



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:38 AM GMT

PDB ID : 3OW2
Title : Crystal Structure of Enhanced Macrolide Bound to 50S Ribosomal Subunit
Authors : Kanyo, Z.F.
Deposited on : 2010-09-17
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

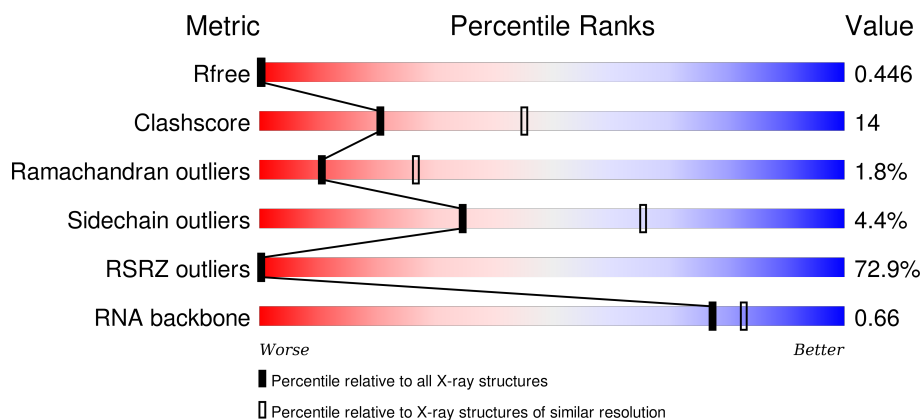
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)
RNA backbone	2183	1069 (3.10-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	2902	<div> <div>68%</div> <div> <div>55%</div> <div>35%</div> <div>5%</div> <div>5%</div> </div> </div>
2	9	122	<div> <div>67%</div> <div> <div>51%</div> <div>39%</div> <div>9%</div> <div>.</div> </div> </div>
3	A	237	<div> <div>87%</div> <div> <div>67%</div> <div>28%</div> <div>5%</div> </div> </div>
4	B	337	<div> <div>75%</div> <div> <div>62%</div> <div>34%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	165	
7	E	172	
8	F	119	
9	G	62	
10	H	167	
11	I	142	
12	J	132	
13	K	150	
14	L	194	
15	M	186	
16	N	115	
17	O	143	
18	P	95	
19	Q	150	
20	R	81	
21	S	119	
22	T	53	
23	U	65	
24	V	154	
25	W	82	
26	X	142	
27	Y	73	
28	Z	56	
29	1	48	

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Mol	Chain	Length	Quality of chain
30	2	92	<div> <div>75%</div> <div>76%</div> <div>24%</div> </div>

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
31	MG	0	8001	-	-	-	X
31	MG	0	8003	-	-	-	X
31	MG	0	8009	-	-	-	X
31	MG	0	8011	-	-	-	X
31	MG	0	8012	-	-	-	X
31	MG	0	8018	-	-	-	X
31	MG	0	8021	-	-	-	X
31	MG	0	8024	-	-	-	X
31	MG	0	8028	-	-	-	X
31	MG	0	8032	-	-	-	X
31	MG	0	8033	-	-	-	X
31	MG	0	8034	-	-	-	X
31	MG	0	8037	-	-	-	X
31	MG	0	8038	-	-	-	X
31	MG	0	8043	-	-	-	X
31	MG	0	8047	-	-	-	X
31	MG	0	8053	-	-	-	X
31	MG	J	201	-	-	-	X
31	MG	X	301	-	-	-	X
32	K	0	8056	-	-	-	X
33	NA	0	8057	-	-	-	X
33	NA	0	8059	-	-	-	X
33	NA	0	8061	-	-	-	X
33	NA	0	8062	-	-	-	X
33	NA	0	8064	-	-	-	X
33	NA	0	8067	-	-	-	X
33	NA	0	8070	-	-	-	X
33	NA	0	8072	-	-	-	X
33	NA	0	8073	-	-	-	X
33	NA	0	8074	-	-	-	X
33	NA	0	8075	-	-	-	X
33	NA	9	3202	-	-	-	X
33	NA	C	301	-	-	-	X
33	NA	I	201	-	-	-	X
33	NA	L	201	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	NA	P	101	-	-	-	X
33	NA	Q	201	-	-	-	X
33	NA	Q	202	-	-	-	X
34	CL	I	203	-	-	-	X
34	CL	L	202	-	-	-	X
34	CL	N	201	-	-	-	X
35	SR	O	8138	-	-	-	X
35	SR	O	8141	-	-	-	X
35	SR	A	305	-	-	-	X
35	SR	B	402	-	-	-	X
36	EMK	O	8163	-	-	X	X

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 90725 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59016	26346	10878	19047	2745			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	?	-	U	DELETION	GB 3377779
0	?	-	C	DELETION	GB 3377779
0	560	C	U	CONFLICT	GB 3377779
0	2099	A	G	CONFLICT	GB 3377779

- Molecule 2 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2600	1160	472	847	121			

- Molecule 3 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	237	Total	C	N	O	S	0	0	0
			1755	1072	352	326	5			

- Molecule 4 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 5 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 6 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	140	Total	C	N	O	S	0	0	0
			1095	685	195	211	4			

- Molecule 7 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	172	Total	C	N	O	S	0	0	0
			1358	840	224	290	4			

- Molecule 8 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	119	Total	C	N	O	S	0	0	0
			886	552	141	192	1			

- Molecule 9 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	29	Total	C	N	O	S	0	0	0
			241	149	39	52	1			

- Molecule 10 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	156	Total	C	N	O	S	0	0	0
			1216	766	233	213	4			

- Molecule 11 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 12 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	132	Total	C	N	O	S	0	0	0
			994	609	189	192	4			

- Molecule 13 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	145	Total	C	N	O		0	0	0
			1119	670	222	227				

- Molecule 14 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	194	Total	C	N	O	S	0	0	0
			1606	988	346	267	5			

- Molecule 15 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 16 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	115	Total	C	N	O		0	0	0
			865	529	161	175				

- Molecule 17 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	O	143	Total	C	N	O		0	0	0
			1134	680	230	224				

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	71	LYS	TYR	CONFLICT	UNP P14119

- Molecule 18 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 19 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Q	150	Total	C	N	O	S	0	0	0
			1150	713	209	224	4			

- Molecule 20 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	81	Total	C	N	O	S	0	0	0
			642	389	111	139	3			

- Molecule 21 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	S	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 22 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	T	53	Total	C	N	O	S	0	0	0
			411	244	75	87	5			

- Molecule 23 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	U	65	Total	C	N	O	S	0	0	0
			500	304	94	101	1			

- Molecule 24 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	V	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 25 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	W	82	Total	C	N	O	S	0	0	0
			655	402	129	123	1			

- Molecule 26 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	X	142	Total	C	N	O		0	0	0
			1131	686	228	217				

- Molecule 27 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y	73	Total	C	N	O	S	0	0	0
			564	359	111	87	7			

- Molecule 28 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 29 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	46	Total	C	N	O	S	0	0	0
			394	238	86	69	1			

- Molecule 30 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
31	0	55	Total	Mg	0	0
			55	55		
31	J	1	Total	Mg	0	0
			1	1		
31	K	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
31	B	1	Total 1	Mg 1	0	0
31	X	1	Total 1	Mg 1	0	0
31	9	1	Total 1	Mg 1	0	0
31	S	1	Total 1	Mg 1	0	0

- Molecule 32 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	1	Total 1	K 1	0	0

- Molecule 33 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	19	Total 19	Na 19	0	0
33	P	1	Total 1	Na 1	0	0
33	Q	2	Total 2	Na 2	0	0
33	I	1	Total 1	Na 1	0	0
33	C	1	Total 1	Na 1	0	0
33	9	1	Total 1	Na 1	0	0
33	L	1	Total 1	Na 1	0	0

- Molecule 34 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	5	Total 5	Cl 5	0	0
34	Q	1	Total 1	Cl 1	0	0
34	D	1	Total 1	Cl 1	0	0

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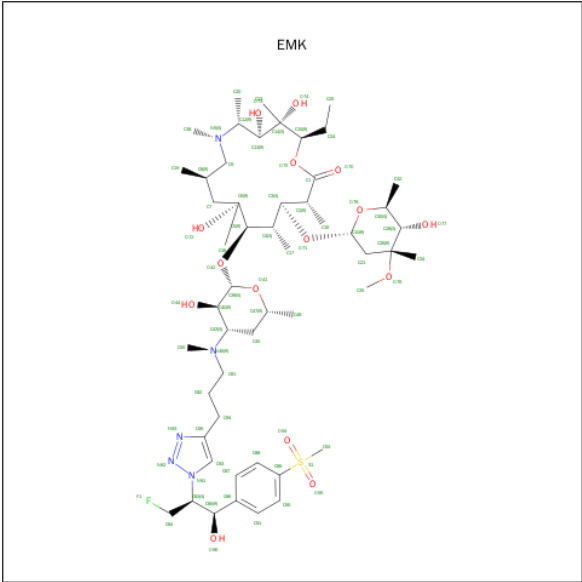
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	I	2	Total 2	Cl 2	0	0
34	A	1	Total 1	Cl 1	0	0
34	N	1	Total 1	Cl 1	0	0
34	X	1	Total 1	Cl 1	0	0
34	L	1	Total 1	Cl 1	0	0

- Molecule 35 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	82	Total 82	Sr 82	0	0
35	Q	1	Total 1	Sr 1	0	0
35	B	2	Total 2	Sr 2	0	0
35	Z	2	Total 2	Sr 2	0	0
35	A	4	Total 4	Sr 4	0	0
35	R	1	Total 1	Sr 1	0	0
35	9	3	Total 3	Sr 3	0	0
35	2	2	Total 2	Sr 2	0	0
35	F	1	Total 1	Sr 1	0	0

- Molecule 36 is (2R,3S,4R,5R,8R,10R,11R,12S,13S,14R)-2-ETHYL-3,4,10-TRIHYDROXY-3,5,6,8,10,12,14-HEPTAMETHYL-15-OXO-11-[(3,4,6-TRIDEOXY-3-{[3-(1-{(1S,2R)-1-(FLUOROMETHYL)-2-HYDROXY-2-[4-(METHYLSULFONYL)PHENYL]ETHYL}-1H-1,2,3-TRIAZOL-4-YL)PROPYL](METHYL)AMINO}-BETA-D-XYLO-HEXOPYRANOSYL)OXY]-1-OXA-6-AZACYCLOPENTADECAN-13-YL 2,6-DIDEOXY-3-C-METHYL-3-O-METHYL-ALPHA-L-RIBO-HEXOPYRANOSIDE (three-letter code: EMK) (formula: C₅₂H₈₈FN₅O₁₅S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	F	N	O	S		
36	0	1	74	52	1	5	15	1	0	0

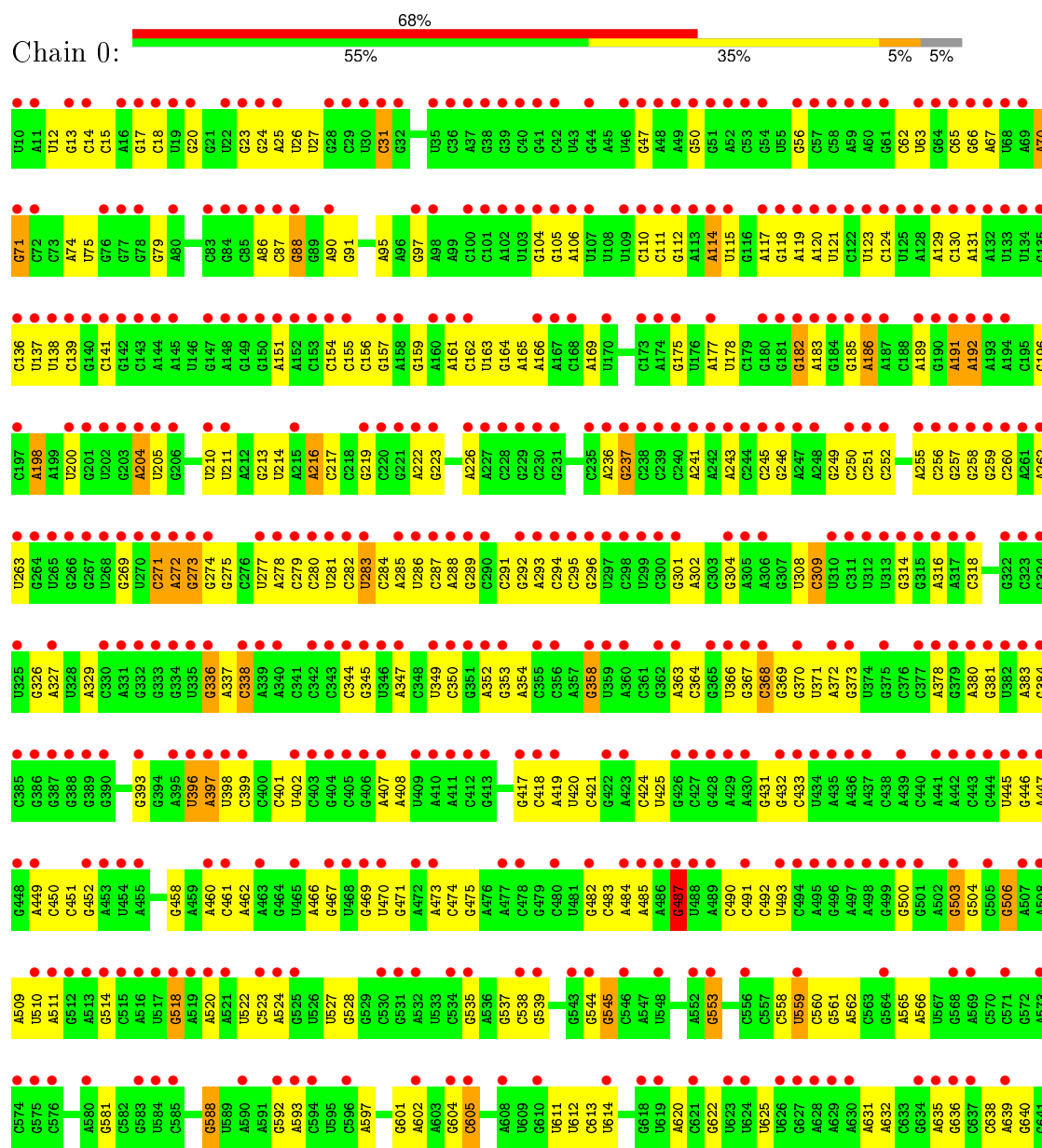
- Molecule 37 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	Z	1	Total	Cd	0	0
			1	1		
37	Y	1	Total	Cd	0	0
			1	1		
37	T	1	Total	Cd	0	0
			1	1		
37	2	1	Total	Cd	0	0
			1	1		

3 Residue-property plots

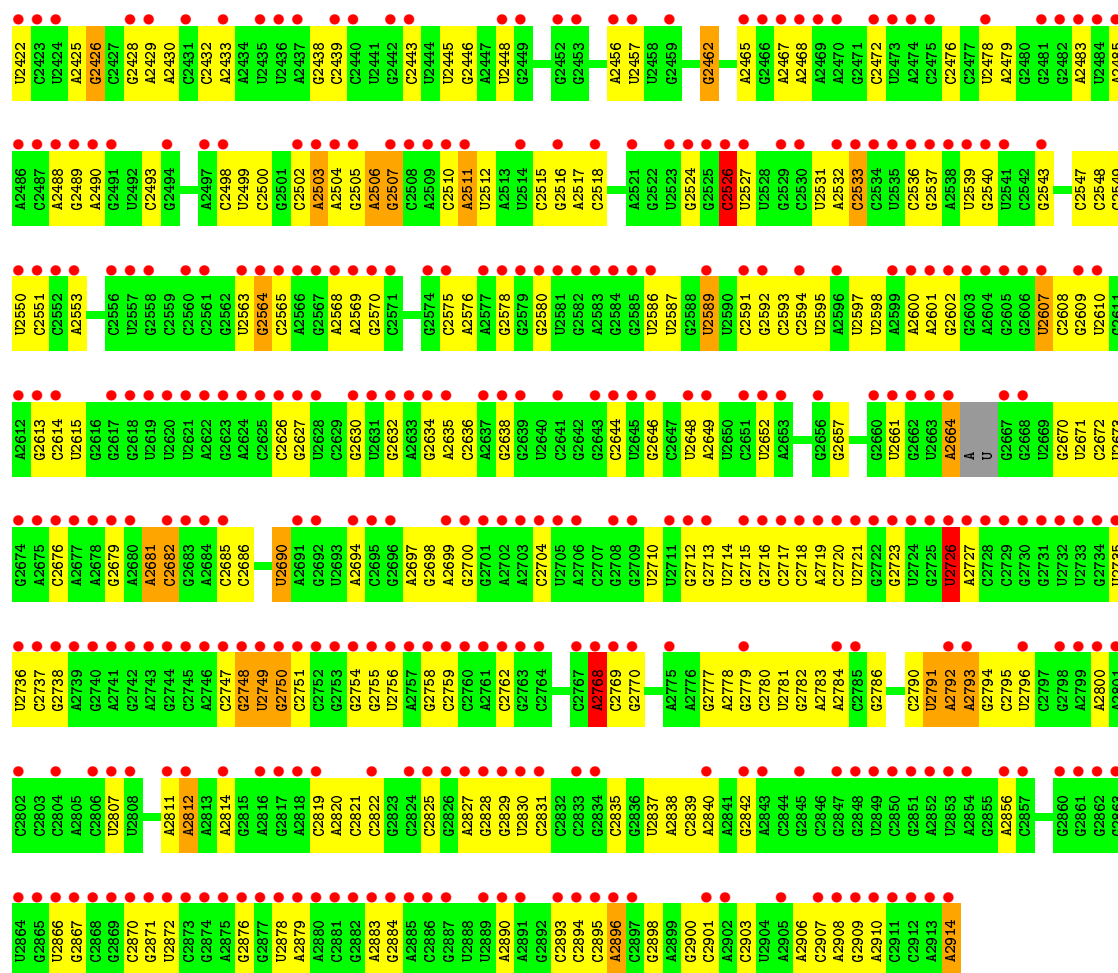
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 23S RIBOSOMAL RNA

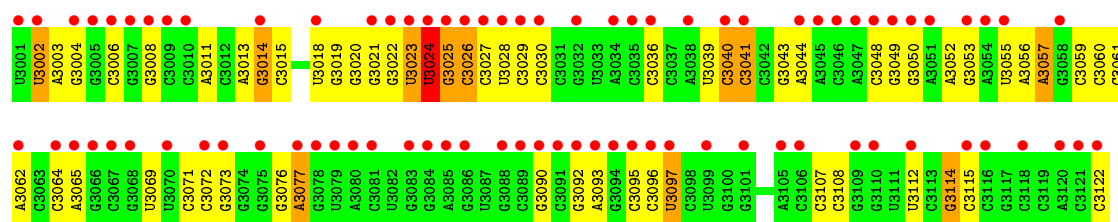




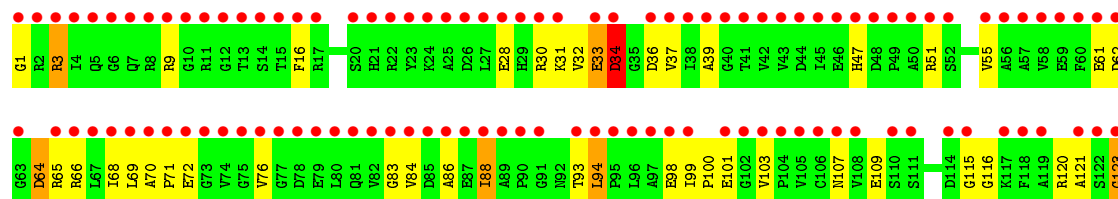
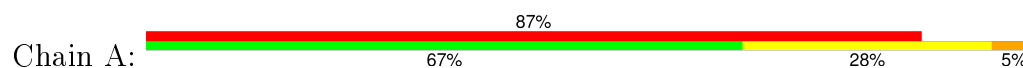
A2356	U2290	G	A	G2110	C2040	U1980	A1919	A1858	C1798	A1737	U1677	G1617	C1557
G2357	A2291	U	C	G2111	G2041	A1981	C1920	A1859	G1799	C1738	A1678	G1618	C1558
C2360	G2292	G	A	A2112	U2042	C1982	A1921	C1860	G1800	C1739	A1679	G1619	A1559
A2361	G2293	A	C	G2113	U2043	C1983	A1922	C1861	A1801	U1740	C1680	G1620	U
A2362	G2294	C	U	G2114	G2044	U1984	A1923	C1862	G1802	U1741	G1681	G1621	C1561
C2363	G2295	U	A	C2115	G2045	U1985	A1924	C1863	C1803	A1742	A1682	G1622	C1562
A2364	C2296	C	C	U2116	G2046	C1986	A1925	C1864	A1804	G1743	G1683	C1623	C1563
A2367	G2297	C	C	U2117	C2047	C1987	A1926	A1865	G1805	G1744	A1684	C1624	C1564
A2368	A2300	A	C	A2118	G2048	C1988	A1927	A1866	G1806	G1745	A1685	U1625	C1565
A2369	A2301	G	A	C2119	G2049	C1989	C1928	G1867	G1807	A1746	C1686	G1626	C1566
A2370	A2302	U	G	U2120	G2050	C1990	C1929	G1868	C1808	A1747	C1687	G1627	U1567
G2371	A2303	U	U	G2121	G2051	A1991	A1930	A1869	G1809	U1748	G1688	G1628	U1568
A2372	U2242	U	A	C2122	U2052	U1992	A1931	C1870	C1810	U1749	A1689	G1629	U1569
U2373	C2243	C	C	A2123	G2053	C1993	G1932	U1871	A1811	C1750	C1690	A1630	C1570
A2374	A2244	C	C	G2124	A2054	A1994	G1933	C1872	G1812	G1751	C1691	A1631	G1571
G2375	C2245	C	C	G2125	U2055	U1996	A1934	G1873	U1813	G1752	C1692	A1632	A1572
C2376	U2246	C	C	C2126	U2056	C1997	U1937	A1874	G1814	C1753	A1693	G1633	A1573
U2377	C2247	C	C	U2127	G2057	C1998	G1938	C1875	A1815	A1754	G1694	G1634	C1574
U2378	C2248	G	C	G2128	G2058	G1999	U1939	C1876	C1816	A1755	G1695	U1635	C1575
A2379	G2249	C	C	U2129	U2063	G2000	U1940	C1877	U1817	G1756	U1696	G1636	U1576
G2380	G2250	U	C	C2130	U2064	G2001	A1941	U1878	G1818	U1757	G1697	A1637	U1577
C2381	G2251	A	A	G2131	C2065	C2002	A1942	C1880	G1819	U1758	C1698	U1638	C1578
C2382	A2252	G	C	C2132	C2066	U2003	G1943	A1881	A1820	A1759	C1699	U1639	C1579
C2383	G2253	C	C	U2133	U2069	U2004	G1944	C1882	A1821	G1760	C1700	C1640	A1580
U2384	G2254	G	G	G2134	A2074	G2005	G1945	U1883	A1822	U1761	A1701	A1641	A1581
C2385	A2255	G	G	A2135	G2070	C2006	C1946	C1884	G1823	C1762	U1702	A1642	C1582
G2386	G2256	C	C	G2136	C2071	A2007	G1947	A1885	U1824	C1763	G1703	C1643	C1583
U2387	G2257	C	A	C	G2072	U2008	G1948	A1886	U1825	G1764	G1704	C1644	U1584
C2388	A2258	C	C	C	G2073	G2009	G1949	U1887	G1826	U1765	G1705	U1645	C1585
U2389	G2259	C	C	U	A2074	A2010	G1950	C1892	G1828	A1767	G1707	G1647	U1587
U2390	A2260	C	C	U	C2077	A2011	G1951	U1890	A1829	C1768	C1708	G1648	U1588
C2391	C2261	C	C	G	U2078	U2012	U	G1891	U1830	U1769	G1709	G1649	C1589
A2395	U2330	C	A	U	G2079	G2013	A	C1892	U1831	U1770	A1710	C1650	A1590
A2398	C2331	C	G	C	G2080	G2014	A	C1893	G1832	U1771	C1651	C1652	A1591
C2399	A2332	U	U	G	A2081	A2015	C	A1895	U1833	G1772	A1712	A1653	C1592
G2400	C2333	C	C	C	G2082	U2016	U	C1896	C1834	G1773	G1713	C1654	C1593
A2401	C2334	C	C	C	A2083	U2017	A	G1897	U1835	G1774	C1714	U1654	C1594
A2402	C2335	C	C	C	G2084	A2018	U	U1898	G1836	A1775	G1715	G1655	C1595
A2405	C2336	C	A	C	A2085	A2019	G	C1899	G1837	A1776	C1716	G1656	U1596
C2406	G2337	C	A	U	C2086	C2020	A	A1900	U1838	G1777	A1657	A1657	A1597
U2407	A2338	U	G	U	A2089	C2021	C	G1901	A1839	A1778	G1718	A1658	U1598
G2408	C	U	U	C	G2090	A2022	C	A1840	A1840	A1779	G1719	A1659	U1599
A2409	A	C	C	C	G2091	G2023	U1964	C1842	C1842	G1780	C1720	A1660	U1600
G2410	G2344	C	C	C	G2092	A2024	C1965	U1903	A1843	A1783	C1721	A1661	G1601
C2411	A2345	C	C	C	G2093	G2025	U1966	A1904	C1844	U1784	U1722	C1662	C1602
G2412	C2346	C	C	C	G2094	C2026	U1967	C1905	U1845	G1785	G1723	G1663	A1603
A2413	C2347	C	C	C	A2095	U2027	A1968	U1907	A1846	C1786	U1724	A1664	G1604
A2414	C2348	C	C	C	A2096	U2028	A1969	G1908	A1847	C1787	G1725	G1665	C1605
A2415	G2349	C	C	C	A2097	G2029	G1970	A1909	G1848	U1788	G1726	C1666	A1606
G2416	U2282	C	U	C	A2100	A2030	G1971	U1910	G1849	U1789	G1727	A1667	U1607
G2417	G2350	C	C	C	A2101	G2031	U1972	A1911	C1850	C1790	G1728	U1668	G1608
G2418	C2351	C	C	C	G2102	U2032	A1973	A1912	U1851	U1791	A1729	A1669	C1609
U2419	G2352	C	C	C	A2103	G2033	G1974	C1913	A1852	G1792	G1730	G1670	G1610
G2420	A2353	C	C	C	G2104	U2034	U1975	U1914	A1853	C1793	A1732	U1671	A1611
A2354	C2287	U	C	C	C2105	C2036	G1976	U1915	C1854	G1794	A1733	U1672	A1612
G2355	G2288	C	C	C	C2106	C2037	U1977	C1916	G1855	G1795	C1734	U1673	C1613
	G2289	C	C	C	U2107	A2038	A1978	G1917	C1856	A1796	C1735	C1674	A1614
						A2039	G1979	U1918	A1857	A1797	A1736	G1675	A1615
												G1676	A1616

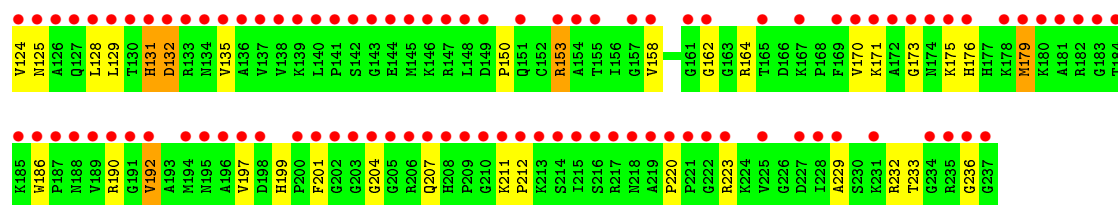


• Molecule 2: 5S RIBOSOMAL RNA

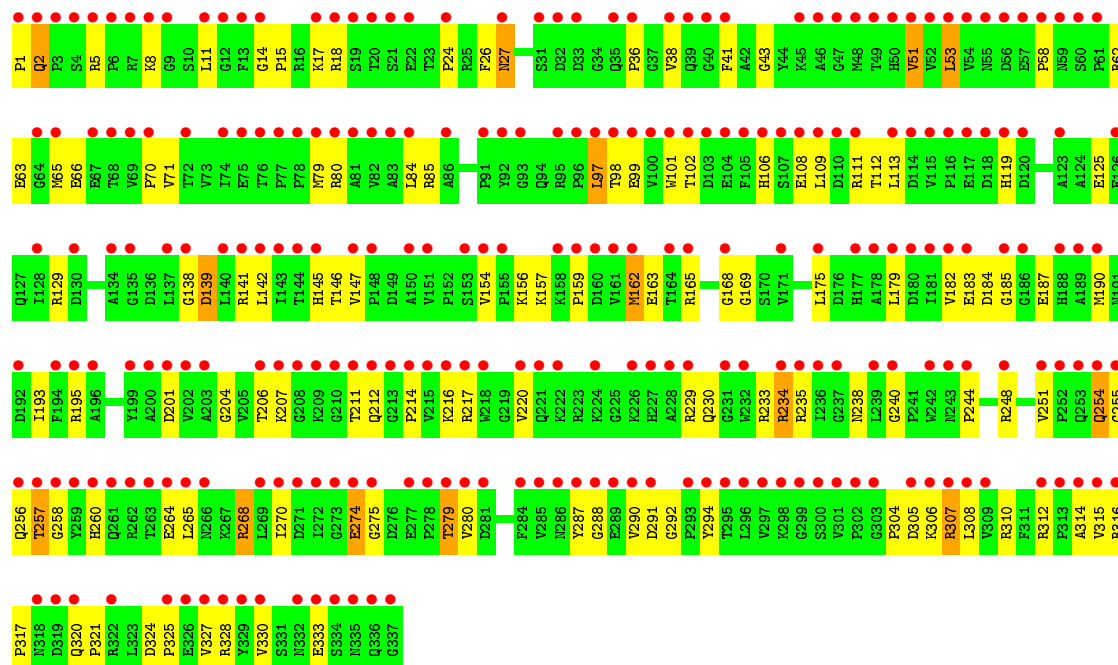
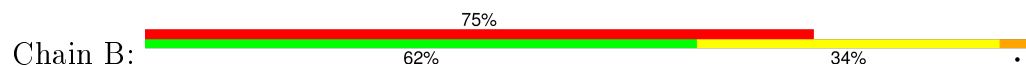


• Molecule 3: 50S ribosomal protein L2P

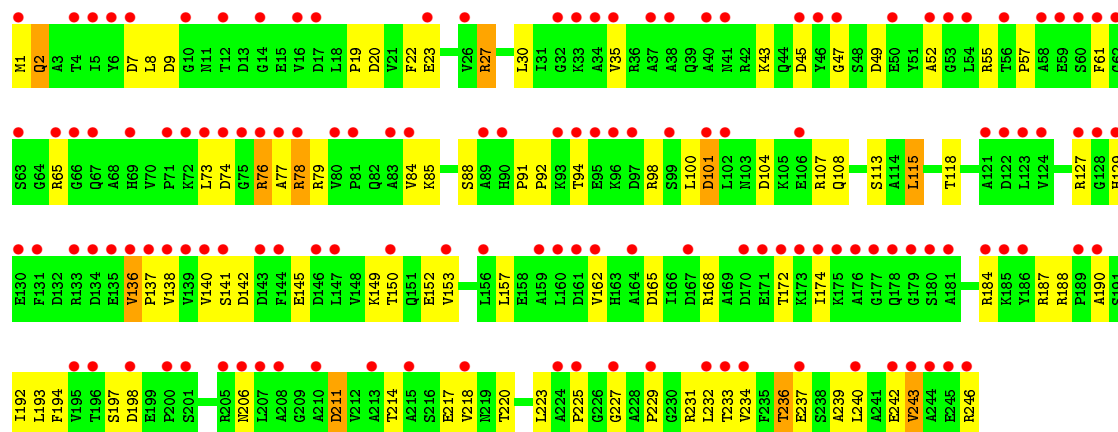




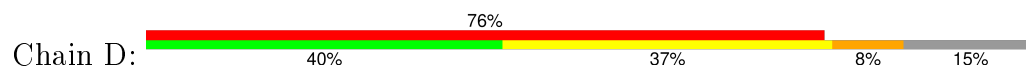
• Molecule 4: 50S ribosomal protein L3P

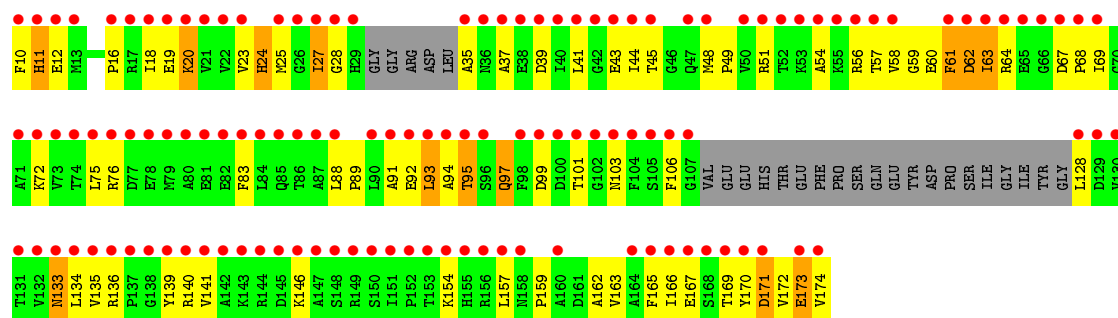


• Molecule 5: 50S ribosomal protein L4P

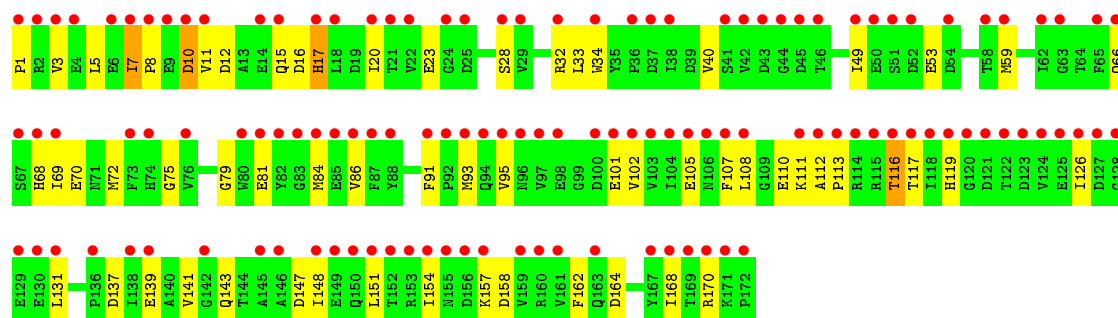


• Molecule 6: 50S ribosomal protein L5P

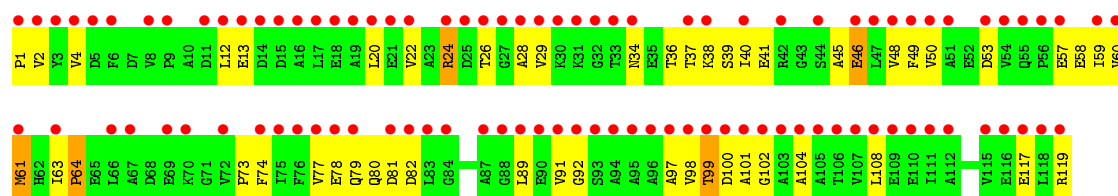
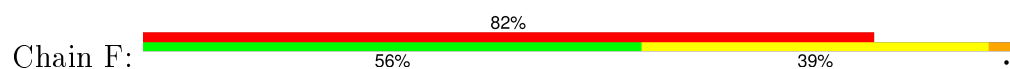




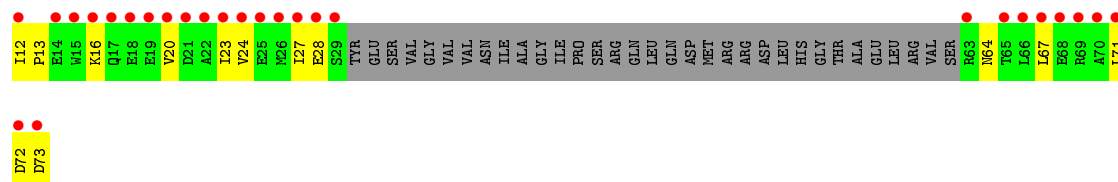
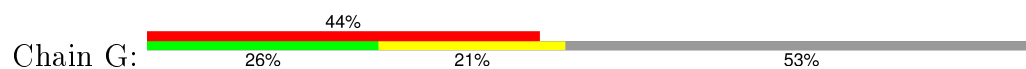
• Molecule 7: 50S ribosomal protein L6P



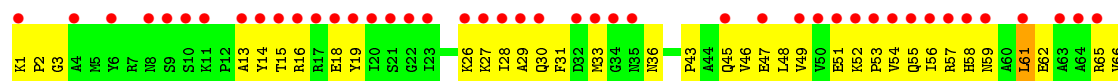
• Molecule 8: 50S ribosomal protein L7Ae

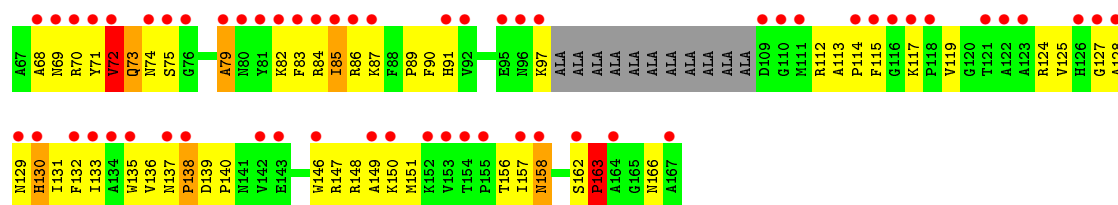


• Molecule 9: 50S ribosomal protein L10E

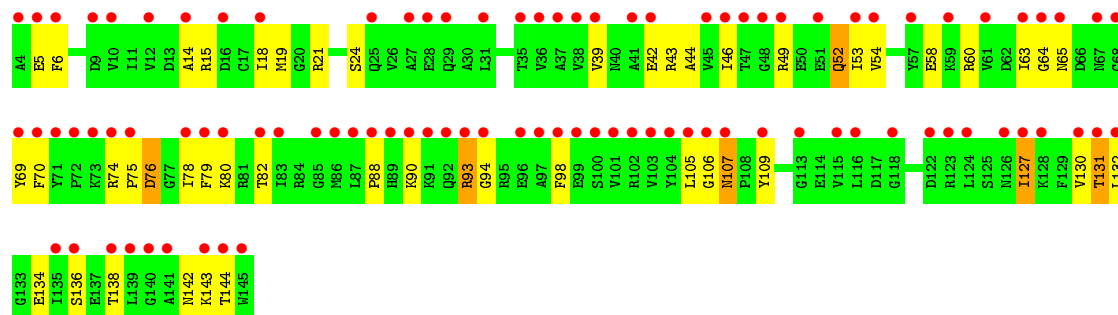


• Molecule 10: 50S ribosomal protein L10e

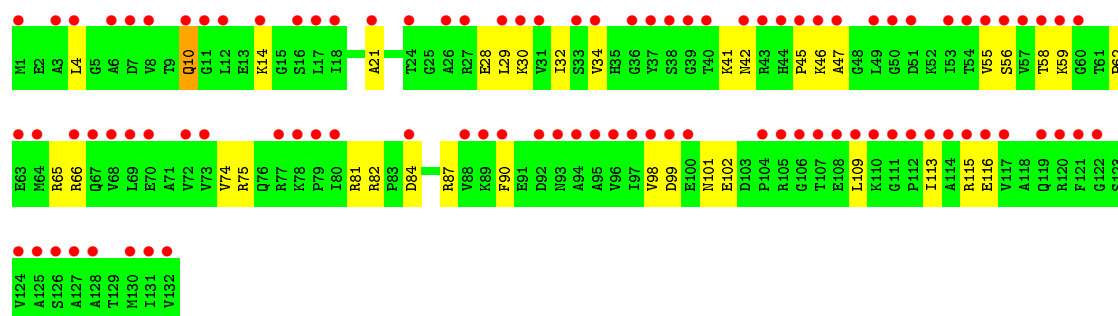




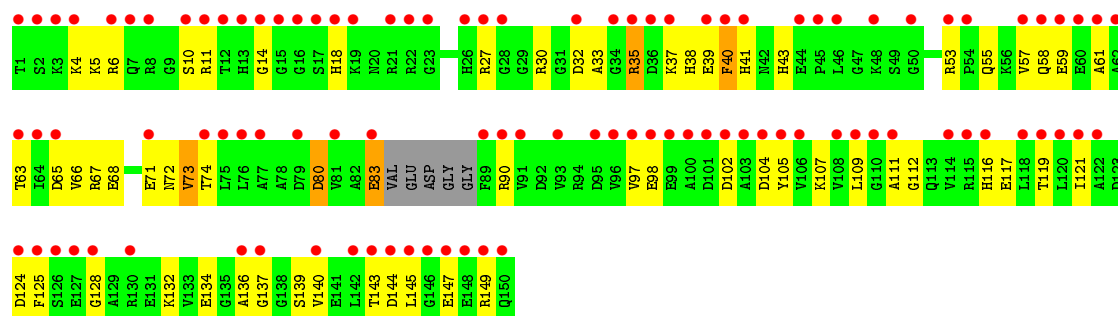
• Molecule 11: 50S ribosomal protein L13P



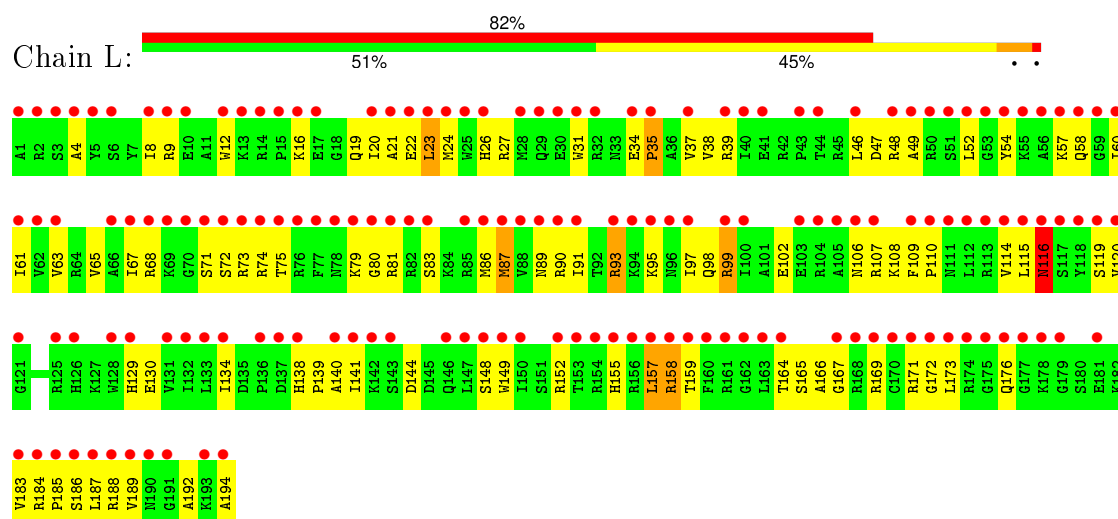
• Molecule 12: 50S ribosomal protein L14P



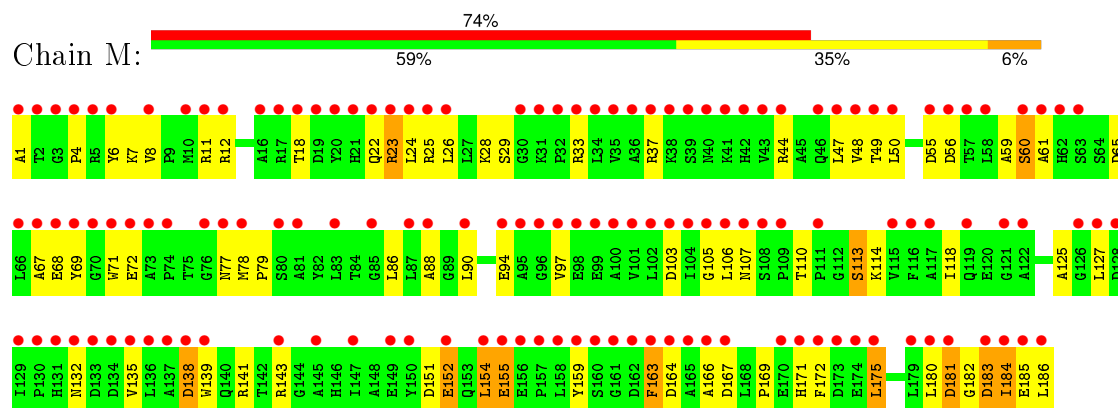
• Molecule 13: 50S ribosomal protein L15P



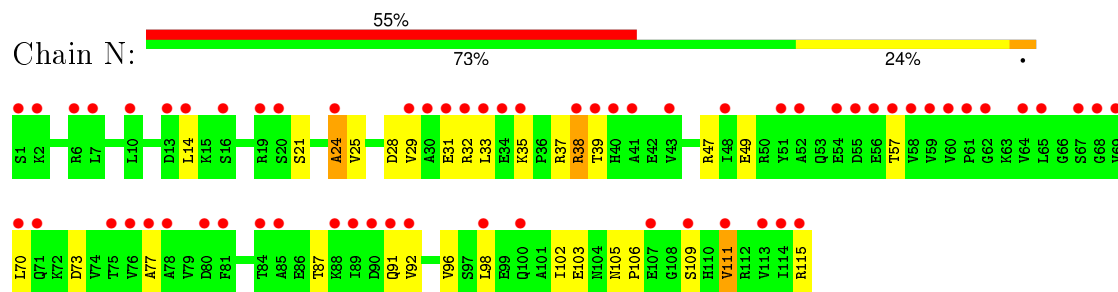
• Molecule 14: 50S ribosomal protein L15e



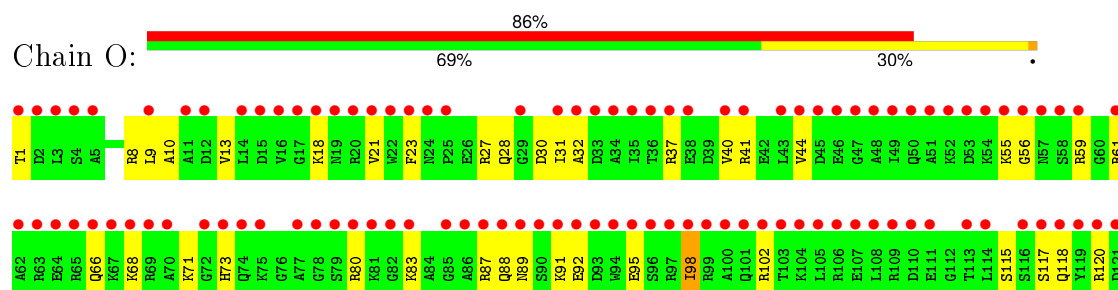
• Molecule 15: 50S ribosomal protein L18P

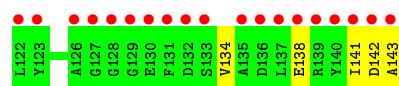


• Molecule 16: 50S ribosomal protein L18e

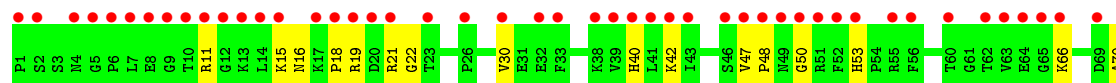
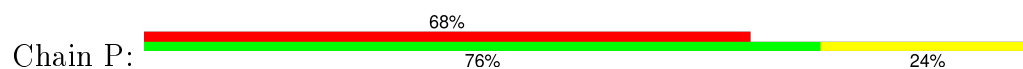


• Molecule 17: 50S ribosomal protein L19e

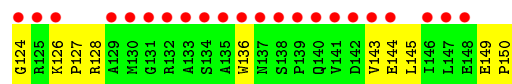
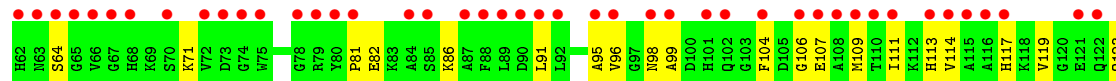
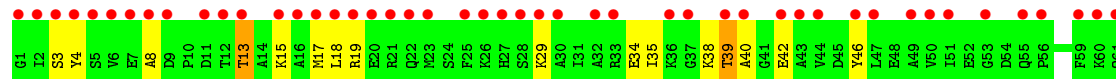
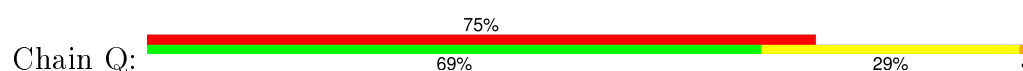




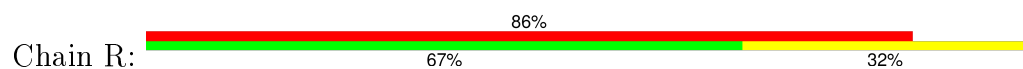
• Molecule 18: 50S ribosomal protein L21e



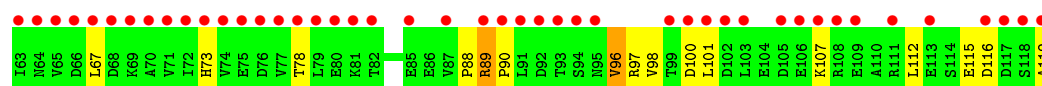
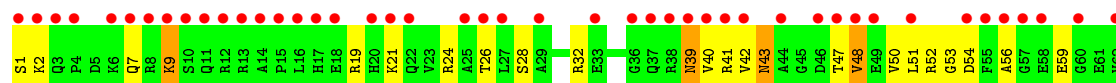
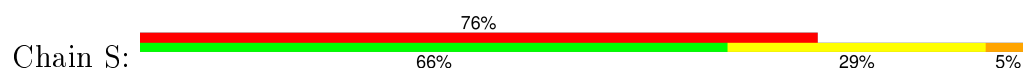
• Molecule 19: 50S ribosomal protein L22P



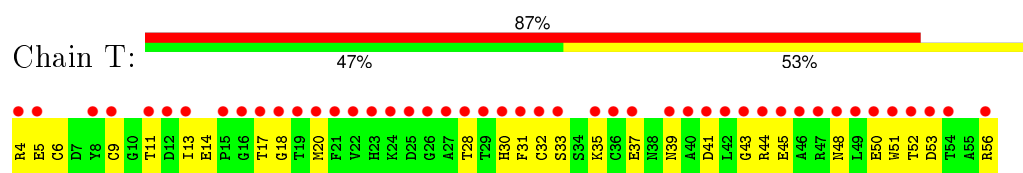
• Molecule 20: 50S ribosomal protein L23P



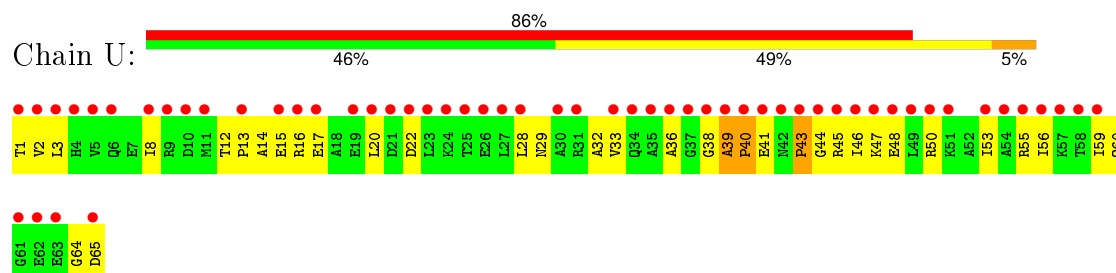
• Molecule 21: 50S ribosomal protein L24P



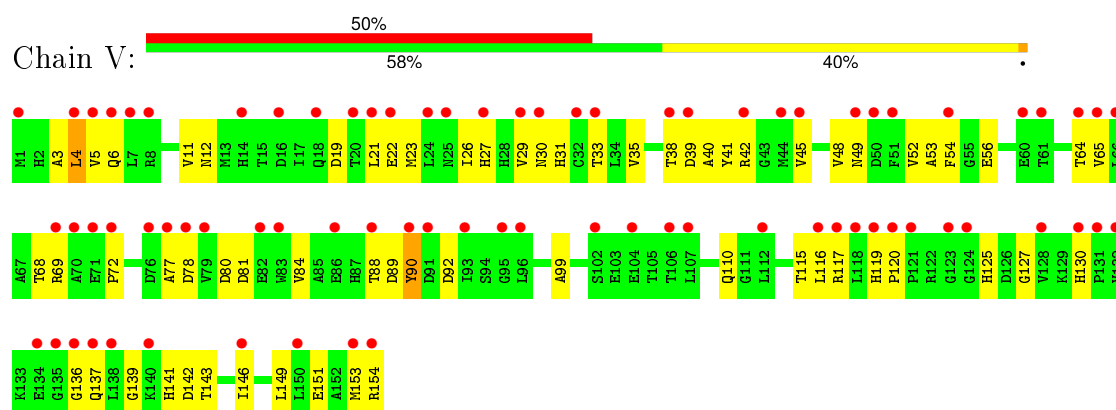
• Molecule 22: 50S ribosomal protein L24e



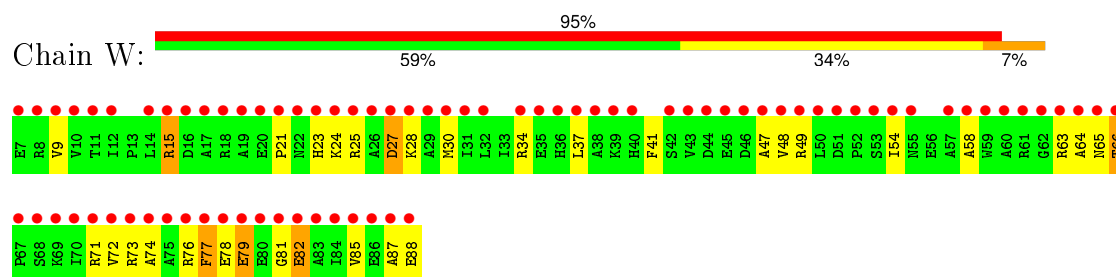
• Molecule 23: 50S ribosomal protein L29P



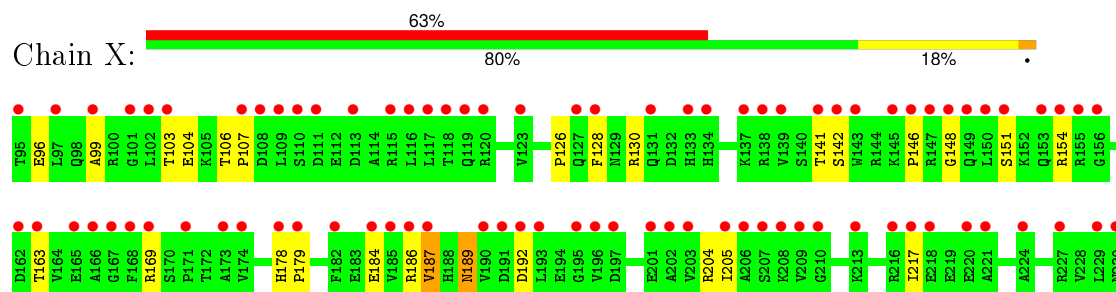
• Molecule 24: 50S ribosomal protein L30P

