



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 01:09 AM UTC

PDB ID : 3JCM / pdb_00003jcm
EMDB ID : EMD-6561
Title : Cryo-EM structure of the spliceosomal U4/U6.U5 tri-snRNP
Authors : Wan, R.; Yan, C.; Bai, R.; Wang, L.; Huang, M.; Wong, C.C.; Shi, Y.
Deposited on : 2015-12-23
Resolution : 3.80 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:

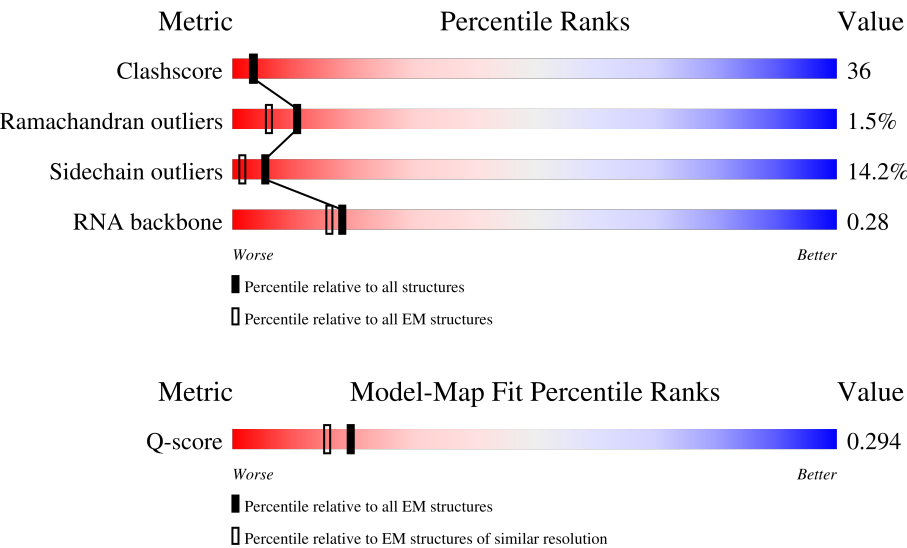
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 3.80 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.



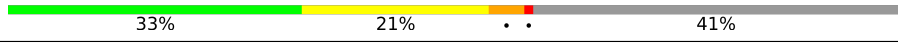
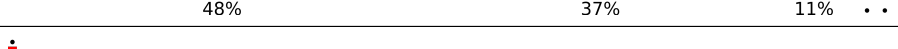
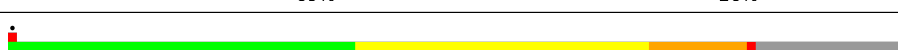
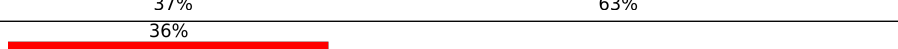
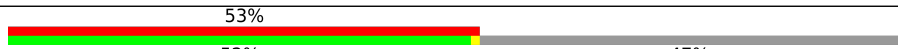
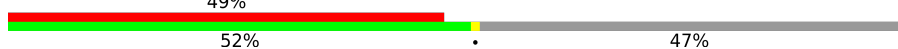
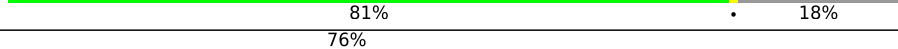
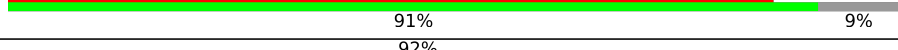
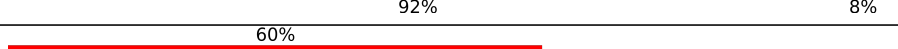
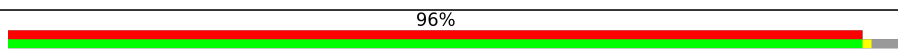
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9193 (3.31 - 4.31)

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

Mol	Chain	Length	Quality of chain
1	A	2413	11% 52% 30% 8% 10%
2	B	465	38% 43% 10% 8%
3	I	494	40% 33% 11% 16%

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Mol	Chain	Length	Quality of chain
4	G	899	
5	K	469	
6	L	143	
7	M	126	
8	H	1008	
9	N	2163	
10	J	101	
10	R	101	
11	O	196	
11	S	196	
12	P	146	
12	T	146	
13	Q	110	
13	U	110	
14	V	94	
14	Y	94	
15	W	86	
15	Z	86	
16	X	77	
16	a	77	
17	b	109	
18	c	95	
19	d	89	
20	e	86	
21	f	93	

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Mol	Chain	Length	Quality of chain
22	g	115	
23	h	187	
24	C	20	
25	D	112	
26	E	160	
27	F	214	

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
28	GTP	H	1500	-	-	X	-

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 58253 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2174	Total	C	N	O	S	0	0
			16889	10715	2978	3138	58		

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3378	2102	610	652	14		

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	416	Total	C	N	O	S	0	0
			3171	2001	573	585	12		

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	734	Total	C	N	O	S	0	0
			4927	3063	911	939	14		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	279	Total	C	N	O	S	0	0
			2328	1476	422	416	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	139	Total	C	N	O	S	0	0
			1146	725	199	211	11		

- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	1686	Total	C	N	O	0	0
			6744	3372	1686	1686		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	79	Total	C	N	O	0	0
			316	158	79	79		
10	J	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	S	73	Total	C	N	O	0	0
			292	146	73	73		
11	O	73	Total	C	N	O	0	0
			292	146	73	73		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	77	Total	C	N	O	0	0
			308	154	77	77		
12	P	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	90	Total	C	N	O	0	0
			360	180	90	90		
13	Q	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	72	Total	C	N	O	0	0
			288	144	72	72		
14	Y	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	70	Total	C	N	O	0	0
			280	140	70	70		
15	Z	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	X	70	Total	C	N	O	0	0
			280	140	70	70		
16	a	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	f	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	g	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 24 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	20	Total	C	N	O	P	0	0
			429	193	79	137	20		

- Molecule 25 is a RNA chain called SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	45	Total	C	N	O	P	0	0
			945	422	170	308	45		

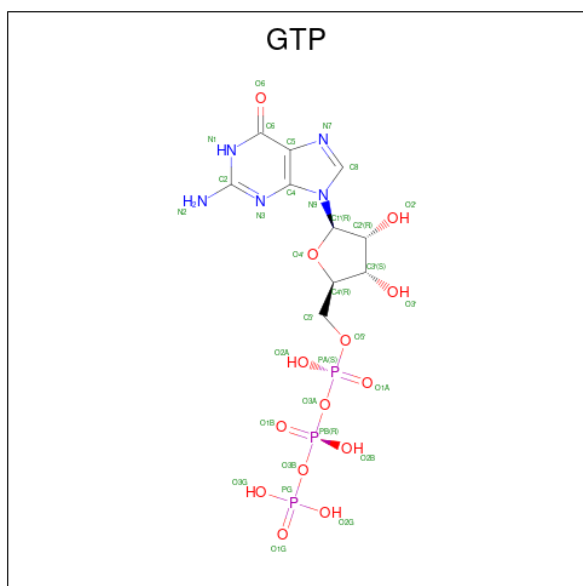
- Molecule 26 is a RNA chain called SNR14 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

- Molecule 27 is a RNA chain called SNR7-L snRNA.

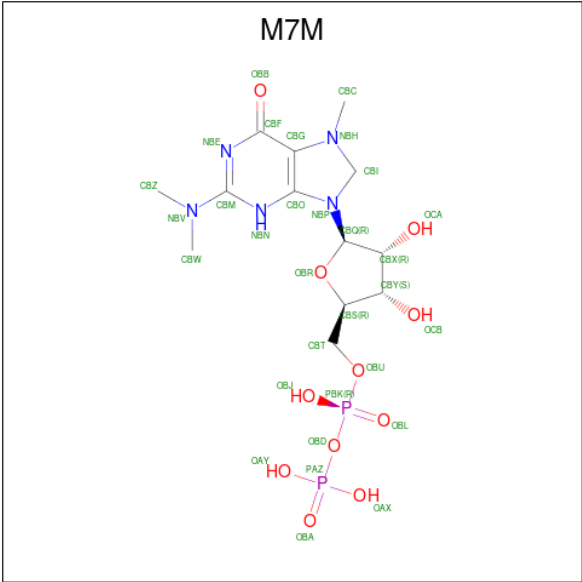
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



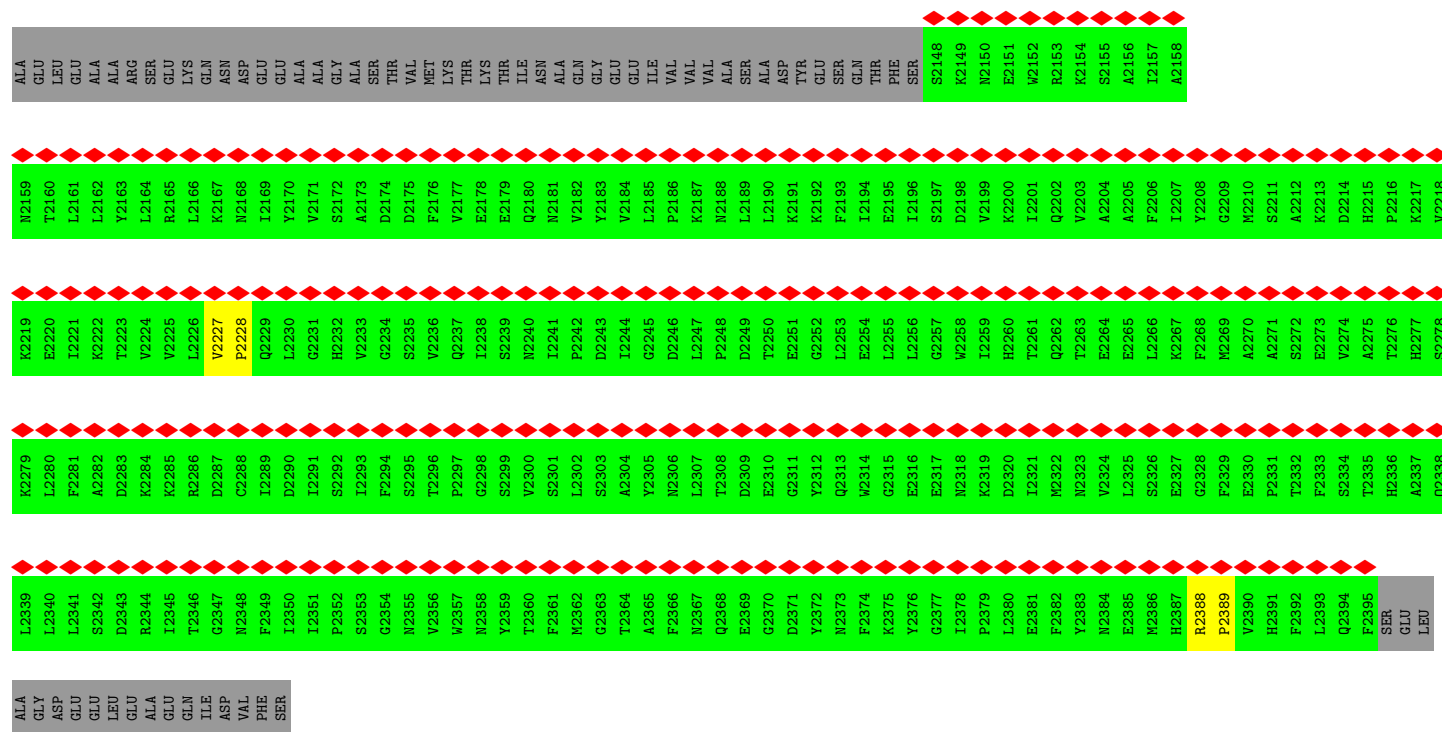
Mol	Chain	Residues	Atoms					AltConf
28	H	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 29 is N,N,7-trimethylguanosine 5'-(trihydrogen diphosphate) (CCD ID: M7M) (formula: $C_{13}H_{23}N_5O_{11}P_2$).



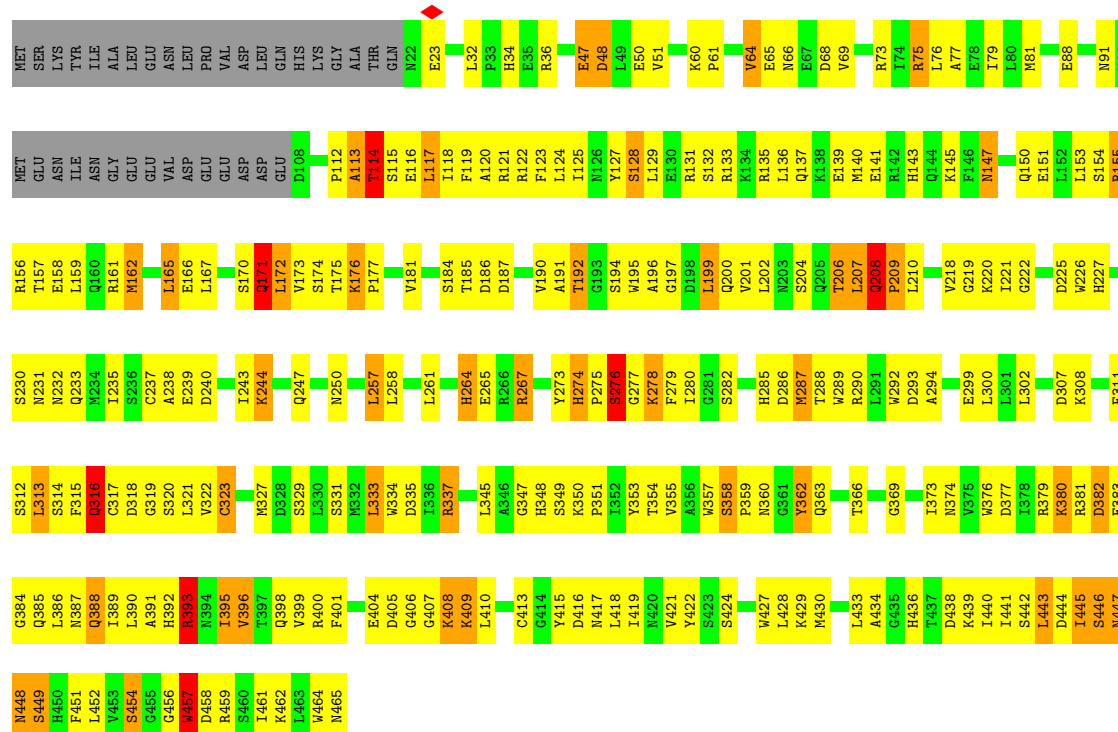
Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	





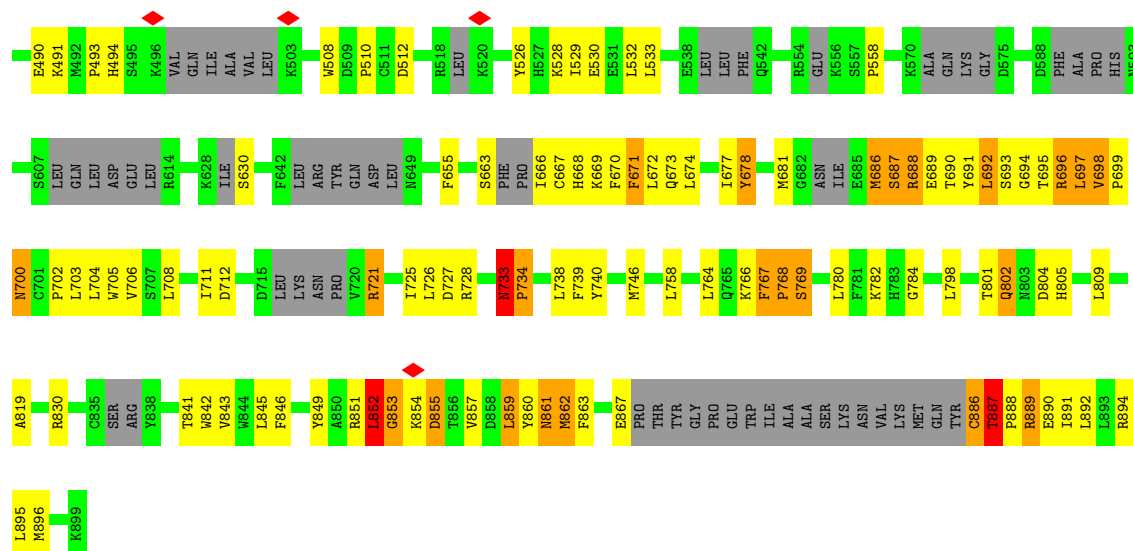
- Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

Chain B: 38% 43% 10% 8%

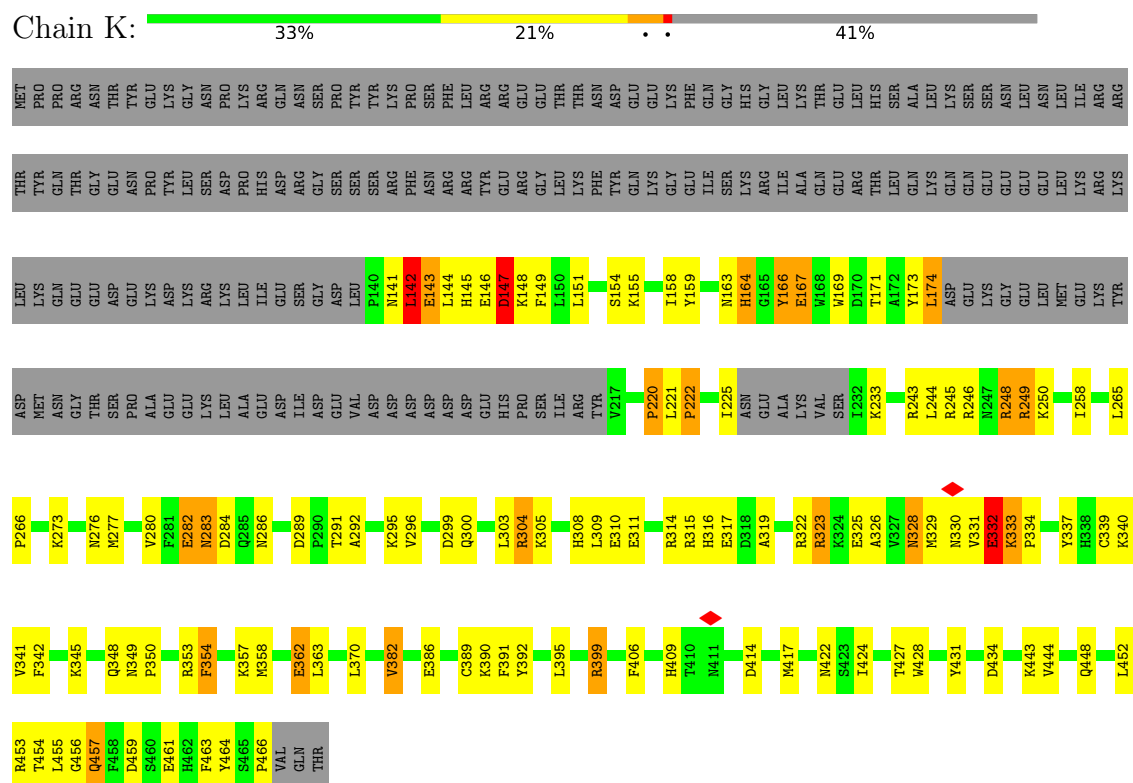


- Molecule 3: Pre-mRNA-processing factor 31

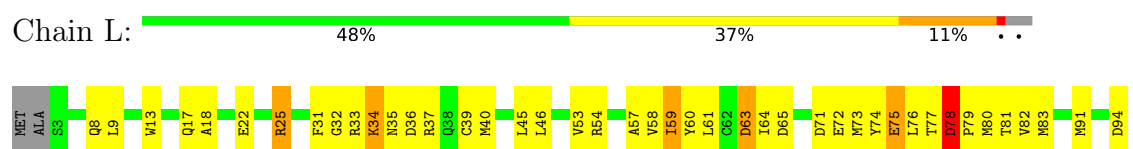




• Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3



• Molecule 6: Spliceosomal protein DIB1

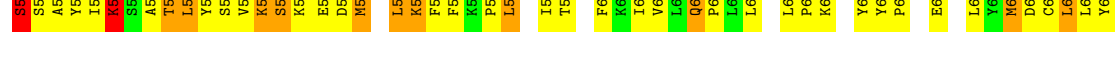
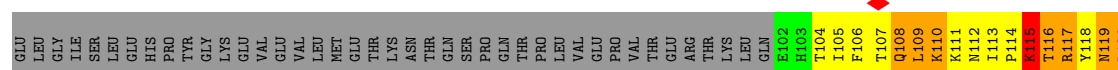


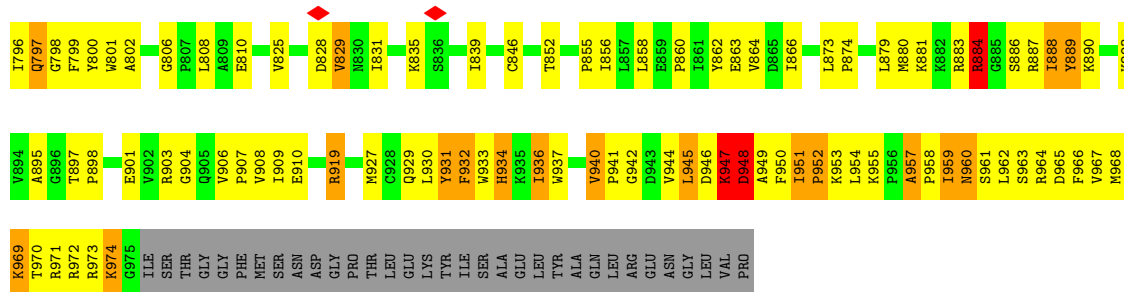


- Molecule 7: 13 kDa ribonucleoprotein-associated protein

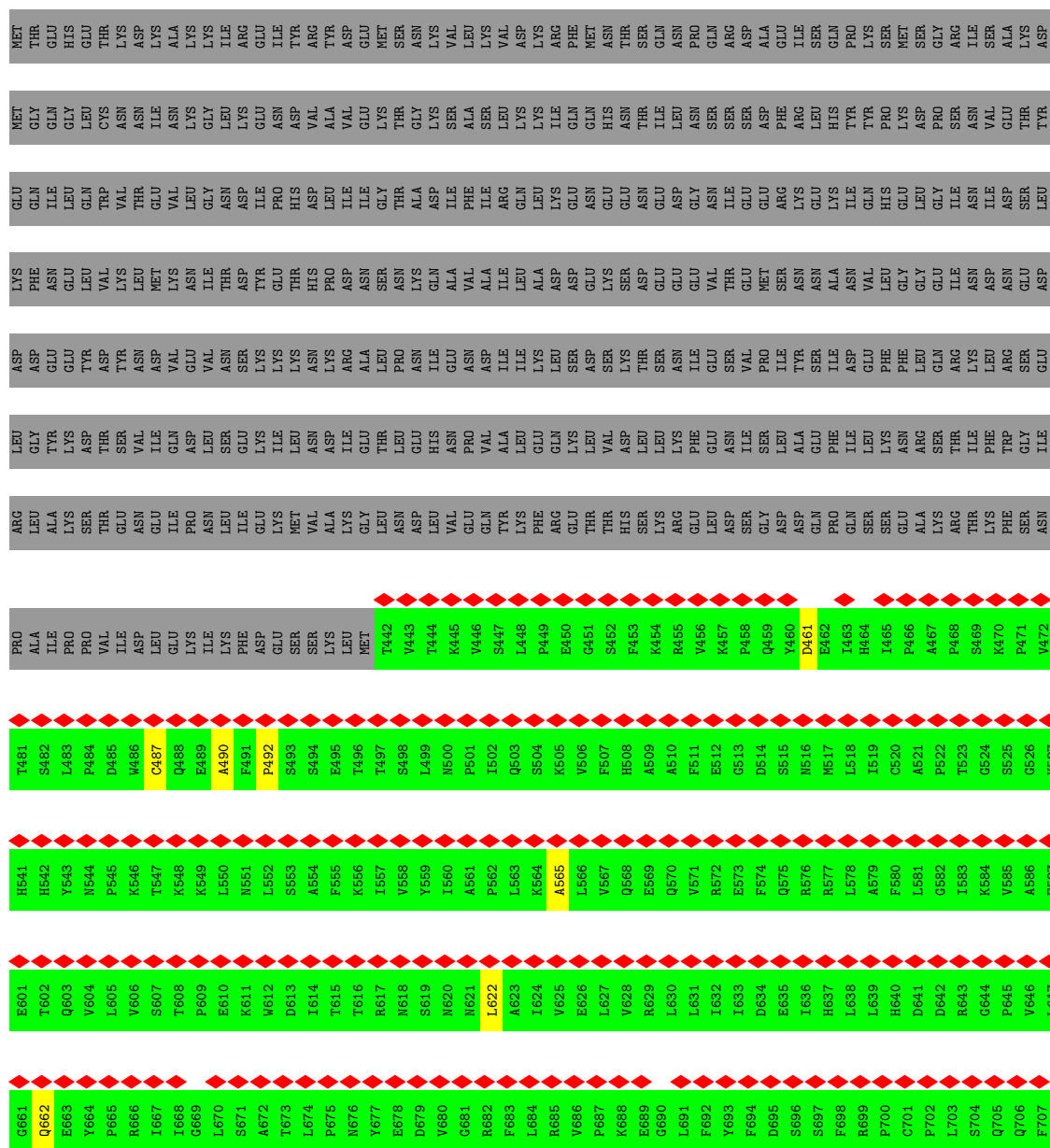
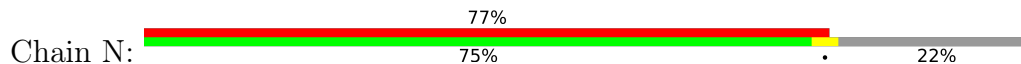


- Molecule 8: Pre-mRNA-splicing factor SNU114





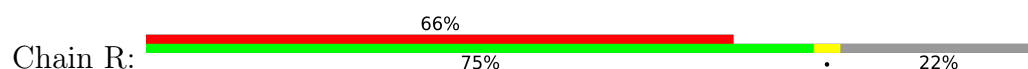
• Molecule 9: Pre-mRNA-splicing helicase BRR2

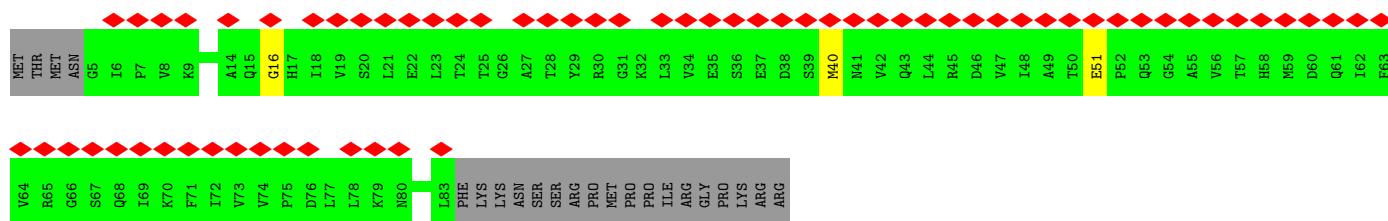




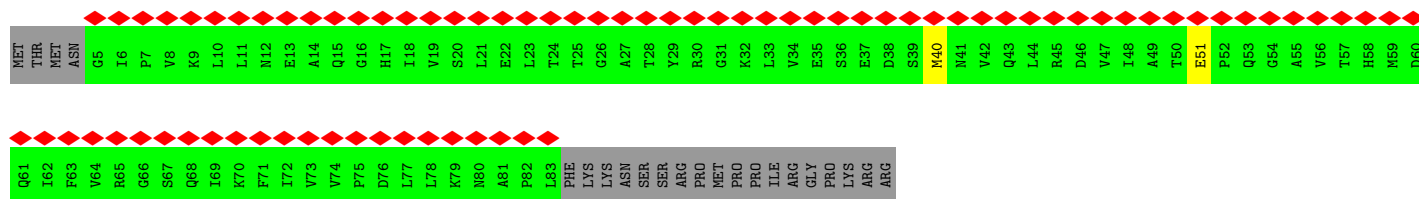
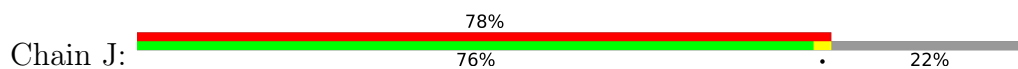
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K1504	L1564	L1624	G1684	S1744	S1804	Q1864	F1924	I1984	F2044	G2104
L1505	Q1565	T1625	T1685	Y1745	M1805	S1865	K1925	Q1985	V2045	E2105
I1506	T1566	D1626	M1686	L1746	L1806	F1866	V1926	G1986	M2046	V2106
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F1508	F1568	H1628	Y1688	Y1748	E1808	S1868	L1928	V1988	Y2048	K2108
V1509	E1569	L1629	D1689	I1749	L1809	S1869	L1929	L1989	P2049	K2109
C1510	A1570	R1630	G1690	I1750	C1810	L1870	L1930	V1990	M2050	E2110
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S1512	A1572	P1632	E1692	T1752	M1812	M1872	A1932	M1992	E2052	Y2112
M1513	A1573	L1633	H1693	T1753	D1813	N1873	Y1933	P1993	L2053	A2113
C1514	A1574	K1634	Y1695	L1754	L1814	S1874	F1934	L1994	T2054	L2114
L1515	A1575	H1635	M1696	M1755	V1815	T1875	S1935	R1995	Y2055	K2115
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M1517	N1577	V1637	P1698	E1757	S1817	K1877	L1937	I1997	L2057	L2117
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R1519	N1579	I1639	T1699	A1759	F1819	M1879	L1939	H1999	N2059	L2119
D1520	S1580	L1640	I1700	M1760	I1820	L1880	P1940	F2000	S2060	N2120
F1521	S1581	Y1641	M1701	S1761	E1821	Y1881	V1941	N2001	D2061	K2121
G1522	S1582	K1642	E1702	I1762	I1822	Y1882	D1942	N2002	S2062	E2122
E1523	V1583	G1643	L1703	I1763	D1823	L1883	F1943	K2003	L2063	T2123
W1524	F1584	M1644	L1704	Q1764	D1824	S1884	Q1944	I2004	T2064	Q2124
A1525	L1585	E1645	E1705	S1765	L1825	T1885	M1945	L2005	S2065	Q2125
G1526	P1586	S1646	M1706	K1766	GLU	A1886	D1946	E2006	G2066	Q2126
M1527	S1587	M1647	V1707	Q1767	ALA	V1887	L1947	K2007	V2067	E2127
T1528	R1588	D1648	G1708	D1768	VAL	E1888	K1948	C2008	K2068	L2128
K1529	X1589	E1649	L1709	C1769	THR	F1889	D1949	K2009	Q2069	F2129
S1530	D1590	R1650	A1710	V1770	ALA	E1890	I1950	E2010	K2070	E2130
M1531	C1591	I1651	S1711	D1771	VAL	S1891	L1951	I2011	I2071	D2131
T1532	M1592	V1652	G1712	W1772	ASN	V1892	E1952	N2012	T2072	T2132
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N1534	V1594	R1654	D1714	T1774	GLY	L1894	V1954	E2014	Q2074	P2134
F1535	A1595	L1655	S1715	Y1775	ASP	R1895	V1955	T2015	L2075	S2135
S1536	S1596	Y1656	M1716	S1776	GLU	K1896	P1956	V2016	T2076	G2136
P1537	A1597	E1657	A1717	Y1777	ALA	G1897	L1957	D2017	R2077	K2137
S1538	F1598	Q1658	G1718	F1778	THR	D1898	I1958	D2018	D2078	H2138
E1539	M1599	G1659	K1719	Y1779	GLU	R1899	M1959	I2019	V2079	M2139
R1540	K1600	A1660	V1720	R1780	SER	A1900	V1960	M2020	E2080	L2140
I1541	F1601	V1661	L1721	R1781	THR	L1901	V1961	A2021	P2081	T2141
E1542	S1602	S1662	I1722	I1782	L1847	L1902	V1962	E2022	E2082	T2142
P1543	K1603	V1663	L1723	H1783	S1848	V1903	D1963	E2023	N2083	W2143
L1544	A1604	L1664	T1724	V1784	M1849	K1904	I1964	D2024	L2084	C2144
E1545	I1605	L1665	S1725	M1785	G1850	L1905	L1965	E2025	Q2085	V2145
T1546	E1606	T1666	H1726	P1786	L1851	S1906	S1966	E2026	V2086	C2146
M1547	W1607	S1667	N1727	S1787	T1852	K1907	A1967	R2027	T2087	D2147
T1548	D1608	K1668	M1728	Y1788	L1853	R1908	N1968	D2028	S2088	S2148
Q1549	M1609	D1669	K1729	Y1789	S1854	L1909	G1969	E2029	E2089	Y2149
S1550	L1610	C1670	A1730	G1790	S1854	P1910	Y1970	I2030	K2090	L2150
F1551	N1611	S1671	Y1731	V1791	H1855	L1911	L1971	L2031	Y2091	D2151
K1552	V1612	A1672	Y1732	Y1792	Y1856	R1912	M1972	T2032	P2092	A2152
D1553	E1613	F1673	K1733	D1793	G1857	F1913	A1973	L2033	F2093	D2153
V1554	E1614	A1674	K1734	T1794	S1858	P1914	T1974	T2034	D2094	K2154
E1555	E1615	C1675	F1735	S1795	S1859	E1915	T1975	D2035	K2095	E2155
H1556	Q1616	K1676	L1736	P1796	F1860	H1916	A1976	S2036	L2096	L2156
I1557	I1617	T1677	I1737	H1797		T1917	M1977	Q2037	E2097	S2157
S1558	V1618	D1678	E1738	G1798		S1918	D1978	T2038	S2098	F2158
F1559	P1619	E1679	P1739	I1799		S1919	L1979	A2039	W2099	E2159
N1560	Y1620	V1680	L1740	S1800		G1920		Q2040	W2100	T2160

● Molecule 10: Small nuclear ribonucleoprotein Sm D3

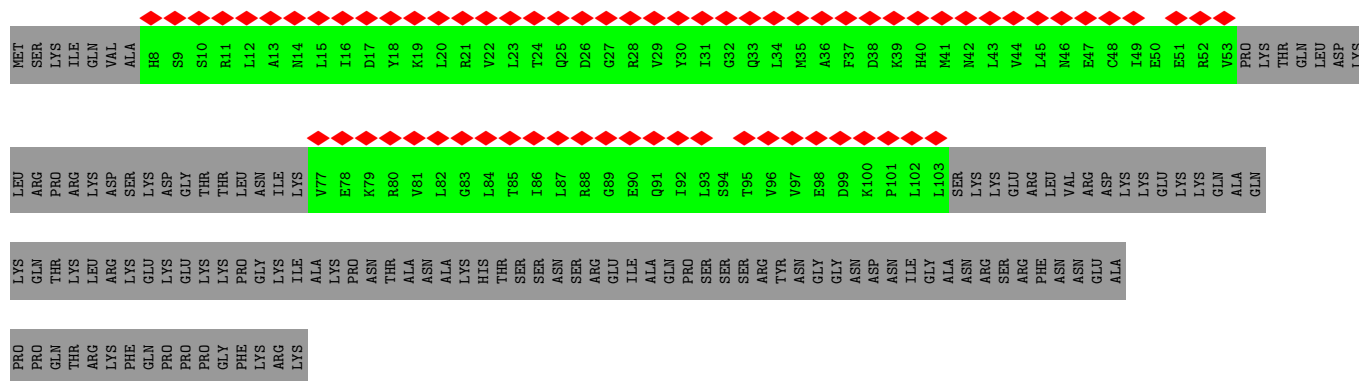




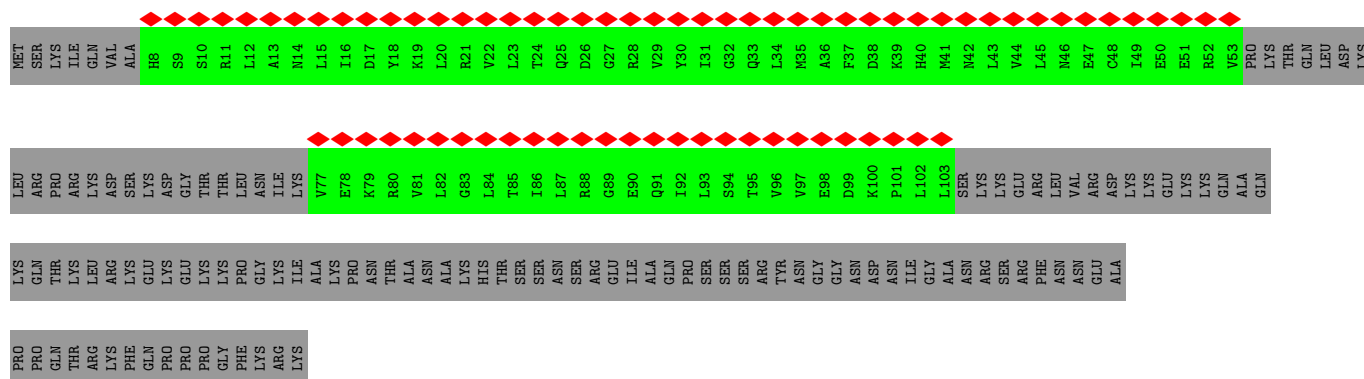
• Molecule 10: Small nuclear ribonucleoprotein Sm D3



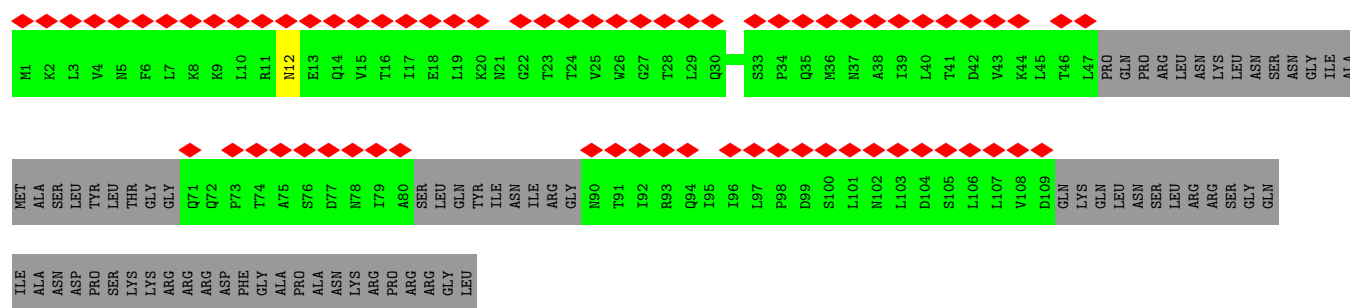
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B

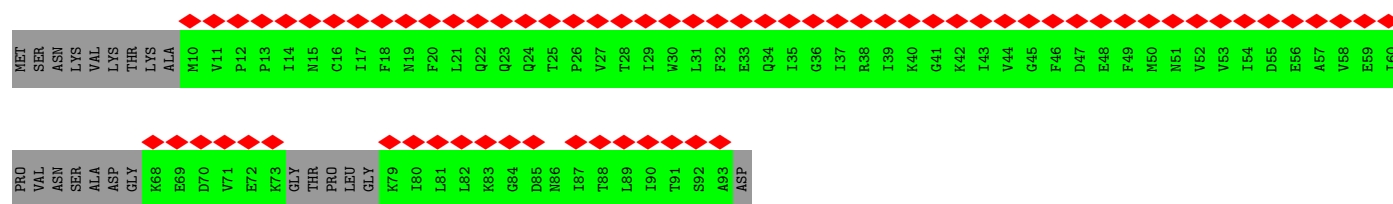
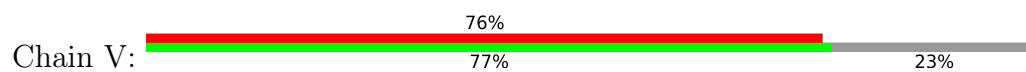


• Molecule 11: Small nuclear ribonucleoprotein-associated protein B

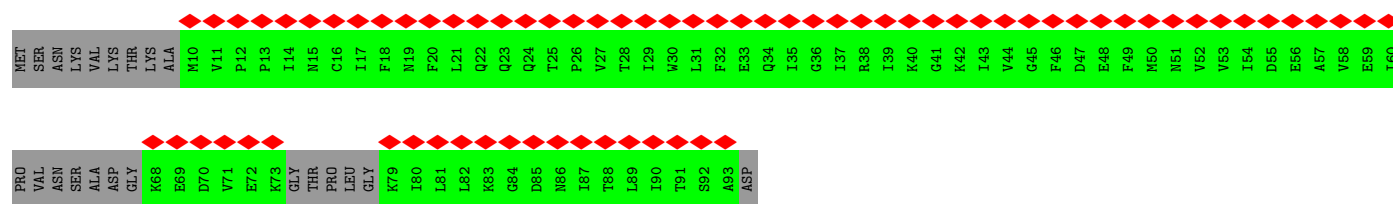
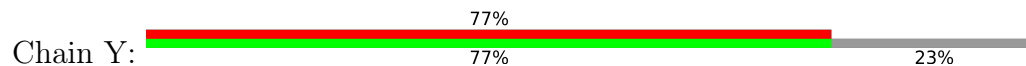


• Molecule 12: Small nuclear ribonucleoprotein Sm D1

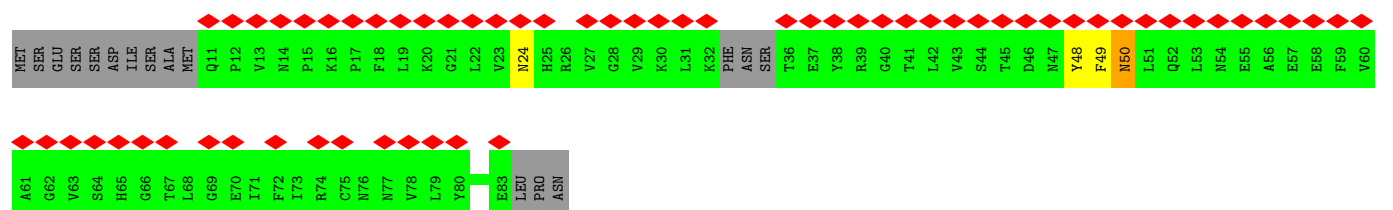
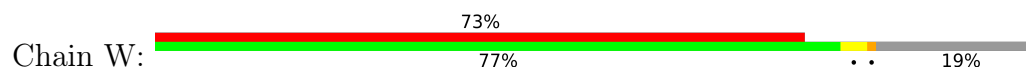




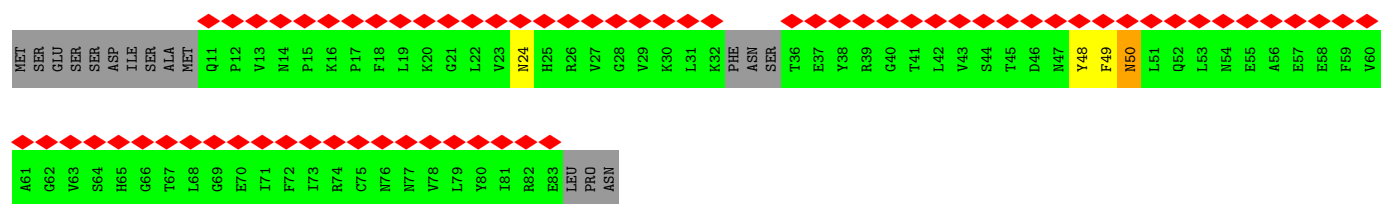
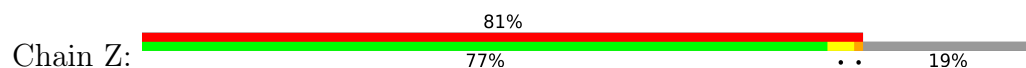
• Molecule 14: Small nuclear ribonucleoprotein E



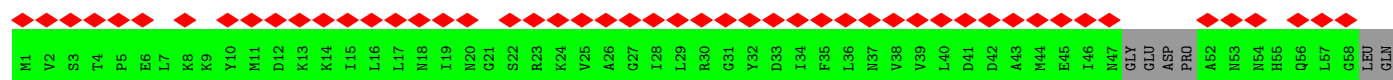
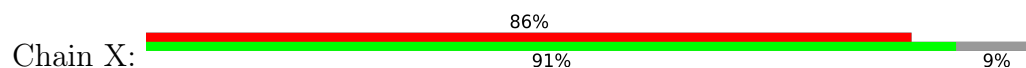
• Molecule 15: Small nuclear ribonucleoprotein F



• Molecule 15: Small nuclear ribonucleoprotein F

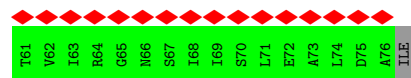


• Molecule 16: Small nuclear ribonucleoprotein G

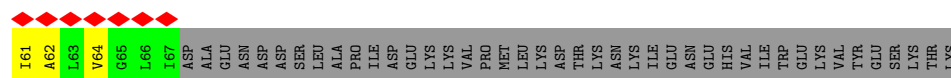
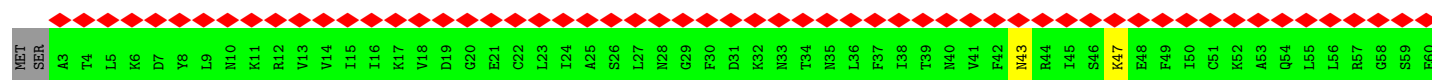




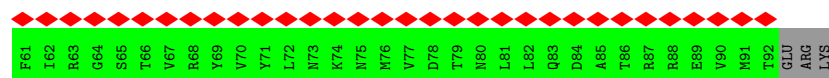
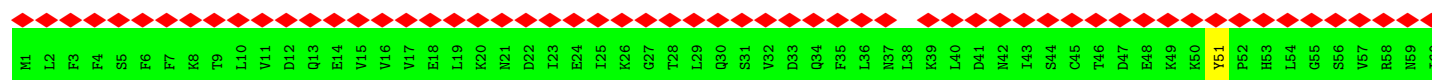
- Molecule 16: Small nuclear ribonucleoprotein G



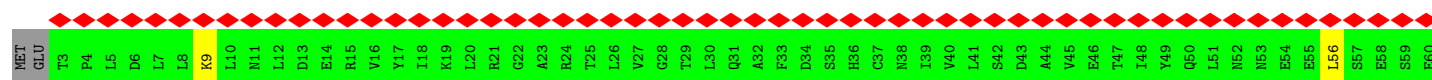
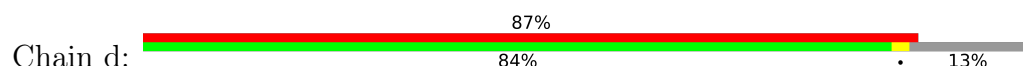
- Molecule 17: U6 snRNA-associated Sm-like protein LSm8



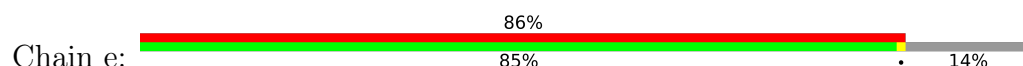
- Molecule 18: U6 snRNA-associated Sm-like protein LSm2

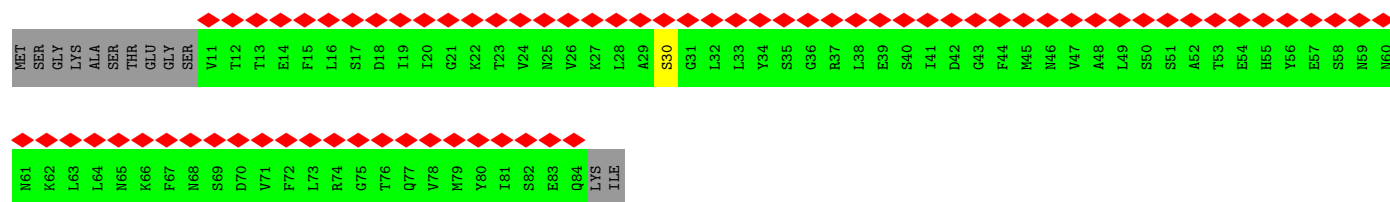


- Molecule 19: U6 snRNA-associated Sm-like protein LSm3

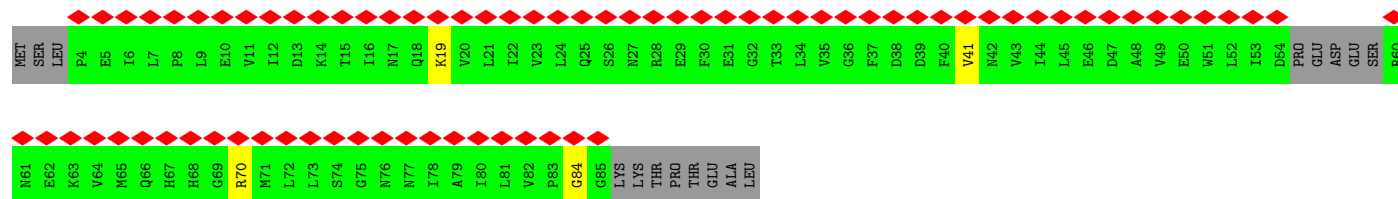
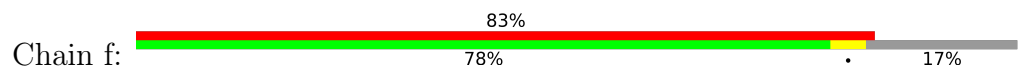


- Molecule 20: U6 snRNA-associated Sm-like protein LSm6

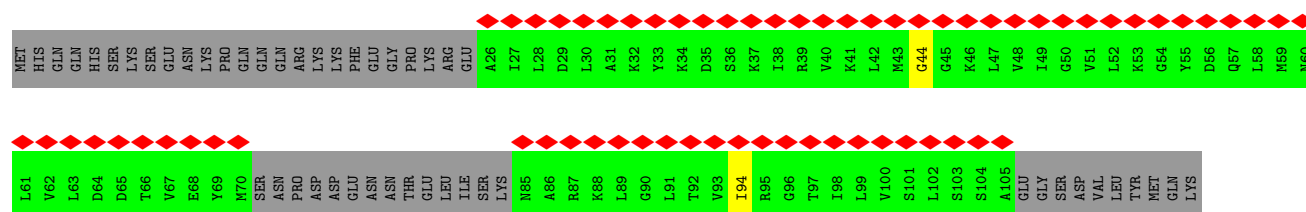




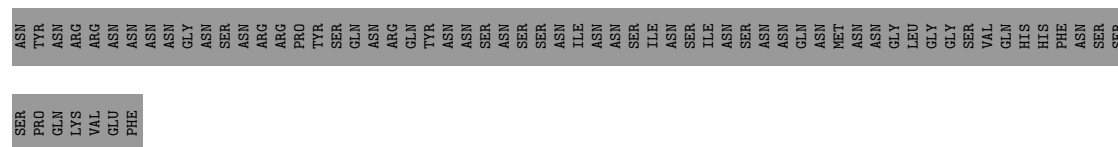
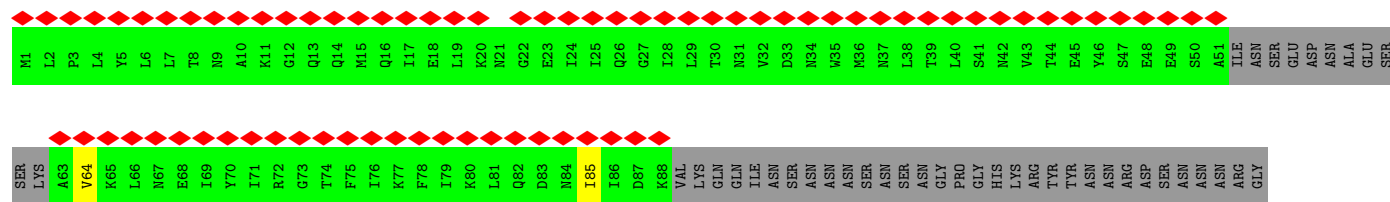
• Molecule 21: U6 snRNA-associated Sm-like protein LSm5



• Molecule 22: U6 snRNA-associated Sm-like protein LSm7

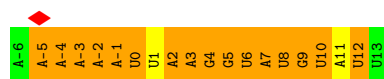


• Molecule 23: U6 snRNA-associated Sm-like protein LSm4



• Molecule 24: pre-mRNA

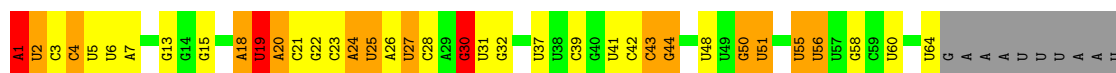
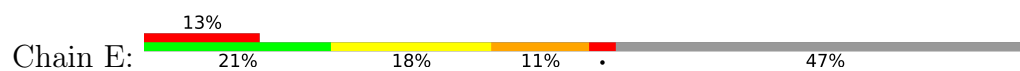




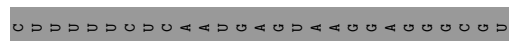
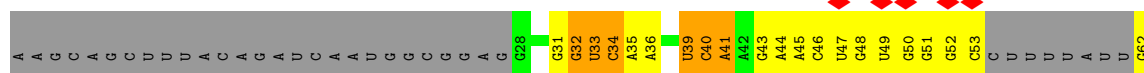
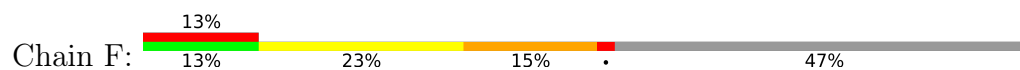
• Molecule 25: SNR6 snRNA



• Molecule 26: SNR14 snRNA



• Molecule 27: SNR7-L snRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	172134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0147	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, M7M

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	1.10	42/17296 (0.2%)	1.18	66/23336 (0.3%)
2	B	0.96	3/3434 (0.1%)	1.10	11/4635 (0.2%)
3	I	1.12	3/3219 (0.1%)	1.24	10/4332 (0.2%)
4	G	0.83	5/4967 (0.1%)	1.17	29/6746 (0.4%)
5	K	0.88	1/2376 (0.0%)	1.10	8/3183 (0.3%)
6	L	0.98	1/1167 (0.1%)	1.04	1/1571 (0.1%)
7	M	1.40	6/963 (0.6%)	1.27	6/1310 (0.5%)
8	H	0.74	8/6874 (0.1%)	1.18	47/9305 (0.5%)
9	N	0.91	0/6738	1.21	13/8412 (0.2%)
10	J	0.47	0/315	0.92	0/392
10	R	0.47	0/315	0.92	0/392
11	O	0.50	0/290	0.86	0/359
11	S	0.50	0/290	0.86	0/359
12	P	0.49	0/305	0.89	0/376
12	T	0.49	0/305	0.89	0/376
13	Q	0.49	0/354	0.95	2/439 (0.5%)
13	U	0.49	0/358	0.95	2/444 (0.5%)
14	V	0.52	0/285	0.85	0/351
14	Y	0.52	0/285	0.85	0/351
15	W	0.53	0/278	0.80	0/344
15	Z	0.53	0/278	0.80	0/344
16	X	0.42	0/277	0.83	0/341
16	a	0.44	0/281	0.83	0/346
17	b	0.77	0/259	1.35	4/322 (1.2%)
18	c	0.83	0/367	1.31	2/457 (0.4%)
19	d	0.98	0/307	1.46	2/382 (0.5%)
20	e	0.82	0/295	1.41	2/367 (0.5%)
21	f	0.81	0/306	1.26	1/379 (0.3%)
22	g	0.83	0/262	1.22	2/324 (0.6%)
23	h	0.79	0/306	1.39	2/379 (0.5%)
24	C	0.41	0/481	0.74	0/747
25	D	0.60	0/1054	0.87	0/1634

