Full wwPDB EM Validation Report (i)

May 17, 2025 – 11:39 PM EDT

PDB ID	:	8ETG / pdb_00008etg
EMDB ID	:	EMD-24397
Title	:	Fkbp39 associated 60S nascent ribosome State 3
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-17
Resolution	:	3.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

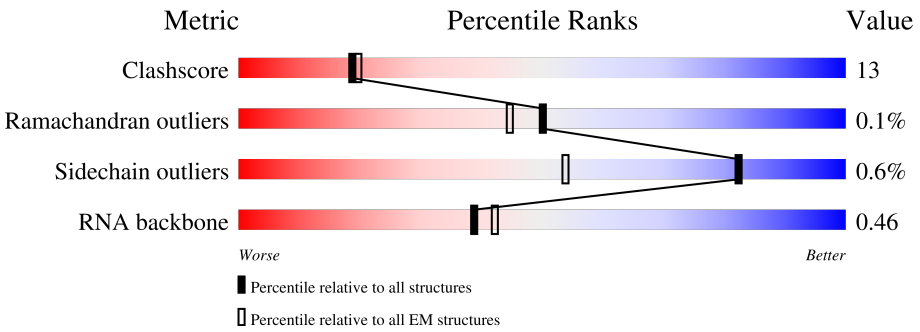
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	1	3497	17% 28% 23% 6% 42%
2	2	165	10% 55% 29% • 12%
3	3	302	11% 23% 17% 60%
4	A	295	31% 65% • 34%
5	B	388	23% 60% 27% 14%
6	C	363	11% 69% 29% •
7	D	578	7% 14% 86%

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Mol	Chain	Length	Quality of chain
8	E	195	18% 45% 29% 26%
9	F	250	58% 27% 14%
10	G	259	10% 55% 16% 29%
11	H	190	51% 51% 45%
12	K	373	46% 59% 38%
13	L	208	41% 15% 43%
14	M	134	13% 53% 38% 7%
15	N	201	63% 20% 17%
16	O	197	14% 69% 26% 5%
17	P	187	19% 38% 34% 27%
18	Q	187	6% 51% 18% 30%
19	R	193	30% 18% 12% 70%
20	S	176	32% 54% 44%
21	U	117	84% 82% 16%
22	V	139	92% 58% 35% 7%
23	W	241	80% 77% 20%
24	X	141	85% 64% 28% 8%
25	Y	126	6% 57% 42%
26	Z	136	95% 88% 7% 5%
27	a	148	52% 39% 24% 36%
28	b	642	50% 58% 41%
29	c	117	56% 53% 44%
30	d	113	83% 30% 51% 17%
31	e	127	60% 31% 8%
32	f	108	6% 75% 23%

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Mol	Chain	Length	Quality of chain
33	g	112	78% 76% 22%
34	h	122	11% 73% 26%
35	i	99	6% 55% 24% 21%
36	j	91	49% 29% 22%
37	k	74	95% 93% 5%
38	m	740	59% 55% 11% 35%
39	n	607	65% 47% 21% 31%
40	o	276	24% 20% 20% 61%
41	p	440	65% 53% 12% 35%
42	r	260	53% 45% 14% 41%
43	t	249	83% 65% 29% 6%
44	u	192	35% 51% 48%
45	v	209	15% 51% 16% 33%
46	y	244	80% 89% 8%
47	T	160	7% 8% 88%
48	6	300	6% 7% 10% 79%

2 Entry composition (i)

There are 49 unique types of molecules in this entry. The entry contains 99257 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (1912-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2018	43202	19298	7842	14044	2018	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	146	3102	1388	547	1021	146	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	120	1015	642	190	177	6	0	0

- Molecule 4 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	A	196	1015	610	201	204	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	334	2653	1682	491	471	9	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	359	2795	1765	536	491	3	0	0

- Molecule 7 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	D	82	408	244	82	82	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	145	1126	723	208	192	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	214	1745	1124	320	298	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	184	1452	934	262	254	2	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	183	1451	914	266	265	6	0	0

- Molecule 12 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	K	231	1145	683	231	231	0	0

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	118	962	603	204	154	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	M	124	1000	639	190	167	4	0	0

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	N	166	1406	883	291	229	3	0	0

- Molecule 16 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	O	187	1483	956	281	242	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	P	136	1080	690	196	191	3	0	0

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Q	130	1020	646	196	177	1	0	0

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	R	57	456	282	93	78	3	0	0

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	S	174	1434	925	269	235	5	0	0

- Molecule 21 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	U	98	484	288	98	98	0	0

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	129	976	617	179	172	8	0	0

- Molecule 23 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	W	193	948	562	193	193	0	0

- Molecule 24 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	130	1032	658	192	181	1	0	0

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Y	125	998	622	201	173	2	0	0

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	Z	129	637	378	129	130	0	0

- Molecule 27 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	a	94	747	474	142	131	0	0

- Molecule 28 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	b	378	1875	1119	378	378	0	0

- Molecule 29 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	c	66	325	193	66	66	0	0

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	d	94	787	500	156	128	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	e	117	939	588	190	156	5	0	0

- Molecule 32 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	106	839	534	162	140	3	0	0

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	g	87	428	254	87	87	0	0

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	h	121	999	629	194	176	0	0

- Molecule 35 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	i	78	637	394	135	107	1	0	0

- Molecule 36 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	j	71	563	346	121	90	6	0	0

- Molecule 37 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	k	70	349	209	70	70	0	0

- Molecule 38 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	m	484	2881	1757	557	566	1	0	0

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	n	416	3389	2186	587	604	12	0	0

- Molecule 40 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	o	109	897	579	162	150	6	0	0

- Molecule 41 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	p	287	1416	842	287	287	0	0

- Molecule 42 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	r	154	1009	613	208	187	1	0	0

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	t	235	1948	1242	367	334	5	0	0

- Molecule 44 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	u	99	491	293	99	99	0	0

- Molecule 45 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	v	140	1143	721	220	199	3	0	0

- Molecule 46 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
46	y	225	1107	657	225	225	0	0

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	T	19	147	93	26	28	0	0

- Molecule 48 is a RNA chain called RNA (62-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	6	62	1315	590	229	434	62	0	0

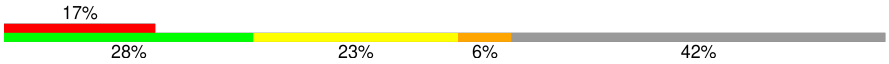
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

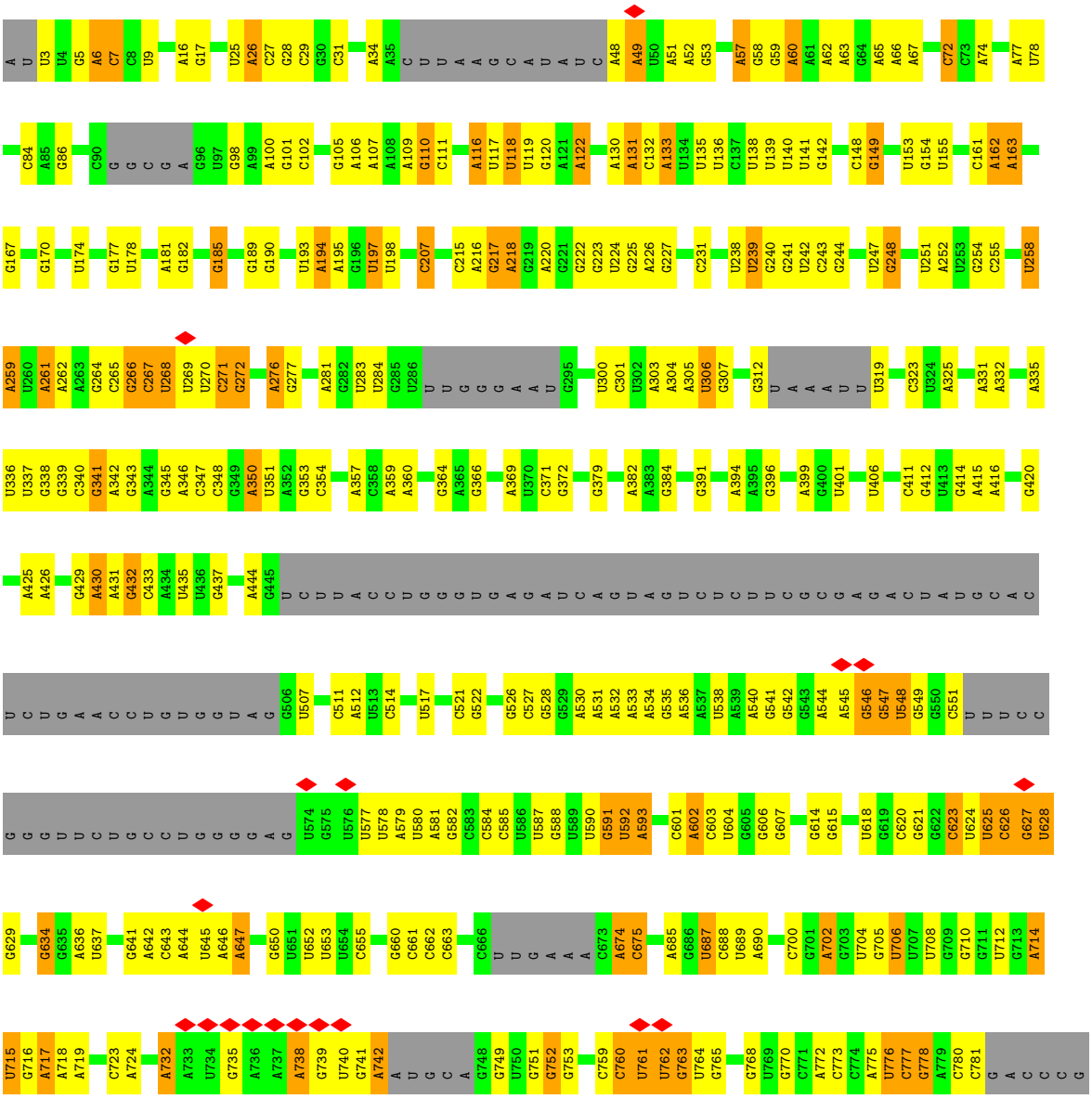
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
49	j	1	1	1	0

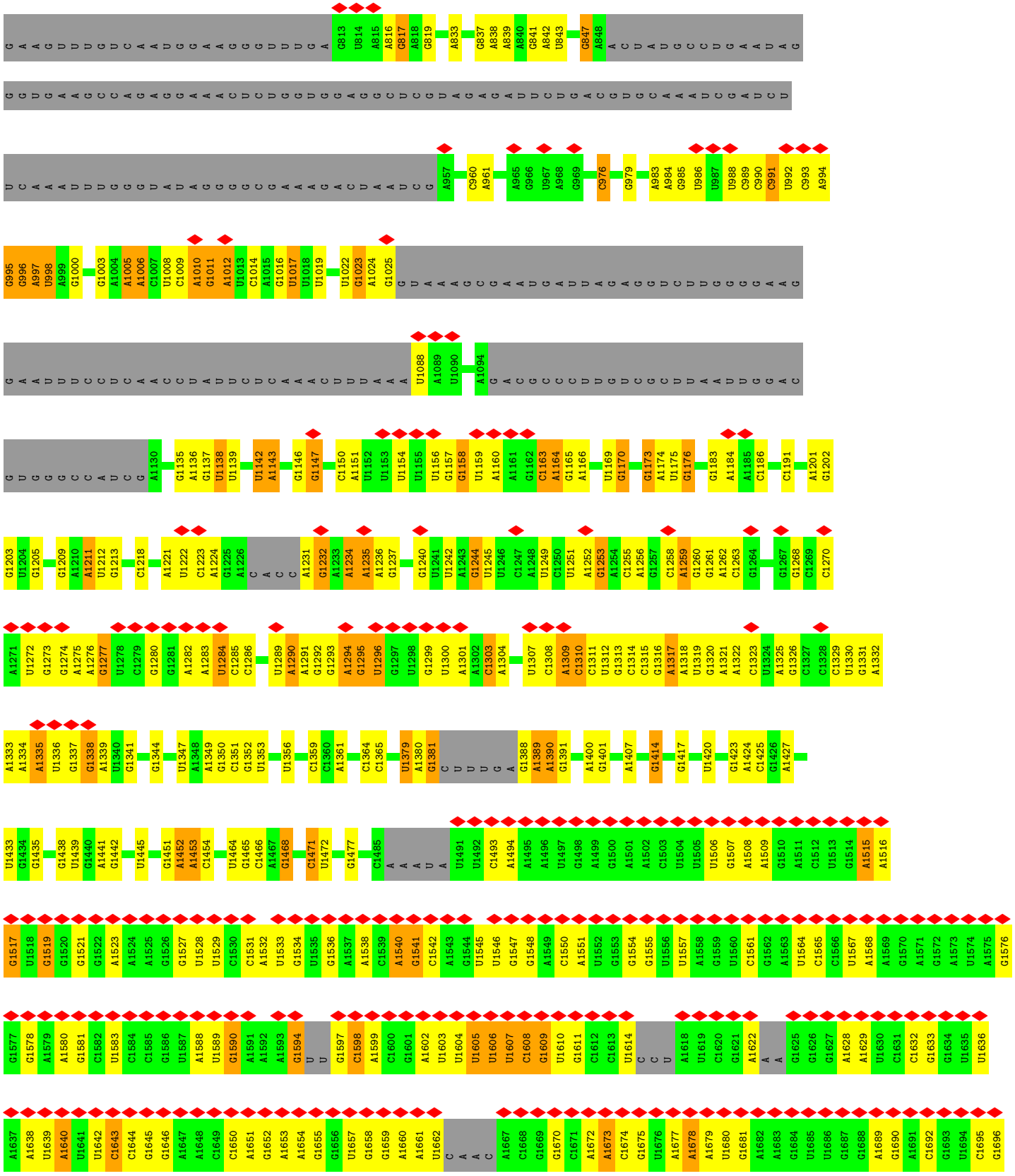
3 Residue-property plots (i)

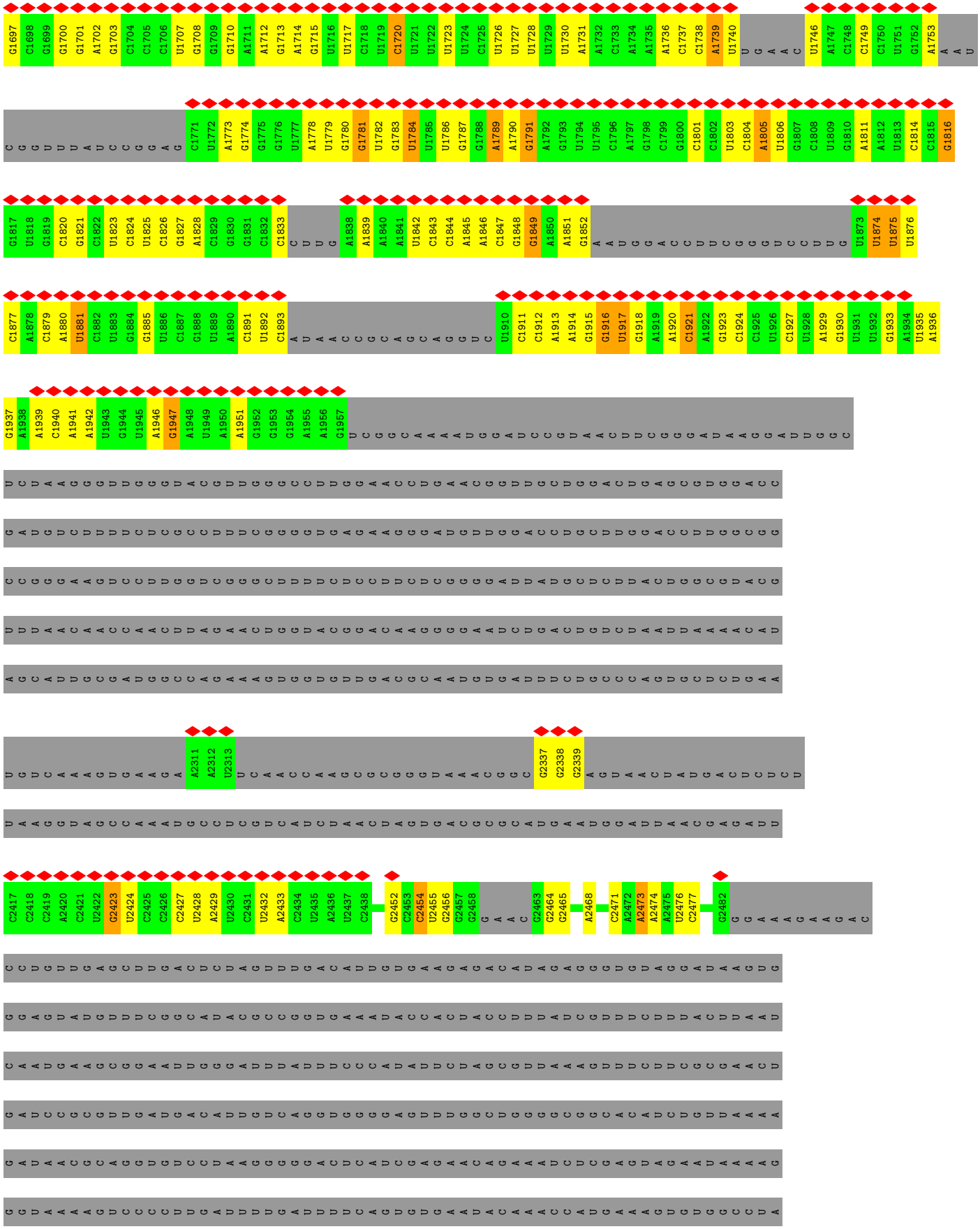
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: RNA (1912-MER)

Chain 1: 






G1697 C1698 G1699 G1700 G1701 A1702 G1703 C1704 C1705 C1706 U1707 G1708 G1709 G1710 A1711 A1712 G1713 A1714 G1715 U1716 U1717 C1718 U1719 C1720 U1721 U1722 U1723 U1724 C1725 U1726 U1727 U1728 U1729 U1730 A1731 A1732 C1733 A1734 A1735 A1736 C1737 C1738 A1739 U1740 U G A A C U1746 A1747 C1748 C1749 C1750 U1751 G1752 A1753 A A U
C G G U U A U C C G G A G C1771 U1772 A1773 G1774 G1775 G1776 U1777 A1778 U1779 G1780 G1781 U1782 G1783 U1784 U1785 U1786 G1787 G1788 A1789 A1790 G1791 A1792 G1793 U1794 U1795 C1796 A1797 G1798 C1799 G1800 C1801 C1802 U1803 C1804 A1805 U1806 G1807 C1808 U1809 G1810 A1811 A1812 U1813 C1814 C1815 G1816
G1817 U1818 G1819 C1820 G1821 C1822 U1823 C1824 U1825 C1826 G1827 A1828 C1829 G1830 G1831 C1832 C1833 C U U G A1838 A1839 A1840 A1841 U1842 C1843 C1844 A1845 A1846 C1847 G1848 G1849 A1850 A1851 G1852 A A U G G A C C U U C G G G U C C U U G U1873 U1874 U1875 U1876
C1877 A1878 C1879 A1880 U1881 C1882 U1883 G1884 G1885 U1886 C1887 G1888 U1889 A1890 C1891 U1892 C1893 A U A A C C G C A G C A G G U C U1910 C1911 C1912 A1913 A1914 G1915 G1916 U1917 G1918 A1919 A1920 C1921 A1922 G1923 C1924 C1925 U1926 C1927 U1928 A1929 G1930 U1931 U1932 G1933 A1934 U1935 A1936
G1937 A1938 A1939 C1940 A1941 A1942 U1943 G1944 U1945 A1946 G1947 A1948 U1949 A1950 A1951 G1952 G1953 G1954 A1955 A1956 G1957 U C G G C A A A A U G G A U C C G U A A C U U C G G G G A U A A G G A U U G G C
U C U A A G G G U U U G G G U A C G U U G G G C C U U G A A G G U U G G A C C
G A U G G U C U U U C U C G C C U U U C G G G G U G A G A A G G A U U G G A C C
C C U G G G G U U U U U C C U U G G C A A A C C U U G G C C U U U A A C U G G C G U A C G
U U U A A C A A C C A A C U G G U A C C U G A A G G G G A A U C U G A A A A C A U
A G C A U U G C G A U G G C C A G A A A G U G G U G G U G A C G G C A A U G U U C U G C U G A A
U G U C A A G A A A G A A2311 A2312 U2313 U C A A C C A A G C G C G G G U A A A C G G C A G2337 G2338 G2339 A G U A A C U A U G A C U C U U C U
U A A G U A G C C A A A U G C C U C G U C A U C U A A C U A U G C G C A U G A A A U G G A A U U A A A C G A G A U U
C2417 C2418 C2419 A2420 C2421 U2422 G2423 U2424 C2425 C2426 C2427 U2428 A2429 U2430 C2431 U2432 A2433 C2434 U2435 A2436 U2437 C2438 G2452 C2453 C2454 U2455 C2456 G2457 G2458 G A A C G2463 G2464 G2465 A2468 C2471 A2472 A2473 A2474 A2475 U2476 C2477 G2482 G G A A A G A A G A C
C C U G U U G A G C U U G A C U C U A A G U G U A U C A U U G U G A A G A C C A U A A G U G
G G A A G U A U G G U U U C G G C A U A C G U A C C U A C C U U U A A U C G U U U C U U U C G A C U
C A A U G A A G C G G A A U G G A U U U C C C A U A U U C U A G C G U U A A A G G C G A A C U
G A U C G C G C G U U G A U G C A C U G G G G A G U U G G G A C A U C U G G C G A A G U A A A A
G A U A A C G C A G G U G U C C U A G G G G A A A C A G A A A U C U G A G A A A U G A G A A A A G
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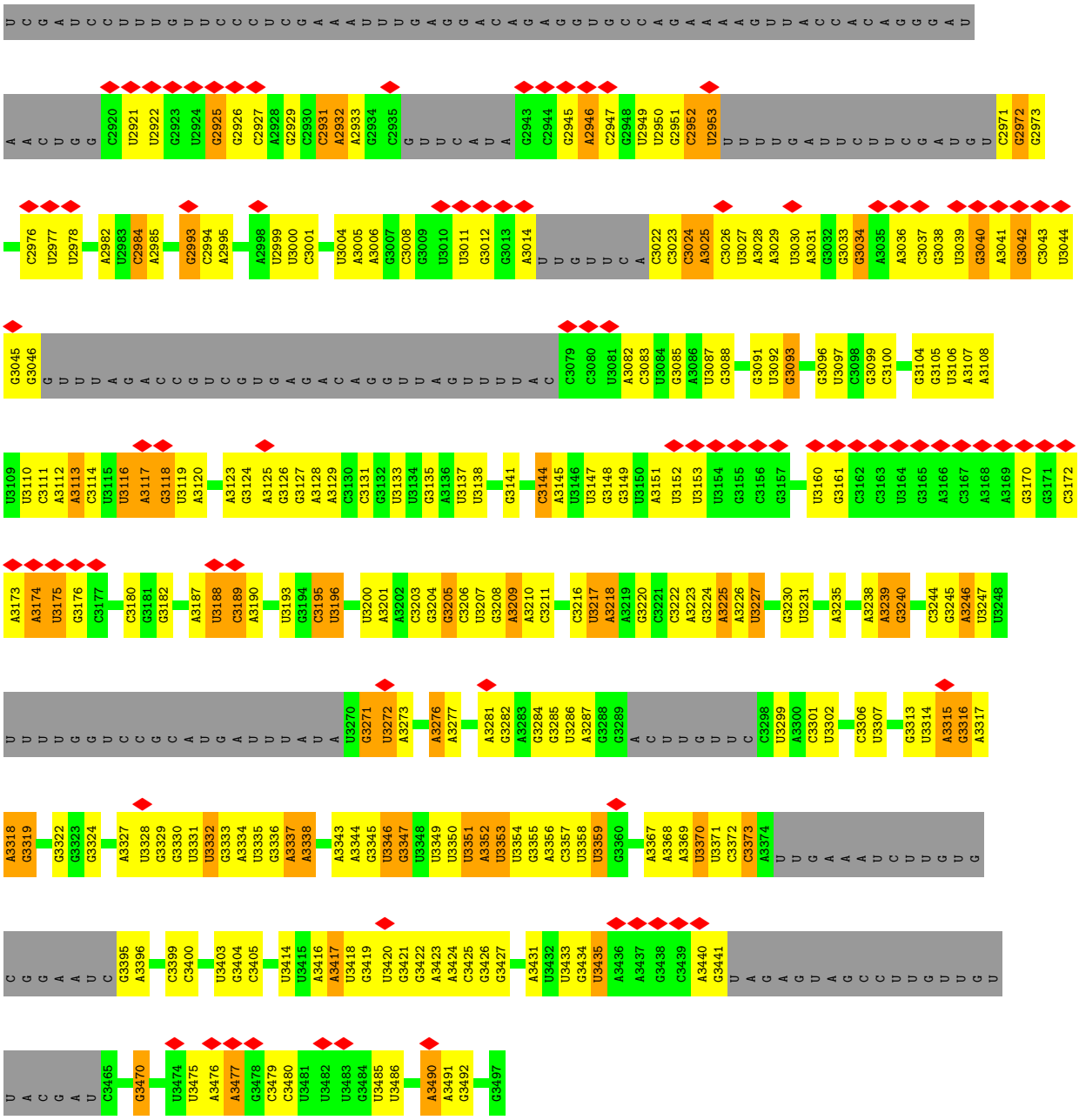
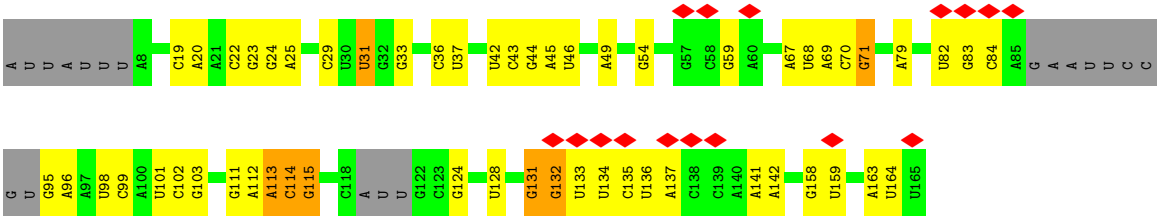


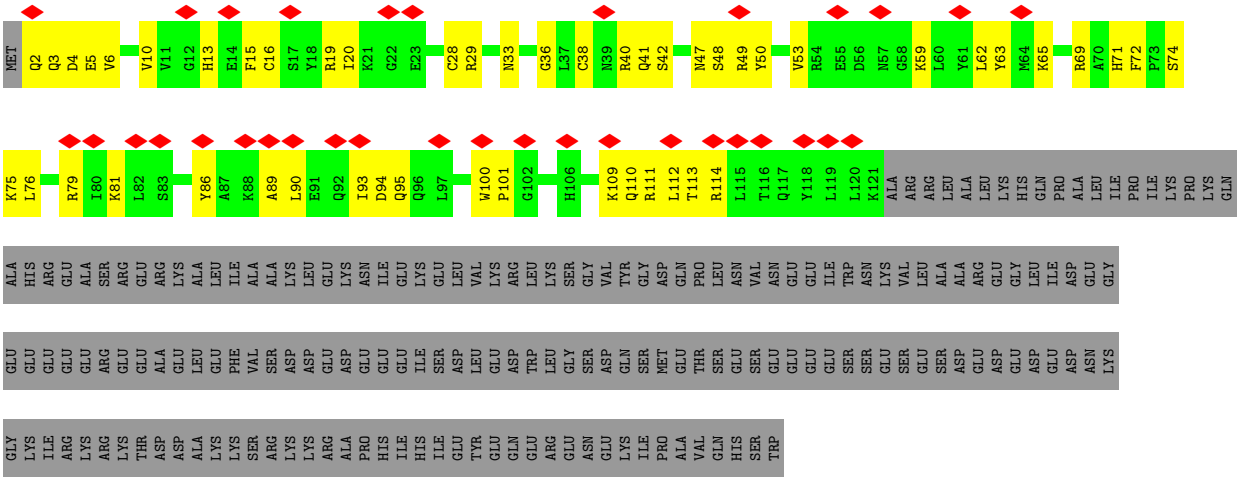
• Molecule 2: RNA (146-MER)

Chain 2:



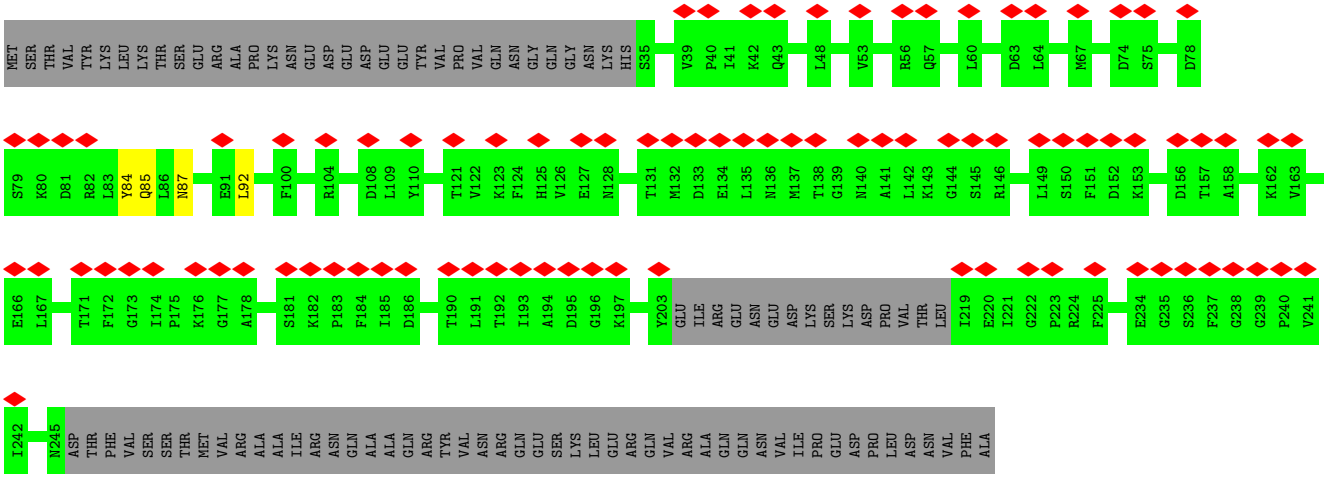
• Molecule 3: Protein mak16

Chain 3:



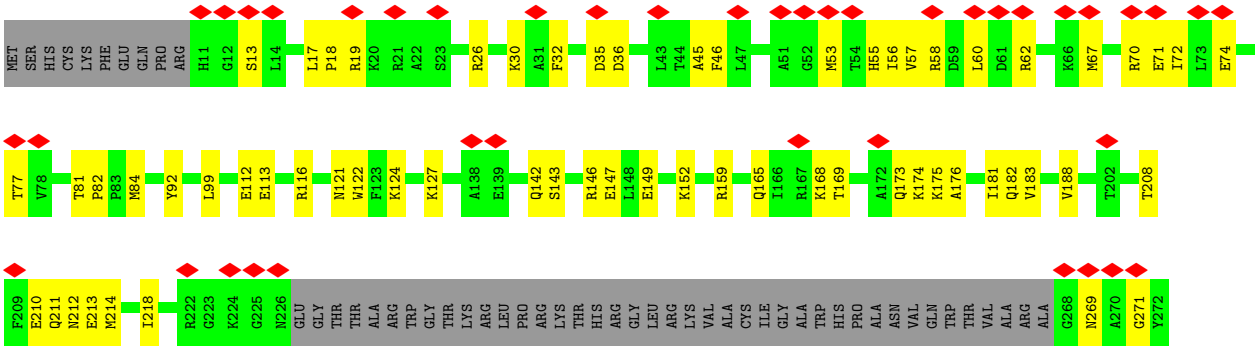
- Molecule 4: Ribosome biogenesis protein brx1

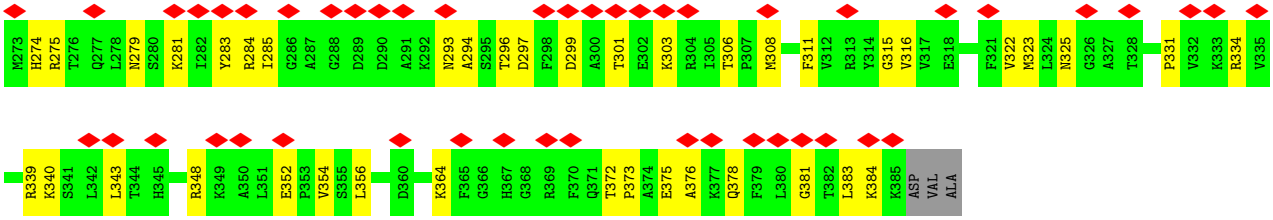
Chain A:



- Molecule 5: 60S ribosomal protein L3-A

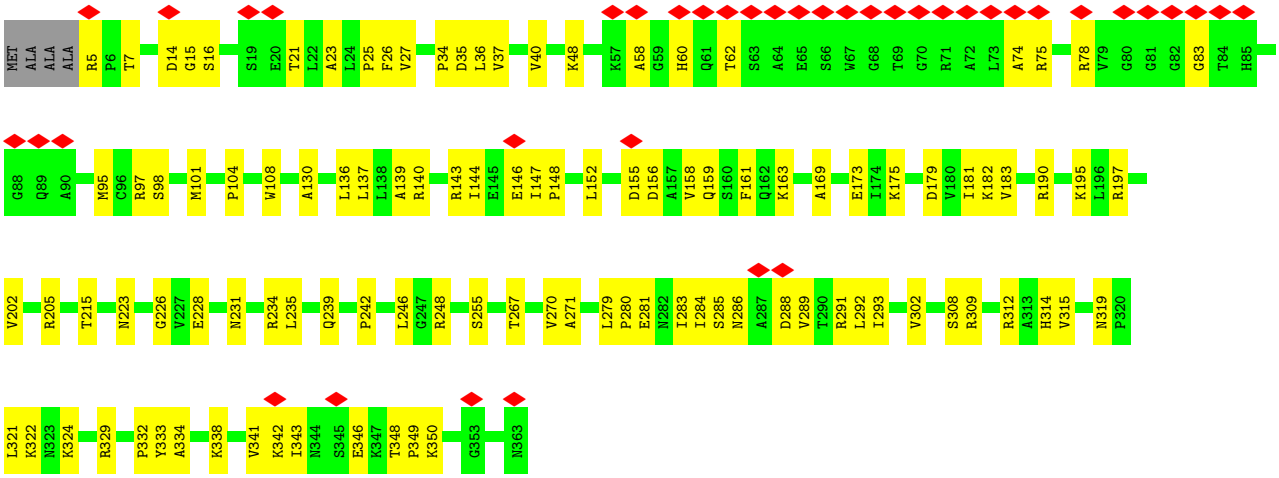
Chain B:





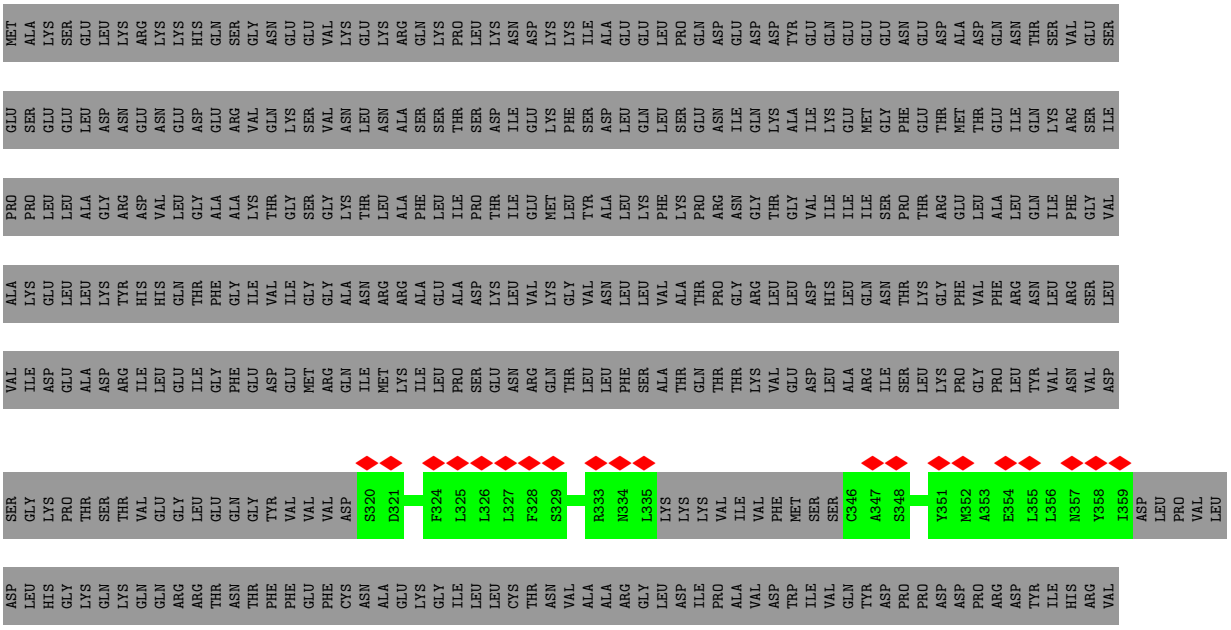
• Molecule 6: 60S ribosomal protein L4-B

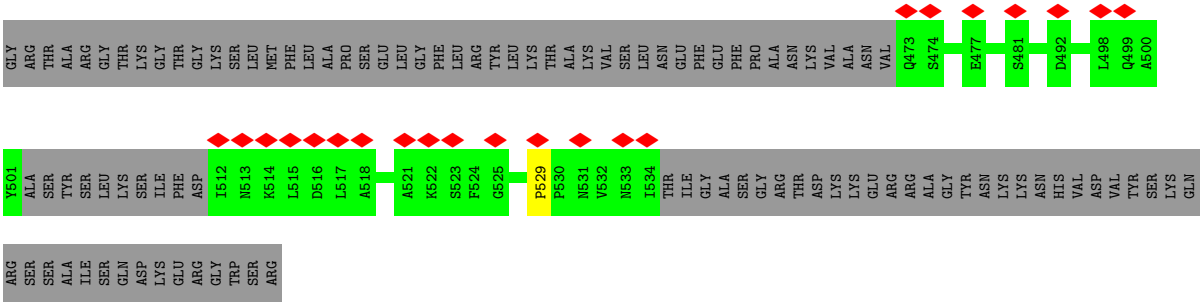
Chain C:



