584:LEU:H	35:2:584:LEU:HD12	1.66	0.61
2:B:99:C:H2'	2:B:100:C:H6	1.64	0.61
7:G:-4:G:O2'	7:G:-3:A:O5'	2.18	0.61
8:H:46:U:H6	33:w:394:TYR:CG	2.14	0.61
22:1:522:LYS:HD3	22:1:525:GLU:CD	2.25	0.61
1:A:519:ASP:OD1	1:A:522:PHE:N	2.34	0.61
1:A:855:ARG:HG3	1:A:856:LEU:H	1.66	0.61
1:A:1308:PRO:HB2	1:A:1548:TYR:HD2	1.50	0.61
1:A:1601:LEU:HA	1:A:1606:ILE:HD12	1.80	0.61
3:C:388:VAL:HA	3:C:392:LEU:HD12	1.82	0.61
6:F:1:G:H2'	6:F:2:U:C6	2.36	0.61
11:K:33:LYS:HD2	11:K:44:HIS:CE1	2.36	0.61
22:1:953:ASP:O	22:1:956:SER:OG	2.10	0.61
23:3:566:PHE:HD2	23:3:574:LEU:HD23	1.65	0.61
40:9:416:ASP:O	40:9:420:ASP:N	2.31	0.61
2:B:37:G:N2	2:B:46:U:H1'	2.16	0.61
3:C:384:VAL:HA	3:C:392:LEU:HD11	1.82	0.61
6:F:42:C:H2'	6:F:43:A:C8	2.36	0.61
7:G:98:U:H3'	7:G:99:C:H5''	1.82	0.61
11:K:142:ILE:O	11:K:144:ARG:NH2	2.34	0.61
20:Y:86:ASP:O	20:Y:89:SER:OG	2.19	0.61
22:1:516:LEU:O	22:1:520:THR:OG1	2.17	0.61
23:3:642:ILE:O	23:3:703:ARG:NH2	2.33	0.61
35:2:524:LEU:HD13	35:2:528:ILE:CG2	2.31	0.61
3:C:208:HIS:HB3	3:C:211:PHE:HD2	1.63	0.60
3:C:808:ILE:HA	3:C:811:THR:HG22	1.82	0.60
23:3:146:ARG:CD	23:3:150:ALA:HA	2.31	0.60
1:A:828:PRO:O	1:A:882:LYS:NZ	2.33	0.60
3:C:799:GLU:HB2	3:C:802:HIS:HB3	1.82	0.60
8:H:43:U:H2'	8:H:44:U:C6	2.36	0.60
8:H:46:U:C6	33:w:394:TYR:CB	2.85	0.60
18:T:213:GLU:O	18:T:472:GLN:NE2	2.30	0.60
23:3:174:ASP:OD2	23:3:240:GLY:N	2.32	0.60
30:k:22:ASN:N	30:k:66:SER:O	2.34	0.60
1:A:372:PRO:HD3	3:C:341:LYS:HD3	1.84	0.60
1:A:717:TRP:HZ3	1:A:747:ALA:HB2	1.65	0.60
1:A:1457:HIS:CD2	17:R:420:SER:HB3	2.36	0.60
6:F:36:A:C6	7:G:10:U:N3	2.69	0.60
6:F:40:U:N3	6:F:41:A:N7	2.49	0.60
18:T:375:VAL:HG22	18:T:391:SER:HB2	1.84	0.60
23:3:689:THR:OG1	23:3:690:ARG:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1007:GLU:O	23:3:1008:SER:HB2	2.00	0.60
35:2:532:GLY:C	35:2:534:GLN:N	2.58	0.60
40:9:306:ASN:OD1	40:9:345:TYR:N	2.24	0.60
1:A:182:ILE:HA	1:A:185:VAL:HG22	1.82	0.60
1:A:530:LEU:HB3	1:A:534:GLU:HB3	1.82	0.60
5:E:93:TRP:HA	5:E:101:ASN:HA	1.83	0.60
22:1:529:GLY:O	22:1:533:ASN:ND2	2.35	0.60
22:1:1135:GLU:O	22:1:1138:VAL:HG22	2.01	0.60
33:w:383:LEU:HD23	33:w:397:TYR:CD2	2.37	0.60
1:A:405:LEU:HD11	3:C:385:VAL:HG11	1.83	0.60
1:A:1256:PHE:H	1:A:1531:ASN:ND2	2.00	0.60
1:A:1433:ASP:OD1	1:A:1439:ARG:NH2	2.34	0.60
1:A:1639:VAL:HG13	1:A:1717:ASN:HB3	1.83	0.60
3:C:190:LEU:O	3:C:198:TYR:N	2.35	0.60
3:C:636:TYR:O	3:C:640:VAL:HG23	2.01	0.60
11:K:42:LYS:O	11:K:46:MET:HG2	2.01	0.60
12:L:16:ASP:OD2	12:L:54:LEU:HD21	2.01	0.60
18:T:311:THR:OG1	18:T:312:ALA:N	2.32	0.60
22:1:620:MET:O	22:1:625:ARG:NH1	2.34	0.60
23:3:1027:ASP:OD2	23:3:1031:ARG:NH1	2.33	0.60
1:A:363:HIS:CE1	3:C:291:MET:HE3	2.36	0.60
1:A:1712:HIS:CE1	1:A:1734:MET:HG3	2.36	0.60
5:E:133:VAL:HG22	5:E:154:VAL:HG11	1.83	0.60
7:G:108:U:H4'	7:G:109:U:OP2	2.01	0.60
17:R:150:ALA:HB1	18:T:360:VAL:HG21	1.83	0.60
1:A:1332:HIS:NE2	1:A:1358:SER:O	2.35	0.60
3:C:302:PRO:HB2	3:C:320:LEU:HD13	1.84	0.60
7:G:115:C:N3	20:Y:116:ARG:HB2	2.16	0.60
17:R:148:ARG:HB3	17:R:148:ARG:NH2	2.17	0.60
22:1:1126:PHE:CE1	35:2:576:PHE:CZ	2.90	0.60
23:3:1040:ASP:N	23:3:1040:ASP:OD1	2.32	0.60
35:2:515:ARG:HD3	43:v:60:LEU:O	2.02	0.60
1:A:1416:ILE:HG22	1:A:1417:PRO:HD3	1.84	0.60
1:A:1539:SER:O	1:A:1541:THR:N	2.34	0.60
2:B:14:U:H2'	2:B:15:C:C6	2.37	0.60
8:H:161:U:O2	8:H:163:G:N2	2.35	0.60
20:Y:113:SER:HG	20:Y:114:ASN:HD22	1.50	0.60
23:3:616:ILE:O	23:3:628:LEU:N	2.23	0.60
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.83	0.60
23:3:899:THR:OG1	23:3:900:GLY:N	2.34	0.60
25:p:152:ILE:CB	33:w:498:GLN:HE22	2.11	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:i:21:VAL:O	27:i:28:GLU:HA	2.02	0.60
30:k:21:LEU:HA	30:k:67:ILE:HA	1.81	0.60
1:A:261:LYS:HB3	1:A:328:HIS:HB3	1.83	0.60
3:C:888:ARG:HD2	3:C:896:PHE:HD1	1.67	0.60
6:F:81:C:H4'	6:F:82:A:C8	2.37	0.60
11:K:63:GLN:HG3	11:K:64:PHE:N	2.17	0.60
16:Q:515:VAL:N	16:Q:540:THR:O	2.34	0.60
40:9:236:LEU:HD22	40:9:452:GLN:NE2	2.17	0.60
1:A:564:TYR:HB2	1:A:574:LEU:HB2	1.82	0.60
1:A:768:ASP:OD1	1:A:769:LYS:N	2.35	0.60
3:C:516:LEU:HD21	3:C:573:GLU:HA	1.83	0.60
8:H:46:U:C6	33:w:394:TYR:HB2	2.37	0.60
1:A:221:ASN:ND2	2:B:12:U:OP1	2.34	0.59
1:A:888:GLN:O	1:A:889:ARG:NE	2.31	0.59
2:B:18:C:H2'	2:B:19:A:H8	1.67	0.59
3:C:94:ILE:HB	18:T:276:GLU:HG3	1.84	0.59
3:C:140:HIS:NE2	3:C:233:GLU:OE1	2.31	0.59
3:C:618:THR:HB	3:C:630:LEU:HB2	1.83	0.59
6:F:36:A:O2'	6:F:37:C:H5''	2.02	0.59
18:T:223:SER:HG	18:T:225:ASP:H	1.50	0.59
22:1:1145:ASN:ND2	22:1:1183:VAL:CG1	2.65	0.59
22:1:1273:TYR:O	22:1:1277:GLN:HB3	2.00	0.59
40:9:368:MET:O	40:9:394:HIS:ND1	2.35	0.59
41:8:45:LEU:O	41:8:48:ILE:N	2.35	0.59
3:C:495:ARG:HB3	3:C:549:TRP:CD1	2.33	0.59
23:3:27:GLN:HE21	23:3:45:PRO:HG3	1.67	0.59
23:3:545:VAL:N	23:3:557:ALA:O	2.28	0.59
23:3:1043:THR:HG21	23:3:1057:ARG:HH21	1.67	0.59
1:A:941:LYS:HE2	1:A:1071:PHE:CD1	2.37	0.59
10:J:267:ARG:O	10:J:271:VAL:HG23	2.02	0.59
10:J:308:ARG:HG3	17:R:231:HIS:O	2.02	0.59
23:3:369:GLU:N	23:3:369:GLU:OE1	2.34	0.59
23:3:895:ARG:HD3	23:3:903:TRP:CE2	2.37	0.59
23:3:1203:GLU:HA	23:3:1203:GLU:OE2	2.01	0.59
40:9:268:GLU:O	40:9:271:LEU:N	2.35	0.59
1:A:768:ASP:HB3	1:A:771:VAL:HG12	1.83	0.59
1:A:1106:ALA:O	1:A:1110:ILE:HG13	2.01	0.59
4:D:1378:TYR:HA	4:D:1452:VAL:O	2.02	0.59
6:F:60:C:H2'	6:F:61:C:O4'	2.01	0.59
18:T:439:TRP:CE3	18:T:446:ASN:HB2	2.37	0.59
22:1:588:TYR:HD1	38:7:96:THR:HG22	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:v:92:GLU:HA	43:v:92:GLU:OE1	1.94	0.59
1:A:67:ARG:NE	1:A:491:GLU:OE2	2.35	0.59
1:A:101:LYS:HG3	1:A:473:PHE:CE2	2.36	0.59
1:A:136:ILE:HG13	1:A:225:TYR:CE1	2.37	0.59
1:A:261:LYS:HA	1:A:328:HIS:HD2	1.68	0.59
1:A:885:LEU:O	1:A:889:ARG:NH2	2.36	0.59
3:C:209:VAL:HB	3:C:898:LEU:HD21	1.84	0.59
3:C:683:ASN:OD1	3:C:797:ALA:N	2.35	0.59
6:F:33:G:N1	7:G:14:A:N6	2.45	0.59
17:R:137:GLU:OE1	17:R:137:GLU:N	2.35	0.59
22:1:1103:VAL:O	22:1:1105:GLU:N	2.36	0.59
41:8:55:ARG:O	41:8:59:ILE:HG13	2.03	0.59
1:A:251:ASP:HB2	1:A:334:THR:OG1	2.03	0.59
1:A:339:PHE:HE1	1:A:406:TRP:HB2	1.68	0.59
1:A:1307:MET:HA	1:A:1307:MET:HE2	1.84	0.59
3:C:591:ALA:HB2	3:C:940:ARG:HH21	1.66	0.59
6:F:23:U:H2'	6:F:24:A:O4'	2.01	0.59
7:G:94:C:H2'	7:G:95:U:H6	1.68	0.59
18:T:216:ASN:ND2	18:T:473:SER:H	2.00	0.59
22:1:1144:GLN:OE1	43:v:51:LEU:CD2	2.50	0.59
23:3:538:THR:HG22	23:3:558:LEU:HD11	1.84	0.59
23:3:791:HIS:C	23:3:791:HIS:CD2	2.80	0.59
40:9:326:ARG:HG3	40:9:327:ASN:OD1	2.03	0.59
1:A:367:SER:OG	3:C:299:ILE:HG21	2.03	0.59
3:C:603:MET:HG3	3:C:653:ILE:HG12	1.83	0.59
5:E:65:HIS:CD2	5:E:83:SER:HG	2.18	0.59
14:O:64:ARG:N	14:O:160:ASN:O	2.27	0.59
18:T:460:ASP:OD1	18:T:461:SER:N	2.35	0.59
36:4:165:GLN:O	36:4:172:ILE:N	2.35	0.59
1:A:851:SER:OG	1:A:852:VAL:N	2.36	0.59
2:B:15:C:H2'	2:B:16:U:H6	1.68	0.59
7:G:104:C:H4'	7:G:105:C:OP2	2.02	0.59
22:1:619:ASN:ND2	22:1:624:VAL:HG21	2.17	0.59
23:3:459:VAL:HG23	23:3:476:VAL:HA	1.84	0.59
23:3:669:LEU:HD22	23:3:673:VAL:HG22	1.85	0.59
23:3:1081:LEU:HD22	23:3:1081:LEU:C	2.28	0.59
1:A:995:ARG:HG3	17:R:291:LEU:HD13	1.84	0.59
2:B:58:U:H2'	2:B:59:G:C8	2.37	0.59
5:E:329:SER:O	5:E:347:SER:N	2.29	0.59
22:1:903:GLN:HE22	22:1:910:MET:HE3	1.68	0.59
23:3:374:SER:OG	23:3:375:SER:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:406:PRO:O	23:3:427:CYS:HB2	2.02	0.59
23:3:808:THR:HG22	23:3:884:GLN:OE1	2.02	0.59
29:l:30:GLY:HA3	29:l:46:ILE:HA	1.85	0.59
1:A:308:ILE:HG22	1:A:313:LYS:HE3	1.84	0.59
7:G:101:U:C2	7:G:102:G:H8	2.20	0.59
10:J:301:ARG:O	10:J:305:THR:OG1	2.21	0.59
22:1:117:ASP:O	22:1:121:LYS:HG3	2.03	0.59
22:1:118:GLU:HG2	22:1:121:LYS:HD2	1.85	0.59
22:1:484:GLU:HA	22:1:487:LEU:HD12	1.85	0.59
23:3:463:ARG:HD3	23:3:468:ASP:HB3	1.85	0.59
40:9:360:HIS:ND1	40:9:391:ASP:OD1	2.36	0.59
2:B:97:G:H2'	2:B:98:G:C8	2.38	0.58
3:C:955:ASP:HB3	3:C:957:MET:HE2	1.83	0.58
8:H:126:A:H2'	8:H:127:G:H8	1.67	0.58
22:1:1137:ARG:HH21	35:2:524:LEU:HD12	1.68	0.58
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.42	0.58
23:3:12:THR:O	23:3:12:THR:OG1	2.17	0.58
35:2:530:ARG:HD3	35:2:530:ARG:C	2.24	0.58
40:9:295:LEU:HD22	40:9:397:PHE:HB2	1.84	0.58
1:A:62:PRO:HG2	1:A:65:HIS:HB2	1.84	0.58
1:A:781:ARG:HG2	1:A:1022:MET:CE	2.33	0.58
1:A:1597:PHE:CE1	1:A:1725:LEU:HD21	2.38	0.58
3:C:143:THR:OG1	3:C:204:ASP:OD2	2.21	0.58
5:E:241:LEU:HB3	5:E:250:LEU:HD11	1.84	0.58
12:L:102:PHE:HD2	12:L:103:LEU:HD23	1.68	0.58
22:1:1197:LEU:HD11	38:7:78:GLN:HE21	1.67	0.58
22:1:1301:ASP:N	22:1:1301:ASP:OD1	2.35	0.58
27:i:72:ILE:O	31:j:78:MET:N	2.29	0.58
1:A:776:LEU:O	1:A:780:THR:HG22	2.03	0.58
1:A:798:GLY:HA2	17:R:284:PHE:CE2	2.37	0.58
1:A:1310:ARG:HB2	1:A:1547:VAL:HG23	1.85	0.58
1:A:1553:VAL:CG1	7:G:2:U:O2'	2.50	0.58
3:C:328:ALA:O	3:C:332:GLY:HA2	2.03	0.58
3:C:584:THR:OG1	3:C:585:THR:N	2.36	0.58
16:Q:440:PRO:HG2	16:Q:1108:ALA:HB1	1.85	0.58
22:1:559:ILE:HG13	22:1:563:LEU:HD13	1.85	0.58
22:1:785:LYS:HG2	22:1:818:PHE:HE1	1.68	0.58
24:o:46:ALA:HA	24:o:68:THR:O	2.02	0.58
35:2:530:ARG:CB	35:2:578:TRP:CZ3	2.86	0.58
3:C:122:LEU:HD13	3:C:199:LEU:HB2	1.85	0.58
5:E:139:GLU:OE2	28:a:11:GLN:CA	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:118:GLY:HA2	23:3:132:ILE:HD11	1.84	0.58
40:9:360:HIS:HB2	40:9:387:CYS:O	2.03	0.58
1:A:314:ILE:O	1:A:330:THR:HG21	2.03	0.58
1:A:794:TYR:HD1	1:A:800:TYR:HE2	1.50	0.58
1:A:1026:ASN:O	1:A:1026:ASN:ND2	2.35	0.58
1:A:2177:TRP:O	1:A:2213:ILE:HA	2.03	0.58
5:E:60:MET:HB2	5:E:353:MET:HB2	1.85	0.58
22:1:952:ALA:HA	22:1:955:ILE:HD12	1.85	0.58
23:3:712:VAL:HG23	23:3:713:LEU:O	2.03	0.58
24:o:100:LEU:O	24:o:125:VAL:N	2.37	0.58
41:8:44:ASN:OD1	41:8:45:LEU:N	2.36	0.58
1:A:1402:ARG:HB3	17:R:406:GLN:HB2	1.84	0.58
1:A:1551:PHE:H	1:A:1551:PHE:HD2	1.49	0.58
2:B:65:G:H2'	2:B:66:A:H8	1.68	0.58
22:1:784:MET:O	22:1:788:VAL:HG13	2.04	0.58
23:3:454:GLY:O	23:3:456:PRO:HD3	2.04	0.58
41:8:31:ALA:HB3	41:8:34:LEU:HD13	1.85	0.58
1:A:645:THR:O	1:A:649:GLU:HG3	2.03	0.58
3:C:133:THR:HB	3:C:225:VAL:HG23	1.85	0.58
3:C:183:SER:H	3:C:214:GLU:HB3	1.68	0.58
3:C:755:ASP:HB2	3:C:759:LEU:HD23	1.85	0.58
7:G:8:C:H2'	7:G:9:C:C6	2.38	0.58
35:2:453:LYS:HE2	35:2:456:ARG:HB2	1.86	0.58
37:6:17:VAL:HG23	37:6:91:TYR:CE1	2.39	0.58
1:A:781:ARG:HG2	1:A:1022:MET:HE3	1.84	0.58
3:C:145:PHE:HA	3:C:312:SER:HB2	1.85	0.58
3:C:465:MET:HE2	3:C:475:MET:HG3	1.85	0.58
3:C:916:ILE:HD13	3:C:928:HIS:HB3	1.86	0.58
11:K:112:TRP:CD1	11:K:118:PHE:HA	2.38	0.58
22:1:1212:LEU:HB2	22:1:1237:LEU:HD13	1.85	0.58
41:8:52:ILE:O	41:8:56:VAL:HG22	2.04	0.58
5:E:157:CYS:HA	5:E:168:CYS:O	2.04	0.58
6:F:78:A:H5''	6:F:79:C:C5	2.37	0.58
7:G:-4:G:C2	7:G:-3:A:C5	2.91	0.58
22:1:586:ASP:OD1	22:1:589:ALA:N	2.28	0.58
23:3:377:MET:HE3	23:3:378:PRO:HD2	1.84	0.58
1:A:547:CYS:SG	1:A:548:ARG:N	2.77	0.58
1:A:612:ILE:O	1:A:616:PHE:HB2	2.03	0.58
1:A:2237:TRP:O	1:A:2241:ASN:CB	2.52	0.58
5:E:312:TRP:CD1	5:E:319:ILE:HG13	2.39	0.58
10:J:343:GLU:HG3	10:J:369:PHE:HE1	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:106:HIS:ND1	11:K:108:ASN:HB2	2.19	0.58
18:T:418:THR:OG1	18:T:468:CYS:SG	2.58	0.58
22:1:1212:LEU:HB2	22:1:1237:LEU:CD1	2.34	0.58
23:3:1193:VAL:O	23:3:1196:GLU:N	2.37	0.58
7:G:86:A:H2'	7:G:87:U:C6	2.39	0.57
8:H:56:A:O2'	35:2:481:THR:CG2	2.49	0.57
11:K:33:LYS:CG	11:K:44:HIS:HE1	2.17	0.57
11:K:168:LYS:HA	11:K:171:LYS:HD2	1.86	0.57
17:R:407:TYR:HB2	17:R:412:PHE:CE1	2.39	0.57
19:X:222:GLU:HG2	20:Y:69:ARG:NH1	2.19	0.57
19:X:338:PHE:HB3	19:X:341:ASN:HA	1.85	0.57
22:1:885:ASP:OD1	22:1:887:LYS:N	2.36	0.57
22:1:1179:ASP:OD1	22:1:1184:HIS:HD2	1.86	0.57
23:3:197:THR:OG1	23:3:199:GLU:HG3	2.04	0.57
23:3:206:GLN:HE21	23:3:231:HIS:HA	1.67	0.57
23:3:747:SER:O	23:3:751:PRO:HA	2.04	0.57
41:8:111:SER:OG	41:8:121:SER:N	2.33	0.57
1:A:1130:ASN:OD1	1:A:1130:ASN:N	2.37	0.57
1:A:1551:PHE:HD2	1:A:1551:PHE:N	2.02	0.57
3:C:237:LEU:HD13	3:C:898:LEU:HD13	1.86	0.57
6:F:36:A:C6	7:G:10:U:C2	2.91	0.57
11:K:262:ASP:CB	22:1:761:TYR:HE1	2.17	0.57
23:3:84:SER:OG	23:3:85:GLY:N	2.31	0.57
23:3:205:GLN:NE2	23:3:205:GLN:H	2.01	0.57
31:j:64:ILE:HA	31:j:70:SER:O	2.03	0.57
40:9:360:HIS:CE1	40:9:396:ILE:HD11	2.39	0.57
1:A:73:HIS:NE2	1:A:84:ASP:OD2	2.37	0.57
1:A:1553:VAL:HG12	1:A:1553:VAL:O	2.04	0.57
3:C:227:LEU:HD21	3:C:239:THR:HG23	1.86	0.57
3:C:556:ASP:O	3:C:612:LYS:NZ	2.29	0.57
10:J:439:ALA:O	10:J:443:ILE:HG12	2.03	0.57
11:K:262:ASP:CB	22:1:761:TYR:CE1	2.86	0.57
15:P:205:LYS:HD3	15:P:208:LYS:HE3	1.84	0.57
22:1:757:MET:HB3	22:1:762:ALA:HB2	1.85	0.57
23:3:267:ILE:HD12	23:3:322:VAL:HG22	1.86	0.57
33:w:459:TRP:CE3	33:w:459:TRP:HA	2.39	0.57
40:9:233:VAL:HG22	40:9:265:ALA:HB2	1.86	0.57
1:A:762:ARG:NH1	15:P:226:LYS:HZ1	2.03	0.57
3:C:130:ARG:NH2	3:C:440:SER:HB3	2.19	0.57
3:C:606:GLY:HA2	3:C:609:LYS:HG3	1.86	0.57
3:C:770:PHE:HA	3:C:816:VAL:HG21	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.85	0.57
3:C:836:VAL:HB	3:C:871:ILE:HB	1.86	0.57
9:I:231:ASN:O	9:I:233:ASP:N	2.35	0.57
18:T:442:ARG:HE	18:T:443:THR:HG22	1.70	0.57
22:1:718:PRO:O	22:1:719:TYR:CG	2.58	0.57
23:3:42:ARG:HH21	23:3:53:LEU:HD11	1.70	0.57
23:3:70:LEU:HD12	23:3:146:ARG:NH2	2.18	0.57
33:w:383:LEU:HD11	33:w:394:TYR:HA	1.85	0.57
35:2:517:ILE:HD12	35:2:517:ILE:H	1.68	0.57
1:A:226:GLN:HE22	1:A:417:ARG:HH21	1.51	0.57
1:A:658:ARG:HH22	6:F:65:G:H3'	1.69	0.57
1:A:755:HIS:HE1	15:P:220:HIS:CE1	2.23	0.57
1:A:821:ARG:HG2	1:A:821:ARG:HH11	1.67	0.57
2:B:51:A:H2'	2:B:52:U:H6	1.68	0.57
3:C:150:ILE:HD13	3:C:167:TYR:CD2	2.40	0.57
3:C:192:ASP:HB2	3:C:432:ASP:OD1	2.04	0.57
3:C:208:HIS:CE1	3:C:635:LEU:HD23	2.39	0.57
3:C:237:LEU:HD21	3:C:835:GLU:HB3	1.86	0.57
3:C:785:ARG:HH12	3:C:904:TRP:CD1	2.23	0.57
8:H:180:G:N2	29:l:53:GLY:HA3	2.19	0.57
19:X:313:TYR:N	19:X:321:GLY:O	2.24	0.57
22:1:1182:LEU:HD12	22:1:1182:LEU:N	2.03	0.57
23:3:1032:TRP:CD1	23:3:1032:TRP:H	2.22	0.57
1:A:405:LEU:HD21	3:C:385:VAL:HG12	1.87	0.57
1:A:1651:VAL:HB	1:A:1653:ASP:OD1	2.03	0.57
6:F:44:G:N2	7:G:5:G:H1	2.02	0.57
6:F:66:C:H2'	6:F:67:G:C8	2.40	0.57
8:H:72:U:H2'	8:H:73:C:C6	2.40	0.57
11:K:168:LYS:HE3	23:3:1214:ARG:HH21	1.69	0.57
12:L:64:SER:OG	12:L:66:GLU:OE1	2.22	0.57
17:R:134:ARG:HG3	18:T:385:TYR:CD1	2.39	0.57
22:1:403:GLU:O	22:1:407:MET:HG2	2.04	0.57
22:1:1291:ASP:OD1	22:1:1292:LYS:N	2.37	0.57
23:3:818:GLN:NE2	23:3:822:GLU:OE2	2.38	0.57
1:A:522:PHE:HB2	1:A:552:ARG:HG3	1.87	0.57
1:A:1330:MET:HG3	1:A:1330:MET:O	2.05	0.57
1:A:1545:ALA:CA	1:A:1563:HIS:CD2	2.87	0.57
2:B:15:C:H2'	2:B:16:U:C6	2.40	0.57
3:C:141:GLY:O	3:C:145:PHE:HB2	2.05	0.57
3:C:888:ARG:HG2	3:C:895:ALA:O	2.04	0.57
18:T:466:PHE:CE2	18:T:482:ALA:HB2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1189:LYS:HA	23:3:1192:ASN:ND2	2.18	0.57
1:A:232:LEU:HD21	3:C:412:ILE:HD11	1.86	0.57
1:A:1199:LYS:HA	1:A:1203:SER:OG	2.05	0.57
1:A:1551:PHE:N	1:A:1551:PHE:CD2	2.72	0.57
2:B:36:C:N3	2:B:47:A:C6	2.73	0.57
22:1:850:ILE:O	22:1:854:VAL:HG13	2.05	0.57
23:3:722:SER:HB2	23:3:731:LEU:HD12	1.87	0.57
38:7:51:TYR:CG	38:7:52:GLY:N	2.72	0.57
40:9:365:ILE:O	40:9:382:ILE:HA	2.04	0.57
1:A:464:PRO:HD3	2:B:24:G:N7	2.20	0.57
1:A:488:ASP:OD2	1:A:565:ARG:NH1	2.35	0.57
1:A:599:MET:HA	1:A:602:ILE:HB	1.86	0.57
6:F:40:U:H2'	6:F:41:A:C8	2.40	0.57
8:H:24:A:H5'	8:H:25:G:H5''	1.86	0.57
19:X:371:HIS:H	19:X:374:SER:HG	1.51	0.57
22:1:1258:ALA:HB3	22:1:1261:VAL:HG13	1.86	0.57
23:3:979:ARG:HH21	33:w:476:GLU:HB3	1.70	0.57
1:A:584:HIS:O	1:A:588:LEU:HG	2.05	0.57
1:A:770:THR:OG1	1:A:771:VAL:N	2.36	0.57
12:L:38:LEU:HD23	12:L:38:LEU:N	2.19	0.57
17:R:150:ALA:HA	17:R:153:LYS:HD2	1.86	0.57
17:R:256:ASN:OD1	17:R:256:ASN:N	2.37	0.57
22:1:160:HIS:CD2	22:1:163:LYS:HE2	2.40	0.57
22:1:1063:LEU:HD11	22:1:1096:THR:OG1	2.05	0.57
23:3:866:ILE:HD13	23:3:907:VAL:HG21	1.87	0.57
23:3:1058:LEU:HD23	23:3:1062:THR:HG21	1.87	0.57
35:2:586:ILE:HD13	35:2:586:ILE:C	2.29	0.57
40:9:259:THR:O	40:9:259:THR:OG1	2.23	0.57
41:8:55:ARG:NH1	41:8:58:GLU:OE2	2.37	0.57
1:A:83:HIS:O	1:A:87:VAL:HG23	2.04	0.56
1:A:405:LEU:O	3:C:413:ARG:NH1	2.35	0.56
1:A:2123:GLN:O	1:A:2152:GLY:HA3	2.05	0.56
3:C:477:HIS:CE1	3:C:577:PHE:HB2	2.40	0.56
3:C:692:LEU:HD11	3:C:744:ILE:HG13	1.86	0.56
11:K:148:THR:HG22	11:K:151:ARG:HH21	1.70	0.56
18:T:395:ILE:HD12	18:T:395:ILE:H	1.69	0.56
22:1:1120:ALA:HA	22:1:1128:VAL:HG11	1.86	0.56
22:1:1182:LEU:H	22:1:1182:LEU:CD1	1.99	0.56
23:3:870:ASN:ND2	23:3:873:GLN:H	2.02	0.56
28:m:16:ARG:HA	28:m:30:THR:HA	1.87	0.56
1:A:592:TYR:HB3	1:A:598:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1298:ARG:HB3	1:A:1298:ARG:HH21	1.68	0.56
3:C:347:ILE:HG13	3:C:357:THR:O	2.06	0.56
4:D:1658:ALA:O	4:D:1692:ASN:N	2.38	0.56
5:E:329:SER:OG	5:E:347:SER:OG	2.12	0.56
22:1:579:GLU:HB3	22:1:627:THR:OG1	2.05	0.56
22:1:1098:LEU:C	22:1:1100:ASN:H	2.14	0.56
41:8:46:GLU:CD	41:8:46:GLU:H	2.13	0.56
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.70	0.56
1:A:1586:HIS:O	1:A:1590:VAL:HG23	2.04	0.56
1:A:1708:ALA:C	1:A:1709:TYR:HD2	2.13	0.56
3:C:159:LYS:HG2	3:C:161:TYR:H	1.70	0.56
3:C:734:ALA:HB3	3:C:767:VAL:HG21	1.87	0.56
3:C:859:GLN:HB3	3:C:872:LYS:HB2	1.86	0.56
8:H:106:G:N2	8:H:107:A:N1	2.41	0.56
10:J:235:ILE:O	10:J:239:ARG:HD3	2.05	0.56
18:T:308:ARG:HG2	18:T:308:ARG:HH11	1.69	0.56
22:1:949:GLN:HB3	22:1:989:VAL:HA	1.86	0.56
22:1:1090:PRO:N	22:1:1090:PRO:C	2.58	0.56
23:3:213:LEU:HD23	23:3:214:ASP:H	1.70	0.56
23:3:473:TYR:HE1	23:3:497:SER:HB2	1.70	0.56
40:9:274:GLN:O	40:9:277:LYS:HE2	2.04	0.56
1:A:106:MET:O	1:A:114:ARG:NH1	2.36	0.56
3:C:70:GLU:H	3:C:70:GLU:CD	2.13	0.56
10:J:436:TYR:HD1	10:J:437:LYS:HD2	1.70	0.56
12:L:85:ILE:O	12:L:88:ILE:N	2.35	0.56
22:1:124:ARG:C	22:1:126:MET:H	2.12	0.56
23:3:180:PRO:HD2	23:3:213:LEU:HB3	1.87	0.56
23:3:254:ASN:O	23:3:271:ILE:HG13	2.05	0.56
36:4:104:ILE:HA	36:4:173:THR:O	2.06	0.56
3:C:181:ILE:O	3:C:211:PHE:HB3	2.05	0.56
3:C:664:GLU:HB3	3:C:820:PHE:HZ	1.70	0.56
5:E:180:ASP:HB2	5:E:183:LYS:HD3	1.88	0.56
10:J:286:GLU:HG3	10:J:298:ILE:HD12	1.87	0.56
10:J:343:GLU:HG3	10:J:369:PHE:CE1	2.41	0.56
19:X:357:VAL:HA	19:X:367:TYR:O	2.04	0.56
22:1:698:GLN:HB3	22:1:701:VAL:HG12	1.87	0.56
23:3:446:GLU:OE1	23:3:763:ARG:HD3	2.05	0.56
32:n:19:LEU:HA	32:n:65:ILE:HA	1.88	0.56
40:9:363:ARG:NH2	40:9:407:LEU:HG	2.21	0.56
1:A:383:PHE:HB3	3:C:331:PHE:CD1	2.40	0.56
1:A:827:PHE:CB	1:A:1002:ASP:OD2	2.46	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1056:HIS:O	1:A:1059:SER:OG	2.22	0.56
3:C:136:GLY:HA2	3:C:227:LEU:HD12	1.87	0.56
5:E:158:TYR:HD2	5:E:201:PHE:H	1.54	0.56
18:T:257:ARG:NH1	18:T:299:THR:O	2.37	0.56
22:1:907:ASP:OD1	22:1:907:ASP:N	2.36	0.56
22:1:936:VAL:HG12	22:1:937:LEU:HD12	1.88	0.56
22:1:944:SER:HB2	22:1:948:ARG:NE	2.21	0.56
33:w:385:LEU:HD13	33:w:386:GLY:H	1.71	0.56
1:A:1460:HIS:H	1:A:1460:HIS:CD2	2.22	0.56
3:C:78:GLU:OE2	18:T:198:ARG:NE	2.38	0.56
3:C:699:ASP:OD2	3:C:722:TYR:OH	2.22	0.56
21:Z:587:VAL:O	21:Z:589:ARG:NH1	2.38	0.56
22:1:1208:LEU:HB3	22:1:1241:ILE:HD11	1.86	0.56
1:A:516:LEU:HD11	1:A:538:SER:HB2	1.88	0.56
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.39	0.56
5:E:62:LEU:HD12	5:E:351:LEU:HB2	1.88	0.56
9:I:428:GLN:HA	9:I:469:TYR:H	1.70	0.56
12:L:65:ARG:NH2	12:L:68:GLU:OE1	2.39	0.56
17:R:138:GLU:HA	17:R:141:LYS:HD3	1.87	0.56
18:T:220:VAL:HG12	18:T:252:VAL:HG21	1.86	0.56
18:T:331:ASN:OD1	18:T:332:ALA:N	2.35	0.56
18:T:460:ASP:O	18:T:463:SER:OG	2.21	0.56
24:o:92:GLU:HA	24:o:117:TYR:O	2.06	0.56
33:w:459:TRP:HA	33:w:459:TRP:HE3	1.71	0.56
1:A:119:LEU:HD11	1:A:482:PHE:HB3	1.87	0.56
1:A:436:PRO:HB2	1:A:439:GLN:CD	2.31	0.56
1:A:857:ASN:OD1	1:A:858:GLN:N	2.39	0.56
3:C:137:HIS:HB3	3:C:140:HIS:CE1	2.41	0.56
3:C:213:ASP:HB3	3:C:616:SER:HB3	1.87	0.56
6:F:63:C:H2'	6:F:64:U:H6	1.71	0.56
22:1:489:PRO:HB2	22:1:491:GLU:OE2	2.06	0.56
23:3:542:LYS:NZ	23:3:562:GLU:OE1	2.34	0.56
1:A:150:MET:HG3	1:A:572:PHE:CE1	2.38	0.56
1:A:1199:LYS:HE2	1:A:1206:GLU:HB2	1.87	0.56
22:1:760:GLU:OE2	22:1:761:TYR:N	2.38	0.56
22:1:929:LEU:O	22:1:932:ILE:HB	2.05	0.56
22:1:1126:PHE:CE1	35:2:576:PHE:CE2	2.94	0.56
23:3:815:ARG:NH2	23:3:819:MET:SD	2.79	0.56
1:A:112:GLN:NE2	1:A:189:GLU:OE1	2.39	0.55
1:A:549:GLU:HG3	1:A:594:TYR:HE2	1.70	0.55
1:A:739:ILE:HG22	1:A:740:LEU:HD23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:275:TYR:HB2	3:C:374:LEU:HD12	1.87	0.55
3:C:313:GLN:HB2	45:C:1500:GTP:C6	2.42	0.55
6:F:33:G:N2	7:G:13:C:N4	2.54	0.55
6:F:63:C:N4	6:F:72:G:O6	2.39	0.55
6:F:86:U:O2	8:H:12:G:C6	2.59	0.55
7:G:94:C:H2'	7:G:95:U:C6	2.41	0.55
10:J:242:ILE:HG22	10:J:245:TRP:CD1	2.41	0.55
11:K:119:THR:OG1	11:K:120:LYS:N	2.39	0.55
22:1:399:LEU:O	37:6:46:ARG:NH2	2.39	0.55
22:1:1257:PRO:CB	35:2:481:THR:OG1	2.54	0.55
23:3:554:VAL:CG1	23:3:556:ILE:HG23	2.36	0.55
40:9:294:GLU:O	40:9:398:GLY:HA3	2.04	0.55
1:A:362:ARG:NH1	3:C:284:GLU:OE1	2.39	0.55
1:A:557:VAL:HG22	1:A:581:ILE:HD13	1.87	0.55
1:A:854:SER:OG	1:A:855:ARG:N	2.39	0.55
2:B:65:G:H2'	2:B:66:A:C8	2.41	0.55
3:C:700:ILE:O	3:C:740:THR:OG1	2.25	0.55
5:E:336:HIS:HD1	5:E:337:PRO:HD2	1.70	0.55
9:I:428:GLN:HA	9:I:469:TYR:N	2.21	0.55
10:J:332:VAL:HA	10:J:335:ARG:HD3	1.88	0.55
22:1:588:TYR:HA	22:1:591:VAL:HG12	1.87	0.55
22:1:883:ASP:OD2	22:1:883:ASP:N	2.39	0.55
23:3:383:ASP:OD1	23:3:384:THR:N	2.39	0.55
23:3:482:THR:OG1	23:3:501:GLY:O	2.24	0.55
40:9:302:LYS:HD3	40:9:350:PHE:HB2	1.88	0.55
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.38	0.55
2:B:98:G:H2'	2:B:99:C:H6	1.71	0.55
7:G:99:C:N4	8:H:32:U:C4	2.65	0.55
16:Q:54:ILE:O	16:Q:59:PHE:N	2.24	0.55
17:R:250:CYS:SG	17:R:252:SER:OG	2.64	0.55
18:T:358:ASP:OD2	18:T:361:ALA:N	2.39	0.55
20:Y:1:MET:HE2	22:1:783:GLU:HG2	1.88	0.55
22:1:907:ASP:HB2	22:1:909:VAL:HG12	1.87	0.55
22:1:1212:LEU:HD22	22:1:1246:MET:HE1	1.88	0.55
23:3:725:TYR:N	23:3:728:ARG:O	2.39	0.55
35:2:587:HIS:C	35:2:587:HIS:CD2	2.84	0.55
43:v:33:LEU:C	43:v:33:LEU:HD22	2.32	0.55
1:A:1074:PHE:CD2	1:A:1080:GLU:HB2	2.42	0.55
1:A:1301:ILE:O	1:A:1301:ILE:HG23	2.05	0.55
3:C:132:VAL:HA	3:C:224:GLY:O	2.06	0.55
5:E:236:ASP:HB2	5:E:256:ASP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:351:ASN:CB	10:J:355:ARG:HH21	2.20	0.55
22:1:586:ASP:OD1	22:1:588:TYR:N	2.40	0.55
23:3:928:TYR:HD1	23:3:937:LEU:HB3	1.71	0.55
28:m:80:MET:O	32:n:58:LEU:HA	2.06	0.55
35:2:471:ARG:HH21	35:2:474:VAL:HG23	1.71	0.55
40:9:339:GLY:O	40:9:379:GLN:NE2	2.39	0.55
1:A:304:ILE:O	3:C:924:GLN:NE2	2.39	0.55
1:A:1473:ASP:OD1	1:A:1473:ASP:N	2.38	0.55
1:A:2161:GLY:N	1:A:2290:PRO:O	2.40	0.55
2:B:40:U:H3	7:G:0:G:H22	1.55	0.55
3:C:707:ILE:HD11	3:C:734:ALA:HA	1.88	0.55
10:J:294:HIS:HA	10:J:297:ASN:ND2	2.21	0.55
13:N:119:CYS:O	13:N:142:CYS:N	2.37	0.55
17:R:230:MET:O	18:T:370:ASN:HA	2.07	0.55
22:1:960:VAL:O	22:1:964:THR:OG1	2.23	0.55
22:1:1252:GLN:HE22	35:2:492:LYS:HA	1.70	0.55
23:3:271:ILE:HD13	23:3:287:PHE:HE2	1.71	0.55
25:p:184:PRO:HG3	33:w:487:VAL:HG12	1.76	0.55
25:p:203:ALA:O	25:p:207:LEU:CB	2.55	0.55
37:6:21:LEU:HB2	37:6:62:VAL:HG23	1.89	0.55
38:7:22:LEU:O	38:7:66:VAL:HG22	2.06	0.55
1:A:378:PHE:HZ	3:C:335:ASN:HB3	1.71	0.55
1:A:429:ASN:ND2	1:A:432:ARG:HD3	2.21	0.55
1:A:1298:ARG:NH2	1:A:1298:ARG:CB	2.69	0.55
22:1:624:VAL:HA	22:1:627:THR:HG22	1.89	0.55
1:A:1501:LEU:HD22	1:A:1503:TRP:HE1	1.71	0.55
2:B:33:U:HO2'	18:T:279:LYS:HZ2	1.50	0.55
2:B:61:A:H2'	2:B:62:G:O4'	2.06	0.55
3:C:174:GLU:OE1	3:C:174:GLU:N	2.40	0.55
3:C:183:SER:O	3:C:482:TYR:OH	2.19	0.55
3:C:842:CYS:HB3	3:C:891:THR:HG21	1.89	0.55
22:1:1262:ARG:HH12	35:2:483:GLN:HE21	1.55	0.55
1:A:641:MET:HA	1:A:644:ILE:HG12	1.86	0.55
1:A:1132:LYS:HA	1:A:1139:ARG:HE	1.72	0.55
1:A:1360:GLU:N	1:A:1363:GLN:OE1	2.39	0.55
7:G:6:A:C8	7:G:7:G:N7	2.74	0.55
8:H:47:U:O2	8:H:47:U:H2'	2.07	0.55
10:J:275:ASN:HB3	10:J:278:LEU:HB2	1.89	0.55
10:J:431:ARG:HA	10:J:434:VAL:HG12	1.89	0.55
11:K:36:ARG:HB3	11:K:37:ASP:OD1	2.06	0.55
12:L:30:GLN:HE22	17:R:256:ASN:ND2	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:287:PHE:HD1	23:3:303:ALA:HB1	1.69	0.55
40:9:220:ILE:O	40:9:224:THR:OG1	2.19	0.55
40:9:363:ARG:HH21	40:9:407:LEU:HG	1.71	0.55
1:A:1199:LYS:HZ3	1:A:1206:GLU:CD	2.15	0.55
1:A:1371:TYR:N	1:A:1371:TYR:CD1	2.75	0.55
3:C:724:TRP:CZ2	3:C:732:ILE:HD11	2.42	0.55
4:D:1671:GLY:HA3	4:D:1860:ILE:O	2.07	0.55
5:E:161:ARG:NH2	5:E:245:SER:HA	2.22	0.55
8:H:82:G:H2'	8:H:83:A:C8	2.41	0.55
11:K:115:LEU:O	11:K:119:THR:HG23	2.07	0.55
23:3:82:SER:OG	23:3:83:ASP:N	2.38	0.55
23:3:374:SER:OG	23:3:376:ALA:N	2.30	0.55
23:3:736:TYR:OH	23:3:763:ARG:HD2	2.06	0.55
23:3:1009:PHE:HZ	23:3:1046:GLY:HA3	1.71	0.55
23:3:1028:THR:HG22	23:3:1028:THR:O	2.06	0.55
26:h:69:ASN:N	26:h:97:SER:O	2.40	0.55
40:9:269:ASP:HA	40:9:272:ARG:HE	1.71	0.55
1:A:179:ALA:HA	1:A:183:LEU:HD22	1.88	0.55
1:A:1310:ARG:CZ	1:A:1310:ARG:CB	2.85	0.55
3:C:481:MET:SD	3:C:612:LYS:HG2	2.46	0.55
9:I:255:LEU:O	9:I:259:TRP:CB	2.54	0.55
17:R:137:GLU:HA	17:R:140:ILE:HD13	1.89	0.55
17:R:239:VAL:O	17:R:243:GLN:HG3	2.07	0.55
22:1:1295:TYR:CE2	39:5:28:LYS:HE2	2.42	0.55
23:3:362:ALA:O	23:3:363:HIS:ND1	2.40	0.55
35:2:576:PHE:CD2	35:2:576:PHE:N	2.75	0.55
40:9:352:ASP:HA	40:9:376:ASN:HD21	1.72	0.55
1:A:755:HIS:CE1	15:P:220:HIS:ND1	2.75	0.54
1:A:1264:ASN:O	1:A:1268:ILE:HG12	2.07	0.54
11:K:39:ASN:O	11:K:41:PHE:N	2.40	0.54
12:L:63:TRP:HB3	12:L:68:GLU:HG3	1.89	0.54
40:9:361:THR:HG23	40:9:386:SER:HB2	1.89	0.54
1:A:118:VAL:O	1:A:484:SER:HA	2.07	0.54
1:A:140:TYR:OH	1:A:421:ALA:O	2.24	0.54
1:A:143:GLN:O	1:A:147:MET:HG2	2.07	0.54
1:A:1310:ARG:HH21	1:A:1310:ARG:CG	2.18	0.54
3:C:320:LEU:HD23	3:C:343:LEU:HB3	1.89	0.54
6:F:41:A:H2'	6:F:42:C:H6	1.72	0.54
10:J:306:LEU:HD13	10:J:312:PHE:HE2	1.72	0.54
11:K:26:TRP:HB2	11:K:35:CYS:O	2.07	0.54
17:R:132:LEU:O	18:T:385:TYR:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:337:ARG:HG3	18:T:378:VAL:HG23	1.88	0.54
20:Y:9:LEU:HD12	22:1:782:GLU:HG3	1.89	0.54
22:1:967:GLU:O	22:1:971:MET:N	2.34	0.54
23:3:894:CYS:HB3	23:3:954:PRO:HB3	1.89	0.54
1:A:91:ALA:HB2	1:A:125:ALA:HB1	1.89	0.54
1:A:119:LEU:HB2	1:A:130:ASN:HD22	1.72	0.54
1:A:814:VAL:HG23	1:A:999:LEU:HD13	1.89	0.54
1:A:1418:ARG:O	1:A:1420:ASN:N	2.40	0.54
1:A:1657:THR:HG22	1:A:1658:GLN:H	1.71	0.54
7:G:85:G:N9	33:w:395:TRP:CH2	2.73	0.54
11:K:151:ARG:NH2	11:K:152:GLN:HG2	2.22	0.54
12:L:39:HIS:HB2	43:v:26:ARG:NH1	2.22	0.54
32:n:20:LYS:N	32:n:64:ASN:O	2.25	0.54
33:w:486:VAL:HG23	33:w:486:VAL:O	2.06	0.54
43:v:79:GLN:OE1	43:v:79:GLN:HA	2.07	0.54
1:A:406:TRP:CH2	3:C:265:LEU:HB2	2.43	0.54
1:A:1558:THR:HB	1:A:1582:TRP:CE3	2.43	0.54
2:B:41:U:H2'	2:B:42:U:C6	2.43	0.54
3:C:142:LYS:O	3:C:146:VAL:HG23	2.07	0.54
3:C:441:PRO:CB	3:C:495:ARG:HH22	2.18	0.54
3:C:490:PHE:CD2	3:C:612:LYS:HD2	2.43	0.54
3:C:788:LYS:HD3	3:C:790:LYS:HG3	1.89	0.54
7:G:85:G:C1'	33:w:395:TRP:CZ3	2.90	0.54
16:Q:1027:LEU:O	16:Q:1032:ALA:N	2.38	0.54
22:1:412:TYR:HB3	37:6:49:ARG:HB3	1.89	0.54
22:1:420:GLY:O	22:1:424:ILE:N	2.33	0.54
37:6:17:VAL:HG21	37:6:71:LYS:HB2	1.90	0.54
43:v:42:LYS:HG3	43:v:42:LYS:O	2.08	0.54
1:A:71:ARG:HD3	13:N:34:THR:HA	1.89	0.54
1:A:414:ARG:HG3	3:C:411:ASN:HA	1.90	0.54
1:A:1256:PHE:HB3	1:A:1299:ILE:HG21	1.90	0.54
3:C:769:GLY:HA3	3:C:812:ALA:HB3	1.89	0.54
5:E:65:HIS:CD2	5:E:351:LEU:HD11	2.42	0.54
38:7:30:CYS:SG	38:7:33:CYS:N	2.81	0.54
1:A:1308:PRO:HG3	1:A:1548:TYR:HE2	1.69	0.54
1:A:1371:TYR:N	1:A:1371:TYR:HD1	2.05	0.54
1:A:1758:PRO:HA	22:1:938:TRP:CD1	2.42	0.54
3:C:317:CYS:SG	3:C:430:PHE:HB2	2.48	0.54
5:E:218:LYS:HD3	5:E:220:TRP:CZ2	2.42	0.54
18:T:209:CYS:SG	18:T:252:VAL:HG22	2.48	0.54
23:3:791:HIS:HD2	23:3:793:GLU:H	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:k:46:VAL:HA	30:k:56:ASN:HA	1.89	0.54
1:A:1382:SER:OG	1:A:1416:ILE:N	2.34	0.54
2:B:55:C:H2'	2:B:56:C:H6	1.72	0.54
6:F:38:G:C2	6:F:39:A:C5	2.96	0.54
8:H:172:C:H2'	8:H:173:C:C6	2.42	0.54
10:J:224:LYS:HE2	10:J:255:LEU:HD13	1.90	0.54
10:J:367:GLU:OE2	10:J:401:ARG:NH2	2.41	0.54
23:3:318:ASP:O	23:3:320:ASP:N	2.41	0.54
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.40	0.54
23:3:670:GLN:HA	23:3:698:PRO:HA	1.89	0.54
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.43	0.54
35:2:586:ILE:CD1	35:2:586:ILE:H	2.20	0.54
40:9:325:ILE:HB	40:9:328:PHE:HB3	1.89	0.54
41:8:38:VAL:HG11	41:8:109:LEU:HD13	1.90	0.54
1:A:675:GLN:NE2	1:A:676:ARG:HG3	2.22	0.54
1:A:706:ALA:O	1:A:709:ILE:N	2.41	0.54
5:E:178:LEU:HB2	5:E:188:GLN:HG2	1.90	0.54
6:F:15:A:H2'	6:F:16:G:H8	1.72	0.54
8:H:27:U:H2'	8:H:28:C:C6	2.43	0.54
8:H:157:G:OP1	24:o:152:LEU:N	2.27	0.54
10:J:226:ARG:O	10:J:230:THR:HG23	2.07	0.54
17:R:390:GLU:H	17:R:390:GLU:CD	2.16	0.54
22:1:862:GLU:OE1	22:1:904:THR:OG1	2.24	0.54
1:A:154:GLU:HG2	1:A:572:PHE:CG	2.43	0.54
1:A:508:ILE:HG13	1:A:513:LEU:HD12	1.89	0.54
1:A:698:PRO:O	1:A:699:GLU:HB2	2.08	0.54
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.41	0.54
2:B:117:A:C2	27:d:26:GLY:HA3	2.43	0.54
22:1:816:LYS:HE3	22:1:817:HIS:CE1	2.43	0.54
40:9:380:PHE:HZ	40:9:428:ILE:HD11	1.72	0.54
1:A:171:ASP:OD1	1:A:521:ASN:ND2	2.40	0.54
1:A:769:LYS:HE2	1:A:773:LYS:HE3	1.89	0.54
1:A:1285:LEU:O	1:A:1289:VAL:HG23	2.07	0.54
3:C:109:LEU:HD21	3:C:539:ILE:HG13	1.89	0.54
5:E:112:VAL:HA	5:E:128:SER:OG	2.08	0.54
8:H:46:U:O2	8:H:46:U:O2'	2.15	0.54
9:I:406:GLU:HA	9:I:410:GLN:HA	1.88	0.54
22:1:973:HIS:O	22:1:977:VAL:HG23	2.08	0.54
22:1:1167:TYR:CE1	35:2:581:LYS:HB2	2.43	0.54
40:9:361:THR:HA	40:9:386:SER:HA	1.89	0.54
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.90	0.53
1:A:827:PHE:C	1:A:827:PHE:CD2	2.86	0.53
1:A:1737:ASN:OD1	1:A:1740:LEU:HG	2.08	0.53
3:C:140:HIS:ND1	3:C:229:ILE:HA	2.23	0.53
3:C:673:LYS:HB3	3:C:686:THR:HG23	1.91	0.53
6:F:45:A:H4'	6:F:46:G:OP2	2.03	0.53
18:T:369:THR:O	18:T:369:THR:OG1	2.23	0.53
22:1:1056:MET:HE3	22:1:1092:ASP:HB2	1.90	0.53
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	1.90	0.53
26:h:41:GLN:HA	26:h:55:ARG:HA	1.90	0.53
40:9:292:ASN:HB2	40:9:402:GLY:N	2.23	0.53
1:A:203:VAL:HG22	1:A:207:PHE:HB2	1.90	0.53
1:A:561:HIS:CE1	1:A:574:LEU:HD21	2.43	0.53
2:B:8:G:H1	2:B:69:A:H61	0.60	0.53
3:C:123:MET:SD	3:C:545:PRO:HD2	2.48	0.53
3:C:605:ASP:OD1	3:C:608:ARG:NH2	2.41	0.53
3:C:829:GLU:OE2	3:C:876:PRO:HB3	2.08	0.53
5:E:93:TRP:CD2	5:E:101:ASN:HB2	2.43	0.53
7:G:7:G:H2'	7:G:8:C:O4'	2.07	0.53
8:H:139:C:H5'	28:m:56:SER:H	1.73	0.53
10:J:224:LYS:HD3	10:J:228:ARG:NH2	2.23	0.53
18:T:371:HIS:NE2	18:T:389:SER:OG	2.41	0.53
22:1:979:TYR:HA	22:1:982:LEU:HD22	1.88	0.53
39:5:46:HIS:C	39:5:48:ASP:H	2.16	0.53
1:A:391:THR:HG21	3:C:395:THR:HG23	1.90	0.53
1:A:1019:TYR:O	1:A:1021:ASP:N	2.42	0.53
1:A:1399:GLN:C	1:A:1401:ARG:H	2.16	0.53
1:A:1820:LYS:HA	1:A:1914:MET:HA	1.91	0.53
5:E:156:SER:O	5:E:169:THR:HA	2.07	0.53
7:G:85:G:C5	33:w:395:TRP:CZ2	2.97	0.53
10:J:357:LYS:HE3	10:J:359:VAL:HG22	1.90	0.53
11:K:82:ARG:HE	22:1:1051:SER:HA	1.73	0.53
40:9:352:ASP:N	40:9:374:ASN:OD1	2.36	0.53
1:A:280:GLU:HB2	2:B:48:A:O5'	2.08	0.53
1:A:1248:LEU:HD22	1:A:1298:ARG:HG3	1.90	0.53
1:A:1638:ASN:HB3	1:A:1656:THR:HG22	1.90	0.53
4:D:1225:VAL:O	4:D:1234:LEU:N	2.37	0.53
5:E:167:VAL:HB	5:E:179:TRP:HB2	1.89	0.53
18:T:394:ASN:HB2	18:T:409:LEU:O	2.08	0.53
23:3:603:ARG:HG2	23:3:604:PHE:CE2	2.43	0.53
23:3:1003:SER:O	23:3:1003:SER:OG	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1382:SER:HA	1:A:1415:GLY:HA2	1.90	0.53
1:A:1428:HIS:NE2	22:1:94:ILE:HG21	2.24	0.53
2:B:38:C:H5'	2:B:39:C:H6	1.71	0.53
2:B:44:A:C2	2:B:45:C:H1'	2.43	0.53
10:J:376:VAL:O	10:J:380:ILE:HG13	2.09	0.53
11:K:83:ARG:HB2	11:K:84:PHE:CE2	2.43	0.53
22:1:458:ASP:N	22:1:458:ASP:OD1	2.41	0.53
22:1:563:LEU:H	22:1:563:LEU:HD12	1.74	0.53
23:3:139:LYS:O	23:3:140:LEU:HD23	2.07	0.53
23:3:613:THR:OG1	23:3:615:ARG:NH1	2.28	0.53
25:p:184:PRO:CD	33:w:487:VAL:HG11	2.38	0.53
35:2:488:LEU:O	35:2:488:LEU:HD23	2.09	0.53
36:4:14:THR:HA	36:4:60:GLU:HA	1.89	0.53
1:A:391:THR:OG1	3:C:398:GLU:OE2	2.27	0.53
1:A:462:ARG:NH2	1:A:465:LYS:HG2	2.23	0.53
1:A:1562:MET:C	1:A:1564:GLY:H	2.16	0.53
2:B:51:A:O2'	2:B:52:U:H5'	2.09	0.53
3:C:142:LYS:HA	3:C:228:PHE:CD2	2.43	0.53
3:C:335:ASN:HD22	3:C:338:GLU:HG2	1.73	0.53
3:C:506:PRO:HA	3:C:526:THR:HA	1.90	0.53
6:F:91:A:H2'	6:F:92:A:C8	2.44	0.53
18:T:261:LEU:HB3	18:T:275:LEU:HD21	1.91	0.53
22:1:1257:PRO:HG3	35:2:482:ALA:HB2	1.91	0.53
23:3:981:CYS:HA	33:w:471:TRP:CH2	2.42	0.53
29:l:19:THR:HA	29:l:29:ARG:HA	1.90	0.53
28:a:37:HIS:O	28:a:74:GLY:HA3	2.08	0.53
1:A:67:ARG:CZ	1:A:67:ARG:HB2	2.38	0.53
1:A:213:LEU:O	1:A:216:SER:OG	2.22	0.53
2:B:14:U:H2'	2:B:15:C:H6	1.74	0.53
3:C:306:ASN:HB3	3:C:437:HIS:CD2	2.43	0.53
3:C:856:HIS:CE1	3:C:874:PHE:HB2	2.43	0.53
8:H:121:A:C2	8:H:122:U:H5'	2.43	0.53
11:K:7:LEU:HG	11:K:8:THR:H	1.72	0.53
22:1:483:ASP:O	22:1:486:THR:OG1	2.25	0.53
35:2:535:GLU:HA	35:2:535:GLU:OE2	2.09	0.53
43:v:54:TYR:OH	43:v:66:GLU:CG	2.56	0.53
1:A:823:SER:O	1:A:823:SER:OG	2.25	0.53
3:C:220:ARG:HH22	3:C:580:LEU:HA	1.73	0.53
6:F:58:G:H3'	6:F:58:G:OP2	2.09	0.53
8:H:165:A:H61	25:p:84:ALA:HB1	1.73	0.53
11:K:68:PHE:CD2	11:K:109:ALA:HB1	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:70:GLU:O	11:K:71:GLU:C	2.52	0.53
11:K:88:ARG:HD2	11:K:138:TYR:HB3	1.91	0.53
19:X:262:TYR:CZ	19:X:370:LEU:HD12	2.44	0.53
19:X:337:THR:O	19:X:343:ARG:HA	2.07	0.53
19:X:372:GLU:HG2	19:X:373:SER:N	2.24	0.53
23:3:180:PRO:HD3	23:3:215:LEU:HD11	1.91	0.53
23:3:606:ALA:HA	23:3:616:ILE:HD12	1.91	0.53
37:6:112:LEU:O	37:6:116:LYS:HB2	2.08	0.53
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.90	0.53
1:A:1293:ASN:HB2	1:A:1357:MET:CE	2.39	0.53
2:B:18:C:H2'	2:B:19:A:C8	2.44	0.53
3:C:64:LYS:CE	15:P:206:LYS:HB3	2.39	0.53
3:C:183:SER:HA	3:C:205:THR:HA	1.91	0.53
3:C:680:ASN:O	3:C:682:LYS:N	2.42	0.53
17:R:148:ARG:NH2	17:R:148:ARG:CB	2.72	0.53
21:Z:574:ASN:N	21:Z:574:ASN:OD1	2.41	0.53
22:1:476:ASP:HB2	37:6:24:ARG:NH2	2.23	0.53
22:1:1252:GLN:HE21	35:2:492:LYS:HA	1.71	0.53
23:3:192:ALA:HA	23:3:200:ALA:HB3	1.90	0.53
23:3:207:THR:O	23:3:207:THR:OG1	2.24	0.53
23:3:328:LYS:HZ2	23:3:365:GLY:C	2.15	0.53
40:9:420:ASP:N	40:9:420:ASP:OD1	2.41	0.53
41:8:63:GLU:OE1	41:8:63:GLU:N	2.31	0.53
27:d:16:GLY:N	27:d:33:LEU:O	2.38	0.53
1:A:339:PHE:CE1	1:A:406:TRP:HB2	2.44	0.53
1:A:385:GLU:HG2	1:A:386:PRO:HD2	1.89	0.53
1:A:1758:PRO:HA	22:1:938:TRP:NE1	2.24	0.53
5:E:67:GLY:C	5:E:349:LYS:HG2	2.34	0.53
23:3:246:SER:OG	23:3:247:GLY:N	2.41	0.53
37:6:22:TYR:OH	37:6:24:ARG:HD3	2.09	0.53
39:5:63:ARG:HD2	39:5:67:ASN:HD21	1.73	0.53
40:9:58:GLY:O	40:9:158:LEU:HA	2.09	0.53
1:A:1203:SER:OG	1:A:1203:SER:O	2.24	0.52
1:A:1298:ARG:HH21	1:A:1298:ARG:CB	2.21	0.52
1:A:1597:PHE:CZ	1:A:1725:LEU:HD21	2.44	0.52
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.91	0.52
3:C:674:CYS:HB3	3:C:818:SER:OG	2.09	0.52
3:C:813:ARG:HH21	3:C:952:PHE:HE1	1.56	0.52
6:F:58:G:H1	6:F:76:A:H61	1.57	0.52
8:H:19:G:O2'	8:H:20:G:O4'	2.23	0.52
10:J:261:ALA:HA	10:J:264:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:318:TYR:O	10:J:322:MET:HG3	2.09	0.52
11:K:41:PHE:HA	11:K:44:HIS:HD2	1.73	0.52
19:X:246:TYR:OH	19:X:307:GLN:OE1	2.27	0.52
20:Y:1:MET:HE1	20:Y:6:LYS:HG3	1.90	0.52
22:1:1178:MET:CE	35:2:591:TYR:CZ	2.91	0.52
35:2:453:LYS:O	35:2:453:LYS:HD3	2.08	0.52
35:2:581:LYS:NZ	35:2:581:LYS:CB	2.73	0.52
1:A:119:LEU:HD21	1:A:476:PHE:HB3	1.91	0.52
1:A:266:SER:HB2	1:A:314:ILE:HD11	1.90	0.52
1:A:963:GLN:NE2	1:A:964:ASP:OD1	2.38	0.52
6:F:38:G:C6	7:G:9:C:N3	2.76	0.52
7:G:89:U:H4'	7:G:90:C:OP2	2.08	0.52
11:K:28:CYS:HA	11:K:41:PHE:HE2	1.73	0.52
19:X:222:GLU:O	20:Y:69:ARG:NH1	2.43	0.52
24:o:23:GLU:HA	24:o:46:ALA:O	2.09	0.52
35:2:578:TRP:N	35:2:578:TRP:CD1	2.76	0.52
38:7:21:ARG:NH2	38:7:68:ASP:OD1	2.42	0.52
43:v:32:GLN:NE2	43:v:32:GLN:CA	2.72	0.52
43:v:34:ALA:HA	43:v:37:THR:H	1.74	0.52
1:A:82:ARG:H	1:A:85:LYS:NZ	2.00	0.52
1:A:156:ARG:HG3	1:A:620:PRO:HB2	1.91	0.52
1:A:1256:PHE:H	1:A:1531:ASN:HD21	1.56	0.52
2:B:52:U:H2'	2:B:53:U:C6	2.43	0.52
2:B:97:G:N2	2:B:117:A:H62	2.07	0.52
3:C:220:ARG:NH1	3:C:578:ARG:O	2.42	0.52
7:G:15:U:H3'	7:G:16:G:C8	2.45	0.52
18:T:250:ARG:NH2	18:T:266:GLU:OE2	2.43	0.52
22:1:170:GLN:HG2	22:1:171:GLN:NE2	2.25	0.52
23:3:530:ASP:O	23:3:532:ARG:N	2.42	0.52
40:9:284:LEU:O	40:9:290:ASP:HA	2.10	0.52
1:A:819:SER:O	1:A:819:SER:OG	2.20	0.52
1:A:1002:ASP:OD1	1:A:1004:ASN:N	2.38	0.52
3:C:898:LEU:HD23	3:C:899:SER:N	2.23	0.52
5:E:92:LEU:HB3	5:E:102:TYR:CZ	2.44	0.52
6:F:40:U:C2	6:F:41:A:N7	2.77	0.52
18:T:387:PHE:O	18:T:398:TRP:HD1	1.92	0.52
19:X:296:HIS:ND1	19:X:298:SER:OG	2.32	0.52
22:1:166:ARG:HH22	22:1:620:MET:HG2	1.75	0.52
22:1:823:MET:SD	22:1:829:ASN:ND2	2.82	0.52
39:5:46:HIS:O	39:5:48:ASP:N	2.41	0.52
40:9:322:HIS:CE1	40:9:334:ASP:HB2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:8:34:LEU:HA	41:8:106:TRP:CD1	2.45	0.52
1:A:88:TYR:HB3	1:A:503:MET:SD	2.50	0.52
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.40	0.52
1:A:1630:LEU:HD21	1:A:1696:PRO:HG3	1.91	0.52
3:C:82:GLN:HE21	3:C:82:GLN:HA	1.74	0.52
3:C:461:LEU:HB3	3:C:465:MET:HE3	1.92	0.52
3:C:772:TRP:CZ2	40:9:130:ALA:HA	2.44	0.52
3:C:829:GLU:HG2	3:C:907:VAL:HG22	1.91	0.52
5:E:74:PHE:HE1	5:E:95:VAL:HG21	1.74	0.52
6:F:50:A:H4'	6:F:51:U:OP1	2.09	0.52
8:H:129:U:H2'	8:H:130:U:H5'	1.92	0.52
8:H:155:C:H2'	8:H:156:U:C6	2.45	0.52
10:J:228:ARG:HG2	10:J:248:TYR:OH	2.10	0.52
11:K:80:LEU:HD12	11:K:84:PHE:CD2	2.45	0.52
12:L:11:TRP:HB2	12:L:49:ARG:HH21	1.74	0.52
12:L:37:LEU:HD23	43:v:30:LEU:HG	1.92	0.52
17:R:416:LYS:HD3	21:Z:607:VAL:HG22	1.92	0.52
33:w:131:THR:O	33:w:135:GLY:N	2.23	0.52
39:5:48:ASP:O	39:5:51:ASN:N	2.42	0.52
40:9:329:VAL:HG12	40:9:383:THR:HA	1.91	0.52
1:A:678:GLU:OE1	1:A:678:GLU:N	2.42	0.52
1:A:969:SER:OG	1:A:970:GLU:N	2.39	0.52
3:C:914:LYS:HD3	3:C:931:ARG:HH22	1.75	0.52
5:E:220:TRP:CD2	5:E:227:LEU:HD13	2.44	0.52
10:J:245:TRP:HH2	10:J:267:ARG:HE	1.58	0.52
10:J:368:ARG:O	10:J:372:VAL:HG23	2.10	0.52
11:K:86:THR:HG22	11:K:141:TYR:O	2.10	0.52
22:1:900:PHE:HE2	22:1:954:LEU:HD22	1.74	0.52
23:3:21:ASN:OD1	23:3:69:ARG:NH2	2.43	0.52
23:3:465:HIS:O	23:3:468:ASP:HB2	2.10	0.52
25:p:154:PHE:O	25:p:220:ILE:HA	2.10	0.52
40:9:360:HIS:CE1	40:9:391:ASP:HA	2.45	0.52
1:A:102:LEU:HD22	1:A:496:VAL:HG21	1.90	0.52
1:A:306:GLN:HG3	3:C:879:ASP:HB3	1.91	0.52
5:E:249:TYR:CE2	5:E:263:ASP:HB3	2.45	0.52
7:G:85:G:N7	33:w:395:TRP:CZ2	2.78	0.52
18:T:385:TYR:CZ	18:T:400:PHE:HB3	2.44	0.52
23:3:552:ARG:HD3	23:3:600:GLN:HB3	1.91	0.52
40:9:305:GLU:HG2	40:9:309:ARG:HD3	1.90	0.52
40:9:343:GLU:H	40:9:378:SER:HB3	1.75	0.52
1:A:634:TRP:O	1:A:638:LEU:HG	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.90	0.52
2:B:51:A:H2'	2:B:52:U:C6	2.44	0.52
3:C:225:VAL:O	3:C:254:THR:OG1	2.24	0.52
5:E:73:LYS:HG3	5:E:115:LEU:O	2.09	0.52
17:R:134:ARG:NH2	18:T:382:PRO:O	2.43	0.52
22:1:123:ARG:HG3	22:1:124:ARG:HG3	1.90	0.52
22:1:609:MET:O	22:1:613:MET:HG2	2.10	0.52
22:1:1154:LEU:O	22:1:1158:ILE:HG23	2.10	0.52
23:3:23:SER:OG	23:3:29:GLU:OE2	2.19	0.52
35:2:586:ILE:CD1	35:2:586:ILE:N	2.72	0.52
31:e:36:TYR:N	31:e:83:ASN:O	2.42	0.52
1:A:108:MET:HE1	1:A:144:TRP:HZ2	1.74	0.52
2:B:36:C:N4	2:B:47:A:H61	2.08	0.52
2:B:47:A:OP2	2:B:47:A:H2'	2.10	0.52
3:C:286:ASN:HB3	3:C:299:ILE:CG2	2.40	0.52
3:C:602:LYS:HB3	3:C:651:ILE:HD11	1.92	0.52
4:D:1211:ASP:O	4:D:1215:HIS:N	2.41	0.52
5:E:133:VAL:HG21	5:E:169:THR:HG21	1.92	0.52
6:F:46:G:H5'	6:F:47:A:C4'	2.40	0.52
12:L:24:MET:CE	43:v:40:ILE:HD11	2.39	0.52
22:1:614:ARG:HG3	22:1:647:PHE:CZ	2.42	0.52
23:3:172:GLY:O	23:3:237:THR:OG1	2.28	0.52
23:3:616:ILE:HG22	23:3:628:LEU:HB2	1.91	0.52
23:3:673:VAL:HA	23:3:690:ARG:HA	1.91	0.52
1:A:1642:PRO:HA	1:A:1716:GLY:O	2.10	0.52
3:C:719:GLN:HA	3:C:724:TRP:H	1.75	0.52
3:C:724:TRP:HE1	3:C:728:ALA:HB3	1.74	0.52
4:D:1558:PRO:HA	4:D:1642:GLN:O	2.10	0.52
4:D:1583:ASP:O	4:D:1585:GLN:N	2.43	0.52
5:E:294:SER:CB	5:E:299:LYS:H	2.23	0.52