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	E	0.71	3/2016 (0.1%)	0.96	13/3136 (0.4%)
27	F	0.50	2/2659 (0.1%)	0.87	2/4131 (0.0%)
All	All	0.92	74/59562 (0.1%)	1.13	225/80302 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
2	B	0	2
3	I	0	1
4	G	0	7
5	K	0	1
7	M	0	4
8	H	0	2
All	All	0	20

All (74) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1608	LEU	CA-C	-9.28	1.41	1.52
4	G	148	ALA	CA-C	-8.04	1.43	1.53
1	A	1335	TRP	CG-CD2	-7.95	1.29	1.43
4	G	147	ALA	CA-C	-7.94	1.43	1.52
7	M	79	VAL	CA-C	-7.93	1.42	1.52
1	A	1088	VAL	CA-C	-7.39	1.43	1.52
4	G	146	TYR	CA-C	-7.25	1.43	1.52
7	M	101	SER	N-CA	-6.95	1.38	1.46
1	A	1516	GLN	CA-C	-6.78	1.44	1.52
1	A	1526	TRP	CA-C	-6.74	1.43	1.52
6	L	131	VAL	N-CA	-6.66	1.38	1.46
1	A	1506	ARG	CA-C	-6.58	1.44	1.52
1	A	1300	ALA	CA-C	-6.55	1.44	1.52
26	E	151	G	C1'-N9	-6.51	1.37	1.47
27	F	175	G	C1'-N9	-6.50	1.37	1.47
1	A	1090	ILE	CA-C	-6.42	1.44	1.52
26	E	155	A	C1'-N9	-6.41	1.38	1.48
3	I	368	ALA	CA-C	-6.38	1.45	1.52
26	E	142	G	C1'-N9	-6.37	1.37	1.47
1	A	1312	PHE	CA-CB	-6.35	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	F	76	U	C1'-N1	6.32	1.56	1.47
1	A	1268	ARG	CA-C	-6.26	1.45	1.52
1	A	1098	VAL	CA-CB	-6.25	1.47	1.54
8	H	370	TYR	C-N	6.25	1.41	1.33
1	A	1158	ILE	CA-C	-6.20	1.46	1.52
8	H	957	ALA	C-N	6.18	1.41	1.33
1	A	1162	THR	CA-C	-6.15	1.45	1.52
1	A	1335	TRP	CE2-CZ2	-6.06	1.27	1.39
1	A	1964	PRO	N-CA	-6.02	1.42	1.47
1	A	1251	TYR	CA-C	-5.90	1.45	1.52
8	H	129	ILE	C-N	5.88	1.41	1.34
1	A	1270	LEU	CA-C	-5.80	1.46	1.52
3	I	372	PHE	CA-CB	-5.73	1.43	1.53
5	K	382	VAL	CA-C	-5.67	1.45	1.52
1	A	1302	LEU	CA-C	-5.66	1.46	1.52
1	A	284	ARG	C-N	5.62	1.41	1.33
1	A	962	ARG	N-CA	-5.62	1.39	1.46
1	A	1355	PRO	C-O	-5.58	1.17	1.24
7	M	51	PHE	C-O	-5.57	1.17	1.23
7	M	77	PRO	CA-C	-5.55	1.46	1.52
1	A	1298	ALA	CA-C	-5.53	1.45	1.52
1	A	1062	ASP	CA-C	-5.53	1.46	1.52
1	A	1012	TRP	CG-CD2	-5.52	1.33	1.43
7	M	78	TYR	C-O	-5.51	1.17	1.23
4	G	149	PRO	N-CA	-5.47	1.41	1.47
1	A	1538	ASN	CA-C	-5.47	1.46	1.52
1	A	1524	PRO	N-CA	-5.40	1.40	1.47
1	A	1107	LEU	CA-C	-5.36	1.46	1.52
1	A	1343	PHE	CA-C	-5.34	1.46	1.52
1	A	1380	PRO	N-CA	-5.29	1.40	1.47
8	H	958	PRO	N-CD	5.29	1.55	1.47
4	G	128	PHE	CA-C	-5.29	1.46	1.52
3	I	367	ARG	CA-C	-5.28	1.46	1.52
1	A	168	LEU	C-N	5.27	1.41	1.34
2	B	393	ARG	CA-C	-5.23	1.46	1.52
1	A	1088	VAL	N-CA	-5.23	1.39	1.46
8	H	445	PRO	N-CD	5.23	1.55	1.47
2	B	454	SER	C-O	-5.22	1.17	1.23
1	A	967	VAL	N-CA	-5.22	1.40	1.46
2	B	457	TRP	CA-C	-5.22	1.45	1.52
1	A	926	LYS	CA-C	-5.20	1.46	1.52
1	A	1344	THR	CA-CB	-5.20	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1163	ARG	CA-C	-5.19	1.46	1.52
1	A	1246	ALA	C-O	-5.17	1.17	1.24
1	A	1610	TRP	CD2-CE3	-5.15	1.32	1.40
1	A	1523	SER	CA-C	-5.13	1.47	1.52
1	A	169	PRO	N-CD	5.11	1.54	1.47
1	A	1505	ASP	CA-C	-5.11	1.46	1.52
8	H	444	GLN	C-N	5.10	1.41	1.34
7	M	90	ALA	C-O	-5.09	1.17	1.24
1	A	285	PRO	N-CD	5.08	1.54	1.47
8	H	130	PRO	N-CD	5.05	1.54	1.47
1	A	797	ILE	N-CA	-5.04	1.42	1.47
8	H	675	THR	CA-C	-5.00	1.46	1.52

All (225) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	852	LEU	N-CA-C	15.26	132.89	112.90
5	K	142	LEU	N-CA-C	14.01	130.59	114.62
4	G	853	GLY	N-CA-C	13.53	145.25	113.18
4	G	143	ARG	N-CA-C	11.96	124.32	111.28
1	A	1383	PHE	CA-C-N	-10.18	112.23	119.66
1	A	1383	PHE	C-N-CA	-10.18	112.23	119.66
1	A	698	GLY	CA-C-N	9.80	132.09	119.84
1	A	698	GLY	C-N-CA	9.80	132.09	119.84
5	K	143	GLU	N-CA-C	-9.22	102.16	113.41
8	H	773	VAL	N-CA-C	9.09	120.34	108.35
4	G	493	PRO	N-CA-CB	9.07	112.22	103.51
4	G	558	PRO	N-CA-CB	8.40	111.31	103.41
27	F	83	C	C4'-C3'-O3'	8.26	125.39	113.00
1	A	203	ASN	N-CA-C	8.06	120.15	111.36
8	H	464	PRO	N-CA-CB	8.01	110.44	103.31
1	A	240	PRO	CA-C-N	7.89	128.62	119.47
1	A	240	PRO	C-N-CA	7.89	128.62	119.47
4	G	417	PRO	N-CA-CB	7.87	111.07	103.51
5	K	354	PHE	N-CA-C	7.69	119.45	111.14
4	G	510	PRO	N-CA-CB	7.63	111.27	103.25
26	E	30	G	C1'-C2'-O2'	-7.58	100.43	111.80
5	K	222	PRO	N-CA-CB	7.57	111.20	103.25
4	G	396	PRO	N-CA-CB	7.54	111.51	103.52
3	I	48	PRO	N-CA-CB	7.50	111.12	103.25
4	G	155	GLY	N-CA-C	7.47	121.94	112.83
3	I	259	ILE	CB-CA-C	-7.46	102.08	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	SER	CA-C-N	7.43	129.13	119.84
1	A	482	SER	C-N-CA	7.43	129.13	119.84
4	G	442	SER	N-CA-C	7.42	119.06	110.97
4	G	414	PRO	N-CA-CB	7.37	110.99	103.25
4	G	399	PRO	N-CA-CB	7.36	111.42	103.33
5	K	220	PRO	N-CA-CB	7.35	110.97	103.25
4	G	156	ASN	N-CA-C	7.32	119.34	111.36
8	H	948	ASP	N-CA-C	7.32	119.26	111.28
8	H	949	ALA	N-CA-C	7.27	119.20	111.28
4	G	286	GLU	N-CA-C	7.25	119.82	111.11
26	E	18	A	C1'-C2'-O2'	7.24	119.26	108.40
9	N	1541	ILE	N-CA-C	7.20	117.99	110.72
3	I	75	PRO	N-CA-CB	7.18	110.78	103.25
4	G	366	PRO	N-CA-CB	7.13	110.86	103.23
4	G	455	PRO	N-CA-CB	7.07	111.03	103.39
8	H	957	ALA	CA-C-N	-7.06	113.04	120.03
8	H	957	ALA	C-N-CA	-7.06	113.04	120.03
1	A	157	ASP	N-CA-C	7.01	125.73	110.80
1	A	811	ILE	CB-CA-C	-6.95	102.76	112.14
8	H	370	TYR	CA-C-N	-6.91	113.19	120.03
8	H	370	TYR	C-N-CA	-6.91	113.19	120.03
1	A	135	PRO	CA-C-N	6.90	126.59	119.56
1	A	135	PRO	C-N-CA	6.90	126.59	119.56
8	H	951	ILE	C-N-CD	-6.84	96.95	125.00
26	E	1	A	O3'-P-O5'	6.83	114.25	104.00
1	A	1378	LYS	N-CA-C	6.82	118.79	111.36
4	G	13	ALA	N-CA-C	-6.80	102.05	110.41
1	A	775	ARG	N-CA-C	6.76	118.30	111.07
3	I	43	PRO	N-CA-CB	6.75	111.00	103.44
9	N	1224	ALA	N-CA-C	-6.70	98.85	109.23
1	A	405	ASN	CA-C-N	6.68	128.19	119.84
1	A	405	ASN	C-N-CA	6.68	128.19	119.84
19	d	9	LYS	N-CA-C	-6.66	103.83	112.23
9	N	787	ASN	N-CA-C	6.62	118.15	111.07
18	c	51	TYR	CA-C-N	6.58	128.06	119.84
18	c	51	TYR	C-N-CA	6.58	128.06	119.84
5	K	246	ARG	N-CA-C	6.54	118.21	111.14
7	M	79	VAL	CB-CA-C	-6.54	98.70	110.48
8	H	448	LEU	N-CA-C	6.52	118.46	111.36
27	F	84	A	C1'-C2'-O2'	6.50	118.14	108.40
9	N	831	THR	N-CA-C	-6.47	101.21	110.59
1	A	1089	VAL	N-CA-C	-6.45	95.92	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	940	VAL	CA-C-N	6.44	127.89	119.84
8	H	940	VAL	C-N-CA	6.44	127.89	119.84
8	H	806	GLY	CA-C-N	6.43	126.05	119.56
8	H	806	GLY	C-N-CA	6.43	126.05	119.56
1	A	394	ARG	CA-C-N	6.42	126.94	120.14
1	A	394	ARG	C-N-CA	6.42	126.94	120.14
2	B	176	LYS	N-CA-C	-6.39	99.87	108.11
8	H	703	LEU	CA-C-N	6.34	127.77	119.84
8	H	703	LEU	C-N-CA	6.34	127.77	119.84
1	A	779	ALA	N-CA-C	6.33	117.98	111.14
8	H	770	ASN	N-CA-C	-6.33	104.11	112.72
7	M	77	PRO	CB-CA-C	-6.31	102.98	111.12
4	G	335	PRO	N-CA-CB	6.29	109.86	103.25
4	G	9	GLN	N-CA-C	6.28	117.92	111.14
26	E	19	U	C4'-C3'-O3'	6.26	122.39	113.00
4	G	768	PRO	N-CA-C	6.25	122.09	113.65
13	Q	29	GLY	CA-C-N	6.22	125.71	119.24
13	Q	29	GLY	C-N-CA	6.22	125.71	119.24
13	U	29	GLY	CA-C-N	6.18	125.67	119.24
13	U	29	GLY	C-N-CA	6.18	125.67	119.24
8	H	825	VAL	CA-C-N	6.12	126.47	119.93
8	H	825	VAL	C-N-CA	6.12	126.47	119.93
9	N	803	THR	N-CA-C	-6.08	100.09	109.52
26	E	19	U	O4'-C1'-C2'	-6.06	101.54	107.60
26	E	1	A	N9-C1'-C2'	-6.05	102.92	112.00
9	N	1909	LEU	CA-C-N	6.05	125.93	119.28
9	N	1909	LEU	C-N-CA	6.05	125.93	119.28
8	H	743	ASN	CA-C-N	6.04	126.48	119.47
8	H	743	ASN	C-N-CA	6.04	126.48	119.47
3	I	432	GLY	N-CA-C	6.01	119.92	112.64
3	I	269	SER	N-CA-C	6.00	118.31	111.11
8	H	697	ARG	N-CA-C	5.97	119.64	110.20
1	A	1354	GLU	CA-C-N	-5.96	112.88	119.19
1	A	1354	GLU	C-N-CA	-5.96	112.88	119.19
8	H	168	VAL	CB-CA-C	-5.94	104.03	112.22
26	E	50	G	C1'-C2'-O2'	5.93	117.29	108.40
2	B	209	PRO	N-CA-C	5.91	122.56	113.75
5	K	221	LEU	N-CA-C	5.89	119.21	110.32
4	G	767	PHE	CA-C-N	5.89	125.75	119.28
4	G	767	PHE	C-N-CA	5.89	125.75	119.28
1	A	543	ASN	N-CA-C	5.88	117.69	111.28
1	A	284	ARG	CA-C-N	-5.88	112.81	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	284	ARG	C-N-CA	-5.88	112.81	119.28
1	A	1113	ILE	CB-CA-C	-5.85	104.24	112.14
23	h	85	ILE	N-CA-C	5.85	116.50	110.36
1	A	1546	VAL	CB-CA-C	-5.84	104.17	112.22
1	A	1233	ARG	N-CA-C	5.82	117.71	111.36
2	B	265	GLU	N-CA-C	5.82	117.43	111.14
1	A	954	ILE	CB-CA-C	-5.81	104.30	112.14
9	N	1430	ASN	CA-C-N	-5.80	115.39	122.64
9	N	1430	ASN	C-N-CA	-5.80	115.39	122.64
17	b	64	VAL	CA-C-N	-5.80	118.18	122.18
17	b	64	VAL	C-N-CA	-5.80	118.18	122.18
1	A	353	GLU	CA-C-N	5.79	125.48	119.05
1	A	353	GLU	C-N-CA	5.79	125.48	119.05
1	A	246	GLU	CA-C-N	5.78	126.33	120.38
1	A	246	GLU	C-N-CA	5.78	126.33	120.38
1	A	179	MET	CA-C-N	5.75	125.43	119.56
1	A	179	MET	C-N-CA	5.75	125.43	119.56
4	G	148	ALA	CA-C-N	-5.74	114.84	120.52
4	G	148	ALA	C-N-CA	-5.74	114.84	120.52
1	A	168	LEU	CA-C-N	-5.74	112.68	119.05
1	A	168	LEU	C-N-CA	-5.74	112.68	119.05
8	H	170	LEU	N-CA-C	5.74	117.21	111.07
8	H	323	THR	N-CA-C	-5.72	100.82	109.85
9	N	849	GLY	N-CA-C	5.71	120.48	113.79
1	A	293	VAL	N-CA-C	5.70	117.06	108.96
1	A	512	GLU	N-CA-C	5.70	117.57	111.36
3	I	113	HIS	N-CA-C	-5.70	104.76	110.97
7	M	102	ILE	CB-CA-C	-5.66	102.65	111.26
1	A	1263	CYS	CA-CB-SG	-5.65	101.40	114.40
2	B	278	LYS	N-CA-C	5.65	117.44	111.28
1	A	2017	THR	CB-CA-C	5.64	121.65	110.42
26	E	1	A	P-O3'-C3'	-5.64	111.74	120.20
8	H	839	ILE	O-C-N	5.62	124.02	120.42
1	A	258	ILE	N-CA-C	5.61	117.02	110.62
8	H	573	LYS	CB-CA-C	-5.60	110.13	116.63
8	H	784	SER	CA-C-N	5.60	125.12	119.19
8	H	784	SER	C-N-CA	5.60	125.12	119.19
4	G	887	THR	CA-C-N	-5.59	113.26	119.19
4	G	887	THR	C-N-CA	-5.59	113.26	119.19
8	H	671	SER	N-CA-C	5.59	118.53	109.86
7	M	48	ILE	CB-CA-C	-5.57	104.29	111.20
3	I	259	ILE	N-CA-C	5.56	116.29	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1885	LYS	N-CA-C	5.55	117.33	111.28
2	B	250	ASN	CB-CA-C	-5.53	110.18	116.54
1	A	134	MET	CA-C-N	5.53	126.07	120.38
1	A	134	MET	C-N-CA	5.53	126.07	120.38
8	H	279	LEU	CA-C-N	-5.52	115.68	119.66
8	H	279	LEU	C-N-CA	-5.52	115.68	119.66
8	H	568	SER	N-CA-C	5.51	117.29	111.28
1	A	1056	GLU	N-CA-C	-5.51	101.50	109.59
8	H	629	TYR	CA-C-N	5.50	125.17	119.56
8	H	629	TYR	C-N-CA	5.50	125.17	119.56
1	A	1108	LYS	N-CA-C	5.50	117.28	111.28
26	E	41	U	C2'-C3'-O3'	-5.50	105.45	113.70
20	e	30	SER	CA-C-N	-5.50	117.47	123.30
20	e	30	SER	C-N-CA	-5.50	117.47	123.30
9	N	662	GLN	N-CA-C	5.50	122.50	110.80
26	E	31	U	C4'-C3'-O3'	5.47	117.61	109.40
8	H	444	GLN	CA-C-N	-5.47	112.98	119.05
8	H	444	GLN	C-N-CA	-5.47	112.98	119.05
9	N	1954	VAL	N-CA-C	5.47	118.76	111.44
1	A	1095	MET	CG-SD-CE	-5.46	88.88	100.90
1	A	1073	ILE	N-CA-CB	-5.44	104.15	112.15
1	A	1120	VAL	CB-CA-C	-5.44	105.01	111.81
1	A	387	PHE	CA-C-N	5.43	125.52	119.87
1	A	387	PHE	C-N-CA	5.43	125.52	119.87
8	H	336	ILE	N-CA-C	5.43	114.97	108.45
4	G	767	PHE	N-CA-C	5.40	121.75	109.81
1	A	642	GLY	N-CA-C	-5.40	107.33	115.32
1	A	960	THR	N-CA-C	5.38	120.34	113.18
1	A	1206	CYS	N-CA-C	5.36	117.12	111.28
1	A	1207	TRP	N-CA-CB	-5.35	103.54	109.74
1	A	1261	SER	N-CA-C	5.34	117.12	108.41
2	B	114	THR	N-CA-C	5.33	117.15	110.91
8	H	655	LEU	CB-CA-C	-5.33	102.51	110.88
26	E	18	A	P-O5'-C5'	-5.31	112.93	120.90
7	M	78	TYR	N-CA-C	5.31	116.92	108.79
6	L	131	VAL	N-CA-C	-5.30	100.96	108.65
1	A	1608	LEU	N-CA-CB	5.30	117.69	110.01
8	H	129	ILE	CA-C-N	-5.29	113.08	118.85
8	H	129	ILE	C-N-CA	-5.29	113.08	118.85
1	A	1018	SER	N-CA-C	5.28	118.98	112.54
26	E	64	U	C1'-C2'-O2'	5.28	116.32	108.40
17	b	62	ALA	N-CA-C	-5.27	107.50	114.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	308	HIS	N-CA-C	-5.26	105.44	111.07
1	A	614	ARG	N-CA-C	-5.25	102.42	110.30
1	A	360	GLU	N-CA-C	5.25	117.08	111.36
2	B	393	ARG	N-CA-C	-5.22	101.25	109.50
7	M	60	PRO	N-CA-C	5.22	123.23	112.47
8	H	672	ASP	CA-C-N	5.20	126.33	119.84
8	H	672	ASP	C-N-CA	5.20	126.33	119.84
1	A	824	VAL	CB-CA-C	-5.19	105.28	112.24
2	B	396	VAL	N-CA-C	-5.19	101.50	108.35
22	g	44	GLY	N-CA-C	-5.19	107.90	115.63
17	b	61	ILE	N-CA-C	5.15	116.22	109.58
3	I	355	ALA	N-CA-C	5.14	117.28	108.90
9	N	1481	GLN	N-CA-C	5.14	119.19	113.02
8	H	611	LEU	CA-C-N	5.13	124.74	119.56
8	H	611	LEU	C-N-CA	5.13	124.74	119.56
1	A	199	ILE	N-CA-C	5.12	115.02	107.75
1	A	546	LYS	N-CA-C	5.11	121.67	110.80
4	G	733	ASN	CA-C-N	5.10	126.22	119.84
4	G	733	ASN	C-N-CA	5.10	126.22	119.84
2	B	274	HIS	CA-C-N	-5.09	113.41	119.05
2	B	274	HIS	C-N-CA	-5.09	113.41	119.05
23	h	64	VAL	N-CA-C	5.08	115.90	108.58
8	H	800	TYR	N-CA-C	-5.07	105.75	111.28
8	H	947	LYS	N-CA-C	5.07	116.89	111.36
19	d	56	LEU	N-CA-C	5.05	116.96	108.73
21	f	70	ARG	N-CA-C	5.04	117.28	108.76
22	g	94	ILE	N-CA-C	5.03	115.53	108.89
26	E	44	G	C1'-C2'-O2'	5.02	119.33	111.80
3	I	298	VAL	N-CA-CB	-5.01	106.53	112.39
2	B	317	CYS	N-CA-C	5.00	118.48	112.38
1	A	1199	ILE	CB-CA-C	-5.00	105.57	111.97

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1867	GLU	Peptide
1	A	694	ASN	Peptide
2	B	208	GLN	Peptide
2	B	316	GLN	Peptide
4	G	12	PRO	Peptide

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Mol	Chain	Res	Type	Group
4	G	123	PRO	Peptide
4	G	733	ASN	Mainchain,Peptide
4	G	767	PHE	Mainchain,Peptide
4	G	802	GLN	Peptide
8	H	160	ARG	Peptide
8	H	171	GLY	Peptide
3	I	410	LEU	Peptide
5	K	282	GLU	Peptide
7	M	59	GLU	Mainchain,Peptide
7	M	9	PHE	Mainchain,Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16889	0	16134	1167	0
2	B	3378	0	3342	377	0
3	I	3171	0	3140	285	0
4	G	4927	0	4006	395	0
5	K	2328	0	2314	164	0
6	L	1146	0	1133	127	0
7	M	950	0	1004	28	0
8	H	6732	0	6904	888	0
9	N	6744	0	1759	36	0
10	J	316	0	86	0	0
10	R	316	0	86	2	0
11	O	292	0	78	0	0
11	S	292	0	78	0	0
12	P	308	0	78	0	0
12	T	308	0	78	0	0
13	Q	356	0	88	0	0
13	U	360	0	89	0	0
14	V	288	0	74	0	0
14	Y	288	0	74	0	0
15	W	280	0	77	1	0
15	Z	280	0	77	1	0
16	X	280	0	79	0	0
16	a	284	0	82	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	b	260	0	72	1	0
18	c	368	0	99	0	0
19	d	308	0	80	0	0
20	e	296	0	83	0	0
21	f	308	0	85	3	0
22	g	264	0	76	0	0
23	h	308	0	85	0	0
24	C	429	0	214	48	0
25	D	945	0	478	73	0
26	E	1806	0	907	49	0
27	F	2385	0	1209	209	0
28	H	32	0	12	10	0
29	E	31	0	20	6	0
All	All	58253	0	44280	3674	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 36.