• Molecule 7: ATP-dependent RNA helicase has1

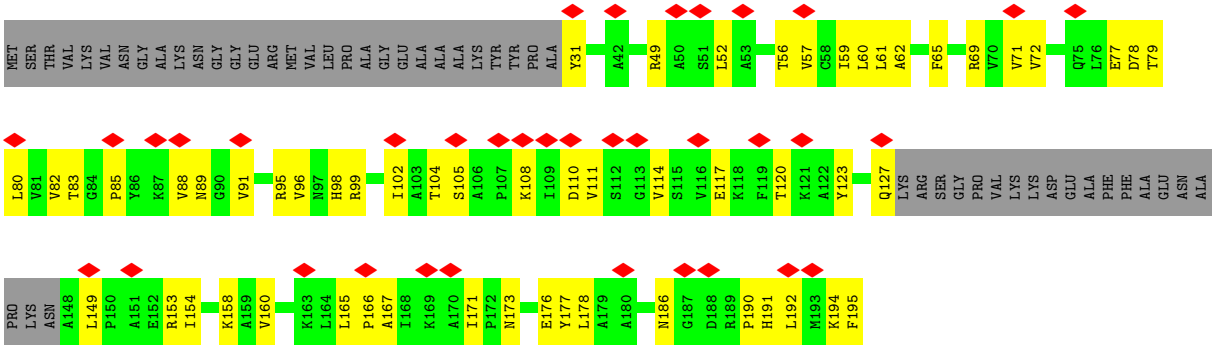
Chain D:





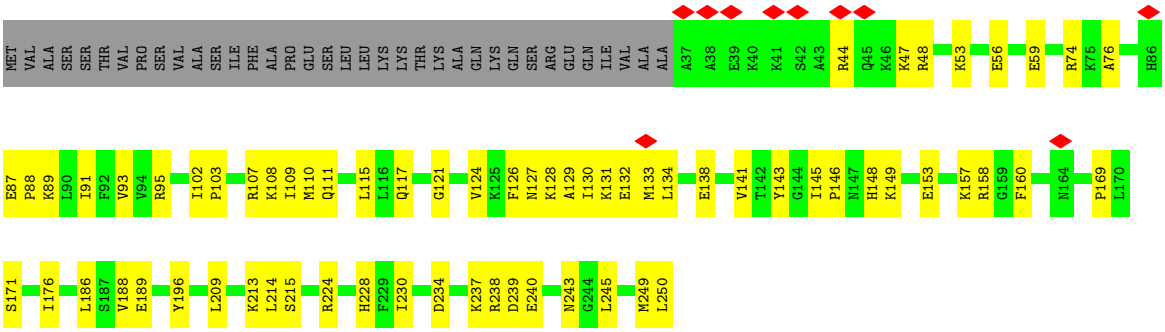
- Molecule 8: 60S ribosomal protein L6

Chain E:



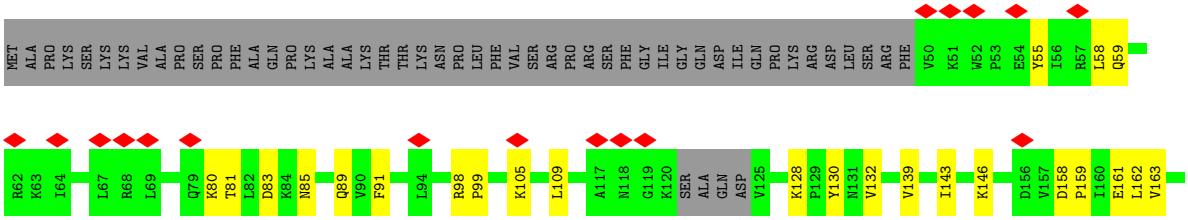
- Molecule 9: 60S ribosomal protein L7-B

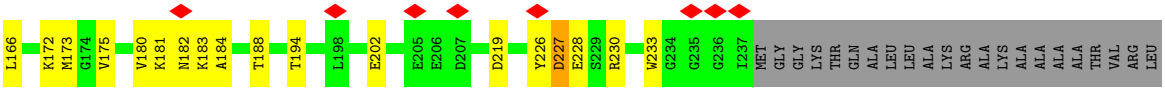
Chain F:



- Molecule 10: 60S ribosomal protein L8

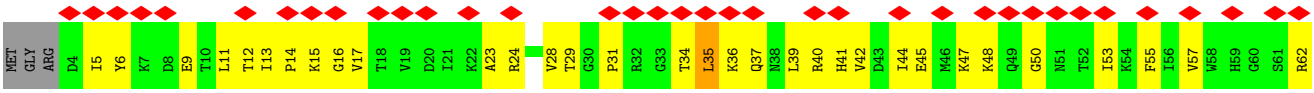
Chain G:

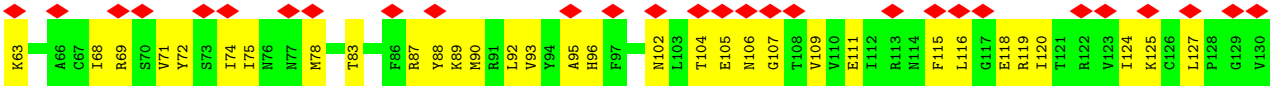


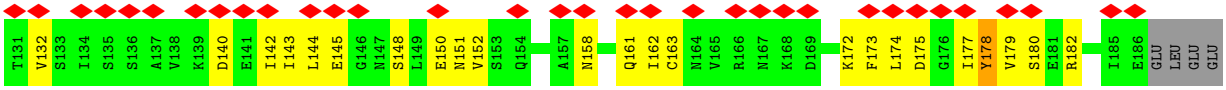


- Molecule 11: 60S ribosomal protein L9-A

Chain H:

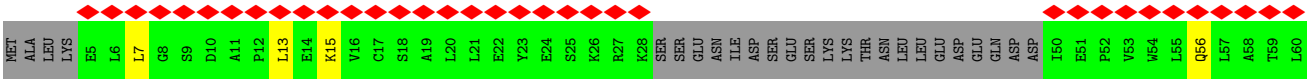


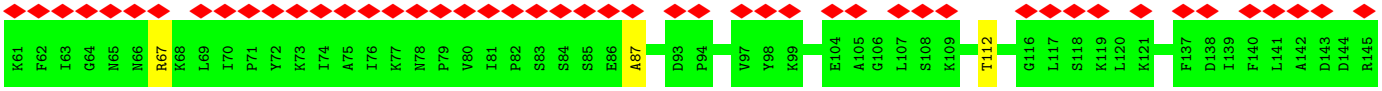


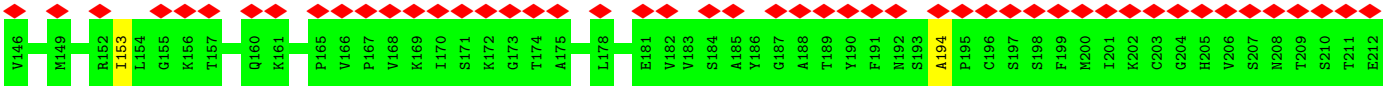


- Molecule 12: Putative ribosome biogenesis protein C8F11.04

Chain K:

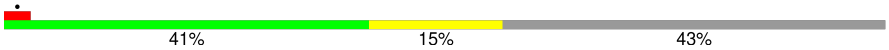


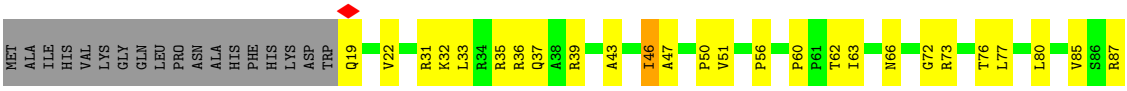


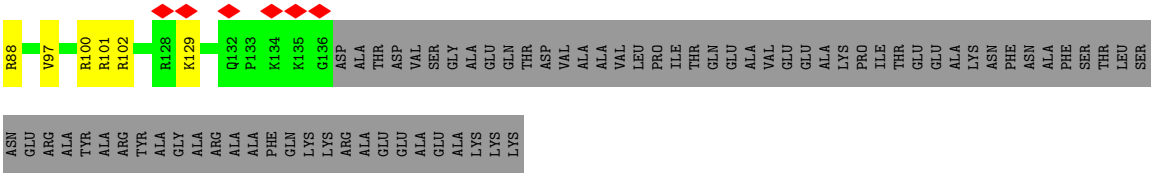


- Molecule 13: 60S ribosomal protein L13

Chain L:

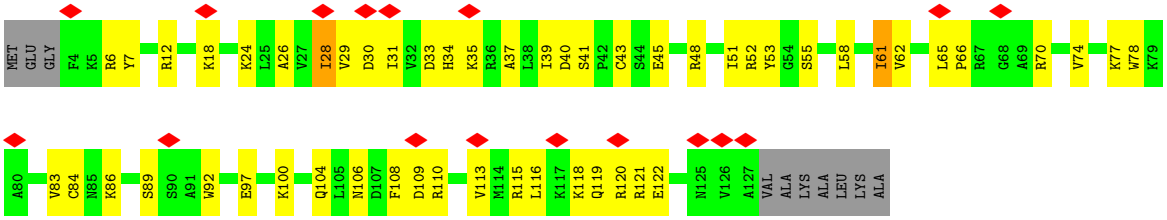






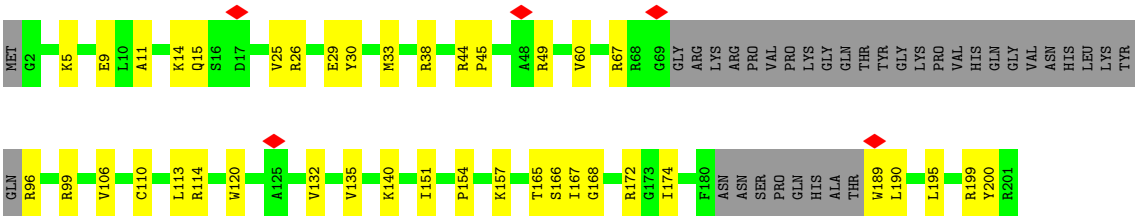
- Molecule 14: 60S ribosomal protein L14

Chain M:



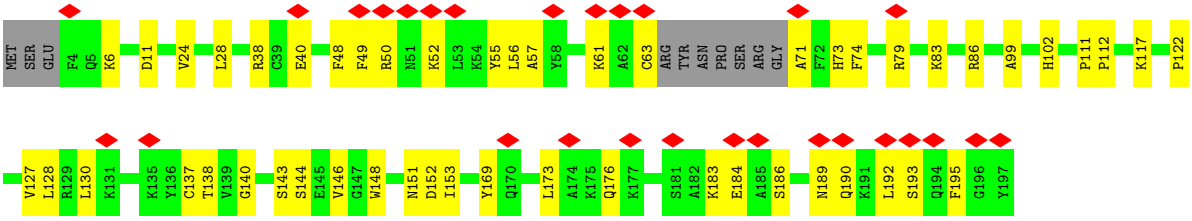
- Molecule 15: 60S ribosomal protein L15-A

Chain N:



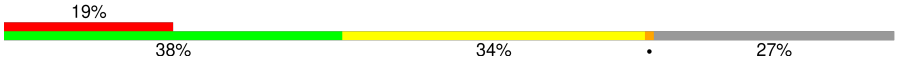
- Molecule 16: 60S ribosomal protein L16-B

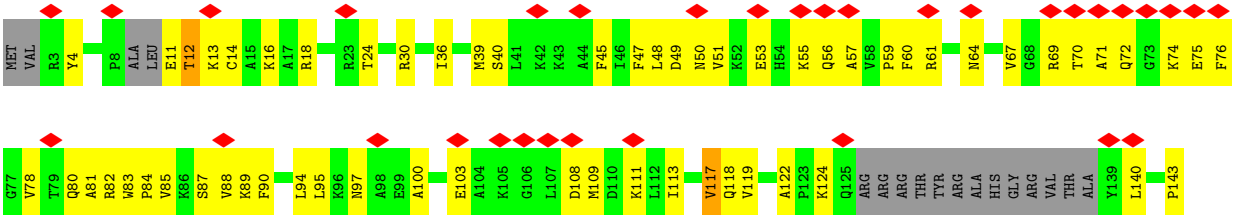
Chain O:

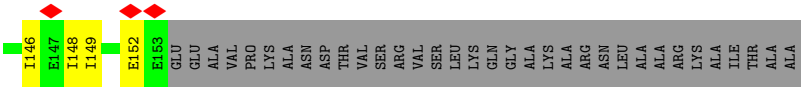


- Molecule 17: 60S ribosomal protein L17-A

Chain P:

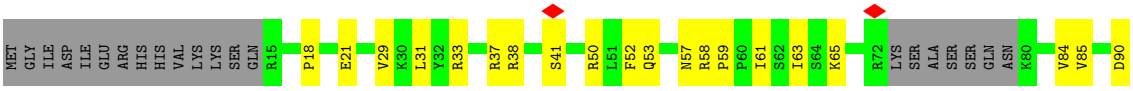


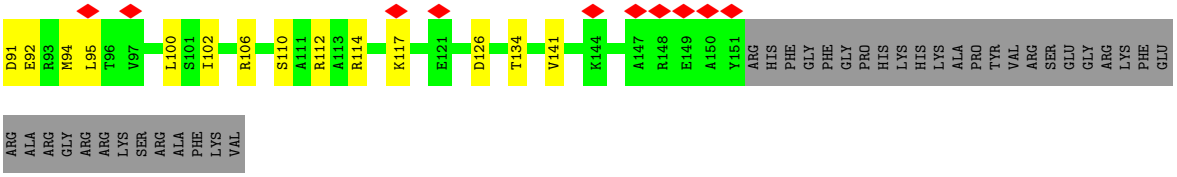




- Molecule 18: 60S ribosomal protein L18-A

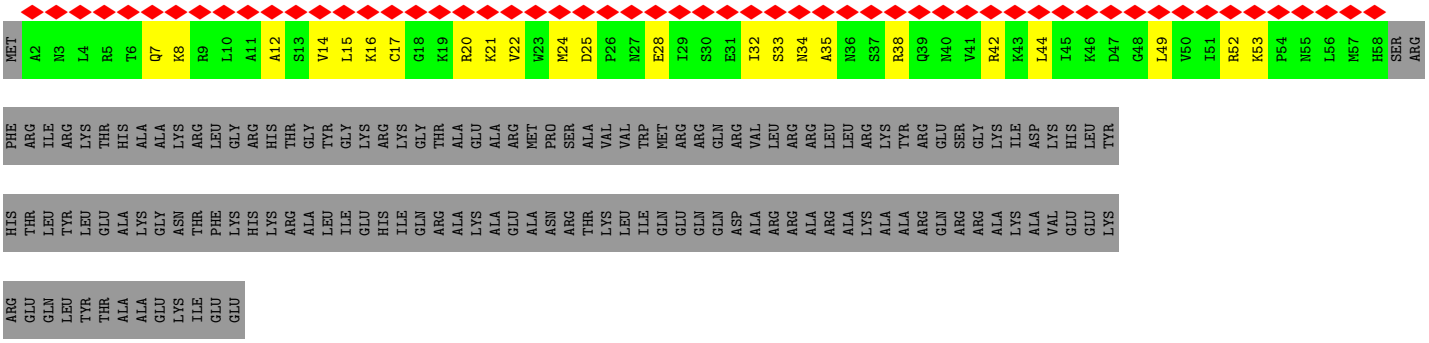
Chain Q:





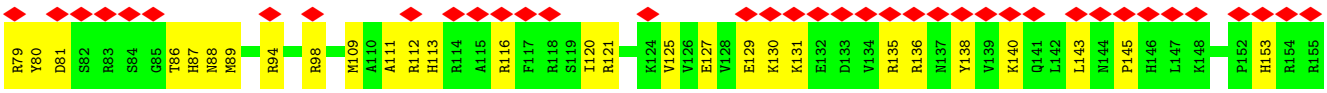
- Molecule 19: 60S ribosomal protein L19-A

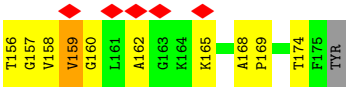
Chain R:



- Molecule 20: 60S ribosomal protein L20-A

Chain S:



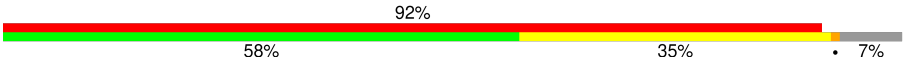


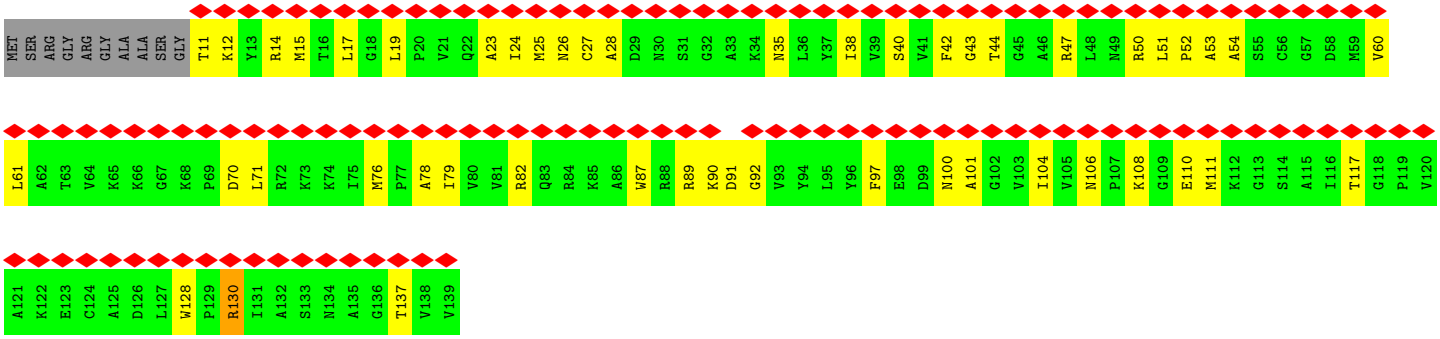
- Molecule 21: 60S ribosomal protein L22

Chain U:

- Molecule 22: 60S ribosomal protein L23-A

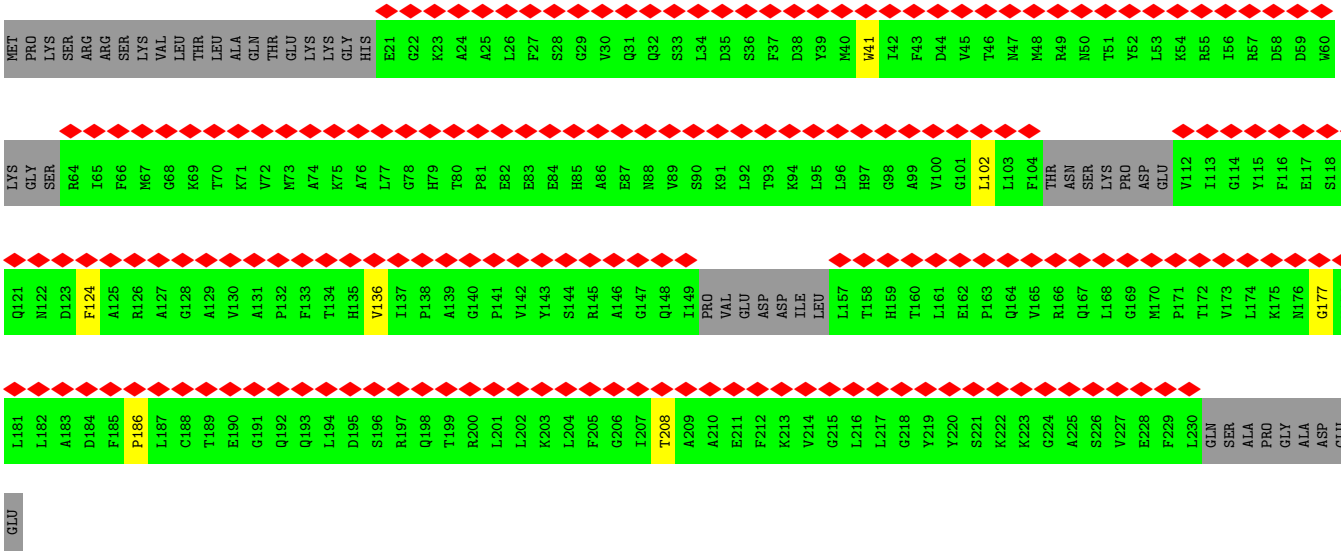
Chain V:





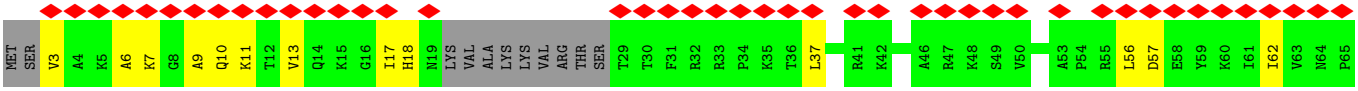
- Molecule 23: Ribosome assembly factor mrt4

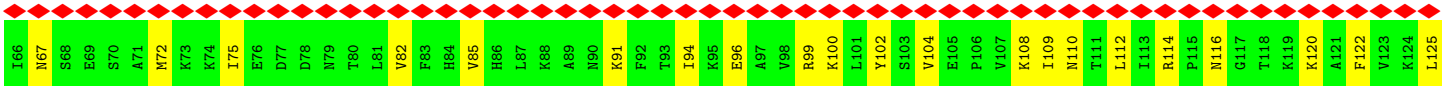
Chain W:

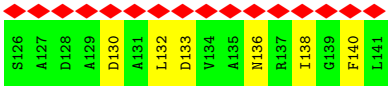


- Molecule 24: 60S ribosomal protein L25-A

Chain X:

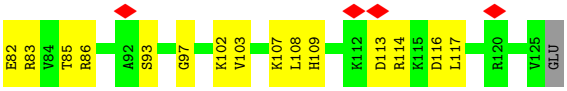






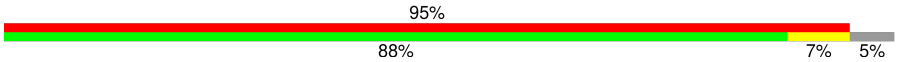
• Molecule 25: 60S ribosomal protein L26

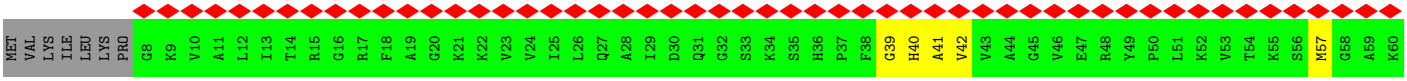
Chain Y:

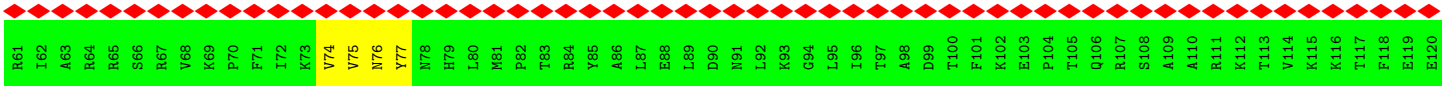


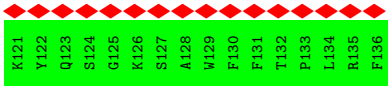
• Molecule 26: 60S ribosomal protein L27-A

Chain Z:



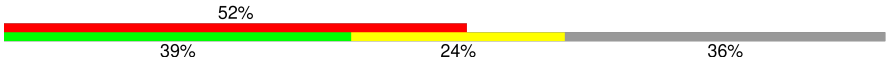


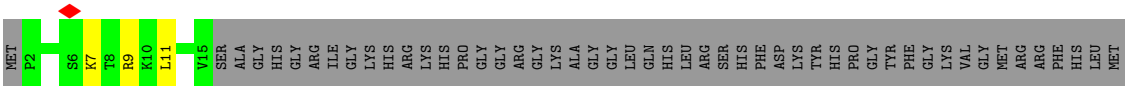


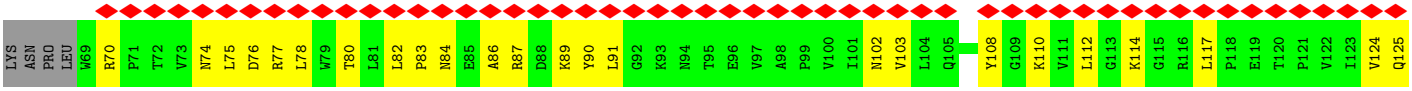


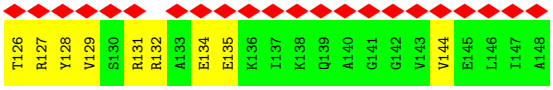
• Molecule 27: 60S ribosomal protein L28-A

Chain a:









• Molecule 28: Probable nucleolar GTP-binding protein 1

Chain b: 50% 58% • 41%

MET ALA THR ALA VAL PHE LYS ASN ILE T10 P11 I12 P13 D14 V15 N16 L19 T26 Q27 R28 K29 T30 P31 T32 V33 I34 R35 S36 G37 F38 K39 I40 S41 R42 I43 R44 G45 F46 Y47 G48 R49 K52 F53 T54 Q55 D56 T59 E60 K61 L62 D63 S64 I65 L66 Q67 E68

F69 P70 K71 L72 N73 D74 I75 H76 P77 F78 H79 A80 D81 L82 L83 N84 I85 L86 Y87 D88 R89 D90 K93 I94 A95 L96 S97 Q98 H104 L105 V106 E107 N108 V109 A110 R111 D112 Y113 I114 R115 L116 L117 K118 Y119 G120 D121 S122 L123 C126 L129 K130 R131 A132 A133 L134 G135

R136 M137 I140 Q144 K145 S146 S147 L148 E149 F150 L151 E152 Q153 V154 R155 L158 S159 R160 L161 P162 A163 I164 D165 P166 N167 T168 R169 T170 L171 L172 V173 C174 G175 Y176 P177 N178 V179 G180 K181 S182 S183 F184 M185 N186 K187 V188 T189 R190 A191 Q192 V193 D194 V195 Q196 P197 Y198 A199

F200 T201 T202 K203 S204 L205 F206 V207 G208 H209 F210 D211 Y212 K213 Y214 L215 R216 W217 Q218 V219 I220 D221 T222 P223 G224 I225 LEU ASP HIS PRO LEU GLU GLN MET ASN T235 I236 E237 M238 Q239 S240 I241 T242 A243 M244 A245 H246 L247 R248 S249 A250 V251 L252 Y253 F254 M255 D256 L257 S258 E259

M260 C261 G262 Y263 S264 V265 A266 A267 Q268 V269 K270 L271 Y272 H273 S274 T275 K276 P277 L278 F279 A280 N281 K282 V283 T284 I285 L286 V287 L288 N289 K290 T291 ASP ALA MET ARG PRO GLU ASP LEU ASP GLN LYS ASN GLN GLU LEU LEU GLN THR ILE ILE ASP ASP GLY ASN VAL K317 V318 V319

Q320 T321 S322 C323 V324 Q325 D326 I327 G328 V329 M330 D331 V332 R333 T334 T335 A336 C337 E338 A339 L340 L341 ALA ALA ARG VAL GLU GLN LYS LEU LYS GLY SER ARG VAL ASN ASN VAL LEU ASN ARG ILE HIS LEU ALA GLU PRO ALA ALA ARG ASP GLU VAL A373 R374 P375 A376 C377 I378 P379

D380 S381 V382 K383 T384 ARG ARG ALA TYR ASP ALA ASN ASP PRO ASN ARG ARG ILE L398 A399 R400 D401 I402 E403 A404 A405 N406 G407 G408 A409 G410 V411 Y412 N413 V414 E415 L416 R417 D418 K419 L422 Q423 D424 P425 S426 W427 K428 Y429 D430 R431 M432 P433 E434 L435 L436 D437 G438 K439 N440

V441 A442 D443 F444 V445 D446 P447 E448 I449 E450 A451 K452 L453 L454 A455 L456 D457 E458 E459 E460 E461 R462 L463 E464 R465 GLU GLY TYR TYR ASP SER ASP GLN GLU ILE GLU ASP ALA ASP GLU GLU GLU VAL LEU GLU LYS ALA SER ARG ILE ARG GLU LYS ASN LYS LEU THR MET LEU ALA

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

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

VAL ILE ALA ALA LYS PRO LYS HIS LEU LEU SER GLY LYS ARG GLY ASN GLY LYS THR GLN ARG ARG

- Molecule 29: 60S ribosomal protein L30-2

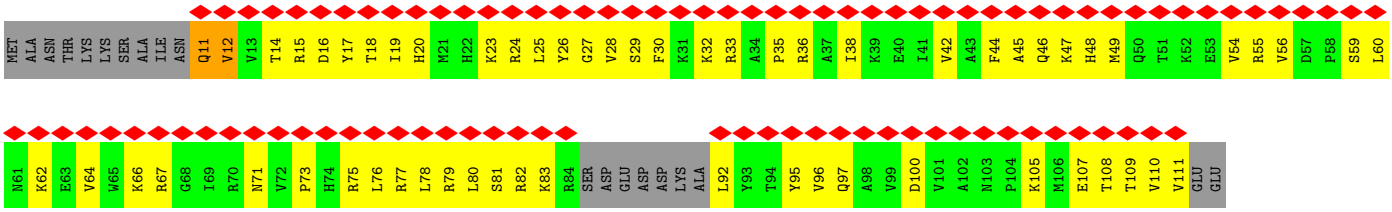
Chain c: 56% 53% • 44%

MET SER ALA ALA PRO THR THR ALA PRO VAL ALA ALA VAL SER LYS LYS GLY LYS LYS SER GLY ASP THR ILE ASN SER LYS LEU ALA LEU THR MET LYS S34 G35 K36 Y37 V38 L39 G40 Y41 K42 S43 T44 L45 K46 T47 L48 R49 S50 G51 K52 A53 K54 L55 I56 L57 I58 A59 A60

N61 A62 P63 P64 L65 R66 K67 S68 E69 L70 E71 Y72 Y73 A74 M75 L76 S77 R78 C79 S80 V81 H82 H83 Y84 S85 GLY ASN ASN ILE ASP LEU GLY THR ALA CYS GLY LYS LEU PHE ARG V101 G102 V103 L104 A105 V106 I107 D108 A109 G110 D111 S112 D113 I114 LEU ALA ALA

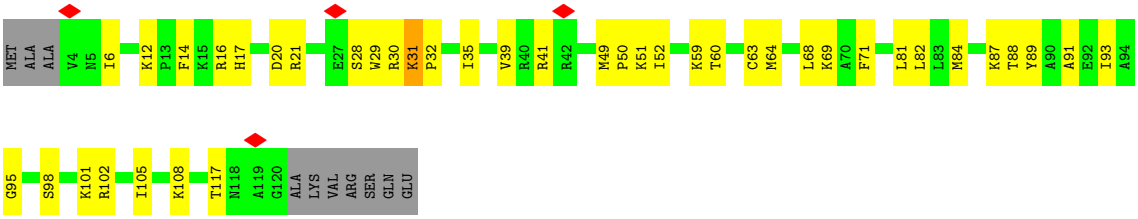
- Molecule 30: 60S ribosomal protein L31

Chain d:



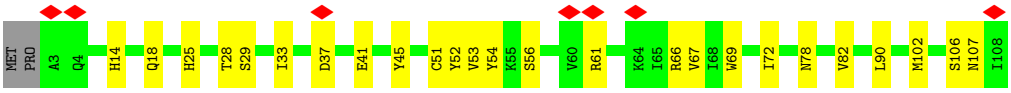
- Molecule 31: 60S ribosomal protein L32-A

Chain e:



- Molecule 32: 60S ribosomal protein L33-B

Chain f:

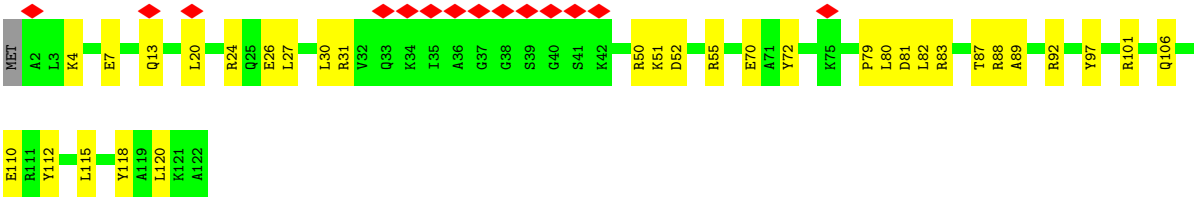


- Molecule 33: 60S ribosomal protein L34-A

Chain g:

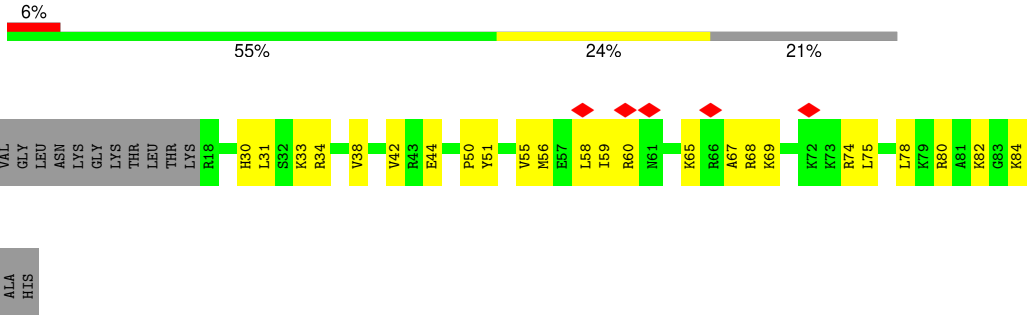
- Molecule 34: 60S ribosomal protein L35

Chain h:



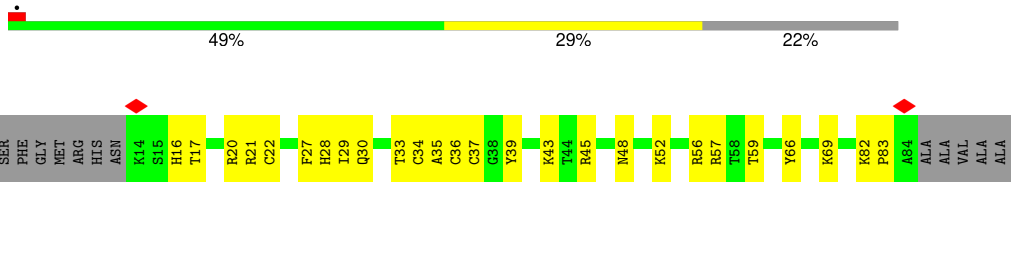
- Molecule 35: 60S ribosomal protein L36-B

Chain i:



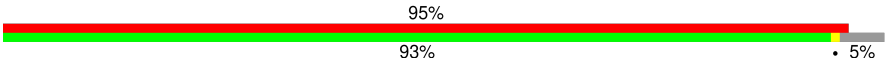
- Molecule 36: 60S ribosomal protein L37-B

Chain j:



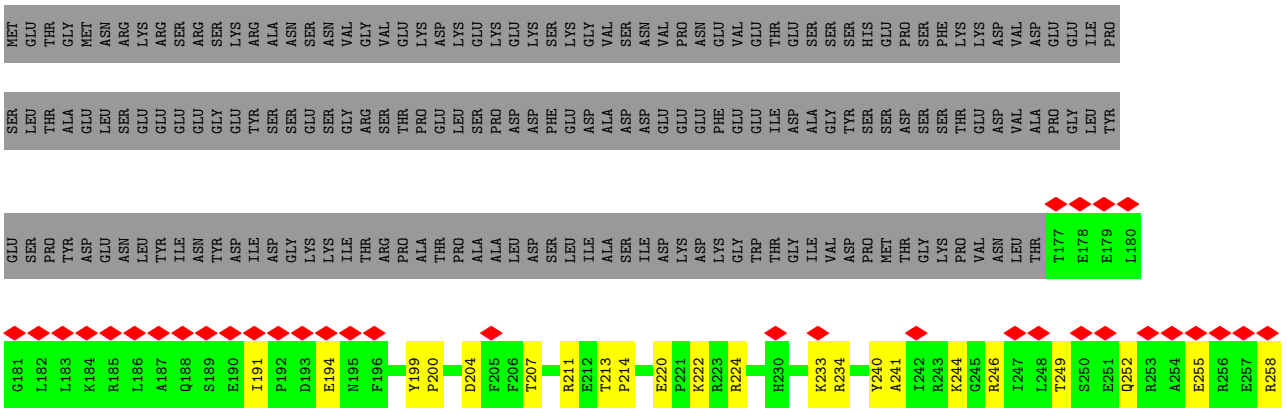
- Molecule 37: 60S ribosomal protein L38-1

Chain k:



- Molecule 38: Ribosome biogenesis protein erb1

Chain m:



E259 S260 Q261 S262 N263 Y264 A265 D266 H267 D268 L269 W270 A271 ASP ASP ASP GLN ALA THR VAL ASN GLN ARG LYS LEU ASP TYR A286 P287 A288 P289 K290 L291 P292 P293 P294 S295 H296 E297 E298 S299 Y300 N301 P302 P303 E304 E305 Y306 LEU LYS GLN SER SER ASP PHE P314 K315 K316 Y317 K318

S319 L320 R321 V322 V323 P324 A325 Y326 S327 N328 L329 I330 K331 E332 K333 F334 E335 R336 C337 L338 D339 L340 Y341 L342 A343 P344 R345 V346 R347 R348 T349 K350 LEU ASN ILE ASP PRO GLU SER LEU LEU PRO LYS LEU PRO THR PRO SER GLU LEU R369 P370 F371 P372 T373 R374 C375 T376 N377 V378

F379 I380 G381 H382 K383 G384 R385 V386 R387 C388 L389 S390 V391 H392 V393 S394 G395 N396 W397 L398 A399 S400 G401 G402 D403 D404 G405 V406 L407 R408 I409 W410 E411 V412 M413 T414 G415 R416 C417 V418 W419 K420 C421 S422 L423 ASP SER PHE GLY ASN ALA HIS ASN ILE ASP SER ASP GLU ASP ALA

VAL ASN GLU SER LEU SER HIS SER THR LYS SER SER I451 I452 Q453 S454 L455 A456 W457 G458 P459 L460 S461 D462 S463 P464 V465 L466 A467 V468 A469 V470 D471 E472 T473 V474 Y475 F476 I477 T478 P479 P480 I481 F482 S483 D484 E485 Q486 I487 E488 A489 S490 K491 E492 L493 F494 T495 SER ALA PRO

TYR GLN GLU SER S503 A504 I505 W506 R507 R508 GLY ALA LYS GLN SER LEU GLN L516 H517 G518 G519 I520 V521 H522 A523 T524 V525 S526 T527 P528 S529 S530 I531 K532 S533 L534 S535 W536 H537 R538 R539 G540 D541 Y542 L543 A544 T545 S546 S547 P548 T549 S550 S551 S552 Q553 A554 V555 L556 I557 H558