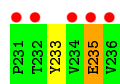


• Molecule 25: 50S ribosomal protein L31e

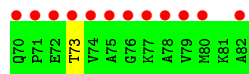
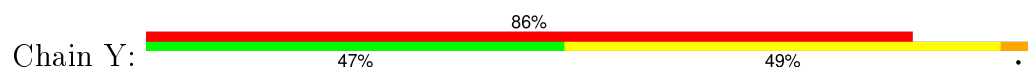


• Molecule 26: 50S ribosomal protein L32e

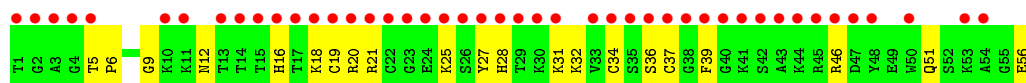
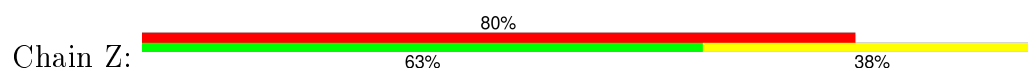




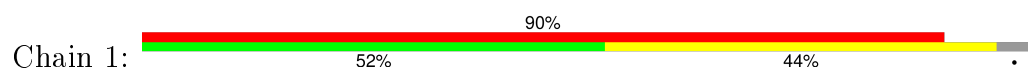
- Molecule 27: 50S ribosomal protein L37Ae



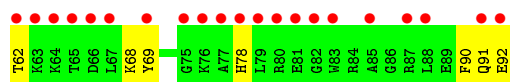
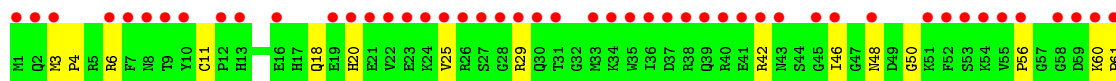
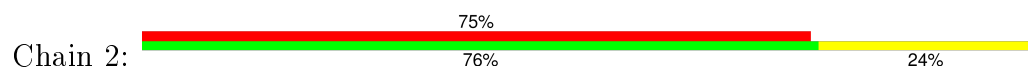
- Molecule 28: 50S ribosomal protein L37e



- Molecule 29: 50S ribosomal protein L39e



- Molecule 30: 50S ribosomal protein L44E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.85Å 298.00Å 574.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 49.90 – 2.72	Depositor EDS
% Data completeness (in resolution range)	92.9 (50.00-2.70) 90.9 (49.90-2.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.73Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.222 , 0.253 0.456 , 0.446	Depositor DCC
R_{free} test set	3128 reflections (0.71%)	DCC
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 454618 reflections	Xtriage
F_o, F_c correlation	0.58	EDS
Total number of atoms	90725	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CL, NA, K, EMK, CD, SR

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	0	0.41	0/66075	0.69	18/103050 (0.0%)
2	9	0.37	0/2905	0.72	2/4528 (0.0%)
3	A	0.36	0/1788	0.66	0/2409
4	B	0.39	0/2690	0.67	0/3652
5	C	0.39	0/1884	0.65	0/2551
6	D	0.32	0/1112	0.58	0/1498
7	E	0.35	0/1383	0.59	0/1880
8	F	0.37	0/897	0.58	0/1219
9	G	0.30	0/242	0.45	0/324
10	H	0.40	0/1247	0.74	1/1686 (0.1%)
11	I	0.38	0/1136	0.63	0/1530
12	J	0.39	0/1004	0.70	0/1351
13	K	0.39	0/1131	0.68	0/1509
14	L	0.39	0/1634	0.69	1/2180 (0.0%)
15	M	0.32	0/1474	0.61	0/1999
16	N	0.33	0/874	0.62	0/1181
17	O	0.37	0/1144	0.57	0/1521
18	P	0.38	0/749	0.72	0/1005
19	Q	0.36	0/1173	0.63	0/1578
20	R	0.36	0/649	0.58	0/875
21	S	0.35	0/958	0.65	0/1289
22	T	0.39	0/418	0.59	0/562
23	U	0.31	0/503	0.52	0/675
24	V	0.36	0/1219	0.65	0/1655
25	W	0.36	0/665	0.60	0/895
26	X	0.38	0/1147	0.66	0/1536
27	Y	0.40	0/576	0.71	0/763
28	Z	0.49	0/438	0.70	0/578
29	1	0.37	0/399	0.60	0/527
30	2	0.41	0/771	0.60	0/1024
All	All	0.40	0/98285	0.68	22/147030 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	75
2	9	1	2
24	V	0	1
All	All	1	78

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	9	3024	U	C2'-C3'-O3'	9.36	130.09	109.50
1	0	1559	A	C2'-C3'-O3'	8.36	127.88	109.50
1	0	2338	G	C2'-C3'-O3'	7.19	125.32	109.50
1	0	1120	U	C5'-C4'-C3'	-6.74	105.22	116.00
1	0	777	U	O4'-C1'-N1	6.46	113.37	108.20
1	0	1829	A	N9-C1'-C2'	-6.38	104.98	112.00
1	0	2316	G	O4'-C1'-N9	5.97	112.97	108.20
1	0	1504	A	N9-C1'-C2'	5.85	121.60	114.00
14	L	157	LEU	CB-CG-CD1	-5.60	101.49	111.00
1	0	2914	A	C2'-C3'-O3'	5.57	122.62	113.70
1	0	2313	C	C5'-C4'-O4'	5.56	115.77	109.10
1	0	2526	C	N1-C1'-C2'	5.33	120.94	114.00
1	0	2726	U	N1-C1'-C2'	5.32	120.92	114.00
1	0	1971	G	N9-C1'-C2'	5.32	120.92	114.00
1	0	2607	U	N1-C1'-C2'	5.20	120.77	114.00
1	0	2316	G	C5'-C4'-C3'	-5.20	107.69	116.00
2	9	3024	U	C4'-C3'-O3'	5.16	123.32	113.00
10	H	74	ASN	N-CA-C	-5.13	97.15	111.00
1	0	883	U	N1-C1'-C2'	5.10	120.63	114.00
1	0	2313	C	C5'-C4'-C3'	5.09	124.14	116.00
1	0	535	G	N9-C1'-C2'	5.09	120.61	114.00
1	0	2664	A	N9-C1'-C2'	5.04	120.55	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	9	3024	U	C3'

All (78) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1055	G	Sidechain
1	0	1078	A	Sidechain
1	0	1134	G	Sidechain
1	0	1310	U	Sidechain
1	0	1327	G	Sidechain
1	0	1342	C	Sidechain
1	0	1359	U	Sidechain
1	0	1368	U	Sidechain
1	0	1417	G	Sidechain
1	0	1435	U	Sidechain
1	0	1473	U	Sidechain
1	0	1647	G	Sidechain
1	0	1681	G	Sidechain
1	0	1696	U	Sidechain
1	0	1714	C	Sidechain
1	0	1771	U	Sidechain
1	0	1777	G	Sidechain
1	0	1809	G	Sidechain
1	0	182	G	Sidechain
1	0	1828	G	Sidechain
1	0	1829	A	Sidechain
1	0	1848	G	Sidechain
1	0	1863	G	Sidechain
1	0	1867	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1885	A	Sidechain
1	0	1979	G	Sidechain
1	0	2102	G	Sidechain
1	0	2103	A	Sidechain
1	0	216	A	Sidechain
1	0	2313	C	Sidechain
1	0	2316	G	Sidechain
1	0	2412	G	Sidechain
1	0	2426	G	Sidechain
1	0	2448	U	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2543	G	Sidechain
1	0	2607	U	Sidechain
1	0	2610	U	Sidechain

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Mol	Chain	Res	Type	Group
1	0	2630	G	Sidechain
1	0	2632	G	Sidechain
1	0	2679	G	Sidechain
1	0	2690	U	Sidechain
1	0	2710	U	Sidechain
1	0	2768	A	Sidechain
1	0	2793	A	Sidechain
1	0	2842	G	Sidechain
1	0	314	G	Sidechain
1	0	396	U	Sidechain
1	0	458	G	Sidechain
1	0	460	A	Sidechain
1	0	462	A	Sidechain
1	0	469	G	Sidechain
1	0	471	G	Sidechain
1	0	482	G	Sidechain
1	0	487	G	Sidechain
1	0	50	G	Sidechain
1	0	503	G	Sidechain
1	0	506	G	Sidechain
1	0	518	G	Sidechain
1	0	686	A	Sidechain
1	0	722	G	Sidechain
1	0	742	G	Sidechain
1	0	761	A	Sidechain
1	0	774	C	Sidechain
1	0	795	G	Sidechain
1	0	817	G	Sidechain
1	0	818	A	Sidechain
1	0	868	G	Sidechain
1	0	872	U	Sidechain
1	0	952	G	Sidechain
2	9	3090	G	Sidechain
2	9	3097	U	Sidechain
24	V	90	TYR	Sidechain

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	0	59016	0	29808	892	0
2	9	2600	0	1326	67	0
3	A	1755	0	1763	77	0
4	B	2625	0	2533	124	0
5	C	1859	0	1816	85	0
6	D	1095	0	1085	84	0
7	E	1358	0	1266	53	0
8	F	886	0	854	50	0
9	G	241	0	231	8	0
10	H	1216	0	1215	132	0
11	I	1120	0	1098	57	0
12	J	994	0	1027	37	0
13	K	1119	0	1076	57	0
14	L	1606	0	1676	123	0
15	M	1445	0	1401	69	0
16	N	865	0	873	23	0
17	O	1134	0	1127	42	0
18	P	735	0	729	17	0
19	Q	1150	0	1122	53	0
20	R	642	0	605	25	0
21	S	950	0	924	31	0
22	T	411	0	364	22	0
23	U	500	0	511	32	0
24	V	1196	0	1137	69	0
25	W	655	0	653	35	0
26	X	1131	0	1133	26	0
27	Y	564	0	598	46	0
28	Z	431	0	426	24	0
29	1	394	0	406	24	0
30	2	755	0	729	22	0
31	0	55	0	0	0	0
31	9	1	0	0	0	0
31	B	1	0	0	0	0
31	J	1	0	0	0	0
31	K	1	0	0	0	0
31	S	1	0	0	0	0
31	X	1	0	0	0	0
32	0	1	0	0	0	0
33	0	19	0	0	0	0
33	9	1	0	0	0	0
33	C	1	0	0	0	0
33	I	1	0	0	0	0
33	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	P	1	0	0	0	0
33	Q	2	0	0	0	0
34	0	5	0	0	0	0
34	A	1	0	0	0	0
34	D	1	0	0	0	0
34	I	2	0	0	0	0
34	L	1	0	0	1	0
34	N	1	0	0	0	0
34	Q	1	0	0	0	0
34	X	1	0	0	0	0
35	0	82	0	0	0	0
35	2	2	0	0	0	0
35	9	3	0	0	0	0
35	A	4	0	0	0	0
35	B	2	0	0	0	0
35	F	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	Z	2	0	0	0	0
36	0	74	0	88	30	0
37	2	1	0	0	0	0
37	T	1	0	0	0	0
37	Y	1	0	0	0	0
37	Z	1	0	0	0	0
All	All	90725	0	59600	2169	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 14.