All (3674) 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)
8:H:856:ILE:HA	8:H:944:VAL:CG1	1.17	1.58
4:G:672:LEU:HD21	4:G:704:LEU:CD2	1.29	1.58
8:H:168:VAL:HG13	8:H:173:LYS:CD	1.09	1.56
8:H:364:PHE:CB	8:H:369:LYS:HG3	1.34	1.54
4:G:672:LEU:CD2	4:G:704:LEU:CD2	1.82	1.52
4:G:274:SER:HB3	4:G:277:ILE:CD1	1.38	1.52
4:G:274:SER:CB	4:G:277:ILE:HD11	1.30	1.50
8:H:168:VAL:CG1	8:H:173:LYS:HD3	1.39	1.50
8:H:500:ARG:CD	8:H:534:THR:HG21	1.40	1.49
8:H:364:PHE:HB2	8:H:369:LYS:CG	1.42	1.49
9:N:807:GLY:CA	9:N:1093:ALA:H	1.28	1.46
8:H:500:ARG:NE	8:H:534:THR:HG21	1.31	1.41
8:H:364:PHE:HD2	8:H:369:LYS:CD	1.33	1.41
8:H:855:PRO:C	8:H:944:VAL:HG11	1.43	1.41
6:L:105:PHE:CB	6:L:141:ARG:HG2	1.52	1.38
9:N:807:GLY:HA2	9:N:1093:ALA:N	1.10	1.38
5:K:354:PHE:CE1	5:K:358:MET:HE3	1.58	1.38
1:A:781:THR:CA	1:A:784:GLN:OE1	1.71	1.37
8:H:488:ILE:CG2	8:H:558:LYS:HA	1.54	1.37
8:H:856:ILE:CA	8:H:944:VAL:CG1	2.00	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ASP:OD2	1:A:292:LYS:N	1.59	1.36
2:B:389:ILE:CD1	2:B:427:TRP:HB3	1.54	1.35
8:H:168:VAL:CG1	8:H:173:LYS:CD	1.97	1.35
8:H:458:ILE:CG2	8:H:459:PRO:HD2	1.56	1.35
4:G:846:PHE:CE1	4:G:859:LEU:HD21	1.62	1.35
1:A:285:PRO:HD2	1:A:298:TYR:OH	1.27	1.34
4:G:268:CYS:SG	4:G:278:TRP:CH2	2.21	1.34
1:A:162:LEU:HD21	1:A:730:ILE:CG2	0.88	1.33
8:H:500:ARG:CD	8:H:534:THR:CG2	2.07	1.33
8:H:855:PRO:O	8:H:944:VAL:CG1	1.75	1.33
8:H:856:ILE:CA	8:H:944:VAL:HG11	1.56	1.33
3:I:197:ILE:O	3:I:201:ASN:ND2	1.61	1.32
4:G:672:LEU:CD2	4:G:704:LEU:HD21	1.50	1.32
4:G:630:SER:CB	4:G:670:PHE:CZ	2.11	1.32
1:A:162:LEU:CD2	1:A:730:ILE:HG21	0.85	1.32
9:N:807:GLY:CA	9:N:1093:ALA:N	1.86	1.31
8:H:856:ILE:N	8:H:944:VAL:HG11	1.45	1.30
8:H:810:GLU:OE2	8:H:974:LYS:HG3	1.13	1.28
4:G:863:PHE:CZ	4:G:892:LEU:HD21	1.67	1.28
27:F:73:U:C2'	27:F:74:U:H5'	1.64	1.27
1:A:289:ASP:O	1:A:293:VAL:HG12	1.29	1.27
8:H:486:VAL:CG1	8:H:564:ILE:HD11	1.65	1.27
6:L:105:PHE:CZ	6:L:137:TYR:CE2	2.23	1.26
1:A:611:LYS:CE	24:C:4:G:OP1	1.85	1.25
9:N:807:GLY:CA	9:N:1093:ALA:CA	2.14	1.25
25:D:48:C:O3'	25:D:49:A:C8	1.89	1.24
1:A:165:LEU:HD12	1:A:578:MET:SD	1.78	1.24
1:A:195:THR:HG23	1:A:556:TYR:O	1.34	1.24
8:H:364:PHE:CD2	8:H:369:LYS:HD2	1.73	1.24
8:H:500:ARG:HD3	8:H:534:THR:CG2	1.66	1.23
9:N:807:GLY:HA2	9:N:1093:ALA:CA	1.67	1.23
5:K:350:PRO:HA	5:K:353:ARG:CG	1.68	1.22
8:H:364:PHE:CD2	8:H:369:LYS:CD	2.22	1.22
3:I:226:ALA:HA	3:I:317:ASP:OD2	1.31	1.22
8:H:330:TYR:HE1	8:H:430:ARG:NH2	1.36	1.22
24:C:8:U:C6	25:D:51:A:N6	2.05	1.22
6:L:105:PHE:CE1	6:L:137:TYR:CE2	2.28	1.21
8:H:889:TYR:CD1	8:H:890:LYS:HG2	1.77	1.20
5:K:354:PHE:HE1	5:K:358:MET:CE	1.52	1.20
4:G:630:SER:CB	4:G:670:PHE:CE2	2.24	1.20
4:G:672:LEU:CD2	4:G:704:LEU:HD23	1.48	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:846:PHE:HE1	4:G:859:LEU:CD2	1.55	1.20
6:L:105:PHE:CZ	6:L:137:TYR:CD2	2.29	1.20
8:H:454:ALA:O	8:H:457:SER:O	1.55	1.20
25:D:48:C:H3'	25:D:49:A:N7	1.57	1.19
3:I:123:ARG:HD3	3:I:189:LEU:CD1	1.70	1.19
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD12	1.78	1.19
1:A:1748:ILE:HG22	1:A:1752:VAL:HG22	1.21	1.19
4:G:655:PHE:CB	4:G:674:LEU:HD21	1.71	1.19
8:H:116:THR:HG23	8:H:158:HIS:CD2	1.78	1.18
25:D:48:C:C3'	25:D:49:A:C8	2.25	1.18
8:H:492:LEU:HD21	8:H:557:HIS:ND1	1.57	1.18
27:F:75:A:C8	27:F:77:A:H5'	1.78	1.18
1:A:286:LEU:HD21	1:A:292:LYS:HB2	1.25	1.17
8:H:510:ARG:HB2	8:H:591:PHE:CE2	1.78	1.17
2:B:389:ILE:HD11	2:B:427:TRP:CB	1.73	1.17
1:A:1755:LYS:O	1:A:1759:TYR:HD2	1.22	1.17
5:K:350:PRO:HA	5:K:353:ARG:HG2	1.20	1.16
1:A:1035:LEU:HD12	1:A:1038:ILE:HG21	1.17	1.16
8:H:354:TYR:CB	8:H:359:PHE:HB3	1.76	1.16
8:H:855:PRO:O	8:H:944:VAL:CG2	1.94	1.15
8:H:163:ASP:OD2	8:H:548:ARG:NH1	1.79	1.15
2:B:316:GLN:HB2	2:B:357:TRP:CD2	1.81	1.15
1:A:468:LEU:HD13	1:A:469:ILE:HD13	1.21	1.15
8:H:117:ARG:HD2	8:H:157:SER:O	1.42	1.15
1:A:162:LEU:HD21	1:A:730:ILE:HG22	1.22	1.15
1:A:1880:PHE:CE2	1:A:1889:LEU:HD21	1.81	1.15
8:H:501:ILE:CD1	8:H:567:ILE:CG2	2.24	1.15
24:C:-3:A:H8	24:C:-2:A:C6	1.65	1.14
6:L:105:PHE:CE1	6:L:137:TYR:CD2	2.35	1.14
1:A:252:GLU:O	1:A:256:GLU:HG2	1.48	1.14
1:A:779:ALA:HA	1:A:782:ILE:HD12	1.30	1.14
1:A:781:THR:HA	1:A:784:GLN:OE1	0.97	1.14
8:H:364:PHE:HD2	8:H:369:LYS:HD2	1.01	1.13
8:H:488:ILE:CD1	8:H:560:GLN:HG2	1.78	1.13
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	1.62	1.13
1:A:1654:TRP:CZ3	1:A:1779:LEU:CD1	2.30	1.13
27:F:44:A:H2'	27:F:45:A:C8	1.83	1.13
8:H:501:ILE:HD11	8:H:567:ILE:CG2	1.78	1.12
8:H:330:TYR:CE1	8:H:430:ARG:NH2	2.17	1.12
8:H:810:GLU:OE2	8:H:974:LYS:CG	1.97	1.12
6:L:105:PHE:HB3	6:L:141:ARG:CG	1.79	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:44:A:H2'	27:F:45:A:H8	0.96	1.11
4:G:272:PRO:HB3	4:G:302:PHE:CD1	1.85	1.11
8:H:330:TYR:HE1	8:H:430:ARG:CZ	1.63	1.11
8:H:332:TYR:OH	8:H:376:PHE:HB3	1.50	1.11
8:H:488:ILE:HD12	8:H:560:GLN:HG2	1.29	1.11
25:D:48:C:O3'	25:D:49:A:H8	1.22	1.11
1:A:141:LYS:HA	1:A:144:ASN:ND2	1.64	1.11
1:A:362:GLU:HB3	1:A:1209:LYS:CE	1.81	1.11
2:B:329:SER:HB3	2:B:348:HIS:O	1.47	1.11
8:H:470:ALA:HB1	8:H:486:VAL:HG21	1.26	1.11
4:G:691:TYR:HB3	4:G:708:LEU:HD12	1.15	1.10
1:A:297:SER:HB3	27:F:32:G:OP1	1.48	1.10
8:H:486:VAL:HG12	8:H:564:ILE:HD11	1.13	1.10
1:A:162:LEU:HD23	1:A:730:ILE:HG21	1.20	1.10
8:H:168:VAL:HG13	8:H:173:LYS:HD2	1.18	1.10
8:H:677:PHE:CE1	8:H:966:PHE:CD2	2.39	1.10
1:A:2077:THR:O	1:A:2080:LYS:HG2	1.52	1.09
2:B:159:LEU:HD13	2:B:430:MET:HE2	1.29	1.09
4:G:286:GLU:HB2	4:G:292:CYS:SG	1.90	1.09
8:H:364:PHE:HD2	8:H:369:LYS:HD3	1.17	1.08
1:A:141:LYS:HA	1:A:144:ASN:HD21	0.95	1.08
24:C:-3:A:H8	24:C:-2:A:C5	1.70	1.08
3:I:184:LYS:HD2	3:I:186:LYS:H	1.14	1.08
8:H:582:SER:CB	8:H:585:ASP:OD2	2.01	1.07
1:A:290:SER:OG	1:A:291:LYS:NZ	1.88	1.07
8:H:468:LEU:HD21	8:H:577:LEU:HD21	1.33	1.07
8:H:468:LEU:HD11	8:H:493:LEU:HD21	1.31	1.07
27:F:75:A:C8	27:F:77:A:C5'	2.37	1.07
2:B:323:CYS:SG	2:B:355:VAL:HG11	1.95	1.06
8:H:488:ILE:HD12	8:H:560:GLN:CG	1.82	1.06
4:G:252:GLU:HG2	4:G:256:LYS:HG3	1.37	1.06
8:H:598:ILE:HG22	8:H:933:TRP:CZ3	1.91	1.06
1:A:503:LYS:HA	1:A:506:PHE:CZ	1.89	1.06
8:H:197:THR:CG2	8:H:545:LEU:CD1	2.32	1.06
3:I:123:ARG:CD	3:I:189:LEU:HD13	1.84	1.06
4:G:668:HIS:HB3	4:G:698:VAL:HG11	1.32	1.06
4:G:672:LEU:HD23	4:G:704:LEU:CD2	1.68	1.06
8:H:458:ILE:HG23	8:H:459:PRO:HD2	1.08	1.06
1:A:404:ASN:OD1	8:H:927:MET:HE3	1.56	1.06
3:I:135:LEU:HD23	3:I:136:GLN:N	1.70	1.06
5:K:428:TRP:HZ2	5:K:463:PHE:CE2	1.74	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:168:VAL:HG13	8:H:173:LYS:CG	1.85	1.06
1:A:218:SER:N	1:A:318:LEU:HD21	1.71	1.05
4:G:274:SER:HB2	4:G:277:ILE:HD11	1.34	1.05
8:H:365:GLU:OE2	8:H:366:ASN:N	1.88	1.05
8:H:501:ILE:HD11	8:H:567:ILE:HG23	1.09	1.05
1:A:1755:LYS:O	1:A:1759:TYR:CD2	2.09	1.05
8:H:133:ILE:O	8:H:134:ILE:HG23	1.55	1.05
1:A:1751:TYR:CE1	1:A:1755:LYS:HD3	1.92	1.05
1:A:1755:LYS:HG3	1:A:1759:TYR:HE2	1.19	1.05
6:L:116:ILE:HD11	6:L:137:TYR:OH	1.57	1.05
6:L:81:THR:HG21	6:L:102:LYS:HZ1	1.21	1.04
6:L:140:LYS:HG2	6:L:141:ARG:NH1	1.72	1.04
8:H:488:ILE:HG21	8:H:557:HIS:C	1.81	1.04
25:D:83:A:H1'	25:D:84:C:C5	1.93	1.04
24:C:-3:A:C8	24:C:-2:A:C6	2.45	1.04
8:H:501:ILE:CD1	8:H:567:ILE:HG23	1.87	1.04
4:G:846:PHE:CE1	4:G:859:LEU:CD2	2.35	1.04
1:A:611:LYS:HE2	24:C:4:G:OP1	1.55	1.03
1:A:1998:ARG:O	1:A:1999:ILE:HG13	1.58	1.03
1:A:1058:ALA:HB2	1:A:1114:PHE:HE1	1.23	1.03
8:H:500:ARG:NE	8:H:534:THR:CG2	2.15	1.03
2:B:389:ILE:HD11	2:B:427:TRP:HB3	1.04	1.03
8:H:510:ARG:HB2	8:H:591:PHE:HE2	0.86	1.03
1:A:611:LYS:HE3	24:C:4:G:OP1	1.54	1.02
8:H:488:ILE:HG22	8:H:558:LYS:CA	1.88	1.02
8:H:504:THR:HA	8:H:507:SER:OG	1.59	1.02
1:A:1748:ILE:O	1:A:1752:VAL:HG23	1.58	1.02
3:I:112:MET:HB3	3:I:204:LEU:HD21	1.38	1.02
4:G:695:THR:HB	4:G:705:TRP:NE1	1.73	1.02
8:H:227:VAL:HG11	8:H:474:LYS:HG3	1.37	1.02
1:A:1365:THR:O	1:A:1369:ASN:ND2	1.92	1.02
4:G:695:THR:O	4:G:699:PRO:HG3	1.58	1.02
27:F:78:A:O2'	27:F:79:C:O5'	1.76	1.02
1:A:1035:LEU:HD12	1:A:1038:ILE:CG2	1.90	1.02
3:I:217:TYR:HE1	3:I:221:LYS:NZ	1.58	1.02
8:H:110:LYS:HE2	8:H:552:PRO:HG2	1.42	1.02
1:A:294:ASN:HB2	1:A:299:LYS:O	1.59	1.02
9:N:807:GLY:N	9:N:1093:ALA:CA	2.22	1.02
1:A:470:LEU:O	1:A:473:THR:HG22	1.60	1.01
1:A:837:GLY:CA	1:A:1317:ARG:NH1	2.23	1.01
5:K:350:PRO:O	5:K:353:ARG:HG3	1.60	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:388:ALA:HA	8:H:396:LEU:HD11	1.42	1.01
27:F:95:C:O2'	27:F:96:U:H5'	1.60	1.01
8:H:472:VAL:HG11	8:H:571:TYR:CE2	1.96	1.01
8:H:855:PRO:C	8:H:944:VAL:CG1	2.26	1.01
2:B:127:TYR:CE2	2:B:276:SER:HB2	1.96	1.01
4:G:721:ARG:CD	4:G:725:ILE:HD11	1.90	1.01
8:H:354:TYR:HB2	8:H:359:PHE:HB3	1.40	1.01
8:H:504:THR:O	8:H:507:SER:OG	1.79	1.01
8:H:793:GLU:HA	8:H:796:ILE:HG22	1.39	1.01
4:G:283:ARG:HD2	4:G:284:LEU:HD22	1.43	1.00
8:H:608:GLN:HE22	8:H:641:GLU:HG2	1.25	1.00
1:A:192:LEU:HD11	1:A:557:PHE:HB3	1.42	1.00
2:B:446:SER:OG	2:B:451:PHE:HD2	1.42	1.00
27:F:43:G:H2'	27:F:44:A:C8	1.96	1.00
4:G:691:TYR:O	4:G:695:THR:HG23	1.62	1.00
27:F:39:U:H2'	27:F:40:C:H5'	1.43	1.00
1:A:837:GLY:HA3	1:A:1317:ARG:NH1	1.77	1.00
8:H:488:ILE:CG2	8:H:558:LYS:CA	2.39	1.00
27:F:73:U:H2'	27:F:74:U:C5'	1.90	1.00
1:A:1008:LEU:CD2	1:A:1073:ILE:HD11	1.91	0.99
8:H:862:TYR:HE1	8:H:908:VAL:HB	1.27	0.99
8:H:500:ARG:HD3	8:H:534:THR:HG23	1.42	0.99
4:G:663:SER:C	4:G:667:CYS:SG	2.45	0.99
8:H:481:ALA:HB3	8:H:565:LYS:HZ1	1.25	0.99
8:H:187:ARG:NH1	8:H:653:ASP:OD2	1.95	0.99
8:H:582:SER:HB2	8:H:585:ASP:HB2	1.44	0.99
8:H:133:ILE:O	8:H:134:ILE:CG2	2.11	0.99
8:H:304:PHE:HD2	8:H:310:ASN:CB	1.76	0.99
8:H:576:THR:HG22	8:H:592:PHE:HB2	1.40	0.99
8:H:901:GLU:OE2	8:H:903:ARG:NH2	1.95	0.99
1:A:912:LEU:HD11	1:A:951:LEU:HD21	1.42	0.98
4:G:274:SER:CB	4:G:277:ILE:CD1	2.13	0.98
8:H:387:TYR:O	8:H:391:MET:HB2	1.62	0.98
8:H:500:ARG:HE	8:H:534:THR:HG21	1.21	0.98
27:F:73:U:C2'	27:F:74:U:C5'	2.39	0.98
2:B:388:GLN:OE1	2:B:388:GLN:N	1.96	0.98
8:H:572:ILE:HD12	8:H:573:LYS:HG3	1.45	0.98
8:H:863:GLU:HB3	8:H:931:TYR:CE1	1.97	0.98
2:B:398:GLN:OE1	2:B:442:SER:OG	1.80	0.98
8:H:855:PRO:O	8:H:944:VAL:HG11	1.45	0.98
1:A:168:LEU:HB2	1:A:199:ILE:HD12	1.41	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:497:GLN:O	1:A:709:ARG:HD2	1.62	0.98
6:L:96:GLY:O	6:L:138:ASN:HB3	1.63	0.98
8:H:227:VAL:HG11	8:H:474:LYS:CG	1.92	0.98
8:H:677:PHE:HE1	8:H:966:PHE:CE2	1.82	0.98
4:G:230:LEU:HD12	4:G:247:SER:HA	1.40	0.98
8:H:168:VAL:CG1	8:H:173:LYS:CG	2.41	0.97
8:H:889:TYR:CE1	8:H:890:LYS:CG	2.47	0.97
3:I:358:ILE:HG23	3:I:359:PRO:HD2	1.44	0.97
8:H:855:PRO:HG2	8:H:944:VAL:HG21	1.42	0.97
8:H:465:GLU:OE1	8:H:466:GLY:N	1.97	0.97
1:A:322:VAL:HG21	1:A:327:TYR:CE2	1.99	0.97
2:B:235:ILE:CD1	2:B:280:ILE:HD13	1.95	0.97
3:I:266:LYS:HG3	3:I:267:HIS:H	1.26	0.97
24:C:-4:A:HI'	24:C:-3:A:OP1	1.64	0.97
6:L:140:LYS:C	6:L:141:ARG:HD2	1.90	0.97
8:H:304:PHE:HD2	8:H:310:ASN:HB3	1.25	0.97
27:F:43:G:H2'	27:F:44:A:H8	1.26	0.97
1:A:781:THR:HA	1:A:784:GLN:CD	1.89	0.97
25:D:78:G:N2	26:E:4:C:C2	2.33	0.97
4:G:251:GLU:OE1	4:G:260:ALA:HB2	1.65	0.97
4:G:672:LEU:HD21	4:G:704:LEU:CG	1.93	0.97
3:I:282:GLU:HG2	3:I:286:PHE:CG	2.00	0.96
6:L:116:ILE:CD1	6:L:137:TYR:OH	2.13	0.96
8:H:677:PHE:CE1	8:H:966:PHE:CE2	2.53	0.96
4:G:846:PHE:HE1	4:G:859:LEU:HD21	0.91	0.96
8:H:492:LEU:CD2	8:H:557:HIS:ND1	2.28	0.96
1:A:773:SER:OG	1:A:774:ILE:CD1	2.13	0.96
8:H:576:THR:HG21	8:H:592:PHE:H	1.26	0.96
8:H:863:GLU:HB3	8:H:931:TYR:HE1	1.27	0.96
8:H:481:ALA:HB3	8:H:565:LYS:NZ	1.80	0.96
2:B:197:GLY:HA2	2:B:221:ILE:HG13	1.47	0.96
3:I:123:ARG:CD	3:I:189:LEU:CD1	2.41	0.96
8:H:324:ILE:O	8:H:328:VAL:HG23	1.66	0.96
1:A:1008:LEU:HD22	1:A:1073:ILE:HD11	1.46	0.95
3:I:226:ALA:CA	3:I:317:ASP:OD2	2.13	0.95
6:L:81:THR:HG21	6:L:102:LYS:NZ	1.80	0.95
6:L:105:PHE:CZ	6:L:137:TYR:HE2	1.72	0.95
8:H:126:MET:HE1	8:H:132:ARG:HH12	1.31	0.95
8:H:458:ILE:CG2	8:H:459:PRO:CD	2.43	0.95
27:F:77:A:H4'	27:F:78:A:H5''	1.49	0.95
8:H:106:PHE:CE2	8:H:554:HIS:CE1	2.55	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:44:A:C2'	27:F:45:A:H8	1.78	0.95
4:G:663:SER:CA	4:G:667:CYS:SG	2.55	0.95
4:G:666:ILE:O	4:G:670:PHE:CD2	2.19	0.95
8:H:364:PHE:CD2	8:H:369:LYS:HD3	1.96	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE3	1.45	0.95
1:A:1654:TRP:HZ3	1:A:1779:LEU:HD12	1.29	0.95
8:H:131:GLU:OE1	8:H:445:PRO:HG3	1.66	0.95
8:H:458:ILE:HG22	8:H:459:PRO:HD2	1.47	0.95
8:H:501:ILE:CD1	8:H:567:ILE:HG22	1.95	0.95
25:D:49:A:H2'	25:D:50:G:H5''	1.46	0.95
8:H:331:TYR:CE1	8:H:404:PHE:HD1	1.84	0.95
8:H:372:THR:HG22	8:H:376:PHE:CD1	2.01	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE2	1.47	0.94
27:F:99:U:O2'	27:F:100:A:OP1	1.84	0.94
27:F:175:G:N2	27:F:176:A:H62	1.65	0.94
1:A:1658:HIS:HA	1:A:1661:ILE:HD12	1.49	0.94
8:H:168:VAL:HG11	8:H:173:LYS:HD3	1.46	0.94
4:G:107:LEU:O	4:G:110:SER:OG	1.86	0.94
6:L:105:PHE:CB	6:L:141:ARG:CG	2.42	0.94
1:A:366:GLU:HB2	1:A:372:ARG:NH1	1.81	0.94
1:A:1490:ARG:HH12	1:A:1536:LEU:HA	1.33	0.94
8:H:383:LYS:O	8:H:387:TYR:HB2	1.68	0.94
26:E:151:G:N2	26:E:152:A:H62	1.65	0.94
27:F:175:G:N2	27:F:176:A:N6	2.16	0.94
2:B:235:ILE:HD12	2:B:280:ILE:HD13	1.47	0.94
8:H:488:ILE:CD1	8:H:560:GLN:CG	2.42	0.94
8:H:608:GLN:NE2	8:H:641:GLU:HG2	1.82	0.94
27:F:73:U:H2'	27:F:74:U:H5'	0.95	0.94
1:A:162:LEU:HG	1:A:734:PHE:HE2	1.32	0.94
1:A:165:LEU:O	1:A:168:LEU:HB3	1.68	0.94
4:G:692:LEU:CD2	4:G:708:LEU:HD11	1.98	0.94
2:B:290:ARG:NE	2:B:302:LEU:HD13	1.82	0.93
3:I:199:GLU:O	3:I:203:ILE:HG13	1.68	0.93
8:H:332:TYR:HH	8:H:376:PHE:HD2	1.06	0.93
1:A:168:LEU:HA	1:A:199:ILE:HD11	1.48	0.93
1:A:1022:PRO:HD3	1:A:1345:TYR:HE1	1.32	0.93
3:I:123:ARG:HD3	3:I:189:LEU:HD13	0.94	0.93
8:H:197:THR:CG2	8:H:545:LEU:HD13	1.96	0.93
24:C:2:A:H2	27:F:98:U:H3	1.06	0.93
6:L:96:GLY:O	6:L:138:ASN:CB	2.16	0.93
26:E:151:G:N2	26:E:152:A:N6	2.16	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:489:TYR:HD2	8:H:592:PHE:HZ	1.11	0.93
4:G:286:GLU:O	4:G:288:ASP:N	2.02	0.93
8:H:219:VAL:HG21	8:H:931:TYR:HB3	1.51	0.93
8:H:486:VAL:HG12	8:H:564:ILE:CD1	1.99	0.93
25:D:48:C:H3'	25:D:49:A:C8	1.99	0.93
1:A:212:VAL:HG11	1:A:285:PRO:HB3	1.46	0.93
8:H:192:LYS:HA	8:H:224:GLU:OE1	1.67	0.93
8:H:855:PRO:O	8:H:944:VAL:HG21	1.67	0.93
6:L:74:TYR:CG	6:L:83:MET:HE1	2.04	0.93
4:G:843:VAL:HG21	4:G:895:LEU:HD13	1.51	0.93
5:K:341:VAL:HG21	5:K:428:TRP:HE1	1.32	0.93
8:H:510:ARG:CB	8:H:591:PHE:HE2	1.80	0.93
27:F:45:A:C2	27:F:46:C:C5	2.56	0.93
8:H:449:PHE:CE1	8:H:453:THR:HG21	2.04	0.92
1:A:1621:VAL:HG12	1:A:1622:GLY:H	1.34	0.92
6:L:105:PHE:HZ	6:L:137:TYR:CE2	1.82	0.92
27:F:98:U:H4'	27:F:99:U:OP1	1.69	0.92
1:A:703:PHE:CE1	1:A:706:PRO:HD3	2.04	0.92
1:A:455:PRO:HB2	1:A:457:ASP:OD1	1.70	0.92
1:A:773:SER:OG	1:A:774:ILE:HD12	1.68	0.92
2:B:358:SER:OG	2:B:401:PHE:CE1	2.20	0.92
3:I:112:MET:CB	3:I:204:LEU:HD21	2.00	0.92
4:G:285:HIS:CE1	4:G:291:TYR:CE2	2.57	0.92
8:H:468:LEU:HD21	8:H:577:LEU:CD2	1.99	0.92
1:A:1748:ILE:HG22	1:A:1752:VAL:CG2	1.98	0.92
5:K:154:SER:O	5:K:158:ILE:HG23	1.68	0.92
3:I:282:GLU:CD	3:I:286:PHE:CD2	2.48	0.92
8:H:506:GLN:O	8:H:509:SER:HB2	1.69	0.92
8:H:500:ARG:HE	8:H:534:THR:CG2	1.77	0.92
8:H:856:ILE:HA	8:H:944:VAL:HG12	0.94	0.92
8:H:968:MET:HE2	8:H:968:MET:HA	1.50	0.92
4:G:274:SER:HB3	4:G:277:ILE:HD12	1.50	0.92
8:H:458:ILE:HG23	8:H:459:PRO:CD	1.99	0.92
2:B:115:SER:HA	2:B:118:ILE:CD1	1.99	0.91
6:L:74:TYR:CD1	6:L:83:MET:HE1	2.06	0.91
8:H:330:TYR:CE1	8:H:430:ARG:CZ	2.52	0.91
8:H:372:THR:CG2	8:H:376:PHE:CE1	2.52	0.91
8:H:889:TYR:CE1	8:H:890:LYS:HG2	2.04	0.91
1:A:1256:PRO:HA	1:A:1274:ARG:HH21	1.31	0.91
4:G:668:HIS:CB	4:G:698:VAL:HG11	2.00	0.91
4:G:663:SER:HA	4:G:667:CYS:SG	2.09	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1755:LYS:HG3	1:A:1759:TYR:CE2	2.06	0.91
8:H:132:ARG:HG2	8:H:132:ARG:HH11	1.35	0.91
8:H:488:ILE:HG22	8:H:558:LYS:HA	0.93	0.91
8:H:582:SER:HB2	8:H:585:ASP:OD2	1.69	0.91
1:A:286:LEU:CD2	1:A:292:LYS:HB2	2.01	0.91
3:I:282:GLU:CD	3:I:286:PHE:CE2	2.49	0.91
8:H:489:TYR:CD2	8:H:592:PHE:HZ	1.88	0.91
1:A:288:GLU:OE1	1:A:288:GLU:N	2.04	0.91
4:G:105:ALA:O	4:G:108:LYS:HG3	1.71	0.91
8:H:889:TYR:CD1	8:H:890:LYS:CG	2.53	0.90
7:M:95:ARG:HG2	7:M:95:ARG:HH11	1.34	0.90
8:H:329:SER:HA	8:H:333:ALA:HB2	1.53	0.90
1:A:298:TYR:O	1:A:493:MET:HG3	1.70	0.90
1:A:412:GLN:OE1	1:A:412:GLN:N	2.05	0.90
2:B:389:ILE:HD13	2:B:427:TRP:HB3	1.53	0.90
4:G:695:THR:HB	4:G:705:TRP:HE1	1.33	0.90
8:H:185:ILE:HD13	27:F:75:A:OP2	1.72	0.90
2:B:173:VAL:HG13	2:B:200:GLN:OE1	1.70	0.90
1:A:317:PRO:HG2	1:A:318:LEU:HD12	1.51	0.90
1:A:322:VAL:HG21	1:A:327:TYR:CD2	2.06	0.90
27:F:75:A:N7	27:F:77:A:C5'	2.35	0.90
1:A:769:MET:HE2	4:G:112:ALA:HA	1.52	0.90
2:B:313:LEU:CD1	2:B:322:VAL:HG23	2.02	0.90
4:G:668:HIS:O	4:G:672:LEU:HG	1.72	0.90
27:F:75:A:O2'	27:F:76:U:OP2	1.89	0.90
2:B:316:GLN:HB2	2:B:357:TRP:CE2	2.07	0.90
8:H:481:ALA:CB	8:H:565:LYS:NZ	2.35	0.90
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.51	0.89
8:H:168:VAL:HG13	8:H:173:LYS:HD3	0.93	0.89
3:I:184:LYS:CE	3:I:186:LYS:HB2	2.03	0.89
4:G:695:THR:O	4:G:699:PRO:CG	2.20	0.89
8:H:355:HIS:O	8:H:356:LYS:CG	2.19	0.89
1:A:218:SER:CA	1:A:318:LEU:HD21	2.02	0.89
4:G:272:PRO:HB3	4:G:302:PHE:HD1	1.35	0.89
6:L:105:PHE:CZ	6:L:137:TYR:HD2	1.84	0.89
6:L:33:ARG:HD3	6:L:65:ASP:CG	1.98	0.89
8:H:598:ILE:HG22	8:H:933:TRP:HZ3	1.32	0.89
8:H:674:LEU:HD13	8:H:973:ARG:HH12	1.35	0.89
6:L:105:PHE:HB3	6:L:141:ARG:HG2	0.89	0.89
25:D:48:C:H4'	25:D:49:A:OP1	1.73	0.89
8:H:500:ARG:CG	8:H:534:THR:HG21	2.03	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:721:ARG:HD3	4:G:725:ILE:HD11	1.53	0.89
8:H:855:PRO:O	8:H:944:VAL:CB	2.21	0.89
5:K:354:PHE:HE1	5:K:358:MET:HE3	0.74	0.88
4:G:266:ASN:O	4:G:269:GLN:HG3	1.73	0.88
8:H:889:TYR:CE1	8:H:890:LYS:HG3	2.06	0.88
1:A:294:ASN:CB	1:A:299:LYS:O	2.22	0.88
1:A:923:TYR:CE1	1:A:933:GLU:HG3	2.08	0.88
2:B:274:HIS:HD2	2:B:276:SER:H	1.20	0.88
8:H:855:PRO:O	8:H:944:VAL:HG13	1.72	0.88
25:D:83:A:O2'	25:D:84:C:OP2	1.92	0.88
4:G:277:ILE:HD12	4:G:277:ILE:H	1.36	0.88
5:K:428:TRP:CZ2	5:K:463:PHE:CE2	2.61	0.88
8:H:304:PHE:CD2	8:H:310:ASN:HB3	2.07	0.88
24:C:7:A:O2'	24:C:8:U:O5'	1.92	0.88
25:D:50:G:O2'	25:D:51:A:O5'	1.91	0.88
2:B:124:LEU:O	2:B:128:SER:OG	1.90	0.88
3:I:373:ARG:HB3	3:I:373:ARG:HH11	1.38	0.88
8:H:855:PRO:CG	8:H:944:VAL:HG21	2.03	0.88
1:A:466:GLU:N	1:A:466:GLU:OE2	2.06	0.88
1:A:850:GLY:O	1:A:853:THR:HG22	1.73	0.88
2:B:393:ARG:HG2	2:B:393:ARG:HH21	1.37	0.88
3:I:98:PHE:HE2	3:I:217:TYR:CD2	1.91	0.88
8:H:582:SER:HB2	8:H:585:ASP:CB	2.03	0.88
1:A:501:LEU:HD12	1:A:501:LEU:H	1.38	0.88
4:G:702:PRO:HB3	4:G:739:PHE:CZ	2.09	0.88
6:L:101:ASN:O	6:L:102:LYS:HG2	1.73	0.88
6:L:105:PHE:HB2	6:L:141:ARG:HG2	1.56	0.88
8:H:364:PHE:HB3	8:H:369:LYS:HG3	1.53	0.88
8:H:415:TYR:O	8:H:416:ASP:OD1	1.92	0.88
8:H:501:ILE:HD13	8:H:567:ILE:HG22	1.55	0.88
2:B:124:LEU:HD21	2:B:274:HIS:CE1	2.08	0.88
8:H:189:LEU:HD12	8:H:190:SER:N	1.89	0.88
1:A:297:SER:HB2	27:F:32:G:O5'	1.74	0.87
4:G:696:ARG:C	4:G:699:PRO:HD3	1.98	0.87
4:G:891:ILE:O	4:G:894:ARG:N	2.07	0.87
8:H:168:VAL:CG1	8:H:173:LYS:HG3	2.04	0.87
2:B:380:LYS:O	2:B:381:ARG:HG2	1.73	0.87
2:B:395:ILE:HG22	2:B:396:VAL:H	1.38	0.87
1:A:141:LYS:CA	1:A:144:ASN:HD21	1.86	0.87
1:A:674:MET:HE2	1:A:678:ARG:HD3	1.56	0.87
2:B:446:SER:OG	2:B:451:PHE:CD2	2.19	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:212:VAL:H	4:G:215:LEU:HD23	1.39	0.87
4:G:282:ILE:O	4:G:286:GLU:HG2	1.73	0.87
4:G:691:TYR:HB3	4:G:708:LEU:CD1	2.03	0.87
5:K:350:PRO:HA	5:K:353:ARG:CD	2.04	0.87
5:K:141:ASN:OD1	5:K:142:LEU:N	2.07	0.87
1:A:266:LEU:HD23	1:A:267:PRO:HD2	1.55	0.87
1:A:358:ARG:HB3	1:A:358:ARG:HH11	1.37	0.87
4:G:692:LEU:HD23	4:G:708:LEU:HD11	1.55	0.87
24:C:8:U:C5	25:D:51:A:N6	2.34	0.87
8:H:306:PRO:HG2	8:H:349:TRP:CZ3	2.09	0.87
27:F:98:U:O2'	27:F:99:U:O5'	1.92	0.87
1:A:1353:THR:O	1:A:1357:LEU:HD12	1.73	0.87
1:A:1373:LEU:HD13	6:L:139:HIS:HE1	1.36	0.86
3:I:282:GLU:OE2	3:I:286:PHE:CD2	2.27	0.86
8:H:250:GLU:HB3	8:H:298:PHE:CE2	2.09	0.86
1:A:168:LEU:HB2	1:A:199:ILE:CD1	2.03	0.86
1:A:837:GLY:HA3	1:A:1317:ARG:HH12	1.37	0.86
2:B:274:HIS:CD2	2:B:276:SER:HB3	2.10	0.86
1:A:1364:GLU:OE1	1:A:1389:TYR:OH	1.92	0.86
6:L:33:ARG:CD	6:L:65:ASP:CG	2.49	0.86
2:B:177:PRO:HB3	2:B:457:TRP:HA	1.56	0.86
3:I:191:ILE:H	3:I:191:ILE:HD12	1.38	0.86
8:H:488:ILE:HD13	8:H:557:HIS:O	1.74	0.86
8:H:489:TYR:CD2	8:H:592:PHE:CZ	2.64	0.86
6:L:140:LYS:HB3	6:L:141:ARG:HD2	1.55	0.86
2:B:313:LEU:HD13	2:B:322:VAL:HG23	1.57	0.86
4:G:892:LEU:O	4:G:896:MET:HG2	1.75	0.86
1:A:1373:LEU:CD1	6:L:139:HIS:HE1	1.88	0.86
1:A:149:MET:HB3	1:A:154:TYR:HD2	1.39	0.86
3:I:231:PHE:CD2	3:I:330:ALA:HB1	2.10	0.86
4:G:886:CYS:SG	4:G:888:PRO:HD2	2.16	0.86
8:H:197:THR:HG23	8:H:545:LEU:O	1.76	0.86
8:H:489:TYR:HD2	8:H:592:PHE:CZ	1.93	0.86
8:H:810:GLU:CD	8:H:974:LYS:HG3	2.00	0.86
1:A:162:LEU:CD2	1:A:730:ILE:CG2	1.74	0.85
1:A:1490:ARG:NH1	1:A:1536:LEU:HD23	1.91	0.85
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.41	0.85
2:B:159:LEU:HD13	2:B:430:MET:CE	2.05	0.85
2:B:162:MET:HE2	2:B:162:MET:N	1.90	0.85
4:G:688:ARG:HH12	4:G:721:ARG:HE	1.24	0.85
8:H:481:ALA:CB	8:H:565:LYS:HZ3	1.89	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:LEU:HD21	1:A:292:LYS:CB	2.05	0.85
1:A:823:TRP:HZ3	1:A:855:LEU:HD21	1.39	0.85
2:B:197:GLY:HA2	2:B:221:ILE:CG1	2.07	0.85
8:H:197:THR:CG2	8:H:545:LEU:HD12	2.06	0.85
8:H:608:GLN:HE22	8:H:641:GLU:CG	1.89	0.85
1:A:936:GLU:O	1:A:940:ILE:HD12	1.77	0.85
1:A:1275:MET:HE1	1:A:1299:LYS:CE	2.06	0.85
8:H:117:ARG:CD	8:H:157:SER:O	2.23	0.85
4:G:691:TYR:CB	4:G:708:LEU:HD12	2.04	0.85
1:A:1756:PHE:O	1:A:1760:THR:HG23	1.75	0.85
2:B:115:SER:HA	2:B:118:ILE:HD12	1.57	0.85
8:H:120:ARG:HG3	8:H:551:TYR:CE1	2.11	0.85
8:H:235:VAL:HG22	8:H:261:VAL:HG12	1.59	0.85
8:H:586:MET:O	8:H:589:LEU:HD23	1.77	0.85
1:A:224:MET:HG3	1:A:701:CYS:O	1.77	0.85
1:A:928:ARG:HH21	4:G:145:THR:HG21	1.42	0.85
8:H:106:PHE:HE2	8:H:554:HIS:CE1	1.93	0.85
8:H:951:ILE:HB	8:H:952:PRO:HD2	1.58	0.85
1:A:162:LEU:HD21	1:A:730:ILE:CB	2.06	0.85
1:A:166:LYS:O	1:A:169:PRO:HD2	1.76	0.85
1:A:1498:ASP:OD1	1:A:1502:LEU:CD1	2.25	0.85
8:H:247:PHE:HA	8:H:250:GLU:OE1	1.76	0.85
8:H:855:PRO:HG2	8:H:944:VAL:CG2	2.05	0.85
1:A:176:LEU:HD23	1:A:708:TRP:HE1	1.42	0.84
2:B:117:LEU:HD23	2:B:300:LEU:HB3	1.58	0.84
2:B:124:LEU:CD2	2:B:274:HIS:CE1	2.60	0.84
8:H:605:ILE:HG13	8:H:652:MET:SD	2.17	0.84
3:I:158:PHE:HA	3:I:161:LEU:HD12	1.57	0.84
8:H:449:PHE:HE1	8:H:453:THR:HG21	1.40	0.84
8:H:486:VAL:HG11	8:H:564:ILE:HD11	1.57	0.84
8:H:501:ILE:HD13	8:H:567:ILE:CG2	2.05	0.84
8:H:951:ILE:O	8:H:952:PRO:O	1.95	0.84
1:A:251:TYR:HA	1:A:255:ILE:HD12	1.58	0.84
4:G:278:TRP:CZ2	4:G:298:THR:HB	2.12	0.84
8:H:793:GLU:HA	8:H:796:ILE:CG2	2.06	0.84
1:A:691:PHE:CZ	1:A:701:CYS:HA	2.13	0.84
1:A:703:PHE:HE1	1:A:706:PRO:HD3	1.40	0.84
8:H:862:TYR:HE1	8:H:908:VAL:CB	1.90	0.84
1:A:175:LEU:HD12	1:A:175:LEU:O	1.76	0.84
1:A:1877:GLY:O	1:A:1894:ILE:N	2.11	0.84
2:B:320:SER:HB2	2:B:337:ARG:NH2	1.92	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:320:SER:HB2	2:B:337:ARG:HH22	1.42	0.84
4:G:888:PRO:O	4:G:892:LEU:HD23	1.77	0.84
8:H:504:THR:CA	8:H:507:SER:OG	2.25	0.84
27:F:39:U:C2'	27:F:40:C:H5'	2.06	0.84
27:F:175:G:H21	27:F:176:A:H62	1.23	0.84
25:D:86:G:H8	25:D:86:G:H5''	1.41	0.84
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.56	0.84
8:H:332:TYR:OH	8:H:376:PHE:CB	2.25	0.84
1:A:195:THR:CG2	1:A:556:TYR:O	2.24	0.84
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	1.78	0.84
8:H:449:PHE:O	8:H:453:THR:HG23	1.77	0.84
8:H:576:THR:CG2	8:H:592:PHE:HB2	2.07	0.84
1:A:160:ALA:HB1	1:A:194:HIS:CE1	2.12	0.84
1:A:176:LEU:CD2	1:A:708:TRP:HE1	1.90	0.84
1:A:218:SER:N	1:A:318:LEU:CD2	2.41	0.84
1:A:585:ARG:HD2	1:A:733:GLN:CD	2.03	0.84
1:A:1909:ALA:O	1:A:1913:THR:HG23	1.78	0.84
3:I:98:PHE:CE2	3:I:217:TYR:CD2	2.65	0.84
3:I:401:LEU:HD12	4:G:214:SER:HB3	1.58	0.84
24:C:-3:A:C8	24:C:-2:A:C5	2.61	0.84
27:F:78:A:N1	27:F:81:A:C5	2.46	0.84
3:I:197:ILE:C	3:I:201:ASN:HD22	1.85	0.84
4:G:122:ILE:HG13	4:G:123:PRO:HD2	1.57	0.84
8:H:542:ILE:O	8:H:553:VAL:HB	1.77	0.84
1:A:170:HIS:ND1	1:A:547:LEU:HD23	1.93	0.83
1:A:286:LEU:CD2	1:A:292:LYS:CB	2.56	0.83
1:A:1459:ALA:O	1:A:1463:THR:HG23	1.78	0.83
2:B:380:LYS:C	2:B:381:ARG:HG2	2.02	0.83
6:L:105:PHE:HE1	6:L:137:TYR:CE2	1.92	0.83
8:H:576:THR:HG21	8:H:592:PHE:N	1.92	0.83
4:G:863:PHE:HB3	4:G:889:ARG:HH22	1.41	0.83
5:K:350:PRO:CA	5:K:353:ARG:HG2	2.06	0.83
4:G:863:PHE:CE2	4:G:892:LEU:HD21	2.13	0.83
27:F:75:A:C5	27:F:77:A:H5''	2.13	0.83
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	1.78	0.83
2:B:335:ASP:OD1	2:B:337:ARG:HD2	1.77	0.83
8:H:576:THR:HB	8:H:592:PHE:HD2	1.41	0.83
27:F:75:A:N7	27:F:77:A:H5'	1.91	0.83
1:A:1453:ASP:O	1:A:1456:ARG:HG2	1.77	0.83
8:H:120:ARG:HG3	8:H:551:TYR:CZ	2.13	0.83
1:A:923:TYR:CE1	1:A:933:GLU:CG	2.62	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:441:ILE:HD11	2:B:457:TRP:HE1	1.42	0.83
3:I:373:ARG:HH11	3:I:373:ARG:CB	1.91	0.83
4:G:268:CYS:SG	4:G:278:TRP:CZ2	2.72	0.83
9:N:807:GLY:N	9:N:1093:ALA:N	2.23	0.83
26:E:151:G:H21	26:E:152:A:H62	1.23	0.83
27:F:33:U:O2'	27:F:34:C:P	2.37	0.83
2:B:47:GLU:O	2:B:51:VAL:HG23	1.78	0.83
2:B:197:GLY:HA2	2:B:221:ILE:CD1	2.08	0.83
8:H:307:ILE:HD12	8:H:324:ILE:HD11	1.59	0.83
1:A:753:TYR:HE1	6:L:37:ARG:HB3	1.44	0.83
3:I:98:PHE:O	3:I:101:ILE:HG22	1.78	0.83
25:D:62:A:C2	26:E:58:G:C2	2.66	0.83
5:K:341:VAL:HG21	5:K:428:TRP:NE1	1.93	0.82
5:K:146:GLU:HA	5:K:149:PHE:CD2	2.14	0.82
1:A:289:ASP:OD2	1:A:292:LYS:CG	2.27	0.82
5:K:428:TRP:HZ2	5:K:463:PHE:HE2	1.27	0.82
8:H:372:THR:HG23	8:H:376:PHE:CE1	2.12	0.82
8:H:116:THR:HG23	8:H:158:HIS:HD2	1.37	0.82
27:F:103:A:O2'	27:F:104:G:O5'	1.96	0.82
1:A:795:ALA:HA	1:A:1095:MET:CE	2.09	0.82
2:B:170:SER:O	2:B:171:GLN:HB2	1.79	0.82
2:B:389:ILE:HD11	2:B:427:TRP:CG	2.14	0.82
4:G:251:GLU:OE2	4:G:259:VAL:HB	1.79	0.82
8:H:488:ILE:HG21	8:H:558:LYS:HA	1.59	0.82
2:B:387:ASN:C	2:B:388:GLN:OE1	2.22	0.82
8:H:230:ALA:CB	8:H:595:LEU:HD21	2.09	0.82
25:D:62:A:H2'	25:D:63:G:H5'	1.61	0.82
2:B:419:ILE:HD11	2:B:443:LEU:CD1	2.10	0.82
5:K:164:HIS:ND1	5:K:164:HIS:O	2.13	0.82
8:H:674:LEU:CD1	8:H:973:ARG:HH12	1.93	0.82
8:H:797:GLN:HA	8:H:797:GLN:NE2	1.94	0.82
1:A:1350:ILE:HG23	1:A:1356:LEU:CD1	2.09	0.82
2:B:446:SER:OG	2:B:451:PHE:HB2	1.78	0.82
3:I:184:LYS:HD2	3:I:186:LYS:N	1.93	0.82
8:H:113:ILE:HG22	8:H:114:PRO:HD2	1.62	0.82
1:A:218:SER:CA	1:A:318:LEU:CD2	2.55	0.82
1:A:1313:ASP:CG	1:A:1359:ILE:HD13	2.05	0.82
2:B:202:LEU:HD23	2:B:207:LEU:CD2	2.09	0.82
1:A:149:MET:HG2	1:A:154:TYR:CE2	2.15	0.82
1:A:1415:SER:OG	1:A:1746:HIS:NE2	2.12	0.82
1:A:923:TYR:HE1	1:A:933:GLU:HG3	1.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1908:LEU:HD12	1:A:1908:LEU:O	1.80	0.81
2:B:323:CYS:SG	2:B:355:VAL:CG1	2.68	0.81
4:G:283:ARG:HD2	4:G:284:LEU:CD2	2.09	0.81
8:H:194:ASN:OD1	8:H:547:GLY:HA2	1.80	0.81
1:A:404:ASN:OD1	8:H:927:MET:CE	2.28	0.81
1:A:809:LYS:O	1:A:813:GLU:HG2	1.80	0.81
2:B:459:ARG:NH2	4:G:758:LEU:HD22	1.95	0.81
5:K:350:PRO:CA	5:K:353:ARG:CG	2.56	0.81
8:H:373:PHE:CD1	8:H:377:ILE:HD12	2.14	0.81
4:G:104:PHE:O	4:G:107:LEU:N	2.14	0.81
4:G:702:PRO:HB3	4:G:739:PHE:CE1	2.16	0.81
8:H:230:ALA:HB2	8:H:595:LEU:HD21	1.60	0.81
8:H:492:LEU:CD2	8:H:557:HIS:CG	2.62	0.81
2:B:51:VAL:HG13	2:B:76:LEU:CD1	2.09	0.81
5:K:354:PHE:CE1	5:K:358:MET:CE	2.40	0.81
21:f:19:LYS:O	21:f:84:GLY:N	2.13	0.81
3:I:184:LYS:CD	3:I:186:LYS:HB2	2.10	0.81
1:A:289:ASP:O	1:A:293:VAL:CG1	2.24	0.81
1:A:1496:GLN:O	1:A:1499:ARG:HG2	1.81	0.81
2:B:195:TRP:O	2:B:219:GLY:O	1.99	0.81
2:B:286:ASP:C	2:B:287:MET:HG2	2.05	0.81
4:G:721:ARG:HD2	4:G:725:ILE:HD11	1.60	0.81
8:H:183:GLN:OE1	8:H:657:TYR:CD2	2.34	0.81
8:H:946:ASP:O	8:H:964:ARG:HG2	1.80	0.81
1:A:176:LEU:HD23	1:A:176:LEU:O	1.79	0.81
8:H:471:HIS:O	8:H:486:VAL:HG23	1.81	0.81
8:H:504:THR:C	8:H:507:SER:HG	1.88	0.81
25:D:49:A:H2'	25:D:50:G:C5'	2.11	0.81
27:F:32:G:H5'	27:F:32:G:C8	2.15	0.81
8:H:175:LEU:HD23	8:H:176:ARG:N	1.96	0.81
27:F:95:C:C4'	27:F:96:U:OP1	2.29	0.81
4:G:144:LYS:NZ	26:E:55:U:O5'	2.14	0.80
1:A:149:MET:HG2	1:A:154:TYR:HE2	1.46	0.80
1:A:361:GLU:N	1:A:361:GLU:OE2	2.13	0.80
25:D:48:C:C3'	25:D:49:A:N7	2.34	0.80
1:A:217:TRP:C	1:A:318:LEU:HD21	2.05	0.80
6:L:140:LYS:HB3	6:L:141:ARG:CD	2.11	0.80
8:H:568:SER:HA	8:H:571:TYR:HE1	1.45	0.80
8:H:769:TYR:CE1	8:H:799:PHE:HE2	1.99	0.80
8:H:336:ILE:HD11	8:H:341:ILE:HG22	1.61	0.80
8:H:369:LYS:HE2	8:H:369:LYS:O	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:598:ILE:CG2	8:H:933:TRP:CZ3	2.64	0.80
1:A:301:TRP:CD1	1:A:491:GLY:O	2.34	0.80
3:I:268:LEU:HD12	3:I:271:GLU:CG	2.11	0.80
4:G:295:LEU:O	4:G:298:THR:OG1	1.98	0.80
8:H:468:LEU:CD1	8:H:493:LEU:HD21	2.09	0.80
1:A:289:ASP:OD2	1:A:292:LYS:HG2	1.81	0.80
1:A:703:PHE:HE1	1:A:705:GLN:HB3	1.45	0.80
8:H:296:ASN:HD21	8:H:304:PHE:H	1.26	0.80
8:H:793:GLU:CA	8:H:796:ILE:HG22	2.11	0.80
2:B:446:SER:HB2	2:B:451:PHE:H	1.46	0.80
8:H:133:ILE:C	8:H:134:ILE:HG23	2.07	0.80
8:H:470:ALA:HB1	8:H:486:VAL:CG2	2.10	0.80
8:H:769:TYR:CE1	8:H:799:PHE:CE2	2.70	0.80
1:A:162:LEU:CG	1:A:730:ILE:CG2	2.58	0.80
4:G:846:PHE:CD1	4:G:859:LEU:HD21	2.17	0.80
8:H:121:ASP:OD1	8:H:122:TYR:N	2.15	0.80
1:A:781:THR:N	1:A:784:GLN:OE1	2.14	0.80
1:A:912:LEU:CD1	1:A:951:LEU:HD21	2.12	0.80
2:B:441:ILE:HD11	2:B:457:TRP:NE1	1.97	0.80
8:H:168:VAL:HG12	8:H:173:LYS:HG3	1.63	0.80
8:H:470:ALA:HB3	8:H:577:LEU:HB3	1.61	0.80
27:F:78:A:C6	27:F:81:A:N7	2.50	0.80
1:A:305:LEU:HD11	1:A:476:ALA:HB2	1.63	0.80
1:A:1654:TRP:CH2	1:A:1779:LEU:HD12	2.17	0.80
4:G:688:ARG:HH12	4:G:721:ARG:NE	1.79	0.80
1:A:166:LYS:HD3	1:A:167:TYR:CE1	2.17	0.79
1:A:837:GLY:CA	1:A:1317:ARG:HH11	1.95	0.79
2:B:316:GLN:HG3	2:B:357:TRP:CZ2	2.16	0.79
3:I:46:ILE:O	3:I:97:PHE:CZ	2.35	0.79
4:G:696:ARG:O	4:G:699:PRO:CD	2.30	0.79
4:G:863:PHE:CE2	4:G:892:LEU:HG	2.17	0.79
27:F:32:G:H1	27:F:121:U:H3	1.31	0.79
4:G:251:GLU:OE2	4:G:259:VAL:CG1	2.30	0.79
4:G:695:THR:O	4:G:699:PRO:CD	2.30	0.79
4:G:691:TYR:HE2	4:G:711:ILE:HD11	1.47	0.79
8:H:488:ILE:HG21	8:H:558:LYS:CA	2.10	0.79
8:H:488:ILE:HG21	8:H:558:LYS:N	1.97	0.79
1:A:1264:GLY:HA3	1:A:1308:GLU:OE1	1.83	0.79
3:I:123:ARG:NH1	3:I:187:GLU:O	2.14	0.79
8:H:856:ILE:HA	8:H:944:VAL:HG13	1.59	0.79
8:H:856:ILE:CA	8:H:944:VAL:HG12	1.85	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:968:MET:HE2	8:H:968:MET:CA	2.12	0.79
1:A:456:GLU:OE1	1:A:456:GLU:N	2.14	0.79
2:B:389:ILE:CD1	2:B:427:TRP:CB	2.46	0.79
3:I:217:TYR:HE1	3:I:221:LYS:HZ3	0.81	0.79
4:G:672:LEU:CG	4:G:704:LEU:HD21	2.13	0.79
8:H:189:LEU:HD13	28:H:1500:GTP:O1G	1.82	0.79
4:G:691:TYR:CE2	4:G:711:ILE:CD1	2.66	0.79
4:G:691:TYR:CE2	4:G:711:ILE:HD11	2.18	0.79
8:H:449:PHE:CE1	8:H:453:THR:CG2	2.65	0.79
8:H:504:THR:C	8:H:507:SER:OG	2.26	0.79
4:G:274:SER:HB3	4:G:277:ILE:HD11	0.79	0.79
5:K:159:TYR:O	5:K:163:ASN:ND2	2.16	0.79
25:D:83:A:H1'	25:D:84:C:H5	1.47	0.79
1:A:285:PRO:CD	1:A:298:TYR:OH	2.21	0.78
4:G:98:SER:OG	4:G:99:ASN:ND2	2.16	0.78
6:L:140:LYS:CG	6:L:141:ARG:NH1	2.46	0.78
8:H:197:THR:HG21	8:H:545:LEU:HD12	1.64	0.78
8:H:500:ARG:HE	8:H:534:THR:CB	1.96	0.78
7:M:93:VAL:HG12	7:M:95:ARG:H	1.48	0.78
8:H:167:ASN:ND2	8:H:173:LYS:HG2	1.98	0.78
27:F:77:A:C4'	27:F:78:A:H5''	2.14	0.78
1:A:1038:ILE:HD11	1:A:1039:TRP:CD2	2.17	0.78
8:H:468:LEU:HD11	8:H:493:LEU:CD2	2.09	0.78
2:B:51:VAL:HG13	2:B:76:LEU:HD11	1.66	0.78
3:I:138:SER:HA	3:I:141:ILE:HD12	1.64	0.78
8:H:467:THR:O	8:H:490:SER:HB3	1.82	0.78
1:A:923:TYR:HE1	1:A:933:GLU:CG	1.95	0.78
2:B:290:ARG:HE	2:B:302:LEU:HD13	1.45	0.78
8:H:863:GLU:CB	8:H:931:TYR:HE1	1.96	0.78
1:A:1275:MET:HE1	1:A:1299:LYS:CD	2.14	0.78
1:A:1755:LYS:CG	1:A:1759:TYR:HE2	1.96	0.78
3:I:266:LYS:HG3	3:I:267:HIS:N	1.98	0.78
6:L:33:ARG:HD2	6:L:65:ASP:OD2	1.83	0.78
9:N:565:ALA:CA	9:N:837:GLY:HA2	2.13	0.78
1:A:770:MET:HE1	1:A:778:LYS:CB	2.14	0.78
3:I:184:LYS:HD2	3:I:186:LYS:HB2	1.63	0.78
1:A:2079:ILE:HA	1:A:2082:ILE:HD12	1.64	0.78
3:I:266:LYS:CG	3:I:267:HIS:H	1.96	0.78
4:G:863:PHE:CE2	4:G:892:LEU:CG	2.67	0.78
1:A:1468:ALA:HB1	1:A:1473:ARG:O	1.83	0.78
5:K:457:GLN:OE1	5:K:457:GLN:N	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:116:THR:CG2	8:H:158:HIS:CD2	2.65	0.78
8:H:355:HIS:O	8:H:356:LYS:HG3	1.82	0.78
1:A:287:GLU:HB2	1:A:288:GLU:OE1	1.84	0.78
4:G:251:GLU:OE2	4:G:259:VAL:HG12	1.84	0.78
4:G:702:PRO:O	4:G:706:VAL:HG23	1.83	0.78
8:H:472:VAL:CG1	8:H:571:TYR:CE2	2.67	0.78
27:F:78:A:N1	27:F:81:A:C4	2.53	0.77
1:A:1697:SER:OG	1:A:1759:TYR:CD1	2.37	0.77
6:L:25:ARG:HB2	6:L:25:ARG:HH11	1.49	0.77
8:H:769:TYR:CZ	8:H:799:PHE:HE2	2.01	0.77
1:A:511:ASP:HB2	1:A:514:TYR:CE1	2.19	0.77
4:G:282:ILE:HA	4:G:295:LEU:HD12	1.66	0.77
8:H:862:TYR:CE1	8:H:908:VAL:HB	2.18	0.77
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.67	0.77
1:A:1877:GLY:O	1:A:1894:ILE:HB	1.83	0.77
5:K:428:TRP:CZ2	5:K:463:PHE:HE2	2.01	0.77
27:F:75:A:O2'	27:F:76:U:P	2.41	0.77
1:A:212:VAL:HG11	1:A:285:PRO:CB	2.15	0.77
1:A:823:TRP:CZ3	1:A:855:LEU:HD21	2.19	0.77
4:G:212:VAL:HG13	4:G:215:LEU:HB3	1.66	0.77
6:L:139:HIS:NE2	27:F:96:U:C5'	2.48	0.77
8:H:195:GLY:HA3	8:H:545:LEU:HD22	1.66	0.77
1:A:273:ASP:HB3	1:A:276:VAL:CG2	2.14	0.77
27:F:31:G:C2	27:F:32:G:H1'	2.19	0.77
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD11	2.17	0.77
4:G:695:THR:CB	4:G:705:TRP:HE1	1.98	0.77
8:H:794:GLN:OE1	8:H:835:LYS:HG3	1.84	0.77
8:H:947:LYS:CD	8:H:947:LYS:H	1.98	0.77
1:A:168:LEU:HA	1:A:199:ILE:CD1	2.14	0.77
5:K:146:GLU:O	5:K:148:LYS:N	2.18	0.77
1:A:1490:ARG:HH11	1:A:1536:LEU:HA	1.47	0.77
2:B:64:VAL:HG12	2:B:65:GLU:H	1.49	0.77
2:B:316:GLN:HG3	2:B:357:TRP:CE2	2.20	0.77
4:G:252:GLU:HG2	4:G:256:LYS:CG	2.15	0.77
8:H:151:ASP:OD1	8:H:175:LEU:HD22	1.85	0.77
1:A:317:PRO:HG2	1:A:318:LEU:CD1	2.15	0.77
1:A:2064:GLY:O	1:A:2068:ASN:N	2.18	0.77
9:N:1198:ARG:CA	9:N:1227:ILE:H	1.96	0.77
2:B:459:ARG:CZ	4:G:758:LEU:HD22	2.14	0.76
3:I:245:ALA:HB1	3:I:250:GLU:HB3	1.66	0.76
4:G:285:HIS:HE1	4:G:291:TYR:CE2	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:883:ARG:O	8:H:884:ARG:HB2	1.81	0.76
1:A:912:LEU:HD11	1:A:951:LEU:CD2	2.16	0.76
8:H:189:LEU:HD21	8:H:218:HIS:HB2	1.67	0.76
8:H:265:PHE:CE2	8:H:295:ILE:HD12	2.20	0.76
8:H:492:LEU:HD23	8:H:557:HIS:HA	1.66	0.76
9:N:807:GLY:H	9:N:1093:ALA:CA	1.97	0.76
5:K:350:PRO:HB3	25:D:84:C:C5	2.21	0.76
8:H:492:LEU:HD21	8:H:557:HIS:CG	2.20	0.76
3:I:268:LEU:HD12	3:I:271:GLU:HG3	1.66	0.76
8:H:697:ARG:NE	8:H:697:ARG:HA	2.00	0.76
8:H:951:ILE:O	8:H:951:ILE:HD12	1.85	0.76
8:H:242:VAL:HG21	8:H:272:ARG:HD3	1.67	0.76
1:A:315:SER:C	1:A:317:PRO:HD2	2.11	0.76
1:A:795:ALA:HA	1:A:1095:MET:HE3	1.66	0.76
8:H:355:HIS:O	8:H:356:LYS:HG2	1.86	0.76
8:H:545:LEU:HD12	8:H:545:LEU:H	1.51	0.76
8:H:942:GLY:HA3	8:H:961:SER:HA	1.67	0.76
27:F:75:A:N7	27:F:77:A:H5''	2.00	0.76
27:F:106:A:C2'	27:F:107:C:H5'	2.16	0.76
1:A:162:LEU:HG	1:A:734:PHE:CE2	2.17	0.76
1:A:1073:ILE:HD12	1:A:1116:TYR:CE1	2.19	0.76
1:A:1902:GLN:O	1:A:1905:LEU:HD21	1.85	0.76
1:A:2079:ILE:HG22	1:A:2083:ILE:HD11	1.65	0.76
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	1.85	0.76
4:G:251:GLU:OE2	4:G:259:VAL:CB	2.34	0.76
1:A:165:LEU:HD12	1:A:578:MET:CG	2.15	0.76
3:I:265:ASN:OD1	3:I:266:LYS:N	2.17	0.76
4:G:257:PHE:CG	4:G:258:SER:N	2.52	0.76
8:H:338:SER:HA	8:H:341:ILE:HD13	1.66	0.76
8:H:372:THR:HG22	8:H:376:PHE:CE1	2.16	0.76
1:A:218:SER:HA	1:A:318:LEU:HD21	1.66	0.76
8:H:197:THR:HG23	8:H:545:LEU:HD13	1.68	0.75
8:H:576:THR:HB	8:H:592:PHE:CD2	2.21	0.75
1:A:258:ILE:O	1:A:259:GLU:HB2	1.86	0.75
1:A:928:ARG:NH2	4:G:145:THR:HG21	2.00	0.75
1:A:1035:LEU:CD1	1:A:1038:ILE:HG21	2.09	0.75
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.67	0.75
2:B:154:SER:OG	2:B:155:ARG:HD3	1.85	0.75
1:A:253:GLN:O	1:A:257:ASN:ND2	2.19	0.75
8:H:118:TYR:HD1	8:H:119:ASN:O	1.69	0.75
8:H:468:LEU:CD1	8:H:493:LEU:CD2	2.63	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:THR:CG2	27:F:33:U:OP2	2.34	0.75
1:A:543:ASN:HD22	1:A:544:LYS:N	1.83	0.75
8:H:233:ASP:OD1	8:H:487:ARG:NH2	2.17	0.75
2:B:345:LEU:HD13	2:B:376:TRP:CD2	2.20	0.75
8:H:146:LYS:HE2	28:H:1500:GTP:O3G	1.85	0.75
1:A:219:ALA:O	1:A:266:LEU:CD1	2.35	0.75
1:A:1058:ALA:HB2	1:A:1114:PHE:CE1	2.15	0.75
1:A:1647:GLN:HG2	25:D:52:G:OP2	1.86	0.75
8:H:304:PHE:CD2	8:H:310:ASN:CB	2.66	0.75
8:H:860:PRO:HB3	8:H:937:TRP:CZ3	2.21	0.75
1:A:276:VAL:HG11	1:A:310:ASN:HB3	1.68	0.75
1:A:322:VAL:CG2	1:A:327:TYR:CD2	2.69	0.75
4:G:672:LEU:HD21	4:G:704:LEU:HD23	1.15	0.75
6:L:139:HIS:CD2	27:F:96:U:H5''	2.21	0.75
8:H:331:TYR:CE1	8:H:404:PHE:CD1	2.73	0.75
8:H:456:LEU:N	8:H:456:LEU:HD23	2.02	0.75
1:A:1038:ILE:HD11	1:A:1039:TRP:CE3	2.21	0.75
3:I:151:LYS:O	3:I:152:ASN:HB2	1.85	0.75
1:A:806:ALA:O	1:A:810:LYS:HG2	1.87	0.75
8:H:510:ARG:HD3	8:H:591:PHE:CE2	2.21	0.75
21:f:19:LYS:O	21:f:84:GLY:CA	2.35	0.75
1:A:180:PRO:HA	1:A:187:LYS:CD	2.17	0.74
2:B:121:ARG:O	2:B:125:ILE:HG13	1.86	0.74
2:B:155:ARG:O	2:B:159:LEU:HG	1.85	0.74
3:I:401:LEU:CD1	4:G:214:SER:HA	2.17	0.74
27:F:31:G:H2'	27:F:32:G:O4'	1.85	0.74
1:A:192:LEU:HD12	1:A:558:GLN:O	1.87	0.74
1:A:1035:LEU:HD21	1:A:1160:LEU:HD11	1.69	0.74
1:A:1629:LEU:HD23	1:A:1630:THR:HG23	1.68	0.74
3:I:192:LYS:O	3:I:195:THR:OG1	2.05	0.74
4:G:863:PHE:HB3	4:G:889:ARG:NH2	2.02	0.74
8:H:458:ILE:HG22	8:H:459:PRO:CD	2.14	0.74
1:A:1256:PRO:HA	1:A:1274:ARG:NH2	2.03	0.74
1:A:180:PRO:HA	1:A:187:LYS:HD3	1.67	0.74
1:A:289:ASP:OD2	1:A:292:LYS:CB	2.34	0.74
4:G:863:PHE:HZ	4:G:892:LEU:HD21	1.47	0.74
5:K:315:ARG:NH1	25:D:72:C:O2	2.18	0.74
8:H:105:ILE:HA	8:H:108:GLN:CD	2.12	0.74
8:H:476:VAL:CG1	8:H:478:TYR:HD1	2.01	0.74
8:H:489:TYR:CE2	8:H:592:PHE:CE1	2.76	0.74
24:C:2:A:H2	27:F:98:U:N3	1.84	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:93:LYS:HA	3:I:93:LYS:HZ2	1.53	0.74
8:H:306:PRO:HG2	8:H:349:TRP:CE3	2.22	0.74
1:A:299:LYS:HA	1:A:493:MET:HG2	1.69	0.74
1:A:1922:ARG:HE	1:A:1951:PHE:HZ	1.35	0.74
2:B:195:TRP:O	2:B:220:LYS:HA	1.86	0.74
26:E:139:A:O2'	26:E:140:G:OP2	2.05	0.74
4:G:281:ASN:ND2	4:G:295:LEU:CD1	2.51	0.74
24:C:-5:A:H4'	24:C:-4:A:OP2	1.88	0.74
1:A:173:LEU:HD11	1:A:712:LEU:HD11	1.68	0.74
1:A:773:SER:OG	1:A:774:ILE:HD11	1.87	0.74
1:A:874:ILE:O	1:A:875:THR:OG1	2.06	0.74
2:B:410:LEU:HB2	2:B:422:TYR:HB2	1.68	0.74
3:I:231:PHE:HD2	3:I:330:ALA:HB1	1.50	0.74
3:I:272:LEU:O	3:I:272:LEU:HD13	1.87	0.74
4:G:863:PHE:CZ	4:G:892:LEU:CD2	2.61	0.74
5:K:146:GLU:HA	5:K:149:PHE:CE2	2.21	0.74
6:L:91:MET:HE1	6:L:128:LYS:O	1.87	0.74
1:A:174:LYS:HD2	1:A:202:VAL:O	1.88	0.73
8:H:305:SER:OG	8:H:307:ILE:HG22	1.87	0.73
8:H:545:LEU:HD12	8:H:545:LEU:N	2.03	0.73
8:H:798:GLY:O	8:H:801:TRP:HB3	1.88	0.73
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.70	0.73
2:B:115:SER:HA	2:B:118:ILE:CG1	2.17	0.73
8:H:372:THR:HG23	8:H:376:PHE:HE1	1.53	0.73
1:A:297:SER:CB	27:F:32:G:OP1	2.33	0.73
1:A:365:ASN:OD1	1:A:366:GLU:N	2.22	0.73
2:B:374:ASN:HB3	2:B:376:TRP:HE1	1.53	0.73
8:H:354:TYR:CA	8:H:359:PHE:HB3	2.17	0.73
8:H:582:SER:HB2	8:H:585:ASP:CG	2.12	0.73
8:H:117:ARG:HD2	8:H:157:SER:C	2.13	0.73
8:H:132:ARG:HG2	8:H:132:ARG:NH1	2.01	0.73
8:H:326:GLU:HG3	8:H:434:GLY:HA3	1.71	0.73
26:E:2:U:C5	26:E:3:C:C5	2.76	0.73
1:A:930:ASN:HB3	1:A:933:GLU:OE1	1.89	0.73
2:B:232:ASN:HB3	2:B:247:GLN:HE22	1.51	0.73
8:H:495:ARG:HH21	8:H:541:GLU:CD	1.96	0.73
1:A:1498:ASP:OD1	1:A:1502:LEU:HD11	1.87	0.73
8:H:274:ILE:HG21	8:H:385:PHE:CE2	2.23	0.73
8:H:500:ARG:CG	8:H:534:THR:CG2	2.62	0.73
27:F:33:U:O2'	27:F:34:C:O5'	2.05	0.73
1:A:1065:LEU:HD23	1:A:1069:LEU:HD13	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:99:ASN:O	4:G:103:GLN:HG3	1.88	0.73
4:G:666:ILE:C	4:G:670:PHE:CD2	2.67	0.73
1:A:1857:VAL:O	1:A:1877:GLY:HA3	1.89	0.73
3:I:123:ARG:O	3:I:183:PHE:HB2	1.89	0.73
5:K:303:LEU:C	5:K:303:LEU:HD23	2.13	0.73
4:G:655:PHE:CB	4:G:674:LEU:CD2	2.60	0.73
8:H:336:ILE:CD1	8:H:341:ILE:HG22	2.18	0.73
8:H:568:SER:HA	8:H:571:TYR:CE1	2.23	0.73
8:H:863:GLU:CB	8:H:931:TYR:CE1	2.71	0.73
24:C:8:U:H2'	24:C:9:G:H5'	1.68	0.73
1:A:151:SER:OG	1:A:152:LYS:N	2.22	0.73
1:A:289:ASP:OD2	1:A:292:LYS:CA	2.36	0.73
1:A:1275:MET:HE1	1:A:1299:LYS:HD2	1.70	0.73
4:G:281:ASN:HD22	4:G:295:LEU:CD1	2.01	0.73
5:K:333:LYS:HE2	5:K:333:LYS:N	2.04	0.73
8:H:489:TYR:HE2	8:H:592:PHE:CE1	2.06	0.73
1:A:1414:TRP:HZ3	1:A:1416:LYS:HB2	1.54	0.72
2:B:127:TYR:CE2	2:B:276:SER:CB	2.71	0.72
2:B:359:PRO:HB2	2:B:406:GLY:C	2.14	0.72
9:N:1122:GLY:HA3	9:N:1249:ASP:CA	2.18	0.72
1:A:585:ARG:HD2	1:A:733:GLN:NE2	2.03	0.72
1:A:1195:PHE:HB3	1:A:1217:ARG:NH1	2.04	0.72
1:A:1461:TYR:CE2	1:A:1494:LEU:HD11	2.24	0.72
2:B:385:GLN:OE1	2:B:385:GLN:HA	1.88	0.72
27:F:44:A:C4	27:F:45:A:C8	2.76	0.72
1:A:751:ASP:OD1	1:A:752:ALA:N	2.22	0.72
1:A:842:LYS:O	1:A:842:LYS:HD2	1.89	0.72
1:A:1907:GLN:O	1:A:1910:LYS:HG2	1.89	0.72
8:H:197:THR:HG22	8:H:545:LEU:CD1	2.20	0.72
8:H:581:LYS:HZ2	8:H:581:LYS:HB3	1.52	0.72
8:H:959:ILE:CD1	8:H:960:ASN:H	2.00	0.72
1:A:1373:LEU:HD13	6:L:139:HIS:CE1	2.22	0.72
1:A:1464:LYS:O	1:A:1475:LEU:HD21	1.90	0.72
2:B:230:SER:HB2	2:B:232:ASN:HD22	1.53	0.72
8:H:274:ILE:HD13	8:H:274:ILE:O	1.90	0.72
8:H:336:ILE:CG1	8:H:341:ILE:HG22	2.19	0.72
8:H:476:VAL:HG12	8:H:478:TYR:HD1	1.55	0.72
24:C:2:A:C2	27:F:98:U:N3	2.57	0.72
1:A:286:LEU:HD12	1:A:287:GLU:N	2.05	0.72
2:B:199:LEU:N	2:B:199:LEU:HD23	2.04	0.72
8:H:197:THR:HG22	8:H:545:LEU:HD13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:307:ILE:CD1	8:H:324:ILE:HD11	2.18	0.72
8:H:461:LYS:HD2	8:H:461:LYS:C	2.15	0.72
27:F:94:C:N4	27:F:96:U:O2'	2.22	0.72
1:A:468:LEU:HD13	1:A:469:ILE:CD1	2.10	0.72
1:A:1846:ASN:HA	1:A:1885:LYS:NZ	2.03	0.72
2:B:197:GLY:CA	2:B:221:ILE:HG13	2.18	0.72
8:H:577:LEU:HD23	8:H:577:LEU:C	2.15	0.72
2:B:374:ASN:OD1	2:B:388:GLN:HG3	1.90	0.72
3:I:346:GLU:O	3:I:347:ALA:HB3	1.87	0.72
8:H:947:LYS:HG2	8:H:948:ASP:OD1	1.90	0.72
27:F:95:C:O4'	27:F:96:U:OP1	2.07	0.72
1:A:778:LYS:HA	1:A:778:LYS:CE	2.20	0.72
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.72	0.72
1:A:1008:LEU:HD21	1:A:1073:ILE:HD11	1.70	0.72
1:A:1880:PHE:CE1	1:A:1882:LEU:HD12	2.25	0.72
8:H:967:VAL:HG12	8:H:968:MET:CE	2.20	0.72
1:A:175:LEU:HD12	1:A:175:LEU:C	2.15	0.71
2:B:369:GLY:HA2	2:B:395:ILE:HG23	1.72	0.71
1:A:298:TYR:O	1:A:493:MET:CG	2.37	0.71
1:A:1069:LEU:HB3	1:A:1116:TYR:HE2	1.55	0.71
1:A:1651:ALA:C	1:A:1652:HIS:CD2	2.68	0.71
1:A:1751:TYR:CZ	1:A:1755:LYS:HD3	2.25	0.71
8:H:347:ARG:O	8:H:352:VAL:HG11	1.90	0.71
27:F:73:U:O2'	27:F:74:U:C5'	2.39	0.71
1:A:779:ALA:HA	1:A:782:ILE:CD1	2.15	0.71
1:A:1216:ILE:HD12	1:A:1254:ASN:HB3	1.72	0.71
1:A:1629:LEU:HD23	1:A:1630:THR:CG2	2.20	0.71
1:A:1653:LEU:HD12	1:A:1653:LEU:O	1.90	0.71
2:B:135:ARG:NH1	2:B:139:GLU:OE2	2.23	0.71
2:B:153:LEU:O	2:B:157:THR:HG23	1.90	0.71
3:I:401:LEU:HD11	4:G:214:SER:HA	1.72	0.71
8:H:168:VAL:HG12	8:H:173:LYS:CG	2.18	0.71
2:B:220:LYS:HB3	2:B:239:GLU:HB3	1.71	0.71
8:H:415:TYR:C	8:H:416:ASP:OD1	2.33	0.71
2:B:127:TYR:CD2	2:B:276:SER:HB2	2.26	0.71
3:I:135:LEU:CD2	3:I:136:GLN:HG3	2.20	0.71
3:I:427:SER:OG	3:I:428:ARG:N	2.20	0.71
8:H:189:LEU:HD12	8:H:189:LEU:C	2.14	0.71
8:H:944:VAL:HG23	8:H:945:LEU:HG	1.71	0.71
1:A:778:LYS:O	1:A:782:ILE:HG13	1.90	0.71
2:B:443:LEU:O	2:B:443:LEU:HD23	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:350:PRO:O	5:K:353:ARG:CG	2.37	0.71
8:H:265:PHE:CD2	8:H:295:ILE:HD12	2.25	0.71
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.25	0.71
2:B:313:LEU:CD1	2:B:322:VAL:CG2	2.68	0.71
2:B:415:TYR:OH	7:M:126:ILE:HA	1.91	0.71
4:G:666:ILE:HG22	4:G:667:CYS:N	2.05	0.71
6:L:139:HIS:NE2	27:F:96:U:H5''	2.06	0.71
27:F:75:A:C8	27:F:77:A:H5''	2.22	0.71
8:H:332:TYR:CZ	8:H:376:PHE:HB3	2.26	0.71
8:H:799:PHE:CE1	8:H:846:CYS:SG	2.84	0.71
27:F:77:A:H1'	27:F:78:A:H5'	1.71	0.71
1:A:410:ILE:HG13	8:H:276:ASP:OD1	1.90	0.71
1:A:1415:SER:OG	1:A:1746:HIS:CD2	2.43	0.71
2:B:446:SER:CB	2:B:451:PHE:HB2	2.20	0.71
3:I:197:ILE:C	3:I:201:ASN:ND2	2.44	0.71
8:H:354:TYR:HA	8:H:359:PHE:HA	1.72	0.71
8:H:677:PHE:CE1	8:H:966:PHE:HD2	2.08	0.71
2:B:359:PRO:HD2	2:B:407:GLY:HA3	1.73	0.70
4:G:696:ARG:O	4:G:699:PRO:HD3	1.89	0.70
27:F:94:C:H6	27:F:94:C:C5'	2.04	0.70
1:A:162:LEU:HD23	1:A:730:ILE:HD13	1.71	0.70
1:A:614:ARG:CZ	24:C:3:A:OP1	2.39	0.70
6:L:33:ARG:HD2	6:L:65:ASP:CG	2.15	0.70
8:H:129:ILE:N	8:H:129:ILE:HD12	2.06	0.70
8:H:501:ILE:HG21	8:H:570:ALA:HB3	1.73	0.70
1:A:774:ILE:HG23	1:A:777:LYS:HE3	1.73	0.70
2:B:359:PRO:HB2	2:B:406:GLY:O	1.91	0.70
2:B:390:LEU:HG	2:B:390:LEU:O	1.91	0.70
5:K:154:SER:O	5:K:158:ILE:CG2	2.39	0.70
1:A:823:TRP:CZ2	1:A:851:ARG:HG2	2.26	0.70
1:A:1489:PRO:O	1:A:1533:ASP:O	2.10	0.70
1:A:1877:GLY:O	1:A:1894:ILE:CB	2.38	0.70
1:A:2071:ILE:O	1:A:2071:ILE:HD13	1.91	0.70
4:G:143:ARG:HB3	4:G:143:ARG:CZ	2.20	0.70
5:K:350:PRO:HG3	5:K:353:ARG:CZ	2.21	0.70
8:H:855:PRO:C	8:H:944:VAL:HG21	2.16	0.70
27:F:39:U:H3	27:F:115:G:H1	1.38	0.70
1:A:2080:LYS:HA	1:A:2083:ILE:HD12	1.74	0.70
2:B:446:SER:HG	2:B:451:PHE:HD2	0.72	0.70
8:H:488:ILE:HG21	8:H:557:HIS:O	1.91	0.70
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1748:ILE:CG2	1:A:1752:VAL:HG22	2.12	0.70
3:I:145:GLU:OE2	3:I:145:GLU:HA	1.90	0.70
4:G:630:SER:CB	4:G:670:PHE:HZ	1.95	0.70
8:H:364:PHE:CB	8:H:369:LYS:CG	2.27	0.70
4:G:863:PHE:HE2	4:G:892:LEU:CG	2.04	0.70
27:F:31:G:C2	27:F:32:G:C4	2.80	0.70
1:A:149:MET:HB3	1:A:154:TYR:CD2	2.25	0.70
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.22	0.70
1:A:1615:ASN:HD21	1:A:1634:LEU:HD23	1.56	0.70
2:B:362:TYR:HD1	2:B:362:TYR:H	1.38	0.70
4:G:863:PHE:CE2	4:G:892:LEU:CD2	2.74	0.70
8:H:586:MET:HA	8:H:589:LEU:HD23	1.73	0.70
24:C:8:U:OP1	24:C:8:U:H4'	1.91	0.70
1:A:1275:MET:HE1	1:A:1299:LYS:HE3	1.74	0.70
1:A:1647:GLN:O	1:A:1650:ARG:HG2	1.92	0.70
2:B:380:LYS:O	2:B:381:ARG:CG	2.39	0.70
4:G:98:SER:OG	4:G:99:ASN:N	2.24	0.70
6:L:31:PHE:O	6:L:80:MET:HA	1.92	0.70
1:A:1022:PRO:HD3	1:A:1345:TYR:CE1	2.22	0.69
8:H:132:ARG:O	8:H:133:ILE:HG12	1.91	0.69
8:H:135:ASN:HD22	8:H:487:ARG:NH2	1.90	0.69
4:G:251:GLU:OE2	4:G:260:ALA:N	2.25	0.69
4:G:666:ILE:HG22	4:G:667:CYS:H	1.57	0.69
8:H:474:LYS:NZ	8:H:630:PRO:HD3	2.06	0.69
8:H:580:VAL:HG22	8:H:582:SER:H	1.57	0.69
27:F:74:U:O2'	27:F:75:A:H5'	1.92	0.69
27:F:78:A:H61	27:F:81:A:N6	1.90	0.69
1:A:1756:PHE:CE1	1:A:1760:THR:HG21	2.27	0.69
4:G:862:MET:N	4:G:862:MET:SD	2.65	0.69
8:H:113:ILE:HG23	8:H:549:TYR:CD1	2.27	0.69
8:H:131:GLU:HA	8:H:131:GLU:OE2	1.92	0.69
26:E:4:C:O2'	26:E:5:U:H5'	1.92	0.69
1:A:1654:TRP:HZ3	1:A:1779:LEU:CD1	1.91	0.69
3:I:93:LYS:O	3:I:96:PRO:HD2	1.91	0.69
8:H:187:ARG:NH2	8:H:654:CYS:SG	2.66	0.69
8:H:959:ILE:N	8:H:959:ILE:HD12	2.06	0.69
27:F:78:A:C6	27:F:81:A:C5	2.80	0.69
1:A:305:LEU:HD11	1:A:476:ALA:CB	2.22	0.69
1:A:998:TYR:CE1	1:A:1002:GLU:HG3	2.28	0.69
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.75	0.69
8:H:143:HIS:HA	28:H:1500:GTP:O3B	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:161:ILE:HG23	8:H:162:PRO:HD2	1.75	0.69
2:B:115:SER:HA	2:B:118:ILE:HG13	1.75	0.69
2:B:177:PRO:HD2	2:B:195:TRP:CD1	2.28	0.69
2:B:274:HIS:CD2	2:B:276:SER:H	2.07	0.69
6:L:53:VAL:HG12	6:L:57:ALA:HB3	1.75	0.69
27:F:106:A:H2'	27:F:107:C:H5'	1.75	0.69
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.21	0.69
1:A:1647:GLN:O	1:A:1650:ARG:CG	2.40	0.69
4:G:666:ILE:O	4:G:670:PHE:HD2	1.73	0.69
8:H:488:ILE:HD12	8:H:560:GLN:HG3	1.73	0.69
27:F:32:G:H4'	27:F:33:U:OP2	1.92	0.69
1:A:1574:PHE:CE1	3:I:390:ARG:HD3	2.27	0.69
2:B:235:ILE:HD12	2:B:280:ILE:CD1	2.20	0.69
4:G:851:ARG:O	4:G:852:LEU:HD12	1.92	0.69
5:K:141:ASN:HD21	5:K:144:LEU:HD23	1.58	0.69
9:N:807:GLY:HA2	9:N:1093:ALA:H	0.66	0.69
1:A:431:ILE:HD11	8:H:287:LYS:HA	1.74	0.69
2:B:176:LYS:HB3	2:B:195:TRP:HB2	1.75	0.69
8:H:349:TRP:HZ3	8:H:373:PHE:CE2	2.10	0.69
2:B:117:LEU:HG	2:B:300:LEU:O	1.93	0.69
3:I:217:TYR:CE1	3:I:221:LYS:NZ	2.45	0.69
8:H:572:ILE:HD12	8:H:573:LYS:CG	2.22	0.69
8:H:948:ASP:OD1	8:H:948:ASP:N	2.26	0.69
25:D:109:U:H3'	25:D:110:U:H5''	1.75	0.69
1:A:1882:LEU:O	1:A:1882:LEU:HD13	1.93	0.68
4:G:19:ILE:HD12	4:G:20:GLY:N	2.07	0.68
27:F:33:U:O2'	27:F:34:C:OP2	2.11	0.68
1:A:354:PRO:O	1:A:355:LEU:HB3	1.93	0.68
1:A:428:LEU:HD13	8:H:279:LEU:HD11	1.74	0.68
2:B:274:HIS:HD2	2:B:276:SER:N	1.89	0.68
4:G:687:SER:O	4:G:690:THR:HG22	1.92	0.68
5:K:350:PRO:HG3	5:K:353:ARG:NH1	2.07	0.68
6:L:101:ASN:O	6:L:102:LYS:CG	2.41	0.68
8:H:495:ARG:HG2	8:H:540:GLU:O	1.94	0.68
1:A:168:LEU:CA	1:A:199:ILE:HD11	2.21	0.68
1:A:431:ILE:HA	8:H:895:ALA:HB1	1.74	0.68
8:H:332:TYR:OH	8:H:376:PHE:CD2	2.44	0.68
27:F:78:A:N6	27:F:81:A:C5	2.61	0.68
1:A:209:ILE:CG1	1:A:493:MET:HE1	2.24	0.68
2:B:419:ILE:HD11	2:B:443:LEU:HD12	1.73	0.68
3:I:183:PHE:CE2	3:I:185:ASN:ND2	2.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:470:ALA:HB3	8:H:577:LEU:HD22	1.76	0.68
3:I:98:PHE:CE2	3:I:217:TYR:HD2	2.09	0.68
4:G:166:ARG:O	4:G:169:LEU:N	2.27	0.68
6:L:25:ARG:HH11	6:L:25:ARG:CB	2.07	0.68
8:H:105:ILE:O	8:H:109:LEU:HD23	1.93	0.68
1:A:2075:THR:HG22	1:A:2077:THR:H	1.58	0.68
3:I:124:PHE:CE2	3:I:127:LEU:HB2	2.28	0.68
3:I:268:LEU:CD1	3:I:271:GLU:HG2	2.24	0.68
1:A:837:GLY:HA2	1:A:1317:ARG:HH11	1.56	0.68
4:G:264:ILE:HG21	4:G:281:ASN:HA	1.75	0.68
8:H:477:ASP:HB2	8:H:628:TYR:CE1	2.29	0.68
8:H:444:GLN:HE21	8:H:444:GLN:HA	1.57	0.68
1:A:753:TYR:CE1	6:L:37:ARG:HB3	2.28	0.68
4:G:693:SER:O	4:G:697:LEU:HG	1.94	0.68
5:K:354:PHE:CE1	5:K:358:MET:SD	2.87	0.68
6:L:39:CYS:SG	6:L:80:MET:HB3	2.34	0.68
8:H:113:ILE:HD11	8:H:550:VAL:O	1.94	0.68
8:H:142:LEU:HD12	8:H:929:GLN:HE21	1.57	0.68
8:H:330:TYR:HE1	8:H:430:ARG:NE	1.91	0.68
27:F:40:C:O2'	27:F:41:A:H5''	1.93	0.68
27:F:78:A:N6	27:F:81:A:N7	2.41	0.68
1:A:176:LEU:CD2	1:A:708:TRP:NE1	2.56	0.68
1:A:358:ARG:HH11	1:A:358:ARG:CB	2.07	0.68
3:I:225:ILE:C	3:I:325:ARG:HH12	2.01	0.68
4:G:886:CYS:C	4:G:888:PRO:HD2	2.19	0.68
1:A:276:VAL:HG13	1:A:310:ASN:HD22	1.59	0.67
1:A:296:THR:HG21	27:F:33:U:OP2	1.94	0.67
1:A:376:ARG:O	1:A:377:VAL:HB	1.93	0.67
2:B:374:ASN:HB3	2:B:376:TRP:NE1	2.09	0.67
8:H:317:LYS:HB2	28:H:1500:GTP:C6	2.29	0.67
8:H:855:PRO:O	8:H:944:VAL:HG22	1.92	0.67
1:A:325:LYS:HB3	1:A:405:ASN:ND2	2.09	0.67
3:I:179:MET:HG3	3:I:183:PHE:CE1	2.28	0.67
4:G:666:ILE:C	4:G:670:PHE:HD2	2.02	0.67
8:H:197:THR:HG23	8:H:545:LEU:CD1	2.20	0.67
1:A:939:LEU:HD11	3:I:441:MET:CE	2.24	0.67
4:G:238:PRO:HD2	4:G:239:THR:H	1.59	0.67
4:G:281:ASN:ND2	4:G:295:LEU:HD13	2.10	0.67
8:H:246:THR:O	8:H:250:GLU:HG3	1.94	0.67
9:N:1122:GLY:CA	9:N:1249:ASP:CA	2.73	0.67
1:A:276:VAL:HG11	1:A:310:ASN:CB	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:691:PHE:HZ	1:A:701:CYS:HA	1.55	0.67
1:A:774:ILE:HG23	1:A:777:LYS:CE	2.24	0.67
1:A:1654:TRP:CH2	1:A:1779:LEU:CD1	2.78	0.67
4:G:703:LEU:HD13	4:G:703:LEU:C	2.19	0.67
8:H:116:THR:OG1	8:H:120:ARG:NH2	2.24	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CB	2.21	0.67
8:H:488:ILE:CD1	8:H:560:GLN:HG3	2.23	0.67
8:H:936:ILE:HD13	8:H:936:ILE:H	1.59	0.67
4:G:863:PHE:HE2	4:G:892:LEU:HG	1.58	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CD	2.22	0.67
8:H:677:PHE:CZ	8:H:966:PHE:CD2	2.82	0.67
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.27	0.67
1:A:2000:SER:OG	5:K:277:MET:HE1	1.94	0.67
3:I:312:LEU:HB3	3:I:333:TRP:CH2	2.29	0.67
1:A:674:MET:HE2	1:A:678:ARG:CD	2.24	0.67
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.60	0.67
3:I:280:ARG:NH2	26:E:37:U:OP2	2.27	0.67
3:I:433:ASN:O	3:I:434:GLN:C	2.37	0.67
4:G:224:GLN:O	4:G:228:THR:HG23	1.95	0.67
8:H:105:ILE:HA	8:H:108:GLN:OE1	1.95	0.67
8:H:126:MET:HE1	8:H:132:ARG:NH1	2.07	0.67
8:H:959:ILE:HD12	8:H:960:ASN:H	1.58	0.67
1:A:165:LEU:CD1	1:A:578:MET:SD	2.72	0.67
3:I:92:ILE:HD12	3:I:92:ILE:N	2.09	0.67
6:L:105:PHE:HZ	6:L:137:TYR:HE2	1.18	0.67
8:H:330:TYR:CE1	8:H:430:ARG:NE	2.61	0.67
8:H:338:SER:O	8:H:341:ILE:HG12	1.95	0.67
27:F:48:G:H1	27:F:67:U:H3	1.41	0.67
27:F:77:A:H4'	27:F:78:A:OP1	1.95	0.67
3:I:123:ARG:CD	3:I:189:LEU:HD12	2.23	0.67
8:H:486:VAL:CG1	8:H:564:ILE:CD1	2.59	0.67
1:A:780:ARG:C	1:A:784:GLN:OE1	2.38	0.67
1:A:1703:MET:HB2	1:A:1732:MET:HB2	1.75	0.67
5:K:350:PRO:CB	25:D:84:C:C5	2.78	0.67
8:H:316:THR:OG1	28:H:1500:GTP:N7	2.28	0.67
27:F:32:G:H5''	27:F:32:G:H8	1.60	0.67
1:A:371:ASP:O	8:H:969:LYS:HG3	1.94	0.66
1:A:511:ASP:HB2	1:A:514:TYR:HE1	1.60	0.66
1:A:1892:LYS:HD2	1:A:1916:GLU:CG	2.25	0.66
4:G:672:LEU:HD23	4:G:704:LEU:HD21	1.41	0.66
4:G:688:ARG:HH22	4:G:721:ARG:NH2	1.93	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:271:ASP:O	8:H:274:ILE:HG22	1.94	0.66
8:H:331:TYR:OH	8:H:428:ILE:HG23	1.95	0.66
1:A:362:GLU:HB2	1:A:1209:LYS:HG2	1.77	0.66
1:A:909:THR:CG2	1:A:910:LYS:N	2.57	0.66
2:B:360:ASN:HB3	2:B:362:TYR:CE1	2.31	0.66
3:I:231:PHE:CD2	3:I:330:ALA:CB	2.78	0.66
4:G:692:LEU:HD22	4:G:708:LEU:HD11	1.75	0.66
4:G:721:ARG:CD	4:G:725:ILE:CD1	2.72	0.66
5:K:292:ALA:O	5:K:296:VAL:HG23	1.94	0.66
8:H:329:SER:O	8:H:333:ALA:HB3	1.96	0.66
27:F:31:G:N2	27:F:32:G:H1'	2.10	0.66
27:F:31:G:N3	27:F:32:G:H1'	2.10	0.66
2:B:202:LEU:HD23	2:B:207:LEU:HD22	1.77	0.66
3:I:112:MET:HB3	3:I:204:LEU:CD2	2.22	0.66
3:I:358:ILE:HG23	3:I:359:PRO:CD	2.21	0.66
8:H:329:SER:HA	8:H:333:ALA:CB	2.25	0.66
1:A:939:LEU:HD11	3:I:441:MET:HE2	1.76	0.66
8:H:472:VAL:HG11	8:H:571:TYR:CZ	2.30	0.66
9:N:807:GLY:C	9:N:1093:ALA:H	2.00	0.66
1:A:1417:GLN:OE1	1:A:1422:ILE:HD11	1.96	0.66
2:B:380:LYS:O	2:B:382:ASP:OD1	2.13	0.66
2:B:456:GLY:O	2:B:459:ARG:N	2.21	0.66
4:G:215:LEU:C	4:G:215:LEU:HD12	2.20	0.66
8:H:219:VAL:CG2	8:H:931:TYR:HB3	2.25	0.66
8:H:317:LYS:HB2	28:H:1500:GTP:C5	2.30	0.66
8:H:354:TYR:HB3	8:H:359:PHE:HB3	1.75	0.66
8:H:458:ILE:HB	8:H:590:LYS:HD3	1.76	0.66
2:B:314:SER:OG	2:B:355:VAL:O	2.10	0.66
8:H:471:HIS:C	8:H:486:VAL:HG23	2.19	0.66
8:H:495:ARG:CG	8:H:540:GLU:O	2.43	0.66
25:D:51:A:H4'	25:D:51:A:OP1	1.96	0.66
1:A:558:GLN:OE1	1:A:558:GLN:HA	1.95	0.66
1:A:862:GLU:HA	1:A:862:GLU:OE2	1.96	0.66
2:B:177:PRO:HD2	2:B:195:TRP:HD1	1.61	0.66
8:H:444:GLN:HA	8:H:444:GLN:NE2	2.11	0.66
21:f:19:LYS:O	21:f:84:GLY:HA2	1.95	0.66
25:D:109:U:H4'	25:D:110:U:OP2	1.95	0.66
1:A:362:GLU:CB	1:A:1209:LYS:HE2	2.22	0.66
1:A:923:TYR:CE1	1:A:933:GLU:HG2	2.30	0.66
1:A:1657:ILE:O	1:A:1661:ILE:HG13	1.95	0.66
2:B:274:HIS:CD2	2:B:275:PRO:HD2	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:313:LEU:HD11	2:B:322:VAL:CG2	2.26	0.66
27:F:50:G:H1	27:F:65:U:H3	1.41	0.66
1:A:366:GLU:HB2	1:A:372:ARG:HH11	1.59	0.66
1:A:1038:ILE:CD1	1:A:1039:TRP:CE3	2.78	0.66
1:A:1041:VAL:HG11	1:A:1253:LYS:N	2.11	0.66
2:B:316:GLN:CB	2:B:357:TRP:CE2	2.78	0.66
4:G:256:LYS:HG2	4:G:257:PHE:H	1.61	0.66
5:K:141:ASN:O	5:K:142:LEU:HD22	1.96	0.66
1:A:842:LYS:HD2	1:A:842:LYS:C	2.19	0.66
1:A:956:LYS:HD2	1:A:956:LYS:C	2.21	0.66
3:I:124:PHE:CD2	3:I:127:LEU:HB2	2.30	0.66
3:I:393:PHE:CD1	3:I:393:PHE:C	2.73	0.66
5:K:349:ASN:HB2	5:K:406:PHE:CE1	2.31	0.66
8:H:564:ILE:CG2	8:H:567:ILE:HG12	2.26	0.66
25:D:78:G:N2	26:E:4:C:O2	2.28	0.66
27:F:73:U:O2'	27:F:74:U:H5''	1.96	0.66
1:A:547:LEU:C	1:A:547:LEU:HD12	2.20	0.65
1:A:325:LYS:HB3	1:A:405:ASN:HD22	1.59	0.65
1:A:987:LEU:HG	3:I:441:MET:HE1	1.76	0.65
5:K:154:SER:O	5:K:158:ILE:CG1	2.44	0.65
5:K:155:LYS:O	5:K:158:ILE:HG13	1.96	0.65
8:H:110:LYS:HE2	8:H:552:PRO:CG	2.20	0.65
8:H:797:GLN:HA	8:H:797:GLN:HE21	1.61	0.65
1:A:319:ARG:NH1	1:A:485:PRO:HG2	2.11	0.65
2:B:227:HIS:HD2	2:B:273:TYR:CE1	2.14	0.65
3:I:197:ILE:CG2	3:I:201:ASN:HD21	2.09	0.65
5:K:154:SER:O	5:K:158:ILE:HG12	1.97	0.65
8:H:165:SER:OG	8:H:168:VAL:HG22	1.96	0.65
25:D:48:C:C2'	25:D:49:A:C8	2.79	0.65