Q559 L560 S561 R562 G563 A564 S565 Q566 S567 P568 F569 S570 K571 S572 K573 G574 S575 V576 Q577 A578 V579 T580 F581 H582 P583 T584 M585 P586 Y587 L588 L589 V590 A591 T592 Q593 R594 Y595 V596 R597 I598 Y599 N600 L601 V602 K603 Q604 E605 L606 V607 K608 T609 L610 L611 T612 G613 V614 K615 W616 V617 S618

S619 L620 S621 V622 H623 S624 S625 G626 D627 H628 V629 S630 I631 G632 S633 Y634 D635 K636 R637 L638 C639 W640 F641 D642 L643 D644 F645 S646 S647 K648 P649 Y650 K651 N652 L653 R654 Y655 H656 S657 R658 A659 L660 R661 D662 V663 S664 Y665 H666 P667 S668 L669 P670 L671 F672 G673 S674 G675 S676 D677 D678

G679 D680 V681 Q682 V683 F684 H685 G686 R687 V688 Y689 S690 D691 L692 L693 A694 N695 P696 L697 I698 V699 P700 L701 K702 I703 L704 R705 N706 H707 K708 V709 V710 D711 N712 V713 G714 V715 L716 S717 T718 C719 W720 H721 P722 K723 E724 A725 W726 L727 F728 S729 A730 G731 A732 G733 G734 E735 I736 R737 M738

W739 T740

- Molecule 39: Pescadillo homolog

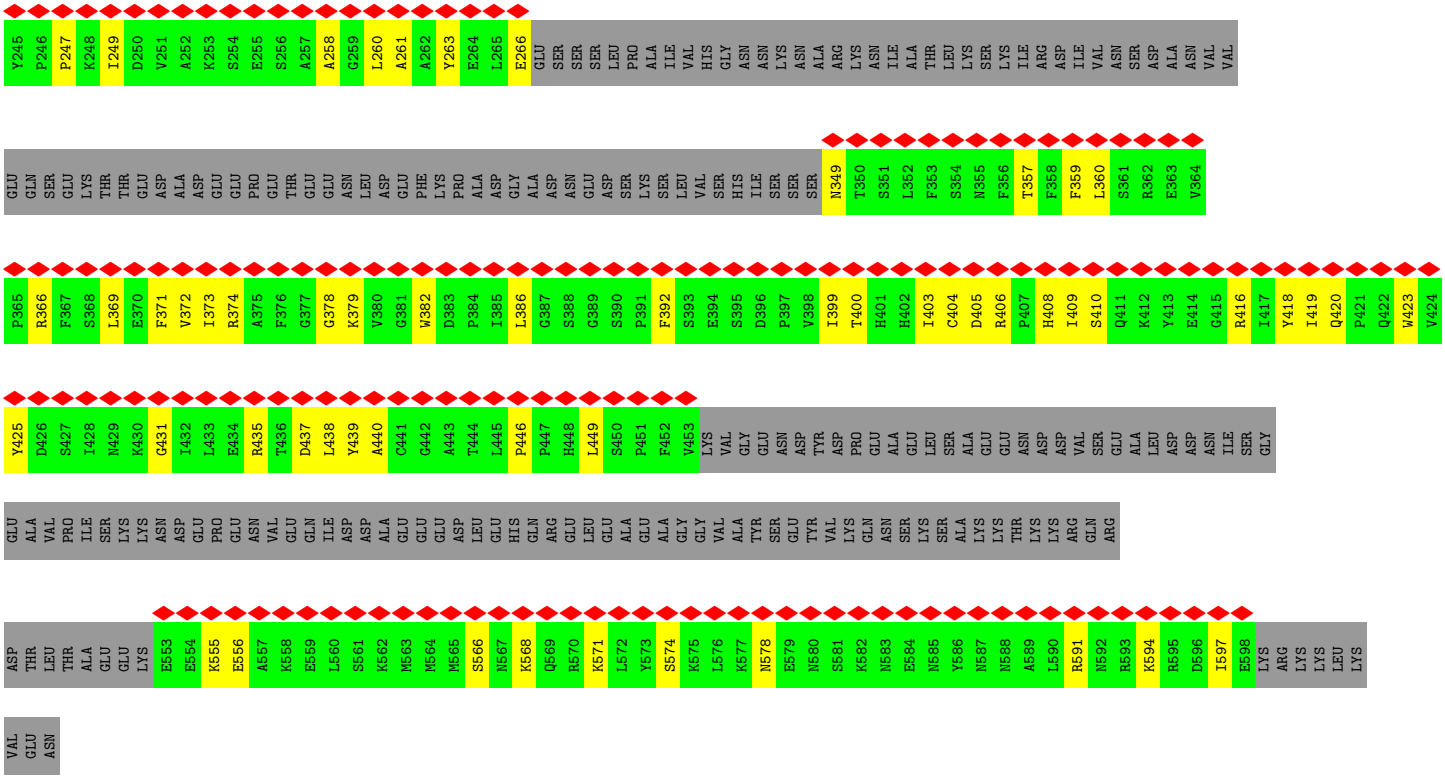
Chain n:

MET A2 R3 V4 K5 Q6 K7 G8 K9 A10 G11 A12 A13 Y16 I17 T18 R19 N20 Q21 A22 L23 K24 K25 L26 Q27 L28 T29 L30 A31 D32 F33 R34 R35 I36 C37 I38 L39 K40 G41 V42 Y43 P44 R45 E46 P47 K48 N49 K50 K51 K52 A53 N54 K55 G56 S57 T58 A59 P60 V61

T62 F63 Y64 Y65 T66 K67 D68 I69 Q70 Y71 L72 L73 H74 E75 P76 I77 V78 Q79 K80 F81 R82 E83 Y84 K85 R89 S92 K93 A94 L95 G96 K97 G98 E99 L100 E101 T102 A103 K104 R105 L106 E107 A108 R109 K110 P111 T112 Y113 S114 L115 D116 H117 I118 I119 K120 E121 R122 Y123 P124

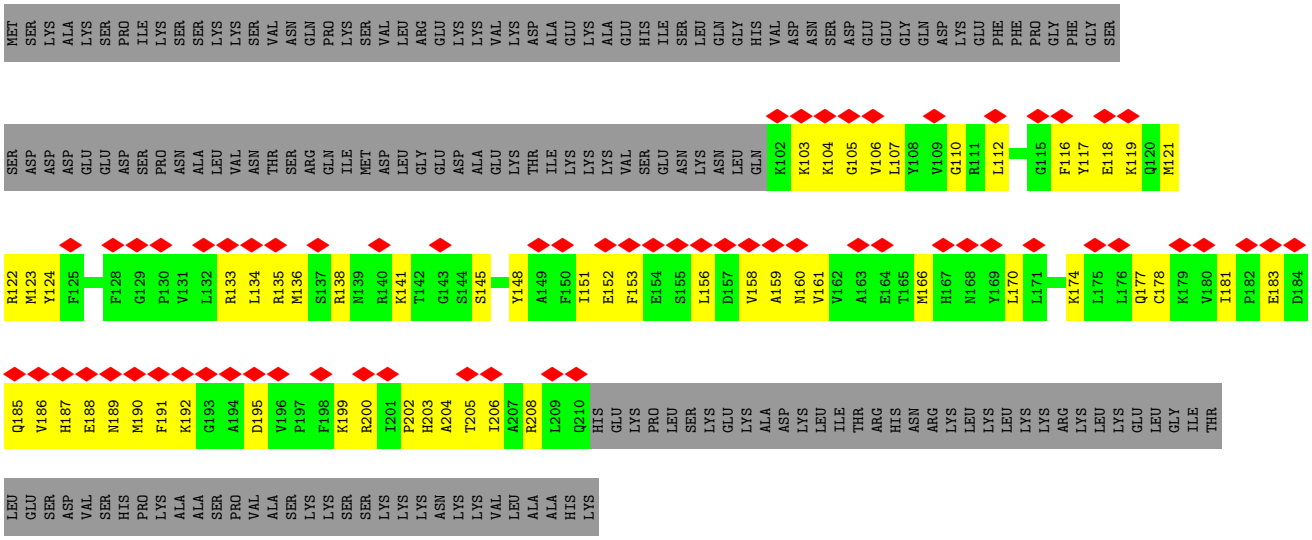
T125 F126 H127 D128 A129 L130 K131 D132 T133 D134 D135 A136 L137 S138 M139 L140 F141 L142 F143 S144 T145 M146 P147 V148 T149 D150 K151 I152 G153 A154 A155 T156 V157 A158 N159 C160 E161 R162 L163 C164 A165 E166 F167 Q168 H169 Y170 V171 I172 R173 S174 N175 S176 L177 R178 K179 A180 F181 L182 S183 I184

K185 G186 I187 I188 Y189 Q190 A191 E192 I193 F194 G195 E196 Q197 I198 T199 W200 I201 V202 P203 Y204 K205 F206 A207 Q208 S209 V210 P211 T212 D213 V214 D215 F216 R217 I218 M219 H220 T221 F222 L223 E224 F225 Y226 Q227 A228 L229 M230 G231 F232 V233 N234 F235 K236 L237 Y238 N239 T240 L241 G242 L243 R244



• Molecule 40: Uncharacterized RNA-binding protein C1827.05c

Chain o:



• Molecule 41: Ribosome biogenesis protein ytm1

Chain p:

GLN GLY GLN LEU LEU LYS THR THR LEU ASP GLU TYR ILE VAL GLN ASN GLY LEU SER THR GLU SER ILE LEU ASP ILE GLU TYR ILE GLN SER THR LEU PRO P95 A96 Y97 L98 A99 S100 F101 S102 H103 D104 D105 W106 I107 S108 G109 I110 Q111 L112 T113 S114 D115 T116 I117 L118 T119 S120

S121 Y122 D123 G124 I125 A126 R127 V128 W129 D130 K131 S132 G133 E134 I135 K136 F137 Q138 S139 T140 G141 C142 G143 S144 S145 L146 K147 S148 A149 S150 W151 H152 I153 P154 N155 Q156 S157 F158 L159 T160 A161 S162 L163 D164 Q165 K166 I167 F168 H169 W170 V171 I172 GLU GLU PRO GLU SER MET LEU ASP

ALA GLU LYS LYS SER S186 G187 I188 L189 Q190 T191 L192 F193 V194 G195 H196 K197 D198 I199 V200 E201 R202 V203 R204 S205 L206 E207 S208 S209 S210 V211 F212 I213 S214 A215 S216 A217 D218 N219 T220 V221 G222 I223 W224 D225 F226 E227 R228 S229 P230 E231 THR THR LEU GLU SER PHE SER SER SER

ILE SER LYS LYS ARG ARG ARG LYS ASN ALA GLU PHE THR PRO GLN ALA GLY A258 R259 S260 P261 L262 I263 L264 C265 E266 G267 H268 T269 G270 P271 V272 M273 D274 I275 V276 F277 S278 D279 D280 P281 S282 V283 A284 Y285 S286 V287 G288 Q289 D290 H291 T292 I293 K294 T295 W296 D297 L298 I299 T300

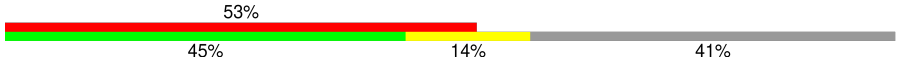
G301 Q302 N303 V304 D305 S306 K307 I308 T309 K310 A311 P312 L313 L314 C315 V316 E317 K318 L319 T320 D321 L322 H323 L324 V325 I326 C327 G328 S329 S330 A331 R332 H333 I334 V335 V336 H337 D338 P339 R340 ALA GLY SER ASP LYS ILE V347 S348 H349 T350 L351 S352 G353 H354 K355 N356 L357 V358 S359 G360

L361 S362 A363 S364 P365 E366 N367 P368 Y369 M370 F371 A372 S373 V374 S375 H376 D377 N378 T379 C380 R381 V382 W383 D384 V385 R386 A387 T388 S389 G390 S391 I392 Y393 T394 I395 S396 R397 A398 GLU LYS THR GLY SER GLN W405 D406 K407 L408 F409 A410 V411 D412 W413 N414 K415 S416 I417 G418 I419 V420

T421 G422 G423 T424 D425 K426 Q427 L428 Q429 T430 N431 Q432 SER SER SER PHE GLY LYS SER GLU

- Molecule 42: Ribosome biogenesis protein nsa2

Chain r:



MET P2 Q3 N4 E5 Y6 E9 S10 K13 H14 G15 R16 R17 F18 D19 H20 E21 E22 R23 K24 R25 K26 K27 A28 A29 R30 E31 A32 H33 D34 A35 S36 L37 Y38 A39 Q40 K41 T42 R43 G44 I45 K46 A47 K48 L49 Y50 Q51 E52 K53 R54 R55 K56 E57 K58 I59 Q60 M61 K62

K63 T64 I65 K66 Q67 H68 GLU GLU ARG ASN ALA THR GLN ARG GLY SER ASP ALA GLN THR GLN GLY ALA VAL PRO THR TYR LEU LEU ASP ARG GLU GLN GLU SER GLN ALA LYS MET LEU SER SER ALA VAL LYS GLN LYS ARG LYS GLU LYS ALA ALA LYS TYR SER VAL PRO LEU PRO

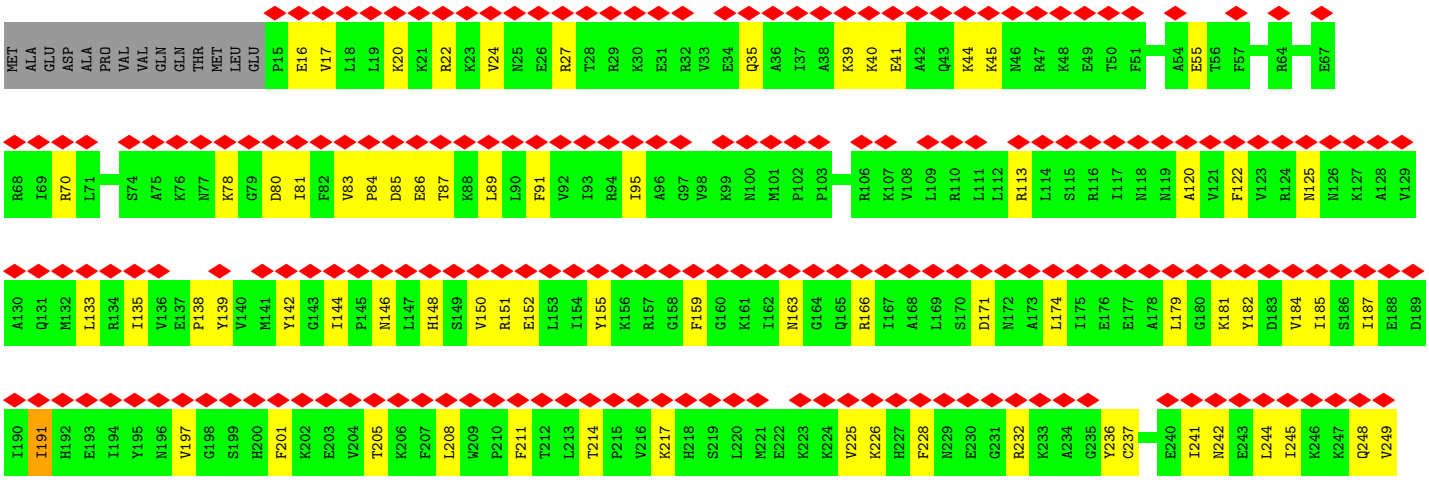
GLN VAL ARG GLY VAL ALA GLU GLU GLU MET PHE LYS VAL ILE ARG THR GLY LYS SER LYS LYS ASN SER TRP K147 R148 M149 I150 T151 K152 A153 T154 F155 V156 GLY ASP GLY PHE THR ARG ARG PRO VAL LYS TYR GLU ARG F170 I171 R172 P173 M174 A175 L176 R177 Q178 K179 K180 A181 N182

V183 T184 H185 K186 E187 L188 G189 V190 T191 M192 Q193 L194 P195 I196 I197 G198 V199 K200 K201 N202 P203 Q204 S205 P206 T207 Y208 T209 Q210 L211 G212 V213 L214 T215 K216 G217 T218 V219 I220 E221 V222 N223 V224 S225 E226 L227 GLY LEU VAL THR SER GLY GLY LYS VAL VAL TRP GLY K240 Y241 A242

Q243 I244 T245 N246 N247 P248 E249 L250 D251 G252 C253 V254 N255 A256 L257 L258 LEU THR

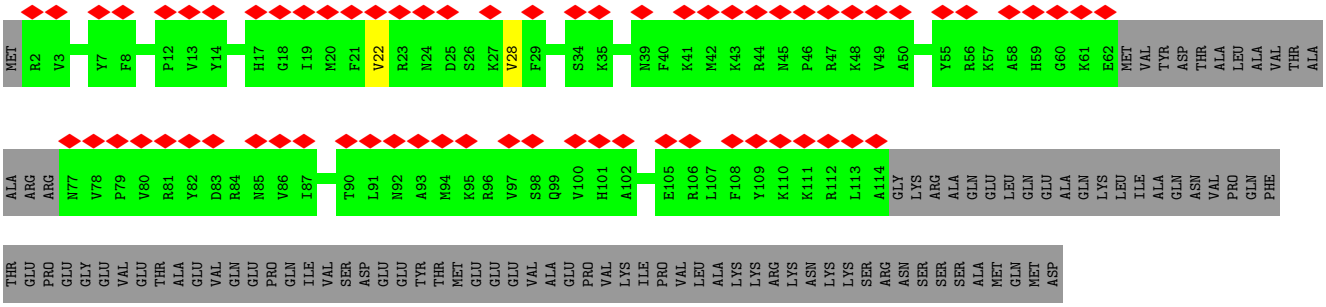
- Molecule 43: 60S ribosomal protein L7-A

Chain t:



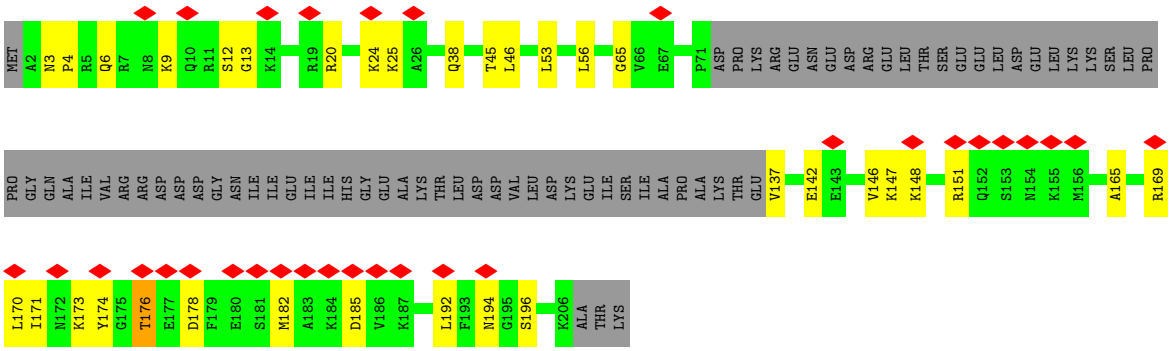
- Molecule 44: Ribosome biogenesis protein rlp24

Chain u:



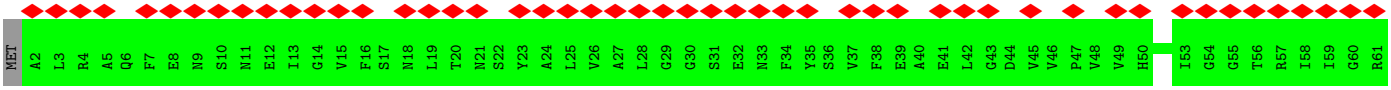
- Molecule 45: Nucleolar protein 16

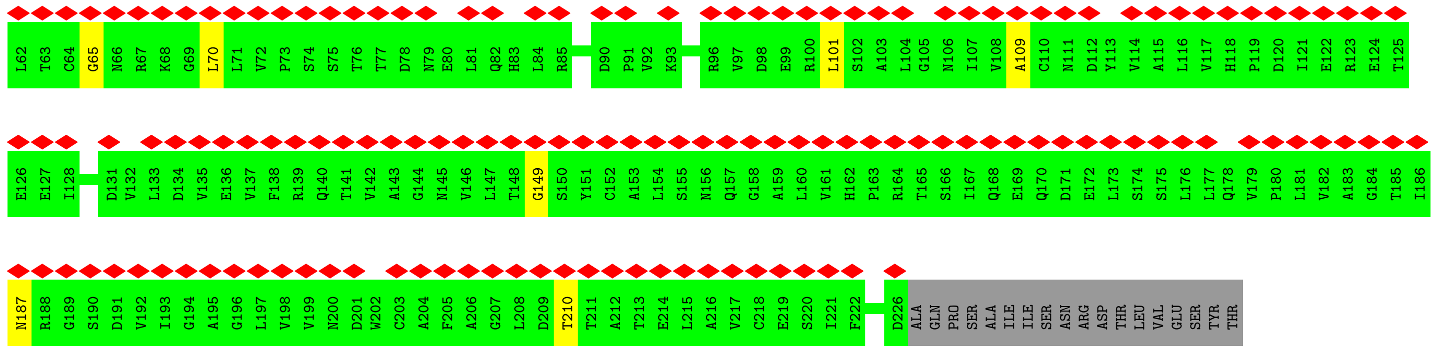
Chain v:



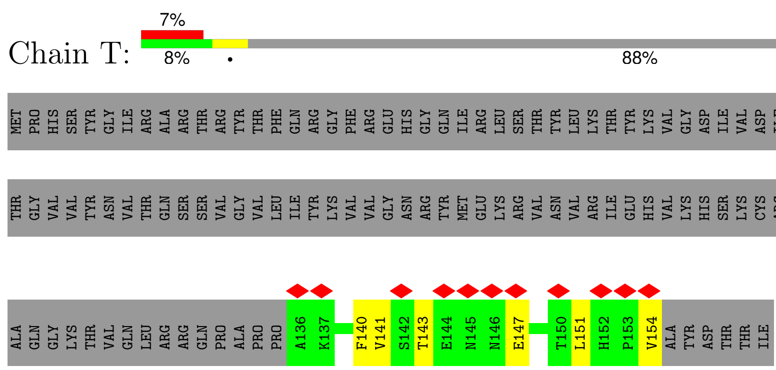
- Molecule 46: Eukaryotic translation initiation factor 6

Chain y:

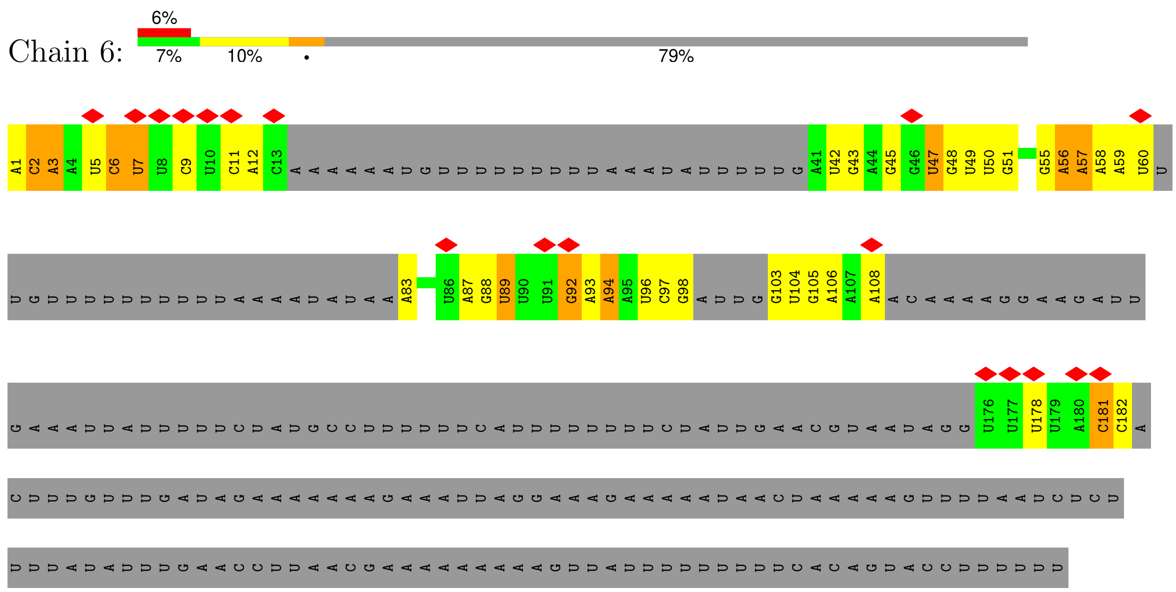




• Molecule 47: 60S ribosomal protein L21-A



• Molecule 48: RNA (62-MER)



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.532	Depositor
Minimum map value	-0.304	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	1	0.17	0/48337	0.26	0/75284
2	2	0.23	0/3465	0.31	0/5390
3	3	0.18	0/1037	0.40	0/1396
4	A	0.06	0/1015	0.23	0/1406
5	B	0.15	0/2706	0.33	0/3635
6	C	0.22	0/2848	0.39	0/3842
7	D	0.06	0/404	0.16	0/558
8	E	0.14	0/1146	0.34	0/1545
9	F	0.19	0/1781	0.34	0/2389
10	G	0.22	0/1474	0.34	0/1987
11	H	0.15	0/1470	0.36	0/1982
12	K	0.10	0/1143	0.25	0/1591
13	L	0.33	1/980 (0.1%)	0.42	0/1314
14	M	0.17	0/1017	0.32	0/1365
15	N	0.27	0/1436	0.35	0/1920
16	O	0.17	0/1511	0.30	0/2023
17	P	0.16	0/1101	0.34	0/1475
18	Q	0.18	0/1031	0.33	0/1384
19	R	0.23	0/460	0.43	0/614
20	S	0.17	0/1470	0.35	0/1977
21	U	0.05	0/483	0.19	0/671
22	V	0.12	0/992	0.33	0/1337
23	W	0.06	0/944	0.23	0/1305
24	X	0.18	0/1048	0.39	0/1406
25	Y	0.22	0/1008	0.37	0/1341
26	Z	0.05	0/636	0.16	0/882
27	a	0.26	0/760	0.47	0/1026
28	b	0.05	0/1870	0.18	0/2601
29	c	0.06	0/323	0.18	0/446
30	d	0.30	0/801	0.52	0/1075
31	e	0.21	0/953	0.32	0/1271
32	f	0.20	0/859	0.34	0/1152

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	g	0.05	0/427	0.18	0/592
34	h	0.20	0/1008	0.29	0/1340
35	i	0.15	0/643	0.32	0/852
36	j	0.22	0/575	0.35	0/761
37	k	0.05	0/348	0.18	0/485
38	m	0.19	0/2910	0.27	0/3993
39	n	0.15	0/3468	0.29	0/4670
40	o	0.18	0/919	0.42	0/1232
41	p	0.07	0/1411	0.20	0/1956
42	r	0.15	0/1014	0.38	0/1361
43	t	0.14	0/1979	0.31	0/2645
44	u	0.06	0/489	0.19	0/679
45	v	0.19	0/1161	0.39	0/1552
46	y	0.05	0/1106	0.19	0/1536
47	T	0.14	0/151	0.39	0/207
48	6	0.09	0/1466	0.16	0/2270
All	All	0.17	1/105584 (0.0%)	0.29	0/153721

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	L	60	PRO	CA-C	-6.40	1.48	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	43202	0	21751	685	0
2	2	3102	0	1570	32	0
3	3	1015	0	1015	46	0
4	A	1015	0	495	6	0
5	B	2653	0	2736	86	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	2795	0	2918	105	0
7	D	408	0	181	1	0
8	E	1126	0	1207	52	0
9	F	1745	0	1818	56	0
10	G	1452	0	1557	31	0
11	H	1451	0	1511	72	0
12	K	1145	0	504	5	0
13	L	962	0	1033	28	0
14	M	1000	0	1063	46	0
15	N	1406	0	1441	34	0
16	O	1483	0	1584	41	0
17	P	1080	0	1095	53	0
18	Q	1020	0	1114	30	0
19	R	456	0	493	25	0
20	S	1434	0	1497	70	0
21	U	484	0	222	1	0
22	V	976	0	1026	41	0
23	W	948	0	440	4	0
24	X	1032	0	1102	37	0
25	Y	998	0	1090	44	0
26	Z	637	0	296	5	0
27	a	747	0	790	32	0
28	b	1875	0	831	6	0
29	c	325	0	154	2	0
30	d	787	0	837	66	0
31	e	939	0	1000	39	0
32	f	839	0	866	23	0
33	g	428	0	193	1	0
34	h	999	0	1092	23	0
35	i	637	0	696	20	0
36	j	563	0	578	19	0
37	k	349	0	156	1	0
38	m	2881	0	1917	80	0
39	n	3389	0	3436	98	0
40	o	897	0	914	47	0
41	p	1416	0	627	27	0
42	r	1009	0	791	33	0
43	t	1948	0	2066	62	0
44	u	491	0	217	1	0
45	v	1143	0	1192	30	0
46	y	1107	0	514	4	0
47	T	147	0	140	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	6	1315	0	666	20	0
49	j	1	0	0	0	0
All	All	99257	0	70432	1928	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 13.