All (2169) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:0:8163:EMK:C15	36:0:8163:EMK:C14	1.75	1.63
36:0:8163:EMK:C20	36:0:8163:EMK:C12	1.76	1.58
36:0:8163:EMK:C13	36:0:8163:EMK:C14	1.78	1.58
36:0:8163:EMK:C8	36:0:8163:EMK:C9	1.75	1.57
36:0:8163:EMK:N9	36:0:8163:EMK:C12	1.71	1.49
36:0:8163:EMK:C26	36:0:8163:EMK:O76	1.63	1.47
36:0:8163:EMK:O78	36:0:8163:EMK:C10	1.66	1.42
1:0:1160:G:H5'	1:0:1161:A:H5'	1.28	1.14
2:9:3023:U:H3'	2:9:3024:U:H5''	1.20	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3056:A:H2'	2:9:3057:A:H5''	1.35	1.06
4:B:212:GLN:HB2	4:B:257:THR:HG21	1.40	1.03
3:A:153:ARG:HH11	3:A:153:ARG:HB2	1.24	1.02
12:J:29:LEU:HB3	12:J:55:VAL:HG11	1.36	1.02
1:0:1451:C:H5'	1:0:1505:U:H3	1.17	1.02
10:H:27:LYS:H	10:H:58:HIS:HD2	1.03	1.02
1:0:1242:A:H5'	11:I:82:THR:HG23	1.39	1.01
10:H:55:GLN:NE2	10:H:124:ARG:HE	1.59	1.01
36:0:8163:EMK:C9	36:0:8163:EMK:C7	2.39	1.00
1:0:156:C:H5''	14:L:171:ARG:HD3	1.45	0.99
10:H:86:ARG:NH1	10:H:133:ILE:HG13	1.79	0.98
1:0:1666:C:C2'	1:0:1667:A:H5''	1.95	0.97
2:9:3076:G:H3'	2:9:3077:A:H5''	1.47	0.96
28:Z:25:LYS:HD2	29:1:49:GLU:H	1.30	0.96
5:C:236:THR:HG22	5:C:239:ALA:H	1.27	0.96
20:R:51:GLN:HE21	20:R:53:ASN:HD21	1.07	0.95
4:B:162:MET:HE2	4:B:310:ARG:HD3	1.47	0.94
19:Q:99:ALA:HB1	19:Q:109:MET:HE1	1.48	0.93
12:J:10:GLN:H	12:J:10:GLN:HE21	0.98	0.93
1:0:2812:A:H2	1:0:2814:A:H62	1.18	0.92
15:M:184:ILE:HG22	15:M:185:GLU:H	1.34	0.92
24:V:137:GLN:HE21	24:V:141:HIS:HE1	1.14	0.91
7:E:20:ILE:HD11	7:E:40:VAL:HG11	1.50	0.91
12:J:10:GLN:NE2	12:J:10:GLN:H	1.68	0.90
19:Q:39:THR:HG22	19:Q:42:GLU:H	1.36	0.90
10:H:55:GLN:HE21	10:H:124:ARG:HE	1.13	0.90
10:H:86:ARG:HH11	10:H:133:ILE:HG13	1.33	0.90
14:L:107:ARG:HG3	14:L:107:ARG:HH11	1.34	0.90
10:H:47:GLU:HB3	10:H:133:ILE:HD13	1.54	0.90
10:H:14:TYR:H	10:H:91:HIS:CE1	1.89	0.90
23:U:12:THR:HB	23:U:15:GLU:HG3	1.53	0.90
1:0:288:A:H61	1:0:364:C:H42	1.21	0.89
17:O:59:ARG:NH2	17:O:66:GLN:HE22	1.70	0.89
27:Y:38:LYS:HE3	27:Y:45:LYS:HE2	1.54	0.89
24:V:4:LEU:HD13	24:V:52:VAL:HG21	1.52	0.89
1:0:1666:C:H2'	1:0:1667:A:H5''	1.51	0.89
2:9:3025:G:H3'	2:9:3026:C:H5'	1.55	0.88
2:9:3023:U:C3'	2:9:3024:U:H5''	2.03	0.88
25:W:37:LEU:HD13	25:W:85:VAL:HG11	1.56	0.88
3:A:199:HIS:HD2	3:A:201:PHE:H	1.16	0.88
10:H:13:ALA:HA	10:H:91:HIS:HE1	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:36:PRO:HA	4:B:168:GLY:HA3	1.58	0.86
6:D:28:GLY:HA2	6:D:69:ILE:HG23	1.57	0.86
1:0:289:G:H22	1:0:363:A:H2	1.22	0.86
8:F:63:ILE:HB	8:F:64:PRO:HD3	1.57	0.86
1:0:1119:G:H2'	11:I:52:GLN:NE2	1.91	0.86
17:O:59:ARG:HH22	17:O:66:GLN:HE22	1.24	0.85
10:H:139:ASP:N	10:H:140:PRO:HD3	1.91	0.85
14:L:102:GLU:OE1	14:L:164:THR:HG21	1.76	0.85
30:2:60:LYS:HG3	30:2:61:PRO:HD2	1.59	0.85
7:E:15:GLN:HE21	7:E:20:ILE:HG12	1.41	0.84
14:L:87:MET:HB3	30:2:46:ILE:HD13	1.58	0.84
5:C:1:MET:HG2	5:C:2:GLN:H	1.41	0.84
1:0:2506:A:O2'	1:0:2507:G:H8	1.59	0.84
2:9:3056:A:C2'	2:9:3057:A:H5''	2.08	0.84
1:0:1451:C:H5'	1:0:1505:U:N3	1.93	0.84
1:0:2502:C:H4'	10:H:151:MET:HG3	1.60	0.83
1:0:2506:A:HO2'	1:0:2507:G:H8	0.84	0.83
29:1:41:HIS:H	29:1:45:ASN:HD22	1.24	0.83
1:0:558:C:C2'	1:0:559:U:H5''	2.09	0.83
19:Q:18:LEU:HB2	19:Q:143:VAL:HG12	1.61	0.83
10:H:36:ASN:HA	10:H:82:LYS:NZ	1.93	0.83
1:0:1701:A:H4'	1:0:1702:U:H5''	1.57	0.83
5:C:162:VAL:HG12	5:C:192:ILE:HD11	1.59	0.83
24:V:88:THR:HG22	24:V:90:TYR:HD1	1.42	0.83
24:V:21:LEU:HD21	24:V:48:VAL:HG11	1.60	0.82
12:J:98:VAL:CG1	12:J:102:GLU:HA	2.08	0.82
12:J:10:GLN:N	12:J:10:GLN:HE21	1.76	0.82
1:0:1160:G:H5'	1:0:1161:A:C5'	2.09	0.82
26:X:235:GLU:CD	26:X:235:GLU:H	1.82	0.82
3:A:199:HIS:CD2	3:A:201:PHE:H	1.96	0.81
19:Q:8:ALA:HB1	19:Q:13:THR:HG21	1.62	0.81
1:0:2003:U:H4'	1:0:2004:U:H5	1.46	0.81
1:0:282:C:O2'	1:0:283:U:H4'	1.80	0.81
14:L:106:ASN:ND2	34:L:202:CL:CL	2.51	0.81
1:0:545:G:H8	1:0:545:G:H5'	1.45	0.81
10:H:86:ARG:HH11	10:H:133:ILE:CG1	1.93	0.81
1:0:2586:U:H3	1:0:2592:G:H22	1.24	0.81
1:0:182:G:H4'	14:L:157:LEU:HD13	1.62	0.81
1:0:1116:U:HO2'	1:0:1118:A:H2	0.84	0.81
23:U:56:ILE:O	23:U:60:GLN:HG3	1.80	0.80
27:Y:29:VAL:O	27:Y:33:HIS:HB2	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:134:LEU:HD11	6:D:166:ILE:HD11	1.62	0.80
15:M:94:GLU:HG3	15:M:186:LEU:O	1.82	0.80
26:X:187:VAL:HG12	26:X:205:ILE:HA	1.64	0.80
13:K:73:VAL:HG23	13:K:74:THR:H	1.46	0.80
27:Y:38:LYS:HE3	27:Y:45:LYS:CE	2.11	0.80
10:H:26:LYS:HD2	10:H:28:ILE:HD12	1.62	0.80
1:O:1002:G:H2'	1:O:1003:U:H5''	1.62	0.80
4:B:217:ARG:HG3	4:B:257:THR:HB	1.64	0.79
1:O:1119:G:H2'	11:I:52:GLN:HE22	1.47	0.79
1:O:949:U:H4'	18:P:95:GLU:HA	1.62	0.79
10:H:27:LYS:H	10:H:58:HIS:CD2	1.96	0.79
10:H:26:LYS:HG2	10:H:28:ILE:H	1.47	0.79
1:O:1160:G:C5'	1:O:1161:A:H5'	2.10	0.79
1:O:2271:G:H5'	3:A:223:ARG:HH21	1.48	0.79
10:H:29:ALA:HB3	10:H:65:ARG:HH12	1.48	0.79
3:A:153:ARG:CB	3:A:153:ARG:HH11	1.96	0.79
1:O:877:G:H5'	1:O:878:G:OP1	1.81	0.79
2:9:3025:G:H3'	2:9:3026:C:C5'	2.11	0.79
26:X:189:ASN:HA	26:X:217:ILE:HD11	1.65	0.79
1:O:1603:A:H5'	1:O:1605:G:O4'	1.83	0.78
19:Q:99:ALA:HB1	19:Q:109:MET:CE	2.13	0.78
1:O:1119:G:N2	1:O:1246:A:C2	2.52	0.78
1:O:111:C:O2'	28:Z:20:ARG:HG2	1.84	0.78
10:H:13:ALA:HA	10:H:91:HIS:CE1	2.18	0.78
1:O:2661:U:H3	1:O:2812:A:H62	1.31	0.78
8:F:13:GLU:OE2	8:F:78:GLU:HG2	1.83	0.78
1:O:1118:A:H3'	1:O:1118:A:C8	2.18	0.78
1:O:2005:G:H3'	1:O:2005:G:OP2	1.83	0.78
17:O:115:SER:H	17:O:118:GLN:NE2	1.81	0.77
1:O:1118:A:H3'	1:O:1118:A:H8	1.47	0.77
4:B:125:GLU:O	4:B:129:ARG:HG3	1.83	0.77
1:O:1209:C:H2'	1:O:1210:G:H8	1.50	0.77
6:D:135:VAL:HG21	6:D:139:TYR:CD1	2.20	0.76
1:O:560:C:H42	1:O:597:A:H61	1.31	0.76
36:O:8163:EMK:C9	36:O:8163:EMK:C12	2.63	0.76
10:H:137:ASN:O	10:H:139:ASP:N	2.17	0.76
19:Q:18:LEU:HB2	19:Q:143:VAL:CG1	2.15	0.76
22:T:14:GLU:O	22:T:17:THR:HB	1.84	0.76
10:H:56:ILE:HG21	10:H:61:LEU:HD13	1.68	0.76
10:H:53:PRO:HG3	10:H:127:GLY:H	1.51	0.76
1:O:2533:C:H5'	1:O:2533:C:H6	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:2:25:VAL:HG22	30:2:68:LYS:HG3	1.67	0.76
1:0:1835:U:H5	1:0:1840:A:N7	1.84	0.76
14:L:35:PRO:HD2	14:L:38:VAL:HG21	1.68	0.75
4:B:265:LEU:HD21	4:B:316:ARG:HD3	1.66	0.75
1:0:861:A:H4'	1:0:1697:G:H4'	1.68	0.75
7:E:116:THR:HG22	7:E:151:LEU:HD22	1.68	0.75
12:J:28:GLU:HB3	12:J:59:LYS:HB2	1.67	0.75
24:V:6:GLN:HB2	24:V:26:ILE:HD12	1.69	0.75
1:0:1669:A:H2'	1:0:1670:G:C8	2.21	0.75
2:9:3023:U:H3'	2:9:3024:U:C5'	2.11	0.75
14:L:37:VAL:HG13	14:L:63:VAL:HG11	1.68	0.75
29:1:36:ASN:H	29:1:39:ARG:HH21	1.35	0.75
3:A:109:GLU:HG2	3:A:116:GLY:H	1.52	0.75
6:D:19:GLU:O	6:D:20:LYS:HB3	1.86	0.74
24:V:149:LEU:HG	24:V:153:MET:HE2	1.67	0.74
3:A:88:ILE:HD13	3:A:100:PRO:HD3	1.68	0.74
5:C:47:GLY:HA2	5:C:92:PRO:HB2	1.69	0.74
14:L:99:ARG:HD2	14:L:167:GLY:HA2	1.67	0.74
12:J:74:VAL:HG11	12:J:113:ILE:HG12	1.70	0.73
24:V:21:LEU:HD22	24:V:26:ILE:HD11	1.68	0.73
17:O:91:LYS:O	17:O:95:GLU:HG3	1.88	0.73
10:H:82:LYS:HB2	10:H:135:TRP:HB2	1.70	0.73
4:B:51:VAL:CG1	4:B:53:LEU:HD13	2.18	0.73
15:M:71:TRP:CE3	15:M:175:LEU:HD22	2.24	0.73
1:0:1666:C:O2'	1:0:1667:A:H5''	1.87	0.73
1:0:282:C:H1'	1:0:368:C:N4	2.03	0.73
27:Y:37:HIS:HB2	27:Y:47:LEU:HB2	1.70	0.73
15:M:184:ILE:HG22	15:M:185:GLU:N	2.03	0.72
14:L:87:MET:HG2	30:2:46:ILE:HG21	1.71	0.72
10:H:55:GLN:HE21	10:H:124:ARG:NE	1.87	0.72
1:0:2635:A:O2'	1:0:2636:C:H5'	1.88	0.72
10:H:47:GLU:HB3	10:H:133:ILE:CD1	2.19	0.72
1:0:1666:C:H2'	1:0:1667:A:C5'	2.18	0.72
2:9:3029:C:H2'	2:9:3030:C:H5'	1.72	0.72
1:0:289:G:N2	1:0:363:A:H2	1.86	0.72
1:0:2468:A:H61	30:2:48:ASN:HD21	1.38	0.72
1:0:559:U:H5'	1:0:559:U:H6	1.54	0.71
22:T:45:GLU:HB2	22:T:48:ASN:ND2	2.05	0.71
19:Q:18:LEU:HD12	19:Q:143:VAL:HG11	1.71	0.71
1:0:2769:C:O2'	1:0:2770:G:H5'	1.88	0.71
15:M:169:PRO:O	15:M:172:PHE:HB3	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:32:ARG:HE	16:N:35:LYS:HD2	1.54	0.71
9:G:12:ILE:N	9:G:13:PRO:HD3	2.05	0.71
1:0:2721:U:H4'	12:J:87:ARG:HG3	1.71	0.71
15:M:48:VAL:CG1	15:M:55:ASP:HB3	2.21	0.71
8:F:37:THR:O	8:F:41:GLU:HG3	1.90	0.71
12:J:32:ILE:HD11	12:J:56:SER:HB3	1.72	0.71
1:0:1116:U:O2'	1:0:1118:A:H2	1.66	0.71
1:0:1877:G:OP1	3:A:164:ARG:NH2	2.22	0.71
25:W:78:GLU:HG2	25:W:79:GLU:H	1.56	0.71
3:A:153:ARG:NH1	3:A:153:ARG:HB2	2.02	0.71
24:V:88:THR:HG23	24:V:110:GLN:NE2	2.06	0.71
14:L:172:GLY:O	14:L:183:VAL:HG11	1.88	0.71
6:D:25:MET:HE1	6:D:37:ALA:HB1	1.73	0.71
13:K:53:ARG:NH2	13:K:57:VAL:HG12	2.06	0.71
10:H:49:VAL:O	10:H:157:ILE:HG23	1.90	0.71
4:B:154:VAL:HG12	4:B:156:LYS:HG2	1.72	0.71
15:M:110:THR:HB	15:M:113:SER:OG	1.91	0.71
2:9:3014:G:H8	2:9:3014:G:H5'	1.54	0.71
10:H:33:MET:HB2	10:H:83:PHE:HB3	1.72	0.70
1:0:2716:G:H5''	4:B:206:THR:HG21	1.72	0.70
1:0:396:U:O2'	1:0:418:C:H4'	1.90	0.70
1:0:1204:C:H3'	1:0:1205:U:H5''	1.74	0.70
1:0:2840:A:OP1	4:B:211:THR:HG23	1.90	0.70
24:V:137:GLN:HE21	24:V:141:HIS:CE1	2.03	0.70
26:X:186:ARG:HG2	26:X:186:ARG:HH11	1.57	0.70
3:A:86:ALA:HB3	3:A:94:LEU:HD22	1.72	0.70
6:D:25:MET:HE2	6:D:41:LEU:HG	1.72	0.70
1:0:2420:G:O2'	1:0:2421:G:H5'	1.91	0.70
25:W:15:ARG:HH11	25:W:15:ARG:HB3	1.55	0.70
36:0:8163:EMK:C10	36:0:8163:EMK:C30	2.70	0.70
1:0:558:C:H2'	1:0:559:U:H5''	1.72	0.70
21:S:50:VAL:HG12	21:S:56:ALA:HA	1.73	0.70
6:D:170:TYR:O	6:D:171:ASP:HB3	1.91	0.70
1:0:470:U:O2'	28:Z:16:HIS:HD2	1.75	0.70
1:0:1377:C:H6	1:0:1377:C:H5'	1.57	0.70
14:L:80:GLY:O	14:L:81:ARG:HD2	1.91	0.69
10:H:48:LEU:HG	10:H:157:ILE:HG21	1.73	0.69
1:0:2372:A:H2'	1:0:2373:U:C6	2.27	0.69
1:0:657:G:OP1	5:C:27:ARG:NH2	2.24	0.69
4:B:212:GLN:CB	4:B:257:THR:HG21	2.19	0.69
4:B:162:MET:CE	4:B:310:ARG:HD3	2.19	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:52:VAL:HG22	24:V:53:ALA:N	2.08	0.69
14:L:139:PRO:C	14:L:141:ILE:H	1.96	0.69
4:B:18:ARG:HG3	4:B:256:GLN:HG3	1.74	0.69
1:O:2578:G:H5'	1:O:2578:G:H8	1.58	0.69
1:O:2780:C:H1'	7:E:143:GLN:HE21	1.57	0.69
12:J:4:LEU:HD22	12:J:116:GLU:HB3	1.74	0.69
25:W:65:ASN:O	25:W:66:THR:HB	1.92	0.69
4:B:109:LEU:HG	4:B:113:LEU:HD11	1.75	0.69
19:Q:18:LEU:HG	19:Q:91:LEU:HD13	1.75	0.69
17:O:80:ARG:HG2	17:O:87:ARG:CZ	2.23	0.69
12:J:29:LEU:HB3	12:J:55:VAL:CG1	2.18	0.69
14:L:139:PRO:O	14:L:140:ALA:HB3	1.91	0.69
27:Y:26:VAL:O	27:Y:30:GLU:HB2	1.92	0.68
1:O:1180:U:H2'	1:O:1181:A:C8	2.27	0.68
1:O:1462:C:H2'	1:O:1463:A:C8	2.28	0.68
20:R:33:SER:O	20:R:37:VAL:HG23	1.93	0.68
26:X:146:PRO:O	26:X:154:ARG:HG3	1.93	0.68
1:O:289:G:H1	1:O:363:A:H2	1.40	0.68
1:O:500:G:H21	19:Q:98:ASN:HD21	1.41	0.68
14:L:87:MET:HB2	14:L:91:ILE:HD11	1.76	0.68
11:I:107:ASN:ND2	11:I:109:TYR:H	1.91	0.68
7:E:23:GLU:HG2	7:E:28:SER:HB2	1.75	0.68
8:F:22:VAL:HG23	8:F:104:ALA:HB2	1.76	0.68
27:Y:38:LYS:HA	27:Y:45:LYS:HA	1.76	0.68
14:L:72:SER:HB2	14:L:93:ARG:HG2	1.75	0.68
30:2:11:CYS:HB2	30:2:20:HIS:CE1	2.29	0.68
10:H:36:ASN:HA	10:H:82:LYS:HZ3	1.56	0.68
1:O:1751:G:H2'	1:O:1752:G:H5''	1.76	0.68
10:H:136:VAL:HG22	10:H:137:ASN:N	2.09	0.68
15:M:90:LEU:HB3	15:M:186:LEU:HD11	1.75	0.68
1:O:2054:A:N3	19:Q:128:ARG:NH2	2.40	0.68
36:0:8163:EMK:C14	36:0:8163:EMK:O73	2.41	0.68
2:9:3006:C:H5''	15:M:37:ARG:NH1	2.09	0.68
1:O:544:G:H2'	1:O:545:G:H5''	1.76	0.67
1:O:1209:C:H2'	1:O:1210:G:C8	2.29	0.67
1:O:1641:A:H2'	1:O:1642:A:H5'	1.77	0.67
36:0:8163:EMK:C14	36:0:8163:EMK:C12	2.71	0.67
10:H:27:LYS:N	10:H:58:HIS:HD2	1.85	0.67
1:O:259:G:H21	14:L:58:GLN:HE22	1.41	0.67
11:I:131:THR:HB	11:I:134:GLU:OE1	1.94	0.67
10:H:30:GLN:H	10:H:65:ARG:NH1	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:450:C:OP1	5:C:184:ARG:NH2	2.25	0.67
2:9:3024:U:O2'	2:9:3025:G:H4'	1.95	0.67
10:H:162:SER:HB2	10:H:163:PRO:HD3	1.76	0.67
1:0:1947:G:H2'	1:0:1948:G:H8	1.58	0.67
1:0:2748:G:OP1	1:0:2749:U:H5''	1.95	0.67
4:B:275:GLY:O	4:B:291:ASP:HA	1.94	0.67
1:0:1118:A:H8	1:0:1119:G:H5''	1.58	0.67
7:E:3:VAL:HG22	7:E:49:ILE:HB	1.76	0.67
11:I:39:VAL:HG13	11:I:106:GLY:O	1.95	0.66
28:Z:28:HIS:CD2	28:Z:31:LYS:HG3	2.30	0.66
1:0:2539:U:C4	36:0:8163:EMK:H84	2.30	0.66
1:0:2502:C:C2'	1:0:2503:A:H5'	2.25	0.66
3:A:109:GLU:HG2	3:A:116:GLY:N	2.11	0.66
24:V:4:LEU:CD1	24:V:52:VAL:HG21	2.23	0.66
1:0:558:C:O2'	1:0:559:U:H5''	1.94	0.66
25:W:9:VAL:HG22	25:W:88:GLU:OE2	1.95	0.66
36:0:8163:EMK:C15	36:0:8163:EMK:C13	2.73	0.66
1:0:2769:C:H2'	1:0:2770:G:O4'	1.95	0.66
4:B:279:THR:HG23	4:B:290:VAL:H	1.60	0.66
2:9:3028:U:H2'	2:9:3029:C:C6	2.31	0.66
2:9:3092:G:H22	10:H:52:LYS:HE2	1.59	0.66
36:0:8163:EMK:C12	36:0:8163:EMK:C38	2.73	0.66
19:Q:106:GLY:HA2	19:Q:109:MET:HE3	1.77	0.66
14:L:37:VAL:CG1	14:L:63:VAL:HG11	2.24	0.66
10:H:46:VAL:HG12	10:H:146:TRP:HZ3	1.61	0.66
14:L:187:LEU:CD2	14:L:194:ALA:HB3	2.25	0.66
13:K:119:THR:HG23	13:K:139:SER:OG	1.95	0.66
23:U:39:ALA:H	23:U:40:PRO:HD2	1.60	0.66
1:0:1701:A:H5''	1:0:1702:U:H3'	1.77	0.66
1:0:544:G:C2'	1:0:545:G:H5''	2.25	0.66
23:U:56:ILE:HG22	23:U:60:GLN:HE21	1.59	0.66
4:B:18:ARG:HE	4:B:256:GLN:NE2	1.94	0.66
1:0:1218:U:H2'	1:0:1219:U:C6	2.30	0.66
8:F:58:GLU:HB3	14:L:8:ILE:HG23	1.76	0.66
11:I:131:THR:HG22	11:I:134:GLU:H	1.60	0.66
10:H:47:GLU:CB	10:H:133:ILE:HD13	2.25	0.66
10:H:147:ARG:O	10:H:151:MET:HG2	1.95	0.66
1:0:1669:A:H2'	1:0:1670:G:H8	1.60	0.66
8:F:58:GLU:HA	8:F:61:MET:HE2	1.78	0.66
36:0:8163:EMK:C13	36:0:8163:EMK:C20	2.73	0.65
1:0:1003:U:HO2'	10:H:90:PHE:HE1	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:289:G:N1	1:0:363:A:C2	2.63	0.65
4:B:179:LEU:O	4:B:183:GLU:HG2	1.97	0.65
6:D:25:MET:HG3	6:D:41:LEU:HD11	1.76	0.65
11:I:75:PRO:HG2	11:I:105:LEU:HD21	1.78	0.65
2:9:3025:G:C3'	2:9:3026:C:H5'	2.27	0.65
29:1:36:ASN:HB3	29:1:39:ARG:HE	1.61	0.65
12:J:14:LYS:HB2	12:J:45:PRO:HG2	1.79	0.65
2:9:3002:U:OP2	2:9:3003:A:H5'	1.95	0.65
12:J:74:VAL:CG1	12:J:113:ILE:HG12	2.27	0.65
4:B:53:LEU:HD11	4:B:327:VAL:HG22	1.79	0.65
11:I:107:ASN:HD21	11:I:109:TYR:HB2	1.61	0.65
20:R:57:THR:HG22	20:R:58:MET:N	2.11	0.65
3:A:36:ASP:CG	3:A:37:VAL:N	2.48	0.65
36:0:8163:EMK:C9	36:0:8163:EMK:H7	2.26	0.65
5:C:1:MET:HG2	5:C:2:GLN:N	2.11	0.65
1:0:485:A:N3	1:0:487:G:H5''	2.11	0.65
1:0:2908:A:C2'	1:0:2909:G:H5'	2.26	0.65
10:H:57:ARG:HB3	10:H:59:ASN:HD22	1.62	0.65
19:Q:39:THR:HG23	19:Q:107:GLU:O	1.97	0.65
24:V:21:LEU:HD21	24:V:48:VAL:CG1	2.26	0.65
1:0:183:A:H5'	14:L:157:LEU:HD12	1.78	0.65
1:0:926:A:O2'	13:K:41:HIS:HD2	1.80	0.65
25:W:74:ALA:HB2	25:W:85:VAL:HG12	1.78	0.65
16:N:32:ARG:HH21	16:N:35:LYS:NZ	1.94	0.65
5:C:127:ARG:HD2	5:C:229:PRO:O	1.97	0.65
6:D:91:ALA:HB2	6:D:106:PHE:CD2	2.32	0.65
1:0:553:G:P	26:X:204:ARG:HH22	2.20	0.65
4:B:58:PRO:HA	4:B:63:GLU:OE1	1.96	0.65
16:N:47:ARG:HH11	16:N:47:ARG:HG3	1.62	0.65
11:I:107:ASN:HD22	11:I:107:ASN:C	2.00	0.65
25:W:30:MET:HE1	25:W:58:ALA:HB3	1.79	0.64
29:1:23:ALA:HA	29:1:26:MET:CE	2.28	0.64
14:L:87:MET:HB3	30:2:46:ILE:HG21	1.79	0.64
10:H:71:TYR:C	10:H:73:GLN:H	2.01	0.64
24:V:88:THR:HG22	24:V:89:ASP:N	2.11	0.64
10:H:45:GLN:H	10:H:163:PRO:HD2	1.62	0.64
14:L:35:PRO:HD2	14:L:38:VAL:CG2	2.27	0.64
1:0:1204:C:C3'	1:0:1205:U:H5''	2.28	0.64
1:0:2515:C:H2'	1:0:2516:G:O4'	1.96	0.64
15:M:132:ASN:O	15:M:135:VAL:HG12	1.98	0.64
2:9:3049:G:O2'	2:9:3050:G:H5'	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:99:ASP:HB3	6:D:103:ASN:HB2	1.78	0.64
30:2:48:ASN:ND2	30:2:50:GLY:H	1.95	0.64
1:0:1185:U:H2'	1:0:1186:C:C6	2.32	0.64
24:V:119:HIS:HD2	24:V:120:PRO:O	1.79	0.64
26:X:187:VAL:HG22	26:X:192:ASP:HB2	1.80	0.64
14:L:184:ARG:HG3	14:L:185:PRO:HA	1.79	0.64
15:M:12:ARG:HD3	15:M:18:THR:OG1	1.98	0.64
5:C:76:ARG:HB3	5:C:76:ARG:HH11	1.63	0.64
36:0:8163:EMK:C26	36:0:8163:EMK:C35	2.75	0.64
10:H:62:GLU:O	10:H:66:VAL:HG23	1.97	0.64
3:A:33:GLU:CD	3:A:33:GLU:H	2.00	0.64
3:A:72:GLU:HG3	27:Y:66:GLY:HA2	1.79	0.64
10:H:69:ASN:O	10:H:72:VAL:HG12	1.98	0.63
14:L:99:ARG:CD	14:L:167:GLY:HA2	2.29	0.63
14:L:60:ILE:C	14:L:61:ILE:HD12	2.17	0.63
21:S:112:LEU:HD23	21:S:119:ALA:HB3	1.80	0.63
24:V:21:LEU:HD22	24:V:26:ILE:CD1	2.28	0.63
1:0:2414:A:H2'	1:0:2415:A:C8	2.33	0.63
15:M:164:ASP:OD2	15:M:167:ASP:HA	1.97	0.63
1:0:2289:G:O2'	1:0:2290:U:H5'	1.98	0.63
1:0:734:U:H2'	1:0:736:A:OP2	1.99	0.63
3:A:94:LEU:HG	3:A:99:ILE:HD11	1.80	0.63
1:0:506:G:H22	1:0:509:A:H5'	1.62	0.63
5:C:127:ARG:NH2	5:C:225:PRO:HB2	2.14	0.63
7:E:5:LEU:HD21	7:E:66:GLN:HG3	1.80	0.63
13:K:143:THR:HG22	13:K:144:ASP:N	2.12	0.63
3:A:192:VAL:HG13	3:A:207:GLN:HB3	1.79	0.63
19:Q:18:LEU:HD12	19:Q:143:VAL:CG1	2.29	0.63
1:0:1098:A:H2'	1:0:1099:G:O4'	1.99	0.63
1:0:475:G:H5'	5:C:73:LEU:HD23	1.81	0.63
28:Z:21:ARG:HD2	28:Z:39:PHE:HB2	1.81	0.63
8:F:53:ASP:OD1	8:F:80:GLN:HB2	1.98	0.63
15:M:90:LEU:CB	15:M:186:LEU:HD11	2.29	0.63
6:D:62:ASP:C	6:D:64:ARG:H	2.01	0.63
10:H:36:ASN:HA	10:H:82:LYS:HZ2	1.62	0.63
5:C:214:THR:HG23	5:C:217:GLU:HG2	1.80	0.63
14:L:71:SER:O	14:L:73:ARG:NH1	2.30	0.63
1:0:2320:U:H4'	1:0:2321:A:O4'	1.99	0.62
4:B:85:ARG:HB2	4:B:99:GLU:HG2	1.79	0.62
14:L:87:MET:CB	30:2:46:ILE:HG21	2.30	0.62
14:L:186:SER:O	14:L:189:VAL:HG12	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:103:THR:HG22	26:X:104:GLU:OE2	1.99	0.62
1:0:156:C:H5''	14:L:171:ARG:CD	2.26	0.62
14:L:107:ARG:HG3	14:L:107:ARG:NH1	2.05	0.62
1:0:1947:G:H2'	1:0:1948:G:C8	2.33	0.62
7:E:107:PHE:O	7:E:110:GLU:HG3	1.98	0.62
1:0:1864:C:OP1	14:L:75:THR:HG23	2.00	0.62
1:0:1242:A:H5'	11:I:82:THR:CG2	2.23	0.62
6:D:165:PHE:HD2	6:D:166:ILE:HD12	1.64	0.62
17:O:115:SER:H	17:O:118:GLN:HE21	1.45	0.62
1:0:259:G:H21	14:L:58:GLN:NE2	1.97	0.62
1:0:2615:U:OP1	4:B:230:GLN:NE2	2.32	0.62
14:L:39:ARG:HA	14:L:63:VAL:HG22	1.80	0.62
1:0:645:U:OP2	13:K:4:LYS:HE2	1.98	0.62
25:W:74:ALA:CB	25:W:85:VAL:HG12	2.29	0.62
6:D:51:ARG:HH11	6:D:68:PRO:HG2	1.65	0.62
1:0:2502:C:H2'	1:0:2503:A:H5'	1.81	0.62
14:L:114:VAL:HB	14:L:159:THR:CG2	2.29	0.62
6:D:146:LYS:NZ	15:M:107:ASN:HD21	1.98	0.62
1:0:1118:A:C8	1:0:1119:G:H5''	2.34	0.62
1:0:2908:A:H2'	1:0:2909:G:O4'	2.00	0.62
1:0:2265:U:H2'	1:0:2266:A:C8	2.35	0.62
1:0:960:G:H2'	1:0:960:G:N3	2.15	0.62
1:0:1118:A:H62	1:0:1244:U:H3	1.46	0.62
1:0:1701:A:H4'	1:0:1702:U:C5'	2.27	0.62
1:0:506:G:H22	1:0:509:A:C5'	2.11	0.62
8:F:91:VAL:HG12	8:F:92:GLY:N	2.15	0.61
17:O:9:LEU:O	17:O:13:VAL:HG12	2.00	0.61
36:0:8163:EMK:C19	36:0:8163:EMK:C9	2.73	0.61
27:Y:38:LYS:HE3	27:Y:45:LYS:NZ	2.15	0.61
1:0:545:G:C8	1:0:545:G:H5'	2.32	0.61
4:B:62:ARG:HA	4:B:65:MET:CE	2.30	0.61
12:J:82:ARG:NH2	12:J:115:ARG:HG2	2.15	0.61
1:0:2896:A:N3	1:0:2896:A:H2'	2.16	0.61
1:0:1789:G:O6	17:O:73:HIS:HE1	1.83	0.61
16:N:39:THR:O	16:N:115:ARG:NH2	2.34	0.61
1:0:1299:G:O6	13:K:6:ARG:HD3	2.01	0.61
5:C:168:ARG:NH2	5:C:190:ALA:O	2.33	0.61
1:0:635:A:H2'	1:0:636:G:H5''	1.81	0.61
14:L:63:VAL:HG21	14:L:109:PHE:CE1	2.35	0.61
24:V:149:LEU:HG	24:V:153:MET:CE	2.30	0.61
1:0:1120:U:H5'	1:0:1121:G:OP2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:115:LEU:HD21	5:C:243:VAL:HG13	1.81	0.61
11:I:75:PRO:HD3	11:I:136:SER:OG	2.00	0.61
24:V:72:PRO:HG2	24:V:77:ALA:HB3	1.82	0.61
11:I:18:ILE:HG22	11:I:21:ARG:H	1.65	0.61
24:V:4:LEU:HB3	24:V:33:THR:HG22	1.83	0.61
14:L:87:MET:CB	30:2:46:ILE:HD13	2.30	0.61
27:Y:42:CYS:SG	27:Y:43:GLY:N	2.74	0.61
2:9:3039:U:H3'	2:9:3040:C:H5''	1.82	0.61
1:0:1687:C:O2	28:Z:9:GLY:HA2	2.01	0.61
15:M:22:GLN:HA	15:M:25:ARG:HH21	1.66	0.61
19:Q:82:GLU:OE1	19:Q:86:LYS:HE3	2.01	0.61
21:S:89:ARG:HG3	21:S:89:ARG:O	1.99	0.61
4:B:66:GLU:OE1	4:B:328:ARG:HD2	2.00	0.61
10:H:131:ILE:HG23	10:H:132:PHE:CD1	2.35	0.61
23:U:64:GLY:O	23:U:65:ASP:HB2	1.99	0.61
1:0:1766:U:O2	1:0:1778:A:H5'	2.01	0.61
7:E:34:TRP:O	11:I:127:ILE:HD11	2.00	0.61
28:Z:36:SER:O	28:Z:46:ARG:HD3	2.01	0.60
6:D:25:MET:CE	6:D:37:ALA:HB1	2.29	0.60
1:0:2615:U:OP1	4:B:230:GLN:CD	2.39	0.60
25:W:15:ARG:NH1	25:W:15:ARG:HB3	2.16	0.60
1:0:256:C:H2'	1:0:257:G:O4'	2.01	0.60
1:0:431:G:P	14:L:48:ARG:HH12	2.24	0.60
7:E:20:ILE:HD11	7:E:40:VAL:CG1	2.26	0.60
10:H:136:VAL:HG22	10:H:137:ASN:H	1.64	0.60
12:J:74:VAL:HG13	12:J:113:ILE:HG23	1.84	0.60
14:L:57:LYS:HD3	14:L:140:ALA:O	2.01	0.60
3:A:121:ALA:O	3:A:124:VAL:HG22	2.01	0.60
2:9:3004:G:H21	15:M:44:ARG:NH1	2.00	0.60
1:0:432:G:OP1	14:L:165:SER:HB3	2.01	0.60
1:0:949:U:O2'	18:P:40:HIS:HE1	1.85	0.60
6:D:20:LYS:HA	6:D:75:LEU:O	2.01	0.60
10:H:57:ARG:CB	10:H:59:ASN:HD22	2.15	0.60
1:0:1966:U:H2'	1:0:1967:U:H2'	1.83	0.60
1:0:12:U:H2'	1:0:13:G:H5'	1.82	0.60
23:U:1:THR:HB	23:U:48:GLU:OE1	2.02	0.60
24:V:41:TYR:O	24:V:45:VAL:HG12	2.01	0.60
5:C:236:THR:HG22	5:C:239:ALA:N	2.08	0.60
27:Y:42:CYS:SG	27:Y:44:PHE:HB2	2.41	0.60
1:0:926:A:O2'	13:K:41:HIS:CD2	2.55	0.60
1:0:2626:C:H2'	1:0:2627:G:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:902:G:N7	13:K:18:HIS:HD2	2.00	0.60
10:H:86:ARG:HH11	10:H:133:ILE:CD1	2.13	0.60
12:J:98:VAL:HG11	12:J:102:GLU:HA	1.83	0.60
1:0:558:C:H2'	1:0:559:U:C5'	2.31	0.60
12:J:58:THR:HG22	12:J:59:LYS:HG3	1.84	0.60
1:0:1778:A:H2'	1:0:1779:A:H5'	1.83	0.60
1:0:1118:A:C8	1:0:1118:A:C3'	2.82	0.60
1:0:185:G:H4'	1:0:186:A:H4'	1.83	0.60
15:M:72:GLU:H	15:M:171:HIS:CE1	2.20	0.60
1:0:2609:G:N2	4:B:238:ASN:HD21	2.00	0.59
1:0:1175:G:H2'	1:0:1176:C:C6	2.37	0.59
10:H:45:GLN:HB3	10:H:163:PRO:HG3	1.84	0.59
2:9:3092:G:H22	10:H:52:LYS:CE	2.15	0.59
3:A:36:ASP:CG	3:A:37:VAL:H	2.04	0.59
10:H:57:ARG:HG3	10:H:57:ARG:HH11	1.67	0.59
17:O:10:ALA:HA	17:O:13:VAL:CG1	2.31	0.59
4:B:14:GLY:HA2	4:B:15:PRO:C	2.23	0.59
2:9:3014:G:C8	2:9:3014:G:H5'	2.37	0.59
1:0:475:G:OP1	5:C:73:LEU:HD22	2.01	0.59
14:L:149:TRP:O	14:L:152:ARG:HG2	2.01	0.59
3:A:131:HIS:O	3:A:132:ASP:HB2	2.03	0.59
25:W:47:ALA:HB1	25:W:82:GLU:HB3	1.85	0.59
6:D:24:HIS:HB2	6:D:72:LYS:CB	2.33	0.59
26:X:106:THR:HG23	26:X:107:PRO:HD2	1.84	0.59
1:0:646:G:H2'	1:0:647:U:C6	2.37	0.59
17:O:59:ARG:HH22	17:O:66:GLN:NE2	1.97	0.59
1:0:2505:G:O2'	1:0:2506:A:H5'	2.02	0.59
5:C:76:ARG:HB3	5:C:76:ARG:NH1	2.16	0.59
1:0:2795:C:O2'	1:0:2796:U:H5'	2.01	0.59
36:0:8163:EMK:C13	36:0:8163:EMK:C23	2.80	0.59
24:V:88:THR:CG2	24:V:90:TYR:HD1	2.13	0.59
4:B:280:VAL:HG13	4:B:333:GLU:O	2.01	0.59
27:Y:62:TYR:CE2	27:Y:64:ILE:HG23	2.38	0.59
10:H:139:ASP:N	10:H:140:PRO:CD	2.65	0.59
8:F:22:VAL:CG2	8:F:104:ALA:HB2	2.33	0.59
1:0:2698:G:H2'	1:0:2699:A:C8	2.38	0.59
13:K:97:VAL:HG12	13:K:98:GLU:O	2.02	0.59
22:T:6:CYS:HA	22:T:13:ILE:HD11	1.84	0.59
8:F:50:VAL:HG13	8:F:60:VAL:HG11	1.84	0.59
5:C:129:HIS:CE1	5:C:231:ARG:HA	2.38	0.59
15:M:72:GLU:H	15:M:171:HIS:HE1	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3114:G:O6	15:M:11:ARG:HD3	2.03	0.59
6:D:58:VAL:HG12	6:D:60:GLU:H	1.67	0.59
1:0:1926:G:H2'	1:0:1927:A:C8	2.37	0.59
1:0:2253:G:O2'	1:0:2254:G:H5'	2.03	0.59
1:0:2547:C:OP2	4:B:5:ARG:NH1	2.36	0.59
23:U:12:THR:HG22	23:U:14:ALA:H	1.67	0.58
8:F:63:ILE:HB	8:F:64:PRO:CD	2.31	0.58
1:0:671:A:O2'	1:0:672:G:H2'	2.03	0.58
24:V:38:THR:HG22	24:V:40:ALA:H	1.68	0.58
25:W:73:ARG:HB2	25:W:88:GLU:OE2	2.02	0.58
13:K:67:ARG:O	13:K:71:GLU:HG3	2.02	0.58
1:0:182:G:O3'	14:L:157:LEU:CD1	2.51	0.58
27:Y:33:HIS:CE1	27:Y:49:ARG:HD2	2.38	0.58
9:G:12:ILE:N	9:G:13:PRO:CD	2.66	0.58
15:M:77:ASN:OD1	15:M:79:PRO:HD2	2.03	0.58
6:D:154:LYS:HD2	6:D:154:LYS:H	1.67	0.58
1:0:285:A:H2'	1:0:286:U:O4'	2.02	0.58
14:L:37:VAL:HG11	14:L:108:LYS:HG3	1.86	0.58
13:K:61:ALA:HB2	13:K:105:TYR:CZ	2.39	0.58
4:B:212:GLN:OE1	4:B:216:LYS:HD3	2.03	0.58
19:Q:39:THR:HB	19:Q:42:GLU:HG3	1.84	0.58
8:F:2:VAL:HG22	8:F:57:GLU:OE1	2.03	0.58
5:C:78:ARG:HG2	5:C:78:ARG:HH11	1.68	0.58
13:K:59:GLU:HA	13:K:104:ASP:OD2	2.03	0.58
4:B:175:LEU:O	4:B:175:LEU:HD23	2.04	0.58
15:M:184:ILE:CG2	15:M:185:GLU:H	2.12	0.58
1:0:1132:A:N6	1:0:1229:C:H2'	2.19	0.58
11:I:74:ARG:O	11:I:78:ILE:HG12	2.03	0.58
14:L:87:MET:CG	30:2:46:ILE:HG21	2.34	0.58
1:0:2878:U:H2'	1:0:2879:A:O4'	2.03	0.58
3:A:107:ASN:OD1	3:A:120:ARG:HD2	2.04	0.58
13:K:90:ARG:NH2	13:K:121:ILE:HD11	2.18	0.58
6:D:136:ARG:NH1	6:D:157:LEU:HA	2.18	0.58
6:D:27:ILE:HD12	6:D:27:ILE:H	1.69	0.58
1:0:775:G:OP1	28:Z:16:HIS:HE1	1.87	0.58
1:0:432:G:O2'	1:0:433:C:H5'	2.04	0.58
10:H:127:GLY:O	10:H:128:ALA:HB3	2.03	0.58
1:0:681:G:N3	1:0:681:G:H5'	2.19	0.58
7:E:102:VAL:HG21	7:E:148:ILE:HG12	1.86	0.58
27:Y:28:ASP:O	27:Y:31:ILE:HG22	2.04	0.58
1:0:2364:A:H5''	18:P:15:LYS:HD3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:344:C:H2'	1:0:345:G:O4'	2.04	0.58
1:0:1289:C:O2'	1:0:1290:G:H5'	2.04	0.58
25:W:78:GLU:HG2	25:W:79:GLU:N	2.18	0.57
1:0:1799:G:H21	17:O:88:GLN:HE22	1.52	0.57
1:0:2027:U:O2'	1:0:2028:U:H5'	2.04	0.57
7:E:15:GLN:HE21	7:E:20:ILE:CG1	2.14	0.57
12:J:109:LEU:HD13	12:J:113:ILE:HD11	1.86	0.57
4:B:305:ASP:O	4:B:306:LYS:HB2	2.05	0.57
24:V:52:VAL:HG22	24:V:53:ALA:H	1.67	0.57
1:0:2720:C:O2	12:J:87:ARG:NH2	2.36	0.57
3:A:9:ARG:HG2	3:A:16:PHE:CD2	2.39	0.57
2:9:3006:C:OP1	15:M:37:ARG:HD2	2.05	0.57
1:0:2694:A:H4'	7:E:91:PHE:CE1	2.38	0.57
1:0:1593:C:P	17:O:117:SER:HB3	2.44	0.57
5:C:153:VAL:O	5:C:157:LEU:HG	2.05	0.57
12:J:98:VAL:HG13	12:J:102:GLU:HA	1.85	0.57
14:L:172:GLY:C	14:L:183:VAL:HG11	2.24	0.57
1:0:1234:U:N3	4:B:244:PRO:HB3	2.19	0.57
1:0:588:G:O6	24:V:154:ARG:NH1	2.38	0.57
8:F:46:GLU:OE1	8:F:100:ASP:HA	2.04	0.57
28:Z:25:LYS:HD2	29:1:49:GLU:N	2.11	0.57
1:0:1183:C:N4	1:0:1184:C:H41	2.02	0.57
13:K:143:THR:HG22	13:K:144:ASP:H	1.69	0.57
2:9:3039:U:H3'	2:9:3040:C:C5'	2.34	0.57
3:A:170:VAL:HG22	27:Y:22:ILE:HG23	1.87	0.57
36:0:8163:EMK:H12	36:0:8163:EMK:C14	2.35	0.57
1:0:2507:G:H2'	1:0:2510:C:H42	1.70	0.57
4:B:125:GLU:HG3	4:B:179:LEU:HD11	1.87	0.57
24:V:39:ASP:HA	24:V:42:ARG:NH1	2.19	0.57
13:K:65:ASP:CG	13:K:111:ALA:HB3	2.25	0.57
1:0:2064:U:H5'	1:0:2652:U:H4'	1.87	0.57
1:0:1667:A:H8	1:0:1667:A:H5'	1.69	0.57
8:F:50:VAL:CG1	8:F:60:VAL:HG11	2.34	0.57
10:H:3:GLY:HA2	10:H:57:ARG:HH12	1.70	0.57
3:A:232:ARG:NH2	3:A:236:GLY:O	2.37	0.57
7:E:8:PRO:HB2	7:E:11:VAL:HG23	1.86	0.57
14:L:165:SER:HB2	14:L:169:ARG:NH2	2.20	0.57
1:0:1641:A:C2'	1:0:1642:A:H5'	2.35	0.57
1:0:1361:C:H2'	1:0:1362:U:C6	2.40	0.57
15:M:143:ARG:HH12	15:M:169:PRO:HB2	1.70	0.56
1:0:1183:C:H41	1:0:1192:A:H5'	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:82:GLU:O	19:Q:86:LYS:HG3	2.05	0.56
18:P:66:LYS:HB2	18:P:70:ALA:O	2.04	0.56
1:0:2829:G:O2'	1:0:2830:U:H5'	2.05	0.56
1:0:2503:A:OP1	10:H:147:ARG:NH2	2.39	0.56
10:H:151:MET:HE3	10:H:151:MET:O	2.05	0.56
11:I:75:PRO:HG2	11:I:105:LEU:CD2	2.35	0.56
1:0:1441:G:O2'	1:0:1442:A:H5'	2.05	0.56
24:V:19:ASP:O	24:V:23:MET:HG3	2.05	0.56
26:X:186:ARG:NH1	26:X:186:ARG:HG2	2.19	0.56
1:0:1377:C:H5'	1:0:1377:C:C6	2.40	0.56
8:F:58:GLU:HG3	8:F:61:MET:HE1	1.86	0.56
11:I:19:MET:CE	11:I:132:LEU:HD11	2.35	0.56
14:L:144:ASP:O	14:L:148:SER:HB3	2.05	0.56
24:V:81:ASP:OD1	24:V:92:ASP:HB2	2.05	0.56
1:0:1511:U:O2'	1:0:1512:G:H5'	2.05	0.56
19:Q:114:VAL:HA	19:Q:144:GLU:O	2.06	0.56
8:F:34:ASN:HA	14:L:4:ALA:HB2	1.87	0.56
1:0:2073:G:OP2	1:0:2490:A:H5'	2.06	0.56
7:E:154:ILE:HD11	7:E:157:LYS:HE2	1.86	0.56
1:0:74:A:H2'	1:0:75:U:C6	2.40	0.56
24:V:130:HIS:O	24:V:136:GLY:HA3	2.05	0.56
23:U:20:LEU:HD22	23:U:60:GLN:HE22	1.71	0.56
5:C:136:VAL:HG22	5:C:137:PRO:HA	1.88	0.56
1:0:2548:C:OP2	4:B:5:ARG:NH2	2.39	0.56
1:0:1173:A:H2'	1:0:1177:A:H62	1.70	0.56
1:0:1632:A:H2'	1:0:1633:C:H5'	1.85	0.56
11:I:107:ASN:HD22	11:I:109:TYR:H	1.52	0.56
21:S:24:ARG:HH21	21:S:39:ASN:ND2	2.02	0.56
1:0:1278:A:H4'	1:0:1279:U:C4	2.40	0.56
2:9:3029:C:C2'	2:9:3030:C:H5'	2.36	0.56
5:C:227:GLY:O	5:C:229:PRO:HD3	2.05	0.56
8:F:48:VAL:CG2	8:F:74:PHE:HB3	2.35	0.56
2:9:3018:U:H2'	2:9:3019:G:H8	1.71	0.56
24:V:29:VAL:O	24:V:30:ASN:HB2	2.05	0.56
1:0:1134:G:H4'	10:H:151:MET:SD	2.46	0.56
12:J:81:ARG:HD3	12:J:87:ARG:NH2	2.21	0.56
5:C:129:HIS:HD2	5:C:165:ASP:OD2	1.88	0.56
1:0:1925:G:O2'	1:0:1926:G:H5'	2.06	0.56
1:0:2827:A:H2'	1:0:2828:G:O4'	2.06	0.56
17:O:40:VAL:O	17:O:44:VAL:HG23	2.06	0.56
1:0:1007:A:H2'	10:H:19:TYR:CZ	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:102:THR:CG2	4:B:182:VAL:HG12	2.36	0.56
1:0:2316:G:H5'	1:0:2317:C:O4'	2.05	0.56
1:0:1733:A:H4'	4:B:212:GLN:HA	1.87	0.56
1:0:2812:A:C2	1:0:2814:A:N6	2.73	0.56
1:0:2252:A:H2'	1:0:2253:G:O4'	2.05	0.56
1:0:121:U:OP2	29:1:10:ARG:NH2	2.33	0.56
3:A:162:GLY:HA3	27:Y:73:THR:HG21	1.87	0.56
13:K:40:PHE:C	13:K:40:PHE:CD1	2.79	0.56
1:0:1342:C:O2'	1:0:1343:C:H5'	2.06	0.56
1:0:1167:G:H2'	1:0:1168:C:O4'	2.06	0.56
3:A:51:ARG:NH1	3:A:120:ARG:O	2.39	0.56
6:D:136:ARG:HH12	6:D:157:LEU:HA	1.69	0.56
4:B:41:PHE:CZ	4:B:79:MET:HG3	2.41	0.56
1:0:2256:G:O2'	1:0:2257:G:H5'	2.05	0.56
1:0:1066:U:H2'	1:0:1067:A:C8	2.40	0.56
5:C:104:ASP:O	5:C:108:GLN:HG3	2.06	0.55
1:0:2676:C:H4'	11:I:70:PHE:CD1	2.41	0.55
8:F:117:GLU:C	8:F:119:ARG:H	2.09	0.55
4:B:254:GLN:HG2	4:B:255:GLY:N	2.20	0.55
1:0:289:G:N1	1:0:363:A:H2	2.01	0.55
14:L:63:VAL:HG21	14:L:109:PHE:CZ	2.41	0.55
13:K:63:THR:HG22	13:K:107:LYS:HB3	1.88	0.55
1:0:292:G:H2'	1:0:358:G:N2	2.20	0.55
23:U:55:ARG:O	23:U:59:ILE:HG12	2.06	0.55
1:0:155:C:OP2	14:L:188:ARG:HD3	2.07	0.55
24:V:4:LEU:HD13	24:V:52:VAL:CG2	2.33	0.55
1:0:1132:A:H2'	1:0:1133:A:C8	2.41	0.55
6:D:99:ASP:N	6:D:103:ASN:O	2.37	0.55
14:L:138:HIS:ND1	14:L:139:PRO:O	2.40	0.55
1:0:137:U:H2'	1:0:139:C:C5	2.41	0.55
5:C:57:PRO:HG2	5:C:73:LEU:HD13	1.87	0.55
10:H:31:PHE:HE2	10:H:87:LYS:O	1.90	0.55
1:0:1909:A:H2'	1:0:1910:A:C8	2.42	0.55
14:L:72:SER:OG	14:L:93:ARG:CZ	2.55	0.55
8:F:48:VAL:HG23	8:F:74:PHE:CB	2.36	0.55
6:D:57:THR:HG23	6:D:63:ILE:HA	1.88	0.55
1:0:951:A:O2'	1:0:952:G:H5'	2.06	0.55
4:B:193:ILE:HD12	4:B:193:ILE:N	2.21	0.55
10:H:14:TYR:N	10:H:91:HIS:CE1	2.67	0.55
1:0:2356:A:H2'	1:0:2357:G:O4'	2.06	0.55
1:0:119:A:H2'	1:0:120:A:H5''	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2676:C:H4'	11:I:70:PHE:CE1	2.41	0.55
7:E:81:GLU:OE1	7:E:170:ARG:NH2	2.40	0.55
14:L:67:ILE:HG21	14:L:97:ILE:HG23	1.89	0.55
4:B:80:ARG:HB2	4:B:145:HIS:CE1	2.41	0.55
4:B:255:GLY:O	4:B:257:THR:HG22	2.07	0.55
22:T:17:THR:CG2	22:T:18:GLY:N	2.69	0.55
15:M:110:THR:HB	15:M:113:SER:HG	1.72	0.55
14:L:138:HIS:O	14:L:141:ILE:HB	2.07	0.55
1:O:2253:G:H2'	1:O:2254:G:H8	1.72	0.55
6:D:27:ILE:HD12	6:D:27:ILE:N	2.22	0.55
1:O:2032:U:O2'	1:O:2033:G:H5''	2.06	0.55
1:O:2531:U:O2'	1:O:2532:A:H5'	2.06	0.55
13:K:10:SER:O	13:K:11:ARG:HB3	2.06	0.55
1:O:1187:U:HO2'	1:O:1189:A:H2	1.53	0.55
14:L:38:VAL:O	14:L:63:VAL:HG13	2.06	0.55
4:B:53:LEU:HD21	4:B:270:ILE:HD12	1.88	0.55
1:O:2372:A:H2'	1:O:2373:U:H6	1.72	0.55
1:O:1768:C:H2'	1:O:1769:C:O4'	2.07	0.55
4:B:106:HIS:CE1	4:B:147:VAL:HG13	2.42	0.55
24:V:125:HIS:HD2	24:V:127:GLY:H	1.54	0.55
2:9:3076:G:C3'	2:9:3077:A:H5''	2.29	0.55
6:D:134:LEU:CD1	6:D:166:ILE:HD11	2.36	0.55
1:O:1003:U:O2'	10:H:90:PHE:HE1	1.90	0.55
1:O:1166:A:H1'	1:O:1192:A:C2	2.42	0.55
3:A:33:GLU:O	3:A:34:ASP:HB2	2.07	0.55
1:O:1874:U:OP1	3:A:51:ARG:HD2	2.06	0.55
10:H:31:PHE:HA	10:H:85:ILE:CG2	2.38	0.55
1:O:65:C:O2'	1:O:66:G:H5'	2.07	0.55
1:O:613:C:H2'	1:O:614:U:H6	1.72	0.55
21:S:41:ARG:O	21:S:43:ASN:ND2	2.40	0.55
1:O:243:A:H61	1:O:269:G:H1'	1.72	0.55
1:O:2592:G:H2'	1:O:2593:C:C6	2.42	0.54
6:D:35:ALA:C	6:D:37:ALA:H	2.10	0.54
5:C:197:SER:HB2	5:C:242:GLU:OE2	2.06	0.54
11:I:49:ARG:O	11:I:53:ILE:HG13	2.06	0.54
1:O:1133:A:H3'	1:O:1134:G:C8	2.42	0.54
1:O:2478:U:O2'	1:O:2479:A:H5'	2.08	0.54
25:W:37:LEU:CD1	25:W:85:VAL:HG11	2.31	0.54
6:D:64:ARG:NE	6:D:67:ASP:HB3	2.21	0.54
2:9:3092:G:H2'	2:9:3093:A:C8	2.42	0.54
1:O:2415:A:H2'	1:O:2416:G:H5'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:19:MET:HE3	11:I:132:LEU:HD21	1.90	0.54
1:O:1886:A:O2'	27:Y:20:LEU:HB2	2.06	0.54
3:A:199:HIS:HD2	3:A:201:PHE:N	1.96	0.54
25:W:71:ARG:HB3	25:W:88:GLU:OE1	2.07	0.54
1:O:952:G:N3	1:O:2302:A:H2'	2.23	0.54
15:M:152:GLU:C	15:M:154:LEU:H	2.11	0.54
1:O:1595:G:O2'	1:O:1596:U:H5'	2.07	0.54
1:O:31:C:H4'	21:S:9:LYS:HD2	1.87	0.54
6:D:10:PHE:CD1	6:D:11:HIS:N	2.74	0.54
13:K:73:VAL:HG21	13:K:116:HIS:NE2	2.23	0.54
1:O:736:A:H2'	1:O:737:A:O4'	2.06	0.54
21:S:78:THR:HG22	21:S:88:PRO:HA	1.88	0.54
1:O:1943:C:O4'	3:A:212:PRO:HA	2.08	0.54
1:O:165:A:H5''	13:K:33:ALA:HB2	1.90	0.54
4:B:258:GLY:H	4:B:260:HIS:CE1	2.25	0.54
15:M:59:ALA:O	15:M:60:SER:HB3	2.08	0.54
22:T:35:LYS:HE2	22:T:51:TRP:CZ2	2.43	0.54
1:O:2870:C:H2'	1:O:2871:G:H8	1.72	0.54
24:V:125:HIS:CD2	24:V:127:GLY:H	2.25	0.54
24:V:68:THR:HG23	24:V:69:ARG:HG2	1.89	0.54
14:L:98:GLN:O	14:L:102:GLU:HG3	2.07	0.54
1:O:861:A:C4'	1:O:1697:G:H4'	2.36	0.54
16:N:32:ARG:O	16:N:32:ARG:HD3	2.07	0.54
1:O:646:G:H2'	1:O:647:U:H6	1.73	0.54
1:O:523:C:H2'	1:O:524:A:C8	2.43	0.54
1:O:2498:C:O2'	1:O:2499:U:H5'	2.07	0.54
10:H:26:LYS:HE3	10:H:28:ILE:HB	1.89	0.54
1:O:111:C:O2'	1:O:112:G:H5'	2.08	0.54
14:L:37:VAL:HG21	14:L:108:LYS:HG3	1.90	0.54
25:W:15:ARG:HH11	25:W:15:ARG:CB	2.19	0.54
24:V:64:THR:O	24:V:68:THR:HG22	2.08	0.54
1:O:2401:A:H2'	1:O:2402:A:C8	2.43	0.54
1:O:236:A:H8	1:O:236:A:OP1	1.91	0.54
10:H:70:ARG:O	10:H:73:GLN:HB2	2.08	0.54
14:L:106:ASN:HD22	14:L:114:VAL:HG23	1.71	0.54
3:A:220:PRO:HD2	3:A:223:ARG:HD2	1.90	0.54
10:H:117:LYS:O	10:H:119:VAL:HG13	2.08	0.54
1:O:56:G:H5''	23:U:50:ARG:NH1	2.23	0.54
30:2:42:ARG:HH11	30:2:42:ARG:HG3	1.73	0.54
10:H:47:GLU:OE1	10:H:133:ILE:HD12	2.07	0.53
3:A:190:ARG:NH2	3:A:207:GLN:OE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:96:GLU:O	26:X:235:GLU:HA	2.08	0.53
14:L:37:VAL:CB	14:L:108:LYS:HG3	2.38	0.53
24:V:35:VAL:HG23	24:V:41:TYR:CD2	2.43	0.53
1:0:2038:A:O2'	1:0:2039:A:H5'	2.07	0.53
1:0:1333:U:H2'	1:0:1334:C:C6	2.42	0.53
5:C:149:LYS:HB2	5:C:152:GLU:HG3	1.91	0.53
6:D:18:ILE:HG12	6:D:134:LEU:CD2	2.39	0.53
10:H:30:GLN:H	10:H:65:ARG:HH11	1.55	0.53
23:U:44:GLY:O	23:U:48:GLU:HG2	2.08	0.53
1:0:2807:U:P	4:B:27:ASN:HD21	2.31	0.53
1:0:2353:A:H4'	1:0:2354:A:O5'	2.07	0.53
7:E:119:HIS:HE1	7:E:147:ASP:OD2	1.92	0.53
1:0:2112:A:H2'	1:0:2113:G:C8	2.42	0.53
24:V:139:GLY:O	24:V:141:HIS:HD2	1.92	0.53
1:0:289:G:C2	1:0:363:A:H2	2.26	0.53
1:0:1119:G:OP2	11:I:49:ARG:HD3	2.08	0.53
1:0:2682:C:OP2	4:B:316:ARG:NH2	2.40	0.53
14:L:61:ILE:N	14:L:61:ILE:HD12	2.23	0.53
23:U:1:THR:HG23	23:U:3:LEU:H	1.72	0.53
1:0:2597:U:H2'	1:0:2598:U:H5'	1.89	0.53
1:0:2456:A:H2'	1:0:2457:U:C6	2.43	0.53
20:R:8:PRO:HD2	23:U:32:ALA:HA	1.90	0.53
1:0:821:U:H2'	1:0:822:C:H6	1.74	0.53
6:D:68:PRO:C	6:D:69:ILE:HD12	2.28	0.53
1:0:2511:A:O2'	1:0:2512:U:H5'	2.09	0.53
25:W:41:PHE:CZ	25:W:74:ALA:HB3	2.44	0.53
13:K:53:ARG:HH22	13:K:57:VAL:HG12	1.74	0.53
1:0:776:A:OP1	28:Z:28:HIS:HE1	1.92	0.53
15:M:22:GLN:CA	15:M:25:ARG:HH21	2.21	0.53
1:0:1632:A:C2'	1:0:1633:C:H5'	2.39	0.53
4:B:41:PHE:HA	4:B:79:MET:HE2	1.90	0.53
14:L:120:VAL:CG1	14:L:130:GLU:HG3	2.38	0.53
1:0:638:C:H2'	1:0:639:A:C8	2.44	0.53
29:1:48:ASP:O	29:1:49:GLU:HB2	2.08	0.53
5:C:162:VAL:HG12	5:C:192:ILE:CD1	2.36	0.53
11:I:74:ARG:NH1	11:I:144:THR:HG21	2.23	0.53
1:0:1042:U:O2'	1:0:1043:C:H5'	2.09	0.53
6:D:64:ARG:CD	6:D:67:ASP:HB3	2.39	0.53
29:1:36:ASN:N	29:1:39:ARG:HH21	2.03	0.53
1:0:2265:U:H2'	1:0:2266:A:H8	1.74	0.53
1:0:1573:A:H2'	1:0:1574:C:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:771:G:H2'	1:0:772:G:C8	2.44	0.53
17:O:141:ILE:C	17:O:143:ALA:H	2.10	0.53
10:H:56:ILE:CG2	10:H:61:LEU:HD13	2.37	0.53
1:0:136:C:H2'	1:0:137:U:O4'	2.07	0.53
1:0:123:U:O2'	1:0:124:C:H5'	2.08	0.53
9:G:16:LYS:O	9:G:20:VAL:HG23	2.09	0.53
24:V:4:LEU:HD22	24:V:54:PHE:HB3	1.91	0.53
1:0:1462:C:H2'	1:0:1463:A:H8	1.72	0.53
1:0:797:A:C4'	27:Y:10:ARG:N	2.71	0.53
10:H:13:ALA:CA	10:H:91:HIS:HE1	2.16	0.53
1:0:2591:C:H2'	1:0:2592:G:O4'	2.09	0.53
5:C:84:VAL:O	5:C:85:LYS:HB2	2.09	0.53
4:B:38:VAL:HG22	4:B:142:LEU:HD12	1.91	0.53
1:0:277:U:O2'	1:0:278:A:H5'	2.10	0.53
5:C:35:VAL:HG23	5:C:220:THR:HG22	1.90	0.53
24:V:88:THR:HG23	24:V:110:GLN:HE21	1.74	0.52
22:T:17:THR:HG22	22:T:18:GLY:N	2.24	0.52
13:K:38:HIS:HD2	13:K:39:GLU:HG3	1.73	0.52
1:0:1298:U:H2'	1:0:1299:G:H8	1.73	0.52
7:E:32:ARG:O	7:E:33:LEU:HD23	2.09	0.52
1:0:695:C:H2'	1:0:696:C:C6	2.45	0.52
1:0:1423:C:O2'	1:0:1424:A:H5'	2.09	0.52
1:0:2274:A:H1'	14:L:86:MET:SD	2.49	0.52
8:F:108:LEU:HD12	8:F:108:LEU:C	2.29	0.52
12:J:55:VAL:HG12	12:J:56:SER:N	2.24	0.52
20:R:51:GLN:NE2	20:R:53:ASN:HD21	1.90	0.52
1:0:2838:A:H2'	1:0:2839:C:C6	2.44	0.52
4:B:320:GLN:HE21	4:B:321:PRO:CD	2.22	0.52
20:R:44:GLN:OE1	20:R:44:GLN:HA	2.09	0.52
10:H:166:ASN:N	10:H:166:ASN:HD22	2.06	0.52
10:H:157:ILE:HG22	10:H:158:ASN:N	2.24	0.52
1:0:475:G:C5'	5:C:73:LEU:HD23	2.38	0.52
1:0:2089:A:O2'	1:0:2090:G:H5'	2.09	0.52
1:0:790:A:H1'	1:0:1710:A:H2'	1.90	0.52
1:0:1505:U:O2	1:0:1505:U:H2'	2.10	0.52
4:B:314:ALA:HB3	4:B:317:PRO:HG3	1.91	0.52
5:C:49:ASP:HB3	5:C:52:ALA:HB2	1.91	0.52
1:0:1198:U:H1'	1:0:1201:C:H5	1.74	0.52
10:H:45:GLN:HB3	10:H:163:PRO:HD3	1.91	0.52
1:0:1166:A:H61	1:0:1180:U:H3	1.57	0.52
2:9:3050:G:H5"	15:M:159:TYR:HE1	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:134:VAL:O	17:O:138:GLU:HG3	2.10	0.52
1:O:2837:U:H1'	4:B:307:ARG:HH12	1.74	0.52
1:O:1178:G:H2'	1:O:1179:C:C6	2.44	0.52
1:O:876:A:N3	1:O:876:A:H2'	2.25	0.52
13:K:83:GLU:CD	13:K:83:GLU:H	2.13	0.52
1:O:559:U:H2'	1:O:560:C:O4'	2.09	0.52
29:1:36:ASN:H	29:1:39:ARG:NH2	2.03	0.52
1:O:2769:C:C2'	1:O:2770:G:H5'	2.39	0.52
7:E:11:VAL:HG12	7:E:12:ASP:N	2.25	0.52
8:F:28:ALA:CB	8:F:99:THR:HG23	2.39	0.52
25:W:24:LYS:HA	25:W:63:ARG:HG2	1.91	0.52
1:O:2900:G:H2'	1:O:2901:C:O4'	2.09	0.52
1:O:447:A:OP1	21:S:2:LYS:HG2	2.09	0.52
1:O:1080:C:H4'	1:O:1081:A:OP1	2.10	0.52
1:O:1634:G:H2'	1:O:1635:U:C6	2.44	0.52
10:H:45:GLN:HB3	10:H:163:PRO:CD	2.39	0.52
11:I:130:VAL:HG12	11:I:131:THR:N	2.24	0.52
15:M:72:GLU:O	15:M:72:GLU:HG2	2.10	0.52
5:C:7:ASP:OD2	5:C:9:ASP:HB2	2.09	0.52
1:O:2594:C:O2'	1:O:2595:U:H5'	2.10	0.52
7:E:101:GLU:HB3	7:E:117:THR:HA	1.91	0.52
11:I:42:GLU:HG2	11:I:43:ARG:HG3	1.92	0.52
1:O:449:A:N7	5:C:43:LYS:HG2	2.24	0.52
1:O:2406:U:O2'	1:O:2407:G:H5'	2.09	0.52
7:E:84:MET:HG2	7:E:168:ILE:HA	1.91	0.52
1:O:1835:U:C5	1:O:1840:A:N7	2.73	0.52
15:M:143:ARG:NH1	15:M:169:PRO:HB2	2.24	0.52
25:W:78:GLU:CG	25:W:79:GLU:H	2.22	0.52
11:I:6:PHE:HB3	11:I:109:TYR:OH	2.09	0.52
10:H:3:GLY:HA2	10:H:57:ARG:NH1	2.25	0.52
29:1:23:ALA:HA	29:1:26:MET:HE2	1.92	0.52
10:H:72:VAL:HG13	10:H:72:VAL:O	2.08	0.52
4:B:175:LEU:C	4:B:175:LEU:HD23	2.30	0.52
6:D:11:HIS:O	6:D:12:GLU:HB3	2.10	0.52
4:B:320:GLN:HE21	4:B:321:PRO:HD3	1.75	0.52
2:9:3072:C:H2'	2:9:3073:G:H8	1.75	0.52
25:W:76:ARG:O	25:W:77:PHE:HB3	2.10	0.52
1:O:799:C:O2'	1:O:800:G:H5'	2.10	0.52
19:Q:39:THR:HG22	19:Q:42:GLU:N	2.15	0.52
1:O:2506:A:O2'	1:O:2507:G:O5'	2.27	0.52
3:A:93:THR:C	3:A:94:LEU:HD23	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:1:23:ALA:HA	29:1:26:MET:HE3	1.89	0.52
1:0:2456:A:H2'	1:0:2457:U:H6	1.75	0.52
1:0:858:U:H2'	1:0:859:C:H6	1.74	0.52
6:D:95:THR:HG21	6:D:174:VAL:HG22	1.92	0.52
3:A:30:ARG:HG2	3:A:31:LYS:N	2.25	0.52
1:0:1370:G:OP1	19:Q:64:SER:HB3	2.09	0.52
24:V:3:ALA:O	24:V:54:PHE:HA	2.10	0.52
1:0:1133:A:H3'	1:0:1134:G:H8	1.75	0.52
1:0:2533:C:C6	1:0:2533:C:H5'	2.38	0.52
1:0:2908:A:O2'	1:0:2909:G:H5'	2.10	0.52
4:B:41:PHE:CD1	4:B:79:MET:HE2	2.44	0.52
1:0:2717:C:O2'	1:0:2718:C:H5'	2.09	0.52
1:0:2894:C:O2'	1:0:2895:C:H5'	2.10	0.52
13:K:125:PHE:CZ	13:K:140:VAL:HG13	2.45	0.52
1:0:2361:A:H2'	1:0:2362:A:C8	2.45	0.52
1:0:2363:G:O2'	18:P:11:ARG:HG3	2.10	0.52
6:D:101:THR:O	6:D:101:THR:HG22	2.10	0.52
6:D:128:LEU:C	6:D:128:LEU:HD23	2.31	0.52
14:L:24:MET:SD	14:L:27:ARG:NH1	2.83	0.51
21:S:24:ARG:HH21	21:S:39:ASN:HD22	1.56	0.51
1:0:611:U:H2'	1:0:612:U:C6	2.45	0.51
1:0:820:G:H5'	1:0:821:U:H5'	1.92	0.51
1:0:685:C:O2	1:0:748:C:H4'	2.10	0.51
28:Z:5:THR:HB	28:Z:6:PRO:HD3	1.92	0.51
2:9:3057:A:C8	6:D:141:VAL:HG21	2.45	0.51
1:0:1116:U:H3	1:0:1246:A:H62	1.58	0.51
1:0:1641:A:H2'	1:0:1642:A:C5'	2.40	0.51
25:W:30:MET:CE	25:W:58:ALA:HB3	2.40	0.51
8:F:91:VAL:CG1	8:F:92:GLY:N	2.73	0.51
6:D:94:ALA:HB3	6:D:174:VAL:CA	2.40	0.51
23:U:12:THR:HG23	23:U:13:PRO:HD2	1.92	0.51
10:H:46:VAL:O	10:H:146:TRP:HH2	1.92	0.51
23:U:39:ALA:O	23:U:41:GLU:N	2.43	0.51
1:0:1218:U:H2'	1:0:1219:U:H6	1.75	0.51
1:0:1755:A:H2'	1:0:1756:G:O4'	2.10	0.51
1:0:2237:G:O2'	1:0:2238:A:C8	2.63	0.51
1:0:204:A:C2'	1:0:205:U:H5'	2.40	0.51
30:2:3:MET:O	30:2:90:PHE:HA	2.10	0.51
17:O:71:LYS:HG3	17:O:71:LYS:O	2.09	0.51
1:0:706:G:HO2'	1:0:707:C:H6	1.57	0.51
25:W:27:ASP:N	25:W:27:ASP:OD2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:5:VAL:O	24:V:52:VAL:HG23	2.10	0.51
26:X:235:GLU:N	26:X:235:GLU:CD	2.56	0.51
8:F:57:GLU:HB2	14:L:23:LEU:HD11	1.93	0.51
4:B:62:ARG:HA	4:B:65:MET:HE3	1.93	0.51
3:A:84:VAL:HG13	3:A:98:GLU:HG3	1.92	0.51
1:0:667:C:H2'	1:0:668:C:H6	1.75	0.51
1:0:216:A:O2'	1:0:217:C:H5'	2.10	0.51
8:F:36:THR:HG23	8:F:97:ALA:HB2	1.92	0.51
1:0:1803:C:H2'	1:0:1804:A:C8	2.46	0.51
23:U:56:ILE:HG22	23:U:60:GLN:NE2	2.24	0.51
13:K:57:VAL:O	13:K:57:VAL:HG12	2.10	0.51
6:D:58:VAL:CG1	6:D:60:GLU:HG2	2.40	0.51
20:R:44:GLN:HE21	23:U:28:LEU:CD2	2.24	0.51
15:M:138:ASP:O	15:M:138:ASP:CG	2.48	0.51
10:H:45:GLN:HB3	10:H:163:PRO:CG	2.40	0.51
20:R:57:THR:CG2	20:R:58:MET:N	2.74	0.51
3:A:170:VAL:HG22	27:Y:22:ILE:CG2	2.41	0.51
1:0:797:A:H4'	27:Y:10:ARG:N	2.25	0.51
5:C:35:VAL:CG2	5:C:220:THR:HG22	2.40	0.51
1:0:870:G:OP2	3:A:3:ARG:HD3	2.10	0.51
10:H:53:PRO:HA	10:H:125:VAL:O	2.10	0.51
12:J:28:GLU:OE2	12:J:58:THR:HG21	2.11	0.51
8:F:102:GLY:C	8:F:104:ALA:H	2.12	0.51
4:B:8:LYS:HG3	4:B:220:VAL:HG12	1.93	0.51
1:0:1878:G:O2'	1:0:1879:U:OP2	2.27	0.51
1:0:2563:U:H2'	1:0:2565:C:O5'	2.11	0.51
1:0:1505:U:C2'	1:0:1505:U:O2	2.59	0.51
24:V:6:GLN:HB2	24:V:26:ILE:CD1	2.38	0.51
18:P:94:GLN:O	18:P:95:GLU:HB2	2.10	0.51
26:X:151:SER:HB3	26:X:154:ARG:HB2	1.92	0.51
1:0:1878:G:O2'	1:0:1879:U:P	2.68	0.51
1:0:2890:A:H1'	22:T:56:ARG:NH2	2.25	0.51
1:0:1667:A:C8	1:0:1667:A:H5'	2.46	0.51
10:H:46:VAL:CG1	10:H:146:TRP:HZ3	2.24	0.51
17:O:10:ALA:HA	17:O:13:VAL:HG12	1.93	0.51
8:F:28:ALA:HB3	8:F:99:THR:O	2.11	0.51
1:0:2081:A:H4'	11:I:69:TYR:CE1	2.46	0.51
1:0:682:A:H2'	1:0:683:G:O4'	2.10	0.51
11:I:14:ALA:HB1	11:I:44:ALA:HB2	1.92	0.51
9:G:64:ASN:N	9:G:64:ASN:HD22	2.08	0.51
2:9:3023:U:C3'	2:9:3024:U:C5'	2.81	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:55:TRP:HB2	27:Y:64:ILE:HG13	1.92	0.51
12:J:115:ARG:HG3	12:J:116:GLU:N	2.26	0.50
1:0:951:A:C2'	1:0:952:G:H5'	2.41	0.50
4:B:145:HIS:HD2	4:B:146:THR:O	1.93	0.50
10:H:97:LYS:HD3	10:H:117:LYS:HD3	1.93	0.50
6:D:94:ALA:O	6:D:95:THR:O	2.29	0.50
19:Q:111:ILE:HG23	19:Q:145:LEU:HD11	1.93	0.50
24:V:22:GLU:HG2	24:V:27:HIS:CD2	2.46	0.50
24:V:6:GLN:HG2	24:V:29:VAL:HA	1.92	0.50
13:K:73:VAL:HG21	13:K:116:HIS:CD2	2.47	0.50
13:K:73:VAL:HG23	13:K:74:THR:N	2.23	0.50
14:L:35:PRO:HB2	14:L:38:VAL:HG23	1.91	0.50
1:0:2896:A:OP1	25:W:15:ARG:NH1	2.44	0.50
1:0:1470:A:OP1	14:L:93:ARG:HD2	2.11	0.50
1:0:1279:U:O2	1:0:1279:U:H2'	2.09	0.50
1:0:2871:G:H2'	1:0:2872:U:C6	2.47	0.50
1:0:407:A:O2'	1:0:408:A:H5'	2.11	0.50
3:A:179:MET:HG2	3:A:186:TRP:CG	2.46	0.50
5:C:172:THR:HG22	5:C:188:ARG:CZ	2.41	0.50
4:B:154:VAL:CG1	4:B:156:LYS:HG2	2.40	0.50
1:0:2908:A:H2'	1:0:2909:G:C5'	2.42	0.50
1:0:2908:A:H2'	1:0:2909:G:H5'	1.93	0.50
5:C:127:ARG:HH22	5:C:225:PRO:HB2	1.76	0.50
1:0:1616:A:H2'	1:0:1618:G:C8	2.46	0.50
1:0:907:A:H2'	1:0:908:A:H8	1.75	0.50
1:0:1700:C:H5''	1:0:1701:A:OP2	2.12	0.50
10:H:48:LEU:HD13	10:H:146:TRP:HB3	1.92	0.50
15:M:154:LEU:O	15:M:155:GLU:CB	2.58	0.50
1:0:858:U:H2'	1:0:859:C:C6	2.45	0.50
1:0:1787:C:OP1	17:O:68:LYS:HE2	2.12	0.50
1:0:164:G:H4'	13:K:30:ARG:HD2	1.92	0.50
1:0:625:U:H5''	1:0:1044:C:N4	2.26	0.50
11:I:93:ARG:HB3	11:I:93:ARG:HH11	1.76	0.50
4:B:26:PHE:CE1	4:B:310:ARG:HB3	2.46	0.50
14:L:107:ARG:O	14:L:110:PRO:HD3	2.12	0.50
4:B:214:PRO:C	4:B:220:VAL:HG22	2.32	0.50
5:C:172:THR:HG22	5:C:188:ARG:NH1	2.26	0.50
10:H:112:ARG:O	10:H:113:ALA:C	2.49	0.50
1:0:766:A:O2'	1:0:767:A:H5''	2.11	0.50
24:V:56:GLU:O	24:V:143:THR:HG23	2.12	0.50
20:R:73:ASP:HB3	20:R:76:GLU:OE1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:25:VAL:HG11	16:N:111:VAL:HG11	1.93	0.50
16:N:57:THR:HB	16:N:111:VAL:HG23	1.94	0.50
15:M:163:PHE:HD2	15:M:163:PHE:H	1.59	0.50
36:O:8163:EMK:C20	36:O:8163:EMK:N9	2.73	0.50
1:O:1242:A:OP2	11:I:60:ARG:NH2	2.42	0.50
10:H:86:ARG:NH1	10:H:133:ILE:CG1	2.59	0.50
6:D:165:PHE:CD2	6:D:166:ILE:HD12	2.47	0.50
1:O:1298:U:H2'	1:O:1299:G:C8	2.46	0.50
1:O:1165:G:H21	1:O:1173:A:H5''	1.76	0.50
1:O:2090:G:H2'	1:O:2091:G:C8	2.47	0.50
17:O:98:ILE:HD12	17:O:102:ARG:NE	2.26	0.50
4:B:312:ARG:HD3	4:B:315:VAL:HG13	1.93	0.50
1:O:1064:U:H2'	1:O:1065:G:C8	2.47	0.50
1:O:263:U:O4'	8:F:59:ILE:HD13	2.12	0.50
14:L:173:LEU:HD23	14:L:183:VAL:HG12	1.94	0.50
1:O:1677:U:OP2	29:1:8:LYS:NZ	2.44	0.50
1:O:1250:C:O2'	1:O:1251:C:H5'	2.12	0.50
27:Y:30:GLU:HA	27:Y:33:HIS:HB3	1.94	0.50
10:H:57:ARG:HG3	10:H:57:ARG:NH1	2.27	0.50
17:O:13:VAL:HG21	17:O:41:ARG:HG2	1.93	0.50
4:B:307:ARG:CG	4:B:307:ARG:HH11	2.24	0.50
16:N:87:THR:O	16:N:91:GLN:HG3	2.11	0.50
5:C:233:THR:HG22	5:C:234:VAL:N	2.26	0.50
4:B:141:ARG:HG2	4:B:165:ARG:HA	1.94	0.50
20:R:51:GLN:HE21	20:R:53:ASN:ND2	1.91	0.50
6:D:146:LYS:HZ3	15:M:107:ASN:HD21	1.58	0.50
28:Z:19:CYS:HB2	28:Z:27:TYR:HB2	1.94	0.50
18:P:30:VAL:O	18:P:30:VAL:HG12	2.11	0.50
4:B:84:LEU:HD13	4:B:84:LEU:O	2.12	0.50
8:F:61:MET:HB3	14:L:19:GLN:OE1	2.11	0.49
25:W:47:ALA:HB1	25:W:82:GLU:CB	2.42	0.49
6:D:58:VAL:HG12	6:D:60:GLU:HG2	1.94	0.49
1:O:2039:A:H2'	1:O:2040:C:C6	2.47	0.49
1:O:2717:C:OP1	4:B:207:LYS:HG3	2.12	0.49
17:O:55:LYS:HG2	17:O:56:GLY:N	2.27	0.49
1:O:1762:C:H2'	1:O:1763:C:H6	1.77	0.49
1:O:1456:C:H2'	1:O:1457:U:C6	2.46	0.49
2:9:3011:A:P	18:P:19:ARG:HH21	2.34	0.49
1:O:731:U:H2'	1:O:732:C:C6	2.47	0.49
10:H:51:GLU:HB2	10:H:156:THR:O	2.11	0.49
10:H:130:HIS:H	10:H:130:HIS:CD2	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:164:THR:CG2	14:L:165:SER:N	2.75	0.49
8:F:28:ALA:HB3	8:F:99:THR:HG23	1.93	0.49
1:0:398:U:H2'	1:0:399:C:C6	2.48	0.49
7:E:1:PRO:HG3	7:E:59:MET:SD	2.53	0.49
1:0:1739:G:H1'	1:0:2726:U:O4	2.11	0.49
27:Y:46:LYS:HD3	27:Y:59:HIS:HB2	1.94	0.49
1:0:1751:G:C2'	1:0:1752:G:H5''	2.43	0.49
1:0:1964:U:H2'	1:0:1965:C:C6	2.47	0.49
5:C:140:VAL:HG12	5:C:141:SER:N	2.27	0.49
10:H:56:ILE:HG22	10:H:61:LEU:HD22	1.95	0.49
4:B:51:VAL:HG22	4:B:330:VAL:HG22	1.93	0.49
4:B:238:ASN:HD22	4:B:240:GLY:H	1.59	0.49
1:0:56:G:H5''	23:U:50:ARG:HH12	1.76	0.49
1:0:1684:A:H1'	29:1:43:ARG:HH22	1.77	0.49
1:0:945:U:H2'	1:0:946:C:C6	2.47	0.49
1:0:565:A:H2'	1:0:566:A:C8	2.47	0.49
1:0:794:U:H3	1:0:819:A:H61	1.60	0.49
3:A:173:GLY:O	3:A:176:HIS:HB3	2.11	0.49
1:0:20:G:H21	19:Q:117:HIS:HD2	1.59	0.49
1:0:969:G:H1	1:0:999:C:N4	2.09	0.49
15:M:139:TRP:HA	15:M:139:TRP:CE3	2.47	0.49
24:V:52:VAL:CG2	24:V:53:ALA:N	2.74	0.49
6:D:62:ASP:O	6:D:64:ARG:N	2.46	0.49
1:0:282:C:HO2'	1:0:283:U:H4'	1.72	0.49
15:M:1:ALA:HA	15:M:6:TYR:CD2	2.47	0.49
4:B:62:ARG:HH11	4:B:62:ARG:HG2	1.77	0.49
1:0:524:A:H5''	19:Q:29:LYS:HE2	1.95	0.49
4:B:312:ARG:HH11	4:B:315:VAL:HG13	1.76	0.49
20:R:17:ASP:HB3	20:R:23:LYS:HB2	1.93	0.49
23:U:29:ASN:O	23:U:33:VAL:HG23	2.13	0.49
29:1:22:PRO:HB2	29:1:25:VAL:HG23	1.95	0.49
36:0:8163:EMK:C24	36:0:8163:EMK:C14	2.83	0.49
10:H:14:TYR:H	10:H:91:HIS:HE1	1.56	0.49
10:H:148:ARG:O	10:H:151:MET:HB2	2.13	0.49
16:N:47:ARG:NH1	16:N:47:ARG:HG3	2.27	0.49
1:0:820:G:C5	3:A:171:LYS:HB2	2.48	0.49
27:Y:10:ARG:HG3	27:Y:11:THR:N	2.26	0.49
13:K:125:PHE:CE1	13:K:140:VAL:HG13	2.47	0.49
20:R:42:GLU:HG2	20:R:49:VAL:HG23	1.94	0.49
1:0:2082:G:O2'	1:0:2083:A:H5'	2.12	0.49
6:D:93:LEU:HD12	6:D:97:GLN:NE2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3096:C:H2'	2:9:3097:U:C6	2.47	0.49
17:O:27:ARG:O	17:O:31:ILE:HG13	2.12	0.49
1:0:372:A:H2'	1:0:373:G:C8	2.48	0.49
1:0:1102:C:HO2'	11:I:24:SER:HG	1.61	0.49
1:0:154:C:H2'	1:0:155:C:C6	2.48	0.49
7:E:23:GLU:HG2	7:E:28:SER:CB	2.41	0.49
1:0:1015:C:H2'	1:0:1016:U:H6	1.77	0.49
5:C:45:ASP:OD2	5:C:98:ARG:HD2	2.13	0.49
26:X:187:VAL:HG22	26:X:192:ASP:CB	2.41	0.49
14:L:38:VAL:C	14:L:63:VAL:HG13	2.32	0.49
1:0:1183:C:C4	1:0:1184:C:N4	2.77	0.49
1:0:841:A:OP2	19:Q:128:ARG:HD2	2.12	0.49
1:0:2032:U:H2'	1:0:2033:G:C5'	2.42	0.49
4:B:268:ARG:HH11	4:B:268:ARG:HG2	1.78	0.49
10:H:130:HIS:CG	10:H:133:ILE:HD11	2.48	0.49
23:U:13:PRO:O	23:U:17:GLU:HG3	2.12	0.49