10:J:300:ASP:O	10:J:304:THR:OG1	2.19	0.52
11:K:33:LYS:HB3	11:K:44:HIS:CE1	2.45	0.52
17:R:126:ASN:HB2	18:T:442:ARG:HD3	1.91	0.52
23:3:715:MET:HG2	23:3:739:LEU:HB2	1.92	0.52
35:2:533:ILE:CD1	35:2:533:ILE:N	2.73	0.52
35:2:586:ILE:HD13	35:2:586:ILE:N	2.24	0.52
1:A:977:LEU:HG	1:A:978:GLU:N	2.23	0.51
1:A:1298:ARG:HB3	1:A:1298:ARG:CZ	2.41	0.51
1:A:1537:TRP:HD1	1:A:1538:TRP:CD1	2.27	0.51
3:C:157:ILE:HD11	3:C:165:LEU:HD11	1.93	0.51
3:C:235:VAL:HG11	3:C:288:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:300:LEU:HA	3:C:306:ASN:ND2	2.24	0.51
3:C:789:PHE:CE2	3:C:816:VAL:HG13	2.45	0.51
3:C:937:THR:O	3:C:941:LYS:HG3	2.10	0.51
10:J:335:ARG:HA	10:J:338:GLU:OE1	2.09	0.51
16:Q:818:LEU:HA	16:Q:1091:TRP:O	2.10	0.51
22:1:1195:MET:O	22:1:1199:VAL:HG23	2.09	0.51
23:3:147:ASP:OD1	23:3:151:ARG:N	2.41	0.51
23:3:727:SER:O	23:3:728:ARG:HG3	2.10	0.51
1:A:429:ASN:HA	1:A:432:ARG:HB2	1.91	0.51
1:A:647:LEU:HD11	1:A:651:TRP:CE2	2.45	0.51
1:A:1482:GLU:HG3	1:A:1483:GLY:H	1.74	0.51
1:A:1635:TYR:O	1:A:1658:GLN:NE2	2.34	0.51
2:B:12:U:H3	2:B:65:G:H1	1.56	0.51
6:F:87:C:C2	8:H:12:G:C6	2.98	0.51
15:P:212:ASN:HD21	18:T:484:LYS:HE3	1.74	0.51
18:T:209:CYS:SG	18:T:252:VAL:N	2.83	0.51
22:1:871:THR:C	22:1:875:ILE:HD12	2.36	0.51
23:3:791:HIS:NE2	23:3:793:GLU:HB2	2.25	0.51
23:3:883:GLU:HG2	23:3:884:GLN:H	1.75	0.51
43:v:91:LYS:NZ	43:v:91:LYS:CB	2.73	0.51
30:f:15:LYS:O	30:f:31:LEU:N	2.38	0.51
1:A:102:LEU:HD22	1:A:496:VAL:HG11	1.91	0.51
1:A:545:HIS:HB3	1:A:594:TYR:CZ	2.45	0.51
1:A:1457:HIS:ND1	1:A:1460:HIS:HD2	2.09	0.51
3:C:226:VAL:HG11	3:C:430:PHE:CE1	2.45	0.51
3:C:281:ILE:O	3:C:285:VAL:HG23	2.10	0.51
4:D:1397:PHE:O	4:D:1402:ASN:N	2.44	0.51
6:F:43:A:H2'	6:F:44:G:C8	2.45	0.51
11:K:129:LYS:NZ	11:K:131:ASP:OD2	2.36	0.51
12:L:50:TRP:CE2	12:L:55:ASP:HB2	2.45	0.51
19:X:245:LYS:HB2	19:X:331:LEU:HD13	1.91	0.51
19:X:260:ARG:HH22	19:X:372:GLU:HA	1.75	0.51
23:3:618:SER:H	23:3:628:LEU:HD13	1.75	0.51
35:2:533:ILE:N	35:2:533:ILE:HD13	2.25	0.51
1:A:332:TYR:HA	3:C:177:ARG:O	2.11	0.51
1:A:863:GLU:O	1:A:867:ILE:HG12	2.11	0.51
3:C:439:PRO:CB	3:C:443:VAL:HG13	2.39	0.51
5:E:140:THR:HG23	5:E:142:GLU:H	1.74	0.51
11:K:106:HIS:CE1	11:K:108:ASN:HB2	2.46	0.51
14:O:258:ILE:HA	14:O:274:PHE:HA	1.92	0.51
22:1:159:GLN:O	22:1:162:THR:OG1	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1098:LEU:HD13	22:1:1135:GLU:HG2	1.92	0.51
23:3:369:GLU:CD	23:3:369:GLU:H	2.18	0.51
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.92	0.51
23:3:864:SER:O	23:3:865:VAL:HG23	2.10	0.51
23:3:1052:ASN:OD1	23:3:1052:ASN:N	2.41	0.51
23:3:1098:GLY:C	23:3:1099:GLU:HG3	2.36	0.51
31:j:31:ILE:O	31:j:44:GLU:HA	2.10	0.51
33:w:481:ASP:HB3	33:w:485:ASN:H	1.75	0.51
1:A:234:MET:O	1:A:238:LEU:HG	2.11	0.51
1:A:445:VAL:O	1:A:449:LYS:HG3	2.11	0.51
1:A:796:LYS:HD2	1:A:797:ASP:OD1	2.09	0.51
2:B:46:U:O4	2:B:47:A:N6	2.43	0.51
6:F:48:A:H5'	6:F:49:G:O5'	2.10	0.51
22:1:822:ARG:HB3	22:1:822:ARG:CZ	2.39	0.51
23:3:102:ILE:HG22	23:3:103:HIS:CD2	2.45	0.51
23:3:316:GLU:HG3	23:3:326:ARG:HD3	1.92	0.51
23:3:644:GLU:HB2	23:3:663:LEU:HD12	1.91	0.51
23:3:1018:GLU:O	23:3:1018:GLU:HG2	2.10	0.51
35:2:453:LYS:HE2	35:2:453:LYS:O	2.11	0.51
40:9:285:HIS:NE2	40:9:432:THR:OG1	2.29	0.51
1:A:171:ASP:HA	1:A:521:ASN:ND2	2.25	0.51
1:A:1063:GLY:HA3	1:A:1069:ASN:OD1	2.11	0.51
1:A:1184:ASN:OD1	1:A:1195:ARG:HD2	2.11	0.51
12:L:98:GLU:HG3	12:L:99:HIS:N	2.25	0.51
18:T:439:TRP:N	18:T:439:TRP:CD1	2.79	0.51
22:1:400:SER:OG	22:1:401:ASP:N	2.43	0.51
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.91	0.51
1:A:703:GLN:C	1:A:705:LYS:H	2.19	0.51
1:A:1295:ILE:O	1:A:1295:ILE:HG12	2.11	0.51
1:A:1298:ARG:HH21	1:A:1298:ARG:CA	2.23	0.51
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.46	0.51
2:B:107:U:H2'	2:B:108:G:O4'	2.10	0.51
5:E:69:VAL:HG23	5:E:349:LYS:HA	1.92	0.51
12:L:49:ARG:HG3	12:L:54:LEU:HD23	1.92	0.51
20:Y:3:PRO:O	20:Y:6:LYS:N	2.43	0.51
22:1:163:LYS:HG3	22:1:164:GLU:N	2.25	0.51
22:1:442:THR:OG1	22:1:443:GLY:N	2.35	0.51
22:1:1126:PHE:O	35:2:575:PHE:CE2	2.63	0.51
22:1:1139:PRO:HB3	43:v:50:HIS:O	2.05	0.51
33:w:32:THR:O	33:w:35:ASP:N	2.44	0.51
1:A:1086:ARG:C	1:A:1087:LEU:HD23	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1103:ALA:O	1:A:1107:ARG:HG3	2.10	0.51
1:A:1412:TRP:O	1:A:1420:ASN:HB3	2.11	0.51
7:G:102:G:H4'	38:7:25:LYS:HZ3	1.76	0.51
8:H:30:A:O2'	12:L:39:HIS:NE2	2.44	0.51
18:T:287:HIS:CE1	18:T:307:SER:HB3	2.46	0.51
18:T:357:TRP:N	18:T:357:TRP:CD1	2.78	0.51
19:X:259:TRP:CE3	19:X:371:HIS:HB3	2.46	0.51
19:X:261:LEU:HD13	19:X:369:LEU:HD13	1.92	0.51
23:3:898:ASN:OD1	23:3:899:THR:HG22	2.10	0.51
31:j:58:LEU:O	31:j:76:ARG:HA	2.11	0.51
35:2:532:GLY:C	35:2:534:GLN:H	2.19	0.51
1:A:818:GLU:HB2	22:1:444:PHE:HD2	1.76	0.51
7:G:91:A:O5'	7:G:91:A:H8	1.94	0.51
11:K:29:GLN:C	11:K:32:GLN:H	2.18	0.51
18:T:189:GLN:HG2	18:T:190:TRP:H	1.75	0.51
18:T:343:PRO:HG3	18:T:356:LEU:HD23	1.93	0.51
18:T:385:TYR:O	18:T:400:PHE:HB2	2.10	0.51
19:X:300:SER:H	19:X:303:HIS:CE1	2.28	0.51
22:1:984:GLU:CD	22:1:986:TYR:H	2.17	0.51
23:3:54:LEU:HD21	23:3:99:PHE:CE2	2.46	0.51
23:3:329:TYR:OH	23:3:332:THR:HG22	2.10	0.51
1:A:390:ASP:OD2	3:C:394:ARG:NH2	2.43	0.51
1:A:1487:HIS:O	1:A:1541:THR:OG1	2.29	0.51
1:A:1643:SER:O	1:A:1715:TYR:HA	2.10	0.51
3:C:203:MET:HB2	3:C:549:TRP:CH2	2.46	0.51
3:C:371:GLU:HA	3:C:375:GLU:HB2	1.93	0.51
3:C:568:PRO:HB2	3:C:569:ARG:HH11	1.76	0.51
3:C:696:LEU:HD21	3:C:744:ILE:HD11	1.92	0.51
10:J:357:LYS:HG3	10:J:359:VAL:HG22	1.93	0.51
22:1:1051:SER:OG	22:1:1054:GLU:HG2	2.11	0.51
22:1:1108:ASN:CB	22:1:1111:CYS:H	2.23	0.51
23:3:876:THR:O	23:3:876:THR:OG1	2.29	0.51
33:w:462:LEU:C	33:w:462:LEU:CD2	2.84	0.51
35:2:656:PRO:HA	35:2:686:VAL:O	2.12	0.51
1:A:535:ARG:HH22	1:A:1551:PHE:HE1	1.54	0.50
1:A:577:GLY:O	1:A:581:ILE:HG13	2.10	0.50
3:C:610:VAL:HG13	3:C:648:TYR:HD2	1.76	0.50
3:C:830:PRO:HA	3:C:904:TRP:HA	1.93	0.50
6:F:1:G:H2'	6:F:2:U:H6	1.76	0.50
10:J:346:TRP:CE3	10:J:369:PHE:HB2	2.46	0.50
12:L:37:LEU:HD21	43:v:30:LEU:HG	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:476:ASP:HB2	37:6:24:ARG:HH22	1.77	0.50
22:1:641:ILE:HD11	22:1:675:MET:HE2	1.93	0.50
22:1:774:ILE:HA	22:1:777:PHE:CE2	2.46	0.50
22:1:1050:VAL:HG12	22:1:1054:GLU:HB2	1.92	0.50
22:1:1257:PRO:HG2	35:2:478:HIS:O	2.10	0.50
23:3:230:GLU:OE1	23:3:230:GLU:N	2.44	0.50
23:3:436:ARG:HH11	23:3:776:GLN:NE2	2.09	0.50
24:o:13:ALA:O	24:o:24:LEU:HA	2.10	0.50
1:A:153:ARG:HG3	1:A:156:ARG:HE	1.76	0.50
1:A:414:ARG:HD3	3:C:410:LEU:O	2.11	0.50
1:A:840:ILE:HG13	22:1:104:PHE:CZ	2.46	0.50
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.26	0.50
1:A:1268:ILE:O	1:A:1272:THR:HG23	2.10	0.50
1:A:1310:ARG:CG	1:A:1310:ARG:NH2	2.73	0.50
3:C:89:LEU:O	18:T:278:ASN:ND2	2.36	0.50
3:C:168:THR:O	3:C:184:THR:HG21	2.11	0.50
3:C:381:LEU:O	3:C:385:VAL:HG13	2.11	0.50
5:E:336:HIS:CB	5:E:341:ILE:HB	2.41	0.50
8:H:153:A:H61	8:H:179:C:N4	2.08	0.50
11:K:145:ASP:O	11:K:149:ILE:HG13	2.11	0.50
11:K:362:GLU:CB	20:Y:71:LYS:HG3	2.35	0.50
14:O:81:CYS:N	14:O:86:LEU:O	2.26	0.50
18:T:412:HIS:NE2	18:T:435:THR:O	2.42	0.50
19:X:260:ARG:HD3	19:X:274:TYR:CE2	2.45	0.50
22:1:130:PRO:HB2	22:1:150:ARG:HD2	1.93	0.50
22:1:656:LYS:CE	41:8:65:ASP:H	2.22	0.50
22:1:984:GLU:OE2	22:1:985:GLU:N	2.44	0.50
22:1:1012:PRO:O	22:1:1015:ASP:N	2.43	0.50
23:3:505:THR:HG21	23:3:508:CYS:SG	2.51	0.50
28:m:47:GLU:O	28:m:64:LYS:HA	2.11	0.50
38:7:33:CYS:SG	38:7:35:SER:HB3	2.51	0.50
38:7:37:VAL:HB	38:7:38:ARG:HG3	1.92	0.50
39:5:1:MET:HE3	39:5:2:THR:HG23	1.92	0.50
40:9:239:ALA:HB3	40:9:264:ALA:HB3	1.92	0.50
2:B:115:C:H2'	2:B:116:U:O4'	2.11	0.50
3:C:507:VAL:HA	3:C:568:PRO:HD3	1.93	0.50
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.94	0.50
4:D:2069:GLY:HA2	4:D:2077:ILE:H	1.75	0.50
5:E:113:MET:HA	5:E:113:MET:HE2	1.94	0.50
6:F:33:G:N2	7:G:14:A:C4	2.79	0.50
10:J:422:PHE:O	10:J:426:GLN:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:14:THR:HG22	43:v:67:GLY:HA3	1.93	0.50
17:R:134:ARG:HH12	18:T:382:PRO:C	2.20	0.50
22:1:1224:PRO:HA	22:1:1227:ILE:HG22	1.92	0.50
43:v:44:PRO:C	43:v:46:PHE:H	2.19	0.50
1:A:210:HIS:CE1	1:A:211:GLN:HG3	2.46	0.50
1:A:1553:VAL:HG13	7:G:2:U:O2'	2.11	0.50
1:A:1639:VAL:HG21	1:A:1699:THR:HB	1.92	0.50
3:C:226:VAL:HG11	3:C:430:PHE:HE1	1.77	0.50
3:C:486:ASP:HB3	3:C:488:VAL:HG23	1.93	0.50
6:F:62:C:N3	6:F:73:A:C2	2.80	0.50
12:L:25:LYS:HD3	12:L:26:TYR:CE2	2.46	0.50
18:T:373:LYS:O	18:T:391:SER:OG	2.25	0.50
22:1:112:ILE:HG13	22:1:115:ARG:HH11	1.76	0.50
22:1:700:LYS:O	22:1:704:ILE:HG22	2.10	0.50
23:3:483:LEU:HG	23:3:493:GLU:HG3	1.93	0.50
39:5:36:HIS:CE1	39:5:76:CYS:SG	3.04	0.50
40:9:334:ASP:OD2	40:9:336:THR:OG1	2.29	0.50
1:A:252:ASP:H	1:A:334:THR:HG21	1.77	0.50
1:A:893:GLU:HB2	1:A:1016:VAL:O	2.12	0.50
3:C:109:LEU:HG	3:C:537:TYR:CE2	2.47	0.50
3:C:673:LYS:HB3	3:C:686:THR:CG2	2.41	0.50
6:F:37:C:H5	7:G:4:A:OP2	1.94	0.50
6:F:40:U:H2'	6:F:41:A:H8	1.76	0.50
6:F:64:U:C4	6:F:65:G:C5	2.99	0.50
16:Q:1181:ASN:HA	16:Q:1305:ALA:O	2.12	0.50
18:T:223:SER:OG	18:T:224:ALA:N	2.39	0.50
20:Y:86:ASP:OD1	20:Y:86:ASP:N	2.40	0.50
20:Y:116:ARG:HA	20:Y:116:ARG:NE	2.26	0.50
22:1:978:LEU:O	22:1:981:TYR:N	2.41	0.50
22:1:1023:ILE:O	22:1:1026:ASN:HB2	2.12	0.50
23:3:185:LEU:HG	23:3:235:LEU:HD11	1.93	0.50
23:3:288:VAL:HG23	23:3:289:CYS:H	1.76	0.50
1:A:378:PHE:CZ	3:C:335:ASN:HB3	2.46	0.50
1:A:1276:GLU:OE2	1:A:1375:TRP:N	2.44	0.50
1:A:1560:ILE:HG22	1:A:1668:TRP:CD1	2.46	0.50
1:A:1670:ASP:CG	1:A:1672:ASP:H	2.19	0.50
3:C:375:GLU:O	3:C:379:LYS:HG3	2.11	0.50
3:C:796:VAL:HB	3:C:803:ARG:HH11	1.76	0.50
3:C:838:ALA:O	3:C:869:TYR:HB2	2.12	0.50
5:E:118:ASN:OD1	5:E:123:MET:HB2	2.12	0.50
6:F:9:U:O2'	6:F:10:U:O4'	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:34:G:C8	7:G:13:C:N4	2.79	0.50
10:J:363:ARG:NH2	10:J:386:GLU:OE1	2.44	0.50
11:K:132:GLU:HG2	11:K:133:THR:N	2.25	0.50
18:T:216:ASN:OD1	18:T:471:ASP:HB2	2.12	0.50
18:T:306:CYS:HB3	18:T:336:VAL:HG12	1.93	0.50
18:T:346:ILE:HD11	18:T:400:PHE:CZ	2.46	0.50
22:1:477:LYS:HB2	22:1:499:LYS:NZ	2.27	0.50
23:3:459:VAL:HA	23:3:475:ILE:O	2.12	0.50
23:3:548:ALA:O	23:3:555:VAL:HB	2.12	0.50
23:3:788:PHE:HB3	23:3:799:ILE:HG23	1.92	0.50
37:6:106:LYS:O	37:6:109:GLN:HG2	2.12	0.50
37:6:112:LEU:O	37:6:116:LYS:CB	2.60	0.50
1:A:82:ARG:HG2	7:G:16:G:O6	2.11	0.50
1:A:121:HIS:ND1	1:A:481:PHE:O	2.45	0.50
1:A:256:TYR:HE1	1:A:331:TRP:H	1.58	0.50
1:A:363:HIS:NE2	3:C:287:GLY:HA3	2.26	0.50
1:A:540:PHE:HB2	1:A:545:HIS:CE1	2.46	0.50
1:A:939:TRP:C	1:A:939:TRP:CD1	2.89	0.50
1:A:979:SER:HB2	1:A:1173:SER:HB3	1.93	0.50
3:C:742:PRO:O	3:C:786:ASN:HA	2.12	0.50
8:H:98:G:C6	26:h:62:HIS:HA	2.47	0.50
10:J:319:MET:HA	10:J:322:MET:HE3	1.94	0.50
10:J:351:ASN:HB2	10:J:355:ARG:HH21	1.77	0.50
18:T:459:LEU:HA	40:9:259:THR:OG1	2.12	0.50
22:1:427:PRO:HA	22:1:430:LYS:CB	2.42	0.50
22:1:884:ILE:HG22	22:1:885:ASP:O	2.12	0.50
22:1:1010:THR:OG1	22:1:1011:PRO:HD3	2.11	0.50
22:1:1262:ARG:NH1	35:2:483:GLN:HE21	2.09	0.50
23:3:16:PHE:HB2	23:3:65:LEU:HD23	1.94	0.50
35:2:518:GLU:OE1	35:2:518:GLU:HA	2.12	0.50
37:6:22:TYR:CZ	37:6:24:ARG:HD3	2.46	0.50
40:9:235:LYS:NZ	40:9:452:GLN:HB2	2.26	0.50
40:9:236:LEU:HD23	40:9:237:ASN:H	1.77	0.50
1:A:150:MET:SD	1:A:193:LEU:HB2	2.51	0.50
1:A:825:ILE:HD13	1:A:929:GLU:HB2	1.93	0.50
1:A:1014:ASN:ND2	12:L:81:GLN:HB3	2.27	0.50
1:A:1019:TYR:O	1:A:1022:MET:N	2.45	0.50
1:A:1022:MET:O	1:A:1023:ASN:ND2	2.42	0.50
1:A:1740:LEU:O	1:A:1744:ARG:HG3	2.12	0.50
1:A:2274:PRO:HA	1:A:2295:GLU:O	2.11	0.50
2:B:32:C:C2	2:B:33:U:C5	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:245:TRP:CZ3	10:J:264:ILE:HG23	2.47	0.50
17:R:138:GLU:CD	17:R:138:GLU:N	2.70	0.50
17:R:413:ASN:OD1	21:Z:603:SER:HB3	2.11	0.50
22:1:1009:MET:HE3	22:1:1011:PRO:HD2	1.92	0.50
23:3:553:GLN:NE2	23:3:601:ARG:HA	2.27	0.50
23:3:593:ALA:HA	23:3:642:ILE:HD13	1.93	0.50
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.11	0.50
1:A:239:TYR:CE1	1:A:408:PRO:HD2	2.46	0.50
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.47	0.50
3:C:207:GLY:N	45:C:1500:GTP:O3G	2.38	0.50
6:F:36:A:N1	7:G:10:U:C4	2.80	0.50
10:J:326:VAL:HG13	10:J:352:PHE:HZ	1.77	0.50
16:Q:408:VAL:O	16:Q:412:GLU:CB	2.60	0.50
16:Q:539:VAL:O	16:Q:624:THR:HA	2.12	0.50
18:T:223:SER:OG	18:T:225:ASP:N	2.33	0.50
19:X:284:GLY:O	19:X:294:ILE:N	2.36	0.50
22:1:856:ASP:HB3	22:1:864:TYR:HE2	1.76	0.50
22:1:1019:ARG:HA	22:1:1019:ARG:HH11	1.77	0.50
30:k:6:PRO:HB3	30:k:36:PRO:HG3	1.93	0.50
1:A:82:ARG:NE	7:G:14:A:OP2	2.45	0.49
1:A:787:GLU:O	1:A:790:ARG:N	2.44	0.49
1:A:931:ASP:OD2	1:A:1434:LYS:NZ	2.29	0.49
1:A:1311:PHE:CD1	1:A:1312:PRO:HD2	2.47	0.49
1:A:1312:PRO:HG3	1:A:1541:THR:CG2	2.41	0.49
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.94	0.49
3:C:225:VAL:HG12	3:C:252:ALA:O	2.11	0.49
3:C:753:GLU:HG2	3:C:756:LYS:HD3	1.93	0.49
5:E:82:ALA:HB1	5:E:115:LEU:HD13	1.94	0.49
5:E:333:VAL:HA	5:E:343:ILE:O	2.12	0.49
6:F:45:A:N1	7:G:4:A:N6	2.60	0.49
8:H:125:G:H2'	8:H:126:A:C8	2.47	0.49
18:T:425:GLY:O	18:T:441:TRP:N	2.35	0.49
19:X:260:ARG:HB3	19:X:272:VAL:HG11	1.93	0.49
22:1:1125:PRO:HG2	22:1:1165:TYR:CE2	2.47	0.49
23:3:802:THR:HG22	23:3:803:ASP:N	2.27	0.49
24:o:116:THR:HA	24:o:142:VAL:HA	1.94	0.49
37:6:81:ASN:HB2	37:6:86:TYR:HE1	1.75	0.49
1:A:770:THR:O	1:A:772:CYS:N	2.45	0.49
1:A:2273:VAL:O	1:A:2297:GLN:N	2.43	0.49
3:C:139:HIS:CE1	3:C:179:VAL:HG23	2.47	0.49
3:C:275:TYR:HA	3:C:278:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:836:VAL:HG22	3:C:897:SER:HB3	1.94	0.49
5:E:242:SER:C	5:E:250:LEU:HD12	2.37	0.49
11:K:177:VAL:HA	23:3:690:ARG:HH22	1.77	0.49
18:T:497:GLU:OE1	18:T:497:GLU:N	2.45	0.49
19:X:260:ARG:HH12	19:X:372:GLU:N	2.10	0.49
20:Y:67:LEU:HD13	20:Y:80:CYS:HB2	1.93	0.49
23:3:249:LEU:HD22	23:3:256:ILE:HD11	1.93	0.49
33:w:383:LEU:CD1	33:w:394:TYR:HA	2.42	0.49
40:9:243:THR:HG23	40:9:262:GLU:O	2.12	0.49
1:A:102:LEU:HA	1:A:129:VAL:HG21	1.94	0.49
1:A:409:ARG:HA	1:A:412:ASN:HD22	1.76	0.49
3:C:137:HIS:HB3	3:C:140:HIS:ND1	2.27	0.49
3:C:137:HIS:CG	3:C:138:LEU:N	2.79	0.49
3:C:497:LEU:HD12	3:C:577:PHE:CZ	2.47	0.49
3:C:590:ILE:HG21	3:C:637:LEU:HD11	1.93	0.49
5:E:69:VAL:HB	5:E:345:ALA:HB1	1.94	0.49
5:E:275:LYS:HD3	5:E:314:THR:O	2.12	0.49
18:T:269:GLN:OE1	18:T:271:LYS:HE2	2.12	0.49
22:1:1107:GLN:OE1	22:1:1107:GLN:HA	2.13	0.49
22:1:1304:LEU:HD12	39:5:52:TYR:CE2	2.48	0.49
23:3:253:GLU:O	23:3:254:ASN:HB2	2.11	0.49
23:3:528:ARG:CB	23:3:532:ARG:HE	2.25	0.49
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	1.93	0.49
1:A:176:LEU:HD11	1:A:562:VAL:HG13	1.95	0.49
1:A:264:PHE:HB2	1:A:328:HIS:CD2	2.48	0.49
2:B:20:G:H4'	2:B:21:A:OP1	2.10	0.49
3:C:224:GLY:HA3	3:C:438:ILE:HG23	1.94	0.49
3:C:230:ASP:HB2	3:C:259:LYS:HZ1	1.77	0.49
3:C:259:LYS:HG2	45:C:1500:GTP:C6	2.46	0.49
3:C:837:GLN:HA	3:C:869:TYR:O	2.11	0.49
4:D:1529:GLY:HA2	4:D:1706:CYS:O	2.13	0.49
19:X:372:GLU:HG2	19:X:373:SER:H	1.75	0.49
22:1:1174:GLU:O	22:1:1178:MET:HG2	2.12	0.49
23:3:111:GLY:O	23:3:113:ARG:N	2.45	0.49
23:3:316:GLU:HB2	23:3:324:GLU:HG2	1.95	0.49
23:3:525:ARG:O	23:3:525:ARG:HG2	2.11	0.49
23:3:666:ASN:HD22	23:3:666:ASN:N	2.11	0.49
40:9:276:VAL:HG13	40:9:437:PRO:HB2	1.93	0.49
1:A:112:GLN:HB3	1:A:187:PRO:HB2	1.94	0.49
1:A:206:TRP:HZ2	1:A:234:MET:HE2	1.76	0.49
1:A:363:HIS:CD2	3:C:287:GLY:HA3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:LEU:HB2	1:A:1175:VAL:HG22	1.95	0.49
1:A:1482:GLU:HG3	1:A:1483:GLY:N	2.27	0.49
2:B:101:U:H2'	2:B:102:U:H6	1.78	0.49
3:C:490:PHE:HD2	3:C:612:LYS:HD2	1.77	0.49
3:C:745:LEU:HD12	3:C:789:PHE:O	2.12	0.49
6:F:31:U:O4	7:G:16:G:H1'	2.13	0.49
7:G:5:G:H5'	11:K:22:GLN:HA	1.95	0.49
19:X:274:TYR:CE1	22:1:436:THR:HA	2.48	0.49
19:X:338:PHE:HB2	19:X:359:LYS:HB3	1.93	0.49
22:1:1055:TRP:HA	22:1:1055:TRP:CE3	2.47	0.49
22:1:1137:ARG:HH21	35:2:524:LEU:CD1	2.26	0.49
23:3:788:PHE:HA	23:3:798:ILE:O	2.12	0.49
23:3:833:GLU:O	23:3:835:ALA:N	2.45	0.49
23:3:1083:ASN:ND2	35:2:471:ARG:HH22	2.10	0.49
35:2:534:GLN:CA	35:2:534:GLN:NE2	2.76	0.49
38:7:10:PHE:HB2	38:7:12:ARG:NE	2.27	0.49
1:A:501:TYR:HD1	1:A:518:LEU:HD23	1.77	0.49
1:A:1234:ASP:O	1:A:1235:GLU:C	2.55	0.49
1:A:2194:THR:HA	1:A:2238:GLY:HA3	1.94	0.49
3:C:453:TYR:CE1	3:C:465:MET:HE1	2.48	0.49
3:C:658:PRO:HB2	3:C:881:PHE:CZ	2.47	0.49
8:H:29:A:N6	43:v:22:SER:HB2	2.28	0.49
11:K:28:CYS:SG	11:K:50:HIS:HE1	2.35	0.49
14:O:75:SER:O	14:O:79:ASN:HA	2.13	0.49
20:Y:54:CYS:O	20:Y:57:SER:OG	2.30	0.49
22:1:1179:ASP:OD1	22:1:1184:HIS:CD2	2.65	0.49
23:3:240:GLY:HA2	23:3:245:PRO:O	2.12	0.49
23:3:312:LYS:NZ	23:3:366:ASP:OD1	2.44	0.49
37:6:29:LYS:HG3	37:6:57:ARG:NH2	2.27	0.49
37:6:47:GLN:HG2	37:6:48:ILE:N	2.27	0.49
1:A:171:ASP:HA	1:A:521:ASN:HD22	1.77	0.49
1:A:319:LEU:HD21	3:C:638:ASP:HA	1.93	0.49
1:A:351:TYR:N	3:C:268:LYS:O	2.45	0.49
1:A:1069:ASN:OD1	1:A:1069:ASN:N	2.43	0.49
1:A:1083:HIS:ND1	1:A:1084:PRO:HD2	2.27	0.49
6:F:82:A:O2'	8:H:16:U:O4	2.22	0.49
8:H:166:G:N3	8:H:166:G:H2'	2.28	0.49
10:J:314:TYR:CE1	10:J:336:TRP:HH2	2.31	0.49
11:K:95:TYR:HB2	11:K:115:LEU:HD21	1.94	0.49
19:X:327:TYR:HB3	19:X:349:TYR:HD1	1.78	0.49
23:3:191:GLU:H	23:3:191:GLU:HG3	1.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:6:16:GLU:CD	37:6:16:GLU:H	2.21	0.49
40:9:369:ALA:HB3	40:9:379:GLN:HB2	1.95	0.49
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.47	0.49
1:A:141:ILE:HG22	1:A:242:ALA:HB1	1.94	0.49
1:A:1303:LEU:HB3	1:A:1566:ILE:HG22	1.95	0.49
1:A:1581:LEU:HD23	1:A:1746:ARG:NH2	2.28	0.49
4:D:1185:GLU:O	4:D:1204:ILE:HA	2.12	0.49
5:E:248:SER:O	5:E:263:ASP:HA	2.13	0.49
5:E:321:TYR:HB3	5:E:323:LEU:HD21	1.95	0.49
6:F:91:A:H2'	6:F:92:A:H8	1.77	0.49
22:1:944:SER:O	22:1:947:VAL:N	2.46	0.49
22:1:953:ASP:OD1	22:1:992:SER:HB3	2.13	0.49
22:1:1091:HIS:ND1	22:1:1091:HIS:C	2.71	0.49
23:3:288:VAL:HG23	23:3:289:CYS:N	2.28	0.49
23:3:305:THR:HG22	23:3:309:ASP:O	2.13	0.49
23:3:512:GLY:HA3	23:3:515:ALA:HB3	1.93	0.49
23:3:981:CYS:SG	23:3:982:GLU:N	2.86	0.49
27:i:70:LEU:O	31:j:80:LYS:N	2.36	0.49
35:2:488:LEU:C	35:2:488:LEU:CD2	2.85	0.49
35:2:520:PRO:HG2	35:2:520:PRO:O	2.12	0.49
35:2:524:LEU:HD13	35:2:528:ILE:HG21	1.93	0.49
1:A:681:PHE:C	1:A:681:PHE:CD2	2.89	0.49
1:A:1306:LYS:NZ	7:G:0:G:N7	2.60	0.49
8:H:114:A:H2'	8:H:115:G:C8	2.48	0.49
11:K:121:TRP:CZ2	11:K:125:GLU:HG3	2.48	0.49
12:L:71:LEU:HD21	12:L:100:TYR:HB2	1.95	0.49
19:X:286:HIS:CD2	19:X:301:LYS:HD3	2.48	0.49
21:Z:574:ASN:ND2	21:Z:578:ILE:H	2.10	0.49
22:1:445:HIS:CG	22:1:445:HIS:O	2.65	0.49
22:1:889:GLU:OE2	22:1:928:TYR:OH	2.21	0.49
23:3:1081:LEU:C	23:3:1081:LEU:CD2	2.85	0.49
39:5:11:LEU:HD12	39:5:12:GLU:N	2.28	0.49
1:A:556:LEU:HD13	1:A:588:LEU:HD13	1.95	0.49
1:A:606:LYS:HG3	1:A:609:LYS:HZ3	1.77	0.49
1:A:661:GLU:N	1:A:661:GLU:OE2	2.43	0.49
1:A:1300:LYS:C	1:A:1302:GLY:N	2.69	0.49
3:C:213:ASP:OD1	3:C:213:ASP:N	2.44	0.49
3:C:220:ARG:NH2	3:C:580:LEU:HA	2.27	0.49
3:C:265:LEU:HD21	3:C:381:LEU:HD13	1.94	0.49
3:C:834:VAL:HA	3:C:898:LEU:O	2.13	0.49
8:H:3:C:H2'	8:H:4:G:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:X:282:LEU:HD23	19:X:290:ALA:HA	1.94	0.49
22:1:129:SEP:O2P	22:1:573:LYS:HG3	2.12	0.49
22:1:129:SEP:P	22:1:573:LYS:NZ	2.84	0.49
22:1:774:ILE:HA	22:1:777:PHE:HE2	1.78	0.49
22:1:1166:ILE:O	22:1:1170:THR:HG23	2.13	0.49
23:3:415:LEU:HD23	23:3:871:PRO:HG3	1.94	0.49
23:3:791:HIS:CD2	23:3:793:GLU:H	2.31	0.49
37:6:35:MET:HE3	37:6:48:ILE:HG21	1.93	0.49
40:9:142:ARG:HA	40:9:149:PRO:HA	1.95	0.49
40:9:233:VAL:HG13	40:9:237:ASN:HB3	1.95	0.49
40:9:410:MET:O	40:9:413:VAL:HG12	2.12	0.49
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.28	0.48
1:A:1258:LYS:HZ3	17:R:428:GLU:CD	2.21	0.48
1:A:1544:ARG:HA	1:A:1670:ASP:OD2	2.13	0.48
1:A:1665:GLN:NE2	1:A:1665:GLN:HA	2.28	0.48
1:A:1699:THR:O	1:A:1699:THR:OG1	2.30	0.48
6:F:87:C:C2	6:F:88:G:C8	3.01	0.48
6:F:93:G:C2	8:H:6:U:C2	3.01	0.48
7:G:86:A:H2'	7:G:87:U:N1	2.27	0.48
8:H:26:A:H2'	8:H:27:U:C6	2.49	0.48
19:X:262:TYR:CE2	19:X:370:LEU:HD12	2.48	0.48
19:X:370:LEU:HB3	19:X:374:SER:O	2.13	0.48
22:1:962:MET:HE3	22:1:974:LEU:HD11	1.94	0.48
23:3:271:ILE:HD13	23:3:287:PHE:CE2	2.47	0.48
23:3:603:ARG:HG2	23:3:604:PHE:CD2	2.48	0.48
23:3:711:ALA:HB1	23:3:722:SER:O	2.13	0.48
27:i:71:TYR:HA	31:j:79:LEU:HA	1.95	0.48
41:8:65:ASP:O	41:8:69:GLU:HG2	2.13	0.48
1:A:200:ASP:HA	1:A:237:THR:CG2	2.43	0.48
1:A:422:LEU:HD22	1:A:638:LEU:HD12	1.93	0.48
1:A:651:TRP:NE1	6:F:66:C:C2	2.81	0.48
1:A:1159:ASN:ND2	15:P:196:ASN:HB2	2.28	0.48
1:A:1530:PRO:O	1:A:1532:ARG:N	2.43	0.48
3:C:148:CYS:HB3	3:C:427:PHE:HE2	1.78	0.48
3:C:606:GLY:HA3	3:C:649:SER:OG	2.12	0.48
5:E:123:MET:HE2	5:E:135:VAL:HG11	1.94	0.48
10:J:370:VAL:O	10:J:374:PRO:HA	2.12	0.48
11:K:30:MET:HE3	11:K:54:LEU:HD12	1.95	0.48
11:K:80:LEU:HA	11:K:84:PHE:CD2	2.49	0.48
16:Q:744:ILE:N	16:Q:745:PRO:HD3	2.28	0.48
17:R:282:GLU:HA	40:9:221:LEU:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:235:SER:O	18:T:237:LYS:HG3	2.12	0.48
18:T:314:ILE:O	18:T:322:SER:HA	2.12	0.48
23:3:666:ASN:N	23:3:666:ASN:ND2	2.61	0.48
23:3:690:ARG:HH11	23:3:690:ARG:HB2	1.77	0.48
23:3:985:HIS:CD2	33:w:469:GLU:HG3	2.48	0.48
23:3:1119:TYR:CD1	23:3:1119:TYR:C	2.91	0.48
36:4:133:MET:O	36:4:142:LYS:N	2.30	0.48
40:9:284:LEU:HD12	40:9:293:LEU:HD11	1.94	0.48
1:A:306:GLN:NE2	3:C:852:ARG:O	2.46	0.48
1:A:883:ARG:O	1:A:887:THR:HG23	2.12	0.48
1:A:1221:THR:OG1	1:A:1223:GLU:OE1	2.23	0.48
1:A:1543:ASN:O	1:A:1563:HIS:CD2	2.66	0.48
1:A:1543:ASN:O	1:A:1563:HIS:HD2	1.96	0.48
3:C:183:SER:OG	3:C:214:GLU:HB3	2.12	0.48
3:C:306:ASN:HA	3:C:433:MET:HG3	1.93	0.48
3:C:767:VAL:HA	3:C:770:PHE:HB3	1.95	0.48
6:F:39:A:H2'	6:F:40:U:O4'	2.13	0.48
8:H:52:G:H2'	8:H:53:U:C6	2.48	0.48
8:H:161:U:H3	25:p:16:ASP:CB	2.26	0.48
17:R:411:LEU:O	17:R:414:GLN:HG3	2.13	0.48
23:3:128:ARG:NH2	23:3:180:PRO:HG3	2.29	0.48
23:3:138:GLN:HG2	23:3:161:HIS:ND1	2.27	0.48
33:w:426:PHE:CZ	33:w:448:ASN:HA	2.49	0.48
41:8:28:LEU:HD23	41:8:30:PHE:CE1	2.48	0.48
1:A:428:LYS:HA	1:A:431:TYR:CZ	2.49	0.48
1:A:599:MET:SD	1:A:602:ILE:HD12	2.53	0.48
1:A:738:MET:HE2	1:A:738:MET:HB3	1.67	0.48
1:A:975:VAL:HG22	1:A:1177:VAL:HG13	1.95	0.48
1:A:1163:ARG:NH1	1:A:1163:ARG:HB2	2.28	0.48
1:A:1403:LEU:HD11	17:R:407:TYR:CD1	2.48	0.48
2:B:11:U:H2'	2:B:12:U:H6	1.78	0.48
2:B:47:A:O2'	2:B:48:A:H5''	2.14	0.48
3:C:131:ASN:HB2	3:C:223:ASP:OD1	2.14	0.48
3:C:139:HIS:HE1	3:C:179:VAL:HG23	1.78	0.48
5:E:233:GLY:HA3	5:E:260:ARG:NH1	2.29	0.48
6:F:40:U:N3	6:F:41:A:C5	2.81	0.48
6:F:63:C:C4	6:F:72:G:N1	2.80	0.48
6:F:85:U:C4	6:F:86:U:C4	3.01	0.48
12:L:21:ALA:O	12:L:24:MET:HG3	2.12	0.48
17:R:147:THR:OG1	18:T:360:VAL:HB	2.14	0.48
17:R:253:ASN:HB2	17:R:254:TRP:CE3	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:203:HIS:CE1	18:T:223:SER:HB3	2.49	0.48
18:T:371:HIS:CE1	18:T:396:LYS:HG3	2.48	0.48
19:X:254:ILE:HG22	19:X:255:PRO:HD2	1.95	0.48
19:X:353:LYS:HG3	19:X:354:GLU:N	2.27	0.48
22:1:1109:ARG:HA	22:1:1112:THR:HG23	1.94	0.48
40:9:322:HIS:O	40:9:421:ARG:HG2	2.14	0.48
32:b:68:PHE:N	26:c:100:PHE:O	2.35	0.48
1:A:66:VAL:HG13	1:A:487:LEU:HD21	1.95	0.48
1:A:508:ILE:O	1:A:513:LEU:HG	2.13	0.48
1:A:617:ASN:N	1:A:617:ASN:OD1	2.46	0.48
1:A:887:THR:OG1	1:A:888:GLN:N	2.45	0.48
3:C:93:ILE:H	3:C:93:ILE:HD12	1.78	0.48
3:C:663:CYS:SG	3:C:785:ARG:NH2	2.87	0.48
5:E:75:HIS:NE2	5:E:121:GLY:HA3	2.28	0.48
6:F:26:U:H3'	6:F:27:A:C5'	2.41	0.48
18:T:284:TYR:N	18:T:284:TYR:CD2	2.81	0.48
22:1:552:LEU:O	22:1:555:VAL:HG13	2.12	0.48
23:3:29:GLU:HG2	23:3:42:ARG:HB2	1.95	0.48
23:3:706:MET:HE1	23:3:767:LEU:HB2	1.94	0.48
23:3:1083:ASN:HB2	35:2:495:ARG:HA	1.96	0.48
40:9:42:CYS:O	40:9:46:LEU:HA	2.13	0.48
40:9:266:ILE:HG23	40:9:267:ASP:H	1.78	0.48
1:A:164:MET:HG3	1:A:577:GLY:HA3	1.96	0.48
1:A:347:LEU:HD22	1:A:351:TYR:CZ	2.48	0.48
1:A:409:ARG:HA	1:A:412:ASN:ND2	2.28	0.48
1:A:652:LEU:O	1:A:655:LEU:HG	2.14	0.48
1:A:1090:ARG:HG2	1:A:1091:TYR:O	2.13	0.48
1:A:1256:PHE:CG	1:A:1299:ILE:HG21	2.47	0.48
1:A:1618:LYS:HG3	1:A:1626:CYS:SG	2.53	0.48
3:C:130:ARG:NE	3:C:435:VAL:HG23	2.28	0.48
6:F:34:G:H2'	6:F:35:A:C4	2.49	0.48
6:F:39:A:C6	6:F:40:U:C4	3.02	0.48
10:J:370:VAL:HB	10:J:379:TRP:CD1	2.48	0.48
18:T:385:TYR:OH	18:T:401:PRO:HB3	2.14	0.48
19:X:225:SER:HB2	19:X:227:GLU:HG3	1.94	0.48
23:3:484:VAL:C	23:3:485:LEU:HD12	2.38	0.48
25:p:73:PRO:HA	25:p:78:PRO:HA	1.95	0.48
40:9:427:ARG:NE	40:9:429:ASP:OD1	2.45	0.48
43:v:34:ALA:CB	43:v:37:THR:HG23	2.44	0.48
1:A:280:GLU:HB2	2:B:48:A:P	2.54	0.48
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:142:LYS:H	45:C:1500:GTP:PB	2.37	0.48
3:C:480:LYS:O	3:C:481:MET:HG3	2.14	0.48
11:K:33:LYS:CD	11:K:44:HIS:HE1	2.25	0.48
11:K:80:LEU:HD12	11:K:84:PHE:HD2	1.79	0.48
18:T:346:ILE:HD11	18:T:400:PHE:HZ	1.78	0.48
20:Y:39:PHE:CD1	20:Y:39:PHE:C	2.91	0.48
22:1:785:LYS:O	22:1:788:VAL:HG22	2.13	0.48
22:1:1108:ASN:HB3	22:1:1110:VAL:N	2.29	0.48
23:3:146:ARG:CG	23:3:146:ARG:NH2	2.72	0.48
23:3:219:HIS:CE1	23:3:221:VAL:HG12	2.49	0.48
23:3:674:LEU:HD12	23:3:675:LEU:N	2.29	0.48
36:4:101:ASN:HA	36:4:148:ASN:HA	1.94	0.48
38:7:23:CYS:SG	38:7:25:LYS:HB3	2.53	0.48
40:9:390:LEU:HD22	40:9:394:HIS:HD2	1.78	0.48
1:A:386:PRO:HG3	3:C:372:PHE:CE1	2.49	0.48
1:A:693:ILE:O	1:A:695:ASP:N	2.47	0.48
1:A:827:PHE:CD2	1:A:828:PRO:HD2	2.48	0.48
1:A:1099:PHE:N	1:A:1099:PHE:CD2	2.80	0.48
1:A:1608:THR:HG23	1:A:1610:GLN:HE22	1.77	0.48
1:A:1730:MET:HE2	1:A:1730:MET:HA	1.95	0.48
3:C:243:ILE:O	3:C:247:VAL:HG23	2.14	0.48
3:C:707:ILE:CD1	3:C:734:ALA:HA	2.43	0.48
3:C:778:PRO:HD3	3:C:817:TYR:CE1	2.48	0.48
5:E:341:ILE:HG23	5:E:354:GLY:O	2.14	0.48
6:F:89:U:H2'	6:F:90:G:C8	2.48	0.48
8:H:71:C:H2'	8:H:72:U:C6	2.49	0.48
11:K:121:TRP:CH2	11:K:125:GLU:HG3	2.49	0.48
16:Q:119:PHE:N	16:Q:120:PRO:HD2	2.29	0.48
16:Q:543:LEU:N	16:Q:621:GLU:O	2.36	0.48
22:1:532:PHE:CE1	22:1:559:ILE:HD11	2.49	0.48
22:1:696:ASP:OD1	22:1:697:GLU:N	2.47	0.48
23:3:146:ARG:HG3	23:3:150:ALA:C	2.39	0.48
23:3:1049:LYS:HE2	39:5:52:TYR:CE1	2.49	0.48
38:7:30:CYS:SG	38:7:32:ILE:N	2.86	0.48
40:9:322:HIS:CE1	40:9:332:GLY:HA2	2.49	0.48
41:8:35:GLU:OE1	41:8:35:GLU:N	2.46	0.48
43:v:33:LEU:C	43:v:33:LEU:CD2	2.85	0.48
1:A:88:TYR:CE1	1:A:125:ALA:HA	2.49	0.48
1:A:787:GLU:O	1:A:788:GLN:C	2.55	0.48
1:A:829:PRO:O	1:A:832:TYR:HB2	2.13	0.48
1:A:1109:LEU:HD23	1:A:1109:LEU:HA	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1332:HIS:ND1	1:A:1357:MET:HB2	2.29	0.48
1:A:1544:ARG:H	1:A:1544:ARG:HG3	1.50	0.48
2:B:63:A:H2'	2:B:64:G:C8	2.49	0.48
3:C:136:GLY:N	3:C:142:LYS:HD3	2.29	0.48
3:C:490:PHE:CE2	3:C:612:LYS:HB3	2.47	0.48
3:C:918:ILE:HG21	3:C:932:GLU:HG3	1.96	0.48
7:G:7:G:H2'	7:G:8:C:C6	2.48	0.48
8:H:171:U:C2	8:H:172:C:C5	3.01	0.48
18:T:307:SER:C	18:T:309:ASP:N	2.70	0.48
19:X:249:PRO:HD2	19:X:307:GLN:OE1	2.14	0.48
22:1:1169:VAL:O	22:1:1170:THR:C	2.56	0.48
23:3:1032:TRP:CD1	23:3:1032:TRP:N	2.82	0.48
31:j:46:CYS:O	31:j:59:ASP:N	2.46	0.48
40:9:352:ASP:CG	40:9:374:ASN:H	2.21	0.48
1:A:151:MET:HE2	1:A:628:GLY:N	2.28	0.48
1:A:170:ASP:OD1	1:A:172:GLU:N	2.24	0.48
1:A:647:LEU:HD11	1:A:651:TRP:CZ2	2.49	0.48
1:A:652:LEU:O	1:A:656:LEU:HD12	2.14	0.48
1:A:1551:PHE:HD1	1:A:1553:VAL:CG2	2.26	0.48
1:A:1681:ARG:O	1:A:1685:LEU:HG	2.14	0.48
3:C:844:SER:O	3:C:848:THR:HG23	2.13	0.48
5:E:319:ILE:H	5:E:319:ILE:HD12	1.79	0.48
6:F:40:U:O2'	6:F:41:A:H5'	2.13	0.48
6:F:50:A:H2'	6:F:50:A:N3	2.28	0.48
8:H:44:U:H2'	8:H:45:C:C5	2.49	0.48
16:Q:28:CYS:HA	16:Q:32:ALA:HB3	1.95	0.48
16:Q:489:VAL:O	16:Q:494:PRO:HD3	2.14	0.48
18:T:395:ILE:HD12	18:T:395:ILE:N	2.29	0.48
18:T:478:LEU:HD22	18:T:488:VAL:HG22	1.95	0.48
21:Z:566:TYR:HB3	21:Z:579:TRP:CD1	2.49	0.48
22:1:130:PRO:CG	22:1:150:ARG:HD2	2.44	0.48
22:1:662:HIS:ND1	22:1:704:ILE:HG21	2.28	0.48
23:3:4:TYR:CE2	23:3:6:LEU:HD21	2.48	0.48
23:3:206:GLN:HE21	23:3:232:GLY:N	2.10	0.48
23:3:364:LEU:HD23	23:3:364:LEU:HA	1.67	0.48
23:3:469:GLU:HB2	23:3:470:PHE:CE2	2.49	0.48
29:l:13:ALA:HB1	29:l:74:PRO:HD2	1.95	0.48
33:w:385:LEU:HD22	33:w:385:LEU:HA	1.71	0.48
40:9:273:TYR:CG	40:9:301:PRO:HB2	2.49	0.48
1:A:228:TRP:H	1:A:228:TRP:CD1	2.32	0.47
1:A:746:LYS:NZ	8:H:22:U:OP1	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1045:GLY:HA3	1:A:1090:ARG:CZ	2.44	0.47
1:A:1104:ASP:OD1	1:A:1104:ASP:N	2.47	0.47
1:A:1683:LYS:HD3	1:A:1683:LYS:HA	1.59	0.47
2:B:54:U:H2'	2:B:55:C:C6	2.49	0.47
2:B:55:C:H2'	2:B:56:C:C6	2.48	0.47
3:C:221:ILE:HD13	3:C:494:GLY:HA2	1.96	0.47
3:C:784:ILE:HG23	3:C:820:PHE:HE1	1.78	0.47
3:C:840:ALA:HA	3:C:869:TYR:CE2	2.49	0.47
5:E:158:TYR:HD2	5:E:201:PHE:HB2	1.78	0.47
16:Q:1225:SER:O	16:Q:1272:LEU:N	2.36	0.47
22:1:944:SER:O	22:1:947:VAL:HG13	2.14	0.47
23:3:19:HIS:HD2	23:3:340:CYS:SG	2.37	0.47
23:3:146:ARG:HD3	23:3:150:ALA:HA	1.95	0.47
23:3:506:LEU:HD22	23:3:544:ILE:HG23	1.96	0.47
23:3:1034:THR:OG1	23:3:1035:THR:N	2.47	0.47
23:3:1203:GLU:C	23:3:1203:GLU:CD	2.82	0.47
33:w:383:LEU:HD22	33:w:392:ILE:CG1	2.44	0.47
33:w:472:GLN:HB2	33:w:475:THR:HB	1.95	0.47
38:7:78:GLN:OE1	38:7:80:LYS:HE2	2.14	0.47
41:8:110:LEU:O	41:8:113:GLN:HG2	2.13	0.47
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.96	0.47
1:A:590:GLY:HA2	1:A:592:TYR:CE2	2.50	0.47
1:A:820:ARG:HD2	1:A:820:ARG:HA	1.61	0.47
1:A:1359:HIS:HB2	1:A:1361:GLU:O	2.13	0.47
1:A:1361:GLU:C	1:A:1363:GLN:H	2.22	0.47
1:A:1615:HIS:ND1	1:A:1618:LYS:HG2	2.29	0.47
1:A:1643:SER:O	1:A:1718:TRP:HZ2	1.97	0.47
2:B:101:U:H2'	2:B:102:U:C6	2.48	0.47
3:C:183:SER:HB2	3:C:203:MET:SD	2.54	0.47
3:C:706:GLN:HB3	3:C:708:THR:HG23	1.96	0.47
6:F:40:U:H3	7:G:7:G:H1	1.61	0.47
8:H:10:C:H2'	8:H:11:G:C8	2.49	0.47
9:I:604:GLU:HA	9:I:612:ALA:HB2	1.94	0.47
11:K:99:ILE:O	11:K:101:HIS:N	2.48	0.47
14:O:87:ASP:O	14:O:91:GLY:N	2.38	0.47
18:T:363:LYS:HD2	18:T:363:LYS:HA	1.57	0.47
22:1:1002:ASN:CG	22:1:1041:ARG:HH21	2.21	0.47
23:3:645:MET:H	23:3:664:TYR:HE2	1.62	0.47
35:2:530:ARG:CB	35:2:578:TRP:HZ3	2.26	0.47
38:7:24:GLU:HG2	38:7:66:VAL:HG11	1.94	0.47
39:5:3:ASP:O	39:5:7:ILE:HG12	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:9:328:PHE:CG	40:9:329:VAL:HG22	2.49	0.47
41:8:115:ASN:OD1	41:8:117:ALA:N	2.43	0.47
1:A:312:TYR:CE2	3:C:882:GLY:HA3	2.50	0.47
1:A:480:LYS:HB3	13:N:109:ARG:O	2.15	0.47
3:C:335:ASN:ND2	3:C:338:GLU:HG2	2.29	0.47
3:C:388:VAL:O	3:C:392:LEU:HB2	2.14	0.47
3:C:507:VAL:HG12	3:C:567:GLU:OE2	2.14	0.47
5:E:69:VAL:C	5:E:331:ASN:HD22	2.21	0.47
5:E:282:HIS:NE2	5:E:289:LEU:HG	2.30	0.47
10:J:245:TRP:CE3	10:J:264:ILE:HG23	2.49	0.47
11:K:29:GLN:O	11:K:32:GLN:N	2.45	0.47
18:T:432:ASP:O	18:T:464:GLY:HA2	2.15	0.47
22:1:871:THR:O	22:1:872:ILE:C	2.58	0.47
22:1:1051:SER:HG	22:1:1054:GLU:H	1.57	0.47
23:3:103:HIS:CE1	23:3:154:ILE:HG22	2.49	0.47
23:3:566:PHE:N	23:3:566:PHE:HD1	2.13	0.47
23:3:854:ALA:C	23:3:856:LYS:HG3	2.38	0.47
41:8:51:TRP:HB2	41:8:123:PHE:HZ	1.78	0.47
1:A:440:PRO:HG2	1:A:443:VAL:HG22	1.95	0.47
1:A:941:LYS:HG3	1:A:951:LEU:HD11	1.95	0.47
1:A:1306:LYS:HB2	1:A:1306:LYS:HE2	1.65	0.47
1:A:1576:ILE:HD11	1:A:1747:ILE:HA	1.97	0.47
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.49	0.47
3:C:655:VAL:HG12	3:C:656:ALA:O	2.14	0.47
3:C:796:VAL:HG23	3:C:798:GLN:HE22	1.79	0.47
6:F:5:U:H2'	6:F:7:G:O4'	2.15	0.47
6:F:36:A:H5'	7:G:11:A:N1	2.30	0.47
7:G:108:U:H5''	7:G:109:U:H5'	1.95	0.47
8:H:51:A:C6	8:H:63:G:C6	3.02	0.47
8:H:150:U:H3	8:H:181:G:H22	1.62	0.47
9:I:140:LEU:N	9:I:141:PRO:HD3	2.30	0.47
12:L:86:ALA:HB1	12:L:91:ARG:O	2.14	0.47
17:R:231:HIS:NE2	18:T:371:HIS:O	2.48	0.47
18:T:243:THR:O	18:T:243:THR:OG1	2.27	0.47
22:1:1221:GLU:OE2	22:1:1222:THR:N	2.44	0.47
23:3:519:VAL:HG13	23:3:524:ILE:HA	1.96	0.47
23:3:535:GLU:HG2	23:3:537:LYS:HZ2	1.79	0.47
23:3:804:HIS:ND1	23:3:805:ASN:HB2	2.28	0.47
37:6:66:ASP:CG	37:6:68:PHE:H	2.22	0.47
40:9:323:ARG:NE	40:9:420:ASP:OD2	2.34	0.47
1:A:178:TYR:CD2	1:A:182:ILE:HB	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:ASN:ND2	3:C:655:VAL:O	2.47	0.47
1:A:426:LEU:H	1:A:426:LEU:HG	1.31	0.47
1:A:1134:TRP:HB3	1:A:1138:ALA:HB3	1.96	0.47
1:A:1179:SER:OG	1:A:1180:LYS:N	2.48	0.47
2:B:51:A:H4'	18:T:277:TYR:CE2	2.49	0.47
2:B:54:U:H2'	2:B:55:C:H6	1.80	0.47
3:C:87:GLN:HG3	18:T:239:LYS:O	2.14	0.47
3:C:318:PHE:CE1	3:C:373:ILE:HD13	2.41	0.47
3:C:839:PRO:HD2	3:C:842:CYS:SG	2.54	0.47
5:E:124:LEU:HB3	5:E:136:TRP:HB2	1.96	0.47
12:L:30:GLN:HE22	17:R:256:ASN:HD21	1.62	0.47
17:R:128:ASP:HB3	17:R:131:ASP:HB2	1.95	0.47
18:T:224:ALA:HA	18:T:248:THR:HG23	1.96	0.47
18:T:240:LEU:HD12	18:T:241:SER:H	1.80	0.47
20:Y:37:TRP:CZ3	20:Y:83:CYS:HB2	2.49	0.47
20:Y:44:PRO:HG2	20:Y:47:LEU:HD13	1.96	0.47
21:Z:566:TYR:CD2	21:Z:580:PRO:HG2	2.50	0.47
22:1:568:ARG:NH1	22:1:608:THR:OG1	2.47	0.47
43:v:54:TYR:CE2	43:v:66:GLU:HG3	2.47	0.47
1:A:303:ILE:HD12	3:C:659:VAL:HG21	1.97	0.47
1:A:614:TYR:O	1:A:618:THR:HG23	2.15	0.47
1:A:1086:ARG:O	1:A:1087:LEU:HD23	2.15	0.47
1:A:1545:ALA:CB	1:A:1563:HIS:NE2	2.68	0.47
1:A:1606:ILE:HA	1:A:1637:TRP:HZ2	1.79	0.47
1:A:1806:ALA:HA	1:A:1820:LYS:O	2.15	0.47
2:B:33:U:C2	2:B:34:U:C5	3.02	0.47
3:C:912:LEU:HD12	3:C:912:LEU:H	1.80	0.47
5:E:65:HIS:CE1	5:E:91:LEU:HD12	2.49	0.47
18:T:419:LEU:HA	18:T:428:VAL:O	2.15	0.47
20:Y:17:GLU:OE1	20:Y:27:SER:HA	2.14	0.47
22:1:869:MET:SD	22:1:910:MET:HA	2.55	0.47
22:1:1097:LEU:HD23	22:1:1097:LEU:HA	1.74	0.47
23:3:74:THR:O	23:3:74:THR:OG1	2.32	0.47
23:3:169:HIS:HD2	23:3:170:VAL:N	2.13	0.47
31:e:34:TRP:O	31:e:85:THR:CA	2.63	0.47
1:A:145:GLY:N	1:A:245:LEU:HD11	2.30	0.47
1:A:598:LEU:HD12	1:A:640:PHE:CZ	2.50	0.47
1:A:1089:CYS:SG	1:A:1189:MET:HE3	2.55	0.47
1:A:1283:GLU:C	1:A:1283:GLU:CD	2.82	0.47
2:B:8:G:C6	2:B:69:A:N6	2.77	0.47
2:B:24:G:C4	2:B:57:G:C2	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:A:N3	2:B:48:A:C8	2.83	0.47
2:B:110:C:H2'	2:B:111:A:C8	2.49	0.47
3:C:181:ILE:HA	3:C:211:PHE:CD2	2.50	0.47
3:C:209:VAL:HG21	3:C:899:SER:O	2.15	0.47
3:C:622:GLU:OE1	3:C:941:LYS:NZ	2.47	0.47
4:D:555:PHE:O	4:D:559:LEU:CB	2.63	0.47
5:E:353:MET:HE2	5:E:353:MET:HB3	1.71	0.47
8:H:6:U:H2'	8:H:7:U:C6	2.50	0.47
8:H:12:G:N7	8:H:13:C:C4	2.83	0.47
8:H:139:C:N4	8:H:140:A:H62	2.13	0.47
8:H:151:C:O2'	29:I:54:ARG:HA	2.15	0.47
9:I:374:ILE:O	9:I:377:THR:N	2.41	0.47
10:J:332:VAL:HG22	10:J:335:ARG:HH11	1.78	0.47
11:K:170:ALA:HA	11:K:173:ILE:HD12	1.97	0.47
17:R:308:VAL:O	17:R:312:MET:HG3	2.14	0.47
18:T:208:ARG:HA	18:T:208:ARG:HD2	1.65	0.47
18:T:301:ASP:C	18:T:317:VAL:HG23	2.40	0.47
18:T:371:HIS:HE2	18:T:389:SER:HG	1.63	0.47
19:X:259:TRP:H	19:X:276:HIS:HB3	1.80	0.47
22:1:118:GLU:HA	22:1:121:LYS:CG	2.44	0.47
22:1:493:LYS:O	22:1:497:ILE:HG22	2.14	0.47
22:1:677:CYS:SG	38:7:48:GLU:HA	2.55	0.47
22:1:785:LYS:HE3	22:1:823:MET:HE2	1.95	0.47
23:3:13:GLY:O	23:3:34:ARG:HD3	2.13	0.47
23:3:206:GLN:NE2	23:3:232:GLY:N	2.58	0.47
23:3:318:ASP:O	23:3:321:MET:N	2.48	0.47
23:3:473:TYR:CE1	23:3:497:SER:HB2	2.49	0.47
23:3:913:LEU:HA	23:3:913:LEU:HD23	1.57	0.47
33:w:474:ASP:N	33:w:474:ASP:OD1	2.47	0.47
37:6:47:GLN:HG2	37:6:48:ILE:H	1.79	0.47
37:6:53:THR:O	37:6:57:ARG:N	2.39	0.47
38:7:30:CYS:SG	38:7:31:VAL:N	2.85	0.47
40:9:239:ALA:HA	40:9:266:ILE:HB	1.97	0.47
40:9:352:ASP:HB3	40:9:354:PHE:CZ	2.49	0.47
41:8:19:ASN:OD1	41:8:22:LYS:N	2.23	0.47
41:8:45:LEU:HA	41:8:48:ILE:HG13	1.97	0.47
43:v:33:LEU:HD22	43:v:33:LEU:O	2.14	0.47
43:v:83:ALA:O	43:v:86:ALA:HB3	2.14	0.47
1:A:233:PRO:O	1:A:237:THR:OG1	2.32	0.47
1:A:242:ALA:O	1:A:246:LEU:HG	2.15	0.47
1:A:301:LYS:HD3	3:C:940:ARG:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:891:PHE:O	12:L:83:ARG:NH2	2.38	0.47
1:A:1209:HIS:CD2	1:A:1210:LYS:H	2.29	0.47
1:A:1529:ILE:HG22	1:A:1530:PRO:HD2	1.96	0.47
1:A:1723:LYS:HE3	1:A:1723:LYS:HB2	1.72	0.47
2:B:100:C:H2'	2:B:101:U:C5	2.50	0.47
3:C:404:THR:O	3:C:408:LEU:HG	2.15	0.47
3:C:785:ARG:HA	3:C:785:ARG:HD3	1.71	0.47
4:D:530:THR:C	4:D:532:ASN:H	2.23	0.47
7:G:7:G:H2'	7:G:8:C:H6	1.79	0.47
7:G:83:A:P	7:G:83:A:C8	3.08	0.47
7:G:88:G:C6	8:H:42:G:C6	3.03	0.47
10:J:399:TYR:HB3	10:J:419:PHE:CE2	2.49	0.47
11:K:33:LYS:CD	11:K:44:HIS:CE1	2.98	0.47
11:K:45:CYS:HA	11:K:50:HIS:HB3	1.97	0.47
11:K:74:ASN:OD1	11:K:74:ASN:N	2.48	0.47
11:K:176:GLN:O	23:3:690:ARG:NH2	2.48	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
23:3:982:GLU:HB3	33:w:471:TRP:CE3	2.49	0.47
35:2:601:LEU:C	35:2:603:GLU:H	2.23	0.47
37:6:19:ARG:O	37:6:63:VAL:HA	2.14	0.47
1:A:386:PRO:HA	3:C:327:TYR:CE1	2.49	0.47
1:A:499:GLN:HA	1:A:502:ASN:ND2	2.29	0.47
1:A:685:LEU:HD11	1:A:742:TYR:HD1	1.79	0.47
1:A:800:TYR:CD1	3:C:59:LEU:HA	2.50	0.47
1:A:1457:HIS:ND1	1:A:1460:HIS:CD2	2.82	0.47
1:A:1684:PHE:CB	1:A:1715:TYR:HD2	2.27	0.47
1:A:1785:VAL:HA	1:A:1806:ALA:H	1.79	0.47
3:C:343:LEU:O	3:C:369:PHE:HB2	2.15	0.47
3:C:531:TRP:CH2	3:C:553:GLU:HB2	2.49	0.47
6:F:68:C:N4	18:T:320:LYS:HD2	2.30	0.47
7:G:93:A:C2	8:H:38:A:C2	3.02	0.47
8:H:27:U:O2'	8:H:28:C:H5'	2.15	0.47
10:J:262:ARG:NH2	10:J:291:GLN:HG2	2.29	0.47
18:T:418:THR:HG21	18:T:467:ALA:HA	1.97	0.47
22:1:477:LYS:HB2	22:1:499:LYS:HZ1	1.78	0.47
22:1:1199:VAL:HG12	22:1:1199:VAL:O	2.15	0.47
23:3:7:THR:OG1	23:3:8:LEU:N	2.47	0.47
23:3:8:LEU:HA	23:3:8:LEU:HD12	1.69	0.47
23:3:255:TYR:CG	23:3:268:ARG:NH2	2.83	0.47
23:3:341:VAL:HG22	23:3:347:LEU:HD12	1.97	0.47
23:3:926:TYR:HB3	23:3:928:TYR:CE2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:8:19:ASN:HD21	41:8:21:GLN:NE2	2.13	0.47
3:C:311:SER:HB2	3:C:316:ILE:HB	1.97	0.47
8:H:52:G:H2'	8:H:53:U:H6	1.80	0.47
11:K:29:GLN:O	11:K:32:GLN:HG3	2.14	0.47
18:T:324:HIS:CE1	18:T:362:GLY:HA3	2.50	0.47
19:X:234:GLU:O	19:X:238:THR:CB	2.62	0.47
22:1:421:TYR:O	22:1:425:ARG:N	2.34	0.47
22:1:692:HIS:C	22:1:692:HIS:CD2	2.92	0.47
23:3:169:HIS:ND1	23:3:234:PHE:HB2	2.30	0.47
23:3:195:ASP:OD2	23:3:200:ALA:N	2.39	0.47
33:w:488:ASN:ND2	33:w:488:ASN:C	2.72	0.47
35:2:534:GLN:C	35:2:534:GLN:NE2	2.72	0.47
39:5:13:HIS:ND1	41:8:15:ASN:HB3	2.29	0.47
40:9:397:PHE:N	40:9:397:PHE:HD1	2.13	0.47
41:8:115:ASN:ND2	41:8:119:ILE:O	2.29	0.47
1:A:265:THR:HG23	1:A:327:VAL:HG13	1.96	0.46
1:A:277:PRO:HD3	1:A:451:LEU:HD13	1.96	0.46
1:A:540:PHE:O	1:A:545:HIS:NE2	2.46	0.46
1:A:1310:ARG:NH2	1:A:1310:ARG:HA	2.31	0.46
3:C:623:GLU:OE2	3:C:941:LYS:HB3	2.15	0.46
6:F:85:U:N3	8:H:14:C:C4	2.78	0.46
10:J:409:GLU:CD	10:J:410:HIS:ND1	2.74	0.46
10:J:429:PHE:CE1	10:J:433:ARG:HG2	2.49	0.46
17:R:280:ILE:HG22	17:R:281:ASN:O	2.15	0.46
22:1:445:HIS:O	22:1:445:HIS:ND1	2.49	0.46
22:1:878:ASN:OD1	22:1:878:ASN:N	2.47	0.46
22:1:981:TYR:O	22:1:983:GLY:N	2.48	0.46
23:3:21:ASN:ND2	23:3:28:GLN:HG3	2.29	0.46
23:3:524:ILE:HD13	23:3:566:PHE:HZ	1.80	0.46
23:3:727:SER:OG	23:3:728:ARG:NH1	2.47	0.46
35:2:585:THR:HB	35:2:589:ASP:CG	2.37	0.46
37:6:81:ASN:HB2	37:6:86:TYR:CE1	2.49	0.46
40:9:406:VAL:HG12	40:9:410:MET:HE3	1.95	0.46
1:A:1271:MET:HE1	1:A:1278:VAL:HG11	1.96	0.46
1:A:1661:TRP:O	1:A:1700:GLY:CA	2.63	0.46
1:A:1662:ILE:HD12	1:A:1701:VAL:HG12	1.97	0.46
1:A:1779:PHE:O	1:A:1809:ILE:HA	2.15	0.46
2:B:88:A:H4'	2:B:94:U:O4	2.15	0.46
3:C:620:LYS:NZ	3:C:630:LEU:HD11	2.31	0.46
3:C:779:LEU:HD11	3:C:911:PRO:HG3	1.97	0.46
5:E:336:HIS:ND1	5:E:337:PRO:HD2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:102:G:N2	7:G:103:U:H2'	2.31	0.46
17:R:150:ALA:HA	17:R:153:LYS:CD	2.46	0.46
22:1:539:LEU:HD12	22:1:539:LEU:HA	1.67	0.46
22:1:850:ILE:H	22:1:850:ILE:HG12	1.49	0.46
22:1:1062:LEU:HA	22:1:1062:LEU:HD23	1.67	0.46
22:1:1197:LEU:HD23	22:1:1197:LEU:HA	1.73	0.46
23:3:169:HIS:CD2	23:3:170:VAL:N	2.83	0.46
1:A:488:ASP:O	1:A:492:VAL:HG23	2.14	0.46
1:A:595:LYS:HE2	1:A:597:LYS:HB2	1.95	0.46
1:A:1454:TRP:H	1:A:1454:TRP:CD1	2.33	0.46
1:A:1640:SER:CA	1:A:1652:MET:HA	2.44	0.46
1:A:1732:LYS:HA	1:A:1732:LYS:HD2	1.71	0.46
3:C:127:GLU:O	3:C:130:ARG:NH2	2.46	0.46
3:C:168:THR:HG22	3:C:184:THR:HG21	1.98	0.46
7:G:15:U:H3'	7:G:16:G:H8	1.80	0.46