1:A:1998:ARG:C	1:A:1999:ILE:HG13	2.21	0.65
1:A:875:THR:OG1	1:A:878:GLU:HB2	1.96	0.65
2:B:316:GLN:HB2	2:B:357:TRP:CE3	2.30	0.65
6:L:141:ARG:HD2	6:L:141:ARG:N	2.11	0.65
7:M:95:ARG:HG3	7:M:96:PRO:HD2	1.78	0.65
8:H:114:PRO:C	8:H:115:LYS:HG3	2.20	0.65
8:H:129:ILE:HG12	10:R:16:GLY:HA3	1.78	0.65
8:H:888:ILE:H	8:H:888:ILE:HD12	1.60	0.65
1:A:809:LYS:O	1:A:813:GLU:CG	2.43	0.65
2:B:202:LEU:HB3	2:B:207:LEU:HD23	1.79	0.65
3:I:120:TYR:HE2	3:I:141:ILE:HG12	1.59	0.65
2:B:147:ASN:HB3	2:B:150:GLN:OE1	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:280:ILE:O	2:B:292:TRP:N	2.29	0.65
2:B:329:SER:CB	2:B:348:HIS:O	2.36	0.65
3:I:358:ILE:CG2	3:I:360:GLU:H	2.10	0.65
4:G:212:VAL:CG1	4:G:215:LEU:HB3	2.25	0.65
5:K:457:GLN:CD	5:K:457:GLN:H	1.98	0.65
8:H:274:ILE:O	8:H:278:LYS:HA	1.96	0.65
1:A:404:ASN:HA	8:H:919:ARG:HH12	1.61	0.65
1:A:1279:VAL:HG11	1:A:1301:TYR:OH	1.96	0.65
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.78	0.65
4:G:278:TRP:CH2	4:G:298:THR:HB	2.31	0.65
8:H:306:PRO:HG2	8:H:349:TRP:CH2	2.31	0.65
1:A:366:GLU:HB2	1:A:372:ARG:HH12	1.59	0.65
1:A:770:MET:HE1	1:A:778:LYS:HB3	1.78	0.65
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.78	0.65
3:I:179:MET:HG3	3:I:183:PHE:HE1	1.62	0.65
8:H:799:PHE:HE1	8:H:846:CYS:SG	2.20	0.65
1:A:173:LEU:HD11	1:A:712:LEU:CD1	2.27	0.65
1:A:770:MET:CE	1:A:775:ARG:O	2.45	0.65
1:A:875:THR:OG1	1:A:878:GLU:OE1	2.15	0.65
2:B:381:ARG:HG3	2:B:382:ASP:OD1	1.97	0.65
8:H:503:ASP:OD1	8:H:571:TYR:HB2	1.97	0.65
1:A:1145:MET:O	1:A:1146:GLN:HG3	1.97	0.64
2:B:218:VAL:HG21	2:B:238:ALA:HB3	1.80	0.64
2:B:454:SER:OG	2:B:464:TRP:NE1	2.29	0.64
4:G:843:VAL:HG21	4:G:895:LEU:CD1	2.27	0.64
8:H:160:ARG:HB3	8:H:161:ILE:HA	1.78	0.64
27:F:95:C:O2'	27:F:96:U:C5'	2.43	0.64
27:F:97:U:C6	27:F:97:U:H5''	2.33	0.64
1:A:767:LEU:HD21	1:A:779:ALA:CB	2.27	0.64
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.31	0.64
3:I:184:LYS:HE2	3:I:186:LYS:HB2	1.78	0.64
1:A:168:LEU:CB	1:A:199:ILE:CD1	2.74	0.64
1:A:173:LEU:HD12	1:A:173:LEU:O	1.98	0.64
1:A:174:LYS:NZ	1:A:177:GLU:OE2	2.30	0.64
1:A:207:ARG:NH1	1:A:299:LYS:HG2	2.13	0.64
8:H:500:ARG:NE	8:H:534:THR:CB	2.57	0.64
8:H:599:THR:CG2	8:H:933:TRP:CZ3	2.80	0.64
8:H:599:THR:HG22	8:H:932:PHE:O	1.98	0.64
8:H:862:TYR:OH	8:H:908:VAL:HG23	1.98	0.64
1:A:250:SER:O	1:A:254:HIS:HB2	1.96	0.64
1:A:676:GLN:N	1:A:676:GLN:OE1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:ARG:O	1:A:784:GLN:OE1	2.15	0.64
2:B:124:LEU:C	2:B:128:SER:HG	1.98	0.64
2:B:313:LEU:HD11	2:B:322:VAL:HG23	1.78	0.64
3:I:266:LYS:CG	3:I:267:HIS:N	2.56	0.64
4:G:99:ASN:ND2	4:G:99:ASN:H	1.94	0.64
5:K:146:GLU:HA	5:K:149:PHE:HD2	1.62	0.64
6:L:76:LEU:HD12	6:L:76:LEU:N	2.11	0.64
27:F:44:A:N3	27:F:45:A:C8	2.66	0.64
1:A:1017:ASP:O	1:A:1509:ARG:NH1	2.31	0.64
2:B:48:ASP:OD2	2:B:69:VAL:HG21	1.96	0.64
2:B:235:ILE:HD13	2:B:280:ILE:HD13	1.78	0.64
2:B:374:ASN:CB	2:B:376:TRP:HE1	2.11	0.64
2:B:393:ARG:HH21	2:B:393:ARG:CG	2.09	0.64
3:I:393:PHE:C	3:I:393:PHE:HD1	2.05	0.64
3:I:401:LEU:HD12	4:G:214:SER:CB	2.27	0.64
7:M:125:LEU:O	7:M:126:ILE:C	2.39	0.64
8:H:129:ILE:HD12	8:H:129:ILE:H	1.59	0.64
26:E:24:A:C2	26:E:50:G:C2	2.86	0.64
1:A:273:ASP:O	1:A:276:VAL:HG22	1.97	0.64
1:A:784:GLN:O	1:A:788:GLU:HG2	1.98	0.64
1:A:1876:ASN:OD1	1:A:1896:THR:HG23	1.97	0.64
2:B:311:PHE:CE2	7:M:126:ILE:HD13	2.32	0.64
2:B:316:GLN:CG	2:B:357:TRP:CE2	2.81	0.64
4:G:281:ASN:ND2	4:G:295:LEU:HD11	2.13	0.64
4:G:721:ARG:HD3	4:G:725:ILE:CD1	2.26	0.64
8:H:197:THR:HG21	8:H:545:LEU:CD1	2.21	0.64
26:E:1:A:N6	29:E:201:M7M:HBZB	2.13	0.64
8:H:164:MET:HG2	8:H:175:LEU:HD12	1.80	0.64
8:H:292:ILE:O	8:H:295:ILE:HG12	1.97	0.64
27:F:76:U:OP2	27:F:76:U:H4'	1.97	0.64
1:A:294:ASN:OD1	1:A:300:LYS:CE	2.45	0.64
1:A:703:PHE:CE1	1:A:705:GLN:HB3	2.30	0.64
8:H:167:ASN:HD21	8:H:173:LYS:HG2	1.62	0.64
1:A:506:PHE:HA	1:A:522:TYR:CE1	2.33	0.64
4:G:286:GLU:HB2	4:G:292:CYS:HG	1.61	0.64
5:K:304:ARG:NH1	26:E:13:G:OP1	2.31	0.64
5:K:325:GLU:HA	5:K:328:ASN:OD1	1.97	0.64
8:H:470:ALA:CB	8:H:577:LEU:HD22	2.28	0.64
1:A:332:ASP:C	1:A:332:ASP:OD1	2.41	0.64
1:A:456:GLU:CD	1:A:456:GLU:H	1.97	0.64
1:A:1591:THR:HG22	1:A:1592:HIS:N	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:120:TYR:CE2	3:I:141:ILE:HG12	2.33	0.64
4:G:693:SER:HA	4:G:696:ARG:HD2	1.80	0.64
26:E:23:C:O2'	26:E:24:A:H5'	1.97	0.64
1:A:1076:PRO:O	1:A:1080:ASP:OD2	2.16	0.63
1:A:1458:TRP:CZ3	1:A:1461:TYR:CD2	2.86	0.63
2:B:415:TYR:HD2	2:B:439:LYS:HD3	1.61	0.63
4:G:843:VAL:CG2	4:G:895:LEU:HD13	2.27	0.63
8:H:105:ILE:HA	8:H:108:GLN:NE2	2.13	0.63
1:A:273:ASP:N	1:A:273:ASP:OD1	2.31	0.63
1:A:293:VAL:HG13	1:A:295:GLY:N	2.13	0.63
1:A:767:LEU:HD21	1:A:779:ALA:HB2	1.78	0.63
8:H:227:VAL:O	8:H:473:LEU:HD13	1.99	0.63
25:D:62:A:C2'	25:D:63:G:H5'	2.28	0.63
1:A:1613:THR:O	1:A:1616:ARG:HD3	1.97	0.63
2:B:114:THR:O	2:B:118:ILE:HG13	1.99	0.63
2:B:273:TYR:CZ	2:B:280:ILE:HD11	2.33	0.63
3:I:197:ILE:HG23	3:I:201:ASN:HD21	1.61	0.63
8:H:118:TYR:CD1	8:H:119:ASN:O	2.50	0.63
8:H:463:THR:CB	8:H:585:ASP:OD1	2.47	0.63
8:H:880:MET:HB3	8:H:886:SER:HA	1.81	0.63
8:H:947:LYS:H	8:H:947:LYS:HD3	1.62	0.63
1:A:173:LEU:CD1	1:A:712:LEU:CD1	2.76	0.63
1:A:176:LEU:HD23	1:A:176:LEU:C	2.22	0.63
2:B:159:LEU:CD1	2:B:430:MET:HE2	2.19	0.63
2:B:456:GLY:O	2:B:457:TRP:C	2.42	0.63
4:G:170:LEU:C	4:G:170:LEU:HD13	2.24	0.63
6:L:25:ARG:HH11	6:L:25:ARG:CG	2.10	0.63
6:L:75:GLU:C	6:L:76:LEU:HD12	2.24	0.63
8:H:484:SER:HB3	8:H:571:TYR:OH	1.97	0.63
24:C:10:U:O2'	24:C:11:A:H5'	1.99	0.63
25:D:49:A:C2'	25:D:50:G:H5''	2.23	0.63
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.81	0.63
3:I:98:PHE:CZ	3:I:217:TYR:HD2	2.15	0.63
4:G:134:ARG:HB3	4:G:134:ARG:CZ	2.28	0.63
8:H:945:LEU:HD12	8:H:945:LEU:H	1.63	0.63
27:F:40:C:H3'	27:F:40:C:OP2	1.99	0.63
1:A:175:LEU:HD11	1:A:564:TRP:CZ2	2.33	0.63
1:A:1317:ARG:HH21	1:A:1366:ARG:HH22	1.45	0.63
3:I:206:ASN:O	3:I:209:LYS:HG2	1.98	0.63
3:I:320:GLN:HG2	3:I:325:ARG:HA	1.80	0.63
3:I:358:ILE:HG22	3:I:360:GLU:H	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:469:TRP:CD1	8:H:578:TYR:HB3	2.34	0.63
1:A:1618:ASN:N	1:A:1618:ASN:OD1	2.31	0.63
2:B:230:SER:OG	2:B:233:GLN:OE1	2.16	0.63
2:B:391:ALA:O	2:B:392:HIS:HB2	1.97	0.63
3:I:268:LEU:HD12	3:I:271:GLU:HG2	1.80	0.63
3:I:402:ASP:OD1	3:I:403:SER:N	2.31	0.63
8:H:363:PRO:O	8:H:364:PHE:HB3	1.98	0.63
8:H:889:TYR:HE1	8:H:890:LYS:HG3	1.57	0.63
27:F:94:C:H6	27:F:94:C:H5''	1.63	0.63
1:A:393:SER:O	1:A:394:ARG:HG2	1.98	0.63
1:A:1658:HIS:CA	1:A:1661:ILE:HD12	2.27	0.63
1:A:1748:ILE:O	1:A:1752:VAL:CG2	2.41	0.63
2:B:239:GLU:HA	2:B:267:ARG:HB2	1.81	0.63
3:I:429:ARG:CB	3:I:429:ARG:HH11	2.11	0.63
4:G:279:LEU:N	4:G:279:LEU:HD23	2.13	0.63
5:K:452:LEU:O	5:K:456:GLY:N	2.31	0.63
1:A:874:ILE:HD11	1:A:1062:ASP:HB2	1.81	0.63
1:A:1118:GLY:HA3	1:A:1163:ARG:NH2	2.14	0.63
4:G:702:PRO:HA	4:G:739:PHE:CE2	2.33	0.63
8:H:942:GLY:O	8:H:963:SER:OG	2.17	0.63
27:F:92:U:H6	27:F:92:U:H5''	1.64	0.63
1:A:297:SER:CB	27:F:32:G:O5'	2.47	0.62
1:A:1916:GLU:HA	1:A:1916:GLU:OE2	1.98	0.62
24:C:2:A:H8	24:C:2:A:O5'	1.82	0.62
1:A:1653:LEU:HD21	1:A:1815:LEU:HD23	1.80	0.62
4:G:859:LEU:O	4:G:862:MET:HG2	1.99	0.62
8:H:178:LEU:N	8:H:178:LEU:HD23	2.14	0.62
8:H:959:ILE:CD1	8:H:960:ASN:N	2.61	0.62
1:A:261:LEU:C	1:A:261:LEU:HD12	2.23	0.62
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.00	0.62
2:B:197:GLY:C	2:B:221:ILE:HD11	2.24	0.62
2:B:405:ASP:OD2	2:B:408:LYS:HD3	1.98	0.62
3:I:102:ILE:HB	3:I:103:PRO:HD3	1.81	0.62
6:L:96:GLY:O	6:L:138:ASN:HB2	1.96	0.62
8:H:126:MET:SD	8:H:132:ARG:NH1	2.72	0.62
8:H:936:ILE:H	8:H:936:ILE:CD1	2.12	0.62
9:N:807:GLY:H	9:N:1093:ALA:N	1.93	0.62
3:I:146:ASN:ND2	3:I:148:ASN:ND2	2.47	0.62
3:I:282:GLU:OE1	3:I:286:PHE:CE2	2.52	0.62
4:G:268:CYS:SG	4:G:278:TRP:HH2	2.15	0.62
5:K:141:ASN:ND2	5:K:144:LEU:HD23	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:129:ILE:HB	8:H:132:ARG:HB2	1.81	0.62
8:H:793:GLU:O	8:H:796:ILE:HG22	1.99	0.62
24:C:3:A:H8	24:C:3:A:O5'	1.81	0.62
1:A:1880:PHE:CD2	1:A:1889:LEU:HD21	2.32	0.62
2:B:278:LYS:C	2:B:279:PHE:HD1	2.08	0.62
2:B:286:ASP:C	2:B:287:MET:CG	2.72	0.62
3:I:321:LYS:HD2	3:I:324:ASP:HB3	1.79	0.62
4:G:124:ASP:N	4:G:124:ASP:OD1	2.32	0.62
4:G:223:LEU:HD23	4:G:223:LEU:O	2.00	0.62
5:K:166:TYR:OH	5:K:174:LEU:HD12	2.00	0.62
1:A:376:ARG:NE	8:H:910:GLU:OE2	2.32	0.62
2:B:292:TRP:CD1	2:B:299:GLU:HA	2.34	0.62
3:I:373:ARG:HB3	3:I:373:ARG:NH1	2.14	0.62
3:I:433:ASN:O	3:I:434:GLN:O	2.18	0.62
4:G:857:VAL:O	4:G:860:TYR:HB2	1.99	0.62
8:H:202:ASP:N	8:H:202:ASP:OD1	2.31	0.62
8:H:483:TRP:CH2	8:H:565:LYS:HG3	2.34	0.62
24:C:5:G:H4'	24:C:6:U:OP1	1.98	0.62
1:A:219:ALA:O	1:A:266:LEU:HD12	1.99	0.62
1:A:1022:PRO:CD	1:A:1345:TYR:HE1	2.09	0.62
3:I:147:GLU:CD	3:I:147:GLU:H	2.07	0.62
4:G:167:GLU:HG3	4:G:168:LYS:N	2.13	0.62
8:H:379:ILE:O	8:H:383:LYS:HG3	1.99	0.62
8:H:931:TYR:O	8:H:931:TYR:HD1	1.83	0.62
1:A:1458:TRP:CE3	1:A:1461:TYR:HD2	2.18	0.62
1:A:1887:GLY:HA3	1:A:1992:TYR:HD1	1.64	0.62
5:K:311:GLU:HA	5:K:311:GLU:OE1	2.00	0.62
1:A:175:LEU:CD1	1:A:564:TRP:CE2	2.83	0.62
1:A:286:LEU:CD2	1:A:292:LYS:HB3	2.28	0.62
2:B:165:LEU:N	2:B:165:LEU:HD23	2.14	0.62
4:G:688:ARG:HD3	4:G:692:LEU:HD21	1.81	0.62
8:H:326:GLU:OE1	8:H:330:TYR:HD2	1.82	0.62
8:H:582:SER:OG	8:H:585:ASP:OD2	2.17	0.62
8:H:674:LEU:CD1	8:H:973:ARG:HH22	2.12	0.62
9:N:487:CYS:O	9:N:490:ALA:N	2.33	0.62
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.82	0.62
4:G:281:ASN:HD22	4:G:295:LEU:HD13	1.65	0.62
5:K:280:VAL:O	5:K:286:ASN:ND2	2.33	0.62
5:K:282:GLU:O	5:K:284:ASP:N	2.32	0.62
6:L:34:LYS:HD2	6:L:35:ASN:H	1.64	0.62
8:H:129:ILE:HG12	10:R:16:GLY:CA	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1658:HIS:HA	1:A:1661:ILE:CD1	2.26	0.61
4:G:230:LEU:HD12	4:G:247:SER:CA	2.23	0.61
4:G:285:HIS:CE1	4:G:291:TYR:CZ	2.87	0.61
5:K:147:ASP:OD1	5:K:147:ASP:N	2.31	0.61
8:H:389:LEU:N	8:H:389:LEU:HD23	2.15	0.61
1:A:367:PHE:C	1:A:367:PHE:CD1	2.78	0.61
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.81	0.61
2:B:124:LEU:CD2	2:B:274:HIS:HE1	2.10	0.61
2:B:192:THR:HB	2:B:461:ILE:HD11	1.82	0.61
2:B:313:LEU:HD13	2:B:322:VAL:CG2	2.26	0.61
3:I:400:VAL:HG21	4:G:154:PRO:HG2	1.81	0.61
4:G:9:GLN:C	4:G:10:GLU:HG3	2.24	0.61
4:G:671:PHE:CE2	4:G:694:GLY:HA2	2.35	0.61
4:G:721:ARG:HD2	4:G:725:ILE:CD1	2.30	0.61
4:G:888:PRO:O	4:G:892:LEU:CD2	2.48	0.61
8:H:373:PHE:CE1	8:H:377:ILE:HD12	2.34	0.61
8:H:881:LYS:HA	8:H:886:SER:CB	2.30	0.61
27:F:31:G:N1	27:F:32:G:C4	2.68	0.61
1:A:840:VAL:O	1:A:840:VAL:HG22	2.00	0.61
3:I:184:LYS:CD	3:I:186:LYS:H	2.01	0.61
8:H:168:VAL:HG12	8:H:173:LYS:O	2.00	0.61
8:H:581:LYS:HB3	8:H:581:LYS:NZ	2.11	0.61
24:C:11:A:H8	24:C:11:A:O5'	1.83	0.61
1:A:207:ARG:NH1	1:A:299:LYS:CG	2.63	0.61
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.34	0.61
1:A:1464:LYS:C	1:A:1475:LEU:HD21	2.25	0.61
1:A:1907:GLN:O	1:A:1910:LYS:CG	2.48	0.61
2:B:395:ILE:HD11	7:M:123:THR:HG23	1.80	0.61
3:I:93:LYS:HA	3:I:93:LYS:NZ	2.15	0.61
3:I:263:GLY:O	3:I:283:GLY:HA2	2.00	0.61
3:I:450:GLN:HG3	3:I:451:GLN:N	2.14	0.61
4:G:143:ARG:HH21	4:G:143:ARG:CG	2.14	0.61
1:A:843:THR:HG21	6:L:108:ASP:HB3	1.83	0.61
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.18	0.61
4:G:6:PHE:CD1	4:G:7:LEU:N	2.68	0.61
4:G:238:PRO:CD	4:G:239:THR:H	2.14	0.61
8:H:674:LEU:HD13	8:H:973:ARG:NH1	2.13	0.61
1:A:147:SER:O	1:A:150:ALA:HB2	2.00	0.61
1:A:322:VAL:CG2	1:A:327:TYR:CE2	2.80	0.61
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.83	0.61
1:A:892:SER:CB	1:A:1128:GLN:HE22	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1890:PHE:HB3	1:A:1986:MET:HE1	1.83	0.61
8:H:139:ILE:HD12	8:H:252:LEU:HD22	1.81	0.61
8:H:379:ILE:HG22	8:H:383:LYS:HE3	1.81	0.61
1:A:141:LYS:CA	1:A:144:ASN:ND2	2.54	0.61
1:A:769:MET:CE	4:G:112:ALA:HA	2.29	0.61
1:A:1350:ILE:HG23	1:A:1356:LEU:HD12	1.81	0.61
2:B:206:THR:HB	2:B:208:GLN:OE1	2.00	0.61
2:B:320:SER:CB	2:B:337:ARG:HH22	2.13	0.61
2:B:456:GLY:O	2:B:458:ASP:N	2.34	0.61
8:H:106:PHE:O	8:H:110:LYS:HG2	2.00	0.61
27:F:32:G:O2'	27:F:33:U:OP1	2.19	0.61
1:A:217:TRP:CD1	1:A:703:PHE:CE2	2.89	0.61
1:A:1468:ALA:CB	1:A:1473:ARG:O	2.49	0.61
8:H:606:VAL:HG21	8:H:973:ARG:HH21	1.66	0.61
24:C:11:A:O2'	24:C:12:U:H5'	2.01	0.61
27:F:74:U:H5'	27:F:74:U:H6	1.65	0.61
1:A:355:LEU:HD13	1:A:356:TYR:N	2.16	0.61
1:A:495:ARG:CZ	1:A:497:GLN:HE21	2.12	0.61
1:A:1282:ASP:O	1:A:1285:VAL:HG23	2.01	0.61
1:A:1830:VAL:HG11	1:A:1958:PRO:HG3	1.80	0.61
8:H:132:ARG:HH21	8:H:206:LYS:HG3	1.66	0.61
8:H:235:VAL:HG22	8:H:261:VAL:CG1	2.29	0.61
8:H:369:LYS:NZ	8:H:369:LYS:H	1.99	0.61
8:H:883:ARG:NH2	8:H:910:GLU:O	2.34	0.61
1:A:293:VAL:HG22	1:A:294:ASN:H	1.65	0.61
1:A:355:LEU:HD13	1:A:355:LEU:C	2.26	0.61
1:A:1887:GLY:HA3	1:A:1992:TYR:CD1	2.35	0.61
3:I:135:LEU:HD23	3:I:136:GLN:HG3	1.83	0.61
3:I:402:ASP:O	3:I:405:GLY:N	2.33	0.61
4:G:668:HIS:HB3	4:G:698:VAL:CG1	2.21	0.61
4:G:696:ARG:C	4:G:699:PRO:CD	2.74	0.61
4:G:702:PRO:CB	4:G:739:PHE:CZ	2.83	0.61
5:K:334:PRO:HG2	5:K:337:TYR:CE1	2.36	0.61
8:H:576:THR:CB	8:H:592:PHE:HD2	2.11	0.61
1:A:547:LEU:HD12	1:A:547:LEU:O	2.00	0.60
2:B:175:THR:HA	2:B:459:ARG:HD2	1.83	0.60
2:B:389:ILE:HD11	2:B:427:TRP:CD1	2.36	0.60
8:H:862:TYR:CE1	8:H:908:VAL:HG23	2.36	0.60
1:A:497:GLN:O	1:A:709:ARG:CD	2.46	0.60
1:A:1158:ILE:HG13	1:A:1172:PHE:HE1	1.65	0.60
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:158:PHE:HA	3:I:161:LEU:CD1	2.28	0.60
1:A:293:VAL:HG13	1:A:295:GLY:H	1.65	0.60
1:A:358:ARG:CD	1:A:360:GLU:HB2	2.31	0.60
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.66	0.60
4:G:6:PHE:CE1	4:G:7:LEU:HD12	2.36	0.60
4:G:692:LEU:HD23	4:G:692:LEU:N	2.17	0.60
7:M:95:ARG:HG2	7:M:95:ARG:NH1	2.01	0.60
1:A:325:LYS:HE2	1:A:325:LYS:HA	1.83	0.60
2:B:127:TYR:CE2	2:B:276:SER:CA	2.85	0.60
2:B:320:SER:HB2	2:B:337:ARG:CZ	2.30	0.60
4:G:630:SER:CA	4:G:670:PHE:CZ	2.84	0.60
4:G:804:ASP:CG	4:G:805:HIS:H	2.10	0.60
6:L:71:ASP:HA	6:L:76:LEU:HD13	1.82	0.60
1:A:770:MET:HE3	1:A:775:ARG:O	2.01	0.60
3:I:123:ARG:HD2	3:I:189:LEU:CD1	2.31	0.60
5:K:244:LEU:O	5:K:248:ARG:HB2	2.02	0.60
24:C:8:U:C5	25:D:51:A:C6	2.90	0.60
27:F:44:A:C4	27:F:45:A:N7	2.69	0.60
27:F:102:C:O5'	27:F:102:C:H6	1.85	0.60
1:A:1275:MET:CE	1:A:1299:LYS:HD2	2.31	0.60
2:B:187:ASP:OD2	2:B:447:ASN:HB3	2.01	0.60
3:I:135:LEU:HD23	3:I:136:GLN:H	1.62	0.60
4:G:855:ASP:N	4:G:855:ASP:OD1	2.34	0.60
5:K:341:VAL:CG2	5:K:428:TRP:NE1	2.65	0.60
8:H:113:ILE:HG23	8:H:549:TYR:CG	2.37	0.60
8:H:352:VAL:HG13	8:H:372:THR:OG1	2.02	0.60
2:B:331:SER:HB3	2:B:345:LEU:HB2	1.83	0.60
3:I:123:ARG:HD2	3:I:189:LEU:HD12	1.83	0.60
8:H:113:ILE:HG22	8:H:114:PRO:CD	2.30	0.60
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.83	0.60
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.41	0.60
2:B:47:GLU:HB2	2:B:50:GLU:HG3	1.82	0.60
3:I:282:GLU:CG	3:I:286:PHE:CG	2.80	0.60
4:G:702:PRO:HB3	4:G:739:PHE:CE2	2.37	0.60
8:H:349:TRP:HZ3	8:H:373:PHE:HE2	1.47	0.60
24:C:8:U:N1	25:D:51:A:N6	2.48	0.60
27:F:32:G:N2	27:F:122:C:C2	2.70	0.60
27:F:97:U:C6	27:F:97:U:C5'	2.85	0.60
1:A:209:ILE:HG12	1:A:493:MET:HE1	1.83	0.60
1:A:1882:LEU:C	1:A:1882:LEU:HD22	2.26	0.60
4:G:143:ARG:HH21	4:G:143:ARG:HG3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:126:MET:CE	8:H:132:ARG:HH12	2.09	0.60
8:H:324:ILE:O	8:H:328:VAL:CG2	2.46	0.60
1:A:173:LEU:CD1	1:A:712:LEU:HD11	2.32	0.59
1:A:266:LEU:HD23	1:A:267:PRO:CD	2.32	0.59
1:A:1025:VAL:O	1:A:1029:THR:HG23	2.01	0.59
1:A:1354:GLU:N	1:A:1354:GLU:OE2	2.35	0.59
3:I:135:LEU:HD23	3:I:135:LEU:C	2.25	0.59
3:I:265:ASN:O	3:I:266:LYS:HB2	2.02	0.59
4:G:6:PHE:CZ	6:L:18:ALA:HB2	2.37	0.59
5:K:342:PHE:HB3	5:K:424:ILE:HD11	1.84	0.59
6:L:71:ASP:OD1	6:L:76:LEU:HB2	2.02	0.59
8:H:209:MET:HE1	8:H:544:LEU:HD13	1.83	0.59
8:H:492:LEU:HD22	8:H:557:HIS:CG	2.36	0.59
27:F:97:U:H5"	27:F:97:U:H6	1.67	0.59
1:A:505:TRP:CZ3	1:A:690:LYS:HG3	2.37	0.59
1:A:1275:MET:CE	1:A:1299:LYS:CE	2.80	0.59
1:A:1450:GLU:HB3	1:A:1488:ILE:HD11	1.83	0.59
2:B:177:PRO:HB2	2:B:195:TRP:HE1	1.66	0.59
2:B:177:PRO:CD	2:B:195:TRP:CD1	2.85	0.59
4:G:863:PHE:HE2	4:G:892:LEU:CD1	2.16	0.59
1:A:1458:TRP:CZ3	1:A:1461:TYR:HD2	2.20	0.59
1:A:1857:VAL:O	1:A:1877:GLY:CA	2.49	0.59
3:I:98:PHE:CE2	3:I:217:TYR:CE2	2.91	0.59
3:I:184:LYS:HD2	3:I:186:LYS:CB	2.31	0.59
3:I:347:ALA:HB1	3:I:348:PRO:CD	2.31	0.59
5:K:350:PRO:HB3	5:K:353:ARG:HD2	1.84	0.59
2:B:177:PRO:HB2	2:B:195:TRP:NE1	2.17	0.59
3:I:98:PHE:HE2	3:I:217:TYR:CE2	2.19	0.59
8:H:332:TYR:OH	8:H:376:PHE:HD2	1.81	0.59
8:H:364:PHE:HB2	8:H:369:LYS:HG3	0.63	0.59
2:B:131:ARG:HG2	2:B:131:ARG:HH11	1.67	0.59
2:B:227:HIS:CD2	2:B:273:TYR:CE1	2.90	0.59
2:B:320:SER:CB	2:B:337:ARG:NH2	2.65	0.59
3:I:282:GLU:OE2	3:I:286:PHE:CE2	2.52	0.59
4:G:104:PHE:O	4:G:105:ALA:C	2.45	0.59
6:L:34:LYS:HD2	6:L:35:ASN:N	2.18	0.59
8:H:132:ARG:C	8:H:133:ILE:HG23	2.27	0.59
1:A:294:ASN:OD1	1:A:300:LYS:HE2	2.01	0.59
1:A:362:GLU:OE2	1:A:1209:LYS:HE3	2.01	0.59
1:A:1846:ASN:HA	1:A:1885:LYS:HZ1	1.68	0.59
3:I:112:MET:CB	3:I:204:LEU:CD2	2.79	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:500:ARG:HD3	8:H:534:THR:CB	2.32	0.59
1:A:175:LEU:CD1	1:A:564:TRP:NE1	2.64	0.59
2:B:124:LEU:O	2:B:128:SER:N	2.31	0.59
3:I:301:GLN:OE1	3:I:344:LEU:HD13	2.01	0.59
4:G:671:PHE:HZ	4:G:693:SER:OG	1.86	0.59
5:K:146:GLU:O	5:K:149:PHE:N	2.33	0.59
8:H:385:PHE:O	8:H:389:LEU:HG	2.03	0.59
8:H:608:GLN:HG3	8:H:609:PRO:HD2	1.85	0.59
1:A:766:ILE:O	1:A:770:MET:HG2	2.03	0.59
2:B:177:PRO:CD	2:B:195:TRP:HD1	2.15	0.59
3:I:233:VAL:HG12	3:I:237:ILE:HB	1.84	0.59
1:A:1892:LYS:HD2	1:A:1916:GLU:CD	2.28	0.59
8:H:230:ALA:HB3	8:H:473:LEU:HD13	1.84	0.59
8:H:323:THR:OG1	8:H:326:GLU:HB2	2.03	0.59
8:H:369:LYS:HE2	8:H:369:LYS:H	1.67	0.59
8:H:932:PHE:O	8:H:933:TRP:CE3	2.56	0.59
1:A:149:MET:O	1:A:153:MET:CG	2.51	0.59
1:A:316:THR:N	1:A:317:PRO:CD	2.66	0.59
1:A:390:LEU:HD13	8:H:652:MET:SD	2.42	0.59
1:A:546:LYS:O	1:A:550:SER:OG	2.18	0.59
1:A:1414:TRP:CZ3	1:A:1416:LYS:HB2	2.37	0.59
2:B:51:VAL:HG13	2:B:76:LEU:HD12	1.85	0.59
3:I:94:LEU:HD13	3:I:98:PHE:CZ	2.38	0.59
4:G:277:ILE:HD12	4:G:277:ILE:N	2.15	0.59
5:K:141:ASN:HD21	5:K:144:LEU:CD2	2.15	0.59
5:K:249:ARG:HG2	5:K:249:ARG:HH11	1.67	0.59
8:H:959:ILE:HD13	8:H:960:ASN:N	2.17	0.59
27:F:44:A:C2'	27:F:45:A:C8	2.67	0.59
27:F:45:A:C2	27:F:46:C:C4	2.91	0.59
1:A:425:ASP:OD2	1:A:426:PRO:HD2	2.03	0.58
4:G:702:PRO:HG3	4:G:738:LEU:HB2	1.85	0.58
6:L:33:ARG:NE	6:L:64:ILE:HB	2.18	0.58
8:H:567:ILE:HD13	8:H:567:ILE:N	2.18	0.58
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.38	0.58
1:A:1158:ILE:CG1	1:A:1172:PHE:CE1	2.86	0.58
1:A:1628:ASP:HB3	25:D:50:G:N2	2.18	0.58
2:B:405:ASP:OD2	2:B:408:LYS:CD	2.52	0.58
2:B:415:TYR:OH	7:M:126:ILE:CA	2.51	0.58
4:G:12:PRO:HB2	4:G:13:ALA:O	2.03	0.58
8:H:268:ASN:HD21	8:H:316:THR:CG2	2.17	0.58
8:H:362:LYS:HE2	8:H:365:GLU:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:386:SER:O	8:H:390:SER:HB3	2.03	0.58
8:H:449:PHE:CD1	8:H:453:THR:CG2	2.86	0.58
25:D:109:U:C3'	25:D:110:U:H5''	2.31	0.58
1:A:297:SER:HB3	27:F:32:G:P	2.41	0.58
2:B:115:SER:CA	2:B:118:ILE:HG13	2.32	0.58
1:A:165:LEU:CD2	1:A:730:ILE:HD11	2.29	0.58
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.38	0.58
1:A:1758:ASP:O	1:A:1762:ASP:HB2	2.04	0.58
1:A:1880:PHE:HE2	1:A:1889:LEU:HD21	1.57	0.58
2:B:127:TYR:OH	2:B:131:ARG:NH1	2.35	0.58
3:I:367:ARG:NH2	26:E:58:G:N7	2.52	0.58
8:H:191:ILE:HG23	8:H:221:PHE:CE1	2.38	0.58
8:H:881:LYS:HA	8:H:886:SER:HB2	1.84	0.58
8:H:968:MET:HE2	8:H:968:MET:N	2.18	0.58
1:A:168:LEU:CA	1:A:199:ILE:CD1	2.81	0.58
1:A:506:PHE:HA	1:A:522:TYR:CD1	2.39	0.58
1:A:1664:ASP:O	1:A:1668:ILE:HG13	2.04	0.58
1:A:1854:ASP:OD1	1:A:1879:ILE:HG23	2.04	0.58
5:K:363:LEU:HD11	5:K:391:PHE:HD2	1.68	0.58
5:K:455:LEU:C	5:K:457:GLN:OE1	2.47	0.58
8:H:145:GLY:N	28:H:1500:GTP:O2B	2.31	0.58
8:H:177:TYR:C	8:H:178:LEU:HD23	2.29	0.58
8:H:476:VAL:CG1	8:H:478:TYR:CD1	2.85	0.58
8:H:780:PRO:HA	8:H:783:ILE:HB	1.85	0.58
2:B:201:VAL:C	2:B:202:LEU:HD12	2.28	0.58
3:I:113:HIS:HD2	3:I:134:PRO:HA	1.68	0.58
4:G:891:ILE:O	4:G:892:LEU:C	2.45	0.58
1:A:1496:GLN:O	1:A:1499:ARG:CG	2.51	0.58
2:B:446:SER:HB2	2:B:451:PHE:N	2.16	0.58
3:I:423:ALA:O	3:I:424:THR:HB	2.03	0.58
4:G:630:SER:CA	4:G:670:PHE:HZ	2.16	0.58
4:G:849:TYR:O	4:G:853:GLY:N	2.35	0.58
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.38	0.58
8:H:572:ILE:HD12	8:H:572:ILE:O	2.03	0.58
24:C:-1:A:N3	24:C:-1:A:H2'	2.18	0.58
1:A:255:ILE:O	1:A:258:ILE:HG22	2.03	0.58
1:A:457:ASP:OD1	1:A:457:ASP:N	2.37	0.58
1:A:839:HIS:NE2	27:F:96:U:C4	2.71	0.58
1:A:1998:ARG:O	1:A:1999:ILE:CG1	2.44	0.58
3:I:282:GLU:HG2	3:I:286:PHE:CD1	2.36	0.58
6:L:133:SER:OG	6:L:135:TYR:O	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:307:ILE:CD1	8:H:324:ILE:CD1	2.81	0.58
8:H:369:LYS:HE2	8:H:369:LYS:CA	2.33	0.58
8:H:489:TYR:CE2	8:H:592:PHE:HE1	2.20	0.58
8:H:862:TYR:HD2	8:H:930:LEU:HB3	1.67	0.58
1:A:149:MET:CG	1:A:154:TYR:HE2	2.16	0.58
1:A:286:LEU:O	1:A:287:GLU:O	2.22	0.58
1:A:1256:PRO:CA	1:A:1274:ARG:HH21	2.12	0.58
1:A:1313:ASP:OD2	1:A:1359:ILE:HD13	2.03	0.58
5:K:295:LYS:O	5:K:299:ASP:HB2	2.04	0.58
8:H:296:ASN:HD21	8:H:304:PHE:N	2.00	0.58
8:H:507:SER:O	8:H:510:ARG:N	2.37	0.58
1:A:249:LEU:HD23	1:A:249:LEU:H	1.69	0.58
1:A:1751:TYR:CE1	1:A:1755:LYS:CD	2.77	0.58
3:I:421:VAL:HG21	4:G:250:LEU:CD1	2.33	0.58
4:G:278:TRP:HA	4:G:278:TRP:CE3	2.38	0.58
4:G:401:ILE:O	4:G:405:SER:N	2.35	0.58
4:G:672:LEU:HD23	4:G:704:LEU:HD23	1.45	0.58
4:G:697:LEU:N	4:G:697:LEU:HD23	2.17	0.58
1:A:239:PHE:O	1:A:240:PRO:C	2.47	0.57
1:A:837:GLY:C	1:A:1317:ARG:NH1	2.62	0.57
1:A:1073:ILE:CG2	1:A:1074:VAL:HG23	2.29	0.57
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.87	0.57
4:G:248:ALA:HB1	4:G:264:ILE:HD11	1.86	0.57
4:G:867:GLU:OE2	4:G:888:PRO:CG	2.52	0.57
8:H:354:TYR:HA	8:H:359:PHE:CB	2.33	0.57
8:H:489:TYR:HE2	8:H:592:PHE:HE1	1.52	0.57
8:H:586:MET:CA	8:H:589:LEU:HD23	2.33	0.57
26:E:19:U:O2'	26:E:20:A:OP2	2.21	0.57
1:A:141:LYS:HA	1:A:144:ASN:CG	2.19	0.57
1:A:552:LYS:HG3	1:A:553:ASN:N	2.19	0.57
1:A:1256:PRO:CA	1:A:1274:ARG:NH2	2.67	0.57
2:B:264:HIS:HE1	2:B:290:ARG:HD2	1.69	0.57
4:G:764:LEU:O	4:G:768:PRO:HB3	2.04	0.57
4:G:846:PHE:CE1	4:G:859:LEU:HD23	2.36	0.57
8:H:349:TRP:CZ3	8:H:373:PHE:CE2	2.92	0.57
8:H:353:TYR:O	8:H:359:PHE:HB2	2.04	0.57
8:H:500:ARG:HG2	8:H:534:THR:CG2	2.33	0.57
1:A:833:ARG:HH21	1:A:840:VAL:HG23	1.69	0.57
2:B:443:LEU:HD11	2:B:452:LEU:HD11	1.86	0.57
1:A:1283:GLU:HG2	1:A:1351:VAL:HB	1.84	0.57
6:L:119:THR:HG22	6:L:131:VAL:CG1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:336:ILE:HG13	8:H:341:ILE:HG22	1.85	0.57
2:B:127:TYR:CE2	2:B:276:SER:HA	2.38	0.57
2:B:131:ARG:HG2	2:B:131:ARG:NH1	2.18	0.57
3:I:189:LEU:HD23	3:I:193:THR:OG1	2.03	0.57
3:I:346:GLU:O	3:I:347:ALA:CB	2.53	0.57
4:G:695:THR:CB	4:G:705:TRP:NE1	2.57	0.57
5:K:163:ASN:O	5:K:164:HIS:HB3	2.03	0.57
8:H:129:ILE:H	8:H:129:ILE:CD1	2.18	0.57
25:D:51:A:O2'	25:D:52:G:O5'	2.22	0.57
1:A:251:TYR:CE2	1:A:566:GLU:OE1	2.58	0.57
1:A:1049:LEU:HD13	1:A:1260:PHE:HB3	1.87	0.57
1:A:2007:ARG:NH2	5:K:291:THR:OG1	2.35	0.57
1:A:2050:THR:O	1:A:2053:SER:OG	2.20	0.57
3:I:217:TYR:O	3:I:220:SER:OG	2.18	0.57
5:K:144:LEU:HD22	5:K:144:LEU:H	1.69	0.57
6:L:74:TYR:HB2	6:L:76:LEU:HD11	1.86	0.57
8:H:132:ARG:NH2	8:H:206:LYS:HG3	2.19	0.57
8:H:369:LYS:H	8:H:369:LYS:CE	2.16	0.57
8:H:580:VAL:HG11	8:H:586:MET:HG2	1.85	0.57
1:A:224:MET:CE	1:A:702:GLY:HA3	2.34	0.57
1:A:301:TRP:CE2	1:A:491:GLY:HA3	2.40	0.57
4:G:698:VAL:N	4:G:699:PRO:HD3	2.20	0.57
8:H:227:VAL:CG1	8:H:474:LYS:HG3	2.25	0.57
8:H:306:PRO:O	8:H:324:ILE:HD13	2.04	0.57
1:A:258:ILE:O	1:A:259:GLU:CB	2.53	0.57
1:A:430:PRO:O	1:A:431:ILE:HG22	2.05	0.57
1:A:1621:VAL:HG12	1:A:1622:GLY:N	2.07	0.57
3:I:155:ASP:N	3:I:155:ASP:OD1	2.35	0.57
3:I:344:LEU:HD23	3:I:344:LEU:N	2.20	0.57
4:G:83:LYS:C	4:G:85:ARG:H	2.12	0.57
4:G:678:TYR:CZ	4:G:686:MET:HG2	2.40	0.57
4:G:846:PHE:CB	4:G:896:MET:SD	2.93	0.57
6:L:22:GLU:OE2	6:L:58:VAL:HG11	2.04	0.57
7:M:39:GLU:HB2	26:E:32:G:O6	2.05	0.57
8:H:488:ILE:HD13	8:H:560:GLN:HG2	1.81	0.57
1:A:165:LEU:CD2	1:A:726:ILE:HG21	2.35	0.57
1:A:543:ASN:ND2	1:A:544:LYS:N	2.53	0.57
1:A:691:PHE:C	1:A:691:PHE:CD1	2.82	0.57
1:A:2068:ASN:N	1:A:2068:ASN:OD1	2.38	0.57
8:H:369:LYS:HE2	8:H:369:LYS:C	2.30	0.57
8:H:697:ARG:HA	8:H:697:ARG:CZ	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:942:GLY:C	8:H:963:SER:OG	2.47	0.57
27:F:99:U:HO2'	27:F:100:A:P	2.23	0.57
1:A:358:ARG:HD2	1:A:360:GLU:HB2	1.87	0.57
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.87	0.57
1:A:1378:LYS:O	1:A:1379:MET:CB	2.53	0.57
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.87	0.57
8:H:133:ILE:O	8:H:134:ILE:HG22	2.01	0.57
8:H:251:GLN:HG2	8:H:933:TRP:CE2	2.39	0.57
8:H:331:TYR:HE1	8:H:404:PHE:HD1	1.50	0.57
8:H:468:LEU:CD1	8:H:493:LEU:HD23	2.35	0.57
1:A:299:LYS:HA	1:A:493:MET:CG	2.33	0.56
1:A:389:HIS:HB2	8:H:653:ASP:OD1	2.05	0.56
1:A:1020:ILE:HD13	1:A:1488:ILE:HG21	1.87	0.56
1:A:1158:ILE:HG13	1:A:1172:PHE:CE1	2.40	0.56
1:A:1342:LEU:C	1:A:1342:LEU:HD23	2.30	0.56
2:B:362:TYR:HB2	2:B:379:ARG:HD2	1.85	0.56
3:I:158:PHE:CA	3:I:161:LEU:HD12	2.34	0.56
8:H:251:GLN:HG2	8:H:933:TRP:CZ2	2.40	0.56
8:H:307:ILE:HD13	8:H:324:ILE:CD1	2.35	0.56
8:H:599:THR:HG23	8:H:933:TRP:CZ3	2.40	0.56
8:H:884:ARG:HD3	8:H:884:ARG:C	2.30	0.56
1:A:219:ALA:O	1:A:266:LEU:HD11	2.05	0.56
1:A:1073:ILE:HG23	1:A:1074:VAL:CG2	2.33	0.56
3:I:191:ILE:HD12	3:I:191:ILE:N	2.14	0.56
4:G:296:VAL:HG12	4:G:300:ILE:HD12	1.86	0.56
5:K:146:GLU:CA	5:K:149:PHE:HD2	2.18	0.56
27:F:103:A:O2'	27:F:104:G:P	2.63	0.56
1:A:170:HIS:ND1	1:A:547:LEU:CD2	2.68	0.56
1:A:180:PRO:HA	1:A:187:LYS:HD2	1.87	0.56
1:A:208:VAL:HG22	1:A:494:VAL:O	2.05	0.56
1:A:209:ILE:HG13	1:A:493:MET:HE1	1.86	0.56
1:A:325:LYS:HA	1:A:325:LYS:CE	2.35	0.56
1:A:770:MET:CE	1:A:778:LYS:CB	2.84	0.56
1:A:779:ALA:O	1:A:782:ILE:HB	2.04	0.56
1:A:909:THR:HG22	1:A:910:LYS:N	2.20	0.56
1:A:1038:ILE:HD11	1:A:1039:TRP:CE2	2.39	0.56
1:A:1468:ALA:HB1	1:A:1473:ARG:C	2.29	0.56
1:A:1498:ASP:HB2	4:G:159:LEU:HB2	1.86	0.56
1:A:1628:ASP:CB	25:D:50:G:N2	2.68	0.56
3:I:227:PRO:HG3	3:I:325:ARG:HB3	1.86	0.56
3:I:418:GLN:NE2	3:I:425:SER:HB2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:296:VAL:O	5:K:300:GLN:HB2	2.05	0.56
6:L:53:VAL:CG1	6:L:57:ALA:HB3	2.35	0.56
6:L:82:VAL:HB	6:L:103:LEU:HB3	1.87	0.56
6:L:116:ILE:HD12	6:L:137:TYR:OH	2.02	0.56
8:H:146:LYS:CE	28:H:1500:GTP:O3G	2.51	0.56
8:H:268:ASN:HD21	8:H:316:THR:HG23	1.69	0.56
8:H:328:VAL:O	8:H:333:ALA:N	2.38	0.56
8:H:476:VAL:HG11	8:H:478:TYR:CD1	2.40	0.56
25:D:49:A:N6	25:D:50:G:C5	2.73	0.56
1:A:794:LYS:O	1:A:1095:MET:HE1	2.05	0.56
1:A:1115:GLN:HA	1:A:1115:GLN:NE2	2.20	0.56
1:A:1773:VAL:HG22	1:A:1788:GLY:HA2	1.86	0.56
2:B:117:LEU:C	2:B:117:LEU:HD13	2.31	0.56
8:H:328:VAL:HG21	8:H:345:THR:HG22	1.87	0.56
8:H:468:LEU:CD2	8:H:577:LEU:CD2	2.80	0.56
8:H:495:ARG:NH2	8:H:541:GLU:OE2	2.38	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CB	2.80	0.56
24:C:-3:A:C8	24:C:-2:A:N6	2.73	0.56
1:A:272:ASP:HB2	1:A:273:ASP:OD1	2.05	0.56
1:A:1275:MET:O	1:A:1277:GLU:O	2.24	0.56
1:A:1364:GLU:O	1:A:1368:GLN:HG3	2.06	0.56
2:B:192:THR:CB	2:B:461:ILE:HD11	2.35	0.56
5:K:300:GLN:OE1	5:K:300:GLN:HA	2.06	0.56
7:M:95:ARG:CG	7:M:96:PRO:HD2	2.36	0.56
8:H:307:ILE:HA	8:H:324:ILE:HD11	1.87	0.56
8:H:369:LYS:HE2	8:H:369:LYS:N	2.20	0.56
8:H:489:TYR:CE2	8:H:592:PHE:CZ	2.94	0.56
9:N:461:ASP:O	9:N:709:GLY:N	2.35	0.56
17:b:43:ASN:O	17:b:47:LYS:N	2.37	0.56
25:D:86:G:H5''	25:D:86:G:C8	2.32	0.56
27:F:41:A:H5'	27:F:41:A:H8	1.71	0.56
1:A:273:ASP:HB3	1:A:276:VAL:HG22	1.86	0.56
2:B:115:SER:O	2:B:118:ILE:HB	2.06	0.56
2:B:127:TYR:HE2	2:B:276:SER:HB2	1.63	0.56
8:H:132:ARG:HH21	8:H:206:LYS:CD	2.18	0.56
1:A:406:PRO:HG2	28:H:1500:GTP:O2'	2.04	0.56
2:B:162:MET:CG	2:B:421:VAL:HG11	2.35	0.56
3:I:95:LEU:HA	3:I:98:PHE:HB2	1.88	0.56
3:I:217:TYR:HE1	3:I:221:LYS:CE	2.18	0.56
6:L:109:ASP:OD1	6:L:110:LYS:N	2.38	0.56
7:M:11:LEU:HD23	7:M:12:ALA:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:582:SER:CB	8:H:585:ASP:HB2	2.28	0.56
8:H:586:MET:C	8:H:589:LEU:HD23	2.30	0.56
8:H:901:GLU:OE2	8:H:903:ARG:CZ	2.53	0.56
25:D:46:U:H2'	25:D:47:A:H8	1.69	0.56
1:A:148:ASP:OD1	1:A:148:ASP:N	2.38	0.56
1:A:360:GLU:OE1	1:A:360:GLU:HA	2.06	0.56
1:A:371:ASP:OD2	8:H:972:ARG:NH1	2.38	0.56
1:A:1379:MET:HG3	1:A:1380:PRO:HD2	1.87	0.56
1:A:1846:ASN:HA	1:A:1885:LYS:HZ2	1.71	0.56
4:G:9:GLN:C	4:G:11:PRO:HD3	2.30	0.56
5:K:316:HIS:C	5:K:316:HIS:CD2	2.83	0.56
5:K:350:PRO:C	5:K:353:ARG:HG3	2.30	0.56
8:H:118:TYR:CD1	8:H:119:ASN:N	2.74	0.56
8:H:307:ILE:HD11	8:H:345:THR:C	2.30	0.56
1:A:165:LEU:CD1	1:A:578:MET:HB3	2.35	0.56
2:B:206:THR:O	2:B:207:LEU:HB2	2.05	0.56
3:I:95:LEU:HD23	3:I:98:PHE:HD2	1.69	0.56
4:G:288:ASP:OD1	4:G:291:TYR:HB2	2.05	0.56
8:H:341:ILE:O	8:H:344:PHE:HB3	2.06	0.56
1:A:167:TYR:N	1:A:167:TYR:CD1	2.73	0.56
1:A:176:LEU:O	1:A:179:MET:HG3	2.06	0.56
1:A:749:ARG:HD2	1:A:750:LEU:N	2.20	0.56
1:A:1389:TYR:CE2	1:A:1401:SER:HB3	2.40	0.56
2:B:320:SER:HB2	2:B:337:ARG:NH1	2.21	0.56
6:L:74:TYR:CD1	6:L:83:MET:CE	2.86	0.56
8:H:572:ILE:CD1	8:H:573:LYS:HG3	2.28	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CG2	2.89	0.56
25:D:77:G:N2	26:E:4:C:O2	2.29	0.56
1:A:428:LEU:CD1	8:H:279:LEU:HD11	2.36	0.55
1:A:549:LYS:HG2	27:F:35:A:H5'	1.88	0.55
1:A:770:MET:CE	1:A:778:LYS:HB2	2.37	0.55
2:B:348:HIS:CD2	2:B:374:ASN:ND2	2.74	0.55
2:B:415:TYR:OH	7:M:126:ILE:C	2.49	0.55
4:G:526:TYR:O	4:G:530:GLU:N	2.35	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.21	0.55
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.22	0.55
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.41	0.55
3:I:329:LEU:HD12	3:I:333:TRP:CZ2	2.41	0.55
8:H:483:TRP:CZ3	8:H:565:LYS:CG	2.89	0.55
8:H:862:TYR:CZ	8:H:908:VAL:HG23	2.41	0.55
9:N:1502:LEU:O	9:N:1503:GLU:C	2.47	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:1795:SER:O	9:N:1798:GLY:N	2.39	0.55
27:F:33:U:O2	27:F:33:U:H2'	2.05	0.55
27:F:44:A:N1	27:F:71:A:N1	2.54	0.55
1:A:149:MET:O	1:A:153:MET:HG2	2.07	0.55
1:A:749:ARG:HD2	1:A:750:LEU:H	1.71	0.55
1:A:992:ASP:OD2	1:A:1109:PHE:CE2	2.60	0.55
2:B:389:ILE:HD12	2:B:427:TRP:O	2.05	0.55
8:H:229:LEU:HD21	8:H:235:VAL:HG11	1.87	0.55
25:D:48:C:C4'	25:D:49:A:OP1	2.52	0.55
27:F:78:A:N1	27:F:81:A:C8	2.74	0.55
27:F:95:C:H4'	27:F:96:U:OP1	2.05	0.55
1:A:503:LYS:HA	1:A:506:PHE:CE1	2.38	0.55
1:A:849:LEU:HG	1:A:973:GLU:HB3	1.88	0.55
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.05	0.55
1:A:1831:GLN:HG2	1:A:1832:GLU:N	2.20	0.55
4:G:282:ILE:O	4:G:286:GLU:CG	2.51	0.55
4:G:298:THR:O	4:G:302:PHE:HD2	1.88	0.55
8:H:332:TYR:CE2	8:H:376:PHE:HB3	2.41	0.55
8:H:605:ILE:CG1	8:H:652:MET:SD	2.92	0.55
25:D:44:A:H2'	25:D:45:A:H8	1.71	0.55
1:A:382:GLU:OE1	1:A:382:GLU:N	2.34	0.55
1:A:1065:LEU:HD23	1:A:1065:LEU:O	2.06	0.55
2:B:360:ASN:CB	2:B:362:TYR:HE1	2.20	0.55
4:G:695:THR:O	4:G:699:PRO:HD3	2.06	0.55
8:H:285:TYR:CD1	8:H:285:TYR:C	2.84	0.55
8:H:380:PRO:HA	8:H:383:LYS:HG3	1.88	0.55
8:H:430:ARG:O	8:H:431:GLN:O	2.23	0.55
8:H:586:MET:O	8:H:589:LEU:CD2	2.52	0.55
8:H:951:ILE:CD1	8:H:955:LYS:HB2	2.37	0.55
1:A:536:PRO:HG2	27:F:76:U:O4	2.06	0.55
1:A:1356:LEU:O	1:A:1356:LEU:HD22	2.06	0.55
1:A:2065:ARG:CD	1:A:2066:LYS:HE2	2.36	0.55
2:B:389:ILE:CD1	2:B:427:TRP:O	2.54	0.55
8:H:305:SER:C	8:H:307:ILE:H	2.15	0.55
8:H:468:LEU:HB3	8:H:579:SER:HB3	1.89	0.55
8:H:506:GLN:O	8:H:509:SER:CB	2.49	0.55
1:A:160:ALA:CB	1:A:194:HIS:CE1	2.89	0.55
1:A:1163:ARG:NH1	1:A:1165:LEU:O	2.39	0.55
1:A:1341:SER:HA	1:A:1525:PHE:HE1	1.72	0.55
2:B:166:GLU:O	2:B:465:ASN:N	2.39	0.55
5:K:350:PRO:HB3	25:D:84:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:452:LEU:HB3	5:K:461:GLU:HG2	1.88	0.55
8:H:133:ILE:C	8:H:134:ILE:CG2	2.72	0.55
8:H:387:TYR:HB3	8:H:396:LEU:HD21	1.88	0.55
8:H:564:ILE:HG21	8:H:567:ILE:CG1	2.36	0.55
8:H:793:GLU:C	8:H:796:ILE:HG22	2.31	0.55
1:A:297:SER:CB	27:F:32:G:P	2.95	0.55
1:A:322:VAL:CB	1:A:327:TYR:CD2	2.90	0.55
1:A:672:LYS:O	1:A:674:MET:N	2.39	0.55
1:A:1074:VAL:HG12	1:A:1075:ASP:N	2.21	0.55
2:B:141:GLU:OE1	2:B:141:GLU:HA	2.07	0.55
4:G:161:LYS:HA	4:G:161:LYS:HE3	1.89	0.55
5:K:332:GLU:O	5:K:332:GLU:HG2	2.05	0.55
8:H:272:ARG:HG3	8:H:276:ASP:HB2	1.89	0.55
1:A:1038:ILE:CD1	1:A:1039:TRP:CD2	2.90	0.55
2:B:446:SER:HB2	2:B:451:PHE:HB2	1.89	0.55
6:L:140:LYS:CB	6:L:141:ARG:HD2	2.32	0.55
8:H:354:TYR:HA	8:H:359:PHE:CA	2.35	0.55
1:A:150:ALA:O	1:A:153:MET:HG2	2.07	0.55
1:A:289:ASP:CG	1:A:292:LYS:CG	2.80	0.55
1:A:1389:TYR:HE2	1:A:1401:SER:HB3	1.72	0.55
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.07	0.55
1:A:1627:LEU:HB2	1:A:1630:THR:OG1	2.07	0.55
2:B:275:PRO:HG3	2:B:319:GLY:CA	2.37	0.55
2:B:363:GLN:HG2	2:B:377:ASP:HB3	1.89	0.55
2:B:452:LEU:HB3	2:B:464:TRP:HB2	1.89	0.55
3:I:282:GLU:OE1	3:I:286:PHE:CZ	2.60	0.55
4:G:230:LEU:CD1	4:G:247:SER:HA	2.25	0.55
4:G:691:TYR:CD2	4:G:711:ILE:CD1	2.90	0.55
5:K:289:ASP:HB3	5:K:292:ALA:HB3	1.89	0.55
8:H:461:LYS:HD2	8:H:462:SER:N	2.22	0.55
8:H:829:VAL:O	8:H:829:VAL:HG12	2.07	0.55
1:A:373:VAL:O	8:H:969:LYS:HG2	2.07	0.54
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.42	0.54
1:A:1458:TRP:HZ3	1:A:1461:TYR:CE2	2.24	0.54
2:B:441:ILE:HD11	2:B:457:TRP:CD1	2.41	0.54
3:I:338:SER:O	3:I:342:ARG:HG3	2.07	0.54
8:H:337:PRO:O	8:H:341:ILE:HG23	2.07	0.54
1:A:1264:GLY:HA3	1:A:1308:GLU:CD	2.33	0.54
1:A:1910:LYS:HG3	1:A:1911:TRP:N	2.22	0.54
3:I:146:ASN:HD21	3:I:148:ASN:ND2	2.04	0.54
3:I:418:GLN:HE22	3:I:425:SER:HB2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:140:LYS:HB3	6:L:141:ARG:HH11	1.70	0.54
8:H:303:VAL:HG23	8:H:303:VAL:O	2.07	0.54
1:A:410:ILE:HD12	1:A:410:ILE:N	2.22	0.54
2:B:206:THR:CG2	2:B:208:GLN:HE22	2.21	0.54
3:I:267:HIS:HE1	3:I:273:HIS:CE1	2.25	0.54
4:G:528:LYS:O	4:G:532:LEU:N	2.39	0.54
4:G:668:HIS:NE2	4:G:669:LYS:HG3	2.21	0.54
8:H:379:ILE:CG2	8:H:383:LYS:CE	2.86	0.54
8:H:582:SER:HB3	8:H:585:ASP:OD2	2.03	0.54
8:H:767:SER:OG	8:H:796:ILE:HD11	2.07	0.54
1:A:256:GLU:HG3	1:A:257:ASN:N	2.22	0.54
1:A:770:MET:SD	4:G:119:TRP:CZ3	3.01	0.54
2:B:36:ARG:HG2	2:B:81:MET:HE1	1.89	0.54
2:B:135:ARG:NH2	5:K:167:GLU:OE2	2.40	0.54
4:G:6:PHE:CD1	4:G:6:PHE:C	2.85	0.54
4:G:688:ARG:O	4:G:692:LEU:HG	2.07	0.54
8:H:564:ILE:HG21	8:H:567:ILE:HG12	1.89	0.54
25:D:87:U:P	25:D:87:U:H3'	2.47	0.54
27:F:40:C:H3'	27:F:40:C:P	2.48	0.54
1:A:293:VAL:HG22	1:A:294:ASN:N	2.22	0.54
1:A:296:THR:HG22	27:F:33:U:OP2	2.06	0.54
1:A:363:ASP:N	1:A:363:ASP:OD1	2.39	0.54
1:A:413:ASN:ND2	1:A:413:ASN:H	2.06	0.54
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.72	0.54
4:G:846:PHE:HB2	4:G:896:MET:SD	2.48	0.54
1:A:221:TRP:CZ2	1:A:691:PHE:HB3	2.42	0.54
1:A:264:ILE:O	1:A:265:ASN:HB2	2.08	0.54
1:A:860:GLU:HA	1:A:860:GLU:OE1	2.07	0.54
3:I:191:ILE:H	3:I:191:ILE:CD1	2.14	0.54
5:K:141:ASN:OD1	5:K:144:LEU:HD23	2.08	0.54
8:H:430:ARG:O	8:H:431:GLN:C	2.50	0.54
8:H:470:ALA:CB	8:H:486:VAL:HG21	2.19	0.54
8:H:810:GLU:OE2	8:H:974:LYS:CB	2.56	0.54
1:A:158:LYS:HG2	1:A:159:LYS:N	2.23	0.54
1:A:1365:THR:C	1:A:1369:ASN:ND2	2.63	0.54
1:A:1995:TRP:CZ3	1:A:2007:ARG:HD2	2.43	0.54
2:B:161:ARG:O	2:B:165:LEU:HD21	2.07	0.54
4:G:863:PHE:CE2	4:G:892:LEU:HD11	2.43	0.54
5:K:249:ARG:HG2	5:K:249:ARG:NH1	2.22	0.54
5:K:276:ASN:OD1	25:D:61:C:OP1	2.26	0.54
8:H:589:LEU:HD11	8:H:591:PHE:CE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:944:VAL:CG2	8:H:945:LEU:HG	2.37	0.54
27:F:74:U:C5'	27:F:74:U:H6	2.20	0.54
6:L:72:GLU:OE2	6:L:72:GLU:HA	2.08	0.54
6:L:140:LYS:HG2	6:L:141:ARG:CZ	2.37	0.54
25:D:78:G:C2	26:E:4:C:C2	2.96	0.54
1:A:322:VAL:HB	1:A:327:TYR:CD2	2.42	0.54
2:B:64:VAL:HG12	2:B:65:GLU:N	2.20	0.54
2:B:415:TYR:CD2	2:B:439:LYS:HD3	2.42	0.54
3:I:392:GLU:HB2	3:I:412:MET:SD	2.48	0.54
3:I:433:ASN:ND2	3:I:433:ASN:H	2.04	0.54
4:G:842:TRP:HA	4:G:845:LEU:HD12	1.90	0.54
8:H:769:TYR:CE1	8:H:799:PHE:CD2	2.96	0.54
8:H:862:TYR:HE1	8:H:908:VAL:CG2	2.20	0.54
8:H:968:MET:CA	8:H:968:MET:CE	2.85	0.54
27:F:31:G:C2	27:F:32:G:C1'	2.89	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CD	2.38	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CG	2.25	0.54
8:H:502:LEU:O	8:H:575:ALA:HB1	2.08	0.54
27:F:78:A:C6	27:F:81:A:C8	2.95	0.54
1:A:266:LEU:CD2	1:A:267:PRO:HD2	2.33	0.53
1:A:614:ARG:NH1	24:C:3:A:OP1	2.41	0.53
1:A:1038:ILE:HD11	1:A:1039:TRP:CZ3	2.44	0.53
1:A:2071:ILE:HD13	1:A:2071:ILE:C	2.33	0.53
2:B:267:ARG:HG3	2:B:285:HIS:CD2	2.42	0.53
2:B:279:PHE:N	2:B:279:PHE:CD1	2.76	0.53
3:I:257:CYS:HB2	26:E:42:C:H41	1.72	0.53
3:I:421:VAL:O	3:I:421:VAL:HG12	2.06	0.53
8:H:578:TYR:CD2	8:H:589:LEU:HD13	2.43	0.53
24:C:7:A:HO2'	24:C:8:U:P	2.26	0.53
27:F:72:C:H2'	27:F:73:U:H6	1.73	0.53
1:A:166:LYS:HE3	1:A:723:GLU:HB3	1.90	0.53
1:A:176:LEU:HD21	1:A:708:TRP:CD1	2.43	0.53
1:A:224:MET:HE3	1:A:702:GLY:HA3	1.91	0.53
1:A:1379:MET:HG3	1:A:1380:PRO:CD	2.39	0.53
1:A:1586:GLN:HG2	1:A:1595:ARG:NH1	2.23	0.53
5:K:167:GLU:HB3	5:K:169:TRP:CE3	2.43	0.53
6:L:33:ARG:HE	6:L:64:ILE:HB	1.73	0.53
8:H:307:ILE:CD1	8:H:345:THR:O	2.55	0.53
8:H:331:TYR:OH	8:H:428:ILE:CG2	2.57	0.53
8:H:494:LYS:HE2	8:H:555:GLU:OE1	2.08	0.53
24:C:11:A:C2'	24:C:12:U:H5'	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:TYR:O	1:A:201:PHE:HE1	1.91	0.53
1:A:284:ARG:NH1	27:F:33:U:O4	2.40	0.53
7:M:60:PRO:HB2	7:M:62:GLU:OE1	2.09	0.53
8:H:862:TYR:CD2	8:H:930:LEU:HB3	2.42	0.53
27:F:31:G:C2	27:F:32:G:N9	2.76	0.53
1:A:168:LEU:CB	1:A:199:ILE:HD11	2.38	0.53
1:A:770:MET:HE1	1:A:778:LYS:C	2.33	0.53
1:A:1880:PHE:HE1	1:A:1882:LEU:HD12	1.71	0.53
5:K:167:GLU:HB3	5:K:169:TRP:HE3	1.73	0.53
8:H:114:PRO:O	8:H:115:LYS:O	2.27	0.53
8:H:447:GLU:HA	8:H:447:GLU:OE2	2.08	0.53
8:H:468:LEU:CD2	8:H:577:LEU:HD21	2.23	0.53
8:H:578:TYR:CD1	8:H:578:TYR:C	2.86	0.53
8:H:873:LEU:HB3	8:H:874:PRO:HD3	1.90	0.53
1:A:755:ASP:OD2	1:A:819:LYS:HE3	2.08	0.53
3:I:123:ARG:O	3:I:183:PHE:CB	2.56	0.53
3:I:376:LYS:O	3:I:377:GLU:C	2.51	0.53
1:A:469:ILE:O	1:A:470:LEU:HD22	2.09	0.53
1:A:2074:LEU:N	1:A:2074:LEU:HD23	2.22	0.53
2:B:199:LEU:HD23	2:B:199:LEU:H	1.73	0.53
2:B:322:VAL:HG13	2:B:334:TRP:HB2	1.91	0.53
2:B:360:ASN:HB3	2:B:362:TYR:CD1	2.44	0.53
4:G:292:CYS:O	4:G:296:VAL:HG23	2.09	0.53
4:G:708:LEU:HD22	4:G:725:ILE:HG21	1.90	0.53
5:K:354:PHE:CD1	5:K:358:MET:HE3	2.33	0.53
8:H:113:ILE:CG2	8:H:114:PRO:HD2	2.34	0.53
8:H:599:THR:HG22	8:H:933:TRP:CZ3	2.43	0.53
8:H:677:PHE:HE1	8:H:966:PHE:HE2	1.45	0.53
8:H:697:ARG:NE	8:H:697:ARG:CA	2.71	0.53
26:E:19:U:C6	26:E:19:U:H3'	2.44	0.53
1:A:468:LEU:N	1:A:468:LEU:HD12	2.24	0.53
1:A:1500:HIS:HB2	4:G:160:ASN:HD21	1.74	0.53
2:B:75:ARG:HG2	2:B:75:ARG:HH21	1.74	0.53
3:I:357:PRO:O	3:I:358:ILE:HG13	2.08	0.53
4:G:158:ASP:OD1	4:G:158:ASP:N	2.40	0.53
4:G:688:ARG:NH1	4:G:721:ARG:NE	2.54	0.53
4:G:691:TYR:CD2	4:G:711:ILE:HD12	2.44	0.53
25:D:49:A:C2'	25:D:50:G:C5'	2.84	0.53
1:A:954:ILE:HG23	1:A:991:THR:HG22	1.89	0.53
2:B:176:LYS:HB2	2:B:194:SER:OG	2.09	0.53
4:G:672:LEU:HD21	4:G:704:LEU:HG	1.83	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:846:PHE:HB3	4:G:896:MET:SD	2.49	0.53
5:K:141:ASN:C	5:K:142:LEU:HD22	2.33	0.53
5:K:350:PRO:C	5:K:353:ARG:CG	2.81	0.53
8:H:222:MET:HE3	8:H:252:LEU:HD21	1.90	0.53
8:H:504:THR:OG1	8:H:594:PRO:HG3	2.09	0.53
27:F:64:C:H2'	27:F:65:U:H6	1.74	0.53
27:F:73:U:C3'	27:F:74:U:C5'	2.87	0.53
1:A:242:PHE:CE1	1:A:249:LEU:HD21	2.44	0.53
1:A:553:ASN:C	1:A:554:THR:HG23	2.33	0.53
1:A:774:ILE:HD12	1:A:774:ILE:N	2.24	0.53
1:A:944:TYR:O	4:G:166:ARG:NH1	2.41	0.53
4:G:104:PHE:O	4:G:106:ASP:N	2.41	0.53
5:K:146:GLU:C	5:K:148:LYS:N	2.66	0.53
8:H:227:VAL:HG11	8:H:474:LYS:CB	2.39	0.53
1:A:166:LYS:HD3	1:A:167:TYR:CZ	2.43	0.53
1:A:1125:LEU:HD21	1:A:1234:VAL:HG23	1.90	0.53
1:A:1577:LYS:HE2	3:I:391:MET:HE2	1.90	0.53
1:A:2065:ARG:HD2	1:A:2066:LYS:HE2	1.91	0.53
2:B:386:LEU:C	2:B:386:LEU:HD12	2.34	0.53
3:I:358:ILE:HG22	3:I:360:GLU:N	2.24	0.53
4:G:170:LEU:HD13	4:G:171:GLN:N	2.24	0.53
8:H:176:ARG:O	8:H:548:ARG:NH2	2.41	0.53
8:H:326:GLU:OE1	8:H:330:TYR:CD2	2.61	0.53
8:H:488:ILE:CD1	8:H:557:HIS:O	2.51	0.53
1:A:721:LEU:HD11	27:F:85:U:O2'	2.09	0.52
1:A:1511:ARG:NH2	1:A:1511:ARG:HG3	2.24	0.52
3:I:82:ARG:O	3:I:86:GLN:N	2.35	0.52
3:I:257:CYS:SG	26:E:44:G:O6	2.61	0.52
4:G:630:SER:HA	4:G:670:PHE:HZ	1.72	0.52
5:K:349:ASN:HB2	5:K:406:PHE:CD1	2.44	0.52
6:L:33:ARG:HD3	6:L:65:ASP:N	2.24	0.52
8:H:265:PHE:HE2	8:H:295:ILE:HB	1.73	0.52
1:A:881:THR:O	1:A:885:VAL:HG23	2.08	0.52
1:A:928:ARG:HH21	4:G:145:THR:CG2	2.17	0.52
1:A:1262:MET:O	1:A:1263:CYS:HB2	2.09	0.52
1:A:1577:LYS:NZ	3:I:397:GLU:OE2	2.36	0.52
1:A:1908:LEU:HD12	1:A:1908:LEU:C	2.34	0.52
2:B:316:GLN:O	2:B:316:GLN:NE2	2.42	0.52
2:B:358:SER:OG	2:B:401:PHE:CZ	2.48	0.52
4:G:126:THR:HB	4:G:128:PHE:CZ	2.44	0.52
4:G:666:ILE:CG2	4:G:667:CYS:H	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:64:U:H5''	25:D:64:U:H6	1.74	0.52
1:A:315:SER:C	1:A:317:PRO:CD	2.82	0.52
1:A:778:LYS:HA	1:A:778:LYS:HE2	1.90	0.52
1:A:921:ASP:HB3	3:I:403:SER:HB2	1.91	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CE1	2.45	0.52
1:A:1468:ALA:O	1:A:1473:ARG:N	2.37	0.52
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.09	0.52
3:I:327:THR:O	3:I:328:VAL:HG23	2.09	0.52
3:I:347:ALA:HA	4:G:130:ARG:HH11	1.74	0.52
3:I:417:LEU:HD22	4:G:226:MET:HE2	1.91	0.52
5:K:143:GLU:HA	5:K:145:HIS:CE1	2.45	0.52
8:H:106:PHE:HE2	8:H:554:HIS:NE2	2.06	0.52
8:H:674:LEU:CD1	8:H:973:ARG:NH1	2.69	0.52
1:A:305:LEU:C	1:A:305:LEU:HD23	2.34	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CD1	2.44	0.52
1:A:1613:THR:O	1:A:1616:ARG:CD	2.57	0.52
4:G:252:GLU:CG	4:G:256:LYS:HG3	2.26	0.52
4:G:283:ARG:NH1	4:G:284:LEU:HD21	2.24	0.52
4:G:672:LEU:HD21	4:G:704:LEU:HD21	1.28	0.52
7:M:95:ARG:HG3	7:M:96:PRO:CD	2.40	0.52
25:D:44:A:H2'	25:D:45:A:C8	2.44	0.52
26:E:19:U:O2'	26:E:20:A:P	2.67	0.52
26:E:19:U:C6	26:E:19:U:C3'	2.93	0.52
1:A:1065:LEU:CD2	1:A:1069:LEU:HD13	2.39	0.52
1:A:1902:GLN:O	1:A:1905:LEU:CD2	2.56	0.52
3:I:336:GLU:O	3:I:340:LYS:HB2	2.09	0.52
3:I:398:GLN:NE2	3:I:419:GLN:HG3	2.25	0.52
4:G:234:ARG:O	4:G:237:ASP:O	2.28	0.52
4:G:288:ASP:OD1	4:G:291:TYR:CB	2.58	0.52
4:G:671:PHE:CE1	4:G:690:THR:O	2.62	0.52
5:K:314:ARG:NH2	5:K:314:ARG:HG2	2.23	0.52
6:L:140:LYS:HB3	6:L:141:ARG:NH1	2.25	0.52
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.91	0.52
24:C:-4:A:C1'	24:C:-3:A:OP1	2.49	0.52
1:A:770:MET:HB2	1:A:775:ARG:HG3	1.92	0.52
1:A:1458:TRP:HZ3	1:A:1461:TYR:CD2	2.25	0.52
3:I:99:ASN:O	3:I:103:PRO:HD2	2.09	0.52
5:K:354:PHE:CE1	5:K:358:MET:HG2	2.45	0.52
6:L:140:LYS:CB	6:L:141:ARG:NH1	2.73	0.52
8:H:682:SER:HA	8:H:714:PRO:HG3	1.92	0.52
1:A:261:LEU:HD12	1:A:262:ASP:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:VAL:CG1	1:A:378:PRO:HD2	2.37	0.52
1:A:514:TYR:HD1	1:A:514:TYR:H	1.58	0.52
1:A:814:ARG:NH1	4:G:103:GLN:O	2.43	0.52
3:I:400:VAL:HG12	4:G:215:LEU:HA	1.92	0.52
4:G:712:ASP:OD2	4:G:721:ARG:HB3	2.09	0.52
4:G:863:PHE:HE2	4:G:892:LEU:HD11	1.73	0.52
5:K:282:GLU:C	5:K:284:ASP:H	2.16	0.52
27:F:95:C:O3'	27:F:96:U:C4'	2.58	0.52
8:H:175:LEU:HD23	8:H:175:LEU:C	2.34	0.52
8:H:332:TYR:CZ	8:H:376:PHE:HD2	2.27	0.52
1:A:362:GLU:CB	1:A:1209:LYS:CE	2.72	0.52
1:A:477:MET:HE2	8:H:278:LYS:HD3	1.91	0.52
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.91	0.52
1:A:1899:TRP:CH2	1:A:1909:ALA:HB2	2.45	0.52
2:B:68:ASP:OD1	5:K:322:ARG:NH1	2.41	0.52
2:B:286:ASP:O	2:B:288:THR:HG23	2.10	0.52
2:B:438:ASP:HB2	2:B:458:ASP:HB3	1.91	0.52
3:I:101:ILE:O	3:I:105:ILE:HG13	2.10	0.52
3:I:217:TYR:CE1	3:I:221:LYS:CE	2.92	0.52
4:G:169:LEU:O	4:G:173:GLN:HG3	2.10	0.52
5:K:314:ARG:HG2	5:K:314:ARG:HH21	1.75	0.52
8:H:265:PHE:N	8:H:265:PHE:CD1	2.77	0.52
8:H:270:LEU:HD11	8:H:313:PHE:HB3	1.92	0.52
27:F:103:A:HO2'	27:F:104:G:P	2.29	0.52
1:A:644:VAL:O	1:A:645:ASP:HB2	2.10	0.52
1:A:703:PHE:HD1	1:A:704:TRP:N	2.08	0.52
1:A:1285:VAL:O	1:A:1448:GLU:OE2	2.29	0.52
1:A:1730:ASN:C	1:A:1731:LYS:HG3	2.35	0.52
2:B:316:GLN:HB2	2:B:357:TRP:CG	2.42	0.52
3:I:127:LEU:HD11	3:I:131:ILE:HD12	1.90	0.52
4:G:702:PRO:CA	4:G:739:PHE:CZ	2.93	0.52
6:L:78:ASP:CG	6:L:79:PRO:HD3	2.34	0.52
8:H:168:VAL:HA	8:H:173:LYS:HG3	1.92	0.52
8:H:483:TRP:CZ3	8:H:565:LYS:HG2	2.45	0.52
1:A:321:GLU:HA	1:A:508:GLN:OE1	2.11	0.51
1:A:471:PRO:HG2	1:A:472:ASN:OD1	2.10	0.51
1:A:1992:TYR:CD2	1:A:2004:ALA:HB1	2.44	0.51
3:I:184:LYS:CD	3:I:186:LYS:CB	2.87	0.51
4:G:360:LYS:O	4:G:364:PHE:N	2.38	0.51
27:F:77:A:H4'	27:F:78:A:C5'	2.32	0.51
27:F:100:A:H5'	27:F:101:C:OP2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:ARG:O	1:A:377:VAL:CB	2.56	0.51
2:B:360:ASN:CB	2:B:362:TYR:CE1	2.93	0.51
3:I:347:ALA:HB1	3:I:348:PRO:HD2	1.92	0.51
4:G:143:ARG:NH2	4:G:143:ARG:CB	2.73	0.51
8:H:227:VAL:HG13	8:H:473:LEU:HB3	1.90	0.51
8:H:497:ASP:O	8:H:538:GLU:HA	2.09	0.51
1:A:217:TRP:CD1	1:A:703:PHE:CZ	2.98	0.51
1:A:228:LYS:CD	1:A:691:PHE:HE1	2.23	0.51
1:A:286:LEU:HD12	1:A:287:GLU:H	1.72	0.51
1:A:840:VAL:C	1:A:841:GLU:HG3	2.34	0.51
1:A:1342:LEU:HD23	1:A:1350:ILE:HD11	1.91	0.51
1:A:2013:ARG:HG3	1:A:2083:ILE:O	2.11	0.51
2:B:275:PRO:CG	2:B:319:GLY:CA	2.88	0.51
8:H:369:LYS:CE	8:H:369:LYS:N	2.73	0.51
8:H:478:TYR:HB2	8:H:483:TRP:HD1	1.76	0.51
9:N:1928:LEU:O	9:N:1931:GLN:N	2.40	0.51
1:A:249:LEU:HD23	1:A:249:LEU:N	2.25	0.51
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.45	0.51
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.25	0.51
1:A:1416:LYS:HG2	1:A:1417:GLN:N	2.25	0.51
1:A:1464:LYS:NZ	1:A:1479:GLU:HB3	2.25	0.51
2:B:206:THR:HB	2:B:208:GLN:CD	2.35	0.51
4:G:19:ILE:HD12	4:G:20:GLY:CA	2.40	0.51
4:G:327:VAL:O	4:G:331:LEU:N	2.39	0.51
8:H:135:ASN:HD22	8:H:487:ARG:HH21	1.57	0.51
8:H:354:TYR:CE1	8:H:376:PHE:HZ	2.28	0.51
8:H:478:TYR:HB2	8:H:483:TRP:CD1	2.45	0.51
8:H:860:PRO:HB3	8:H:937:TRP:HZ3	1.74	0.51
1:A:250:SER:HB2	1:A:252:GLU:OE1	2.11	0.51
1:A:815:TYR:CD1	1:A:815:TYR:C	2.88	0.51
1:A:1313:ASP:OD2	1:A:1359:ILE:CD1	2.59	0.51
1:A:1339:LEU:CD2	1:A:1440:ILE:HD12	2.40	0.51
3:I:455:PHE:O	3:I:458:SER:OG	2.19	0.51
6:L:135:TYR:N	6:L:135:TYR:CD1	2.79	0.51
8:H:113:ILE:CG2	8:H:114:PRO:CD	2.89	0.51
8:H:232:SER:OG	8:H:234:LEU:O	2.28	0.51
8:H:951:ILE:CB	8:H:952:PRO:CD	2.88	0.51
8:H:959:ILE:HD13	8:H:960:ASN:H	1.72	0.51
27:F:62:G:H2'	27:F:63:C:H6	1.75	0.51
1:A:166:LYS:O	1:A:169:PRO:CD	2.53	0.51
1:A:170:HIS:C	1:A:170:HIS:CD2	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:ASP:C	1:A:321:GLU:HG3	2.34	0.51
1:A:366:GLU:HG3	1:A:367:PHE:N	2.26	0.51
1:A:1651:ALA:C	1:A:1652:HIS:HD2	2.16	0.51
2:B:171:GLN:O	2:B:172:LEU:CD1	2.59	0.51
2:B:436:HIS:CD2	2:B:440:ILE:HD11	2.45	0.51
3:I:401:LEU:HD12	4:G:214:SER:HA	1.93	0.51
4:G:101:LYS:O	4:G:105:ALA:N	2.36	0.51
6:L:94:ASP:OD1	6:L:132:VAL:HA	2.10	0.51
8:H:354:TYR:HA	8:H:359:PHE:HB3	1.90	0.51
8:H:461:LYS:NZ	8:H:464:PRO:CB	2.73	0.51
1:A:291:LYS:NZ	1:A:291:LYS:H	2.09	0.51
1:A:497:GLN:HB3	1:A:712:LEU:HD23	1.92	0.51
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.92	0.51
1:A:1065:LEU:CD2	1:A:1069:LEU:HD22	2.40	0.51
1:A:2067:TYR:N	1:A:2067:TYR:CD1	2.78	0.51
3:I:376:LYS:O	3:I:378:LYS:N	2.43	0.51
8:H:167:ASN:ND2	8:H:167:ASN:C	2.69	0.51
8:H:178:LEU:HD12	8:H:214:ASP:HB2	1.92	0.51
8:H:379:ILE:CG2	8:H:383:LYS:HE2	2.40	0.51
8:H:953:LYS:O	8:H:954:LEU:HB2	2.10	0.51
1:A:273:ASP:HB3	1:A:276:VAL:HG21	1.92	0.51
1:A:298:TYR:O	1:A:493:MET:SD	2.69	0.51
1:A:522:TYR:CE2	1:A:686:ILE:HD12	2.46	0.51
27:F:74:U:H2'	27:F:75:A:H3'	1.92	0.51
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.76	0.51
1:A:1756:PHE:CD1	1:A:1756:PHE:C	2.89	0.51
2:B:274:HIS:HD2	2:B:276:SER:HB3	1.72	0.51
3:I:112:MET:HB2	3:I:204:LEU:HD21	1.91	0.51
3:I:265:ASN:O	3:I:266:LYS:CB	2.57	0.51
8:H:449:PHE:CD1	8:H:449:PHE:C	2.88	0.51
8:H:697:ARG:NH1	8:H:852:THR:OG1	2.44	0.51
8:H:883:ARG:CZ	8:H:910:GLU:O	2.59	0.51
8:H:945:LEU:O	8:H:945:LEU:HD13	2.11	0.51
24:C:11:A:C2	24:C:12:U:C4	2.99	0.51
27:F:64:C:C2	27:F:65:U:C5	2.99	0.51
1:A:621:LEU:HD12	1:A:666:ILE:HD11	1.91	0.51
1:A:774:ILE:CG2	1:A:777:LYS:HE3	2.38	0.51
1:A:1511:ARG:HH21	1:A:1511:ARG:CG	2.22	0.51
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.46	0.51
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.11	0.51
2:B:121:ARG:HD2	2:B:337:ARG:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:274:HIS:CD2	2:B:275:PRO:CD	2.93	0.51
3:I:112:MET:HE2	3:I:203:ILE:HD12	1.92	0.51
7:M:46:ARG:NH1	26:E:43:C:OP1	2.44	0.51
8:H:143:HIS:HA	28:H:1500:GTP:PB	2.51	0.51
8:H:160:ARG:HB3	8:H:161:ILE:CA	2.40	0.51
8:H:376:PHE:CD1	8:H:376:PHE:N	2.79	0.51
27:F:72:C:C2	27:F:73:U:C5	2.98	0.51
1:A:767:LEU:CD2	1:A:779:ALA:HB2	2.40	0.50
1:A:806:ALA:N	1:A:807:PRO:HD2	2.26	0.50
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.44	0.50
2:B:127:TYR:HE2	2:B:276:SER:CB	2.19	0.50
2:B:167:LEU:O	4:G:728:ARG:NH2	2.44	0.50
2:B:243:ILE:HD12	2:B:292:TRP:CZ3	2.46	0.50
3:I:301:GLN:OE1	3:I:344:LEU:CD1	2.60	0.50
3:I:447:GLU:OE2	3:I:448:ALA:N	2.45	0.50
4:G:143:ARG:CG	4:G:143:ARG:NH2	2.73	0.50
4:G:851:ARG:C	4:G:852:LEU:HD12	2.36	0.50
8:H:116:THR:CG2	8:H:157:SER:OG	2.59	0.50
8:H:247:PHE:CB	8:H:931:TYR:OH	2.59	0.50
8:H:353:TYR:CE2	8:H:371:PRO:HG3	2.47	0.50
1:A:418:ASP:N	1:A:418:ASP:OD1	2.44	0.50
1:A:1477:PHE:O	1:A:1481:GLU:N	2.44	0.50
1:A:1498:ASP:OD1	1:A:1502:LEU:HD12	2.07	0.50
2:B:354:THR:HG21	2:B:399:VAL:H	1.75	0.50
3:I:210:LEU:O	3:I:214:ILE:HG13	2.12	0.50
3:I:447:GLU:HA	3:I:450:GLN:HG2	1.93	0.50
4:G:887:THR:N	4:G:888:PRO:CD	2.74	0.50
8:H:135:ASN:ND2	8:H:487:ARG:NH2	2.60	0.50
15:Z:48:TYR:O	15:Z:50:ASN:N	2.45	0.50
27:F:63:C:C2	27:F:64:C:C5	3.00	0.50
27:F:117:G:H2'	27:F:118:U:O4'	2.12	0.50
1:A:149:MET:CG	1:A:154:TYR:CE2	2.89	0.50
1:A:251:TYR:CA	1:A:255:ILE:HD12	2.34	0.50
1:A:774:ILE:O	1:A:774:ILE:HG22	2.11	0.50
1:A:1627:LEU:HD22	1:A:1632:ILE:HB	1.94	0.50
2:B:360:ASN:ND2	2:B:406:GLY:O	2.43	0.50
2:B:419:ILE:HD11	2:B:443:LEU:HD13	1.91	0.50
3:I:184:LYS:HZ3	3:I:186:LYS:CB	2.25	0.50
4:G:215:LEU:HD12	4:G:216:SER:O	2.11	0.50
5:K:453:ARG:O	5:K:457:GLN:CD	2.54	0.50
6:L:78:ASP:CG	6:L:79:PRO:CD	2.85	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:62:A:H2'	25:D:63:G:C5'	2.38	0.50
1:A:299:LYS:O	1:A:300:LYS:HB2	2.12	0.50
1:A:505:TRP:O	1:A:522:TYR:HE1	1.93	0.50
1:A:754:TYR:CE2	1:A:758:LEU:CD2	2.94	0.50
1:A:764:ASP:O	1:A:768:GLU:N	2.44	0.50
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.46	0.50
1:A:1336:ASN:O	1:A:1340:ILE:HG13	2.10	0.50
1:A:1373:LEU:HD21	1:A:1379:MET:SD	2.51	0.50
1:A:1461:TYR:CE2	1:A:1494:LEU:CD1	2.95	0.50
1:A:1709:TRP:HD1	1:A:1730:ASN:O	1.94	0.50
1:A:1735:ASP:O	1:A:1775:ILE:N	2.37	0.50
1:A:1880:PHE:CE2	1:A:1889:LEU:CD2	2.74	0.50
1:A:1882:LEU:HD22	1:A:1883:ASN:N	2.27	0.50
1:A:1892:LYS:HG3	1:A:1916:GLU:HG3	1.93	0.50
2:B:127:TYR:CZ	2:B:276:SER:HA	2.47	0.50
2:B:171:GLN:O	2:B:172:LEU:HD13	2.12	0.50
2:B:376:TRP:N	2:B:376:TRP:CD1	2.78	0.50
3:I:410:LEU:O	3:I:410:LEU:HD12	2.12	0.50
4:G:6:PHE:HE1	4:G:7:LEU:HD12	1.75	0.50
4:G:223:LEU:HD23	4:G:223:LEU:C	2.36	0.50
8:H:302:ASN:OD1	8:H:303:VAL:N	2.44	0.50
8:H:580:VAL:O	8:H:580:VAL:HG13	2.11	0.50
8:H:794:GLN:OE1	8:H:835:LYS:CG	2.57	0.50
1:A:1650:ARG:O	1:A:1651:ALA:HB3	2.12	0.50
6:L:32:GLY:O	6:L:63:ASP:HA	2.10	0.50
8:H:354:TYR:CA	8:H:359:PHE:CB	2.86	0.50
8:H:769:TYR:CD1	8:H:799:PHE:HD2	2.29	0.50
1:A:165:LEU:HD21	1:A:726:ILE:HG21	1.93	0.50
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.11	0.50
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.46	0.50
1:A:1778:ASP:HB2	1:A:1783:MET:HB2	1.94	0.50
4:G:252:GLU:O	4:G:256:LYS:HB2	2.11	0.50
4:G:274:SER:HB2	4:G:277:ILE:CD1	2.15	0.50
4:G:702:PRO:CB	4:G:739:PHE:CE2	2.95	0.50
5:K:144:LEU:HD22	5:K:144:LEU:N	2.27	0.50
6:L:140:LYS:HG2	6:L:141:ARG:HH12	1.69	0.50
8:H:126:MET:CE	8:H:132:ARG:NH1	2.73	0.50
8:H:160:ARG:NH1	8:H:160:ARG:HG3	2.26	0.50
8:H:349:TRP:CZ3	8:H:373:PHE:CD2	2.99	0.50
15:W:48:TYR:O	15:W:50:ASN:N	2.45	0.50
25:D:81:G:C6	25:D:82:A:N7	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:39:U:O2'	27:F:40:C:H5'	2.11	0.50
1:A:286:LEU:HD21	1:A:289:ASP:HB3	1.92	0.50
1:A:367:PHE:O	1:A:367:PHE:HD1	1.95	0.50
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.44	0.50
2:B:390:LEU:HD12	5:K:428:TRP:CD1	2.46	0.50
4:G:143:ARG:CZ	4:G:143:ARG:CB	2.86	0.50
4:G:241:PRO:HG3	4:G:274:SER:OG	2.12	0.50
8:H:133:ILE:HA	8:H:209:MET:O	2.11	0.50
8:H:379:ILE:HG22	8:H:383:LYS:CE	2.42	0.50
8:H:862:TYR:OH	8:H:908:VAL:CG2	2.59	0.50
1:A:547:LEU:O	1:A:551:LEU:HB2	2.12	0.50
2:B:290:ARG:NE	2:B:299:GLU:OE2	2.42	0.50
2:B:446:SER:OG	2:B:451:PHE:CB	2.54	0.50
2:B:462:LYS:HE2	4:G:727:ASP:OD2	2.12	0.50
4:G:161:LYS:O	4:G:165:GLU:HB2	2.12	0.50
26:E:139:A:O2'	26:E:140:G:P	2.69	0.50
27:F:97:U:O2	27:F:97:U:H2'	2.11	0.50
1:A:221:TRP:CH2	1:A:691:PHE:HB3	2.47	0.50
1:A:395:PRO:O	1:A:396:ARG:HG3	2.11	0.50
1:A:1008:LEU:HD21	1:A:1073:ILE:CD1	2.40	0.50
2:B:308:LYS:HB3	2:B:327:MET:HE2	1.94	0.50
4:G:141:LEU:O	4:G:141:LEU:HD13	2.11	0.50
4:G:299:ALA:O	4:G:303:ASN:N	2.43	0.50
5:K:363:LEU:HD11	5:K:391:PHE:CD2	2.47	0.50
6:L:140:LYS:CG	6:L:141:ARG:CZ	2.90	0.50
8:H:132:ARG:HH21	8:H:206:LYS:CG	2.25	0.50
8:H:347:ARG:HG3	8:H:359:PHE:CZ	2.47	0.50
8:H:501:ILE:HG21	8:H:570:ALA:CB	2.41	0.50
27:F:32:G:O3'	27:F:33:U:H4'	2.11	0.50
27:F:73:U:C2'	27:F:74:U:H5''	2.38	0.50
27:F:75:A:O2'	27:F:76:U:C3'	2.59	0.50
1:A:291:LYS:NZ	1:A:291:LYS:N	2.60	0.49
1:A:452:PHE:CZ	8:H:343:ASP:HB3	2.46	0.49
1:A:909:THR:HG22	1:A:910:LYS:H	1.77	0.49
1:A:1275:MET:CE	1:A:1299:LYS:NZ	2.75	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.27	0.49
3:I:275:LEU:N	3:I:275:LEU:HD23	2.27	0.49
4:G:798:LEU:O	4:G:802:GLN:HA	2.12	0.49
5:K:319:ALA:O	5:K:323:ARG:N	2.44	0.49
8:H:250:GLU:HB3	8:H:298:PHE:CD2	2.47	0.49
8:H:274:ILE:HD13	8:H:274:ILE:C	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:PHE:CE2	1:A:551:LEU:HD21	2.47	0.49
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.47	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
1:A:1759:TYR:HB3	1:A:1767:TYR:OH	2.12	0.49
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.48	0.49
1:A:2065:ARG:NE	1:A:2066:LYS:HE2	2.26	0.49
2:B:143:HIS:CE1	5:K:151:LEU:HD22	2.47	0.49
2:B:447:ASN:ND2	2:B:447:ASN:C	2.70	0.49
3:I:401:LEU:HD12	4:G:214:SER:CA	2.42	0.49
4:G:886:CYS:SG	4:G:888:PRO:CD	2.97	0.49
8:H:118:TYR:O	8:H:119:ASN:CB	2.60	0.49
8:H:503:ASP:OD1	8:H:571:TYR:CB	2.59	0.49
1:A:149:MET:O	1:A:153:MET:HG3	2.11	0.49
1:A:1490:ARG:HH11	1:A:1536:LEU:HD23	1.76	0.49
1:A:1591:THR:HG22	1:A:1592:HIS:H	1.76	0.49
2:B:448:ASN:O	2:B:449:SER:HB2	2.12	0.49
8:H:379:ILE:CG2	8:H:383:LYS:HE3	2.42	0.49
25:D:50:G:HO2'	25:D:51:A:P	2.27	0.49
26:E:141:G:O2'	26:E:142:G:OP2	2.27	0.49
27:F:62:G:C4	27:F:63:C:C5	3.00	0.49
1:A:770:MET:HE1	1:A:779:ALA:N	2.27	0.49
1:A:1118:GLY:HA3	1:A:1163:ARG:CZ	2.42	0.49
2:B:357:TRP:CD1	2:B:358:SER:H	2.29	0.49
4:G:671:PHE:CZ	4:G:693:SER:OG	2.64	0.49
5:K:141:ASN:CG	5:K:144:LEU:HD23	2.37	0.49
8:H:336:ILE:HG13	8:H:341:ILE:CG2	2.43	0.49
1:A:356:TYR:HE2	1:A:396:ARG:HB2	1.76	0.49
1:A:470:LEU:HB2	1:A:473:THR:HB	1.95	0.49
1:A:908:ASP:HB3	1:A:951:LEU:HD11	1.94	0.49
1:A:912:LEU:CG	1:A:951:LEU:HD21	2.43	0.49
1:A:956:LYS:C	1:A:956:LYS:CD	2.83	0.49
1:A:1014:LYS:HD3	1:A:1024:LEU:HD13	1.95	0.49
1:A:1074:VAL:HG12	1:A:1075:ASP:H	1.77	0.49
1:A:1385:PRO:HG3	1:A:1407:ILE:HA	1.95	0.49
1:A:1590:LEU:HB2	1:A:1595:ARG:HH21	1.76	0.49
1:A:1922:ARG:NE	1:A:1951:PHE:HZ	2.06	0.49