14:L:164:THR:HG22	14:L:166:ALA:N	2.28	0.49
1:0:159:G:H5''	14:L:74:ARG:NH2	2.28	0.49
10:H:45:GLN:H	10:H:163:PRO:CD	2.26	0.49
24:V:88:THR:CG2	24:V:89:ASP:N	2.75	0.49
1:0:2856:A:OP1	25:W:15:ARG:NH2	2.46	0.49
28:Z:28:HIS:O	28:Z:32:LYS:N	2.39	0.49
1:0:797:A:O4'	27:Y:10:ARG:N	2.46	0.49
7:E:1:PRO:HD2	7:E:53:GLU:O	2.13	0.49
1:0:316:A:N3	1:0:336:G:O2'	2.44	0.49
1:0:2389:U:H4'	18:P:53:HIS:CD2	2.48	0.49
1:0:2506:A:O2'	1:0:2507:G:P	2.71	0.49
3:A:100:PRO:HG2	3:A:103:VAL:HG21	1.94	0.49
22:T:45:GLU:HB2	22:T:48:ASN:HD22	1.78	0.49
20:R:33:SER:OG	20:R:36:GLU:HG3	2.12	0.49
13:K:67:ARG:HB2	13:K:112:GLY:HA3	1.94	0.49
1:0:2870:C:H2'	1:0:2871:G:C8	2.48	0.49
1:0:371:U:H2'	1:0:372:A:H8	1.77	0.49
1:0:1894:C:N4	1:0:1939:U:H2'	2.28	0.49
1:0:1039:G:H2'	1:0:1040:A:O4'	2.13	0.49
14:L:31:TRP:O	14:L:34:GLU:HB2	2.12	0.49
5:C:88:SER:OG	5:C:91:PRO:HB3	2.13	0.49
6:D:54:ALA:HB2	6:D:69:ILE:HG12	1.94	0.48
1:0:2504:A:H4'	10:H:70:ARG:HD3	1.95	0.48
26:X:178:HIS:CG	26:X:179:PRO:HD2	2.47	0.48
2:9:3061:C:H2'	2:9:3062:A:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1419:U:H2'	1:0:1685:A:C2	2.48	0.48
1:0:1791:U:H2'	1:0:1792:C:H6	1.78	0.48
1:0:2820:A:OP1	4:B:98:THR:HG22	2.13	0.48
1:0:1528:A:H2'	1:0:1529:G:O4'	2.13	0.48
1:0:95:A:H5''	1:0:97:G:O4'	2.13	0.48
1:0:2346:C:H6	1:0:2346:C:O5'	1.95	0.48
36:0:8163:EMK:H12	36:0:8163:EMK:H23B	1.94	0.48
1:0:154:C:H2'	1:0:155:C:H6	1.77	0.48
5:C:211:ASP:HB2	5:C:231:ARG:HH22	1.78	0.48
6:D:94:ALA:HB3	6:D:174:VAL:HA	1.95	0.48
17:O:98:ILE:O	17:O:98:ILE:HD13	2.14	0.48
9:G:23:ILE:O	9:G:27:ILE:HG13	2.13	0.48
1:0:1838:U:O2'	1:0:2644:C:H5'	2.13	0.48
1:0:466:A:H2'	1:0:467:G:O4'	2.13	0.48
19:Q:39:THR:CG2	19:Q:42:GLU:HG3	2.43	0.48
24:V:90:TYR:N	24:V:90:TYR:CD1	2.81	0.48
5:C:211:ASP:HB2	5:C:231:ARG:NH2	2.28	0.48
1:0:2883:A:H2'	1:0:2884:G:O4'	2.14	0.48
20:R:2:TRP:CZ2	20:R:31:ARG:HB2	2.48	0.48
30:2:69:TYR:HB2	30:2:78:HIS:CE1	2.48	0.48
1:0:175:G:H2'	14:L:192:ALA:HB3	1.96	0.48
1:0:1819:G:H4'	1:0:1819:G:OP1	2.13	0.48
28:Z:28:HIS:CE1	28:Z:31:LYS:HE2	2.48	0.48
1:0:2266:A:H2'	1:0:2267:G:C8	2.48	0.48
2:9:3008:G:O6	15:M:11:ARG:NH1	2.47	0.48
1:0:1515:A:H2'	1:0:1516:C:C6	2.48	0.48
1:0:2768:A:C8	4:B:316:ARG:HB2	2.47	0.48
1:0:1926:G:H2'	1:0:1927:A:H8	1.74	0.48
1:0:2828:G:O2'	1:0:2829:G:H5'	2.13	0.48
21:S:43:ASN:HD22	21:S:43:ASN:N	2.11	0.48
1:0:1762:C:H2'	1:0:1763:C:C6	2.49	0.48
1:0:24:G:N2	1:0:518:G:H1'	2.28	0.48
1:0:280:C:H2'	1:0:281:U:O4'	2.14	0.48
26:X:99:ALA:HB2	26:X:233:TYR:CE2	2.47	0.48
8:F:26:THR:HG22	8:F:102:GLY:HA3	1.96	0.48
27:Y:31:ILE:HG23	27:Y:32:LYS:N	2.28	0.48
1:0:684:G:H2'	1:0:685:C:C6	2.48	0.48
1:0:1803:C:H2'	1:0:1804:A:H8	1.78	0.48
1:0:1791:U:H2'	1:0:1792:C:C6	2.48	0.48
6:D:172:VAL:HG12	6:D:173:GLU:N	2.27	0.48
18:P:77:ASP:HB3	18:P:82:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:869:G:OP2	14:L:79:LYS:HE3	2.13	0.48
3:A:39:ALA:HB3	3:A:61:GLU:OE2	2.13	0.48
17:O:8:ARG:HG2	17:O:8:ARG:HH11	1.78	0.48
1:O:1451:C:C5'	1:O:1505:U:H3	2.07	0.48
11:I:39:VAL:HG11	11:I:107:ASN:CB	2.43	0.48
8:F:48:VAL:HG23	8:F:74:PHE:HB3	1.92	0.48
1:O:1333:U:H2'	1:O:1334:C:H6	1.79	0.48
14:L:120:VAL:HG11	14:L:130:GLU:HG3	1.95	0.48
1:O:757:C:OP1	13:K:27:ARG:HD2	2.13	0.48
11:I:54:VAL:O	11:I:58:GLU:HG3	2.12	0.48
1:O:1398:G:H2'	1:O:1399:A:C8	2.49	0.48
6:D:23:VAL:HG21	6:D:45:THR:HG21	1.95	0.48
21:S:47:THR:HB	21:S:100:ASP:HB3	1.94	0.48
1:O:812:A:H2'	1:O:813:C:C6	2.48	0.48
1:O:271:C:C2	1:O:273:G:O4'	2.67	0.48
10:H:132:PHE:O	10:H:133:ILE:HD13	2.14	0.48
10:H:29:ALA:HB3	10:H:65:ARG:NH1	2.24	0.48
3:A:88:ILE:HD13	3:A:100:PRO:CD	2.39	0.48
1:O:470:U:O2'	28:Z:16:HIS:CD2	2.64	0.48
1:O:960:G:N3	1:O:960:G:C2'	2.77	0.48
15:M:180:LEU:O	15:M:181:ASP:HB3	2.13	0.48
9:G:71:LEU:C	9:G:73:ASP:H	2.17	0.48
2:9:3057:A:H8	6:D:141:VAL:HG21	1.79	0.48
10:H:71:TYR:C	10:H:73:GLN:N	2.67	0.48
1:O:120:A:H2'	1:O:120:A:N3	2.28	0.48
1:O:2072:G:C6	1:O:2533:C:H1'	2.49	0.48
2:9:3013:A:H3'	2:9:3014:G:H5'	1.96	0.48
1:O:2780:C:H1'	7:E:143:GLN:NE2	2.27	0.48
1:O:1181:A:C2'	1:O:1182:C:H5'	2.44	0.48
14:L:67:ILE:CG2	14:L:97:ILE:HG23	2.44	0.48
20:R:44:GLN:HE21	23:U:28:LEU:HD22	1.78	0.48
1:O:1576:G:H2'	1:O:1577:U:C6	2.49	0.48
8:F:20:LEU:HD13	8:F:49:PHE:CE1	2.49	0.48
13:K:55:GLN:HA	13:K:58:GLN:NE2	2.29	0.48
1:O:2549:C:H1'	4:B:248:ARG:NH2	2.29	0.48
1:O:2737:C:OP2	17:O:61:ARG:NH2	2.39	0.48
27:Y:38:LYS:HG3	27:Y:45:LYS:HB3	1.94	0.48
14:L:114:VAL:HG21	14:L:159:THR:HG21	1.94	0.48
2:9:3013:A:O2'	2:9:3014:G:H5''	2.14	0.48
14:L:139:PRO:C	14:L:141:ILE:N	2.63	0.48
1:O:138:U:OP2	1:O:139:C:H5	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:60:VAL:O	8:F:61:MET:C	2.53	0.48
16:N:29:VAL:O	16:N:33:LEU:HG	2.13	0.48
4:B:312:ARG:HD3	4:B:315:VAL:CG1	2.44	0.48
12:J:99:ASP:OD1	12:J:101:ASN:N	2.45	0.48
1:0:656:G:OP2	16:N:37:ARG:HD2	2.13	0.48
1:0:1008:C:H5''	10:H:16:ARG:HH12	1.79	0.48
20:R:77:VAL:O	20:R:80:ARG:HG2	2.14	0.48
2:9:3020:G:O2'	2:9:3021:G:H5'	2.14	0.48
4:B:53:LEU:CD1	4:B:327:VAL:HG22	2.44	0.47
1:0:1205:U:H2'	1:0:1206:U:O4'	2.13	0.47
14:L:139:PRO:O	14:L:140:ALA:CB	2.57	0.47
24:V:151:GLU:O	24:V:154:ARG:HB3	2.14	0.47
4:B:307:ARG:HH11	4:B:307:ARG:HG3	1.78	0.47
1:0:758:A:H2'	1:0:759:C:O4'	2.14	0.47
1:0:2685:C:H2'	1:0:2686:C:C6	2.50	0.47
1:0:1307:A:H2'	1:0:1308:A:C8	2.48	0.47
1:0:161:A:H2'	1:0:162:C:C6	2.48	0.47
1:0:2507:G:H2'	1:0:2510:C:N4	2.28	0.47
27:Y:25:ARG:O	27:Y:29:VAL:HG23	2.14	0.47
3:A:101:GLU:OE2	3:A:131:HIS:HB2	2.14	0.47
1:0:338:C:H4'	5:C:174:ILE:CD1	2.44	0.47
6:D:51:ARG:HH11	6:D:68:PRO:CG	2.26	0.47
11:I:39:VAL:HG11	11:I:107:ASN:HB2	1.96	0.47
2:9:3114:G:H2'	2:9:3115:C:C6	2.50	0.47
5:C:78:ARG:HG2	5:C:78:ARG:NH1	2.29	0.47
16:N:25:VAL:O	16:N:29:VAL:HG23	2.15	0.47
1:0:2866:U:H2'	22:T:50:GLU:OE1	2.14	0.47
1:0:2281:C:C2'	1:0:2282:U:H5'	2.44	0.47
1:0:558:C:C2'	1:0:559:U:C5'	2.88	0.47
27:Y:47:LEU:HD23	27:Y:57:CYS:HA	1.95	0.47
2:9:3092:G:H2'	2:9:3093:A:H8	1.80	0.47
1:0:2415:A:O2'	15:M:29:SER:HB3	2.14	0.47
1:0:1501:A:OP2	17:O:37:ARG:HD2	2.14	0.47
4:B:145:HIS:HD2	4:B:159:PRO:HB3	1.78	0.47
24:V:65:VAL:HA	24:V:68:THR:HG22	1.97	0.47
1:0:523:C:H2'	1:0:524:A:H8	1.79	0.47
4:B:304:PRO:HD2	4:B:307:ARG:HD2	1.95	0.47
6:D:39:ASP:O	6:D:43:GLU:HG3	2.14	0.47
1:0:1268:C:O2'	26:X:169:ARG:HB2	2.14	0.47
1:0:1714:C:O2'	1:0:1715:C:H5'	2.14	0.47
1:0:88:G:N7	29:1:28:LYS:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:99:ARG:HD2	14:L:167:GLY:CA	2.40	0.47
1:0:1116:U:O2'	1:0:1118:A:C2	2.51	0.47
1:0:475:G:H5'	5:C:74:ASP:OD2	2.14	0.47
21:S:21:LYS:HA	21:S:24:ARG:HG3	1.96	0.47
3:A:179:MET:HG2	3:A:186:TRP:CB	2.45	0.47
1:0:371:U:H2'	1:0:372:A:C8	2.49	0.47
1:0:2783:A:H2'	1:0:2784:A:C8	2.50	0.47
1:0:2791:U:H1'	1:0:2792:A:H5''	1.96	0.47
10:H:68:ALA:HB2	10:H:149:ALA:HB2	1.95	0.47
4:B:314:ALA:CB	4:B:317:PRO:HG3	2.44	0.47
1:0:1182:C:O2'	1:0:1192:A:H8	1.98	0.47
4:B:307:ARG:NH1	4:B:307:ARG:HG3	2.29	0.47
1:0:2044:G:OP1	25:W:23:HIS:HE1	1.96	0.47
1:0:1213:C:O2'	1:0:1214:G:H5'	2.15	0.47
1:0:522:U:O2'	1:0:1366:C:H5'	2.14	0.47
15:M:49:THR:HG22	15:M:50:LEU:N	2.29	0.47
1:0:177:A:H2'	1:0:178:U:O4'	2.13	0.47
1:0:1849:G:H1'	1:0:2011:A:N1	2.30	0.47
1:0:2114:C:O2'	1:0:2115:U:H5'	2.14	0.47
1:0:1666:C:C2'	1:0:1667:A:C5'	2.79	0.47
29:1:48:ASP:O	29:1:49:GLU:CB	2.62	0.47
4:B:43:GLY:O	4:B:308:LEU:HD12	2.14	0.47
25:W:54:ILE:HD12	25:W:85:VAL:HG23	1.95	0.47
10:H:136:VAL:CG2	10:H:137:ASN:N	2.77	0.47
6:D:162:ALA:O	6:D:166:ILE:HD13	2.14	0.47
6:D:25:MET:CE	6:D:41:LEU:HG	2.43	0.47
2:9:3014:G:H1'	15:M:1:ALA:HB2	1.96	0.47
1:0:1181:A:N1	1:0:1192:A:O2'	2.48	0.47
8:F:57:GLU:O	8:F:61:MET:HG3	2.15	0.47
1:0:926:A:H5'	13:K:39:GLU:OE2	2.15	0.47
14:L:48:ARG:NH1	14:L:52:LEU:HD21	2.29	0.47
1:0:255:A:H2'	1:0:256:C:C6	2.50	0.47
19:Q:113:HIS:HE1	19:Q:144:GLU:CD	2.18	0.47
1:0:1165:G:O3'	1:0:1174:A:H4'	2.14	0.47
24:V:11:VAL:O	24:V:12:ASN:HB2	2.14	0.47
1:0:1187:U:H1'	1:0:1189:A:H2	1.79	0.47
1:0:1422:U:H2'	1:0:1423:C:C6	2.50	0.47
4:B:201:ASP:OD2	4:B:312:ARG:NH1	2.48	0.47
4:B:97:LEU:O	4:B:98:THR:HG23	2.14	0.47
1:0:222:A:H2'	1:0:223:G:O4'	2.14	0.47
17:O:89:ASN:HB3	17:O:92:GLU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:602:A:O2'	1:0:605:C:H4'	2.14	0.47
22:T:33:SER:O	22:T:37:GLU:HG3	2.15	0.47
21:S:98:VAL:HG11	21:S:101:LEU:CD2	2.45	0.47
3:A:66:ARG:HH11	3:A:66:ARG:HB2	1.80	0.47
7:E:16:ASP:O	7:E:17:HIS:HB2	2.13	0.47
3:A:76:VAL:HG23	27:Y:63:LYS:HB3	1.97	0.47
7:E:10:ASP:O	7:E:10:ASP:OD1	2.33	0.47
6:D:140:ARG:HH11	6:D:140:ARG:HG3	1.79	0.47
5:C:194:PHE:CD2	5:C:234:VAL:HG11	2.49	0.47
1:0:2524:G:H21	1:0:2526:C:H5	1.60	0.47
1:0:778:C:C2	1:0:881:C:H5'	2.48	0.47
1:0:2657:G:OP1	4:B:17:LYS:HB2	2.14	0.47
1:0:451:C:O2'	1:0:452:G:H5'	2.14	0.47
16:N:98:LEU:O	16:N:102:ILE:HG13	2.15	0.47
24:V:52:VAL:CG2	24:V:53:ALA:H	2.27	0.47
6:D:19:GLU:O	6:D:133:ASN:HB3	2.15	0.47
12:J:74:VAL:HG12	12:J:75:ARG:HG3	1.97	0.47
13:K:41:HIS:H	13:K:41:HIS:CD2	2.31	0.47
4:B:5:ARG:HD2	4:B:8:LYS:NZ	2.29	0.47
11:I:19:MET:HE3	11:I:132:LEU:CG	2.44	0.47
21:S:42:VAL:C	21:S:43:ASN:HD22	2.18	0.47
7:E:126:ILE:HB	7:E:131:LEU:CD2	2.44	0.47
22:T:31:PHE:CG	22:T:37:GLU:HG2	2.49	0.47
5:C:61:PHE:CD1	5:C:65:ARG:HD2	2.50	0.47
1:0:1760:G:H5'	1:0:1818:C:O2'	2.14	0.47
1:0:949:U:C4'	18:P:95:GLU:HA	2.38	0.47
2:9:3092:G:H22	10:H:52:LYS:NZ	2.12	0.47
26:X:184:GLU:OE2	26:X:204:ARG:HD2	2.15	0.47
1:0:474:C:O3'	5:C:73:LEU:HD21	2.15	0.47
1:0:474:C:O2'	5:C:73:LEU:HD21	2.15	0.47
11:I:74:ARG:NH2	11:I:76:ASP:OD2	2.47	0.47
7:E:8:PRO:HB2	7:E:11:VAL:CG2	2.45	0.47
1:0:1512:G:O2'	1:0:1513:C:H5'	2.15	0.47
19:Q:113:HIS:HE1	19:Q:144:GLU:OE1	1.97	0.47
3:A:123:GLY:HA3	3:A:162:GLY:HA2	1.96	0.47
1:0:79:G:H22	1:0:97:G:H1'	1.80	0.47
1:0:105:G:O2'	1:0:106:A:H5'	2.14	0.47
1:0:2488:A:O2'	1:0:2489:G:H5'	2.15	0.47
23:U:43:PRO:O	23:U:46:ILE:HG22	2.14	0.47
1:0:2133:U:H4'	1:0:2134:G:H5'	1.95	0.47
36:0:8163:EMK:H12	36:0:8163:EMK:C23	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:84:ARG:NH2	10:H:135:TRP:HH2	2.14	0.46
6:D:167:GLU:C	6:D:169:THR:H	2.18	0.46
1:0:431:G:OP1	14:L:48:ARG:NH1	2.48	0.46
1:0:20:G:O3'	19:Q:3:SER:HB2	2.15	0.46
9:G:67:LEU:O	9:G:71:LEU:HG	2.15	0.46
1:0:1565:C:H2'	1:0:1566:C:H6	1.80	0.46
12:J:62:PRO:HG3	12:J:65:ARG:NH2	2.30	0.46
3:A:94:LEU:HG	3:A:99:ILE:CD1	2.46	0.46
14:L:19:GLN:O	14:L:22:GLU:HB3	2.15	0.46
14:L:52:LEU:HD13	14:L:116:ASN:HB3	1.97	0.46
4:B:14:GLY:CA	4:B:15:PRO:C	2.84	0.46
8:F:1:PRO:H3	8:F:4:VAL:HG23	1.80	0.46
4:B:162:MET:HE1	4:B:308:LEU:HD21	1.97	0.46
19:Q:104:PHE:HB3	19:Q:109:MET:CE	2.45	0.46
27:Y:57:CYS:SG	27:Y:60:CYS:SG	3.02	0.46
1:0:2721:U:C4'	12:J:87:ARG:HG3	2.45	0.46
1:0:2781:U:H1'	7:E:139:GLU:OE2	2.15	0.46
2:9:3050:G:H5''	15:M:159:TYR:CE1	2.50	0.46
1:0:503:G:H2'	1:0:504:G:H8	1.80	0.46
1:0:703:G:O2'	1:0:704:C:H5'	2.15	0.46
13:K:128:GLY:O	13:K:132:LYS:HG3	2.16	0.46
1:0:2104:C:O2	1:0:2485:A:N1	2.48	0.46
36:0:8163:EMK:H5	36:0:8163:EMK:H30	1.96	0.46
3:A:192:VAL:HA	3:A:201:PHE:O	2.14	0.46
6:D:35:ALA:C	6:D:37:ALA:N	2.68	0.46
13:K:124:ASP:OD1	13:K:149:ARG:NH2	2.48	0.46
6:D:57:THR:CG2	6:D:63:ILE:HA	2.46	0.46
1:0:612:U:H2'	1:0:613:C:C6	2.51	0.46
4:B:268:ARG:NH2	4:B:325:PRO:HG3	2.30	0.46
1:0:162:C:H2'	1:0:163:U:H5'	1.98	0.46
1:0:1321:A:H2'	1:0:1322:G:C8	2.51	0.46
1:0:622:G:P	26:X:148:GLY:HA3	2.55	0.46
1:0:2750:G:H2'	1:0:2751:C:C6	2.50	0.46
26:X:130:ARG:HB2	26:X:142:SER:O	2.16	0.46
16:N:21:SER:OG	16:N:106:PRO:HB2	2.15	0.46
10:H:15:THR:HG22	10:H:91:HIS:HA	1.97	0.46
10:H:131:ILE:HG23	10:H:132:PHE:HD1	1.79	0.46
20:R:51:GLN:HB3	20:R:67:ARG:NH1	2.30	0.46
5:C:136:VAL:HA	5:C:137:PRO:C	2.35	0.46
11:I:19:MET:HE3	11:I:132:LEU:HD11	1.95	0.46
21:S:26:THR:HG23	21:S:97:ARG:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:40:ILE:HD11	8:F:48:VAL:HG11	1.98	0.46
1:0:1335:C:H2'	1:0:1336:U:C6	2.50	0.46
1:0:70:A:H4'	1:0:71:G:O5'	2.16	0.46
1:0:473:A:OP1	28:Z:51:GLN:NE2	2.49	0.46
1:0:26:U:H2'	1:0:27:U:C6	2.51	0.46
1:0:1119:G:N2	1:0:1246:A:N1	2.63	0.46
15:M:67:ALA:HA	15:M:71:TRP:HB3	1.97	0.46
10:H:49:VAL:C	10:H:157:ILE:HG23	2.35	0.46
1:0:138:U:H5''	1:0:139:C:OP2	2.15	0.46
1:0:601:G:O2'	1:0:602:A:H5'	2.15	0.46
1:0:848:C:H2'	1:0:849:C:C6	2.50	0.46
3:A:70:ALA:HA	3:A:71:PRO:HD3	1.78	0.46
1:0:561:G:O2'	1:0:562:A:H5'	2.15	0.46
19:Q:4:TYR:CE1	19:Q:15:LYS:HD3	2.51	0.46
1:0:2472:C:O2'	1:0:2634:G:H4'	2.16	0.46
1:0:2379:G:N7	1:0:2408:A:N1	2.64	0.46
19:Q:106:GLY:HA2	19:Q:109:MET:CE	2.44	0.46
25:W:72:VAL:CG2	25:W:85:VAL:HB	2.45	0.46
5:C:162:VAL:HG13	5:C:232:LEU:HD21	1.98	0.46
7:E:7:ILE:HD11	7:E:11:VAL:O	2.15	0.46
1:0:2032:U:H2'	1:0:2033:G:H5'	1.97	0.46
1:0:1942:A:O2'	1:0:1943:C:H5'	2.15	0.46
1:0:1198:U:H1'	1:0:1201:C:C5	2.51	0.46
1:0:492:C:O2'	1:0:493:U:H5'	2.16	0.46
1:0:1654:U:H2'	3:A:47:HIS:HD2	1.79	0.46
6:D:159:PRO:O	6:D:163:VAL:HG23	2.15	0.46
1:0:1029:U:O2'	1:0:1273:C:OP1	2.30	0.46
1:0:2670:G:O2'	1:0:2671:U:H5'	2.16	0.46
1:0:1160:G:HO2'	1:0:1190:G:H8	1.63	0.46
19:Q:39:THR:HB	19:Q:42:GLU:CG	2.46	0.46
1:0:1845:A:OP2	3:A:190:ARG:NH1	2.49	0.46
1:0:2510:C:H42	1:0:2564:G:H22	1.63	0.46
14:L:37:VAL:HG13	14:L:63:VAL:CG1	2.43	0.46
4:B:62:ARG:HA	4:B:65:MET:HE1	1.98	0.46
1:0:638:C:H2'	1:0:639:A:H8	1.81	0.46
10:H:166:ASN:N	10:H:166:ASN:ND2	2.64	0.46
11:I:15:ARG:CZ	11:I:43:ARG:NH1	2.79	0.46
1:0:2389:U:H4'	18:P:53:HIS:HD2	1.81	0.46
1:0:702:G:O2'	1:0:703:G:H5'	2.15	0.46
10:H:75:SER:C	10:H:79:ALA:HB2	2.37	0.46
1:0:380:A:OP2	14:L:9:ARG:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:28:SER:O	21:S:32:ARG:HG3	2.16	0.46
5:C:142:ASP:OD1	5:C:237:GLU:HB3	2.15	0.46
1:O:2672:C:O2'	1:O:2673:U:H5'	2.16	0.46
8:F:79:GLN:HB2	8:F:82:ASP:OD2	2.16	0.46
3:A:190:ARG:HH11	3:A:190:ARG:HG3	1.81	0.46
14:L:114:VAL:CG2	14:L:159:THR:HG21	2.46	0.46
1:O:2704:C:O2	7:E:110:GLU:HB3	2.16	0.46
7:E:126:ILE:HB	7:E:131:LEU:HD23	1.98	0.46
1:O:372:A:H2'	1:O:373:G:H8	1.81	0.46
1:O:1527:A:H1'	1:O:1528:A:C8	2.51	0.46
14:L:155:HIS:CE1	14:L:158:ARG:HH21	2.34	0.46
1:O:2429:A:H2'	1:O:2430:A:C8	2.51	0.46
1:O:1304:U:H2'	1:O:1305:C:C6	2.51	0.46
1:O:17:G:O2'	1:O:18:C:H5'	2.16	0.46
1:O:1353:C:N3	13:K:5:LYS:NZ	2.63	0.46
15:M:69:TYR:N	15:M:69:TYR:CD1	2.83	0.46
1:O:2121:G:O2'	1:O:2122:C:H5'	2.16	0.46
3:A:64:ASP:OD2	3:A:64:ASP:N	2.49	0.46
28:Z:25:LYS:O	28:Z:25:LYS:HG2	2.16	0.46
6:D:166:ILE:N	6:D:166:ILE:HD12	2.30	0.46
1:O:862:U:O2'	1:O:863:G:H5'	2.16	0.46
5:C:145:GLU:OE1	5:C:198:ASP:HB2	2.15	0.46
1:O:932:U:H2'	1:O:933:C:C6	2.51	0.46
18:P:21:ARG:HG2	18:P:22:GLY:N	2.31	0.46
10:H:55:GLN:HE21	10:H:124:ARG:HG2	1.81	0.45
1:O:286:U:H2'	1:O:287:C:C6	2.52	0.45
14:L:102:GLU:CD	14:L:164:THR:HG21	2.34	0.45
10:H:53:PRO:O	10:H:54:VAL:HG13	2.16	0.45
5:C:193:LEU:HD12	5:C:211:ASP:O	2.15	0.45
15:M:78:MET:HB2	15:M:79:PRO:HD3	1.98	0.45
27:Y:20:LEU:O	27:Y:24:VAL:HG23	2.16	0.45
1:O:263:U:C2	8:F:59:ILE:CD1	2.99	0.45
1:O:2011:A:H4'	1:O:2012:U:O5'	2.16	0.45
15:M:69:TYR:HE2	15:M:183:ASP:OD2	1.99	0.45
20:R:10:VAL:HG11	23:U:36:ALA:HA	1.98	0.45
1:O:1636:G:O2'	1:O:1637:A:H5'	2.16	0.45
29:1:40:ARG:HG3	29:1:45:ASN:CB	2.46	0.45
1:O:2681:A:H4'	1:O:2682:C:H5'	1.98	0.45
1:O:1182:C:H4'	1:O:1192:A:N7	2.31	0.45
23:U:39:ALA:N	23:U:40:PRO:HD2	2.30	0.45
13:K:38:HIS:CD2	13:K:39:GLU:HG3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:19:MET:CE	11:I:132:LEU:HD21	2.46	0.45
27:Y:31:ILE:CG2	27:Y:32:LYS:N	2.79	0.45
1:0:1318:A:H4'	1:0:1343:C:H4'	1.99	0.45
19:Q:95:ALA:HB2	19:Q:145:LEU:HD23	1.98	0.45
6:D:93:LEU:HD12	6:D:97:GLN:HE22	1.80	0.45
1:0:279:C:H42	1:0:370:G:H1	1.64	0.45
1:0:1008:C:H2'	1:0:1009:U:C6	2.51	0.45
6:D:48:MET:HA	6:D:49:PRO:HD3	1.81	0.45
4:B:195:ARG:HD2	4:B:324:ASP:OD1	2.16	0.45
11:I:88:PRO:HG2	11:I:94:GLY:HA3	1.98	0.45
6:D:62:ASP:C	6:D:64:ARG:N	2.69	0.45
1:0:2003:U:H4'	1:0:2004:U:C5	2.37	0.45
1:0:1002:G:C2'	1:0:1003:U:H5''	2.40	0.45
12:J:81:ARG:HD3	12:J:87:ARG:CZ	2.47	0.45
1:0:1463:A:O5'	1:0:1463:A:H8	1.98	0.45
3:A:36:ASP:HA	3:A:83:GLY:HA3	1.97	0.45
1:0:2112:A:H2'	1:0:2113:G:H8	1.80	0.45
6:D:92:GLU:O	6:D:93:LEU:O	2.35	0.45
1:0:2329:C:O2'	1:0:2330:U:H5'	2.15	0.45
25:W:34:ARG:NH1	25:W:48:VAL:O	2.48	0.45
1:0:1220:U:H2'	1:0:1221:G:H8	1.81	0.45
1:0:631:A:C6	1:0:2074:A:H5'	2.52	0.45
1:0:1131:G:C6	1:0:1230:A:C4	3.04	0.45
9:G:24:VAL:O	9:G:28:GLU:HG3	2.16	0.45
6:D:88:LEU:N	6:D:89:PRO:CD	2.80	0.45
1:0:249:G:O2'	1:0:250:C:H5'	2.16	0.45
4:B:162:MET:HE2	4:B:310:ARG:CD	2.33	0.45
17:O:37:ARG:HG2	17:O:37:ARG:HH11	1.82	0.45
21:S:24:ARG:NH2	21:S:39:ASN:HD22	2.15	0.45
1:0:1596:U:H2'	1:0:1598:A:OP2	2.17	0.45
1:0:2274:A:O2'	1:0:2275:G:H5'	2.16	0.45
1:0:2690:U:O2'	7:E:111:LYS:HD2	2.16	0.45
1:0:1471:A:H2'	1:0:1472:C:C6	2.51	0.45
15:M:7:LYS:HE2	15:M:8:VAL:O	2.16	0.45
17:O:18:LYS:O	17:O:21:VAL:HG13	2.15	0.45
1:0:883:U:H2'	1:0:883:U:O2	2.17	0.45
23:U:13:PRO:HA	23:U:16:ARG:NH1	2.31	0.45
1:0:368:C:H2'	1:0:369:G:O4'	2.16	0.45
20:R:37:VAL:O	20:R:41:VAL:HG23	2.16	0.45
28:Z:21:ARG:HD2	28:Z:37:CYS:SG	2.56	0.45
1:0:876:A:N3	1:0:876:A:C2'	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1225:C:H2'	1:0:1226:G:O4'	2.17	0.45
1:0:329:A:OP2	5:C:206:ASN:HB2	2.16	0.45
25:W:25:ARG:HD3	25:W:64:ALA:O	2.17	0.45
1:0:295:C:O2'	1:0:296:G:H5'	2.17	0.45
12:J:34:VAL:HG22	12:J:47:ALA:HB2	1.97	0.45
19:Q:104:PHE:CB	19:Q:109:MET:HE1	2.47	0.45
10:H:84:ARG:CZ	10:H:135:TRP:CH2	2.99	0.45
10:H:45:GLN:NE2	10:H:135:TRP:HE1	2.15	0.45
24:V:90:TYR:CE2	24:V:99:ALA:HB2	2.52	0.45
1:0:2839:C:H2'	1:0:2840:A:H5''	1.98	0.45
14:L:138:HIS:C	14:L:139:PRO:O	2.55	0.45
14:L:47:ASP:CG	14:L:48:ARG:N	2.69	0.45
22:T:6:CYS:HB2	22:T:32:CYS:HB3	1.99	0.45
10:H:31:PHE:HD2	10:H:85:ILE:O	2.00	0.45
4:B:157:LYS:O	4:B:159:PRO:HD3	2.17	0.45
1:0:1943:C:H4'	3:A:211:LYS:O	2.17	0.45
1:0:1249:U:H2'	1:0:1250:C:C6	2.51	0.45
10:H:75:SER:O	10:H:79:ALA:HB2	2.17	0.45
1:0:1006:A:N1	1:0:2311:A:H1'	2.31	0.45
1:0:1794:G:N2	1:0:1796:A:H3'	2.32	0.45
22:T:9:CYS:CB	22:T:52:THR:HG22	2.47	0.45
1:0:1041:U:H4'	1:0:1295:G:H5'	1.98	0.45
7:E:108:LEU:HD13	7:E:164:ASP:HB2	1.98	0.45
12:J:90:PHE:CD1	12:J:90:PHE:N	2.85	0.45
8:F:58:GLU:HA	8:F:61:MET:CE	2.44	0.45
13:K:66:VAL:HG23	13:K:67:ARG:N	2.31	0.45
14:L:83:SER:HA	14:L:86:MET:HE2	1.98	0.45
1:0:2362:A:H2'	1:0:2363:G:C8	2.52	0.45
1:0:999:C:H2'	1:0:1000:C:O4'	2.16	0.45
15:M:182:GLY:O	15:M:183:ASP:O	2.35	0.45
1:0:2125:G:H2'	1:0:2126:C:C6	2.51	0.45
1:0:835:U:P	4:B:229:ARG:HH12	2.39	0.45
1:0:2517:A:O2'	1:0:2518:C:H5'	2.16	0.45
12:J:55:VAL:CG1	12:J:56:SER:N	2.79	0.45
1:0:544:G:C3'	1:0:545:G:H5''	2.46	0.45
14:L:12:TRP:HH2	14:L:24:MET:HE1	1.81	0.45
1:0:836:G:OP1	4:B:230:GLN:CD	2.55	0.45
1:0:2694:A:H4'	7:E:91:PHE:HE1	1.82	0.45
8:F:46:GLU:O	8:F:73:PRO:HD2	2.16	0.45
4:B:102:THR:HG23	4:B:182:VAL:HG12	1.98	0.45
6:D:63:ILE:HD12	6:D:63:ILE:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:65:ARG:O	12:J:66:ARG:HB2	2.17	0.45
1:0:1142:C:O2'	1:0:1143:G:H5'	2.17	0.45
1:0:1155:G:H2'	1:0:1156:C:C6	2.52	0.45
1:0:1829:A:H61	27:Y:18:TYR:H	1.63	0.45
13:K:145:LEU:HD23	13:K:145:LEU:O	2.17	0.45
1:0:1160:G:H5'	1:0:1161:A:C4'	2.46	0.45
11:I:107:ASN:ND2	11:I:107:ASN:C	2.66	0.45
4:B:145:HIS:CD2	4:B:146:THR:O	2.69	0.45
1:0:1328:A:OP1	26:X:169:ARG:HD2	2.17	0.45
15:M:151:ASP:OD1	15:M:166:ALA:HA	2.16	0.45
1:0:1415:G:H5'	28:Z:12:ASN:O	2.17	0.45
1:0:2831:C:O3'	19:Q:71:LYS:HE2	2.16	0.45
26:X:126:PRO:HD2	26:X:128:PHE:CE1	2.52	0.45
21:S:19:ARG:HD3	21:S:67:LEU:O	2.17	0.45
4:B:294:TYR:C	4:B:294:TYR:CD1	2.90	0.45
1:0:1930:A:H2'	1:0:1931:A:C8	2.52	0.45
14:L:107:ARG:NH1	14:L:107:ARG:CG	2.73	0.45
6:D:51:ARG:HD3	6:D:68:PRO:HB3	1.99	0.45
2:9:3014:G:C2'	2:9:3015:C:H5'	2.47	0.45
2:9:3014:G:H2'	2:9:3015:C:H5'	1.99	0.45
1:0:2909:G:H2'	1:0:2910:A:H8	1.82	0.45
21:S:112:LEU:CD2	21:S:119:ALA:HB3	2.46	0.45
5:C:115:LEU:O	5:C:118:THR:HB	2.15	0.45
1:0:1927:A:O2'	1:0:1928:C:H5'	2.17	0.45
11:I:142:ASN:O	11:I:144:THR:N	2.50	0.45
1:0:1334:C:O2'	1:0:1335:C:H5'	2.16	0.45
1:0:667:C:H2'	1:0:668:C:C6	2.52	0.45
1:0:407:A:H2'	1:0:408:A:C8	2.52	0.45
17:O:55:LYS:CG	17:O:56:GLY:N	2.80	0.45
20:R:38:ALA:O	20:R:42:GLU:HG3	2.17	0.45
1:0:2281:C:H2'	1:0:2282:U:H5'	2.00	0.45
1:0:1945:G:O2'	1:0:1946:C:H5'	2.17	0.45
1:0:226:A:H1'	1:0:393:G:C5	2.52	0.45
18:P:50:GLY:HA3	18:P:87:THR:OG1	2.17	0.45
1:0:293:A:O2'	1:0:294:C:H5'	2.17	0.45
1:0:2388:C:H5'	18:P:83:THR:O	2.16	0.45
5:C:19:PRO:HG2	5:C:22:PHE:CE1	2.51	0.45
14:L:167:GLY:O	14:L:171:ARG:HG3	2.17	0.44
23:U:64:GLY:O	23:U:65:ASP:CB	2.65	0.44
1:0:1210:G:O2'	1:0:1211:G:H5'	2.17	0.44
6:D:103:ASN:HD21	6:D:133:ASN:HD22	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:32:ARG:HH21	16:N:35:LYS:HZ2	1.63	0.44
1:0:2781:U:C2'	1:0:2782:G:H5'	2.47	0.44
27:Y:32:LYS:HA	27:Y:35:LYS:HE3	1.99	0.44
1:0:1419:U:H5'	1:0:1420:C:OP2	2.17	0.44
1:0:79:G:N2	1:0:97:G:H1'	2.32	0.44
1:0:1486:A:C5	29:1:2:LYS:HG3	2.51	0.44
4:B:138:GLY:O	4:B:139:ASP:O	2.35	0.44
1:0:1400:C:O2'	1:0:1401:G:H5'	2.17	0.44
1:0:793:A:H5''	17:O:83:LYS:HG2	2.00	0.44
1:0:895:A:H2'	1:0:896:C:C6	2.52	0.44
7:E:68:HIS:O	7:E:72:MET:HG3	2.16	0.44
1:0:2754:G:H2'	1:0:2755:G:O4'	2.17	0.44
1:0:830:G:O2'	1:0:831:U:H5'	2.17	0.44
2:9:3107:C:O2'	2:9:3108:C:H5'	2.18	0.44
10:H:55:GLN:HE21	10:H:124:ARG:CG	2.31	0.44
19:Q:96:VAL:HG13	19:Q:106:GLY:HA3	1.99	0.44
10:H:45:GLN:NE2	10:H:135:TRP:NE1	2.65	0.44
14:L:138:HIS:HD1	14:L:139:PRO:N	2.16	0.44
1:0:1163:G:N1	1:0:1184:C:C4	2.86	0.44
1:0:258:G:O2'	1:0:259:G:H5'	2.18	0.44
7:E:5:LEU:HD21	7:E:66:GLN:CG	2.45	0.44
5:C:118:THR:HG22	5:C:137:PRO:HB3	1.99	0.44
1:0:907:A:H2'	1:0:908:A:C8	2.51	0.44
1:0:1761:U:H2'	1:0:1762:C:C6	2.52	0.44
1:0:1847:A:OP1	3:A:175:LYS:HG3	2.17	0.44
1:0:843:A:C2	1:0:846:A:C8	3.05	0.44
24:V:31:HIS:HB3	24:V:115:THR:HG21	1.98	0.44
1:0:2735:U:H2'	1:0:2736:U:C6	2.52	0.44
22:T:4:ARG:HG2	22:T:5:GLU:N	2.33	0.44
1:0:2123:A:H5'	14:L:89:ASN:HD21	1.83	0.44
1:0:1060:C:H6	1:0:1060:C:H5'	1.82	0.44
14:L:74:ARG:HD3	14:L:91:ILE:HD12	1.98	0.44
10:H:84:ARG:NH2	10:H:135:TRP:CH2	2.86	0.44
1:0:1211:G:O2'	1:0:1212:C:H5'	2.18	0.44
1:0:1181:A:H2'	1:0:1182:C:H5'	1.99	0.44
7:E:66:GLN:O	7:E:70:GLU:HG3	2.17	0.44
1:0:1942:A:H5''	3:A:233:THR:OG1	2.18	0.44
1:0:750:A:O3'	5:C:101:ASP:HB2	2.17	0.44
3:A:125:ASN:CB	3:A:158:VAL:HG12	2.47	0.44
1:0:2269:C:C2'	1:0:2270:G:H5'	2.47	0.44
1:0:1426:C:C5	1:0:1435:U:H5''	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:128:LEU:HD12	3:A:129:LEU:H	1.82	0.44
5:C:127:ARG:HH11	5:C:127:ARG:HG2	1.82	0.44
8:F:81:ASP:HA	8:F:92:GLY:HA2	2.00	0.44
1:0:2032:U:C2'	1:0:2033:G:H5''	2.47	0.44
8:F:36:THR:O	8:F:39:SER:HB3	2.17	0.44
1:0:1268:C:O2'	1:0:1269:G:H5'	2.17	0.44
3:A:128:LEU:HD12	3:A:129:LEU:N	2.32	0.44
1:0:958:G:O2'	1:0:959:C:H5'	2.17	0.44
1:0:1386:G:O2'	1:0:1387:G:H5'	2.17	0.44
7:E:20:ILE:CD1	7:E:40:VAL:HG11	2.36	0.44
3:A:192:VAL:HG23	3:A:201:PHE:HB3	1.99	0.44
12:J:28:GLU:HG2	12:J:58:THR:HB	2.00	0.44
1:0:259:G:O2'	1:0:260:C:H5'	2.17	0.44
1:0:1015:C:H2'	1:0:1016:U:C6	2.52	0.44
1:0:1481:G:H2'	1:0:1482:A:O4'	2.18	0.44
1:0:1869:A:H2'	1:0:1870:C:O4'	2.18	0.44
2:9:3069:U:OP1	15:M:4:PRO:HG3	2.17	0.44
24:V:88:THR:HG22	24:V:89:ASP:H	1.83	0.44
1:0:2592:G:H2'	1:0:2593:C:H6	1.82	0.44
14:L:57:LYS:HB3	14:L:60:ILE:HD12	1.99	0.44
1:0:1181:A:O2'	1:0:1182:C:H5'	2.17	0.44
1:0:1384:C:H5'	25:W:30:MET:HG2	2.00	0.44
1:0:2697:A:H2'	1:0:2698:G:O4'	2.17	0.44
1:0:309:C:OP1	21:S:97:ARG:NH2	2.50	0.44
17:O:27:ARG:HH21	17:O:30:ASP:CG	2.21	0.44
2:9:3036:C:N4	2:9:3048:C:H1'	2.33	0.44
1:0:2898:G:O3'	4:B:288:GLY:HA2	2.17	0.44
2:9:3052:A:O2'	2:9:3053:G:H5'	2.17	0.44
1:0:2821:C:H2'	1:0:2822:C:H6	1.82	0.44
7:E:158:ASP:O	7:E:162:PHE:HD1	2.01	0.44
14:L:37:VAL:HG22	14:L:65:VAL:HG22	2.00	0.44
2:9:3049:G:C2'	2:9:3050:G:H5'	2.48	0.44
13:K:144:ASP:HA	13:K:147:GLU:HG3	1.98	0.44
5:C:88:SER:O	5:C:91:PRO:HD3	2.18	0.44
1:0:326:G:O2'	1:0:327:A:H5'	2.17	0.44
1:0:1482:A:O2'	1:0:1483:C:H5'	2.18	0.44
19:Q:34:GLU:HG2	19:Q:46:TYR:OH	2.17	0.44
4:B:101:TRP:HB2	4:B:119:HIS:CD2	2.53	0.44
5:C:55:ARG:NH2	28:Z:56:GLU:OE2	2.45	0.44
28:Z:25:LYS:CD	29:1:49:GLU:H	2.17	0.44
24:V:139:GLY:O	24:V:141:HIS:CD2	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2462:G:N7	30:2:60:LYS:NZ	2.66	0.44
26:X:99:ALA:HB2	26:X:233:TYR:CZ	2.53	0.44
16:N:14:LEU:CD2	16:N:102:ILE:HD11	2.48	0.44
1:0:1741:U:O2'	1:0:2723:G:H4'	2.18	0.44
2:9:3065:A:H61	2:9:3112:U:H2'	1.81	0.44
1:0:2276:U:H2'	1:0:2277:U:C6	2.53	0.44
1:0:445:U:O2'	1:0:446:G:H5'	2.17	0.44
1:0:2015:A:H2'	1:0:2016:U:O4'	2.18	0.44
6:D:166:ILE:O	6:D:169:THR:N	2.51	0.44
1:0:1166:A:H1'	1:0:1192:A:H2	1.81	0.44
4:B:79:MET:O	4:B:187:GLU:HA	2.17	0.44
1:0:23:G:H1'	1:0:520:A:N6	2.33	0.44
8:F:20:LEU:HD12	8:F:98:VAL:HG22	2.00	0.44
1:0:161:A:H2'	1:0:162:C:H6	1.82	0.44
1:0:2712:G:O2'	1:0:2713:G:H5'	2.18	0.44
1:0:2906:A:H5'	1:0:2907:C:O4'	2.17	0.44
1:0:420:U:H2'	1:0:421:C:C6	2.52	0.44
1:0:920:C:OP1	13:K:37:LYS:NZ	2.51	0.44
1:0:2568:A:H2'	1:0:2569:A:O4'	2.18	0.44
36:0:8163:EMK:C13	36:0:8163:EMK:H15	2.48	0.43
10:H:55:GLN:HE22	10:H:91:HIS:CD2	2.36	0.43
1:0:2504:A:H2'	1:0:2505:G:O4'	2.18	0.43
14:L:37:VAL:CG1	14:L:108:LYS:HG3	2.46	0.43
25:W:78:GLU:CG	25:W:79:GLU:N	2.81	0.43
1:0:396:U:O2'	1:0:397:A:P	2.76	0.43
1:0:1204:C:H2'	1:0:1205:U:C4'	2.48	0.43
2:9:3002:U:P	2:9:3003:A:H5'	2.58	0.43
5:C:77:ALA:O	5:C:78:ARG:HG2	2.18	0.43
10:H:85:ILE:HG23	10:H:85:ILE:O	2.18	0.43
5:C:140:VAL:CG1	5:C:141:SER:N	2.81	0.43
17:O:8:ARG:HG2	17:O:8:ARG:NH1	2.31	0.43
1:0:1946:C:H2'	1:0:1971:G:C8	2.53	0.43
1:0:2432:C:O2'	1:0:2433:A:H5'	2.18	0.43
11:I:80:LYS:HE2	11:I:98:PHE:CE1	2.52	0.43
1:0:2300:A:H4'	1:0:2301:A:O5'	2.18	0.43
14:L:114:VAL:HB	14:L:159:THR:HG23	1.98	0.43
3:A:88:ILE:HG22	3:A:88:ILE:O	2.18	0.43
3:A:94:LEU:N	3:A:94:LEU:HD23	2.33	0.43
30:2:3:MET:HG3	30:2:4:PRO:HD2	2.00	0.43
1:0:731:U:O2'	1:0:732:C:H5'	2.18	0.43
2:9:3041:C:H5''	6:D:48:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:77:ALA:HA	16:N:96:VAL:O	2.18	0.43
12:J:41:LYS:O	12:J:42:ASN:HB2	2.18	0.43
1:0:241:A:C2	1:0:378:A:H4'	2.53	0.43
1:0:2314:G:C2'	1:0:2315:C:H5'	2.48	0.43
25:W:28:LYS:HA	25:W:28:LYS:HE3	2.00	0.43
1:0:2646:G:C8	36:0:8163:EMK:H17A	2.54	0.43
1:0:287:C:H2'	1:0:288:A:C8	2.53	0.43
11:I:52:GLN:HG3	11:I:53:ILE:N	2.34	0.43
24:V:88:THR:HG22	24:V:90:TYR:CD1	2.34	0.43
23:U:20:LEU:HD11	23:U:53:ILE:HG23	2.00	0.43
7:E:102:VAL:HG22	7:E:116:THR:HG23	1.99	0.43
1:0:2781:U:O2'	1:0:2782:G:H5'	2.18	0.43
6:D:27:ILE:H	6:D:27:ILE:CD1	2.31	0.43
4:B:41:PHE:CE1	4:B:79:MET:HG3	2.53	0.43
5:C:233:THR:HG22	5:C:234:VAL:H	1.83	0.43
4:B:141:ARG:HD2	4:B:163:GLU:OE2	2.19	0.43
1:0:327:A:H2'	5:C:150:THR:OG1	2.18	0.43
4:B:108:GLU:HB3	4:B:111:ARG:HD2	1.99	0.43
1:0:1158:G:O2'	1:0:1159:G:H5'	2.18	0.43
1:0:527:U:H2'	1:0:528:G:H8	1.83	0.43
1:0:2105:C:H2'	1:0:2106:C:C6	2.53	0.43
24:V:48:VAL:HG12	24:V:52:VAL:CG1	2.48	0.43
3:A:164:ARG:HB2	27:Y:68:CYS:SG	2.58	0.43
10:H:48:LEU:CG	10:H:157:ILE:HG21	2.44	0.43
14:L:23:LEU:O	14:L:26:HIS:HB2	2.18	0.43
1:0:506:G:H22	1:0:509:A:H5''	1.83	0.43
1:0:1739:G:O2'	1:0:1740:U:H5'	2.18	0.43
29:1:25:VAL:O	29:1:29:THR:HG23	2.17	0.43
1:0:327:A:H4'	1:0:329:A:C8	2.54	0.43
1:0:2793:A:H2'	1:0:2794:G:H5'	2.00	0.43
1:0:677:C:O2'	1:0:678:G:H5'	2.18	0.43
1:0:690:G:H4'	1:0:741:C:O2	2.18	0.43
2:9:3044:A:O4'	6:D:76:ARG:NE	2.52	0.43
4:B:24:PRO:CG	4:B:204:GLY:HA2	2.49	0.43
1:0:196:G:H1'	1:0:198:A:N7	2.34	0.43
1:0:1840:A:H4'	1:0:1841:C:O5'	2.18	0.43
1:0:1204:C:H2'	1:0:1205:U:H5''	2.00	0.43
8:F:102:GLY:C	8:F:104:ALA:N	2.71	0.43
5:C:57:PRO:HG2	5:C:73:LEU:CD1	2.48	0.43
1:0:2266:A:OP2	14:L:90:ARG:NH2	2.51	0.43
5:C:193:LEU:HA	5:C:211:ASP:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1167:G:H2'	1:0:1168:C:C6	2.54	0.43
1:0:2256:G:C2'	1:0:2257:G:H5'	2.48	0.43
1:0:2091:G:O3'	4:B:235:ARG:HD3	2.17	0.43
1:0:1295:G:H5''	13:K:14:GLY:O	2.19	0.43
1:0:661:G:C5	1:0:686:A:C2	3.06	0.43
21:S:48:VAL:O	21:S:59:GLU:HG3	2.18	0.43
21:S:48:VAL:HG22	21:S:96:VAL:HG22	2.01	0.43
5:C:218:VAL:O	5:C:246:ARG:NH2	2.52	0.43
1:0:90:A:H2'	1:0:91:G:O4'	2.18	0.43
1:0:1525:G:H5'	1:0:1526:A:OP2	2.19	0.43
19:Q:17:MET:HE1	19:Q:19:ARG:NH2	2.33	0.43
1:0:1538:C:O2'	1:0:1539:U:H5'	2.18	0.43
1:0:1524:U:OP1	1:0:1524:U:H4'	2.18	0.43
6:D:67:ASP:O	6:D:69:ILE:HD13	2.19	0.43
29:1:40:ARG:HG3	29:1:45:ASN:HB2	2.00	0.43
15:M:90:LEU:HD13	15:M:186:LEU:HD21	2.00	0.43
5:C:27:ARG:HG2	5:C:30:LEU:HG	1.99	0.43
30:2:11:CYS:HB2	30:2:20:HIS:HE1	1.82	0.43
1:0:291:C:H2'	1:0:292:G:O4'	2.19	0.43
1:0:1154:A:H2'	1:0:1155:G:C8	2.54	0.43
1:0:1257:C:O2'	1:0:1258:G:H5'	2.19	0.43
22:T:39:ASN:ND2	22:T:44:ARG:HH11	2.16	0.43
1:0:1171:A:H2'	1:0:1172:G:O4'	2.19	0.43
1:0:366:U:H2'	1:0:367:G:O4'	2.18	0.43
1:0:1603:A:H5''	1:0:1604:G:H3'	2.00	0.43
1:0:1211:G:H2'	1:0:1212:C:C6	2.53	0.43
1:0:861:A:H2'	1:0:862:U:C6	2.54	0.43
15:M:37:ARG:NH2	15:M:103:ASP:OD1	2.52	0.43
10:H:57:ARG:HB3	10:H:59:ASN:ND2	2.30	0.43
1:0:185:G:C4'	1:0:186:A:H4'	2.49	0.43
1:0:790:A:H2'	1:0:791:A:O4'	2.19	0.43
25:W:21:PRO:HG2	25:W:24:LYS:HD2	2.00	0.43
21:S:48:VAL:HG21	21:S:96:VAL:CG1	2.48	0.43
2:9:3059:C:H2'	2:9:3060:C:C6	2.54	0.43
7:E:105:GLU:HG2	7:E:113:PRO:HB3	2.00	0.43
15:M:33:ARG:O	15:M:47:LEU:HA	2.18	0.43
1:0:1535:G:H2'	1:0:1536:C:C6	2.53	0.43
1:0:2758:G:H2'	1:0:2759:C:C6	2.53	0.43
6:D:51:ARG:NH1	6:D:68:PRO:HG2	2.33	0.43
1:0:1119:G:H8	11:I:52:GLN:NE2	2.17	0.43
14:L:37:VAL:HG21	14:L:108:LYS:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:41:VAL:HG12	27:Y:42:CYS:N	2.33	0.43
1:0:1072:G:OP2	26:X:154:ARG:NH2	2.50	0.43
1:0:1306:U:OP1	5:C:184:ARG:HD2	2.19	0.43
1:0:1909:A:N1	1:0:2128:G:H1'	2.34	0.43
1:0:945:U:H2'	1:0:946:C:H6	1.84	0.43
1:0:301:G:O2'	1:0:302:A:H5'	2.19	0.43
13:K:68:GLU:O	13:K:72:ASN:ND2	2.50	0.43
1:0:1985:U:C2	1:0:1996:U:O4'	2.72	0.43
13:K:134:GLU:O	13:K:137:GLY:N	2.48	0.43
1:0:2587:U:H2'	1:0:2589:U:H5''	2.00	0.43
1:0:111:C:C2'	1:0:112:G:H5'	2.49	0.43
1:0:2716:G:C5'	4:B:206:THR:HG21	2.44	0.43
1:0:2415:A:C2'	1:0:2416:G:H5'	2.48	0.43
14:L:115:LEU:HB2	14:L:134:ILE:HG12	2.00	0.43
1:0:1594:C:C5	17:O:120:ARG:NH1	2.87	0.43
6:D:10:PHE:CG	6:D:11:HIS:N	2.87	0.43
1:0:2039:A:OP2	4:B:234:ARG:NH2	2.51	0.43
1:0:1267:C:O2'	1:0:1268:C:H5'	2.19	0.43
1:0:751:U:H5''	5:C:100:LEU:HD22	2.01	0.43
1:0:2580:G:N3	1:0:2600:A:H2	2.16	0.43
1:0:2425:A:H5'	1:0:2426:G:OP2	2.19	0.43
1:0:2348:C:H2'	1:0:2349:G:H8	1.84	0.43
1:0:963:C:H2'	1:0:964:G:C8	2.54	0.43
1:0:2385:G:H2'	1:0:2386:U:C6	2.54	0.43
1:0:1367:A:C2'	1:0:1368:U:H5'	2.49	0.43
36:0:8163:EMK:H9	36:0:8163:EMK:C7	2.44	0.43
23:U:16:ARG:NH1	23:U:65:ASP:O	2.52	0.43
1:0:1134:G:C8	1:0:1134:G:O5'	2.71	0.43
1:0:2502:C:H2'	1:0:2503:A:C5'	2.47	0.43
24:V:89:ASP:HB2	24:V:90:TYR:CE1	2.52	0.43
4:B:51:VAL:HG12	4:B:53:LEU:HD13	1.97	0.43
15:M:23:ARG:NH2	15:M:55:ASP:OD2	2.52	0.43
1:0:2443:C:H5'	13:K:57:VAL:HG21	2.00	0.43
5:C:27:ARG:N	5:C:113:SER:OG	2.51	0.43
14:L:23:LEU:HD22	14:L:27:ARG:CZ	2.49	0.43
1:0:797:A:H5'	27:Y:10:ARG:HG2	2.01	0.43
8:F:39:SER:OG	8:F:45:ALA:HB2	2.19	0.43
1:0:17:G:H2'	1:0:18:C:C6	2.54	0.43
11:I:63:ILE:HG22	11:I:64:GLY:N	2.33	0.43
1:0:1056:U:H2'	1:0:1057:A:O4'	2.18	0.43
5:C:20:ASP:O	5:C:23:GLU:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:74:ARG:NH1	14:L:74:ARG:HG3	2.34	0.42
1:O:1211:G:H2'	1:O:1212:C:H6	1.83	0.42
20:R:57:THR:HG22	20:R:59:ASP:H	1.84	0.42
15:M:26:LEU:HA	15:M:26:LEU:HD12	1.87	0.42
1:O:1734:C:OP1	4:B:234:ARG:HD3	2.19	0.42
2:9:3072:C:H2'	2:9:3073:G:C8	2.54	0.42
12:J:34:VAL:HG21	12:J:46:LYS:O	2.19	0.42
7:E:69:ILE:HG12	7:E:72:MET:HE3	2.00	0.42
24:V:31:HIS:HB3	24:V:115:THR:CG2	2.49	0.42
1:O:660:A:H4'	1:O:661:G:O5'	2.19	0.42
7:E:75:GLY:O	7:E:79:GLY:HA2	2.19	0.42
4:B:274:GLU:HA	4:B:292:GLY:O	2.19	0.42
16:N:49:GLU:OE1	16:N:70:LEU:HA	2.19	0.42
1:O:1689:A:OP2	1:O:1689:A:H8	2.02	0.42
12:J:30:LYS:O	12:J:55:VAL:HG13	2.18	0.42
1:O:1244:U:H4'	1:O:1246:A:O4'	2.19	0.42
4:B:214:PRO:HB2	4:B:220:VAL:HG21	2.01	0.42
1:O:2499:U:H2'	1:O:2500:C:H6	1.84	0.42
17:O:142:ASP:O	17:O:143:ALA:O	2.37	0.42
1:O:483:C:C4	1:O:484:A:C6	3.07	0.42
1:O:245:C:H2'	1:O:246:G:H5'	2.00	0.42
1:O:2550:U:O2'	1:O:2551:C:H5'	2.19	0.42
1:O:654:A:OP2	16:N:38:ARG:HD3	2.19	0.42
22:T:41:ASP:C	22:T:43:GLY:H	2.21	0.42
1:O:2779:G:H21	7:E:143:GLN:NE2	2.17	0.42
14:L:187:LEU:HD23	14:L:194:ALA:HB3	2.00	0.42
3:A:32:VAL:O	3:A:33:GLU:C	2.56	0.42
15:M:22:GLN:O	15:M:26:LEU:HB2	2.19	0.42
6:D:24:HIS:HB2	6:D:72:LYS:HB3	1.99	0.42
7:E:7:ILE:HA	7:E:8:PRO:HD3	1.91	0.42
13:K:107:LYS:HE3	13:K:124:ASP:OD2	2.19	0.42
1:O:204:A:H2'	1:O:205:U:H5'	2.00	0.42
5:C:194:PHE:HA	5:C:234:VAL:HG13	2.02	0.42
1:O:1964:U:H2'	1:O:1965:C:H6	1.84	0.42
1:O:1102:C:H2'	1:O:1103:C:C6	2.54	0.42
1:O:527:U:H2'	1:O:528:G:C8	2.54	0.42
1:O:1020:A:H2'	1:O:1021:G:C8	2.54	0.42
1:O:592:G:H5''	1:O:593:A:OP1	2.18	0.42
3:A:135:VAL:HA	3:A:150:PRO:HD3	2.01	0.42
15:M:61:ALA:HB3	15:M:88:ALA:HB2	2.01	0.42
18:P:92:ARG:HA	18:P:92:ARG:HD2	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:164:THR:HG22	14:L:166:ALA:H	1.83	0.42
24:V:88:THR:C	24:V:90:TYR:H	2.22	0.42
6:D:25:MET:HG3	6:D:41:LEU:CD1	2.48	0.42
10:H:150:LYS:HB2	10:H:157:ILE:HD12	2.01	0.42
15:M:37:ARG:NH2	15:M:105:GLY:N	2.67	0.42
1:O:2699:A:H2'	1:O:2700:G:O4'	2.19	0.42
27:Y:31:ILE:O	27:Y:35:LYS:HG3	2.20	0.42
1:O:20:G:H21	19:Q:117:HIS:CD2	2.35	0.42
22:T:20:MET:HE2	22:T:28:THR:HG21	2.01	0.42
30:2:91:GLN:O	30:2:92:GLU:HB2	2.20	0.42
1:O:1096:U:O2'	1:O:1097:A:H5'	2.18	0.42
15:M:114:LYS:O	15:M:118:ILE:HG13	2.19	0.42
1:O:25:A:O2'	1:O:640:G:H5'	2.20	0.42
1:O:189:A:OP1	14:L:171:ARG:NH2	2.52	0.42
4:B:316:ARG:N	4:B:317:PRO:HD3	2.34	0.42
27:Y:39:CYS:O	27:Y:42:CYS:O	2.37	0.42
27:Y:42:CYS:SG	27:Y:44:PHE:N	2.81	0.42
20:R:5:ILE:HD11	20:R:41:VAL:HG22	2.00	0.42
15:M:22:GLN:HA	15:M:25:ARG:HE	1.83	0.42
27:Y:56:MET:HA	27:Y:62:TYR:O	2.18	0.42
6:D:59:GLY:C	6:D:61:PHE:H	2.21	0.42
1:O:710:G:O2'	1:O:711:G:H5'	2.19	0.42
1:O:1170:U:H2'	1:O:1172:G:OP2	2.19	0.42
1:O:941:G:C5	1:O:942:U:C4	3.07	0.42
1:O:210:U:O2'	1:O:211:U:H5'	2.20	0.42
1:O:1503:U:H2'	1:O:1504:A:O4'	2.19	0.42
14:L:49:ALA:C	14:L:54:TYR:HB3	2.40	0.42
1:O:383:A:H2'	1:O:384:G:O4'	2.19	0.42
16:N:24:ALA:O	16:N:28:ASP:HB2	2.20	0.42
1:O:304:G:H1'	1:O:347:A:N6	2.33	0.42
21:S:51:LEU:O	21:S:52:ARG:HG2	2.20	0.42
2:9:3026:C:O2'	2:9:3027:C:H5'	2.20	0.42
19:Q:104:PHE:HB3	19:Q:109:MET:HE1	2.01	0.42
1:O:2782:G:O6	1:O:2790:C:H5''	2.20	0.42
28:Z:34:CYS:HB3	28:Z:39:PHE:H	1.84	0.42
1:O:1310:U:OP2	5:C:168:ARG:NH1	2.53	0.42
1:O:1342:C:C2'	1:O:1343:C:H5'	2.49	0.42
2:9:3095:C:O2'	2:9:3096:C:H5'	2.20	0.42
1:O:370:G:O2'	1:O:371:U:H5'	2.18	0.42
1:O:2685:C:H2'	1:O:2686:C:H6	1.85	0.42
1:O:1169:U:H2'	1:O:1170:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:97:VAL:HG12	15:M:127:LEU:HD11	2.01	0.42
6:D:44:ILE:HG12	6:D:83:PHE:HE1	1.85	0.42
1:0:1345:A:H2'	1:0:1346:U:C6	2.54	0.42
7:E:137:ASP:O	7:E:141:VAL:HG23	2.19	0.42
1:0:2780:C:H2'	1:0:2781:U:C6	2.55	0.42
15:M:164:ASP:CG	15:M:167:ASP:HA	2.39	0.42
25:W:76:ARG:HG3	25:W:76:ARG:HH11	1.84	0.42
10:H:114:PRO:O	10:H:115:PHE:C	2.58	0.42
1:0:2133:U:H4'	1:0:2134:G:C5'	2.49	0.42
1:0:401:C:H2'	1:0:402:U:C6	2.55	0.42
1:0:2714:U:H2'	1:0:2715:G:C8	2.54	0.42
1:0:1808:C:O2'	1:0:1809:G:H5'	2.19	0.42
1:0:352:A:H2'	1:0:353:G:C8	2.55	0.42
17:O:28:GLN:O	17:O:32:ALA:N	2.46	0.42
27:Y:33:HIS:HA	27:Y:69:TYR:O	2.20	0.42
5:C:165:ASP:O	5:C:168:ARG:HB3	2.19	0.42
14:L:48:ARG:HH11	14:L:52:LEU:HD21	1.83	0.42
11:I:15:ARG:NH1	11:I:43:ARG:NH1	2.67	0.42
1:0:316:A:H5'	21:S:54:ASP:OD2	2.19	0.42
1:0:23:G:C6	1:0:24:G:N1	2.88	0.42
3:A:55:VAL:CG2	3:A:68:ILE:O	2.68	0.42
19:Q:119:VAL:O	19:Q:119:VAL:CG1	2.68	0.42
13:K:117:GLU:HG3	13:K:117:GLU:O	2.20	0.42
29:1:41:HIS:HD2	29:1:44:ARG:H	1.67	0.42
1:0:1183:C:N4	1:0:1184:C:N4	2.67	0.42
1:0:1184:C:HO2'	1:0:1185:U:H6	1.66	0.42
1:0:2289:G:H21	1:0:2291:A:H2	1.63	0.42
1:0:1594:C:OP2	17:O:120:ARG:HD2	2.20	0.42
1:0:696:C:O2'	1:0:697:G:H5'	2.19	0.42
1:0:920:C:H4'	1:0:921:G:C2	2.55	0.42
1:0:213:G:O2'	1:0:214:U:OP2	2.38	0.42
1:0:14:C:H2'	1:0:15:C:C6	2.54	0.42
19:Q:18:LEU:HB2	19:Q:143:VAL:HG13	1.99	0.42
1:0:1204:C:H2'	1:0:1205:U:O4'	2.20	0.42
1:0:901:G:OP2	13:K:18:HIS:HE1	2.03	0.42
4:B:305:ASP:O	4:B:306:LYS:CB	2.66	0.42
1:0:2893:C:O2'	1:0:2894:C:H5'	2.19	0.42
3:A:66:ARG:HH11	3:A:66:ARG:CB	2.33	0.42
1:0:1434:A:O2'	1:0:1435:U:H2'	2.20	0.42
10:H:86:ARG:HG2	10:H:86:ARG:H	1.70	0.41
19:Q:39:THR:CB	19:Q:42:GLU:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2635:A:HO2'	1:0:2636:C:H5'	1.83	0.41
26:X:151:SER:HB3	26:X:154:ARG:CB	2.50	0.41
2:9:3006:C:H5''	15:M:37:ARG:HH11	1.82	0.41
15:M:154:LEU:O	15:M:155:GLU:HB3	2.19	0.41
4:B:320:GLN:NE2	4:B:321:PRO:HD3	2.34	0.41
2:9:3071:C:O2'	2:9:3072:C:H5'	2.20	0.41
1:0:710:G:H5'	16:N:25:VAL:HG22	2.02	0.41
1:0:2634:G:OP2	3:A:204:GLY:N	2.30	0.41
19:Q:124:GLY:HA3	19:Q:136:TRP:O	2.19	0.41
1:0:349:U:O2'	1:0:350:C:H5'	2.20	0.41
3:A:197:VAL:O	3:A:197:VAL:HG22	2.20	0.41
1:0:47:G:N3	1:0:114:A:C2	2.88	0.41
10:H:151:MET:HE3	10:H:151:MET:CA	2.50	0.41
10:H:127:GLY:O	10:H:128:ALA:CB	2.68	0.41
1:0:926:A:C4'	13:K:39:GLU:HG2	2.50	0.41
1:0:2614:C:O2'	1:0:2615:U:H5'	2.20	0.41
1:0:644:G:O2'	13:K:4:LYS:HE3	2.20	0.41
1:0:12:U:C2'	1:0:13:G:H5'	2.50	0.41
1:0:1369:A:H5''	19:Q:64:SER:OG	2.20	0.41
1:0:1514:C:H2'	1:0:1515:A:C8	2.55	0.41
1:0:2115:U:H2'	1:0:2116:U:C6	2.54	0.41
1:0:2330:U:H4'	1:0:2331:C:OP1	2.19	0.41
1:0:2125:G:H2'	1:0:2126:C:H6	1.85	0.41
1:0:2269:C:H2'	1:0:2270:G:H5'	2.01	0.41
1:0:2065:C:H2'	1:0:2066:C:C6	2.55	0.41
1:0:2445:U:H2'	1:0:2446:G:C8	2.56	0.41
24:V:80:ASP:O	24:V:84:VAL:HG23	2.21	0.41
1:0:1520:G:H2'	1:0:1521:C:C6	2.55	0.41
1:0:251:C:H2'	1:0:252:C:C6	2.55	0.41
1:0:1816:C:H2'	1:0:1817:U:O4'	2.20	0.41
1:0:274:G:H2'	1:0:275:G:H8	1.85	0.41
1:0:1826:C:O2'	1:0:1827:G:H5'	2.20	0.41
1:0:262:A:C6	8:F:89:LEU:HD21	2.55	0.41
13:K:35:ARG:HD3	13:K:35:ARG:C	2.40	0.41
24:V:4:LEU:CD2	24:V:54:PHE:HB3	2.49	0.41
27:Y:29:VAL:O	27:Y:33:HIS:CB	2.63	0.41
8:F:13:GLU:OE1	8:F:77:VAL:HG13	2.20	0.41
1:0:861:A:H4'	1:0:1697:G:C4'	2.45	0.41
1:0:1287:A:O4'	24:V:117:ARG:HD3	2.19	0.41
11:I:54:VAL:HG11	11:I:138:THR:HG21	2.02	0.41
11:I:88:PRO:O	11:I:94:GLY:HA3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:834:G:H3'	1:0:835:U:H4'	2.02	0.41
1:0:1141:U:O2'	1:0:1142:C:H5'	2.20	0.41
19:Q:126:LYS:HA	19:Q:127:PRO:HD3	1.94	0.41
19:Q:149:GLU:HA	19:Q:150:PRO:HD3	1.94	0.41
16:N:105:ASN:HD21	16:N:109:SER:N	2.17	0.41
36:0:8163:EMK:O72	36:0:8163:EMK:H9	2.19	0.41
10:H:136:VAL:CG2	10:H:137:ASN:H	2.31	0.41
1:0:282:C:C2'	1:0:283:U:H4'	2.50	0.41
27:Y:30:GLU:HA	27:Y:33:HIS:CB	2.50	0.41
6:D:146:LYS:HG2	15:M:106:LEU:HB2	2.03	0.41
14:L:115:LEU:O	14:L:116:ASN:HB2	2.18	0.41
4:B:238:ASN:HD22	4:B:240:GLY:N	2.18	0.41
25:W:47:ALA:O	25:W:82:GLU:HB2	2.19	0.41
19:Q:114:VAL:HG13	19:Q:114:VAL:O	2.20	0.41
1:0:1790:C:H5	17:O:71:LYS:HE3	1.85	0.41
1:0:2819:C:H2'	1:0:2820:A:C8	2.55	0.41
1:0:1514:C:O2'	1:0:1515:A:H5'	2.20	0.41
22:T:9:CYS:HB2	22:T:52:THR:HG22	2.01	0.41
19:Q:17:MET:CE	19:Q:19:ARG:NH2	2.83	0.41
1:0:1367:A:H2'	1:0:1368:U:H5'	2.01	0.41
22:T:20:MET:CG	22:T:28:THR:HG23	2.50	0.41
1:0:353:G:O2'	1:0:354:A:H5'	2.20	0.41
1:0:764:C:H2'	1:0:765:G:O4'	2.19	0.41
1:0:1586:G:O2'	1:0:1587:U:H5'	2.20	0.41
21:S:1:SER:O	21:S:7:GLN:NE2	2.43	0.41
1:0:1913:C:H2'	1:0:1914:C:C6	2.55	0.41
10:H:14:TYR:N	10:H:91:HIS:HE1	2.15	0.41
1:0:155:C:O2'	1:0:156:C:H5'	2.20	0.41
1:0:283:U:C5	1:0:284:C:N3	2.89	0.41
10:H:26:LYS:HD3	10:H:89:PRO:CG	2.50	0.41
1:0:1697:G:O2'	1:0:1698:U:H5'	2.21	0.41
27:Y:62:TYR:CE2	27:Y:64:ILE:CG2	3.02	0.41
1:0:121:U:O4	28:Z:18:LYS:HD3	2.19	0.41
1:0:1594:C:O2'	1:0:1595:G:H5'	2.19	0.41
5:C:138:VAL:O	5:C:234:VAL:HA	2.20	0.41
1:0:97:G:C6	21:S:107:LYS:HE3	2.56	0.41
4:B:24:PRO:HG3	4:B:204:GLY:HA2	2.02	0.41
21:S:48:VAL:HG21	21:S:96:VAL:HG13	2.03	0.41
11:I:63:ILE:CG2	11:I:64:GLY:N	2.83	0.41
1:0:1202:A:H2'	1:0:1203:G:O4'	2.21	0.41
1:0:117:A:H2'	1:0:118:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2241:C:O2'	1:0:2242:U:H5'	2.20	0.41
15:M:24:LEU:O	15:M:28:LYS:HG2	2.21	0.41
24:V:21:LEU:HA	24:V:21:LEU:HD23	1.81	0.41
13:K:53:ARG:NH2	13:K:57:VAL:CG1	2.82	0.41
1:0:664:U:O4	1:0:681:G:H5''	2.21	0.41
1:0:2316:G:OP1	1:0:2317:C:H1'	2.20	0.41
7:E:95:VAL:O	7:E:126:ILE:HD13	2.21	0.41
11:I:80:LYS:HE2	11:I:98:PHE:CZ	2.56	0.41
22:T:20:MET:HE2	22:T:30:HIS:CE1	2.56	0.41
1:0:1924:A:O2'	30:2:29:ARG:NH1	2.54	0.41
14:L:16:LYS:C	14:L:21:ALA:HB2	2.41	0.41
1:0:2575:C:H2'	1:0:2576:A:O4'	2.20	0.41
19:Q:39:THR:O	19:Q:40:ALA:C	2.58	0.41
1:0:1928:C:H2'	1:0:1929:G:O4'	2.21	0.41
24:V:39:ASP:HA	24:V:42:ARG:HH12	1.84	0.41
1:0:1067:A:O2'	24:V:12:ASN:HA	2.20	0.41
21:S:40:VAL:HG22	21:S:41:ARG:N	2.35	0.41
5:C:35:VAL:HG23	5:C:220:THR:CG2	2.51	0.41
10:H:113:ALA:N	10:H:114:PRO:HD3	2.35	0.41
1:0:1791:U:O2'	1:0:1792:C:H5'	2.21	0.41
7:E:112:ALA:HA	7:E:113:PRO:HD3	1.94	0.41
3:A:1:GLY:HA2	3:A:197:VAL:HG23	2.02	0.41
21:S:73:HIS:HE1	21:S:90:PRO:HG3	1.86	0.41
8:F:12:LEU:HD23	8:F:12:LEU:O	2.20	0.41
24:V:26:ILE:HG13	24:V:26:ILE:O	2.20	0.41
2:9:3049:G:H2'	2:9:3050:G:O4'	2.21	0.41
7:E:154:ILE:HG23	7:E:154:ILE:O	2.21	0.41
23:U:8:ILE:HG21	23:U:59:ILE:HG13	2.03	0.41
1:0:1421:C:O2'	1:0:1422:U:H5'	2.20	0.41
3:A:65:ARG:C	3:A:66:ARG:HG3	2.41	0.41
2:9:3048:C:H4'	15:M:141:ARG:HH21	1.86	0.41
16:N:73:ASP:HA	16:N:92:VAL:O	2.21	0.41
19:Q:35:ILE:HA	19:Q:38:LYS:HD2	2.02	0.41
10:H:139:ASP:H	10:H:140:PRO:HD3	1.76	0.41
24:V:110:GLN:NE2	24:V:110:GLN:HA	2.36	0.41
14:L:37:VAL:CG2	14:L:108:LYS:HG3	2.50	0.41
14:L:183:VAL:HG12	14:L:184:ARG:N	2.35	0.41
1:0:2578:G:C8	1:0:2578:G:H5'	2.45	0.41
1:0:2909:G:H2'	1:0:2910:A:C8	2.56	0.41
13:K:143:THR:CG2	13:K:144:ASP:N	2.80	0.41
26:X:106:THR:CG2	26:X:107:PRO:HD2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:26:THR:HA	21:S:39:ASN:HB3	2.01	0.41
24:V:65:VAL:HG12	24:V:116:LEU:HD13	2.02	0.41
24:V:69:ARG:HD2	24:V:117:ARG:O	2.21	0.41
1:0:2237:G:O2'	1:0:2238:A:H8	2.03	0.41
1:0:870:G:OP2	3:A:3:ARG:NH1	2.50	0.41
19:Q:111:ILE:HG23	19:Q:145:LEU:CD1	2.50	0.41
1:0:1565:C:O4'	1:0:2738:G:H1'	2.21	0.41
1:0:911:G:H5'	1:0:932:U:OP1	2.21	0.41
2:9:3064:C:H2'	2:9:3065:A:H5'	2.02	0.41
1:0:490:C:O2'	1:0:491:C:H5'	2.21	0.41
1:0:1139:U:H2'	1:0:1140:C:C6	2.55	0.41
30:2:6:ARG:HG2	30:2:6:ARG:HH11	1.85	0.41
1:0:510:U:O5'	1:0:510:U:H6	2.04	0.41
1:0:2777:G:O2'	1:0:2778:A:H5'	2.20	0.41
20:R:11:THR:H	20:R:14:ALA:HB3	1.85	0.41
1:0:1293:U:O2'	1:0:1294:A:H5'	2.21	0.41
7:E:93:MET:HB2	7:E:93:MET:HE2	1.89	0.41
1:0:1396:C:H1'	17:O:1:THR:O	2.21	0.41
1:0:2661:U:C2	1:0:2812:A:N6	2.89	0.41
1:0:1603:A:H5''	1:0:1605:G:H5'	2.02	0.41
27:Y:39:CYS:HA	27:Y:47:LEU:HD11	2.03	0.41
1:0:2416:G:H2'	1:0:2417:C:C6	2.56	0.41
6:D:58:VAL:HG12	6:D:59:GLY:N	2.36	0.41
11:I:132:LEU:HA	11:I:132:LEU:HD23	1.84	0.41
1:0:449:A:C8	5:C:43:LYS:HG2	2.56	0.41
7:E:84:MET:HB2	7:E:131:LEU:HB2	2.03	0.41
1:0:2866:U:H4'	1:0:2867:G:H5'	2.01	0.41
1:0:2016:U:H2'	1:0:2017:U:C6	2.56	0.41
19:Q:119:VAL:HG12	19:Q:119:VAL:O	2.20	0.41
1:0:424:C:H2'	1:0:425:U:C6	2.55	0.41
15:M:86:LEU:HD12	15:M:125:ALA:HB2	2.03	0.41
1:0:2428:G:N7	30:2:60:LYS:HE2	2.36	0.40
10:H:45:GLN:O	10:H:163:PRO:HD3	2.21	0.40
1:0:862:U:H2'	1:0:863:G:H8	1.86	0.40
10:H:158:ASN:OD1	10:H:158:ASN:C	2.60	0.40
1:0:840:U:H2'	19:Q:128:ARG:NH1	2.36	0.40
2:9:3093:A:N1	10:H:52:LYS:HD2	2.36	0.40
15:M:22:GLN:CB	15:M:25:ARG:HH21	2.34	0.40
1:0:1165:G:H4'	1:0:1174:A:O2'	2.21	0.40
1:0:2317:C:OP2	30:2:62:THR:HB	2.21	0.40
1:0:820:G:O2'	1:0:856:G:H4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:15:ARG:CZ	11:I:43:ARG:HH11	2.34	0.40
1:O:2310:G:OP2	10:H:114:PRO:HD2	2.22	0.40
20:R:73:ASP:OD1	20:R:76:GLU:HG3	2.21	0.40
1:O:757:C:H2'	1:O:758:A:C8	2.55	0.40
1:O:1398:G:H5'	17:O:23:PHE:O	2.21	0.40
1:O:1104:C:H4'	11:I:88:PRO:HD3	2.03	0.40
22:T:9:CYS:SG	22:T:11:THR:HG23	2.61	0.40
1:O:1477:C:H4'	1:O:1868:G:H5''	2.03	0.40
1:O:419:A:H1'	1:O:1921:A:C2	2.56	0.40
1:O:192:A:C4'	14:L:176:GLN:HE22	2.34	0.40
10:H:1:LYS:HA	10:H:2:PRO:HD3	1.92	0.40
3:A:28:GLU:HA	3:A:115:GLY:O	2.21	0.40
23:U:45:ARG:C	23:U:47:LYS:N	2.74	0.40
1:O:157:G:H4'	14:L:95:LYS:HG3	2.02	0.40
1:O:110:C:H2'	1:O:111:C:H6	1.86	0.40
1:O:1204:C:C2'	1:O:1205:U:H5''	2.51	0.40
23:U:39:ALA:O	23:U:41:GLU:HG3	2.22	0.40
14:L:20:ILE:HA	14:L:23:LEU:HB2	2.03	0.40
8:F:34:ASN:ND2	8:F:38:LYS:HE2	2.35	0.40
1:O:2083:A:H61	11:I:90:LYS:HD3	1.87	0.40
1:O:272:A:H5'	1:O:273:G:OP2	2.21	0.40
1:O:1825:U:O2'	1:O:1826:C:H5'	2.21	0.40
1:O:1145:G:H2'	1:O:1146:C:O4'	2.22	0.40
4:B:1:PRO:O	4:B:2:GLN:O	2.38	0.40
2:9:3024:U:O2'	2:9:3025:G:C4'	2.68	0.40
1:O:120:A:H5'	28:Z:20:ARG:HH21	1.86	0.40
1:O:137:U:OP1	1:O:259:G:O2'	2.40	0.40
3:A:36:ASP:OD1	3:A:37:VAL:N	2.54	0.40
1:O:2908:A:H2'	1:O:2909:G:C4'	2.52	0.40
1:O:737:A:O5'	1:O:737:A:H8	2.04	0.40
1:O:1362:U:H1'	5:C:84:VAL:HG21	2.04	0.40
1:O:74:A:C4	1:O:104:G:N2	2.90	0.40
6:D:140:ARG:NH1	6:D:140:ARG:HG3	2.37	0.40
1:O:327:A:H4'	1:O:329:A:N7	2.37	0.40
22:T:11:THR:HG22	22:T:53:ASP:OD2	2.21	0.40
1:O:653:C:H2'	1:O:654:A:C8	2.56	0.40
1:O:62:C:C4	1:O:63:U:C4	3.09	0.40
18:P:47:VAL:HA	18:P:48:PRO:HD3	1.88	0.40
1:O:2326:U:H2'	1:O:2327:A:C8	2.57	0.40
8:F:24:ARG:HB2	8:F:29:VAL:HG21	2.04	0.40
14:L:119:SER:HA	14:L:129:HIS:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:191:A:C4	1:0:237:G:N7	2.90	0.40
10:H:129:ASN:N	10:H:129:ASN:HD22	2.17	0.40
4:B:109:LEU:CG	4:B:113:LEU:HD11	2.49	0.40
4:B:279:THR:HG22	4:B:280:VAL:H	1.85	0.40
1:0:1593:C:OP1	17:O:117:SER:HB3	2.20	0.40
13:K:134:GLU:C	13:K:136:ALA:N	2.75	0.40
1:0:1827:G:H2'	1:0:1828:G:C8	2.56	0.40
1:0:2719:A:C2	4:B:70:PRO:HB3	2.56	0.40
1:0:2438:G:H2'	1:0:2439:C:O4'	2.21	0.40
1:0:2084:C:H2'	1:0:2085:A:C8	2.56	0.40
4:B:233:ARG:HH11	4:B:233:ARG:HG2	1.85	0.40
1:0:1883:U:OP2	3:A:190:ARG:NE	2.46	0.40
5:C:1:MET:CG	5:C:2:GLN:H	2.24	0.40
1:0:1134:G:H8	1:0:1134:G:O5'	2.05	0.40
1:0:283:U:H5	1:0:284:C:N3	2.19	0.40
1:0:2756:U:O2	1:0:2896:A:H2	2.04	0.40
20:R:57:THR:HG22	20:R:58:MET:H	1.84	0.40
1:0:836:G:OP1	4:B:230:GLN:NE2	2.55	0.40
17:O:37:ARG:O	17:O:41:ARG:HG3	2.21	0.40
23:U:1:THR:HG23	23:U:2:VAL:N	2.37	0.40
11:I:19:MET:HE1	11:I:78:ILE:HG22	2.02	0.40
13:K:65:ASP:OD1	13:K:109:LEU:HB2	2.22	0.40
1:0:816:G:H5'	1:0:1598:A:H4'	2.03	0.40
1:0:695:C:H2'	1:0:696:C:H6	1.83	0.40
6:D:23:VAL:O	6:D:23:VAL:HG23	2.21	0.40
1:0:678:G:OP2	5:C:107:ARG:NH2	2.55	0.40
1:0:1076:G:C2	1:0:1084:C:C2	3.10	0.40
29:1:14:LEU:HD13	29:1:47:THR:CG2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
3	A	235/237 (99%)	209 (89%)	21 (9%)	5 (2%)	9	23
4	B	335/337 (99%)	309 (92%)	20 (6%)	6 (2%)	11	27
5	C	244/246 (99%)	229 (94%)	13 (5%)	2 (1%)	24	51
6	D	134/165 (81%)	103 (77%)	20 (15%)	11 (8%)	1	1
7	E	170/172 (99%)	160 (94%)	9 (5%)	1 (1%)	30	59
8	F	117/119 (98%)	101 (86%)	14 (12%)	2 (2%)	11	29
9	G	25/62 (40%)	23 (92%)	1 (4%)	1 (4%)	4	8
10	H	152/167 (91%)	134 (88%)	13 (9%)	5 (3%)	5	11
11	I	140/142 (99%)	130 (93%)	7 (5%)	3 (2%)	9	23
12	J	130/132 (98%)	122 (94%)	7 (5%)	1 (1%)	24	51
13	K	141/150 (94%)	117 (83%)	22 (16%)	2 (1%)	14	35
14	L	192/194 (99%)	174 (91%)	16 (8%)	2 (1%)	19	45
15	M	184/186 (99%)	159 (86%)	17 (9%)	8 (4%)	3	7
16	N	113/115 (98%)	107 (95%)	5 (4%)	1 (1%)	21	49
17	O	141/143 (99%)	137 (97%)	4 (3%)	0	100	100
18	P	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	17	42
19	Q	148/150 (99%)	138 (93%)	9 (6%)	1 (1%)	26	55
20	R	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
21	S	117/119 (98%)	111 (95%)	4 (3%)	2 (2%)	11	29
22	T	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
23	U	63/65 (97%)	58 (92%)	1 (2%)	4 (6%)	2	2
24	V	152/154 (99%)	145 (95%)	6 (4%)	1 (1%)	26	55
25	W	80/82 (98%)	71 (89%)	5 (6%)	4 (5%)	3	5
26	X	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
27	Y	71/73 (97%)	63 (89%)	5 (7%)	3 (4%)	3	7
28	Z	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
29	1	42/48 (88%)	40 (95%)	2 (5%)	0	100	100
30	2	90/92 (98%)	86 (96%)	3 (3%)	1 (1%)	17	42
All	All	3633/3777 (96%)	3317 (91%)	249 (7%)	67 (2%)	11	27