10:J:436:TYR:CD1	10:J:437:LYS:HD2	2.51	0.46
11:K:157:LYS:HA	11:K:157:LYS:HD3	1.72	0.46
18:T:326:LEU:HB3	18:T:357:TRP:CE3	2.50	0.46
19:X:353:LYS:HE2	19:X:353:LYS:HB2	1.63	0.46
22:1:120:LYS:O	22:1:123:ARG:HB3	2.16	0.46
22:1:508:THR:OG1	22:1:510:PRO:HD2	2.15	0.46
22:1:940:LEU:HD12	22:1:940:LEU:HA	1.70	0.46
22:1:1133:MET:HE1	35:2:528:ILE:HD12	1.96	0.46
23:3:609:LEU:HD12	23:3:611:ASP:OD2	2.16	0.46
37:6:93:ASN:O	37:6:95:ASN:N	2.49	0.46
41:8:51:TRP:HB2	41:8:123:PHE:CZ	2.50	0.46
1:A:79:ARG:HD3	1:A:82:ARG:HH11	1.80	0.46
1:A:263:PHE:CZ	1:A:277:PRO:HD2	2.50	0.46
1:A:770:THR:C	1:A:772:CYS:N	2.73	0.46
1:A:1554:GLN:O	1:A:1554:GLN:HG2	2.15	0.46
1:A:1580:HIS:CB	1:A:1584:LYS:HE3	2.45	0.46
1:A:1614:ILE:HG23	1:A:1618:LYS:HB2	1.96	0.46
3:C:325:LYS:O	3:C:325:LYS:HD3	2.15	0.46
3:C:375:GLU:HG3	3:C:379:LYS:NZ	2.29	0.46
3:C:825:PRO:HG2	3:C:912:LEU:HD11	1.96	0.46
6:F:85:U:C2'	6:F:86:U:H5'	2.45	0.46
7:G:112:U:H2'	7:G:113:U:O4'	2.16	0.46
8:H:102:U:O2	28:m:74:GLY:N	2.47	0.46
11:K:70:GLU:O	11:K:73:ARG:N	2.48	0.46
12:L:77:LEU:HD13	17:R:284:PHE:HB3	1.96	0.46
17:R:150:ALA:HB3	18:T:360:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:216:ASN:HD21	18:T:473:SER:H	1.63	0.46
18:T:316:ASP:OD1	18:T:318:ARG:N	2.49	0.46
19:X:303:HIS:CE1	19:X:333:SER:HB2	2.51	0.46
23:3:1043:THR:HG22	23:3:1057:ARG:HE	1.81	0.46
31:j:44:GLU:O	31:j:61:ALA:HA	2.16	0.46
33:w:496:LYS:HA	33:w:501:LEU:C	2.40	0.46
38:7:49:CYS:HB3	38:7:87:LYS:HD3	1.98	0.46
40:9:292:ASN:ND2	40:9:402:GLY:HA3	2.31	0.46
42:y:33:THR:N	42:y:53:GLU:O	2.37	0.46
43:v:59:CYS:SG	43:v:81:ASN:ND2	2.85	0.46
1:A:485:THR:OG1	1:A:486:LYS:N	2.45	0.46
1:A:856:LEU:HD23	1:A:856:LEU:HA	1.70	0.46
1:A:1053:LEU:HD11	1:A:1088:PHE:CD2	2.50	0.46
1:A:1210:LYS:C	1:A:1212:GLY:N	2.74	0.46
1:A:1243:ARG:HH11	1:A:1243:ARG:HG3	1.80	0.46
1:A:1551:PHE:CD1	1:A:1553:VAL:CG2	2.98	0.46
1:A:2124:ILE:O	1:A:2179:HIS:HA	2.16	0.46
3:C:187:THR:HG23	3:C:201:ASN:OD1	2.16	0.46
3:C:232:ALA:HB3	3:C:262:ARG:NH2	2.31	0.46
5:E:304:SER:O	5:E:330:ILE:N	2.45	0.46
8:H:48:A:H2'	8:H:49:U:C6	2.49	0.46
8:H:118:G:O6	8:H:140:A:N6	2.48	0.46
10:J:238:ASN:C	10:J:240:THR:H	2.23	0.46
22:1:1009:MET:HE3	22:1:1009:MET:HB3	1.74	0.46
23:3:524:ILE:HG21	23:3:566:PHE:CE2	2.51	0.46
23:3:566:PHE:N	23:3:566:PHE:CD1	2.82	0.46
23:3:631:GLN:HE21	23:3:632:ALA:C	2.18	0.46
36:4:33:PHE:HA	36:4:36:ALA:HB3	1.97	0.46
38:7:39:PRO:HB2	38:7:70:TYR:CD1	2.50	0.46
40:9:299:LEU:HD21	40:9:357:ASN:OD1	2.16	0.46
31:e:34:TRP:O	31:e:85:THR:N	2.48	0.46
1:A:464:PRO:CB	1:A:467:GLN:HE21	2.29	0.46
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.49	0.46
1:A:1300:LYS:C	1:A:1302:GLY:H	2.22	0.46
2:B:46:U:C4	2:B:47:A:N6	2.82	0.46
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.98	0.46
5:E:133:VAL:O	5:E:147:LEU:HG	2.16	0.46
6:F:47:A:H5''	6:F:48:A:O5'	2.15	0.46
7:G:102:G:H4'	38:7:25:LYS:HE2	1.97	0.46
7:G:105:C:OP2	7:G:105:C:H3'	2.15	0.46
8:H:64:A:H2'	8:H:65:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:216:ASN:OD1	18:T:472:GLN:N	2.36	0.46
19:X:255:PRO:HD2	19:X:276:HIS:O	2.16	0.46
22:1:834:VAL:HG13	22:1:871:THR:HG22	1.98	0.46
22:1:903:GLN:OE1	22:1:910:MET:HG3	2.15	0.46
22:1:1133:MET:CE	35:2:528:ILE:CD1	2.93	0.46
22:1:1211:LEU:HD23	22:1:1211:LEU:HA	1.74	0.46
23:3:328:LYS:NZ	23:3:370:GLU:OE1	2.48	0.46
23:3:519:VAL:HG22	23:3:524:ILE:HG23	1.98	0.46
23:3:630:MET:HE3	23:3:630:MET:HB2	1.79	0.46
23:3:753:GLY:HA3	23:3:765:LEU:O	2.15	0.46
28:m:42:LEU:O	28:m:69:LEU:HA	2.15	0.46
32:n:39:HIS:HA	32:n:59:SER:HA	1.98	0.46
37:6:17:VAL:HG23	37:6:91:TYR:CZ	2.51	0.46
40:9:268:GLU:O	40:9:269:ASP:C	2.59	0.46
1:A:79:ARG:NH2	6:F:29:A:H5'	2.27	0.46
1:A:110:TRP:HB2	1:A:208:TYR:CD1	2.50	0.46
1:A:499:GLN:O	1:A:502:ASN:HB2	2.15	0.46
1:A:587:GLN:O	1:A:588:LEU:HD23	2.16	0.46
1:A:794:TYR:HD1	1:A:800:TYR:CE2	2.31	0.46
1:A:1418:ARG:HD3	1:A:1418:ARG:HA	1.32	0.46
1:A:1485:LEU:HD13	1:A:1490:PHE:CD2	2.50	0.46
2:B:40:U:H3	7:G:0:G:N2	2.14	0.46
5:E:249:TYR:CD2	5:E:263:ASP:HB3	2.51	0.46
10:J:381:LYS:HA	10:J:381:LYS:HE3	1.98	0.46
10:J:393:ALA:O	10:J:397:LYS:HG3	2.16	0.46
11:K:33:LYS:HD2	11:K:44:HIS:HE1	1.81	0.46
11:K:112:TRP:HA	11:K:117:ASP:OD2	2.16	0.46
11:K:159:LYS:O	11:K:163:LEU:HD12	2.15	0.46
17:R:416:LYS:HE2	17:R:416:LYS:HB2	1.72	0.46
22:1:876:MET:HE2	22:1:917:VAL:HG22	1.97	0.46
23:3:780:PRO:O	23:3:781:LEU:HD23	2.15	0.46
23:3:970:TYR:HD1	23:3:977:LEU:HB3	1.80	0.46
35:2:453:LYS:HD3	35:2:453:LYS:C	2.41	0.46
35:2:456:ARG:HA	35:2:459:ARG:NE	2.30	0.46
40:9:330:ILE:HG21	40:9:407:LEU:HD11	1.97	0.46
40:9:367:SER:HA	40:9:396:ILE:HA	1.97	0.46
1:A:88:TYR:CZ	1:A:125:ALA:HA	2.51	0.46
1:A:283:VAL:O	1:A:284:ARG:HB2	2.15	0.46
1:A:564:TYR:HB3	1:A:574:LEU:HD13	1.97	0.46
1:A:566:LEU:HB3	1:A:568:ASN:ND2	2.31	0.46
1:A:1144:LYS:HA	1:A:1147:VAL:CG1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1229:PHE:N	1:A:1229:PHE:HD1	2.14	0.46
1:A:1411:SER:O	1:A:1413:ASP:N	2.49	0.46
1:A:1712:HIS:ND1	1:A:1734:MET:HG3	2.31	0.46
3:C:142:LYS:HB2	45:C:1500:GTP:O2B	2.15	0.46
3:C:231:ALA:O	3:C:277:LYS:HE3	2.15	0.46
3:C:833:PHE:O	3:C:899:SER:HA	2.16	0.46
5:E:175:THR:HB	5:E:189:THR:HG23	1.97	0.46
5:E:277:PHE:HE1	5:E:317:ARG:HG2	1.80	0.46
5:E:348:ASP:O	5:E:350:ARG:HG3	2.16	0.46
7:G:-1:C:H2'	7:G:0:G:O4'	2.16	0.46
8:H:51:A:C4	8:H:52:G:C8	3.03	0.46
8:H:59:A:H2'	8:H:60:U:O4'	2.15	0.46
17:R:252:SER:HB3	17:R:255:LYS:H	1.81	0.46
22:1:900:PHE:CE2	22:1:954:LEU:HD22	2.50	0.46
23:3:665:LEU:HD21	23:3:667:ILE:HG13	1.97	0.46
43:v:88:LYS:HA	43:v:91:LYS:NZ	2.30	0.46
1:A:68:LYS:NZ	13:N:45:SER:O	2.20	0.46
1:A:462:ARG:HB3	1:A:465:LYS:HD2	1.97	0.46
1:A:1298:ARG:HD2	1:A:1298:ARG:HA	1.42	0.46
2:B:30:A:C4	2:B:31:U:C5	3.04	0.46
3:C:371:GLU:O	3:C:371:GLU:HG2	2.14	0.46
3:C:434:CYS:O	3:C:438:ILE:N	2.39	0.46
4:D:1803:SER:O	4:D:1810:VAL:HA	2.15	0.46
5:E:91:LEU:HD13	5:E:93:TRP:CZ2	2.50	0.46
7:G:15:U:H2'	7:G:16:G:O4'	2.16	0.46
7:G:19:G:H2'	7:G:19:G:N3	2.31	0.46
8:H:157:G:H2'	8:H:158:G:C8	2.51	0.46
10:J:235:ILE:HG21	10:J:245:TRP:CE2	2.51	0.46
11:K:35:CYS:HB2	11:K:44:HIS:NE2	2.31	0.46
16:Q:1136:GLN:H	16:Q:1156:ASN:HA	1.81	0.46
16:Q:1226:ILE:O	16:Q:1257:VAL:HA	2.16	0.46
22:1:400:SER:H	22:1:403:GLU:HB2	1.81	0.46
22:1:1126:PHE:HE1	35:2:576:PHE:HZ	1.64	0.46
23:3:260:ASN:CG	23:3:261:PHE:N	2.74	0.46
23:3:624:CYS:SG	23:3:625:LEU:HG	2.56	0.46
23:3:999:ARG:NH1	23:3:1024:PHE:HZ	2.12	0.46
40:9:269:ASP:HA	40:9:272:ARG:HB2	1.98	0.46
41:8:111:SER:O	41:8:114:GLU:HG3	2.16	0.46
1:A:139:VAL:HG11	1:A:212:PRO:HG3	1.98	0.46
1:A:518:LEU:HD12	1:A:523:ASN:C	2.42	0.46
1:A:821:ARG:HH11	1:A:821:ARG:CG	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1619:SER:OG	1:A:1620:TYR:N	2.49	0.46
1:A:1706:ASP:O	1:A:1710:ASN:N	2.49	0.46
7:G:98:U:H5''	7:G:99:C:OP2	2.16	0.46
8:H:47:U:H1'	8:H:48:A:C8	2.50	0.46
8:H:72:U:H2'	8:H:73:C:H6	1.80	0.46
8:H:172:C:H2'	8:H:173:C:H6	1.79	0.46
18:T:303:LEU:HA	18:T:303:LEU:HD23	1.67	0.46
18:T:308:ARG:HA	18:T:332:ALA:HB1	1.97	0.46
22:1:164:GLU:O	22:1:168:ILE:HG12	2.15	0.46
22:1:170:GLN:HG2	22:1:171:GLN:HE21	1.79	0.46
22:1:565:ASP:O	22:1:567:VAL:N	2.49	0.46
22:1:1098:LEU:C	22:1:1100:ASN:N	2.73	0.46
22:1:1126:PHE:CE2	35:2:572:HIS:CD2	2.89	0.46
22:1:1151:LEU:HD23	22:1:1151:LEU:HA	1.57	0.46
33:w:394:TYR:CZ	33:w:398:LYS:HE3	2.51	0.46
37:6:22:TYR:CE2	37:6:24:ARG:HD3	2.51	0.46
1:A:356:ILE:HD13	3:C:267:LEU:HD22	1.97	0.45
1:A:516:LEU:HD23	1:A:526:PRO:HA	1.98	0.45
1:A:843:LEU:HA	1:A:843:LEU:HD23	1.75	0.45
1:A:974:ASN:OD1	1:A:974:ASN:N	2.49	0.45
1:A:1002:ASP:OD1	1:A:1002:ASP:C	2.59	0.45
1:A:1571:ILE:HD11	11:K:16:ILE:HD11	1.97	0.45
2:B:108:G:H3'	2:B:109:G:H8	1.81	0.45
3:C:561:LYS:NZ	3:C:617:LEU:O	2.40	0.45
3:C:645:ARG:NH2	3:C:655:VAL:HG23	2.31	0.45
3:C:911:PRO:O	3:C:931:ARG:HD3	2.16	0.45
8:H:13:C:H6	8:H:14:C:H41	1.64	0.45
10:J:242:ILE:HA	10:J:245:TRP:HB2	1.97	0.45
10:J:292:VAL:O	10:J:296:ARG:HG3	2.16	0.45
18:T:189:GLN:HG2	18:T:190:TRP:N	2.31	0.45
18:T:308:ARG:HA	18:T:332:ALA:CB	2.45	0.45
20:Y:69:ARG:HB3	20:Y:76:SER:HA	1.98	0.45
22:1:112:ILE:HG23	22:1:115:ARG:HE	1.80	0.45
22:1:728:LEU:O	22:1:731:LEU:HB2	2.15	0.45
22:1:1080:THR:HA	22:1:1083:TYR:CD2	2.51	0.45
35:2:584:LEU:HD12	35:2:584:LEU:N	2.31	0.45
1:A:195:LEU:HB2	1:A:204:LEU:HD12	1.97	0.45
1:A:311:GLU:H	1:A:311:GLU:HG3	1.39	0.45
1:A:1303:LEU:HB3	1:A:1566:ILE:CG2	2.45	0.45
1:A:1312:PRO:O	1:A:1312:PRO:HG2	2.15	0.45
1:A:1455:TRP:H	1:A:1455:TRP:CD1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:167:TYR:CE2	3:C:535:ALA:HB3	2.51	0.45
3:C:470:PRO:HB3	3:C:545:PRO:CB	2.46	0.45
4:D:560:ALA:O	4:D:563:GLY:N	2.49	0.45
4:D:1205:THR:HA	4:D:1248:ASP:O	2.16	0.45
6:F:42:C:O2'	6:F:43:A:H5'	2.17	0.45
11:K:73:ARG:NH2	11:K:74:ASN:OD1	2.48	0.45
11:K:151:ARG:HH11	11:K:155:LEU:HD12	1.80	0.45
18:T:316:ASP:N	18:T:321:ALA:O	2.35	0.45
20:Y:37:TRP:HA	20:Y:82:LEU:O	2.16	0.45
22:1:112:ILE:H	22:1:112:ILE:HD12	1.81	0.45
23:3:53:LEU:HA	23:3:53:LEU:HD23	1.56	0.45
23:3:399:ASP:CG	23:3:400:GLU:N	2.74	0.45
23:3:1049:LYS:HE2	39:5:52:TYR:HE1	1.81	0.45
23:3:1096:HIS:HD2	23:3:1166:TYR:HB3	1.82	0.45
23:3:1168:PHE:N	23:3:1168:PHE:CD2	2.83	0.45
38:7:93:SER:O	38:7:96:THR:OG1	2.34	0.45
1:A:161:PHE:O	1:A:625:PRO:HG2	2.16	0.45
1:A:350:PHE:CZ	3:C:382:ALA:HB2	2.51	0.45
1:A:608:LEU:HD23	1:A:608:LEU:HA	1.78	0.45
1:A:1606:ILE:CG2	1:A:1631:LEU:HB3	2.47	0.45
3:C:154:HIS:HB2	3:C:157:ILE:HG22	1.99	0.45
3:C:181:ILE:HG23	3:C:211:PHE:CE1	2.51	0.45
3:C:287:GLY:O	3:C:291:MET:HG3	2.16	0.45
3:C:610:VAL:HA	3:C:613:SER:OG	2.17	0.45
6:F:53:A:H8	6:F:53:A:OP2	2.00	0.45
7:G:95:U:C2	8:H:36:G:N2	2.85	0.45
11:K:79:LEU:HD13	11:K:98:TYR:HA	1.98	0.45
11:K:121:TRP:CA	11:K:124:ARG:HH21	2.27	0.45
18:T:329:HIS:HD1	18:T:351:ASP:CG	2.16	0.45
19:X:261:LEU:O	19:X:263:PRO:HD3	2.16	0.45
22:1:939:ARG:HD2	22:1:939:ARG:HA	1.58	0.45
22:1:1010:THR:O	22:1:1012:PRO:HD3	2.17	0.45
22:1:1267:LYS:HE2	22:1:1267:LYS:HB2	1.24	0.45
23:3:131:MET:HB2	23:3:141:VAL:HG22	1.98	0.45
23:3:148:ALA:C	23:3:150:ALA:H	2.23	0.45
23:3:1121:THR:OG1	23:3:1122:LEU:N	2.47	0.45
40:9:266:ILE:HG23	40:9:267:ASP:N	2.31	0.45
32:b:42:ALA:N	32:b:56:GLU:O	2.49	0.45
1:A:255:PHE:CZ	1:A:432:ARG:HB3	2.51	0.45
1:A:414:ARG:HH11	3:C:415:LEU:HD11	1.82	0.45
1:A:717:TRP:O	1:A:718:ARG:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:755:HIS:CD2	15:P:219:PHE:HE2	2.34	0.45
1:A:1307:MET:SD	1:A:1308:PRO:N	2.84	0.45
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.98	0.45
2:B:18:C:C2	2:B:60:G:C2	3.04	0.45
2:B:18:C:N4	2:B:59:G:O6	2.49	0.45
2:B:35:U:O4	2:B:36:C:N4	2.49	0.45
3:C:189:VAL:HG13	3:C:197:SER:HB3	1.97	0.45
3:C:230:ASP:OD2	3:C:233:GLU:HB2	2.16	0.45
3:C:288:LEU:HA	3:C:291:MET:SD	2.56	0.45
5:E:71:CYS:HA	5:E:332:GLU:OE1	2.17	0.45
5:E:116:HIS:O	5:E:124:LEU:HD12	2.17	0.45
6:F:5:U:O3'	6:F:6:C:H4'	2.16	0.45
7:G:-3:A:C2	7:G:-2:A:C5	3.05	0.45
7:G:10:U:O4	7:G:11:A:N6	2.49	0.45
9:I:342:PRO:C	9:I:344:LEU:H	2.23	0.45
11:K:33:LYS:HB3	11:K:44:HIS:HE1	1.81	0.45
11:K:148:THR:CG2	11:K:151:ARG:HH21	2.28	0.45
12:L:38:LEU:H	12:L:38:LEU:CD2	2.20	0.45
22:1:151:THR:O	22:1:155:VAL:HG23	2.17	0.45
22:1:578:ILE:HD13	22:1:578:ILE:HA	1.73	0.45
22:1:751:GLY:HA3	22:1:791:VAL:HG22	1.97	0.45
22:1:1019:ARG:NH1	22:1:1019:ARG:O	2.49	0.45
22:1:1172:LEU:O	22:1:1175:ASP:N	2.48	0.45
22:1:1281:ILE:HA	22:1:1281:ILE:HD13	1.58	0.45
23:3:8:LEU:HB2	23:3:1126:ILE:O	2.17	0.45
23:3:457:ASN:ND2	23:3:479:VAL:HA	2.31	0.45
26:h:77:VAL:HA	26:h:89:PRO:HA	1.97	0.45
33:w:471:TRP:O	33:w:471:TRP:CD1	2.69	0.45
38:7:74:GLU:O	38:7:77:ILE:N	2.44	0.45
40:9:328:PHE:CD2	40:9:329:VAL:HG13	2.52	0.45
41:8:106:TRP:N	41:8:107:PRO:HD2	2.31	0.45
1:A:409:ARG:N	1:A:410:PRO:HD2	2.31	0.45
1:A:634:TRP:HE1	1:A:638:LEU:HD11	1.80	0.45
1:A:685:LEU:HD12	1:A:685:LEU:HA	1.75	0.45
1:A:1426:ASP:O	1:A:1427:ARG:C	2.58	0.45
1:A:1576:ILE:O	1:A:1746:ARG:NH2	2.46	0.45
3:C:183:SER:HB3	3:C:205:THR:HG22	1.98	0.45
3:C:222:SER:OG	3:C:251:LEU:HD11	2.16	0.45
3:C:518:ASP:HB3	3:C:520:GLU:CD	2.41	0.45
3:C:599:GLU:HG3	3:C:602:LYS:HB2	1.98	0.45
3:C:833:PHE:CZ	3:C:835:GLU:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:965:ASP:HA	4:D:970:VAL:O	2.17	0.45
6:F:36:A:N1	7:G:9:C:N3	2.64	0.45
6:F:41:A:O2'	6:F:42:C:H5'	2.16	0.45
6:F:43:A:H2'	6:F:44:G:N9	2.31	0.45
6:F:62:C:N3	6:F:73:A:H2	2.15	0.45
6:F:63:C:N3	6:F:72:G:N1	2.65	0.45
11:K:129:LYS:HG2	11:K:131:ASP:OD1	2.17	0.45
12:L:74:LEU:HD23	12:L:74:LEU:HA	1.60	0.45
16:Q:82:SER:O	16:Q:86:SER:N	2.50	0.45
21:Z:587:VAL:HG12	21:Z:589:ARG:NH1	2.32	0.45
22:1:613:MET:HG3	22:1:632:PHE:CE2	2.52	0.45
22:1:1024:LEU:HD23	22:1:1024:LEU:HA	1.69	0.45
33:w:448:ASN:CG	35:2:477:MET:HE2	2.36	0.45
39:5:69:MET:HE2	39:5:69:MET:HB2	1.71	0.45
40:9:287:ASN:HD21	40:9:426:ILE:HA	1.82	0.45
41:8:23:LYS:C	41:8:27:GLN:HE21	2.24	0.45
43:v:66:GLU:CD	43:v:66:GLU:N	2.71	0.45
1:A:378:PHE:CE1	3:C:338:GLU:HB2	2.52	0.45
1:A:1425:LYS:N	17:R:415:SER:O	2.42	0.45
1:A:1817:LEU:O	1:A:1916:LEU:HA	2.16	0.45
2:B:88:A:H2'	2:B:88:A:N3	2.32	0.45
3:C:86:THR:OG1	18:T:239:LYS:HA	2.16	0.45
3:C:510:LEU:HD22	3:C:514:TYR:CZ	2.51	0.45
8:H:121:A:N3	8:H:121:A:H2'	2.32	0.45
12:L:23:VAL:HG11	12:L:50:TRP:CH2	2.51	0.45
18:T:196:LEU:HD21	18:T:199:VAL:HG23	1.98	0.45
18:T:387:PHE:CE1	18:T:398:TRP:HB2	2.51	0.45
19:X:260:ARG:HH12	19:X:372:GLU:HA	1.82	0.45
22:1:415:LEU:HD22	37:6:32:ALA:HB2	1.97	0.45
22:1:807:LYS:HA	22:1:811:LEU:CD1	2.46	0.45
22:1:922:GLY:O	22:1:925:VAL:HG12	2.16	0.45
22:1:962:MET:SD	22:1:970:LEU:HD21	2.56	0.45
22:1:1027:ARG:HH22	22:1:1067:LYS:HZ2	1.63	0.45
22:1:1110:VAL:O	22:1:1113:THR:HB	2.17	0.45
22:1:1153:PHE:O	22:1:1157:TYR:HD2	1.99	0.45
23:3:519:VAL:HG11	23:3:544:ILE:HD13	1.98	0.45
23:3:1195:GLU:C	23:3:1198:ASP:H	2.25	0.45
35:2:533:ILE:HD13	35:2:533:ILE:H	1.82	0.45
1:A:642:ARG:NH2	2:B:55:C:O2	2.39	0.45
1:A:822:PHE:C	1:A:822:PHE:CD2	2.94	0.45
1:A:1232:VAL:HG22	1:A:1274:PHE:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1393:ARG:HG2	17:R:405:VAL:HG11	1.98	0.45
2:B:20:G:H2'	2:B:20:G:N3	2.31	0.45
3:C:684:LYS:HE3	3:C:793:ASP:OD2	2.17	0.45
7:G:12:G:N2	7:G:13:C:H1'	2.31	0.45
8:H:7:U:H2'	8:H:8:C:H6	1.81	0.45
10:J:396:ARG:O	10:J:400:GLU:HG2	2.17	0.45
11:K:280:TRP:C	11:K:282:GLN:H	2.23	0.45
11:K:360:ILE:O	20:Y:72:LYS:CG	2.64	0.45
17:R:299:ARG:NH1	22:1:448:THR:OG1	2.50	0.45
18:T:297:HIS:HB3	18:T:300:ILE:O	2.16	0.45
18:T:454:VAL:HB	18:T:458:SER:OG	2.16	0.45
20:Y:37:TRP:CH2	20:Y:83:CYS:HB2	2.50	0.45
22:1:677:CYS:C	22:1:679:ILE:H	2.24	0.45
22:1:956:SER:OG	22:1:957:ARG:N	2.49	0.45
22:1:1062:LEU:HD23	22:1:1065:LEU:HD12	1.99	0.45
23:3:128:ARG:NH2	23:3:178:GLU:O	2.49	0.45
23:3:556:ILE:O	23:3:556:ILE:HG13	2.17	0.45
23:3:644:GLU:HA	23:3:662:PHE:O	2.17	0.45
1:A:136:ILE:HG21	1:A:230:PHE:CE2	2.52	0.45
1:A:755:HIS:CD2	15:P:219:PHE:CE2	3.05	0.45
1:A:1210:LYS:C	1:A:1212:GLY:H	2.24	0.45
1:A:1215:ASN:HB3	1:A:1224:ARG:HE	1.81	0.45
1:A:1552:GLN:O	1:A:1554:GLN:N	2.50	0.45
3:C:143:THR:HG21	3:C:169:ASP:OD1	2.16	0.45
3:C:373:ILE:C	3:C:376:PRO:HD2	2.41	0.45
3:C:824:THR:O	3:C:824:THR:OG1	2.32	0.45
5:E:89:LEU:HD13	5:E:91:LEU:HG	1.98	0.45
5:E:166:LEU:HD23	5:E:201:PHE:HE1	1.81	0.45
5:E:224:GLN:NE2	5:E:228:THR:OG1	2.50	0.45
8:H:118:G:H2'	8:H:119:G:C8	2.52	0.45
10:J:225:LEU:O	10:J:229:LYS:HG3	2.16	0.45
21:Z:600:ARG:HG2	21:Z:600:ARG:HH11	1.80	0.45
22:1:169:ARG:HH11	22:1:397:ARG:HG2	1.80	0.45
22:1:643:SER:OG	22:1:644:LEU:N	2.50	0.45
22:1:685:SER:HA	22:1:688:GLU:OE1	2.16	0.45
22:1:948:ARG:NH2	22:1:984:GLU:OE1	2.49	0.45
22:1:1048:GLU:HG2	22:1:1049:TYR:N	2.31	0.45
23:3:442:LEU:HB2	23:3:734:LEU:HD22	1.98	0.45
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.99	0.45
23:3:817:GLN:HA	23:3:843:LEU:HD11	1.98	0.45
23:3:1022:ILE:HD13	23:3:1022:ILE:HA	1.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2:532:GLY:O	35:2:534:GLN:N	2.49	0.45
38:7:9:ILE:O	38:7:88:ILE:HA	2.17	0.45
43:v:63:HIS:CE1	43:v:72:HIS:CB	2.99	0.45
1:A:400:ASN:ND2	1:A:400:ASN:H	2.14	0.45
1:A:1016:VAL:HG22	1:A:1025:THR:HG22	1.98	0.45
1:A:1539:SER:O	1:A:1542:ILE:N	2.49	0.45
1:A:1661:TRP:O	1:A:1662:ILE:HD13	2.16	0.45
3:C:315:SER:O	3:C:420:CYS:HB3	2.17	0.45
3:C:416:LEU:HA	3:C:419:VAL:HG12	1.99	0.45
5:E:113:MET:N	5:E:127:ALA:O	2.49	0.45
5:E:118:ASN:CG	5:E:123:MET:HB2	2.42	0.45
8:H:7:U:H2'	8:H:8:C:C6	2.52	0.45
8:H:42:G:C6	8:H:43:U:C4	3.05	0.45
10:J:326:VAL:HG13	10:J:352:PHE:CZ	2.51	0.45
10:J:363:ARG:HH21	10:J:386:GLU:CD	2.23	0.45
16:Q:360:ASP:O	16:Q:413:ARG:N	2.48	0.45
19:X:262:TYR:CE2	19:X:370:LEU:HB2	2.52	0.45
19:X:317:ASP:OD1	19:X:317:ASP:N	2.37	0.45
21:Z:575:ARG:HG3	21:Z:597:ARG:NH1	2.32	0.45
22:1:157:ARG:O	22:1:161:LEU:HD22	2.17	0.45
22:1:579:GLU:HB2	22:1:580:PRO:HD3	1.98	0.45
22:1:838:VAL:HG12	22:1:842:ASN:HD21	1.81	0.45
22:1:860:GLU:O	22:1:865:ARG:NH2	2.46	0.45
23:3:42:ARG:NH2	23:3:53:LEU:HD11	2.32	0.45
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.52	0.45
35:2:654:ASN:O	35:2:685:ASP:N	2.36	0.45
41:8:26:LYS:HA	41:8:26:LYS:HD3	1.64	0.45
1:A:591:MET:HA	1:A:594:TYR:CD2	2.52	0.45
1:A:597:LYS:O	1:A:600:ARG:HG2	2.17	0.45
1:A:796:LYS:HG3	17:R:279:HIS:HD2	1.82	0.45
1:A:1299:ILE:HD13	1:A:1316:PHE:HE1	1.76	0.45
1:A:1538:TRP:O	1:A:1542:ILE:HG13	2.16	0.45
2:B:19:A:C2	2:B:59:G:C4	3.05	0.45
6:F:72:G:C6	6:F:73:A:C6	3.05	0.45
10:J:350:ILE:HD12	10:J:350:ILE:HA	1.84	0.45
10:J:359:VAL:HG11	10:J:391:TYR:OH	2.16	0.45
10:J:359:VAL:O	10:J:363:ARG:HG2	2.17	0.45
11:K:151:ARG:O	11:K:155:LEU:HB2	2.17	0.45
16:Q:525:PRO:HB3	16:Q:531:TRP:O	2.17	0.45
18:T:297:HIS:CE1	18:T:300:ILE:HG13	2.52	0.45
18:T:356:LEU:N	18:T:356:LEU:HD12	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1140:GLU:OE1	22:1:1140:GLU:HA	2.17	0.45
23:3:305:THR:OG1	23:3:306:GLU:N	2.50	0.45
23:3:1026:ASP:OD1	23:3:1026:ASP:N	2.48	0.45
33:w:496:LYS:O	33:w:501:LEU:N	2.49	0.45
33:w:497:ARG:O	33:w:499:GLY:N	2.39	0.45
40:9:346:TRP:C	40:9:348:LYS:H	2.25	0.45
1:A:95:MET:O	1:A:99:VAL:HG23	2.17	0.44
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.82	0.44
1:A:402:ILE:HA	1:A:405:LEU:HD12	2.00	0.44
2:B:36:C:H42	2:B:47:A:H61	1.65	0.44
3:C:277:LYS:O	3:C:281:ILE:HG13	2.17	0.44
3:C:620:LYS:HE3	3:C:620:LYS:HB2	1.81	0.44
3:C:766:ILE:HG13	3:C:808:ILE:HG22	1.99	0.44
3:C:909:GLY:HA3	3:C:930:ALA:H	1.82	0.44
5:E:237:SER:O	5:E:255:MET:HG3	2.17	0.44
6:F:36:A:C2'	6:F:36:A:N3	2.80	0.44
8:H:118:G:C6	8:H:140:A:N6	2.86	0.44
16:Q:559:HIS:N	16:Q:597:ILE:O	2.50	0.44
22:1:465:PRO:HD2	22:1:502:LEU:HD21	1.99	0.44
22:1:807:LYS:HA	22:1:811:LEU:HD12	1.98	0.44
22:1:1139:PRO:CA	43:v:50:HIS:O	2.63	0.44
22:1:1197:LEU:HD13	38:7:74:GLU:HB3	1.99	0.44
22:1:1251:LEU:HA	22:1:1251:LEU:HD23	1.62	0.44
23:3:77:TYR:HE1	23:3:91:GLU:OE1	2.00	0.44
23:3:212:GLU:HG2	23:3:213:LEU:O	2.17	0.44
33:w:481:ASP:HB3	33:w:485:ASN:CA	2.47	0.44
41:8:38:VAL:HG22	41:8:113:GLN:OE1	2.16	0.44
1:A:92:LEU:HD12	1:A:503:MET:HB3	1.99	0.44
1:A:409:ARG:HD3	1:A:409:ARG:C	2.43	0.44
1:A:647:LEU:HD21	1:A:651:TRP:CH2	2.52	0.44
1:A:1120:PRO:HA	40:9:77:PRO:O	2.18	0.44
1:A:1206:GLU:OE2	1:A:1224:ARG:CZ	2.66	0.44
1:A:1433:ASP:HB3	1:A:1460:HIS:HE1	1.83	0.44
1:A:1661:TRP:O	1:A:1700:GLY:HA3	2.17	0.44
5:E:176:VAL:HG22	5:E:196:VAL:HG11	1.98	0.44
7:G:-1:C:C4	7:G:0:G:C6	3.06	0.44
7:G:5:G:C5'	11:K:22:GLN:HA	2.47	0.44
8:H:57:A:H2'	8:H:58:U:O4'	2.16	0.44
18:T:254:VAL:HA	18:T:261:LEU:HD12	1.98	0.44
22:1:562:LYS:HA	22:1:562:LYS:HD3	1.79	0.44
22:1:1126:PHE:CZ	35:2:572:HIS:HD2	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1273:TYR:CD2	22:1:1273:TYR:C	2.96	0.44
23:3:769:LYS:HA	23:3:769:LYS:HD3	1.79	0.44
23:3:1087:GLN:H	23:3:1087:GLN:HG2	1.64	0.44
23:3:1178:LEU:HA	23:3:1178:LEU:HD12	1.53	0.44
33:w:477:GLU:HG2	33:w:479:TYR:CE2	2.52	0.44
40:9:291:LEU:HD23	40:9:291:LEU:HA	1.84	0.44
1:A:158:ARG:HH22	1:A:570:ASP:HB3	1.82	0.44
1:A:822:PHE:CD2	1:A:822:PHE:O	2.70	0.44
1:A:1386:TRP:NE1	1:A:1417:PRO:HD2	2.32	0.44
1:A:1436:TRP:HH2	1:A:1437:ARG:NH2	2.16	0.44
3:C:450:GLU:HA	3:C:457:VAL:HG22	2.00	0.44
3:C:465:MET:CE	3:C:475:MET:HG3	2.47	0.44
3:C:678:THR:O	3:C:681:LYS:HD3	2.18	0.44
5:E:61:LEU:HD13	5:E:352:TYR:CZ	2.52	0.44
5:E:309:VAL:HG22	5:E:330:ILE:HG21	1.99	0.44
10:J:279:TRP:CE3	10:J:302:ALA:HB2	2.52	0.44
11:K:27:TYR:CD2	11:K:34:GLN:HB2	2.52	0.44
22:1:555:VAL:O	22:1:556:ILE:C	2.61	0.44
22:1:700:LYS:HD3	22:1:700:LYS:HA	1.66	0.44
22:1:901:GLN:HA	22:1:939:ARG:NH2	2.28	0.44
22:1:1280:LEU:HD23	22:1:1280:LEU:HA	1.59	0.44
23:3:817:GLN:HE21	23:3:818:GLN:HA	1.81	0.44
23:3:833:GLU:OE1	23:3:833:GLU:N	2.50	0.44
23:3:911:LYS:HB3	23:3:922:GLY:O	2.17	0.44
23:3:995:THR:HB	23:3:1000:VAL:HG22	1.98	0.44
23:3:1096:HIS:HD2	23:3:1166:TYR:CB	2.30	0.44
33:w:387:TRP:CD1	33:w:387:TRP:O	2.70	0.44
41:8:34:LEU:N	41:8:35:GLU:OE1	2.50	0.44
1:A:112:GLN:HE21	1:A:190:ALA:H	1.65	0.44
1:A:380:LEU:HG	3:C:334:ILE:HD12	2.00	0.44
1:A:609:LYS:HB3	1:A:609:LYS:HE2	1.73	0.44
1:A:1267:LEU:HD12	1:A:1267:LEU:HA	1.68	0.44
1:A:1485:LEU:HA	1:A:1485:LEU:HD23	1.69	0.44
2:B:55:C:C2	2:B:56:C:C5	3.06	0.44
3:C:589:LYS:O	3:C:658:PRO:HB3	2.17	0.44
3:C:684:LYS:HB3	3:C:684:LYS:HE2	1.60	0.44
3:C:908:PRO:HD2	3:C:929:LEU:HD12	1.98	0.44
5:E:249:TYR:HB3	5:E:261:VAL:HG13	1.99	0.44
6:F:93:G:H2'	6:F:94:C:H6	1.83	0.44
7:G:109:U:H2'	7:G:109:U:O2	2.17	0.44
8:H:152:G:C6	8:H:180:G:C6	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:433:ARG:HD2	10:J:433:ARG:HA	1.44	0.44
11:K:82:ARG:HH21	22:1:1051:SER:N	2.15	0.44
16:Q:1065:ALA:O	16:Q:1101:PRO:HA	2.18	0.44
18:T:232:ASP:HB2	18:T:239:LYS:HD2	1.99	0.44
18:T:250:ARG:HG2	18:T:292:TYR:HA	1.98	0.44
18:T:351:ASP:O	18:T:352:THR:OG1	2.25	0.44
19:X:277:ARG:HH22	22:1:437:PRO:HA	1.80	0.44
22:1:503:LYS:HG2	22:1:511:MET:HB3	1.99	0.44
23:3:644:GLU:OE2	23:3:662:PHE:HD2	2.01	0.44
23:3:942:LYS:HB2	23:3:942:LYS:HE3	1.65	0.44
23:3:1088:LYS:HB3	23:3:1088:LYS:HE2	1.71	0.44
24:o:16:THR:HA	24:o:21:ASP:O	2.17	0.44
30:k:19:LEU:HA	30:k:70:LEU:HA	1.98	0.44
32:n:40:LEU:N	32:n:58:LEU:O	2.48	0.44
40:9:298:ASP:OD1	40:9:299:LEU:N	2.50	0.44
40:9:360:HIS:O	40:9:387:CYS:N	2.47	0.44
41:8:37:LYS:HG2	41:8:38:VAL:N	2.33	0.44
41:8:55:ARG:HG3	41:8:59:ILE:HD11	1.98	0.44
43:v:34:ALA:HB2	43:v:37:THR:HG23	1.99	0.44
1:A:119:LEU:HB2	1:A:130:ASN:ND2	2.33	0.44
1:A:1229:PHE:N	1:A:1229:PHE:CD1	2.84	0.44
1:A:1395:GLU:O	1:A:1399:GLN:HG2	2.18	0.44
1:A:1436:TRP:CH2	1:A:1437:ARG:NH2	2.86	0.44
1:A:1443:LYS:HD3	1:A:1443:LYS:HA	1.57	0.44
3:C:688:ILE:O	3:C:789:PHE:HA	2.18	0.44
3:C:745:LEU:HD13	3:C:770:PHE:CD1	2.52	0.44
3:C:745:LEU:HD22	3:C:770:PHE:HB2	2.00	0.44
3:C:784:ILE:HG23	3:C:820:PHE:CE1	2.52	0.44
3:C:789:PHE:CD2	3:C:816:VAL:HG22	2.52	0.44
5:E:65:HIS:NE2	5:E:91:LEU:HD12	2.33	0.44
5:E:289:LEU:HD11	5:E:330:ILE:O	2.17	0.44
6:F:36:A:OP2	7:G:11:A:N6	2.39	0.44
6:F:63:C:C2	6:F:72:G:C2	3.05	0.44
7:G:102:G:H4'	38:7:25:LYS:NZ	2.32	0.44
8:H:9:U:C4	8:H:10:C:C4	3.05	0.44
8:H:52:G:C2	8:H:62:U:C2	3.06	0.44
11:K:119:THR:HA	11:K:122:LEU:HD12	1.99	0.44
12:L:14:THR:HG23	43:v:67:GLY:C	2.43	0.44
17:R:237:MET:HA	17:R:241:GLU:OE2	2.16	0.44
22:1:774:ILE:HD13	22:1:777:PHE:HE2	1.83	0.44
22:1:1257:PRO:HB3	35:2:481:THR:C	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1266:TRP:CZ3	39:5:22:GLY:HA3	2.52	0.44
23:3:608:GLY:HA2	23:3:614:VAL:HG23	2.00	0.44
23:3:908:GLY:O	23:3:909:VAL:HG23	2.17	0.44
31:j:41:MET:HA	31:j:65:HIS:HA	1.99	0.44
37:6:22:TYR:OH	37:6:24:ARG:NH2	2.50	0.44
40:9:135:ASN:HA	40:9:140:ASN:O	2.17	0.44
40:9:269:ASP:HB3	40:9:272:ARG:HH21	1.82	0.44
41:8:24:LEU:O	41:8:28:LEU:HB2	2.17	0.44
1:A:256:TYR:OH	1:A:315:ALA:HB1	2.17	0.44
1:A:539:ARG:HH12	7:G:-1:C:C5'	2.23	0.44
1:A:998:ARG:NH1	1:A:1003:HIS:HB2	2.33	0.44
1:A:1593:LEU:O	1:A:1597:PHE:HD2	2.01	0.44
2:B:38:C:H5'	2:B:39:C:C6	2.51	0.44
3:C:231:ALA:HB1	3:C:263:LEU:HD11	1.98	0.44
3:C:368:SER:O	3:C:372:PHE:HB2	2.18	0.44
3:C:410:LEU:HB3	3:C:414:PRO:HB2	2.00	0.44
3:C:687:MET:HE2	3:C:791:ILE:HG12	1.99	0.44
3:C:870:THR:C	3:C:871:ILE:HD12	2.42	0.44
4:D:1228:VAL:HA	4:D:1265:GLN:O	2.18	0.44
4:D:2103:ASN:HA	4:D:2123:SER:HA	1.99	0.44
6:F:92:A:H2'	6:F:93:G:H8	1.81	0.44
8:H:51:A:C6	8:H:63:G:N1	2.86	0.44
8:H:125:G:H2'	8:H:126:A:H8	1.82	0.44
17:R:390:GLU:C	19:X:348:ARG:HG3	2.42	0.44
19:X:369:LEU:HD12	19:X:370:LEU:N	2.33	0.44
22:1:1272:ILE:O	22:1:1274:ILE:N	2.51	0.44
23:3:745:PHE:CB	23:3:755:VAL:HG23	2.44	0.44
35:2:524:LEU:HD13	35:2:528:ILE:HG22	1.99	0.44
35:2:536:MET:HG3	35:2:566:ILE:HG13	1.99	0.44
38:7:102:ARG:NE	38:7:102:ARG:HA	2.32	0.44
1:A:122:ILE:HD12	1:A:122:ILE:HA	1.84	0.44
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.53	0.44
1:A:406:TRP:HH2	3:C:265:LEU:HB2	1.80	0.44
1:A:1218:ASN:OD1	1:A:1219:GLU:N	2.51	0.44
1:A:1402:ARG:HD2	17:R:406:GLN:HB2	1.99	0.44
1:A:1439:ARG:NH1	1:A:1439:ARG:HG3	2.31	0.44
3:C:70:GLU:OE1	3:C:70:GLU:N	2.30	0.44
3:C:664:GLU:OE1	3:C:778:PRO:HD2	2.18	0.44
3:C:938:ARG:CZ	3:C:943:LEU:HB3	2.48	0.44
3:C:945:GLU:OE1	3:C:945:GLU:N	2.50	0.44
5:E:73:LYS:NZ	5:E:332:GLU:OE2	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:87:C:H2'	6:F:88:G:C8	2.52	0.44
16:Q:851:ILE:O	16:Q:1036:ALA:HA	2.17	0.44
17:R:403:ASN:ND2	19:X:251:GLU:HA	2.33	0.44
22:1:453:MET:O	22:1:456:VAL:HG12	2.17	0.44
22:1:681:PRO:HB3	23:3:219:HIS:CD2	2.53	0.44
22:1:717:THR:HA	22:1:756:LEU:HD11	2.00	0.44
22:1:1075:ARG:HE	22:1:1075:ARG:HB2	1.24	0.44
23:3:162:LYS:HZ2	23:3:162:LYS:HG2	1.66	0.44
23:3:477:SER:HA	23:3:482:THR:HG22	1.99	0.44
23:3:488:GLY:C	23:3:490:THR:H	2.24	0.44
23:3:631:GLN:HG2	23:3:632:ALA:N	2.33	0.44
23:3:1155:LEU:HA	23:3:1155:LEU:HD12	1.59	0.44
39:5:44:MET:HE1	39:5:69:MET:HE1	2.00	0.44
1:A:95:MET:N	1:A:96:PRO:HD2	2.33	0.44
1:A:142:SER:HA	1:A:242:ALA:HB2	1.99	0.44
1:A:226:GLN:HE22	1:A:417:ARG:NH2	2.14	0.44
1:A:227:ARG:HA	1:A:417:ARG:HA	2.00	0.44
1:A:441:VAL:O	1:A:445:VAL:HG23	2.17	0.44
1:A:693:ILE:HG23	1:A:697:MET:CB	2.48	0.44
2:B:106:U:H2'	2:B:107:U:C6	2.53	0.44
3:C:65:TYR:CD2	3:C:65:TYR:N	2.85	0.44
3:C:261:ASP:CG	45:C:1500:GTP:HN1	2.26	0.44
6:F:33:G:C2	7:G:14:A:C5	3.06	0.44
6:F:40:U:C4	6:F:41:A:N7	2.86	0.44
6:F:40:U:O4	6:F:41:A:N6	2.51	0.44
8:H:160:A:H2'	8:H:161:U:C6	2.53	0.44
10:J:310:ASN:ND2	10:J:342:GLU:OE2	2.49	0.44
17:R:319:LYS:HD2	17:R:319:LYS:C	2.43	0.44
18:T:194:TRP:CZ2	18:T:491:GLU:HG3	2.53	0.44
18:T:338:CYS:HA	18:T:344:GLN:O	2.17	0.44
19:X:230:GLY:O	19:X:234:GLU:N	2.36	0.44
19:X:285:ARG:HD2	19:X:297:PRO:HA	2.00	0.44
20:Y:70:ASP:O	20:Y:74:GLY:N	2.51	0.44
22:1:1213:ASN:OD1	22:1:1249:TYR:OH	2.29	0.44
23:3:88:VAL:HG23	23:3:90:LEU:HD13	1.98	0.44
40:9:143:ASP:N	40:9:148:GLU:O	2.43	0.44
40:9:414:GLU:O	40:9:423:LYS:HG2	2.18	0.44
1:A:69:ILE:HA	1:A:72:ASP:OD2	2.18	0.44
1:A:79:ARG:HD3	1:A:82:ARG:NH1	2.33	0.44
1:A:140:TYR:HA	1:A:143:GLN:OE1	2.17	0.44
1:A:189:GLU:OE2	1:A:192:GLN:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:TYR:CZ	1:A:611:LEU:HD13	2.53	0.44
1:A:1411:SER:O	1:A:1412:TRP:C	2.61	0.44
2:B:62:G:C4	2:B:63:A:C8	3.06	0.44
3:C:591:ALA:HB2	3:C:940:ARG:NH2	2.32	0.44
3:C:788:LYS:HZ3	3:C:790:LYS:HE3	1.83	0.44
3:C:884:GLU:H	3:C:884:GLU:HG2	1.45	0.44
5:E:113:MET:HG2	5:E:129:THR:HG23	2.00	0.44
6:F:37:C:N4	7:G:5:G:P	2.91	0.44
6:F:41:A:H2'	6:F:42:C:O4'	2.18	0.44
6:F:49:G:H21	11:K:15:ARG:HG3	1.83	0.44
7:G:103:U:OP1	38:7:63:GLY:HA3	2.18	0.44
10:J:297:ASN:HB3	10:J:301:ARG:NH1	2.32	0.44
11:K:48:GLU:O	11:K:51:GLN:HB2	2.17	0.44
11:K:80:LEU:HA	11:K:84:PHE:HD2	1.83	0.44
22:1:676:GLY:O	22:1:678:ALA:N	2.51	0.44
22:1:1126:PHE:HE1	35:2:576:PHE:CZ	2.34	0.44
23:3:22:PHE:HE1	23:3:78:ILE:HG12	1.82	0.44
23:3:399:ASP:CG	23:3:400:GLU:H	2.26	0.44
23:3:565:TYR:CD1	23:3:619:LEU:HD13	2.53	0.44
40:9:283:ARG:HB2	40:9:434:PHE:CZ	2.53	0.44
1:A:155:LYS:HB3	1:A:616:PHE:HE1	1.82	0.43
1:A:201:ALA:HA	1:A:204:LEU:HB2	1.99	0.43
1:A:511:LYS:HB3	1:A:513:LEU:HD21	2.00	0.43
1:A:731:LEU:O	40:9:241:TYR:HB3	2.18	0.43
1:A:1557:LEU:HD13	1:A:1557:LEU:HA	1.68	0.43
3:C:515:THR:HA	3:C:575:GLN:HE22	1.83	0.43
3:C:533:SER:HA	3:C:538:HIS:ND1	2.33	0.43
7:G:85:G:H2'	7:G:86:A:C8	2.53	0.43
8:H:181:G:H2'	8:H:182:U:C6	2.53	0.43
17:R:137:GLU:HA	17:R:140:ILE:HG23	2.00	0.43
18:T:466:PHE:CD2	18:T:482:ALA:HB2	2.53	0.43
19:X:238:THR:HA	19:X:243:VAL:HA	2.00	0.43
22:1:169:ARG:NH1	22:1:397:ARG:HG2	2.32	0.43
23:3:102:ILE:HD12	23:3:102:ILE:HG23	1.75	0.43
23:3:603:ARG:HH11	23:3:603:ARG:HG3	1.82	0.43
23:3:1096:HIS:CE1	23:3:1098:GLY:HA2	2.53	0.43
29:l:20:CYS:HA	29:l:71:LEU:HA	1.99	0.43
30:k:44:GLU:N	30:k:58:GLY:O	2.51	0.43
33:w:472:GLN:HG3	33:w:475:THR:HB	2.00	0.43
36:4:41:ASN:O	36:4:59:VAL:HA	2.18	0.43
37:6:44:PRO:HB2	37:6:65:GLU:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:9:294:GLU:OE2	40:9:401:VAL:HG11	2.18	0.43
1:A:202:PRO:O	1:A:234:MET:HG2	2.17	0.43
1:A:304:ILE:H	3:C:924:GLN:HE22	1.65	0.43
1:A:1034:LEU:H	1:A:1034:LEU:HG	1.65	0.43
1:A:1215:ASN:ND2	1:A:1215:ASN:H	2.16	0.43
1:A:1256:PHE:CD2	1:A:1531:ASN:ND2	2.86	0.43
1:A:1295:ILE:HD13	1:A:1296:GLN:N	2.33	0.43
1:A:1358:SER:C	1:A:1359:HIS:ND1	2.76	0.43
1:A:1502:PHE:CZ	1:A:1505:LYS:HD3	2.53	0.43
1:A:1640:SER:HA	1:A:1652:MET:HA	2.00	0.43
3:C:173:THR:HG23	3:C:177:ARG:HE	1.84	0.43
5:E:207:GLN:HA	5:E:220:TRP:O	2.18	0.43
5:E:215:ASN:HB3	5:E:234:HIS:O	2.18	0.43
6:F:36:A:N3	6:F:36:A:H2'	2.33	0.43
6:F:38:G:P	6:F:38:G:H8	2.41	0.43
6:F:63:C:H2'	6:F:64:U:C6	2.53	0.43
6:F:69:A:H3'	6:F:70:A:C8	2.39	0.43
6:F:87:C:H2'	6:F:88:G:H8	1.84	0.43
14:O:55:PHE:O	14:O:67:LYS:CA	2.51	0.43
19:X:221:LYS:HE2	19:X:223:LYS:HE3	2.00	0.43
22:1:909:VAL:HG13	22:1:910:MET:N	2.33	0.43
22:1:1139:PRO:O	43:v:51:LEU:CA	2.63	0.43
22:1:1206:ASP:OD1	22:1:1207:SER:N	2.51	0.43
23:3:135:ILE:HD13	23:3:135:ILE:HG21	1.74	0.43
33:w:459:TRP:CZ2	33:w:463:LYS:HE2	2.53	0.43
40:9:243:THR:HG22	40:9:264:ALA:HA	2.00	0.43
40:9:350:PHE:CZ	40:9:376:ASN:HB3	2.52	0.43
40:9:416:ASP:HB3	40:9:419:THR:HG22	1.98	0.43
1:A:462:ARG:HE	1:A:465:LYS:HD2	1.82	0.43
1:A:694:LEU:HD13	1:A:706:ALA:HB1	2.00	0.43
1:A:705:LYS:O	1:A:708:THR:N	2.51	0.43
1:A:1030:ILE:HG12	1:A:1031:ILE:N	2.31	0.43
1:A:1474:MET:O	1:A:1475:ILE:C	2.61	0.43
1:A:1562:MET:C	1:A:1564:GLY:N	2.77	0.43
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.52	0.43
2:B:66:A:H2'	2:B:67:A:C8	2.54	0.43
2:B:66:A:H2'	2:B:67:A:H8	1.83	0.43
3:C:103:THR:OG1	3:C:485:ASP:OD1	2.25	0.43
3:C:134:LEU:HD13	3:C:226:VAL:HB	1.99	0.43
3:C:216:THR:HB	3:C:580:LEU:HD21	2.00	0.43
3:C:448:LYS:NZ	3:C:497:LEU:HD22	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:61:LEU:HD12	5:E:351:LEU:O	2.17	0.43
5:E:152:SER:HB2	5:E:173:ASP:N	2.32	0.43
6:F:33:G:C2	7:G:14:A:N1	2.85	0.43
9:I:565:ILE:CB	9:I:576:ALA:HB1	2.48	0.43
18:T:190:TRP:HD1	18:T:502:VAL:HG23	1.82	0.43
19:X:327:TYR:CZ	19:X:351:GLU:HB2	2.54	0.43
20:Y:30:SER:O	20:Y:33:LYS:HG3	2.18	0.43
22:1:998:LYS:HD2	22:1:1002:ASN:OD1	2.19	0.43
23:3:234:PHE:C	23:3:234:PHE:CD2	2.96	0.43
23:3:362:ALA:C	23:3:363:HIS:ND1	2.77	0.43
23:3:485:LEU:HG	23:3:493:GLU:HA	2.00	0.43
40:9:131:VAL:O	40:9:135:ASN:CB	2.67	0.43
40:9:352:ASP:HB3	40:9:354:PHE:CE1	2.54	0.43
1:A:67:ARG:HE	1:A:491:GLU:CD	2.26	0.43
1:A:1601:LEU:O	1:A:1606:ILE:HG13	2.18	0.43
2:B:25:C:H4'	2:B:26:A:H5''	2.00	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
3:C:211:PHE:HA	3:C:213:ASP:OD1	2.18	0.43
5:E:136:TRP:CZ3	5:E:143:ARG:HB3	2.53	0.43
8:H:15:U:P	8:H:15:U:H6	2.42	0.43
10:J:231:PHE:O	10:J:235:ILE:HD12	2.18	0.43
22:1:1138:VAL:O	22:1:1140:GLU:N	2.51	0.43
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.43
23:3:440:HIS:CE1	23:3:1217:PHE:HB3	2.53	0.43
27:i:49:GLU:O	27:i:56:SER:N	2.23	0.43
39:5:11:LEU:HD13	39:5:23:HIS:CG	2.53	0.43
41:8:35:GLU:N	41:8:35:GLU:CD	2.76	0.43
41:8:44:ASN:OD1	41:8:44:ASN:C	2.61	0.43
1:A:63:PRO:O	1:A:66:VAL:HG13	2.18	0.43
1:A:384:VAL:HA	3:C:331:PHE:CD2	2.54	0.43
1:A:420:ARG:HH12	2:B:56:C:C2'	2.29	0.43
1:A:428:LYS:O	1:A:432:ARG:HG3	2.19	0.43
1:A:476:PHE:O	1:A:479:THR:OG1	2.29	0.43
1:A:640:PHE:CE1	1:A:644:ILE:HG21	2.54	0.43
1:A:652:LEU:HD23	1:A:655:LEU:HD21	1.99	0.43
1:A:981:PHE:HD1	1:A:981:PHE:HA	1.72	0.43
1:A:1016:VAL:HA	1:A:1024:HIS:O	2.19	0.43
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.36	0.43
1:A:1375:TRP:O	1:A:1376:GLU:C	2.61	0.43
1:A:1416:ILE:HG22	1:A:1417:PRO:CD	2.48	0.43
2:B:36:C:N3	2:B:47:A:N6	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:449:ILE:HG23	3:C:453:TYR:HB3	1.99	0.43
5:E:130:ASP:OD1	5:E:130:ASP:N	2.51	0.43
7:G:115:C:O2	20:Y:118:PRO:HG3	2.19	0.43
10:J:376:VAL:HG21	10:J:415:LEU:HB2	2.00	0.43
11:K:8:THR:O	11:K:12:ILE:HG12	2.18	0.43
17:R:129:ASP:O	17:R:133:GLN:HG2	2.19	0.43
20:Y:29:HIS:ND1	20:Y:91:ILE:HG12	2.33	0.43
22:1:124:ARG:C	22:1:126:MET:N	2.76	0.43
22:1:148:ASN:CB	37:6:100:LYS:HD2	2.49	0.43
22:1:498:MET:HE3	22:1:498:MET:HB2	1.58	0.43
22:1:1148:LEU:HD23	22:1:1148:LEU:HA	1.67	0.43
23:3:232:GLY:HA2	23:3:252:SER:HA	2.00	0.43
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.18	0.43
37:6:36:TYR:CD2	37:6:45:ILE:HD13	2.53	0.43
40:9:302:LYS:HG3	40:9:346:TRP:CH2	2.53	0.43
41:8:51:TRP:HZ3	41:8:105:LEU:HD12	1.83	0.43
41:8:101:PHE:C	41:8:101:PHE:CD2	2.97	0.43
1:A:318:TYR:HD1	3:C:645:ARG:NH1	2.10	0.43
1:A:609:LYS:HE3	1:A:610:HIS:CD2	2.54	0.43
1:A:642:ARG:HD3	2:B:28:A:H1'	2.01	0.43
1:A:705:LYS:O	1:A:706:ALA:C	2.61	0.43
1:A:767:VAL:HG12	1:A:1249:MET:HE2	1.99	0.43
1:A:1576:ILE:HD13	1:A:1747:ILE:HG12	1.99	0.43
3:C:433:MET:O	3:C:436:GLN:HB3	2.19	0.43
3:C:480:LYS:HB3	3:C:493:PHE:HD2	1.84	0.43
5:E:166:LEU:HD23	5:E:201:PHE:CE1	2.54	0.43
6:F:16:G:H2'	6:F:17:C:O4'	2.18	0.43
6:F:47:A:H2'	6:F:47:A:N3	2.33	0.43
7:G:18:A:H3'	7:G:19:G:C8	2.54	0.43
7:G:19:G:N2	7:G:20:A:H1'	2.32	0.43
8:H:9:U:H2'	8:H:10:C:C6	2.53	0.43
8:H:34:U:C2	8:H:35:A:C8	3.06	0.43
8:H:173:C:H2'	8:H:174:A:O4'	2.18	0.43
12:L:104:LEU:HD23	12:L:104:LEU:HA	1.76	0.43
20:Y:40:LEU:HD23	20:Y:43:LEU:HD21	2.00	0.43
22:1:397:ARG:HD2	22:1:397:ARG:HA	1.81	0.43
22:1:552:LEU:HD23	22:1:552:LEU:HA	1.67	0.43
22:1:698:GLN:HB3	22:1:701:VAL:CG1	2.49	0.43
22:1:729:LYS:HD3	22:1:729:LYS:HA	1.61	0.43
22:1:735:ILE:HD13	22:1:735:ILE:HA	1.58	0.43
22:1:1137:ARG:NH2	35:2:524:LEU:HD12	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1300:LEU:HA	22:1:1300:LEU:HD23	1.58	0.43
23:3:1105:GLN:HG3	23:3:1106:LYS:N	2.29	0.43
32:n:29:ILE:HA	32:n:40:LEU:HA	1.99	0.43
37:6:24:ARG:HB2	37:6:88:VAL:HB	2.00	0.43
40:9:323:ARG:CZ	40:9:325:ILE:HD11	2.49	0.43
1:A:264:PHE:CE1	1:A:459:LEU:HB2	2.54	0.43
1:A:471:TYR:O	1:A:475:SER:OG	2.36	0.43
1:A:637:TRP:CE3	1:A:637:TRP:HA	2.53	0.43
1:A:641:MET:HA	1:A:644:ILE:CG1	2.49	0.43
1:A:1215:ASN:HB3	1:A:1224:ARG:NE	2.34	0.43
1:A:1257:THR:HG23	1:A:1320:LYS:NZ	2.34	0.43
1:A:1298:ARG:NH2	1:A:1298:ARG:C	2.72	0.43
3:C:182:LYS:C	3:C:206:PRO:HD3	2.43	0.43
3:C:185:PRO:HB2	3:C:533:SER:OG	2.19	0.43
4:D:560:ALA:C	4:D:563:GLY:H	2.26	0.43
5:E:118:ASN:O	5:E:121:GLY:N	2.50	0.43
6:F:40:U:C2'	6:F:41:A:H5'	2.48	0.43
6:F:60:C:H6	6:F:75:G:N7	2.16	0.43
6:F:69:A:H2'	6:F:70:A:O4'	2.19	0.43
6:F:83:A:H4'	6:F:84:A:O4'	2.18	0.43
6:F:95:G:C6	8:H:4:G:C6	3.06	0.43
7:G:103:U:C2	7:G:104:C:C5	3.07	0.43
8:H:47:U:O2	8:H:47:U:C2'	2.67	0.43
11:K:121:TRP:HA	11:K:124:ARG:HE	1.82	0.43
14:O:56:ARG:HA	14:O:66:LYS:O	2.18	0.43
17:R:399:PRO:O	17:R:401:THR:N	2.52	0.43
18:T:373:LYS:HG3	18:T:393:ASP:OD1	2.18	0.43
18:T:415:ILE:H	18:T:415:ILE:HG13	1.47	0.43
22:1:411:GLY:O	37:6:51:GLY:HA2	2.19	0.43
22:1:479:LEU:HD23	37:6:24:ARG:NH1	2.33	0.43
22:1:488:SER:N	22:1:489:PRO:HD2	2.34	0.43
22:1:648:LEU:O	22:1:649:LYS:C	2.61	0.43
22:1:1266:TRP:O	22:1:1270:ASN:ND2	2.52	0.43
23:3:162:LYS:HZ2	23:3:222:ARG:NH1	2.17	0.43
35:2:523:GLU:O	35:2:523:GLU:HG3	2.13	0.43
38:7:54:TYR:HA	38:7:57:ARG:HG2	2.00	0.43
41:8:23:LYS:O	41:8:27:GLN:HG2	2.18	0.43
1:A:137:GLU:OE2	1:A:419:ARG:N	2.47	0.43
1:A:138:PRO:HB2	1:A:238:LEU:HD13	2.01	0.43
1:A:500:GLY:HA3	1:A:551:LEU:HD11	2.00	0.43
1:A:518:LEU:HG	1:A:519:ASP:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:693:ILE:HG22	1:A:694:LEU:HG	2.00	0.43
1:A:713:LEU:HD12	1:A:713:LEU:HA	1.63	0.43
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.83	0.43
1:A:1439:ARG:HG3	1:A:1439:ARG:HH11	1.84	0.43
2:B:27:U:O2'	2:B:28:A:O5'	2.35	0.43
2:B:35:U:C4	2:B:36:C:N4	2.87	0.43
3:C:450:GLU:HA	3:C:457:VAL:CG2	2.49	0.43
3:C:496:VAL:O	3:C:497:LEU:HD23	2.18	0.43
3:C:666:VAL:O	3:C:691:PRO:HB3	2.19	0.43
3:C:778:PRO:HD3	3:C:817:TYR:CD1	2.54	0.43
4:D:1406:VAL:O	4:D:1425:ILE:HA	2.19	0.43
5:E:61:LEU:HD11	5:E:350:ARG:HB3	1.99	0.43
5:E:92:LEU:HD23	5:E:92:LEU:HA	1.89	0.43
5:E:108:HIS:NE2	5:E:134:ALA:HB3	2.34	0.43
8:H:52:G:C6	8:H:53:U:C4	3.07	0.43
11:K:24:LEU:HD13	11:K:25:ARG:N	2.34	0.43
16:Q:1193:PRO:HD2	16:Q:1197:PHE:O	2.18	0.43
16:Q:1358:MET:N	16:Q:1359:PRO:HD2	2.33	0.43
17:R:287:LEU:HA	17:R:287:LEU:HD12	1.76	0.43
18:T:423:SER:HB2	18:T:474:GLU:OE1	2.18	0.43
20:Y:40:LEU:HD21	20:Y:56:PHE:CZ	2.53	0.43
20:Y:57:SER:OG	21:Z:584:TRP:HA	2.19	0.43
22:1:166:ARG:NH2	22:1:620:MET:HG2	2.34	0.43
22:1:501:LEU:HD23	22:1:501:LEU:HA	1.75	0.43
22:1:1140:GLU:O	22:1:1144:GLN:HG3	2.18	0.43
23:3:475:ILE:HG13	23:3:508:CYS:SG	2.58	0.43
23:3:495:THR:C	23:3:497:SER:H	2.27	0.43
23:3:1096:HIS:C	23:3:1096:HIS:ND1	2.77	0.43
23:3:1175:ASP:OD1	23:3:1175:ASP:C	2.61	0.43
24:o:147:PHE:O	25:p:75:TYR:N	2.35	0.43
35:2:495:ARG:HE	35:2:495:ARG:HB3	1.67	0.43
37:6:27:PRO:HG3	37:6:85:ARG:HD3	1.99	0.43
37:6:51:GLY:HA3	37:6:56:THR:O	2.19	0.43
40:9:281:TYR:HA	40:9:293:LEU:O	2.17	0.43
41:8:45:LEU:HB3	41:8:49:LYS:NZ	2.34	0.43
1:A:136:ILE:HG12	1:A:228:TRP:CB	2.48	0.43
1:A:414:ARG:NH1	3:C:408:LEU:O	2.49	0.43
1:A:684:GLU:CD	18:T:308:ARG:NH2	2.75	0.43
1:A:1287:LEU:HA	1:A:1287:LEU:HD12	1.78	0.43
1:A:1359:HIS:O	1:A:1360:GLU:C	2.61	0.43
1:A:1527:ASN:OD1	1:A:1527:ASN:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1575:GLN:HE21	1:A:1575:GLN:HA	1.84	0.43
3:C:724:TRP:HD1	3:C:725:ASP:O	2.02	0.43
3:C:850:LEU:O	3:C:853:ARG:N	2.47	0.43
6:F:92:A:H2'	6:F:93:G:C8	2.54	0.43
7:G:101:U:C5'	22:1:1070:LYS:HZ1	2.31	0.43
8:H:19:G:N2	8:H:20:G:N7	2.67	0.43
9:I:550:TRP:O	9:I:552:ASN:N	2.52	0.43
10:J:242:ILE:H	10:J:242:ILE:HG12	1.59	0.43
11:K:49:SER:O	11:K:53:GLN:HG3	2.19	0.43
11:K:159:LYS:HZ3	11:K:159:LYS:HG3	1.73	0.43
16:Q:734:LYS:O	16:Q:778:ILE:HA	2.19	0.43
20:Y:46:GLU:CD	20:Y:103:LYS:HZ3	2.24	0.43
20:Y:55:VAL:HG12	20:Y:56:PHE:CD2	2.54	0.43
22:1:472:ILE:HA	22:1:472:ILE:HD13	1.58	0.43
22:1:506:ASN:OD1	22:1:506:ASN:N	2.50	0.43
23:3:57:GLU:HG2	23:3:59:PHE:CE1	2.54	0.43
23:3:102:ILE:HD13	23:3:102:ILE:HA	1.76	0.43
23:3:254:ASN:C	23:3:271:ILE:HG13	2.44	0.43
23:3:579:GLU:HG2	23:3:581:LYS:HB2	2.00	0.43
23:3:623:ASP:OD2	23:3:628:LEU:HD11	2.18	0.43
23:3:983:ASN:OD1	23:3:983:ASN:C	2.62	0.43
33:w:496:LYS:HA	33:w:501:LEU:CA	2.48	0.43
37:6:101:MET:HE1	37:6:106:LYS:HG2	2.00	0.43
39:5:5:TYR:O	39:5:9:SER:OG	2.36	0.43
40:9:224:THR:H	40:9:224:THR:HG1	1.57	0.43
40:9:406:VAL:O	40:9:410:MET:HG3	2.19	0.43
41:8:14:ASP:OD1	41:8:15:ASN:N	2.52	0.43
1:A:67:ARG:CD	1:A:179:ALA:HB2	2.49	0.43
1:A:352:PHE:CE1	1:A:359:ILE:HD11	2.54	0.43
1:A:386:PRO:HA	3:C:327:TYR:HE1	1.84	0.43
1:A:405:LEU:HD13	3:C:265:LEU:HD13	2.00	0.43
1:A:532:THR:OG1	1:A:533:LYS:N	2.52	0.43
1:A:544:PHE:CZ	1:A:548:ARG:HD3	2.53	0.43
1:A:574:LEU:O	1:A:578:LEU:HG	2.19	0.43
1:A:1608:THR:OG1	1:A:1609:VAL:N	2.51	0.43
1:A:1633:ALA:HA	1:A:1637:TRP:CZ2	2.54	0.43
2:B:33:U:H2'	2:B:34:U:H6	1.83	0.43
3:C:191:PRO:HA	3:C:196:LYS:O	2.19	0.43
3:C:284:GLU:O	3:C:288:LEU:HG	2.18	0.43
3:C:377:LEU:O	3:C:381:LEU:HG	2.19	0.43
3:C:920:PRO:HB2	3:C:921:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1065:ALA:O	4:D:1070:LEU:N	2.45	0.43
10:J:242:ILE:HD12	10:J:278:LEU:HD13	2.00	0.43
10:J:411:MET:SD	10:J:415:LEU:HD23	2.59	0.43
17:R:148:ARG:CG	17:R:148:ARG:NH2	2.73	0.43