All (1928) 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)
30:d:49:MET:HE1	30:d:82:ARG:HE	1.15	1.05
5:B:331:PRO:HD2	5:B:334:ARG:HE	1.33	0.91
1:1:607:G:H4'	32:f:107:ASN:HD21	1.36	0.88
38:m:249:THR:HG23	38:m:252:GLN:HE22	1.36	0.88
11:H:93:VAL:HB	11:H:178:TYR:HE1	1.40	0.86
1:1:3352:A:H3'	1:1:3353:U:H5"	1.60	0.84
1:1:238:U:H5'	1:1:240:G:H5'	1.60	0.83
17:P:30:ARG:HA	17:P:119:VAL:HG21	1.60	0.83
36:j:36:CYS:SG	36:j:57:ARG:NH2	2.53	0.82
30:d:25:LEU:HD21	30:d:33:ARG:HD2	1.62	0.81
1:1:621:G:H5"	9:F:44:ARG:HH21	1.45	0.80
27:a:82:LEU:HD21	27:a:86:ALA:HB3	1.63	0.80
1:1:1010:A:H4'	1:1:1011:G:H5'	1.65	0.79
39:n:139:MET:HE1	39:n:219:MET:SD	2.23	0.79
14:M:33:ASP:OD1	14:M:34:HIS:N	2.15	0.79
6:C:101:MET:HE2	6:C:104:PRO:HA	1.64	0.79
1:1:1879:C:H2'	1:1:1880:A:H8	1.48	0.79
18:Q:92:GLU:OE1	18:Q:92:GLU:N	2.14	0.78
2:2:49:A:HO2'	36:j:59:THR:HG1	1.31	0.78
24:X:13:VAL:HG13	24:X:17:ILE:HG22	1.66	0.78
1:1:1605:U:H3	1:1:1607:U:H2'	1.49	0.78
30:d:49:MET:HE1	30:d:82:ARG:NE	1.98	0.77
42:r:149:MET:HA	42:r:171:ILE:H	1.50	0.77
6:C:7:THR:OG1	6:C:21:THR:HB	1.85	0.77
19:R:20:ARG:HG3	19:R:21:LYS:HD3	1.68	0.76
42:r:55:ARG:HH22	42:r:56:LYS:HG3	1.50	0.76
34:h:4:LYS:HB2	34:h:7:GLU:HG3	1.68	0.76
1:1:2931:C:H3'	1:1:2932:A:H8	1.50	0.76
40:o:187:HIS:H	40:o:190:MET:HE1	1.52	0.75
5:B:92:TYR:HB3	5:B:99:LEU:HD12	1.68	0.75
5:B:218:ILE:HD11	5:B:339:ARG:HH12	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:45:LYS:HZ3	20:S:51:LYS:HA	1.52	0.75
1:1:312:G:H1	1:1:319:U:H3	1.31	0.74
1:1:533:A:OP1	6:C:350:LYS:NZ	2.20	0.74
5:B:285:ILE:HG22	5:B:322:VAL:HG12	1.69	0.74
17:P:61:ARG:O	17:P:64:ASN:ND2	2.20	0.74
31:e:21:ARG:NH1	31:e:21:ARG:O	2.20	0.74
1:1:27:C:H3'	1:1:28:G:H21	1.51	0.74
1:1:760:C:N4	1:1:763:G:OP2	2.20	0.74
1:1:1730:U:O2'	1:1:1789:A:N1	2.20	0.74
11:H:93:VAL:HB	11:H:178:TYR:CE1	2.22	0.74
22:V:42:PHE:CE1	22:V:61:LEU:HD11	2.23	0.74
22:V:24:ILE:HD11	22:V:35:ASN:HB3	1.69	0.74
11:H:90:MET:HB3	11:H:142:ILE:HB	1.69	0.74
19:R:21:LYS:HA	19:R:53:LYS:HZ1	1.53	0.73
1:1:3196:U:H3	1:1:3230:G:H1	1.36	0.73
39:n:4:VAL:O	39:n:6:GLN:NE2	2.21	0.73
17:P:70:THR:HG22	17:P:72:GLN:H	1.52	0.73
36:j:30:GLN:OE1	36:j:30:GLN:N	2.21	0.73
20:S:44:LEU:HD21	20:S:50:VAL:HB	1.70	0.73
35:i:75:LEU:HD23	35:i:80:ARG:HB3	1.71	0.73
1:1:366:G:N2	1:1:369:A:OP2	2.20	0.73
1:1:3092:U:H3'	1:1:3093:G:H5'	1.69	0.73
5:B:211:GLN:NE2	5:B:283:TYR:O	2.20	0.73
11:H:104:THR:OG1	11:H:105:GLU:OE1	2.07	0.72
38:m:306:TYR:HB3	38:m:316:LYS:HD2	1.70	0.72
1:1:190:G:H1	1:1:242:U:H3	1.37	0.72
25:Y:54:GLN:HB3	25:Y:107:LYS:HB3	1.70	0.72
22:V:106:ASN:HD21	22:V:110:GLU:HB3	1.54	0.72
1:1:26:A:N3	1:1:336:U:O2'	2.23	0.72
1:1:1692:C:N4	1:1:1839:A:OP2	2.21	0.72
15:N:5:LYS:HG3	35:i:38:VAL:HG11	1.69	0.72
5:B:375:GLU:HA	5:B:378:GLN:HE22	1.54	0.72
1:1:116:A:OP1	35:i:34:ARG:NH2	2.23	0.71
1:1:3027:U:H5'	22:V:43:GLY:HA2	1.72	0.71
1:1:1270:C:H42	1:1:1280:G:H1	1.37	0.71
5:B:281:LYS:O	5:B:325:ASN:ND2	2.22	0.71
6:C:140:ARG:HG3	6:C:140:ARG:HH11	1.55	0.71
6:C:5:ARG:HD2	6:C:23:ALA:HB1	1.71	0.71
38:m:249:THR:H	38:m:252:GLN:HE22	1.38	0.71
1:1:31:C:O2'	15:N:96:ARG:NH1	2.23	0.71
1:1:1930:G:N7	19:R:20:ARG:NH1	2.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:607:G:H4'	32:f:107:ASN:ND2	2.05	0.71
19:R:8:LYS:HD2	19:R:22:VAL:HG21	1.71	0.71
39:n:23:LEU:HD11	39:n:30:LEU:HD13	1.72	0.71
1:1:2933:A:N6	1:1:2945:G:O2'	2.24	0.71
38:m:334:PHE:HD1	39:n:219:MET:HE1	1.54	0.71
1:1:2423:G:N2	1:1:2427:C:O2'	2.23	0.71
6:C:338:LYS:NZ	6:C:341:VAL:HG12	2.06	0.71
40:o:188:GLU:OE2	40:o:188:GLU:N	2.21	0.71
6:C:179:ASP:OD1	6:C:182:LYS:NZ	2.21	0.71
1:1:401:U:O3'	25:Y:86:ARG:NH2	2.22	0.70
1:1:1175:U:OP2	31:e:41:ARG:NH1	2.24	0.70
43:t:55:GLU:OE1	43:t:55:GLU:N	2.23	0.70
1:1:3480:C:H4'	5:B:315:GLY:HA2	1.71	0.70
2:2:137:A:H5"	39:n:10:ALA:HB1	1.72	0.70
39:n:141:PHE:HD2	39:n:202:VAL:HG22	1.56	0.70
1:1:3138:U:H5"	22:V:47:ARG:HD2	1.73	0.70
3:3:100:TRP:CD1	3:3:101:PRO:HD2	2.27	0.70
6:C:37:VAL:HG21	6:C:246:LEU:HD21	1.74	0.70
42:r:21:GLU:OE1	42:r:21:GLU:N	2.20	0.70
42:r:52:GLU:HB2	42:r:55:ARG:HH21	1.57	0.70
36:j:21:ARG:NH2	36:j:43:LYS:O	2.25	0.70
42:r:9:GLU:N	42:r:9:GLU:OE2	2.24	0.70
3:3:114:ARG:HH21	31:e:84:MET:HE1	1.56	0.69
17:P:109:MET:HE2	17:P:109:MET:HA	1.74	0.69
34:h:27:LEU:HD11	34:h:50:ARG:HG3	1.72	0.69
1:1:1531:C:H2'	1:1:1532:A:H8	1.56	0.69
6:C:302:VAL:HG23	18:Q:38:ARG:HB3	1.72	0.69
45:v:173:LYS:NZ	45:v:174:TYR:CE2	2.60	0.69
1:1:3012:G:H1	1:1:3024:C:H5	1.39	0.69
5:B:58:ARG:NH1	5:B:74:GLU:OE2	2.24	0.69
11:H:92:LEU:HB3	11:H:140:ASP:HB2	1.75	0.69
20:S:78:ILE:HD11	20:S:109:MET:HE2	1.74	0.69
6:C:338:LYS:HZ3	6:C:341:VAL:HG12	1.58	0.69
18:Q:21:GLU:N	18:Q:21:GLU:OE2	2.26	0.69
1:1:1639:U:O2	1:1:1639:U:H2'	1.92	0.69
20:S:78:ILE:CD1	20:S:109:MET:HE2	2.23	0.69
20:S:80:TYR:CD2	20:S:109:MET:HE3	2.27	0.69
31:e:63:CYS:SG	31:e:69:LYS:NZ	2.64	0.69
1:1:1598:C:OP2	39:n:24:LYS:NZ	2.26	0.69
32:f:53:VAL:HG22	32:f:67:VAL:HG22	1.73	0.69
1:1:3209:A:H4'	11:H:69:ARG:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:52:LYS:O	16:O:56:LEU:HD22	1.93	0.68
35:i:78:LEU:HG	35:i:82:LYS:HE2	1.76	0.68
16:O:117:LYS:NZ	20:S:169:PRO:O	2.27	0.68
3:3:20:ILE:HD11	3:3:29:ARG:HB2	1.75	0.68
15:N:114:ARG:NH1	15:N:151:ILE:O	2.26	0.68
1:1:1438:G:N2	1:1:1441:A:OP2	2.22	0.68
45:v:194:ASN:ND2	45:v:196:SER:OG	2.27	0.68
16:O:63:CYS:HG	16:O:71:ALA:N	1.91	0.68
40:o:112:LEU:HD12	40:o:116:PHE:HB3	1.74	0.67
40:o:122:ARG:HG3	40:o:134:LEU:HD13	1.77	0.67
17:P:119:VAL:HG12	17:P:146:ILE:HG12	1.76	0.67
18:Q:92:GLU:H	18:Q:92:GLU:CD	2.00	0.67
39:n:159:ASN:OD1	39:n:162:ARG:NH2	2.27	0.67
5:B:383:LEU:HD23	5:B:384:LYS:H	1.59	0.67
10:G:161:GLU:OE2	15:N:26:ARG:NH2	2.27	0.67
1:1:1244:G:H5'	20:S:136:ARG:HH21	1.59	0.67
1:1:2947:C:H1'	42:r:59:ILE:HD13	1.76	0.67
17:P:4:TYR:HE1	17:P:18:ARG:HE	1.41	0.67
24:X:3:VAL:HG12	40:o:158:VAL:HG23	1.75	0.67
38:m:290:LYS:HG3	43:t:17:VAL:HG23	1.77	0.67
1:1:1284:U:H5"	1:1:1285:C:H5'	1.77	0.67
30:d:25:LEU:HD23	30:d:25:LEU:O	1.95	0.67
5:B:284:ARG:NH1	5:B:294:ALA:O	2.28	0.66
3:3:110:GLN:HB3	3:3:114:ARG:HH22	1.59	0.66
18:Q:94:MET:O	18:Q:114:ARG:NH2	2.26	0.66
1:1:1218:C:H5	1:1:1350:G:H1	1.43	0.66
3:3:16:CYS:HB3	3:3:19:ARG:HG2	1.78	0.66
10:G:163:VAL:HG12	10:G:166:LEU:HD12	1.77	0.66
43:t:171:ASP:HB2	43:t:174:LEU:HG	1.77	0.66
1:1:3272:U:O2	16:O:6:LYS:NZ	2.28	0.66
1:1:3435:U:N3	1:1:3470:G:O2'	2.27	0.66
9:F:87:GLU:OE2	9:F:89:LYS:HG3	1.95	0.66
16:O:127:VAL:HG23	16:O:128:LEU:HD12	1.78	0.66
48:6:6:C:N3	48:6:48:G:O2'	2.29	0.66
1:1:847:G:OP1	36:j:16:HIS:NE2	2.26	0.66
20:S:7:GLN:OE1	20:S:61:ASN:ND2	2.23	0.66
9:F:245:LEU:HD21	9:F:249:MET:HE3	1.76	0.66
1:1:1146:G:N2	1:1:1146:G:OP2	2.27	0.66
1:1:3315:A:N1	8:E:176:GLU:HB2	2.10	0.66
30:d:24:ARG:HG2	30:d:24:ARG:HH11	1.61	0.66
38:m:191:ILE:H	38:m:191:ILE:HD12	1.62	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:239:U:O4	45:v:25:LYS:NZ	2.20	0.65
25:Y:5:ARG:HG3	45:v:24:LYS:HG3	1.78	0.65
1:1:1242:U:O2'	20:S:112:ARG:NH1	2.29	0.65
36:j:20:ARG:NH2	36:j:39:TYR:OH	2.28	0.65
2:2:79:A:O2'	25:Y:51:ARG:NH2	2.29	0.65
9:F:234:ASP:OD2	9:F:238:ARG:NH2	2.28	0.65
17:P:67:VAL:O	17:P:80:GLN:NE2	2.29	0.65
25:Y:55:ILE:HD11	25:Y:81:ILE:HG12	1.79	0.65
18:Q:53:GLN:O	18:Q:58:ARG:NH1	2.30	0.65
38:m:249:THR:CG2	38:m:252:GLN:HE22	2.09	0.65
1:1:1379:U:OP2	18:Q:37:ARG:NH1	2.30	0.65
4:A:92:LEU:HD11	35:i:69:LYS:HB3	1.78	0.65
5:B:146:ARG:NH1	5:B:149:GLU:OE1	2.30	0.65
24:X:72:MET:HE3	24:X:72:MET:HA	1.77	0.65
2:2:71:G:O2'	34:h:51:LYS:NZ	2.30	0.65
3:3:3:GLN:HG3	3:3:4:ASP:H	1.61	0.65
5:B:116:ARG:O	5:B:175:LYS:NZ	2.29	0.65
24:X:6:ALA:HA	24:X:10:GLN:HB2	1.79	0.64
1:1:3315:A:OP2	14:M:118:LYS:NZ	2.29	0.64
14:M:65:LEU:HD12	14:M:66:PRO:HD2	1.78	0.64
22:V:28:ALA:O	22:V:117:THR:HG23	1.98	0.64
1:1:3203:C:H2'	1:1:3204:G:H8	1.63	0.64
39:n:146:MET:HA	39:n:208:GLN:HE22	1.61	0.64
1:1:3285:G:H1	1:1:3302:U:H3	1.45	0.64
1:1:3475:U:OP2	30:d:75:ARG:NH2	2.29	0.64
9:F:130:ILE:HA	9:F:133:MET:HB2	1.78	0.64
38:m:334:PHE:HD1	39:n:219:MET:CE	2.10	0.64
13:L:87:ARG:HH21	13:L:88:ARG:HH12	1.46	0.64
20:S:11:ARG:HD2	20:S:21:PRO:HG2	1.79	0.64
39:n:258:ALA:HB1	39:n:261:ALA:HB3	1.79	0.64
40:o:187:HIS:N	40:o:190:MET:HE1	2.12	0.64
40:o:189:ASN:HB2	40:o:192:LYS:HB2	1.80	0.64
1:1:372:G:OP2	36:j:52:LYS:NZ	2.30	0.64
11:H:23:ALA:O	11:H:40:ARG:NH2	2.31	0.64
24:X:85:VAL:HG11	24:X:94:ILE:HD11	1.78	0.64
10:G:162:LEU:HD11	15:N:45:PRO:HG3	1.79	0.64
11:H:116:LEU:HD23	11:H:116:LEU:O	1.97	0.64
1:1:252:A:OP1	45:v:148:LYS:NZ	2.30	0.64
1:1:528:G:OP1	9:F:74:ARG:NH2	2.31	0.64
1:1:712:U:OP2	13:L:36:ARG:NH2	2.31	0.64
3:3:19:ARG:NH1	3:3:28:CYS:SG	2.71	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:7:LYS:HE3	40:o:161:VAL:HG22	1.80	0.64
35:i:51:TYR:OH	35:i:84:LYS:NZ	2.31	0.63
39:n:137:LEU:HD22	39:n:230:MET:HE1	1.80	0.63
3:3:69:ARG:HD2	3:3:75:LYS:HD2	1.80	0.63
8:E:89:ASN:ND2	8:E:178:LEU:O	2.30	0.63
20:S:65:GLU:OE2	20:S:72:LYS:NZ	2.30	0.63
39:n:75:GLU:HB3	39:n:78:VAL:HG23	1.80	0.63
1:1:396:G:H1'	17:P:97:ASN:HD21	1.63	0.63
1:1:1009:C:N4	1:1:1136:A:N1	2.47	0.63
14:M:31:ILE:O	20:S:94:ARG:NH2	2.30	0.63
1:1:732:A:N6	1:1:742:A:OP2	2.31	0.63
10:G:172:LYS:HE3	38:m:211:ARG:HB2	1.79	0.63
1:1:1417:G:OP1	6:C:205:ARG:NH1	2.27	0.63
17:P:16:LYS:HG2	17:P:149:ILE:HG12	1.80	0.63
1:1:351:U:H1'	6:C:97:ARG:HG3	1.80	0.62
5:B:378:GLN:N	5:B:378:GLN:OE1	2.32	0.62
6:C:147:ILE:HD11	6:C:152:LEU:HB2	1.79	0.62
18:Q:92:GLU:HB2	27:a:80:THR:HG21	1.81	0.62
28:b:404:ALA:HA	28:b:408:GLY:HA2	1.79	0.62
30:d:47:LYS:HZ2	30:d:48:HIS:HA	1.64	0.62
1:1:174:U:O2'	1:1:259:A:N6	2.29	0.62
39:n:142:LEU:HA	39:n:203:PRO:HG3	1.82	0.62
10:G:146:LYS:NZ	10:G:173:MET:O	2.33	0.62
43:t:81:ILE:HG13	43:t:83:VAL:H	1.64	0.62
14:M:24:LYS:HE2	14:M:45:GLU:HG3	1.81	0.62
38:m:335:GLU:O	43:t:22:ARG:NH2	2.32	0.62
40:o:112:LEU:HD23	40:o:148:TYR:HA	1.80	0.62
45:v:171:ILE:HD11	45:v:176:THR:HA	1.81	0.62
1:1:650:G:N2	1:1:1435:G:OP1	2.26	0.62
1:1:3040:G:N2	1:1:3044:U:OP2	2.33	0.62
39:n:366:ARG:NH2	39:n:386:LEU:O	2.32	0.62
1:1:262:A:N3	34:h:112:TYR:OH	2.30	0.62
17:P:11:GLU:O	17:P:13:LYS:N	2.33	0.62
42:r:16:ARG:HD3	42:r:17:ARG:H	1.64	0.62
1:1:48:A:H4'	1:1:49:A:H5'	1.81	0.62
1:1:1222:U:OP2	16:O:50:ARG:NH1	2.33	0.62
6:C:183:VAL:HG21	6:C:226:GLY:HA3	1.81	0.62
1:1:1636:U:OP1	19:R:42:ARG:NH2	2.30	0.62
20:S:57:ILE:HG21	20:S:60:ILE:HD11	1.82	0.62
22:V:137:THR:HG22	46:y:101:LEU:HA	1.82	0.62
31:e:88:THR:HG23	31:e:89:TYR:HD1	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:576:VAL:HA	38:m:592:THR:HA	1.82	0.61
43:t:245:ILE:O	43:t:249:VAL:N	2.30	0.61
1:1:2993:G:OP2	1:1:2994:C:N4	2.30	0.61
27:a:132:ARG:HA	27:a:135:GLU:OE2	2.00	0.61
36:j:27:PHE:HA	36:j:34:CYS:HA	1.82	0.61
1:1:1390:A:N7	3:3:13:HIS:NE2	2.48	0.61
1:1:1536:G:N2	1:1:1547:G:N7	2.47	0.61
6:C:329:ARG:NH1	9:F:171:SER:O	2.33	0.61
22:V:82:ARG:HD3	22:V:97:PHE:HD2	1.65	0.61
38:m:344:PRO:HG2	43:t:20:LYS:HB2	1.82	0.61
1:1:163:A:N6	1:1:272:G:O2'	2.32	0.61
1:1:223:G:OP1	25:Y:15:ARG:NH1	2.34	0.61
1:1:1424:A:N6	1:1:1452:A:O2'	2.34	0.61
1:1:2972:G:H1	1:1:3044:U:H3	1.48	0.61
11:H:11:LEU:HB2	11:H:72:TYR:HE1	1.66	0.61
1:1:216:A:OP1	6:C:163:LYS:NZ	2.34	0.61
1:1:3145:A:H4'	5:B:364:LYS:HE3	1.83	0.61
1:1:3203:C:H2'	1:1:3204:G:C8	2.36	0.61
42:r:16:ARG:HD3	42:r:17:ARG:N	2.15	0.61
1:1:1379:U:OP1	18:Q:38:ARG:NH1	2.33	0.61
1:1:3133:U:OP1	5:B:348:ARG:NH1	2.33	0.61
1:1:3318:A:O2'	1:1:3319:G:OP2	2.17	0.61
2:2:45:A:OP2	34:h:88:ARG:NH1	2.33	0.60
43:t:78:LYS:NZ	43:t:80:ASP:O	2.33	0.60
1:1:63:A:N3	1:1:78:U:O2'	2.31	0.60
6:C:228:GLU:HG3	6:C:248:ARG:HH22	1.66	0.60
27:a:132:ARG:HA	27:a:135:GLU:CD	2.26	0.60
30:d:16:ASP:OD2	30:d:77:ARG:NE	2.35	0.60
40:o:122:ARG:NH2	40:o:195:ASP:OD2	2.30	0.60
42:r:55:ARG:NH2	42:r:56:LYS:HG3	2.16	0.60
1:1:587:U:H2'	1:1:588:G:H8	1.66	0.60
15:N:11:ALA:O	15:N:14:LYS:NZ	2.27	0.60
16:O:52:LYS:HG3	16:O:56:LEU:HD21	1.83	0.60
17:P:117:VAL:HG22	17:P:148:ILE:HG12	1.82	0.60
20:S:62:GLU:OE1	20:S:62:GLU:N	2.34	0.60
1:1:1364:C:OP1	9:F:117:GLN:NE2	2.33	0.60
6:C:285:SER:N	18:Q:126:ASP:OD2	2.34	0.60
34:h:52:ASP:OD1	34:h:55:ARG:NH1	2.35	0.60
19:R:38:ARG:HB3	19:R:42:ARG:HH12	1.65	0.60
31:e:84:MET:HA	31:e:84:MET:HE2	1.83	0.60
40:o:153:PHE:HD2	40:o:159:ALA:HA	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1454:C:OP2	6:C:195:LYS:NZ	2.34	0.60
1:1:1700:G:H1	1:1:1825:U:H3	1.50	0.60
3:3:5:GLU:CD	6:C:289:VAL:H	2.08	0.60
1:1:1578:G:H1	1:1:1583:U:H3	1.50	0.60
19:R:24:MET:N	19:R:24:MET:SD	2.75	0.60
38:m:249:THR:HG23	38:m:252:GLN:NE2	2.12	0.60
1:1:197:U:O4	25:Y:102:LYS:NZ	2.34	0.60
1:1:749:G:H1	1:1:776:U:H3	1.48	0.60
5:B:124:LYS:HD2	5:B:124:LYS:H	1.65	0.60
16:O:52:LYS:HG3	16:O:56:LEU:CD2	2.31	0.60
1:1:3107:A:H62	5:B:13:SER:HA	1.65	0.60
41:p:313:LEU:HA	41:p:329:SER:HA	1.82	0.60
1:1:1332:A:N7	42:r:45:ILE:HD11	2.17	0.59
11:H:124:ILE:HD11	11:H:162:ILE:HD13	1.83	0.59
42:r:22:GLU:OE2	42:r:22:GLU:N	2.28	0.59
1:1:741:G:N7	27:a:110:LYS:NZ	2.40	0.59
2:2:101:U:H2'	2:2:102:C:O4'	2.02	0.59
24:X:114:ARG:HH21	24:X:116:ASN:HD21	1.50	0.59
1:1:960:C:H2'	1:1:961:A:C8	2.38	0.59
22:V:111:MET:N	22:V:111:MET:SD	2.75	0.59
1:1:371:C:OP2	36:j:56:ARG:NH2	2.36	0.59
1:1:674:A:H2'	1:1:675:C:C6	2.37	0.59
18:Q:90:ASP:OD1	18:Q:91:ASP:N	2.35	0.59
1:1:742:A:H8	27:a:114:LYS:HD3	1.68	0.59
1:1:1016:G:N2	1:1:1170:G:OP1	2.28	0.59
5:B:112:GLU:HG3	5:B:122:TRP:CH2	2.36	0.59
10:G:226:TYR:O	10:G:228:GLU:N	2.36	0.59
17:P:4:TYR:HE2	17:P:16:LYS:HB3	1.67	0.59
1:1:1244:G:OP1	20:S:138:TYR:OH	2.20	0.59
15:N:135:VAL:HG21	15:N:151:ILE:HG21	1.84	0.59
35:i:30:HIS:CG	35:i:31:LEU:H	2.20	0.59
1:1:1025:G:H22	1:1:1088:U:H3	1.49	0.59
1:1:3314:U:OP2	14:M:121:ARG:NH2	2.34	0.59
8:E:99:ARG:NH1	32:f:106:SER:O	2.34	0.59
13:L:36:ARG:HH22	45:v:45:THR:HG21	1.66	0.59
1:1:1262:A:H4'	1:1:1292:G:H8	1.68	0.59
1:1:1598:C:H2'	1:1:1599:A:H8	1.68	0.59
39:n:555:LYS:NZ	39:n:556:GLU:OE2	2.35	0.59
1:1:1606:U:H3	39:n:221:THR:HG22	1.67	0.59
9:F:157:LYS:HD3	9:F:250:LEU:HD22	1.84	0.59
38:m:249:THR:H	38:m:252:GLN:NE2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:574:SER:O	39:n:578:ASN:ND2	2.36	0.59
1:1:1681:G:N2	1:1:1849:G:O2'	2.32	0.59
8:E:71:VAL:HG13	8:E:178:LEU:HD11	1.85	0.59
8:E:77:GLU:OE1	8:E:78:ASP:N	2.17	0.59
26:Z:40:HIS:HA	26:Z:76:ASN:HA	1.85	0.59
39:n:140:LEU:HD22	39:n:230:MET:HG3	1.85	0.59
39:n:179:LYS:HE3	39:n:190:GLN:HG2	1.85	0.59
1:1:252:A:OP1	45:v:151:ARG:NH2	2.36	0.58
1:1:379:G:N1	1:1:382:A:OP2	2.36	0.58
5:B:301:THR:HG23	28:b:437:ASP:H	1.66	0.58
10:G:83:ASP:OD1	10:G:85:ASN:N	2.36	0.58
14:M:61:ILE:HD11	14:M:83:VAL:HG22	1.84	0.58
15:N:38:ARG:HH12	15:N:60:VAL:HG22	1.68	0.58
16:O:74:PHE:HB3	16:O:79:ARG:HB3	1.85	0.58
1:1:1517:G:H2'	1:1:1519:G:C8	2.38	0.58
1:1:1714:A:H2'	1:1:1715:G:H8	1.67	0.58
13:L:80:LEU:HD11	13:L:97:VAL:HG22	1.84	0.58
17:P:40:SER:HA	17:P:113:ILE:HG22	1.85	0.58
1:1:369:A:O3'	36:j:45:ARG:NH2	2.35	0.58
4:A:84:TYR:O	4:A:87:ASN:ND2	2.35	0.58
13:L:63:ILE:HD12	13:L:66:ASN:HD21	1.69	0.58
25:Y:116:ASP:OD1	25:Y:117:LEU:N	2.37	0.58
36:j:82:LYS:HD3	36:j:83:PRO:HD2	1.84	0.58
43:t:159:PHE:HB3	43:t:166:ARG:HH12	1.69	0.58
1:1:984:A:O2'	1:1:1000:G:N2	2.37	0.58
2:2:128:U:P	39:n:74:HIS:HE2	2.26	0.58
39:n:349:ASN:ND2	39:n:431:GLY:O	2.36	0.58
1:1:1803:U:OP1	1:1:1805:A:N6	2.36	0.58
1:1:3217:U:H1'	1:1:3218:A:H5"	1.86	0.58
1:1:3306:C:O2	14:M:6:ARG:NH1	2.34	0.58
27:a:103:VAL:HG12	27:a:108:TYR:HB2	1.86	0.58
39:n:113:TYR:OH	39:n:224:GLU:OE1	2.20	0.58
1:1:194:A:N3	1:1:215:C:O2'	2.35	0.58
3:3:47:ASN:OD1	3:3:48:SER:N	2.36	0.58
6:C:288:ASP:CG	6:C:291:ARG:HB2	2.28	0.58
6:C:314:HIS:CE1	9:F:169:PRO:HG2	2.38	0.58
11:H:88:TYR:HB3	11:H:144:LEU:HB2	1.85	0.58
14:M:86:LYS:O	14:M:89:SER:OG	2.20	0.58
31:e:17:HIS:CG	31:e:39:VAL:HG21	2.38	0.58
1:1:764:U:H3'	1:1:765:G:H8	1.69	0.58
1:1:1527:G:N2	1:1:1527:G:OP2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:79:THR:HG21	8:E:95:ARG:HD2	1.85	0.58
39:n:244:ARG:NH1	39:n:266:GLU:OE1	2.37	0.58
41:p:222:GLY:HA2	41:p:264:LEU:HA	1.86	0.58
43:t:41:GLU:OE1	43:t:45:LYS:NZ	2.32	0.58
1:1:364:G:O2'	6:C:83:GLY:O	2.22	0.58
1:1:1739:A:OP2	1:1:1780:G:N1	2.30	0.58
38:m:387:ARG:H	38:m:402:GLY:HA2	1.69	0.58
1:1:717:A:OP2	6:C:48:LYS:NZ	2.36	0.58
1:1:1472:U:OP1	6:C:78:ARG:NH2	2.36	0.58
3:3:74:SER:HB3	6:C:148:PRO:HA	1.85	0.58
19:R:20:ARG:HE	19:R:21:LYS:HE3	1.69	0.58
40:o:106:VAL:HG13	40:o:181:ILE:HG23	1.85	0.58
1:1:1557:U:OP1	1:1:1642:U:N3	2.35	0.57
25:Y:58:ILE:HG22	25:Y:59:ARG:HG2	1.85	0.57
38:m:578:ALA:HB3	38:m:591:ALA:HB3	1.86	0.57
1:1:3210:A:N1	42:r:33:HIS:NE2	2.47	0.57
6:C:156:ASP:OD2	6:C:255:SER:OG	2.22	0.57
1:1:34:A:N3	1:1:842:A:O2'	2.37	0.57
14:M:12:ARG:HG3	14:M:62:VAL:HG22	1.85	0.57
18:Q:90:ASP:OD2	18:Q:110:SER:OG	2.22	0.57
27:a:82:LEU:HD23	27:a:83:PRO:N	2.19	0.57
40:o:148:TYR:OH	48:6:98:G:OP1	2.20	0.57
40:o:183:GLU:HA	40:o:186:VAL:HG13	1.85	0.57
41:p:97:TYR:HA	41:p:431:ASN:HA	1.85	0.57
1:1:3135:G:OP1	5:B:62:ARG:NH1	2.37	0.57
1:1:3172:C:OP1	30:d:71:ASN:ND2	2.28	0.57
5:B:159:ARG:NE	5:B:182:GLN:OE1	2.28	0.57
22:V:17:LEU:HB3	22:V:53:ALA:HB3	1.86	0.57
25:Y:2:LYS:HD3	25:Y:9:SER:HB2	1.86	0.57
30:d:18:THR:HB	30:d:77:ARG:HH11	1.69	0.57
42:r:184:THR:HA	42:r:191:THR:HA	1.86	0.57
1:1:614:G:OP1	31:e:59:LYS:NZ	2.33	0.57
33:g:43:ARG:HA	33:g:50:PRO:HA	1.87	0.57
45:v:174:TYR:HE2	45:v:185:ASP:HB2	1.69	0.57
6:C:97:ARG:NH1	6:C:98:SER:OG	2.38	0.57
20:S:13:VAL:N	20:S:54:THR:O	2.33	0.57
43:t:214:THR:O	43:t:248:GLN:NE2	2.37	0.57
1:1:444:A:H61	1:1:647:A:H62	1.52	0.57
5:B:274:HIS:O	5:B:275:ARG:NH1	2.35	0.57
1:1:2428:U:H2'	1:1:2429:A:H8	1.70	0.57
1:1:3318:A:OP2	1:1:3319:G:N2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:153:HIS:O	20:S:156:THR:OG1	2.23	0.57
22:V:42:PHE:CD1	22:V:61:LEU:HD21	2.40	0.57
40:o:104:LYS:HE3	40:o:152:GLU:OE1	2.04	0.57
40:o:133:ARG:NH2	40:o:191:PHE:HB2	2.19	0.57
1:1:58:G:H5"	15:N:154:PRO:HB2	1.85	0.57
1:1:2993:G:H22	42:r:5:GLU:HA	1.70	0.57
2:2:95:G:OP1	34:h:4:LYS:NZ	2.38	0.57
16:O:152:ASP:OD2	16:O:153:ILE:N	2.37	0.57
24:X:72:MET:HE3	24:X:75:ILE:HD11	1.87	0.57
39:n:594:LYS:HA	39:n:597:ILE:HD12	1.87	0.57
8:E:78:ASP:OD1	8:E:79:THR:N	2.38	0.56
9:F:110:MET:HE3	9:F:115:LEU:HB2	1.87	0.56
20:S:157:GLY:C	20:S:159:VAL:H	2.12	0.56
35:i:58:LEU:HB3	35:i:67:ALA:HB2	1.87	0.56
1:1:1731:A:OP2	1:1:1789:A:N6	2.33	0.56
11:H:78:MET:N	11:H:78:MET:SD	2.78	0.56
26:Z:39:GLY:O	26:Z:77:TYR:N	2.38	0.56
38:m:249:THR:N	38:m:252:GLN:OE1	2.38	0.56
38:m:348:ARG:N	43:t:16:GLU:O	2.34	0.56
47:T:143:THR:OG1	47:T:147:GLU:OE2	2.23	0.56
1:1:27:C:N4	1:1:57:A:H61	2.04	0.56
8:E:60:LEU:HD23	8:E:65:PHE:HB2	1.88	0.56
8:E:120:THR:HG23	8:E:123:TYR:H	1.70	0.56
11:H:95:ALA:H	11:H:175:ASP:HB2	1.70	0.56
42:r:52:GLU:OE1	42:r:52:GLU:N	2.39	0.56
1:1:1515:A:N6	1:1:1927:C:O2	2.38	0.56
9:F:47:LYS:HE3	9:F:186:LEU:HD13	1.85	0.56
27:a:131:ARG:NH1	27:a:134:GLU:OE2	2.39	0.56
1:1:710:G:OP1	13:L:39:ARG:NH2	2.32	0.56
11:H:90:MET:HE1	11:H:179:VAL:HA	1.88	0.56
1:1:1142:U:O2'	1:1:1143:A:O5'	2.21	0.56
1:1:1338:G:H5'	16:O:61:LYS:HE3	1.86	0.56
1:1:3175:U:C5	30:d:30:PHE:HE2	2.23	0.56
8:E:52:LEU:HD13	8:E:80:LEU:HD11	1.86	0.56
30:d:100:ASP:OD1	30:d:100:ASP:N	2.35	0.56
31:e:20:ASP:OD1	31:e:21:ARG:N	2.39	0.56
41:p:372:ALA:HA	41:p:382:VAL:HA	1.88	0.56
1:1:216:A:N3	6:C:223:ASN:ND2	2.54	0.56
1:1:1011:G:H2'	1:1:1012:A:H4'	1.87	0.56
1:1:3225:A:N6	1:1:3227:U:O2	2.38	0.56
10:G:109:LEU:HD23	38:m:234:ARG:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:36:ILE:HA	17:P:39:MET:SD	2.46	0.56
39:n:235:PHE:O	39:n:239:ASN:ND2	2.39	0.56
42:r:55:ARG:O	42:r:59:ILE:HG22	2.05	0.56
1:1:1202:G:P	9:F:224:ARG:HH22	2.29	0.56
1:1:1557:U:O2'	24:X:110:ASN:OD1	2.22	0.56
1:1:1567:U:H2'	1:1:1568:A:H8	1.70	0.56
1:1:3477:A:C4	30:d:26:TYR:HD2	2.24	0.56
14:M:65:LEU:HD21	14:M:74:VAL:HG22	1.88	0.56
25:Y:78:LEU:HD13	25:Y:97:GLY:HA3	1.88	0.56
30:d:24:ARG:HG2	30:d:24:ARG:NH1	2.21	0.56
38:m:319:SER:OG	39:n:405:ASP:OD2	2.24	0.56
40:o:174:LYS:NZ	48:6:94:A:OP2	2.33	0.56
13:L:62:THR:HG22	13:L:63:ILE:H	1.71	0.56
25:Y:85:THR:HG21	25:Y:93:SER:HB3	1.86	0.56
45:v:9:LYS:HA	45:v:12:SER:HB3	1.88	0.56
8:E:72:VAL:HA	8:E:82:VAL:HG23	1.87	0.56
27:a:127:ARG:HH21	27:a:128:TYR:HE2	1.53	0.56
45:v:3:ASN:OD1	45:v:4:PRO:HD2	2.06	0.56
1:1:1658:G:OP1	39:n:566:SER:OG	2.23	0.55
1:1:3316:G:N1	1:1:3359:U:O2	2.39	0.55
1:1:1201:A:H5"	9:F:224:ARG:HH21	1.71	0.55
43:t:138:PRO:HG2	43:t:139:TYR:CE1	2.41	0.55
1:1:741:G:O6	27:a:70:ARG:NH1	2.39	0.55
1:1:1531:C:H2'	1:1:1532:A:C8	2.39	0.55
1:1:1640:A:O2'	1:1:1642:U:OP2	2.23	0.55
1:1:2477:C:H1'	17:P:69:ARG:HH12	1.72	0.55
1:1:3193:U:H4'	5:B:279:ASN:HB3	1.88	0.55
3:3:49:ARG:HG3	3:3:100:TRP:HE1	1.69	0.55
6:C:108:TRP:CD1	13:L:22:VAL:HG21	2.41	0.55
45:v:38:GLN:OE1	45:v:38:GLN:HA	2.06	0.55
1:1:347:C:OP1	1:1:1414:G:O2'	2.25	0.55
1:1:545:A:N6	1:1:547:G:N3	2.53	0.55
1:1:991:C:O2'	1:1:994:A:N6	2.40	0.55
1:1:1643:C:OP1	24:X:108:LYS:NZ	2.29	0.55
1:1:2925:G:H2'	1:1:2926:G:C8	2.41	0.55
8:E:77:GLU:CD	8:E:78:ASP:H	2.12	0.55
23:W:136:VAL:HA	23:W:186:PRO:HA	1.89	0.55
39:n:39:LEU:O	39:n:122:ARG:NH1	2.39	0.55
6:C:283:ILE:HD11	18:Q:106:ARG:HE	1.71	0.55
8:E:105:SER:N	8:E:195:PHE:O	2.38	0.55
9:F:108:LYS:NZ	9:F:111:GLN:OE1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:132:ARG:HA	27:a:135:GLU:OE1	2.06	0.55
42:r:6:TYR:HA	42:r:9:GLU:OE1	2.06	0.55
1:1:425:A:H2'	1:1:426:A:C8	2.41	0.55
1:1:718:A:N1	2:2:36:C:O2'	2.39	0.55
1:1:1352:G:H21	20:S:111:ALA:HB2	1.71	0.55
1:1:3210:A:O3'	11:H:62:ARG:NH1	2.40	0.55
2:2:83:G:H2'	2:2:84:C:C6	2.41	0.55
6:C:14:ASP:OD1	6:C:16:SER:N	2.29	0.55
14:M:43:CYS:HB3	14:M:45:GLU:CD	2.32	0.55
39:n:437:ASP:OD1	39:n:438:LEU:N	2.40	0.55
1:1:1262:A:O2'	1:1:1292:G:H1'	2.07	0.55
1:1:1546:U:H2'	1:1:1547:G:H8	1.71	0.55
1:1:1701:G:H2'	1:1:1702:A:C8	2.42	0.55
1:1:3147:U:H2'	1:1:3148:G:H8	1.71	0.55
6:C:140:ARG:HG3	6:C:140:ARG:NH1	2.19	0.55
11:H:87:ARG:HE	11:H:89:LYS:HE3	1.71	0.55
41:p:231:GLU:HA	41:p:259:ARG:HA	1.89	0.55
1:1:3416:A:N6	5:B:121:ASN:OD1	2.40	0.55
1:1:3426:G:H2'	1:1:3427:G:H8	1.72	0.55
3:3:16:CYS:HA	6:C:139:ALA:HB1	1.88	0.55
5:B:283:TYR:CZ	5:B:325:ASN:HB3	2.41	0.55
6:C:283:ILE:HG22	6:C:284:ILE:HG23	1.89	0.55
14:M:7:TYR:O	14:M:12:ARG:NE	2.40	0.55
15:N:110:CYS:HB3	15:N:113:LEU:HD12	1.89	0.55
1:1:3039:U:H2'	1:1:3042:G:N7	2.22	0.55
10:G:130:TYR:HE1	10:G:202:GLU:HG2	1.72	0.55
13:L:77:LEU:HD22	13:L:87:ARG:HD3	1.89	0.55
24:X:112:LEU:HD21	24:X:120:LYS:HD2	1.88	0.55
1:1:1353:U:OP1	20:S:116:ARG:NH1	2.30	0.55
1:1:3222:C:O2'	11:H:158:ASN:OD1	2.25	0.55
3:3:10:VAL:HG22	6:C:34:PRO:HG3	1.89	0.55
18:Q:61:ILE:HD11	18:Q:65:LYS:HG2	1.88	0.55
25:Y:31:SER:HA	25:Y:48:PRO:HA	1.88	0.55
27:a:89:LYS:HG3	27:a:90:TYR:CD2	2.42	0.55
30:d:42:VAL:HG23	30:d:54:VAL:HG21	1.89	0.55
39:n:591:ARG:HA	39:n:594:LYS:HE3	1.88	0.55
1:1:985:G:H21	1:1:1147:G:H1	1.54	0.54
1:1:1231:A:O2'	1:1:1232:G:N2	2.40	0.54
1:1:1701:G:H2'	1:1:1702:A:H8	1.72	0.54
1:1:3033:G:H2'	1:1:3034:G:C8	2.42	0.54
20:S:162:ALA:HB3	20:S:165:LYS:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:19:ILE:HG21	30:d:76:LEU:HD13	1.88	0.54
1:1:985:G:N2	1:1:1147:G:H1	2.04	0.54
1:1:3244:C:H2'	1:1:3245:G:C8	2.42	0.54
11:H:115:PHE:HE2	11:H:163:CYS:HA	1.71	0.54
38:m:618:SER:H	38:m:633:SER:HA	1.71	0.54
1:1:1696:G:H2'	1:1:1697:G:C8	2.42	0.54
8:E:89:ASN:HB3	8:E:91:VAL:HG23	1.88	0.54
19:R:38:ARG:HB3	19:R:42:ARG:NH1	2.22	0.54
39:n:141:PHE:CD2	39:n:202:VAL:HG22	2.41	0.54
1:1:1156:U:H2'	1:1:1157:G:H8	1.72	0.54
1:1:1715:G:H1	1:1:1723:U:H3	1.56	0.54
1:1:1780:G:H4'	1:1:1781:G:H21	1.72	0.54
2:2:131:G:H2'	2:2:132:G:C8	2.43	0.54
32:f:37:ASP:OD1	32:f:37:ASP:N	2.41	0.54
39:n:166:GLU:O	39:n:238:TYR:OH	2.25	0.54
39:n:183:SER:O	39:n:204:TYR:OH	2.20	0.54
41:p:106:TRP:O	41:p:122:TYR:N	2.40	0.54
2:2:54:G:O2'	2:2:69:A:N1	2.35	0.54
6:C:228:GLU:OE1	6:C:239:GLN:NE2	2.41	0.54
14:M:120:ARG:HD2	16:O:183:LYS:HD2	1.89	0.54
18:Q:63:ILE:HG22	18:Q:90:ASP:HA	1.89	0.54
25:Y:37:GLU:HA	25:Y:40:GLU:OE2	2.08	0.54
1:1:58:G:N2	1:1:60:A:N3	2.56	0.54
1:1:1827:G:H2'	1:1:1828:A:C8	2.43	0.54
1:1:3351:U:H2'	1:1:3352:A:C8	2.43	0.54
32:f:51:CYS:SG	32:f:102:MET:HE3	2.48	0.54
32:f:56:SER:OG	32:f:66:ARG:NE	2.32	0.54
38:m:373:THR:N	38:m:740:THR:O	2.39	0.54
8:E:194:LYS:O	14:M:110:ARG:NH2	2.40	0.54
22:V:51:LEU:H	22:V:51:LEU:HD12	1.73	0.54
24:X:130:ASP:OD1	24:X:132:LEU:N	2.41	0.54
38:m:339:ASP:OD1	43:t:22:ARG:NH1	2.38	0.54
1:1:167:G:H5'	38:m:222:LYS:HD2	1.89	0.54
3:3:49:ARG:HA	3:3:65:LYS:HG3	1.90	0.54
27:a:77:ARG:O	27:a:80:THR:OG1	2.24	0.54
4:A:92:LEU:HD13	35:i:68:ARG:HE	1.72	0.54
9:F:149:LYS:HE2	9:F:153:GLU:OE2	2.08	0.54
20:S:78:ILE:HB	20:S:120:ILE:HD11	1.90	0.54
25:Y:35:SER:OG	25:Y:37:GLU:OE2	2.25	0.54
1:1:178:U:H3	1:1:254:G:H1	1.56	0.54
1:1:1262:A:H5"	1:1:1263:C:H5'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1299:G:H1'	1:1:1304:A:H61	1.73	0.54
1:1:3033:G:H2'	1:1:3034:G:H8	1.74	0.54
2:2:29:C:OP1	6:C:195:LYS:HE2	2.08	0.54
14:M:51:ILE:HD12	14:M:52:ARG:H	1.73	0.54
14:M:97:GLU:HA	14:M:100:LYS:HB3	1.89	0.54
46:y:109:ALA:HB2	46:y:149:GLY:HA2	1.90	0.54
1:1:1915:G:H2'	1:1:1916:G:H8	1.73	0.53
38:m:339:ASP:CG	43:t:22:ARG:HH22	2.16	0.53
39:n:164:CYS:SG	39:n:165:ALA:N	2.81	0.53
41:p:201:GLU:H	41:p:216:SER:HA	1.73	0.53
42:r:19:ASP:OD2	42:r:19:ASP:N	2.33	0.53
1:1:995:G:H2'	1:1:996:G:H8	1.73	0.53
1:1:1644:C:N4	1:1:1645:G:O6	2.41	0.53
1:1:2925:G:H2'	1:1:2926:G:H8	1.74	0.53
1:1:3284:G:H2'	1:1:3285:G:H8	1.73	0.53
11:H:11:LEU:HD23	11:H:12:THR:C	2.34	0.53
20:S:78:ILE:HD11	20:S:109:MET:CE	2.38	0.53
12:K:56:GLN:N	12:K:240:HIS:O	2.40	0.53
14:M:97:GLU:H	14:M:97:GLU:CD	2.17	0.53
22:V:70:ASP:OD1	22:V:71:LEU:N	2.41	0.53
30:d:78:LEU:HD12	30:d:96:VAL:CG2	2.37	0.53
38:m:241:ALA:HB1	38:m:246:ARG:HB2	1.89	0.53
39:n:134:ASP:OD1	39:n:134:ASP:N	2.40	0.53
1:1:276:A:N6	1:1:304:A:OP2	2.34	0.53
1:1:323:C:P	13:L:102:ARG:HH22	2.31	0.53
5:B:372:THR:HG23	5:B:375:GLU:H	1.74	0.53
1:1:1277:G:H1'	1:1:1295:G:H2'	1.91	0.53
1:1:1941:A:H2'	1:1:1942:A:C8	2.43	0.53
1:1:3208:G:O6	1:1:3216:C:H5"	2.09	0.53
1:1:3373:C:H4'	8:E:62:ALA:HB1	1.90	0.53
6:C:289:VAL:O	6:C:293:ILE:HG12	2.08	0.53
8:E:57:VAL:O	8:E:104:THR:OG1	2.22	0.53
8:E:114:VAL:HG21	8:E:160:VAL:HG13	1.91	0.53
11:H:48:LYS:NZ	11:H:50:GLY:O	2.37	0.53
30:d:67:ARG:HG3	30:d:73:PRO:HD3	1.91	0.53
1:1:283:U:H2'	1:1:284:U:H6	1.73	0.53
2:2:31:U:H1'	25:Y:16:LYS:HG3	1.89	0.53
11:H:90:MET:HE2	11:H:90:MET:HA	1.90	0.53
20:S:121:ARG:NH1	47:T:154:VAL:O	2.41	0.53
22:V:82:ARG:HB2	22:V:101:ALA:H	1.74	0.53
31:e:6:ILE:HD13	31:e:60:THR:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:n:194:PHE:HZ	39:n:240:THR:HG21	1.73	0.53
39:n:399:ILE:HB	39:n:416:ARG:HD3	1.89	0.53
1:1:1739:A:N6	1:1:1780:G:O4'	2.42	0.53
1:1:3123:A:H2'	1:1:3124:G:O4'	2.09	0.53
14:M:26:ALA:HB3	14:M:39:ILE:HD12	1.89	0.53
1:1:1253:G:H21	1:1:1317:A:H2	1.55	0.53
1:1:2931:C:H5	1:1:2947:C:H41	1.56	0.53
1:1:3235:A:OP2	5:B:30:LYS:NZ	2.32	0.53
11:H:29:THR:HG22	11:H:34:THR:HG23	1.90	0.53
19:R:12:ALA:HA	19:R:15:LEU:HB3	1.90	0.53
43:t:144:ILE:O	43:t:242:ASN:ND2	2.40	0.53
1:1:1826:C:H2'	1:1:1827:G:H8	1.74	0.53
17:P:50:ASN:HB3	17:P:55:LYS:HB2	1.90	0.53
20:S:80:TYR:OH	20:S:113:HIS:O	2.26	0.53
25:Y:6:ASP:OD1	45:v:20:ARG:HG3	2.09	0.53
38:m:299:SER:H	38:m:302:PRO:HG3	1.74	0.53
40:o:119:LYS:O	40:o:123:MET:HG3	2.09	0.53
1:1:1365:C:H5"	9:F:213:LYS:HB3	1.90	0.53
1:1:3247:U:H4'	1:1:3395:G:H1'	1.90	0.53
5:B:299:ASP:O	5:B:301:THR:OG1	2.24	0.53
10:G:158:ASP:HB3	10:G:159:PRO:HD3	1.91	0.53
30:d:77:ARG:HH22	30:d:108:THR:HA	1.74	0.53
1:1:641:G:H2'	1:1:642:A:H8	1.73	0.52
1:1:761:U:H1'	1:1:762:U:H5'	1.91	0.52
13:L:31:ARG:HD3	13:L:35:ARG:NH1	2.24	0.52
39:n:357:THR:O	39:n:400:THR:N	2.40	0.52
40:o:202:PRO:HB2	40:o:205:THR:OG1	2.09	0.52
1:1:714:A:H5'	1:1:717:A:N7	2.24	0.52
14:M:40:ASP:OD1	14:M:41:SER:N	2.41	0.52
41:p:273:MET:H	41:p:288:GLY:HA2	1.74	0.52
48:6:87:A:H2'	48:6:88:G:O4'	2.08	0.52
1:1:530:A:N1	20:S:64:SER:N	2.57	0.52
1:1:1695:C:H2'	1:1:1696:G:H8	1.74	0.52
1:1:3104:G:H2'	1:1:3105:G:H8	1.75	0.52
1:1:3423:A:H2'	1:1:3424:A:C8	2.43	0.52
3:3:62:LEU:HD22	3:3:93:ILE:HD12	1.91	0.52
8:E:83:THR:OG1	8:E:91:VAL:O	2.28	0.52
8:E:117:GLU:OE1	8:E:117:GLU:N	2.24	0.52
24:X:37:LEU:HD11	39:n:82:ARG:NH1	2.24	0.52
39:n:141:PHE:CE1	39:n:164:CYS:HB2	2.45	0.52
39:n:369:LEU:HA	39:n:372:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:227:ASP:HA	10:G:230:ARG:HH11	1.75	0.52
27:a:102:ASN:HA	27:a:125:GLN:HB2	1.92	0.52
41:p:296:TRP:HA	41:p:303:ASN:HA	1.91	0.52
1:1:216:A:H4'	1:1:218:A:N7	2.25	0.52
1:1:837:G:H4'	6:C:75:ARG:HB2	1.91	0.52
1:1:1308:C:O2'	1:1:1309:A:O5'	2.24	0.52
6:C:314:HIS:ND1	6:C:314:HIS:O	2.43	0.52
13:L:50:PRO:HD2	34:h:118:TYR:CE2	2.44	0.52
17:P:48:LEU:HD12	17:P:88:VAL:HB	1.90	0.52
25:Y:30:MET:HE3	25:Y:77:PHE:HA	1.91	0.52
16:O:184:GLU:OE1	16:O:184:GLU:N	2.38	0.52
19:R:17:CYS:SG	19:R:52:ARG:NH1	2.79	0.52
30:d:66:LYS:HB3	30:d:67:ARG:HH21	1.75	0.52
38:m:337:CYS:HB3	39:n:222:PHE:CE2	2.44	0.52
1:1:1918:G:H1	1:1:1921:C:P	2.32	0.52
38:m:503:SER:N	38:m:565:SER:O	2.42	0.52
1:1:2931:C:H3'	1:1:2932:A:C8	2.37	0.52
1:1:3284:G:H2'	1:1:3285:G:C8	2.45	0.52
1:1:3417:A:H1'	1:1:3490:A:H4'	1.92	0.52
41:p:192:LEU:O	41:p:258:ALA:N	2.43	0.52
1:1:621:G:H5"	9:F:44:ARG:NH2	2.21	0.52
1:1:1714:A:H2'	1:1:1715:G:C8	2.45	0.52
1:1:3112:A:O2'	1:1:3113:A:H8	1.93	0.52
32:f:72:ILE:HD12	32:f:82:VAL:HG21	1.92	0.52
38:m:338:LEU:HB2	43:t:22:ARG:NH2	2.25	0.52
39:n:357:THR:HG22	39:n:379:LYS:HB3	1.92	0.52
41:p:151:TRP:HA	41:p:158:PHE:HA	1.91	0.52
1:1:1260:G:H2'	1:1:1261:G:H8	1.74	0.52
2:2:111:G:OP2	2:2:113:A:O2'	2.28	0.52
3:3:71:HIS:C	3:3:72:PHE:HD2	2.18	0.52
3:3:110:GLN:O	3:3:113:THR:OG1	2.27	0.52
40:o:200:ARG:NH1	48:6:181:C:O4'	2.43	0.52
1:1:522:G:H1	1:1:604:U:H3	1.58	0.51
1:1:1773:A:H2'	1:1:1774:G:H8	1.74	0.51
3:3:19:ARG:NH2	3:3:38:CYS:SG	2.77	0.51
1:1:700:C:O2'	1:1:704:U:OP1	2.23	0.51
1:1:1389:A:H4'	1:1:1390:A:O5'	2.10	0.51
8:E:165:LEU:HG	8:E:166:PRO:HD3	1.92	0.51
9:F:138:GLU:OE2	9:F:228:HIS:NE2	2.43	0.51
9:F:237:LYS:HD2	9:F:239:ASP:H	1.76	0.51
31:e:35:ILE:O	31:e:41:ARG:NH2	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:26:GLU:O	34:h:30:LEU:N	2.38	0.51
43:t:89:LEU:HD11	43:t:122:PHE:HB3	1.92	0.51
43:t:179:LEU:HB3	43:t:184:VAL:HB	1.92	0.51
6:C:281:GLU:OE1	18:Q:112:ARG:NE	2.43	0.51
8:E:59:ILE:HG12	8:E:69:ARG:HG2	1.93	0.51
20:S:41:TRP:HH2	20:S:55:GLY:HA3	1.75	0.51
1:1:174:U:HO2'	1:1:259:A:H61	1.59	0.51
1:1:391:G:N2	1:1:394:A:OP2	2.30	0.51
1:1:1277:G:N3	1:1:1295:G:O2'	2.38	0.51
17:P:4:TYR:CE2	17:P:16:LYS:HB3	2.46	0.51
25:Y:26:ARG:O	25:Y:30:MET:HG3	2.10	0.51
27:a:7:LYS:HG2	27:a:11:LEU:HD12	1.93	0.51
42:r:154:THR:HA	42:r:213:VAL:HA	1.92	0.51
1:1:1695:C:H2'	1:1:1696:G:C8	2.45	0.51
1:1:3147:U:H2'	1:1:3148:G:C8	2.45	0.51
5:B:82:PRO:HG2	5:B:169:THR:HG22	1.91	0.51
38:m:331:LYS:NZ	39:n:213:ASP:OD2	2.37	0.51
41:p:109:GLY:HA3	41:p:148:SER:HA	1.91	0.51
1:1:118:U:N3	1:1:122:A:OP2	2.22	0.51
1:1:1259:A:H2'	1:1:1260:G:C8	2.46	0.51
1:1:1605:U:O4	1:1:1608:C:H5"	2.10	0.51
1:1:2925:G:H5'	28:b:135:GLY:HA3	1.92	0.51
1:1:3148:G:H2'	1:1:3149:G:H8	1.76	0.51
13:L:80:LEU:HB3	13:L:85:VAL:HG23	1.91	0.51
16:O:122:PRO:HG3	20:S:168:ALA:HB2	1.92	0.51
21:U:51:VAL:HA	21:U:65:ALA:HA	1.93	0.51
30:d:14:THR:HG23	30:d:81:SER:HB3	1.93	0.51
30:d:59:SER:O	30:d:62:LYS:HB2	2.09	0.51
40:o:110:GLY:N	40:o:177:GLN:O	2.39	0.51
1:1:601:C:OP2	9:F:149:LYS:HE3	2.10	0.51
1:1:1156:U:H2'	1:1:1157:G:C8	2.45	0.51
1:1:1183:G:OP2	1:1:1183:G:N2	2.25	0.51
1:1:1309:A:HO2'	1:1:1310:C:P	2.34	0.51
1:1:1312:U:H2'	1:1:1313:G:H8	1.76	0.51
1:1:1629:A:H1'	1:1:1650:C:H1'	1.93	0.51
1:1:2432:U:H2'	1:1:2433:A:C8	2.46	0.51
1:1:3000:U:H2'	1:1:3001:C:C6	2.46	0.51
24:X:132:LEU:O	24:X:136:ASN:ND2	2.42	0.51
41:p:363:ALA:HA	41:p:371:PHE:HA	1.92	0.51
42:r:182:ASN:HA	42:r:193:GLN:HA	1.92	0.51
1:1:1710:G:H1	1:1:1728:U:H3	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:28:CYS:N	3:3:36:GLY:O	2.43	0.51
8:E:31:TYR:HB2	31:e:87:LYS:HB3	1.93	0.51
17:P:4:TYR:CE2	17:P:16:LYS:HD2	2.45	0.51
18:Q:41:SER:OG	18:Q:134:THR:O	2.27	0.51
24:X:62:ILE:HD13	24:X:85:VAL:HG23	1.93	0.51
30:d:49:MET:HG3	30:d:80:LEU:HD21	1.92	0.51
34:h:87:THR:HG22	34:h:89:ALA:H	1.76	0.51
38:m:326:TYR:CE2	39:n:185:LYS:HD3	2.46	0.51
48:6:58:A:H2'	48:6:59:A:C8	2.46	0.51
1:1:59:G:H4'	1:1:60:A:OP1	2.11	0.51
1:1:715:U:H4'	25:Y:3:PHE:CE1	2.46	0.51
1:1:997:A:O2'	1:1:998:U:OP1	2.24	0.51
1:1:1341:G:O2'	1:1:2468:A:O2'	2.21	0.51
1:1:2454:C:H2'	1:1:2455:U:H6	1.75	0.51
20:S:157:GLY:O	20:S:159:VAL:N	2.44	0.51
39:n:260:LEU:HD12	39:n:374:ARG:HH21	1.76	0.51
1:1:1213:G:N2	1:1:1356:U:O2	2.44	0.51
1:1:1915:G:H2'	1:1:1916:G:C8	2.46	0.51
5:B:306:THR:HG21	5:B:316:VAL:HG22	1.93	0.51
6:C:159:GLN:O	6:C:215:THR:OG1	2.29	0.51
8:E:49:ARG:NH1	8:E:98:HIS:O	2.35	0.51
23:W:124:PHE:HA	23:W:208:THR:HA	1.93	0.51
24:X:9:ALA:HA	24:X:13:VAL:HG23	1.91	0.51
38:m:260:SER:OG	38:m:261:GLN:N	2.43	0.51
1:1:526:G:OP1	6:C:342:LYS:NZ	2.44	0.50
1:1:1564:U:OP2	1:1:1565:C:N4	2.40	0.50
1:1:1598:C:H2'	1:1:1599:A:C8	2.46	0.50
20:S:31:PRO:HD2	20:S:35:VAL:HG11	1.93	0.50
42:r:199:VAL:HA	42:r:220:ILE:HA	1.94	0.50
1:1:1674:C:H2'	1:1:1675:G:H8	1.75	0.50
1:1:3276:A:H2'	1:1:3277:A:O4'	2.10	0.50
1:1:3337:A:H2'	1:1:3338:A:C8	2.46	0.50
1:1:3425:C:H4'	30:d:18:THR:HG23	1.93	0.50
2:2:20:A:H4'	17:P:4:TYR:O	2.12	0.50
5:B:143:SER:O	5:B:147:GLU:HG2	2.11	0.50
41:p:383:TRP:HA	41:p:392:ILE:H	1.75	0.50
1:1:531:A:C2	6:C:349:PRO:HD2	2.47	0.50
1:1:1674:C:H2'	1:1:1675:G:C8	2.46	0.50
1:1:1826:C:H2'	1:1:1827:G:C8	2.46	0.50
1:1:1917:U:H3	1:1:1923:G:H1	1.58	0.50
5:B:281:LYS:NZ	5:B:352:GLU:O	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:137:LEU:HD23	6:C:144:ILE:HD13	1.93	0.50
30:d:47:LYS:HG3	30:d:48:HIS:CD2	2.47	0.50
34:h:20:LEU:O	34:h:24:ARG:HG2	2.12	0.50
34:h:106:GLN:O	34:h:110:GLU:HG2	2.11	0.50
6:C:338:LYS:HZ3	6:C:341:VAL:HA	1.75	0.50
10:G:81:THR:HG1	10:G:181:LYS:HZ3	1.52	0.50
24:X:114:ARG:NH2	24:X:116:ASN:HD21	2.08	0.50
42:r:61:MET:HE2	42:r:61:MET:HA	1.93	0.50
1:1:1017:U:O2'	9:F:109:ILE:HD11	2.11	0.50
1:1:1580:A:O2'	15:N:96:ARG:NH2	2.44	0.50
1:1:717:A:N6	45:v:25:LYS:HE2	2.26	0.50
1:1:764:U:H3'	1:1:765:G:C8	2.46	0.50
1:1:1941:A:H2'	1:1:1942:A:H8	1.76	0.50
1:1:3117:A:N6	1:1:3129:A:OP2	2.39	0.50
3:3:3:GLN:CG	3:3:4:ASP:H	2.23	0.50
9:F:158:ARG:NH1	9:F:214:LEU:HA	2.26	0.50
16:O:57:ALA:O	16:O:61:LYS:HG2	2.12	0.50
17:P:14:CYS:O	17:P:16:LYS:HG3	2.11	0.50
20:S:174:THR:O	20:S:174:THR:HG22	2.11	0.50
43:t:146:ASN:O	43:t:150:VAL:HG23	2.11	0.50
1:1:735:G:N2	1:1:738:A:OP2	2.43	0.50
1:1:995:G:H2'	1:1:996:G:C8	2.47	0.50
1:1:1005:A:N6	1:1:1006:A:N6	2.59	0.50
1:1:1309:A:O2'	1:1:1310:C:O5'	2.30	0.50
5:B:331:PRO:HD2	5:B:334:ARG:NE	2.15	0.50
17:P:108:ASP:OD1	17:P:109:MET:N	2.45	0.50
1:1:258:U:H3'	1:1:259:A:H5'	1.94	0.50
20:S:11:ARG:NH1	20:S:56:GLU:OE2	2.44	0.50
22:V:54:ALA:HB2	22:V:60:VAL:HG11	1.94	0.50
26:Z:57:MET:HA	43:t:27:ARG:HH12	1.77	0.50
36:j:28:HIS:CE1	36:j:30:GLN:HB2	2.47	0.50
38:m:302:PRO:O	38:m:316:LYS:NZ	2.45	0.50
1:1:702:A:O2'	27:a:77:ARG:NH1	2.45	0.50
1:1:1533:U:H2'	1:1:1534:G:C8	2.47	0.50
1:1:1879:C:H2'	1:1:1880:A:C8	2.38	0.50
11:H:106:ASN:ND2	11:H:106:ASN:O	2.45	0.50
17:P:12:THR:OG1	17:P:13:LYS:N	2.43	0.50
20:S:59:ALA:C	20:S:60:ILE:HD13	2.37	0.50
35:i:55:VAL:O	35:i:59:ILE:HG12	2.12	0.50
1:1:155:U:OP2	15:N:49:ARG:NH2	2.43	0.49
5:B:208:THR:O	5:B:340:LYS:NZ	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:15:LEU:CD2	19:R:17:CYS:HB2	2.41	0.49
31:e:14:PHE:CG	31:e:50:PRO:HG3	2.47	0.49
39:n:373:ILE:HG22	39:n:378:GLY:HA3	1.94	0.49
41:p:96:ALA:O	41:p:432:GLN:N	2.43	0.49
1:1:1274:G:N3	1:1:1301:A:O2'	2.45	0.49
44:u:22:VAL:HA	44:u:28:VAL:HA	1.95	0.49
48:6:7:U:N3	48:6:47:U:OP1	2.32	0.49
1:1:620:C:O2	6:C:329:ARG:HD3	2.11	0.49
1:1:3421:G:H2'	1:1:3422:G:H8	1.77	0.49
8:E:69:ARG:HD3	8:E:177:TYR:CE1	2.46	0.49
1:1:1509:A:H5'	30:d:62:LYS:HZ2	1.77	0.49
1:1:1610:U:H2'	1:1:1611:G:H8	1.77	0.49
1:1:1670:G:N2	1:1:1673:A:OP2	2.25	0.49
5:B:293:ASN:OD1	5:B:294:ALA:N	2.44	0.49
6:C:190:ARG:HB3	6:C:195:LYS:HB3	1.94	0.49
9:F:91:ILE:HG23	9:F:124:VAL:HB	1.93	0.49
24:X:112:LEU:HD23	24:X:112:LEU:H	1.78	0.49
39:n:406:ARG:HH12	39:n:409:ILE:HG23	1.77	0.49
1:1:372:G:OP1	6:C:62:THR:HG23	2.13	0.49
1:1:511:C:H2'	1:1:512:A:C8	2.47	0.49
1:1:742:A:OP2	27:a:112:LEU:HB3	2.11	0.49
1:1:1533:U:H2'	1:1:1534:G:H8	1.77	0.49
1:1:1632:C:H2'	1:1:1633:G:C8	2.47	0.49
1:1:2454:C:H2'	1:1:2455:U:C6	2.47	0.49
27:a:76:ASP:OD1	27:a:77:ARG:N	2.45	0.49
1:1:1262:A:N6	1:1:1307:U:OP2	2.45	0.49
1:1:1321:A:H2'	1:1:1322:A:H8	1.77	0.49
1:1:3024:C:O2'	1:1:3025:A:O5'	2.27	0.49
1:1:3099:G:O2'	5:B:92:TYR:OH	2.30	0.49
1:1:3160:U:H2'	1:1:3161:G:H8	1.77	0.49
6:C:319:ASN:HD22	6:C:322:LYS:HE2	1.77	0.49
9:F:91:ILE:HD11	9:F:143:TYR:HD2	1.78	0.49
9:F:103:PRO:O	9:F:107:ARG:HG3	2.12	0.49
15:N:99:ARG:HB3	15:N:167:ILE:HG12	1.95	0.49
20:S:80:TYR:CD2	20:S:109:MET:CE	2.93	0.49
22:V:14:ARG:HD2	22:V:15:MET:N	2.27	0.49
22:V:76:MET:HE1	22:V:104:ILE:HG23	1.95	0.49
1:1:620:C:H2'	1:1:621:G:O4'	2.12	0.49
1:1:646:A:HO2'	1:1:647:A:H8	1.60	0.49
1:1:1164:A:H2'	1:1:1165:G:C8	2.48	0.49
1:1:1424:A:OP1	1:1:1425:C:O2'	2.17	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1608:C:H1'	1:1:1609:G:C8	2.47	0.49
1:1:3131:C:O4'	11:H:120:ILE:HD11	2.13	0.49
9:F:127:ASN:OD1	9:F:129:ALA:N	2.46	0.49
17:P:57:ALA:HB3	17:P:81:ALA:HB1	1.93	0.49
19:R:44:LEU:HD21	19:R:49:LEU:HB3	1.95	0.49
30:d:15:ARG:HG2	30:d:110:VAL:HA	1.95	0.49
30:d:26:TYR:HD1	30:d:27:GLY:N	2.11	0.49
43:t:113:ARG:NH1	43:t:205:THR:O	2.46	0.49
1:1:3306:C:N4	14:M:92:TRP:HB2	2.27	0.49
6:C:239:GLN:O	6:C:248:ARG:HD3	2.12	0.49
16:O:11:ASP:OD2	16:O:38:ARG:NH2	2.46	0.49
16:O:61:LYS:O	16:O:73:HIS:NE2	2.40	0.49
38:m:326:TYR:HE2	39:n:185:LYS:HD3	1.78	0.49
41:p:203:VAL:HA	41:p:214:SER:HA	1.95	0.49
1:1:189:G:H1	1:1:243:C:H41	1.60	0.49
1:1:216:A:O2'	1:1:218:A:OP2	2.21	0.49
1:1:1471:C:O2'	6:C:95:MET:HE1	2.13	0.49
1:1:1713:G:H2'	1:1:1714:A:C8	2.48	0.49
6:C:333:TYR:HE2	9:F:59:GLU:HG2	1.78	0.49
11:H:109:VAL:HG22	11:H:125:LYS:HA	1.93	0.49
19:R:25:ASP:HB2	19:R:28:GLU:OE1	2.13	0.49
24:X:85:VAL:HG21	24:X:94:ILE:HG12	1.95	0.49
39:n:38:ILE:HD12	39:n:222:PHE:CZ	2.48	0.49
1:1:3:U:O4	24:X:18:HIS:ND1	2.39	0.49
1:1:306:U:H4'	1:1:307:G:H5'	1.94	0.49
1:1:340:C:OP2	45:v:6:GLN:NE2	2.42	0.49
1:1:538:U:O2	1:1:588:G:N2	2.42	0.49
1:1:1778:A:H2'	1:1:1779:U:C6	2.48	0.49
1:1:1946:A:H2'	1:1:1947:G:C8	2.48	0.49
1:1:3025:A:H2'	1:1:3026:C:C6	2.48	0.49
6:C:140:ARG:HH21	6:C:242:PRO:HG2	1.77	0.49
6:C:288:ASP:O	6:C:288:ASP:OD2	2.31	0.49
8:E:56:THR:OG1	8:E:108:LYS:NZ	2.33	0.49
11:H:44:ILE:HD12	11:H:68:ILE:HD11	1.94	0.49
24:X:96:GLU:HA	24:X:96:GLU:OE2	2.13	0.49
38:m:336:ARG:O	38:m:339:ASP:HB2	2.13	0.49
43:t:133:LEU:HD11	43:t:142:TYR:CG	2.48	0.49
1:1:271:C:H2'	1:1:272:G:H8	1.78	0.48
1:1:2927:C:H42	1:1:2951:G:H1	1.61	0.48
1:1:2951:G:O2'	42:r:191:THR:N	2.32	0.48
16:O:24:VAL:O	16:O:28:LEU:HD23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:7:GLN:NE2	19:R:35:ALA:O	2.32	0.48
38:m:334:PHE:CD1	39:n:219:MET:CE	2.93	0.48
39:n:379:LYS:HG3	39:n:392:PHE:HZ	1.78	0.48
39:n:438:LEU:HG	39:n:446:PRO:HG3	1.95	0.48
43:t:87:THR:OG1	43:t:89:LEU:O	2.31	0.48
1:1:1439:U:H1'	31:e:51:LYS:O	2.13	0.48
1:1:2432:U:H2'	1:1:2433:A:H8	1.79	0.48
5:B:81:THR:O	5:B:81:THR:OG1	2.24	0.48
6:C:147:ILE:HG13	6:C:152:LEU:HD22	1.96	0.48
8:E:149:LEU:HD23	8:E:149:LEU:H	1.78	0.48
16:O:40:GLU:CD	16:O:40:GLU:H	2.20	0.48
41:p:146:LEU:HA	41:p:162:SER:HA	1.95	0.48
43:t:55:GLU:HG2	48:6:2:C:C6	2.49	0.48
1:1:139:U:P	1:1:140:U:H3	2.36	0.48
1:1:182:G:N2	1:1:251:U:O2	2.46	0.48
1:1:1011:G:H21	1:1:1136:A:H1'	1.78	0.48
8:E:59:ILE:HB	8:E:102:ILE:HB	1.95	0.48
9:F:146:PRO:HA	9:F:243:ASN:OD1	2.13	0.48
10:G:143:ILE:HG23	10:G:175:VAL:HG21	1.95	0.48
11:H:88:TYR:CE1	11:H:182:ARG:HG3	2.48	0.48
17:P:122:ALA:HB3	17:P:143:PRO:HB2	1.94	0.48
1:1:623:C:H2'	1:1:624:U:O4'	2.12	0.48
1:1:687:U:H2'	1:1:688:C:C6	2.48	0.48
1:1:994:A:H2'	1:1:995:G:O4'	2.13	0.48
1:1:3113:A:H2'	1:1:3114:C:C6	2.49	0.48
19:R:15:LEU:O	19:R:15:LEU:HD23	2.13	0.48
30:d:49:MET:O	30:d:49:MET:HE3	2.14	0.48
38:m:252:GLN:HA	38:m:255:GLU:HG2	1.95	0.48
38:m:321:ARG:HD2	43:t:185:ILE:HG22	1.94	0.48
38:m:677:ASP:HA	38:m:714:GLY:H	1.78	0.48
43:t:225:VAL:HG23	43:t:228:PHE:HB2	1.94	0.48
45:v:147:LYS:NZ	45:v:151:ARG:HE	2.11	0.48
1:1:1824:C:H2'	1:1:1825:U:C6	2.48	0.48
1:1:3174:A:OP1	1:1:3176:G:H5'	2.14	0.48
17:P:57:ALA:HB2	17:P:83:TRP:NE1	2.28	0.48
18:Q:84:VAL:HB	18:Q:141:VAL:HG23	1.95	0.48
20:S:80:TYR:HB3	20:S:87:HIS:HB2	1.96	0.48
25:Y:4:SER:OG	25:Y:6:ASP:HB2	2.13	0.48
29:c:56:ILE:O	29:c:82:HIS:N	2.45	0.48
30:d:20:HIS:O	30:d:24:ARG:HG3	2.14	0.48
38:m:349:THR:O	38:m:349:THR:OG1	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:86:G:O2'	1:1:98:G:O6	2.30	0.48
1:1:433:C:N3	1:1:660:G:N2	2.61	0.48
1:1:644:A:H4'	1:1:645:U:OP2	2.14	0.48
1:1:705:G:H2'	1:1:706:U:H5'	1.96	0.48
1:1:1380:A:H3'	1:1:1380:A:N3	2.27	0.48
1:1:1658:G:H2'	1:1:1659:G:H8	1.78	0.48
1:1:1784:U:O2	1:1:1784:U:H2'	2.12	0.48
1:1:3118:G:H22	1:1:3127:G:H3'	1.78	0.48
5:B:17:LEU:HD13	5:B:18:PRO:HA	1.94	0.48
8:E:173:ASN:ND2	8:E:176:GLU:OE2	2.37	0.48
10:G:91:PHE:CZ	10:G:180:VAL:HG11	2.48	0.48
10:G:98:ARG:NH2	10:G:188:THR:O	2.47	0.48
11:H:15:LYS:NZ	11:H:16:GLY:O	2.37	0.48
22:V:19:LEU:HD21	22:V:100:ASN:HD22	1.78	0.48
24:X:102:TYR:CE1	24:X:138:ILE:HD11	2.49	0.48
30:d:67:ARG:HG3	30:d:73:PRO:CD	2.44	0.48
31:e:88:THR:HG23	31:e:89:TYR:CD1	2.46	0.48
38:m:341:TYR:CD1	39:n:38:ILE:HD11	2.48	0.48
40:o:103:LYS:HG3	40:o:156:LEU:HD23	1.94	0.48
40:o:107:LEU:HB3	40:o:151:ILE:HG13	1.95	0.48
41:p:145:SER:O	41:p:163:LEU:N	2.43	0.48
1:1:261:A:O2'	38:m:233:LYS:NZ	2.24	0.48
3:3:40:ARG:O	3:3:50:TYR:OH	2.30	0.48
17:P:57:ALA:HB2	17:P:83:TRP:CE2	2.49	0.48
25:Y:58:ILE:O	25:Y:63:LYS:HG3	2.13	0.48
32:f:33:ILE:H	32:f:33:ILE:HD12	1.79	0.48
1:1:546:G:C6	20:S:143:LEU:HD13	2.49	0.48
1:1:1234:A:H4'	1:1:1235:A:O5'	2.13	0.48
1:1:1466:C:O2'	1:1:1468:G:OP2	2.28	0.48
1:1:1516:A:OP2	1:1:1913:A:O2'	2.23	0.48
1:1:3195:C:H42	1:1:3231:U:H3	1.61	0.48
11:H:90:MET:SD	11:H:177:ILE:HG13	2.54	0.48
20:S:56:GLU:OE1	20:S:56:GLU:N	2.46	0.48
22:V:82:ARG:HB2	22:V:101:ALA:N	2.29	0.48
22:V:82:ARG:NH2	22:V:117:THR:O	2.27	0.48
29:c:53:ALA:HA	29:c:107:ILE:HA	1.95	0.48
30:d:75:ARG:NH1	30:d:105:LYS:HE3	2.28	0.48
38:m:469:ALA:HA	38:m:474:VAL:HA	1.96	0.48
41:p:211:VAL:HA	41:p:225:ASP:HA	1.95	0.48
1:1:3188:U:O3'	22:V:50:ARG:NH2	2.47	0.48
1:1:3369:A:H4'	1:1:3370:U:H5'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:338:LYS:HZ3	6:C:341:VAL:CG1	2.23	0.48
12:K:87:ALA:O	12:K:112:THR:N	2.42	0.48
20:S:116:ARG:O	20:S:120:ILE:HG22	2.13	0.48
43:t:181:LYS:CG	43:t:182:TYR:CE1	2.96	0.48
48:6:50:U:H2'	48:6:51:G:C8	2.49	0.48
3:3:114:ARG:HH21	31:e:84:MET:CE	2.23	0.48
4:A:92:LEU:HD12	35:i:65:LYS:HG2	1.96	0.48
6:C:36:LEU:O	6:C:40:VAL:HG23	2.14	0.48
8:E:177:TYR:HE2	14:M:108:PHE:HA	1.79	0.48
16:O:40:GLU:O	16:O:140:GLY:N	2.45	0.48
40:o:185:GLN:N	40:o:185:GLN:OE1	2.47	0.48
1:1:251:U:H2'	1:1:252:A:H8	1.79	0.47
1:1:341:G:OP2	45:v:9:LYS:HE3	2.14	0.47
1:1:548:U:H2'	1:1:549:G:H8	1.79	0.47
1:1:1321:A:H2'	1:1:1322:A:C8	2.49	0.47
1:1:1678:A:H2'	1:1:1679:A:N3	2.29	0.47