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	139	ASP
6	D	63	ILE
6	D	93	LEU
6	D	95	THR
6	D	173	GLU
10	H	163	PRO
13	K	80	ASP
15	M	154	LEU
15	M	183	ASP
25	W	66	THR
4	B	2	GLN
6	D	11	HIS
6	D	27	ILE
6	D	56	ARG
6	D	171	ASP
11	I	5	GLU
11	I	143	LYS
13	K	73	VAL
21	S	53	GLY
3	A	34	ASP
4	B	169	GLY
4	B	185	GLY
5	C	8	LEU
6	D	97	GLN
8	F	101	ALA
10	H	72	VAL
10	H	79	ALA
10	H	138	PRO
14	L	35	PRO
14	L	116	ASN
15	M	113	SER
15	M	155	GLU
15	M	181	ASP
16	N	24	ALA
23	U	40	PRO
24	V	49	ASN
25	W	87	ALA
30	2	56	PRO
3	A	229	ALA
5	C	79	ARG
6	D	16	PRO
8	F	61	MET
11	I	65	ASN

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Mol	Chain	Res	Type
15	M	60	SER
23	U	39	ALA
23	U	43	PRO
25	W	77	PHE
27	Y	20	LEU
3	A	132	ASP
4	B	287	TYR
7	E	17	HIS
15	M	68	GLU
19	Q	81	PRO
21	S	116	ASP
27	Y	67	GLY
4	B	184	ASP
6	D	20	LYS
9	G	72	ASP
12	J	21	ALA
18	P	18	PRO
25	W	81	GLY
10	H	43	PRO
23	U	38	GLY
27	Y	41	VAL
3	A	123	GLY
3	A	88	ILE
15	M	184	ILE

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 X-ray entries followed by that with respect to entries of similar resolution.

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	
3	A	179/179 (100%)	168 (94%)	11 (6%)	23	49
4	B	282/282 (100%)	264 (94%)	18 (6%)	22	47
5	C	193/193 (100%)	179 (93%)	14 (7%)	17	39
6	D	117/138 (85%)	113 (97%)	4 (3%)	44	75
7	E	152/152 (100%)	148 (97%)	4 (3%)	54	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	F	92/92 (100%)	88 (96%)	4 (4%)	35	66
9	G	27/55 (49%)	27 (100%)	0	100	100
10	H	122/122 (100%)	113 (93%)	9 (7%)	17	39
11	I	118/118 (100%)	110 (93%)	8 (7%)	20	43
12	J	106/106 (100%)	104 (98%)	2 (2%)	65	88
13	K	113/116 (97%)	106 (94%)	7 (6%)	23	49
14	L	166/166 (100%)	158 (95%)	8 (5%)	31	62
15	M	149/149 (100%)	142 (95%)	7 (5%)	32	63
16	N	93/93 (100%)	89 (96%)	4 (4%)	35	66
17	O	113/113 (100%)	112 (99%)	1 (1%)	84	95
18	P	79/79 (100%)	77 (98%)	2 (2%)	55	84
19	Q	117/117 (100%)	114 (97%)	3 (3%)	54	83
20	R	71/71 (100%)	70 (99%)	1 (1%)	74	92
21	S	105/105 (100%)	98 (93%)	7 (7%)	20	44
22	T	44/44 (100%)	44 (100%)	0	100	100
23	U	51/51 (100%)	50 (98%)	1 (2%)	63	87
24	V	130/130 (100%)	126 (97%)	4 (3%)	47	78
25	W	66/66 (100%)	61 (92%)	5 (8%)	16	37
26	X	120/120 (100%)	115 (96%)	5 (4%)	36	68
27	Y	56/56 (100%)	55 (98%)	1 (2%)	66	89
28	Z	46/46 (100%)	46 (100%)	0	100	100
29	1	42/44 (96%)	41 (98%)	1 (2%)	57	85
30	2	79/79 (100%)	78 (99%)	1 (1%)	76	92
All	All	3028/3082 (98%)	2896 (96%)	132 (4%)	35	65

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	3	ARG
3	A	33	GLU
3	A	34	ASP
3	A	62	ASP
3	A	64	ASP
3	A	69	LEU

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Mol	Chain	Res	Type
3	A	94	LEU
3	A	131	HIS
3	A	153	ARG
3	A	179	MET
3	A	192	VAL
4	B	11	LEU
4	B	27	ASN
4	B	51	VAL
4	B	53	LEU
4	B	71	VAL
4	B	97	LEU
4	B	112	THR
4	B	162	MET
4	B	190	MET
4	B	234	ARG
4	B	251	VAL
4	B	254	GLN
4	B	257	THR
4	B	264	GLU
4	B	268	ARG
4	B	274	GLU
4	B	279	THR
4	B	307	ARG
5	C	2	GLN
5	C	27	ARG
5	C	76	ARG
5	C	78	ARG
5	C	94	THR
5	C	101	ASP
5	C	115	LEU
5	C	136	VAL
5	C	187	ARG
5	C	211	ASP
5	C	223	LEU
5	C	236	THR
5	C	240	LEU
5	C	243	VAL
6	D	24	HIS
6	D	61	PHE
6	D	62	ASP
6	D	133	ASN
7	E	7	ILE

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Mol	Chain	Res	Type
7	E	10	ASP
7	E	86	VAL
7	E	116	THR
8	F	24	ARG
8	F	46	GLU
8	F	64	PRO
8	F	99	THR
10	H	18	GLU
10	H	61	LEU
10	H	72	VAL
10	H	73	GLN
10	H	85	ILE
10	H	130	HIS
10	H	138	PRO
10	H	158	ASN
10	H	163	PRO
11	I	46	ILE
11	I	52	GLN
11	I	76	ASP
11	I	79	PHE
11	I	93	ARG
11	I	107	ASN
11	I	127	ILE
11	I	131	THR
12	J	10	GLN
12	J	84	ASP
13	K	32	ASP
13	K	35	ARG
13	K	40	PHE
13	K	43	HIS
13	K	80	ASP
13	K	83	GLU
13	K	102	ASP
14	L	23	LEU
14	L	46	LEU
14	L	68	ARG
14	L	87	MET
14	L	93	ARG
14	L	99	ARG
14	L	116	ASN
14	L	158	ARG
15	M	23	ARG

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Mol	Chain	Res	Type
15	M	56	ASP
15	M	65	ASP
15	M	138	ASP
15	M	152	GLU
15	M	163	PHE
15	M	175	LEU
16	N	31	GLU
16	N	38	ARG
16	N	103	GLU
16	N	111	VAL
17	O	98	ILE
18	P	16	ASN
18	P	42	LYS
19	Q	13	THR
19	Q	39	THR
19	Q	123	GLN
20	R	80	ARG
21	S	9	LYS
21	S	39	ASN
21	S	43	ASN
21	S	48	VAL
21	S	89	ARG
21	S	96	VAL
21	S	115	GLU
23	U	22	ASP
24	V	4	LEU
24	V	78	ASP
24	V	142	ASP
24	V	146	ILE
25	W	15	ARG
25	W	27	ASP
25	W	49	ARG
25	W	79	GLU
25	W	82	GLU
26	X	141	THR
26	X	163	THR
26	X	187	VAL
26	X	189	ASN
26	X	235	GLU
27	Y	42	CYS
29	1	18	ASN
30	2	18	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	47	HIS
3	A	199	HIS
4	B	27	ASN
4	B	106	HIS
4	B	145	HIS
4	B	238	ASN
4	B	256	GLN
4	B	260	HIS
4	B	320	GLN
4	B	332	ASN
5	C	2	GLN
5	C	39	GLN
5	C	129	HIS
5	C	163	HIS
6	D	29	HIS
6	D	47	GLN
6	D	103	ASN
6	D	133	ASN
7	E	15	GLN
7	E	94	GLN
7	E	106	ASN
7	E	119	HIS
7	E	143	GLN
9	G	64	ASN
10	H	8	ASN
10	H	55	GLN
10	H	58	HIS
10	H	69	ASN
10	H	74	ASN
10	H	80	ASN
10	H	91	HIS
10	H	129	ASN
10	H	137	ASN
10	H	166	ASN
11	I	25	GLN
11	I	52	GLN
11	I	107	ASN
12	J	10	GLN
13	K	18	HIS
13	K	41	HIS
13	K	42	ASN

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Mol	Chain	Res	Type
14	L	58	GLN
14	L	89	ASN
14	L	176	GLN
15	M	93	GLN
15	M	107	ASN
17	O	50	GLN
17	O	66	GLN
17	O	73	HIS
17	O	88	GLN
17	O	101	GLN
17	O	118	GLN
18	P	40	HIS
19	Q	61	GLN
19	Q	94	ASN
19	Q	98	ASN
19	Q	113	HIS
19	Q	117	HIS
20	R	9	HIS
20	R	21	GLN
20	R	44	GLN
20	R	53	ASN
21	S	11	GLN
21	S	39	ASN
21	S	43	ASN
21	S	73	HIS
22	T	39	ASN
22	T	48	ASN
23	U	60	GLN
24	V	12	ASN
24	V	27	HIS
24	V	59	GLN
24	V	87	HIS
24	V	110	GLN
24	V	119	HIS
24	V	125	HIS
24	V	141	HIS
25	W	22	ASN
25	W	23	HIS
25	W	36	HIS
26	X	119	GLN
26	X	134	HIS
26	X	149	GLN

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Mol	Chain	Res	Type
26	X	189	ASN
27	Y	33	HIS
27	Y	70	GLN
28	Z	8	GLN
28	Z	16	HIS
28	Z	28	HIS
29	1	18	ASN
29	1	41	HIS
29	1	45	ASN
30	2	15	ASN
30	2	30	GLN
30	2	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2902 (94%)	233 (8%)	22 (0%)
2	9	121/122 (99%)	14 (11%)	2 (1%)
All	All	2866/3024 (94%)	247 (8%)	24 (0%)

All (247) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	70	A
1	0	71	G
1	0	86	A
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	130	C
1	0	131	A
1	0	141	C
1	0	151	A
1	0	166	A
1	0	169	A
1	0	186	A
1	0	191	A
1	0	192	A

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Mol	Chain	Res	Type
1	0	198	A
1	0	200	U
1	0	204	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	308	U
1	0	309	C
1	0	318	C
1	0	336	G
1	0	337	A
1	0	358	G
1	0	368	C
1	0	381	G
1	0	397	A
1	0	417	G
1	0	461	C
1	0	487	G
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	545	G
1	0	553	G
1	0	559	U
1	0	581	G
1	0	588	G
1	0	604	G
1	0	605	C
1	0	620	A
1	0	632	A
1	0	660	A
1	0	688	A
1	0	701	U
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U

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Mol	Chain	Res	Type
1	0	840	U
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	875	A
1	0	877	G
1	0	878	G
1	0	885	G
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1003	U
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1087	G
1	0	1088	A
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1131	G
1	0	1137	G
1	0	1164	U
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1192	A
1	0	1193	A
1	0	1205	U

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Mol	Chain	Res	Type
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1287	A
1	0	1289	C
1	0	1331	A
1	0	1342	C
1	0	1351	G
1	0	1353	C
1	0	1357	A
1	0	1360	C
1	0	1377	C
1	0	1378	G
1	0	1407	A
1	0	1488	U
1	0	1505	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1528	A
1	0	1562	C
1	0	1564	C
1	0	1592	G
1	0	1603	A
1	0	1625	U
1	0	1626	A
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1730	G
1	0	1731	C
1	0	1752	G

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Mol	Chain	Res	Type
1	0	1774	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1873	G
1	0	1879	U
1	0	1919	A
1	0	1942	A
1	0	1971	G
1	0	1974	G
1	0	1978	A
1	0	1979	G
1	0	1996	U
1	0	2004	U
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2034	U
1	0	2063	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2103	A
1	0	2110	G
1	0	2238	A
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2354	A
1	0	2361	A

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Mol	Chain	Res	Type
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2467	A
1	0	2476	C
1	0	2483	A
1	0	2507	G
1	0	2511	A
1	0	2526	C
1	0	2527	U
1	0	2533	C
1	0	2537	G
1	0	2540	G
1	0	2553	A
1	0	2564	G
1	0	2570	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2638	G
1	0	2648	U
1	0	2649	A
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2726	U
1	0	2727	A
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2812	A
1	0	2825	C

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Mol	Chain	Res	Type
1	0	2835	C
1	0	2876	G
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U
2	9	3014	G
2	9	3022	G
2	9	3023	U
2	9	3024	U
2	9	3025	G
2	9	3026	C
2	9	3040	C
2	9	3041	C
2	9	3043	G
2	9	3057	A
2	9	3077	A
2	9	3114	G
2	9	3122	C

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	129	A
1	0	169	A
1	0	338	C
1	0	604	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	877	G
1	0	1080	C
1	0	1232	A
1	0	1237	U
1	0	1352	A
1	0	1684	A
1	0	1752	G
1	0	1856	C
1	0	2011	A
1	0	2313	C
1	0	2467	A
1	0	2526	C

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Mol	Chain	Res	Type
1	0	2536	C
1	0	2726	U
1	0	2791	U
2	9	3024	U
2	9	3055	U

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 204 ligands modelled in this entry, 203 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
36	EMK	0	8163	-	76,78,78	5.74	57 (75%)	103,118,118	3.39	39 (37%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	EMK	0	8163	-	-	0/92/133/133	0/5/5/5

All (57) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	0	8163	EMK	O42-C5	-11.11	1.13	1.44
36	0	8163	EMK	O73-C13	2.00	1.47	1.42
36	0	8163	EMK	N82-N81	2.06	1.38	1.34
36	0	8163	EMK	C93-N81	2.16	1.38	1.35
36	0	8163	EMK	O76-C35	2.47	1.51	1.43
36	0	8163	EMK	C26-C28	2.48	1.59	1.53
36	0	8163	EMK	C92-S1	2.67	1.87	1.74
36	0	8163	EMK	C95-N83	2.87	1.37	1.33
36	0	8163	EMK	C40-C43	2.93	1.59	1.53
36	0	8163	EMK	O96-C85	3.09	1.48	1.42
36	0	8163	EMK	C4-C5	3.35	1.62	1.54
36	0	8163	EMK	C85-C83	3.36	1.58	1.54
36	0	8163	EMK	C24-C15	3.51	1.65	1.53
36	0	8163	EMK	O41-C39	3.69	1.51	1.41
36	0	8163	EMK	O95-S1	4.08	1.57	1.44
36	0	8163	EMK	C89-S1	4.09	1.82	1.77
36	0	8163	EMK	C86-C85	4.20	1.58	1.51
36	0	8163	EMK	C45-C47	4.49	1.60	1.51
36	0	8163	EMK	C2-C1	4.58	1.62	1.51
36	0	8163	EMK	C2-C3	4.63	1.66	1.55
36	0	8163	EMK	C16-C2	4.71	1.64	1.53
36	0	8163	EMK	O94-S1	4.74	1.59	1.44
36	0	8163	EMK	O78-C30	4.79	1.56	1.44
36	0	8163	EMK	C90-C89	4.82	1.46	1.38
36	0	8163	EMK	C88-C89	4.83	1.46	1.38
36	0	8163	EMK	C93-C95	4.95	1.43	1.36
36	0	8163	EMK	C7-C6	4.99	1.63	1.54
36	0	8163	EMK	C34-C26	5.27	1.64	1.52
36	0	8163	EMK	O71-C3	5.28	1.57	1.43
36	0	8163	EMK	C43-N46	5.32	1.60	1.48
36	0	8163	EMK	C90-C91	5.33	1.48	1.38
36	0	8163	EMK	C9-C8	5.51	1.75	1.53
36	0	8163	EMK	C88-C87	5.64	1.48	1.38
36	0	8163	EMK	C30-C28	5.72	1.67	1.53
36	0	8163	EMK	C45-C43	5.74	1.67	1.53
36	0	8163	EMK	C21-C26	5.79	1.66	1.52
36	0	8163	EMK	C91-C86	5.95	1.48	1.39
36	0	8163	EMK	O75-C15	6.12	1.57	1.46
36	0	8163	EMK	C17-C4	6.42	1.68	1.53
36	0	8163	EMK	C87-C86	7.32	1.51	1.39
36	0	8163	EMK	O71-C10	7.34	1.61	1.41
36	0	8163	EMK	C6-C5	7.43	1.73	1.55
36	0	8163	EMK	C38-N9	7.93	1.62	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	0	8163	EMK	O75-C1	8.09	1.53	1.34
36	0	8163	EMK	C23-C14	8.32	1.68	1.52
36	0	8163	EMK	C21-C10	8.73	1.70	1.51
36	0	8163	EMK	O76-C26	8.82	1.63	1.44
36	0	8163	EMK	C14-C13	8.83	1.78	1.55
36	0	8163	EMK	C18-C6	8.83	1.68	1.52
36	0	8163	EMK	O70-C1	9.05	1.44	1.21
36	0	8163	EMK	O72-C6	9.21	1.61	1.44
36	0	8163	EMK	O78-C10	9.26	1.66	1.42
36	0	8163	EMK	O77-C28	9.58	1.63	1.42
36	0	8163	EMK	C14-C15	10.26	1.75	1.54
36	0	8163	EMK	O74-C14	10.60	1.63	1.44
36	0	8163	EMK	C20-C12	13.34	1.76	1.52
36	0	8163	EMK	C12-N9	13.34	1.71	1.49

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	0	8163	EMK	C7-C8-C9	-14.23	91.72	112.39
36	0	8163	EMK	C81-N46-C43	-8.91	96.03	112.72
36	0	8163	EMK	C6-C7-C8	-7.80	100.28	117.42
36	0	8163	EMK	O73-C13-C14	-6.79	95.36	106.79
36	0	8163	EMK	C15-O75-C1	-5.75	108.43	118.12
36	0	8163	EMK	C3-C2-C1	-5.28	99.53	109.86
36	0	8163	EMK	C6-C5-C4	-5.16	106.87	114.11
36	0	8163	EMK	C20-C12-N9	-4.54	103.70	113.63
36	0	8163	EMK	C15-C14-C13	-3.94	101.52	108.11
36	0	8163	EMK	C95-C93-N81	-3.83	100.83	107.14
36	0	8163	EMK	C81-C82-C94	-3.81	105.35	113.61
36	0	8163	EMK	O72-C6-C18	-3.80	100.12	108.51
36	0	8163	EMK	C39-C40-C43	-3.74	102.66	109.25
36	0	8163	EMK	O95-S1-C92	-3.48	102.84	108.53
36	0	8163	EMK	O76-C26-C34	-3.46	105.47	110.88
36	0	8163	EMK	O75-C1-O70	-3.45	116.79	123.89
36	0	8163	EMK	C45-C43-C40	-3.25	105.29	110.03
36	0	8163	EMK	C94-C95-C93	-3.21	124.58	129.55
36	0	8163	EMK	C26-C21-C10	-3.11	109.70	115.03
36	0	8163	EMK	C23-C14-C13	-3.08	108.17	113.28
36	0	8163	EMK	O95-S1-C89	-2.40	106.21	108.31
36	0	8163	EMK	C45-C43-N46	-2.24	108.88	115.63
36	0	8163	EMK	O71-C3-C2	-2.11	107.15	111.10
36	0	8163	EMK	C87-C86-C85	2.13	123.83	120.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	0	8163	EMK	C3-C4-C5	2.14	114.83	110.85
36	0	8163	EMK	C23-C14-C15	2.81	115.50	111.29
36	0	8163	EMK	O76-C26-C28	2.90	108.34	103.86
36	0	8163	EMK	C10-O71-C3	3.41	122.01	114.73
36	0	8163	EMK	C50-N46-C43	3.65	119.71	113.78
36	0	8163	EMK	O75-C15-C14	3.73	113.51	107.23
36	0	8163	EMK	O75-C1-C2	3.86	119.40	111.47
36	0	8163	EMK	C25-C24-C15	4.34	125.04	113.22
36	0	8163	EMK	O42-C5-C6	4.57	112.28	106.44
36	0	8163	EMK	C50-N46-C81	4.92	117.56	110.50
36	0	8163	EMK	O72-C6-C7	4.93	121.65	108.34
36	0	8163	EMK	O71-C3-C4	5.32	114.88	108.19
36	0	8163	EMK	O74-C14-C15	5.81	116.37	107.14
36	0	8163	EMK	C92-S1-C89	8.38	114.82	104.68
36	0	8163	EMK	C39-O42-C5	12.69	139.06	116.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	0	8163	EMK	30	0

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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2754/2902 (94%)	2.74	1966 (71%) 0 0	18, 37, 79, 130	0
2	9	122/122 (100%)	2.40	82 (67%) 0 0	30, 54, 76, 135	0
3	A	237/237 (100%)	3.85	206 (86%) 0 0	21, 41, 70, 88	0
4	B	337/337 (100%)	3.18	252 (74%) 0 0	21, 42, 67, 79	0
5	C	246/246 (100%)	2.33	136 (55%) 0 0	20, 37, 59, 70	0
6	D	140/165 (84%)	4.35	125 (89%) 0 0	49, 82, 103, 111	0
7	E	172/172 (100%)	2.98	122 (70%) 0 0	37, 55, 72, 78	0
8	F	119/119 (100%)	3.98	97 (81%) 0 0	39, 60, 86, 91	0
9	G	29/62 (46%)	4.18	27 (93%) 0 0	65, 81, 86, 91	0
10	H	156/167 (93%)	2.71	102 (65%) 0 0	28, 47, 72, 78	0
11	I	142/142 (100%)	2.92	94 (66%) 0 0	29, 40, 56, 75	0
12	J	132/132 (100%)	3.14	96 (72%) 0 0	26, 38, 60, 71	0
13	K	145/150 (96%)	2.94	101 (69%) 0 0	21, 52, 89, 104	0
14	L	194/194 (100%)	3.34	160 (82%) 0 0	27, 37, 51, 58	0
15	M	186/186 (100%)	3.09	138 (74%) 0 0	34, 52, 93, 104	0
16	N	115/115 (100%)	2.30	63 (54%) 0 0	33, 45, 60, 65	0
17	O	143/143 (100%)	4.04	123 (86%) 0 0	29, 42, 54, 64	0
18	P	95/95 (100%)	2.73	65 (68%) 0 0	29, 38, 53, 66	0
19	Q	150/150 (100%)	3.15	113 (75%) 0 0	24, 35, 52, 60	0
20	R	81/81 (100%)	3.89	70 (86%) 0 0	35, 49, 69, 77	0
21	S	119/119 (100%)	3.20	90 (75%) 0 0	33, 44, 66, 91	0
22	T	53/53 (100%)	3.94	46 (86%) 0 0	34, 42, 60, 70	0
23	U	65/65 (100%)	4.32	56 (86%) 0 0	44, 64, 98, 105	0
24	V	154/154 (100%)	2.23	77 (50%) 0 0	28, 39, 56, 63	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	82/82 (100%)	4.67	78 (95%) 0 0	34, 46, 69, 87	0
26	X	142/142 (100%)	2.65	89 (62%) 0 0	22, 34, 55, 73	0
27	Y	73/73 (100%)	4.57	63 (86%) 0 0	39, 52, 64, 74	0
28	Z	56/56 (100%)	2.78	45 (80%) 0 0	21, 27, 32, 42	0
29	1	46/48 (95%)	4.28	43 (93%) 0 0	27, 45, 63, 80	0
30	2	92/92 (100%)	3.14	69 (75%) 0 0	25, 44, 55, 66	0
All	All	6577/6801 (96%)	3.02	4794 (72%) 0 0	18, 41, 80, 135	0

All (4794) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	W	58	ALA	16.2
25	W	10	VAL	15.0
25	W	85	VAL	14.6
8	F	20	LEU	13.7
27	Y	19	GLY	13.7
20	R	14	ALA	13.0
23	U	38	GLY	12.8
23	U	1	THR	12.6
3	A	31	LYS	12.5
3	A	40	GLY	12.0
27	Y	33	HIS	11.8
6	D	92	GLU	11.5
11	I	94	GLY	11.4
8	F	16	ALA	11.4
1	0	1195	G	11.3
3	A	82	VAL	11.1
8	F	91	VAL	11.0
19	Q	49	ALA	10.9
26	X	236	VAL	10.8
27	Y	26	VAL	10.5
4	B	186	GLY	10.5
6	D	63	ILE	10.4
25	W	72	VAL	10.4
23	U	3	LEU	10.1
25	W	50	LEU	10.0
27	Y	82	ALA	10.0
13	K	97	VAL	9.8
20	R	58	MET	9.7
3	A	1	GLY	9.4

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Mol	Chain	Res	Type	RSRZ
27	Y	25	ARG	9.4
19	Q	88	PHE	9.4
3	A	36	ASP	9.4
1	0	2829	G	9.3
3	A	99	ILE	9.3
23	U	36	ALA	9.3
1	0	1176	C	9.2
1	0	1951	G	9.2
17	O	50	GLN	9.2
29	1	22	PRO	9.1
1	0	1199	A	9.1
17	O	25	PRO	9.0
2	9	3001	U	8.9
21	S	119	ALA	8.9
6	D	88	LEU	8.9
1	0	1172	G	8.9
8	F	105	ALA	8.8
17	O	62	ALA	8.8
23	U	37	GLY	8.8
6	D	128	LEU	8.8
13	K	102	ASP	8.8
4	B	105	PHE	8.7
8	F	24	ARG	8.7
1	0	2344	G	8.6
27	Y	79	VAL	8.6
1	0	1202	A	8.6
4	B	150	ALA	8.6
4	B	81	ALA	8.5
20	R	68	LEU	8.5
1	0	1171	A	8.5
4	B	272	ILE	8.5
13	K	100	ALA	8.5
25	W	74	ALA	8.4
6	D	50	VAL	8.3
12	J	111	GLY	8.3
8	F	66	LEU	8.3
17	O	140	TYR	8.2
1	0	1947	G	8.2
22	T	24	LYS	8.2
7	E	108	LEU	8.1
17	O	49	ILE	8.1
4	B	104	GLU	8.1

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Mol	Chain	Res	Type	RSRZ
9	G	21	ASP	8.0
29	1	35	ARG	8.0
25	W	24	LYS	8.0
8	F	108	LEU	8.0
14	L	75	THR	8.0
6	D	134	LEU	7.9
22	T	18	GLY	7.9
26	X	217	ILE	7.9
1	0	1170	U	7.9
17	O	105	LEU	7.9
4	B	116	PRO	7.9
6	D	26	GLY	7.9
25	W	31	ILE	7.8
3	A	74	VAL	7.8
19	Q	6	VAL	7.8
17	O	48	ALA	7.8
4	B	290	VAL	7.8
15	M	115	VAL	7.8
3	A	15	THR	7.8
11	I	98	PHE	7.8
17	O	137	LEU	7.7
30	2	56	PRO	7.7
9	G	66	LEU	7.7
21	S	2	LYS	7.7
6	D	130	VAL	7.7
17	O	44	VAL	7.7
1	0	735	C	7.7
3	A	42	VAL	7.7
11	I	4	ALA	7.7
12	J	95	ALA	7.7
4	B	214	PRO	7.6
7	E	146	ALA	7.6
22	T	31	PHE	7.6
12	J	47	ALA	7.6
22	T	44	ARG	7.6
18	P	20	ASP	7.6
26	X	116	LEU	7.5
6	D	56	ARG	7.5
1	0	1179	C	7.5
1	0	1604	G	7.5
12	J	58	THR	7.5
27	Y	14	PHE	7.5

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Mol	Chain	Res	Type	RSRZ
3	A	39	ALA	7.5
23	U	39	ALA	7.5
3	A	216	SER	7.5
6	D	131	THR	7.4
15	M	186	LEU	7.4
12	J	78	LYS	7.4
21	S	74	VAL	7.4
17	O	114	LEU	7.4
1	0	1165	G	7.4
8	F	112	ALA	7.3
25	W	19	ALA	7.3
6	D	77	ASP	7.3
17	O	23	PHE	7.3
29	1	19	SER	7.3
19	Q	141	VAL	7.3
8	F	3	TYR	7.3
19	Q	91	LEU	7.2
14	L	114	VAL	7.2
22	T	8	TYR	7.2
1	0	1207	A	7.2
22	T	42	LEU	7.2
17	O	119	TYR	7.2
6	D	158	ASN	7.2
22	T	12	ASP	7.2
4	B	195	ARG	7.2
17	O	95	GLU	7.2
7	E	160	ARG	7.1
27	Y	15	GLY	7.1
14	L	87	MET	7.1
20	R	18	MET	7.1
25	W	88	GLU	7.1
7	E	120	GLY	7.1
15	M	160	SER	7.1
5	C	244	ALA	7.1
23	U	5	VAL	7.1
1	0	1624	A	7.1
21	S	85	GLU	7.1
3	A	60	PHE	7.1
8	F	95	ALA	7.1
25	W	66	THR	7.0
10	H	167	ALA	7.0
27	Y	18	TYR	7.0

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Mol	Chain	Res	Type	RSRZ
3	A	75	GLY	7.0
1	0	1965	C	7.0
4	B	51	VAL	7.0
11	I	75	PRO	7.0
12	J	124	VAL	7.0
15	M	154	LEU	7.0
6	D	138	GLY	7.0
23	U	43	PRO	7.0
1	0	2748	G	7.0
14	L	152	ARG	7.0
13	K	61	ALA	7.0
1	0	1711	A	7.0
1	0	1978	A	7.0
17	O	64	GLU	7.0
6	D	86	THR	7.0
27	Y	21	LYS	6.9
1	0	300	C	6.9
3	A	80	LEU	6.9
10	H	35	ASN	6.9
4	B	278	PRO	6.9
6	D	41	LEU	6.9
1	0	808	A	6.9
6	D	169	THR	6.9
25	W	59	TRP	6.9
4	B	91	PRO	6.9
17	O	66	GLN	6.9
17	O	68	LYS	6.9
6	D	66	GLY	6.9
14	L	132	ILE	6.9
8	F	79	GLN	6.9
8	F	96	ALA	6.8
8	F	13	GLU	6.8
8	F	6	PHE	6.8
10	H	137	ASN	6.8
17	O	89	ASN	6.8
6	D	102	GLY	6.8
27	Y	23	ARG	6.8
23	U	59	ILE	6.8
6	D	69	ILE	6.8
27	Y	47	LEU	6.8
12	J	6	ALA	6.8
23	U	46	ILE	6.8

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Mol	Chain	Res	Type	RSRZ
1	0	2910	A	6.8
29	1	10	ARG	6.8
4	B	330	VAL	6.8
21	S	62	VAL	6.8
20	R	77	VAL	6.8
25	W	81	GLY	6.8
1	0	1161	A	6.7
1	0	796	A	6.7
23	U	58	THR	6.7
26	X	147	ARG	6.7
7	E	97	VAL	6.7
19	Q	87	ALA	6.7
15	M	20	TYR	6.7
17	O	129	GLY	6.7
25	W	65	ASN	6.7
3	A	20	SER	6.7
15	M	166	ALA	6.7
26	X	234	VAL	6.7
15	M	184	ILE	6.7
17	O	130	GLU	6.7
6	D	107	GLY	6.7
17	O	141	ILE	6.7
25	W	11	THR	6.7
8	F	106	THR	6.6
1	0	1497	G	6.6
6	D	135	VAL	6.6
17	O	113	THR	6.6
14	L	71	SER	6.6
1	0	1797	A	6.6
30	2	82	GLY	6.6
3	A	85	ASP	6.6
6	D	104	PHE	6.6
13	K	2	SER	6.6
3	A	137	VAL	6.6
1	0	1626	A	6.6
8	F	19	ALA	6.6
6	D	38	GLU	6.6
22	T	22	VAL	6.6
3	A	228	ILE	6.5
7	E	51	SER	6.5
3	A	229	ALA	6.5
1	0	1948	G	6.5