18:T:203:HIS:NE2	18:T:229:LYS:HD2	2.34	0.43
18:T:442:ARG:HD2	18:T:442:ARG:C	2.44	0.43
22:1:412:TYR:HA	37:6:50:VAL:O	2.18	0.43
22:1:540:MET:HB3	22:1:540:MET:HE3	1.67	0.43
22:1:617:ILE:HD13	22:1:617:ILE:HA	1.77	0.43
22:1:1212:LEU:HD12	22:1:1212:LEU:C	2.37	0.43
22:1:1241:ILE:HD12	22:1:1241:ILE:HG23	1.64	0.43
26:h:70:VAL:CB	26:h:96:ILE:O	2.67	0.43
37:6:20:ILE:HB	37:6:92:TYR:HB3	2.01	0.43
39:5:71:LYS:O	39:5:73:LEU:N	2.51	0.43
40:9:291:LEU:HD23	40:9:403:GLY:HA3	2.01	0.43
40:9:302:LYS:HG3	40:9:346:TRP:HH2	1.84	0.43
40:9:334:ASP:OD2	40:9:339:GLY:N	2.49	0.43
40:9:364:GLY:O	40:9:399:ARG:HA	2.19	0.43
1:A:155:LYS:HB2	1:A:626:GLY:O	2.19	0.42
1:A:845:ARG:HE	1:A:845:ARG:HB2	1.45	0.42
1:A:1424:GLN:HE22	1:A:1459:ARG:HD2	1.83	0.42
1:A:1664:ILE:HD12	1:A:1664:ILE:HA	1.77	0.42
1:A:1785:VAL:HA	1:A:1806:ALA:N	2.34	0.42
2:B:18:C:O2'	2:B:19:A:O5'	2.35	0.42
2:B:19:A:H1'	2:B:59:G:N2	2.34	0.42
3:C:142:LYS:HB3	3:C:204:ASP:OD1	2.17	0.42
3:C:319:THR:HG22	3:C:320:LEU:N	2.34	0.42
3:C:473:PRO:HB3	3:C:571:ASN:ND2	2.34	0.42
5:E:206:ASP:O	5:E:222:LEU:HG	2.19	0.42
8:H:140:A:H2'	8:H:141:C:H6	1.83	0.42
12:L:73:HIS:HD2	40:9:220:ILE:HB	1.84	0.42
17:R:126:ASN:HD22	18:T:442:ARG:HH11	1.66	0.42
22:1:652:CYS:HB2	22:1:692:HIS:HE1	1.84	0.42
22:1:694:LEU:HD23	22:1:705:SER:OG	2.19	0.42
22:1:759:ALA:O	22:1:763:ASN:HB2	2.19	0.42
22:1:1120:ALA:HB2	22:1:1128:VAL:HG21	2.00	0.42
37:6:105:LYS:HA	37:6:108:GLU:OE2	2.19	0.42
1:A:518:LEU:HD21	1:A:522:PHE:HD1	1.83	0.42
1:A:1581:LEU:HD23	1:A:1746:ARG:CZ	2.50	0.42
2:B:19:A:H2'	2:B:20:G:H5''	2.01	0.42
2:B:63:A:H2'	2:B:64:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:223:ASP:OD2	3:C:441:PRO:HD3	2.19	0.42
3:C:589:LYS:HG3	3:C:630:LEU:CD2	2.47	0.42
6:F:38:G:O6	7:G:9:C:N4	2.51	0.42
8:H:139:C:C5'	28:m:56:SER:H	2.31	0.42
12:L:72:LEU:HA	12:L:72:LEU:HD23	1.70	0.42
17:R:315:LYS:HE3	17:R:315:LYS:HB2	1.79	0.42
22:1:133:LEU:HB2	22:1:149:ALA:HB1	2.00	0.42
22:1:413:LYS:HB2	22:1:413:LYS:HE3	1.78	0.42
22:1:490:GLU:O	22:1:494:GLU:HG2	2.19	0.42
22:1:865:ARG:HA	22:1:868:VAL:HG22	2.01	0.42
22:1:1126:PHE:HA	35:2:575:PHE:CE2	2.54	0.42
22:1:1272:ILE:O	22:1:1273:TYR:C	2.62	0.42
23:3:604:PHE:HE1	23:3:681:PRO:HA	1.84	0.42
23:3:942:LYS:HG3	23:3:942:LYS:O	2.19	0.42
23:3:999:ARG:NH1	23:3:1024:PHE:CZ	2.87	0.42
29:l:61:VAL:HA	30:k:71:GLU:HA	2.02	0.42
33:w:481:ASP:HB3	33:w:485:ASN:N	2.34	0.42
35:2:542:GLU:HA	35:2:545:GLU:HB2	2.02	0.42
39:5:50:LEU:HA	39:5:50:LEU:HD12	1.33	0.42
40:9:323:ARG:HB3	40:9:331:GLN:HB3	2.01	0.42
1:A:304:ILE:HB	3:C:923:PRO:HA	2.00	0.42
1:A:428:LYS:HE2	1:A:432:ARG:HD2	2.01	0.42
1:A:546:LEU:CD2	1:A:591:MET:HB3	2.49	0.42
1:A:596:TYR:OH	7:G:-4:G:O4'	2.37	0.42
1:A:683:LEU:HA	1:A:683:LEU:HD12	1.74	0.42
1:A:814:VAL:HG23	1:A:999:LEU:CD1	2.48	0.42
1:A:841:LEU:HA	1:A:841:LEU:HD23	1.63	0.42
1:A:929:GLU:O	1:A:932:LYS:N	2.52	0.42
1:A:1218:ASN:HB2	1:A:1225:THR:HG21	2.00	0.42
1:A:1663:ASP:OD1	1:A:1664:ILE:N	2.53	0.42
3:C:138:LEU:HD12	3:C:138:LEU:HA	1.80	0.42
3:C:142:LYS:HD2	3:C:205:THR:O	2.19	0.42
3:C:746:VAL:O	3:C:791:ILE:HG13	2.20	0.42
3:C:914:LYS:NZ	3:C:931:ARG:HH12	2.17	0.42
3:C:938:ARG:HH21	3:C:944:SER:H	1.67	0.42
5:E:348:ASP:OD2	5:E:350:ARG:NE	2.47	0.42
6:F:23:U:H3'	6:F:24:A:C8	2.53	0.42
10:J:386:GLU:HB3	10:J:395:ALA:HB2	2.02	0.42
11:K:39:ASN:OD1	11:K:39:ASN:C	2.62	0.42
12:L:17:GLU:OE1	12:L:20:LYS:HE2	2.19	0.42
15:P:193:VAL:HG23	15:P:194:PHE:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:224:ALA:HA	18:T:248:THR:HA	2.00	0.42
18:T:483:ASP:OD1	18:T:485:THR:OG1	2.36	0.42
22:1:584:ASP:OD1	22:1:585:GLU:N	2.53	0.42
22:1:789:LEU:HA	22:1:789:LEU:HD12	1.66	0.42
22:1:914:PHE:HZ	22:1:932:ILE:HD12	1.83	0.42
22:1:1000:ILE:O	22:1:1004:ILE:HG22	2.19	0.42
22:1:1019:ARG:HH12	22:1:1022:PRO:CG	2.32	0.42
23:3:135:ILE:HD11	39:5:44:MET:HE2	2.01	0.42
23:3:146:ARG:HG3	23:3:150:ALA:CA	2.45	0.42
23:3:159:GLU:OE2	38:7:14:GLN:HB2	2.19	0.42
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.55	0.42
23:3:379:LEU:HD22	23:3:383:ASP:OD1	2.19	0.42
23:3:506:LEU:HD12	23:3:506:LEU:HA	1.86	0.42
23:3:715:MET:N	23:3:715:MET:SD	2.92	0.42
40:9:235:LYS:HZ1	40:9:452:GLN:HB2	1.83	0.42
43:v:34:ALA:HB1	43:v:38:ILE:HD13	2.01	0.42
1:A:402:ILE:HD13	3:C:268:LYS:HD3	2.01	0.42
1:A:712:HIS:CE1	17:R:250:CYS:HA	2.54	0.42
1:A:764:GLY:O	1:A:765:ALA:C	2.61	0.42
1:A:780:THR:O	1:A:781:ARG:C	2.61	0.42
1:A:1045:GLY:O	1:A:1046:LEU:C	2.62	0.42
1:A:1458:GLN:CB	17:R:421:GLY:H	2.32	0.42
1:A:1628:ASP:HB3	1:A:1662:ILE:O	2.19	0.42
3:C:135:CYS:O	3:C:227:LEU:HA	2.19	0.42
3:C:743:ASN:OD1	3:C:784:ILE:HG22	2.20	0.42
11:K:121:TRP:CZ3	11:K:122:LEU:HD23	2.54	0.42
17:R:316:GLU:O	17:R:319:LYS:HG3	2.20	0.42
17:R:323:LYS:HD2	17:R:324:LEU:HD23	2.00	0.42
18:T:334:ALA:H	18:T:349:SER:HA	1.84	0.42
18:T:423:SER:N	18:T:474:GLU:OE2	2.47	0.42
18:T:465:ILE:HG12	18:T:481:GLU:HG2	2.01	0.42
22:1:516:LEU:HD12	22:1:516:LEU:HA	1.77	0.42
22:1:547:GLN:O	22:1:548:GLU:C	2.63	0.42
22:1:578:ILE:HG13	22:1:596:ILE:HD11	2.01	0.42
22:1:645:LEU:HA	22:1:645:LEU:HD12	1.87	0.42
22:1:909:VAL:HG13	22:1:910:MET:H	1.84	0.42
22:1:1115:ALA:O	22:1:1119:VAL:HG23	2.19	0.42
23:3:2:PHE:O	23:3:3:LEU:HD23	2.20	0.42
23:3:22:PHE:CE1	23:3:78:ILE:HG12	2.53	0.42
23:3:121:LEU:HD12	23:3:121:LEU:HA	1.70	0.42
23:3:168:TYR:HD2	23:3:168:TYR:N	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:441:GLY:HA2	23:3:733:PRO:O	2.18	0.42
23:3:664:TYR:HA	23:3:677:THR:O	2.19	0.42
23:3:791:HIS:C	23:3:791:HIS:HD2	2.26	0.42
23:3:870:ASN:HD21	23:3:873:GLN:H	1.67	0.42
23:3:1081:LEU:HD13	23:3:1082:LEU:HB2	2.01	0.42
32:n:14:THR:O	32:n:71:PRO:HG3	2.19	0.42
35:2:586:ILE:C	35:2:586:ILE:CD1	2.90	0.42
35:2:587:HIS:CD2	35:2:587:HIS:O	2.73	0.42
41:8:44:ASN:CG	41:8:47:VAL:HG12	2.44	0.42
41:8:51:TRP:CZ2	41:8:104:GLU:HG3	2.54	0.42
41:8:73:ASN:HA	41:8:76:GLU:HG2	2.02	0.42
1:A:66:VAL:CG1	1:A:487:LEU:HD21	2.48	0.42
1:A:121:HIS:HB3	1:A:125:ALA:H	1.83	0.42
1:A:195:LEU:HD13	1:A:204:LEU:HA	2.01	0.42
1:A:318:TYR:CE1	3:C:645:ARG:HD3	2.55	0.42
1:A:531:THR:HG21	6:F:37:C:O2'	2.19	0.42
1:A:685:LEU:HD11	1:A:742:TYR:CD1	2.54	0.42
1:A:770:THR:C	1:A:772:CYS:H	2.28	0.42
1:A:864:LEU:HA	1:A:864:LEU:HD23	1.63	0.42
1:A:978:GLU:HA	1:A:1095:ILE:O	2.19	0.42
1:A:1064:PRO:HG2	1:A:1067:MET:HB2	2.01	0.42
1:A:1627:ALA:HB2	1:A:1696:PRO:HD3	2.00	0.42
3:C:308:CYS:SG	3:C:310:SER:OG	2.66	0.42
3:C:847:TYR:CE1	3:C:857:VAL:HG21	2.54	0.42
5:E:281:VAL:HB	5:E:306:ASP:HB3	2.01	0.42
6:F:58:G:O3'	6:F:59:G:H3'	2.18	0.42
7:G:-2:A:O2'	7:G:-1:C:H5'	2.20	0.42
7:G:-1:C:N4	7:G:0:G:O6	2.52	0.42
10:J:231:PHE:HE2	10:J:251:TRP:CD1	2.37	0.42
10:J:347:HIS:HA	10:J:350:ILE:HG22	2.01	0.42
12:L:35:ALA:HB2	12:L:43:ALA:HA	2.02	0.42
12:L:102:PHE:CD2	12:L:102:PHE:C	2.96	0.42
18:T:239:LYS:HB3	18:T:239:LYS:HE3	1.69	0.42
18:T:301:ASP:O	18:T:317:VAL:HG23	2.20	0.42
19:X:260:ARG:HH12	19:X:371:HIS:C	2.27	0.42
22:1:656:LYS:HE2	41:8:65:ASP:CB	2.50	0.42
22:1:1149:LYS:O	22:1:1152:SER:N	2.53	0.42
22:1:1197:LEU:HD11	38:7:78:GLN:NE2	2.33	0.42
23:3:126:LYS:HB2	23:3:128:ARG:HH11	1.85	0.42
23:3:673:VAL:HG23	23:3:674:LEU:N	2.34	0.42
23:3:791:HIS:ND1	23:3:930:LEU:HD21	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5:32:LEU:HD13	39:5:32:LEU:HA	1.77	0.42
40:9:285:HIS:O	40:9:429:ASP:HB2	2.20	0.42
40:9:352:ASP:OD2	40:9:374:ASN:N	2.43	0.42
1:A:387:PHE:CE2	3:C:399:LEU:HD23	2.55	0.42
1:A:780:THR:O	1:A:783:TYR:N	2.53	0.42
1:A:1418:ARG:CB	1:A:1462:GLY:HA3	2.50	0.42
1:A:1551:PHE:CD1	1:A:1553:VAL:HG23	2.55	0.42
3:C:643:ASP:O	3:C:647:MET:HG2	2.19	0.42
3:C:660:VAL:HG11	3:C:877:ALA:CB	2.49	0.42
3:C:674:CYS:SG	3:C:819:ALA:HA	2.59	0.42
3:C:685:ILE:HD12	3:C:815:VAL:HG21	2.01	0.42
5:E:217:ILE:HD11	5:E:234:HIS:CD2	2.55	0.42
7:G:108:U:H5	22:1:828:ARG:NH2	2.17	0.42
9:I:456:LEU:O	9:I:460:THR:CB	2.68	0.42
11:K:363:LYS:N	20:Y:71:LYS:CB	2.83	0.42
12:L:77:LEU:HD23	12:L:77:LEU:HA	1.77	0.42
18:T:191:HIS:CD2	18:T:440:ASP:HB2	2.54	0.42
18:T:308:ARG:HH11	18:T:308:ARG:CG	2.29	0.42
18:T:334:ALA:HB2	18:T:350:HIS:CE1	2.55	0.42
20:Y:26:VAL:HB	22:1:861:ALA:HB2	2.00	0.42
22:1:714:GLU:O	38:7:51:TYR:OH	2.37	0.42
22:1:1170:THR:O	22:1:1173:LEU:N	2.52	0.42
23:3:257:THR:HA	23:3:267:ILE:O	2.20	0.42
23:3:544:ILE:HD11	23:3:547:CYS:HB3	2.01	0.42
23:3:550:ASN:CB	23:3:592:LEU:HG	2.50	0.42
23:3:914:ILE:HD13	23:3:914:ILE:HA	1.84	0.42
23:3:1187:PRO:HA	23:3:1190:GLN:HB2	2.02	0.42
37:6:107:GLU:HG3	37:6:108:GLU:N	2.33	0.42
40:9:308:ILE:HD12	40:9:438:TYR:CE2	2.55	0.42
40:9:346:TRP:HZ3	40:9:350:PHE:HB3	1.84	0.42
43:v:75:GLY:O	43:v:78:HIS:N	2.52	0.42
1:A:148:TRP:HZ3	1:A:612:ILE:HG23	1.85	0.42
1:A:393:LEU:O	3:C:379:LYS:HA	2.20	0.42
1:A:520:TYR:O	1:A:555:LYS:HD3	2.20	0.42
1:A:1197:LEU:HD12	1:A:1197:LEU:HA	1.75	0.42
1:A:1399:GLN:C	1:A:1401:ARG:N	2.75	0.42
1:A:1638:ASN:ND2	1:A:1652:MET:HB3	2.35	0.42
6:F:37:C:H4'	6:F:38:G:OP2	2.19	0.42
6:F:43:A:C2	7:G:6:A:N1	2.88	0.42
7:G:9:C:H2'	7:G:10:U:C6	2.55	0.42
11:K:172:PHE:HZ	23:3:1214:ARG:CZ	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:38:LEU:HD12	12:L:41:LYS:HB2	2.01	0.42
19:X:289:ILE:HG12	19:X:290:ALA:N	2.34	0.42
20:Y:1:MET:HE2	22:1:783:GLU:CG	2.49	0.42
22:1:489:PRO:O	22:1:492:GLN:HB3	2.19	0.42
22:1:709:ILE:HG23	22:1:709:ILE:HD12	1.78	0.42
22:1:791:VAL:O	22:1:792:VAL:C	2.60	0.42
22:1:939:ARG:HE	22:1:947:VAL:HB	1.85	0.42
22:1:1125:PRO:O	22:1:1126:PHE:C	2.62	0.42
23:3:331:ASP:OD2	23:3:395:LEU:HD12	2.20	0.42
23:3:459:VAL:HB	23:3:757:ILE:HG12	2.01	0.42
23:3:1082:LEU:HD12	23:3:1082:LEU:HA	1.77	0.42
29:l:13:ALA:CB	29:l:74:PRO:HD2	2.49	0.42
33:w:479:TYR:CG	33:w:489:LYS:HG2	2.54	0.42
37:6:14:PRO:HA	37:6:15:PRO:HD3	1.92	0.42
37:6:23:ILE:HD13	37:6:89:VAL:HA	2.02	0.42
1:A:68:LYS:HE2	13:N:35:GLU:CB	2.50	0.42
1:A:575:ALA:HA	1:A:630:TRP:HE1	1.85	0.42
1:A:675:GLN:HE21	1:A:675:GLN:HB2	1.49	0.42
1:A:924:GLN:OE1	1:A:1439:ARG:NH2	2.53	0.42
1:A:1091:TYR:O	1:A:1092:ILE:C	2.62	0.42
1:A:1460:HIS:CD2	1:A:1460:HIS:N	2.87	0.42
2:B:43:U:H3'	2:B:44:A:H8	1.84	0.42
3:C:692:LEU:HA	3:C:692:LEU:HD23	1.79	0.42
10:J:224:LYS:HD3	10:J:228:ARG:HH22	1.84	0.42
10:J:376:VAL:HB	10:J:406:PHE:CE2	2.55	0.42
11:K:121:TRP:HA	11:K:124:ARG:NH2	2.28	0.42
14:O:236:VAL:O	14:O:269:CYS:HA	2.19	0.42
17:R:386:ARG:HH22	19:X:353:LYS:HB3	1.85	0.42
22:1:614:ARG:NH1	41:8:64:ASP:OD1	2.53	0.42
22:1:849:ILE:H	22:1:849:ILE:HG12	1.61	0.42
22:1:972:GLY:O	22:1:976:VAL:HG12	2.20	0.42
22:1:982:LEU:HD12	22:1:982:LEU:HA	1.74	0.42
22:1:1145:ASN:ND2	22:1:1183:VAL:HG12	2.35	0.42
23:3:168:TYR:N	23:3:168:TYR:CD2	2.88	0.42
23:3:219:HIS:ND1	23:3:219:HIS:C	2.77	0.42
23:3:310:ILE:HG22	23:3:311:PHE:N	2.34	0.42
23:3:515:ALA:HB1	23:3:526:HIS:NE2	2.35	0.42
23:3:674:LEU:C	23:3:675:LEU:HD12	2.45	0.42
23:3:999:ARG:HH21	23:3:1041:TYR:HE2	1.68	0.42
23:3:1040:ASP:OD2	35:2:707:PRO:HA	2.19	0.42
23:3:1081:LEU:HB3	23:3:1082:LEU:H	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1102:LEU:HA	23:3:1102:LEU:HD23	1.46	0.42
24:o:68:THR:HA	24:o:92:GLU:O	2.19	0.42
39:5:2:THR:O	39:5:6:THR:HG22	2.20	0.42
40:9:358:LEU:HD22	40:9:399:ARG:HH12	1.84	0.42
41:8:36:LYS:H	41:8:36:LYS:HD2	1.85	0.42
1:A:318:TYR:HB2	3:C:638:ASP:CG	2.45	0.42
1:A:388:LEU:HD22	1:A:391:THR:OG1	2.20	0.42
1:A:441:VAL:HG22	1:A:444:ARG:NH2	2.35	0.42
1:A:929:GLU:O	1:A:930:ALA:C	2.61	0.42
1:A:1730:MET:O	1:A:1734:MET:HG2	2.20	0.42
2:B:36:C:H2'	2:B:37:G:C8	2.55	0.42
2:B:69:A:H2'	2:B:69:A:N3	2.35	0.42
3:C:264:ILE:HG23	3:C:378:TYR:CD2	2.54	0.42
3:C:468:CYS:SG	3:C:546:ALA:HB1	2.60	0.42
3:C:480:LYS:HB3	3:C:493:PHE:CD2	2.55	0.42
3:C:907:VAL:HG11	3:C:933:PHE:CE2	2.55	0.42
5:E:235:ALA:HB3	5:E:256:ASP:OD1	2.20	0.42
7:G:10:U:N3	7:G:11:A:C5	2.87	0.42
10:J:294:HIS:HA	10:J:297:ASN:HD22	1.85	0.42
10:J:343:GLU:CD	10:J:378:ASN:HD21	2.20	0.42
18:T:225:ASP:OD2	18:T:227:THR:OG1	2.24	0.42
18:T:292:TYR:HH	18:T:308:ARG:HD3	1.79	0.42
18:T:394:ASN:HB2	18:T:410:SER:HA	2.02	0.42
22:1:412:TYR:CZ	37:6:61:TYR:HE2	2.38	0.42
22:1:413:LYS:CB	37:6:52:ASN:HD21	2.33	0.42
22:1:672:ALA:HB2	22:1:712:LEU:HD23	2.02	0.42
22:1:752:TYR:O	22:1:755:PRO:HD2	2.20	0.42
22:1:912:ASN:OD1	22:1:957:ARG:NH2	2.50	0.42
22:1:914:PHE:C	22:1:914:PHE:CD2	2.98	0.42
22:1:942:ASN:ND2	22:1:942:ASN:C	2.77	0.42
23:3:444:VAL:HG22	23:3:765:LEU:HD22	2.01	0.42
23:3:679:LEU:HD12	23:3:679:LEU:HA	1.68	0.42
28:m:53:PRO:HG3	28:m:60:GLU:HA	2.02	0.42
30:k:14:ASP:N	30:k:31:LEU:O	2.41	0.42
37:6:68:PHE:HD1	37:6:68:PHE:HA	1.72	0.42
41:8:34:LEU:HD23	41:8:82:SER:HB2	2.02	0.42
41:8:55:ARG:HE	41:8:59:ILE:HD11	1.84	0.42
43:v:161:PRO:HA	43:v:162:PRO:HD3	1.84	0.42
1:A:82:ARG:NH2	7:G:14:A:OP2	2.53	0.42
1:A:107:PRO:HA	1:A:114:ARG:CZ	2.49	0.42
1:A:114:ARG:HG2	1:A:116:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:ILE:HG21	1:A:230:PHE:CZ	2.55	0.42
1:A:1397:ILE:HG12	17:R:405:VAL:N	2.35	0.42
2:B:44:A:H2	7:G:-4:G:O6	2.02	0.42
3:C:66:TYR:HD1	3:C:66:TYR:HA	1.69	0.42
3:C:118:PHE:O	3:C:121:ASP:HB3	2.20	0.42
3:C:262:ARG:O	3:C:266:GLU:HB2	2.20	0.42
3:C:392:LEU:HD23	3:C:392:LEU:HA	1.66	0.42
11:K:163:LEU:HA	11:K:166:GLU:CD	2.44	0.42
18:T:233:LEU:O	18:T:233:LEU:HD12	2.20	0.42
19:X:308:TYR:HB3	19:X:324:VAL:HG23	2.02	0.42
22:1:1206:ASP:OD1	22:1:1206:ASP:N	2.52	0.42
23:3:617:ILE:HG23	23:3:626:GLN:O	2.19	0.42
23:3:791:HIS:HA	23:3:792:PRO:HD3	1.95	0.42
33:w:488:ASN:OD1	33:w:490:LYS:CB	2.53	0.42
37:6:26:LEU:HA	37:6:26:LEU:HD12	1.73	0.42
37:6:111:LYS:O	37:6:115:GLU:HG3	2.20	0.42
40:9:205:ARG:HE	40:9:205:ARG:HB3	1.61	0.42
41:8:28:LEU:HD12	41:8:28:LEU:HA	1.83	0.42
41:8:56:VAL:O	41:8:57:THR:C	2.62	0.42
1:A:318:TYR:HE1	3:C:645:ARG:HD3	1.84	0.41
1:A:872:ASP:HB2	1:A:873:ASN:OD1	2.20	0.41
1:A:954:LYS:HD3	1:A:954:LYS:HA	1.75	0.41
1:A:1035:GLN:H	1:A:1035:GLN:HG2	1.50	0.41
1:A:1072:LEU:HD23	1:A:1072:LEU:HA	1.59	0.41
1:A:1154:PHE:CD2	1:A:1154:PHE:C	2.97	0.41
1:A:1268:ILE:HG12	1:A:1268:ILE:H	1.54	0.41
1:A:1391:LEU:HD22	1:A:1391:LEU:HA	1.90	0.41
1:A:1612:GLU:O	1:A:1614:ILE:HD12	2.20	0.41
5:E:299:LYS:HB2	5:E:335:PHE:CZ	2.55	0.41
6:F:38:G:H2'	6:F:39:A:H8	1.85	0.41
6:F:50:A:H1'	6:F:51:U:H5'	2.01	0.41
6:F:82:A:H4'	8:H:16:U:O4	2.20	0.41
8:H:148:C:N4	8:H:149:A:N6	2.68	0.41
18:T:274:ASP:HB2	18:T:281:ILE:HD13	2.02	0.41
18:T:297:HIS:CG	18:T:298:PRO:HD2	2.55	0.41
18:T:372:LYS:HB2	18:T:393:ASP:OD2	2.20	0.41
22:1:172:LEU:HD11	37:6:117:TYR:HD2	1.85	0.41
22:1:571:VAL:O	22:1:574:ILE:N	2.52	0.41
22:1:1304:LEU:HA	22:1:1304:LEU:HD23	1.85	0.41
23:3:328:LYS:NZ	23:3:365:GLY:O	2.37	0.41
23:3:804:HIS:HB2	23:3:862:TRP:CZ3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:6:36:TYR:HD2	37:6:45:ILE:HD13	1.83	0.41
1:A:179:ALA:HA	1:A:183:LEU:HB2	2.02	0.41
1:A:363:HIS:CE1	3:C:287:GLY:HA3	2.55	0.41
1:A:728:VAL:HA	1:A:729:PRO:HD3	1.94	0.41
1:A:832:TYR:HB3	1:A:835:ASP:HB3	2.02	0.41
1:A:951:LEU:HD23	1:A:951:LEU:HA	1.69	0.41
1:A:1237:MET:SD	1:A:1283:GLU:OE1	2.79	0.41
1:A:1495:PHE:HE1	1:A:1748:ARG:HG2	1.85	0.41
3:C:319:THR:HG22	3:C:320:LEU:H	1.85	0.41
4:D:1223:ILE:HA	4:D:1269:ARG:O	2.19	0.41
5:E:264:VAL:HG13	5:E:272:ARG:NH2	2.35	0.41
8:H:106:G:N2	8:H:107:A:C6	2.88	0.41
15:P:204:GLN:HB3	15:P:206:LYS:HE3	2.01	0.41
17:R:299:ARG:HH12	22:1:448:THR:HA	1.86	0.41
18:T:393:ASP:OD1	18:T:393:ASP:N	2.51	0.41
21:Z:612:TYR:O	21:Z:615:SER:N	2.53	0.41
22:1:427:PRO:O	22:1:430:LYS:CB	2.68	0.41
22:1:860:GLU:O	22:1:861:ALA:C	2.63	0.41
23:3:195:ASP:O	23:3:197:THR:N	2.53	0.41
23:3:246:SER:O	23:3:258:TYR:OH	2.24	0.41
23:3:444:VAL:CG2	23:3:765:LEU:HD22	2.50	0.41
23:3:485:LEU:HB3	23:3:491:VAL:HG12	2.02	0.41
23:3:736:TYR:CG	23:3:737:GLU:N	2.88	0.41
23:3:806:ALA:HB1	23:3:856:LYS:HD3	2.02	0.41
23:3:993:ILE:O	23:3:993:ILE:HG12	2.20	0.41
33:w:458:LEU:HD12	33:w:458:LEU:HA	1.73	0.41
37:6:100:LYS:H	37:6:100:LYS:HG3	1.69	0.41
40:9:288:LYS:NZ	40:9:424:GLU:OE2	2.50	0.41
41:8:105:LEU:O	41:8:106:TRP:C	2.63	0.41
1:A:134:TRP:HE3	1:A:419:ARG:C	2.28	0.41
1:A:441:VAL:HG13	1:A:444:ARG:HH21	1.84	0.41
1:A:693:ILE:HG13	1:A:738:MET:SD	2.60	0.41
1:A:755:HIS:HE1	15:P:220:HIS:ND1	2.16	0.41
1:A:1256:PHE:CE1	1:A:1299:ILE:HG22	2.55	0.41
1:A:1846:ALA:HB1	1:A:2220:PRO:CB	2.50	0.41
3:C:128:LEU:HD23	3:C:197:SER:O	2.21	0.41
3:C:500:THR:HG23	3:C:544:VAL:C	2.45	0.41
3:C:855:GLY:HA2	3:C:874:PHE:O	2.20	0.41
3:C:938:ARG:NH1	3:C:943:LEU:HD23	2.36	0.41
4:D:686:GLU:O	4:D:866:GLU:HA	2.19	0.41
5:E:202:ASN:CG	5:E:207:GLN:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:88:G:N2	8:H:11:G:C4	2.89	0.41
10:J:228:ARG:NH2	10:J:257:GLU:OE2	2.54	0.41
12:L:37:LEU:CD2	43:v:30:LEU:CD2	2.98	0.41
15:P:214:THR:OG1	15:P:215:LEU:N	2.53	0.41
18:T:220:VAL:HG22	18:T:230:ILE:HG13	2.02	0.41
18:T:335:THR:OG1	18:T:336:VAL:N	2.53	0.41
18:T:360:VAL:HG13	18:T:361:ALA:H	1.85	0.41
22:1:1129:LEU:HA	22:1:1129:LEU:HD23	1.61	0.41
22:1:1199:VAL:HG11	22:1:1204:CYS:HB2	2.02	0.41
22:1:1210:HIS:CE1	35:2:585:THR:HG1	2.39	0.41
22:1:1253:GLY:HA3	22:1:1265:TYR:CD1	2.55	0.41
23:3:126:LYS:HB2	23:3:128:ARG:NH1	2.36	0.41
23:3:379:LEU:HD13	23:3:383:ASP:O	2.20	0.41
23:3:477:SER:HB2	23:3:504:PRO:CA	2.48	0.41
23:3:667:ILE:HB	23:3:675:LEU:HB2	2.02	0.41
23:3:781:LEU:HB3	23:3:801:GLU:OE1	2.20	0.41
25:p:155:LEU:O	25:p:189:ILE:HA	2.20	0.41
35:2:535:GLU:OE2	35:2:535:GLU:CA	2.68	0.41
37:6:13:LEU:O	37:6:13:LEU:HD12	2.20	0.41
39:5:46:HIS:C	39:5:48:ASP:N	2.75	0.41
39:5:72:MET:HE2	39:5:72:MET:HB3	1.73	0.41
40:9:353:GLU:HB3	40:9:355:ARG:NH2	2.35	0.41
40:9:416:ASP:HB3	40:9:419:THR:CG2	2.50	0.41
1:A:141:ILE:HG21	1:A:246:LEU:HD21	2.02	0.41
1:A:636:VAL:HA	1:A:639:PHE:CD2	2.55	0.41
1:A:827:PHE:CG	1:A:828:PRO:HD2	2.55	0.41
1:A:1361:GLU:O	1:A:1363:GLN:N	2.53	0.41
1:A:1381:ASP:OD2	1:A:1414:ARG:NH1	2.52	0.41
1:A:1498:TRP:HB2	1:A:1501:LEU:HD12	2.02	0.41
3:C:94:ILE:HB	18:T:276:GLU:CG	2.51	0.41
3:C:709:TRP:N	3:C:709:TRP:CD1	2.89	0.41
3:C:772:TRP:CH2	3:C:813:ARG:HD3	2.55	0.41
3:C:788:LYS:NZ	3:C:790:LYS:HE3	2.35	0.41
6:F:84:A:C8	6:F:84:A:H3'	2.55	0.41
7:G:-3:A:N3	7:G:-2:A:C8	2.88	0.41
7:G:99:C:N3	8:H:32:U:O2	2.53	0.41
10:J:417:VAL:O	10:J:421:LYS:HG2	2.21	0.41
11:K:20:GLY:O	11:K:22:GLN:NE2	2.53	0.41
11:K:160:LYS:HA	11:K:163:LEU:HD12	2.01	0.41
12:L:54:LEU:HA	12:L:54:LEU:HD13	1.62	0.41
18:T:264:CYS:SG	18:T:294:LEU:HD22	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:283:HIS:CD2	18:T:283:HIS:C	2.98	0.41
18:T:412:HIS:CG	18:T:437:HIS:CG	3.09	0.41
22:1:413:LYS:HB3	37:6:52:ASN:HD21	1.86	0.41
22:1:446:MET:HE2	22:1:446:MET:HB3	1.65	0.41
22:1:694:LEU:HD23	22:1:694:LEU:HA	1.80	0.41
22:1:846:ALA:O	22:1:847:ALA:C	2.63	0.41
22:1:997:LEU:HA	22:1:997:LEU:HD23	1.80	0.41
23:3:30:ILE:O	23:3:40:LEU:HD12	2.21	0.41
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.86	0.41
23:3:407:ILE:HB	23:3:1121:THR:O	2.20	0.41
23:3:709:GLN:HG3	23:3:710:GLU:O	2.20	0.41
37:6:21:LEU:HD13	37:6:64:TYR:CE2	2.55	0.41
38:7:32:ILE:HD11	38:7:71:TYR:HE1	1.84	0.41
43:v:88:LYS:HA	43:v:91:LYS:HZ2	1.85	0.41
1:A:513:LEU:HA	1:A:515:TYR:CE2	2.56	0.41
1:A:557:VAL:HG13	1:A:578:LEU:HD22	2.02	0.41
1:A:941:LYS:HD2	1:A:941:LYS:HA	1.74	0.41
1:A:1637:TRP:HZ3	1:A:1660:TYR:HB2	1.85	0.41
1:A:1721:GLY:O	1:A:1724:PRO:HD2	2.21	0.41
1:A:1730:MET:O	1:A:1731:ALA:C	2.63	0.41
2:B:46:U:H2'	2:B:47:A:C8	2.56	0.41
3:C:82:GLN:HA	3:C:82:GLN:NE2	2.36	0.41
3:C:173:THR:CG2	3:C:177:ARG:HE	2.33	0.41
3:C:522:SER:OG	3:C:523:GLN:N	2.54	0.41
3:C:756:LYS:HA	3:C:759:LEU:HB2	2.01	0.41
3:C:853:ARG:NH1	3:C:883:PHE:HA	2.34	0.41
6:F:44:G:N2	7:G:5:G:N1	2.67	0.41
12:L:14:THR:CG2	43:v:67:GLY:C	2.93	0.41
15:P:205:LYS:HD2	15:P:208:LYS:HG3	2.02	0.41
16:Q:967:PHE:O	16:Q:969:PRO:HD3	2.20	0.41
17:R:386:ARG:HH11	17:R:386:ARG:CB	2.33	0.41
20:Y:44:PRO:HD2	20:Y:47:LEU:HD22	2.02	0.41
22:1:621:ASP:OD1	22:1:621:ASP:C	2.64	0.41
22:1:679:ILE:O	22:1:680:LEU:C	2.63	0.41
22:1:830:TYR:OH	22:1:870:GLU:OE1	2.23	0.41
22:1:871:THR:O	22:1:875:ILE:HD12	2.20	0.41
22:1:970:LEU:O	22:1:973:HIS:HB2	2.20	0.41
22:1:1003:VAL:HG13	22:1:1004:ILE:N	2.36	0.41
22:1:1132:LEU:HA	22:1:1132:LEU:HD23	1.87	0.41
22:1:1227:ILE:HA	22:1:1227:ILE:HD12	1.72	0.41
22:1:1252:GLN:OE1	35:2:499:PRO:CA	2.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1303:ILE:HD13	22:1:1303:ILE:HA	1.72	0.41
23:3:181:MET:HG2	23:3:212:GLU:HB2	2.02	0.41
23:3:273:ARG:HA	23:3:273:ARG:HD3	1.76	0.41
23:3:915:LEU:HD12	23:3:915:LEU:HA	1.56	0.41
23:3:1006:GLN:O	23:3:1006:GLN:HG3	2.21	0.41
24:o:50:SER:HA	24:o:72:ASN:O	2.21	0.41
35:2:471:ARG:HE	35:2:471:ARG:HB3	1.73	0.41
35:2:538:GLU:N	35:2:538:GLU:OE2	2.53	0.41
35:2:596:GLU:HG2	35:2:597:PHE:CD1	2.56	0.41
38:7:24:GLU:HG2	38:7:66:VAL:HG21	2.03	0.41
1:A:261:LYS:NZ	3:C:176:GLU:HG2	2.36	0.41
1:A:282:LEU:HG	2:B:49:A:H5''	2.01	0.41
1:A:589:THR:OG1	1:A:590:GLY:N	2.53	0.41
1:A:602:ILE:HG23	7:G:-5:C:N4	2.36	0.41
1:A:616:PHE:CD1	1:A:621:VAL:HG21	2.55	0.41
1:A:726:TRP:O	40:9:247:SER:OG	2.34	0.41
1:A:966:TRP:CE3	1:A:1198:PRO:HG3	2.56	0.41
1:A:1232:VAL:HG12	1:A:1237:MET:HG2	2.03	0.41
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.48	0.41
1:A:1610:GLN:O	1:A:1630:LEU:HB2	2.21	0.41
2:B:95:G:H21	2:B:96:A:H5''	1.86	0.41
3:C:129:ILE:HG13	3:C:441:PRO:HD2	2.02	0.41
3:C:259:LYS:HD2	3:C:262:ARG:HH11	1.85	0.41
3:C:623:GLU:HB2	3:C:941:LYS:O	2.21	0.41
3:C:692:LEU:HB2	3:C:786:ASN:CG	2.46	0.41
3:C:821:LEU:HD13	3:C:948:SER:O	2.20	0.41
4:D:1407:LEU:HA	4:D:1426:ILE:O	2.19	0.41
5:E:95:VAL:HG11	5:E:336:HIS:NE2	2.35	0.41
7:G:87:U:H2'	7:G:88:G:O4'	2.21	0.41
7:G:112:U:H2'	7:G:113:U:C6	2.56	0.41
8:H:168:A:H5''	8:H:169:C:C5	2.56	0.41
11:K:52:ARG:O	11:K:55:LEU:HB3	2.21	0.41
11:K:145:ASP:HA	11:K:146:PRO:HD3	1.93	0.41
15:P:207:ASP:OD2	15:P:222:LYS:NZ	2.43	0.41
18:T:430:GLY:HA3	18:T:465:ILE:HG21	2.02	0.41
20:Y:36:ALA:O	20:Y:83:CYS:HA	2.21	0.41
20:Y:37:TRP:CE3	20:Y:83:CYS:HB2	2.55	0.41
22:1:968:GLU:OE1	22:1:968:GLU:N	2.51	0.41
23:3:486:SER:OG	23:3:494:VAL:HG11	2.21	0.41
23:3:727:SER:O	23:3:727:SER:OG	2.32	0.41
24:o:14:GLN:HA	24:o:23:GLU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:p:156:ASN:O	25:p:218:MET:HA	2.21	0.41
33:w:479:TYR:CD1	33:w:489:LYS:HG2	2.55	0.41
37:6:66:ASP:OD2	37:6:68:PHE:HB2	2.21	0.41
1:A:84:ASP:HA	1:A:87:VAL:HB	2.03	0.41
1:A:182:ILE:HG22	1:A:565:ARG:NH2	2.35	0.41
1:A:260:LEU:HB3	1:A:264:PHE:CE2	2.56	0.41
1:A:548:ARG:HH22	1:A:549:GLU:CD	2.28	0.41
1:A:1131:LYS:O	1:A:1132:LYS:HD2	2.20	0.41
1:A:1684:PHE:HB3	1:A:1715:TYR:CD2	2.45	0.41
2:B:23:C:HO2'	2:B:24:G:P	2.44	0.41
3:C:214:GLU:HG3	3:C:480:LYS:HZ3	1.86	0.41
5:E:213:ILE:HG22	5:E:237:SER:OG	2.20	0.41
5:E:343:ILE:HD13	5:E:353:MET:HA	2.02	0.41
6:F:45:A:H4'	6:F:45:A:OP1	2.20	0.41
10:J:266:GLU:OE1	10:J:269:LEU:HD13	2.21	0.41
16:Q:1176:ASP:O	16:Q:1300:GLY:HA2	2.21	0.41
22:1:148:ASN:HB3	37:6:100:LYS:HD2	2.02	0.41
22:1:509:PRO:HB2	22:1:510:PRO:HD3	2.02	0.41
22:1:1028:HIS:HB3	22:1:1031:VAL:CG2	2.51	0.41
22:1:1179:ASP:OD2	22:1:1179:ASP:C	2.64	0.41
22:1:1272:ILE:O	22:1:1275:GLY:O	2.38	0.41
23:3:34:ARG:CZ	23:3:39:GLU:OE1	2.68	0.41
23:3:423:LEU:HD13	23:3:774:PHE:HE1	1.86	0.41
23:3:843:LEU:HA	23:3:843:LEU:HD12	1.71	0.41
23:3:930:LEU:HD12	23:3:930:LEU:HA	1.72	0.41
24:o:8:LEU:O	24:o:12:ALA:HB2	2.21	0.41
36:4:166:TYR:HA	36:4:171:PRO:HA	2.03	0.41
40:9:354:PHE:C	40:9:355:ARG:HD3	2.46	0.41
1:A:265:THR:HG22	1:A:269:LEU:HD12	2.02	0.41
1:A:578:LEU:HD12	1:A:630:TRP:NE1	2.36	0.41
1:A:613:TYR:HE1	1:A:627:CYS:HB3	1.85	0.41
1:A:997:LEU:HD23	1:A:997:LEU:HA	1.77	0.41
1:A:1210:LYS:O	1:A:1212:GLY:N	2.54	0.41
1:A:1403:LEU:O	1:A:1403:LEU:HD12	2.21	0.41
1:A:1499:GLU:OE1	1:A:1499:GLU:N	2.53	0.41
3:C:73:TYR:HE2	18:T:199:VAL:HG11	1.84	0.41
3:C:814:ARG:HG3	3:C:952:PHE:HD1	1.86	0.41
3:C:823:ALA:O	3:C:825:PRO:HD3	2.21	0.41
3:C:829:GLU:O	3:C:905:GLN:N	2.47	0.41
6:F:39:A:N6	7:G:8:C:N3	2.68	0.41
7:G:99:C:C4	7:G:100:C:N4	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:44:HIS:O	11:K:50:HIS:HB2	2.21	0.41
11:K:172:PHE:HZ	23:3:1214:ARG:NH2	2.19	0.41
18:T:262:PHE:CD1	18:T:303:LEU:HD11	2.55	0.41
18:T:381:HIS:CD2	18:T:441:TRP:CE2	3.09	0.41
18:T:383:ARG:HG3	18:T:384:HIS:CE1	2.55	0.41
19:X:245:LYS:HE3	19:X:302:GLN:HB2	2.02	0.41
19:X:284:GLY:O	19:X:293:PRO:HA	2.21	0.41
22:1:112:ILE:HG23	22:1:115:ARG:NE	2.35	0.41
22:1:115:ARG:HB2	22:1:585:GLU:OE1	2.21	0.41
22:1:686:LEU:O	22:1:689:ILE:HB	2.21	0.41
22:1:1258:ALA:CB	22:1:1261:VAL:HG13	2.50	0.41
23:3:474:ILE:C	23:3:475:ILE:HD13	2.45	0.41
23:3:595:VAL:HG22	23:3:596:PRO:O	2.20	0.41
23:3:1210:ASP:O	23:3:1213:THR:N	2.53	0.41
25:p:37:VAL:HA	25:p:55:ILE:O	2.21	0.41
28:m:86:PRO:HA	28:m:87:PRO:HD3	1.86	0.41
33:w:469:GLU:OE2	33:w:469:GLU:CA	2.69	0.41
33:w:469:GLU:OE2	33:w:469:GLU:HA	2.20	0.41
39:5:44:MET:HE3	39:5:44:MET:HB3	1.59	0.41
1:A:67:ARG:HH21	1:A:487:LEU:HD23	1.86	0.41
1:A:108:MET:HE1	1:A:144:TRP:CZ2	2.54	0.41
1:A:141:ILE:HG22	1:A:242:ALA:CB	2.51	0.41
1:A:308:ILE:CG2	1:A:320:TYR:HB3	2.50	0.41
1:A:451:LEU:HD23	1:A:454:TYR:HD2	1.86	0.41
1:A:574:LEU:HD11	1:A:578:LEU:HD11	2.01	0.41
1:A:590:GLY:O	1:A:593:ARG:HB2	2.21	0.41
1:A:828:PRO:HA	1:A:829:PRO:HD3	1.96	0.41
1:A:839:LEU:HA	1:A:839:LEU:HD12	1.77	0.41
1:A:964:ASP:OD1	1:A:964:ASP:N	2.54	0.41
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	2.02	0.41
1:A:1503:TRP:CZ3	1:A:1533:ARG:HD3	2.56	0.41
1:A:1709:TYR:N	1:A:1709:TYR:CD2	2.89	0.41
2:B:16:U:C2	2:B:62:G:N2	2.89	0.41
2:B:49:A:H2'	2:B:50:G:C8	2.56	0.41
3:C:123:MET:HE2	3:C:123:MET:HB3	1.75	0.41
3:C:142:LYS:HA	3:C:228:PHE:CE2	2.56	0.41
3:C:211:PHE:HZ	3:C:635:LEU:HG	1.86	0.41
3:C:237:LEU:H	3:C:237:LEU:HD12	1.85	0.41
3:C:350:ASN:HD21	3:C:352:LYS:HE2	1.86	0.41
3:C:412:ILE:H	3:C:412:ILE:HD12	1.86	0.41
5:E:306:ASP:O	5:E:308:PHE:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:313:ASP:HB2	5:E:320:LEU:HD11	2.02	0.41
7:G:-4:G:C2	7:G:-3:A:N7	2.89	0.41
7:G:12:G:H4'	7:G:13:C:OP1	2.21	0.41
7:G:14:A:H2'	7:G:15:U:H6	1.86	0.41
10:J:220:LEU:HD11	10:J:224:LYS:HE3	2.01	0.41
10:J:306:LEU:HB3	10:J:309:VAL:HG23	2.03	0.41
11:K:24:LEU:O	11:K:26:TRP:N	2.53	0.41
11:K:70:GLU:OE1	11:K:73:ARG:NE	2.53	0.41
12:L:37:LEU:HD23	43:v:30:LEU:CG	2.51	0.41
12:L:71:LEU:O	12:L:72:LEU:C	2.64	0.41
16:Q:877:LEU:N	16:Q:1034:ILE:O	2.54	0.41
17:R:281:ASN:HD21	17:R:283:ASN:ND2	2.18	0.41
18:T:194:TRP:CH2	18:T:491:GLU:HG3	2.56	0.41
18:T:324:HIS:ND1	18:T:362:GLY:HA3	2.35	0.41
18:T:440:ASP:OD2	18:T:443:THR:HG23	2.21	0.41
18:T:496:THR:OG1	18:T:498:GLU:HG3	2.20	0.41
18:T:499:THR:HB	18:T:500:HIS:ND1	2.36	0.41
20:Y:32:TYR:C	20:Y:34:ASP:H	2.29	0.41
22:1:118:GLU:HA	22:1:121:LYS:HB2	2.02	0.41
22:1:124:ARG:O	22:1:126:MET:N	2.54	0.41
22:1:130:PRO:HD2	22:1:150:ARG:HD2	2.02	0.41
22:1:578:ILE:O	22:1:579:GLU:C	2.64	0.41
22:1:686:LEU:HD23	22:1:686:LEU:HA	1.79	0.41
22:1:815:PHE:HA	22:1:819:TRP:HD1	1.86	0.41
22:1:969:LYS:HE2	22:1:969:LYS:HB2	1.78	0.41
22:1:1144:GLN:O	22:1:1147:VAL:HG13	2.20	0.41
22:1:1261:VAL:O	22:1:1262:ARG:C	2.62	0.41
23:3:319:GLU:H	23:3:319:GLU:CD	2.29	0.41
23:3:404:LEU:HD23	23:3:407:ILE:HD11	2.03	0.41
23:3:718:ARG:NH2	23:3:735:SER:HA	2.35	0.41
23:3:817:GLN:HE21	23:3:818:GLN:CA	2.34	0.41
23:3:982:GLU:HG3	23:3:983:ASN:N	2.34	0.41
23:3:1049:LYS:HE3	23:3:1049:LYS:HB2	1.56	0.41
23:3:1082:LEU:HG	35:2:496:ASN:HA	2.03	0.41
23:3:1096:HIS:CD2	23:3:1166:TYR:HB2	2.56	0.41
35:2:540:LEU:N	35:2:540:LEU:HD23	2.35	0.41
37:6:18:ASN:CG	37:6:20:ILE:HG13	2.45	0.41
37:6:46:ARG:N	37:6:65:GLU:HG2	2.36	0.41
38:7:11:CYS:N	38:7:87:LYS:O	2.53	0.41
38:7:46:CYS:N	38:7:85:CYS:SG	2.73	0.41
40:9:310:LEU:HD13	40:9:315:TYR:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:9:391:ASP:C	40:9:392:LYS:HD2	2.46	0.41
41:8:90:THR:HG23	41:8:95:GLY:HA2	2.03	0.41
1:A:545:HIS:O	1:A:549:GLU:HG2	2.21	0.41
1:A:549:GLU:HG3	1:A:594:TYR:CE2	2.54	0.41
1:A:981:PHE:CZ	1:A:1095:ILE:HD11	2.56	0.41
1:A:1412:TRP:CH2	1:A:1423:PHE:HD2	2.39	0.41
1:A:1685:LEU:HD21	1:A:1715:TYR:HE2	1.85	0.41
3:C:141:GLY:O	3:C:145:PHE:CB	2.68	0.41
3:C:550:VAL:HB	3:C:552:ILE:HD11	2.02	0.41
6:F:37:C:H41	7:G:5:G:P	2.43	0.41
6:F:42:C:H2'	6:F:43:A:O4'	2.21	0.41
8:H:38:A:O2'	8:H:39:U:H5'	2.21	0.41
8:H:41:U:H2'	8:H:42:G:O4'	2.21	0.41
9:I:473:SER:O	9:I:475:PRO:HD3	2.21	0.41
11:K:78:GLU:O	11:K:82:ARG:HG3	2.21	0.41
11:K:178:ARG:HD2	11:K:182:GLU:OE1	2.21	0.41
18:T:220:VAL:CG1	18:T:252:VAL:HG21	2.50	0.41
22:1:641:ILE:N	22:1:642:PRO:HD2	2.36	0.41
22:1:656:LYS:HE2	41:8:65:ASP:HB2	2.02	0.41
22:1:978:LEU:O	22:1:979:TYR:C	2.64	0.41
23:3:86:ARG:HH11	23:3:86:ARG:HD2	1.73	0.41
23:3:170:VAL:HG22	23:3:184:CYS:HB2	2.02	0.41
23:3:550:ASN:HB2	23:3:592:LEU:HG	2.03	0.41
23:3:550:ASN:O	23:3:551:GLN:C	2.64	0.41
23:3:644:GLU:HG2	23:3:645:MET:HB2	2.03	0.41
23:3:791:HIS:HD1	23:3:930:LEU:HD21	1.86	0.41
23:3:823:MET:HE1	23:3:838:MET:HB2	2.03	0.41
23:3:1084:GLY:HA3	35:2:495:ARG:HH21	1.86	0.41
39:5:8:HIS:O	39:5:11:LEU:HG	2.21	0.41
40:9:352:ASP:OD2	40:9:370:ASN:ND2	2.54	0.41
41:8:56:VAL:O	41:8:59:ILE:N	2.54	0.41
1:A:156:ARG:HD2	1:A:620:PRO:HG2	2.03	0.40
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.85	0.40
1:A:417:ARG:HG2	1:A:418:THR:H	1.86	0.40
1:A:1183:PRO:N	1:A:1201:ARG:HH21	2.18	0.40
1:A:1307:MET:HB2	2:B:40:U:C4	2.56	0.40
3:C:168:THR:O	3:C:170:ILE:HG12	2.20	0.40
3:C:531:TRP:HH2	3:C:553:GLU:HB2	1.85	0.40
3:C:811:THR:O	3:C:815:VAL:HG22	2.21	0.40
3:C:916:ILE:HB	3:C:931:ARG:HG2	2.03	0.40
5:E:115:LEU:HD23	5:E:115:LEU:HA	1.78	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:126:SER:HG	5:E:136:TRP:HD1	1.62	0.40
5:E:194:TYR:HD2	5:E:214:ASP:HB3	1.86	0.40
6:F:86:U:C2	8:H:14:C:N4	2.90	0.40
8:H:171:U:H2'	8:H:172:C:C6	2.57	0.40
8:H:172:C:C2	8:H:173:C:C5	3.09	0.40
11:K:73:ARG:O	11:K:77:LEU:HG	2.21	0.40
17:R:418:MET:HE3	17:R:418:MET:HB2	1.75	0.40
18:T:371:HIS:CD2	18:T:375:VAL:HG21	2.56	0.40
18:T:394:ASN:HD21	18:T:408:ASN:CG	2.29	0.40
21:Z:600:ARG:HH22	21:Z:601:LEU:CD1	2.33	0.40
22:1:146:LYS:HB3	22:1:146:LYS:HE3	1.80	0.40
22:1:487:LEU:HD23	22:1:492:GLN:HE21	1.85	0.40
22:1:531:LEU:HD12	22:1:531:LEU:HA	1.59	0.40
22:1:551:LEU:O	22:1:555:VAL:HG12	2.22	0.40
22:1:1210:HIS:CE1	35:2:585:THR:OG1	2.74	0.40
23:3:407:ILE:HG23	23:3:425:VAL:HG13	2.02	0.40
23:3:1016:ARG:HG3	23:3:1017:ASN:H	1.86	0.40
23:3:1210:ASP:O	23:3:1211:ILE:C	2.64	0.40
37:6:48:ILE:HG12	37:6:62:VAL:HG12	2.03	0.40
38:7:21:ARG:HH21	38:7:21:ARG:HG2	1.86	0.40
40:9:221:LEU:H	40:9:221:LEU:HG	1.25	0.40
41:8:69:GLU:HG2	41:8:69:GLU:H	1.71	0.40
41:8:89:LEU:HB3	41:8:93:LEU:HD12	2.03	0.40
41:8:106:TRP:O	41:8:110:LEU:HG	2.21	0.40
41:8:123:PHE:HA	41:8:126:LEU:HB3	2.03	0.40
1:A:106:MET:HE3	1:A:630:TRP:CZ3	2.56	0.40
1:A:164:MET:HE3	1:A:569:VAL:HG21	2.03	0.40
1:A:192:GLN:H	1:A:192:GLN:HG2	1.54	0.40
1:A:256:TYR:CD1	1:A:256:TYR:C	2.99	0.40
1:A:260:LEU:H	1:A:260:LEU:HD12	1.86	0.40
1:A:590:GLY:HA2	1:A:592:TYR:CZ	2.56	0.40
1:A:1183:PRO:CA	1:A:1201:ARG:HH21	2.33	0.40
2:B:39:C:H4'	2:B:40:U:OP1	2.21	0.40
3:C:183:SER:H	3:C:214:GLU:CB	2.34	0.40
3:C:220:ARG:HH12	3:C:579:PRO:C	2.30	0.40
3:C:350:ASN:OD1	3:C:352:LYS:HG2	2.21	0.40
3:C:452:THR:O	3:C:578:ARG:N	2.33	0.40
3:C:914:LYS:HA	3:C:931:ARG:HH21	1.86	0.40
6:F:10:U:H2'	6:F:11:C:O4'	2.20	0.40
6:F:60:C:H3'	6:F:60:C:OP2	2.21	0.40
11:K:25:ARG:HD3	11:K:26:TRP:CH2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:253:ASN:HB2	17:R:254:TRP:CZ3	2.56	0.40
22:1:912:ASN:OD1	22:1:957:ARG:NH1	2.50	0.40
22:1:1167:TYR:CD1	35:2:581:LYS:HB2	2.54	0.40
23:3:147:ASP:CG	23:3:151:ARG:HG2	2.46	0.40
23:3:477:SER:OG	23:3:477:SER:O	2.37	0.40
23:3:886:GLU:OE2	23:3:911:LYS:HD3	2.21	0.40
24:o:137:TYR:CB	24:o:158:ALA:HB1	2.51	0.40
40:9:213:LYS:HD2	40:9:213:LYS:C	2.46	0.40
40:9:327:ASN:HB3	40:9:385:ARG:HH11	1.85	0.40
42:y:11:GLY:HA2	42:y:49:PHE:HA	2.04	0.40
1:A:713:LEU:HD13	1:A:739:ILE:HG12	2.03	0.40
1:A:717:TRP:O	1:A:720:TRP:N	2.54	0.40
1:A:769:LYS:HD2	1:A:769:LYS:HA	1.78	0.40
1:A:776:LEU:HD12	1:A:776:LEU:HA	1.80	0.40
1:A:946:GLU:HB3	1:A:950:LEU:HD23	2.02	0.40
1:A:960:ASN:ND2	1:A:1216:LEU:O	2.54	0.40
1:A:1296:GLN:HA	1:A:1299:ILE:CD1	2.51	0.40
1:A:1312:PRO:O	1:A:1312:PRO:CG	2.70	0.40
2:B:103:G:N1	2:B:111:A:C6	2.89	0.40
3:C:79:THR:C	3:C:80:ILE:HD12	2.47	0.40
3:C:495:ARG:CB	3:C:549:TRP:HD1	2.29	0.40
3:C:607:LEU:HD12	3:C:627:HIS:CD2	2.56	0.40
3:C:659:VAL:HG22	3:C:660:VAL:H	1.86	0.40
5:E:174:GLY:HA2	5:E:194:TYR:O	2.21	0.40
6:F:37:C:N4	7:G:5:G:OP2	2.53	0.40
6:F:38:G:OP1	6:F:38:G:C8	2.75	0.40
6:F:41:A:C6	6:F:42:C:C4	3.10	0.40
6:F:83:A:C8	6:F:84:A:C5	3.09	0.40
9:I:205:ASN:C	9:I:207:GLU:H	2.30	0.40
10:J:216:ASP:O	10:J:220:LEU:HB3	2.20	0.40
10:J:224:LYS:O	10:J:228:ARG:HB2	2.21	0.40
11:K:33:LYS:CB	11:K:44:HIS:HE1	2.34	0.40
11:K:155:LEU:HD23	11:K:158:LYS:HD2	2.03	0.40
11:K:180:GLY:HA3	23:3:690:ARG:NH2	2.37	0.40
12:L:34:ILE:O	12:L:37:LEU:HB2	2.21	0.40
12:L:73:HIS:CD2	40:9:220:ILE:HB	2.57	0.40
16:Q:979:GLN:O	16:Q:980:PRO:C	2.65	0.40
17:R:291:LEU:HD23	17:R:291:LEU:HA	1.79	0.40
19:X:229:SER:HB3	20:Y:51:ASP:OD2	2.22	0.40
22:1:171:GLN:O	22:1:174:GLU:N	2.53	0.40
22:1:548:GLU:H	22:1:548:GLU:HG2	1.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:628:THR:O	22:1:629:ALA:C	2.63	0.40
22:1:642:PRO:HD3	22:1:682:HIS:NE2	2.35	0.40
22:1:721:ILE:O	22:1:721:ILE:HG13	2.20	0.40
22:1:1262:ARG:NH1	35:2:483:GLN:NE2	2.65	0.40
23:3:14:ILE:HD13	23:3:32:VAL:HG11	2.03	0.40
23:3:149:ALA:HB3	23:3:151:ARG:HD3	2.03	0.40
23:3:356:HIS:HB2	23:3:401:LEU:HB2	2.04	0.40
23:3:412:ILE:HG12	23:3:423:LEU:HG	2.04	0.40
23:3:447:MET:HG2	23:3:750:CYS:HB2	2.03	0.40
23:3:450:SER:HB3	23:3:762:LEU:HD23	2.04	0.40
23:3:535:GLU:HG3	23:3:536:TRP:N	2.36	0.40
23:3:543:THR:O	23:3:559:THR:HG23	2.22	0.40
23:3:791:HIS:HD2	23:3:793:GLU:N	2.18	0.40
23:3:1015:LYS:NZ	23:3:1067:ASP:HB2	2.37	0.40
31:j:29:SER:O	31:j:46:CYS:HA	2.21	0.40
33:w:495:LEU:C	33:w:501:LEU:HB2	2.47	0.40
40:9:324:SER:HB3	40:9:415:SER:OG	2.20	0.40
41:8:14:ASP:OD2	41:8:16:ARG:NH2	2.46	0.40
1:A:226:GLN:NE2	1:A:417:ARG:HH21	2.18	0.40
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.21	0.40
1:A:489:TRP:CZ3	1:A:558:VAL:HG22	2.57	0.40
1:A:541:GLY:HA3	6:F:66:C:P	2.61	0.40
1:A:826:PRO:O	1:A:826:PRO:CD	2.70	0.40
1:A:1392:LYS:HB2	1:A:1392:LYS:HE2	1.71	0.40
1:A:1404:THR:N	1:A:1407:ASP:OD2	2.54	0.40
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.21	0.40
3:C:289:ILE:O	3:C:292:TYR:N	2.54	0.40
3:C:316:ILE:HD11	3:C:420:CYS:SG	2.62	0.40
3:C:658:PRO:HB2	3:C:881:PHE:CE2	2.57	0.40
3:C:669:THR:OG1	3:C:689:ALA:O	2.35	0.40
4:D:1031:GLU:HA	4:D:1034:LYS:CB	2.51	0.40
5:E:133:VAL:HB	5:E:147:LEU:HD12	2.03	0.40
5:E:224:GLN:HE21	5:E:226:LYS:C	2.25	0.40
6:F:46:G:H5'	6:F:47:A:H4'	2.02	0.40
7:G:116:C:C4	20:Y:117:ALA:O	2.75	0.40
8:H:22:U:H5'	8:H:23:A:OP2	2.21	0.40
10:J:286:GLU:HB3	10:J:295:ALA:HB2	2.03	0.40
19:X:338:PHE:HA	19:X:342:LYS:O	2.22	0.40
20:Y:22:VAL:HG12	20:Y:26:VAL:HG23	2.03	0.40
22:1:539:LEU:HD23	22:1:577:VAL:HG11	2.02	0.40
22:1:866:LYS:CG	22:1:909:VAL:HG11	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1048:GLU:C	22:1:1050:VAL:H	2.29	0.40
22:1:1270:ASN:O	22:1:1271:SER:C	2.63	0.40
23:3:58:VAL:O	23:3:59:PHE:C	2.62	0.40
23:3:78:ILE:HD13	23:3:78:ILE:HG21	1.86	0.40
23:3:268:ARG:CZ	23:3:268:ARG:HB3	2.52	0.40
23:3:272:PRO:HG2	23:3:311:PHE:CZ	2.56	0.40
23:3:471:ASP:OD1	23:3:471:ASP:N	2.54	0.40
23:3:609:LEU:HD11	23:3:615:ARG:HD2	2.02	0.40
23:3:709:GLN:HA	23:3:709:GLN:OE1	2.21	0.40
23:3:833:GLU:O	23:3:836:ALA:N	2.53	0.40
23:3:906:LEU:HD12	23:3:906:LEU:N	2.37	0.40
37:6:101:MET:HB2	37:6:101:MET:HE2	1.78	0.40
40:9:398:GLY:C	40:9:399:ARG:HD2	2.46	0.40
41:8:39:ASP:HA	41:8:78:LYS:O	2.22	0.40
30:f:14:ASP:N	30:f:31:LEU:O	2.54	0.40
1:A:111:GLU:OE2	1:A:210:HIS:HA	2.21	0.40
1:A:119:LEU:HD13	1:A:477:LYS:HD3	2.02	0.40
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.52	0.40
1:A:264:PHE:CE1	1:A:455:VAL:HG13	2.56	0.40
1:A:359:ILE:HG21	3:C:276:TYR:C	2.47	0.40
1:A:368:GLN:HG2	1:A:369:GLU:H	1.87	0.40
1:A:941:LYS:HG2	1:A:1071:PHE:CE1	2.56	0.40
1:A:1248:LEU:HD23	1:A:1248:LEU:HA	1.81	0.40
1:A:1489:LEU:HD23	1:A:1489:LEU:HA	1.89	0.40
1:A:1490:PHE:CE2	1:A:1498:TRP:HB3	2.57	0.40
1:A:1566:ILE:H	1:A:1566:ILE:HG12	1.52	0.40
1:A:1664:ILE:HD13	1:A:1703:ILE:HG13	2.03	0.40
1:A:1699:THR:HA	1:A:1717:ASN:ND2	2.37	0.40
3:C:219:LEU:HD23	3:C:219:LEU:HA	1.93	0.40
3:C:501:ILE:HB	3:C:544:VAL:CG1	2.52	0.40
3:C:676:ALA:HA	3:C:954:ASP:OD1	2.22	0.40
3:C:772:TRP:CZ2	3:C:813:ARG:HD3	2.56	0.40
5:E:343:ILE:HD13	5:E:343:ILE:HA	1.91	0.40
6:F:70:A:C6	6:F:71:G:N7	2.90	0.40
6:F:86:U:H3	8:H:13:C:H5	1.67	0.40
10:J:222:ASP:O	10:J:226:ARG:HG3	2.21	0.40
22:1:517:ARG:HE	22:1:517:ARG:HB3	1.57	0.40
22:1:774:ILE:O	22:1:777:PHE:HD2	2.04	0.40
22:1:896:ILE:HA	22:1:896:ILE:HD13	1.74	0.40
22:1:954:LEU:O	22:1:958:THR:HG23	2.22	0.40
22:1:986:TYR:HD1	22:1:986:TYR:HA	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:1:1051:SER:OG	22:1:1053:ARG:N	2.55	0.40
22:1:1091:HIS:C	22:1:1091:HIS:HD1	2.29	0.40
22:1:1098:LEU:O	22:1:1100:ASN:N	2.55	0.40
22:1:1140:GLU:HB2	22:1:1143:VAL:HG12	2.04	0.40
23:3:534:ASN:OD1	23:3:534:ASN:N	2.55	0.40
23:3:794:SER:O	23:3:795:ASN:HB2	2.21	0.40
23:3:827:ALA:HA	23:3:834:LEU:HD21	2.02	0.40
23:3:861:GLN:HE21	23:3:861:GLN:HB3	1.47	0.40
23:3:1198:ASP:C	23:3:1199:ARG:HG2	2.45	0.40
38:7:54:TYR:CD1	38:7:54:TYR:N	2.89	0.40
40:9:302:LYS:CD	40:9:350:PHE:HB2	2.51	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	2135/2335 (91%)	1880 (88%)	240 (11%)	15 (1%)	18	47
3	C	892/972 (92%)	827 (93%)	65 (7%)	0	100	100
4	D	1720/2136 (80%)	1602 (93%)	114 (7%)	4 (0%)	43	71
5	E	297/357 (83%)	274 (92%)	23 (8%)	0	100	100
9	I	591/855 (69%)	494 (84%)	93 (16%)	4 (1%)	18	47
10	J	245/848 (29%)	226 (92%)	17 (7%)	2 (1%)	16	44
11	K	308/393 (78%)	292 (95%)	14 (4%)	2 (1%)	21	50
12	L	97/802 (12%)	94 (97%)	3 (3%)	0	100	100
13	N	132/144 (92%)	123 (93%)	9 (7%)	0	100	100
14	O	267/420 (64%)	255 (96%)	12 (4%)	0	100	100
15	P	40/229 (18%)	31 (78%)	9 (22%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	1319/1485 (89%)	1256 (95%)	62 (5%)	1 (0%)	48	78
17	R	184/536 (34%)	172 (94%)	12 (6%)	0	100	100
18	T	318/514 (62%)	281 (88%)	36 (11%)	1 (0%)	36	65
19	X	152/396 (38%)	142 (93%)	10 (7%)	0	100	100
20	Y	116/322 (36%)	106 (91%)	10 (9%)	0	100	100
21	Z	53/619 (9%)	48 (91%)	5 (9%)	0	100	100
22	1	984/1304 (76%)	872 (89%)	102 (10%)	10 (1%)	12	40
23	3	1168/1217 (96%)	1023 (88%)	141 (12%)	4 (0%)	36	65
24	o	160/255 (63%)	148 (92%)	12 (8%)	0	100	100
25	p	165/225 (73%)	152 (92%)	13 (8%)	0	100	100
26	c	95/118 (80%)	84 (88%)	11 (12%)	0	100	100
26	h	91/118 (77%)	86 (94%)	4 (4%)	1 (1%)	11	38
27	d	72/86 (84%)	66 (92%)	6 (8%)	0	100	100
27	i	70/86 (81%)	65 (93%)	5 (7%)	0	100	100
28	a	82/240 (34%)	77 (94%)	5 (6%)	0	100	100
28	m	80/240 (33%)	75 (94%)	5 (6%)	0	100	100
29	g	77/126 (61%)	70 (91%)	7 (9%)	0	100	100
29	l	81/126 (64%)	74 (91%)	7 (9%)	0	100	100
30	f	72/76 (95%)	67 (93%)	5 (7%)	0	100	100
30	k	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
31	e	75/92 (82%)	68 (91%)	7 (9%)	0	100	100
31	j	79/92 (86%)	70 (89%)	9 (11%)	0	100	100
32	b	80/119 (67%)	75 (94%)	5 (6%)	0	100	100
32	n	78/119 (66%)	72 (92%)	6 (8%)	0	100	100
33	w	428/501 (85%)	403 (94%)	23 (5%)	2 (0%)	24	54
34	u	183/793 (23%)	175 (96%)	8 (4%)	0	100	100
35	2	225/895 (25%)	205 (91%)	17 (8%)	3 (1%)	9	33
36	4	157/424 (37%)	145 (92%)	12 (8%)	0	100	100
37	6	107/125 (86%)	98 (92%)	9 (8%)	0	100	100
38	7	103/110 (94%)	89 (86%)	14 (14%)	0	100	100
39	5	79/86 (92%)	70 (89%)	9 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	9	378/520 (73%)	343 (91%)	34 (9%)	1 (0%)	36	65
41	8	113/904 (12%)	104 (92%)	9 (8%)	0	100	100
42	y	77/301 (26%)	73 (95%)	4 (5%)	0	100	100
43	v	158/464 (34%)	143 (90%)	15 (10%)	0	100	100
All	All	14454/23201 (62%)	13162 (91%)	1242 (9%)	50 (0%)	37	65