1:1:3332:U:H2'	1:1:3333:G:C8	2.49	0.47
4:A:92:LEU:HD13	35:i:68:ARG:NE	2.29	0.47
17:P:47:PHE:HD2	17:P:48:LEU:HD22	1.78	0.47
31:e:16:ARG:HB2	31:e:28:SER:O	2.14	0.47
43:t:85:ASP:CG	43:t:86:GLU:N	2.71	0.47
1:1:1236:A:N1	1:1:1330:U:H5	2.11	0.47
1:1:3123:A:H8	28:b:209:HIS:H	1.61	0.47
5:B:183:VAL:HG23	5:B:183:VAL:O	2.14	0.47
11:H:124:ILE:HD11	11:H:162:ILE:HG21	1.96	0.47
14:M:78:TRP:HE1	14:M:84:CYS:H	1.61	0.47
39:n:126:PHE:CG	39:n:236:LYS:HD3	2.49	0.47
41:p:273:MET:N	41:p:287:VAL:O	2.47	0.47
42:r:60:GLN:O	42:r:64:THR:HG23	2.14	0.47
1:1:339:G:P	45:v:6:GLN:HE21	2.37	0.47
1:1:3333:G:H1	1:1:3354:U:H3	1.62	0.47
2:2:141:A:H2'	2:2:142:A:C8	2.49	0.47
8:E:191:HIS:CD2	8:E:192:LEU:HG	2.49	0.47
11:H:127:LEU:H	11:H:127:LEU:HD12	1.79	0.47
38:m:194:GLU:CD	38:m:194:GLU:H	2.23	0.47
1:1:1295:G:N2	1:1:1296:U:O4	2.40	0.47
1:1:1465:G:N7	27:a:9:ARG:NH1	2.63	0.47
1:1:1540:A:O2'	1:1:1541:G:OP1	2.29	0.47
1:1:1652:G:H2'	1:1:1653:A:H8	1.78	0.47
1:1:2995:A:H4'	11:H:172:LYS:HD3	1.96	0.47
2:2:95:G:N1	25:Y:113:ASP:OD2	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:291:ARG:HH11	6:C:291:ARG:HG3	1.79	0.47
10:G:80:LYS:HB3	10:G:226:TYR:CZ	2.50	0.47
14:M:119:GLN:HA	14:M:122:GLU:OE1	2.13	0.47
20:S:12:LYS:HG2	20:S:21:PRO:HB3	1.95	0.47
22:V:79:ILE:HD13	22:V:128:TRP:CD1	2.48	0.47
27:a:124:VAL:HG22	27:a:126:THR:HG23	1.95	0.47
32:f:14:HIS:CD2	32:f:29:SER:HB3	2.49	0.47
43:t:148:HIS:NE2	43:t:152:GLU:OE2	2.47	0.47
1:1:3099:G:P	5:B:26:ARG:HH22	2.37	0.47
5:B:122:TRP:HE1	5:B:127:LYS:HG3	1.78	0.47
8:E:85:PRO:HB2	8:E:88:VAL:HB	1.97	0.47
17:P:84:PRO:HB2	17:P:87:SER:HB2	1.96	0.47
20:S:76:ILE:HG23	20:S:125:VAL:HG22	1.97	0.47
1:1:3331:U:H3	1:1:3356:A:N6	2.11	0.47
3:3:29:ARG:HA	31:e:81:LEU:HD11	1.97	0.47
5:B:92:TYR:HE2	5:B:159:ARG:HD2	1.79	0.47
6:C:312:ARG:NH2	6:C:315:VAL:HG23	2.29	0.47
8:E:117:GLU:H	8:E:117:GLU:CD	2.15	0.47
9:F:133:MET:HE2	9:F:133:MET:HA	1.94	0.47
32:f:18:GLN:HB3	32:f:28:THR:HG23	1.96	0.47
34:h:79:PRO:HD2	34:h:82:LEU:HD12	1.96	0.47
39:n:172:ILE:HD11	39:n:371:PHE:HA	1.96	0.47
43:t:120:ALA:HB3	43:t:211:PHE:HD2	1.80	0.47
1:1:27:C:H2'	1:1:28:G:H5'	1.95	0.47
1:1:527:C:H5"	6:C:343:ILE:HD11	1.96	0.47
1:1:1209:G:N3	1:1:1359:C:O2'	2.47	0.47
1:1:1260:G:H2'	1:1:1261:G:C8	2.50	0.47
1:1:1594:G:O2'	1:1:1597:G:H5"	2.14	0.47
1:1:2952:C:O2'	1:1:2953:U:H5'	2.14	0.47
2:2:83:G:OP2	25:Y:73:TYR:OH	2.31	0.47
3:3:47:ASN:HB3	3:3:50:TYR:CE2	2.49	0.47
3:3:79:ARG:NH1	3:3:81:LYS:HB2	2.30	0.47
6:C:74:ALA:O	6:C:78:ARG:NH1	2.36	0.47
10:G:80:LYS:HB3	10:G:226:TYR:CE1	2.48	0.47
10:G:183:LYS:HB2	10:G:194:THR:HG23	1.95	0.47
31:e:29:TRP:CZ2	31:e:50:PRO:HD2	2.49	0.47
34:h:13:GLN:NE2	34:h:13:GLN:O	2.47	0.47
43:t:181:LYS:HG3	43:t:182:TYR:CE1	2.49	0.47
1:1:3333:G:H2'	1:1:3334:A:C8	2.49	0.47
1:1:3359:U:O4	14:M:115:ARG:NH2	2.43	0.47
5:B:35:ASP:OD1	5:B:36:ASP:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:311:PHE:N	5:B:315:GLY:O	2.45	0.47
22:V:11:THR:OG1	22:V:12:LYS:N	2.47	0.47
48:6:1:A:O2'	48:6:3:A:N7	2.39	0.47
10:G:55:TYR:O	10:G:59:GLN:HG3	2.14	0.47
11:H:145:GLU:OE1	11:H:145:GLU:N	2.48	0.47
34:h:80:LEU:HA	34:h:83:ARG:HD2	1.97	0.47
45:v:45:THR:HG22	45:v:46:LEU:H	1.79	0.47
1:1:58:G:OP1	15:N:157:LYS:NZ	2.34	0.47
1:1:207:C:OP2	25:Y:59:ARG:NH2	2.38	0.47
1:1:420:G:N3	17:P:118:GLN:NE2	2.63	0.47
1:1:548:U:H2'	1:1:549:G:C8	2.50	0.47
1:1:590:U:O5'	1:1:591:G:H5"	2.15	0.47
1:1:1201:A:H5"	9:F:224:ARG:NH2	2.29	0.47
1:1:1658:G:H2'	1:1:1659:G:C8	2.50	0.47
1:1:1672:A:O2'	1:1:1749:C:O2'	2.28	0.47
1:1:3043:C:H2'	1:1:3044:U:C6	2.50	0.47
5:B:53:MET:HB3	5:B:77:THR:HA	1.96	0.47
11:H:150:GLU:OE1	11:H:150:GLU:N	2.48	0.47
17:P:45:PHE:HE1	17:P:95:LEU:HB3	1.80	0.47
18:Q:94:MET:SD	18:Q:114:ARG:NH2	2.88	0.47
38:m:270:TRP:CH2	39:n:129:ALA:HB2	2.49	0.47
1:1:222:G:OP1	25:Y:11:ARG:NH1	2.46	0.46
1:1:752:G:H3'	1:1:753:G:H8	1.80	0.46
1:1:1222:U:C4	16:O:49:PHE:HD1	2.33	0.46
11:H:148:SER:O	11:H:152:VAL:HG23	2.15	0.46
13:L:129:LYS:HD3	13:L:129:LYS:HA	1.77	0.46
14:M:78:TRP:HE1	14:M:84:CYS:N	2.14	0.46
18:Q:95:LEU:HD13	27:a:91:LEU:HD21	1.97	0.46
40:o:106:VAL:HG23	40:o:191:PHE:HZ	1.80	0.46
42:r:20:HIS:CE1	42:r:24:LYS:HD3	2.50	0.46
1:1:1388:G:OP1	3:3:41:GLN:NE2	2.48	0.46
1:1:1791:G:H21	37:k:71:GLY:HA3	1.79	0.46
11:H:71:VAL:O	11:H:75:ILE:HG12	2.15	0.46
14:M:12:ARG:O	14:M:28:ILE:HG22	2.15	0.46
20:S:33:GLU:HG2	20:S:34:SER:N	2.30	0.46
30:d:19:ILE:HD13	30:d:44:PHE:CE2	2.49	0.46
30:d:38:ILE:HD11	30:d:64:VAL:HG11	1.97	0.46
43:t:155:TYR:HE1	43:t:187:ILE:HB	1.79	0.46
1:1:1262:A:H4'	1:1:1292:G:C8	2.48	0.46
5:B:32:PHE:CG	5:B:182:GLN:HG3	2.51	0.46
5:B:57:VAL:HG13	5:B:71:GLU:CD	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:132:GLU:OE1	9:F:132:GLU:N	2.46	0.46
11:H:5:ILE:HG21	14:M:34:HIS:CE1	2.50	0.46
17:P:60:PHE:O	17:P:64:ASN:HB3	2.16	0.46
38:m:347:ARG:HA	43:t:17:VAL:HA	1.96	0.46
41:p:157:SER:HA	41:p:171:VAL:HA	1.98	0.46
48:6:11:C:H2'	48:6:12:A:C8	2.50	0.46
1:1:283:U:H2'	1:1:284:U:C6	2.49	0.46
1:1:1008:U:N3	1:1:1009:C:N3	2.63	0.46
6:C:285:SER:OG	6:C:286:ASN:N	2.48	0.46
16:O:86:ARG:HG2	16:O:86:ARG:HH11	1.81	0.46
20:S:25:ARG:HH22	20:S:27:ARG:HD2	1.80	0.46
24:X:6:ALA:HB1	40:o:161:VAL:HG11	1.98	0.46
25:Y:2:LYS:O	25:Y:2:LYS:HG3	2.15	0.46
30:d:16:ASP:OD2	30:d:16:ASP:C	2.59	0.46
1:1:742:A:C8	27:a:114:LYS:HD3	2.48	0.46
1:1:1606:U:N3	39:n:221:THR:HG22	2.29	0.46
3:3:63:TYR:CE1	3:3:79:ARG:HB2	2.51	0.46
11:H:36:LYS:HE3	11:H:36:LYS:HB2	1.81	0.46
11:H:127:LEU:HB2	11:H:151:ASN:OD1	2.15	0.46
20:S:11:ARG:HH12	20:S:14:PRO:HD3	1.81	0.46
31:e:71:PHE:HD2	31:e:82:LEU:HD11	1.81	0.46
38:m:249:THR:O	38:m:252:GLN:OE1	2.33	0.46
39:n:55:LYS:HA	39:n:55:LYS:HD3	1.84	0.46
40:o:117:TYR:O	40:o:121:MET:HG3	2.16	0.46
1:1:353:G:O2'	2:2:33:G:N3	2.49	0.46
1:1:740:U:H2'	1:1:741:G:O4'	2.16	0.46
5:B:46:PHE:CE1	5:B:84:MET:HE1	2.49	0.46
9:F:53:LYS:O	9:F:56:GLU:HG2	2.15	0.46
10:G:139:VAL:O	10:G:143:ILE:HD12	2.15	0.46
17:P:71:ALA:O	17:P:74:LYS:HG2	2.15	0.46
18:Q:29:VAL:O	18:Q:33:ARG:N	2.47	0.46
30:d:11:GLN:O	30:d:12:VAL:C	2.59	0.46
30:d:19:ILE:HD13	30:d:44:PHE:HE2	1.81	0.46
30:d:19:ILE:N	30:d:76:LEU:O	2.44	0.46
34:h:97:TYR:O	34:h:101:ARG:HG2	2.15	0.46
38:m:334:PHE:CD1	39:n:214:VAL:HG23	2.50	0.46
1:1:1344:G:OP1	16:O:83:LYS:NZ	2.41	0.46
1:1:1347:U:OP1	16:O:130:LEU:HA	2.15	0.46
1:1:1509:A:O3'	30:d:66:LYS:NZ	2.48	0.46
1:1:1712:A:H2'	1:1:1713:G:C8	2.51	0.46
1:1:1914:A:H2'	1:1:1915:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3148:G:H2'	1:1:3149:G:C8	2.50	0.46
1:1:3333:G:H2'	1:1:3334:A:H8	1.80	0.46
3:3:65:LYS:HE3	3:3:76:LEU:HD21	1.96	0.46
6:C:140:ARG:NH2	6:C:242:PRO:HG2	2.30	0.46
6:C:312:ARG:CZ	6:C:315:VAL:HG23	2.44	0.46
11:H:74:ILE:O	11:H:78:MET:HE1	2.15	0.46
13:L:36:ARG:NH2	45:v:45:THR:HG21	2.31	0.46
15:N:165:THR:HG22	15:N:166:SER:H	1.79	0.46
16:O:48:PHE:HA	16:O:137:CYS:HB2	1.97	0.46
22:V:42:PHE:CZ	22:V:61:LEU:HD11	2.50	0.46
24:X:96:GLU:HG3	24:X:100:LYS:NZ	2.31	0.46
30:d:82:ARG:HG2	30:d:92:LEU:HD22	1.98	0.46
38:m:204:ASP:OD1	38:m:204:ASP:N	2.47	0.46
1:1:976:C:N4	27:a:9:ARG:O	2.41	0.46
1:1:1284:U:O2'	1:1:1294:A:N3	2.41	0.46
1:1:1842:U:H2'	1:1:1843:C:C6	2.51	0.46
1:1:3160:U:H2'	1:1:3161:G:C8	2.50	0.46
1:1:3203:C:N3	1:1:3224:G:N2	2.64	0.46
3:3:109:LYS:HA	3:3:112:LEU:HD12	1.97	0.46
8:E:110:ASP:OD2	8:E:110:ASP:C	2.58	0.46
39:n:143:PHE:CD1	39:n:223:LEU:HD21	2.50	0.46
39:n:169:HIS:CD2	39:n:260:LEU:HD22	2.51	0.46
40:o:103:LYS:HG3	40:o:156:LEU:CD2	2.46	0.46
1:1:1234:A:H5'	1:1:1235:A:C4	2.51	0.46
1:1:1381:G:H3'	3:3:41:GLN:HG2	1.98	0.46
1:1:1951:A:H61	1:1:2427:C:H42	1.64	0.46
1:1:3141:G:OP1	5:B:19:ARG:NH2	2.49	0.46
3:3:94:ASP:OD1	3:3:95:GLN:N	2.49	0.46
6:C:332:PRO:HB3	9:F:48:ARG:CZ	2.46	0.46
11:H:11:LEU:HD23	11:H:11:LEU:C	2.40	0.46
19:R:15:LEU:HD13	19:R:22:VAL:HG12	1.97	0.46
20:S:79:ARG:NH2	20:S:86:THR:OG1	2.48	0.46
30:d:77:ARG:NH2	30:d:107:GLU:O	2.48	0.46
42:r:245:THR:H	42:r:256:ALA:HA	1.81	0.46
43:t:236:TYR:HD1	43:t:237:CYS:N	2.14	0.46
1:1:167:G:N2	1:1:268:U:O2	2.48	0.46
1:1:1325:A:H2'	1:1:1326:G:C8	2.51	0.46
1:1:1707:U:H3	1:1:1816:G:H1	1.63	0.46
1:1:1874:U:H2'	1:1:1875:U:C6	2.50	0.46
1:1:3349:U:H2'	1:1:3350:U:C6	2.51	0.46
1:1:3403:U:H1'	1:1:3414:U:O2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:80:TYR:HD1	20:S:81:ASP:N	2.14	0.46
39:n:163:LEU:HD13	39:n:230:MET:HB2	1.98	0.46
47:T:141:VAL:HG23	47:T:141:VAL:O	2.16	0.46
1:1:240:G:O2'	1:1:241:G:H5"	2.16	0.45
1:1:674:A:O2'	1:1:675:C:OP1	2.33	0.45
1:1:1319:U:H2'	1:1:1320:G:H8	1.80	0.45
1:1:1494:A:H5"	30:d:55:ARG:HE	1.81	0.45
1:1:1567:U:H1'	1:1:1839:A:H2	1.80	0.45
1:1:1740:U:N3	1:1:1827:G:O2'	2.43	0.45
1:1:3200:U:H2'	1:1:3201:A:H8	1.81	0.45
1:1:3217:U:N3	1:1:3220:G:N7	2.64	0.45
8:E:60:LEU:HD11	8:E:96:VAL:HG21	1.97	0.45
11:H:9:GLU:HB3	11:H:55:PHE:HD1	1.81	0.45
18:Q:100:LEU:HB3	18:Q:102:ILE:HD11	1.97	0.45
20:S:98:ARG:NH2	20:S:127:GLU:OE2	2.49	0.45
38:m:558:HIS:HA	38:m:565:SER:HA	1.98	0.45
1:1:1918:G:N2	1:1:1921:C:OP2	2.40	0.45
1:1:2971:C:O2'	1:1:2972:G:H5'	2.17	0.45
7:D:529:PRO:O	38:m:214:PRO:HD3	2.16	0.45
11:H:11:LEU:HB3	11:H:53:ILE:HB	1.97	0.45
15:N:189:TRP:CE3	15:N:190:LEU:HG	2.52	0.45
17:P:94:LEU:HB3	17:P:148:ILE:HD12	1.98	0.45
30:d:83:LYS:NZ	30:d:95:TYR:HB3	2.31	0.45
45:v:53:LEU:HD22	45:v:137:VAL:HG21	1.98	0.45
45:v:171:ILE:CD1	45:v:176:THR:HA	2.45	0.45
1:1:1508:A:O3'	30:d:62:LYS:NZ	2.47	0.45
1:1:1702:A:H2'	1:1:1703:G:C8	2.51	0.45
1:1:3004:U:H2'	1:1:3005:A:O4'	2.17	0.45
9:F:76:ALA:HB2	47:T:140:PHE:HE2	1.81	0.45
9:F:176:ILE:HD11	9:F:188:VAL:HG22	1.98	0.45
16:O:28:LEU:HD12	16:O:99:ALA:O	2.15	0.45
28:b:290:LYS:H	28:b:323:CYS:H	1.63	0.45
31:e:29:TRP:CE2	31:e:50:PRO:HD2	2.52	0.45
35:i:30:HIS:O	35:i:31:LEU:HB2	2.17	0.45
39:n:129:ALA:O	39:n:133:ILE:HB	2.16	0.45
1:1:1445:U:OP1	31:e:95:GLY:N	2.40	0.45
1:1:1653:A:OP2	39:n:7:LYS:NZ	2.50	0.45
1:1:1827:G:H2'	1:1:1828:A:H8	1.81	0.45
1:1:3367:A:OP1	1:1:3368:A:N6	2.50	0.45
3:3:100:TRP:O	3:3:101:PRO:C	2.60	0.45
8:E:105:SER:HB3	14:M:106:ASN:HD22	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:174:LEU:N	11:H:174:LEU:HD12	2.31	0.45
31:e:82:LEU:HD13	31:e:91:ALA:HB2	1.98	0.45
46:y:187:ASN:HA	46:y:210:THR:HA	1.99	0.45
1:1:185:G:C2	1:1:248:G:C8	3.04	0.45
1:1:414:G:H1'	2:2:24:G:N2	2.31	0.45
1:1:3351:U:H2'	1:1:3352:A:H8	1.82	0.45
16:O:169:TYR:O	16:O:173:LEU:N	2.38	0.45
17:P:124:LYS:HD3	17:P:140:LEU:HD13	1.99	0.45
30:d:78:LEU:HD12	30:d:96:VAL:HG22	1.97	0.45
43:t:87:THR:HG21	43:t:144:ILE:HG12	1.98	0.45
43:t:236:TYR:HD1	43:t:237:CYS:H	1.64	0.45
45:v:12:SER:OG	45:v:13:GLY:N	2.49	0.45
1:1:343:G:N2	2:2:37:U:O2	2.50	0.45
1:1:1740:U:H3	1:1:1827:G:HO2'	1.61	0.45
1:1:1847:C:H3'	1:1:1848:G:H8	1.81	0.45
1:1:1880:A:H2'	1:1:1881:U:H5'	1.98	0.45
1:1:3271:G:H2'	8:E:186:ASN:ND2	2.31	0.45
9:F:239:ASP:OD2	9:F:240:GLU:N	2.50	0.45
14:M:116:LEU:HD23	16:O:192:LEU:HD22	1.98	0.45
25:Y:37:GLU:OE2	25:Y:38:LEU:HD23	2.17	0.45
30:d:11:GLN:HB3	30:d:12:VAL:H	1.59	0.45
48:6:103:G:H2'	48:6:104:U:C6	2.52	0.45
1:1:53:G:OP2	36:j:48:ASN:ND2	2.48	0.45
1:1:817:G:N2	18:Q:91:ASP:OD1	2.50	0.45
1:1:3100:C:O2'	5:B:99:LEU:O	2.20	0.45
1:1:3173:A:H5"	1:1:3174:A:H5'	1.99	0.45
1:1:3419:G:H1'	1:1:3421:G:O4'	2.17	0.45
5:B:122:TRP:CD1	5:B:122:TRP:C	2.93	0.45
13:L:43:ALA:HB2	13:L:51:VAL:HG22	1.99	0.45
30:d:25:LEU:HD21	30:d:33:ARG:CD	2.39	0.45
38:m:287:PRO:HD2	39:n:43:TYR:OH	2.17	0.45
1:1:1352:G:N2	20:S:111:ALA:HB2	2.32	0.45
1:1:1509:A:C4'	30:d:62:LYS:HZ3	2.29	0.45
1:1:1547:G:H4'	1:1:1548:G:H21	1.82	0.45
1:1:2428:U:H2'	1:1:2429:A:C8	2.51	0.45
1:1:3022:C:H2'	1:1:3023:C:O4'	2.17	0.45
6:C:14:ASP:OD1	6:C:15:GLY:N	2.50	0.45
11:H:24:ARG:HH11	11:H:24:ARG:HB2	1.81	0.45
13:L:19:GLN:HA	15:N:195:LEU:HD21	1.98	0.45
17:P:85:VAL:O	17:P:89:LYS:HG2	2.17	0.45
22:V:87:TRP:HZ3	22:V:89:ARG:HB2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:75:LEU:HD23	27:a:78:LEU:HD13	1.98	0.45
30:d:47:LYS:NZ	30:d:48:HIS:HA	2.30	0.45
1:1:542:G:H1	1:1:584:C:H42	1.63	0.45
1:1:1025:G:N2	1:1:1088:U:H3	2.15	0.45
1:1:1672:A:H2'	1:1:1673:A:C4	2.52	0.45
1:1:1707:U:H2'	1:1:1708:G:H8	1.82	0.45
5:B:67:MET:CE	5:B:70:ARG:HB3	2.47	0.45
6:C:314:HIS:CD2	9:F:171:SER:HB3	2.51	0.45
9:F:145:ILE:O	9:F:243:ASN:ND2	2.45	0.45
14:M:18:LYS:HB2	14:M:55:SER:HB2	1.98	0.45
14:M:109:ASP:HB3	16:O:195:PHE:CE1	2.52	0.45
30:d:79:ARG:HD3	30:d:111:VAL:HG21	1.97	0.45
38:m:220:GLU:OE1	38:m:224:ARG:NH1	2.48	0.45
40:o:105:GLY:O	40:o:153:PHE:N	2.27	0.45
1:1:1150:C:H2'	1:1:1151:A:C8	2.52	0.45
1:1:1417:G:H21	3:3:15:PHE:HE1	1.65	0.45
1:1:1717:U:O2'	1:1:1720:C:N4	2.43	0.45
3:3:111:ARG:HG2	31:e:84:MET:HE1	1.98	0.45
41:p:108:SER:N	41:p:120:SER:O	2.50	0.45
48:6:56:A:H2'	48:6:57:A:C8	2.51	0.45
15:N:44:ARG:NH2	15:N:120:TRP:O	2.31	0.44
17:P:67:VAL:HG13	17:P:82:ARG:HG3	1.98	0.44
18:Q:126:ASP:OD1	18:Q:126:ASP:N	2.42	0.44
20:S:79:ARG:HD3	20:S:88:ASN:OD1	2.16	0.44
22:V:25:MET:SD	22:V:26:ASN:N	2.90	0.44
39:n:403:ILE:HD12	39:n:419:ILE:HG13	1.98	0.44
41:p:408:LEU:HA	41:p:423:GLY:HA3	1.99	0.44
2:2:19:C:H2'	2:2:20:A:O4'	2.16	0.44
6:C:58:ALA:C	6:C:60:HIS:H	2.26	0.44
6:C:279:LEU:HD23	6:C:280:PRO:HD2	1.98	0.44
15:N:38:ARG:HH11	15:N:60:VAL:HG13	1.81	0.44
22:V:26:ASN:OD1	22:V:27:CYS:N	2.50	0.44
38:m:339:ASP:HA	43:t:22:ARG:HH12	1.82	0.44
1:1:138:U:N3	34:h:70:GLU:OE1	2.35	0.44
1:1:1019:U:O3'	9:F:128:LYS:NZ	2.42	0.44
1:1:1523:A:N6	1:1:1893:C:O2	2.50	0.44
1:1:1547:G:O2'	1:1:1548:G:N3	2.50	0.44
1:1:1554:G:H2'	1:1:1555:G:H8	1.81	0.44
1:1:1644:C:H2'	1:1:1645:G:C8	2.52	0.44
1:1:3239:A:H4'	1:1:3240:G:O5'	2.17	0.44
5:B:212:ASN:HD21	5:B:354:VAL:H	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:131:LYS:HB3	9:F:131:LYS:HE2	1.77	0.44
14:M:51:ILE:HD12	14:M:52:ARG:N	2.31	0.44
14:M:78:TRP:CD1	14:M:83:VAL:HB	2.53	0.44
15:N:38:ARG:NH1	15:N:60:VAL:HG13	2.32	0.44
17:P:24:THR:HB	17:P:90:PHE:CE2	2.53	0.44
20:S:11:ARG:HH21	47:T:141:VAL:HG12	1.83	0.44
31:e:101:LYS:O	31:e:105:ILE:HG13	2.17	0.44
48:6:92:G:O2'	48:6:93:A:H5'	2.16	0.44
1:1:254:G:H2'	1:1:255:C:C6	2.53	0.44
1:1:266:G:H5'	1:1:267:C:OP2	2.16	0.44
1:1:335:A:OP1	13:L:31:ARG:NH2	2.49	0.44
1:1:587:U:H2'	1:1:588:G:C8	2.50	0.44
1:1:625:U:O2'	1:1:626:C:O5'	2.32	0.44
1:1:1400:A:H2'	1:1:1401:G:O4'	2.17	0.44
1:1:1506:U:H2'	1:1:1507:G:H8	1.82	0.44
5:B:269:ASN:ND2	5:B:271:GLY:O	2.48	0.44
10:G:80:LYS:HE2	10:G:80:LYS:HB2	1.70	0.44
11:H:45:GLU:OE2	11:H:47:LYS:HB2	2.17	0.44
13:L:62:THR:HG22	13:L:63:ILE:N	2.31	0.44
15:N:140:LYS:HD3	15:N:140:LYS:HA	1.73	0.44
20:S:24:PHE:HB3	47:T:151:LEU:HD22	1.99	0.44
20:S:41:TRP:CH2	20:S:55:GLY:HA3	2.51	0.44
30:d:42:VAL:O	30:d:46:GLN:N	2.50	0.44
31:e:31:LYS:HE3	31:e:49:MET:CE	2.46	0.44
32:f:18:GLN:O	32:f:25:HIS:HB2	2.17	0.44
32:f:69:TRP:CH2	32:f:102:MET:HE1	2.52	0.44
1:1:615:G:N2	1:1:637:U:OP1	2.48	0.44
1:1:1259:A:H2'	1:1:1260:G:H8	1.83	0.44
1:1:1330:U:H2'	1:1:1331:G:H8	1.83	0.44
1:1:1506:U:P	19:R:8:LYS:HZ1	2.41	0.44
1:1:1508:A:C2'	30:d:62:LYS:HZ1	2.30	0.44
1:1:1645:G:H2'	1:1:1646:G:C8	2.53	0.44
1:1:1659:G:O2'	1:1:1678:A:N1	2.46	0.44
9:F:93:VAL:O	9:F:121:GLY:HA2	2.18	0.44
14:M:35:LYS:HA	14:M:53:TYR:HD2	1.82	0.44
26:Z:41:ALA:N	26:Z:75:VAL:O	2.50	0.44
42:r:45:ILE:HD13	42:r:45:ILE:N	2.31	0.44
1:1:723:C:O2'	1:1:724:A:O5'	2.32	0.44
1:1:1164:A:H2'	1:1:1165:G:H8	1.82	0.44
1:1:1389:A:H5"	1:1:1391:G:H1'	1.99	0.44
5:B:210:GLU:C	5:B:212:ASN:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:296:THR:HG23	5:B:303:LYS:HZ3	1.83	0.44
5:B:323:MET:HE2	5:B:323:MET:HB2	1.89	0.44
6:C:5:ARG:NH1	6:C:26:PHE:CZ	2.82	0.44
8:E:191:HIS:HD2	8:E:192:LEU:HG	1.83	0.44
11:H:47:LYS:HA	11:H:47:LYS:HD3	1.68	0.44
16:O:55:TYR:CD1	16:O:146:VAL:HG11	2.53	0.44
16:O:74:PHE:HD2	16:O:79:ARG:HG3	1.83	0.44
24:X:56:LEU:HD12	24:X:56:LEU:HA	1.78	0.44
38:m:345:ARG:HD2	39:n:43:TYR:CG	2.52	0.44
38:m:387:ARG:N	38:m:401:GLY:O	2.51	0.44
43:t:22:ARG:HB2	43:t:24:VAL:HG22	2.00	0.44
1:1:517:U:OP1	6:C:319:ASN:HB2	2.18	0.44
1:1:585:C:OP1	20:S:70:LYS:NZ	2.43	0.44
1:1:984:A:C6	1:1:985:G:C4	3.06	0.44
1:1:1163:C:H2'	1:1:1164:A:H8	1.83	0.44
1:1:1427:A:N3	1:1:1453:A:O2'	2.46	0.44
1:1:1590:G:OP2	1:1:1590:G:H4'	2.17	0.44
1:1:1786:U:H2'	1:1:1787:G:C8	2.53	0.44
3:3:53:VAL:HG11	3:3:112:LEU:HD21	1.99	0.44
10:G:173:MET:HE1	38:m:211:ARG:HD3	1.99	0.44
14:M:29:VAL:HG11	14:M:48:ARG:HH12	1.83	0.44
16:O:190:GLN:O	16:O:193:SER:OG	2.29	0.44
24:X:67:ASN:HB3	24:X:140:PHE:HD2	1.82	0.44
25:Y:2:LYS:NZ	25:Y:4:SER:O	2.51	0.44
30:d:60:LEU:HD21	30:d:97:GLN:HA	2.00	0.44
43:t:217:LYS:HG2	43:t:228:PHE:CE2	2.53	0.44
43:t:226:LYS:NZ	48:6:1:A:OP2	2.43	0.44
1:1:426:A:O2'	1:1:655:C:OP1	2.29	0.44
1:1:592:U:H1'	6:C:346:GLU:O	2.18	0.44
1:1:723:C:H1'	45:v:65:GLY:HA3	1.99	0.44
1:1:841:G:H2'	1:1:842:A:C8	2.53	0.44
1:1:1023:G:H2'	1:1:1024:A:C8	2.53	0.44
1:1:1843:C:H2'	1:1:1844:C:C6	2.52	0.44
1:1:1936:A:H2'	1:1:1937:G:H8	1.83	0.44
19:R:7:GLN:HE22	19:R:33:SER:C	2.25	0.44
27:a:74:ASN:HB3	27:a:114:LYS:HB2	2.00	0.44
27:a:129:VAL:HG21	27:a:144:VAL:HG11	1.99	0.44
39:n:45:ARG:HD3	39:n:65:TYR:CD1	2.53	0.44
45:v:170:LEU:HD12	45:v:182:MET:HB3	2.00	0.44
1:1:271:C:H2'	1:1:272:G:C8	2.52	0.44
1:1:621:G:OP2	9:F:44:ARG:NE	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:777:C:H2'	1:1:778:G:H5"	1.99	0.44
1:1:1557:U:P	1:1:1642:U:H3	2.40	0.44
1:1:1712:A:H2'	1:1:1713:G:H8	1.83	0.44
1:1:2932:A:H2	1:1:2945:G:H3'	1.83	0.44
1:1:3137:U:H2'	1:1:3138:U:C6	2.53	0.44
1:1:3435:U:H3	1:1:3470:G:HO2'	1.63	0.44
5:B:122:TRP:HE1	5:B:127:LYS:CG	2.31	0.44
9:F:189:GLU:OE2	9:F:189:GLU:HA	2.18	0.44
17:P:75:GLU:OE1	17:P:75:GLU:N	2.50	0.44
20:S:135:ARG:HB2	20:S:136:ARG:HH11	1.82	0.44
24:X:109:ILE:C	24:X:110:ASN:HD22	2.26	0.44
32:f:51:CYS:HB2	32:f:67:VAL:HG13	2.00	0.44
32:f:52:TYR:CE2	32:f:54:TYR:CD1	3.06	0.44
1:1:130:A:H2'	1:1:131:A:O4'	2.18	0.43
1:1:148:C:H2'	1:1:149:G:O4'	2.18	0.43
1:1:674:A:H2'	1:1:675:C:H6	1.79	0.43
3:3:5:GLU:OE2	6:C:289:VAL:N	2.29	0.43
8:E:123:TYR:OH	8:E:153:ARG:NE	2.51	0.43
16:O:74:PHE:CD2	16:O:79:ARG:HG3	2.53	0.43
20:S:51:LYS:HB2	20:S:54:THR:HG22	2.00	0.43
22:V:40:SER:HB3	22:V:61:LEU:HD23	2.00	0.43
30:d:83:LYS:HZ3	30:d:95:TYR:HB3	1.83	0.43
35:i:33:LYS:HE2	35:i:33:LYS:HB2	1.71	0.43
38:m:578:ALA:O	38:m:591:ALA:N	2.46	0.43
1:1:841:G:H2'	1:1:842:A:H8	1.82	0.43
1:1:1423:G:OP1	31:e:98:SER:OG	2.24	0.43
1:1:1550:C:H2'	1:1:1551:A:H8	1.83	0.43
3:3:29:ARG:HG3	31:e:81:LEU:HD21	2.00	0.43
15:N:15:GLN:HB3	35:i:50:PRO:HD2	2.00	0.43
17:P:100:ALA:HA	17:P:103:GLU:OE2	2.18	0.43
34:h:72:TYR:CE2	34:h:79:PRO:HD3	2.53	0.43
38:m:661:ARG:H	38:m:676:SER:HA	1.83	0.43
40:o:166:MET:HB2	40:o:178:CYS:SG	2.57	0.43
48:6:88:G:H2'	48:6:89:U:O4'	2.18	0.43
1:1:102:C:HO2'	13:L:62:THR:HG1	1.51	0.43
1:1:107:A:O2'	1:1:332:A:N3	2.50	0.43
1:1:993:C:H2'	1:1:994:A:N9	2.33	0.43
1:1:1332:A:N7	1:1:2922:U:N3	2.65	0.43
1:1:3332:U:H2'	1:1:3333:G:H8	1.83	0.43
17:P:4:TYR:HE2	17:P:16:LYS:HD2	1.82	0.43
19:R:7:GLN:NE2	19:R:32:ILE:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:f:61:ARG:HA	32:f:61:ARG:HD2	1.59	0.43
34:h:88:ARG:O	34:h:92:ARG:HD2	2.18	0.43
38:m:344:PRO:HA	39:n:44:PRO:O	2.18	0.43
8:E:167:ALA:O	8:E:171:ILE:HG12	2.19	0.43
8:E:194:LYS:NZ	14:M:104:GLN:O	2.36	0.43
10:G:99:PRO:HD3	10:G:132:VAL:HG12	2.00	0.43
10:G:158:ASP:HB3	10:G:159:PRO:CD	2.49	0.43
11:H:17:VAL:HB	11:H:29:THR:OG1	2.18	0.43
38:m:265:ALA:HA	39:n:232:PHE:CE1	2.53	0.43
40:o:136:MET:HE2	40:o:145:SER:HB3	2.00	0.43
40:o:181:ILE:CD1	40:o:185:GLN:HE21	2.31	0.43
40:o:203:HIS:NE2	48:6:83:A:H5'	2.34	0.43
43:t:197:VAL:HA	43:t:201:PHE:CD1	2.53	0.43
48:6:93:A:H4'	48:6:94:A:C2	2.54	0.43
1:1:546:G:O3'	20:S:145:PRO:HB3	2.18	0.43
1:1:838:A:H2'	1:1:839:A:N3	2.34	0.43
1:1:1773:A:H2'	1:1:1774:G:C8	2.51	0.43
1:1:2337:G:H2'	1:1:2338:G:H8	1.83	0.43
1:1:3368:A:N1	8:E:154:ILE:HG23	2.33	0.43
1:1:3477:A:N3	30:d:23:LYS:HA	2.33	0.43
3:3:2:GLN:HB2	3:3:6:VAL:HG11	1.99	0.43
6:C:158:VAL:HG23	6:C:161:PHE:CZ	2.53	0.43
11:H:28:VAL:HG11	11:H:78:MET:HG2	2.01	0.43
15:N:30:TYR:HA	15:N:33:MET:HE3	2.01	0.43
15:N:168:GLY:O	15:N:172:ARG:HG2	2.18	0.43
30:d:15:ARG:HB3	30:d:17:TYR:CE2	2.53	0.43
39:n:419:ILE:HA	39:n:440:ALA:HA	2.00	0.43
40:o:200:ARG:HG3	40:o:200:ARG:O	2.18	0.43
41:p:200:VAL:HA	41:p:216:SER:HA	2.00	0.43
1:1:77:A:H5'	13:L:100:ARG:NH2	2.33	0.43
1:1:641:G:H2'	1:1:642:A:C8	2.51	0.43
1:1:1240:G:OP1	42:r:36:SER:OG	2.24	0.43
1:1:2474:A:H61	1:1:3088:G:H2'	1.83	0.43
14:M:115:ARG:HA	14:M:115:ARG:HD3	1.80	0.43
15:N:189:TRP:HE3	15:N:190:LEU:HG	1.83	0.43
16:O:144:SER:HB2	16:O:151:ASN:HB2	2.01	0.43
40:o:199:LYS:HD2	40:o:199:LYS:O	2.18	0.43
1:1:1157:G:H2'	1:1:1158:G:O4'	2.18	0.43
1:1:1442:G:P	31:e:30:ARG:HH22	2.42	0.43
1:1:1493:C:H2'	1:1:1494:A:C8	2.53	0.43
1:1:1739:A:H2	1:1:1781:G:H1	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3026:C:H2'	1:1:3027:U:O4'	2.18	0.43
1:1:3470:G:H1	5:B:381:GLY:N	2.16	0.43
5:B:45:ALA:HB3	5:B:181:ILE:HG23	1.99	0.43
9:F:88:PRO:O	9:F:126:PHE:HB3	2.19	0.43
10:G:233:TRP:NE1	38:m:200:PRO:O	2.52	0.43
17:P:13:LYS:H	17:P:13:LYS:HG2	1.64	0.43
22:V:108:LYS:HE2	22:V:108:LYS:HB2	1.85	0.43
30:d:32:LYS:C	30:d:35:PRO:HD2	2.44	0.43
30:d:45:ALA:O	30:d:49:MET:HB2	2.19	0.43
38:m:317:TYR:CE2	38:m:324:PRO:HD3	2.54	0.43
40:o:135:ARG:HH22	48:6:98:G:H5'	1.83	0.43
42:r:54:ARG:HD2	42:r:57:GLU:OE1	2.18	0.43
1:1:110:G:OP2	13:L:73:ARG:NH2	2.34	0.43
1:1:430:A:H2'	1:1:431:A:C8	2.54	0.43
1:1:643:C:H2'	1:1:644:A:C8	2.53	0.43
1:1:1211:A:H5"	32:f:78:ASN:HB2	2.01	0.43
1:1:1417:G:H4'	6:C:242:PRO:HB2	2.01	0.43
5:B:297:ASP:N	5:B:297:ASP:OD1	2.51	0.43
8:E:127:GLN:H	8:E:127:GLN:CD	2.25	0.43
11:H:13:ILE:HG22	11:H:14:PRO:O	2.18	0.43
18:Q:50:ARG:HB3	18:Q:85:VAL:HG21	2.01	0.43
38:m:297:GLU:OE2	39:n:449:LEU:HD13	2.18	0.43
38:m:334:PHE:HA	39:n:219:MET:HE1	2.01	0.43
39:n:166:GLU:OE2	39:n:247:PRO:HD2	2.19	0.43
40:o:160:ASN:C	40:o:160:ASN:OD1	2.61	0.43
40:o:185:GLN:CD	40:o:185:GLN:H	2.27	0.43
43:t:237:CYS:SG	43:t:241:ILE:HB	2.59	0.43
1:1:9:U:O2	2:2:158:G:N2	2.51	0.43
1:1:162:A:H8	1:1:162:A:OP1	2.01	0.43
1:1:372:G:O6	36:j:56:ARG:HD3	2.18	0.43
1:1:584:C:P	14:M:70:ARG:HE	2.42	0.43
1:1:593:A:OP1	6:C:348:THR:OG1	2.36	0.43
1:1:979:G:H5"	31:e:52:ILE:HB	2.01	0.43
1:1:3244:C:H2'	1:1:3245:G:H8	1.84	0.43
1:1:3354:U:H2'	1:1:3355:G:C8	2.54	0.43
13:L:76:THR:HG22	13:L:101:ARG:HB3	2.01	0.43
17:P:78:VAL:HG12	17:P:80:GLN:H	1.84	0.43
20:S:16:GLU:HG2	20:S:17:HIS:ND1	2.34	0.43
39:n:182:LEU:HD11	39:n:425:TYR:CD2	2.54	0.43
41:p:130:ASP:N	41:p:134:GLU:O	2.47	0.43
1:1:435:U:OP1	31:e:12:LYS:NZ	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3355:G:H2'	1:1:3356:A:O4'	2.18	0.43
5:B:60:LEU:HD23	5:B:67:MET:HB3	2.00	0.43
8:E:61:LEU:HD23	8:E:61:LEU:HA	1.78	0.43
9:F:95:ARG:NH1	9:F:115:LEU:O	2.49	0.43
17:P:61:ARG:HH21	17:P:76:PHE:HB3	1.84	0.43
20:S:15:THR:HG23	20:S:18:GLU:H	1.84	0.43
32:f:51:CYS:HB3	32:f:69:TRP:CZ3	2.53	0.43
38:m:600:ASN:O	38:m:604:GLN:N	2.52	0.43
39:n:210:VAL:HG12	39:n:212:THR:H	1.84	0.43
1:1:6:A:H5'	1:1:7:C:OP2	2.19	0.42
1:1:52:A:H1'	1:1:843:U:O2'	2.19	0.42
1:1:719:A:OP1	15:N:199:ARG:NH2	2.52	0.42
1:1:985:G:C6	1:1:1173:G:C5	3.07	0.42
1:1:1657:U:H2'	1:1:1658:G:C8	2.54	0.42
1:1:3175:U:C6	30:d:30:PHE:HE2	2.36	0.42
6:C:267:THR:OG1	6:C:281:GLU:HG2	2.19	0.42
12:K:67:ARG:HA	12:K:194:ALA:HA	2.00	0.42
17:P:49:ASP:O	17:P:53:GLU:HG2	2.19	0.42
20:S:131:LYS:NZ	20:S:140:LYS:O	2.52	0.42
27:a:82:LEU:HD23	27:a:82:LEU:C	2.42	0.42
32:f:90:LEU:HD23	32:f:90:LEU:HA	1.80	0.42
38:m:211:ARG:NH2	38:m:213:THR:OG1	2.52	0.42
39:n:30:LEU:HD12	39:n:30:LEU:HA	1.80	0.42
43:t:70:ARG:NH2	43:t:135:ILE:O	2.43	0.42
1:1:251:U:H2'	1:1:252:A:C8	2.54	0.42
1:1:264:G:C6	1:1:265:C:C4	3.07	0.42
1:1:1237:G:O3'	42:r:54:ARG:NH1	2.52	0.42
1:1:1335:A:C5	1:1:3034:G:H1'	2.54	0.42
1:1:1652:G:H2'	1:1:1653:A:C8	2.54	0.42
1:1:2338:G:H2'	1:1:2339:G:H8	1.83	0.42
1:1:3144:C:H5'	5:B:53:MET:HE2	2.01	0.42
1:1:3180:C:O2'	1:1:3433:U:OP1	2.31	0.42
5:B:67:MET:HE1	5:B:70:ARG:HB3	2.01	0.42
5:B:213:GLU:HG2	5:B:214:MET:H	1.83	0.42
8:E:177:TYR:CE2	14:M:108:PHE:HA	2.54	0.42
9:F:134:LEU:HB3	9:F:143:TYR:CE1	2.54	0.42
14:M:28:ILE:HD13	14:M:37:ALA:HB1	2.01	0.42
27:a:84:ASN:HA	27:a:87:ARG:HD3	2.01	0.42
30:d:80:LEU:HD23	30:d:81:SER:N	2.34	0.42
31:e:64:MET:HG3	31:e:68:LEU:O	2.17	0.42
40:o:124:TYR:CE1	40:o:166:MET:HE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:t:91:PHE:CZ	43:t:120:ALA:HB1	2.55	0.42
1:1:189:G:H1	1:1:243:C:N4	2.17	0.42
1:1:1651:A:H2'	1:1:1652:G:C8	2.54	0.42
1:1:1885:G:H5"	24:X:91:LYS:HD2	2.01	0.42
1:1:1929:A:P	19:R:21:LYS:HZ3	2.41	0.42
1:1:3120:A:H5"	11:H:96:HIS:CE1	2.54	0.42
1:1:3414:U:H4'	5:B:173:GLN:HG3	2.00	0.42
3:3:33:ASN:OD1	3:3:42:SER:HB2	2.18	0.42
10:G:105:LYS:HB2	10:G:105:LYS:HE3	1.75	0.42
20:S:73:VAL:HG22	20:S:94:ARG:HB2	2.01	0.42
24:X:96:GLU:OE2	24:X:99:ARG:HD2	2.19	0.42
40:o:118:GLU:OE2	40:o:138:ARG:NE	2.35	0.42
40:o:141:LYS:HD3	40:o:141:LYS:HA	1.84	0.42
43:t:217:LYS:HG2	43:t:228:PHE:HE2	1.84	0.42
45:v:178:ASP:O	45:v:182:MET:HG3	2.19	0.42
1:1:1506:U:H2'	1:1:1507:G:C8	2.54	0.42
1:1:1557:U:H1'	24:X:110:ASN:HB3	2.01	0.42
1:1:2455:U:N3	1:1:2456:G:N7	2.67	0.42
1:1:3433:U:H2'	1:1:3434:G:O4'	2.19	0.42
6:C:14:ASP:OD1	6:C:14:ASP:C	2.63	0.42
6:C:155:ASP:OD1	6:C:155:ASP:N	2.50	0.42
6:C:270:VAL:HG22	6:C:271:ALA:O	2.19	0.42
6:C:291:ARG:HG3	6:C:291:ARG:NH1	2.32	0.42
11:H:35:LEU:HB3	11:H:37:GLN:HE22	1.84	0.42
11:H:102:ASN:HB2	11:H:111:GLU:HG3	2.01	0.42
38:m:263:ASN:O	38:m:263:ASN:ND2	2.45	0.42
38:m:334:PHE:CG	39:n:214:VAL:HG23	2.54	0.42
39:n:170:TYR:CE1	39:n:237:LEU:HB3	2.55	0.42
1:1:135:U:O2	1:1:140:U:N3	2.53	0.42
1:1:305:A:C8	1:1:307:G:H1'	2.54	0.42
1:1:2477:C:H1'	17:P:69:ARG:NH1	2.33	0.42
1:1:3116:U:H4'	11:H:119:ARG:HH11	1.85	0.42
1:1:3217:U:H4'	1:1:3218:A:OP1	2.17	0.42
1:1:3331:U:H3	1:1:3356:A:H61	1.68	0.42
5:B:165:GLN:NE2	5:B:168:LYS:HG2	2.34	0.42
6:C:35:ASP:OD1	6:C:36:LEU:N	2.52	0.42
9:F:148:HIS:HB2	9:F:196:TYR:CE2	2.55	0.42
12:K:7:LEU:HA	12:K:233:ALA:HB1	2.01	0.42
16:O:28:LEU:CD1	16:O:102:HIS:HB2	2.49	0.42
25:Y:53:ASP:OD1	25:Y:109:HIS:N	2.52	0.42
45:v:165:ALA:O	45:v:169:ARG:HD3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:535:G:H2'	1:1:536:A:C8	2.54	0.42
1:1:1307:U:H2'	1:1:1308:C:C6	2.55	0.42
1:1:1325:A:H2'	1:1:1326:G:H8	1.83	0.42
1:1:1929:A:N7	19:R:20:ARG:NH2	2.67	0.42
5:B:116:ARG:NE	5:B:122:TRP:CZ3	2.87	0.42
10:G:89:GLN:HG3	40:o:170:LEU:CD2	2.50	0.42
10:G:219:ASP:OD1	10:G:219:ASP:C	2.63	0.42
11:H:116:LEU:O	11:H:118:GLU:N	2.52	0.42
11:H:174:LEU:O	11:H:178:TYR:OH	2.37	0.42
14:M:77:LYS:HD3	14:M:77:LYS:HA	1.90	0.42
36:j:66:TYR:CE1	36:j:69:LYS:HD2	2.55	0.42
39:n:408:HIS:NE2	39:n:410:SER:HB3	2.35	0.42
43:t:35:GLN:HG2	43:t:39:LYS:HE2	2.02	0.42
43:t:133:LEU:HD21	43:t:142:TYR:CZ	2.55	0.42
1:1:84:C:O2'	1:1:101:G:O6	2.29	0.42
1:1:1300:U:H1'	1:1:1303:C:C5	2.55	0.42
1:1:1638:A:OP1	19:R:38:ARG:NH1	2.48	0.42
1:1:1786:U:H2'	1:1:1787:G:H8	1.85	0.42
1:1:1951:A:H61	1:1:2427:C:N4	2.17	0.42
1:1:2976:C:H2'	1:1:2977:U:C6	2.55	0.42
1:1:3096:G:H2'	1:1:3097:U:C6	2.55	0.42
1:1:3399:C:H2'	1:1:3400:C:C6	2.55	0.42
6:C:314:HIS:HD2	9:F:171:SER:HB3	1.84	0.42
8:E:56:THR:O	8:E:72:VAL:HG12	2.20	0.42
11:H:39:LEU:HA	11:H:41:HIS:CD2	2.55	0.42
14:M:30:ASP:OD2	14:M:31:ILE:N	2.52	0.42
15:N:25:VAL:O	15:N:29:GLU:HG3	2.19	0.42
18:Q:117:LYS:HB3	18:Q:117:LYS:HE3	1.79	0.42
20:S:26:MET:HB3	20:S:28:LEU:HD22	2.01	0.42
22:V:100:ASN:N	22:V:100:ASN:OD1	2.52	0.42
22:V:106:ASN:ND2	22:V:110:GLU:HB3	2.29	0.42
31:e:29:TRP:O	31:e:30:ARG:NH1	2.52	0.42
36:j:22:CYS:HB3	36:j:37:CYS:SG	2.59	0.42
38:m:339:ASP:HA	43:t:22:ARG:NH1	2.35	0.42
43:t:91:PHE:CE1	43:t:120:ALA:HB1	2.54	0.42
43:t:138:PRO:HG2	43:t:139:TYR:CD1	2.54	0.42
1:1:634:G:O2'	6:C:315:VAL:HG12	2.20	0.42
1:1:1202:G:H2'	1:1:1203:G:O4'	2.20	0.42
1:1:1329:C:N4	1:1:1330:U:O4	2.53	0.42
1:1:1420:U:OP2	6:C:143:ARG:NH2	2.53	0.42
1:1:1494:A:H5'	30:d:56:VAL:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1567:U:H1'	1:1:1839:A:C2	2.55	0.42
1:1:1726:U:H2'	1:1:1727:U:C6	2.54	0.42
1:1:2932:A:O2'	1:1:2946:A:N6	2.50	0.42
8:E:111:VAL:O	8:E:114:VAL:HG12	2.19	0.42
20:S:11:ARG:HB2	20:S:21:PRO:HB2	2.00	0.42
22:V:23:ALA:O	22:V:38:ILE:HG22	2.20	0.42
35:i:56:MET:HE1	35:i:60:ARG:HD2	2.02	0.42
38:m:255:GLU:HA	38:m:258:ARG:HE	1.84	0.42
39:n:568:LYS:O	39:n:571:LYS:NZ	2.28	0.42
1:1:993:C:H2'	1:1:994:A:C4	2.54	0.42
1:1:2477:C:H5'	17:P:80:GLN:NE2	2.35	0.42
1:1:3025:A:H2'	1:1:3026:C:H6	1.84	0.42
1:1:3485:U:H2'	1:1:3486:U:C6	2.55	0.42
2:2:114:C:H4'	2:2:115:G:H5"	2.01	0.42
5:B:152:LYS:HA	5:B:188:VAL:HG12	2.00	0.42
6:C:25:PRO:HB2	6:C:27:VAL:HG12	2.01	0.42
6:C:292:LEU:HD13	18:Q:31:LEU:HD22	2.02	0.42
11:H:68:ILE:HD13	11:H:68:ILE:HA	1.80	0.42
11:H:69:ARG:HA	11:H:69:ARG:HD2	1.79	0.42
14:M:58:LEU:HA	14:M:58:LEU:HD13	1.83	0.42
17:P:59:PRO:HD3	17:P:76:PHE:CE2	2.55	0.42
20:S:45:LYS:O	20:S:49:LYS:HD2	2.20	0.42
20:S:129:GLU:HG2	20:S:130:LYS:HG2	2.00	0.42
25:Y:42:TYR:HE1	25:Y:108:LEU:HD12	1.84	0.42
42:r:9:GLU:H	42:r:9:GLU:CD	2.26	0.42
43:t:95:ILE:HD12	43:t:232:ARG:HD3	2.01	0.42
43:t:232:ARG:NH2	43:t:244:LEU:HD11	2.34	0.42
1:1:27:C:H3'	1:1:28:G:N2	2.28	0.42
1:1:132:C:H2'	1:1:133:A:O4'	2.20	0.42
1:1:431:A:H2'	1:1:432:G:O4'	2.20	0.42
1:1:1255:C:H2'	1:1:1256:A:O4'	2.20	0.42
1:1:1493:C:H2'	1:1:1494:A:H8	1.85	0.42
1:1:1578:G:OP1	15:N:67:ARG:NH1	2.52	0.42
1:1:1689:A:H2'	1:1:1690:G:O4'	2.20	0.42
1:1:2984:C:HO2'	1:1:3029:A:HO2'	1.66	0.42
1:1:3195:C:N4	1:1:3231:U:H3	2.17	0.42
6:C:338:LYS:NZ	6:C:341:VAL:HA	2.35	0.42
11:H:6:TYR:HA	11:H:57:VAL:O	2.20	0.42
12:K:13:LEU:O	12:K:15:LYS:N	2.51	0.42
13:L:33:LEU:O	13:L:37:GLN:HG3	2.19	0.42
16:O:143:SER:OG	16:O:148:TRP:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:44:THR:HG21	22:V:52:PRO:HG3	2.01	0.42
25:Y:82:GLU:O	25:Y:83:ARG:HG2	2.19	0.42
30:d:28:VAL:HG11	30:d:36:ARG:HG3	2.02	0.42
40:o:183:GLU:HA	40:o:186:VAL:CG1	2.50	0.42
43:t:113:ARG:NH2	43:t:208:LEU:O	2.30	0.42
1:1:348:C:OP2	6:C:197:ARG:NH1	2.45	0.41
1:1:689:U:H2'	1:1:690:A:C8	2.55	0.41
1:1:1508:A:O2'	30:d:62:LYS:NZ	2.50	0.41
1:1:3204:G:H2'	1:1:3205:G:O4'	2.21	0.41
1:1:3281:A:O2'	11:H:44:ILE:N	2.53	0.41
2:2:79:A:C2	2:2:96:A:H1'	2.55	0.41
6:C:158:VAL:HA	6:C:161:PHE:CE1	2.56	0.41
9:F:108:LYS:HB2	9:F:108:LYS:HE2	1.91	0.41
15:N:174:ILE:HD13	15:N:174:ILE:HA	1.88	0.41
24:X:7:LYS:O	24:X:11:LYS:HB3	2.19	0.41
39:n:404:CYS:SG	39:n:418:TYR:HD2	2.42	0.41
43:t:84:PRO:O	43:t:125:ASN:ND2	2.48	0.41
1:1:141:U:H2'	1:1:142:G:O4'	2.19	0.41
1:1:197:U:O4'	1:1:231:C:H5'	2.20	0.41
1:1:1221:A:N3	1:1:1221:A:H2'	2.35	0.41
1:1:1643:C:OP2	1:1:1643:C:H3'	2.21	0.41
1:1:1845:A:H2'	1:1:1846:A:H8	1.85	0.41
1:1:2337:G:H2'	1:1:2338:G:C8	2.55	0.41
1:1:3187:A:O2'	1:1:3189:C:H2'	2.19	0.41
5:B:373:PRO:HA	5:B:376:ALA:HB3	2.01	0.41
6:C:293:ILE:HD11	18:Q:31:LEU:HA	2.02	0.41
8:E:190:PRO:HD2	32:f:45:TYR:OH	2.19	0.41
11:H:9:GLU:HB3	11:H:55:PHE:CD1	2.54	0.41
11:H:9:GLU:OE2	11:H:69:ARG:NH1	2.54	0.41
16:O:137:CYS:SG	16:O:138:THR:N	2.93	0.41
17:P:50:ASN:HB3	17:P:56:GLN:OE1	2.20	0.41
19:R:14:VAL:O	19:R:16:LYS:NZ	2.53	0.41
20:S:80:TYR:HD2	20:S:89:MET:HE1	1.85	0.41
25:Y:33:PRO:HD2	25:Y:103:VAL:O	2.20	0.41
31:e:31:LYS:HD2	31:e:32:PRO:HD2	2.02	0.41
38:m:453:GLN:N	38:m:469:ALA:O	2.53	0.41
43:t:151:ARG:HA	43:t:191:ILE:HD13	2.01	0.41
1:1:16:A:H2'	1:1:17:G:O4'	2.20	0.41
1:1:1245:U:P	20:S:136:ARG:HH22	2.43	0.41
1:1:1290:A:N3	1:1:1311:C:O2'	2.51	0.41
1:1:1713:G:H2'	1:1:1714:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:321:LEU:HD11	9:F:153:GLU:HA	2.02	0.41
13:L:32:LYS:O	13:L:36:ARG:HG3	2.20	0.41
16:O:86:ARG:HG2	16:O:86:ARG:NH1	2.36	0.41
17:P:108:ASP:OD1	17:P:108:ASP:C	2.63	0.41
36:j:17:THR:HG23	36:j:29:ILE:HD11	2.02	0.41
39:n:159:ASN:ND2	39:n:227:GLN:HB3	2.35	0.41
39:n:435:ARG:HD3	39:n:437:ASP:H	1.84	0.41
1:1:1176:G:H4'	31:e:41:ARG:O	2.21	0.41
1:1:3245:G:C6	1:1:3246:A:C6	3.09	0.41
1:1:3352:A:N3	1:1:3352:A:H2'	2.36	0.41
3:3:59:LYS:NZ	3:3:81:LYS:HD3	2.35	0.41
6:C:231:ASN:HB3	6:C:234:ARG:HG2	2.02	0.41
11:H:41:HIS:CE1	11:H:42:VAL:HG22	2.54	0.41
20:S:160:GLY:O	20:S:165:LYS:NZ	2.41	0.41
22:V:42:PHE:CE1	22:V:61:LEU:HD21	2.55	0.41
27:a:75:LEU:HB3	27:a:117:LEU:HD21	2.03	0.41
31:e:64:MET:HE1	31:e:117:THR:HG22	2.02	0.41
39:n:423:TRP:HD1	39:n:439:TYR:CD1	2.38	0.41
1:1:1350:G:C6	1:1:1351:C:C4	3.09	0.41
1:1:2931:C:H5	1:1:2947:C:N4	2.17	0.41
1:1:3239:A:H4'	1:1:3240:G:C5'	2.51	0.41
3:3:93:ILE:HG13	3:3:112:LEU:HD21	2.01	0.41
5:B:165:GLN:HE22	5:B:168:LYS:NZ	2.18	0.41
8:E:158:LYS:HB2	8:E:158:LYS:HE3	1.78	0.41
16:O:186:SER:OG	16:O:189:ASN:OD1	2.36	0.41
22:V:60:VAL:O	22:V:78:ALA:N	2.47	0.41
31:e:108:LYS:HE2	31:e:108:LYS:HB2	1.81	0.41
39:n:403:ILE:HD11	39:n:420:GLN:C	2.45	0.41
42:r:198:GLY:O	42:r:221:GLU:N	2.53	0.41
43:t:40:LYS:HB3	43:t:44:LYS:NZ	2.36	0.41
1:1:223:G:H2'	1:1:224:U:O4'	2.20	0.41
1:1:652:U:H2'	1:1:653:U:C6	2.56	0.41
1:1:985:G:N3	1:1:1147:G:N1	2.69	0.41
1:1:1005:A:N6	1:1:1138:U:O4	2.54	0.41
1:1:1642:U:O2'	1:1:1643:C:H5'	2.20	0.41
1:1:3044:U:H2'	1:1:3045:G:C8	2.56	0.41
1:1:3206:C:H2'	1:1:3207:U:C6	2.56	0.41
3:3:86:TYR:O	3:3:90:LEU:HG	2.21	0.41
5:B:116:ARG:HG2	5:B:122:TRP:CE3	2.55	0.41
6:C:130:ALA:HB1	6:C:136:LEU:HD12	2.02	0.41
11:H:87:ARG:HG3	11:H:143:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:107:GLY:HA3	11:H:132:VAL:O	2.20	0.41
11:H:173:PHE:C	11:H:174:LEU:HD12	2.45	0.41
24:X:96:GLU:O	24:X:100:LYS:NZ	2.46	0.41
25:Y:47:LEU:HD23	25:Y:47:LEU:HA	1.86	0.41
30:d:15:ARG:HB3	30:d:17:TYR:HE2	1.85	0.41
39:n:439:TYR:CZ	39:n:446:PRO:HG2	2.56	0.41
46:y:65:GLY:HA3	46:y:70:LEU:HA	2.02	0.41
1:1:29:C:H4'	1:1:62:A:H4'	2.01	0.41
1:1:1319:U:H2'	1:1:1320:G:C8	2.55	0.41
1:1:3271:G:H2'	8:E:186:ASN:HD22	1.84	0.41
9:F:95:ARG:HA	9:F:141:VAL:HG12	2.02	0.41
11:H:31:PRO:HD2	11:H:83:THR:HA	2.01	0.41
11:H:63:LYS:HE3	11:H:63:LYS:HB2	1.89	0.41
14:M:12:ARG:HD2	14:M:58:LEU:HD12	2.02	0.41
16:O:173:LEU:O	16:O:176:GLN:NE2	2.53	0.41
20:S:79:ARG:HG3	20:S:121:ARG:NH1	2.36	0.41
24:X:57:ASP:OD1	24:X:57:ASP:N	2.42	0.41
26:Z:42:VAL:HA	26:Z:74:VAL:HA	2.02	0.41
31:e:87:LYS:HA	31:e:87:LYS:HD3	1.67	0.41
1:1:72:C:H5'	13:L:63:ILE:HD13	2.02	0.41
1:1:120:G:C8	10:G:128:LYS:HG3	2.56	0.41
1:1:1916:G:H2'	1:1:1917:U:C6	2.55	0.41
1:1:2473:A:C5	1:1:3239:A:H8	2.39	0.41
2:2:163:A:C6	2:2:164:U:C4	3.08	0.41
5:B:149:GLU:HA	5:B:152:LYS:HG2	2.03	0.41
8:E:191:HIS:CD2	32:f:41:GLU:OE2	2.74	0.41
18:Q:18:PRO:HD3	18:Q:52:PHE:CE1	2.55	0.41
20:S:22:LYS:HZ2	20:S:24:PHE:HA	1.85	0.41
23:W:41:TRP:O	23:W:102:LEU:HA	2.21	0.41
30:d:78:LEU:HD13	30:d:97:GLN:O	2.21	0.41
43:t:155:TYR:CE1	43:t:187:ILE:HD12	2.56	0.41
1:1:541:G:H2'	1:1:542:G:H8	1.86	0.41
1:1:990:C:C2	1:1:996:G:C2	3.09	0.41
1:1:1268:G:H1'	1:1:1294:A:N6	2.36	0.41
1:1:1320:G:H2'	1:1:1321:A:H8	1.86	0.41
1:1:1823:U:H2'	1:1:1824:C:C6	2.56	0.41
1:1:3346:U:H5'	1:1:3347:G:O4'	2.21	0.41
2:2:44:G:C5	34:h:88:ARG:HD3	2.55	0.41
3:3:89:ALA:O	3:3:93:ILE:HG12	2.21	0.41
4:A:85:GLN:OE1	35:i:82:LYS:NZ	2.52	0.41
5:B:211:GLN:NE2	5:B:211:GLN:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:308:MET:HE3	5:B:308:MET:HB3	1.88	0.41
6:C:146:GLU:HG3	6:C:175:LYS:HG3	2.03	0.41
6:C:190:ARG:NH2	6:C:202:VAL:HG12	2.36	0.41
6:C:235:LEU:HD23	6:C:235:LEU:HA	1.87	0.41
6:C:324:LYS:HA	6:C:324:LYS:HD3	1.93	0.41
10:G:184:ALA:O	10:G:188:THR:HG23	2.21	0.41
10:G:233:TRP:CD2	38:m:199:TYR:HB3	2.56	0.41
13:L:46:ILE:H	13:L:46:ILE:HG13	1.66	0.41
14:M:113:VAL:HA	14:M:116:LEU:HB2	2.01	0.41
15:N:9:GLU:O	35:i:42:VAL:HG11	2.21	0.41
15:N:199:ARG:CZ	15:N:200:TYR:HE1	2.34	0.41
17:P:51:VAL:HG11	17:P:88:VAL:HG11	2.03	0.41
19:R:21:LYS:HA	19:R:53:LYS:NZ	2.29	0.41
25:Y:44:ILE:HD12	25:Y:44:ILE:HA	1.88	0.41
27:a:82:LEU:HD23	27:a:83:PRO:O	2.21	0.41
32:f:69:TRP:CZ3	32:f:102:MET:HE1	2.56	0.41
34:h:120:LEU:HB3	45:v:56:LEU:HB2	2.02	0.41
36:j:35:ALA:O	36:j:45:ARG:NE	2.54	0.41
38:m:329:LEU:O	38:m:332:GLU:HG3	2.21	0.41
39:n:24:LYS:HB2	39:n:24:LYS:HE3	1.97	0.41
39:n:143:PHE:CE2	39:n:223:LEU:HD11	2.56	0.41
39:n:208:GLN:OE1	39:n:208:GLN:N	2.54	0.41
40:o:134:LEU:HG	40:o:151:ILE:HG22	2.03	0.41
43:t:133:LEU:HD21	43:t:142:TYR:CE1	2.55	0.41
45:v:142:GLU:O	45:v:146:VAL:HG22	2.21	0.41
1:1:181:A:H2'	1:1:182:G:C8	2.55	0.41
1:1:541:G:H2'	1:1:542:G:C8	2.56	0.41
1:1:1274:G:H1	1:1:1275:A:H62	1.69	0.41
1:1:1825:U:H2'	1:1:1826:C:C6	2.56	0.41
1:1:1891:C:H2'	1:1:1892:U:C6	2.56	0.41
1:1:1911:C:H2'	1:1:1912:C:C6	2.56	0.41
1:1:2949:U:H2'	1:1:2950:U:C6	2.56	0.41
1:1:3106:U:O2'	1:1:3107:A:H2'	2.21	0.41
1:1:3301:C:H2'	1:1:3302:U:C6	2.55	0.41
5:B:116:ARG:HD2	5:B:174:LYS:O	2.21	0.41
5:B:343:LEU:H	5:B:343:LEU:HD23	1.86	0.41
8:E:60:LEU:HD12	8:E:60:LEU:HA	1.77	0.41
13:L:56:PRO:HG2	13:L:72:GLY:HA3	2.03	0.41
16:O:111:PRO:N	16:O:112:PRO:HD2	2.36	0.41
17:P:111:LYS:HB3	17:P:152:GLU:OE1	2.21	0.41
30:d:66:LYS:HD3	30:d:66:LYS:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:27:LEU:HD21	34:h:31:ARG:HH12	1.86	0.41
36:j:33:THR:HA	36:j:39:TYR:O	2.21	0.41
45:v:192:LEU:HD23	45:v:192:LEU:HA	1.92	0.41
1:1:350:A:OP2	2:2:29:C:N4	2.54	0.40
1:1:627:G:H2'	1:1:628:U:H5'	2.02	0.40
1:1:1235:A:H61	1:1:1331:G:H1'	1.86	0.40
1:1:1610:U:H2'	1:1:1611:G:C8	2.56	0.40
1:1:3286:U:H2'	1:1:3287:A:C8	2.56	0.40
2:2:22:C:H2'	2:2:23:G:O4'	2.21	0.40
6:C:179:ASP:O	6:C:183:VAL:HG13	2.21	0.40
11:H:11:LEU:HD23	11:H:12:THR:N	2.36	0.40
25:Y:30:MET:O	25:Y:49:VAL:HG22	2.21	0.40
25:Y:48:PRO:O	25:Y:114:ARG:NH2	2.54	0.40
34:h:81:ASP:OD1	34:h:82:LEU:HG	2.21	0.40
38:m:268:ASP:OD1	38:m:270:TRP:HD1	2.04	0.40
38:m:270:TRP:CD1	38:m:270:TRP:H	2.38	0.40
38:m:350:LYS:HB3	43:t:16:GLU:HB2	2.03	0.40
39:n:249:ILE:HD12	39:n:263:TYR:CZ	2.56	0.40
1:1:301:C:O3'	35:i:74:ARG:NH1	2.55	0.40
1:1:602:A:H1'	6:C:334:ALA:HB1	2.03	0.40
1:1:983:A:H5"	1:1:1174:A:N6	2.36	0.40
1:1:3110:U:H2'	1:1:3111:C:C6	2.56	0.40
2:2:82:U:C3'	25:Y:75:LYS:HZ1	2.33	0.40
5:B:121:ASN:O	5:B:122:TRP:C	2.64	0.40
9:F:160:PHE:CE2	9:F:169:PRO:HG3	2.56	0.40
9:F:209:LEU:HD23	9:F:209:LEU:HA	1.97	0.40
11:H:89:LYS:HB2	11:H:180:SER:OG	2.21	0.40
22:V:110:GLU:HA	22:V:130:ARG:HD2	2.02	0.40
24:X:104:VAL:HG21	24:X:125:LEU:HD23	2.03	0.40
24:X:112:LEU:HD23	24:X:112:LEU:N	2.36	0.40
25:Y:15:ARG:O	25:Y:19:PHE:HD2	2.05	0.40
25:Y:46:SER:OG	25:Y:47:LEU:N	2.55	0.40
25:Y:50:ARG:HD2	25:Y:51:ARG:H	1.84	0.40
25:Y:68:LYS:H	25:Y:82:GLU:HG2	1.86	0.40
1:1:281:A:N1	1:1:300:U:H5	2.19	0.40
1:1:985:G:N2	1:1:1173:G:H2'	2.37	0.40
1:1:1365:C:H1'	9:F:215:SER:HB2	2.04	0.40
1:1:2985:A:H61	1:1:3008:C:H42	1.70	0.40
1:1:2994:C:H6	1:1:2994:C:H2'	1.73	0.40
1:1:3223:A:H2'	1:1:3224:G:O4'	2.21	0.40
5:B:301:THR:OG1	28:b:436:LEU:HA	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:308:SER:O	6:C:309:ARG:C	2.63	0.40
9:F:228:HIS:ND1	9:F:230:ILE:HG12	2.36	0.40
15:N:38:ARG:NH1	15:N:60:VAL:HG22	2.36	0.40
15:N:167:ILE:HA	15:N:167:ILE:HD12	1.85	0.40
20:S:116:ARG:HA	20:S:116:ARG:HD3	1.95	0.40
22:V:89:ARG:HG2	22:V:91:ASP:OD1	2.21	0.40
25:Y:9:SER:O	25:Y:9:SER:OG	2.35	0.40
32:f:51:CYS:SG	32:f:102:MET:CE	3.09	0.40
38:m:240:TYR:CZ	38:m:244:LYS:HG3	2.56	0.40
39:n:141:PHE:CD1	39:n:164:CYS:HB2	2.56	0.40
39:n:146:MET:HG2	39:n:208:GLN:NE2	2.36	0.40
40:o:204:ALA:O	40:o:208:ARG:HG2	2.21	0.40
43:t:163:ASN:O	43:t:163:ASN:CG	2.64	0.40
1:1:3145:A:O2'	5:B:55:HIS:ND1	2.50	0.40
1:1:3337:A:O2'	1:1:3338:A:P	2.80	0.40
5:B:72:ILE:HD11	22:V:90:LYS:HB3	2.02	0.40
5:B:142:GLN:HE21	5:B:142:GLN:C	2.23	0.40
6:C:169:ALA:O	6:C:173:GLU:HG2	2.21	0.40
17:P:64:ASN:HB2	17:P:80:GLN:OE1	2.22	0.40
18:Q:57:ASN:C	18:Q:59:PRO:HD3	2.46	0.40
20:S:11:ARG:HG3	20:S:56:GLU:OE2	2.21	0.40
22:V:91:ASP:OD1	22:V:92:GLY:N	2.54	0.40
22:V:111:MET:SD	22:V:130:ARG:HD2	2.62	0.40
24:X:82:VAL:HG22	24:X:122:PHE:HD1	1.86	0.40
35:i:44:GLU:OE2	38:m:207:THR:OG1	2.30	0.40
39:n:28:LEU:HD22	39:n:32:ASP:HB2	2.03	0.40
39:n:360:LEU:HB2	39:n:382:TRP:HA	2.03	0.40
1:1:217:G:OP2	6:C:163:LYS:HD3	2.22	0.40
1:1:415:A:C2	2:2:25:A:H1'	2.56	0.40
1:1:1303:C:H3'	1:1:1304:A:H8	1.86	0.40
1:1:2999:U:H2'	1:1:3000:U:H6	1.86	0.40
1:1:3204:G:H21	11:H:161:GLN:HE22	1.69	0.40
1:1:3207:U:O4	1:1:3216:C:H4'	2.21	0.40
1:1:3330:G:H1	1:1:3357:C:H42	1.69	0.40
3:3:50:TYR:HA	3:3:100:TRP:CZ2	2.56	0.40
5:B:56:ILE:HD12	5:B:356:LEU:HD22	2.03	0.40
5:B:57:VAL:HG13	5:B:71:GLU:OE2	2.22	0.40
5:B:113:GLU:HB2	5:B:176:ALA:HB2	2.03	0.40
15:N:106:VAL:HG21	15:N:132:VAL:HG21	2.04	0.40
22:V:19:LEU:HB2	22:V:54:ALA:O	2.21	0.40
23:W:177:GLY:N	42:r:13:LYS:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:133:ASP:OD2	24:X:133:ASP:C	2.64	0.40
25:Y:78:LEU:HD23	25:Y:78:LEU:HA	1.92	0.40
27:a:74:ASN:OD1	27:a:114:LYS:HB2	2.22	0.40
31:e:93:ILE:HG21	31:e:102:ARG:HG2	2.03	0.40
39:n:359:PHE:O	39:n:403:ILE:HG22	2.21	0.40
40:o:156:LEU:HA	40:o:159:ALA:HB3	2.04	0.40
40:o:206:ILE:C	40:o:206:ILE:HD12	2.46	0.40
41:p:117:ILE:N	41:p:129:TRP:O	2.52	0.40
41:p:337:HIS:HA	41:p:348:SER:HA	2.04	0.40
43:t:95:ILE:HD12	43:t:232:ARG:HB3	2.03	0.40
48:6:42:U:H2'	48:6:43:G:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	118/302 (39%)	108 (92%)	10 (8%)	0	100	100
4	A	192/295 (65%)	188 (98%)	4 (2%)	0	100	100
5	B	330/388 (85%)	307 (93%)	23 (7%)	0	100	100
6	C	357/363 (98%)	329 (92%)	28 (8%)	0	100	100
7	D	74/578 (13%)	74 (100%)	0	0	100	100
8	E	141/195 (72%)	133 (94%)	8 (6%)	0	100	100
9	F	212/250 (85%)	202 (95%)	10 (5%)	0	100	100
10	G	180/259 (70%)	170 (94%)	8 (4%)	2 (1%)	12	37
11	H	181/190 (95%)	166 (92%)	15 (8%)	0	100	100
12	K	227/373 (61%)	213 (94%)	13 (6%)	1 (0%)	30	60
13	L	116/208 (56%)	108 (93%)	7 (6%)	1 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	122/134 (91%)	116 (95%)	6 (5%)	0	100	100
15	N	160/201 (80%)	147 (92%)	13 (8%)	0	100	100
16	O	183/197 (93%)	180 (98%)	3 (2%)	0	100	100
17	P	130/187 (70%)	115 (88%)	14 (11%)	1 (1%)	16	44
18	Q	126/187 (67%)	119 (94%)	7 (6%)	0	100	100
19	R	55/193 (28%)	51 (93%)	4 (7%)	0	100	100
20	S	172/176 (98%)	160 (93%)	10 (6%)	2 (1%)	11	35
21	U	96/117 (82%)	92 (96%)	4 (4%)	0	100	100
22	V	127/139 (91%)	124 (98%)	3 (2%)	0	100	100
23	W	185/241 (77%)	176 (95%)	9 (5%)	0	100	100
24	X	126/141 (89%)	121 (96%)	5 (4%)	0	100	100
25	Y	123/126 (98%)	117 (95%)	6 (5%)	0	100	100
26	Z	127/136 (93%)	125 (98%)	2 (2%)	0	100	100
27	a	90/148 (61%)	87 (97%)	3 (3%)	0	100	100
28	b	368/642 (57%)	360 (98%)	8 (2%)	0	100	100
29	c	62/117 (53%)	60 (97%)	2 (3%)	0	100	100
30	d	90/113 (80%)	82 (91%)	7 (8%)	1 (1%)	12	37
31	e	115/127 (91%)	109 (95%)	6 (5%)	0	100	100
32	f	104/108 (96%)	96 (92%)	8 (8%)	0	100	100
33	g	85/112 (76%)	84 (99%)	1 (1%)	0	100	100
34	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
35	i	76/99 (77%)	73 (96%)	3 (4%)	0	100	100
36	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
37	k	68/74 (92%)	67 (98%)	1 (2%)	0	100	100
38	m	470/740 (64%)	450 (96%)	20 (4%)	0	100	100
39	n	410/607 (68%)	388 (95%)	22 (5%)	0	100	100
40	o	107/276 (39%)	102 (95%)	5 (5%)	0	100	100
41	p	277/440 (63%)	270 (98%)	7 (2%)	0	100	100
42	r	146/260 (56%)	143 (98%)	3 (2%)	0	100	100
43	t	233/249 (94%)	219 (94%)	14 (6%)	0	100	100
44	u	95/192 (50%)	90 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	v	136/209 (65%)	127 (93%)	9 (7%)	0	100	100
46	y	223/244 (91%)	219 (98%)	4 (2%)	0	100	100
47	T	17/160 (11%)	17 (100%)	0	0	100	100
All	All	7220/10706 (67%)	6868 (95%)	344 (5%)	8 (0%)	50	78