2:B:276:SER:OG	2:B:277:GLY:N	2.46	0.49
3:I:98:PHE:O	3:I:102:ILE:HG12	2.12	0.49
5:K:331:VAL:O	5:K:332:GLU:HG2	2.13	0.49
8:H:160:ARG:HG3	8:H:160:ARG:HH11	1.77	0.49
8:H:191:ILE:HG23	8:H:221:PHE:CZ	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:539:VAL:HG13	8:H:564:ILE:HG23	1.93	0.49
27:F:31:G:N3	27:F:32:G:C1'	2.74	0.49
27:F:48:G:H2'	27:F:49:U:H6	1.77	0.49
27:F:73:U:H2'	27:F:74:U:H6	1.78	0.49
1:A:165:LEU:HD21	1:A:726:ILE:CG2	2.42	0.49
1:A:176:LEU:CD2	1:A:176:LEU:C	2.85	0.49
1:A:218:SER:HB2	1:A:317:PRO:HG2	1.95	0.49
1:A:272:ASP:CB	1:A:273:ASP:OD1	2.61	0.49
1:A:874:ILE:C	1:A:875:THR:OG1	2.55	0.49
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.12	0.49
1:A:1464:LYS:HZ3	1:A:1479:GLU:HB3	1.76	0.49
2:B:116:GLU:CD	2:B:117:LEU:N	2.70	0.49
2:B:264:HIS:CE1	2:B:290:ARG:HD2	2.47	0.49
4:G:688:ARG:HH11	4:G:712:ASP:CG	2.20	0.49
6:L:119:THR:HG22	6:L:131:VAL:HG11	1.94	0.49
8:H:470:ALA:HB3	8:H:577:LEU:CB	2.38	0.49
8:H:492:LEU:CD2	8:H:557:HIS:CE1	2.95	0.49
27:F:92:U:C4	27:F:93:G:N7	2.80	0.49
1:A:201:PHE:CE2	1:A:551:LEU:CD2	2.96	0.49
1:A:1204:ARG:HD2	1:A:1259:LEU:HB3	1.93	0.49
1:A:1373:LEU:CD1	6:L:139:HIS:CE1	2.80	0.49
4:G:672:LEU:HD22	4:G:703:LEU:HD12	1.93	0.49
4:G:712:ASP:OD2	4:G:721:ARG:HD2	2.13	0.49
4:G:843:VAL:CG2	4:G:895:LEU:CD1	2.88	0.49
8:H:571:TYR:HD2	8:H:573:LYS:O	1.96	0.49
8:H:864:VAL:HG12	8:H:866:ILE:HG13	1.94	0.49
24:C:11:A:N1	24:C:12:U:C4	2.81	0.49
25:D:83:A:HO2'	25:D:84:C:P	2.27	0.49
27:F:77:A:H1'	27:F:78:A:C5'	2.41	0.49
1:A:505:TRP:CD1	1:A:505:TRP:H	2.30	0.49
1:A:749:ARG:O	1:A:750:LEU:CB	2.61	0.49
3:I:93:LYS:HA	3:I:93:LYS:CE	2.43	0.49
8:H:268:ASN:ND2	8:H:316:THR:HG23	2.28	0.49
8:H:369:LYS:NZ	8:H:369:LYS:N	2.60	0.49
8:H:492:LEU:CD2	8:H:557:HIS:HA	2.39	0.49
1:A:165:LEU:CD2	1:A:726:ILE:CG2	2.90	0.49
1:A:277:LYS:HG3	1:A:278:ASP:N	2.28	0.49
1:A:543:ASN:HD22	1:A:543:ASN:C	2.21	0.49
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.34	0.49
2:B:117:LEU:HD22	2:B:117:LEU:O	2.13	0.49
3:I:217:TYR:CE1	3:I:221:LYS:HE2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:400:VAL:HB	4:G:214:SER:HB2	1.94	0.49
4:G:101:LYS:O	4:G:105:ALA:CB	2.61	0.49
4:G:276:ASP:OD1	4:G:276:ASP:N	2.38	0.49
6:L:105:PHE:CE1	6:L:137:TYR:HE2	2.01	0.49
8:H:589:LEU:HD11	8:H:591:PHE:HE1	1.78	0.49
27:F:63:C:H2'	27:F:64:C:H6	1.78	0.49
1:A:302:SER:HA	1:A:489:THR:O	2.13	0.49
1:A:1067:ASN:OD1	3:I:270:HIS:HB3	2.11	0.49
4:G:170:LEU:HD22	4:G:170:LEU:O	2.12	0.49
5:K:159:TYR:CG	5:K:163:ASN:ND2	2.77	0.49
8:H:383:LYS:O	8:H:387:TYR:CB	2.51	0.49
8:H:967:VAL:C	8:H:968:MET:HE2	2.38	0.49
1:A:175:LEU:CD1	1:A:564:TRP:CZ2	2.96	0.48
1:A:276:VAL:CG1	1:A:310:ASN:CB	2.89	0.48
1:A:1038:ILE:HG13	1:A:1039:TRP:N	2.28	0.48
1:A:1629:LEU:H	1:A:1629:LEU:CD2	2.26	0.48
2:B:197:GLY:CA	2:B:221:ILE:CD1	2.87	0.48
4:G:166:ARG:O	4:G:167:GLU:C	2.56	0.48
5:K:265:LEU:HD12	5:K:266:PRO:HD2	1.94	0.48
5:K:354:PHE:CE1	5:K:358:MET:CG	2.96	0.48
5:K:448:GLN:HE21	5:K:464:TYR:HE2	1.61	0.48
8:H:165:SER:H	8:H:168:VAL:CG2	2.26	0.48
24:C:-4:A:H1'	24:C:-3:A:P	2.52	0.48
1:A:140:ARG:NH2	1:A:252:GLU:HB3	2.28	0.48
1:A:613:SER:O	1:A:614:ARG:C	2.55	0.48
2:B:282:SER:O	2:B:290:ARG:N	2.40	0.48
3:I:263:GLY:C	3:I:283:GLY:HA2	2.38	0.48
4:G:136:ARG:NH1	26:E:51:U:OP2	2.46	0.48
8:H:306:PRO:O	8:H:324:ILE:CD1	2.60	0.48
8:H:677:PHE:CZ	8:H:966:PHE:CE2	3.00	0.48
8:H:791:TYR:O	8:H:795:ILE:HG13	2.13	0.48
1:A:192:LEU:HG	1:A:557:PHE:CD2	2.48	0.48
1:A:839:HIS:CE1	27:F:96:U:C5	3.02	0.48
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.48	0.48
1:A:1461:TYR:CZ	1:A:1494:LEU:HD13	2.48	0.48
1:A:1594:GLN:N	1:A:1594:GLN:HE21	2.11	0.48
4:G:99:ASN:H	4:G:99:ASN:HD22	1.61	0.48
4:G:780:LEU:O	4:G:784:GLY:N	2.45	0.48
8:H:177:TYR:O	8:H:178:LEU:HG	2.13	0.48
8:H:353:TYR:N	8:H:353:TYR:CD1	2.81	0.48
8:H:945:LEU:HD12	8:H:945:LEU:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:1198:ARG:CA	9:N:1227:ILE:N	2.71	0.48
27:F:45:A:H2'	27:F:45:A:N3	2.28	0.48
1:A:140:ARG:HH21	1:A:252:GLU:HB3	1.77	0.48
1:A:1336:ASN:OD1	1:A:1400:ILE:HG13	2.13	0.48
1:A:1557:LEU:O	1:A:1560:THR:OG1	2.27	0.48
2:B:447:ASN:C	2:B:447:ASN:HD22	2.22	0.48
8:H:161:ILE:HB	8:H:164:MET:SD	2.54	0.48
8:H:161:ILE:CG2	8:H:162:PRO:HD2	2.41	0.48
8:H:489:TYR:O	8:H:558:LYS:HG3	2.13	0.48
8:H:674:LEU:HD11	8:H:973:ARG:HH22	1.77	0.48
8:H:936:ILE:HD13	8:H:936:ILE:N	2.27	0.48
9:N:1105:ALA:O	9:N:1106:GLY:C	2.54	0.48
24:C:8:U:H2'	24:C:9:G:C5'	2.42	0.48
27:F:46:C:H2'	27:F:47:U:H6	1.79	0.48
27:F:74:U:C2'	27:F:75:A:H5'	2.44	0.48
1:A:1183:THR:HG22	1:A:1184:ASP:N	2.29	0.48
1:A:1353:THR:O	1:A:1357:LEU:CD1	2.56	0.48
2:B:60:LYS:HG3	2:B:79:ILE:HD13	1.96	0.48
3:I:462:ASN:OD1	4:G:830:ARG:NE	2.47	0.48
8:H:881:LYS:HA	8:H:886:SER:HB3	1.95	0.48
8:H:884:ARG:CB	8:H:910:GLU:HG3	2.44	0.48
8:H:947:LYS:CD	8:H:947:LYS:N	2.73	0.48
24:C:8:U:C5	25:D:51:A:N1	2.81	0.48
1:A:1335:TRP:CZ2	1:A:1339:LEU:CD1	2.97	0.48
1:A:1650:ARG:HD2	25:D:52:G:P	2.53	0.48
1:A:1705:SER:HB3	1:A:1709:TRP:CD1	2.49	0.48
2:B:177:PRO:HG2	2:B:195:TRP:HE1	1.79	0.48
6:L:76:LEU:N	6:L:76:LEU:CD1	2.77	0.48
8:H:490:SER:HA	8:H:558:LYS:HG3	1.96	0.48
27:F:48:G:C4	27:F:49:U:C5	3.02	0.48
1:A:228:LYS:HD2	1:A:691:PHE:HE1	1.78	0.48
1:A:290:SER:HG	1:A:291:LYS:NZ	2.05	0.48
1:A:774:ILE:HG23	1:A:777:LYS:NZ	2.28	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CE3	2.48	0.48
2:B:357:TRP:CD1	2:B:358:SER:N	2.82	0.48
2:B:359:PRO:CD	2:B:407:GLY:HA3	2.41	0.48
3:I:130:LEU:HD22	3:I:174:VAL:HG11	1.96	0.48
6:L:81:THR:CG2	6:L:102:LYS:NZ	2.66	0.48
8:H:566:GLY:C	8:H:567:ILE:HD13	2.39	0.48
8:H:858:LEU:HB3	8:H:937:TRP:HB2	1.96	0.48
8:H:950:PHE:CZ	8:H:952:PRO:O	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:64:U:H5''	25:D:64:U:C6	2.49	0.48
27:F:46:C:C2	27:F:47:U:C5	3.01	0.48
1:A:1657:ILE:O	1:A:1661:ILE:CD1	2.62	0.48
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.18	0.48
2:B:173:VAL:CG1	2:B:200:GLN:OE1	2.54	0.48
2:B:350:LYS:HE3	5:K:431:TYR:CG	2.49	0.48
5:K:159:TYR:CD2	5:K:163:ASN:ND2	2.82	0.48
7:M:42:LYS:NZ	26:E:44:G:O6	2.47	0.48
8:H:449:PHE:CD1	8:H:453:THR:HG21	2.45	0.48
8:H:491:GLY:O	8:H:492:LEU:HD23	2.14	0.48
27:F:52:G:C4	27:F:53:C:C5	3.01	0.48
27:F:71:A:H2'	27:F:72:C:H6	1.79	0.48
1:A:754:TYR:CE2	1:A:758:LEU:HD21	2.49	0.48
1:A:1061:ILE:HG12	1:A:1117:TYR:CE2	2.49	0.48
2:B:177:PRO:CB	2:B:195:TRP:HE1	2.27	0.48
2:B:293:ASP:OD1	2:B:294:ALA:N	2.46	0.48
2:B:320:SER:HB2	2:B:337:ARG:HH12	1.79	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CG	2.49	0.48
2:B:395:ILE:HG22	2:B:396:VAL:N	2.18	0.48
4:G:886:CYS:CB	4:G:888:PRO:HD2	2.44	0.48
5:K:146:GLU:C	5:K:148:LYS:H	2.21	0.48
8:H:538:GLU:H	8:H:538:GLU:HG2	1.47	0.48
1:A:292:LYS:NZ	1:A:307:GLU:OE2	2.35	0.48
1:A:755:ASP:CG	1:A:819:LYS:HE3	2.39	0.48
1:A:1276:GLU:H	1:A:1276:GLU:CD	2.21	0.48
2:B:312:SER:HB2	2:B:353:TYR:O	2.14	0.48
3:I:248:VAL:O	3:I:252:SER:OG	2.30	0.48
4:G:284:LEU:CD2	4:G:284:LEU:N	2.77	0.48
26:E:1:A:OP2	29:E:201:M7M:HBI	2.13	0.48
27:F:78:A:HO2'	27:F:79:C:C5'	2.15	0.48
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.49	0.47
2:B:60:LYS:HB3	2:B:61:PRO:HD2	1.95	0.47
2:B:404:GLU:O	2:B:405:ASP:HB3	2.13	0.47
3:I:79:ASP:O	3:I:83:ILE:N	2.31	0.47
4:G:721:ARG:O	4:G:725:ILE:HD12	2.14	0.47
8:H:355:HIS:C	8:H:356:LYS:CG	2.86	0.47
8:H:888:ILE:HA	8:H:904:GLY:HA2	1.96	0.47
26:E:24:A:O2'	26:E:25:U:OP1	2.28	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.96	0.47
1:A:874:ILE:O	1:A:874:ILE:HG22	2.15	0.47
1:A:1009:PHE:CE1	1:A:1115:GLN:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.39	0.47
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.30	0.47
1:A:1593:ALA:CB	6:L:118:GLU:OE1	2.63	0.47
3:I:95:LEU:HD23	3:I:98:PHE:CD2	2.49	0.47
3:I:184:LYS:HZ3	3:I:186:LYS:HB3	1.79	0.47
4:G:809:LEU:HD12	4:G:841:THR:HG22	1.96	0.47
6:L:118:GLU:OE2	6:L:122:ARG:NH2	2.26	0.47
8:H:132:ARG:HE	8:H:206:LYS:HD2	1.80	0.47
8:H:265:PHE:CE2	8:H:295:ILE:HB	2.49	0.47
8:H:577:LEU:HD23	8:H:577:LEU:O	2.13	0.47
9:N:1203:SER:N	9:N:1223:ILE:O	2.39	0.47
27:F:73:U:O2'	27:F:74:U:H5'	2.02	0.47
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.50	0.47
1:A:1731:LYS:O	1:A:1771:THR:OG1	2.32	0.47
1:A:1877:GLY:O	1:A:1894:ILE:CA	2.62	0.47
2:B:77:ALA:O	2:B:81:MET:HG2	2.14	0.47
4:G:702:PRO:CA	4:G:739:PHE:CE2	2.98	0.47
6:L:18:ALA:HB1	6:L:60:TYR:CE2	2.49	0.47
8:H:444:GLN:NE2	8:H:444:GLN:CA	2.73	0.47
9:N:990:ASP:O	9:N:994:ASP:N	2.45	0.47
27:F:36:A:H61	27:F:118:U:H3	1.61	0.47
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.80	0.47
1:A:1586:GLN:CG	1:A:1595:ARG:NH1	2.77	0.47
1:A:2046:GLU:HG2	1:A:2049:ILE:HD12	1.96	0.47
2:B:446:SER:CB	2:B:451:PHE:H	2.22	0.47
3:I:209:LYS:HG3	3:I:210:LEU:N	2.29	0.47
4:G:740:TYR:OH	4:G:766:LYS:NZ	2.42	0.47
4:G:852:LEU:CD1	4:G:852:LEU:N	2.76	0.47
8:H:233:ASP:HA	8:H:452:LYS:NZ	2.29	0.47
8:H:373:PHE:CE1	8:H:377:ILE:CD1	2.97	0.47
8:H:889:TYR:N	8:H:903:ARG:O	2.47	0.47
27:F:32:G:HO2'	27:F:33:U:P	2.37	0.47
1:A:689:TYR:C	1:A:689:TYR:CD1	2.93	0.47
1:A:719:ILE:N	1:A:720:PRO:HD2	2.28	0.47
1:A:1065:LEU:HG	3:I:177:MET:HE1	1.95	0.47
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.37	0.47
1:A:1468:ALA:C	1:A:1473:ARG:O	2.57	0.47
1:A:1607:THR:O	1:A:1611:SER:N	2.47	0.47
4:G:120:MET:O	4:G:122:ILE:N	2.44	0.47
4:G:291:TYR:O	4:G:291:TYR:HD1	1.97	0.47
4:G:697:LEU:C	4:G:699:PRO:HD3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:350:PRO:CA	5:K:353:ARG:CD	2.85	0.47
8:H:118:TYR:O	8:H:119:ASN:HB3	2.14	0.47
8:H:247:PHE:CD1	8:H:903:ARG:NH1	2.83	0.47
8:H:769:TYR:CD1	8:H:799:PHE:CD2	3.02	0.47
8:H:801:TRP:CD1	8:H:801:TRP:C	2.92	0.47
8:H:828:ASP:O	8:H:829:VAL:C	2.57	0.47
8:H:860:PRO:HB3	8:H:937:TRP:CE3	2.48	0.47
8:H:941:PRO:HG2	8:H:962:LEU:HD12	1.97	0.47
25:D:86:G:H8	25:D:86:G:C5'	2.19	0.47
1:A:454:LEU:HD22	8:H:336:ILE:HB	1.96	0.47
1:A:495:ARG:NH1	1:A:497:GLN:HE21	2.12	0.47
1:A:790:TRP:CD2	1:A:819:LYS:HD3	2.49	0.47
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.50	0.47
2:B:123:PHE:CD1	2:B:123:PHE:C	2.93	0.47
8:H:104:THR:O	8:H:108:GLN:HG3	2.14	0.47
8:H:305:SER:C	8:H:307:ILE:N	2.72	0.47
25:D:62:A:N3	26:E:58:G:N2	2.62	0.47
27:F:52:G:H2'	27:F:53:C:H6	1.79	0.47
27:F:71:A:C4	27:F:72:C:C5	3.02	0.47
1:A:301:TRP:CZ2	1:A:491:GLY:HA3	2.50	0.47
1:A:553:ASN:O	1:A:554:THR:HG23	2.15	0.47
1:A:703:PHE:CD1	1:A:703:PHE:C	2.93	0.47
1:A:1262:MET:O	1:A:1263:CYS:CB	2.61	0.47
1:A:1508:HIS:HA	1:A:1511:ARG:NH2	2.29	0.47
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.40	0.47
2:B:119:PHE:CD1	2:B:119:PHE:C	2.93	0.47
2:B:162:MET:HE2	2:B:162:MET:H	1.76	0.47
2:B:321:LEU:HD22	2:B:335:ASP:HA	1.97	0.47
2:B:362:TYR:CD2	2:B:379:ARG:HD2	2.49	0.47
2:B:413:CYS:SG	2:B:440:ILE:HG21	2.55	0.47
4:G:15:TYR:CE1	6:L:13:TRP:HD1	2.32	0.47
4:G:127:ASP:C	4:G:127:ASP:OD1	2.57	0.47
4:G:368:SER:O	4:G:372:LEU:N	2.47	0.47
4:G:672:LEU:HD13	4:G:703:LEU:HD12	1.97	0.47
4:G:853:GLY:O	4:G:854:LYS:HB2	2.14	0.47
5:K:348:GLN:OE1	5:K:417:MET:HE2	2.15	0.47
8:H:492:LEU:HD22	8:H:557:HIS:ND1	2.24	0.47
8:H:577:LEU:CD2	8:H:577:LEU:C	2.85	0.47
8:H:581:LYS:NZ	8:H:581:LYS:CB	2.73	0.47
8:H:964:ARG:O	8:H:968:MET:HG2	2.15	0.47
1:A:174:LYS:O	1:A:178:ASN:ND2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:PHE:CB	1:A:240:PRO:CD	2.92	0.47
1:A:767:LEU:HA	1:A:770:MET:HG3	1.96	0.47
1:A:1217:ARG:HD3	1:A:1217:ARG:HA	1.75	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.50	0.47
1:A:1591:THR:CG2	1:A:1592:HIS:N	2.78	0.47
2:B:120:ALA:HB1	2:B:279:PHE:CE2	2.50	0.47
2:B:187:ASP:OD2	2:B:447:ASN:CB	2.63	0.47
2:B:225:ASP:OD1	2:B:226:TRP:N	2.48	0.47
2:B:275:PRO:HG3	2:B:319:GLY:N	2.30	0.47
4:G:144:LYS:O	4:G:145:THR:OG1	2.18	0.47
6:L:105:PHE:CB	6:L:141:ARG:CD	2.92	0.47
8:H:307:ILE:HD13	8:H:345:THR:O	2.15	0.47
8:H:336:ILE:HD11	8:H:341:ILE:CG2	2.38	0.47
27:F:66:A:C4	27:F:67:U:C5	3.02	0.47
1:A:175:LEU:HD11	1:A:564:TRP:CE2	2.50	0.47
1:A:470:LEU:H	1:A:473:THR:CG2	2.27	0.47
1:A:470:LEU:H	1:A:473:THR:HG21	1.80	0.47
1:A:691:PHE:HZ	1:A:701:CYS:CA	2.26	0.47
1:A:760:ASN:ND2	6:L:40:MET:HE2	2.30	0.47
1:A:1115:GLN:NE2	1:A:1115:GLN:CA	2.78	0.47
1:A:1369:ASN:O	1:A:1373:LEU:HG	2.15	0.47
1:A:1623:PHE:CZ	24:C:5:G:C5	3.02	0.47
2:B:181:VAL:HA	2:B:191:ALA:O	2.15	0.47
2:B:243:ILE:HD12	2:B:292:TRP:HZ3	1.78	0.47
2:B:261:LEU:HD13	2:B:292:TRP:CE3	2.50	0.47
3:I:225:ILE:C	3:I:325:ARG:NH1	2.72	0.47
3:I:277:SER:HB3	3:I:279:VAL:HG23	1.97	0.47
4:G:251:GLU:CD	4:G:260:ALA:HB2	2.37	0.47
4:G:288:ASP:O	4:G:292:CYS:SG	2.72	0.47
4:G:490:GLU:O	4:G:494:HIS:N	2.48	0.47
4:G:672:LEU:HD22	4:G:703:LEU:CD1	2.45	0.47
5:K:340:LYS:HE2	5:K:389:CYS:HB3	1.97	0.47
5:K:370:LEU:HD21	5:K:454:THR:HG21	1.95	0.47
1:A:845:VAL:HG21	1:A:1321:MET:CE	2.44	0.47
1:A:853:THR:OG1	1:A:971:MET:HG2	2.14	0.47
1:A:1145:MET:CE	1:A:1160:LEU:HD13	2.44	0.47
1:A:2388:ARG:O	1:A:2389:PRO:C	2.57	0.47
2:B:161:ARG:O	2:B:165:LEU:CD2	2.62	0.47
2:B:275:PRO:O	2:B:276:SER:C	2.57	0.47
2:B:275:PRO:O	2:B:276:SER:O	2.33	0.47
4:G:698:VAL:N	4:G:699:PRO:CD	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:861:ASN:ND2	4:G:862:MET:SD	2.88	0.47
6:L:13:TRP:CH2	6:L:17:GLN:NE2	2.83	0.47
1:A:251:TYR:HA	1:A:255:ILE:CD1	2.37	0.46
1:A:289:ASP:HB3	1:A:292:LYS:HB2	1.97	0.46
1:A:2014:ALA:HB3	1:A:2055:MET:HE3	1.97	0.46
3:I:214:ILE:O	3:I:218:ILE:HG12	2.15	0.46
3:I:401:LEU:HD12	3:I:401:LEU:H	1.79	0.46
4:G:101:LYS:O	4:G:105:ALA:HB2	2.15	0.46
6:L:108:ASP:N	6:L:108:ASP:OD1	2.48	0.46
8:H:375:GLU:CG	8:H:376:PHE:CE1	2.99	0.46
8:H:500:ARG:CD	8:H:534:THR:HG23	2.10	0.46
8:H:564:ILE:HG22	8:H:567:ILE:HG12	1.95	0.46
8:H:572:ILE:HD12	8:H:572:ILE:C	2.40	0.46
8:H:855:PRO:CD	8:H:944:VAL:HG21	2.44	0.46
8:H:897:THR:HB	8:H:898:PRO:HD2	1.97	0.46
27:F:35:A:C4	27:F:120:G:N2	2.82	0.46
27:F:43:G:C2	27:F:44:A:C5	3.02	0.46
1:A:1115:GLN:N	1:A:1115:GLN:HE21	2.12	0.46
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.29	0.46
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.97	0.46
2:B:350:LYS:HB3	2:B:351:PRO:HD2	1.98	0.46
4:G:298:THR:O	4:G:302:PHE:CD2	2.67	0.46
5:K:395:LEU:HD13	5:K:399:ARG:CZ	2.45	0.46
8:H:941:PRO:HD2	8:H:962:LEU:HB2	1.98	0.46
25:D:48:C:H2'	25:D:49:A:C8	2.50	0.46
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.80	0.46
2:B:171:GLN:CD	2:B:172:LEU:H	2.23	0.46
2:B:218:VAL:HG23	2:B:240:ASP:CG	2.40	0.46
2:B:362:TYR:HD2	2:B:379:ARG:HD2	1.81	0.46
2:B:387:ASN:CA	2:B:388:GLN:OE1	2.64	0.46
4:G:83:LYS:C	4:G:85:ARG:N	2.73	0.46
4:G:325:ARG:O	4:G:329:LYS:N	2.37	0.46
5:K:334:PRO:HG2	5:K:337:TYR:HE1	1.79	0.46
8:H:488:ILE:HD11	8:H:556:ALA:HB1	1.97	0.46
8:H:500:ARG:HE	8:H:534:THR:HB	1.75	0.46
27:F:165:A:O2'	27:F:166:U:OP2	2.27	0.46
1:A:474:LYS:C	1:A:474:LYS:CD	2.89	0.46
1:A:505:TRP:HZ3	1:A:690:LYS:HG3	1.78	0.46
1:A:703:PHE:HD1	1:A:703:PHE:C	2.23	0.46
1:A:1284:GLY:HA2	1:A:1348:GLU:HB3	1.96	0.46
1:A:1875:ILE:HG21	1:A:1979:MET:HE1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1899:TRP:CH2	1:A:1909:ALA:CB	2.98	0.46
2:B:184:SER:OG	2:B:186:ASP:OD1	2.18	0.46
4:G:122:ILE:CG1	4:G:123:PRO:HD2	2.36	0.46
4:G:691:TYR:CE2	4:G:711:ILE:HD12	2.49	0.46
8:H:296:ASN:OD1	8:H:303:VAL:HA	2.15	0.46
8:H:387:TYR:O	8:H:391:MET:CB	2.50	0.46
1:A:594:ASP:C	1:A:594:ASP:OD1	2.59	0.46
1:A:1402:ALA:O	1:A:1403:SER:CB	2.63	0.46
1:A:2075:THR:HG22	1:A:2076:GLN:N	2.30	0.46
2:B:177:PRO:CG	2:B:195:TRP:HE1	2.27	0.46
2:B:279:PHE:HD1	2:B:279:PHE:N	2.12	0.46
2:B:307:ASP:OD1	5:K:225:ILE:HA	2.16	0.46
2:B:313:LEU:HD11	2:B:322:VAL:HG21	1.98	0.46
2:B:408:LYS:O	2:B:424:SER:HB3	2.15	0.46
3:I:281:GLN:NE2	26:E:37:U:O4	2.48	0.46
3:I:433:ASN:ND2	3:I:433:ASN:N	2.61	0.46
4:G:13:ALA:O	4:G:15:TYR:N	2.48	0.46
6:L:45:LEU:HD11	6:L:110:LYS:HA	1.97	0.46
8:H:507:SER:C	8:H:509:SER:N	2.71	0.46
1:A:166:LYS:C	1:A:169:PRO:HD2	2.39	0.46
1:A:286:LEU:HD22	1:A:292:LYS:HB3	1.96	0.46
1:A:514:TYR:N	1:A:514:TYR:CD1	2.84	0.46
1:A:1216:ILE:HD12	1:A:1254:ASN:CB	2.44	0.46
1:A:1593:ALA:HB3	6:L:118:GLU:OE1	2.16	0.46
1:A:1995:TRP:CE3	1:A:2007:ARG:HD2	2.50	0.46
8:H:544:LEU:HG	8:H:553:VAL:HG21	1.97	0.46
8:H:801:TRP:O	8:H:801:TRP:HD1	1.98	0.46
1:A:247:PRO:HB2	1:A:248:PRO:HD2	1.98	0.46
1:A:291:LYS:N	1:A:291:LYS:HZ1	2.14	0.46
1:A:294:ASN:C	1:A:294:ASN:ND2	2.73	0.46
1:A:674:MET:CE	1:A:678:ARG:HD3	2.38	0.46
1:A:810:LYS:HA	1:A:810:LYS:HE3	1.98	0.46
1:A:901:PRO:HD3	1:A:1078:ILE:HD11	1.98	0.46
1:A:1125:LEU:HD21	1:A:1234:VAL:CG2	2.46	0.46
1:A:1417:GLN:OE1	1:A:1422:ILE:CG1	2.64	0.46
2:B:290:ARG:CZ	2:B:302:LEU:HD13	2.45	0.46
8:H:247:PHE:HB3	8:H:931:TYR:OH	2.15	0.46
8:H:578:TYR:C	8:H:578:TYR:HD1	2.24	0.46
24:C:-4:A:Cl'	24:C:-3:A:P	3.04	0.46
1:A:318:LEU:HD12	1:A:318:LEU:N	2.31	0.46
1:A:656:ILE:O	1:A:660:ILE:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1038:ILE:HD12	1:A:1039:TRP:CE3	2.51	0.46
1:A:1204:ARG:CD	1:A:1259:LEU:HB3	2.46	0.46
1:A:1287:ASP:OD2	1:A:1296:ARG:NH1	2.49	0.46
2:B:321:LEU:HD13	2:B:333:LEU:HD23	1.98	0.46
2:B:422:TYR:HD1	2:B:429:LYS:HA	1.81	0.46
2:B:456:GLY:C	2:B:458:ASP:N	2.71	0.46
3:I:136:GLN:NE2	3:I:166:LYS:O	2.49	0.46
3:I:226:ALA:CB	3:I:317:ASP:OD2	2.62	0.46
4:G:144:LYS:HE3	26:E:19:U:OP1	2.16	0.46
7:M:51:PHE:CE2	7:M:53:ILE:HD11	2.50	0.46
8:H:571:TYR:CD2	8:H:573:LYS:O	2.69	0.46
8:H:967:VAL:HG12	8:H:971:ARG:HG3	1.97	0.46
1:A:665:GLY:O	1:A:668:ARG:HG2	2.15	0.46
2:B:171:GLN:OE1	2:B:172:LEU:O	2.34	0.46
2:B:196:ALA:C	2:B:219:GLY:O	2.58	0.46
3:I:143:ILE:HG23	3:I:149:TYR:HE2	1.81	0.46
4:G:16:VAL:HG13	4:G:17:PRO:HD2	1.98	0.46
4:G:103:GLN:O	4:G:106:ASP:OD1	2.34	0.46
8:H:362:LYS:HE2	8:H:365:GLU:CB	2.45	0.46
24:C:10:U:H2'	24:C:11:A:C8	2.50	0.46
26:E:2:U:C6	26:E:3:C:C5	3.03	0.46
27:F:89:U:C4	27:F:90:C:C5	3.04	0.46
1:A:175:LEU:HD12	1:A:564:TRP:NE1	2.31	0.46
1:A:275:TYR:O	1:A:279:TRP:CE2	2.69	0.46
1:A:532:ASN:ND2	27:F:83:C:O3'	2.49	0.46
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.79	0.46
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.97	0.46
1:A:1521:ARG:CZ	3:I:404:TYR:CD2	2.99	0.46
1:A:1625:VAL:O	1:A:1633:PHE:HA	2.15	0.46
1:A:1790:TRP:CE3	1:A:1795:LYS:HG3	2.51	0.46
3:I:268:LEU:CD1	3:I:271:GLU:CG	2.83	0.46
4:G:281:ASN:HD22	4:G:281:ASN:C	2.23	0.46
4:G:692:LEU:O	4:G:696:ARG:HG3	2.15	0.46
4:G:769:SER:O	4:G:801:THR:HG22	2.15	0.46
4:G:851:ARG:C	4:G:852:LEU:CD1	2.89	0.46
5:K:303:LEU:C	5:K:303:LEU:CD2	2.84	0.46
8:H:831:ILE:O	8:H:831:ILE:HG22	2.16	0.46
26:E:32:G:N2	26:E:44:G:N3	2.64	0.46
1:A:672:LYS:C	1:A:674:MET:N	2.72	0.45
1:A:853:THR:OG1	1:A:971:MET:CG	2.64	0.45
1:A:1461:TYR:CD1	1:A:1461:TYR:C	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.31	0.45
5:K:159:TYR:CE1	5:K:163:ASN:ND2	2.83	0.45
6:L:36:ASP:HB2	6:L:39:CYS:HB2	1.99	0.45
6:L:139:HIS:NE2	27:F:96:U:O5'	2.49	0.45
8:H:328:VAL:HG21	8:H:345:THR:CG2	2.45	0.45
8:H:933:TRP:C	8:H:934:HIS:CG	2.92	0.45
27:F:73:U:C2	27:F:74:U:C5	3.03	0.45
1:A:1878:CYS:O	1:A:1878:CYS:SG	2.73	0.45
2:B:244:LYS:HG2	2:B:257:LEU:HD23	1.97	0.45
2:B:261:LEU:HB3	2:B:292:TRP:CZ3	2.51	0.45
2:B:267:ARG:NH1	2:B:285:HIS:NE2	2.64	0.45
3:I:123:ARG:HB2	3:I:189:LEU:CD1	2.46	0.45
3:I:359:PRO:O	6:L:122:ARG:NH1	2.50	0.45
7:M:40:ALA:O	7:M:43:THR:OG1	2.34	0.45
8:H:204:GLU:OE1	8:H:204:GLU:HA	2.17	0.45
8:H:963:SER:O	8:H:967:VAL:HG23	2.17	0.45
26:E:21:C:H2'	26:E:22:G:O4'	2.15	0.45
27:F:75:A:C4	27:F:77:A:H5''	2.50	0.45
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.98	0.45
1:A:495:ARG:CZ	1:A:497:GLN:NE2	2.78	0.45
1:A:1839:ASN:ND2	1:A:1842:GLU:OE1	2.50	0.45
3:I:98:PHE:CZ	3:I:217:TYR:CD2	2.98	0.45
3:I:424:THR:HG22	3:I:425:SER:N	2.30	0.45
4:G:487:GLN:O	4:G:491:LYS:N	2.43	0.45
5:K:337:TYR:CE2	5:K:434:ASP:HA	2.51	0.45
1:A:362:GLU:CB	1:A:1209:LYS:HG2	2.45	0.45
1:A:770:MET:HE1	1:A:778:LYS:HB2	1.93	0.45
1:A:883:PHE:HB2	3:I:177:MET:SD	2.56	0.45
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.52	0.45
1:A:1589:LYS:O	1:A:1590:LEU:HD13	2.16	0.45
1:A:2066:LYS:HB2	1:A:2067:TYR:HD1	1.80	0.45
2:B:135:ARG:HD3	2:B:360:ASN:O	2.16	0.45
2:B:443:LEU:CD1	2:B:452:LEU:HD11	2.47	0.45
4:G:219:THR:HG22	4:G:221:GLU:H	1.81	0.45
4:G:255:ARG:HH11	4:G:255:ARG:HG3	1.80	0.45
4:G:285:HIS:HE1	4:G:291:TYR:HE2	1.56	0.45
4:G:668:HIS:HB2	4:G:698:VAL:HG11	1.95	0.45
4:G:691:TYR:HE2	4:G:711:ILE:CD1	2.14	0.45
5:K:144:LEU:CD2	5:K:144:LEU:H	2.29	0.45
5:K:273:LYS:O	5:K:277:MET:HB2	2.16	0.45
6:L:46:LEU:HD21	6:L:113:MET:HE3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:67:LEU:HB2	7:M:68:PRO:HD3	1.98	0.45
8:H:247:PHE:CD1	8:H:250:GLU:OE1	2.70	0.45
8:H:379:ILE:HG23	8:H:383:LYS:HE2	1.98	0.45
1:A:162:LEU:CD2	1:A:730:ILE:HD13	2.42	0.45
1:A:874:ILE:O	1:A:875:THR:O	2.34	0.45
1:A:974:ASN:C	1:A:976:GLN:H	2.23	0.45
1:A:1453:ASP:O	1:A:1457:VAL:HG23	2.16	0.45
2:B:155:ARG:CD	2:B:155:ARG:N	2.79	0.45
3:I:237:ILE:O	3:I:240:GLN:N	2.49	0.45
4:G:733:ASN:HB2	4:G:734:PRO:HA	1.99	0.45
6:L:102:LYS:CG	6:L:103:LEU:N	2.78	0.45
27:F:77:A:C1'	27:F:78:A:C5'	2.95	0.45
1:A:251:TYR:O	1:A:255:ILE:HB	2.16	0.45
1:A:366:GLU:O	1:A:372:ARG:HD2	2.16	0.45
1:A:795:ALA:O	1:A:796:ASN:HB2	2.17	0.45
1:A:820:ALA:O	1:A:824:VAL:HG23	2.16	0.45
2:B:428:LEU:HD11	5:K:466:PRO:HD2	1.97	0.45
3:I:245:ALA:CB	3:I:250:GLU:HB3	2.40	0.45
4:G:252:GLU:CG	4:G:256:LYS:HE3	2.47	0.45
8:H:113:ILE:CG2	8:H:549:TYR:CD1	2.99	0.45
8:H:121:ASP:O	8:H:125:SER:N	2.49	0.45
8:H:270:LEU:CD1	8:H:313:PHE:HB3	2.45	0.45
8:H:306:PRO:HD2	8:H:349:TRP:CE2	2.51	0.45
8:H:586:MET:C	8:H:586:MET:SD	3.00	0.45
1:A:373:VAL:CG1	1:A:374:ILE:N	2.80	0.45
1:A:1974:LEU:O	1:A:1978:VAL:HG23	2.17	0.45
2:B:88:GLU:HA	2:B:91:ASN:HB3	1.98	0.45
2:B:192:THR:CG2	2:B:200:GLN:HG3	2.47	0.45
2:B:202:LEU:N	2:B:202:LEU:CD1	2.80	0.45
3:I:92:ILE:O	3:I:96:PRO:HD3	2.16	0.45
8:H:272:ARG:O	8:H:276:ASP:HB2	2.16	0.45
8:H:675:THR:HG22	8:H:909:ILE:HD13	1.98	0.45
27:F:66:A:H2'	27:F:67:U:H6	1.81	0.45
27:F:102:C:H2'	27:F:103:A:H5'	1.99	0.45
1:A:776:GLN:HG2	1:A:777:LYS:N	2.32	0.45
1:A:1611:SER:N	1:A:1612:PRO:HD2	2.32	0.45
3:I:66:SER:O	3:I:70:THR:N	2.50	0.45
3:I:402:ASP:O	3:I:403:SER:C	2.60	0.45
4:G:703:LEU:HD13	4:G:703:LEU:O	2.16	0.45
5:K:409:HIS:ND1	5:K:414:ASP:OD1	2.44	0.45
8:H:500:ARG:HG2	8:H:534:THR:HG21	1.87	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:578:TYR:CD1	8:H:578:TYR:O	2.70	0.45
9:N:1343:PHE:O	9:N:1345:PHE:N	2.49	0.45
25:D:49:A:H2'	25:D:50:G:O5'	2.16	0.45
27:F:84:A:C2	27:F:111:C:C2	3.05	0.45
1:A:151:SER:H	1:A:577:ASN:ND2	2.14	0.45
1:A:505:TRP:H	1:A:505:TRP:HD1	1.64	0.45
1:A:505:TRP:CE3	1:A:690:LYS:HG3	2.50	0.45
2:B:419:ILE:CG2	2:B:433:LEU:HB2	2.47	0.45
3:I:46:ILE:O	3:I:97:PHE:CE1	2.69	0.45
3:I:358:ILE:CG2	3:I:359:PRO:CD	2.94	0.45
4:G:890:GLU:OE1	4:G:890:GLU:HA	2.17	0.45
8:H:167:ASN:ND2	8:H:173:LYS:CG	2.76	0.45
8:H:471:HIS:O	8:H:486:VAL:HA	2.17	0.45
8:H:950:PHE:CE1	8:H:951:ILE:O	2.70	0.45
8:H:968:MET:HE1	8:H:971:ARG:HG3	1.99	0.45
9:N:833:THR:O	9:N:834:LEU:C	2.58	0.45
9:N:1795:SER:O	9:N:1796:PRO:C	2.60	0.45
29:E:201:M7M:NBN	29:E:201:M7M:HBX	2.32	0.45
27:F:107:C:H2'	27:F:108:C:O4'	2.16	0.45
1:A:298:TYR:O	1:A:298:TYR:CD1	2.70	0.45
1:A:298:TYR:CE1	1:A:493:MET:CE	3.00	0.45
1:A:1748:ILE:C	1:A:1752:VAL:HG23	2.39	0.45
24:C:11:A:C2	25:D:47:A:C6	3.05	0.45
1:A:205:THR:O	1:A:205:THR:HG23	2.16	0.44
1:A:484:PHE:CD1	27:F:81:A:C6	3.05	0.44
1:A:860:GLU:OE2	1:A:863:ARG:NH1	2.51	0.44
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.44
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	1.98	0.44
2:B:357:TRP:HD1	2:B:358:SER:N	2.15	0.44
2:B:393:ARG:CG	2:B:393:ARG:NH2	2.74	0.44
8:H:133:ILE:HG13	8:H:134:ILE:N	2.32	0.44
8:H:234:LEU:HD23	8:H:234:LEU:H	1.82	0.44
8:H:470:ALA:HB3	8:H:577:LEU:CD2	2.46	0.44
8:H:481:ALA:HB2	8:H:565:LYS:HZ3	1.77	0.44
8:H:539:VAL:HG22	8:H:567:ILE:HD11	1.99	0.44
8:H:889:TYR:CD1	8:H:889:TYR:C	2.94	0.44
8:H:967:VAL:HB	8:H:968:MET:HE3	2.00	0.44
27:F:78:A:HO2'	27:F:79:C:P	2.30	0.44
27:F:79:C:O2	27:F:79:C:H3'	2.17	0.44
1:A:176:LEU:HD21	1:A:708:TRP:NE1	2.31	0.44
1:A:1620:TYR:O	1:A:1621:VAL:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1910:LYS:O	1:A:1913:THR:OG1	2.29	0.44
1:A:2006:SER:O	1:A:2009:THR:OG1	2.29	0.44
3:I:113:HIS:HD2	3:I:134:PRO:CA	2.30	0.44
3:I:400:VAL:CG2	4:G:154:PRO:HG2	2.47	0.44
3:I:401:LEU:HA	3:I:407:GLU:HA	1.97	0.44
5:K:341:VAL:HG21	5:K:428:TRP:CD1	2.51	0.44
8:H:110:LYS:HA	8:H:110:LYS:HD3	1.79	0.44
8:H:354:TYR:CD1	8:H:354:TYR:O	2.70	0.44
8:H:599:THR:HG23	8:H:933:TRP:HZ3	1.80	0.44
8:H:919:ARG:NH1	8:H:927:MET:HE1	2.32	0.44
8:H:942:GLY:HA2	8:H:960:ASN:O	2.17	0.44
24:C:-3:A:H1'	24:C:-2:A:C8	2.52	0.44
25:D:83:A:O2'	25:D:84:C:P	2.75	0.44
27:F:103:A:C4	27:F:104:G:N7	2.86	0.44
1:A:165:LEU:HD23	1:A:726:ILE:HG21	1.99	0.44
1:A:1020:ILE:HD12	1:A:1020:ILE:N	2.32	0.44
1:A:1364:GLU:OE1	1:A:1405:ILE:HD11	2.17	0.44
1:A:1378:LYS:O	1:A:1379:MET:HB2	2.16	0.44
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.17	0.44
1:A:2076:GLN:HA	1:A:2079:ILE:HD12	1.98	0.44
3:I:429:ARG:HH11	3:I:429:ARG:HA	1.82	0.44
4:G:286:GLU:OE2	4:G:292:CYS:SG	2.69	0.44
5:K:143:GLU:O	5:K:145:HIS:CE1	2.70	0.44
6:L:133:SER:HA	6:L:134:PRO:HD2	1.84	0.44
6:L:140:LYS:CB	6:L:141:ARG:HH11	2.30	0.44
8:H:145:GLY:O	8:H:146:LYS:C	2.59	0.44
8:H:449:PHE:O	8:H:449:PHE:CD1	2.70	0.44
27:F:50:G:H2'	27:F:51:G:H8	1.82	0.44
27:F:95:C:O3'	27:F:96:U:H4'	2.17	0.44
1:A:802:PRO:O	1:A:803:GLY:C	2.60	0.44
1:A:840:VAL:C	1:A:841:GLU:CG	2.90	0.44
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.53	0.44
1:A:1373:LEU:HD11	27:F:96:U:OP1	2.17	0.44
1:A:1417:GLN:HE22	1:A:1783:MET:HA	1.83	0.44
1:A:1851:PHE:O	1:A:1881:THR:HA	2.17	0.44
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.47	0.44
1:A:1880:PHE:CD2	1:A:1889:LEU:CD2	3.00	0.44
2:B:32:LEU:HD23	2:B:34:HIS:H	1.82	0.44
2:B:359:PRO:HG2	2:B:407:GLY:CA	2.47	0.44
2:B:390:LEU:CD1	5:K:428:TRP:CD1	3.01	0.44
2:B:393:ARG:HG2	2:B:393:ARG:NH2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:456:LEU:HD23	3:I:456:LEU:O	2.18	0.44
6:L:81:THR:HG21	6:L:102:LYS:HZ3	1.76	0.44
8:H:120:ARG:HA	8:H:120:ARG:HD3	1.67	0.44
8:H:354:TYR:HB2	8:H:359:PHE:CB	2.28	0.44
8:H:472:VAL:CG1	8:H:571:TYR:HE2	2.29	0.44
8:H:595:LEU:HD13	8:H:595:LEU:HA	1.83	0.44
24:C:7:A:N6	25:D:51:A:C8	2.85	0.44
1:A:162:LEU:CG	1:A:734:PHE:CE2	2.96	0.44
1:A:275:TYR:CD1	1:A:275:TYR:N	2.72	0.44
1:A:298:TYR:CE1	1:A:493:MET:HE2	2.53	0.44
1:A:325:LYS:CE	1:A:325:LYS:CA	2.96	0.44
1:A:807:PRO:O	1:A:811:ILE:HG13	2.18	0.44
1:A:1073:ILE:HD12	1:A:1116:TYR:HE1	1.77	0.44
8:H:375:GLU:HB3	8:H:376:PHE:CD1	2.52	0.44
8:H:950:PHE:CZ	8:H:951:ILE:O	2.70	0.44
27:F:102:C:C2'	27:F:103:A:H5'	2.47	0.44
1:A:170:HIS:CD2	1:A:170:HIS:O	2.70	0.44
1:A:358:ARG:CB	1:A:358:ARG:NH1	2.80	0.44
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.98	0.44
1:A:751:ASP:OD2	1:A:844:MET:HE3	2.17	0.44
1:A:1346:PHE:O	1:A:1347:ARG:C	2.61	0.44
2:B:293:ASP:HB2	2:B:300:LEU:HD11	1.99	0.44
3:I:137:TYR:O	3:I:141:ILE:HG13	2.17	0.44
3:I:398:GLN:OE1	3:I:414:ASN:ND2	2.49	0.44
4:G:19:ILE:HD12	4:G:19:ILE:C	2.41	0.44
4:G:111:LEU:O	4:G:113:ALA:N	2.51	0.44
6:L:25:ARG:CG	6:L:25:ARG:NH1	2.75	0.44
8:H:229:LEU:CD2	8:H:235:VAL:HG11	2.48	0.44
8:H:230:ALA:HB3	8:H:473:LEU:CD1	2.48	0.44
8:H:372:THR:O	8:H:373:PHE:C	2.58	0.44
8:H:769:TYR:CZ	8:H:799:PHE:CE2	2.92	0.44
8:H:964:ARG:NH1	8:H:968:MET:HE3	2.33	0.44
9:N:1382:LEU:O	9:N:1385:LEU:N	2.50	0.44
26:E:151:G:C2	26:E:152:A:N6	2.84	0.44
1:A:164:ALA:HB2	1:A:194:HIS:CD2	2.53	0.44
1:A:807:PRO:HB2	4:G:111:LEU:HD23	1.99	0.44
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.98	0.44
1:A:1661:ILE:HB	1:A:1736:VAL:HG11	2.00	0.44
2:B:154:SER:O	2:B:158:GLU:HG3	2.18	0.44
2:B:416:ASP:O	2:B:417:ASN:HB2	2.18	0.44
3:I:277:SER:CB	3:I:279:VAL:HG23	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:867:GLU:OE2	4:G:888:PRO:HG2	2.17	0.44
5:K:345:LYS:HB2	5:K:422:ASN:HA	2.00	0.44
8:H:132:ARG:O	8:H:133:ILE:HG23	2.17	0.44
8:H:304:PHE:N	8:H:304:PHE:CD1	2.86	0.44
8:H:460:GLY:HA3	8:H:461:LYS:HA	1.67	0.44
8:H:461:LYS:HZ2	8:H:464:PRO:CB	2.31	0.44
1:A:171:ALA:HB2	1:A:201:PHE:CE1	2.51	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.17	0.44
1:A:781:THR:C	1:A:784:GLN:OE1	2.52	0.44
2:B:171:GLN:NE2	2:B:172:LEU:H	2.15	0.44
2:B:448:ASN:O	2:B:449:SER:CB	2.65	0.44
4:G:6:PHE:CE1	4:G:7:LEU:CD1	2.99	0.44
8:H:222:MET:HE1	8:H:248:VAL:CG2	2.48	0.44
8:H:484:SER:O	8:H:564:ILE:HD12	2.17	0.44
26:E:6:U:H2'	26:E:7:A:H8	1.83	0.44
27:F:99:U:O2'	27:F:100:A:P	2.73	0.44
1:A:175:LEU:C	1:A:175:LEU:CD1	2.86	0.44
1:A:413:ASN:ND2	1:A:413:ASN:N	2.66	0.44
1:A:1276:GLU:N	1:A:1276:GLU:OE2	2.50	0.44
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.83	0.44
3:I:282:GLU:CG	3:I:286:PHE:CD2	3.00	0.44
3:I:400:VAL:HG21	4:G:154:PRO:CG	2.46	0.44
4:G:161:LYS:HA	4:G:161:LYS:CE	2.48	0.44
4:G:212:VAL:HG22	4:G:214:SER:H	1.83	0.44
4:G:272:PRO:CB	4:G:302:PHE:CD1	2.77	0.44
6:L:25:ARG:HH11	6:L:25:ARG:HG3	1.82	0.44
8:H:123:MET:SD	8:H:123:MET:C	3.01	0.44
8:H:185:ILE:CD1	27:F:75:A:OP2	2.55	0.44
8:H:306:PRO:HG2	8:H:349:TRP:CD2	2.52	0.44
8:H:354:TYR:CD1	8:H:376:PHE:HZ	2.36	0.44
8:H:368:GLU:C	8:H:368:GLU:CD	2.86	0.44
8:H:449:PHE:C	8:H:449:PHE:HD1	2.25	0.44
27:F:175:G:H4'	27:F:176:A:O4'	2.18	0.44
1:A:379:ILE:HG22	1:A:379:ILE:O	2.17	0.43
1:A:689:TYR:CD1	1:A:689:TYR:O	2.71	0.43
1:A:900:PHE:CZ	1:A:959:LEU:HD12	2.52	0.43
1:A:939:LEU:CD1	3:I:441:MET:HE2	2.43	0.43
1:A:1285:VAL:HA	1:A:1300:ALA:O	2.18	0.43
1:A:1393:GLU:HG2	3:I:395:LYS:O	2.18	0.43
2:B:316:GLN:O	2:B:319:GLY:N	2.45	0.43
3:I:267:HIS:CE1	3:I:273:HIS:CE1	3.05	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:702:PRO:HB3	4:G:739:PHE:CD1	2.52	0.43
6:L:95:PHE:CE2	6:L:103:LEU:HD13	2.53	0.43
8:H:347:ARG:C	8:H:352:VAL:HG11	2.42	0.43
25:D:84:C:O2	25:D:84:C:C2'	2.66	0.43
27:F:175:G:C2	27:F:176:A:N6	2.84	0.43
1:A:1065:LEU:HA	3:I:177:MET:HE1	2.00	0.43
1:A:1501:THR:HG21	4:G:163:THR:HG21	1.99	0.43
1:A:1894:ILE:HG21	1:A:1899:TRP:CZ2	2.52	0.43
1:A:2067:TYR:N	1:A:2067:TYR:HD1	2.15	0.43
2:B:316:GLN:CG	2:B:357:TRP:CZ2	2.97	0.43
5:K:144:LEU:HB3	5:K:146:GLU:OE2	2.18	0.43
5:K:341:VAL:CG2	5:K:428:TRP:CD1	3.01	0.43
8:H:347:ARG:HG3	8:H:359:PHE:HZ	1.81	0.43
8:H:488:ILE:HD11	8:H:560:GLN:CG	2.42	0.43
1:A:505:TRP:CD1	1:A:505:TRP:N	2.86	0.43
1:A:513:GLU:CD	1:A:513:GLU:N	2.77	0.43
1:A:750:LEU:HG	1:A:751:ASP:N	2.34	0.43
2:B:357:TRP:O	2:B:401:PHE:CD2	2.72	0.43
2:B:395:ILE:CG2	2:B:396:VAL:H	2.16	0.43
2:B:409:LYS:HA	2:B:422:TYR:O	2.18	0.43
3:I:298:VAL:O	3:I:298:VAL:HG12	2.18	0.43
3:I:327:THR:O	3:I:328:VAL:CB	2.67	0.43
3:I:391:MET:SD	3:I:397:GLU:HG3	2.58	0.43
5:K:333:LYS:HD2	5:K:333:LYS:O	2.17	0.43
8:H:120:ARG:HD3	8:H:123:MET:HE3	2.00	0.43
8:H:160:ARG:HH11	8:H:160:ARG:C	2.26	0.43
27:F:44:A:H61	27:F:71:A:H61	1.66	0.43
1:A:395:PRO:C	1:A:396:ARG:HG3	2.43	0.43
1:A:415:GLU:OE1	1:A:416:GLU:HB2	2.18	0.43
1:A:1019:GLU:HA	1:A:1023:LEU:HD23	2.00	0.43
1:A:1335:TRP:CD1	1:A:1367:ILE:CD1	3.01	0.43
1:A:1342:LEU:HD23	1:A:1350:ILE:CD1	2.49	0.43
1:A:1393:GLU:CD	1:A:1543:ARG:HH12	2.25	0.43
2:B:127:TYR:HE2	2:B:276:SER:CA	2.31	0.43
3:I:450:GLN:HG3	3:I:451:GLN:H	1.83	0.43
4:G:231:LYS:HA	4:G:234:ARG:HD3	2.00	0.43
4:G:886:CYS:C	4:G:888:PRO:CD	2.90	0.43
8:H:144:SER:HA	8:H:240:ASP:OD2	2.18	0.43
8:H:247:PHE:HA	8:H:250:GLU:CD	2.41	0.43
8:H:330:TYR:HE1	8:H:430:ARG:HH21	1.25	0.43
8:H:373:PHE:O	8:H:377:ILE:HB	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:C:-4:A:H4'	24:C:-3:A:OP2	2.18	0.43
27:F:47:U:H2'	27:F:48:G:H8	1.83	0.43
27:F:67:U:H2'	27:F:68:A:H8	1.82	0.43
1:A:162:LEU:HD11	1:A:730:ILE:HG22	2.01	0.43
1:A:1283:GLU:CD	1:A:1351:VAL:HG11	2.44	0.43
1:A:1381:THR:OG1	1:A:1382:ARG:HG3	2.19	0.43
1:A:1664:ASP:O	1:A:1668:ILE:CG1	2.66	0.43
1:A:1739:ARG:HD2	1:A:1751:TYR:CD2	2.53	0.43
1:A:1843:LEU:HA	1:A:1849:LYS:HZ3	1.84	0.43
2:B:192:THR:HG23	2:B:200:GLN:CG	2.48	0.43
2:B:337:ARG:HD3	5:K:173:TYR:OH	2.18	0.43
3:I:137:TYR:CE2	3:I:141:ILE:HD11	2.54	0.43
3:I:183:PHE:CD2	3:I:185:ASN:ND2	2.86	0.43
6:L:33:ARG:HD3	6:L:65:ASP:H	1.84	0.43
8:H:349:TRP:CZ3	8:H:373:PHE:HE2	2.31	0.43
8:H:360:ARG:HG2	8:H:362:LYS:H	1.82	0.43
1:A:1168:ILE:O	1:A:1169:TYR:CD1	2.72	0.43
1:A:1580:GLY:HA3	3:I:389:ASN:ND2	2.33	0.43
1:A:1697:SER:OG	1:A:1759:TYR:CE1	2.64	0.43
2:B:222:GLY:N	2:B:237:CYS:O	2.44	0.43
3:I:143:ILE:HG23	3:I:149:TYR:CE2	2.52	0.43
3:I:380:ARG:CZ	3:I:380:ARG:CB	2.96	0.43
3:I:447:GLU:OE2	3:I:447:GLU:C	2.62	0.43
8:H:769:TYR:HE1	8:H:774:LEU:HB2	1.84	0.43
9:N:1343:PHE:C	9:N:1345:PHE:H	2.26	0.43
25:D:109:U:H3'	25:D:110:U:C5'	2.47	0.43
26:E:151:G:H4'	26:E:152:A:O4'	2.18	0.43
27:F:31:G:C6	27:F:32:G:C5	3.06	0.43
27:F:83:C:H4'	27:F:84:A:OP1	2.18	0.43
27:F:102:C:N4	27:F:103:A:H62	2.16	0.43
1:A:367:PHE:C	1:A:367:PHE:HD1	2.22	0.43
1:A:479:LEU:O	1:A:480:TYR:C	2.62	0.43
1:A:484:PHE:HB3	1:A:485:PRO:HD3	2.00	0.43
1:A:839:HIS:CE1	27:F:96:U:C6	3.07	0.43
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.76	0.43
1:A:1732:MET:HE1	1:A:1789:ASN:HB2	2.01	0.43
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.34	0.43
1:A:2076:GLN:OE1	5:K:283:ASN:O	2.37	0.43
2:B:382:ASP:OD1	2:B:382:ASP:N	2.50	0.43
3:I:93:LYS:CE	3:I:93:LYS:CA	2.95	0.43
3:I:416:SER:HA	3:I:419:GLN:OE1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:153:ILE:HG23	4:G:154:PRO:HD2	1.99	0.43
4:G:529:ILE:O	4:G:533:LEU:N	2.52	0.43
4:G:666:ILE:N	4:G:668:HIS:CD2	2.86	0.43
5:K:382:VAL:HG11	5:K:392:TYR:CE2	2.53	0.43
8:H:132:ARG:NH1	8:H:132:ARG:CG	2.73	0.43
8:H:364:PHE:CG	8:H:369:LYS:CD	2.94	0.43
8:H:571:TYR:CB	8:H:575:ALA:HB2	2.49	0.43
8:H:964:ARG:NH1	8:H:968:MET:CE	2.82	0.43
9:N:1082:SER:O	9:N:1083:TYR:C	2.60	0.43
26:E:150:G:C2	26:E:152:A:H4'	2.54	0.43
29:E:201:M7M:HBX	29:E:201:M7M:HNBN	1.82	0.43
1:A:222:ILE:HB	1:A:266:LEU:HD11	2.01	0.43
1:A:287:GLU:HB2	1:A:288:GLU:H	1.64	0.43
1:A:672:LYS:C	1:A:674:MET:H	2.27	0.43
1:A:960:THR:HG21	3:I:455:PHE:CZ	2.54	0.43
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	2.01	0.43
1:A:2002:TYR:HB3	5:K:277:MET:HE3	2.00	0.43
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	2.01	0.43
2:B:73:ARG:O	2:B:76:LEU:HB2	2.19	0.43
2:B:202:LEU:HD12	2:B:202:LEU:N	2.33	0.43
5:K:337:TYR:HE2	5:K:434:ASP:HA	1.82	0.43
6:L:25:ARG:NH1	6:L:25:ARG:HG3	2.34	0.43
8:H:379:ILE:O	8:H:383:LYS:CG	2.65	0.43
27:F:174:G:C2	27:F:176:A:H4'	2.54	0.43
1:A:207:ARG:NH1	1:A:299:LYS:HG3	2.34	0.43
1:A:883:PHE:O	1:A:887:VAL:HG23	2.19	0.43
1:A:1262:MET:C	1:A:1263:CYS:SG	3.01	0.43
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.19	0.43
1:A:1451:PHE:O	1:A:1455:GLN:OE1	2.35	0.43
1:A:1647:GLN:O	1:A:1650:ARG:HG3	2.17	0.43
1:A:1657:ILE:O	1:A:1661:ILE:CG1	2.64	0.43
1:A:1992:TYR:HD2	1:A:2004:ALA:HB1	1.83	0.43
2:B:208:GLN:HA	2:B:209:PRO:HA	1.66	0.43
5:K:142:LEU:HD13	5:K:142:LEU:HA	1.74	0.43
5:K:146:GLU:O	5:K:147:ASP:C	2.61	0.43
5:K:146:GLU:O	5:K:149:PHE:HD2	2.01	0.43
5:K:328:ASN:ND2	5:K:328:ASN:C	2.76	0.43
6:L:33:ARG:HD3	6:L:65:ASP:CB	2.49	0.43
8:H:488:ILE:HD11	8:H:560:GLN:HG3	1.99	0.43
8:H:858:LEU:HB3	8:H:937:TRP:CB	2.48	0.43
27:F:62:G:H2'	27:F:63:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:98:U:O2'	27:F:99:U:P	2.76	0.43
1:A:410:ILE:N	1:A:410:ILE:CD1	2.82	0.43
1:A:617:ASN:ND2	27:F:99:U:O2'	2.46	0.43
1:A:1087:ASN:ND2	3:I:274:THR:OG1	2.45	0.43
1:A:1474:ARG:HG2	1:A:1475:LEU:N	2.33	0.43
1:A:1511:ARG:HG3	1:A:1511:ARG:HH21	1.81	0.43
1:A:1882:LEU:HD13	1:A:1882:LEU:C	2.43	0.43
2:B:458:ASP:OD2	2:B:462:LYS:NZ	2.52	0.43
3:I:188:PRO:O	3:I:189:LEU:C	2.62	0.43
3:I:321:LYS:O	3:I:324:ASP:O	2.35	0.43
3:I:429:ARG:HH11	3:I:429:ARG:CG	2.32	0.43
4:G:127:ASP:OD1	4:G:128:PHE:N	2.52	0.43
8:H:373:PHE:HE1	8:H:377:ILE:HG21	1.84	0.43
8:H:598:ILE:CG2	8:H:933:TRP:CH2	3.01	0.43
9:N:1539:GLU:O	9:N:1540:ARG:C	2.62	0.43
24:C:6:U:O2	24:C:6:U:O2'	2.28	0.43
26:E:6:U:H2'	26:E:7:A:C8	2.53	0.43
1:A:294:ASN:HB2	1:A:300:LYS:HB2	2.01	0.42
1:A:547:LEU:C	1:A:547:LEU:CD1	2.90	0.42
1:A:815:TYR:O	1:A:818:SER:OG	2.34	0.42
1:A:1020:ILE:HD12	1:A:1020:ILE:H	1.84	0.42
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.19	0.42
2:B:446:SER:OG	2:B:451:PHE:CG	2.69	0.42
3:I:120:TYR:OH	3:I:141:ILE:HG23	2.19	0.42
4:G:702:PRO:HA	4:G:739:PHE:CZ	2.54	0.42
5:K:155:LYS:HA	5:K:158:ILE:HG12	1.99	0.42
6:L:8:GLN:HG2	6:L:61:LEU:HB2	2.01	0.42
8:H:114:PRO:O	8:H:115:LYS:HG3	2.18	0.42
8:H:862:TYR:N	8:H:862:TYR:CD1	2.87	0.42
8:H:884:ARG:HD3	8:H:884:ARG:O	2.19	0.42
8:H:940:VAL:HA	8:H:941:PRO:HD3	1.89	0.42
1:A:268:LEU:HD12	1:A:268:LEU:O	2.19	0.42
1:A:289:ASP:CG	1:A:292:LYS:HG2	2.44	0.42
1:A:770:MET:SD	4:G:119:TRP:HZ3	2.41	0.42
1:A:883:PHE:CD1	3:I:177:MET:SD	3.13	0.42
1:A:940:ILE:O	1:A:943:ALA:HB3	2.18	0.42
1:A:1615:ASN:ND2	1:A:1634:LEU:HD23	2.31	0.42
2:B:247:GLN:HB2	2:B:258:LEU:HD21	1.99	0.42
2:B:349:SER:O	2:B:350:LYS:HG3	2.19	0.42
2:B:353:TYR:HE2	2:B:395:ILE:HG21	1.84	0.42
2:B:422:TYR:CD1	2:B:429:LYS:HA	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:245:ILE:HG23	4:G:280:GLU:HG2	2.01	0.42
8:H:129:ILE:N	8:H:129:ILE:CD1	2.73	0.42
8:H:160:ARG:HA	8:H:160:ARG:HD2	1.70	0.42
8:H:189:LEU:CD1	8:H:190:SER:O	2.66	0.42
8:H:236:LEU:HD23	8:H:266:VAL:HG21	2.00	0.42
8:H:408:LEU:HD21	8:H:427:LEU:HD22	2.01	0.42
25:D:62:A:C2	26:E:58:G:N1	2.87	0.42
27:F:73:U:H2'	27:F:74:U:C6	2.54	0.42
1:A:396:ARG:O	1:A:398:VAL:HG23	2.19	0.42
1:A:674:MET:HE2	1:A:678:ARG:NE	2.34	0.42
1:A:901:PRO:HG3	1:A:998:TYR:CD2	2.54	0.42
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.18	0.42
2:B:321:LEU:CD2	2:B:335:ASP:HA	2.49	0.42
3:I:376:LYS:HE2	26:E:56:U:OP2	2.20	0.42
3:I:400:VAL:O	3:I:400:VAL:HG23	2.19	0.42
4:G:264:ILE:HG22	4:G:281:ASN:OD1	2.19	0.42
4:G:364:PHE:O	4:G:368:SER:N	2.38	0.42
5:K:323:ARG:O	5:K:326:ALA:HB3	2.19	0.42
5:K:333:LYS:O	5:K:333:LYS:CE	2.67	0.42
8:H:124:LEU:HD12	8:H:124:LEU:O	2.18	0.42
8:H:470:ALA:N	8:H:577:LEU:O	2.48	0.42
8:H:483:TRP:CH2	8:H:565:LYS:CG	3.01	0.42
8:H:933:TRP:HB2	8:H:934:HIS:CE1	2.55	0.42
1:A:224:MET:HE2	1:A:702:GLY:HA3	2.01	0.42
1:A:1206:CYS:HB2	1:A:1266:GLU:OE1	2.19	0.42
1:A:1213:MET:HE1	1:A:1250:VAL:HB	2.02	0.42
1:A:1275:MET:O	1:A:1276:GLU:C	2.62	0.42
1:A:1846:ASN:CA	1:A:1885:LYS:NZ	2.79	0.42
2:B:315:PHE:CE1	2:B:322:VAL:HB	2.54	0.42
3:I:135:LEU:HD21	3:I:136:GLN:HG3	2.01	0.42
3:I:168:THR:O	3:I:172:ILE:HD12	2.19	0.42
3:I:385:ARG:CZ	4:G:153:ILE:HD11	2.50	0.42
4:G:134:ARG:CZ	4:G:134:ARG:CB	2.96	0.42
4:G:275:SER:O	4:G:279:LEU:HG	2.19	0.42
5:K:141:ASN:CG	5:K:142:LEU:N	2.76	0.42
5:K:443:LYS:HG2	5:K:444:VAL:H	1.84	0.42
8:H:167:ASN:HD22	8:H:168:VAL:N	2.16	0.42
1:A:1559:HIS:ND1	1:A:1613:THR:HG21	2.34	0.42
1:A:1697:SER:CB	1:A:1759:TYR:CE1	3.02	0.42
1:A:2227:VAL:O	1:A:2228:PRO:C	2.62	0.42
2:B:112:PRO:O	2:B:113:ALA:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:125:ILE:HA	2:B:128:SER:OG	2.20	0.42
4:G:846:PHE:CD1	4:G:859:LEU:CD2	2.88	0.42
5:K:164:HIS:O	5:K:164:HIS:CG	2.71	0.42
5:K:309:LEU:HD23	5:K:309:LEU:HA	1.79	0.42
8:H:234:LEU:HD23	8:H:234:LEU:N	2.34	0.42
8:H:510:ARG:HD3	8:H:591:PHE:CZ	2.54	0.42
8:H:652:MET:HA	8:H:655:LEU:HD12	2.01	0.42
8:H:957:ALA:HB2	8:H:965:ASP:OD2	2.19	0.42
27:F:95:C:C1'	27:F:96:U:OP1	2.67	0.42
1:A:410:ILE:CG1	8:H:276:ASP:OD1	2.65	0.42
1:A:779:ALA:CA	1:A:782:ILE:HD12	2.23	0.42
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.53	0.42
2:B:124:LEU:HD22	2:B:274:HIS:HE1	1.84	0.42
2:B:313:LEU:CD1	2:B:313:LEU:C	2.92	0.42
2:B:320:SER:O	2:B:321:LEU:HD23	2.20	0.42
3:I:95:LEU:O	3:I:98:PHE:HB2	2.20	0.42
3:I:227:PRO:HG3	3:I:325:ARG:HG2	2.02	0.42
8:H:365:GLU:CD	8:H:366:ASN:N	2.73	0.42
8:H:968:MET:CE	8:H:971:ARG:HG3	2.49	0.42
1:A:173:LEU:CD1	1:A:712:LEU:HD12	2.50	0.42
1:A:298:TYR:CD1	1:A:493:MET:HE2	2.54	0.42
1:A:939:LEU:HA	1:A:939:LEU:HD23	1.85	0.42
1:A:1335:TRP:HZ3	1:A:1400:ILE:O	2.03	0.42
1:A:1344:THR:HG22	1:A:1347:ARG:HH21	1.83	0.42
1:A:1586:GLN:HB3	1:A:1595:ARG:HH12	1.84	0.42
5:K:143:GLU:HA	5:K:145:HIS:HE1	1.84	0.42
6:L:33:ARG:HD3	6:L:65:ASP:OD1	2.17	0.42
8:H:500:ARG:HD3	8:H:534:THR:OG1	2.19	0.42
8:H:964:ARG:HA	8:H:964:ARG:HD2	1.77	0.42
24:C:-1:A:O2'	24:C:0:U:C6	2.73	0.42
26:E:26:A:O2'	26:E:27:U:P	2.78	0.42
1:A:193:TYR:CZ	1:A:558:GLN:HB3	2.55	0.42
1:A:370:ILE:HD12	8:H:953:LYS:HD2	2.00	0.42
1:A:908:ASP:HB3	1:A:951:LEU:CD1	2.49	0.42
1:A:1274:ARG:O	1:A:1277:GLU:OE1	2.37	0.42
1:A:1629:LEU:CD2	1:A:1629:LEU:N	2.82	0.42
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	2.00	0.42
1:A:2066:LYS:HB2	1:A:2067:TYR:CD1	2.54	0.42
2:B:159:LEU:N	2:B:159:LEU:HD23	2.34	0.42
2:B:418:LEU:CD2	2:B:434:ALA:HB2	2.50	0.42
3:I:93:LYS:HD2	3:I:93:LYS:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:102:ILE:HB	3:I:103:PRO:CD	2.48	0.42
4:G:15:TYR:O	4:G:15:TYR:CD1	2.72	0.42
4:G:238:PRO:CD	4:G:239:THR:N	2.79	0.42
4:G:508:TRP:O	4:G:512:ASP:N	2.52	0.42
4:G:678:TYR:HD1	4:G:678:TYR:HA	1.74	0.42
8:H:271:ASP:OD2	8:H:318:LEU:HG	2.20	0.42
9:N:757:LEU:O	9:N:758:LYS:C	2.63	0.42
1:A:1629:LEU:HD23	1:A:1630:THR:HG22	1.98	0.42
1:A:1652:HIS:CD2	1:A:1652:HIS:N	2.87	0.42
1:A:1715:SER:HB2	1:A:1719:GLU:OE1	2.19	0.42
1:A:1755:LYS:C	1:A:1759:TYR:HD2	2.11	0.42
1:A:2075:THR:CG2	1:A:2076:GLN:N	2.82	0.42
1:A:2079:ILE:HG22	1:A:2083:ILE:CD1	2.44	0.42
2:B:345:LEU:HB3	2:B:376:TRP:CH2	2.54	0.42
3:I:123:ARG:HB2	3:I:189:LEU:HD11	2.02	0.42
3:I:424:THR:CG2	3:I:425:SER:N	2.83	0.42
4:G:282:ILE:HG12	4:G:295:LEU:HB3	2.01	0.42
4:G:349:ALA:O	4:G:353:GLN:N	2.48	0.42
5:K:280:VAL:HG12	5:K:282:GLU:H	1.85	0.42
5:K:350:PRO:CB	5:K:353:ARG:HD2	2.48	0.42
8:H:449:PHE:O	8:H:449:PHE:HD1	2.02	0.42
8:H:483:TRP:CZ3	8:H:565:LYS:HG3	2.54	0.42
8:H:722:ASP:OD2	8:H:755:TYR:OH	2.34	0.42
9:N:1482:GLY:O	9:N:1483:VAL:C	2.62	0.42
1:A:146:HIS:ND1	1:A:146:HIS:C	2.78	0.42
1:A:276:VAL:CG1	1:A:310:ASN:HB2	2.49	0.42
1:A:465:GLU:HG3	8:H:387:TYR:OH	2.20	0.42
1:A:655:TYR:CD1	1:A:655:TYR:C	2.98	0.42
1:A:843:THR:HG21	6:L:108:ASP:CB	2.49	0.42
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.78	0.42
1:A:1453:ASP:O	1:A:1456:ARG:CG	2.58	0.42
1:A:1851:PHE:HB2	1:A:1882:LEU:HD13	2.01	0.42
1:A:2026:LEU:HD11	1:A:2040:TRP:HZ3	1.85	0.42
2:B:151:GLU:O	2:B:154:SER:OG	2.37	0.42
2:B:316:GLN:NE2	2:B:316:GLN:C	2.77	0.42
4:G:19:ILE:HD12	4:G:20:GLY:HA2	2.02	0.42
4:G:252:GLU:HG3	4:G:284:LEU:CD1	2.50	0.42
6:L:78:ASP:OD2	6:L:79:PRO:HD2	2.20	0.42
8:H:475:THR:HG22	8:H:483:TRP:O	2.20	0.42
8:H:798:GLY:O	8:H:802:ALA:N	2.53	0.42
1:A:358:ARG:HD3	1:A:360:GLU:HB2	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1390:THR:HA	1:A:1391:PRO:HD3	1.75	0.41
2:B:280:ILE:N	2:B:292:TRP:O	2.45	0.41
2:B:445:ILE:HG12	2:B:446:SER:N	2.35	0.41
3:I:429:ARG:HH11	3:I:429:ARG:CA	2.33	0.41
4:G:726:LEU:HD11	4:G:746:MET:HE3	2.01	0.41
5:K:146:GLU:CA	5:K:149:PHE:CD2	2.91	0.41
6:L:53:VAL:O	6:L:54:ARG:C	2.62	0.41
7:M:95:ARG:NH1	7:M:95:ARG:CG	2.73	0.41
9:N:1610:LEU:O	9:N:1660:ALA:O	2.38	0.41
27:F:48:G:H2'	27:F:49:U:C6	2.55	0.41
1:A:774:ILE:CG2	1:A:777:LYS:NZ	2.83	0.41
1:A:958:LEU:HD22	1:A:1081:TYR:CD2	2.56	0.41
2:B:335:ASP:OD1	2:B:337:ARG:CD	2.58	0.41
3:I:390:ARG:O	3:I:412:MET:HG2	2.20	0.41
4:G:397:GLN:O	4:G:401:ILE:N	2.38	0.41
5:K:300:GLN:OE1	5:K:300:GLN:CA	2.68	0.41
6:L:39:CYS:SG	6:L:79:PRO:O	2.78	0.41
6:L:59:ILE:HG22	6:L:60:TYR:N	2.33	0.41
8:H:159:LYS:H	8:H:159:LYS:HG2	1.53	0.41
8:H:191:ILE:O	8:H:224:GLU:OE1	2.38	0.41
8:H:320:PHE:CD1	8:H:320:PHE:C	2.98	0.41
8:H:656:LEU:HD13	8:H:670:ILE:HD13	2.02	0.41
9:N:755:THR:O	9:N:756:TRP:C	2.62	0.41
27:F:77:A:C4'	27:F:78:A:C5'	2.93	0.41
1:A:217:TRP:NE1	1:A:703:PHE:CE1	2.89	0.41
1:A:276:VAL:HG11	1:A:310:ASN:HB2	2.01	0.41
1:A:286:LEU:HD22	1:A:292:LYS:CB	2.47	0.41
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.55	0.41
1:A:458:PHE:CD1	1:A:458:PHE:C	2.97	0.41
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.20	0.41
1:A:1626:GLN:HE22	1:A:1694:MET:HG2	1.84	0.41
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.41
2:B:289:TRP:HB2	2:B:313:LEU:HD23	2.01	0.41
2:B:316:GLN:OE1	2:B:321:LEU:HB2	2.20	0.41
3:I:92:ILE:HB	3:I:93:LYS:HD2	2.01	0.41
3:I:441:MET:SD	3:I:444:ARG:NH2	2.93	0.41
4:G:98:SER:HG	4:G:99:ASN:ND2	2.15	0.41
4:G:115:THR:O	4:G:119:TRP:HD1	2.03	0.41
8:H:108:GLN:OE1	8:H:109:LEU:HD23	2.19	0.41
8:H:571:TYR:H	8:H:571:TYR:HD1	1.69	0.41
8:H:879:LEU:O	8:H:883:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:32:G:O2'	27:F:33:U:P	2.79	0.41
27:F:45:A:N3	27:F:46:C:C5	2.87	0.41
1:A:1115:GLN:CA	1:A:1115:GLN:HE21	2.33	0.41
1:A:1216:ILE:HG21	1:A:1254:ASN:ND2	2.36	0.41
1:A:1738:LEU:HD23	1:A:1777:ILE:HB	2.01	0.41
1:A:2020:GLU:HA	1:A:2023:LYS:HB2	2.01	0.41
3:I:329:LEU:HD12	3:I:333:TRP:CH2	2.55	0.41
4:G:104:PHE:C	4:G:106:ASP:N	2.78	0.41
5:K:354:PHE:CZ	5:K:358:MET:SD	3.14	0.41
5:K:362:GLU:HG2	29:E:201:M7M:NBN	2.35	0.41
7:M:126:ILE:HG22	7:M:126:ILE:O	2.21	0.41
8:H:177:TYR:O	8:H:178:LEU:CB	2.69	0.41
8:H:343:ASP:O	8:H:344:PHE:C	2.62	0.41
8:H:474:LYS:HZ1	8:H:630:PRO:HD3	1.79	0.41
8:H:482:GLU:O	8:H:482:GLU:HG2	2.20	0.41
8:H:608:GLN:NE2	8:H:641:GLU:CG	2.61	0.41
1:A:458:PHE:CD1	1:A:458:PHE:O	2.74	0.41
1:A:484:PHE:N	1:A:485:PRO:CD	2.83	0.41
1:A:1204:ARG:HG3	1:A:1259:LEU:HD13	2.00	0.41
1:A:1383:PHE:O	1:A:1384:PRO:C	2.61	0.41
1:A:1417:GLN:OE1	1:A:1422:ILE:CD1	2.65	0.41
1:A:1678:ILE:HD13	1:A:1703:MET:CE	2.50	0.41
2:B:174:SER:OG	2:B:175:THR:N	2.54	0.41
2:B:316:GLN:HE21	2:B:318:ASP:H	1.67	0.41
2:B:362:TYR:CB	2:B:379:ARG:HD2	2.48	0.41
3:I:141:ILE:HG21	3:I:197:ILE:HG23	2.03	0.41
5:K:159:TYR:CE2	5:K:163:ASN:ND2	2.89	0.41
5:K:386:GLU:HG2	5:K:390:LYS:HE2	2.01	0.41
8:H:193:LEU:CB	8:H:214:ASP:O	2.67	0.41
8:H:325:LYS:HD2	8:H:325:LYS:HA	1.92	0.41
8:H:327:PHE:HE1	8:H:331:TYR:CD2	2.39	0.41
8:H:467:THR:HG23	8:H:579:SER:O	2.21	0.41
8:H:950:PHE:CD1	8:H:951:ILE:N	2.88	0.41
27:F:63:C:H2'	27:F:64:C:C6	2.55	0.41
1:A:294:ASN:ND2	27:F:32:G:OP1	2.53	0.41
1:A:1054:LEU:HD23	1:A:1054:LEU:HA	1.86	0.41
1:A:1175:GLU:O	1:A:1179:GLY:N	2.49	0.41
1:A:1312:PHE:CD1	1:A:1342:LEU:HD12	2.55	0.41
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.56	0.41
1:A:1405:ILE:HB	1:A:1437:ILE:HD12	2.03	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:O	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.48	0.41
1:A:1582:GLU:OE2	1:A:1586:GLN:NE2	2.53	0.41
1:A:1594:GLN:NE2	1:A:1594:GLN:CA	2.83	0.41
1:A:1607:THR:O	1:A:1608:LEU:C	2.60	0.41
2:B:405:ASP:OD2	2:B:408:LYS:HD2	2.21	0.41
4:G:255:ARG:O	4:G:256:LYS:CB	2.68	0.41
5:K:159:TYR:CZ	5:K:163:ASN:ND2	2.88	0.41
7:M:5:ASN:HD21	7:M:61:ILE:HG21	1.85	0.41
7:M:58:CYS:SG	7:M:98:ILE:HG21	2.60	0.41
8:H:362:LYS:CG	8:H:363:PRO:HD2	2.50	0.41
8:H:365:GLU:CD	8:H:366:ASN:H	2.14	0.41
8:H:475:THR:CG2	8:H:483:TRP:O	2.68	0.41
9:N:1913:PHE:O	9:N:1914:PRO:C	2.64	0.41
25:D:87:U:O5'	25:D:87:U:H6	2.04	0.41
27:F:49:U:H2'	27:F:50:G:H8	1.84	0.41
1:A:361:GLU:N	1:A:361:GLU:CD	2.78	0.41
1:A:454:LEU:O	1:A:455:PRO:C	2.62	0.41
1:A:473:THR:HG23	1:A:474:LYS:N	2.35	0.41
1:A:619:PHE:CD1	1:A:619:PHE:C	2.98	0.41
1:A:778:LYS:HE2	1:A:778:LYS:CA	2.50	0.41
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.21	0.41
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.36	0.41
1:A:1308:GLU:OE1	1:A:1346:PHE:CZ	2.70	0.41
2:B:177:PRO:N	2:B:195:TRP:HD1	2.18	0.41
2:B:408:LYS:O	2:B:424:SER:CB	2.68	0.41
4:G:677:ILE:O	4:G:681:MET:HG2	2.20	0.41
5:K:158:ILE:HG13	5:K:159:TYR:N	2.34	0.41
5:K:159:TYR:CD1	5:K:163:ASN:ND2	2.76	0.41
8:H:352:VAL:HG13	8:H:352:VAL:O	2.21	0.41
8:H:365:GLU:O	8:H:366:ASN:HB2	2.20	0.41
8:H:792:LYS:O	8:H:796:ILE:N	2.43	0.41
25:D:49:A:N6	25:D:50:G:C6	2.88	0.41
1:A:258:ILE:HG21	1:A:640:ARG:HG3	2.03	0.41
1:A:691:PHE:CD1	1:A:691:PHE:O	2.73	0.41
1:A:750:LEU:HD23	1:A:752:ALA:HB3	2.03	0.41
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.54	0.41
1:A:1144:PHE:HZ	1:A:1162:THR:HG21	1.85	0.41
1:A:1195:PHE:HB3	1:A:1217:ARG:HH11	1.82	0.41
1:A:1795:LYS:N	1:A:1796:PRO:HD2	2.36	0.41
3:I:259:ILE:HD13	3:I:259:ILE:HG21	1.76	0.41
3:I:321:LYS:HG3	3:I:324:ASP:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:358:ILE:CG2	3:I:359:PRO:N	2.84	0.41
4:G:19:ILE:CD1	4:G:20:GLY:N	2.81	0.41
4:G:669:LYS:O	4:G:673:GLN:HG3	2.21	0.41
4:G:804:ASP:OD1	4:G:805:HIS:N	2.53	0.41
5:K:330:ASN:HD22	5:K:331:VAL:HG23	1.85	0.41
6:L:95:PHE:HD1	6:L:133:SER:CB	2.33	0.41
8:H:132:ARG:O	8:H:133:ILE:CG1	2.66	0.41
8:H:178:LEU:N	8:H:178:LEU:CD2	2.83	0.41
8:H:386:SER:O	8:H:390:SER:CB	2.69	0.41
24:C:9:G:O5'	24:C:9:G:H8	2.04	0.41
25:D:48:C:H2'	25:D:48:C:O2	2.20	0.41
27:F:46:C:H2'	27:F:47:U:C6	2.55	0.41
1:A:331:PHE:CD2	1:A:509:HIS:CE1	3.09	0.41
1:A:767:LEU:HD21	1:A:779:ALA:HB1	2.00	0.41
1:A:882:ILE:HD13	1:A:1238:LEU:HD21	2.03	0.41
1:A:1067:ASN:HD22	1:A:1067:ASN:HA	1.62	0.41
1:A:1174:PHE:HD2	1:A:1222:LEU:HD11	1.85	0.41
1:A:1183:THR:CG2	1:A:1184:ASP:N	2.83	0.41
1:A:1460:GLU:O	1:A:1463:THR:OG1	2.35	0.41
1:A:1581:PHE:CZ	1:A:1585:MET:HE2	2.56	0.41
1:A:1594:GLN:HE21	1:A:1594:GLN:CA	2.33	0.41
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.56	0.41
2:B:68:ASP:OD1	2:B:69:VAL:N	2.53	0.41
2:B:267:ARG:HG3	2:B:285:HIS:HD2	1.82	0.41
2:B:275:PRO:HG3	2:B:319:GLY:HA2	2.02	0.41
2:B:383:GLU:OE1	2:B:383:GLU:HA	2.21	0.41
2:B:404:GLU:CD	2:B:404:GLU:C	2.88	0.41
2:B:419:ILE:HG21	2:B:419:ILE:HD13	1.89	0.41
3:I:40:LYS:O	3:I:44:PHE:N	2.44	0.41
3:I:271:GLU:O	3:I:272:LEU:HB3	2.19	0.41
4:G:111:LEU:O	4:G:112:ALA:C	2.64	0.41
4:G:284:LEU:HD22	4:G:284:LEU:N	2.36	0.41
6:L:33:ARG:CD	6:L:65:ASP:OD2	2.54	0.41
7:M:36:GLY:CA	26:E:30:G:O2'	2.69	0.41
8:H:449:PHE:CD1	8:H:453:THR:HG23	2.56	0.41
8:H:578:TYR:CE2	8:H:589:LEU:CD1	3.04	0.41
8:H:586:MET:O	8:H:586:MET:SD	2.79	0.41
8:H:615:LEU:HB3	8:H:616:PRO:HD3	2.02	0.41
8:H:808:LEU:HD11	8:H:855:PRO:HB2	2.01	0.41
8:H:906:VAL:HA	8:H:907:PRO:HD3	1.97	0.41
8:H:908:VAL:HG13	8:H:909:ILE:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:950:PHE:CG	8:H:951:ILE:N	2.89	0.41
8:H:968:MET:CE	8:H:968:MET:N	2.82	0.41
25:D:49:A:C2'	25:D:50:G:O5'	2.69	0.41
26:E:2:U:C5	26:E:3:C:H5	2.32	0.41
27:F:96:U:P	27:F:96:U:O4'	2.79	0.41
1:A:160:ALA:HB1	1:A:194:HIS:HE1	1.79	0.41
1:A:286:LEU:HD12	1:A:286:LEU:C	2.46	0.41
1:A:294:ASN:OD1	1:A:300:LYS:HE3	2.18	0.41
1:A:376:ARG:C	1:A:377:VAL:HG23	2.46	0.41
1:A:863:ARG:NH2	1:A:1059:GLU:HB3	2.36	0.41
2:B:185:THR:OG1	2:B:231:ASN:OD1	2.31	0.41
2:B:235:ILE:CD1	2:B:280:ILE:HG21	2.51	0.41
2:B:418:LEU:HD23	2:B:434:ALA:HB2	2.02	0.41
5:K:158:ILE:HG13	5:K:159:TYR:H	1.86	0.41
5:K:427:THR:OG1	5:K:428:TRP:N	2.54	0.41
8:H:116:THR:CG2	8:H:158:HIS:HD2	2.16	0.41
8:H:117:ARG:NE	8:H:156:ASP:O	2.54	0.41
8:H:486:VAL:HG22	8:H:487:ARG:N	2.36	0.41
8:H:576:THR:CG2	8:H:592:PHE:H	2.14	0.41
25:D:87:U:H3'	25:D:87:U:H6	1.86	0.41
1:A:543:ASN:ND2	1:A:544:LYS:HB2	2.36	0.40
1:A:867:ILE:O	1:A:867:ILE:HG22	2.21	0.40
1:A:1053:THR:C	1:A:1055:GLY:N	2.79	0.40
1:A:1481:GLU:OE2	4:G:256:LYS:HD3	2.20	0.40
1:A:1623:PHE:CZ	24:C:5:G:C4	3.09	0.40
3:I:272:LEU:HD22	3:I:272:LEU:C	2.45	0.40
6:L:9:LEU:HD11	6:L:60:TYR:CB	2.51	0.40
6:L:97:THR:HG23	6:L:99:ASN:H	1.86	0.40
8:H:122:TYR:HD1	8:H:122:TYR:O	2.05	0.40
8:H:123:MET:SD	8:H:209:MET:SD	3.19	0.40
8:H:164:MET:HG2	8:H:175:LEU:CD1	2.50	0.40
8:H:305:SER:O	8:H:307:ILE:N	2.55	0.40
1:A:175:LEU:HD12	1:A:564:TRP:HE1	1.86	0.40
1:A:574:GLN:HA	1:A:574:GLN:OE1	2.21	0.40
1:A:845:VAL:HG21	1:A:1321:MET:HE2	2.01	0.40
1:A:1029:THR:HG22	1:A:1260:PHE:HZ	1.85	0.40
1:A:1049:LEU:HD11	1:A:1258:LEU:HD21	2.04	0.40
2:B:162:MET:HG3	2:B:421:VAL:HG11	2.03	0.40
2:B:366:THR:O	2:B:373:ILE:HA	2.22	0.40
4:G:302:PHE:O	4:G:303:ASN:OD1	2.39	0.40
8:H:178:LEU:HD13	8:H:194:ASN:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:187:ARG:HD3	8:H:650:LEU:HD11	2.02	0.40
8:H:737:ILE:HG12	8:H:768:PHE:HB3	2.03	0.40
26:E:1:A:C6	29:E:201:M7M:HBZB	2.56	0.40
1:A:1182:LEU:HD23	1:A:1182:LEU:HA	1.91	0.40
1:A:1653:LEU:CD2	1:A:1815:LEU:HD23	2.48	0.40
3:I:161:LEU:HB3	3:I:167:LEU:HD12	2.03	0.40
3:I:222:ILE:HD13	3:I:222:ILE:HA	1.89	0.40
4:G:278:TRP:CE2	4:G:298:THR:HB	2.52	0.40
5:K:328:ASN:C	5:K:328:ASN:HD22	2.30	0.40
6:L:25:ARG:HB2	6:L:25:ARG:NH1	2.27	0.40
6:L:34:LYS:HD2	6:L:34:LYS:N	2.35	0.40
8:H:500:ARG:CD	8:H:534:THR:CB	2.88	0.40
8:H:796:ILE:HD12	8:H:796:ILE:HA	1.87	0.40
8:H:951:ILE:CB	8:H:952:PRO:HD2	2.30	0.40
25:D:62:A:C2'	25:D:63:G:C5'	2.98	0.40
27:F:103:A:C4	27:F:104:G:C8	3.10	0.40
1:A:287:GLU:H	1:A:287:GLU:HG3	1.47	0.40
1:A:297:SER:HB2	27:F:32:G:P	2.59	0.40
1:A:510:PRO:O	1:A:514:TYR:CE1	2.74	0.40
1:A:766:ILE:HG21	1:A:782:ILE:HG21	2.03	0.40
1:A:1790:TRP:CD1	1:A:1795:LYS:HE3	2.56	0.40
1:A:1887:GLY:O	1:A:1990:ASN:HA	2.21	0.40
2:B:173:VAL:HA	2:B:200:GLN:OE1	2.20	0.40
2:B:311:PHE:HE2	7:M:126:ILE:HD13	1.84	0.40
3:I:248:VAL:HG11	3:I:317:ASP:HB3	2.03	0.40
3:I:415:THR:O	3:I:418:GLN:N	2.52	0.40
5:K:159:TYR:C	5:K:163:ASN:ND2	2.77	0.40
5:K:339:CYS:SG	5:K:340:LYS:N	2.94	0.40
8:H:135:ASN:ND2	8:H:487:ARG:HH21	2.18	0.40
8:H:189:LEU:HD12	8:H:190:SER:O	2.22	0.40
8:H:247:PHE:HD1	8:H:903:ARG:NH1	2.18	0.40
8:H:589:LEU:O	8:H:589:LEU:HG	2.20	0.40
27:F:43:G:N3	27:F:44:A:N7	2.69	0.40
27:F:77:A:C1'	27:F:78:A:H5'	2.45	0.40
1:A:143:ILE:HA	1:A:146:HIS:HB3	2.03	0.40
1:A:153:MET:HE3	1:A:153:MET:HB3	1.96	0.40
1:A:168:LEU:N	1:A:169:PRO:HD2	2.36	0.40
1:A:305:LEU:N	1:A:306:PRO:HD2	2.36	0.40
1:A:1203:ASN:OD1	1:A:1203:ASN:N	2.54	0.40
1:A:1229:GLU:O	1:A:1232:SER:OG	2.31	0.40
4:G:256:LYS:O	4:G:257:PHE:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:244:LEU:HD23	5:K:244:LEU:HA	1.69	0.40
8:H:375:GLU:HG2	8:H:376:PHE:CE1	2.57	0.40
8:H:942:GLY:CA	8:H:960:ASN:O	2.70	0.40
25:D:49:A:C3'	25:D:50:G:C5'	2.99	0.40
27:F:94:C:H5''	27:F:94:C:C6	2.50	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	2166/2413 (90%)	2019 (93%)	110 (5%)	37 (2%)	7	34
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	5	31
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	8	36
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	5	30
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	6	33
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	8	36
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	7	35
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	4	29
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	21	54
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	4	27
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	4	27
11	O	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
11	S	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
12	P	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	9	37
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	9	37
13	Q	85/110 (77%)	82 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	U	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
14	V	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
14	Y	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
15	W	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	18
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	2	18
16	X	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
16	a	65/77 (84%)	59 (91%)	6 (9%)	0	100	100
17	b	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
18	c	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
19	d	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
20	e	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
21	f	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	9	37
22	g	62/115 (54%)	62 (100%)	0	0	100	100
23	h	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
All	All	8236/10574 (78%)	7611 (92%)	505 (6%)	120 (2%)	11	36