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	802	THR
1	A	1553	VAL
22	1	430	LYS
22	1	435	PRO
22	1	437	PRO
22	1	1099	ASN
33	w	498	GLN
35	2	510	TYR
1	A	1549	VAL
4	D	531	ILE
4	D	2098	ALA
9	I	375	ILE
22	1	945	ALA
22	1	1104	GLN
23	3	773	VAL
23	3	1008	SER
33	w	500	LEU
35	2	533	ILE
40	9	269	ASP
1	A	1305	SER
11	K	281	LEU
1	A	366	LYS
1	A	1020	LYS
1	A	1311	PHE
4	D	2099	THR
9	I	207	GLU
18	T	308	ARG
1	A	367	SER
1	A	1362	ASP
1	A	1548	TYR
9	I	85	ARG
11	K	40	GLY

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Mol	Chain	Res	Type
22	1	125	THR
22	1	417	PRO
22	1	717	THR
22	1	973	HIS
23	3	319	GLU
23	3	496	ASP
10	J	241	VAL
1	A	826	PRO
1	A	1308	PRO
1	A	1419	ILE
4	D	1584	ILE
1	A	167	PRO
1	A	942	PRO
9	I	385	VAL
10	J	341	PRO
26	h	103	GLY
35	2	474	VAL
16	Q	489	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1476/2108 (70%)	1236 (84%)	240 (16%)	2	10
3	C	792/866 (92%)	719 (91%)	73 (9%)	8	29
5	E	256/300 (85%)	232 (91%)	24 (9%)	8	29
9	I	23/749 (3%)	23 (100%)	0	100	100
10	J	205/751 (27%)	190 (93%)	15 (7%)	13	39
11	K	164/354 (46%)	139 (85%)	25 (15%)	3	10
12	L	86/709 (12%)	72 (84%)	14 (16%)	2	10
15	P	40/203 (20%)	36 (90%)	4 (10%)	7	26
16	Q	71/1336 (5%)	71 (100%)	0	100	100
17	R	160/459 (35%)	133 (83%)	27 (17%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	T	273/441 (62%)	227 (83%)	46 (17%)	2	9
19	X	139/349 (40%)	125 (90%)	14 (10%)	7	25
20	Y	105/291 (36%)	81 (77%)	24 (23%)	1	2
21	Z	40/545 (7%)	37 (92%)	3 (8%)	12	38
22	1	834/1103 (76%)	687 (82%)	147 (18%)	2	8
23	3	1020/1051 (97%)	808 (79%)	212 (21%)	1	4
24	o	6/218 (3%)	6 (100%)	0	100	100
25	p	8/195 (4%)	8 (100%)	0	100	100
26	h	5/110 (4%)	5 (100%)	0	100	100
27	i	4/74 (5%)	4 (100%)	0	100	100
28	m	4/177 (2%)	4 (100%)	0	100	100
29	l	3/101 (3%)	3 (100%)	0	100	100
30	k	3/66 (4%)	3 (100%)	0	100	100
31	j	1/84 (1%)	1 (100%)	0	100	100
32	n	3/101 (3%)	3 (100%)	0	100	100
33	w	112/446 (25%)	93 (83%)	19 (17%)	2	9
34	u	10/709 (1%)	10 (100%)	0	100	100
35	2	134/776 (17%)	96 (72%)	38 (28%)	0	1
37	6	97/109 (89%)	85 (88%)	12 (12%)	4	18
38	7	90/95 (95%)	75 (83%)	15 (17%)	2	9
39	5	72/77 (94%)	63 (88%)	9 (12%)	4	18
40	9	223/456 (49%)	197 (88%)	26 (12%)	5	20
41	8	104/831 (12%)	96 (92%)	8 (8%)	12	37
43	v	73/382 (19%)	55 (75%)	18 (25%)	1	2
All	All	6636/16622 (40%)	5623 (85%)	1013 (15%)	5	10