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	P	12	THR
20	S	158	VAL
10	G	227	ASP
20	S	159	VAL
12	K	153	ILE
30	d	12	VAL
10	G	182	ASN
13	L	47	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	109/271 (40%)	109 (100%)	0	100	100
4	A	11/266 (4%)	11 (100%)	0	100	100
5	B	283/326 (87%)	283 (100%)	0	100	100
6	C	296/297 (100%)	295 (100%)	1 (0%)	91	95
8	E	119/155 (77%)	119 (100%)	0	100	100
9	F	180/210 (86%)	179 (99%)	1 (1%)	84	90
10	G	154/212 (73%)	153 (99%)	1 (1%)	84	90
11	H	164/170 (96%)	162 (99%)	2 (1%)	67	80
13	L	99/167 (59%)	98 (99%)	1 (1%)	73	83
14	M	107/113 (95%)	105 (98%)	2 (2%)	52	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	146/176 (83%)	146 (100%)	0	100	100
16	O	153/162 (94%)	153 (100%)	0	100	100
17	P	112/149 (75%)	111 (99%)	1 (1%)	75	86
18	Q	111/159 (70%)	111 (100%)	0	100	100
19	R	51/162 (32%)	50 (98%)	1 (2%)	50	70
20	S	152/154 (99%)	152 (100%)	0	100	100
22	V	102/107 (95%)	101 (99%)	1 (1%)	73	83
24	X	112/122 (92%)	112 (100%)	0	100	100
25	Y	110/111 (99%)	110 (100%)	0	100	100
27	a	81/122 (66%)	81 (100%)	0	100	100
30	d	86/102 (84%)	83 (96%)	3 (4%)	31	56
31	e	100/107 (94%)	99 (99%)	1 (1%)	73	83
32	f	89/91 (98%)	89 (100%)	0	100	100
34	h	106/107 (99%)	105 (99%)	1 (1%)	75	86
35	i	68/84 (81%)	68 (100%)	0	100	100
36	j	58/71 (82%)	58 (100%)	0	100	100
38	m	132/659 (20%)	131 (99%)	1 (1%)	79	87
39	n	364/532 (68%)	361 (99%)	3 (1%)	79	87
40	o	96/246 (39%)	96 (100%)	0	100	100
42	r	59/224 (26%)	57 (97%)	2 (3%)	32	57
43	t	211/223 (95%)	210 (100%)	1 (0%)	86	91
45	v	120/181 (66%)	119 (99%)	1 (1%)	79	87
47	T	17/139 (12%)	17 (100%)	0	100	100
All	All	4158/6377 (65%)	4134 (99%)	24 (1%)	82	90