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
1	A	157	ASP
1	A	239	PHE
1	A	240	PRO
1	A	259	GLU
1	A	264	ILE
1	A	287	GLU
1	A	546	LYS
1	A	645	ASP
1	A	699	PRO
1	A	1044	GLY
1	A	1403	SER
2	B	113	ALA
2	B	171	GLN
2	B	276	SER
2	B	395	ILE
3	I	266	LYS
3	I	328	VAL

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Mol	Chain	Res	Type
3	I	434	GLN
4	G	10	GLU
4	G	287	SER
4	G	700	ASN
5	K	147	ASP
8	H	115	LYS
8	H	133	ILE
8	H	356	LYS
8	H	364	PHE
8	H	431	GLN
8	H	704	PRO
8	H	829	VAL
8	H	884	ARG
8	H	952	PRO
9	N	766	ILE
9	N	1200	PRO
1	A	156	THR
1	A	554	THR
1	A	803	GLY
1	A	1088	VAL
2	B	449	SER
3	I	152	ASN
4	G	112	ALA
5	K	220	PRO
5	K	332	GLU
8	H	146	LYS
8	H	350	GLY
8	H	366	ASN
8	H	367	VAL
8	H	508	GLU
9	N	1693	HIS
10	R	40	MET
12	T	12	ASN
15	W	24	ASN
15	W	49	PHE
10	J	40	MET
12	P	12	ASN
15	Z	24	ASN
15	Z	49	PHE
1	A	261	LEU
1	A	539	PRO
1	A	750	LEU