All (1013) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	VAL
1	A	92	LEU
1	A	102	LEU
1	A	118	VAL
1	A	123	THR

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Mol	Chain	Res	Type
1	A	176	LEU
1	A	177	ASP
1	A	192	GLN
1	A	193	LEU
1	A	210	HIS
1	A	220	VAL
1	A	237	THR
1	A	245	LEU
1	A	280	GLU
1	A	283	VAL
1	A	304	ILE
1	A	310	THR
1	A	311	GLU
1	A	314	ILE
1	A	325	HIS
1	A	337	VAL
1	A	340	ILE
1	A	342	THR
1	A	344	ASP
1	A	391	THR
1	A	400	ASN
1	A	412	ASN
1	A	413	LEU
1	A	422	LEU
1	A	426	LEU
1	A	427	VAL
1	A	430	TRP
1	A	433	GLU
1	A	475	SER
1	A	479	THR
1	A	487	LEU
1	A	496	VAL
1	A	506	LEU
1	A	507	LEU
1	A	508	ILE
1	A	524	LEU
1	A	547	CYS
1	A	551	LEU
1	A	562	VAL
1	A	574	LEU
1	A	579	GLN
1	A	585	VAL

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Mol	Chain	Res	Type
1	A	591	MET
1	A	596	TYR
1	A	607	ASP
1	A	613	TYR
1	A	617	ASN
1	A	621	VAL
1	A	627	CYS
1	A	637	TRP
1	A	659	GLN
1	A	675	GLN
1	A	689	VAL
1	A	693	ILE
1	A	699	GLU
1	A	701	ILE
1	A	708	THR
1	A	709	ILE
1	A	728	VAL
1	A	731	LEU
1	A	733	THR
1	A	735	ILE
1	A	738	MET
1	A	739	ILE
1	A	740	LEU
1	A	743	VAL
1	A	748	ASP
1	A	751	THR
1	A	753	THR
1	A	766	THR
1	A	767	VAL
1	A	770	THR
1	A	771	VAL
1	A	779	LEU
1	A	780	THR
1	A	784	LEU
1	A	790	ARG
1	A	801	ILE
1	A	807	VAL
1	A	811	THR
1	A	812	THR
1	A	813	THR
1	A	814	VAL
1	A	819	SER