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	C	181	ILE
9	F	102	ILE
10	G	58	LEU
11	H	35	LEU
11	H	178	TYR
13	L	46	ILE

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Mol	Chain	Res	Type
14	M	28	ILE
14	M	61	ILE
17	P	117	VAL
19	R	34	ASN
22	V	130	ARG
30	d	11	GLN
30	d	29	SER
30	d	109	THR
31	e	31	LYS
34	h	115	LEU
38	m	263	ASN
39	n	18	THR
39	n	148	VAL
39	n	221	THR
42	r	19	ASP
42	r	37	LEU
43	t	191	ILE
45	v	176	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	87	ASN
5	B	109	HIS
5	B	165	GLN
5	B	319	ASN
6	C	344	ASN
9	F	69	GLN
9	F	207	ASN
10	G	89	GLN
11	H	37	GLN
11	H	41	HIS
11	H	184	ASN
13	L	28	GLN
13	L	66	ASN
16	O	5	GLN
16	O	43	ASN
16	O	82	GLN
17	P	54	HIS
17	P	80	GLN
18	Q	53	GLN
19	R	55	ASN

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Mol	Chain	Res	Type
24	X	86	HIS
27	a	4	HIS
30	d	48	HIS
32	f	43	GLN
35	i	63	GLN
39	n	239	ASN
39	n	349	ASN
39	n	411	GLN
39	n	580	ASN
39	n	585	ASN
42	r	3	GLN
42	r	4	ASN
42	r	40	GLN
43	t	163	ASN
45	v	37	GLN
47	T	139	HIS
47	T	152	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1981/3497 (56%)	472 (23%)	23 (1%)
2	2	143/165 (86%)	23 (16%)	2 (1%)
48	6	57/300 (19%)	24 (42%)	0
All	All	2181/3962 (55%)	519 (23%)	25 (1%)