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Mol	Chain	Res	Type	RSRZ
20	R	78	ALA	6.5
23	U	20	LEU	6.5
7	E	95	VAL	6.5
18	P	76	VAL	6.5
23	U	24	LYS	6.5
30	2	81	GLU	6.5
14	L	78	ASN	6.5
25	W	8	ARG	6.5
14	L	136	PRO	6.5
19	Q	7	GLU	6.5
3	A	133	ARG	6.5
19	Q	53	GLY	6.5
6	D	13	MET	6.4
1	0	1453	G	6.4
3	A	30	ARG	6.4
4	B	109	LEU	6.4
23	U	62	GLU	6.4
1	0	2914	A	6.4
1	0	1517	U	6.4
1	0	2874	G	6.4
26	X	118	THR	6.4
22	T	4	ARG	6.4
1	0	2876	G	6.4
7	E	159	VAL	6.4
3	A	25	ALA	6.4
13	K	58	GLN	6.4
24	V	140	LYS	6.4
14	L	70	GLY	6.3
3	A	29	HIS	6.3
27	Y	37	HIS	6.3
17	O	108	LEU	6.3
27	Y	75	ALA	6.3
3	A	200	PRO	6.3
19	Q	43	ALA	6.3
17	O	79	SER	6.3
6	D	170	TYR	6.3
1	0	2237	G	6.3
6	D	81	GLU	6.3
1	0	1699	C	6.3
21	S	36	GLY	6.3
1	0	271	C	6.3
1	0	2911	C	6.3

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Mol	Chain	Res	Type	RSRZ
6	D	18	ILE	6.3
16	N	34	GLU	6.3
15	M	159	TYR	6.3
20	R	56	ASN	6.3
1	0	2828	G	6.3
20	R	37	VAL	6.3
27	Y	10	ARG	6.3
17	O	126	ALA	6.2
4	B	182	VAL	6.2
30	2	22	VAL	6.2
1	0	1612	A	6.2
27	Y	30	GLU	6.2
14	L	106	ASN	6.2
19	Q	81	PRO	6.2
27	Y	20	LEU	6.2
3	A	151	GLN	6.2
1	0	497	A	6.2
3	A	38	ILE	6.2
11	I	85	GLY	6.2
1	0	299	U	6.2
4	B	106	HIS	6.2
6	D	47	GLN	6.2
14	L	58	GLN	6.2
7	E	81	GLU	6.2
20	R	74	ALA	6.2
15	M	71	TRP	6.2
27	Y	52	THR	6.2
1	0	1526	A	6.1
20	R	20	PHE	6.1
23	U	48	GLU	6.1
6	D	58	VAL	6.1
14	L	1	ALA	6.1
19	Q	115	ALA	6.1
25	W	7	GLU	6.1
13	K	3	LYS	6.1
15	M	70	GLY	6.1
10	H	56	ILE	6.1
19	Q	95	ALA	6.1
20	R	81	ILE	6.1
6	D	98	PHE	6.1
29	1	47	THR	6.1
15	M	162	ASP	6.1

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Mol	Chain	Res	Type	RSRZ
1	0	1163	G	6.1
22	T	52	THR	6.1
13	K	21	ARG	6.1
23	U	9	ARG	6.1
4	B	302	PRO	6.1
8	F	115	VAL	6.1
17	O	109	ARG	6.1
7	E	155	ASN	6.1
1	0	1966	U	6.1
3	A	187	PRO	6.1
17	O	121	ASP	6.1
19	Q	64	SER	6.1
25	W	71	ARG	6.1
10	H	82	LYS	6.1
19	Q	20	GLU	6.1
19	Q	139	PRO	6.1
25	W	27	ASP	6.1
27	Y	11	THR	6.1
1	0	1592	G	6.0
1	0	1204	C	6.0
8	F	49	PHE	6.0
22	T	16	GLY	6.0
4	B	183	GLU	6.0
14	L	34	GLU	6.0
1	0	1166	A	6.0
1	0	1929	G	6.0
28	Z	50	TRP	6.0
7	E	87	PHE	6.0
13	K	103	ALA	6.0
17	O	43	LEU	6.0
11	I	48	GLY	6.0
1	0	1598	A	6.0
1	0	816	G	6.0
10	H	32	ASP	6.0
8	F	97	ALA	6.0
9	G	70	ALA	6.0
3	A	88	ILE	6.0
3	A	93	THR	6.0
20	R	57	THR	6.0
15	M	105	GLY	6.0
12	J	121	PHE	5.9
21	S	66	ASP	5.9

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Mol	Chain	Res	Type	RSRZ
1	0	2247	C	5.9
29	1	11	LEU	5.9
3	A	16	PHE	5.9
29	1	7	THR	5.9
1	0	1000	C	5.9
21	S	77	VAL	5.9
6	D	90	LEU	5.9
17	O	98	ILE	5.9
27	Y	35	LYS	5.9
18	P	86	VAL	5.9
1	0	1613	C	5.9
17	O	78	GLY	5.9
17	O	143	ALA	5.9
23	U	61	GLY	5.9
1	0	1191	A	5.9
1	0	2024	A	5.9
4	B	297	VAL	5.9
11	I	38	VAL	5.9
11	I	79	PHE	5.9
4	B	215	VAL	5.8
21	S	10	SER	5.8
1	0	1603	A	5.8
12	J	110	LYS	5.8
4	B	1	PRO	5.8
13	K	45	PRO	5.8
8	F	87	ALA	5.8
21	S	1	SER	5.8
6	D	106	PHE	5.8
14	L	109	PHE	5.8
1	0	1547	A	5.8
14	L	56	ALA	5.8
1	0	960	G	5.8
1	0	2747	C	5.8
10	H	13	ALA	5.8
3	A	237	GLY	5.8
3	A	76	VAL	5.8
1	0	798	G	5.8
8	F	76	PHE	5.7
11	I	86	MET	5.7
8	F	99	THR	5.7
1	0	1617	C	5.7
1	0	1571	G	5.7

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Mol	Chain	Res	Type	RSRZ
30	2	26	ARG	5.7
1	0	2850	C	5.7
3	A	57	ALA	5.7
9	G	29	SER	5.7
13	K	147	GLU	5.7
3	A	44	ASP	5.7
4	B	143	ILE	5.7
23	U	27	LEU	5.7
29	1	25	VAL	5.7
1	0	1796	A	5.7
6	D	142	ALA	5.7
15	M	100	ALA	5.7
1	0	1201	C	5.7
17	O	61	ARG	5.7
6	D	129	ASP	5.7
6	D	93	LEU	5.7
13	K	91	VAL	5.7
6	D	20	LYS	5.7
1	0	2637	A	5.7
4	B	192	ASP	5.7
19	Q	140	GLN	5.7
29	1	29	THR	5.7
6	D	75	LEU	5.7
1	0	2627	G	5.7
11	I	109	TYR	5.7
1	0	1169	U	5.7
14	L	72	SER	5.7
3	A	129	LEU	5.7
8	F	90	GLU	5.7
18	P	66	LYS	5.7
4	B	188	HIS	5.6
1	0	1601	G	5.6
12	J	127	ALA	5.6
16	N	14	LEU	5.6
8	F	28	ALA	5.6
17	O	18	LYS	5.6
1	0	1824	C	5.6
25	W	22	ASN	5.6
5	C	53	GLY	5.6
9	G	20	VAL	5.6
21	S	65	VAL	5.6
19	Q	16	ALA	5.6

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Mol	Chain	Res	Type	RSRZ
21	S	67	LEU	5.6
3	A	212	PRO	5.6
4	B	178	ALA	5.6
25	W	76	ARG	5.6
3	A	83	GLY	5.6
11	I	139	LEU	5.6
12	J	29	LEU	5.6
7	E	171	LYS	5.6
10	H	51	GLU	5.6
7	E	168	ILE	5.6
4	B	32	ASP	5.6
26	X	111	ASP	5.6
3	A	205	GLY	5.6
1	0	2004	U	5.6
4	B	52	VAL	5.6
11	I	103	VAL	5.6
17	O	19	ASN	5.6
19	Q	80	TYR	5.6
25	W	80	GLU	5.6
6	D	171	ASP	5.5
1	0	1785	G	5.5
1	0	1820	G	5.5
29	1	21	VAL	5.5
4	B	110	ASP	5.5
29	1	20	ARG	5.5
6	D	155	HIS	5.5
25	W	54	ILE	5.5
1	0	1600	G	5.5
1	0	2701	G	5.5
1	0	1810	C	5.5
21	S	69	LYS	5.5
30	2	62	THR	5.5
8	F	74	PHE	5.5
3	A	143	GLY	5.5
14	L	175	GLY	5.5
8	F	8	VAL	5.5
27	Y	63	LYS	5.5
1	0	1950	G	5.5
8	F	77	VAL	5.5
5	C	76	ARG	5.5
14	L	163	LEU	5.5
22	T	49	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
21	S	117	ASP	5.5
6	D	22	VAL	5.5
6	D	64	ARG	5.5
1	0	1561	U	5.5
7	E	119	HIS	5.5
13	K	26	HIS	5.5
18	P	19	ARG	5.5
11	I	45	VAL	5.5
16	N	98	LEU	5.5
6	D	68	PRO	5.4
13	K	64	ILE	5.4
11	I	141	ALA	5.4
1	0	1731	C	5.4
14	L	80	GLY	5.4
20	R	1	SER	5.4
11	I	145	TRP	5.4
4	B	179	LEU	5.4
20	R	47	VAL	5.4
1	0	793	A	5.4
1	0	1632	A	5.4
13	K	59	GLU	5.4
1	0	1872	C	5.4
1	0	1499	U	5.4
3	A	55	VAL	5.4
18	P	9	GLY	5.4
30	2	76	LYS	5.4
30	2	92	GLU	5.4
4	B	113	LEU	5.4
29	1	28	LYS	5.4
1	0	1599	U	5.4
20	R	43	GLU	5.4
1	0	1655	G	5.4
27	Y	56	MET	5.4
1	0	1886	A	5.4
1	0	1521	C	5.4
4	B	153	SER	5.4
3	A	59	GLU	5.4
23	U	41	GLU	5.4
12	J	12	LEU	5.4
4	B	47	GLY	5.4
3	A	84	VAL	5.4
21	S	14	ALA	5.4

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Mol	Chain	Res	Type	RSRZ
15	M	2	THR	5.4
19	Q	121	GLU	5.4
23	U	13	PRO	5.4
15	M	150	TYR	5.4
4	B	60	SER	5.4
4	B	327	VAL	5.4
6	D	143	LYS	5.4
1	0	1811	A	5.3
4	B	211	THR	5.3
13	K	75	LEU	5.3
14	L	115	LEU	5.3
25	W	63	ARG	5.3
27	Y	40	PRO	5.3
1	0	1505	U	5.3
1	0	1402	G	5.3
1	0	287	C	5.3
6	D	173	GLU	5.3
4	B	181	ILE	5.3
1	0	1190	G	5.3
27	Y	13	ARG	5.3
1	0	1451	C	5.3
1	0	1700	C	5.3
1	0	1631	A	5.3
3	A	78	ASP	5.3
20	R	19	ASP	5.3
3	A	185	LYS	5.3
1	0	1970	G	5.3
27	Y	28	ASP	5.3
1	0	1946	C	5.3
15	M	32	PRO	5.3
1	0	1606	A	5.3
1	0	1885	A	5.3
3	A	62	ASP	5.3
4	B	120	ASP	5.3
8	F	14	ASP	5.3
15	M	128	ASP	5.3
1	0	1184	C	5.3
1	0	1180	U	5.2
3	A	43	VAL	5.2
10	H	127	GLY	5.2
22	T	46	ALA	5.2
24	V	24	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
1	0	2730	G	5.2
25	W	18	ARG	5.2
1	0	1173	A	5.2
22	T	28	THR	5.2
9	G	67	LEU	5.2
13	K	142	LEU	5.2
14	L	149	TRP	5.2
23	U	65	ASP	5.2
1	0	1525	G	5.2
1	0	1618	G	5.2
13	K	62	ALA	5.2
19	Q	50	VAL	5.2
26	X	224	ALA	5.2
10	H	158	ASN	5.2
12	J	3	ALA	5.2
4	B	289	GLU	5.2
12	J	119	GLN	5.2
30	2	3	MET	5.2
1	0	1641	A	5.2
1	0	2880	A	5.2
15	M	129	ILE	5.2
17	O	81	LYS	5.2
9	G	17	GLN	5.2
6	D	101	THR	5.2
17	O	99	ARG	5.2
29	1	30	ASP	5.2
12	J	34	VAL	5.2
7	E	41	SER	5.2
1	0	1640	C	5.2
1	0	1488	U	5.2
1	0	2735	U	5.2
15	M	156	GLU	5.2
1	0	716	G	5.2
25	W	70	ILE	5.2
1	0	1232	A	5.2
1	0	1732	A	5.2
1	0	2913	A	5.2
10	H	19	TYR	5.2
21	S	99	THR	5.2
3	A	206	ARG	5.1
21	S	8	ARG	5.1
3	A	138	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
1	0	792	G	5.1
1	0	810	G	5.1
4	B	145	HIS	5.1
20	R	17	ASP	5.1
12	J	56	SER	5.1
5	C	62	GLY	5.1
27	Y	12	GLY	5.1
1	0	2703	A	5.1
26	X	99	ALA	5.1
6	D	103	ASN	5.1
14	L	133	LEU	5.1
19	Q	104	PHE	5.1
1	0	2725	G	5.1
17	O	51	ALA	5.1
6	D	21	VAL	5.1
6	D	141	VAL	5.1
17	O	133	SER	5.1
7	E	54	ASP	5.1
1	0	1182	C	5.1
14	L	86	MET	5.1
1	0	1614	G	5.1
1	0	1709	G	5.1
3	A	24	LYS	5.1
15	M	21	HIS	5.1
15	M	87	LEU	5.1
29	1	14	LEU	5.1
1	0	1177	A	5.1
21	S	33	GLU	5.1
6	D	160	ALA	5.1
20	R	13	LYS	5.1
29	1	4	SER	5.1
11	I	115	VAL	5.1
1	0	1496	G	5.1
1	0	2619	U	5.1
3	A	28	GLU	5.1
10	H	27	LYS	5.1
14	L	79	LYS	5.1
1	0	2746	A	5.1
15	M	3	GLY	5.1
8	F	29	VAL	5.1
3	A	213	LYS	5.0
1	0	2005	G	5.0

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Mol	Chain	Res	Type	RSRZ
14	L	28	MET	5.0
3	A	46	GLU	5.0
1	0	120	A	5.0
26	X	169	ARG	5.0
19	Q	137	ASN	5.0
1	0	2243	C	5.0
1	0	2287	C	5.0
5	C	75	GLY	5.0
3	A	21	HIS	5.0
3	A	96	LEU	5.0
11	I	70	PHE	5.0
15	M	97	VAL	5.0
8	F	26	THR	5.0
1	0	1712	A	5.0
7	E	112	ALA	5.0
11	I	116	LEU	5.0
27	Y	74	VAL	5.0
13	K	76	LEU	5.0
11	I	6	PHE	5.0
11	I	92	GLN	5.0
4	B	151	VAL	5.0
22	T	51	TRP	5.0
3	A	26	ASP	5.0
13	K	10	SER	5.0
1	0	1563	G	5.0
14	L	5	TYR	5.0
14	L	194	ALA	5.0
19	Q	99	ALA	5.0
20	R	36	GLU	5.0
22	T	40	ALA	5.0
22	T	45	GLU	5.0
1	0	138	U	5.0
3	A	179	MET	5.0
3	A	215	ILE	5.0
27	Y	22	ILE	5.0
25	W	55	ASN	5.0
11	I	93	ARG	5.0
28	Z	31	LYS	5.0
30	2	2	GLN	5.0
30	2	78	HIS	5.0
1	0	1999	C	5.0
13	K	137	GLY	5.0

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Mol	Chain	Res	Type	RSRZ
1	0	1704	G	4.9
1	0	1979	G	4.9
1	0	2353	A	4.9
14	L	150	ILE	4.9
1	0	860	U	4.9
1	0	1760	G	4.9
3	A	106	CYS	4.9
15	M	180	LEU	4.9
1	0	780	A	4.9
1	0	1783	A	4.9
10	H	123	ALA	4.9
10	H	128	ALA	4.9
12	J	36	GLY	4.9
20	R	5	ILE	4.9
6	D	74	THR	4.9
1	0	1570	C	4.9
1	0	2355	G	4.9
15	M	61	ALA	4.9
17	O	75	LYS	4.9
1	0	1717	A	4.9
3	A	114	ASP	4.9
8	F	84	GLY	4.9
8	F	102	GLY	4.9
7	E	101	GLU	4.9
8	F	42	ARG	4.9
12	J	120	ARG	4.9
1	0	2882	G	4.9
5	C	5	ILE	4.9
17	O	123	TYR	4.9
14	L	25	TRP	4.9
1	0	1459	A	4.9
4	B	303	GLY	4.9
4	B	318	ASN	4.9
17	O	111	GLU	4.9
1	0	736	A	4.9
1	0	1407	A	4.9
21	S	64	ASN	4.9
3	A	135	VAL	4.9
3	A	145	MET	4.9
17	O	103	THR	4.9
16	N	31	GLU	4.9
23	U	17	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
6	D	157	LEU	4.9
10	H	91	HIS	4.9
21	S	73	HIS	4.9
6	D	145	ASP	4.9
13	K	89	PHE	4.9
17	O	33	ASP	4.9
29	1	18	ASN	4.9
14	L	183	VAL	4.8
13	K	99	GLU	4.8
1	0	1467	C	4.8
17	O	65	ARG	4.8
30	2	60	LYS	4.8
19	Q	129	ALA	4.8
1	0	1412	U	4.8
1	0	2733	U	4.8
1	0	2885	A	4.8
27	Y	39	CYS	4.8
17	O	15	ASP	4.8
3	A	169	PHE	4.8
19	Q	84	ALA	4.8
30	2	19	GLU	4.8
17	O	116	SER	4.8
19	Q	134	SER	4.8
20	R	49	VAL	4.8
14	L	60	ILE	4.8
1	0	535	G	4.8
14	L	153	THR	4.8
13	K	95	ASP	4.8
6	D	53	LYS	4.8
23	U	54	ALA	4.8
21	S	118	SER	4.8
2	9	3023	U	4.8
6	D	52	THR	4.8
7	E	69	ILE	4.8
7	E	100	ASP	4.8
1	0	2723	G	4.8
1	0	1818	C	4.8
22	T	26	GLY	4.8
12	J	57	VAL	4.8
12	J	18	ILE	4.8
14	L	134	ILE	4.8
4	B	329	TYR	4.8

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Mol	Chain	Res	Type	RSRZ
6	D	29	HIS	4.8
14	L	76	ARG	4.8
5	C	66	GLY	4.8
14	L	167	GLY	4.8
1	0	1527	A	4.8
1	0	2664	A	4.8
1	0	2868	C	4.8
20	R	6	LYS	4.8
10	H	109	ASP	4.8
3	A	11	ARG	4.8
20	R	9	HIS	4.8
17	O	128	GLY	4.8
20	R	40	ALA	4.8
6	D	78	GLU	4.8
4	B	115	VAL	4.8
5	C	97	ASP	4.8
8	F	81	ASP	4.8
21	S	101	LEU	4.8
1	0	1411	A	4.8
1	0	1801	A	4.8
1	0	1977	U	4.8
6	D	42	GLY	4.8
23	U	35	ALA	4.7
8	F	72	VAL	4.7
18	P	11	ARG	4.7
30	2	37	ASP	4.7
25	W	23	HIS	4.7
29	1	45	ASN	4.7
1	0	1827	G	4.7
14	L	179	GLY	4.7
14	L	193	LYS	4.7
3	A	111	SER	4.7
15	M	185	GLU	4.7
1	0	797	A	4.7
20	R	31	ARG	4.7
5	C	139	VAL	4.7
16	N	55	ASP	4.7
7	E	20	ILE	4.7
1	0	10	U	4.7
1	0	1576	G	4.7
1	0	1805	G	4.7
1	0	1406	A	4.7

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Mol	Chain	Res	Type	RSRZ
14	L	147	LEU	4.7
5	C	1	MET	4.7
3	A	50	ALA	4.7
30	2	91	GLN	4.7
1	0	1713	G	4.7
7	E	22	VAL	4.7
6	D	27	ILE	4.7
10	H	85	ILE	4.7
18	P	50	GLY	4.7
29	1	16	ASN	4.7
1	0	278	A	4.7
24	V	77	ALA	4.7
25	W	47	ALA	4.7
1	0	1635	U	4.7
1	0	2012	U	4.7
23	U	19	GLU	4.7
10	H	61	LEU	4.7
1	0	87	C	4.7
1	0	1562	C	4.7
8	F	75	ILE	4.7
9	G	65	THR	4.7
1	0	2525	G	4.7
30	2	52	PHE	4.7
1	0	1616	A	4.7
25	W	38	ALA	4.7
25	W	83	ALA	4.7
1	0	1967	U	4.7
8	F	2	VAL	4.7
1	0	2886	C	4.7
4	B	67	GLU	4.7
1	0	2862	G	4.7
7	E	121	ASP	4.7
1	0	272	A	4.7
1	0	1779	A	4.7
1	0	2258	A	4.7
1	0	2369	A	4.7
1	0	1583	U	4.7
5	C	172	THR	4.7
10	H	30	GLN	4.7
12	J	113	ILE	4.7
29	1	38	LYS	4.6
1	0	39	G	4.6

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Mol	Chain	Res	Type	RSRZ
1	0	1162	G	4.6
4	B	212	GLN	4.6
6	D	132	VAL	4.6
1	0	1625	U	4.6
1	0	2032	U	4.6
13	K	44	GLU	4.6
23	U	63	GLU	4.6
4	B	6	PRO	4.6
1	0	1574	C	4.6
8	F	17	LEU	4.6
12	J	38	SER	4.6
1	0	1498	G	4.6
1	0	1819	G	4.6
1	0	2763	G	4.6
2	9	3073	G	4.6
5	C	61	PHE	4.6
1	0	1909	A	4.6
3	A	153	ARG	4.6
9	G	18	GLU	4.6
14	L	29	GLN	4.6
5	C	162	VAL	4.6
15	M	108	SER	4.6
20	R	52	VAL	4.6
4	B	33	ASP	4.6
1	0	1964	U	4.6
1	0	2662	G	4.6
3	A	70	ALA	4.6
3	A	89	ALA	4.6
15	M	1	ALA	4.6
23	U	26	GLU	4.6
1	0	2030	A	4.6
17	O	14	LEU	4.6
14	L	148	SER	4.6
29	1	41	HIS	4.6
1	0	534	C	4.6
4	B	77	PRO	4.6
1	0	2246	U	4.6
19	Q	15	LYS	4.6
21	S	70	ALA	4.6
1	0	2754	G	4.6
15	M	69	TYR	4.6
16	N	51	TYR	4.6

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Mol	Chain	Res	Type	RSRZ
1	0	285	A	4.6
6	D	65	GLU	4.6
22	T	13	ILE	4.6
25	W	86	GLU	4.6
1	0	2443	C	4.6
4	B	64	GLY	4.6
27	Y	34	LYS	4.6
6	D	37	ALA	4.6
6	D	87	ALA	4.6
20	R	2	TRP	4.6
27	Y	78	ALA	4.6
21	S	103	LEU	4.6
13	K	81	VAL	4.6
1	0	1605	G	4.6
1	0	1486	A	4.6
1	0	1656	A	4.6
13	K	122	ALA	4.6
9	G	69	ARG	4.6
8	F	30	LYS	4.6
15	M	134	ASP	4.6
5	C	177	GLY	4.5
1	0	336	G	4.5
4	B	266	ASN	4.5
1	0	788	A	4.5
3	A	65	ARG	4.5
5	C	65	ARG	4.5
14	L	162	GLY	4.5
21	S	90	PRO	4.5
12	J	116	GLU	4.5
19	Q	148	GLU	4.5
29	1	31	GLU	4.5
1	0	1178	G	4.5
1	0	2734	G	4.5
20	R	21	GLN	4.5
1	0	2049	C	4.5
4	B	259	TYR	4.5
8	F	50	VAL	4.5
10	H	80	ASN	4.5
10	H	122	ALA	4.5
25	W	64	ALA	4.5
17	O	101	GLN	4.5
1	0	387	G	4.5

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Mol	Chain	Res	Type	RSRZ
1	0	786	G	4.5
1	0	1627	G	4.5
1	0	1896	G	4.5
1	0	2003	U	4.5
1	0	2017	U	4.5
1	0	2312	G	4.5
3	A	167	LYS	4.5
4	B	164	THR	4.5
30	2	31	THR	4.5
1	0	2890	A	4.5
3	A	134	ASN	4.5
9	G	27	ILE	4.5
9	G	71	LEU	4.5
24	V	7	LEU	4.5
4	B	4	SER	4.5
17	O	22	TRP	4.5
30	2	66	ASP	4.5
8	F	31	LYS	4.5
1	0	2749	U	4.5
6	D	165	PHE	4.5
19	Q	46	TYR	4.5
30	2	10	TYR	4.5
3	A	218	ASN	4.5
1	0	1628	G	4.5
21	S	37	GLN	4.5
1	0	1404	C	4.5
1	0	1597	A	4.5
15	M	58	LEU	4.5
24	V	49	ASN	4.5
1	0	1206	U	4.5
8	F	59	ILE	4.5
8	F	12	LEU	4.5
1	0	1943	C	4.5
1	0	2294	C	4.5
1	0	352	A	4.5
1	0	957	A	4.5
1	0	1194	A	4.5
4	B	295	THR	4.5
11	I	83	ILE	4.5
4	B	160	ASP	4.5
17	O	110	ASP	4.5
6	D	148	SER	4.5

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Mol	Chain	Res	Type	RSRZ
21	S	49	GLU	4.5
7	E	170	ARG	4.5
28	Z	46	ARG	4.5
1	0	58	C	4.4
1	0	2685	C	4.4
19	Q	130	MET	4.4
1	0	69	A	4.4
1	0	1082	A	4.4
3	A	141	PRO	4.4
12	J	79	PRO	4.4
17	O	21	VAL	4.4
9	G	15	TRP	4.4
18	P	49	ASN	4.4
1	0	851	C	4.4
4	B	309	VAL	4.4
12	J	45	PRO	4.4
27	Y	16	PRO	4.4
4	B	114	ASP	4.4
4	B	308	LEU	4.4
17	O	132	ASP	4.4
27	Y	49	ARG	4.4
12	J	122	GLY	4.4
3	A	136	ALA	4.4
17	O	5	ALA	4.4
1	0	1972	U	4.4
9	G	25	GLU	4.4
13	K	119	THR	4.4
22	T	11	THR	4.4
1	0	298	C	4.4
1	0	1593	C	4.4
11	I	87	LEU	4.4
17	O	31	ILE	4.4
3	A	86	ALA	4.4
3	A	121	ALA	4.4
4	B	189	ALA	4.4
6	D	94	ALA	4.4
22	T	32	CYS	4.4
4	B	5	ARG	4.4
10	H	86	ARG	4.4
4	B	315	VAL	4.4
6	D	152	PRO	4.4
23	U	50	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
12	J	1	MET	4.4
4	B	208	GLY	4.4
19	Q	106	GLY	4.4
7	E	138	ILE	4.4
3	A	186	TRP	4.4
25	W	36	HIS	4.4
14	L	185	PRO	4.4
3	A	63	GLY	4.4
5	C	153	VAL	4.4
17	O	29	GLY	4.4
18	P	2	SER	4.4
1	0	1196	C	4.4
1	0	1768	C	4.4
2	9	3046	C	4.4
1	0	297	U	4.4
1	0	1758	U	4.4
4	B	36	PRO	4.4
3	A	105	VAL	4.4
1	0	150	G	4.4
1	0	812	A	4.4
1	0	869	G	4.4
1	0	2869	G	4.4
15	M	158	LEU	4.4
10	H	64	ALA	4.4
20	R	32	ALA	4.4
6	D	17	ARG	4.4
20	R	67	ARG	4.4
13	K	32	ASP	4.4
1	0	1198	U	4.4
1	0	1698	U	4.4
5	C	160	LEU	4.4
14	L	46	LEU	4.4
1	0	604	G	4.4
1	0	1543	G	4.4
1	0	1607	A	4.4
1	0	2136	G	4.4
1	0	2743	A	4.4
28	Z	48	TYR	4.4
5	C	90	HIS	4.3
3	A	149	ASP	4.3
7	E	36	PRO	4.3
15	M	43	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
21	S	79	LEU	4.3
1	0	1408	U	4.3
17	O	80	ARG	4.3
26	X	155	ARG	4.3
5	C	215	ALA	4.3
17	O	77	ALA	4.3
20	R	45	TYR	4.3
1	0	274	G	4.3
1	0	1944	G	4.3
1	0	2848	G	4.3
3	A	79	GLU	4.3
5	C	237	GLU	4.3
8	F	56	PRO	4.3
4	B	68	THR	4.3
11	I	35	THR	4.3
11	I	131	THR	4.3
7	E	42	VAL	4.3
19	Q	79	ARG	4.3
26	X	123	VAL	4.3
25	W	30	MET	4.3
29	1	26	MET	4.3
1	0	2752	C	4.3
8	F	111	ILE	4.3
9	G	23	ILE	4.3
20	R	27	ALA	4.3
8	F	15	ASP	4.3
25	W	52	PRO	4.3
27	Y	17	ARG	4.3
1	0	1160	G	4.3
1	0	1200	A	4.3
1	0	2750	G	4.3
1	0	2863	G	4.3
16	N	70	LEU	4.3
26	X	109	LEU	4.3
1	0	133	U	4.3
1	0	1185	U	4.3
1	0	1514	C	4.3
1	0	1793	C	4.3
19	Q	90	ASP	4.3
23	U	44	GLY	4.3
7	E	136	PRO	4.3
23	U	40	PRO	4.3

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Mol	Chain	Res	Type	RSRZ
12	J	69	LEU	4.3
18	P	47	VAL	4.3
15	M	174	GLU	4.3
1	0	380	A	4.3
1	0	2694	A	4.3
4	B	12	GLY	4.3
6	D	35	ALA	4.3
13	K	77	ALA	4.3
26	X	195	GLY	4.3
1	0	18	C	4.3
28	Z	25	LYS	4.3
15	M	132	ASN	4.3
3	A	210	GLY	4.3
6	D	54	ALA	4.3
3	A	190	ARG	4.3
19	Q	113	HIS	4.3
1	0	237	G	4.3
1	0	1522	A	4.3
1	0	2827	A	4.3
7	E	6	GLU	4.3
29	1	49	GLU	4.3
4	B	301	VAL	4.3
4	B	255	GLY	4.3
6	D	133	ASN	4.3
17	O	32	ALA	4.3
25	W	12	ILE	4.3
1	0	1639	U	4.3
12	J	49	LEU	4.3
1	0	273	G	4.3
1	0	1392	A	4.3
1	0	1413	A	4.3
1	0	1608	G	4.3
3	A	37	VAL	4.3
11	I	101	VAL	4.3
13	K	53	ARG	4.3
27	Y	58	GLY	4.3
1	0	505	C	4.3
1	0	1584	C	4.3
1	0	2031	C	4.3
1	0	794	U	4.2
28	Z	38	GLY	4.2
29	1	1	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
3	A	48	ASP	4.2
1	0	800	G	4.2
1	0	811	C	4.2
1	0	1798	C	4.2
4	B	107	SER	4.2
30	2	38	ARG	4.2
5	C	198	ASP	4.2
7	E	145	ALA	4.2
8	F	101	ALA	4.2
11	I	78	ILE	4.2
30	2	39	GLN	4.2
1	0	390	G	4.2
1	0	525	G	4.2
1	0	878	G	4.2
1	0	1774	G	4.2
1	0	1997	A	4.2
1	0	2019	A	4.2
1	0	1841	C	4.2
1	0	2753	G	4.2
14	L	95	LYS	4.2
12	J	109	LEU	4.2
3	A	192	VAL	4.2
5	C	84	VAL	4.2
3	A	68	ILE	4.2
4	B	21	SER	4.2
29	1	37	HIS	4.2
21	S	75	GLU	4.2
1	0	698	A	4.2
1	0	887	G	4.2
1	0	1533	A	4.2
1	0	1681	G	4.2
1	0	1687	C	4.2
1	0	2238	A	4.2
1	0	2770	G	4.2
1	0	2826	G	4.2
19	Q	11	ASP	4.2
3	A	103	VAL	4.2
4	B	154	VAL	4.2
7	E	150	GLN	4.2
19	Q	40	ALA	4.2
26	X	173	ALA	4.2
15	M	68	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
4	B	58	PRO	4.2
5	C	207	LEU	4.2
3	A	41	THR	4.2
1	0	1575	C	4.2
1	0	1609	C	4.2
11	I	10	VAL	4.2
1	0	1523	G	4.2
1	0	1777	G	4.2
1	0	1843	A	4.2
1	0	1923	G	4.2
1	0	2333	G	4.2
1	0	2420	G	4.2
1	0	1405	U	4.2
2	9	3024	U	4.2
10	H	68	ALA	4.2
8	F	63	ILE	4.2
8	F	69	GLU	4.2
10	H	126	HIS	4.2
17	O	4	SER	4.2
7	E	44	GLY	4.2
30	2	25	VAL	4.2
1	0	999	C	4.2
1	0	2122	C	4.2
1	0	2281	C	4.2
11	I	27	ALA	4.2
1	0	805	G	4.2
1	0	1701	A	4.2
1	0	1729	A	4.2
7	E	104	ILE	4.2
11	I	127	ILE	4.2
1	0	2683	G	4.2
3	A	71	PRO	4.2
4	B	39	GLN	4.2
20	R	24	LEU	4.2
21	S	15	PRO	4.2
21	S	76	ASP	4.2
14	L	37	VAL	4.2
14	L	88	VAL	4.2
15	M	8	VAL	4.2
15	M	149	GLU	4.2
3	A	180	LYS	4.1
14	L	66	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
18	P	80	LYS	4.1
25	W	68	SER	4.1
27	Y	32	LYS	4.1
7	E	118	ILE	4.1
27	Y	53	GLY	4.1
1	0	200	U	4.1
1	0	970	U	4.1
1	0	1183	C	4.1
20	R	53	ASN	4.1
1	0	795	G	4.1
1	0	1458	A	4.1
1	0	1504	A	4.1
1	0	1930	A	4.1
1	0	2124	G	4.1
14	L	2	ARG	4.1
28	Z	22	CYS	4.1
4	B	220	VAL	4.1
4	B	251	VAL	4.1
7	E	3	VAL	4.1
10	H	142	VAL	4.1
17	O	104	LYS	4.1
20	R	66	VAL	4.1
5	C	77	ALA	4.1
24	V	6	GLN	4.1
6	D	83	PHE	4.1
1	0	1507	C	4.1
1	0	2625	C	4.1
7	E	169	THR	4.1
24	V	88	THR	4.1
1	0	49	A	4.1
1	0	1667	A	4.1
1	0	2867	G	4.1
4	B	69	VAL	4.1
12	J	16	SER	4.1
15	M	161	GLY	4.1
7	E	68	HIS	4.1
7	E	45	ASP	4.1
17	O	12	ASP	4.1
4	B	78	PRO	4.1
4	B	306	LYS	4.1
1	0	14	C	4.1
1	0	40	C	4.1

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Mol	Chain	Res	Type	RSRZ
1	0	238	C	4.1
1	0	1537	C	4.1
1	0	1861	C	4.1
4	B	206	THR	4.1
4	B	100	VAL	4.1
19	Q	65	GLY	4.1
1	0	1636	G	4.1
1	0	770	C	4.1
1	0	2870	C	4.1
16	N	29	VAL	4.1
3	A	126	ALA	4.1
4	B	119	HIS	4.1
4	B	274	GLU	4.1
14	L	107	ARG	4.1
1	0	2289	G	4.1
17	O	83	LYS	4.1
21	S	82	THR	4.1
30	2	9	THR	4.1
14	L	26	HIS	4.1
19	Q	135	ALA	4.1
27	Y	50	ALA	4.1
1	0	2883	A	4.1
1	0	1541	G	4.1
1	0	2001	G	4.1
1	0	1454	U	4.1
3	A	58	VAL	4.1
1	0	1792	C	4.1
1	0	1844	C	4.1
1	0	2769	C	4.1
4	B	108	GLU	4.1
30	2	16	GLU	4.1
30	2	80	ARG	4.1
3	A	52	SER	4.1
7	E	102	VAL	4.0
23	U	2	VAL	4.0
1	0	1587	U	4.0
1	0	2732	U	4.0
1	0	1586	G	4.0
1	0	1780	G	4.0
1	0	2110	G	4.0
1	0	2254	G	4.0
1	0	2452	G	4.0

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Mol	Chain	Res	Type	RSRZ
11	I	59	LYS	4.0
20	R	51	GLN	4.0
26	X	150	LEU	4.0
28	Z	30	LYS	4.0
3	A	144	GLU	4.0
8	F	110	GLU	4.0
21	S	12	ARG	4.0
1	0	859	C	4.0
10	H	111	MET	4.0
11	I	82	THR	4.0
15	M	57	THR	4.0
3	A	132	ASP	4.0
4	B	207	LYS	4.0
10	H	69	ASN	4.0
1	0	1645	U	4.0
4	B	53	LEU	4.0
7	E	129	GLU	4.0
1	0	1318	A	4.0
1	0	2465	A	4.0
1	0	1933	G	4.0
1	0	2887	G	4.0
24	V	124	GLY	4.0
19	Q	138	SER	4.0
1	0	1578	C	4.0
1	0	2130	C	4.0
5	C	171	GLU	4.0
5	C	218	VAL	4.0
6	D	85	GLN	4.0
11	I	65	ASN	4.0
12	J	68	VAL	4.0
12	J	94	ALA	4.0
19	Q	133	ALA	4.0
25	W	87	ALA	4.0
15	M	109	PRO	4.0
23	U	8	ILE	4.0
6	D	72	LYS	4.0
1	0	1174	A	4.0
1	0	2612	A	4.0
20	R	69	SER	4.0
7	E	52	ASP	4.0
7	E	127	ASP	4.0
1	0	618	G	4.0

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Mol	Chain	Res	Type	RSRZ
1	0	2257	G	4.0
1	0	2884	G	4.0
28	Z	13	THR	4.0
3	A	124	VAL	4.0
4	B	312	ARG	4.0
7	E	114	ARG	4.0
8	F	98	VAL	4.0
15	M	5	ARG	4.0
16	N	64	VAL	4.0
1	0	2751	C	4.0
5	C	34	ALA	4.0
17	O	122	LEU	4.0
1	0	2027	U	4.0
12	J	80	ILE	4.0
15	M	167	ASP	4.0
17	O	74	GLN	4.0
5	C	233	THR	4.0
1	0	102	A	4.0
1	0	1572	A	4.0
1	0	2504	A	4.0
3	A	170	VAL	4.0
24	V	14	HIS	4.0
28	Z	28	HIS	4.0
1	0	373	G	4.0
1	0	384	G	4.0
7	E	18	LEU	4.0
23	U	51	LYS	4.0
29	1	6	ALA	4.0
1	0	2409	C	4.0
1	0	2561	C	4.0
10	H	138	PRO	4.0
7	E	7	ILE	4.0
12	J	97	ILE	4.0
1	0	2726	U	4.0
4	B	117	GLU	4.0
12	J	100	GLU	4.0
13	K	71	GLU	4.0
11	I	138	THR	4.0
14	L	170	CYS	4.0
1	0	1124	A	4.0
1	0	1381	A	4.0
1	0	1919	A	4.0

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Mol	Chain	Res	Type	RSRZ
1	0	1851	G	4.0
1	0	122	C	4.0
1	0	2644	C	4.0
8	F	70	LYS	4.0
15	M	95	ALA	4.0
12	J	27	ARG	4.0
26	X	120	ARG	4.0
1	0	86	A	4.0
1	0	411	A	4.0
1	0	489	A	4.0
1	0	516	A	4.0
1	0	2854	A	4.0
3	A	23	TYR	4.0
1	0	813	C	3.9
1	0	1417	G	3.9
1	0	1445	G	3.9
1	0	1703	G	3.9
1	0	1745	G	3.9
1	0	1807	U	3.9
3	A	202	GLY	3.9
4	B	260	HIS	3.9
15	M	47	LEU	3.9
17	O	92	GLU	3.9
4	B	196	ALA	3.9
17	O	11	ALA	3.9
26	X	128	PHE	3.9
14	L	118	TYR	3.9
27	Y	69	TYR	3.9
4	B	76	THR	3.9
1	0	1230	A	3.9
1	0	1839	A	3.9
1	0	2018	A	3.9
1	0	2372	A	3.9
1	0	1854	C	3.9
3	A	208	HIS	3.9
5	C	175	LYS	3.9
13	K	96	VAL	3.9
12	J	66	ARG	3.9
17	O	37	ARG	3.9
4	B	118	ASP	3.9
10	H	28	ILE	3.9
4	B	332	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
14	L	190	ASN	3.9
7	E	117	THR	3.9
27	Y	76	GLY	3.9
21	S	9	LYS	3.9
22	T	23	HIS	3.9
8	F	94	ALA	3.9
19	Q	114	VAL	3.9
1	0	368	C	3.9
1	0	399	C	3.9
1	0	1208	C	3.9
1	0	1913	C	3.9
1	0	2239	C	3.9
1	0	2259	C	3.9
1	0	2891	A	3.9
9	G	73	ASP	3.9
1	0	1167	G	3.9
1	0	2375	G	3.9
1	0	2632	G	3.9
2	9	3004	G	3.9
4	B	74	ILE	3.9
18	P	43	ILE	3.9
4	B	287	TYR	3.9
15	M	76	GLY	3.9
24	V	135	GLY	3.9
4	B	18	ARG	3.9
6	D	153	THR	3.9
1	0	2240	U	3.9
4	B	101	TRP	3.9
27	Y	55	TRP	3.9
1	0	2245	C	3.9
1	0	132	A	3.9
1	0	1934	A	3.9
14	L	96	ASN	3.9
1	0	47	G	3.9
1	0	1706	G	3.9
12	J	77	ARG	3.9
14	L	184	ARG	3.9
8	F	89	LEU	3.9
26	X	163	THR	3.9
30	2	20	HIS	3.9
5	C	195	VAL	3.9
26	X	139	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
26	X	192	ASP	3.9
14	L	77	PHE	3.9
24	V	51	PHE	3.9
1	0	1164	U	3.9
11	I	53	ILE	3.9
15	M	30	GLY	3.9
1	0	1988	C	3.9
1	0	2622	A	3.9
14	L	23	LEU	3.9
17	O	36	THR	3.9
18	P	7	LEU	3.9
24	V	38	THR	3.9
1	0	76	G	3.9
1	0	1540	G	3.9
1	0	1884	G	3.9
4	B	285	VAL	3.9
14	L	57	LYS	3.9
15	M	152	GLU	3.9
5	C	89	ALA	3.9
16	N	92	VAL	3.9
20	R	64	ALA	3.9
30	2	7	PHE	3.9
1	0	858	U	3.9
1	0	1825	U	3.9
2	9	3002	U	3.9
14	L	85	ARG	3.9
1	0	2802	C	3.9
17	O	107	GLU	3.9
26	X	108	ASP	3.9
1	0	790	A	3.9
14	L	21	ALA	3.9
5	C	81	PRO	3.9
8	F	44	SER	3.9
16	N	30	ALA	3.9
1	0	296	G	3.9
1	0	2731	G	3.9
3	A	147	ARG	3.9
14	L	169	ARG	3.9
15	M	46	GLN	3.9
14	L	155	HIS	3.8
19	Q	27	HIS	3.8
26	X	102	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
28	Z	17	THR	3.8
1	0	323	C	3.8
1	0	804	C	3.8
1	0	1157	C	3.8
2	9	3122	C	3.8
3	A	97	ALA	3.8
4	B	256	GLN	3.8
5	C	246	ARG	3.8
16	N	91	GLN	3.8
17	O	127	GLY	3.8
1	0	1427	A	3.8
1	0	1492	A	3.8
1	0	1494	A	3.8
1	0	1710	A	3.8
1	0	1875	A	3.8
1	0	1973	A	3.8
1	0	2007	A	3.8
1	0	2266	A	3.8
1	0	1339	G	3.8
1	0	1672	G	3.8
1	0	2638	G	3.8
1	0	2744	G	3.8
1	0	2830	U	3.8
2	9	3005	G	3.8
15	M	24	LEU	3.8
6	D	62	ASP	3.8
15	M	171	HIS	3.8
10	H	84	ARG	3.8
7	E	86	VAL	3.8
24	V	120	PRO	3.8
27	Y	77	LYS	3.8
1	0	279	C	3.8
7	E	105	GLU	3.8
20	R	50	GLU	3.8
1	0	288	A	3.8
1	0	791	A	3.8
1	0	1461	U	3.8
1	0	1515	A	3.8
3	A	69	LEU	3.8
17	O	2	ASP	3.8
21	S	46	ASP	3.8
30	2	67	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
4	B	20	THR	3.8
1	0	1295	G	3.8
1	0	1410	G	3.8
1	0	1449	G	3.8
1	0	1610	G	3.8
1	0	1718	G	3.8
1	0	2023	G	3.8
25	W	15	ARG	3.8
3	A	110	SER	3.8
7	E	111	LYS	3.8
21	S	109	GLU	3.8
1	0	1894	C	3.8
1	0	2241	C	3.8
3	A	66	ARG	3.8
4	B	291	ASP	3.8
25	W	32	LEU	3.8
1	0	1890	U	3.8
12	J	24	THR	3.8
26	X	103	THR	3.8
1	0	1968	A	3.8
1	0	2768	A	3.8
4	B	210	GLY	3.8
13	K	60	GLU	3.8
16	N	41	ALA	3.8
17	O	16	VAL	3.8
1	0	229	G	3.8
1	0	269	G	3.8
1	0	467	G	3.8
1	0	871	G	3.8
1	0	2336	G	3.8
9	G	16	LYS	3.8
10	H	157	ILE	3.8
17	O	120	ARG	3.8
19	Q	61	GLN	3.8
3	A	67	LEU	3.8
15	M	175	LEU	3.8
1	0	1705	C	3.8
1	0	2475	C	3.8
22	T	37	GLU	3.8
7	E	113	PRO	3.8
1	0	737	A	3.8
1	0	961	A	3.8

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Mol	Chain	Res	Type	RSRZ
1	0	1487	A	3.8
1	0	1518	A	3.8
1	0	2583	A	3.8
6	D	51	ARG	3.8
14	L	174	ARG	3.8
1	0	1555	G	3.8
1	0	1556	G	3.8
1	0	2121	G	3.8
1	0	2713	G	3.8
2	9	3025	G	3.8
5	C	143	ASP	3.8
8	F	82	ASP	3.8
20	R	48	THR	3.8
1	0	2029	C	3.8
1	0	2329	C	3.8
1	0	2571	C	3.8
11	I	61	VAL	3.8
12	J	73	VAL	3.8
13	K	106	VAL	3.8
15	M	6	TYR	3.8
26	X	185	VAL	3.8
7	E	93	MET	3.8
17	O	87	ARG	3.8
17	O	136	ASP	3.8
1	0	151	A	3.8
1	0	1181	A	3.8
1	0	2413	A	3.8
15	M	90	LEU	3.8
5	C	10	GLY	3.8
14	L	186	SER	3.8
19	Q	1	GLY	3.8
1	0	1697	G	3.8
1	0	1773	G	3.8
1	0	2861	G	3.8
2	9	3007	G	3.8
3	A	49	PRO	3.8
6	D	61	PHE	3.8
21	S	25	ALA	3.8
1	0	695	C	3.8
1	0	842	C	3.8
1	0	1342	C	3.8
1	0	1462	C	3.8

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Mol	Chain	Res	Type	RSRZ
1	0	1715	C	3.8
1	0	1724	U	3.8
1	0	2261	C	3.8
5	C	6	TYR	3.8
6	D	48	MET	3.7
5	C	101	ASP	3.7
3	A	6	GLY	3.7
18	P	5	GLY	3.7
1	0	1341	A	3.7
1	0	2814	A	3.7
5	C	56	THR	3.7
4	B	284	PHE	3.7
1	0	13	G	3.7
1	0	2602	G	3.7
1	0	396	U	3.7
1	0	1725	C	3.7
1	0	2129	U	3.7
1	0	2346	C	3.7
21	S	68	ASP	3.7
29	1	2	LYS	3.7
4	B	97	LEU	3.7
6	D	44	ILE	3.7
27	Y	31	ILE	3.7
4	B	257	THR	3.7
6	D	19	GLU	3.7
17	O	138	GLU	3.7
6	D	164	ALA	3.7
1	0	114	A	3.7
1	0	659	A	3.7
1	0	1379	A	3.7
2	9	3045	A	3.7
26	X	209	VAL	3.7
1	0	824	G	3.7
1	0	919	U	3.7
1	0	1050	G	3.7
1	0	1589	G	3.7
1	0	1596	U	3.7
1	0	1873	G	3.7
8	F	83	LEU	3.7
1	0	124	C	3.7
1	0	1651	C	3.7
26	X	207	SER	3.7

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Mol	Chain	Res	Type	RSRZ
8	F	119	ARG	3.7
9	G	63	ARG	3.7
3	A	201	PHE	3.7
5	C	159	ALA	3.7
18	P	52	PHE	3.7
24	V	136	GLY	3.7
1	0	886	A	3.7
1	0	1847	A	3.7
27	Y	68	CYS	3.7
1	0	1544	U	3.7
29	1	43	ARG	3.7
7	E	50	GLU	3.7
26	X	165	GLU	3.7
4	B	128	ILE	3.7
1	0	141	C	3.7
1	0	1535	G	3.7
1	0	1666	C	3.7
3	A	95	PRO	3.7
18	P	1	PRO	3.7
11	I	41	ALA	3.7
16	N	113	VAL	3.7
3	A	10	GLY	3.7
4	B	213	GLY	3.7
24	V	123	GLY	3.7
9	G	28	GLU	3.7
16	N	33	LEU	3.7
26	X	229	LEU	3.7
23	U	42	ASN	3.7
3	A	45	ILE	3.7
1	0	498	A	3.7
3	A	130	THR	3.7
8	F	37	THR	3.7
21	S	26	THR	3.7
1	0	514	G	3.7
1	0	2383	G	3.7
1	0	2857	C	3.7
22	T	21	PHE	3.7
24	V	91	ASP	3.7
2	9	3066	G	3.7
6	D	79	MET	3.7
15	M	42	HIS	3.7
1	0	2628	U	3.7

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Mol	Chain	Res	Type	RSRZ
4	B	72	THR	3.7
13	K	1	THR	3.7
21	S	105	ASP	3.7
25	W	46	ASP	3.7
1	0	2739	A	3.7
4	B	275	GLY	3.7
8	F	21	GLU	3.7
18	P	95	GLU	3.7
24	V	8	ARG	3.7
1	0	1508	C	3.7
1	0	2831	C	3.7
1	0	2912	C	3.7
16	N	43	VAL	3.7
1	0	1197	G	3.7
1	0	2271	G	3.7
3	A	148	LEU	3.7
14	L	141	ILE	3.7
3	A	13	THR	3.7
6	D	57	THR	3.7
1	0	883	U	3.7
14	L	188	ARG	3.7
27	Y	72	GLU	3.7
3	A	204	GLY	3.6
13	K	28	GLY	3.6
21	S	57	GLY	3.6
27	Y	70	GLN	3.6
1	0	80	A	3.6
1	0	1005	A	3.6
1	0	1213	C	3.6
1	0	1664	A	3.6
1	0	1716	A	3.6
1	0	1778	A	3.6
1	0	1804	A	3.6
1	0	2812	A	3.6
5	C	60	SER	3.6
14	L	119	SER	3.6
2	9	3064	C	3.6
15	M	107	ASN	3.6
1	0	1542	G	3.6
1	0	1688	G	3.6
1	0	2505	G	3.6
30	2	36	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
15	M	18	THR	3.6
16	N	6	ARG	3.6
3	A	90	PRO	3.6
1	0	1980	U	3.6
27	Y	65	ALA	3.6
24	V	79	VAL	3.6
6	D	105	SER	3.6
6	D	25	MET	3.6
1	0	1189	A	3.6
1	0	1579	C	3.6
1	0	2040	C	3.6
26	X	216	ARG	3.6
5	C	71	PRO	3.6
12	J	107	THR	3.6
26	X	119	GLN	3.6
1	0	809	G	3.6
1	0	1809	G	3.6
1	0	1823	G	3.6
1	0	2667	G	3.6
5	C	58	ALA	3.6
10	H	149	ALA	3.6
1	0	1205	U	3.6
1	0	2120	U	3.6
4	B	38	VAL	3.6
4	B	286	ASN	3.6
8	F	78	GLU	3.6
30	2	87	ARG	3.6
30	2	1	MET	3.6
7	E	34	TRP	3.6
1	0	290	C	3.6
7	E	1	PRO	3.6
7	E	172	PRO	3.6
13	K	63	THR	3.6
15	M	163	PHE	3.6
1	0	177	A	3.6
1	0	1476	A	3.6
1	0	1693	A	3.6
1	0	2345	A	3.6
12	J	21	ALA	3.6
15	M	41	LYS	3.6
17	O	86	ALA	3.6
3	A	140	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
14	L	187	LEU	3.6
30	2	88	LEU	3.6
1	0	787	G	3.6
1	0	2256	G	3.6
1	0	2263	G	3.6
1	0	2416	G	3.6
14	L	48	ARG	3.6
21	S	22	GLN	3.6
17	O	17	GLY	3.6
17	O	35	ILE	3.6
14	L	110	PRO	3.6
29	1	9	LYS	3.6
1	0	881	C	3.6
4	B	262	ARG	3.6
12	J	117	VAL	3.6
13	K	27	ARG	3.6
17	O	106	ARG	3.6
30	2	48	ASN	3.6
1	0	602	A	3.6
1	0	2645	U	3.6
10	H	45	GLN	3.6
15	M	55	ASP	3.6
1	0	856	G	3.6
1	0	870	G	3.6
1	0	1629	G	3.6
1	0	1649	G	3.6
1	0	2871	G	3.6
26	X	156	GLY	3.6
3	A	178	LYS	3.6
9	G	26	MET	3.6
12	J	64	MET	3.6
13	K	105	TYR	3.6
16	N	81	PHE	3.6
30	2	65	THR	3.6
3	A	172	ALA	3.6
4	B	334	SER	3.6
16	N	32	ARG	3.6
3	A	197	VAL	3.6
9	G	24	VAL	3.6
11	I	67	ASN	3.6
15	M	101	VAL	3.6
15	M	102	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
21	S	7	GLN	3.6
1	0	1772	C	3.6
1	0	1856	C	3.6
1	0	2760	C	3.6
1	0	623	U	3.6
1	0	1569	U	3.6
20	R	62	LYS	3.6
1	0	430	A	3.6
1	0	1528	A	3.6
1	0	1691	A	3.6
1	0	1981	A	3.6
1	0	2800	A	3.6
7	E	58	THR	3.6
18	P	71	TYR	3.6
1	0	820	G	3.6
1	0	1409	G	3.6
1	0	1452	G	3.6
11	I	49	ARG	3.6
30	2	29	ARG	3.6
11	I	132	LEU	3.6
15	M	127	LEU	3.6
21	S	3	GLN	3.6
16	N	76	VAL	3.6
30	2	34	LYS	3.6
10	H	58	HIS	3.6
1	0	1343	C	3.6
1	0	1377	C	3.6
1	0	1456	C	3.6
1	0	2026	C	3.6
1	0	1419	U	3.6
1	0	1548	U	3.6
1	0	2484	U	3.6
7	E	65	PHE	3.5
7	E	107	PHE	3.5
14	L	164	THR	3.5
19	Q	125	ARG	3.6
26	X	107	PRO	3.5
1	0	485	A	3.5
1	0	1590	A	3.5
3	A	154	ALA	3.5
4	B	224	LYS	3.5
5	C	208	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
24	V	96	LEU	3.5
1	0	246	G	3.5
1	0	854	G	3.5
1	0	1707	G	3.5
1	0	1855	G	3.5
1	0	1976	G	3.5
1	0	2009	G	3.5
1	0	2578	G	3.5
14	L	103	GLU	3.5
17	O	72	GLY	3.5
24	V	82	GLU	3.5
1	0	103	U	3.5
1	0	123	U	3.5
1	0	239	C	3.5
1	0	268	U	3.5
1	0	1816	C	3.5
1	0	1911	C	3.5
4	B	8	LYS	3.5
14	L	94	LYS	3.5
18	P	62	THR	3.5
24	V	33	THR	3.5
13	K	111	ALA	3.5
14	L	52	LEU	3.5
24	V	112	LEU	3.5
1	0	372	A	3.5
1	0	2761	A	3.5
4	B	57	GLU	3.5
7	E	11	VAL	3.5
15	M	135	VAL	3.5
26	X	186	ARG	3.5
1	0	56	G	3.5
1	0	381	G	3.5
1	0	496	G	3.5
1	0	1974	G	3.5
1	0	2643	G	3.5
1	0	2877	G	3.5
10	H	118	PRO	3.5
1	0	1770	U	3.5
1	0	2589	U	3.5
1	0	111	C	3.5
1	0	789	C	3.5
1	0	2825	C	3.5