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Mol	Chain	Res	Type
1	A	875	THR
1	A	1015	PRO
2	B	384	GLY
4	G	11	PRO
4	G	105	ALA
4	G	734	PRO
6	L	75	GLU
8	H	488	ILE
9	N	492	PRO
9	N	1936	ARG
1	A	407	VAL
1	A	511	ASP
1	A	538	LEU
1	A	701	CYS
1	A	1087	ASN
1	A	1621	VAL
1	A	2019	GLU
2	B	204	SER
2	B	210	LEU
2	B	347	GLY
4	G	256	LYS
4	G	769	SER
4	G	819	ALA
5	K	283	ASN
8	H	119	ASN
9	N	1555	GLU
9	N	1968	ASN
1	A	300	LYS
1	A	377	VAL
1	A	841	GLU
1	A	1379	MET
1	A	1380	PRO
4	G	782	LYS
8	H	171	GLY
8	H	305	SER
15	W	50	ASN
15	Z	50	ASN
1	A	802	PRO
4	G	239	THR
4	G	257	PHE
4	G	887	THR
6	L	78	ASP

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Mol	Chain	Res	Type
7	M	60	PRO
8	H	134	ILE
9	N	622	LEU
9	N	1202	MET
10	R	51	GLU
10	J	51	GLU
1	A	406	PRO
4	G	698	VAL
7	M	10	PRO
9	N	791	PRO
4	G	414	PRO
1	A	644	VAL
5	K	222	PRO
21	f	41	VAL
1	A	181	HIS
3	I	132	PRO
3	I	347	ALA
8	H	319	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1749/2182 (80%)	1541 (88%)	208 (12%)	5	22
2	B	374/410 (91%)	317 (85%)	57 (15%)	3	16
3	I	327/445 (74%)	259 (79%)	68 (21%)	1	7
4	G	361/813 (44%)	292 (81%)	69 (19%)	1	9
5	K	253/436 (58%)	225 (89%)	28 (11%)	6	24
6	L	129/132 (98%)	112 (87%)	17 (13%)	4	19
7	M	104/104 (100%)	99 (95%)	5 (5%)	23	47
8	H	757/910 (83%)	632 (84%)	125 (16%)	2	14
All	All	4054/5432 (75%)	3477 (86%)	577 (14%)	5	17

All (577) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	147	SER
1	A	148	ASP
1	A	152	LYS
1	A	153	MET
1	A	154	TYR
1	A	156	THR
1	A	158	LYS
1	A	162	LEU
1	A	165	LEU
1	A	166	LYS
1	A	168	LEU
1	A	175	LEU
1	A	177	GLU
1	A	187	LYS
1	A	204	GLU
1	A	224	MET
1	A	229	ARG
1	A	249	LEU
1	A	252	GLU
1	A	256	GLU
1	A	261	LEU
1	A	266	LEU
1	A	268	LEU
1	A	273	ASP
1	A	275	TYR
1	A	283	SER
1	A	287	GLU
1	A	288	GLU
1	A	291	LYS
1	A	294	ASN
1	A	299	LYS
1	A	313	ARG
1	A	321	GLU
1	A	324	ASP
1	A	325	LYS
1	A	328	TYR
1	A	331	PHE
1	A	351	LYS
1	A	353	GLU
1	A	355	LEU
1	A	358	ARG
1	A	360	GLU

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Mol	Chain	Res	Type
1	A	361	GLU
1	A	362	GLU
1	A	363	ASP
1	A	364	TYR
1	A	367	PHE
1	A	371	ASP
1	A	372	ARG
1	A	376	ARG
1	A	408	SER
1	A	412	GLN
1	A	413	ASN
1	A	414	ASP
1	A	416	GLU
1	A	418	ASP
1	A	427	SER
1	A	454	LEU
1	A	456	GLU
1	A	457	ASP
1	A	458	PHE
1	A	462	LEU
1	A	468	LEU
1	A	469	ILE
1	A	472	ASN
1	A	474	LYS
1	A	501	LEU
1	A	503	LYS
1	A	504	LYS
1	A	505	TRP
1	A	507	LEU
1	A	511	ASP
1	A	514	TYR
1	A	543	ASN
1	A	544	LYS
1	A	545	THR
1	A	546	LYS
1	A	547	LEU
1	A	549	LYS
1	A	555	LYS
1	A	558	GLN
1	A	581	LEU
1	A	611	LYS
1	A	614	ARG

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Mol	Chain	Res	Type
1	A	678	ARG
1	A	691	PHE
1	A	749	ARG
1	A	758	LEU
1	A	768	GLU
1	A	774	ILE
1	A	777	LYS
1	A	778	LYS
1	A	783	LEU
1	A	786	LEU
1	A	813	GLU
1	A	815	TYR
1	A	817	LYS
1	A	835	LYS
1	A	841	GLU
1	A	842	LYS
1	A	844	MET
1	A	847	LYS
1	A	849	LEU
1	A	852	LEU
1	A	858	LYS
1	A	861	GLN
1	A	862	GLU
1	A	878	GLU
1	A	880	THR
1	A	909	THR
1	A	932	SER
1	A	933	GLU
1	A	937	LEU
1	A	955	LYS
1	A	956	LYS
1	A	959	LEU
1	A	960	THR
1	A	969	ILE
1	A	992	ASP
1	A	995	LEU
1	A	1002	GLU
1	A	1035	LEU
1	A	1066	LEU
1	A	1067	ASN
1	A	1072	LEU
1	A	1073	ILE

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Mol	Chain	Res	Type
1	A	1083	THR
1	A	1088	VAL
1	A	1095	MET
1	A	1105	ARG
1	A	1109	PHE
1	A	1115	GLN
1	A	1128	GLN
1	A	1170	MET
1	A	1183	THR
1	A	1202	ASN
1	A	1214	ARG
1	A	1217	ARG
1	A	1222	LEU
1	A	1231	GLN
1	A	1233	ARG
1	A	1262	MET
1	A	1275	MET
1	A	1276	GLU
1	A	1314	SER
1	A	1329	THR
1	A	1339	LEU
1	A	1344	THR
1	A	1354	GLU
1	A	1356	LEU
1	A	1358	ASP
1	A	1362	LYS
1	A	1365	THR
1	A	1366	ARG
1	A	1381	THR
1	A	1382	ARG
1	A	1383	PHE
1	A	1405	ILE
1	A	1415	SER
1	A	1416	LYS
1	A	1418	THR
1	A	1455	GLN
1	A	1460	GLU
1	A	1470	GLN
1	A	1473	ARG
1	A	1490	ARG
1	A	1499	ARG
1	A	1500	HIS