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Mol	Chain	Res	Type
1	A	826	PRO
1	A	848	GLU
1	A	852	VAL
1	A	856	LEU
1	A	871	TYR
1	A	873	ASN
1	A	879	SER
1	A	894	VAL
1	A	910	ASP
1	A	911	VAL
1	A	923	ASP
1	A	946	GLU
1	A	956	CYS
1	A	957	GLN
1	A	959	ILE
1	A	963	GLN
1	A	969	SER
1	A	976	MET
1	A	977	LEU
1	A	979	SER
1	A	980	ARG
1	A	990	LEU
1	A	1000	ILE
1	A	1002	ASP
1	A	1010	THR
1	A	1012	LYS
1	A	1021	ASP
1	A	1022	MET
1	A	1027	SER
1	A	1030	ILE
1	A	1034	LEU
1	A	1048	MET
1	A	1051	LEU
1	A	1059	SER
1	A	1069	ASN
1	A	1070	ASP
1	A	1076	ASP
1	A	1085	ILE
1	A	1089	CYS
1	A	1092	ILE
1	A	1095	ILE
1	A	1099	PHE

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Mol	Chain	Res	Type
1	A	1102	THR
1	A	1105	GLU
1	A	1108	ASP
1	A	1114	LEU
1	A	1130	ASN
1	A	1133	CYS
1	A	1137	ASP
1	A	1147	VAL
1	A	1157	ILE
1	A	1158	LYS
1	A	1177	VAL
1	A	1180	LYS
1	A	1181	ASP
1	A	1186	LEU
1	A	1189	MET
1	A	1194	CYS
1	A	1215	ASN
1	A	1223	GLU
1	A	1237	MET
1	A	1255	THR
1	A	1258	LYS
1	A	1268	ILE
1	A	1275	ARG
1	A	1284	LEU
1	A	1293	ASN
1	A	1295	ILE
1	A	1297	THR
1	A	1298	ARG
1	A	1299	ILE
1	A	1301	ILE
1	A	1303	LEU
1	A	1304	ASN
1	A	1306	LYS
1	A	1308	PRO
1	A	1310	ARG
1	A	1314	VAL
1	A	1315	VAL
1	A	1318	THR
1	A	1327	MET
1	A	1329	SER
1	A	1332	HIS
1	A	1334	LEU

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Mol	Chain	Res	Type
1	A	1359	HIS
1	A	1361	GLU
1	A	1363	GLN
1	A	1365	ILE
1	A	1367	ASN
1	A	1368	LEU
1	A	1372	ILE
1	A	1376	GLU
1	A	1377	SER
1	A	1380	ILE
1	A	1385	VAL
1	A	1391	LEU
1	A	1393	ARG
1	A	1402	ARG
1	A	1404	THR
1	A	1405	LEU
1	A	1407	ASP
1	A	1410	ASP
1	A	1416	ILE
1	A	1418	ARG
1	A	1428	HIS
1	A	1438	VAL
1	A	1447	VAL
1	A	1448	LEU
1	A	1458	GLN
1	A	1460	HIS
1	A	1461	ASP
1	A	1471	ARG
1	A	1473	ASP
1	A	1475	ILE
1	A	1488	THR
1	A	1493	THR
1	A	1494	TYR
1	A	1527	ASN
1	A	1529	ILE
1	A	1531	ASN
1	A	1535	THR
1	A	1536	LEU
1	A	1539	SER
1	A	1546	ASN
1	A	1547	VAL
1	A	1551	PHE

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Mol	Chain	Res	Type
1	A	1555	LEU
1	A	1557	LEU
1	A	1562	MET
1	A	1566	ILE
1	A	1574	ILE
1	A	1575	GLN
1	A	1581	LEU
1	A	1606	ILE
1	A	1607	GLU
1	A	1608	THR
1	A	1611	LYS
1	A	1612	GLU
1	A	1614	ILE
1	A	1624	SER
1	A	1629	ILE
1	A	1650	ASP
1	A	1655	THR
1	A	1659	LYS
1	A	1664	ILE
1	A	1681	ARG
1	A	1699	THR
1	A	1703	ILE
1	A	1706	ASP
1	A	1725	LEU
1	A	1745	GLU
3	C	59	LEU
3	C	65	TYR
3	C	68	THR
3	C	80	ILE
3	C	85	ASP
3	C	91	GLU
3	C	126	SER
3	C	129	ILE
3	C	132	VAL
3	C	147	ASP
3	C	148	CYS
3	C	162	ASP
3	C	168	THR
3	C	171	LEU
3	C	188	VAL
3	C	202	ILE
3	C	209	VAL

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Mol	Chain	Res	Type
3	C	213	ASP
3	C	223	ASP
3	C	243	ILE
3	C	251	LEU
3	C	254	THR
3	C	265	LEU
3	C	289	ILE
3	C	306	ASN
3	C	312	SER
3	C	325	LYS
3	C	347	ILE
3	C	399	LEU
3	C	432	ASP
3	C	460	ASP
3	C	468	CYS
3	C	476	CYS
3	C	484	THR
3	C	498	SER
3	C	510	LEU
3	C	516	LEU
3	C	529	ARG
3	C	534	VAL
3	C	551	LEU
3	C	562	THR
3	C	564	THR
3	C	566	THR
3	C	584	THR
3	C	587	VAL
3	C	592	VAL
3	C	602	LYS
3	C	616	SER
3	C	618	THR
3	C	619	THR
3	C	627	HIS
3	C	638	ASP
3	C	639	CYS
3	C	661	THR
3	C	685	ILE
3	C	686	THR
3	C	690	GLU
3	C	707	ILE
3	C	749	THR

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Mol	Chain	Res	Type
3	C	755	ASP
3	C	767	VAL
3	C	779	LEU
3	C	796	VAL
3	C	816	VAL
3	C	824	THR
3	C	850	LEU
3	C	878	ILE
3	C	879	ASP
3	C	884	GLU
3	C	890	HIS
3	C	902	HIS
3	C	907	VAL
3	C	946	ASP
5	E	62	LEU
5	E	63	SER
5	E	71	CYS
5	E	74	PHE
5	E	86	PHE
5	E	113	MET
5	E	116	HIS
5	E	133	VAL
5	E	135	VAL
5	E	144	VAL
5	E	156	SER
5	E	167	VAL
5	E	168	CYS
5	E	173	ASP
5	E	215	ASN
5	E	244	SER
5	E	246	GLU
5	E	259	VAL
5	E	264	VAL
5	E	290	ARG
5	E	300	ILE
5	E	304	SER
5	E	331	ASN
5	E	351	LEU
10	J	220	LEU
10	J	242	ILE
10	J	252	GLU
10	J	258	ILE

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Mol	Chain	Res	Type
10	J	270	ASP
10	J	280	LEU
10	J	303	ILE
10	J	305	THR
10	J	306	LEU
10	J	321	GLU
10	J	359	VAL
10	J	385	PHE
10	J	404	GLU
10	J	405	PHE
10	J	406	PHE
11	K	7	LEU
11	K	8	THR
11	K	16	ILE
11	K	24	LEU
11	K	28	CYS
11	K	35	CYS
11	K	38	GLU
11	K	54	LEU
11	K	56	LEU
11	K	63	GLN
11	K	66	ASP
11	K	74	ASN
11	K	77	LEU
11	K	84	PHE
11	K	93	ILE
11	K	94	VAL
11	K	99	ILE
11	K	108	ASN
11	K	115	LEU
11	K	132	GLU
11	K	139	ILE
11	K	141	TYR
11	K	165	ASP
11	K	174	GLU
11	K	181	LEU
12	L	14	THR
12	L	16	ASP
12	L	23	VAL
12	L	30	GLN
12	L	37	LEU
12	L	38	LEU

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Mol	Chain	Res	Type
12	L	41	LYS
12	L	54	LEU
12	L	55	ASP
12	L	58	ILE
12	L	61	THR
12	L	64	SER
12	L	77	LEU
12	L	103	LEU
15	P	196	ASN
15	P	202	ASP
15	P	214	THR
15	P	224	MET
17	R	132	LEU
17	R	137	GLU
17	R	138	GLU
17	R	140	ILE
17	R	147	THR
17	R	148	ARG
17	R	151	LEU
17	R	157	GLN
17	R	231	HIS
17	R	234	SER
17	R	238	THR
17	R	239	VAL
17	R	256	ASN
17	R	279	HIS
17	R	280	ILE
17	R	307	GLN
17	R	316	GLU
17	R	324	LEU
17	R	386	ARG
17	R	388	ILE
17	R	401	THR
17	R	405	VAL
17	R	406	GLN
17	R	408	ASP
17	R	415	SER
17	R	433	TYR
17	R	434	ASP
18	T	196	LEU
18	T	201	SER
18	T	209	CYS

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Mol	Chain	Res	Type
18	T	210	ILE
18	T	212	VAL
18	T	223	SER
18	T	225	ASP
18	T	228	ILE
18	T	230	ILE
18	T	242	LEU
18	T	246	ILE
18	T	263	SER
18	T	267	ASP
18	T	277	TYR
18	T	281	ILE
18	T	283	HIS
18	T	300	ILE
18	T	305	THR
18	T	309	ASP
18	T	311	THR
18	T	316	ASP
18	T	325	THR
18	T	336	VAL
18	T	349	SER
18	T	355	ARG
18	T	360	VAL
18	T	369	THR
18	T	370	ASN
18	T	373	LYS
18	T	374	SER
18	T	400	PHE
18	T	402	ASP
18	T	415	ILE
18	T	424	ASP
18	T	426	VAL
18	T	432	ASP
18	T	435	THR
18	T	439	TRP
18	T	440	ASP
18	T	443	THR
18	T	459	LEU
18	T	463	SER
18	T	465	ILE
18	T	468	CYS
18	T	486	ILE

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Mol	Chain	Res	Type
18	T	499	THR
19	X	221	LYS
19	X	232	LEU
19	X	234	GLU
19	X	237	ASN
19	X	242	VAL
19	X	261	LEU
19	X	266	ASN
19	X	273	MET
19	X	283	LEU
19	X	287	ARG
19	X	289	ILE
19	X	300	SER
19	X	307	GLN
19	X	344	ILE
20	Y	1	MET
20	Y	2	ASN
20	Y	7	VAL
20	Y	9	LEU
20	Y	13	LEU
20	Y	18	VAL
20	Y	24	ASP
20	Y	34	ASP
20	Y	38	ILE
20	Y	46	GLU
20	Y	51	ASP
20	Y	52	ILE
20	Y	54	CYS
20	Y	57	SER
20	Y	69	ARG
20	Y	85	GLU
20	Y	86	ASP
20	Y	89	SER
20	Y	90	THR
20	Y	91	ILE
20	Y	107	ILE
20	Y	108	ARG
20	Y	109	VAL
20	Y	113	SER
21	Z	574	ASN
21	Z	587	VAL
21	Z	598	PHE

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Mol	Chain	Res	Type
22	1	116	GLU
22	1	123	ARG
22	1	127	ILE
22	1	128	ILE
22	1	131	GLU
22	1	142	THR
22	1	154	ASP
22	1	160	HIS
22	1	161	LEU
22	1	395	ARG
22	1	414	VAL
22	1	446	MET
22	1	458	ASP
22	1	467	LEU
22	1	472	ILE
22	1	478	LEU
22	1	479	LEU
22	1	483	ASP
22	1	488	SER
22	1	491	GLU
22	1	500	LEU
22	1	502	LEU
22	1	504	ILE
22	1	506	ASN
22	1	516	LEU
22	1	519	ILE
22	1	520	THR
22	1	524	ARG
22	1	531	LEU
22	1	535	ILE
22	1	539	LEU
22	1	541	SER
22	1	543	THR
22	1	548	GLU
22	1	551	LEU
22	1	555	VAL
22	1	559	ILE
22	1	577	VAL
22	1	582	LEU
22	1	584	ASP
22	1	585	GLU
22	1	596	ILE

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Mol	Chain	Res	Type
22	1	606	LEU
22	1	612	THR
22	1	614	ARG
22	1	617	ILE
22	1	624	VAL
22	1	635	VAL
22	1	637	SER
22	1	673	ILE
22	1	675	MET
22	1	679	ILE
22	1	680	LEU
22	1	690	ILE
22	1	691	GLU
22	1	694	LEU
22	1	703	THR
22	1	705	SER
22	1	714	GLU
22	1	723	SER
22	1	726	SER
22	1	727	VAL
22	1	728	LEU
22	1	731	LEU
22	1	735	ILE
22	1	750	ILE
22	1	753	LEU
22	1	754	ILE
22	1	758	ASP
22	1	765	TYR
22	1	769	VAL
22	1	776	GLU
22	1	796	CYS
22	1	801	VAL
22	1	806	ILE
22	1	808	THR
22	1	810	ILE
22	1	837	THR
22	1	839	GLU
22	1	850	ILE
22	1	853	ILE
22	1	855	ASP
22	1	872	ILE
22	1	875	ILE

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Mol	Chain	Res	Type
22	1	878	ASN
22	1	883	ASP
22	1	889	GLU
22	1	896	ILE
22	1	905	THR
22	1	921	LEU
22	1	935	THR
22	1	942	ASN
22	1	947	VAL
22	1	950	GLN
22	1	964	THR
22	1	982	LEU
22	1	992	SER
22	1	1000	ILE
22	1	1013	ILE
22	1	1016	LEU
22	1	1020	LEU
22	1	1021	THR
22	1	1023	ILE
22	1	1026	ASN
22	1	1063	LEU
22	1	1084	ILE
22	1	1086	LYS
22	1	1090	PRO
22	1	1092	ASP
22	1	1093	VAL
22	1	1094	LEU
22	1	1096	THR
22	1	1100	ASN
22	1	1109	ARG
22	1	1112	THR
22	1	1113	THR
22	1	1121	GLU
22	1	1128	VAL
22	1	1135	GLU
22	1	1147	VAL
22	1	1150	SER
22	1	1152	SER
22	1	1158	ILE
22	1	1160	GLU
22	1	1169	VAL
22	1	1177	LEU

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Mol	Chain	Res	Type
22	1	1178	MET
22	1	1179	ASP
22	1	1182	LEU
22	1	1184	HIS
22	1	1195	MET
22	1	1223	SER
22	1	1226	VAL
22	1	1227	ILE
22	1	1228	GLN
22	1	1239	VAL
22	1	1252	GLN
22	1	1261	VAL
22	1	1267	LYS
22	1	1271	SER
22	1	1277	GLN
22	1	1281	ILE
22	1	1287	ILE
22	1	1297	ARG
22	1	1299	GLU
22	1	1303	ILE
22	1	1304	LEU
23	3	5	ASN
23	3	6	LEU
23	3	7	THR
23	3	8	LEU
23	3	9	GLN
23	3	12	THR
23	3	21	ASN
23	3	25	THR
23	3	27	GLN
23	3	33	SER
23	3	40	LEU
23	3	42	ARG
23	3	44	ASP
23	3	54	LEU
23	3	55	THR
23	3	56	VAL
23	3	65	LEU
23	3	68	PHE
23	3	69	ARG
23	3	82	SER
23	3	88	VAL

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Mol	Chain	Res	Type
23	3	90	LEU
23	3	106	THR
23	3	116	VAL
23	3	123	VAL
23	3	124	ASP
23	3	130	VAL
23	3	131	MET
23	3	132	ILE
23	3	139	LYS
23	3	143	ILE
23	3	146	ARG
23	3	151	ARG
23	3	155	SER
23	3	156	SER
23	3	164	ASN
23	3	165	THR
23	3	191	GLU
23	3	193	ASP
23	3	205	GLN
23	3	207	THR
23	3	209	THR
23	3	212	GLU
23	3	213	LEU
23	3	219	HIS
23	3	221	VAL
23	3	222	ARG
23	3	225	SER
23	3	226	GLU
23	3	228	LEU
23	3	234	PHE
23	3	237	THR
23	3	256	ILE
23	3	259	LYS
23	3	261	PHE
23	3	263	ASP
23	3	266	ASP
23	3	268	ARG
23	3	285	MET
23	3	290	SER
23	3	297	SER
23	3	298	MET
23	3	305	THR

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Mol	Chain	Res	Type
23	3	309	ASP
23	3	315	LEU
23	3	318	ASP
23	3	320	ASP
23	3	322	VAL
23	3	323	THR
23	3	325	ILE
23	3	328	LYS
23	3	332	THR
23	3	335	VAL
23	3	342	LEU
23	3	344	THR
23	3	347	LEU
23	3	360	GLN
23	3	368	ASP
23	3	374	SER
23	3	384	THR
23	3	394	ASN
23	3	395	LEU
23	3	410	CYS
23	3	418	GLU
23	3	433	SER
23	3	434	SER
23	3	439	ARG
23	3	445	SER
23	3	449	VAL
23	3	466	ILE
23	3	482	THR
23	3	483	LEU
23	3	494	VAL
23	3	497	SER
23	3	505	THR
23	3	508	CYS
23	3	509	SER
23	3	511	LEU
23	3	516	LEU
23	3	518	GLN
23	3	525	ARG
23	3	534	ASN
23	3	549	VAL
23	3	566	PHE
23	3	588	VAL

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Mol	Chain	Res	Type
23	3	589	CYS
23	3	592	LEU
23	3	604	PHE
23	3	609	LEU
23	3	613	THR
23	3	616	ILE
23	3	624	CYS
23	3	633	LEU
23	3	638	GLU
23	3	643	VAL
23	3	665	LEU
23	3	666	ASN
23	3	673	VAL
23	3	674	LEU
23	3	679	LEU
23	3	680	ASP
23	3	683	THR
23	3	686	LEU
23	3	689	THR
23	3	690	ARG
23	3	700	LYS
23	3	704	VAL
23	3	712	VAL
23	3	721	LEU
23	3	724	SER
23	3	762	LEU
23	3	777	VAL
23	3	791	HIS
23	3	799	ILE
23	3	815	ARG
23	3	817	GLN
23	3	824	VAL
23	3	843	LEU
23	3	847	LEU
23	3	851	ILE
23	3	861	GLN
23	3	864	SER
23	3	865	VAL
23	3	867	ARG
23	3	875	ASN
23	3	876	THR
23	3	877	LEU

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Mol	Chain	Res	Type
23	3	886	GLU
23	3	889	PHE
23	3	891	VAL
23	3	897	SER
23	3	899	THR
23	3	909	VAL
23	3	913	LEU
23	3	915	LEU
23	3	920	VAL
23	3	931	VAL
23	3	940	LEU
23	3	943	THR
23	3	948	VAL
23	3	959	VAL
23	3	961	ILE
23	3	963	VAL
23	3	976	LYS
23	3	980	LYS
23	3	984	LYS
23	3	990	ILE
23	3	991	SER
23	3	993	ILE
23	3	994	GLN
23	3	995	THR
23	3	1005	VAL
23	3	1008	SER
23	3	1010	ILE
23	3	1012	VAL
23	3	1022	ILE
23	3	1023	ILE
23	3	1028	THR
23	3	1033	VAL
23	3	1038	LEU
23	3	1040	ASP
23	3	1049	LYS
23	3	1052	ASN
23	3	1053	ILE
23	3	1057	ARG
23	3	1058	LEU
23	3	1081	LEU
23	3	1082	LEU
23	3	1087	GLN

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Mol	Chain	Res	Type
23	3	1088	LYS
23	3	1099	GLU
23	3	1104	LEU
23	3	1105	GLN
23	3	1115	GLU
23	3	1120	THR
23	3	1121	THR
23	3	1128	ILE
23	3	1130	VAL
23	3	1134	SER
23	3	1135	HIS
23	3	1138	HIS
23	3	1145	GLU
23	3	1148	LEU
23	3	1155	LEU
23	3	1162	SER
23	3	1168	PHE
23	3	1181	GLN
23	3	1185	MET
23	3	1195	GLU
23	3	1197	LEU
23	3	1203	GLU
23	3	1214	ARG
33	w	381	LYS
33	w	383	LEU
33	w	385	LEU
33	w	390	LYS
33	w	396	LEU
33	w	459	TRP
33	w	463	LYS
33	w	469	GLU
33	w	471	TRP
33	w	472	GLN
33	w	477	GLU
33	w	478	GLU
33	w	485	ASN
33	w	487	VAL
33	w	488	ASN
33	w	489	LYS
33	w	491	THR
33	w	497	ARG
33	w	500	LEU

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Mol	Chain	Res	Type
35	2	451	LYS
35	2	453	LYS
35	2	454	LEU
35	2	455	ARG
35	2	457	MET
35	2	467	GLN
35	2	473	ASP
35	2	474	VAL
35	2	486	LYS
35	2	488	LEU
35	2	495	ARG
35	2	497	SER
35	2	507	LYS
35	2	508	ARG
35	2	514	LYS
35	2	515	ARG
35	2	517	ILE
35	2	525	PRO
35	2	528	ILE
35	2	533	ILE
35	2	534	GLN
35	2	535	GLU
35	2	536	MET
35	2	537	ARG
35	2	538	GLU
35	2	541	GLN
35	2	542	GLU
35	2	545	GLU
35	2	566	ILE
35	2	570	LYS
35	2	578	TRP
35	2	579	GLN
35	2	581	LYS
35	2	584	LEU
35	2	586	ILE
35	2	587	HIS
35	2	598	GLU
35	2	703	ILE
37	6	16	GLU
37	6	31	THR
37	6	37	ASP
37	6	53	THR

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Mol	Chain	Res	Type
37	6	77	LEU
37	6	78	SER
37	6	88	VAL
37	6	89	VAL
37	6	103	THR
37	6	105	LYS
37	6	107	GLU
37	6	110	LEU
38	7	7	ASP
38	7	30	CYS
38	7	32	ILE
38	7	33	CYS
38	7	35	SER
38	7	37	VAL
38	7	46	CYS
38	7	50	ASN
38	7	54	TYR
38	7	60	ILE
38	7	61	CYS
38	7	72	CYS
38	7	77	ILE
38	7	78	GLN
38	7	88	ILE
39	5	9	SER
39	5	12	GLU
39	5	14	LEU
39	5	27	THR
39	5	33	VAL
39	5	39	SER
39	5	44	MET
39	5	64	VAL
39	5	69	MET
40	9	197	LEU
40	9	200	THR
40	9	221	LEU
40	9	224	THR
40	9	241	TYR
40	9	249	SER
40	9	252	SER
40	9	253	THR
40	9	256	VAL
40	9	260	THR

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Mol	Chain	Res	Type
40	9	261	HIS
40	9	266	ILE
40	9	268	GLU
40	9	283	ARG
40	9	298	ASP
40	9	320	ILE
40	9	336	THR
40	9	346	TRP
40	9	354	PHE
40	9	367	SER
40	9	396	ILE
40	9	397	PHE
40	9	400	VAL
40	9	401	VAL
40	9	420	ASP
40	9	453	LEU
41	8	18	SER
41	8	39	ASP
41	8	44	ASN
41	8	48	ILE
41	8	77	VAL
41	8	82	SER
41	8	90	THR
41	8	105	LEU
43	v	19	SER
43	v	22	SER
43	v	24	ARG
43	v	27	ARG
43	v	29	ARG
43	v	32	GLN
43	v	33	LEU
43	v	35	LEU
43	v	37	THR
43	v	38	ILE
43	v	40	ILE
43	v	42	LYS
43	v	79	GLN
43	v	82	LEU
43	v	85	ARG
43	v	88	LYS
43	v	91	LYS
43	v	92	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (147) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	112	GLN
1	A	210	HIS
1	A	221	ASN
1	A	321	ASN
1	A	326	HIS
1	A	328	HIS
1	A	357	ASN
1	A	363	HIS
1	A	400	ASN
1	A	429	ASN
1	A	467	GLN
1	A	499	GLN
1	A	505	ASN
1	A	514	ASN
1	A	517	HIS
1	A	521	ASN
1	A	568	ASN
1	A	584	HIS
1	A	675	GLN
1	A	755	HIS
1	A	775	ASN
1	A	1003	HIS
1	A	1023	ASN
1	A	1096	HIS
1	A	1117	HIS
1	A	1124	ASN
1	A	1188	ASN
1	A	1209	HIS
1	A	1215	ASN
1	A	1367	ASN
1	A	1373	GLN
1	A	1424	GLN
1	A	1460	HIS
1	A	1527	ASN
1	A	1563	HIS
1	A	1575	GLN
1	A	1665	GLN
1	A	1717	ASN
3	C	137	HIS
3	C	139	HIS

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Mol	Chain	Res	Type
3	C	154	HIS
3	C	208	HIS
3	C	258	ASN
3	C	335	ASN
3	C	436	GLN
3	C	571	ASN
3	C	627	HIS
3	C	798	GLN
3	C	807	GLN
5	E	150	HIS
5	E	165	GLN
5	E	224	GLN
5	E	287	ASN
5	E	331	ASN
10	J	297	ASN
10	J	331	GLN
10	J	389	HIS
11	K	44	HIS
11	K	62	GLN
11	K	92	ASN
11	K	111	GLN
12	L	29	ASN
12	L	30	GLN
15	P	212	ASN
17	R	157	GLN
17	R	279	HIS
17	R	283	ASN
17	R	414	GLN
18	T	283	HIS
18	T	394	ASN
18	T	407	GLN
18	T	408	ASN
18	T	413	ASN
18	T	446	ASN
19	X	278	GLN
19	X	335	ASN
20	Y	58	GLN
20	Y	64	ASN
20	Y	114	ASN
22	1	160	HIS
22	1	171	GLN
22	1	492	GLN

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Mol	Chain	Res	Type
22	1	533	ASN
22	1	534	GLN
22	1	692	HIS
22	1	832	GLN
22	1	842	ASN
22	1	878	ASN
22	1	942	ASN
22	1	1007	HIS
22	1	1184	HIS
22	1	1210	HIS
22	1	1293	ASN
23	3	5	ASN
23	3	9	GLN
23	3	19	HIS
23	3	103	HIS
23	3	164	ASN
23	3	169	HIS
23	3	203	ASN
23	3	205	GLN
23	3	206	GLN
23	3	219	HIS
23	3	231	HIS
23	3	264	GLN
23	3	304	GLN
23	3	411	GLN
23	3	440	HIS
23	3	465	HIS
23	3	612	ASN
23	3	666	ASN
23	3	730	HIS
23	3	775	ASN
23	3	776	GLN
23	3	791	HIS
23	3	796	ASN
23	3	817	GLN
23	3	861	GLN
23	3	870	ASN
23	3	933	ASN
23	3	985	HIS
23	3	988	ASN
23	3	1083	ASN
23	3	1096	HIS

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Mol	Chain	Res	Type
23	3	1192	ASN
33	w	433	HIS
33	w	485	ASN
33	w	488	ASN
35	2	458	ASN
35	2	478	HIS
35	2	483	GLN
35	2	534	GLN
35	2	572	HIS
35	2	587	HIS
37	6	52	ASN
38	7	14	GLN
39	5	67	ASN
40	9	199	ASN
40	9	379	GLN
40	9	452	GLN
41	8	21	GLN
41	8	27	GLN
41	8	97	ASN
43	v	32	GLN
43	v	65	ASN
43	v	81	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	96/117 (82%)	37 (38%)	3 (3%)
6	F	94/107 (87%)	51 (54%)	8 (8%)
7	G	62/220 (28%)	40 (64%)	10 (16%)
8	H	161/188 (85%)	59 (36%)	4 (2%)
All	All	413/632 (65%)	187 (45%)	25 (6%)

All (187) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
2	B	25	C
2	B	28	A
2	B	32	C
2	B	33	U
2	B	35	U
2	B	38	C
2	B	39	C
2	B	40	U
2	B	43	U
2	B	45	C
2	B	47	A
2	B	48	A
2	B	50	G
2	B	57	G
2	B	62	G
2	B	65	G
2	B	71	C
2	B	85	C
2	B	86	C
2	B	87	A
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	98	G
2	B	117	A
6	F	5	U
6	F	6	C
6	F	7	G
6	F	9	U
6	F	10	U
6	F	12	G
6	F	16	G
6	F	19	C
6	F	25	C
6	F	26	U
6	F	27	A

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Mol	Chain	Res	Type
6	F	28	A
6	F	29	A
6	F	31	U
6	F	32	U
6	F	33	G
6	F	34	G
6	F	36	A
6	F	37	C
6	F	38	G
6	F	40	U
6	F	41	A
6	F	42	C
6	F	43	A
6	F	44	G
6	F	45	A
6	F	46	G
6	F	47	A
6	F	48	A
6	F	49	G
6	F	50	A
6	F	51	U
6	F	53	A
6	F	54	G
6	F	58	G
6	F	59	G
6	F	60	C
6	F	62	C
6	F	69	A
6	F	73	A
6	F	74	U
6	F	76	A
6	F	77	C
6	F	78	A
6	F	79	C
6	F	80	G
6	F	81	C
6	F	83	A
6	F	85	U
6	F	86	U
6	F	92	A
7	G	-7	U
7	G	-6	C

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Mol	Chain	Res	Type
7	G	-5	C
7	G	-4	G
7	G	-3	A
7	G	-1	C
7	G	1	G
7	G	2	U
7	G	3	A
7	G	4	A
7	G	5	G
7	G	7	G
7	G	12	G
7	G	13	C
7	G	17	U
7	G	18	A
7	G	20	A
7	G	84	U
7	G	85	G
7	G	88	G
7	G	89	U
7	G	90	C
7	G	97	A
7	G	98	U
7	G	99	C
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	107	U
7	G	109	U
7	G	110	U
7	G	111	U
7	G	112	U
7	G	114	U
7	G	115	C
7	G	116	C
8	H	13	C
8	H	15	U
8	H	18	U
8	H	19	G

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Mol	Chain	Res	Type
8	H	22	U
8	H	23	A
8	H	24	A
8	H	27	U
8	H	28	C
8	H	29	A
8	H	30	A
8	H	31	G
8	H	36	G
8	H	37	U
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	54	U
8	H	61	C
8	H	63	G
8	H	64	A
8	H	65	U
8	H	83	A
8	H	84	C
8	H	98	G
8	H	100	U
8	H	101	U
8	H	103	U
8	H	104	U
8	H	111	G
8	H	116	A
8	H	117	U
8	H	118	G
8	H	121	A
8	H	122	U
8	H	123	A
8	H	124	G
8	H	125	G
8	H	128	C
8	H	129	U
8	H	130	U
8	H	136	G

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Mol	Chain	Res	Type
8	H	137	U
8	H	146	C
8	H	147	G
8	H	156	U
8	H	157	G
8	H	162	U
8	H	164	C
8	H	166	G
8	H	168	A
8	H	169	C
8	H	177	A
8	H	178	A
8	H	179	C

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	27	U
2	B	39	C
2	B	94	U
6	F	5	U
6	F	28	A
6	F	37	C
6	F	45	A
6	F	50	A
6	F	59	G
6	F	77	C
6	F	79	C
7	G	12	G
7	G	16	G
7	G	83	A
7	G	84	U
7	G	88	G
7	G	89	U
7	G	101	U
7	G	104	C
7	G	106	C
7	G	108	U
8	H	29	A
8	H	45	C
8	H	46	U
8	H	47	U

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	$\# Z > 2$
22	SEP	1	129	22	8,9,10	1.17	0	7,12,14	1.54	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
22	SEP	1	129	22	-	1/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	1	129	SEP	OG-CB-CA	-3.43	104.81	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	1	129	SEP	CB-OG-P-O2P

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	1	129	SEP	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
45	GTP	C	1500	46	33,34,34	0.98	2 (6%)	50,54,54	1.56	10 (20%)

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	-	10/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	C	1500	GTP	C2-N3	2.24	1.38	1.33
45	C	1500	GTP	PA-O3A	2.12	1.61	1.59

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C	1500	GTP	C5-C4-N3	-4.55	121.14	128.39
45	C	1500	GTP	C2-N3-C4	4.38	119.85	112.30
45	C	1500	GTP	N9-C4-N3	3.12	132.19	125.95
45	C	1500	GTP	N9-C8-N7	-2.90	108.03	113.40
45	C	1500	GTP	C2-N1-C6	-2.69	120.24	125.11
45	C	1500	GTP	O2A-PA-O3A	2.65	114.44	107.27
45	C	1500	GTP	C8-N7-C5	2.58	108.86	104.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C	1500	GTP	C5-C6-N1	2.42	119.40	113.25
45	C	1500	GTP	O6-C6-C5	-2.40	120.20	126.53
45	C	1500	GTP	O2B-PB-O3B	2.01	112.71	107.27

There are no chirality outliers.