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Mol	Chain	Res	Type	RSRZ
5	C	242	GLU	3.5
9	G	68	GLU	3.5
12	J	128	ALA	3.5
19	Q	92	LEU	3.5
25	W	82	GLU	3.5
7	E	63	GLY	3.5
4	B	227	HIS	3.5
16	N	38	ARG	3.5
25	W	34	ARG	3.5
1	0	1567	A	3.5
3	A	207	GLN	3.5
1	0	834	G	3.5
1	0	1175	G	3.5
1	0	1901	G	3.5
1	0	2630	G	3.5
7	E	49	ILE	3.5
12	J	40	THR	3.5
14	L	22	GLU	3.5
24	V	146	ILE	3.5
1	0	1771	U	3.5
11	I	69	TYR	3.5
12	J	37	TYR	3.5
13	K	128	GLY	3.5
15	M	83	LEU	3.5
28	Z	27	TYR	3.5
1	0	1853	C	3.5
1	0	2020	C	3.5
19	Q	33	ARG	3.5
21	S	87	VAL	3.5
4	B	2	GLN	3.5
16	N	57	THR	3.5
4	B	288	GLY	3.5
5	C	164	ALA	3.5
10	H	117	LYS	3.5
10	H	6	TYR	3.5
15	M	26	LEU	3.5
16	N	85	ALA	3.5
28	Z	44	LYS	3.5
30	2	77	ALA	3.5
1	0	1447	U	3.5
1	0	1799	G	3.5
1	0	1863	G	3.5

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Mol	Chain	Res	Type	RSRZ
1	0	2442	G	3.5
1	0	2660	G	3.5
4	B	261	GLN	3.5
1	0	130	C	3.5
1	0	318	C	3.5
1	0	1862	C	3.5
7	E	139	GLU	3.5
4	B	31	SER	3.5
4	B	158	LYS	3.5
14	L	55	LYS	3.5
11	I	63	ILE	3.5
22	T	41	ASP	3.5
25	W	84	ILE	3.5
14	L	12	TRP	3.5
26	X	227	ARG	3.5
1	0	119	A	3.5
1	0	1550	A	3.5
1	0	2367	A	3.5
1	0	2818	A	3.5
12	J	88	VAL	3.5
1	0	754	G	3.5
1	0	1131	G	3.5
1	0	1292	G	3.5
1	0	1444	G	3.5
1	0	1512	G	3.5
1	0	1670	G	3.5
1	0	2507	G	3.5
10	H	150	LYS	3.5
22	T	36	CYS	3.5
1	0	356	C	3.5
1	0	1720	C	3.5
4	B	313	PRO	3.5
14	L	156	ARG	3.5
18	P	10	THR	3.5
20	R	59	ASP	3.5
26	X	210	GLY	3.5
10	H	23	ILE	3.5
15	M	139	TRP	3.5
25	W	45	GLU	3.5
1	0	60	A	3.5
1	0	468	U	3.5
1	0	861	A	3.5

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Mol	Chain	Res	Type	RSRZ
1	0	1493	A	3.5
1	0	1638	U	3.5
1	0	1702	U	3.5
1	0	1759	A	3.5
1	0	2663	U	3.5
5	C	173	LYS	3.5
1	0	2799	A	3.5
14	L	81	ARG	3.4
5	C	179	GLY	3.4
13	K	36	ASP	3.4
15	M	126	GLY	3.4
1	0	50	G	3.4
1	0	135	G	3.4
1	0	1680	C	3.4
1	0	1695	G	3.4
1	0	1828	G	3.4
1	0	1925	G	3.4
1	0	1940	C	3.4
1	0	1993	C	3.4
1	0	2347	C	3.4
1	0	2352	G	3.4
2	9	3068	G	3.4
26	X	191	ASP	3.4
15	M	147	ILE	3.4
11	I	99	GLU	3.4
17	O	34	ALA	3.4
30	2	83	TRP	3.4
3	A	211	LYS	3.4
11	I	36	VAL	3.4
1	0	855	U	3.4
6	D	76	ARG	3.4
18	P	4	ASN	3.4
1	0	148	A	3.4
1	0	189	A	3.4
1	0	2083	A	3.4
1	0	2244	A	3.4
13	K	125	PHE	3.4
20	R	25	GLN	3.4
21	S	4	PRO	3.4
23	U	6	GLN	3.4
25	W	77	PHE	3.4
7	E	157	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
19	Q	26	LYS	3.4
27	Y	48	LYS	3.4
27	Y	54	ILE	3.4
1	0	345	G	3.4
1	0	1536	C	3.4
1	0	1644	C	3.4
1	0	1752	G	3.4
1	0	2270	G	3.4
1	0	2560	C	3.4
1	0	2570	G	3.4
1	0	2712	G	3.4
11	I	130	VAL	3.4
14	L	63	VAL	3.4
14	L	158	ARG	3.4
7	E	98	GLU	3.4
11	I	88	PRO	3.4
13	K	98	GLU	3.4
13	K	148	GLU	3.4
3	A	165	THR	3.4
1	0	688	A	3.4
1	0	1591	A	3.4
1	0	1642	A	3.4
1	0	1689	A	3.4
1	0	1852	A	3.4
2	9	3051	A	3.4
4	B	46	ALA	3.4
12	J	131	ILE	3.4
1	0	260	C	3.4
1	0	849	C	3.4
1	0	2901	C	3.4
7	E	124	VAL	3.4
1	0	428	G	3.4
1	0	1794	G	3.4
1	0	2041	G	3.4
1	0	2606	G	3.4
1	0	2865	G	3.4
3	A	107	ASN	3.4
5	C	185	LYS	3.4
1	0	1654	U	3.4
1	0	1835	U	3.4
1	0	2736	U	3.4
15	M	4	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
4	B	142	LEU	3.4
24	V	66	LEU	3.4
24	V	20	THR	3.4
27	Y	73	THR	3.4
19	Q	8	ALA	3.4
19	Q	51	ILE	3.4
1	0	25	A	3.4
1	0	1144	A	3.4
1	0	1895	A	3.4
1	0	2100	A	3.4
1	0	2577	A	3.4
2	9	3065	A	3.4
16	N	68	GLY	3.4
1	0	1397	C	3.4
5	C	170	ASP	3.4
5	C	180	SER	3.4
5	C	201	SER	3.4
6	D	39	ASP	3.4
30	2	27	SER	3.4
1	0	266	G	3.4
1	0	389	G	3.4
1	0	1814	G	3.4
1	0	2131	G	3.4
1	0	1130	U	3.4
1	0	1298	U	3.4
1	0	2866	U	3.4
21	S	27	LEU	3.4
10	H	65	ARG	3.4
14	L	154	ARG	3.4
17	O	69	ARG	3.4
29	1	44	ARG	3.4
25	W	39	LYS	3.4
26	X	208	LYS	3.4
8	F	55	GLN	3.4
22	T	5	GLU	3.4
13	K	110	GLY	3.4
4	B	199	TYR	3.4
15	M	183	ASP	3.4
21	S	92	ASP	3.4
1	0	262	A	3.4
1	0	1736	A	3.4
1	0	2490	A	3.4

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Mol	Chain	Res	Type	RSRZ
1	0	2569	A	3.4
4	B	70	PRO	3.4
1	0	173	C	3.4
1	0	2536	C	3.4
1	0	2745	C	3.4
4	B	322	ARG	3.4
24	V	61	THR	3.4
1	0	738	G	3.4
1	0	1354	G	3.4
1	0	1529	G	3.4
3	A	87	GLU	3.4
14	L	100	ILE	3.4
24	V	27	HIS	3.4
30	2	33	MET	3.4
10	H	74	ASN	3.4
19	Q	73	ASP	3.4
25	W	43	VAL	3.4
19	Q	25	PHE	3.4
4	B	11	LEU	3.4
4	B	296	LEU	3.4
1	0	491	C	3.4
1	0	532	A	3.4
1	0	1516	C	3.4
1	0	2301	A	3.4
1	0	2382	A	3.4
1	0	2402	A	3.4
3	A	101	GLU	3.4
4	B	102	THR	3.4
15	M	98	GLU	3.4
18	P	8	GLU	3.4
25	W	78	GLU	3.4
4	B	221	GLN	3.4
1	0	825	U	3.4
1	0	1871	U	3.4
1	0	2378	U	3.4
3	A	115	GLY	3.4
14	L	89	ASN	3.4
24	V	50	ASP	3.4
1	0	1949	G	3.4
1	0	2603	G	3.4
2	9	3088	G	3.4
3	A	235	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
15	M	25	ARG	3.3
4	B	293	PRO	3.3
25	W	14	LEU	3.3
25	W	20	GLU	3.3
30	2	21	GLU	3.3
16	N	39	THR	3.3
5	C	38	ALA	3.3
8	F	92	GLY	3.3
24	V	93	ILE	3.3
1	0	106	A	3.3
1	0	139	C	3.3
1	0	152	A	3.3
1	0	843	A	3.3
1	0	893	C	3.3
1	0	1233	A	3.3
1	0	1836	A	3.3
1	0	2300	A	3.3
1	0	2509	A	3.3
1	0	2530	C	3.3
1	0	2539	U	3.3
4	B	190	MET	3.3
4	B	242	TRP	3.3
7	E	59	MET	3.3
7	E	156	ASP	3.3
25	W	51	ASP	3.3
7	E	76	VAL	3.3
14	L	51	SER	3.3
14	L	117	SER	3.3
5	C	46	TYR	3.3
6	D	139	TYR	3.3
20	R	70	GLU	3.3
1	0	332	G	3.3
1	0	817	G	3.3
1	0	1568	G	3.3
7	E	163	GLN	3.3
12	J	4	LEU	3.3
3	A	175	LYS	3.3
4	B	9	GLY	3.3
4	B	263	THR	3.3
11	I	128	LYS	3.3
14	L	178	LYS	3.3
15	M	165	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
4	B	55	ASN	3.3
8	F	34	ASN	3.3
14	L	171	ARG	3.3
15	M	40	ASN	3.3
17	O	94	TRP	3.3
1	0	283	U	3.3
1	0	1860	U	3.3
1	0	282	C	3.3
1	0	959	C	3.3
1	0	1084	C	3.3
1	0	1509	C	3.3
1	0	1834	C	3.3
3	A	189	VAL	3.3
4	B	277	GLU	3.3
5	C	138	VAL	3.3
1	0	192	A	3.3
1	0	247	A	3.3
1	0	1150	A	3.3
1	0	1922	A	3.3
10	H	83	PHE	3.3
18	P	56	PHE	3.3
24	V	72	PRO	3.3
4	B	216	LYS	3.3
23	U	57	LYS	3.3
12	J	11	GLY	3.3
22	T	17	THR	3.3
22	T	19	THR	3.3
28	Z	14	THR	3.3
1	0	499	G	3.3
1	0	1460	G	3.3
1	0	1588	G	3.3
1	0	2286	G	3.3
4	B	165	ARG	3.3
6	D	136	ARG	3.3
4	B	264	GLU	3.3
12	J	93	ASN	3.3
15	M	133	ASP	3.3
18	P	21	ARG	3.3
19	Q	146	ILE	3.3
29	1	48	ASP	3.3
17	O	46	GLU	3.3
4	B	244	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
11	I	72	PRO	3.3
1	0	1534	C	3.3
1	0	2035	C	3.3
1	0	2729	C	3.3
2	9	3089	C	3.3
1	0	1188	A	3.3
22	T	54	THR	3.3
3	A	188	ASN	3.3
4	B	271	ASP	3.3
7	E	9	GLU	3.3
14	L	49	ALA	3.3
7	E	154	ILE	3.3
1	0	104	G	3.3
1	0	830	G	3.3
1	0	1719	G	3.3
1	0	1878	G	3.3
1	0	2349	G	3.3
2	9	3022	G	3.3
14	L	31	TRP	3.3
30	2	24	LYS	3.3
5	C	102	LEU	3.3
11	I	105	LEU	3.3
18	P	14	LEU	3.3
1	0	1899	C	3.3
14	L	17	GLU	3.3
18	P	81	GLU	3.3
10	H	15	THR	3.3
11	I	97	ALA	3.3
1	0	117	A	3.3
1	0	1414	A	3.3
7	E	66	GLN	3.3
30	2	46	ILE	3.3
11	I	54	VAL	3.3
7	E	131	LEU	3.3
1	0	826	U	3.3
1	0	1500	U	3.3
1	0	2125	G	3.3
1	0	2716	G	3.3
5	C	14	GLY	3.3
30	2	6	ARG	3.3
17	O	54	LYS	3.3
1	0	1582	C	3.3

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Mol	Chain	Res	Type	RSRZ
1	0	2417	C	3.3
14	L	129	HIS	3.3
29	1	42	TRP	3.3
1	0	241	A	3.3
1	0	1192	A	3.3
3	A	158	VAL	3.3
12	J	96	VAL	3.3
14	L	53	GLY	3.3
19	Q	131	GLY	3.3
25	W	61	ARG	3.3
26	X	117	LEU	3.3
29	1	39	ARG	3.3
20	R	39	ASP	3.3
1	0	259	G	3.3
1	0	301	G	3.3
1	0	1647	G	3.3
1	0	2014	G	3.3
1	0	2310	G	3.3
1	0	1186	C	3.2
1	0	1545	C	3.2
1	0	2348	C	3.2
1	0	2533	C	3.2
10	H	146	TRP	3.2
15	M	143	ARG	3.2
28	Z	24	GLU	3.2
3	A	102	GLY	3.2
4	B	40	GLY	3.2
4	B	161	VAL	3.2
3	A	231	LYS	3.2
11	I	143	LYS	3.2
12	J	130	MET	3.2
18	P	17	LYS	3.2
26	X	148	GLY	3.2
1	0	243	A	3.2
1	0	1991	A	3.2
1	0	2095	A	3.2
1	0	2361	A	3.2
1	0	2727	A	3.2
13	K	150	GLN	3.2
3	A	125	ASN	3.2
1	0	1539	U	3.2
1	0	1554	U	3.2

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Mol	Chain	Res	Type	RSRZ
14	L	54	TYR	3.2
5	C	224	ALA	3.2
15	M	145	ALA	3.2
24	V	119	HIS	3.2
7	E	2	ARG	3.2
10	H	95	GLU	3.2
22	T	50	GLU	3.2
25	W	25	ARG	3.2
1	0	351	G	3.2
1	0	1159	G	3.2
1	0	1546	G	3.2
1	0	1917	G	3.2
1	0	2494	G	3.2
26	X	137	LYS	3.2
12	J	17	LEU	3.2
15	M	48	VAL	3.2
18	P	65	GLY	3.2
1	0	1061	C	3.2
12	J	90	PHE	3.2
26	X	182	PHE	3.2
14	L	116	ASN	3.2
15	M	77	ASN	3.2
1	0	59	A	3.2
1	0	248	A	3.2
1	0	2485	A	3.2
1	0	2488	A	3.2
1	0	2532	A	3.2
1	0	2699	A	3.2
1	0	2878	U	3.2
8	F	18	GLU	3.2
12	J	44	HIS	3.2
12	J	114	ALA	3.2
15	M	99	GLU	3.2
15	M	117	ALA	3.2
18	P	40	HIS	3.2
3	A	161	GLY	3.2
14	L	172	GLY	3.2
4	B	252	PRO	3.2
8	F	118	LEU	3.2
14	L	173	LEU	3.2
14	L	189	VAL	3.2
25	W	9	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	0	487	G	3.2
1	0	1260	G	3.2
1	0	1378	G	3.2
1	0	2613	G	3.2
5	C	74	ASP	3.2
1	0	1495	C	3.2
1	0	1769	C	3.2
1	0	2552	C	3.2
3	A	184	THR	3.2
14	L	9	ARG	3.2
23	U	45	ARG	3.2
6	D	147	ALA	3.2
9	G	22	ALA	3.2
11	I	57	TYR	3.2
15	M	137	ALA	3.2
17	O	70	ALA	3.2
25	W	26	ALA	3.2
1	0	121	U	3.2
1	0	445	U	3.2
1	0	1784	U	3.2
3	A	91	GLY	3.2
6	D	151	ILE	3.2
1	0	131	A	3.2
1	0	261	A	3.2
1	0	841	A	3.2
1	0	1775	A	3.2
1	0	2123	A	3.2
1	0	2264	A	3.2
1	0	2468	A	3.2
1	0	2875	A	3.2
4	B	130	ASP	3.2
4	B	201	ASP	3.2
15	M	56	ASP	3.2
10	H	97	LYS	3.2
11	I	107	ASN	3.2
24	V	104	GLU	3.2
28	Z	45	ARG	3.2
1	0	531	G	3.2
1	0	918	G	3.2
1	0	1634	G	3.2
1	0	1926	G	3.2
1	0	2755	G	3.2

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Mol	Chain	Res	Type	RSRZ
16	N	20	SER	3.2
1	0	803	C	3.2
1	0	1763	C	3.2
1	0	1914	C	3.2
1	0	2360	C	3.2
7	E	167	TYR	3.2
1	0	1380	U	3.2
1	0	2290	U	3.2
19	Q	18	LEU	3.2
3	A	171	LYS	3.2
4	B	326	GLU	3.2
5	C	136	VAL	3.2
6	D	99	ASP	3.2
10	H	92	VAL	3.2
14	L	142	LYS	3.2
17	O	40	VAL	3.2
18	P	77	ASP	3.2
1	0	397	A	3.2
1	0	1573	A	3.2
1	0	2600	A	3.2
24	V	30	ASN	3.2
4	B	300	SER	3.2
11	I	106	GLY	3.2
30	2	45	GLY	3.2
1	0	140	G	3.2
1	0	1433	G	3.2
1	0	1739	G	3.2
1	0	1945	G	3.2
1	0	2077	C	3.2
1	0	2251	G	3.2
6	D	146	LYS	3.2
16	N	2	LYS	3.2
19	Q	144	GLU	3.2
1	0	864	U	3.2
1	0	888	U	3.2
6	D	23	VAL	3.2
12	J	115	ARG	3.2
14	L	90	ARG	3.2
18	P	18	PRO	3.2
15	M	78	MET	3.2
1	0	513	A	3.2
1	0	818	A	3.2

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Mol	Chain	Res	Type	RSRZ
1	0	1356	A	3.2
1	0	1581	A	3.2
1	0	1678	A	3.2
1	0	1921	A	3.2
1	0	2741	A	3.2
3	A	131	HIS	3.2
3	A	162	GLY	3.2
7	E	85	GLU	3.2
7	E	43	ASP	3.2
16	N	7	LEU	3.2
21	S	38	ARG	3.2
25	W	49	ARG	3.2
1	0	342	C	3.2
1	0	2824	C	3.2
1	0	393	G	3.2
1	0	1401	G	3.2
1	0	1757	U	3.2
1	0	2648	U	3.2
1	0	2700	G	3.2
11	I	126	ASN	3.2
19	Q	98	ASN	3.2
27	Y	61	GLY	3.2
3	A	181	ALA	3.2
4	B	314	ALA	3.2
13	K	41	HIS	3.2
21	S	78	THR	3.2
1	0	186	A	3.1
1	0	191	A	3.1
1	0	204	A	3.1
1	0	363	A	3.1
1	0	429	A	3.1
1	0	1040	A	3.1
1	0	1079	A	3.1
1	0	1685	A	3.1
1	0	2801	A	3.1
4	B	92	TYR	3.1
6	D	149	ARG	3.1
7	E	62	ILE	3.1
13	K	35	ARG	3.1
21	S	63	ILE	3.1
21	S	100	ASP	3.1
4	B	147	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
20	R	16	ASN	3.1
21	S	40	VAL	3.1
1	0	932	U	3.1
1	0	1721	C	3.1
3	A	142	SER	3.1
11	I	73	LYS	3.1
1	0	661	G	3.1
1	0	1986	G	3.1
1	0	2909	G	3.1
2	9	3094	G	3.1
30	2	28	GLY	3.1
19	Q	116	ALA	3.1
28	Z	20	ARG	3.1
30	2	59	ASP	3.1
14	L	40	ILE	3.1
18	P	84	ILE	3.1
6	D	55	LYS	3.1
10	H	115	PHE	3.1
16	N	88	LYS	3.1
1	0	145	A	3.1
1	0	829	A	3.1
1	0	1081	A	3.1
1	0	2252	A	3.1
1	0	2368	A	3.1
1	0	2649	A	3.1
1	0	2684	A	3.1
5	C	16	VAL	3.1
24	V	132	VAL	3.1
30	2	35	TRP	3.1
1	0	443	C	3.1
1	0	884	C	3.1
1	0	1060	C	3.1
1	0	1623	C	3.1
1	0	1633	C	3.1
1	0	2534	C	3.1
1	0	500	G	3.1
1	0	1552	G	3.1
1	0	1891	G	3.1
1	0	1938	G	3.1
1	0	1971	G	3.1
1	0	2584	G	3.1
26	X	162	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
3	A	220	PRO	3.1
14	L	15	PRO	3.1
8	F	22	VAL	3.1
21	S	58	GLU	3.1
17	O	117	SER	3.1
21	S	94	SER	3.1
28	Z	26	SER	3.1
1	0	125	U	3.1
1	0	1531	U	3.1
1	0	2811	A	3.1
28	Z	16	HIS	3.1
5	C	213	ALA	3.1
1	0	377	C	3.1
1	0	799	C	3.1
1	0	1403	C	3.1
1	0	1553	C	3.1
1	0	2126	C	3.1
1	0	2132	C	3.1
2	9	3029	C	3.1
19	Q	9	ASP	3.1
23	U	10	ASP	3.1
5	C	232	LEU	3.1
6	D	84	LEU	3.1
4	B	270	ILE	3.1
4	B	61	PRO	3.1
1	0	118	G	3.1
1	0	739	G	3.1
1	0	1155	G	3.1
1	0	1484	G	3.1
1	0	1832	G	3.1
1	0	2267	G	3.1
1	0	2399	G	3.1
1	0	2421	G	3.1
4	B	82	VAL	3.1
8	F	27	GLY	3.1
25	W	62	GLY	3.1
7	E	115	ARG	3.1
17	O	41	ARG	3.1
1	0	1432	U	3.1
1	0	1577	U	3.1
1	0	2853	U	3.1
1	0	160	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	0	1580	A	3.1
1	0	2896	A	3.1
5	C	106	GLU	3.1
15	M	50	LEU	3.1
21	S	80	GLU	3.1
30	2	79	LEU	3.1
1	0	839	C	3.1
1	0	879	C	3.1
1	0	2873	C	3.1
14	L	8	ILE	3.1
14	L	20	ILE	3.1
5	C	144	PHE	3.1
5	C	186	TYR	3.1
7	E	92	PRO	3.1
3	A	2	ARG	3.1
3	A	217	ARG	3.1
3	A	223	ARG	3.1
5	C	63	SER	3.1
8	F	93	SER	3.1
18	P	30	VAL	3.1
1	0	182	G	3.1
1	0	2111	G	3.1
4	B	98	THR	3.1
1	0	335	U	3.1
1	0	900	U	3.1
1	0	2016	U	3.1
1	0	2661	U	3.1
2	9	3018	U	3.1
2	9	3112	U	3.1
4	B	27	ASN	3.1
7	E	148	ILE	3.1
15	M	31	LYS	3.1
17	O	139	ARG	3.1
29	1	13	LYS	3.1
1	0	546	C	3.1
1	0	1428	C	3.1
1	0	1690	C	3.1
1	0	1826	C	3.1
1	0	1900	A	3.1
1	0	2015	A	3.1
1	0	2022	A	3.1
1	0	2439	C	3.1

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Mol	Chain	Res	Type	RSRZ
1	0	2775	A	3.1
2	9	3044	A	3.1
8	F	107	VAL	3.1
4	B	86	ALA	3.1
1	0	358	G	3.1
1	0	543	G	3.1
1	0	720	G	3.1
1	0	833	G	3.1
1	0	1415	G	3.1
1	0	1430	G	3.1
1	0	2033	G	3.1
1	0	2798	G	3.1
4	B	217	ARG	3.1
4	B	269	LEU	3.1
11	I	31	LEU	3.1
1	0	1831	U	3.1
1	0	2008	U	3.1
4	B	93	GLY	3.1
3	A	221	PRO	3.1
18	P	6	PRO	3.1
19	Q	66	VAL	3.1
27	Y	24	VAL	3.1
10	H	18	GLU	3.1
1	0	57	C	3.1
1	0	155	C	3.1
1	0	874	A	3.1
1	0	1280	A	3.1
1	0	1357	A	3.1
1	0	2089	A	3.1
1	0	2292	C	3.1
1	0	2641	C	3.1
2	9	3120	A	3.1
14	L	137	ASP	3.1
24	V	78	ASP	3.1
11	I	89	HIS	3.1
13	K	4	LYS	3.0
30	2	54	LYS	3.0
3	A	128	LEU	3.0
17	O	97	ARG	3.0
1	0	205	U	3.0
1	0	270	U	3.0
1	0	406	G	3.0

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Mol	Chain	Res	Type	RSRZ
1	0	1319	G	3.0
1	0	1340	G	3.0
1	0	1694	G	3.0
1	0	2489	G	3.0
1	0	2842	G	3.0
3	A	122	SER	3.0
15	M	111	PRO	3.0
21	S	72	ILE	3.0
3	A	108	VAL	3.0
17	O	118	GLN	3.0
26	X	149	GLN	3.0
5	C	33	LYS	3.0
15	M	164	ASP	3.0
15	M	181	ASP	3.0
3	A	176	HIS	3.0
19	Q	19	ARG	3.0
1	0	778	C	3.0
1	0	2071	C	3.0
2	9	3048	C	3.0
12	J	26	ALA	3.0
20	R	54	THR	3.0
1	0	226	A	3.0
1	0	1231	A	3.0
1	0	1482	A	3.0
1	0	1924	A	3.0
1	0	2680	A	3.0
10	H	21	SER	3.0
19	Q	28	SER	3.0
1	0	1440	U	3.0
1	0	1673	U	3.0
1	0	2541	U	3.0
6	D	154	LYS	3.0
7	E	82	TYR	3.0
1	0	105	G	3.0
1	0	190	G	3.0
1	0	1158	G	3.0
1	0	1663	G	3.0
1	0	1908	G	3.0
1	0	2656	G	3.0
2	9	3014	G	3.0
3	A	9	ARG	3.0
19	Q	75	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
28	Z	21	ARG	3.0
3	A	195	ASN	3.0
5	C	47	GLY	3.0
5	C	240	LEU	3.0
13	K	16	GLY	3.0
15	M	106	LEU	3.0
1	0	2351	C	3.0
1	0	2764	C	3.0
4	B	75	GLU	3.0
5	C	59	GLU	3.0
10	H	143	GLU	3.0
20	R	12	GLU	3.0
12	J	112	PRO	3.0
1	0	1754	A	3.0
17	O	93	ASP	3.0
1	0	1187	U	3.0
19	Q	4	TYR	3.0
16	N	54	GLU	3.0
22	T	48	ASN	3.0
1	0	324	G	3.0
1	0	802	G	3.0
1	0	1137	G	3.0
1	0	1660	G	3.0
1	0	1726	G	3.0
1	0	2013	G	3.0
4	B	144	THR	3.0
4	B	175	LEU	3.0
5	C	40	ALA	3.0
15	M	81	ALA	3.0
19	Q	23	MET	3.0
26	X	131	GLN	3.0
30	2	30	GLN	3.0
30	2	53	SER	3.0
27	Y	71	PRO	3.0
1	0	228	C	3.0
1	0	880	C	3.0
1	0	1753	C	3.0
11	I	122	ASP	3.0
1	0	465	U	3.0
1	0	1321	A	3.0
1	0	1448	A	3.0
1	0	1857	A	3.0

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Mol	Chain	Res	Type	RSRZ
1	0	2112	A	3.0
7	E	142	GLY	3.0
8	F	116	GLU	3.0
14	L	111	ASN	3.0
17	O	100	ALA	3.0
1	0	379	G	3.0
1	0	2847	G	3.0
23	U	31	ARG	3.0
1	0	1787	C	3.0
20	R	34	LYS	3.0
24	V	29	VAL	3.0
3	A	191	GLY	3.0
4	B	185	GLY	3.0
7	E	128	GLY	3.0
1	0	2889	U	3.0
1	0	435	A	3.0
1	0	524	A	3.0
1	0	593	A	3.0
1	0	844	A	3.0
1	0	1658	A	3.0
1	0	2356	A	3.0
6	D	80	ALA	3.0
23	U	23	LEU	3.0
4	B	95	ARG	3.0
6	D	156	ARG	3.0
14	L	104	ARG	3.0
5	C	131	PHE	3.0
13	K	79	ASP	3.0
11	I	51	GLU	3.0
19	Q	126	LYS	3.0
1	0	264	G	3.0
1	0	304	G	3.0
1	0	365	G	3.0
1	0	1532	G	3.0
1	0	1648	G	3.0
1	0	2579	G	3.0
1	0	2646	G	3.0
8	F	4	VAL	3.0
16	N	60	VAL	3.0
22	T	43	GLY	3.0
1	0	1564	C	3.0
3	A	127	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
7	E	94	GLN	3.0
19	Q	102	GLN	3.0
1	0	872	U	3.0
1	0	2756	U	3.0
1	0	2872	U	3.0
7	E	46	THR	3.0
14	L	68	ARG	3.0
18	P	87	THR	3.0
19	Q	12	THR	3.0
3	A	139	LYS	3.0
12	J	59	LYS	3.0
24	V	153	MET	3.0
1	0	484	A	3.0
1	0	846	A	3.0
1	0	939	A	3.0
1	0	1845	A	3.0
1	0	2280	A	3.0
9	G	19	GLU	3.0
25	W	79	GLU	3.0
26	X	231	PRO	3.0
15	M	119	GLN	3.0
20	R	10	VAL	3.0
20	R	41	VAL	3.0
7	E	151	LEU	2.9
15	M	136	LEU	2.9
1	0	38	G	2.9
1	0	51	G	2.9
1	0	2580	G	2.9
1	0	2817	G	2.9
17	O	90	SER	2.9
18	P	13	LYS	2.9
24	V	106	THR	2.9
28	Z	1	THR	2.9
1	0	294	C	2.9
1	0	1585	C	2.9
1	0	2457	U	2.9
1	0	2472	C	2.9
10	H	33	MET	2.9
19	Q	56	PRO	2.9
24	V	1	MET	2.9
14	L	67	ILE	2.9
1	0	255	A	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	410	A	2.9
1	0	472	A	2.9
1	0	1193	A	2.9
1	0	1485	A	2.9
1	0	1659	A	2.9
6	D	144	ARG	2.9
13	K	8	ARG	2.9
19	Q	60	LYS	2.9
19	Q	101	HIS	2.9
24	V	107	LEU	2.9
5	C	50	GLU	2.9
12	J	54	THR	2.9
8	F	5	ASP	2.9
1	0	330	C	2.9
1	0	370	G	2.9
1	0	518	G	2.9
1	0	1646	G	2.9
1	0	1806	G	2.9
1	0	2384	U	2.9
1	0	2849	U	2.9
1	0	2767	C	2.9
2	9	3095	C	2.9
22	T	20	MET	2.9
23	U	11	MET	2.9
4	B	168	GLY	2.9
18	P	75	ILE	2.9
1	0	441	A	2.9
1	0	569	A	2.9
1	0	1248	A	2.9
1	0	2467	A	2.9
4	B	294	TYR	2.9
14	L	143	SER	2.9
19	Q	70	SER	2.9
7	E	21	THR	2.9
18	P	69	ASP	2.9
22	T	29	THR	2.9
26	X	221	ALA	2.9
10	H	53	PRO	2.9
15	M	130	PRO	2.9
1	0	281	U	2.9
1	0	1740	U	2.9
13	K	23	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
24	V	95	GLY	2.9
1	0	31	C	2.9
1	0	418	C	2.9
1	0	925	C	2.9
1	0	1126	C	2.9
1	0	1212	C	2.9
1	0	1450	C	2.9
1	0	1652	C	2.9
1	0	2037	C	2.9
30	2	42	ARG	2.9
1	0	353	G	2.9
1	0	592	G	2.9
1	0	1849	G	2.9
1	0	2428	G	2.9
1	0	2708	G	2.9
1	0	2742	G	2.9
4	B	280	VAL	2.9
7	E	103	VAL	2.9
13	K	93	VAL	2.9
10	H	75	SER	2.9
4	B	83	ALA	2.9
5	C	176	ALA	2.9
10	H	134	ALA	2.9
12	J	51	ASP	2.9
18	P	60	THR	2.9
21	S	54	ASP	2.9
22	T	53	ASP	2.9
25	W	17	ALA	2.9
28	Z	5	THR	2.9
1	0	327	A	2.9
1	0	419	A	2.9
1	0	922	A	2.9
1	0	1437	A	2.9
1	0	1615	A	2.9
1	0	2483	A	2.9
1	0	2604	A	2.9
11	I	91	LYS	2.9
12	J	14	LYS	2.9
14	L	121	GLY	2.9
4	B	48	MET	2.9
1	0	705	C	2.9
1	0	1303	C	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	1882	C	2.9
1	0	1920	C	2.9
1	0	2894	C	2.9
15	M	179	LEU	2.9
1	0	157	G	2.9
1	0	1045	G	2.9
1	0	1398	G	2.9
1	0	2025	G	2.9
2	9	3101	G	2.9
4	B	203	ALA	2.9
4	B	226	LYS	2.9
5	C	45	ASP	2.9
8	F	67	ALA	2.9
15	M	88	ALA	2.9
21	S	11	GLN	2.9
8	F	88	GLY	2.9
11	I	64	GLY	2.9
13	K	40	PHE	2.9
23	U	16	ARG	2.9
24	V	154	ARG	2.9
28	Z	40	GLY	2.9
6	D	167	GLU	2.9
7	E	4	GLU	2.9
24	V	22	GLU	2.9
1	0	129	A	2.9
1	0	167	A	2.9
1	0	521	A	2.9
1	0	1058	A	2.9
1	0	2274	A	2.9
1	0	2395	A	2.9
1	0	277	U	2.9
1	0	325	U	2.9
7	E	126	ILE	2.9
7	E	17	HIS	2.9
15	M	35	VAL	2.9
18	P	53	HIS	2.9
19	Q	143	VAL	2.9
20	R	7	HIS	2.9
26	X	174	VAL	2.9
27	Y	29	VAL	2.9
5	C	161	ASP	2.9
29	1	17	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	0	100	C	2.9
1	0	1513	C	2.9
1	0	1734	C	2.9
1	0	1762	C	2.9
1	0	1990	C	2.9
1	0	2881	C	2.9
5	C	196	THR	2.9
24	V	70	ALA	2.9
1	0	1800	G	2.9
1	0	2134	G	2.9
1	0	2337	G	2.9
4	B	13	PHE	2.9
5	C	41	ASN	2.9
17	O	24	ASN	2.9
20	R	15	MET	2.9
1	0	2373	U	2.9
1	0	2586	U	2.9
4	B	336	GLN	2.9
1	0	767	A	2.9
14	L	59	GLY	2.9
22	T	27	ALA	2.9
1	0	110	C	2.9
1	0	350	C	2.9
1	0	405	C	2.9
1	0	427	C	2.9
1	0	1650	C	2.9
3	A	209	PRO	2.9
20	R	8	PRO	2.9
8	F	38	LYS	2.9
10	H	96	ASN	2.9
12	J	46	LYS	2.9
4	B	65	MET	2.9
1	0	469	G	2.8
1	0	1323	G	2.8
1	0	2412	G	2.8
1	0	2851	G	2.8
3	A	14	SER	2.8
3	A	47	HIS	2.8
15	M	22	GLN	2.8
3	A	34	ASP	2.8
4	B	141	ARG	2.8
6	D	140	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
12	J	126	SER	2.8
17	O	96	SER	2.8
19	Q	96	VAL	2.8
11	I	28	GLU	2.8
12	J	108	GLU	2.8
21	S	111	ARG	2.8
25	W	16	ASP	2.8
15	M	96	GLY	2.8
16	N	24	ALA	2.8
1	0	460	A	2.8
1	0	1345	A	2.8
1	0	1434	A	2.8
1	0	1865	A	2.8
1	0	2135	A	2.8
1	0	2486	A	2.8
1	0	2856	A	2.8
4	B	17	LYS	2.8
21	S	47	THR	2.8
21	S	93	THR	2.8
30	2	43	ASN	2.8
1	0	2065	C	2.8
1	0	2614	C	2.8
19	Q	109	MET	2.8
3	A	51	ARG	2.8
4	B	328	ARG	2.8
5	C	123	LEU	2.8
11	I	123	ARG	2.8
14	L	112	LEU	2.8
16	N	13	ASP	2.8
17	O	45	ASP	2.8
1	0	66	G	2.8
1	0	564	G	2.8
1	0	1235	G	2.8
1	0	1373	G	2.8
1	0	2046	G	2.8
1	0	2091	G	2.8
1	0	2564	G	2.8
1	0	2779	G	2.8
10	H	87	LYS	2.8
1	0	402	U	2.8
1	0	1422	U	2.8
1	0	1722	U	2.8

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Mol	Chain	Res	Type	RSRZ
1	0	2621	U	2.8
5	C	229	PRO	2.8
8	F	1	PRO	2.8
10	H	135	TRP	2.8
26	X	146	PRO	2.8
1	0	806	A	2.8
14	L	168	ARG	2.8
1	0	1620	C	2.8
2	9	3115	C	2.8
14	L	3	SER	2.8
18	P	38	LYS	2.8
18	P	39	VAL	2.8
21	S	107	LYS	2.8
15	M	49	THR	2.8
16	N	75	THR	2.8
26	X	202	ALA	2.8
1	0	359	U	2.8
1	0	434	U	2.8
1	0	2535	U	2.8
1	0	64	G	2.8
1	0	184	G	2.8
1	0	404	G	2.8
1	0	1481	G	2.8
1	0	2080	G	2.8
8	F	9	PRO	2.8
17	O	88	GLN	2.8
14	L	93	ARG	2.8
27	Y	62	TYR	2.8
4	B	209	LYS	2.8
10	H	1	LYS	2.8
21	S	116	ASP	2.8
19	Q	17	MET	2.8
1	0	1942	A	2.8
3	A	77	GLY	2.8
3	A	222	GLY	2.8
4	B	237	GLY	2.8
24	V	45	VAL	2.8
1	0	154	C	2.8
1	0	240	C	2.8
1	0	1864	C	2.8
1	0	2759	C	2.8
1	0	2762	C	2.8

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Mol	Chain	Res	Type	RSRZ
6	D	71	ALA	2.8
6	D	91	ALA	2.8
3	A	98	GLU	2.8
19	Q	107	GLU	2.8
26	X	141	THR	2.8
14	L	99	ARG	2.8
19	Q	21	ARG	2.8
28	Z	39	PHE	2.8
1	0	1524	U	2.8
1	0	1887	U	2.8
1	0	2043	U	2.8
1	0	88	G	2.8
1	0	257	G	2.8
1	0	367	G	2.8
1	0	568	G	2.8
1	0	2585	G	2.8
1	0	2758	G	2.8
2	9	3050	G	2.8
2	9	3110	G	2.8
7	E	38	ILE	2.8
10	H	20	ILE	2.8
10	H	34	GLY	2.8
13	K	109	LEU	2.8
17	O	82	GLY	2.8
18	P	12	GLY	2.8
19	Q	2	ILE	2.8
24	V	4	LEU	2.8
28	Z	4	GLY	2.8
1	0	37	A	2.8
1	0	316	A	2.8
1	0	694	A	2.8
1	0	1910	A	2.8
1	0	2103	A	2.8
1	0	2105	C	2.8
1	0	2440	C	2.8
1	0	2633	A	2.8
1	0	2893	C	2.8
3	A	155	THR	2.8
4	B	235	ARG	2.8
12	J	43	ARG	2.8
13	K	136	ALA	2.8
16	N	78	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
26	X	232	THR	2.8
26	X	143	TRP	2.8
1	0	1041	U	2.8
1	0	2436	U	2.8
1	0	2478	U	2.8
8	F	32	GLY	2.8
10	H	71	TYR	2.8
11	I	68	GLY	2.8
17	O	56	GLY	2.8
11	I	135	ILE	2.8
23	U	56	ILE	2.8
1	0	689	G	2.8
1	0	873	G	2.8
1	0	1386	G	2.8
1	0	2079	G	2.8
11	I	12	VAL	2.8
14	L	32	ARG	2.8
20	R	23	LYS	2.8
23	U	47	LYS	2.8
3	A	119	ALA	2.8
3	A	174	ASN	2.8
5	C	150	THR	2.8
10	H	59	ASN	2.8
5	C	200	PRO	2.8
26	X	171	PRO	2.8
1	0	53	C	2.8
1	0	280	C	2.8
1	0	340	A	2.8
1	0	630	A	2.8
1	0	1858	A	2.8
1	0	1906	C	2.8
1	0	2002	C	2.8
1	0	2370	A	2.8
1	0	2908	A	2.8
26	X	113	ASP	2.8
1	0	1879	U	2.8
12	J	33	SER	2.8
14	L	177	GLY	2.8
4	B	134	ALA	2.8
4	B	335	ASN	2.8
25	W	60	ALA	2.8
1	0	672	G	2.8

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Mol	Chain	Res	Type	RSRZ
1	0	863	G	2.8
1	0	1216	G	2.8
1	0	1389	G	2.8
1	0	1877	G	2.8
1	0	2092	G	2.8
2	9	3078	G	2.8
4	B	325	PRO	2.8
4	B	56	ASP	2.8
10	H	22	GLY	2.8
19	Q	124	GLY	2.8
5	C	245	GLU	2.7
11	I	96	GLU	2.7
25	W	53	SER	2.7
1	0	1643	C	2.7
1	0	1892	C	2.7
1	0	2034	U	2.7
1	0	2262	C	2.7
1	0	2526	C	2.7
1	0	2895	C	2.7
2	9	3072	C	2.7
11	I	71	TYR	2.7
15	M	131	HIS	2.7
1	0	2101	A	2.7
1	0	2380	A	2.7
10	H	72	VAL	2.7
18	P	63	VAL	2.7
14	L	43	PRO	2.7
19	Q	32	ALA	2.7
24	V	131	PRO	2.7
26	X	95	THR	2.7
5	C	146	ASP	2.7
10	H	26	LYS	2.7
11	I	90	LYS	2.7
17	O	52	LYS	2.7
26	X	213	LYS	2.7
7	E	80	TRP	2.7
1	0	292	G	2.7
1	0	1387	G	2.7
1	0	2567	G	2.7
1	0	2582	G	2.7
5	C	178	GLN	2.7
14	L	74	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	349	U	2.7
1	0	1883	U	2.7
1	0	2048	C	2.7
1	0	2127	U	2.7
1	0	2265	U	2.7
1	0	2405	C	2.7
1	0	2897	C	2.7
4	B	59	ASN	2.7
8	F	61	MET	2.7
1	0	608	A	2.7
1	0	819	A	2.7
1	0	895	A	2.7
1	0	916	A	2.7
1	0	1154	A	2.7
1	0	1502	A	2.7
1	0	1767	A	2.7
1	0	2437	A	2.7
10	H	152	LYS	2.7
18	P	42	LYS	2.7
8	F	25	ASP	2.7
11	I	16	ASP	2.7
16	N	90	ASP	2.7
16	N	107	GLU	2.7
19	Q	59	PHE	2.7
25	W	44	ASP	2.7
4	B	307	ARG	2.7
5	C	133	ARG	2.7
13	K	90	ARG	2.7
19	Q	132	ARG	2.7
14	L	157	LEU	2.7
1	0	1595	G	2.7
1	0	2070	G	2.7
1	0	2299	G	2.7
1	0	2524	G	2.7
1	0	2529	G	2.7
16	N	114	ILE	2.7
1	0	2550	U	2.7
1	0	2631	U	2.7
14	L	131	VAL	2.7
1	0	220	C	2.7
1	0	556	C	2.7
1	0	1549	C	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	2086	C	2.7
1	0	2717	C	2.7
2	9	3067	C	2.7
14	L	10	GLU	2.7
19	Q	142	ASP	2.7
21	S	55	PHE	2.7
29	1	12	ALA	2.7
6	D	96	SER	2.7
10	H	9	SER	2.7
15	M	17	ARG	2.7
1	0	2879	A	2.7
28	Z	42	SER	2.7
8	F	117	GLU	2.7
11	I	46	ILE	2.7
16	N	56	GLU	2.7
25	W	48	VAL	2.7
26	X	235	GLU	2.7
1	0	382	U	2.7
1	0	852	U	2.7
1	0	2107	U	2.7
1	0	2448	U	2.7
4	B	253	GLN	2.7
12	J	10	GLN	2.7
14	L	4	ALA	2.7
16	N	80	ASP	2.7
1	0	267	G	2.7
1	0	1299	G	2.7
1	0	1621	G	2.7
1	0	2410	G	2.7
1	0	2692	G	2.7
1	0	2709	G	2.7
8	F	33	THR	2.7
1	0	2487	C	2.7
1	0	2626	C	2.7
6	D	168	SER	2.7
20	R	79	SER	2.7
15	M	66	LEU	2.7
19	Q	117	HIS	2.7
1	0	1866	A	2.7
1	0	1941	A	2.7
1	0	2456	A	2.7
1	0	2596	A	2.7

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Mol	Chain	Res	Type	RSRZ
1	0	2706	A	2.7
5	C	134	ASP	2.7
13	K	130	ARG	2.7
14	L	113	ARG	2.7
2	9	3055	U	2.7
15	M	63	SER	2.7
1	0	101	C	2.7
1	0	235	C	2.7
1	0	621	C	2.7
1	0	727	G	2.7
1	0	877	G	2.7
1	0	1209	C	2.7
1	0	2249	G	2.7
1	0	2556	C	2.7
6	D	43	GLU	2.7
7	E	106	ASN	2.7
26	X	153	GLN	2.7
1	0	128	A	2.7
1	0	305	A	2.7
1	0	437	A	2.7
1	0	511	A	2.7
1	0	2099	A	2.7
1	0	2374	A	2.7
1	0	2702	A	2.7
1	0	2719	A	2.7
2	9	3038	A	2.7
3	A	225	VAL	2.7
5	C	128	GLY	2.7
8	F	48	VAL	2.7
12	J	55	VAL	2.7
12	J	72	VAL	2.7
24	V	65	VAL	2.7
24	V	121	PRO	2.7
30	2	85	ALA	2.7
4	B	19	SER	2.7
7	E	67	SER	2.7
10	H	121	THR	2.7
1	0	777	U	2.7
1	0	1066	U	2.7
1	0	1371	U	2.7
1	0	1383	U	2.7
1	0	2473	U	2.7

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Mol	Chain	Res	Type	RSRZ
7	E	149	GLU	2.7
21	S	91	LEU	2.7
23	U	28	LEU	2.7
17	O	73	HIS	2.7
14	L	161	ARG	2.7
21	S	39	ASN	2.7
1	0	28	G	2.7
1	0	41	G	2.7
1	0	71	G	2.7
1	0	175	G	2.7
1	0	1385	G	2.7
1	0	1441	G	2.7
1	0	2411	C	2.7
1	0	2502	C	2.7
1	0	2591	C	2.7
1	0	2634	G	2.7
1	0	2639	G	2.7
1	0	2676	C	2.7
1	0	2679	G	2.7
26	X	205	ILE	2.7
5	C	4	THR	2.7
6	D	150	SER	2.7
24	V	102	SER	2.7
25	W	57	ALA	2.7
26	X	168	PHE	2.7
30	2	61	PRO	2.7
13	K	39	GLU	2.7
14	L	181	GLU	2.7
1	0	98	A	2.7
1	0	215	A	2.7
1	0	628	A	2.7
1	0	643	A	2.7
1	0	2255	A	2.7
1	0	2260	A	2.7
28	Z	29	THR	2.7
1	0	30	U	2.6
1	0	63	U	2.6
1	0	1457	U	2.6
1	0	1511	U	2.6
1	0	2330	U	2.6
15	M	34	LEU	2.6
18	P	41	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
4	B	234	ARG	2.6
22	T	30	HIS	2.6
30	2	13	HIS	2.6
19	Q	29	LYS	2.6
3	A	227	ASP	2.6
24	V	16	ASP	2.6
1	0	230	C	2.6
1	0	523	C	2.6
1	0	712	C	2.6
1	0	1365	C	2.6
1	0	1477	C	2.6
1	0	2319	C	2.6
1	0	2819	C	2.6
1	0	2822	C	2.6
4	B	202	VAL	2.6
5	C	26	VAL	2.6
14	L	61	ILE	2.6
1	0	77	G	2.6
1	0	610	G	2.6
1	0	1210	G	2.6
1	0	2072	G	2.6
1	0	2740	G	2.6
2	9	3083	G	2.6
4	B	3	PRO	2.6
6	D	137	PRO	2.6
7	E	14	GLU	2.6
10	H	162	SER	2.6
19	Q	85	SER	2.6
11	I	47	THR	2.6
23	U	55	ARG	2.6
30	2	51	LYS	2.6
1	0	293	A	2.6
1	0	486	A	2.6
1	0	1022	A	2.6
1	0	1279	U	2.6
1	0	1294	A	2.6
1	0	1905	U	2.6
1	0	2038	A	2.6
1	0	2620	U	2.6
1	0	2721	U	2.6
1	0	2864	U	2.6
2	9	3077	A	2.6

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Mol	Chain	Res	Type	RSRZ
6	D	36	ASN	2.6
19	Q	136	TRP	2.6
4	B	231	GLY	2.6
6	D	73	VAL	2.6
6	D	166	ILE	2.6
13	K	121	ILE	2.6
17	O	38	GLU	2.6
30	2	55	VAL	2.6
11	I	14	ALA	2.6
1	0	85	C	2.6
1	0	571	C	2.6
1	0	1830	C	2.6
1	0	2785	C	2.6
2	9	3030	C	2.6
13	K	19	LYS	2.6
3	A	27	LEU	2.6
3	A	182	ARG	2.6
1	0	97	G	2.6
1	0	868	G	2.6
1	0	901	G	2.6
1	0	1382	G	2.6
1	0	1756	G	2.6
1	0	1998	G	2.6
1	0	2363	G	2.6
1	0	2400	G	2.6
1	0	2540	G	2.6
1	0	2618	G	2.6
1	0	510	U	2.6
1	0	517	U	2.6
1	0	1846	U	2.6
3	A	198	ASP	2.6
4	B	258	GLY	2.6
7	E	83	GLY	2.6
13	K	144	ASP	2.6
1	0	477	A	2.6
1	0	1014	A	2.6
1	0	1994	A	2.6
1	0	2469	A	2.6
1	0	2792	A	2.6
4	B	298	LYS	2.6
13	K	126	SER	2.6
14	L	16	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
21	S	21	LYS	2.6
15	M	116	PHE	2.6
18	P	26	PRO	2.6
22	T	33	SER	2.6
11	I	102	ARG	2.6
12	J	105	ARG	2.6
14	L	105	ALA	2.6
21	S	56	ALA	2.6
23	U	30	ALA	2.6
25	W	29	ALA	2.6
30	2	69	TYR	2.6
10	H	154	THR	2.6
16	N	84	THR	2.6
19	Q	110	THR	2.6
21	S	51	LEU	2.6
26	X	193	LEU	2.6
1	0	433	C	2.6
1	0	1069	C	2.6
1	0	1085	C	2.6
1	0	1714	C	2.6
3	A	234	GLY	2.6
5	C	130	GLU	2.6
24	V	130	HIS	2.6
1	0	24	G	2.6
1	0	84	G	2.6
1	0	203	G	2.6
1	0	231	G	2.6
1	0	362	G	2.6
1	0	801	U	2.6
1	0	1234	U	2.6
1	0	1491	G	2.6
1	0	1671	U	2.6
1	0	1744	G	2.6
1	0	2272	G	2.6
1	0	2275	G	2.6
1	0	2295	G	2.6
1	0	2623	G	2.6
14	L	69	LYS	2.6
27	Y	46	LYS	2.6
4	B	41	PHE	2.6
7	E	15	GLN	2.6
11	I	74	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
28	Z	3	ALA	2.6
1	0	331	A	2.6
1	0	2085	A	2.6
1	0	2429	A	2.6
1	0	2497	A	2.6
3	A	72	GLU	2.6
22	T	9	CYS	2.6
26	X	97	LEU	2.6
29	1	27	LEU	2.6
4	B	50	HIS	2.6
28	Z	41	LYS	2.6
1	0	480	C	2.6
1	0	853	C	2.6
1	0	1692	C	2.6
1	0	1750	C	2.6
1	0	2737	C	2.6
2	9	3121	C	2.6
1	0	1939	U	2.6
1	0	2069	U	2.6
1	0	2282	U	2.6
16	N	100	GLN	2.6
1	0	2592	G	2.6
4	B	96	PRO	2.6
4	B	159	PRO	2.6
14	L	160	PHE	2.6
24	V	5	VAL	2.6
3	A	56	ALA	2.6
5	C	181	ALA	2.6
5	C	156	LEU	2.6
11	I	144	THR	2.6
24	V	86	GLU	2.6
17	O	9	LEU	2.6
5	C	96	LYS	2.6
1	0	166	A	2.6
1	0	236	A	2.6
1	0	378	A	2.6
25	W	40	HIS	2.6
17	O	20	ARG	2.6
26	X	115	ARG	2.6
4	B	35	GLN	2.6
4	B	320	GLN	2.6
1	0	244	C	2.6