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Mol	Chain	Res	Type
1	A	1509	ARG
1	A	1511	ARG
1	A	1519	LEU
1	A	1521	ARG
1	A	1590	LEU
1	A	1594	GLN
1	A	1616	ARG
1	A	1618	ASN
1	A	1627	LEU
1	A	1629	LEU
1	A	1630	THR
1	A	1652	HIS
1	A	1657	ILE
1	A	1661	ILE
1	A	1663	PHE
1	A	1690	LYS
1	A	1752	VAL
1	A	1755	LYS
1	A	1757	LEU
1	A	1882	LEU
1	A	1885	LYS
1	A	1888	HIS
1	A	1892	LYS
1	A	1893	ILE
1	A	1908	LEU
1	A	1912	LYS
1	A	1915	GLU
1	A	1916	GLU
1	A	1920	LEU
1	A	1973	LYS
1	A	2007	ARG
1	A	2013	ARG
1	A	2062	GLU
1	A	2065	ARG
1	A	2067	TYR
1	A	2068	ASN
1	A	2071	ILE
1	A	2076	GLN
1	A	2078	GLU
2	B	23	GLU
2	B	47	GLU
2	B	48	ASP

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Mol	Chain	Res	Type
2	B	64	VAL
2	B	66	ASN
2	B	75	ARG
2	B	114	THR
2	B	117	LEU
2	B	122	ARG
2	B	128	SER
2	B	129	LEU
2	B	132	SER
2	B	133	ARG
2	B	136	LEU
2	B	137	GLN
2	B	140	MET
2	B	145	LYS
2	B	147	ASN
2	B	155	ARG
2	B	156	ARG
2	B	162	MET
2	B	165	LEU
2	B	171	GLN
2	B	172	LEU
2	B	190	VAL
2	B	192	THR
2	B	199	LEU
2	B	206	THR
2	B	207	LEU
2	B	208	GLN
2	B	244	LYS
2	B	257	LEU
2	B	264	HIS
2	B	267	ARG
2	B	276	SER
2	B	287	MET
2	B	313	LEU
2	B	316	GLN
2	B	323	CYS
2	B	333	LEU
2	B	337	ARG
2	B	358	SER
2	B	362	TYR
2	B	380	LYS
2	B	382	ASP

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Mol	Chain	Res	Type
2	B	388	GLN
2	B	393	ARG
2	B	400	ARG
2	B	408	LYS
2	B	409	LYS
2	B	443	LEU
2	B	444	ASP
2	B	445	ILE
2	B	446	SER
2	B	447	ASN
2	B	448	ASN
2	B	457	TRP
3	I	92	ILE
3	I	93	LYS
3	I	94	LEU
3	I	106	LYS
3	I	107	SER
3	I	117	ILE
3	I	118	SER
3	I	135	LEU
3	I	145	GLU
3	I	155	ASP
3	I	161	LEU
3	I	164	LYS
3	I	173	LEU
3	I	184	LYS
3	I	186	LYS
3	I	187	GLU
3	I	189	LEU
3	I	190	ASP
3	I	191	ILE
3	I	195	THR
3	I	198	LEU
3	I	204	LEU
3	I	205	GLU
3	I	208	TRP
3	I	210	LEU
3	I	236	GLU
3	I	249	LEU
3	I	250	GLU
3	I	252	SER
3	I	253	ARG

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Mol	Chain	Res	Type
3	I	257	CYS
3	I	264	LYS
3	I	268	LEU
3	I	271	GLU
3	I	272	LEU
3	I	273	HIS
3	I	275	LEU
3	I	280	ARG
3	I	281	GLN
3	I	312	LEU
3	I	320	GLN
3	I	321	LYS
3	I	327	THR
3	I	328	VAL
3	I	344	LEU
3	I	346	GLU
3	I	350	ILE
3	I	353	THR
3	I	354	LYS
3	I	358	ILE
3	I	362	GLN
3	I	364	LYS
3	I	370	ARG
3	I	373	ARG
3	I	374	LYS
3	I	376	LYS
3	I	380	ARG
3	I	393	PHE
3	I	401	LEU
3	I	427	SER
3	I	429	ARG
3	I	433	ASN
3	I	436	LYS
3	I	439	LYS
3	I	447	GLU
3	I	450	GLN
3	I	454	GLU
3	I	456	LEU
4	G	5	SER
4	G	7	LEU
4	G	9	GLN
4	G	15	TYR

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Mol	Chain	Res	Type
4	G	24	THR
4	G	99	ASN
4	G	100	VAL
4	G	101	LYS
4	G	102	ARG
4	G	107	LEU
4	G	108	LYS
4	G	124	ASP
4	G	126	THR
4	G	129	THR
4	G	130	ARG
4	G	134	ARG
4	G	138	GLN
4	G	140	GLN
4	G	141	LEU
4	G	143	ARG
4	G	159	LEU
4	G	160	ASN
4	G	161	LYS
4	G	162	LEU
4	G	164	GLU
4	G	165	GLU
4	G	167	GLU
4	G	168	LYS
4	G	170	LEU
4	G	176	GLU
4	G	214	SER
4	G	216	SER
4	G	221	GLU
4	G	222	ASP
4	G	226	MET
4	G	227	ARG
4	G	230	LEU
4	G	232	SER
4	G	249	ARG
4	G	251	GLU
4	G	252	GLU
4	G	268	CYS
4	G	274	SER
4	G	275	SER
4	G	276	ASP
4	G	277	ILE

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Mol	Chain	Res	Type
4	G	279	LEU
4	G	281	ASN
4	G	284	LEU
4	G	295	LEU
4	G	671	PHE
4	G	678	TYR
4	G	686	MET
4	G	687	SER
4	G	688	ARG
4	G	689	GLU
4	G	692	LEU
4	G	696	ARG
4	G	697	LEU
4	G	700	ASN
4	G	721	ARG
4	G	852	LEU
4	G	855	ASP
4	G	859	LEU
4	G	861	ASN
4	G	862	MET
4	G	886	CYS
4	G	887	THR
4	G	889	ARG
5	K	142	LEU
5	K	147	ASP
5	K	164	HIS
5	K	166	TYR
5	K	167	GLU
5	K	171	THR
5	K	174	LEU
5	K	233	LYS
5	K	243	ARG
5	K	245	ARG
5	K	248	ARG
5	K	249	ARG
5	K	250	LYS
5	K	258	ILE
5	K	304	ARG
5	K	305	LYS
5	K	310	GLU
5	K	317	GLU
5	K	323	ARG

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Mol	Chain	Res	Type
5	K	328	ASN
5	K	329	MET
5	K	332	GLU
5	K	333	LYS
5	K	357	LYS
5	K	362	GLU
5	K	399	ARG
5	K	457	GLN
5	K	459	ASP
6	L	25	ARG
6	L	34	LYS
6	L	59	ILE
6	L	63	ASP
6	L	73	MET
6	L	77	THR
6	L	78	ASP
6	L	102	LYS
6	L	108	ASP
6	L	113	MET
6	L	118	GLU
6	L	128	LYS
6	L	133	SER
6	L	135	TYR
6	L	137	TYR
6	L	139	HIS
6	L	140	LYS
7	M	35	LYS
7	M	46	ARG
7	M	94	SER
7	M	95	ARG
7	M	96	PRO
8	H	107	THR
8	H	108	GLN
8	H	109	LEU
8	H	110	LYS
8	H	111	LYS
8	H	112	ASN
8	H	115	LYS
8	H	116	THR
8	H	117	ARG
8	H	120	ARG
8	H	124	LEU

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Mol	Chain	Res	Type
8	H	129	ILE
8	H	131	GLU
8	H	132	ARG
8	H	133	ILE
8	H	160	ARG
8	H	166	LYS
8	H	167	ASN
8	H	168	VAL
8	H	173	LYS
8	H	177	TYR
8	H	178	LEU
8	H	181	LEU
8	H	187	ARG
8	H	189	LEU
8	H	193	LEU
8	H	202	ASP
8	H	203	LEU
8	H	204	GLU
8	H	205	SER
8	H	206	LYS
8	H	208	ARG
8	H	222	MET
8	H	224	GLU
8	H	235	VAL
8	H	236	LEU
8	H	240	ASP
8	H	265	PHE
8	H	269	LYS
8	H	274	ILE
8	H	275	LEU
8	H	296	ASN
8	H	297	SER
8	H	300	LYS
8	H	305	SER
8	H	307	ILE
8	H	326	GLU
8	H	329	SER
8	H	330	TYR
8	H	336	ILE
8	H	339	SER
8	H	342	ASP
8	H	353	TYR

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Mol	Chain	Res	Type
8	H	354	TYR
8	H	364	PHE
8	H	367	VAL
8	H	368	GLU
8	H	369	LYS
8	H	372	THR
8	H	389	LEU
8	H	391	MET
8	H	395	LYS
8	H	416	ASP
8	H	448	LEU
8	H	452	LYS
8	H	456	LEU
8	H	457	SER
8	H	461	LYS
8	H	465	GLU
8	H	469	TRP
8	H	474	LYS
8	H	478	TYR
8	H	487	ARG
8	H	489	TYR
8	H	490	SER
8	H	501	ILE
8	H	503	ASP
8	H	505	SER
8	H	508	GLU
8	H	509	SER
8	H	510	ARG
8	H	536	SER
8	H	538	GLU
8	H	545	LEU
8	H	558	LYS
8	H	564	ILE
8	H	565	LYS
8	H	567	ILE
8	H	568	SER
8	H	569	SER
8	H	573	LYS
8	H	576	THR
8	H	577	LEU
8	H	581	LYS
8	H	582	SER

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Mol	Chain	Res	Type
8	H	583	LYS
8	H	584	GLU
8	H	586	MET
8	H	589	LEU
8	H	590	LYS
8	H	595	LEU
8	H	603	PHE
8	H	608	GLN
8	H	617	LYS
8	H	652	MET
8	H	725	ARG
8	H	797	GLN
8	H	884	ARG
8	H	887	ARG
8	H	888	ILE
8	H	889	TYR
8	H	893	LYS
8	H	919	ARG
8	H	931	TYR
8	H	932	PHE
8	H	934	HIS
8	H	936	ILE
8	H	945	LEU
8	H	947	LYS
8	H	948	ASP
8	H	959	ILE
8	H	960	ASN
8	H	969	LYS
8	H	970	THR
8	H	974	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	181	HIS
1	A	254	HIS
1	A	310	ASN
1	A	413	ASN
1	A	429	ASN
1	A	481	HIS
1	A	497	GLN

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Mol	Chain	Res	Type
1	A	543	ASN
1	A	576	HIS
1	A	592	HIS
1	A	785	HIS
1	A	868	GLN
1	A	907	ASN
1	A	948	HIS
1	A	976	GLN
1	A	1011	ASN
1	A	1033	ASN
1	A	1067	ASN
1	A	1115	GLN
1	A	1128	GLN
1	A	1156	HIS
1	A	1496	GLN
1	A	1594	GLN
1	A	1615	ASN
1	A	1652	HIS
1	A	1809	ASN
1	A	1839	ASN
1	A	1856	ASN
2	B	144	GLN
2	B	171	GLN
2	B	205	GLN
2	B	227	HIS
2	B	232	ASN
2	B	247	GLN
2	B	274	HIS
2	B	316	GLN
2	B	374	ASN
2	B	420	ASN
2	B	447	ASN
2	B	448	ASN
3	I	113	HIS
3	I	146	ASN
3	I	148	ASN
3	I	152	ASN
3	I	201	ASN
3	I	211	GLN
3	I	267	HIS
3	I	281	GLN
3	I	396	GLN

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Mol	Chain	Res	Type
3	I	398	GLN
3	I	414	ASN
3	I	433	ASN
3	I	449	ASN
3	I	461	HIS
4	G	99	ASN
4	G	140	GLN
4	G	160	ASN
4	G	281	ASN
4	G	285	HIS
4	G	668	HIS
4	G	700	ASN
4	G	777	GLN
4	G	805	HIS
5	K	163	ASN
5	K	283	ASN
5	K	316	HIS
5	K	330	ASN
5	K	338	HIS
6	L	14	HIS
6	L	17	GLN
6	L	87	HIS
6	L	139	HIS
7	M	45	ASN
8	H	112	ASN
8	H	135	ASN
8	H	143	HIS
8	H	158	HIS
8	H	167	ASN
8	H	183	GLN
8	H	211	ASN
8	H	255	GLN
8	H	296	ASN
8	H	334	HIS
8	H	355	HIS
8	H	418	GLN
8	H	444	GLN
8	H	554	HIS
8	H	608	GLN
8	H	721	GLN
8	H	797	GLN
8	H	929	GLN

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Mol	Chain	Res	Type
8	H	960	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	C	19/20 (95%)	17 (89%)	2 (10%)
25	D	41/112 (36%)	22 (53%)	4 (9%)
26	E	85/160 (53%)	28 (32%)	7 (8%)
27	F	111/214 (51%)	51 (45%)	14 (12%)
All	All	256/506 (50%)	118 (46%)	27 (10%)

All (118) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	C	-5	A
24	C	-4	A
24	C	-3	A
24	C	-2	A
24	C	-1	A
24	C	0	U
24	C	1	U
24	C	2	A
24	C	3	A
24	C	4	G
24	C	5	G
24	C	6	U
24	C	7	A
24	C	8	U
24	C	9	G
24	C	10	U
24	C	12	U
25	D	48	C
25	D	49	A
25	D	50	G
25	D	51	A
25	D	52	G
25	D	57	U
25	D	62	A
25	D	63	G
25	D	66	C
25	D	72	C

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Mol	Chain	Res	Type
25	D	75	A
25	D	76	A
25	D	77	G
25	D	78	G
25	D	79	A
25	D	83	A
25	D	84	C
25	D	85	C
25	D	86	G
25	D	87	U
25	D	109	U
25	D	110	U
26	E	2	U
26	E	4	C
26	E	15	G
26	E	18	A
26	E	19	U
26	E	20	A
26	E	25	U
26	E	27	U
26	E	28	C
26	E	30	G
26	E	39	C
26	E	43	C
26	E	48	U
26	E	51	U
26	E	55	U
26	E	56	U
26	E	60	U
26	E	140	G
26	E	141	G
26	E	142	G
26	E	143	A
26	E	144	A
26	E	146	U
26	E	147	U
26	E	148	U
26	E	149	U
26	E	150	G
26	E	151	G
27	F	32	G
27	F	33	U

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Mol	Chain	Res	Type
27	F	34	C
27	F	39	U
27	F	40	C
27	F	41	A
27	F	74	U
27	F	75	A
27	F	76	U
27	F	77	A
27	F	78	A
27	F	79	C
27	F	80	G
27	F	81	A
27	F	82	A
27	F	83	C
27	F	84	A
27	F	90	C
27	F	92	U
27	F	93	G
27	F	94	C
27	F	95	C
27	F	96	U
27	F	97	U
27	F	98	U
27	F	99	U
27	F	100	A
27	F	101	C
27	F	103	A
27	F	104	G
27	F	107	C
27	F	108	C
27	F	109	A
27	F	110	U
27	F	113	G
27	F	120	G
27	F	121	U
27	F	126	A
27	F	127	U
27	F	164	C
27	F	165	A
27	F	166	U
27	F	167	A
27	F	168	U

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Mol	Chain	Res	Type
27	F	169	U
27	F	170	U
27	F	171	U
27	F	172	U
27	F	173	U
27	F	174	G
27	F	175	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	C	-4	A
24	C	6	U
25	D	48	C
25	D	50	G
25	D	83	A
25	D	85	C
26	E	1	A
26	E	18	A
26	E	19	U
26	E	24	A
26	E	139	A
26	E	142	G
26	E	148	U
27	F	32	G
27	F	33	U
27	F	75	A
27	F	77	A
27	F	81	A
27	F	83	C
27	F	95	C
27	F	97	U
27	F	98	U
27	F	107	C
27	F	163	C
27	F	166	U
27	F	168	U
27	F	172	U

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
28	GTP	H	1500	-	33,34,34	1.09	3 (9%)	50,54,54	1.71	7 (14%)
29	M7M	E	201	26	31,33,33	1.38	4 (12%)	37,52,52	1.77	5 (13%)

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
28	GTP	H	1500	-	-	4/22/38/38	0/3/3/3
29	M7M	E	201	26	-	6/20/48/48	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	3.82	1.46	1.36
28	H	1500	GTP	C5-C4	3.15	1.47	1.38
29	E	201	M7M	CBF-NBE	-2.92	1.33	1.38
29	E	201	M7M	CBG-NBH	-2.91	1.32	1.35
28	H	1500	GTP	C6-N1	-2.44	1.34	1.38
29	E	201	M7M	CBO-NBN	-2.12	1.33	1.37
28	H	1500	GTP	C5-N7	-2.12	1.34	1.39

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	H	1500	GTP	C5-C4-N3	-6.09	118.69	128.39
29	E	201	M7M	NBP-CBI-NBH	-5.85	95.09	103.37
28	H	1500	GTP	C2-N3-C4	4.83	120.62	112.30
29	E	201	M7M	PBK-OBU-CBT	4.60	147.72	121.35
28	H	1500	GTP	N9-C4-N3	4.29	134.54	125.95
29	E	201	M7M	OBU-PBK-OBL	-3.31	95.83	108.94
28	H	1500	GTP	C6-C5-N7	3.29	136.28	130.29
29	E	201	M7M	OAY-PAZ-OBA	2.90	122.13	110.83
28	H	1500	GTP	C4-C5-N7	-2.88	106.11	110.67
29	E	201	M7M	CBG-CBO-NBN	-2.46	117.72	123.02
28	H	1500	GTP	C3'-C2'-C1'	2.44	106.08	101.46
28	H	1500	GTP	O6-C6-C5	-2.05	121.11	126.53

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
29	E	201	M7M	NBE-CBM-NBV-CBW
29	E	201	M7M	NBE-CBM-NBV-CBZ
29	E	201	M7M	NBN-CBM-NBV-CBZ
29	E	201	M7M	CBS-CBT-OBU-PBK
28	H	1500	GTP	O4'-C4'-C5'-O5'
28	H	1500	GTP	C3'-C4'-C5'-O5'
29	E	201	M7M	NBN-CBM-NBV-CBW
28	H	1500	GTP	PB-O3A-PA-O2A
29	E	201	M7M	CBX-CBQ-NBP-CBI
28	H	1500	GTP	PB-O3A-PA-O1A

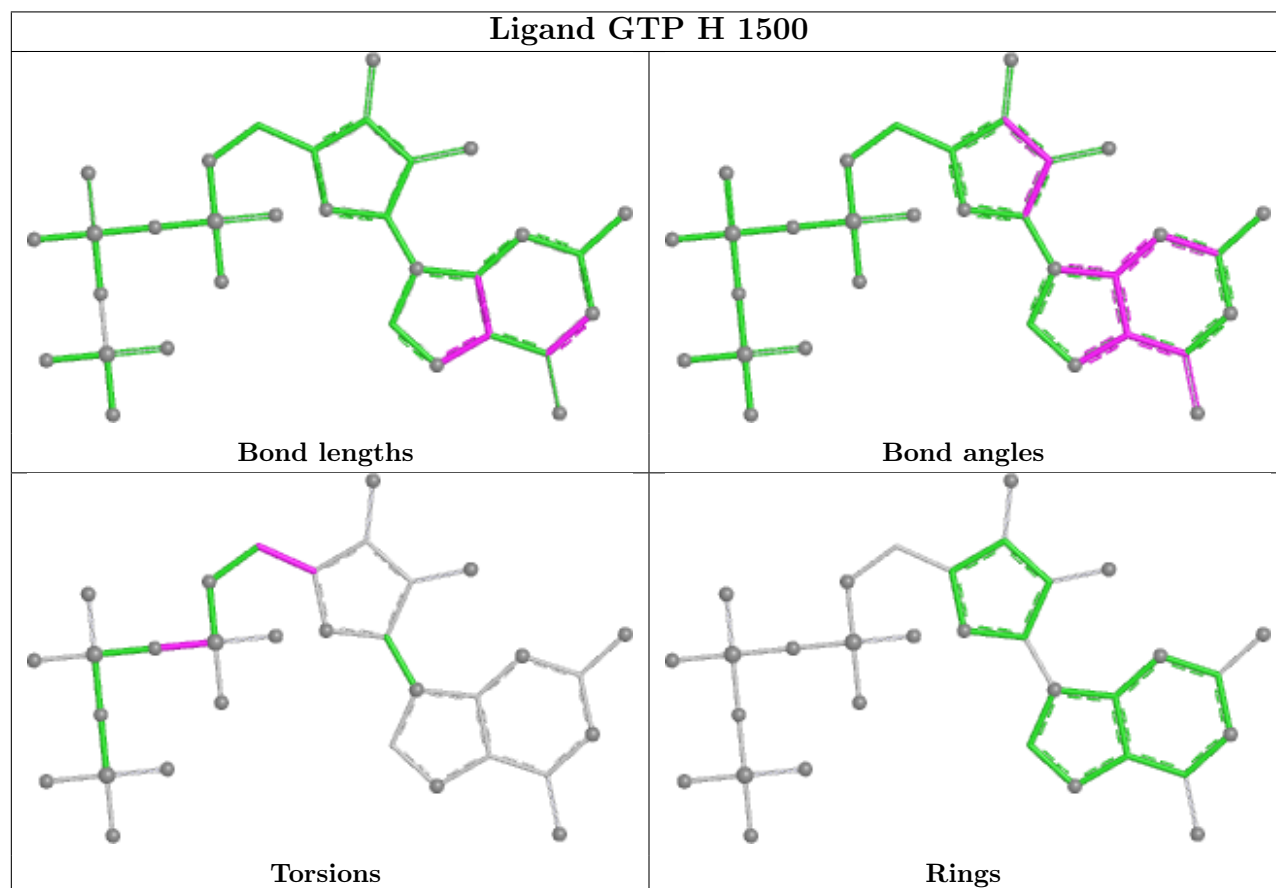
There are no ring outliers.

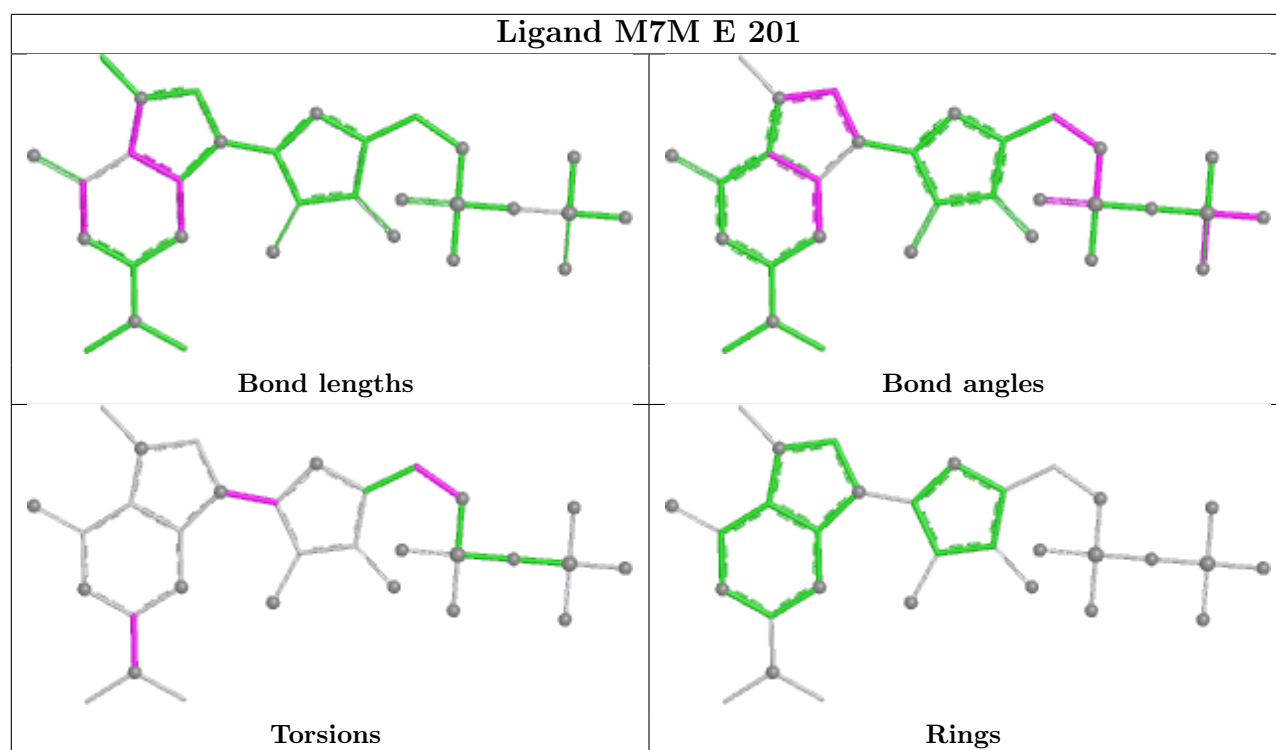
2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	H	1500	GTP	10	0
29	E	201	M7M	6	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.

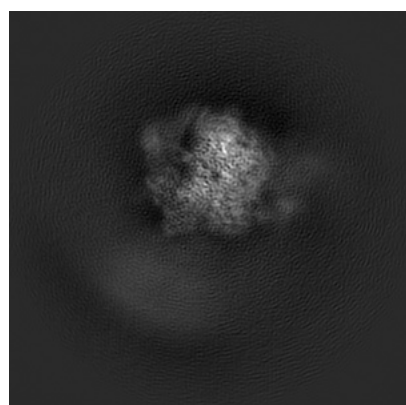
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6561. These allow visual inspection of the internal detail of the map and identification of artifacts.

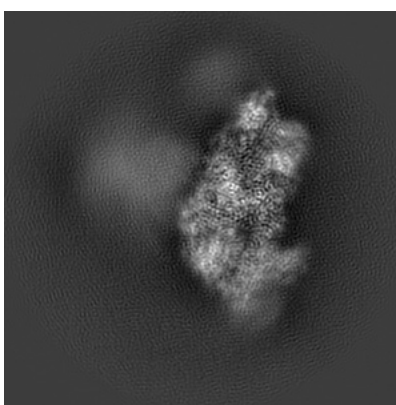
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

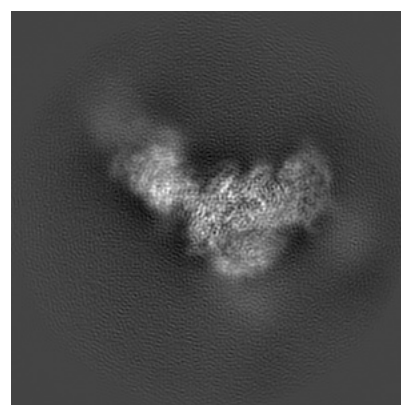
6.1.1 Primary map



X



Y

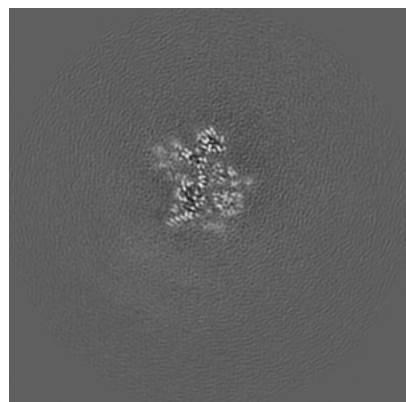


Z

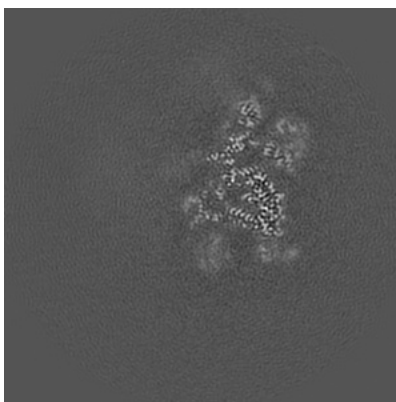
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

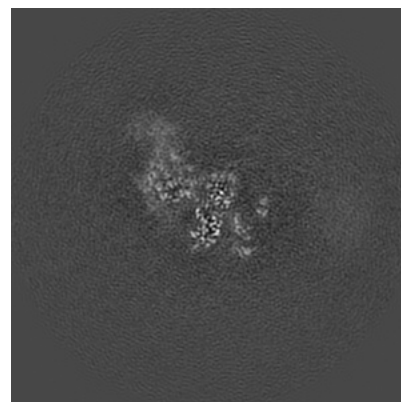
6.2.1 Primary map



X Index: 160



Y Index: 160

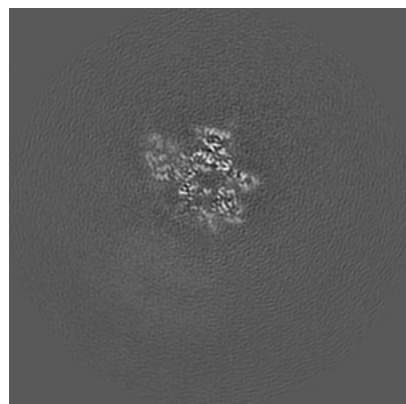


Z Index: 160

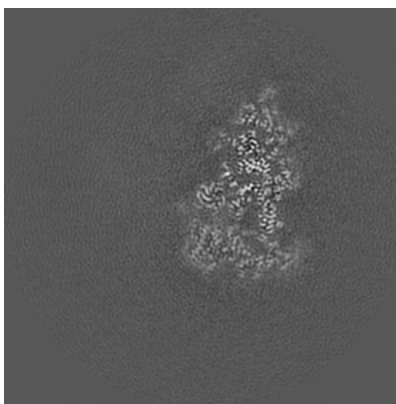
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

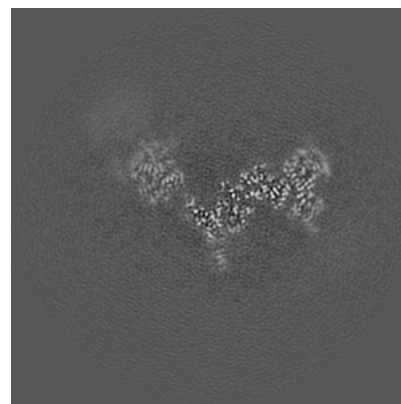
6.3.1 Primary map



X Index: 167



Y Index: 171

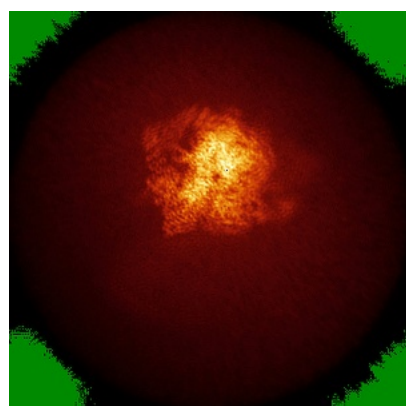


Z Index: 199

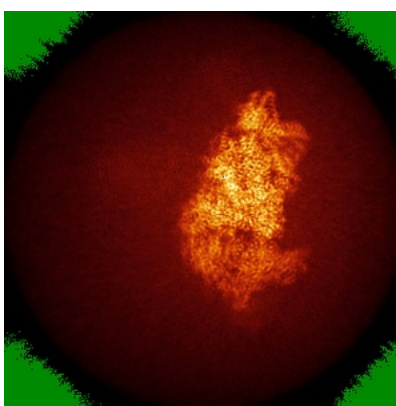
The images above show the largest variance slices of the map in three orthogonal directions.

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

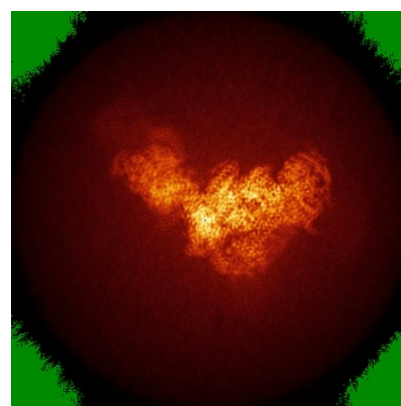
6.4.1 Primary map



X



Y

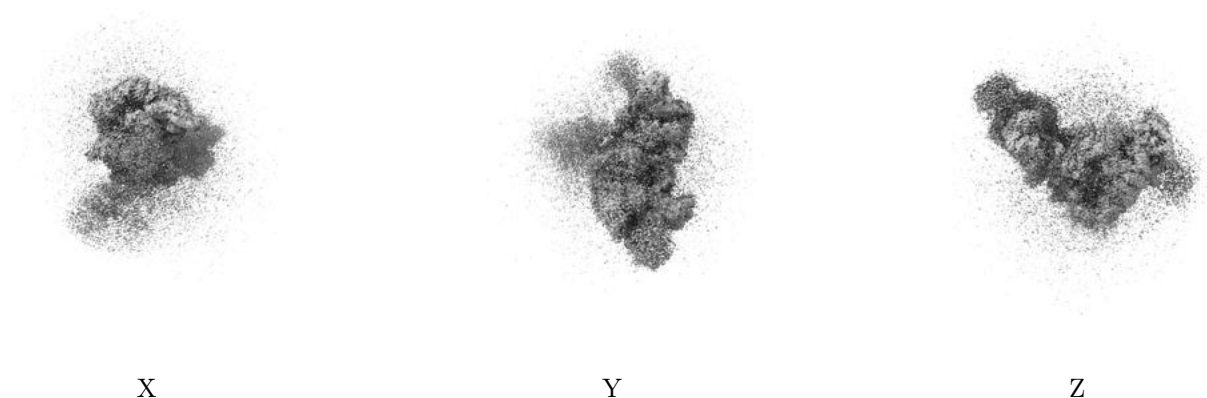


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

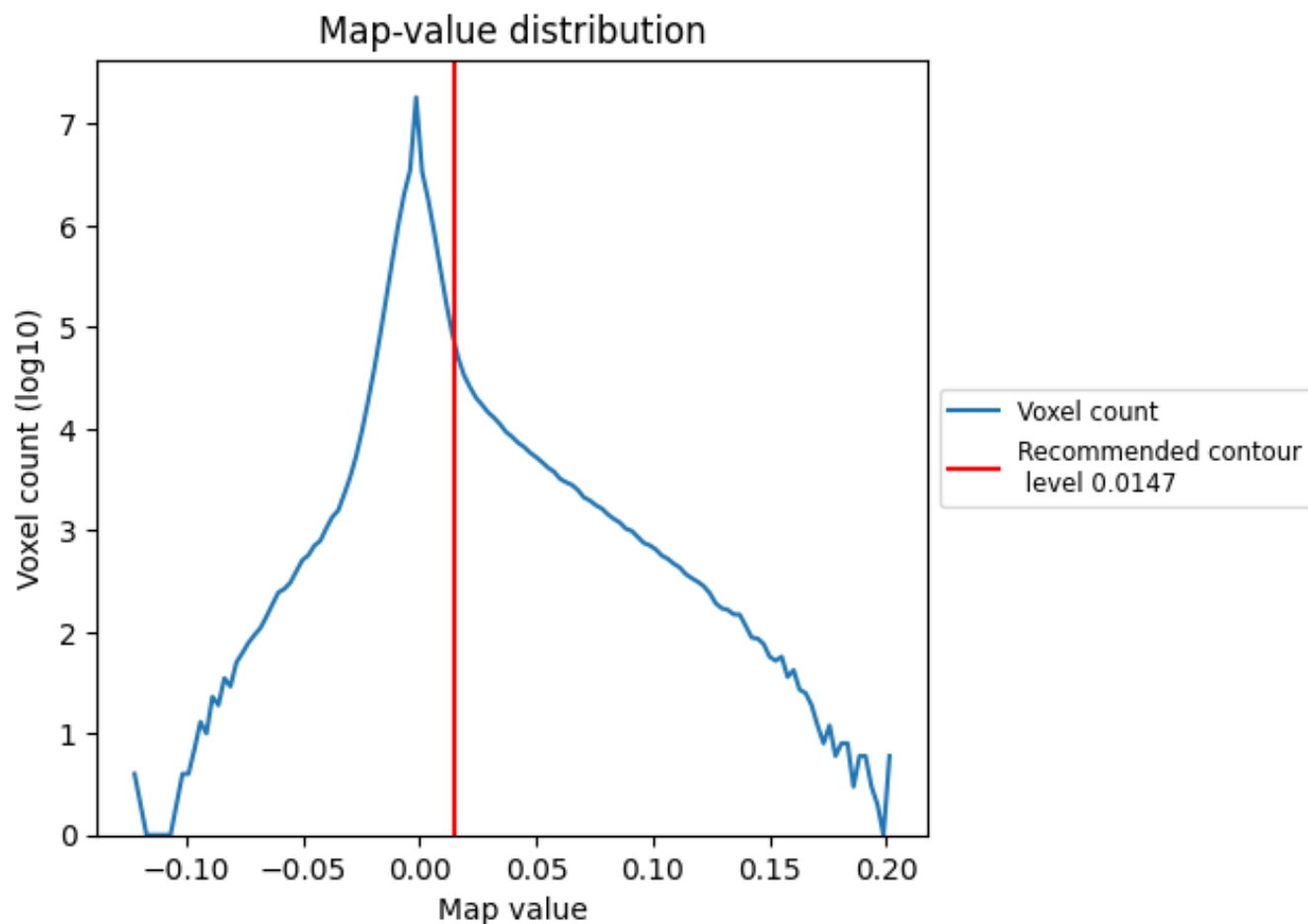
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

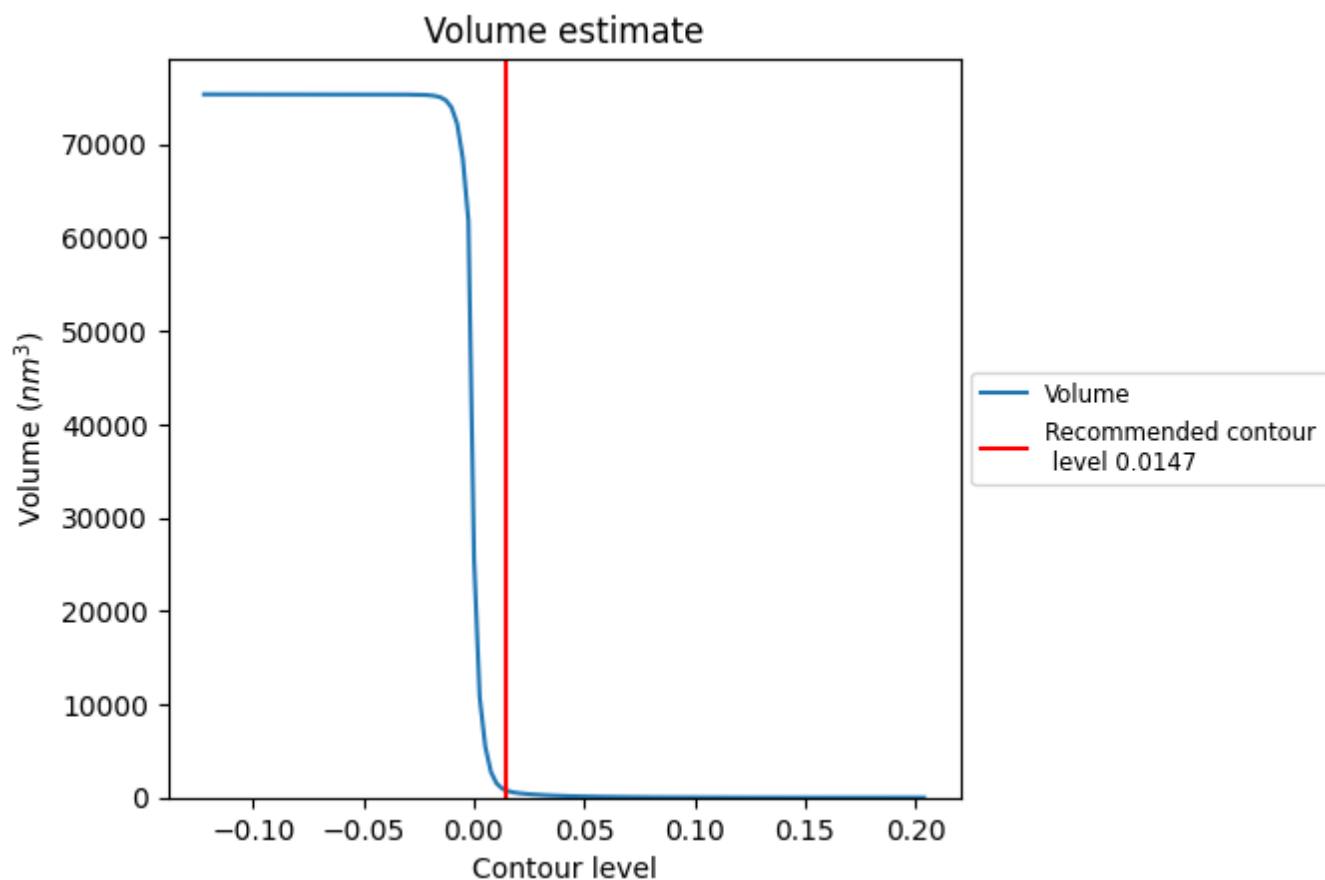
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

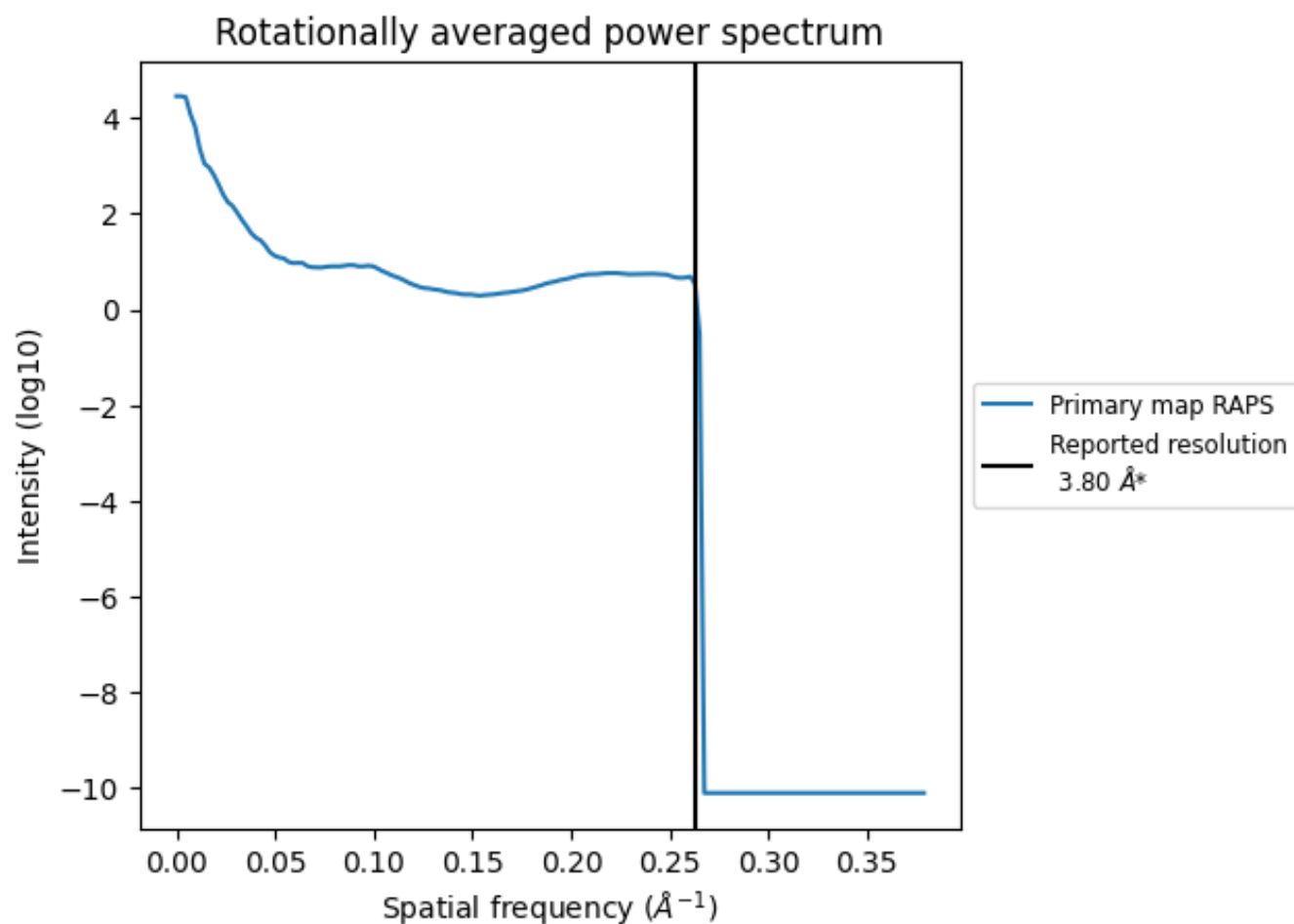
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 773 nm³; this corresponds to an approximate mass of 699 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 0.263 Å⁻¹

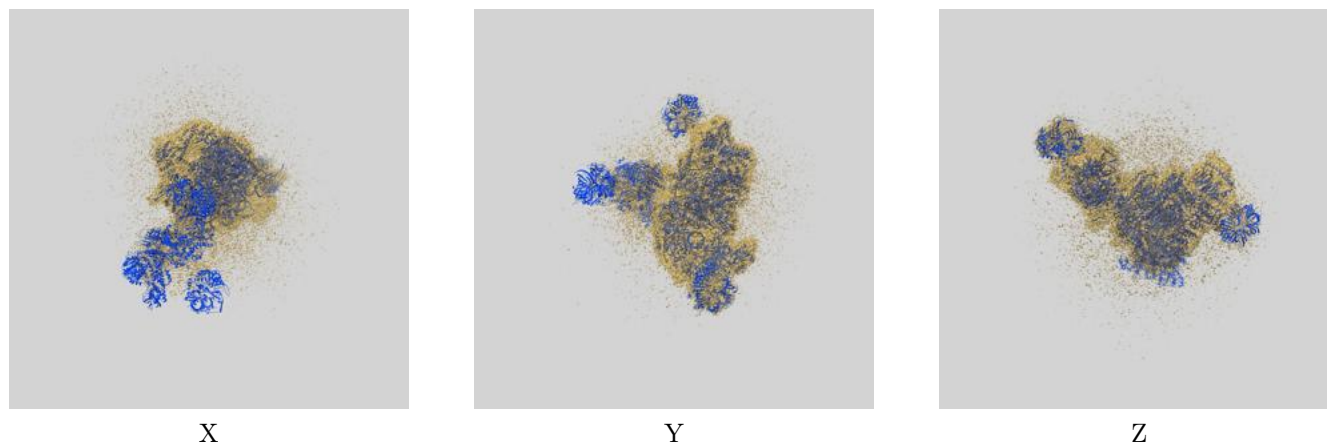
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

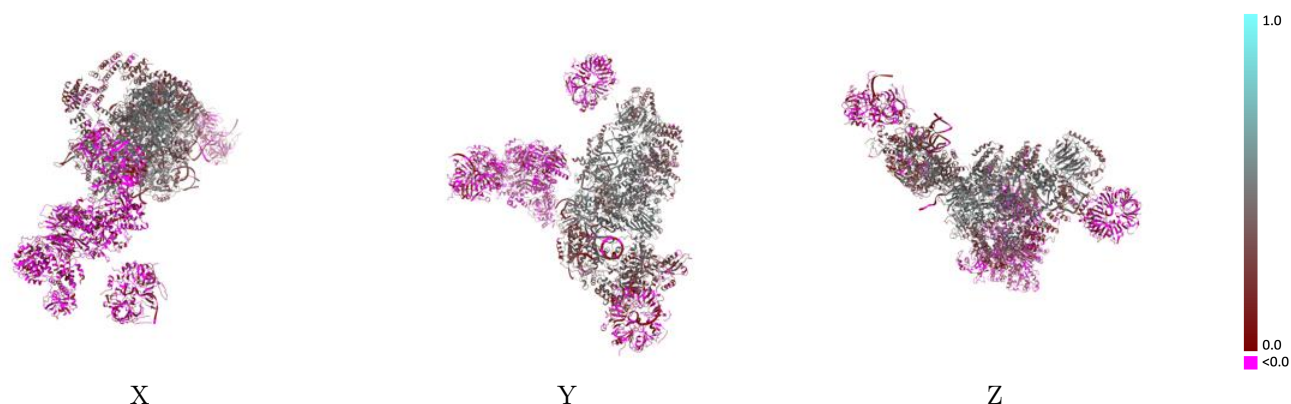
This section contains information regarding the fit between EMDB map EMD-6561 and PDB model 3JCM. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



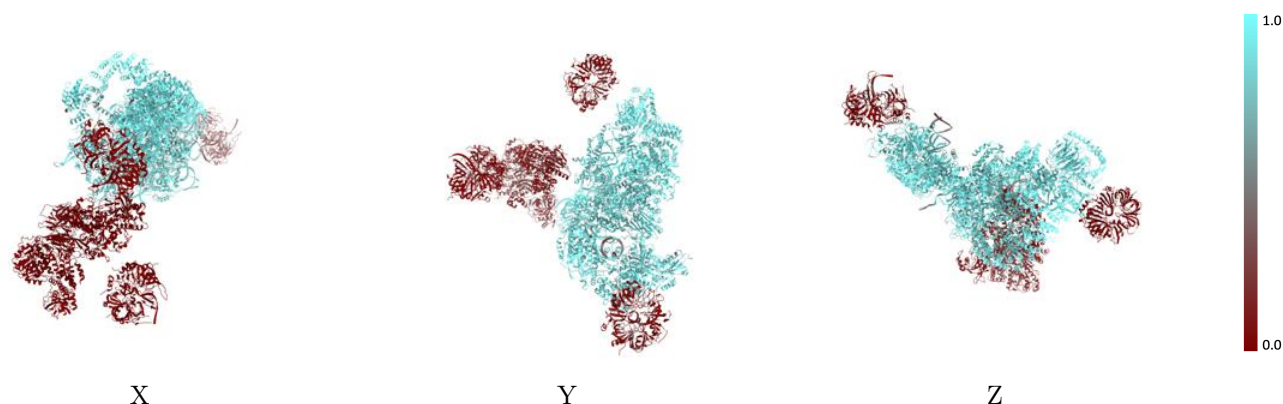
The images above show the 3D surface view of the map at the recommended contour level 0.0147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



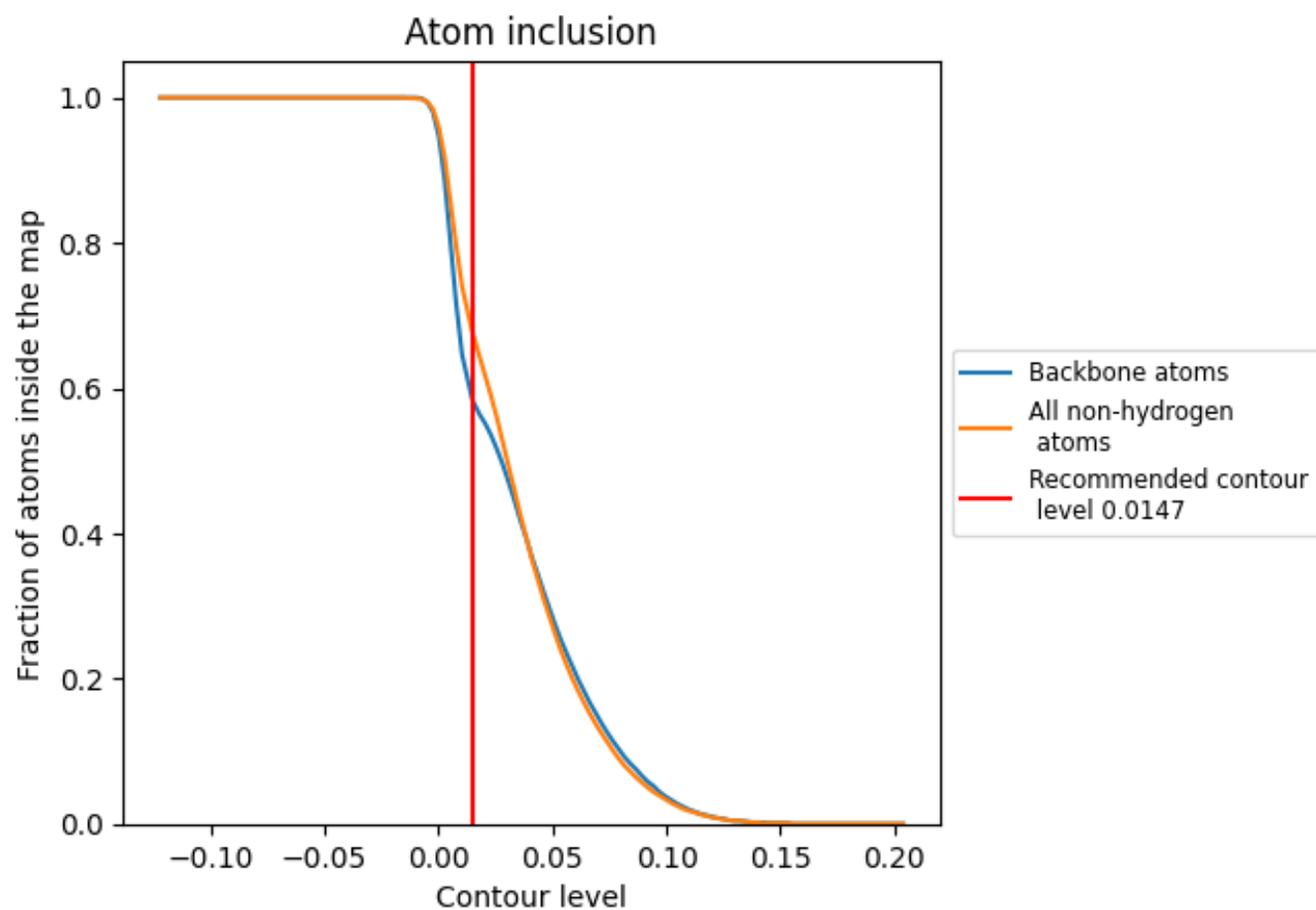
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0147).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 68% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.2940
A	 0.8560	 0.3990
B	 0.9060	 0.4200
C	 0.8700	 0.2880
D	 0.8910	 0.3730
E	 0.7470	 0.3630
F	 0.7110	 0.2090
G	 0.9070	 0.3400
H	 0.8910	 0.3210
I	 0.9220	 0.4400
J	 0.0000	 -0.0190
K	 0.9070	 0.4070
L	 0.9240	 0.4570
M	 0.9270	 0.4890
N	 0.0230	 0.0020
O	 0.0000	 0.0160
P	 0.0030	 0.0440
Q	 0.0000	 0.0460
R	 0.1490	 0.0620
S	 0.0510	 0.0240
T	 0.0910	 0.0940
U	 0.1220	 0.0370
V	 0.0490	 -0.0010
W	 0.1320	 0.0400
X	 0.0500	 0.0310
Y	 0.0000	 -0.0070
Z	 0.0040	 0.0190
a	 0.0000	 0.0330
b	 0.0110	 0.0180
c	 0.0110	 0.0280
d	 0.0100	 0.0140
e	 0.0270	 0.0190
f	 0.0130	 0.0250
g	 0.0110	 0.0220
h	 0.0160	 -0.0580