All (10) torsion outliers are listed below:

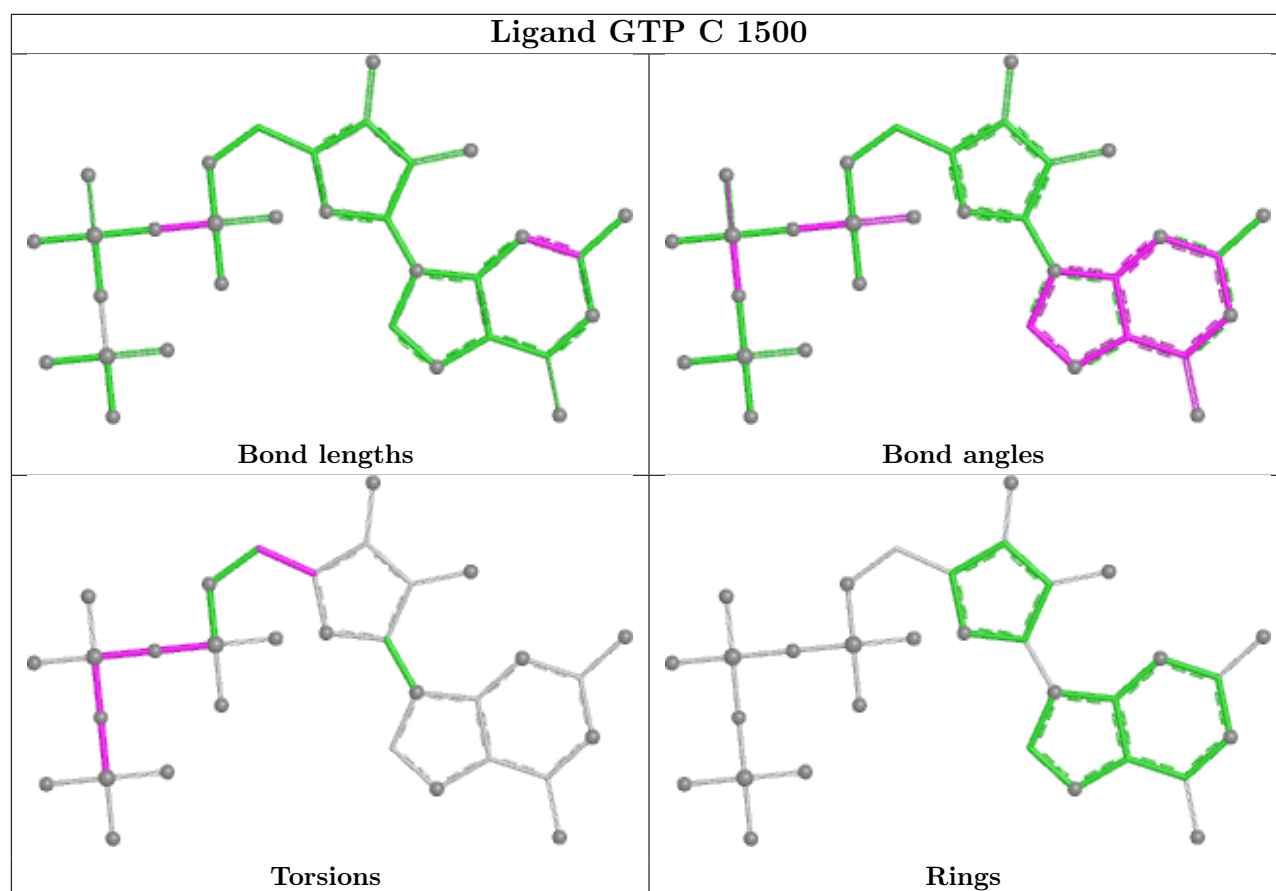
Mol	Chain	Res	Type	Atoms
45	C	1500	GTP	O4'-C4'-C5'-O5'
45	C	1500	GTP	C3'-C4'-C5'-O5'
45	C	1500	GTP	PB-O3B-PG-O1G
45	C	1500	GTP	PG-O3B-PB-O2B
45	C	1500	GTP	PA-O3A-PB-O2B
45	C	1500	GTP	PB-O3B-PG-O2G
45	C	1500	GTP	PB-O3B-PG-O3G
45	C	1500	GTP	PG-O3B-PB-O1B
45	C	1500	GTP	PB-O3A-PA-O2A
45	C	1500	GTP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 8 short contacts:

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

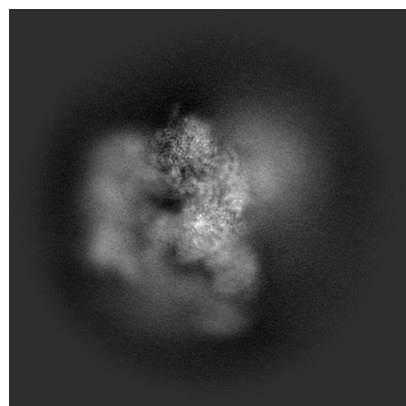
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35105. These allow visual inspection of the internal detail of the map and identification of artifacts.

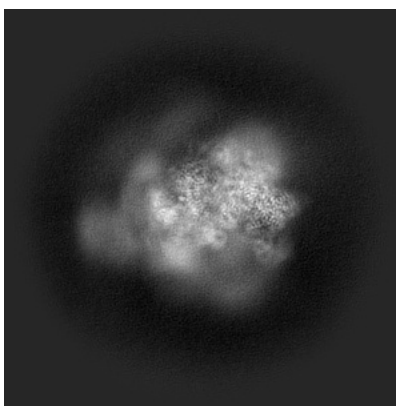
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

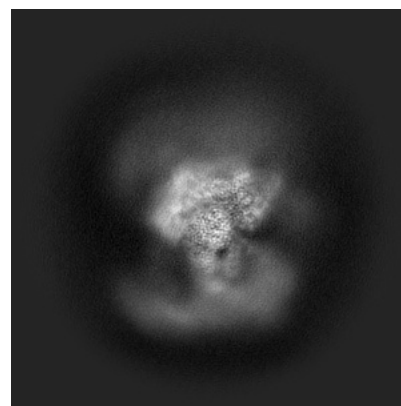
6.1.1 Primary map



X

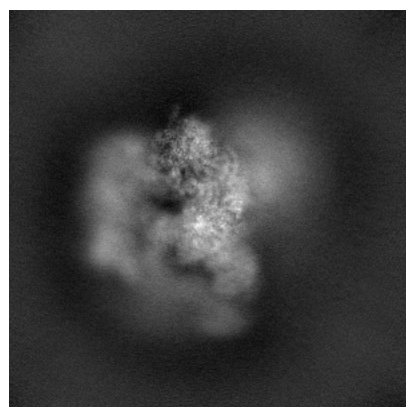


Y

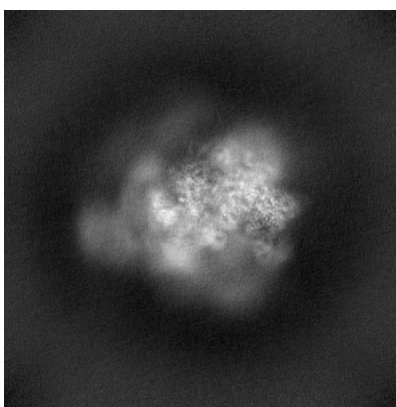


Z

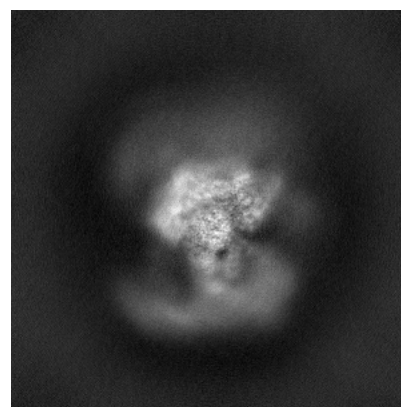
6.1.2 Raw map



X



Y

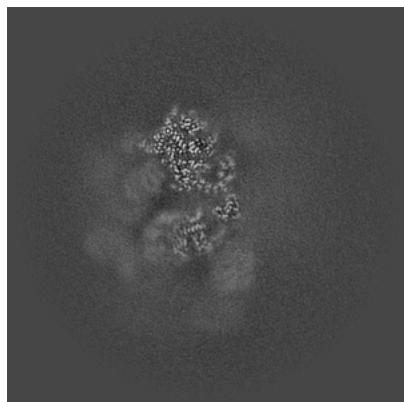


Z

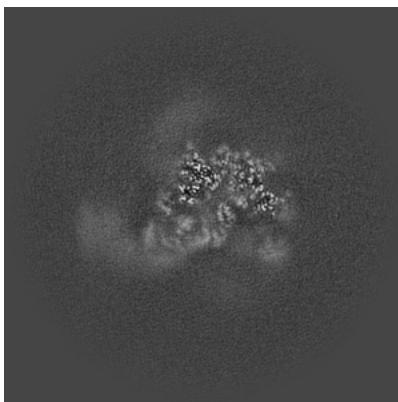
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

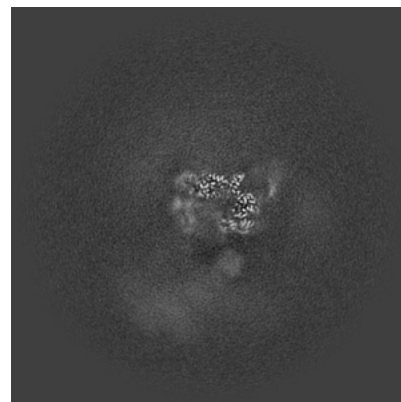
6.2.1 Primary map



X Index: 240

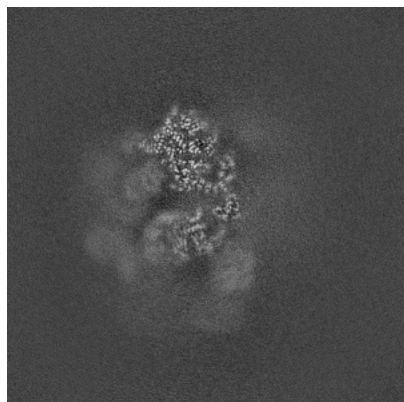


Y Index: 240

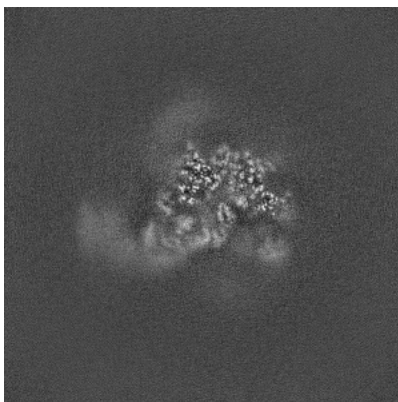


Z Index: 240

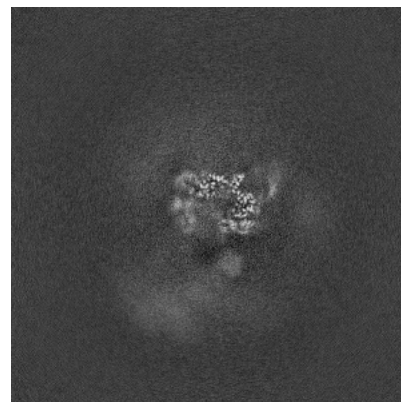
6.2.2 Raw map



X Index: 240



Y Index: 240

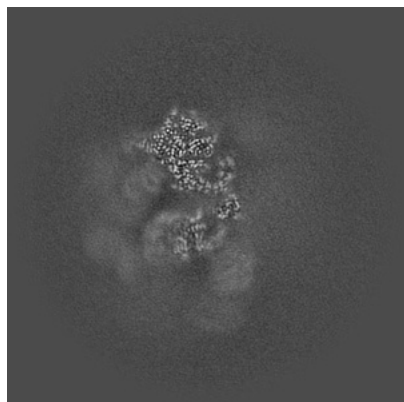


Z Index: 240

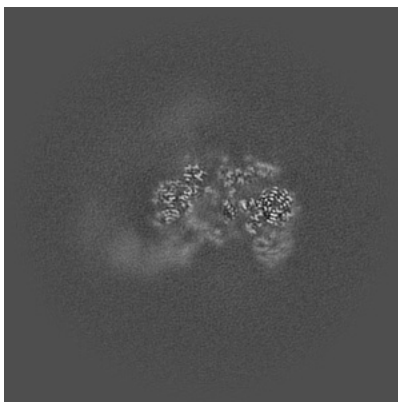
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

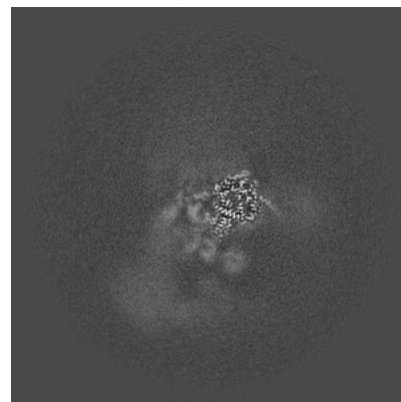
6.3.1 Primary map



X Index: 239

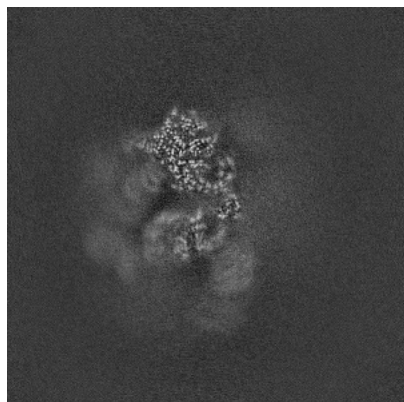


Y Index: 225

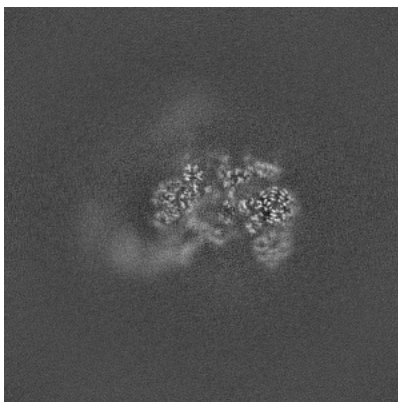


Z Index: 222

6.3.2 Raw map



X Index: 239



Y Index: 226

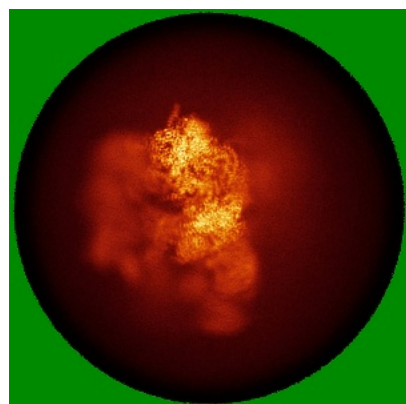


Z Index: 222

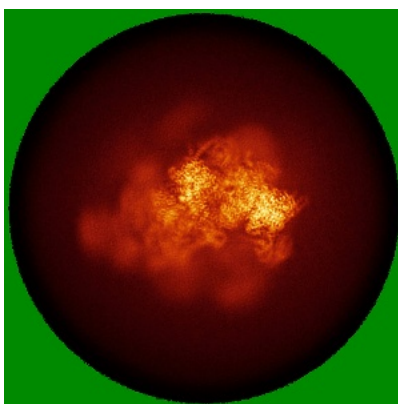
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

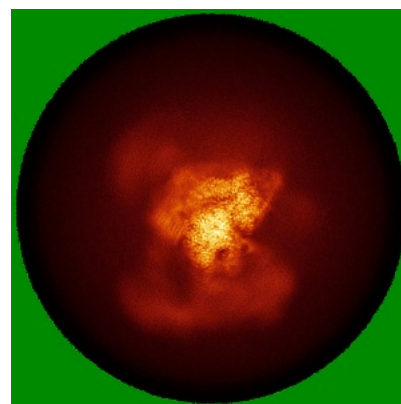
6.4.1 Primary map



X

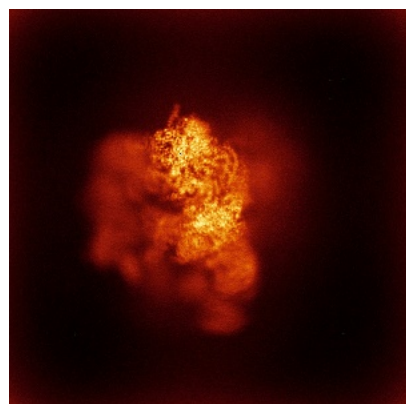


Y

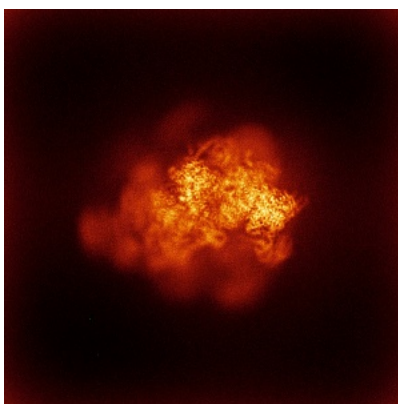


Z

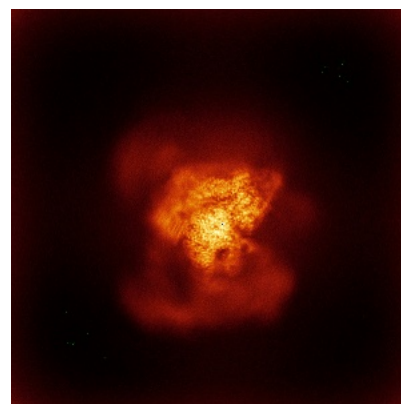
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



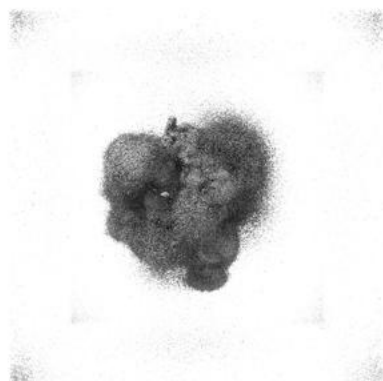
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.19. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

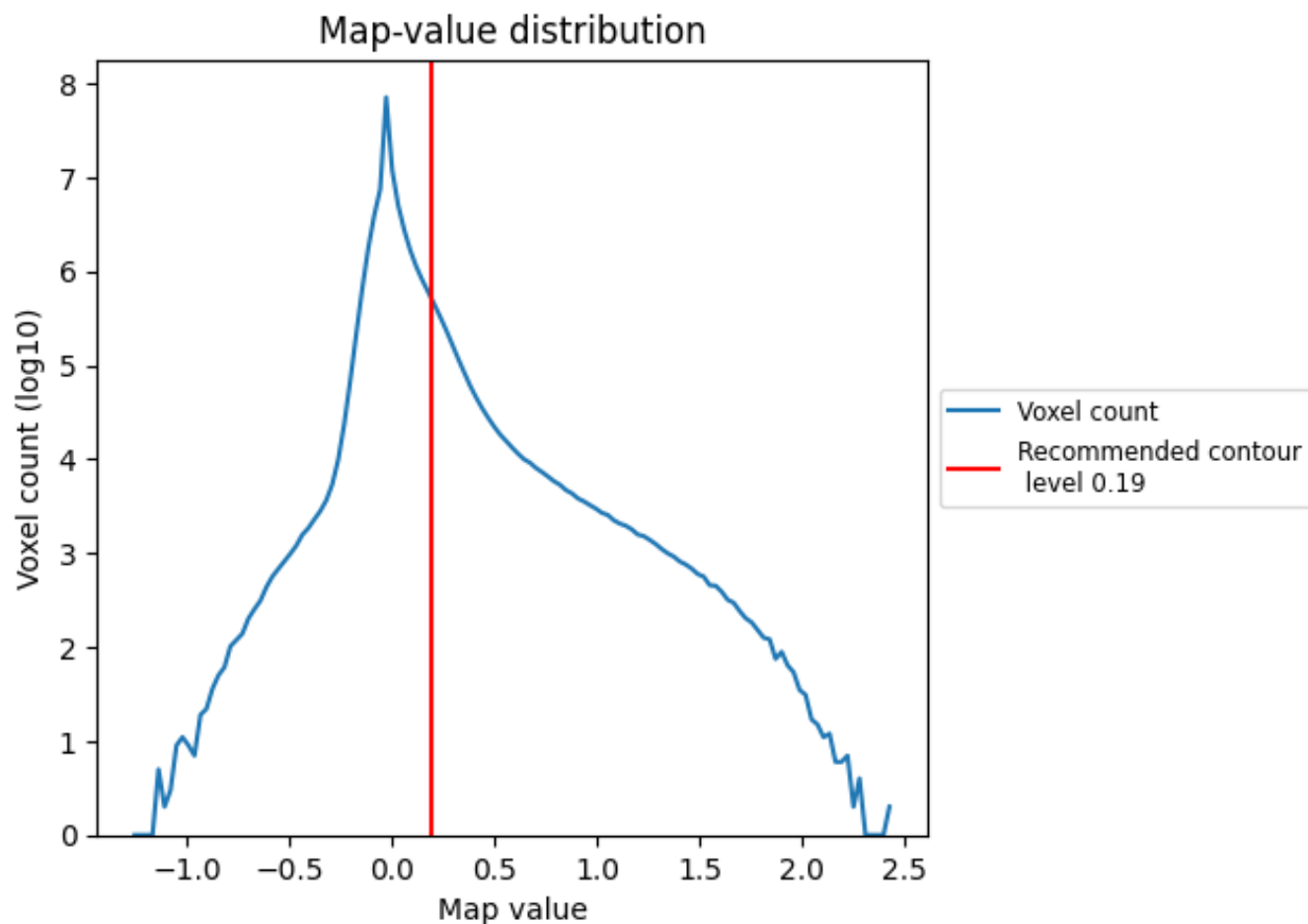
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

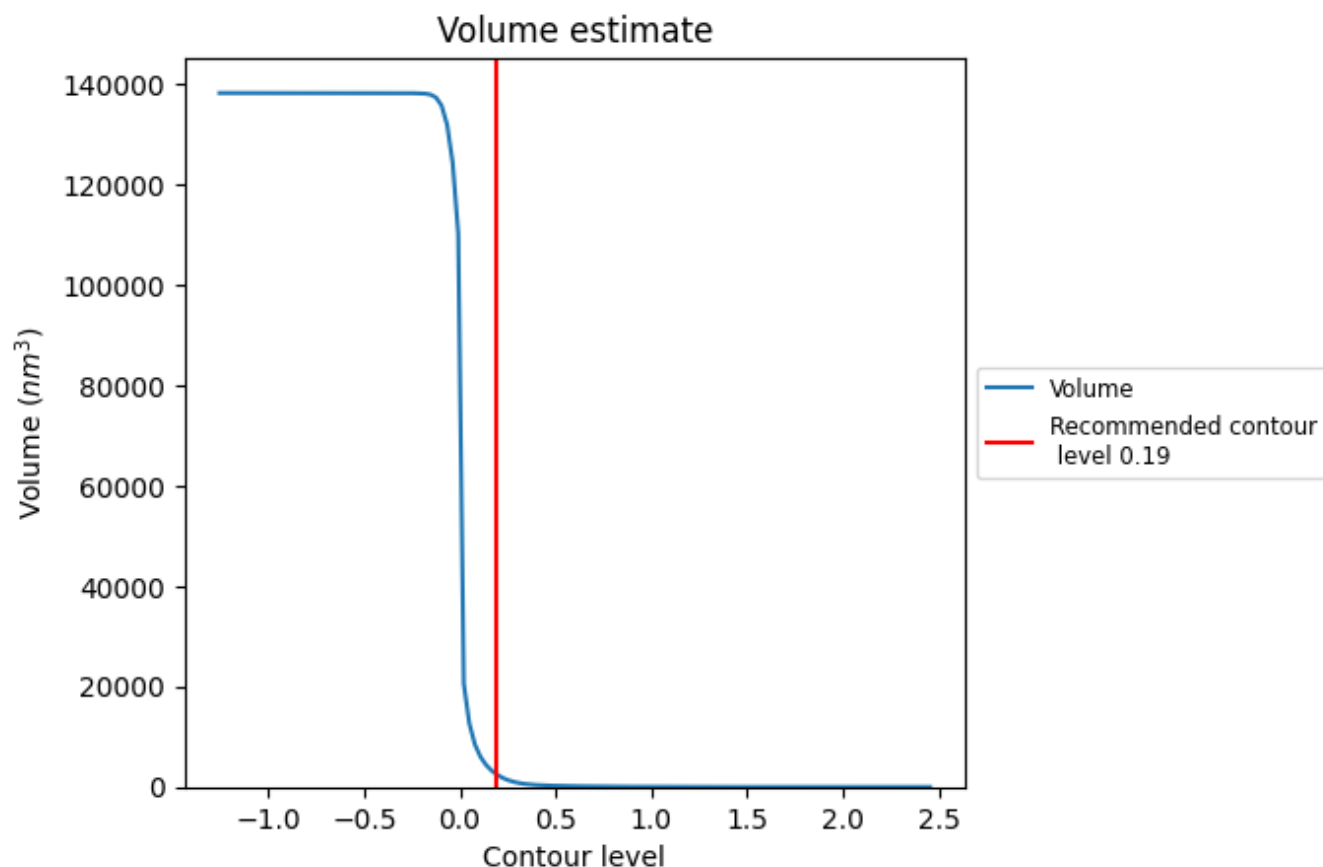
This section contains the results of statistical analysis of the map.

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.

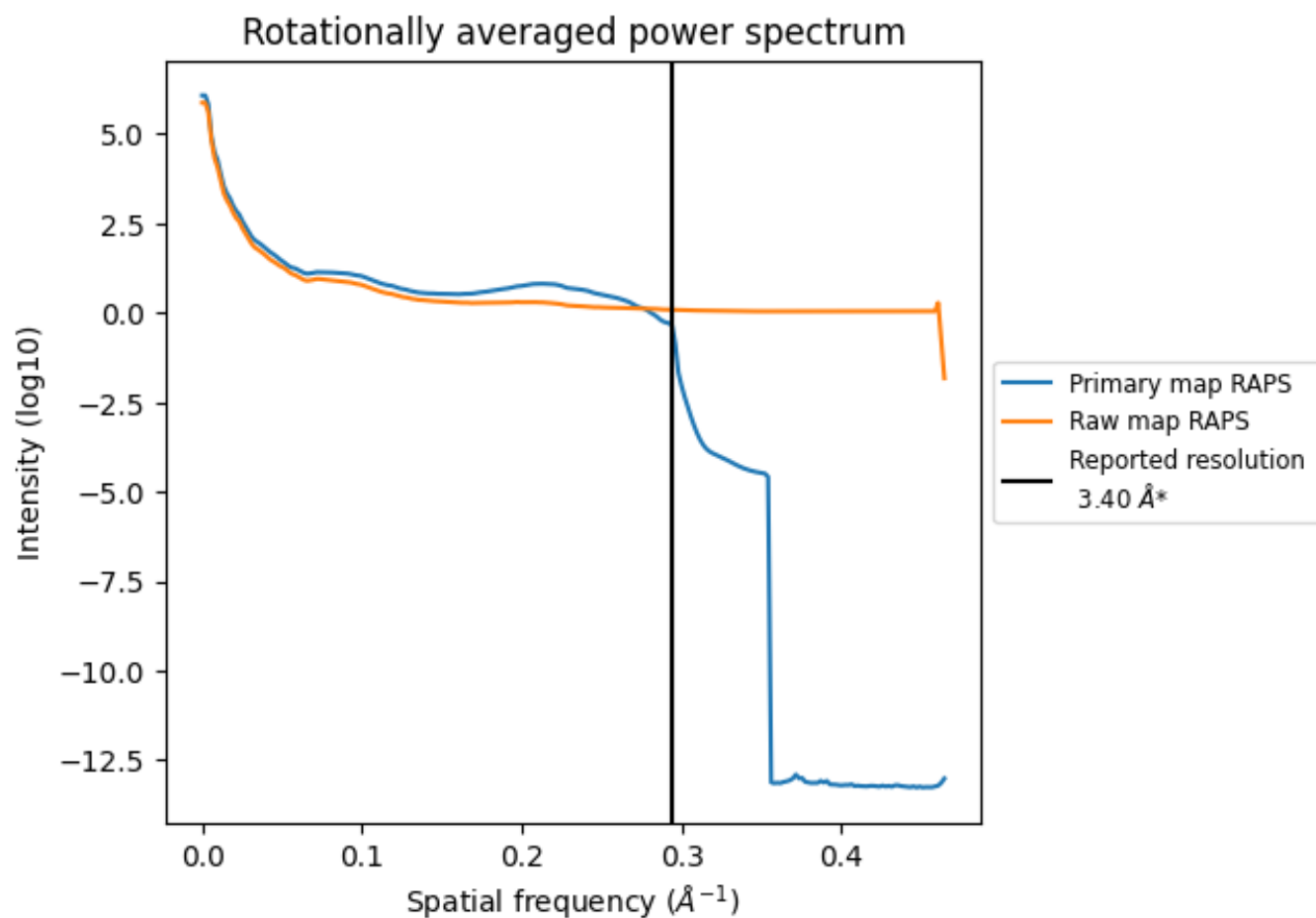
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2577 nm^3 ; this corresponds to an approximate mass of 2328 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

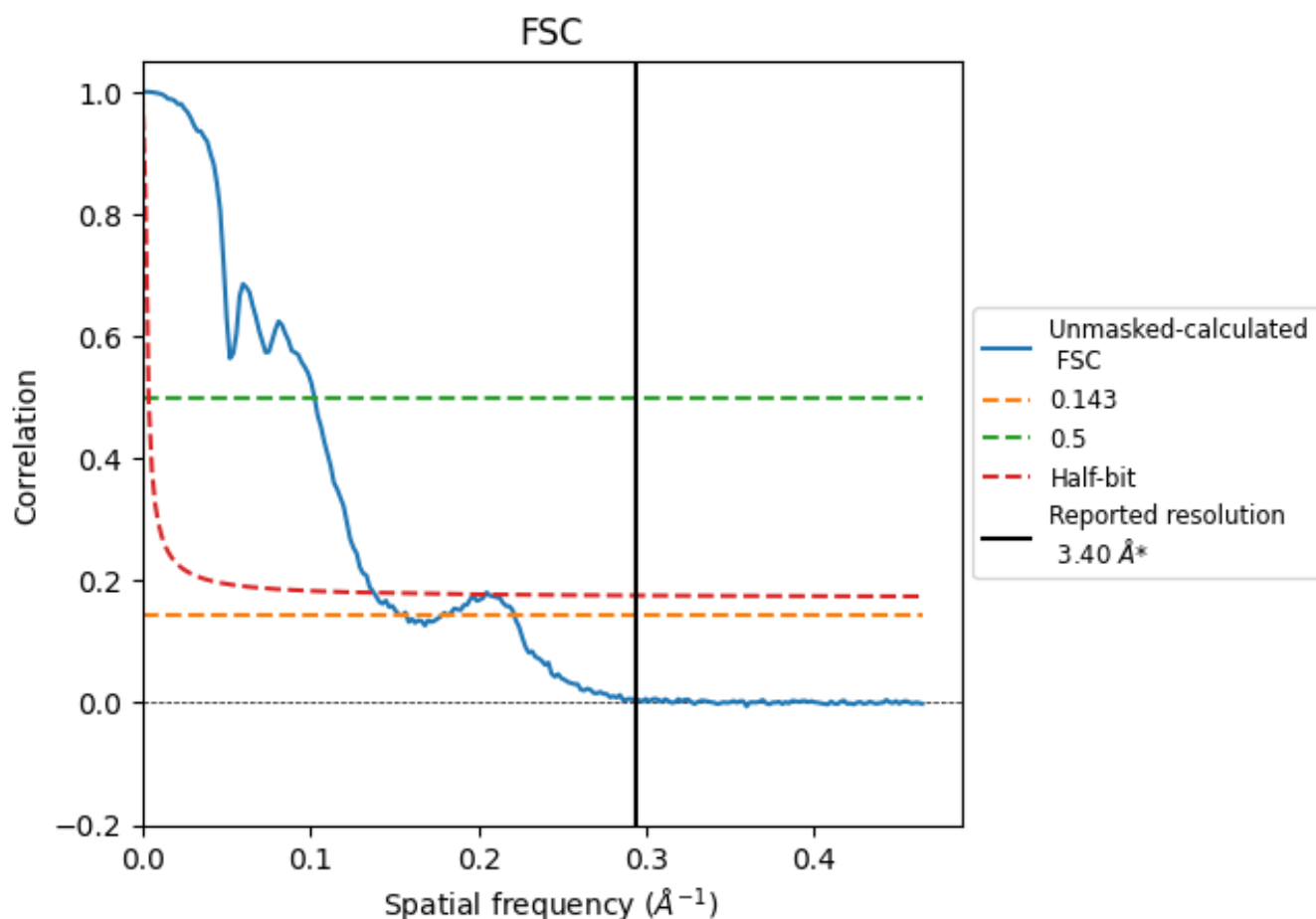


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

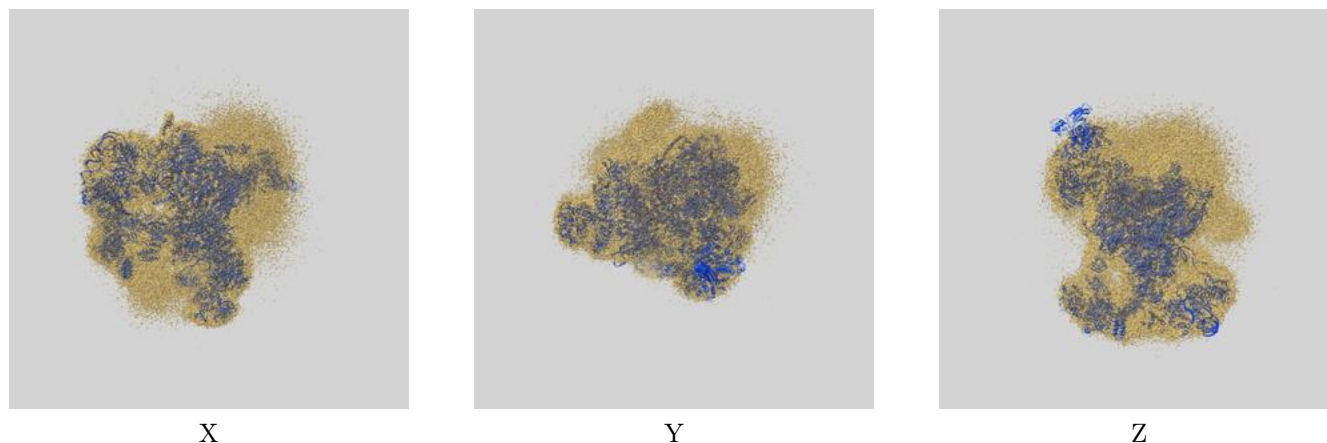
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.48	9.75	7.25

*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 6.48 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

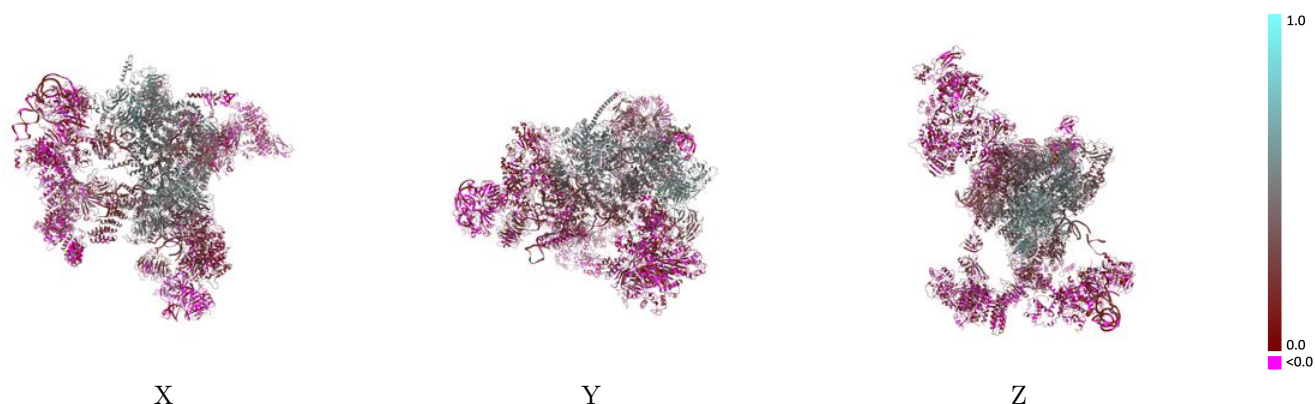
This section contains information regarding the fit between EMDB map EMD-35105 and PDB model 8I0P. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



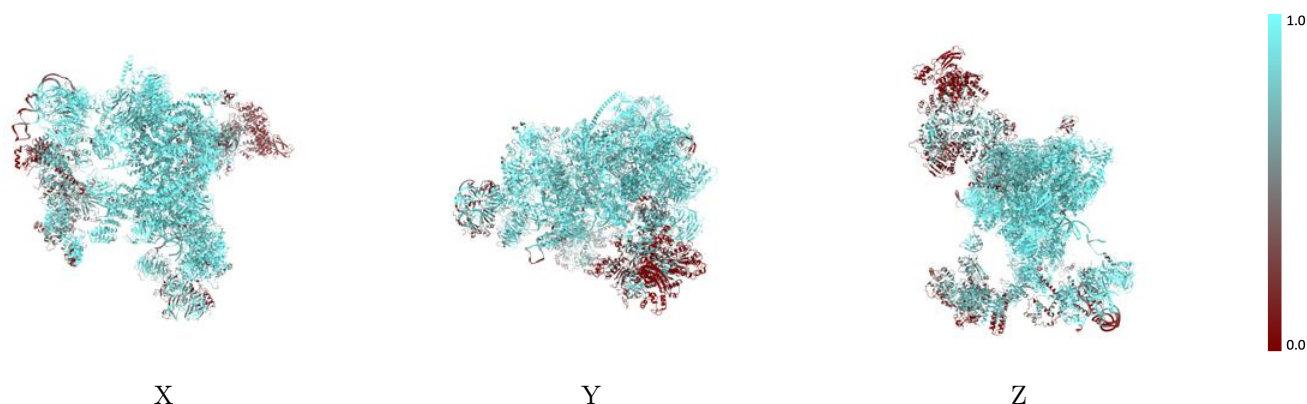
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



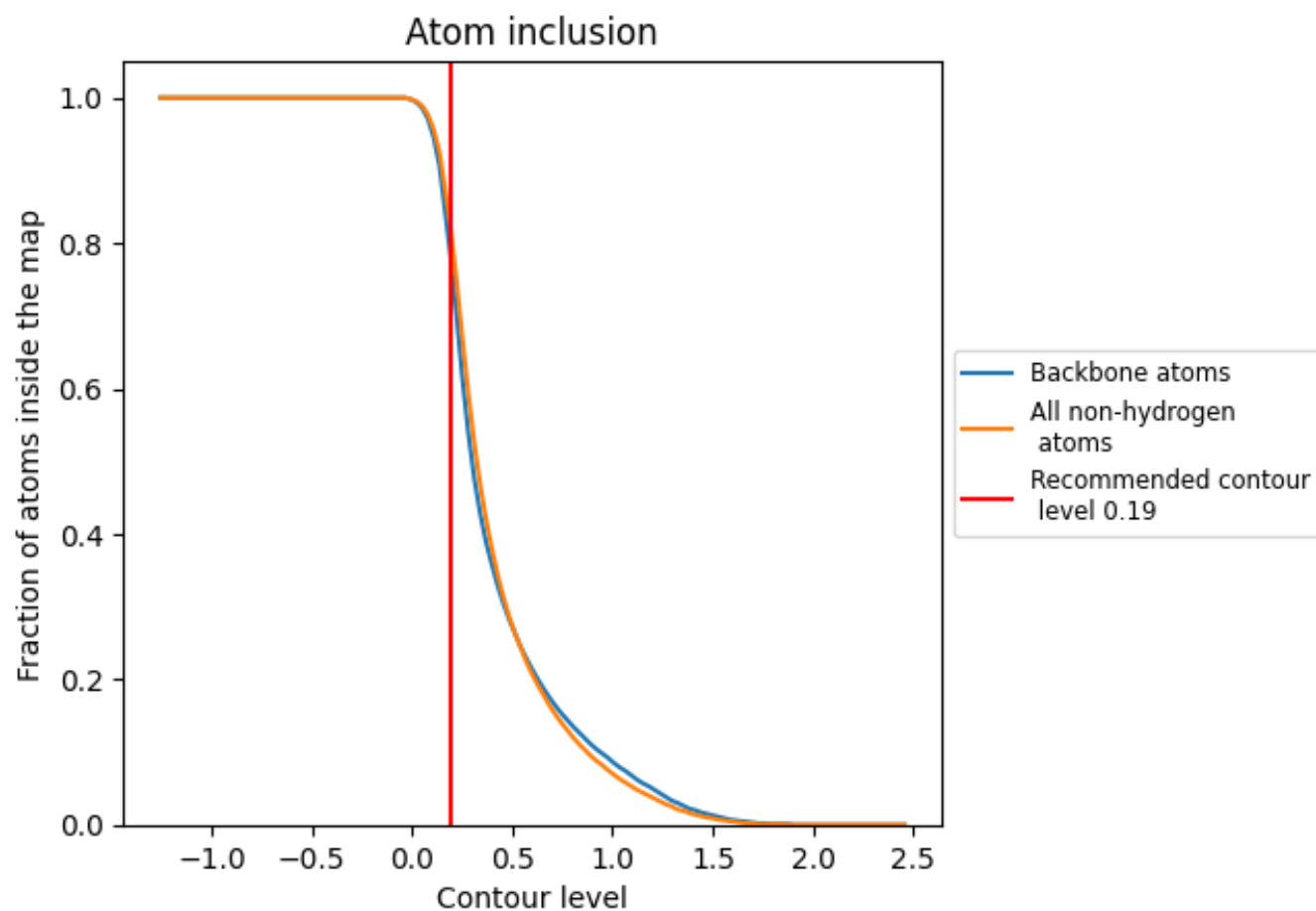
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.19).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 83% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.2870
1	 0.9710	 0.4690
2	 0.9300	 0.3980
3	 0.9870	 0.4850
4	 0.9420	 0.2370
5	 0.9340	 0.5140
6	 0.9910	 0.3740
7	 0.9520	 0.4660
8	 0.9720	 0.4140
9	 0.9100	 0.2660
A	 0.8960	 0.3530
B	 0.9040	 0.1640
C	 0.9010	 0.1980
D	 0.3650	 0.1400
E	 0.8420	 0.1810
F	 0.8960	 0.2350
G	 0.9640	 0.2930
H	 0.7850	 0.2110
I	 0.7100	 0.1150
J	 0.9590	 0.2620
K	 0.8650	 0.2550
L	 0.9840	 0.4810
N	 0.8340	 0.1620
O	 0.8730	 0.1820
P	 0.9520	 0.4780
Q	 0.5540	 0.1340
R	 0.9420	 0.4120
T	 0.9860	 0.4700
X	 0.9680	 0.3540
Y	 0.9680	 0.4810
Z	 0.9670	 0.4700
a	 0.6700	 0.0550
b	 0.5760	 0.0140
c	 0.6260	 0.0030
d	 0.6420	 0.0290



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Chain	Atom inclusion	Q-score
e	 0.6430	 0.0390
f	 0.5850	 0.0300
g	 0.6480	 -0.0220
h	 0.8420	 0.1220
i	 0.8660	 0.1030
j	 0.9280	 0.1720
k	 0.9340	 0.1280
l	 0.8940	 0.1710
m	 0.8860	 0.1450
n	 0.7760	 0.1740
o	 0.8330	 0.1390
p	 0.9010	 0.1850
u	 0.5620	 0.1590
v	 0.7330	 0.2950
w	 0.6850	 0.2220
y	 0.7640	 0.1920
z	 0.9760	 0.3290