All (519) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	7	C
1	1	25	U
1	1	26	A
1	1	49	A
1	1	51	A
1	1	57	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A

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Mol	Chain	Res	Type
1	1	72	C
1	1	74	A
1	1	100	A
1	1	105	G
1	1	106	A
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	119	U
1	1	122	A
1	1	131	A
1	1	133	A
1	1	136	U
1	1	149	G
1	1	153	U
1	1	154	G
1	1	161	C
1	1	162	A
1	1	163	A
1	1	170	G
1	1	177	G
1	1	185	G
1	1	193	U
1	1	194	A
1	1	195	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	217	G
1	1	218	A
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	244	G
1	1	247	U
1	1	248	G
1	1	258	U

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Mol	Chain	Res	Type
1	1	259	A
1	1	261	A
1	1	266	G
1	1	267	C
1	1	268	U
1	1	269	U
1	1	271	C
1	1	272	G
1	1	276	A
1	1	277	G
1	1	303	A
1	1	306	U
1	1	325	A
1	1	331	A
1	1	337	U
1	1	338	G
1	1	341	G
1	1	342	A
1	1	345	G
1	1	346	A
1	1	350	A
1	1	354	C
1	1	357	A
1	1	359	A
1	1	360	A
1	1	384	G
1	1	399	A
1	1	406	U
1	1	411	C
1	1	412	G
1	1	416	A
1	1	429	G
1	1	430	A
1	1	432	G
1	1	437	G
1	1	507	U
1	1	514	C
1	1	521	C
1	1	532	A
1	1	534	A
1	1	540	A
1	1	544	A

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Mol	Chain	Res	Type
1	1	546	G
1	1	547	G
1	1	548	U
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	591	G
1	1	592	U
1	1	593	A
1	1	602	A
1	1	603	C
1	1	606	G
1	1	618	U
1	1	623	C
1	1	625	U
1	1	626	C
1	1	627	G
1	1	628	U
1	1	629	G
1	1	634	G
1	1	636	A
1	1	647	A
1	1	661	C
1	1	662	C
1	1	663	C
1	1	674	A
1	1	675	C
1	1	685	A
1	1	687	U
1	1	702	A
1	1	706	U
1	1	708	U
1	1	714	A
1	1	715	U
1	1	716	G
1	1	717	A
1	1	732	A
1	1	738	A

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Mol	Chain	Res	Type
1	1	739	G
1	1	742	A
1	1	751	G
1	1	752	G
1	1	759	C
1	1	760	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	768	G
1	1	770	G
1	1	772	A
1	1	773	C
1	1	775	A
1	1	776	U
1	1	777	C
1	1	778	G
1	1	780	C
1	1	781	C
1	1	816	A
1	1	817	G
1	1	819	G
1	1	833	A
1	1	847	G
1	1	976	C
1	1	986	U
1	1	988	U
1	1	989	C
1	1	991	C
1	1	992	U
1	1	995	G
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1003	G
1	1	1005	A
1	1	1006	A
1	1	1010	A
1	1	1011	G
1	1	1012	A
1	1	1014	C
1	1	1017	U

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Mol	Chain	Res	Type
1	1	1022	U
1	1	1023	G
1	1	1135	G
1	1	1137	G
1	1	1138	U
1	1	1139	U
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1154	U
1	1	1158	G
1	1	1160	A
1	1	1163	C
1	1	1164	A
1	1	1166	A
1	1	1169	U
1	1	1170	G
1	1	1173	G
1	1	1176	G
1	1	1184	A
1	1	1186	C
1	1	1191	C
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1224	A
1	1	1232	G
1	1	1235	A
1	1	1244	G
1	1	1249	U
1	1	1251	U
1	1	1252	A
1	1	1253	G
1	1	1258	C
1	1	1259	A
1	1	1273	G
1	1	1276	A
1	1	1277	G
1	1	1282	A
1	1	1283	A
1	1	1284	U

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Mol	Chain	Res	Type
1	1	1286	C
1	1	1289	U
1	1	1290	A
1	1	1291	A
1	1	1293	G
1	1	1294	A
1	1	1295	G
1	1	1296	U
1	1	1303	C
1	1	1309	A
1	1	1310	C
1	1	1315	C
1	1	1316	G
1	1	1317	A
1	1	1318	A
1	1	1323	C
1	1	1333	A
1	1	1334	A
1	1	1335	A
1	1	1336	U
1	1	1337	G
1	1	1338	G
1	1	1339	A
1	1	1349	A
1	1	1361	A
1	1	1379	U
1	1	1381	G
1	1	1389	A
1	1	1390	A
1	1	1407	A
1	1	1414	G
1	1	1433	U
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1464	U
1	1	1468	G
1	1	1471	C
1	1	1477	G
1	1	1515	A
1	1	1517	G
1	1	1519	G

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Mol	Chain	Res	Type
1	1	1521	G
1	1	1528	U
1	1	1529	U
1	1	1538	A
1	1	1541	G
1	1	1542	C
1	1	1545	U
1	1	1561	C
1	1	1576	G
1	1	1581	G
1	1	1588	A
1	1	1589	U
1	1	1590	G
1	1	1594	G
1	1	1598	C
1	1	1602	A
1	1	1603	U
1	1	1604	U
1	1	1605	U
1	1	1606	U
1	1	1607	U
1	1	1608	C
1	1	1609	G
1	1	1614	U
1	1	1622	A
1	1	1628	A
1	1	1640	A
1	1	1643	C
1	1	1654	A
1	1	1655	G
1	1	1660	A
1	1	1661	A
1	1	1662	U
1	1	1673	A
1	1	1677	A
1	1	1678	A
1	1	1680	U
1	1	1720	C
1	1	1736	A
1	1	1737	C
1	1	1738	C
1	1	1739	A

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Mol	Chain	Res	Type
1	1	1746	U
1	1	1753	A
1	1	1781	G
1	1	1782	U
1	1	1783	G
1	1	1784	U
1	1	1789	A
1	1	1790	A
1	1	1791	G
1	1	1801	C
1	1	1804	C
1	1	1805	A
1	1	1806	U
1	1	1811	A
1	1	1814	C
1	1	1816	G
1	1	1820	C
1	1	1821	G
1	1	1833	C
1	1	1849	G
1	1	1852	G
1	1	1874	U
1	1	1875	U
1	1	1876	U
1	1	1877	C
1	1	1881	U
1	1	1917	U
1	1	1920	A
1	1	1921	C
1	1	1924	C
1	1	1933	G
1	1	1935	U
1	1	1939	A
1	1	1940	C
1	1	1947	G
1	1	2423	G
1	1	2424	U
1	1	2452	G
1	1	2454	C
1	1	2464	G
1	1	2465	G
1	1	2471	C

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Mol	Chain	Res	Type
1	1	2473	A
1	1	2476	U
1	1	2921	U
1	1	2925	G
1	1	2929	G
1	1	2931	C
1	1	2932	A
1	1	2946	A
1	1	2952	C
1	1	2953	U
1	1	2972	G
1	1	2973	G
1	1	2978	U
1	1	2982	A
1	1	2984	C
1	1	2993	G
1	1	3006	A
1	1	3011	U
1	1	3014	A
1	1	3024	C
1	1	3025	A
1	1	3028	A
1	1	3030	U
1	1	3031	A
1	1	3034	G
1	1	3036	A
1	1	3037	C
1	1	3038	G
1	1	3040	G
1	1	3041	A
1	1	3042	G
1	1	3046	G
1	1	3082	A
1	1	3083	C
1	1	3085	G
1	1	3087	U
1	1	3091	G
1	1	3093	G
1	1	3108	A
1	1	3113	A
1	1	3116	U
1	1	3117	A

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Mol	Chain	Res	Type
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3126	G
1	1	3128	A
1	1	3144	C
1	1	3151	A
1	1	3152	U
1	1	3153	U
1	1	3170	G
1	1	3174	A
1	1	3175	U
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3190	A
1	1	3195	C
1	1	3196	U
1	1	3205	G
1	1	3209	A
1	1	3211	C
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3246	A
1	1	3271	G
1	1	3272	U
1	1	3273	A
1	1	3276	A
1	1	3282	G
1	1	3299	U
1	1	3307	U
1	1	3313	G
1	1	3315	A
1	1	3316	G
1	1	3317	A
1	1	3318	A
1	1	3319	G

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Mol	Chain	Res	Type
1	1	3322	G
1	1	3324	G
1	1	3327	A
1	1	3329	G
1	1	3332	U
1	1	3335	U
1	1	3336	G
1	1	3337	A
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3347	G
1	1	3351	U
1	1	3352	A
1	1	3353	U
1	1	3358	U
1	1	3359	U
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3396	A
1	1	3404	G
1	1	3405	C
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3431	A
1	1	3435	U
1	1	3440	A
1	1	3441	G
1	1	3470	G
1	1	3476	A
1	1	3477	A
1	1	3479	C
1	1	3490	A
1	1	3491	A
1	1	3492	G
2	2	31	U
2	2	42	U

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Mol	Chain	Res	Type
2	2	43	C
2	2	46	U
2	2	59	G
2	2	67	A
2	2	68	U
2	2	70	C
2	2	71	G
2	2	98	U
2	2	99	C
2	2	103	G
2	2	112	A
2	2	113	A
2	2	114	C
2	2	115	G
2	2	124	G
2	2	132	G
2	2	133	U
2	2	134	U
2	2	135	C
2	2	136	U
2	2	159	U
48	6	2	C
48	6	3	A
48	6	5	U
48	6	6	C
48	6	7	U
48	6	9	C
48	6	45	G
48	6	47	U
48	6	49	U
48	6	55	G
48	6	56	A
48	6	57	A
48	6	60	U
48	6	89	U
48	6	92	G
48	6	94	A
48	6	96	U
48	6	97	C
48	6	105	G
48	6	106	A
48	6	108	A

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Mol	Chain	Res	Type
48	6	178	U
48	6	181	C
48	6	182	C

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	270	U
1	1	674	A
1	1	716	G
1	1	761	U
1	1	995	G
1	1	997	A
1	1	1159	U
1	1	1234	A
1	1	1258	C
1	1	1272	U
1	1	1314	C
1	1	1333	A
1	1	1338	G
1	1	1389	A
1	1	1540	A
1	1	1851	A
1	1	1916	G
1	1	3217	U
1	1	3239	A
1	1	3318	A
1	1	3328	U
1	1	3337	A
1	1	3372	C
2	2	103	G
2	2	131	G

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

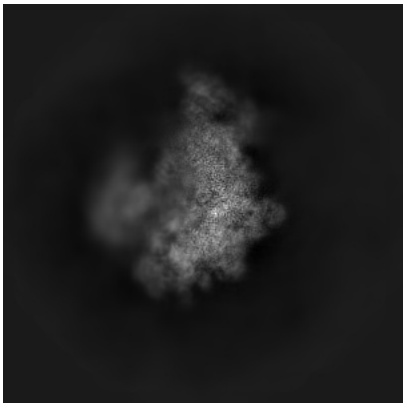
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24397. These allow visual inspection of the internal detail of the map and identification of artifacts.

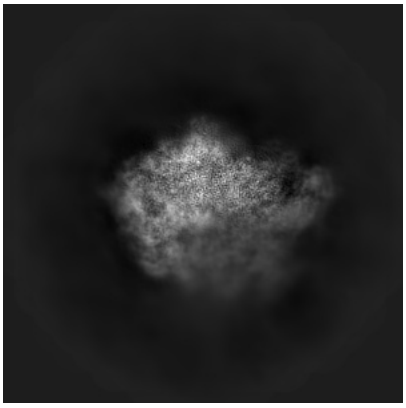
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

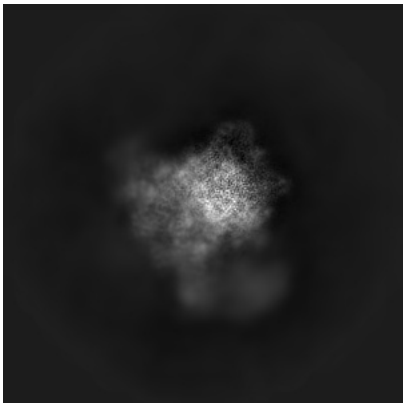
6.1.1 Primary map



X



Y

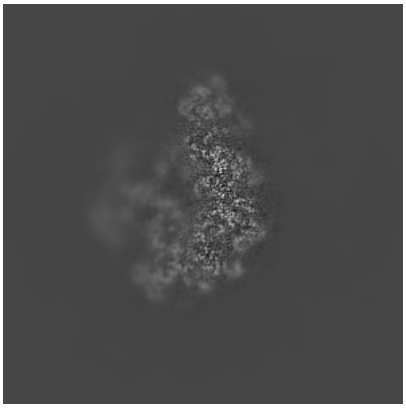


Z

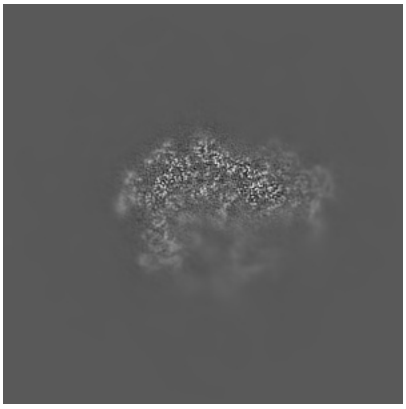
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

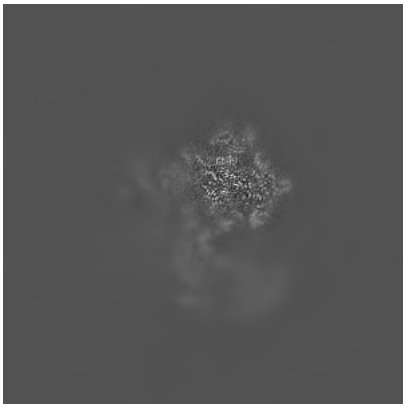
6.2.1 Primary map



X Index: 256



Y Index: 256

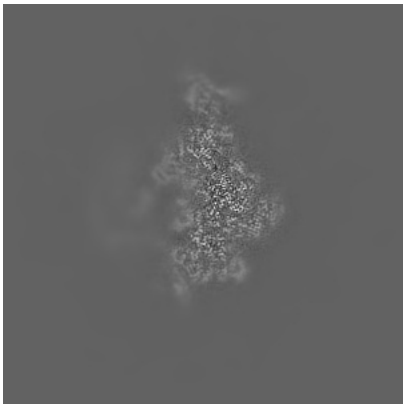


Z Index: 256

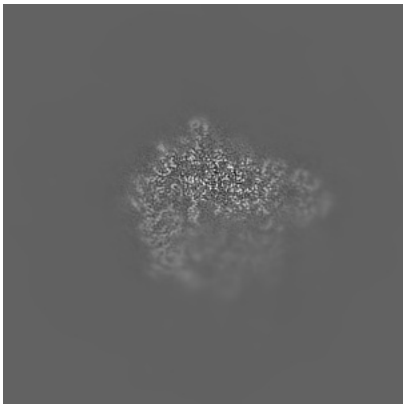
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

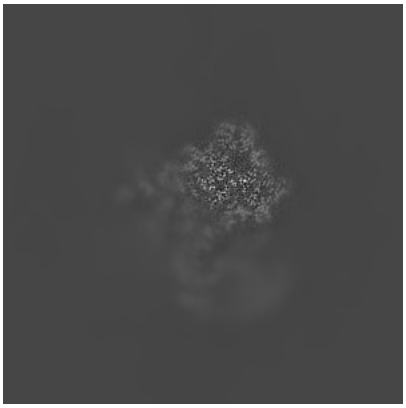
6.3.1 Primary map



X Index: 282



Y Index: 272

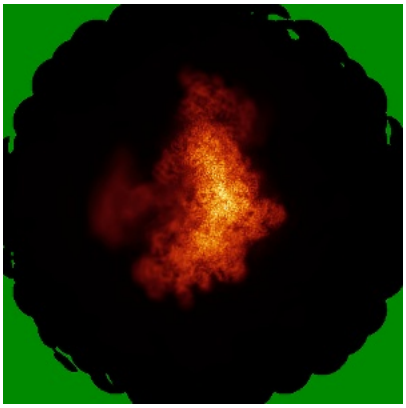


Z Index: 250

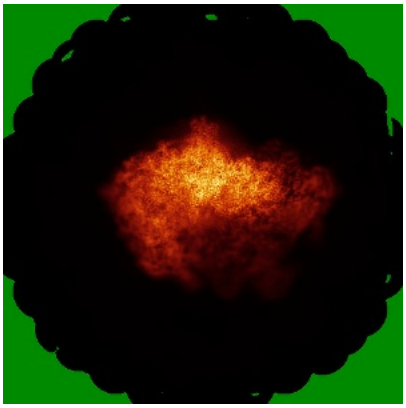
The images above show the largest variance slices of the map in three orthogonal directions.

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

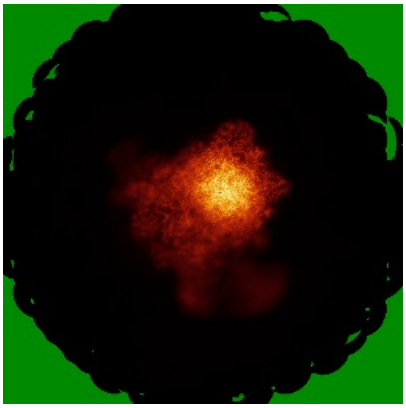
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

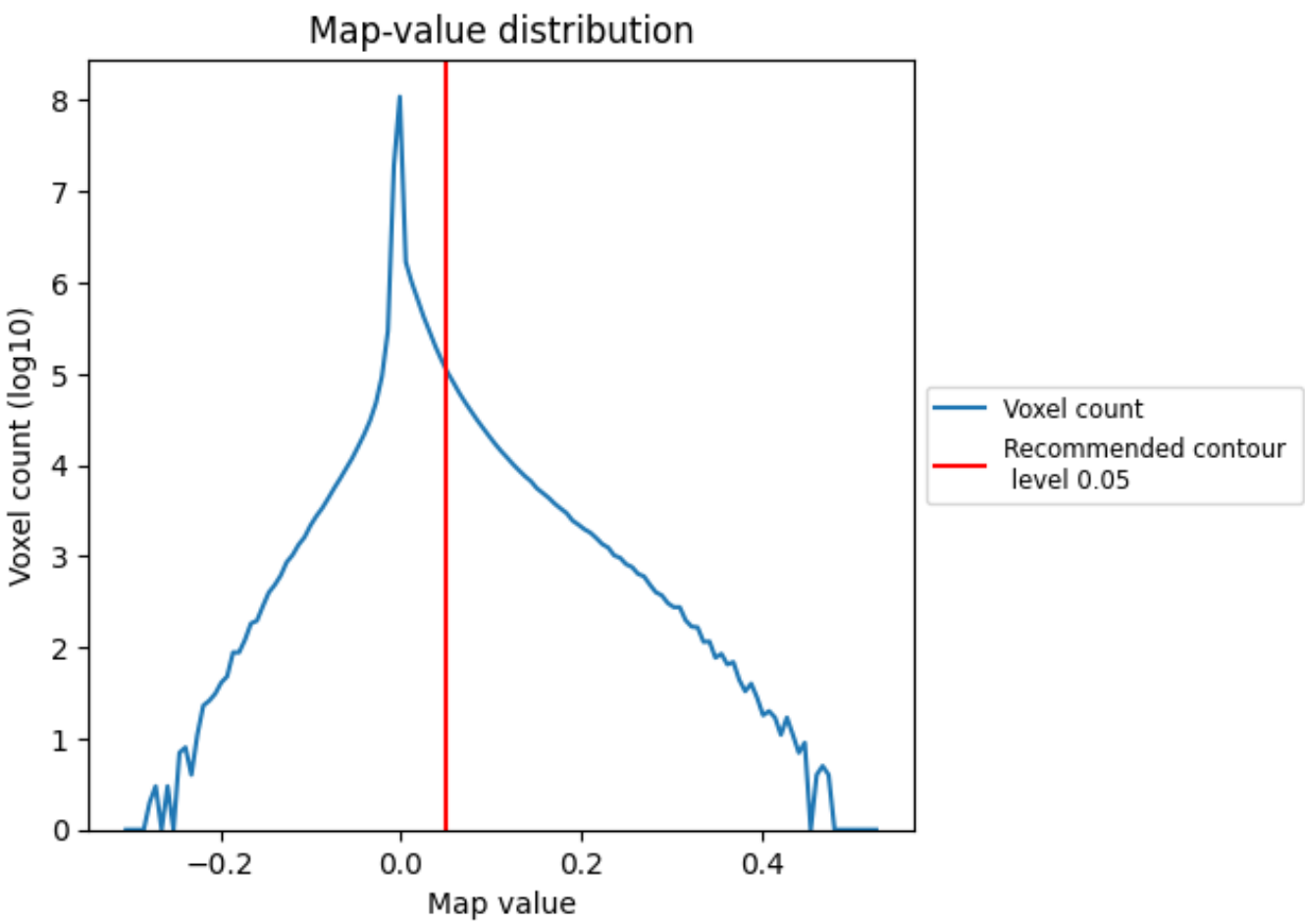
6.6 Mask visualisation (i)

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

7 Map analysis (i)

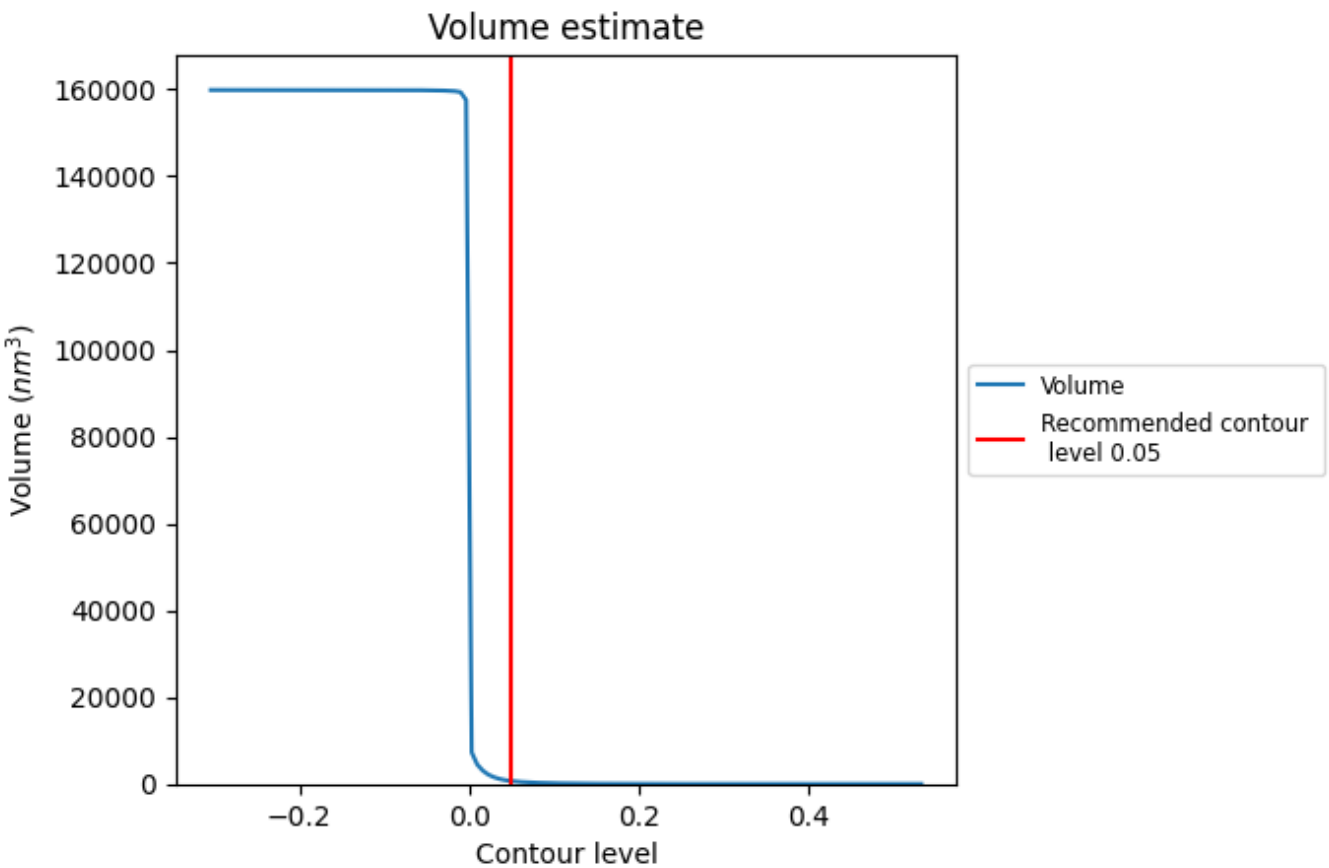
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

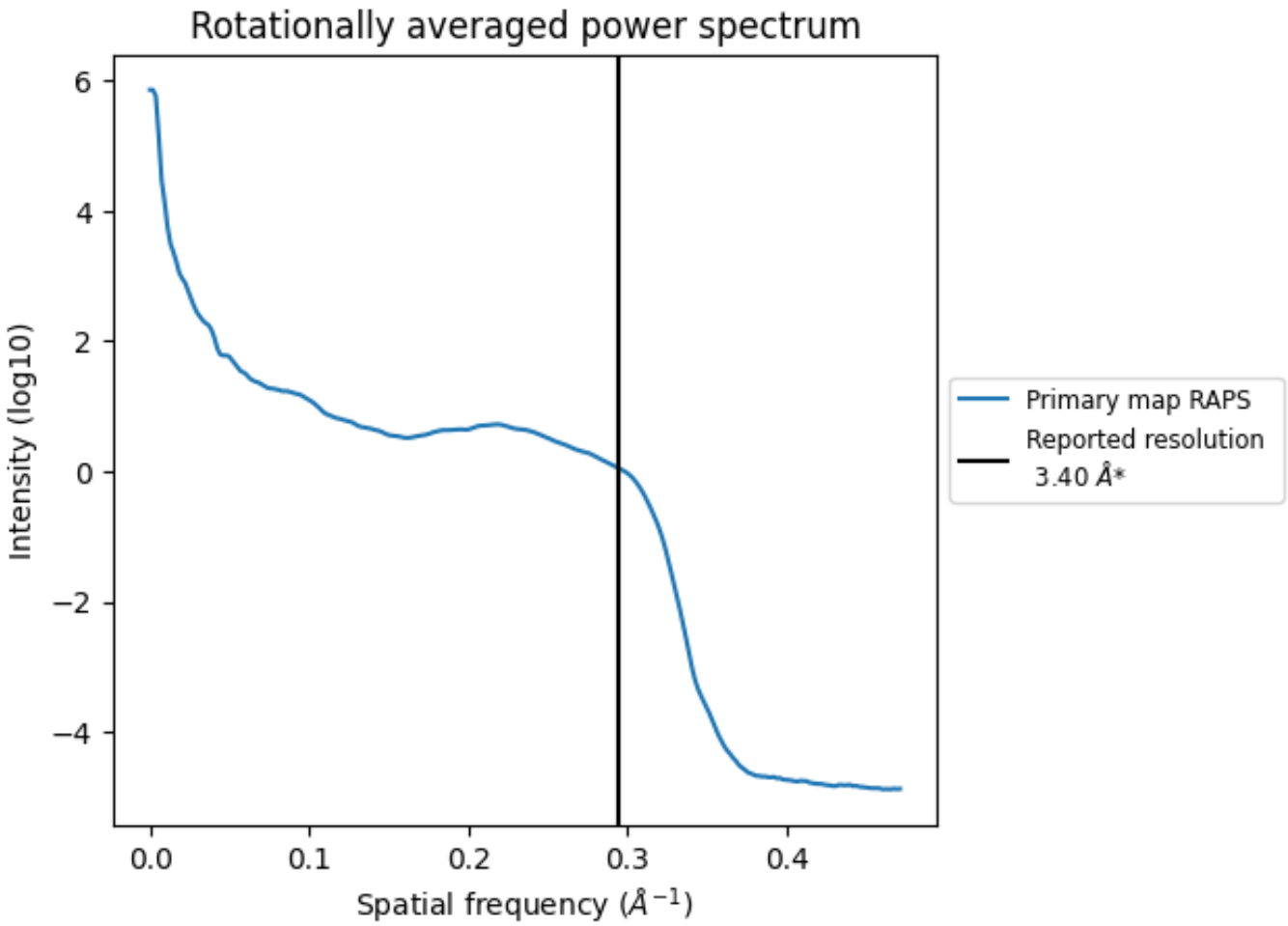
7.2 Volume estimate (i)



The volume at the recommended contour level is 669 nm^3; this corresponds to an approximate mass of 605 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

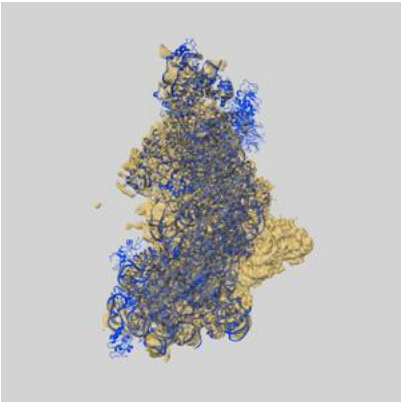
8 Fourier-Shell correlation (i)

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

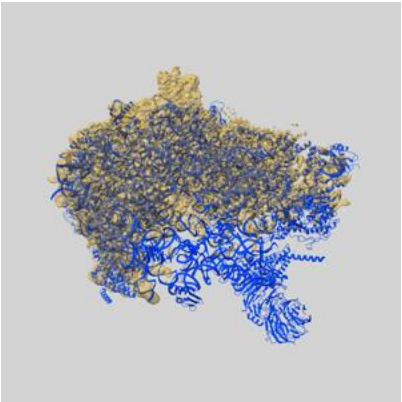
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24397 and PDB model 8ETG. Per-residue inclusion information can be found in section 3 on page 13.

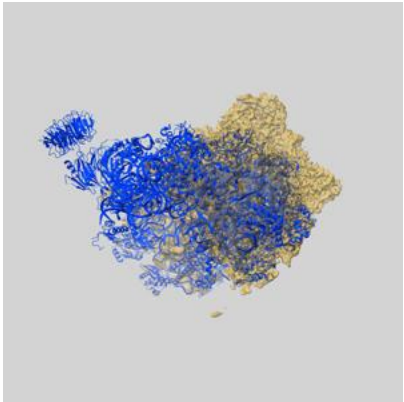
9.1 Map-model overlay (i)



X



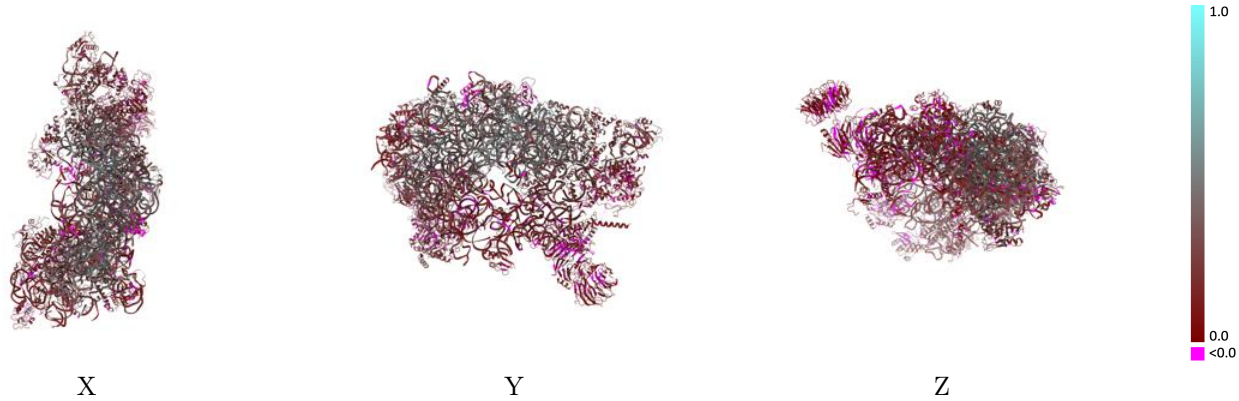
Y



Z

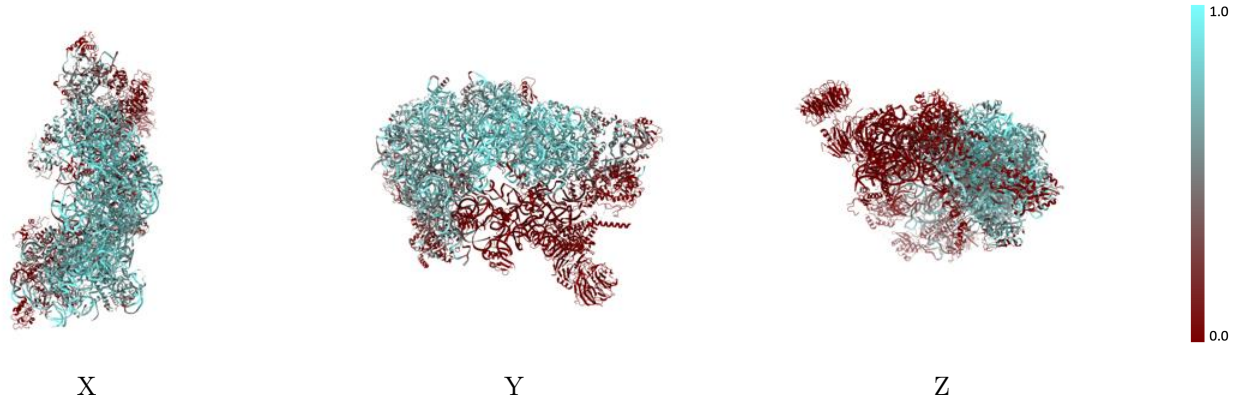
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



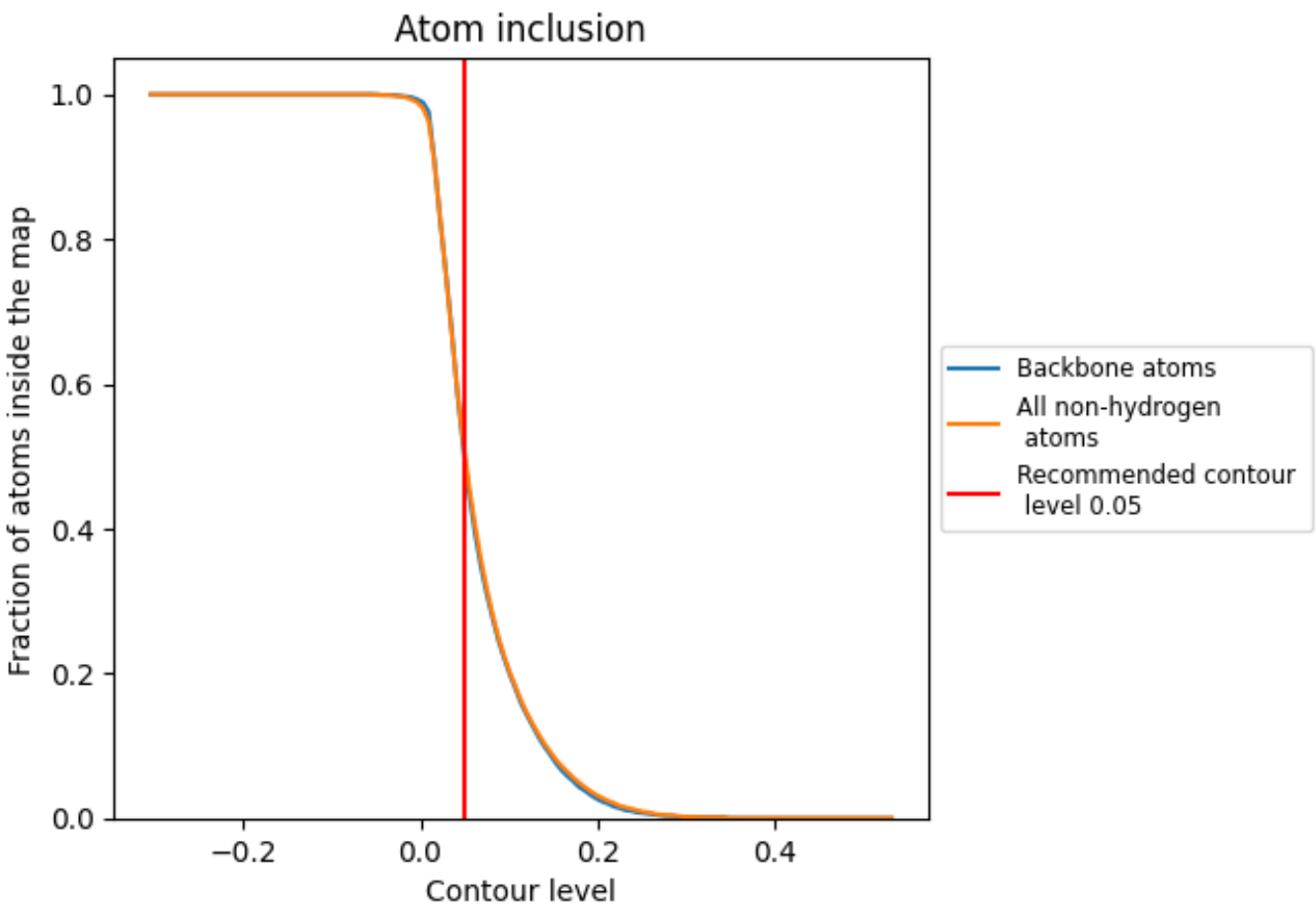
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 50% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5050	0.2580
1	0.6110	0.2740
2	0.7840	0.3630
3	0.5550	0.1600
6	0.4840	0.2490
A	0.4910	0.2160
B	0.5580	0.2520
C	0.7320	0.3730
D	0.4260	0.3090
E	0.5830	0.2080
F	0.7450	0.3850
G	0.6270	0.2970
H	0.3860	0.1750
K	0.2660	0.2550
L	0.8260	0.4420
M	0.6180	0.2650
N	0.7830	0.4010
O	0.6580	0.3360
P	0.5680	0.2640
Q	0.6910	0.3180
R	0.0000	0.1510
S	0.5210	0.2810
T	0.3470	0.2810
U	0.0000	0.1600
V	0.0400	0.0870
W	0.0040	0.1490
X	0.0990	0.2120
Y	0.7310	0.3790
Z	0.0000	0.1140
a	0.1530	0.0820
b	0.1630	0.1630
c	0.0000	0.0820
d	0.0040	0.1560
e	0.7730	0.3970
f	0.7740	0.3980

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Chain	Atom inclusion	Q-score
g	0.0000	0.0670
h	0.6860	0.3740
i	0.6880	0.3140
j	0.8280	0.4290
k	0.0000	0.1790
m	0.1130	0.1280
n	0.0820	0.1570
o	0.3330	0.2010
p	0.0000	0.0760
r	0.1450	0.1580
t	0.1370	0.1360
u	0.3460	0.2140
v	0.6180	0.3110
y	0.1400	0.1250