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Mol	Chain	Res	Type	RSRZ
1	0	311	C	2.6
1	0	1662	C	2.6
1	0	1983	C	2.6
1	0	2682	C	2.6
1	0	170	U	2.6
1	0	909	U	2.6
1	0	1338	U	2.6
1	0	2711	U	2.6
3	A	33	GLU	2.6
5	C	80	VAL	2.6
5	C	234	VAL	2.6
10	H	54	VAL	2.6
16	N	89	ILE	2.6
16	N	111	VAL	2.6
28	Z	33	VAL	2.6
5	C	190	ALA	2.6
19	Q	13	THR	2.6
19	Q	37	GLY	2.6
19	Q	47	LEU	2.6
19	Q	63	ASN	2.6
1	0	142	G	2.6
1	0	553	G	2.6
1	0	627	G	2.6
1	0	1468	G	2.6
1	0	2668	G	2.6
4	B	180	ASP	2.6
5	C	184	ARG	2.6
1	0	317	A	2.6
1	0	882	A	2.6
1	0	1090	A	2.6
1	0	1821	A	2.6
1	0	1869	A	2.6
1	0	1881	A	2.6
1	0	2538	A	2.6
1	0	2624	A	2.6
17	O	58	SER	2.6
19	Q	3	SER	2.6
28	Z	36	SER	2.6
29	1	8	LYS	2.6
4	B	236	ILE	2.6
10	H	114	PRO	2.6
1	0	202	U	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	687	C	2.6
1	0	862	U	2.5
1	0	1519	U	2.5
1	0	1675	C	2.6
1	0	1786	C	2.6
1	0	2269	C	2.6
13	K	108	VAL	2.6
20	R	65	VAL	2.6
1	0	2422	U	2.5
8	F	103	ALA	2.5
10	H	76	GLY	2.5
15	M	16	ALA	2.5
17	O	47	GLY	2.5
29	1	23	ALA	2.5
10	H	14	TYR	2.5
23	U	22	ASP	2.5
29	1	46	ASP	2.5
4	B	7	ARG	2.5
14	L	14	ARG	2.5
1	0	512	G	2.5
1	0	683	G	2.5
1	0	724	G	2.5
1	0	885	G	2.5
1	0	1728	G	2.5
1	0	1802	G	2.5
1	0	2250	G	2.5
1	0	2574	G	2.5
10	H	52	LYS	2.5
18	P	15	LYS	2.5
20	R	76	GLU	2.5
3	A	214	SER	2.5
14	L	91	ILE	2.5
1	0	495	A	2.5
1	0	573	A	2.5
1	0	965	A	2.5
1	0	2784	A	2.5
1	0	2840	A	2.5
5	C	147	LEU	2.5
1	0	295	C	2.5
1	0	835	U	2.5
1	0	1266	U	2.5
1	0	2435	U	2.5

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Mol	Chain	Res	Type	RSRZ
7	E	116	THR	2.5
16	N	115	ARG	2.5
19	Q	39	THR	2.5
11	I	5	GLU	2.5
20	R	63	LYS	2.5
1	0	201	G	2.5
1	0	417	G	2.5
1	0	432	G	2.5
1	0	1727	G	2.5
1	0	1837	G	2.5
1	0	1867	G	2.5
1	0	2459	G	2.5
4	B	84	LEU	2.5
4	B	123	ALA	2.5
4	B	171	VAL	2.5
5	C	243	VAL	2.5
6	D	174	VAL	2.5
10	H	116	GLY	2.5
12	J	31	VAL	2.5
14	L	62	VAL	2.5
14	L	120	VAL	2.5
4	B	239	LEU	2.5
14	L	140	ALA	2.5
15	M	11	ARG	2.5
15	M	37	ARG	2.5
25	W	37	LEU	2.5
26	X	166	ALA	2.5
4	B	279	THR	2.5
12	J	67	GLN	2.5
13	K	7	GLN	2.5
14	L	146	GLN	2.5
8	F	109	GLU	2.5
17	O	91	LYS	2.5
1	0	67	A	2.5
1	0	158	A	2.5
1	0	507	A	2.5
1	0	584	U	2.5
1	0	1092	A	2.5
1	0	1465	A	2.5
1	0	1530	U	2.5
1	0	1813	U	2.5
1	0	1838	U	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	1912	A	2.5
1	0	2074	A	2.5
1	0	2276	U	2.5
21	S	113	GLU	2.5
1	0	848	C	2.5
1	0	1146	C	2.5
1	0	1225	C	2.5
1	0	1253	C	2.5
1	0	2388	C	2.5
5	C	189	PRO	2.5
7	E	8	PRO	2.5
7	E	32	ARG	2.5
5	C	54	LEU	2.5
8	F	47	LEU	2.5
8	F	60	VAL	2.5
10	H	4	ALA	2.5
11	I	39	VAL	2.5
12	J	8	VAL	2.5
13	K	115	ARG	2.5
21	S	108	ARG	2.5
22	T	47	ARG	2.5
15	M	36	ALA	2.5
15	M	122	ALA	2.5
23	U	34	GLN	2.5
26	X	206	ALA	2.5
28	Z	18	LYS	2.5
1	0	20	G	2.5
1	0	112	G	2.5
1	0	413	G	2.5
1	0	446	G	2.5
1	0	448	G	2.5
1	0	657	G	2.5
1	0	697	G	2.5
1	0	1214	G	2.5
1	0	1344	G	2.5
1	0	2053	G	2.5
1	0	2453	G	2.5
1	0	398	U	2.5
1	0	470	U	2.5
1	0	1464	U	2.5
1	0	436	A	2.5
1	0	515	C	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	552	A	2.5
1	0	897	A	2.5
1	0	1987	C	2.5
1	0	2011	A	2.5
1	0	2039	A	2.5
1	0	2398	A	2.5
1	0	2594	C	2.5
2	9	3027	C	2.5
2	9	3081	C	2.5
4	B	273	GLY	2.5
14	L	191	GLY	2.5
28	Z	23	GLY	2.5
3	A	118	PHE	2.5
4	B	254	GLN	2.5
6	D	10	PHE	2.5
8	F	100	ASP	2.5
12	J	7	ASP	2.5
14	L	176	GLN	2.5
18	P	64	GLU	2.5
20	R	71	ASP	2.5
25	W	21	PRO	2.5
25	W	67	PRO	2.5
1	0	539	G	2.5
1	0	771	G	2.5
1	0	772	G	2.5
1	0	958	G	2.5
1	0	1077	G	2.5
1	0	1741	U	2.5
1	0	2045	G	2.5
1	0	2293	G	2.5
2	9	3084	G	2.5
2	9	3099	U	2.5
14	L	13	LYS	2.5
3	A	73	GLY	2.5
13	K	127	GLU	2.5
16	N	71	GLN	2.5
18	P	32	GLU	2.5
1	0	650	C	2.5
1	0	1114	A	2.5
1	0	1168	C	2.5
1	0	1259	A	2.5
1	0	1738	C	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	2114	C	2.5
1	0	2321	A	2.5
1	0	2332	A	2.5
1	0	2354	A	2.5
1	0	2718	C	2.5
10	H	132	PHE	2.5
13	K	124	ASP	2.5
6	D	40	ILE	2.5
8	F	40	ILE	2.5
8	F	51	ALA	2.5
21	S	16	LEU	2.5
17	O	1	THR	2.5
13	K	48	LYS	2.5
15	M	38	LYS	2.5
26	X	145	LYS	2.5
30	2	63	LYS	2.5
3	A	183	GLY	2.5
4	B	138	GLY	2.5
15	M	155	GLU	2.5
25	W	35	GLU	2.5
26	X	218	GLU	2.5
27	Y	51	GLY	2.5
1	0	19	U	2.5
1	0	614	U	2.5
1	0	815	U	2.5
1	0	2064	U	2.5
1	0	185	G	2.5
1	0	315	G	2.5
1	0	1075	G	2.5
1	0	1443	G	2.5
1	0	1743	G	2.5
1	0	2128	G	2.5
20	R	30	ASP	2.5
22	T	39	ASN	2.5
7	E	161	VAL	2.5
24	V	128	VAL	2.5
1	0	530	C	2.5
1	0	576	C	2.5
1	0	2106	C	2.5
1	0	2728	C	2.5
2	9	3041	C	2.5
1	0	48	A	2.5

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Mol	Chain	Res	Type	RSRZ
1	0	242	A	2.5
1	0	1682	A	2.5
1	0	1822	A	2.5
1	0	2691	A	2.5
6	D	45	THR	2.5
17	O	102	ARG	2.5
24	V	117	ARG	2.5
4	B	22	GLU	2.5
28	Z	34	CYS	2.5
3	A	203	GLY	2.5
4	B	240	GLY	2.5
11	I	29	GLN	2.5
28	Z	2	GLY	2.5
1	0	68	U	2.5
1	0	713	U	2.5
1	0	823	U	2.5
1	0	1429	U	2.5
1	0	1503	U	2.5
1	0	2406	U	2.5
1	0	2705	U	2.5
4	B	148	PRO	2.5
3	A	196	ALA	2.4
1	0	386	G	2.4
1	0	902	G	2.4
1	0	1327	G	2.4
1	0	1665	G	2.4
1	0	2285	G	2.4
1	0	2288	G	2.4
2	9	3032	G	2.4
1	0	1228	C	2.4
1	0	1483	C	2.4
1	0	1880	C	2.4
1	0	1975	C	2.4
1	0	2720	C	2.4
1	0	2907	C	2.4
5	C	32	GLY	2.4
10	H	110	GLY	2.4
11	I	100	SER	2.4
15	M	39	SER	2.4
26	X	127	GLN	2.4
1	0	90	A	2.4
1	0	1471	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	1630	A	2.4
2	9	3054	A	2.4
7	E	123	ASP	2.4
11	I	9	ASP	2.4
27	Y	38	LYS	2.4
30	2	8	ASN	2.4
1	0	831	U	2.4
1	0	1219	U	2.4
5	C	135	GLU	2.4
5	C	210	ALA	2.4
17	O	59	ARG	2.4
19	Q	108	ALA	2.4
6	D	28	GLY	2.4
16	N	1	SER	2.4
1	0	322	G	2.4
1	0	334	G	2.4
1	0	501	G	2.4
1	0	1311	G	2.4
1	0	1370	G	2.4
1	0	1376	G	2.4
1	0	2418	G	2.4
1	0	2516	G	2.4
1	0	1156	C	2.4
1	0	2047	C	2.4
2	9	3026	C	2.4
28	Z	10	LYS	2.4
7	E	25	ASP	2.4
20	R	46	ASP	2.4
26	X	230	ASN	2.4
1	0	161	A	2.4
1	0	671	A	2.4
1	0	1242	A	2.4
1	0	1470	A	2.4
1	0	2511	A	2.4
3	A	94	LEU	2.4
7	E	153	ARG	2.4
8	F	46	GLU	2.4
18	P	51	ARG	2.4
26	X	220	GLU	2.4
1	0	346	U	2.4
1	0	409	U	2.4
1	0	2052	U	2.4

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Mol	Chain	Res	Type	RSRZ
5	C	140	VAL	2.4
16	N	52	ALA	2.4
4	B	49	THR	2.4
13	K	12	THR	2.4
21	S	20	HIS	2.4
4	B	222	LYS	2.4
13	K	17	SER	2.4
21	S	60	GLY	2.4
26	X	151	SER	2.4
13	K	65	ASP	2.4
4	B	79	MET	2.4
29	1	36	ASN	2.4
1	0	29	C	2.4
1	0	65	C	2.4
1	0	147	G	2.4
1	0	197	C	2.4
1	0	344	C	2.4
1	0	814	G	2.4
1	0	1065	G	2.4
1	0	1316	G	2.4
1	0	1394	C	2.4
1	0	1870	C	2.4
1	0	2056	C	2.4
1	0	2407	G	2.4
1	0	2423	C	2.4
1	0	2715	G	2.4
1	0	2845	G	2.4
2	9	3035	C	2.4
6	D	16	PRO	2.4
18	P	55	ARG	2.4
19	Q	147	LEU	2.4
24	V	21	LEU	2.4
28	Z	19	CYS	2.4
30	2	12	PRO	2.4
5	C	52	ALA	2.4
10	H	55	GLN	2.4
10	H	49	VAL	2.4
11	I	18	ILE	2.4
12	J	125	ALA	2.4
20	R	55	GLN	2.4
1	0	109	U	2.4
1	0	183	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	508	A	2.4
1	0	1815	A	2.4
1	0	1937	U	2.4
1	0	2327	A	2.4
1	0	2503	A	2.4
1	0	2568	A	2.4
5	C	12	THR	2.4
14	L	6	SER	2.4
14	L	44	THR	2.4
26	X	178	HIS	2.4
15	M	80	SER	2.4
13	K	101	ASP	2.4
26	X	197	ASP	2.4
3	A	8	ARG	2.4
4	B	229	ARG	2.4
24	V	118	LEU	2.4
1	0	168	C	2.4
1	0	1335	C	2.4
1	0	1469	C	2.4
1	0	2651	C	2.4
1	0	78	G	2.4
1	0	375	G	2.4
1	0	575	G	2.4
1	0	755	G	2.4
1	0	865	G	2.4
1	0	1089	G	2.4
1	0	1312	G	2.4
1	0	2834	G	2.4
3	A	173	GLY	2.4
4	B	200	ALA	2.4
4	B	337	GLY	2.4
7	E	29	VAL	2.4
16	N	59	VAL	2.4
25	W	75	ALA	2.4
1	0	22	U	2.4
1	0	35	U	2.4
1	0	211	U	2.4
1	0	840	U	2.4
1	0	1003	U	2.4
1	0	1992	U	2.4
1	0	2028	U	2.4
1	0	2115	U	2.4

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Mol	Chain	Res	Type	RSRZ
1	0	2610	U	2.4
1	0	439	A	2.4
1	0	463	A	2.4
1	0	857	A	2.4
1	0	955	A	2.4
1	0	1859	A	2.4
1	0	2553	A	2.4
1	0	2675	A	2.4
19	Q	42	GLU	2.4
13	K	6	ARG	2.4
15	M	12	ARG	2.4
7	E	88	TYR	2.4
5	C	227	GLY	2.4
12	J	98	VAL	2.4
13	K	140	VAL	2.4
15	M	67	ALA	2.4
17	O	85	GLY	2.4
19	Q	44	VAL	2.4
28	Z	37	CYS	2.4
1	0	256	C	2.4
1	0	1229	C	2.4
1	0	1735	C	2.4
1	0	2273	C	2.4
1	0	2695	C	2.4
2	9	3040	C	2.4
5	C	95	GLU	2.4
5	C	78	ARG	2.4
24	V	76	ASP	2.4
1	0	223	G	2.4
1	0	258	G	2.4
1	0	626	U	2.4
1	0	1284	G	2.4
1	0	1898	G	2.4
1	0	2320	U	2.4
17	O	67	LYS	2.4
24	V	18	GLN	2.4
1	0	11	A	2.4
1	0	453	A	2.4
1	0	746	A	2.4
3	A	194	MET	2.4
5	C	137	PRO	2.4
18	P	33	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
4	B	299	GLY	2.4
21	S	42	VAL	2.4
6	D	95	THR	2.4
7	E	37	ASP	2.4
24	V	32	CYS	2.4
30	2	64	LYS	2.4
1	0	252	C	2.4
1	0	343	C	2.4
1	0	403	C	2.4
1	0	637	C	2.4
1	0	1551	C	2.4
1	0	1708	C	2.4
1	0	2331	C	2.4
1	0	2806	C	2.4
2	9	3036	C	2.4
12	J	42	ASN	2.4
17	O	57	ASN	2.4
1	0	46	U	2.4
1	0	942	U	2.4
1	0	2607	U	2.4
1	0	2652	U	2.4
1	0	2796	U	2.4
1	0	333	G	2.3
1	0	1416	G	2.3
1	0	1611	G	2.3
2	9	3008	G	2.3
22	T	15	PRO	2.3
3	A	157	GLY	2.3
15	M	94	GLU	2.3
1	0	193	A	2.3
1	0	827	A	2.3
1	0	867	A	2.3
2	9	3034	A	2.3
3	A	17	ARG	2.3
3	A	146	LYS	2.3
4	B	316	ARG	2.3
5	C	35	VAL	2.3
11	I	80	LYS	2.3
13	K	18	HIS	2.3
13	K	149	ARG	2.3
4	B	305	ASP	2.3
8	F	53	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
16	N	48	ILE	2.3
20	R	11	THR	2.3
1	0	83	C	2.3
1	0	263	U	2.3
1	0	1748	U	2.3
1	0	2551	C	2.3
4	B	24	PRO	2.3
13	K	46	LEU	2.3
19	Q	36	LYS	2.3
1	0	219	G	2.3
1	0	422	G	2.3
1	0	644	G	2.3
1	0	1765	G	2.3
1	0	2102	G	2.3
1	0	2722	G	2.3
10	H	81	TYR	2.3
20	R	4	VAL	2.3
23	U	25	THR	2.3
1	0	187	A	2.3
1	0	347	A	2.3
1	0	383	A	2.3
1	0	2118	A	2.3
1	0	2566	A	2.3
1	0	2678	A	2.3
2	9	3085	A	2.3
1	0	137	U	2.3
1	0	753	U	2.3
1	0	2326	U	2.3
3	A	104	PRO	2.3
4	B	265	LEU	2.3
11	I	124	LEU	2.3
13	K	14	GLY	2.3
22	T	56	ARG	2.3
1	0	585	C	2.3
1	0	1044	C	2.3
1	0	1674	C	2.3
1	0	1803	C	2.3
1	0	1916	C	2.3
1	0	2298	C	2.3
1	0	2318	C	2.3
5	C	7	ASP	2.3
15	M	73	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
16	N	109	SER	2.3
24	V	137	GLN	2.3
10	H	153	VAL	2.3
19	Q	72	VAL	2.3
1	0	426	G	2.3
1	0	1087	G	2.3
1	0	1217	G	2.3
1	0	1351	G	2.3
1	0	1489	G	2.3
1	0	2696	G	2.3
2	9	3049	G	2.3
24	V	71	GLU	2.3
30	2	23	GLU	2.3
1	0	1098	A	2.3
1	0	1390	A	2.3
1	0	2470	A	2.3
1	0	2843	A	2.3
2	9	3093	A	2.3
10	H	16	ARG	2.3
10	H	57	ARG	2.3
4	B	155	PRO	2.3
15	M	157	PRO	2.3
24	V	150	LEU	2.3
1	0	1282	U	2.3
1	0	1333	U	2.3
1	0	1418	U	2.3
1	0	2063	U	2.3
7	E	84	MET	2.3
5	C	129	HIS	2.3
16	N	77	ALA	2.3
28	Z	54	ALA	2.3
1	0	1421	C	2.3
1	0	2119	C	2.3
1	0	2431	C	2.3
1	0	2498	C	2.3
2	9	3106	C	2.3
12	J	89	LYS	2.3
3	A	3	ARG	2.3
17	O	63	ARG	2.3
19	Q	78	GLY	2.3
4	B	140	LEU	2.3
13	K	120	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
24	V	138	LEU	2.3
1	0	17	G	2.3
1	0	61	G	2.3
1	0	691	G	2.3
1	0	1076	G	2.3
1	0	1438	G	2.3
1	0	1622	G	2.3
7	E	73	PHE	2.3
19	Q	22	GLN	2.3
4	B	281	ASP	2.3
11	I	136	SER	2.3
14	L	24	MET	2.3
21	S	102	ASP	2.3
27	Y	80	MET	2.3
29	1	15	ASP	2.3
1	0	548	U	2.3
1	0	756	A	2.3
1	0	1047	U	2.3
1	0	1657	A	2.3
1	0	1746	A	2.3
1	0	2307	A	2.3
1	0	2362	A	2.3
1	0	2527	U	2.3
4	B	333	GLU	2.3
10	H	164	ALA	2.3
18	P	82	LYS	2.3
21	S	81	LYS	2.3
26	X	134	HIS	2.3
11	I	104	TYR	2.3
13	K	114	VAL	2.3
24	V	83	TRP	2.3
26	X	184	GLU	2.3
4	B	243	ASN	2.3
26	X	196	VAL	2.3
13	K	74	THR	2.3
1	0	36	C	2.3
1	0	444	C	2.3
1	0	461	C	2.3
1	0	704	C	2.3
1	0	725	C	2.3
1	0	838	C	2.3
1	0	1455	C	2.3

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Mol	Chain	Res	Type	RSRZ
2	9	3116	C	2.3
4	B	14	GLY	2.3
13	K	15	GLY	2.3
20	R	80	ARG	2.3
24	V	42	ARG	2.3
26	X	167	GLY	2.3
3	A	7	GLN	2.3
13	K	145	LEU	2.3
1	0	482	G	2.3
1	0	1145	G	2.3
3	A	219	ALA	2.3
13	K	116	HIS	2.3
1	0	107	U	2.3
1	0	286	U	2.3
1	0	312	U	2.3
1	0	845	U	2.3
1	0	1056	U	2.3
1	0	1903	U	2.3
12	J	132	VAL	2.3
26	X	203	VAL	2.3
1	0	666	A	2.3
1	0	1375	A	2.3
1	0	1424	A	2.3
1	0	774	C	2.3
1	0	2508	C	2.3
2	9	3009	C	2.3
2	9	3118	C	2.3
17	O	3	LEU	2.3
24	V	116	LEU	2.3
9	G	14	GLU	2.3
12	J	63	GLU	2.3
8	F	54	VAL	2.3
23	U	33	VAL	2.3
1	0	180	G	2.3
1	0	673	U	2.3
1	0	1350	U	2.3
11	I	118	GLY	2.3
1	0	1363	G	2.3
1	0	2482	G	2.3
1	0	2738	G	2.3
15	M	104	ILE	2.3
19	Q	122	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	52	A	2.2
1	0	306	A	2.2
1	0	875	A	2.2
1	0	2433	A	2.2
1	0	2793	A	2.2
2	9	3062	A	2.2
2	9	3105	A	2.2
10	H	47	GLU	2.2
14	L	41	GLU	2.2
5	C	17	ASP	2.2
15	M	138	ASP	2.2
22	T	25	ASP	2.2
23	U	21	ASP	2.2
26	X	179	PRO	2.2
1	0	250	C	2.2
1	0	338	C	2.2
1	0	494	C	2.2
1	0	1243	C	2.2
1	0	1366	C	2.2
1	0	2325	C	2.2
1	0	2335	C	2.2
15	M	23	ARG	2.2
29	1	40	ARG	2.2
5	C	37	ALA	2.2
14	L	138	HIS	2.2
3	A	12	GLY	2.2
11	I	140	GLY	2.2
16	N	62	GLY	2.2
19	Q	74	GLY	2.2
21	S	6	LYS	2.2
25	W	28	LYS	2.2
4	B	218	TRP	2.2
18	P	85	ILE	2.2
1	0	821	U	2.2
1	0	832	U	2.2
18	P	91	LEU	2.2
1	0	23	G	2.2
1	0	44	G	2.2
1	0	181	G	2.2
1	0	503	G	2.2
1	0	742	G	2.2
1	0	2491	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	2558	G	2.2
2	9	3092	G	2.2
6	D	100	ASP	2.2
20	R	26	PHE	2.2
25	W	42	SER	2.2
28	Z	35	SER	2.2
15	M	33	ARG	2.2
1	0	113	A	2.2
1	0	908	A	2.2
1	0	1296	A	2.2
1	0	1829	A	2.2
1	0	2096	A	2.2
1	0	2601	A	2.2
1	0	2635	A	2.2
1	0	2653	A	2.2
5	C	72	LYS	2.2
5	C	121	ALA	2.2
7	E	74	HIS	2.2
21	S	17	HIS	2.2
22	T	35	LYS	2.2
1	0	42	C	2.2
1	0	1474	C	2.2
1	0	2565	C	2.2
2	9	3006	C	2.2
10	H	63	ALA	2.2
26	X	133	HIS	2.2
12	J	60	GLY	2.2
13	K	146	GLY	2.2
27	Y	43	GLY	2.2
26	X	187	VAL	2.2
14	L	159	THR	2.2
1	0	619	U	2.2
1	0	1766	U	2.2
1	0	2514	U	2.2
5	C	141	SER	2.2
21	S	13	ARG	2.2
24	V	69	ARG	2.2
30	2	40	ARG	2.2
1	0	32	G	2.2
1	0	690	G	2.2
1	0	1391	G	2.2
1	0	1475	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	2113	G	2.2
1	0	2537	G	2.2
2	9	3058	G	2.2
5	C	83	ALA	2.2
10	H	29	ALA	2.2
12	J	50	GLY	2.2
20	R	60	GLY	2.2
15	M	10	MET	2.2
1	0	72	C	2.2
1	0	360	A	2.2
1	0	807	A	2.2
1	0	1080	C	2.2
1	0	1661	A	2.2
1	0	1747	A	2.2
1	0	2334	C	2.2
1	0	2575	C	2.2
10	H	50	VAL	2.2
26	X	190	VAL	2.2
9	G	12	ILE	2.2
4	B	80	ARG	2.2
9	G	72	ASP	2.2
12	J	99	ASP	2.2
13	K	118	LEU	2.2
1	0	115	U	2.2
1	0	954	U	2.2
1	0	1677	U	2.2
1	0	2277	U	2.2
13	K	54	PRO	2.2
16	N	16	SER	2.2
3	A	5	GLN	2.2
10	H	79	ALA	2.2
21	S	44	ALA	2.2
1	0	634	G	2.2
1	0	642	G	2.2
1	0	678	G	2.2
1	0	1059	G	2.2
1	0	1848	G	2.2
1	0	2044	G	2.2
1	0	2051	G	2.2
1	0	2466	G	2.2
14	L	39	ARG	2.2
14	L	50	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
25	W	73	ARG	2.2
1	0	423	A	2.2
1	0	447	A	2.2
1	0	519	A	2.2
1	0	590	A	2.2
1	0	766	A	2.2
1	0	1274	A	2.2
1	0	1393	A	2.2
1	0	2376	C	2.2
1	0	2599	A	2.2
1	0	2677	A	2.2
1	0	2757	A	2.2
1	0	2905	A	2.2
7	E	28	SER	2.2
19	Q	5	SER	2.2
26	X	142	SER	2.2
1	0	701	U	2.2
1	0	1359	U	2.2
1	0	2278	U	2.2
5	C	67	GLN	2.2
10	H	8	ASN	2.2
5	C	69	HIS	2.2
15	M	62	HIS	2.2
4	B	45	LYS	2.2
5	C	93	LYS	2.2
10	H	11	LYS	2.2
11	I	37	ALA	2.2
4	B	248	ARG	2.2
14	L	82	ARG	2.2
16	N	69	VAL	2.2
21	S	71	VAL	2.2
26	X	138	ARG	2.2
12	J	92	ASP	2.2
23	U	53	ILE	2.2
1	0	314	G	2.2
1	0	892	G	2.2
1	0	944	G	2.2
1	0	952	G	2.2
1	0	1052	G	2.2
1	0	1099	G	2.2
1	0	1119	G	2.2
1	0	1322	G	2.2

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Mol	Chain	Res	Type	RSRZ
15	M	72	GLU	2.2
30	2	41	GLU	2.2
1	0	1129	C	2.2
1	0	2315	C	2.2
2	9	3010	C	2.2
11	I	113	GLY	2.2
1	0	580	A	2.2
1	0	635	A	2.2
1	0	923	A	2.2
1	0	1032	A	2.2
1	0	1308	A	2.2
1	0	1330	A	2.2
1	0	1358	A	2.2
1	0	2474	A	2.2
1	0	313	U	2.2
1	0	675	U	2.2
1	0	785	U	2.2
1	0	1001	U	2.2
18	P	88	ALA	2.2
5	C	167	ASP	2.2
24	V	64	THR	2.2
5	C	174	ILE	2.2
10	H	133	ILE	2.2
11	I	42	GLU	2.2
7	E	91	PHE	2.2
10	H	155	PRO	2.2
12	J	39	GLY	2.2
12	J	106	GLY	2.2
24	V	54	PHE	2.2
17	O	55	LYS	2.2
1	0	388	G	2.2
1	0	717	C	2.2
1	0	765	G	2.2
1	0	906	C	2.2
1	0	1015	C	2.2
1	0	1324	G	2.2
1	0	1431	C	2.2
1	0	1565	C	2.2
1	0	2000	G	2.2
1	0	2082	G	2.2
1	0	2317	C	2.2
1	0	2385	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	0	2391	C	2.2
14	L	126	HIS	2.2
23	U	4	HIS	2.2
1	0	265	U	2.2
1	0	2386	U	2.2
1	0	407	A	2.2
1	0	639	A	2.2
1	0	776	A	2.2
1	0	907	A	2.2
1	0	1559	A	2.2
2	9	3047	A	2.2
4	B	99	GLU	2.2
4	B	126	GLU	2.2
5	C	124	VAL	2.2
15	M	103	ASP	2.2
24	V	44	MET	2.2
16	N	10	LEU	2.1
16	N	65	LEU	2.1
13	K	37	LYS	2.1
16	N	61	PRO	2.1
13	K	22	ARG	2.1
16	N	19	ARG	2.1
1	0	153	C	2.1
1	0	310	U	2.1
1	0	355	C	2.1
1	0	454	U	2.1
1	0	594	C	2.1
1	0	781	C	2.1
1	0	1347	U	2.1
1	0	1874	U	2.1
1	0	2313	C	2.1
1	0	2518	C	2.1
1	0	2724	U	2.1
5	C	23	GLU	2.1
24	V	60	GLU	2.1
1	0	149	G	2.1
1	0	1071	G	2.1
1	0	1258	G	2.1
1	0	1795	G	2.1
1	0	2058	G	2.1
2	9	3053	G	2.1
7	E	10	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
17	O	53	ASP	2.1
20	R	3	ASP	2.1
13	K	57	VAL	2.1
16	N	35	LYS	2.1
18	P	73	VAL	2.1
23	U	49	LEU	2.1
1	0	222	A	2.1
1	0	339	A	2.1
1	0	455	A	2.1
1	0	692	A	2.1
1	0	784	A	2.1
1	0	876	A	2.1
5	C	99	SER	2.1
15	M	85	GLY	2.1
14	L	35	PRO	2.1
17	O	131	PHE	2.1
24	V	25	ASN	2.1
3	A	22	ARG	2.1
6	D	11	HIS	2.1
8	F	57	GLU	2.1
12	J	70	GLU	2.1
16	N	40	HIS	2.1
13	K	104	ASP	2.1
20	R	44	GLN	2.1
25	W	69	LYS	2.1
27	Y	45	LYS	2.1
28	Z	11	LYS	2.1
28	Z	47	ASP	2.1
1	0	366	U	2.1
1	0	1791	U	2.1
2	9	3079	U	2.1
5	C	73	LEU	2.1
21	S	48	VAL	2.1
1	0	143	C	2.1
1	0	1395	C	2.1
1	0	1439	C	2.1
1	0	1876	C	2.1
1	0	2804	C	2.1
1	0	2833	C	2.1
3	A	123	GLY	2.1
1	0	544	G	2.1
1	0	969	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	1054	G	2.1
1	0	2324	G	2.1
1	0	2481	G	2.1
2	9	3109	G	2.1
5	C	127	ARG	2.1
15	M	172	PHE	2.1
1	0	227	A	2.1
1	0	629	A	2.1
1	0	1442	A	2.1
1	0	1501	A	2.1
1	0	2408	A	2.1
13	K	83	GLU	2.1
4	B	103	ASP	2.1
15	M	19	ASP	2.1
13	K	50	GLY	2.1
13	K	143	THR	2.1
14	L	83	SER	2.1
18	P	46	SER	2.1
1	0	134	U	2.1
1	0	1029	U	2.1
1	0	2581	U	2.1
19	Q	67	GLY	2.1
4	B	232	TRP	2.1
1	0	136	C	2.1
1	0	251	C	2.1
1	0	385	C	2.1
1	0	478	C	2.1
1	0	538	C	2.1
1	0	748	C	2.1
1	0	1004	C	2.1
1	0	1558	C	2.1
1	0	1602	C	2.1
1	0	1790	C	2.1
2	9	3096	C	2.1
3	A	61	GLU	2.1
6	D	82	GLU	2.1
7	E	130	GLU	2.1
24	V	134	GLU	2.1
28	Z	53	LYS	2.1
1	0	54	G	2.1
1	0	953	G	2.1
1	0	956	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	1063	G	2.1
1	0	1269	G	2.1
1	0	2314	G	2.1
1	0	2609	G	2.1
1	0	2617	G	2.1
1	0	2674	G	2.1
1	0	2860	G	2.1
1	0	1904	A	2.1
1	0	2902	A	2.1
17	O	135	ALA	2.1
4	B	137	LEU	2.1
5	C	205	ARG	2.1
14	L	125	ARG	2.1
7	E	152	THR	2.1
15	M	60	SER	2.1
26	X	154	ARG	2.1
30	2	58	GLY	2.1
12	J	30	LYS	2.1
1	0	493	U	2.1
1	0	624	U	2.1
1	0	649	U	2.1
1	0	779	U	2.1
1	0	967	U	2.1
3	A	81	GLN	2.1
1	0	574	C	2.1
1	0	668	C	2.1
2	9	3091	C	2.1
6	D	67	ASP	2.1
19	Q	68	HIS	2.1
4	B	111	ARG	2.1
1	0	289	G	2.1
1	0	745	G	2.1
1	0	1038	G	2.1
1	0	1100	G	2.1
1	0	1557	G	2.1
1	0	2279	G	2.1
7	E	24	GLY	2.1
6	D	12	GLU	2.1
14	L	30	GLU	2.1
1	0	16	A	2.1
1	0	473	A	2.1
1	0	1215	A	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	1331	A	2.1
1	0	2521	A	2.1
10	H	129	ASN	2.1
28	Z	15	THR	2.1
3	A	4	ILE	2.1
4	B	162	MET	2.1
12	J	53	ILE	2.1
14	L	97	ILE	2.1
19	Q	55	GLN	2.1
19	Q	111	ILE	2.1
1	0	210	U	2.1
1	0	1985	U	2.1
1	0	2523	U	2.1
2	9	3028	U	2.1
4	B	319	ASP	2.1
10	H	17	ARG	2.1
10	H	70	ARG	2.1
14	L	73	ARG	2.1
18	P	93	ARG	2.1
21	S	89	ARG	2.1
1	0	162	C	2.1
1	0	412	C	2.1
1	0	847	C	2.1
27	Y	36	LYS	2.1
18	P	79	GLY	2.1
1	0	636	G	2.1
1	0	722	G	2.1
1	0	1002	G	2.1
1	0	1211	G	2.1
1	0	1995	G	2.1
1	0	2338	G	2.1
2	9	3021	G	2.1
14	L	128	TRP	2.1
18	P	48	PRO	2.1
1	0	144	A	2.1
1	0	1007	A	2.1
1	0	2816	A	2.1
1	0	559	U	2.1
1	0	655	U	2.1
1	0	2807	U	2.1
12	J	84	ASP	2.1
13	K	11	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
15	M	44	ARG	2.1
19	Q	62	HIS	2.1
21	S	41	ARG	2.1
26	X	201	GLU	2.1
3	A	236	GLY	2.1
21	S	29	ALA	2.1
28	Z	43	ALA	2.1
19	Q	89	LEU	2.0
1	0	596	C	2.0
1	0	963	C	2.0
1	0	1238	C	2.0
1	0	2104	C	2.0
1	0	2704	C	2.0
5	C	206	ASN	2.0
7	E	122	THR	2.0
4	B	194	PHE	2.0
12	J	104	PRO	2.0
15	M	74	PRO	2.0
15	M	173	ASP	2.0
24	V	39	ASP	2.0
1	0	206	G	2.0
1	0	702	G	2.0
2	9	3075	G	2.0
2	9	3090	G	2.0
2	9	3097	U	2.0
1	0	442	A	2.0
1	0	449	A	2.0
1	0	1247	A	2.0
1	0	1348	A	2.0
15	M	121	GLY	2.0
18	P	89	ALA	2.0
24	V	90	TYR	2.0
27	Y	57	CYS	2.0
3	A	117	LYS	2.0
4	B	54	VAL	2.0
5	C	94	THR	2.0
16	N	58	VAL	2.0
18	P	23	THR	2.0
1	0	245	C	2.0
1	0	764	C	2.0
17	O	142	ASP	2.0
23	U	15	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
10	H	130	HIS	2.0
1	0	488	U	2.0
1	0	734	U	2.0
1	0	2078	U	2.0
1	0	2390	U	2.0
1	0	2424	U	2.0
1	0	2557	U	2.0
1	0	2563	U	2.0
2	9	3070	U	2.0
10	H	10	SER	2.0
11	I	25	GLN	2.0
16	N	67	SER	2.0
19	Q	30	ALA	2.0
26	X	110	SER	2.0
1	0	452	G	2.0
1	0	583	G	2.0
1	0	964	G	2.0
1	0	1048	G	2.0
1	0	1325	G	2.0
1	0	1364	G	2.0
1	0	2449	G	2.0
1	0	2543	G	2.0
1	0	2605	G	2.0
2	9	3086	G	2.0
1	0	174	A	2.0
1	0	395	A	2.0
1	0	1012	A	2.0
1	0	2852	A	2.0
2	9	3080	A	2.0
15	M	170	GLU	2.0
5	C	122	ASP	2.0
8	F	11	ASP	2.0
1	0	605	C	2.0
1	0	1010	C	2.0
1	0	1227	C	2.0
1	0	2510	C	2.0
4	B	135	GLY	2.0
4	B	177	HIS	2.0
13	K	13	HIS	2.0
13	K	34	GLY	2.0
26	X	101	GLY	2.0
30	2	75	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	0	1788	U	2.0
1	0	1915	U	2.0
1	0	2808	U	2.0
4	B	228	ALA	2.0
7	E	96	ASN	2.0
8	F	104	ALA	2.0
21	S	95	ASN	2.0
7	E	125	GLU	2.0
21	S	18	GLU	2.0
21	S	106	GLU	2.0
1	0	221	G	2.0
1	0	924	G	2.0
1	0	1425	G	2.0
1	0	1723	G	2.0
1	0	1730	G	2.0
5	C	225	PRO	2.0
1	0	194	A	2.0
1	0	520	A	2.0
1	0	1733	A	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	K	0	8056	1/1	0.29	2.09	54.47	88,88,88,88	0
33	NA	0	8064	1/1	-0.30	1.23	24.81	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	0	8075	1/1	0.35	0.96	22.55	63,63,63,63	0
33	NA	9	3202	1/1	0.00	1.04	21.40	93,93,93,93	0
33	NA	0	8057	1/1	0.56	0.84	19.62	46,46,46,46	0
33	NA	0	8072	1/1	0.10	0.84	19.23	61,61,61,61	0
31	MG	0	8028	1/1	0.34	0.97	10.08	48,48,48,48	0
31	MG	0	8033	1/1	0.42	0.72	9.77	62,62,62,62	0
33	NA	0	8070	1/1	0.56	0.65	8.94	69,69,69,69	0
31	MG	0	8047	1/1	0.30	0.63	7.61	49,49,49,49	0
31	MG	0	8003	1/1	0.43	0.56	7.47	43,43,43,43	0
31	MG	0	8043	1/1	0.34	0.67	6.75	63,63,63,63	0
35	SR	0	8141	1/1	0.38	0.59	6.59	160,160,160,160	0
35	SR	B	402	1/1	0.66	0.58	6.46	90,90,90,90	0
33	NA	0	8074	1/1	0.15	0.67	6.36	60,60,60,60	0
31	MG	0	8018	1/1	0.15	0.56	5.89	47,47,47,47	0
33	NA	Q	201	1/1	0.63	0.54	5.50	57,57,57,57	0
34	CL	N	201	1/1	0.36	0.65	5.39	74,74,74,74	0
31	MG	0	8024	1/1	0.72	0.44	5.23	20,20,20,20	0
31	MG	0	8009	1/1	0.57	0.55	5.21	35,35,35,35	0
33	NA	0	8061	1/1	0.40	0.56	5.16	56,56,56,56	0
31	MG	0	8034	1/1	0.37	0.69	4.80	60,60,60,60	0
31	MG	0	8012	1/1	0.15	0.51	4.63	53,53,53,53	0
31	MG	0	8053	1/1	0.58	0.63	4.38	52,52,52,52	0
31	MG	J	201	1/1	0.59	0.51	4.35	32,32,32,32	0
35	SR	0	8138	1/1	0.85	0.63	3.92	137,137,137,137	0
36	EMK	0	8163	74/74	0.68	0.50	3.81	40,48,59,62	0
33	NA	0	8067	1/1	0.48	0.57	3.73	57,57,57,57	0
31	MG	0	8001	1/1	0.24	0.45	3.60	27,27,27,27	0
31	MG	0	8032	1/1	0.68	0.36	3.49	46,46,46,46	0
33	NA	L	201	1/1	0.34	0.78	3.22	62,62,62,62	0
33	NA	I	201	1/1	0.29	0.60	3.09	54,54,54,54	0
31	MG	0	8021	1/1	0.70	0.63	2.84	42,42,42,42	0
31	MG	0	8037	1/1	0.66	0.55	2.26	58,58,58,58	0
31	MG	0	8011	1/1	0.74	0.33	2.23	40,40,40,40	0
33	NA	0	8062	1/1	0.52	0.57	2.07	39,39,39,39	0
33	NA	0	8059	1/1	0.34	0.42	1.99	39,39,39,39	0
31	MG	0	8038	1/1	0.43	0.41	1.63	54,54,54,54	0
34	CL	I	203	1/1	0.76	0.51	1.53	62,62,62,62	0
33	NA	0	8073	1/1	0.57	0.58	1.51	54,54,54,54	0
31	MG	0	8052	1/1	0.54	0.37	1.36	56,56,56,56	0
31	MG	0	8013	1/1	0.64	0.36	1.35	34,34,34,34	0
33	NA	P	101	1/1	0.28	0.54	1.32	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	Q	202	1/1	0.85	0.41	1.24	66,66,66,66	0
34	CL	L	202	1/1	0.74	0.61	1.21	51,51,51,51	0
33	NA	C	301	1/1	0.39	0.47	1.08	35,35,35,35	0
31	MG	X	301	1/1	0.53	0.45	1.06	39,39,39,39	0
31	MG	0	8040	1/1	0.88	0.35	0.84	21,21,21,21	0
35	SR	0	8147	1/1	0.24	0.35	0.81	105,105,105,105	0
35	SR	A	305	1/1	-0.21	0.44	0.64	133,133,133,133	0
31	MG	0	8008	1/1	0.91	0.36	0.57	35,35,35,35	0
33	NA	0	8069	1/1	0.48	0.34	0.50	37,37,37,37	0
35	SR	0	8132	1/1	0.08	0.28	0.26	100,100,100,100	0
31	MG	0	8017	1/1	0.44	0.36	0.17	36,36,36,36	0
34	CL	0	8076	1/1	0.54	0.37	-0.15	58,58,58,58	0
35	SR	0	8154	1/1	0.77	0.30	-0.16	147,147,147,147	0
35	SR	0	8162	1/1	0.26	0.28	-0.30	103,103,103,103	0
31	MG	0	8010	1/1	0.61	0.34	-0.33	42,42,42,42	0
31	MG	K	201	1/1	0.71	0.29	-0.37	3,3,3,3	0
33	NA	0	8066	1/1	0.63	0.33	-0.65	42,42,42,42	0
31	MG	0	8044	1/1	0.57	0.30	-0.65	51,51,51,51	0
31	MG	0	8004	1/1	0.80	0.25	-0.91	38,38,38,38	0
37	CD	2	101	1/1	0.61	0.13	-1.13	87,87,87,87	0
37	CD	T	8701	1/1	0.22	0.20	-1.16	118,118,118,118	0
35	SR	0	8119	1/1	0.83	0.25	-1.48	106,106,106,106	0
35	SR	F	201	1/1	0.75	0.15	-1.61	102,102,102,102	0
31	MG	S	201	1/1	0.76	0.19	-1.71	59,59,59,59	0
35	SR	A	302	1/1	0.68	0.30	-2.13	86,86,86,86	0
35	SR	A	303	1/1	0.09	0.19	-2.15	89,89,89,89	0
31	MG	0	8039	1/1	0.78	0.19	-2.15	36,36,36,36	0
35	SR	0	8148	1/1	0.13	0.26	-2.19	132,132,132,132	0
35	SR	0	8082	1/1	0.51	0.15	-2.27	64,64,64,64	0
37	CD	Y	101	1/1	0.25	0.14	-2.34	112,112,112,112	0
37	CD	Z	101	1/1	0.77	0.20	-2.45	141,141,141,141	0
35	SR	2	102	1/1	0.92	0.14	-2.50	67,67,67,67	0
35	SR	0	8083	1/1	0.82	0.13	-3.05	46,46,46,46	0
35	SR	0	8108	1/1	0.54	0.14	-3.17	63,63,63,63	0
35	SR	0	8115	1/1	0.57	0.16	-3.22	101,101,101,101	0
31	MG	0	8006	1/1	0.86	0.14	-3.30	26,26,26,26	0
35	SR	Q	204	1/1	0.83	0.11	-3.31	70,70,70,70	0
35	SR	0	8097	1/1	0.81	0.20	-3.44	85,85,85,85	0
35	SR	0	8120	1/1	0.46	0.13	-3.69	82,82,82,82	0
35	SR	0	8107	1/1	0.86	0.13	-3.75	62,62,62,62	0
35	SR	0	8153	1/1	0.38	0.17	-4.05	130,130,130,130	0
35	SR	0	8136	1/1	0.75	0.13	-4.07	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	SR	Z	102	1/1	0.92	0.10	-4.15	56,56,56,56	0
35	SR	0	8121	1/1	0.56	0.15	-6.01	79,79,79,79	0
35	SR	0	8117	1/1	0.78	0.19	-6.11	104,104,104,104	0
35	SR	0	8088	1/1	0.82	0.12	-6.63	62,62,62,62	0
35	SR	0	8084	1/1	0.81	0.11	-	49,49,49,49	0
35	SR	0	8152	1/1	0.68	0.17	-	89,89,89,89	0
35	SR	0	8093	1/1	0.54	0.13	-	57,57,57,57	0
33	NA	0	8068	1/1	0.27	0.76	-	42,42,42,42	0
35	SR	0	8159	1/1	0.56	0.24	-	118,118,118,118	0
31	MG	0	8045	1/1	-0.52	1.51	-	75,75,75,75	0
35	SR	0	8150	1/1	0.13	0.34	-	128,128,128,128	0
31	MG	0	8055	1/1	0.61	0.42	-	45,45,45,45	0
35	SR	0	8127	1/1	0.68	0.38	-	96,96,96,96	0
35	SR	0	8089	1/1	0.73	0.13	-	69,69,69,69	0
35	SR	0	8103	1/1	0.59	0.22	-	84,84,84,84	0
34	CL	0	8077	1/1	0.92	0.34	-	55,55,55,55	0
35	SR	0	8126	1/1	0.41	0.17	-	118,118,118,118	0
31	MG	0	8029	1/1	-0.24	0.99	-	54,54,54,54	0
35	SR	0	8096	1/1	0.79	0.14	-	63,63,63,63	0
35	SR	0	8105	1/1	0.51	0.12	-	85,85,85,85	0
35	SR	0	8098	1/1	0.44	0.21	-	71,71,71,71	0
31	MG	0	8002	1/1	-0.40	1.42	-	57,57,57,57	0
31	MG	0	8022	1/1	0.32	0.39	-	43,43,43,43	0
34	CL	D	201	1/1	0.39	0.50	-	49,49,49,49	0
35	SR	0	8128	1/1	0.58	0.15	-	92,92,92,92	0
35	SR	0	8145	1/1	0.56	0.32	-	126,126,126,126	0
35	SR	0	8104	1/1	0.77	0.18	-	77,77,77,77	0
35	SR	0	8114	1/1	0.58	0.19	-	101,101,101,101	0
35	SR	0	8151	1/1	0.57	0.25	-	122,122,122,122	0
33	NA	0	8058	1/1	0.65	0.37	-	62,62,62,62	0
35	SR	0	8095	1/1	0.35	0.16	-	92,92,92,92	0
31	MG	0	8030	1/1	0.39	0.28	-	49,49,49,49	0
31	MG	0	8025	1/1	0.27	0.61	-	56,56,56,56	0
35	SR	0	8133	1/1	0.04	0.52	-	102,102,102,102	0
31	MG	0	8005	1/1	0.77	0.31	-	32,32,32,32	0
35	SR	0	8158	1/1	-0.15	1.00	-	128,128,128,128	0
35	SR	0	8137	1/1	-0.29	0.54	-	151,151,151,151	0
35	SR	0	8122	1/1	0.58	0.23	-	113,113,113,113	0
35	SR	0	8116	1/1	0.69	0.42	-	117,117,117,117	0
31	MG	0	8050	1/1	0.52	0.63	-	78,78,78,78	0
33	NA	0	8065	1/1	-0.17	2.31	-	48,48,48,48	0
31	MG	0	8023	1/1	0.39	0.69	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	SR	0	8125	1/1	0.65	0.35	-	105,105,105,105	0
35	SR	0	8155	1/1	0.52	0.26	-	135,135,135,135	0
35	SR	0	8092	1/1	0.66	0.12	-	75,75,75,75	0
31	MG	0	8015	1/1	0.75	0.46	-	39,39,39,39	0
35	SR	0	8101	1/1	0.90	0.10	-	75,75,75,75	0
35	SR	0	8091	1/1	0.81	0.08	-	81,81,81,81	0
31	MG	0	8048	1/1	0.71	0.59	-	38,38,38,38	0
31	MG	0	8054	1/1	0.32	1.02	-	53,53,53,53	0
31	MG	0	8049	1/1	0.63	0.38	-	51,51,51,51	0
35	SR	0	8099	1/1	0.52	0.17	-	94,94,94,94	0
35	SR	0	8157	1/1	-0.05	1.09	-	125,125,125,125	0
35	SR	B	403	1/1	0.85	0.17	-	106,106,106,106	0
34	CL	I	202	1/1	0.28	0.33	-	58,58,58,58	0
35	SR	A	304	1/1	0.20	0.20	-	95,95,95,95	0
35	SR	0	8129	1/1	0.29	0.20	-	107,107,107,107	0
33	NA	0	8060	1/1	-0.18	0.94	-	46,46,46,46	0
31	MG	B	401	1/1	-0.61	1.23	-	66,66,66,66	0
35	SR	9	3203	1/1	0.07	0.62	-	110,110,110,110	0
35	SR	0	8130	1/1	0.69	0.32	-	106,106,106,106	0
31	MG	0	8007	1/1	0.66	0.32	-	28,28,28,28	0
35	SR	0	8124	1/1	0.24	0.23	-	84,84,84,84	0
31	MG	0	8026	1/1	0.70	0.66	-	56,56,56,56	0
34	CL	A	301	1/1	0.27	0.78	-	74,74,74,74	0
35	SR	9	3205	1/1	-0.41	0.44	-	141,141,141,141	0
31	MG	0	8041	1/1	0.63	0.40	-	52,52,52,52	0
35	SR	0	8142	1/1	-0.13	0.70	-	138,138,138,138	0
35	SR	0	8161	1/1	0.52	0.92	-	137,137,137,137	0
35	SR	0	8144	1/1	0.34	0.23	-	126,126,126,126	0
35	SR	0	8087	1/1	0.81	0.17	-	77,77,77,77	0
35	SR	0	8113	1/1	0.62	0.27	-	75,75,75,75	0
35	SR	R	101	1/1	0.02	0.43	-	119,119,119,119	0
34	CL	Q	203	1/1	0.81	0.72	-	55,55,55,55	0
31	MG	0	8014	1/1	0.49	0.62	-	50,50,50,50	0
35	SR	0	8140	1/1	0.53	0.49	-	108,108,108,108	0
33	NA	0	8071	1/1	0.60	0.40	-	51,51,51,51	0
31	MG	0	8031	1/1	0.84	0.24	-	50,50,50,50	0
35	SR	0	8143	1/1	0.76	0.17	-	63,63,63,63	0
31	MG	0	8019	1/1	0.30	0.36	-	37,37,37,37	0
35	SR	0	8100	1/1	0.87	0.08	-	68,68,68,68	0
31	MG	9	3201	1/1	0.58	0.34	-	46,46,46,46	0
35	SR	0	8102	1/1	0.69	0.15	-	72,72,72,72	0
34	CL	0	8080	1/1	0.47	0.94	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	SR	0	8106	1/1	0.32	0.32	-	128,128,128,128	0
35	SR	0	8146	1/1	0.22	0.29	-	156,156,156,156	0
31	MG	0	8051	1/1	0.04	0.80	-	54,54,54,54	0
35	SR	0	8135	1/1	0.38	0.15	-	99,99,99,99	0
35	SR	0	8111	1/1	0.76	0.21	-	75,75,75,75	0
35	SR	0	8131	1/1	0.07	0.24	-	104,104,104,104	0
35	SR	0	8123	1/1	0.58	0.30	-	96,96,96,96	0
31	MG	0	8042	1/1	0.48	0.44	-	28,28,28,28	0
31	MG	0	8036	1/1	0.74	0.43	-	52,52,52,52	0
35	SR	0	8149	1/1	0.75	0.58	-	200,200,200,200	0
31	MG	0	8035	1/1	0.08	0.60	-	85,85,85,85	0
34	CL	X	302	1/1	0.93	0.17	-	44,44,44,44	0
35	SR	0	8090	1/1	0.52	0.14	-	72,72,72,72	0
35	SR	0	8094	1/1	0.64	0.24	-	56,56,56,56	0
35	SR	0	8112	1/1	0.70	0.15	-	75,75,75,75	0
31	MG	0	8020	1/1	0.74	0.38	-	44,44,44,44	0
31	MG	0	8016	1/1	0.88	0.38	-	40,40,40,40	0
35	SR	2	103	1/1	0.48	0.27	-	74,74,74,74	0
35	SR	9	3204	1/1	-0.29	0.20	-	122,122,122,122	0
35	SR	0	8139	1/1	0.71	0.17	-	101,101,101,101	0
35	SR	0	8156	1/1	0.35	0.47	-	137,137,137,137	0
35	SR	Z	103	1/1	0.83	0.31	-	140,140,140,140	0
31	MG	0	8027	1/1	0.19	0.82	-	51,51,51,51	0
35	SR	0	8109	1/1	0.28	0.31	-	88,88,88,88	0
35	SR	0	8086	1/1	0.84	0.10	-	46,46,46,46	0
35	SR	0	8134	1/1	0.41	0.18	-	94,94,94,94	0
34	CL	0	8079	1/1	0.51	0.45	-	56,56,56,56	0
35	SR	0	8110	1/1	0.73	0.12	-	89,89,89,89	0
33	NA	0	8063	1/1	-0.03	0.91	-	48,48,48,48	0
34	CL	0	8078	1/1	0.87	0.99	-	63,63,63,63	0
35	SR	0	8160	1/1	0.90	0.08	-	59,59,59,59	0
31	MG	0	8046	1/1	0.47	0.42	-	47,47,47,47	0
35	SR	0	8081	1/1	0.16	0.21	-	91,91,91,91	0
35	SR	0	8118	1/1	0.57	0.33	-	96,96,96,96	0
35	SR	0	8085	1/1	0.45	0.16	-	50,50,50,50	0

6.5 Other polymers

There are no such residues in this entry.